ScanProsite tool

Matched UniProtKB entries
Taxonomic Distribution of matched entries

include splice variants (Swiss-Prot)

Output format: Simple view [help]

Hits for USERPAT1{E(20)} motif on all UniProtKB/Swiss-Prot (release 2021_03 of 02-Jun-21: 565254 entries), UniProtKB/TrEMBL (release 2021_03 of 02-Jun-21: 0 entries) databases sequences :

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capping: hit limit [50000] reached; not all results are shown
shown: 50000 hits in 3966 sequences

Graphical view **graphical view with feature detection**
shaded alignment of hits

Hits for **USERPAT1** (user pattern)
Pattern: **E(20)**
Approximate number of expected random matches [Ref: PMID 11535175] in ~ 100'000 sequences (50'000'000 residues): 3.403942e-17

Q7TS75 **AMER1_MOUSE** (1132 aa)
APC membrane recruitment protein 1 (Amer1) (Protein FAM123B). *Mus musculus (Mouse)*

```
MESQQDEAVQTKGASTSSDAQDQGAEKGAKNKTTEATEGPTSEPPLSGPGRLKKTAMKLFGGKKGICTLPSFFGGGRSKG
SGKVSSKKSLNKSKTHDGLSEASQGPEDVVIEETDLSTPLSKSSAQFPSSQSANGALEIGSKHKTSGTEAIEKAGVEKVP
SVHKPKKSLKSFFSSIRRHRKGKTSGADQSVPGAKELEGARTRSHEHVSSISLPSSEEIFRDTRKENAKPQDAPGPKMSP
AQVHFSPTTEKAACKNPEKLTRTCASEFMQPKPVLEGGSLEEPHTSETEGKVVAGEVNPPNGPVGDQLSLLFGDVTSLKS
FDSLTGCGDIIAEQDMDSMTDSMASGGQRANRDGTKRSSCLVTYQGGGEEMALPDDDDNDDEEEEEEEEEEEEEEEEEE
EEEEEEEEELLEDEEEVKDGEENDDLEYLWASAQIYPRFNMNLGYHTAISPSHQGYMLLDPVQSYPNLGLGELLTPQSDQ
QESAPNSDEGYYDSTTPGFEDDSGEALGLAHRDCLPRDSYSGDALYEFYEPDDSLEHSPPGDDCLYDLRGRNSEMLDPFL
NLEPFSSRPPGAMETEEERLVTIQKQLLYWELRREQREAQEACAREAHAREAYARDTHTRESYGRNVRARETQALEAHSQ
EGRVQETKVRQEKPALEYQMRPLGPSVMGLVAGTSGGSQTSHRGTTSAFPATSSSEPDWRDFRPLEKRFEGTCSKKDQST
CLMQLFQSDAMFEPDMQEANFGGSPRKAYPSYSPPEEPEEEEEEKEGNATVSFSQALVEFTSNGNLFTSMSYSSDSDSSF
TQNLPELPPMVTFDIADVERDGEGKCEENPEFNNDEDLTASLEAFELGYYHKHAFNSYHSRFYQGLPWGVSSLPRYLGLP
GVHPRPPPAAMALNRRSRSLDNAESLELELSSSHLAQGYMESDELQAHQEDSDEEGEEEEGEWGRDSPLSLYTEPPGVYD
WPPWAHCPLPVGPGLAWMSPNQLYEPFNQSSYVQATCCVPPVAMPVSVPGRTPGDSVSQLARPSHLPLPMGPCYNLQSQA
SQSGRAKPRDVLLPVDEPSCSSISGANSQSQAKPVGITHGIPQLPRVRPEPFQLQPNHYRASNLDLSKERGEQGASLSTS
YSSTAMNGNLAK
```

382 - 401:	EEEEEEEEEEEEEEEEEEEE
383 - 402:	EEEEEEEEEEEEEEEEEEEE
384 - 403:	EEEEEEEEEEEEEEEEEEEE
385 - 404:	EEEEEEEEEEEEEEEEEEEE
386 - 405:	EEEEEEEEEEEEEEEEEEEE
387 - 406:	EEEEEEEEEEEEEEEEEEEE
388 - 407:	EEEEEEEEEEEEEEEEEEEE
389 - 408:	EEEEEEEEEEEEEEEEEEEE
390 - 409:	EEEEEEEEEEEEEEEEEEEE

Q5VXU3 **CHIC1_HUMAN** (224 aa)
Cysteine-rich hydrophobic domain-containing protein 1 (Brain X-linked protein). *Homo sapiens (Human)*

```
MSILLPNMAEFDTISELEEEEEEEAATSSSSPSSSSSVSGPDDDEEDEEEEEEEEEEEEEEEEEEEEEAPPPPRVVSEEH
LRRYAPDPVLVRGAGHITVFGLSNKFDTEFPSVLTGKVAPEEFKTSIGRVNACLKKALPVNVKWLLCGCLCCCCTLGCSL
WPVICLNKRTRRSIQKLIEWENNRLYHKLALHWKLTKRKCETSNMMEYVILIEFLPKYPIFRPD
```

48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE

Q5VXU3-2 **CHIC1_HUMAN** (204 aa)
Cysteine-rich hydrophobic domain-containing protein 1 (Brain X-linked protein). *Homo sapiens (Human)*

```
MSILLPNMAEFDTISELEEEEEEEAATSSSSPSSSSSVSGPDDDEEDEEEEEEEEEEEEEEEEEEEEAPPPRVVSEEH
LRRYAPDPVLVRGAGHITVFGLSNKFDTEFPSVLTGKVAPEEFKTSIGRVNACLKKALPVNVKWLLCGCLCCCCTLGCSL
WPVICLNKRTRRSIQKLIEWENNRLYHKVILIEFLPKYPIFRPD
```

48 - 67:	EEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEE

P0C7V8 **DC8L2_HUMAN** (631 aa)
DDB1- and CUL4-associated factor 8-like protein 2 (WD repeat-containing protein 42C). *Homo sapiens (Human)*

```
MSHQEGSTDGLPDLGTESLFSSPEEQSGAVAATEASSDIDIATSELSVTVTGDGSDSRDGGFPNDASTENRSSDQESASE
DIELESLEDFEHFLMSGESLFHYPLVGEEETEREEDEEIQEEGGEEEEEEEEEEEEEEEEEEEEEQPRAGPQGSGGNH
EQYSLEEDQALEEWVSSETSALPRPRWQVVTALHQRQLGSRPRFVYEACGARAFVQRFRLQYRLADHVGCVNTVHFNQRG
TRLASSGDDLKVIVWDWVRQRPVLNFESGHTNNVFQAKFLPNCGDSTLAMCARDGQVRVAELINASYFNNTKCVAQHRGP
AHKLALEPDSPYKFLTSGEDAVVFTIDLRQDRPASKVVVTRENDKKVGLYTITVNPANTYQFAVGGQDQFVRIYDQRKID
KKENNGVLKKFTPHHLVNCDFPTNITCVVYSHDGTELLASYNDDDIYLFNSSHSDGAQYSKRFKGHRNNTTVKGVNFYGP
RSEFVVSGSDCGHIFFWEKSSCQIIQFLKGSREGTINCLEPHPYLPVLACSGLDHDVKIWTPTAKAATELTGLKKVIKKN
KWERDEDSLHHGSLFDQYMLWFLLRHVTQRGRHQDWRSGEAEFPDEESDESSSTSETSEEEVQDRVQCMPS
```

126 - 145:	EEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEE

A7TJM9 **DRS1_VANPO** (752 aa)
ATP-dependent RNA helicase DRS1 (EC 3.6.4.13). *Vanderwaltozyma polyspora (strain ATCC 22028 / DSM 70294 / BCRC 21397 / CBS 2163 / NBRC 10782 / NRRL Y-8283 / UCD 57-17) (Kluyveromyces polysporus)*

```
MAVTSDRKNNRKKAITKFNDLDFVPTISDSEEDVPDLDDSDDELLTSENKSVKTPAKSKKGKKNDPVKINGNGDEVAEDL
NPDFRFNIDGGELSTNFQGWDFVGDQKENDDDMKKDVDLDGIIRRKGGLLNMAHIEVAEEEEEEEEEEEEEEEEEEEELA
MDGFGMGATKKNEQEEAGDEDDDDNEEEEEEEVDDDKEDDDEEREEDTAEEMASFYAPESESSEATSTVHSTFNSLTLSR
PVLKGLSDLGYTKPSPIQSATIPIGLSGKDIIAGAVTGSGKTAAFMIPIIERLLYKPAKVASTRVIVLTPTRELAIQIAD
VGKKIGKYVSGLTFGLAVGGLNLRQQEQELKTRPDIVIATPGRFIDHVRNSSSFNVDSVEVLVMDEADRMLEEGFQEELN
EILTLLPSKRQTLLFSATMNSRIKSLISLSLRKPVRIMINPPKQAAARLTQEFVRIRKRDHLKPALLFYLIRKLDGTGQK
RIVVFVARKEMAHKLRIILGLLGMKVGELHGSLTQEQRLQSVNNFKSLEVPVLICTDLASRGLDIPKIEVVINFDMPKSY
EIYLHRVGRTARAGREGRSVTFVGESSQDRSIVRSAIKSVEESSSKNKAVSRNVEWTQIEETNKLVESFGETIDDILVEE
KQEKEILRAEMQLRKGENMIKHKKEIQSRPKRTWFQSEAEKKNAKILDTLQKNKKTVNSKKRKRLEALEDNDNSRSYKKT
QKDRVVDQERSMKKQKIANGKKSKNKKKFNKR
```

139 - 158:	EEEEEEEEEEEEEEEEEEE

A7A0P8 **DRS1_YEAS7** (754 aa)
ATP-dependent RNA helicase DRS1 (EC 3.6.4.13) (Deficiency of ribosomal subunits protein 1). *Saccharomyces cerevisiae (strain YJM789) (Baker's yeast)*

```
MVVGTKKYSNLDFVPTISDSEDDVPILDSSDDEKVEAKKTTKKRKGKNNKKKVSEGDNLDEDVHEDLDAGFKFDLDADDT
TSNFQGWNFLAEGESNKDDAEAFVKKDVDLDKIIRRKGGLVKMAHIDSKQEEETEKEKVEKENDSDDEELAMDGFGMGAP
MNNGDENQSEEEEEEEEEEEEEEEEEEEEEQEEMTLEKGGKDDEIDEEDDSEEAKADFYAPETEGDEAKKQMYENFNSLSL
SRPVLKGLASLGYVKPSPIQSATIPIALLGKDIIAGAVTGSGKTAAFMIPIIERLLYKPAKIASTRVIVLLPTRELAIQV
ADVGKQIARFVSGITFGLAVGGLNLRQQEQMLKSRPDIVIATPGRFIDHIRNSASFNVDSVEILVMDEADRMLEEGFQDE
LNEIMGLLPSNRQNLLFSATMNSKIKSLVSLSLKKPVRIMIDPPKKAATKLTQEFVRIRKRDHLKPALLFNLIRKLDPTG
QKRIVVFVARKETAHRLRIIMGLLGMSVGELHGSLTQEQRLDSVNKFKNLEVPVLICTDLASRGLDIPKIEVVINYDMPK
SYEIYLHRVGRTARAGREGRSVTFVGESSQDRSIVRAAIKSVEENKSLTQGKALGRNVDWVQIEETNKLVESMNDTIEDI
LVEEKEEKEILRAEMQLRKGENMLKHKKEIQARPRRTWFQSESDKKNSKVLGALSRNKKVTNSKKRKREEAKADGNGARS
YRKTKTDRIADQERTFKKQKSTNSNKKKGFKSRR
```

170 - 189:	EEEEEEEEEEEEEEEEEEE

Q96KQ7 **EHMT2_HUMAN** (1210 aa)
Histone-lysine N-methyltransferase EHMT2 (EC 2.1.1.-) (Euchromatic histone-lysine N-methyltransferase 2) (HLA-B-associated transcript 8) (Histone H3-K9 methyltransferase 3) (H3-K9-HMTase 3) (Lysine N-methyltransferase 1C) (Protein G9a). *Homo sapiens (Human)*

```
MAAAAGAAAAAAAEGEAPAEMGALLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGAD
TPVGATPLIGDESENLEGDGDLRGGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGA
AAAGSEPPPATTSPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEIQHFRMSDDVHSLGKVTSDLAKRRKLNSGGGLSEEL
GSARRSGEVTLTKGDPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEE
EEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTL
SPNHAGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVL
CETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGT
AAPAPPPLSQDVPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQE
SERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRT
PLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEV
IRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELR
NKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETS
TMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRL
QLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNII
```

PVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLP
ELGSLPPVNT

300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE

Q96KQ7-2 **EHMT2_HUMAN** (1176 aa)
Histone-lysine N-methyltransferase EHMT2 (EC 2.1.1.-) (Euchromatic histone-lysine N-methyltransferase 2) (HLA-B-associated transcript 8) (Histone H3-K9 methyltransferase 3) (H3-K9-HMTase 3) (Lysine N-methyltransferase 1C) (Protein G9a). *Homo sapiens (Human)*

MAAAAGAAAAAAAEGEAPAEMGALLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGAD
TPVGATPLIGDESENLEGDGDLRGGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGA
AAAGSEPPPATTSPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEIQHFRMSDDVHSLGKVTSDLAKRRKLNSGGGLSEEL
GSARRSGEVTLTKGDPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEE
EEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAPK
IDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFR
VAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLSQDVPGRADTSQPSARMRGHGEPRRP
PCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNL
DPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTC
LHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIA
EVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNR
AIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRC
WYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISD
AEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDY
GDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNT

300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE

Q9Z148 **EHMT2_MOUSE** (1263 aa)
Histone-lysine N-methyltransferase EHMT2 (EC 2.1.1.-) (Euchromatic histone-lysine N-methyltransferase 2) (HLA-B-associated transcript 8) (Histone H3-K9 methyltransferase 3) (H3-K9-HMTase 3) (Protein G9a). *Mus musculus (Mouse)*

MRGLPRGRGLMRARGRGRAAPTGGRGRGRGGAHRGRGRPRSLLSLPRAQASWAPQLPAGLTGPPVPCLPSQGEAPAEMGA
LLLEKEPRGAAERVHSSLGDTPQSEETLPKANPDSLEPAGPSSPASVTVTVGDEGADTPVGAASLIGDEPESLEGDGGRI
VLGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAATAGPEPSPATTAAQEGQPKVHRARKT
MSKPSNGQPPIPEKRPPEVQHFRMSDDMHLGKVTSDVAKRRKLNSGSLSEDLGSAGGSGDIILEKGEPRPLEEWETVVGD
DFSLYYDAYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAKKKWR
KDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEELPLCS
CRMEAPKIDRISERAGHKCMATESVDGELLGCNAAILKRETMRPSSRVALMVLCEAHRARMVKHHCCPGCGYFCTAGTFL
ECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGGTPPIGTAAPALPPLAHDAPGRADTSQPSARMRG
HGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPPGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVI
LMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQLGGCVYSK
EEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIDVIRMLLTRGADVTLTDNEENICLHWASF
TGSAAIAEVLLNAQCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKL
RLGVGNRAVRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLC
GQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRSCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEY
VGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTG
EELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPDLSSLPPINT

352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE

Q9Z148-2 **EHMT2_MOUSE** (1172 aa)
Histone-lysine N-methyltransferase EHMT2 (EC 2.1.1.-) (Euchromatic histone-lysine N-methyltransferase 2) (HLA-B-associated transcript 8) (Histone H3-K9 methyltransferase 3) (H3-K9-HMTase 3) (Protein G9a). *Mus musculus (Mouse)*

MAAAAGAAAAAAAEGEAPAEMGALLLEKEPRGAAERVHSSLGDTPQSEETLPKANPDSLEPAGPSSPASVTVTVGDEGAD
TPVGAASLIGDEPESLEGDGGRIVLGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAATAG
PEPSPATTAAQEGQPKVHRARKTMSKPSNGQPPIPEKRPPEVQHFRMSDDMHLGKVTSDVAKRRKLNSGSLSEDLGSAGG
SGDIILEKGEPRPLEEWETVVGDDFSLYYDAYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEED
EESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAPKIDRI
SERAGHKCMATESVDGELLGCNAAILKRETMRPSSRVALMVLCEAHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHR
FHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGGTPPIGTAAPALPPLAHDAPGRADTSQPSARMRGHGEPRRPPCDP

```
LADTIDSSGPSLTLPNGGCLSAVGLPPGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNF
QSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQLGGCVYSKEEDGSTCLHHA
AKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIDVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLL
NAQCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAVRT
EKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDK
DGRLLQEFNKIEPPLIFECNQACSCWRSCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEAD
VREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRF
WDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPDLSSLPPINT
```

295 - 314:	EEEEEEEEEEEEEEEEEEEE
296 - 315:	EEEEEEEEEEEEEEEEEEEE
297 - 316:	EEEEEEEEEEEEEEEEEEEE
298 - 317:	EEEEEEEEEEEEEEEEEEEE
299 - 318:	EEEEEEEEEEEEEEEEEEEE
300 - 319:	EEEEEEEEEEEEEEEEEEEE

Q9Z148-3 **EHMT2_MOUSE** (1206 aa)
Histone-lysine N-methyltransferase EHMT2 (EC 2.1.1.-) (Euchromatic histone-lysine N-methyltransferase 2) (HLA-B-associated transcript 8) (Histone H3-K9 methyltransferase 3) (H3-K9-HMTase 3) (Protein G9a). *Mus musculus (Mouse)*

```
MAAAAGAAAAAAAAEGEAPAEMGALLLEKEPRGAAERVHSSLGDTPQSEETLPKANPDSLEPAGPSSPASVTVTVGDEGAD
TPVGAASLIGDEPESLEGDGGRIVLGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAATAG
PEPSPATTAAQEGQPKVHRARKTMSKPSNGQPPIPEKRPPEVQHFRMSDDMHLGKVTSDVAKRRKLNSGSLSEDLGSAGG
SGDIILEKGEPRPLEEWETVVGDDFSLYYDAYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEED
EESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNH
AGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELLGCNAAILKRETMRPSSRVALMVLCEAH
RARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGGTPPIGTAAPA
LPPLAHDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPPGPGREALEKALVIQESERR
KKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLME
AVVNNHLEVARYMVQLGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIDVIRML
LTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNAQCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEG
DTAWDLTPERSDVWFALQLNRKLRLGVGNRAVRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNI
DRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRSCKNRVVQSGIKVRLQLYR
TAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRV
FMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPDLSS
LPPINT
```

295 - 314:	EEEEEEEEEEEEEEEEEEEE
296 - 315:	EEEEEEEEEEEEEEEEEEEE
297 - 316:	EEEEEEEEEEEEEEEEEEEE
298 - 317:	EEEEEEEEEEEEEEEEEEEE
299 - 318:	EEEEEEEEEEEEEEEEEEEE
300 - 319:	EEEEEEEEEEEEEEEEEEEE

Q9SY06 **FAF1_ARATH** (271 aa)
Protein FANTASTIC FOUR 1. *Arabidopsis thaliana (Mouse-ear cress)*

```
MSIVVGQAYQHLPKQVSQNPDVGGWSFLQYFSEPKGIVQNREDDTKKTAYVYPIEKRSVAKLSLEMCTESLGTENGSDSG
DEMSLLALEATNISKSPRLTTKPQKETSFMTRENSFPPPLNSVNGFNNSRMVKSYKEDGRLVVQAIRVCSPPRCFVSERR
EGRLRLCLSQNSLNSQDAEEEFEEEDEDDQYDAEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEGIVGNNENFEGKSGNKK
VSNRPKRRCNENGCEPKTMLNWKQQQFWVTT
```

194 - 213:	EEEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEEE
196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE

Q9FX02 **FB38_ARATH** (306 aa)
Putative F-box protein At1g47300. *Arabidopsis thaliana (Mouse-ear cress)*

```
MISDSIPKELILEIMLRLPAKSIARFHCVSKQWASMLSRPYFTELFLTSSSTQPRLLFAIKRNGLWCFFSLPKHQSPYDN
SSSSLVVAADFHMKFLPNKIQMYSSSENRKLSCCYASGLTYFYDMYSEVRVICNPITGRYASLPYLKRYRKELSFFGFDP
IDKQFKEWLKYAYSLRDDKFFTHDVFVVRVTATEMNTIQRVEIQGFGECQHEYDYYRSRVVYVFADHVEDLDVNDPKLLE
SKEEEEEEEEEEEEEEEEEEEEEEEEEEEEESKEREKEKKIETVIGGWIKQYWACFLRKSWELNPHR
```

243 - 262:	EEEEEEEEEEEEEEEEEEEE

244 - 263:	EEEEEEEEEEEEEEEEEEEE
245 - 264:	EEEEEEEEEEEEEEEEEEEE
246 - 265:	EEEEEEEEEEEEEEEEEEEE
247 - 266:	EEEEEEEEEEEEEEEEEEEE
248 - 267:	EEEEEEEEEEEEEEEEEEEE
249 - 268:	EEEEEEEEEEEEEEEEEEEE
250 - 269:	EEEEEEEEEEEEEEEEEEEE
251 - 270:	EEEEEEEEEEEEEEEEEEEE

P13816 **GARP_PLAFF** (678 aa)
Glutamic acid-rich protein. *Plasmodium falciparum (isolate FC27 / Papua New Guinea)*

```
MNVLFLSYNICILFFVVCTLNFSTKCFSNGLLKNQNILNKSFDSITGRLLNETELEKNKDDNSKSETLLKEEKDEKDDVP
TTSNDNLKNAHNNNEISSSTDPTNIINVNDKDNENSVDKKKDKKEKKHKKDKKEKKEKKDKKEKKDKKEKKHKKEKKHKK
DKKKKENSEVMSLYKTGQHKPKNATEHGEENLDEEMVSEINNNAQGGLLLSSPYQYREQGGCGIISSVHETSNDTKDNDK
ENISEDKKEDHQQEEMLKTLDKKERKQKEKEMKEQEKIEKKKKKQEEKEKKKQEKERKKQEKKERKQKEKEMKKQKKIEK
ERKKKEEKEKKKKKHDKENEETMQQPDQTSEETNNEIMVPLPSPLTDVTTPEEHKEGEHKEEEHKEGEHKEGEHKEEEHK
EEEHKKEEHKSKEHKSKGKKDKGKKDKGKHKKAKKEKVKKHVVKNVIEDEDKDGVEIINLEDKEACEEQHITVESRPLSQ
PQCKLIDEPEQLTLMDKSKVEEKNLSIQEQLIGTIGRVNVVPRRDNHKKKMAKIEEAELQKQKHVDKEEDKKEESKEVQE
ESKEVQEDEEEVEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EDDDEDEDEDEEDEEEEEEEEEESEKKIKRNLRKNAKI
```

576 - 595:	EEEEEEEEEEEEEEEEEEEE
577 - 596:	EEEEEEEEEEEEEEEEEEEE
578 - 597:	EEEEEEEEEEEEEEEEEEEE
579 - 598:	EEEEEEEEEEEEEEEEEEEE
580 - 599:	EEEEEEEEEEEEEEEEEEEE
581 - 600:	EEEEEEEEEEEEEEEEEEEE
582 - 601:	EEEEEEEEEEEEEEEEEEEE
583 - 602:	EEEEEEEEEEEEEEEEEEEE
584 - 603:	EEEEEEEEEEEEEEEEEEEE
585 - 604:	EEEEEEEEEEEEEEEEEEEE
586 - 605:	EEEEEEEEEEEEEEEEEEEE

Q54F38 **H3V1_DICDI** (619 aa)
Histone H3.v1. *Dictyostelium discoideum (Slime mold)*

```
MANKPKPSEHLRDLIRSGQRTSPEADLQLKQQQQPRQTQPSRPSSSLTQSYEPPGTTRVPVSPVISTSESSGSSRSPASS
GSSRSSGSSGSSRLSGSSRASVNTIMNLSNIEFNDTPSVTDDSYYTNVMTESPIRKAASQRLPTGVMDSIRGSLENINVS
HNLTPTTPLSKPNTLMYKKGAPAPPRLTPILPSYKTNLKPVVQTPKIQRKTSQIEEESDDDSSSQNNSSDQEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
ESSKQSRVKVSKKPSPLIKKKPAPIKKVTTPTRSKQQQQSPLPPTRRSPLPSEAKKPAASKKVSKNVLSSSSSSPSSSSS
SSSSLTPTKSRRETIVTTPTKTPPSTRSKSITPLSTPTRTPPSTRSKTSSTPSSTPSSLSISTPSSTSISSPVSSRTSTS
ILTPPSTPTSTHSSTSASITTPTTPRIRVQRTTTTPTTPTTPTTPRKKRRRRLVASVIRRLRNSVDFMIPRLPLSRLVREIMC
LFDDGLRITPGALLAIQTTTEAYLTRLMEDSGLLASHAGRKTIRSVDMYAWKRARHFLF
```

232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE
239 - 258:	EEEEEEEEEEEEEEEEEEEE
240 - 259:	EEEEEEEEEEEEEEEEEEEE
241 - 260:	EEEEEEEEEEEEEEEEEEEE
242 - 261:	EEEEEEEEEEEEEEEEEEEE
243 - 262:	EEEEEEEEEEEEEEEEEEEE
244 - 263:	EEEEEEEEEEEEEEEEEEEE
245 - 264:	EEEEEEEEEEEEEEEEEEEE
246 - 265:	EEEEEEEEEEEEEEEEEEEE
247 - 266:	EEEEEEEEEEEEEEEEEEEE

248 - 267:	EEEEEEEEEEEEEEEEEEEE
249 - 268:	EEEEEEEEEEEEEEEEEEEE
250 - 269:	EEEEEEEEEEEEEEEEEEEE
251 - 270:	EEEEEEEEEEEEEEEEEEEE
252 - 271:	EEEEEEEEEEEEEEEEEEEE
253 - 272:	EEEEEEEEEEEEEEEEEEEE
254 - 273:	EEEEEEEEEEEEEEEEEEEE
255 - 274:	EEEEEEEEEEEEEEEEEEEE
256 - 275:	EEEEEEEEEEEEEEEEEEEE
257 - 276:	EEEEEEEEEEEEEEEEEEEE
258 - 277:	EEEEEEEEEEEEEEEEEEEE
259 - 278:	EEEEEEEEEEEEEEEEEEEE
260 - 279:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE
262 - 281:	EEEEEEEEEEEEEEEEEEEE
263 - 282:	EEEEEEEEEEEEEEEEEEEE
264 - 283:	EEEEEEEEEEEEEEEEEEEE
265 - 284:	EEEEEEEEEEEEEEEEEEEE
266 - 285:	EEEEEEEEEEEEEEEEEEEE
267 - 286:	EEEEEEEEEEEEEEEEEEEE

Q5AQ47 **HST1_CANAL** (655 aa)
NAD-dependent protein deacetylase HST1 (EC 2.3.1.286) (Homologous to SIR2 protein 1) (Regulatory protein SIR2 homolog 1). *Candida albicans (strain SC5314 / ATCC MYA-2876) (Yeast)*

```
MPGDNDIVLVDSSSDNEEEREEDDDDESQHREIKKFKPNPNPSQTRDMNESHVINKSNFSTVPFNAVSSSSSSDNDQDND
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEESEINGNQISLSIDDEYDSEGLTKESSRTPIGSNTSDIIINGVTIIT
NNNDSSLVASSSDDDDDDDDDDDKDDDNDDDASDLESDFAFEEIPPSLIMETRKYLKQNGTMKFLEKYLPTAASIENIIK
LILQLGFVPKRKLNNGLDENDIMEYIKILNHAIIKVKSIRERREDITTINDALKLIENSKNIMVITGAGISTSLGIPDFR
SSQGFYSMIQHLGLSDPQEVFDLDLFLNDPNIFYSIAHMILPPNHIYSPLHSFIKLLQDKNKLLRNYTQNIDNLESYAGI
HKENLIQCHGSFATASCITCGYKVDGEIIFPEIKNKEIPYCPKCNEVKQSILKKGKKTKSKSKKKKKKKNKPYDDDDEEE
EEGETYFHESFGVMKPDITFFGEQLPENFKIAINQDINKVDLVLVIGTSLKVAPVADIVGKIPEHIPQILLNKDPINHCQ
FDVSLLGYCDDVASYIANELGESWDLPHPDYNKIRGEKNGENLSVQLLDSTLREYLISNKKNDLSSEQEQNKMGEENRKV
EESGRRPNESGGKSG
```

81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE

Q59ZH9 **MAK5_CANAL** (782 aa)
ATP-dependent RNA helicase MAK5 (EC 3.6.4.13). *Candida albicans (strain SC5314 / ATCC MYA-2876) (Yeast)*

```
MAKQGKNKVSKPRKPPTLKQKLKKESKVVKAKDLQWKLVDIPDNLGDYEGFYGLEEIDGVDVQIVNGKAEFIVRDNGKVE
NKSKKEETNENGENNMDVEDNETPEVEDEKPTEQEEEEEEEEEEEEEEEEEEEEEFAGFEDDENNQEDANTSERVSNND
KDDKLAESNDELNAVSFANLDLPLPDDNEINLPNWQEGDLGSSISAYTLYGLSQLDFKKPTPIQKETIPIALSGKDVIGK
ATTGSGKTLAYGIPILEKYIQSLNLIKQNNKDKKINHPTGIIFAPTRELAHQVVDHLNKLAKYSPLSTRGIVSITGGLSI
QKQQRLLRHGPGIIVATPGRMLELVQGDSELAKRLASIDIIVLDEADRLLQDGHFDEFEKILELFGKNRPKSKSIEWKWQ
TLVFSATFSRDLFRKLDRHQKGKSSSLMGNDEIVQLLNEKLKFKDKKPTLVDANPKEIVSGQITEALVECGPTERDLYLY
YFLLMYKGSTLVFANSIDSVKRLVPLLNNLNIPAFSIHSSMIQKQRLRALEKFKEASQKNEVAVLVASDVAARGLDIPNI
DHVVHYHLPRSADVYIHRSGRTARAGKEGVSVMFCSPQEASGPLRKLRRLVAGNSNKESRLNMHNDVKLLPIEMDLVSQI
KPRVEISSKLADASISSTATRKEDSWVKQAAEDLGLDDLSGLEDFEDDIIKKQRKRKEGKMLSKDETKALKYELKTLLAN
```

```
PIKKNTRKSYITSGLQNLAHQMVTGAHHDDVLGHEKVNALSDLKGSKNKNKKIEKKRISKKK
```

115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE

Q90342 **MYC2_CYPCA** (401 aa)
Transcriptional regulator Myc-2 (c-Myc-2) (c-Myc II). *Cyprinus carpio (Common carp)*

```
MPVSSSLAYKNYDYDYDSIQPYFYFDNDDEDFYHHQQGQTQPPAPSEDIWKKFELLPTPPLSPSRRQSLSTAEQLEMVSE
FLGDDVVNQSFICDADYSQSFIKSIIIQDCMWSGFSAAAKLEKVVSEKLASLHAARKELISDSSSNRLNASYLQDLSTSA
SECIGPSVVFPYPLTESSKSSKVAPSEPMLVLDTPPNSSSSSGSDSEDEEEEEEEEEEEEEEEEEEEEEIDVVTVEKRQKR
NEAEVSDSRYPSPLVLKRCHVSTHQHNYAAHPSTRHDQPAVKRLRLESSSSNNSSSNRQGKQRKCTSPRTSDSEDNDKRR
THNVLERQRRNELKLSFFALRDEIPEVANNEKAAKVVILKKATECIHSMQLDEQRLLSIKEQLRRKSEQLKHRLQQLRSS
H
```

209 - 228:	EEEEEEEEEEEEEEEEEEEE

P49709 **MYC_CARAU** (399 aa)
Transcriptional regulator Myc (c-Myc). *Carassius auratus (Goldfish)*

```
MPVSASLAYKNYDYDYDSIQPYFYFDNDDEDFYHHQQGQPQPPAPSEDIWKKFELLPTPPLSPSRRQSLSTAEQLEMVSE
FLGDDVVNQSFICDADYSQSFIKSIIIQDCMWSGFSAAAKLEKAVSERLASLHAARKELISDSSSNRLSASYLQDLSTSA
SECIDPSVVFPYPLTESSKSNKVAPSQPMLVLDTPPNSSSSSGSDSEDEEEEEEEEEEEEEEEEEEEEEEIDVVTVEKR
QKRNEADVSDSRYPSPLVLKRCHVSTHQHNYAAHPSTRHDQPAVKRLRLETSSSNRHGKQRKCTSPRTSDSEDNDKRRTH
NVLERQRRNELKLSFFALRDEIPEVANNEKAAKVVILKKATECIHSMQLDEQRLLSIKEQLRRKSEQLKHRLQQLRSSH
```

209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE

Q01538 **MYT1_HUMAN** (1121 aa)
Myelin transcription factor 1 (MyT1) (Myelin transcription factor I) (MyTI) (PLPB1) (Proteolipid protein-binding protein). *Homo sapiens (Human)*

```
MSLENEDKRARTRSKALRGPPETTAADLSCPTPGCTGSGHVRGKYSRHRSLQSCPLAKKRKLEGAEAEHLVSKRKSHPLK
LALDEGYGVDSDGSEDTEVKDASVSDESEGTLEGAEAETSGQDEIHRPETAEGRSPVKSHFGSNPIGSATASSKGSYSSY
QGIIATSLLNLGQIAEETLVEEDLGQAAKPGPGIVHLLQEAAEGAASEEGEKGLFIQPEDAEEVVEVTTERSQDLCPQSL
EDAASEESSKQKGILSHEEEDEEEEEEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAAPDVIFQEDTSHT
SAQKAPELRGPESPSPKPEYSVIVEVRSDDDKDEDTHSRKSTVTDESEMQDMMTRGNLGLLEQAIALKAEQVRTVCEPGC
PPAEQSQLGLGEPGKAAKPLDTVRKSYYSKDPSRAEKREIKCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRIPPEILAMH
ENVLKCPTPGCTGQGHVNSNRNTHRSLSGCPIAAAEKLAKSHEKQQPQTGDPSKSSSNSDRILRPMCFVKQLEVPPYGSY
RPNVAPATPRANLAKELEKFSKVTFDYASFDAQVFGKRMLAPKIQTSETSPKAFQCFDYSQDAEAAHMAATAILNLSTRC
WEMPENLSTKPQDLPSKSVDIEVDENGTLDLSMHKHRKRENAFPSSSSCSSSPGVKSPDASQRHSSTSAPSSSMTSPQSS
QASRQDEWDRPLDYTKPSRLREEEPEESEPAAHSFASSEADDQEVSEENFEERKYPGEVTLTNFKLKFLSKDIKKELLTC
PTPGCDGSGHITGNYASHRSLSGCPLADKSLRNLMAAHSADLKCPTPGCDGSGHITGNYASHRSLSGCPRAKKSGVKVAP
TKDDKEDPELMKCPVPGCVGLGHISGKYASHRSASGCPLAARRQKEGSLNGSSFSWKSLKNEGPTCPTPGCDGSGHANGS
FLTHRSLSGCPRATFAGKKGKLSGDEVLSPKFKTSDVLENDEEIKQLNQEIRDLNESNSEMEAAMVQLQSQISSMEKNLK
NIEEENKLIEEQNEALFLELSGLSQALIQSLANIRLPHMEPICEQNFDAYVSTLTDMYSNQDPENKDLLESIKQAVRGIQ
V
```

275 - 294:	EEEEEEEEEEEEEEEEEEEE
276 - 295:	EEEEEEEEEEEEEEEEEEEE
277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE
287 - 306:	EEEEEEEEEEEEEEEEEEEE

Q01538-2 **MYT1_HUMAN** (1148 aa)
Myelin transcription factor 1 (MyT1) (Myelin transcription factor I) (MyTI) (PLPB1) (Proteolipid protein-binding protein). *Homo*

sapiens (Human)

```
MSLENEDKRARTRSKALRGPPETTAADLSCPTPGCTGSGHVRGKYSRHRSLQSCPLAKKRKLEGAEAEHLVSKRKSHPLK
LALDEGYGVDSDGSEDTEVKDASVSDESEGTLEGAEAETSGQDEIHRPETAEGRSPVKSHFGSNPIGSATASSKGSYSSY
QGIIATSLLNLGQIAEETLVEEDLGQAAKPGPGIVHLLQEAAEGAASEEGEKGLFIQPEDAEEVVEVTTERSQDLCPQSL
EDAASEESSKQKGILSHEEEDEEEEEEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAAPDVIFQEDTSHT
SAQKAPELRGPESPSPKPEYSVIVEVRSDDDKDEDTHSRKSTVTDESEMQDMMTRGNLGLLEQAIALKAEQVRTVCEPGC
PPAEQSQLGLGEPGKAAKPLDTVRKSYYSKDPSRAEKREIKCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRIPPEILAMH
ENVLKCPTPGCTGQGHVNSNRNTHRSLSGCPIAAAEKLAKSHEKQQPQTGDPSKSSSNSDRILRPMCFVKQLEVPPYGSY
RPNVAPATPRANLAKELEKFSKVTFDYASFDAQVFGKRMLAPKIQTSETSPKAFQSKPFPKASSPRHSPSSSYVRSTSSS
SAGFDYSQDAEAAHMAATAILNLSTRCWEMPENLSTKPQDLPSKSVDIEVDENGTLDLSMHKHRKRENAFPSSSSCSSSP
GVKSPDASQRHSSTSAPSSSMTSPQSSQASRQDEWDRPLDYTKPSRLREEEPEESEPAAHSFASSEADDQEVSEENFEER
KYPGEVTLTNFKLKFLSKDIKKELLTCPTPGCDGSGHITGNYASHRSLSGCPLADKSLRNLMAAHSADLKCPTPGCDGSG
HITGNYASHRSLSGCPRAKKSGVKVAPTKDDKEDPELMKCPVPGCVGLGHISGKYASHRSASGCPLAARRQKEGSLNGSS
FSWKSLKNEGPTCPTPGCDGSGHANGSFLTHRSLSGCPRATFAGKKGKLSGDEVLSPKFKTSDVLENDEEIKQLNQEIRD
LNESNSEMEAAMVQLQSQISSMEKNLKNIEEENKLIEEQNEALFLELSGLSQALIQSLANIRLPHMEPICEQNFDAYVST
LTDMYSNQDPENKDLLESIKQAVRGIQV
```

275 - 294:	EEEEEEEEEEEEEEEEEEEE
276 - 295:	EEEEEEEEEEEEEEEEEEEE
277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE
287 - 306:	EEEEEEEEEEEEEEEEEEEE

P68874 **P230_PLAF7** (3135 aa)
Gametocyte surface protein P230. *Plasmodium falciparum (isolate 3D7)*

```
MKKIITLKNLFLIILVYIFSEKKDLRCNVIKGNNIKDDEDKRFHLFYYSHNLFKTPETKEKKNKKECFYKNGGIYNLSKE
IRMRKDTSVKIKQRTCPFHKEGSSFEMGSKNITCFYPIVGKKERKTLDTIIIKKNVTNDHVVSSDMHSNVQEKNMILIRN
IDKENKNDIQNVEEKIQRDTYENKDYESDDTLIEWFDDNTNEENFLLTFLKRCLMKIFSSPKRKKTVVQKKHKSNFFINS
SLKYIYMYLTPSDSFNLVRRNRNLDEEDMSPRDNFVIDDEEEEEEEEEEEEEEEEEEEEEEEEYDDYVYEESGDETEEQ
LQEEHQEEVGAESSEESFNDEDEDSVEARDGDMIRVDEYYEDQDGDTYDSTIKNEDVDEEVGEEVGEEVGEEVGEEVGEE
VGEEVGEEVGEEVGEEEGEEVGEGVGEEVGEEEGEEVGEEEGEYVDEKERQGEIYPFGDEEEKDEGGESFTYEKSEVDKT
DLFKFIEGGEGDDVYKVDGSKVLLDDDTISRVSKKHTARDGEYGEYGEAVEDGENVIKIIRSVLQSGALPSVGVDELDKI
DLSYETTESGDTAVSEDSYDKYASNNTNKEYVCDFTDQLKPTESGPKVKKCEVKVNEPLIKVKIICPLKGSVEKLYDNIE
YVPKKSPYVVLTKEETKLKEKLLSKLIYGLLISPTVNEKENNFKEGVIEFTLPPVVHKATVFYFICDNSKTEDDNKKGNR
GIVEVYVEPYGNKINGCAFLDEDEEEEKYGNQIEEDEHNEKIKMKTFFTQNIYKKNNIYPCYMKLYSGDIGGILFPKNIK
STTCFEEMIPYNKEIKWNKENKSLGNLVNNSVVYNKEMNAKYFNVQYVHIPTSYKDTLNLFCSIILKEEESNLISTSYLV
YVSINEELNFSLFDFYESFVPIKKTIQVAQKNVNNKEHDYTCDFTDKLDKTVPSTANGKKLFICRKHLKEFDTFTLKCNV
NKTQYPNIEIFPKTLKDKKEVLKLDLDIQYQMFSKFFKFNTQNAKYLNLYPYYLIFPFNHIGKKELKNNPTYKNHKDVKY
FEQSSVLSPLSSADSLGKLLNFLDTQETVCLTEKIRYLNLSINELGSDNNTFSVTFQVPPYIDIKEPFYFMFGCNNNKGE
GNIGIVELLISKQEEKIKGCNFHESKLDYFNENISSDTHECTLHAYENDIIGFNCLETTHPNEVEVEVEDAEIYLQPENC
FNNVYKGLNSVDITTILKNAQTYNINNKKTPTFLKIPPYNLLEDVEISCQCTIKQVVKKIKVIITKNDTVLLKREVQSES
TLDDKIYKCEHENFINPRVNKTFDENVEYTCNIKIENFFNYIQIFCPAKDLGIYKNIQMYYDIVKPTRVPQFKKFNNEEL
HKLIPNSEMLHKTKEMLILYNEEKVDLLHFYVFLPIYIKDIYEFNIVCDNSKTMWKNQLGGKVIYHITVSKREQKVKGCS
FDNEHAHMFSYNKTNVKNCIIDAKPKDLIGFVCPSGTLKLTNCFKDAIVHTNLTNINGILYLKNNLANFTYKHQFNYMEI
PALMDNDISFKCICVDLKKKKYNVKSPLGPKVLRALYKKLNIKFDNYVTGTDQNKYLMTYMDLHLSHKRNYLKELFHDLG
KKKPADTDANPESIIESLSINESNESGPFPTGDVDAEHLILEGYDTWESLYDEQLEEVIYNDIESLELKDIEQYVLQVNL
KAPKLMMSAQIHNNRHVCDFSKNNLIVPESLKKKEELGGNPVNIHCYALLKPLDTLYVKCPTSKDNYEAAKVNISENDNE
YELQVISLIEKRFHNFETLESKKPGNGDVVVHNGVVDTGPVLDNSTFEKYFKNIKIKPDKFFEKVINEYDDTEEEKDLES
ILPGAIVSPMKVLKKKDPFTSYAAFVVPPIVPKDLHFKVECNNTEYKDENQYISGYNGIIHIDISNSNRKINGCDFSTNN
SSILTSSVKLVNGETKNCEININNNEVFGIICDNETNLDPEKCFHEIYSKDNKTVKKFREVIPNIDIFSLHNSNKKKVAY
AKVPLDYINKLLFSCSCKTSHTNTIGTMKVTLNKDEKEEEDFKTAQGIKHNNVHLCNFFDNPELTFDNNKIVLCKIDAEL
FSEVIIQLPIFGTKNVEEGVQNEEYKKFSLKPSLVFDDNNNDIKVIGKEKNEVSISLALKGVYGNRIFTFDKNGKKGEGI
SFFIPPIKQDTDLKFIINETIDNSNIKQRGLIYIFVRKNVSENSFKLCDFTTGSTSLMELNSQVKEKKCTVKIKKGDIFG
LKCPKGFAIFPQACFSNVLLEYYKSDYEDSEHINYYIHKDKKYNLKPKDVIELMDENFRELQNIQQYTGISNITDVLHFK
NFNLGNLPLNFKNHYSTAYAKVPDTFNSIINFSCNCYNPEKHVYGTMQVESDNRNFDNIKKNENVIKNFLLPNIEKYALL
LDDEERQKKIKQQQEEEQQEQILKDQDDRLSRHDDYNKNHTYILYDSNEHICDYEKNESLISTLPNDTKKIQKSICKINA
KALDVVTIKCPHTKNFTPKDYFPNSSLITNDKKIVITFDKKNFVTYIDPTKKTFSLKDIYIQSFYGVSLDHLNQIKKIHE
EWDDVHLFYPPHNVLHNVVLNNHIVNLSSALEGVLFMKSKVTGDETATKKNTTLPTDGVSSILIPPYVKEDITFHLFCGK
STTKKPNKKNTSLALIHIHISSNRNIIHGCDFLYLENQTNDAISNNNNNSYSIFTHNKNTENNLICDISLIPKTVIGIKC
PNKKLNPQTCFDEVYYVKQEDVPSKTITADKYNTFSKDKIGNILKNAISINNPDEKDNTYTYLILPEKFEEELIDTKKVL
ACTCDNKYIIHMKIEKSTMDKIKIDEKKTIGKDICKYDVTTKVATCEIIDTIDSSVLKEHHTVHYSITLSRWDKLIIKYP
TNEKTHFENFFVNPFNLKDKVLYNYNKPINIEHILPGAITTDIYDTRTKIKQYILRIPPYVHKDIHFSLEFNNSLSLTKQ
NQNIIYGNVAKIFIHINQGYKEIHGCDFTGKYSHLFTYSKKPLPNDDDICNVTIGNNTFSGFACLSHFELKPNNCFSSVY
DYNEANKVKKLFDLSTKVELDHIKQNTSGYTLSYIIFNKESTKLKFSCTCSSNYSNYTIRITFDPNYIIPEPQSRAIIKY
VDLQDKNFAKYLRKL
```

280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE

284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE

P68875 **P230_PLAFO** (3135 aa)
Gametocyte surface protein P230. *Plasmodium falciparum (isolate NF54)*

```
MKKIITLKNLFLIILVYIFSEKKDLRCNVIKGNNIKDDEDKRFHLFYYSHNLFKTPETKEKKNKKECFYKNGGIYNLSKE
IRMRKDTSVKIKQRTCPFHKEGSSFEMGSKNITCFYPIVGKKERKTLDTIIIKKNVTNDHVVSSDMHSNVQEKNMILIRN
IDKENKNDIQNVEEKIQRDTYENKDYESDDTLIEWFDDNTNEENFLLTFLKRCLMKIFSSPKRKKTVVQKKHKSNFFINS
SLKYIYMYLTPSDSFNLVRRNRNLDEEDMSPRDNFVIDDEEEEEEEEEEEEEEEEEEEEEEEYDDYVYEESGDETEEQ
LQEEHQEEVGAESSEESFNDEDEDSVEARDGDMIRVDEYYEDQDGDTYDSTIKNEDVDEEVGEEVGEEVGEEVGEEVGEE
VGEEVGEEVGEEVGEEEGEEVGEGVGEEVGEEEGEEVGEEEGEYVDEKERQGEIYPFGDEEEKDEGGESFTYEKSEVDKT
DLFKFIEGGEGDDVYKVDGSKVLLDDDTISRVSKKHTARDGEYGEYGEAVEDGENVIKIIRSVLQSGALPSVGVDELDKI
DLSYETTESGDTAVSEDSYDKYASNNTNKEYVCDFTDQLKPTESGPKVKKCEVKVNEPLIKVKIICPLKGSVEKLYDNIE
YVPKKSPYVVLTKEETKLKEKLLSKLIYGLLISPTVNEKENNFKEGVIEFTLPPVVHKATVFYFICDNSKTEDDNKKGNR
GIVEVYVEPYGNKINGCAFLDEDEEEEKYGNQIEEDEHNEKIKMKTFFTQNIYKKNNIYPCYMKLYSGDIGGILFPKNIK
STTCFEEMIPYNKEIKWNKENKSLGNLVNNSVVYNKEMNAKYFNVQYVHIPTSYKDTLNLFCSIILKEEESNLISTSYLV
YVSINEELNFSLFDFYESFVPIKKTIQVAQKNVNNKEHDYTCDFTDKLDKTVPSTANGKKLFICRKHLKEFDTFTLKCNV
NKTQYPNIEIFPKTLKDKKEVLKLDLDIQYQMFSKFFKFNTQNAKYLNLYPYYLIFPFNHIGKKELKNNPTYKNHKDVKY
FEQSSVLSPLSSADSLGKLLNFLDTQETVCLTEKIRYLNLSINELGSDNNTFSVTFQVPPYIDIKEPFYFMFGCNNNKGE
GNIGIVELLISKQEEKIKGCNFHESKLDYFNENISSDTHECTLHAYENDIIGFNCLETTHPNEVEVEVEDAEIYLQPENC
FNNVYKGLNSVDITTILKNAQTYNINNKKTPTFLKIPPYNLLEDVEISCQCTIKQVVKKIKVIITKNDTVLLKREVQSES
TLDDKIYKCEHENFINPRVNKTFDENVEYTCNIKIENFFNYIQIFCPAKDLGIYKNIQMYYDIVKPTRVPQFKKFNNEEL
HKLIPNSEMLHKTKEMLILYNEEKVDLLHFYVFLPIYIKDIYEFNIVCDNSKTMWKNQLGGKVIYHITVSKREQKVKGCS
FDNEHAHMFSYNKTNVKNCIIDAKPKDLIGFVCPSGTLKLTNCFKDAIVHTNLTNINGILYLKNNLANFTYKHQFNYMEI
PALMDNDISFKCICVDLKKKKYNVKSPLGPKVLRALYKKLNIKFDNYVTGTDQNKYLMTYMDLHLSHKRNYLKELFHDLG
KKKPADTDANPESIIESLSINESNESGPFPTGDVDAEHLILEGYDTWESLYDEQLEEVIYNDIESLELKDIEQYVLQVNL
KAPKLMMSAQIHNNRHVCDFSKNNLIVPESLKKKEELGGNPVNIHCYALLKPLDTLYVKCPTSKDNYEAAKVNISENDNE
YELQVISLIEKRFHNFETLESKKPGNGDVVVHNGVVDTGPVLDNSTFEKYFKNIKIKPDKFFEKVINEYDDTEEEKDLES
ILPGAIVSPMKVLKKKDPFTSYAAFVVPPIVPKDLHFKVECNNTEYKDENQYISGYNGIIHIDISNSNRKINGCDFSTNN
SSILTSSVKLVNGETKNCEININNNEVFGIICDNETNLDPEKCFHEIYSKDNKTVKKFREVIPNIDIFSLHNSNKKKVAY
AKVPLDYINKLLFSCSCKTSHTNTIGTMKVTLNKDEKEEEDFKTAQGIKHNNVHLCNFFDNPELTFDNNKIVLCKIDAEL
FSEVIIQLPIFGTKNVEEGVQNEEYKKFSLKPSLVFDDNNNDIKVIGKEKNEVSISLALKGVYGNRIFTFDKNGKKGEGI
SFFIPPIKQDTDLKFIINETIDNSNIKQRGLIYIFVRKNVSENSFKLCDFTTGSTSLMELNSQVKEKKCTVKIKKGDIFG
LKCPKGFAIFPQACFSNVLLEYYKSDYEDSEHINYYIHKDKKYNLKPKDVIELMDENFRELQNIQQYTGISNITDVLHFK
NFNLGNLPLNFKNHYSTAYAKVPDTFNSIINFSCNCYNPEKHVYGTMQVESDNRNFDNIKKNENVIKNFLLPNIEKYALL
LDDEERQKKIKQQQEEEQQEQILKDQDDRLSRHDDYNKNHTYILYDSNEHICDYEKNESLISTLPNDTKKIQKSICKINA
KALDVVTIKCPHTKNFTPKDYFPNSSLITNDKKIVITFDKKNFVTYIDPTKKTFSLKDIYIQSFYGVSLDHLNQIKKIHE
EWDDVHLFYPPHNVLHNVVLNNHIVNLSSALEGVLFMKSKVTGDETATKKNTTLPTDGVSSILIPPYVKEDITFHLFCGK
STTKKPNKKNTSLALIHIHISSNRNIIHGCDFLYLENQTNDAISNNNNNSYSIFTHNKNTENNLICDISLIPKTVIGIKC
PNKKLNPQTCFDEVYYVKQEDVPSKTITADKYNTFSKDKIGNILKNAISINNPDEKDNTYTYLILPEKFEEELIDTKKVL
ACTCDNKYIIHMKIEKSTMDKIKIDEKKTIGKDICKYDVTTKVATCEIIDTIDSSVLKEHHTVHYSITLSRWDKLIIKYP
TNEKTHFENFFVNPFNLKDKVLYNYNKPINIEHILPGAITTDIYDTRTKIKQYILRIPPYVHKDIHFSLEFNNSLSLTKQ
NQNIIYGNVAKIFIHINQGYKEIHGCDFTGKYSHLFTYSKKPLPNDDDICNVTIGNNTFSGFACLSHFELKPNNCFSSVY
DYNEANKVKKLFDLSTKVELDHIKQNTSGYTLSYIIFNKESTKLKFSCTCSSNYSNYTIRITFDPNYIIPEPQSRAIIKY
VDLQDKNFAKYLRKL
```

280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE

Q8IZL8 **PELP1_HUMAN** (1130 aa)
Proline-, glutamic acid- and leucine-rich protein 1 (Modulator of non-genomic activity of estrogen receptor) (Transcription factor HMX3). *Homo sapiens (Human)*

```
MAAAVLSGPSAGSAAGVPGGTGGLSAVSSGPRLRLLLLESVSGLLQPRTGSAVAPVHPPNRSAPHLPGLMCLLRLHGSVG
GAQNLSALGALVSLSNARLSSIKTRFEGLCLLSLLVGESPTELFQQHCVSWLRSIQQVLQTQDPPATMELAVAVLRDLLR
YAAQLPALFRDISMNHLPGLLTSLLGLRPECEQSALEGMKACMTYFPRACGSLKGKLASFFLSRVDALSPQLQQLACECY
SRLPSLGAGFSQGLKHTESWEQELHSLLASLHTLLGALYEGAETAPVQNEGPGVEMLLSSEDGDAHVLLQLRQRFSGLAR
CLGLMLSSEFGAPVSVPVQEILDFICRTLSVSSKNISLHGDGPLRLLLLPSIHLEALDLLSALILACGSRLLRFGILIGR
LLPQVLNSWSIGRDSLSPGQERPYSTVRTKVYAILELWVQVCGASAGMLQGGASGEALLTHLLSDISPPADALKLRSPRG
SPDGSLQTGKPSAPKKLKLDVGEAMAPPSHRKGDSNANSDVCAAALRGLSRTILMCGPLIKEETHRRLHDLVLPLVMGVQ
QGEVLGSSPYTSSRCRRELYCLLLALLLAPSPRCPPPLACALQAFSLGQREDSLEVSSFCSEALVTCAALTHPRVPPLQP
MGPTCPTPAPVPPPEAPSPFRAPPFHPPGPMPSVGSMPSAGPMPSAGPMPSAGPVPSARPGPPTTANHLGLSVPGLVSVP
PRLLPGPENHRAGSNEDPILAPSGTPPPTIPPDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDSVVIVPEGLPPLPP
PPPSGATPPPIAPTGPPTASPPVPAKEEPEELPAAPGPLPPPPPPPPPVPGPVTLPPPQLVPEGTPGGGGPPALEEDLTV
ININSSDEEEEEEEEEEEEEEEEEEEEEEEDFEEEEEDEEEYFEEEEEEEEEFEEEFEEEEGELEEEEEEEDEEEEEELEEV
EDLEFGTAGGEVEEGAPPPPTLPPALPPPESPPKVQPEPEPEPGLLLEVEEPGTEEERGADTAPTLAPEALPSQGEVERE
GESPAAGPPPQELVEEEPSAPPTLLEEETEDGSDKVQPPPETPAEEEMETETEAEALQEKEQDDTAAMLADFIDCPPDDE
KPPPPTEPDS
```

888 - 907:	EEEEEEEEEEEEEEEEEEEE
889 - 908:	EEEEEEEEEEEEEEEEEEEE

Q7TPB0 **PLPR3_MOUSE** (716 aa)
Phospholipid phosphatase-related protein type 3 (EC 3.1.3.4) (Lipid phosphate phosphatase-related protein type 3) (Plasticity-related gene 2 protein) (PRG-2). *Mus musculus (Mouse)*

```
MLAMKEKNKTPKDSMTLLPCFYFVELPIVASSIVSLYFLELTDLFKPAKVGFQCYDRALSMPYVETNEELIPLLMLLSLA
```

```
FAAPAASIMVGEGMVYCLQSRLWGRGPGGVEGSINAGGCNFNSFLRRTVRFVGVHVFGLCATALVTDVIQLATGYHTPFF
LTVCKPNYTLLGTSCESNPYITQDICSGHDTHAILSARKTFPSQHATLSAFAAVYVSMYFNAVISDTTKLLKPILVFAFA
IAAGVCGLTQITQYRSHPVDVYAGFLIGAGIAAYLACHAVGNFQAPPAEKVPTPAPAKDALRALTQRGHESMYQQNKSVS
TDELGPPGRLEGVPRPVAREKTSLGSLKRASVDVDLLAPRSPMGKEGMVTFSNTLPRVSTPSLDDPARRHMTIHVPLDAS
RSRQLIGEWKQKSLEGRGLGLPDEASPVHLRAPAEQVAEEEEEEEEEEEEEEEEEEEEGPVPPSLYPTVQARPGLGPRVI
LPPRPGPQPLVHIPEEGVQAGAGLSPKSSSSSVRAKWLSVAEKGGGPVAVAPSQPRVANPPRLLQVIAMSKAAGGPKAET
ASSSSASSDSSQYRSPSDRDSASIVTIDAHAPHHPVVHLSAGSTPWEWKAKVVEGEGSYELGDLARGFRSSCKQPGMGPG
SPVSDVDQEEPRFGAVATVNLATGEGLPPPGASEGALGAGSRESTLRRQVGGLAEREVEAEAESYYRRMQARRYQD
```

439 - 458:	EEEEEEEEEEEEEEEEEEEE

Q7TMB0 **PLPR3_RAT** (716 aa)
Phospholipid phosphatase-related protein type 3 (EC 3.1.3.4) (Lipid phosphate phosphatase-related protein type 3) (Plasticity-related gene 2 protein) (PRG-2). *Rattus norvegicus (Rat)*

```
MIAKKEKNKTPKDSMTLLPCFYFVELPIVASSVVSLYFLELTDLFQPAKVGFQCHDRSLSMPYVETNEELIPLLMLLSLA
FAAPAASIMVGEGMVYCLQSRLWGRGPGGVEGSINAGGCNFNSFLRRTVRFVGVHVFGLCATALVTDVIQLATGYHTPFF
LTVCKPNYTLLGTSCEANPYITQDICSGHDTHAILSARKTFPSQHATLSAFAAVYVSMYFNSVISDATKLLKPILVFAFA
IAAGVCGLTQITQYRSHPVDVYAGFLIGAGIAAYLACHAVGNFQAPPAEKVPTPAPAKDALRVLTQRGHESMYQQNKSVS
TDELGPPGRLEGVPRPVAREKTSLGSLKRASVDVDLLAPRSPMGKEGMVTFSNTLPRVSTPSLDDPSRRHMTIHVPLDAS
RSRQLISEWKQKSLEGRGLGLPDEASPAHLRAPAEQVAEEEEEEEEEEEEEEEEEEEEEGPVPPSLYPTVQARPGLGPRV
ILPPRPGPQPLIHIPEEVVQAGAGLSPKSSASVRAKWLSMVEKGGGPVAVAPPQPRVANPPRLLQVIAMSKAAGGPKAET
ASSSSASSDSSQYRSPSDRDSASIVTIDAHAPHHPVVHLSAGSTPWEWKAKVVEGEGGYELGDLARGFRSSCKQPGIGPG
SPVSDVDQEEPRFGAVATVNLATGEGLPPPGASEGALGAGSRESTLRRQVGALGEREVEAEAESYYRRMQARRYQD
```

439 - 458:	EEEEEEEEEEEEEEEEEEEE
440 - 459:	EEEEEEEEEEEEEEEEEEEE

Q12532 **RQC2_YEAST** (1038 aa)
Ribosome quality control complex subunit 2 (Translation-associated element 2). *Saccharomyces cerevisiae (strain ATCC 204508 / S288c) (Baker's yeast)*

```
MKQRISALDLLLLARELKQDLEGYRLSNIYNIADSSKQFLLKFNKPDSKLNVVVDCGLRIYLTEFSRPIPPTPSGFVVKL
RKHLKAKRLTALKQVDQDRILVLQFADGHFYLVLEFFSAGNVILLDENRRIMALQRVVLEHENKVGQIYEMFDESLFTTN
NESADESIEKNRKAEYTSELVNEWIKAVQAKYESDITVIKQLNIQGKEGAKKKKVKVPSIHKLLLSKVPHLSSDLLSKNL
KVFNIDPSESCLNLLEETDSLAELLNSTQLEYNQLLTTTDRKGYILAKRNENYISEKDTADLEFIYDTFHPFKPYINGGD
TDSSCIIEVEGPYNRTLDKFFSTIESSKYALRIQNQESQAQKKIDDARAENDRKIQALLDVQELNERKGHLIIENAPLIE
EVKLAVQGLIDQQMDWNTIEKLIKSEQKKGNRIAQLLNLPLNLKQNKISVKLDLSSKELNTSSDEDNESEGNTTDSSSDS
DSEDMESSKERSTKSMKRKSNEKINVTIDLGLSAYANATEYFNIKKTSAQKQKKVEKNVGKAMKNIEVKIDQQLKKKLKD
SHSVLKKIRTPYFFEKYSWFISSEGFLVMMGKSPAETDQIYSKYIEDDDIYMSNSFNSHVWIKNPEKTEVPPNTLMQAGI
LCMSSSEAWSKKISSSPWWCFAKNVSKFDGSDNSILPEGAFRLKNENDQNHLPPAQLVMGFGFLWKVKTSGNEDNGDDDE
EEEEEEEEEEEEEEEEEEEEEEEKEEEEKEEEQQQDEDDSNEVNGLEKGGDSNDSTKNNSFEHDNLEKDIEKHCTISSDT
DSDSGNAKAKNDNSSTQRILDEPGVPISLIENINSNVRGKRGKLKKIQKKYADQDETERLLRLEALGTLKGIEKQQQRKK
EEIMKREVREDRKNKREKQRRLQALKFTKKEKARVNYDKHKSELKPSLDKGDVVDDIIPVFAPWPALLKYKYKVKIQPGS
AKKTKTLTEILHYFKSRPLDGSSTDNEMDWPQEHEMIKGLKEQDLVLLLCVDKLKVTIAGQKSTKNGGNSSKKGKKKR
```

720 - 739:	EEEEEEEEEEEEEEEEEEEE
721 - 740:	EEEEEEEEEEEEEEEEEEEE
722 - 741:	EEEEEEEEEEEEEEEEEEEE
723 - 742:	EEEEEEEEEEEEEEEEEEEE
724 - 743:	EEEEEEEEEEEEEEEEEEEE

Q7M732 **RTL1_MOUSE** (1744 aa)
Retrotransposon-like protein 1 (Mammalian retrotransposon derived protein 1) (Paternally expressed gene 11 protein) (Retrotransposon-derived protein PEG11). *Mus musculus (Mouse)*

```
MIEPSEDSFETMMELKNPSSKQMESSEGSSNTVEETPGSSGAQAGAQAGAQAEAQAETQVEAQAEAQAEAQVEAQVEAQA
GSDSGPAQEEKEPPSGPLKEMQELPTNLLQEVEEPSSGPHQEMQELPTDLLQEVEEPSSGPHQEMQELPTDLLREVEEPS
SGPYQEMQELPTDLLREVEEPSSGPYQEMQELPTDLLREVEEPSSGPYQEMQELPTDLLREVEEPSSGPYQEMQELPTDL
LREVEEPSSDPCEASSNDLPQDMEESSDDGSNQESSDGSNHELSNGSNHESSFGSNPESSDVSNLESSGGSNQESSDGSQ
KESSYDSNPELSDNSNQELSDNSNQESSDSSNQSSDISNQEGSEPLSEASDYSMDETINSSETQSDQDDTDLGDDEEEEE
EEGGEEEGQPKNSPEEVVATMGNVISLFLRMQDLKEQQRVAERLMMQAINEGRLPSLRPFSGDRRDYHEFVVLCQMTMQN
YPSMLYNDELRVKFVIRHLTDLALEWANDLVEQNSPVINNFSAFLEAMSEKFEYRQTLRVAEDAMFNIRQGNRCAADYIN
EFRGLIPTLGWPDEVLQAHLCQGLNEEIRHYLFRIPQPNSLDNLIVLVLQLEEKLAERRALLRLPPESRPRSVAWMDAPA
PEKWRVSSWLPNEFHPDIDRDHLFLLLLVRVDPYHSVAVRALVDSGAEGNYMDERFAQEHYVELYEKPYPQIIQGVDGIP
IGNEPVWLCTEPLVCVHQKHYEYIEFDILPSPNFSIVLGMKWLRTHAPEVDWMRGRCTFHSPYCLRNCFTPPPPCIALET
YSISLLPGLPHTYSDLADVFNPREADDETSDQPSSDGSDDLSESEPSELQQAGDSDQSGVFYESGARETLEPVSARMQEK
ARQQEKAREQEEYWILYDMLTDRQDYTQMVPELFDQLHGAAWFTKLELLGIKESEMRHTVTHTEDTWRASFGFGLHQMRC
YRPFTMNSYSDEGNNIVHFILKDILGLFVICHGREVLVYSMSQEEHSQHVRQVLVRFRYHNIYCSLDKTQFHRQTAEILG
FNISPKGVKLNKNLMNLIVGCPVPGSRRCLQSVIDLVYPYRHFVENFAVIAAPLVRQLLSSEPYYWGEEEQEALESLKRA
FRKSPVLYHPKPQNPFYLETDITGSFLSASLVQTDDETGKKSTCAFYSRPLSTMEVEYPRVEMRILPIRAAFMVWCRYLE
NTEEPIMILLNTEDLASLNNDRLTVLLPGHWVFFFSHFNFGVMEMPAEGDTQALFRRCWNQRGFRARFLRPLLLMSIRAN
LRYFDRSSETEDKEDDEEEEEEDGEEEEGEEEEDGEEEEGEEEEDGEEEEEEEEDDEEEEGEEEEDGEEEEGEEEEDGEE
EEGEEEEDGEEEEGEEEGEEEEEGEEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEEEDEEEEDEEEVPSM
VRELLAAIPMDHILNGLLAHFSVAQIRAVVLNFFRGLLYWKSLLGVAAVLVMLRARQPLSPVPAPNLEVARPQHRHTLRL
ILDSTLIASSGMATAIAQLLSQMPPLVGANTLPARELAELFLGPRCWHRNALHSQPPRGMRFTPGFWLTLCEFFGVRVNP
EDDVFPDPYQHRYLELHVVGDEDVVLREALQDDLQRYRQCGLHDGLQDTSQDAQDNDVQEDLFGDQEAVTFRPRNLLDPE
VLDFLNNRLLYTLGTDGRLTLLSRDQVAQALTRFLAMASRMALPSPAREQARLEELSDSDDELD
```

1394 - 1413:	EEEEEEEEEEEEEEEEEEEE

1395 - 1414:	EEEEEEEEEEEEEEEEEEEE
1396 - 1415:	EEEEEEEEEEEEEEEEEEEE
1397 - 1416:	EEEEEEEEEEEEEEEEEEEE
1398 - 1417:	EEEEEEEEEEEEEEEEEEEE
1399 - 1418:	EEEEEEEEEEEEEEEEEEEE
1400 - 1419:	EEEEEEEEEEEEEEEEEEEE
1401 - 1420:	EEEEEEEEEEEEEEEEEEEE
1402 - 1421:	EEEEEEEEEEEEEEEEEEEE
1403 - 1422:	EEEEEEEEEEEEEEEEEEEE
1404 - 1423:	EEEEEEEEEEEEEEEEEEEE

Q9ULL8 **SHRM4_HUMAN** (1493 aa)
Protein Shroom4 (Second homolog of apical protein). *Homo sapiens (Human)*

```
MENRPGSFQYVPVQLQGGAPWGFTLKGGLEHCEPLTVSKIEDGGKAALSQKMRTGDELVNINGTPLYGSRQEALILIKGS
FRILKLIVRRRNAPVSRPHSWHVAKLLEGCPEAATTMHFPSEAFSLSWHSGCNTSDVCVQWCPLSRHCSTEKSSSIGSME
SLEQPGQATYESHLLPIDQNMYPNQRDSAYSSFSASSNASDCALSLRPEEPASTDCIMQGPGPTKAPSGRPNVAETSGGS
RRTNGGHLTPSSQMSSRPQEGYQSGPAKAVRGPPQPPVRRDSLQASRAQLLNGEQRRASEPVVPLPQKEKLSLEPVLPAR
NPNRFCCLSGHDQVTSEGHQNCEFSQPPESSQQGSEHLLMQASTKAVGSPKACDRASSVDSNPLNEASAELAKASFGRPP
HLIGPTGHRHSAPEQLLASHLQHVHLDTRGSKGMELPPVQDGHQWTLSPLHSSHKGKKSPCPPTGGTHDQSSKERKTRQV
DDRSLVLGHQSQSSPPHGEADGHPSEKGFLDPNRTSRAASELANQQPSASGSLVQQATDCSSTTKAASGTEAGEEGDSEP
KECSRMGGRRSGGTRGRSIQNRRKSERFATNLRNEIQRRKAQLQKSKGPLSQLCDTKEPVEETQEPPESPPLTASNTSLL
SSCKKPPSPRDKLFNKSMMLRARSSECLSQAPESHESRTGLEGRISPGQRPGQSSLGLNTWWKAPDPSSSDPEKAHAHCG
VRGGHWRWSPEHNSQPLVAAAMEGPSNPGDNKELKASTAQAGEDAILLPFADRRKFFEESSKSLSTSHLPGLTTHSNKTF
TQRPKPIDQNFQPMSSSCRELRRHPMDQSYHSADQPYHATDQSYHSMSPLQSETPTYSECFASKGLENSMCCKPLHCGDF
DYHRTCSYSCSVQGALVHDPCIYCSGEICPALLKRNMMPNCYNCRCHHHQCIRCSVCYHNPQHSALEDSSLAPGNTWKPR
KLTVQEFPGDKWNPITGNRKTSQSGREMAHSKTSFSWATPFHPCLENPALDLSSYRAISSLDLLGDFKHALKKSEETSVY
EEGSSLASMPHPLRSRAFSESHISLAPQSTRAWGQHRRELFSKGDETQSDLLGARKKAFPPPRPPPPNWEKYRLFRAAQQ
QKQQQQQQKQQEEEEEEEEEEEEEEEEEEEEAEEEEEELPPQYFSSETSGSCALNPEEVLEQPQPLSFGHLEGSRQGSQS
VPAEQESFALHSSDFLPPIRGHLGSQPEQAQPPCYYGIGGLWRTSGQEATESAKQEFQHFSPPSGAPGIPTSYSAYYNIS
VAKAELLNKLKDQPEMAEIGLGEEEVDHELAQKKIQLIESISRKLSVLREAQRGLLEDINANSALGEEVEANLKAVCKSN
EFEKYHLFVGDLDKVVNLLLSLSGRLARVENALNSIDSEANQEKLVLIEKKQQLTGQLADAKELKEHVDRREKLVFGMVS
RYLPQDQLQDYQHFVKMKSALIIEQRELEEKIKLGEEQLKCLRESLLLGPSNF
```

1132 - 1151:	EEEEEEEEEEEEEEEEEEEE

Q9ULL8-2 **SHRM4_HUMAN** (1377 aa)
Protein Shroom4 (Second homolog of apical protein). *Homo sapiens (Human)*

```
MHFPSEAFSLSWHSGCNTSDVCVQWCPLSRHCSTEKSSSIGSMESLEQPGQATYESHLLPIDQNMYPNQRDSAYSSFSAS
SNASDCALSLRPEEPASTDCIMQGPGPTKAPSGRPNVAETSGGSRRTNGGHLTPSSQMSSRPQEGYQSGPAKAVRGPPQP
PVRRDSLQASRAQLLNGEQRRASEPVVPLPQKEKLSLEPVLPARNPNRFCCLSGHDQVTSEGHQNCEFSQPPESSQQGSE
HLLMQASTKAVGSPKACDRASSVDSNPLNEASAELAKASFGRPPHLIGPTGHRHSAPEQLLASHLQHVHLDTRGSKGMEL
PPVQDGHQWTLSPLHSSHKGKKSPCPPTGGTHDQSSKERKTRQVDDRSLVLGHQSQSSPPHGEADGHPSEKGFLDPNRTS
RAASELANQQPSASGSLVQQATDCSSTTKAASGTEAGEEGDSEPKECSRMGGRRSGGTRGRSIQNRRKSERFATNLRNEI
QRRKAQLQKSKGPLSQLCDTKEPVEETQEPPESPPLTASNTSLLSSCKKPPSPRDKLFNKSMMLRARSSECLSQAPESHE
SRTGLEGRISPGQRPGQSSLGLNTWWKAPDPSSSDPEKAHAHCGVRGGHWRWSPEHNSQPLVAAAMEGPSNPGDNKELKA
STAQAGEDAILLPFADRRKFFEESSKSLSTSHLPGLTTHSNKTFTQRPKPIDQNFQPMSSSCRELRRHPMDQSYHSADQP
YHATDQSYHSMSPLQSETPTYSECFASKGLENSMCCKPLHCGDFDYHRTCSYSCSVQGALVHDPCIYCSGEICPALLKRN
MMPNCYNCRCHHHQCIRCSVCYHNPQHSALEDSSLAPGNTWKPRKLTVQEFPGDKWNPITGNRKTSQSGREMAHSKTSFS
WATPFHPCLENPALDLSSYRAISSLDLLGDFKHALKKSEETSVYEEGSSLASMPHPLRSRAFSESHISLAPQSTRAWGQH
RRELFSKGDETQSDLLGARKKAFPPPRPPPPNWEKYRLFRAAQQQKQQQQQQKQQEEEEEEEEEEEEEEEEEEEEAEEEE
EELPPQYFSSETSGSCALNPEEVLEQPQPLSFGHLEGSRQGSQSVPAEQESFALHSSDFLPPIRGHLGSQPEQAQPPCYY
GIGGLWRTSGQEATESAKQEFQHFSPPSGAPGIPTSYSAYYNISVAKAELLNKLKDQPEMAEIGLGEEEVDHELAQKKIQ
LIESISRKLSVLREAQRGLLEDINANSALGEEVEANLKAVCKSNEFEKYHLFVGDLDKVVNLLLSLSGRLARVENALNSI
DSEANQEKLVLIEKKQQLTGQLADAKELKEHVDRREKLVFGMVSRYLPQDQLQDYQHFVKMKSALIIEQRELEEKIKLGE
EQLKCLRESLLLGPSNF
```

1016 - 1035:	EEEEEEEEEEEEEEEEEEEE

M0R8L2-2 **SPXN_RAT** (172 aa)
Spexin (Liver regeneration-related protein LRRGT00060) (NPQ) (Neuropeptide Q) (Spexin hormone) [Cleaved into: Spexin-1; Spexin-2 (NPQ 53-70)]. *Rattus norvegicus (Rat)*

```
MKGPSILAVAALALLLVLSVLENSSGAPQRLSEKRNWTPQAMLYLKGAQGHRFISDQSRRKELADRPPPEMNEVVDRKLL
MFKTCIFTWELLTSTHAHGLAHLCRMSNHFVHNAGQRKEKEGKGQRGRGGETVKLKEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEAKT
```

137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE

143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE

P19351 **TNNT_DROME** (397 aa)
Troponin T, skeletal muscle (Protein intended thorax) (Protein upheld). *Drosophila melanogaster (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETKPPQTPAEGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAK
RKVTRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSS
AAMERNKTKEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQL
RHKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDEISKDSNEKIWNEKKEQYTGRQKSKLPKWFG
ERPGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE

P19351-10 **TNNT_DROME** (306 aa)
Troponin T, skeletal muscle (Protein intended thorax) (Protein upheld). *Drosophila melanogaster (Fruit fly)*

```
MAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSSAAMERNKTKEQ
LEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDP
EALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDEISKDSNEKIWNEKKEQYTGRQKSKLPKWFGERPGKKAGEPE
TPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE
287 - 306:	EEEEEEEEEEEEEEEEEEEE

P19351-11 **TNNT_DROME** (397 aa)
Troponin T, skeletal muscle (Protein intended thorax) (Protein upheld). *Drosophila melanogaster (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETKPPQTPAEGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAK
RKVTRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSS
AAMERNKTKEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQL
RHKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYNTVYAETLEKTWQERQERFTQRTKSKLPKWFG
ERPGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE

370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE

P19351-12 **TNNT_DROME** (388 aa)
Troponin T, skeletal muscle (Protein intended thorax) (Protein upheld). *Drosophila melanogaster (Fruit fly)*

```
MSDDEEYTSEEEEVVEETREETKGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAKRKVTRAEE
EQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGLGLSSAAMERNKTK
EQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGL
DPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDEISKDSNEKIWNEKKEQYTGRQKSKLPKWFGERPGKKAGE
PETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE

P19351-13 **TNNT_DROME** (389 aa)
Troponin T, skeletal muscle (Protein intended thorax) (Protein upheld). *Drosophila melanogaster (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAKRKVTRAEE
EQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSSAAMERNKT
KEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKG
LDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYNTVYAETLEKTWQERQERFTQRTKSKLPKWFGERPGKKAG
EPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE

P19351-2 **TNNT_DROME** (396 aa)
Troponin T, skeletal muscle (Protein intended thorax) (Protein upheld). *Drosophila melanogaster (Fruit fly)*

```
MSDDEEYTSEEEEVVEETREETKPPQTPAEGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAKR
KVTRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSSA
AMERNKTKEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLR
HKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDEISKDSNEKIWNEKKEQYTGRQKSKLPKWFGE
RPGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

367 - 386:	EEEEEEEEEEEEEEEEEEEE

368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE

P19351-3 **TNNT_DROME** (397 aa)
Troponin T, skeletal muscle (Protein intended thorax) (Protein upheld). *Drosophila melanogaster (Fruit fly)*

```
MSDDEEYTSEEEEVVEETREETKKPPQTPAEGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAK
RKVTRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSS
AAMERNKTKEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQL
RHKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDEISKDSNEKIWNEKKEQYTGRQKSKLPKWFG
ERPGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE

P19351-4 **TNNT_DROME** (396 aa)
Troponin T, skeletal muscle (Protein intended thorax) (Protein upheld). *Drosophila melanogaster (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETKPPQTPAEGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAK
RKVTRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGLGLSSA
AMERNKTKEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLR
HKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDEISKDSNEKIWNEKKEQYTGRQKSKLPKWFGE
RPGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE

P19351-5 **TNNT_DROME** (396 aa)
Troponin T, skeletal muscle (Protein intended thorax) (Protein upheld). *Drosophila melanogaster (Fruit fly)*

```
MSDDEEYTSEEEEVVEETREETKKPPQTPAEGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAK
RKVTRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGLGLSSA
AMERNKTKEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLR
HKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDEISKDSNEKIWNEKKEQYTGRQKSKLPKWFGE
RPGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE

P19351-6 **TNNT_DROME** (374 aa)
Troponin T, skeletal muscle (Protein intended thorax) (Protein upheld). *Drosophila melanogaster (Fruit fly)*

```
MSDDEEYTGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAKRKVTRAEEEQKMAQRKKEEEERR
VREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSSAAMERNKTKEQLEEEKKISLSFR
IKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQ
VASKYERRVDTRSYDDKKKLFEGGWDEISKDSNEKIWNEKKEQYTGRQKSKLPKWFGERPGKKAGEPETPEGEEDAKADE
DIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE

P19351-7 **TNNT_DROME** (389 aa)
Troponin T, skeletal muscle (Protein intended thorax) (Protein upheld). *Drosophila melanogaster (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAKRKVTRAEE
EQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSSAAMERNKT
KEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKG
LDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDEISKDSNEKIWNEKKEQYTGRQKSKLPKWFGERPGKKAG
EPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE

P19351-8 **TNNT_DROME** (388 aa)
Troponin T, skeletal muscle (Protein intended thorax) (Protein upheld). *Drosophila melanogaster (Fruit fly)*

```
MSDDEEYTSEEEEVVEETREETGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAKRKVTRAEEE
QKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSSAAMERNKTK
EQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGL
DPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDEISKDSNEKIWNEKKEQYTGRQKSKLPKWFGERPGKKAGE
PETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE

P19351-9 **TNNT_DROME** (374 aa)
Troponin T, skeletal muscle (Protein intended thorax) (Protein upheld). *Drosophila melanogaster (Fruit fly)*

```
MSDDEEYTGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAKRKVTRAEEEQKMAQRKKEEEERR
VREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSSAAMERNKTKEQLEEEKKISLSFR
IKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQ
VASKYERRVDTRSYDDKKKLFEGGYNTVYAETLEKTWQERQERFTQRTKSKLPKWFGERPGKKAGEPETPEGEEDAKADE
DIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE

Q5TCY1 **TTBK1_HUMAN** (1321 aa)
Tau-tubulin kinase 1 (EC 2.7.11.1) (Brain-derived tau kinase). *Homo sapiens (Human)*

```
MQCLAAALKDETNMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTRENVALKVESAQQPKQVLKMEVAV
LKKLQGKDHVCRFIGCGRNEKFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESIEAIHSVGFLHRDIKPSNF
AMGRLPSTYRKCYMLDFGLARQYTNTTGDVRPPRNVAGFRGTVRYASVNAHKNREMGRHDDLWSLFYMLVEFAVGQLPWR
KIKDKEQVGMIKEKYEHRMLLKHMPSEFHLFLDHIASLDYFTKPDYQLIMSVFENSMKERGIAENEAFDWEKAGTDALLS
TSTSTPPQQNTRQTAAMFGVVNVTPVPGDLLRENTEDVLQGEHLSDQENAPPILPGRPSEGLGPSPHLVPHPGGPEAEVW
EETDVNRNKLRINIGKSPCVEEEQSRGMGVPSSPVRAPPDSPTTPVRSLRYRRVNSPESERLSTADGRVELPERRSRMDL
PGSPSRQACSSQPAQMLSVDTGHADRQASGRMDVSASVEQEALSNAFRSVPLAEEEDFDSKEWVIIDKETELKDFPPGAE
PSTSGTTDEEPEELRPLPEEGEERRRLGAEPTVRPRGRSMQALAEEDLQHLPPQPLPPQLSQGDGRSETSQPPTPGSPSH
SPLHSGPRPRRRESDPTGPQRQVFSVAPPFEVNGLPRAVPLSLPYQDFKRDLSDYRERARLLNRVRRVGFSHMLLTTPQV
PLAPVQPQANGKEEEEEEEEDEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEAAAAVALGEVLGPRSGSSSEGSERSTDRS
QEGAPSTLLADDQKESRGRASMADGDLEPEEGSKTLVLVSPGDMKKSPVTAELAPDPDLGTLAALTPQHERPQPTGSQLD
VSEPGTLSSVLKSEPKPPGPGAGLGAGTVTTGVGGVAVTSSPFTKVERTFVHIAEKTHLNVMSSGGQALRSEEFSAGGEL
GLELASDGGAVEEGARAPLENGLALSGLNGAEIEGSALSGAPRETPSEMATNSLPNGPALADGPAPVSPLEPSPEKVATI
SPRRHAMPGSRPRSRIPVLLSEEDTGSEPSGSLSAKERWSKRARPQQDLARLVMEKRQGRLLLRLASGASSSSSEEQRRA
SETLSGTGSEEDTPASEPAAALPRKSGRAAATRSRIPRPIGLRMPMPVAAQQPASRSHGAAPALDTAITSRLQLQTPPGS
ATAADLRPKQPPGRGLGPGRAQAGARPPAPRSPRLPASTSAARNASASPRSQSLSRRESPSPSHQARPGVPPPRGVPPAR
AQPDGTPSPGGSKKGPRGKLQAQRATTKGRAGGAEGRAGAR
```

749 - 768:	EEEEEEEEEEEEEEEEEEEE
750 - 769:	EEEEEEEEEEEEEEEEEEEE
751 - 770:	EEEEEEEEEEEEEEEEEEEE
752 - 771:	EEEEEEEEEEEEEEEEEEEE

Q6PCN3 **TTBK1_MOUSE** (1308 aa)
Tau-tubulin kinase 1 (EC 2.7.11.1). *Mus musculus (Mouse)*

```
MQCLAAALKDETNMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTRENVALKVESAQQPKQVLKMEVAV
LKKLQGKDHVCRFIGCGRNEKFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESIEAIHSVGFLHRDIKPSNF
AMGRLPSTYRKCYMLDFGLARQYTNTTGDVRPPRNVAGFRGTVRYASVNAHKNREMGRHDDLWSLFYMLVEFAVGQLPWR
KIKDKEQVGMIKEKYEHRMLLKHMPSEFHLFLDHIASLDYFTKPDYQLIMSVFENSMKERGIAENEAFDWEKAGTDALLS
TSTSTPPQQNTRQTAAMFGVVNVTPVPGDLLRENTEDVLQGEHLSDQENAPPILPGRPPEGLGPGPHLVPHPGGPEAEVW
EETDVNRNKLRINIGKTPCVEEEQSRGVGVPSSPVRAPPDSPTTPVRSLCYRRVNSPESERLSTAADGRVELQERRSRMD
LPGSPSRQACSSQPAQMLSVDTGHADRQASGRMDVSASVEQEALSNAFRSVPLAEEEDFDSKEWVIIDKETELKDFPPGA
EPSTSGTTDEEPEELRPLPEEGEERRRLGTEPTVRPRGRGMHTLTEEDPRQMLPQPAPPQLSQADGRSETSQPPTPGSPS
HSPLHSGPRPRRRESDPTGPQRQVFSVAPPFEVNGLPRAVPLALPYQDFKRDLSDYRERARLLNRVRRVGFSHMLLTAPQ
VPLAPFQPQANGKEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAGALGEVLGPRSGSSSEGSERSTERSQEGAPS
TLLADDQKEARGRASMADGDLEPEEGSKTLVLVSPGDMKKSPVTAELAPDPDLGTLAALTPQHERPQPTGSQLDVSEPGT
LSSILKSEPKPSGPGAGGGVGLVAPGAGVTAVTSPFTKVERTFVHIAEKSHLNVMSSGGQASRPEELSTGGELGLEVLSE
GGIAEEGAPAPLENGMALAGLDGTEMESCALSGPPGETPSEVVTDSLPNGPALADGPAPASQQEPVTKKGTTISPSRHAM
PGSRPRSRIPVLLSEEDTGSEPSGSLSAKERWSKRARPQQDLARLVMEKRQGRLLLRLASGASSSSSEEQRRASETLSGT
GSEEDTPASEPTTALPRKAVRAATTRSRIPRPISVSMPVEGQQLPGRPHGAASATDLAITSRLQLQKPSGLAPAADLRPK
QSASRGPGPGRAQVSKPAAPRSPGLPASTARHPSGSPRSQSLSRKESSSPSHQARPGVPPSRGVLQVRSQPEASPVAPKK
GPKGKQLQTQRAATKGRAVVSEGRPGAR
```

736 - 755:	EEEEEEEEEEEEEEEEEEEE
737 - 756:	EEEEEEEEEEEEEEEEEEEE
738 - 757:	EEEEEEEEEEEEEEEEEEEE
739 - 758:	EEEEEEEEEEEEEEEEEEEE
740 - 759:	EEEEEEEEEEEEEEEEEEEE
741 - 760:	EEEEEEEEEEEEEEEEEEEE
742 - 761:	EEEEEEEEEEEEEEEEEEEE
743 - 762:	EEEEEEEEEEEEEEEEEEEE
744 - 763:	EEEEEEEEEEEEEEEEEEEE
745 - 764:	EEEEEEEEEEEEEEEEEEEE
746 - 765:	EEEEEEEEEEEEEEEEEEEE
747 - 766:	EEEEEEEEEEEEEEEEEEEE
748 - 767:	EEEEEEEEEEEEEEEEEEEE
749 - 768:	EEEEEEEEEEEEEEEEEEEE

Q8BTT6 **UTP25_MOUSE** (772 aa)
U3 small nucleolar RNA-associated protein 25 homolog (Digestive organ expansion factor homolog) (UTP25 small subunit processor component). *Mus musculus (Mouse)*

```
MGKRRNRGRSQMLSTMTKKQKKHLRDFGEEHPFYDRVSKKEAKPQICQLPESSDSSHSESESESESEQEHVSGYHRLLATLK
NVSEEEEEEEEEEEEEEEEEEEEEEEEEDDSAVGDAEMNEEAGSEDGSVGEAAVSEAAEEAAETQEHMSLADNSKEKDGE
EPPGVSQKSSEEFTDVKHESLFSLETNFLEEDSGGSCSQRPSQDPFQQHVNKELKEKEIQAAASSPPATQQLKWPVLGHL
VFSSKFQKTETFKPPKDIDLKLLHLQKPLESTWAKTNSQFLSGPQKSNSSFTPLQKELFLIMNSYRDLFYPERTALKNGE
EVRHVYCLHAINHVLKANAQVLANNSRRRSQKLGVGEDDDFRDQGLTRPKVLIVVPFREAALRVVQLFISLLEGDSKKKI
IVSNKKRFQGEYGSDPEERPPNLKRPEDYEAVFVGNIDDHFRIGVAILQRSIRLYAPFYSSDILIASPLGLRTIIGGEGE
KKRDFDFLSSVELLIIDQADIYLMQNWEHVLHLMNHMNLLPLDSHGVDFSRVRMWSLNNWSKYYRQTLLFGALQDAQINS
VFNKHCINAQGQVAVRNVPMTGSISHVLVQLPHVFQRMEAQDLSSVIDARFHFFINKILPQYRDAVMSHTLIYVPSYFDF
VRLRNYFKKEELNFTHICEYTQKSGISRARHFFLQGEKQFLLLTERFHFYKRYTIKGIRNLIFYELPTYPHFYSEVCNML
RATSRGEEATWTCTVLYSKYDAQRLAAVVGVERAAQMLQSPKNVHLFVTGEK
```

84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE

Q54Y18 **Y8469_DICDI** (715 aa)
Bromodomain-containing protein DDB_G0278469. *Dictyostelium discoideum (Slime mold)*

```
MEDISTIKKLEGLSVHCEDNNNNNNNNNNKENINNDDNNINPNRNATSSLLKGNIQQVKKKKVFARLHLFNRDGTVKQIV
EMRKYKFIIGSDQKSTDILITRPGVYSNHAEIIYDKEVRKFYLNPLVDPSISDTIRINFIPFINKKEVLGNNDIISIGLR
AFRIEFFAPVYVDNLILPKNIQPQQQQQKQQQQQQQQQQAPTAQKKLKQEVEHILTAATTTPTTTTTKPKKLKTAPPTTV
ASSSTIPKTTTTKKQAIEQPSKSNLKSSQNKLSTTTTTTITSKPPLNKSSIDGDTRSESSKALQGLKPKEQKKDIMKSLI
SSKKANTHEEKEEGESEEEEEEEEEEEEEEEEEEEEEQLEDKQKQTKTPISQNKSASSNIKPLSKTSKSNPPPLSAATKS
NPVVKKITSTTVTRTTKKADTETKQEIKITKSSTTTKQQTQEEIEQELKLESIRKRIEQFINKFEKEINDNDFKDLDEGK
RKIKESLDFISKTKYEFQGTTSNPGDVESTPLDKWFKNIPYEDFVDSFKLKYYSIITEPVSITSILNKLKSGPNYQLAEV
LKDFKQMLINVTLYHKEPNEYWWISHQCNIQFYKSLLETGLITQDQYQIQYQTSNNEIVKLDKTLNLVPKLVVVENNDED
DNNDDEGSKKAVLVDEDEDECLNNQNNPTTYDSDGDFVTKQSDQESDEESDEESDEESDEERDQLSEEEDQEATN
```

337 - 356:	EEEEEEEEEEEEEEEEEEEE

338 - 357:	EEEEEEEEEEEEEEEEEEEE

Q96MU7 **YTDC1_HUMAN** (727 aa)
YTH domain-containing protein 1 (Splicing factor YT521) (YT521-B). *Homo sapiens (Human)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSN
NKRIVSTKGKSATEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEE
EEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSAS
ESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVILI
FSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEI
ELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQR
PGYLKDPRYQEVDRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHH
PVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDRG
ERGRYRR
```

230 - 249:	EEEEEEEEEEEEEEEEEEEE

Q96MU7-2 **YTDC1_HUMAN** (709 aa)
YTH domain-containing protein 1 (Splicing factor YT521) (YT521-B). *Homo sapiens (Human)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSN
NKRIVSTKGKSATEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEE
EEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSAS
ESYADQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVILIFSVRESGKFQGFARLSSE
SHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLLFPPDESI
DLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQRPGYLKDPRYQEVDRRFSG
VRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHHPVPHEARYRDKRVHDYDM
RVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDRGERGRYRR
```

230 - 249:	EEEEEEEEEEEEEEEEEEEE

Q62947 **ZEB1_RAT** (1109 aa)
Zinc finger E-box-binding homeobox 1 (Transcription factor 8) (TCF-8) (Zinc finger homeodomain enhancer-binding protein) (Zfhep). *Rattus norvegicus (Rat)*

```
MADGPRCKRRKQANPRRNNVTNYNTVVEANSDSDDEDKLHIVEEESVTDAADCEGGVPDDELPTDQTVLPGGSDRAGSAK
NCWQDDVKDDECDSDAENEQNHDPNVEEFLQQQDTAVIYPEAPEEDQRQGTPEASGHDDNGTPDAFSQLLTCPYCDRGYK
RFTSLKEHIKYRHEKNEDNFSCSLCSYTFAYRTQLERHMTSHKSGREQRHVTQSGGNRKFKCTECGKAFKYKHHLKEHLR
IHSGEKPYECPNCKKRFSHSGSYSSHISSKKCISLMPVNGRPRSGLKTSQCSSPSLSTSPGSPTRPQIRQKIENKPLQEP
LSVNQIKTEPVDYEFKPIVVASGINCSTPLQNGVFSGGGQLQATSSPQGVVQAVVLPTVGLVSPISINLSDIQNVLKVAV
DGNIIRQVLENNQASLASKEQEAVSASSIQQGGHSVISAISLPLVDQDGTTKIIINYSLEQPGQLQVVPQNLKKENPAPP
KSCKSEKSPEDLTVKSEKDKSFDGAADESTCLLCEDCPGDLNALPELKHYDPEHPAQPPPPAPATEKPESSASSAGNGDL
SPSQPPLKNLLSLLKAYYALNAQPSTEELTKIADSVNLPLDVVKKWFEKMQAGQIPGQSLEPPSPGPGSGNIPAKTEEQP
QPVDGNEPQEDSTRGQSPLKMTSSPVLPVGSAINGSRSCTSSPSPLNLSSARNPQGYSCVSEGTQEEPQVEPLDLSLPKQ
QGELLERSTVSSVYQNSVYSVQEEPLNLSCAKKEPQKDSCVTDSEPVVNVVPPSANPINIAIPTVTAQLPTIVAIADQNS
VPCLRALAANKQTILIPQVAYTYSATVSPAMQEPPVKVIQPNGNQDERQDTSSEGVSVEDQNDSDCTPPKKKTRKAENGM
YACDLCDKIFQKSSSLLRHKYEHTGKRPHECGICRKAFKHKHHLIEHMRLHSGEKPYQCDKCGKRFSHSGSYSQHMNHRY
SYCKRGAEDRDAMEQEDTGPEALPEVLPTELVGARASPSQADSDERESLTREEDEDSEKEEEEEDKEMEELQEDKECENP
QEEEEEEEEEEEEEEEEEEEEAEEAEHEAAAAKTGGAVEEEAAQQAGSFQQKASGSESKRLSEEKTNEA
```

1042 - 1061:	EEEEEEEEEEEEEEEEEEEE

Q62947-2 **ZEB1_RAT** (911 aa)
Zinc finger E-box-binding homeobox 1 (Transcription factor 8) (TCF-8) (Zinc finger homeodomain enhancer-binding protein) (Zfhep). *Rattus norvegicus (Rat)*

```
MTSHKSGREQRHVTQSGGNRKFKCTECGKAFKYKHHLKEHLRIHSGEKPYECPNCKKRFSHSGSYSSHISSKKCISLMPV
NGRPRSGLKTSQCSSPSLSTSPGSPTRPQIRQKIENKPLQEPLSVNQIKTEPVDYEFKPIVVASGINCSTPLQNGVFSGG
GQLQATSSPQGVVQAVVLPTVGLVSPISINLSDIQNVLKVAVDGNIIRQVLENNQASLASKEQEAVSASSIQQGGHSVIS
AISLPLVDQDGTTKIIINYSLEQPGQLQVVPQNLKKENPAPPKSCKSEKSPEDLTVKSEKDKSFDGAADESTCLLCEDCP
GDLNALPELKHYDPEHPAQPPPPAPATEKPESSASSAGNGDLSPSQPPLKNLLSLLKAYYALNAQPSTEELTKIADSVNL
PLDVVKKWFEKMQAGQIPGQSLEPPSPGPGSGNIPAKTEEQPQPVDGNEPQEDSTRGQSPLKMTSSPVLPVGSAINGSRS
CTSSPSPLNLSSARNPQGYSCVSEGTQEEPQVEPLDLSLPKQQGELLERSTVSSVYQNSVYSVQEEPLNLSCAKKEPQKD
SCVTDSEPVVNVVPPSANPINIAIPTVTAQLPTIVAIADQNSVPCLRALAANKQTILIPQVAYTYSATVSPAMQEPPVKV
IQPNGNQDERQDTSSEGVSVEDQNDSDCTPPKKKTRKAENGMYACDLCDKIFQKSSSLLRHKYEHTGKRPHECGICRKAF
KHKHHLIEHMRLHSGEKPYQCDKCGKRFSHSGSYSQHMNHRYSYCKRGAEDRDAMEQEDTGPEALPEVLPTELVGARASP
SQADSDERESLTREEDEDSEKEEEEEDKEMEELQEDKECENPQEEEEEEEEEEEEEEEEEEEEAEEAEHEAAAAKTGGAV
EEEAAQQAGSFQQKASGSESKRLSEEKTNEA
```

844 - 863:	EEEEEEEEEEEEEEEEEEEE

A0A015IU76 **A0A015IU76_RHIIW** (228 aa)
Uncharacterized protein. *Rhizophagus irregularis (strain DAOM 197198w) (Glomus intraradices)*

```
METTKTADAGSKNWLKERAAISAAHRRQKTDPAAARLIEKADQLHKERTQKNLRETVDEDDEAVDEVPETTVKKNEAEDE
DLEDIDAIVSVPPPEEIVVKIAQKPAEEDTIASNHGKETSEDVYRSFAESVLEQGLTTKSELELSFDLKPEDIKIKEEEE
EEEEEEEEEEEEEEEEEEEKGEEETQEDLNEADITEEKVQEKLKDADVEINHNEENKGDVKDQGKMN
```

157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE

A0A015J242 **A0A015J242_RHIIW** (196 aa)
Uncharacterized protein. *Rhizophagus irregularis (strain DAOM 197198w) (Glomus intraradices)*

```
METTKTADAGSKNWLKERAAISAAHRRQKTDPAAARLIEKADQLHKERTQKNLRETVDEDDEAVDEVPETTVKKNEAEDE
DLEDIDAIVSVPPPEEIVVKIAQKPAEEDTIASNHGKETSEDVYRSFAESVLEQGLTTKSELELSFDLKPEDIKIKEEEE
EEEEEEEEEEEEEEEEEEEKGEEETQEGMIKTEHA
```

157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE

A0A015K0C1 **A0A015K0C1_RHIIW** (276 aa)
Uncharacterized protein. *Rhizophagus irregularis (strain DAOM 197198w) (Glomus intraradices)*

```
METTKTADAGSKNWLKERAAISAAHRRQKTDPAAARLIEKADQLHKERTQKNLRETVDEDDEAVDEVPETTVKKNEGRDR
RTNVKSSFRRSVVFSSPLNYSSTPAEDEDLEDIDAIVSVPPPEEIVVKIAQKPAEEDTIASNHGKETSEDVYRSFAESVL
EQGLTTKSELELSFDLKPEDIKIKEEEEEEEEEEEEEEEEEEEEEEEKGEEETQEDLNEADITEEKVQEKLKDADVEIN
HNEENKGDVKDQEDDKSEESTLTKEVDVDTVPKNND
```

185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE

A0A015M1U7 **A0A015M1U7_RHIIW** (248 aa)
Uncharacterized protein. *Rhizophagus irregularis (strain DAOM 197198w) (Glomus intraradices)*

```
METTKTADAGSKNWLKERAAISAAHRRQKTDPAAARLIEKADQLHKERTQKNLRETVDEDDEAVDEVPETTVKKNEAEDE
DLEDIDAIVSVPPPEEIVVKIAQKPAEEDTIASNHGKETSEDVYRSFAESVLEQGLTTKSELELSFDLKPEDIKIKEEEE
EEEEEEEEEEEEEEEEEEEKGEEETQEDLNEADITEEKVQEKLKDADVEINHNEENKGDVKDQEDDKSEESTLTKEVDV
DTVPKNND
```

157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE

A0A016S6F1 **A0A016S6F1_9BILA** (395 aa)
Uncharacterized protein. *Ancylostoma ceylanicum*

```
MGEEDYREEESRPRKRWTLEQLKSGNTFLSMQAATNKFDSQSGMTAPGMPRWNIVRDKQLGYIEPDRRSENVLRVQCGTN
QYASQKGETPIGASRFQVPKITYKKDWETILDKEGEKIIPKQAGDYGLATQSGEVSMGAHRNQVANVRGRLPHDRRTHGV
LVFQNGTNIFASQTGMAAPPGIGAVRQATQRIEGLDMTEDQQRRGTEFTPWYSGQNKFATQAGSGGFLKVRDVLPHTVGG
KEIEEALKQKSEGIVPLQSGTNKLASQRGMTGFGTPRNTMLKSGWKKEWIEEYELALKEWEETKPPGSASSADPFGHYKK
KFEERESSRQSEIDAQSVKVEEEKEAKENEEKAEEEEVRILYLVQFEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE

374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE

A0A016S704 **A0A016S704_9BILA** (386 aa)
Uncharacterized protein. *Ancylostoma ceylanicum*

```
MGEEDYREEESRPRKRWTLEQLKSGNTFLSMQAATNKFDSQSGMTAPGMPRWNIVRDKQLGYIEPDRRSENVLRVQCGTN
QYASQKGETPIGASRFQVPKITYKKDWETILDKEGEKIIPKQAGDYGLATQSGEVSMGAHRNQVANVRGRLPHDRRTHGV
LVFQNGTNIFASQTGMAAPPGIGAVRQATQRIEGLDMTEDQQRRGTEFTPWYSGQNKFATQAGSGGFLKVRDVLPHTVGG
KEIEEALKQKSEGIVPLQSGTNKLASQRGMTGFGTPRNTMLKSGWKKEWIEEYELALKEWEETKPPGSASSADPFGHYKK
KFEERESSRQSEIDAQSVKVEEEKEAKENEEKAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE

A0A016S7L0 **A0A016S7L0_9BILA** (374 aa)
Uncharacterized protein. *Ancylostoma ceylanicum*

```
MGEEDYREEESRPRKRWTLEQLKSGNTFLSMQAATNKFDSQSGMTAPGMPRWNIVRDKQLGYIEPDRRSENVLRVQCGTN
QYASQKGETPIGASRFQVPKITYKKDWETILDKEGEKIIPKQAGDYGLATQSGEVSMGAHRNQVANVRGRLPHDRRTHGV
LVFQNGTNIFASQTGMAAPPGIGAVRQATQRIEGLDMTEDQQRRGTEFTPWYSGQNKFATQAGSGGFLKVRDVLPHTVGG
KEIEEALKQKSEGIVPLQSGTNKLASQRGMTGFGTPRNTMLKSGWKKEWIEEYELALKEWEETKPPGSASSADPFGHYKK
KFEERESSRQSEIDAQSVKVEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE

A0A016UPX7 **A0A016UPX7_9BILA** (240 aa)
Uncharacterized protein. *Ancylostoma ceylanicum*

```
MVEEGSDYGREWRKIKEEQEVEEVGEVGENEEEEKEEEDEEGKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGRREE
RREERREERREERREERREERREERREERREERREERREERREERREERREERREERREERREERREKRREERRGKKKEK
EGKRRKKKEEEGRRRKKKEEEGRRRKKKEEEEEKEEEEEEKEEQEEEQEGREQEEEKDEEERKRERRAKKRKKSEKEEGD
```

45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE

50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE

A0A022Q107 **A0A022Q107_ERYGU** (735 aa)
Uncharacterized protein. *Erythranthe guttata (Yellow monkey flower) (Mimulus guttatus)*

```
MQKHIKLGYLYEIDHTQLPPRTPVQLRSIRVAMVCEMTELNVSVRFPSMESLRAFFNYSSRETHPALDEKFVMGSTLADR
VLIRLVPSEIFSEQKSLVAFWLIGSSAAPDWCTDNVSVGHNNNKGTYLSEALKANGIVRWGIRRQVKYLGRHKDSDNGND
VNGQNNSSSSFVNGVEESQMGLMVNCEEEKLDGGDGSEEIGDDDDGGAESDAESEEKGEGDGEDEDEEDEEEEEEEEEE
EEEEEEEEEEKKIKVSNENLKRKRYPLRNKGGVKKPKIEKIDVKKEKQKKKKKKMKKNQKKKSMGRSRFKEALVLRDPKD
RWSAERYKLAEQNLLAVMKSKEATAEKPILRPQLRAEARKKIGDTGLLDHLLKHMAGKIAPGGEERFRRRHNPDGAMEYW
LENADLVSIRRDAGVADPYWVPPLGWKLGDSPTQDPICARELKLLKDDVSKIKRELEELSSKKREEESQAITITTSRSDI
SQKLDQLATSLVSSKSDFVNAHVSVGKIGKVTPNVEERAMVVVSSLNAEAEMHSKEKSSVAKESKSKEQEVQALNATILS
DENKTAEKEKTAAEEKAARLQRLKSGFRICKPQGTFLWPNMVNNGTPPSVSSSTASAPPQLPFHHPASLVKPLAEKRAVA
VTVSAVSKGTNYEDGSNNYSTTTTALINLNDLPTNQTIMPMLSPSGVYGSRNLIGYSQKEYNTGSCSSITSLPCEVGNWL
ALSTPKSATDESSRG
```

230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE

A0A022R1X8 **A0A022R1X8_ERYGU** (574 aa)
CaM_binding domain-containing protein. *Erythranthe guttata (Yellow monkey flower) (Mimulus guttatus)*

```
MAEESIDPLIIIPEENESVINKMGGKTLVENPSSPKTARGKKPDSSKILPIYLRASTGSCHDLCKFGRKHASDEITRKPL
RLRTAKSVEIVVVDKPKACADSIKKHSLVVNVVKPSRTKTRSLNSPTEKPSSSNPPEIIKREILPSSSGNQMSRTDKTAY
DHSAKRSFVTAKPFNKVKPSFVSDNVDRVHGNRRRYSDVQTSKKMTSSSMSAKKALLPITASSSSPKFVRGKIVISGNTR
KTRTSLKSMSPSKNGSGTHSVGEDCEKILHVVENNAVEESPSLPNYSSNPDFDSSLSREKEKDDERIKYGETEFEDVFVS
DKNIVQPPAESHDYIGNEFAADEIVSISSKEIREETLEMGAENNAVELESSSRSDSASLSSCEDEDEDEDEEEEEEEEEE
EEEEEEEEEEEEEEEEEDEEIKNGDEESKIETTKQNPNKTLRKNKLDLSEDKNRSPINQRKVDQQSDITNTPTRLRFSKAR
ASQRADESKPEDSRRTHRKSGSRDDAGFSVISSRKLVLKHQDLEGKKDDQGLLNNVIEETASKLVETRKSKVKALVGAFE
TVISLQERKPSRRS
```

391 - 410:	EEEEEEEEEEEEEEEEEEEE
392 - 411:	EEEEEEEEEEEEEEEEEEEE
393 - 412:	EEEEEEEEEEEEEEEEEEEE
394 - 413:	EEEEEEEEEEEEEEEEEEEE
395 - 414:	EEEEEEEEEEEEEEEEEEEE
396 - 415:	EEEEEEEEEEEEEEEEEEEE
397 - 416:	EEEEEEEEEEEEEEEEEEEE

A0A022RBZ2 **A0A022RBZ2_ERYGU** (739 aa)
Uncharacterized protein. *Erythranthe guttata (Yellow monkey flower) (Mimulus guttatus)*

```
MARGGEIGHKRKIKNKVQLEKKGSDESDEDYKVEEDEAINVSEDEYCSSLADDDTEESLGAFEEEWVEKKVKKVTRPRGR
KRSQTRKKNGVVKPKRKKVAYSEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEYDEYNRSGATQQKRNKASL
KEEKDDDIESLYRQGDEEFVDVNARKRSRISRKRSRVSRTELSKDSYNEIPRKKDKVSYVEEKEDGDNDDSDDKDDEEFT
PGEEVLKTTRRKPVKKWGLRRKERSNLTKELPHENPTSRKKKMIGGRRRGCGGRKRKYVVNSDSDFVSSGSSDYEYTVSE
EEIEQVRDATQFCKRSRNSTSLKTVKEEELLQPPKPKRPLVRKGKQKVVDMKIELGKQVCGICLSEEGKRTVRGVLNCCS
HHFCFTCIMEWSKVESRCPLCKQRFATISRTAGNELTDAVFPVPQRDQVYQPSEEELRGYLDPYENVLCSECQQGGDDAL
MLLCDLCDSPAHTYCVGLGHEVPDGNWYCDGCRPTALASSNGQPLNPNIHDNNNININVGTNNNLSVGSSPIASVRETFD
LNEEYVPETPLLTQGTNNNVHFQATSPTSGQGAFTLQERRRIQRQIQYLLNNRSRQSDRSFGAGPASEISLFGSPIGQDG
VVRARTGPQNVYLQGRLQDYNTVPPSLYNNSEVFSRRVSSLRGEALPSQASTSTDHSYGGLSLPSEFSGFNGRIGGGLGH
NQQLHPCNGTSNTLPYQFR
```

103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE

112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE

A0A022RQV7 **A0A022RQV7_ERYGU** (193 aa)
Uncharacterized protein (Fragment). *Erythranthe guttata (Yellow monkey flower) (Mimulus guttatus)*

```
MANFSRSSDDDGPNSKRPCIYRTAISPSSSSVPAANSGEVGYGYGKRRGGYNSVIPPSYEAINRVEPPPPFGRLFYFNDI
YYDDEELVAVEEVAEEEVAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERGNNRRRVEEELQSSARGV
NSTAARPVSVNLMDPDLLDCPICLEPLKLPVYQ
```

100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE

A0A023ERF7 **A0A023ERF7_AEDAL** (397 aa)
Putative troponin t skeletal muscle. *Aedes albopictus (Asian tiger mosquito) (Stegomyia albopicta)*

```
MSDDEEYSSEEEEVVEEQHEQKGDDPEFIKRQDQKRSDLDEQLKEYINEWRKQRSKEEDELKRLKEKQAKRKVSRAEEEQ
RMAQRKKEEEERRVREIEEKKQREIDEKRRRLEEAEKKRQAMLQAMKDKDKKGPNFTITKKDSSFGMSNAQMERNKTKEQ
LEEEKKISLSFRIKPLEMDGLSADALRTKATELWETIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDP
EALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGFDTLNKESLEKQWSERKEQYVGRQKSKLPKWFGERPGKKAGDPE
TPEGEDEVKPEDEEVEEVEEVVEEVVSIPEHVSVGNSSNAARSTPTVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE

374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE

A0A023ETB4 **A0A023ETB4_AEDAL** (382 aa)
Putative troponin t skeletal muscle. *Aedes albopictus (Asian tiger mosquito) (Stegomyia albopicta)*

```
MSDDEEYSSEEEEVVEEQHEQKPAAKSEGDDPEFIKRQDQKRSDLDEQLKEYINEWRKQRSKEEDELKRLKEKQAKRKVS
RAEEEQRMAQRKKEEEERRVREIEEKKQREIDEKRRRLEEAEKKRQAMLQAMKDKDKKGPNFTITKKDSSFGMSNAQMER
NKTKEQLEEEKKISLSFRIKPLEMDGLSADALRTKATELWETIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKAL
KKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGFDTLNKESLEKQWSERKEQYVGRQKSKLPKWFGERPGK
KAGDPETPEGEDEVKPEDEEVEEVEEVVEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE

A0A023EVJ1 **A0A023EVJ1_AEDAL** (616 aa)
Putative sarcomere length short (Fragment). *Aedes albopictus (Asian tiger mosquito) (Stegomyia albopicta)*

```
MPVNGSNRPPWLKDRLETVNKNVPPAWARKNPTTTGLDSKDFKSTSKAETSDSSKTAPIVKKPTTAATASAAAKENGEPP
KTSVKLQSREIKVPVVVQQKKPVQPPLTKPEPLIKNTTPQMTVLREPAKPKPKPKEPTPSDSEEEEEEEEEEEEEEEEE
EEEGSTEYETETESEEESPPPPPVKKPQPKREPSPPKPKIPVQLKKVSKSPEKTDTESKSSKSEKSSSPEPKTFIKPPLK
KVIRPQQDEPQKERSKSPEPKGFRVQLRKVPSNLKAPRLKEKLPEVQLKRVEKPLLEEKPKKEEAYPHKPSMLKSESSKR
IPPPPPMPKSNIPPPPPPPPKLAPPSDFKKEEVSEKHKEMIEKLKKRPRRRPDWSDMMKEVEQGKKLRHVECNDRSKPIV
HCKSITKVKDQFIFETEKATAHNVLLKEIQSGVRLKPTKCNDRSKPILEGLRKFRRQMTLEEQLAKSESRANLEAPPPEE
DEVDEMDDIDRVRDDLQSTKQLLAMELRNNEALERENKRLLQRVQNLEAELSRERWNPLSGEEKSSIAGPDAELIHSLKK
EAVEAQQQSKQLEEKYQTVAKELDTATKQNEEQKRKIADLEKKLQSLTDDDFYLKE
```

143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE

A0A023FJI4 **A0A023FJI4_AMBCJ** (391 aa)
Putative troponin t skeletal muscle. *Amblyomma cajennense (Cayenne tick) (Acarus cajennensis)*

```
MTEAEMLMEEKLRKKKEEEEEMWAEYLEQRKKQRAKEEEELRKLKERQAKRKAQRAEQEAKLMEFKKKQEEQRIKEMEEK
KAREAEAKRKRLEEAERKRQAMQAAKEKREQEPVKPNFVITKREGEEMPGSALGGSGFDKFANIMYARGEMGKTKEQMEE
DKKAILSFRIKPLEIEGLTVEQLREKAKQLWEKIVTLESEKYDLEERQKRQDYDLKELAERQRQINRSKALKKGLDPEAL
QGKHPPKIQVASKYERRTDRRTFVDKRDLFSGGLEAMTDAELEKQWEERMLSFKESSRQGLPKWDPENPKNKQVSRARHV
DEDEEEEIEAPVFEPPKPEPPKPAPPKPAPVQQQEEEEEEEEEEEEEEDEEEEEEEEEEEEEEEEEEEEE
```

370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE

A0A023FM62 **A0A023FM62_AMBCJ** (390 aa)
Putative troponin t skeletal muscle. *Amblyomma cajennense (Cayenne tick) (Acarus cajennensis)*

```
MTEAEMLMEEKLRKKKEEEEEMWAEYLEQRKKQRAKEEDELRKLKERQAKRKAQRAEQEAKLMEFKKKQEEQRIKEMEEK
KAREAEAKRKRLEEAERKRQAMQAAKEKREQEPVKPNFVITKREGEEMPGSALGGSGFDKFANIMYARGEMGKTKEQMEE
DKKAILSFRIKPLEIEGLTVEQLREKAKQLWEKIVTLESEKYDLEERQKRQDYDLKELAERQRQINRSKALKKGLDPEAL
QGKHPPKIQVASKYERRTDRRTFTDKRDLFSGGLEAMTDAELEKQWEERMLNFKESSRQGLPKWDPENPKNKQVSRARHV
DEDEEEEIEAPVFEPPKPEPPKPAPPKPAPVQQQEEEEEEEEEEEEEEDEEEEEEEEEEEEEEEEEEEEE
```

370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE

A0A024GK67 **A0A024GK67_9STRA** (215 aa)
Uncharacterized protein. *Albugo candida*

```
MVEHNDSARIIELNKKSRKKIKFFSYNGSSQKRRLALLANLHQANNKKRQLQAQKEKPEEVKAAEEFDCQSPTPDWNGEE
EEVEEEEEEEEEEEEEEEEEEEEEEDKSEGEEEEYRLETDIAQLQKIIAAIQAQLEKEKRGRRRDLLPIKRTHELSSEGG
RSQQPSATKRKEPVIALEDESSEQQGEEGEDEYRMEEDIIGLKEGLKGIQNQKRS
```

84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE

A0A024RCN9 **A0A024RCN9_HUMAN** (1210 aa)
EHMT2 (Euchromatic histone-lysine N-methyltransferase 2, isoform CRA_c). *Homo sapiens (Human)*

```
MAAAAGAAAAAAAEGEAPAEMGALLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGAD
TPVGATPLIGDESENLEGDGDLRGGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGA
AAAGSEPPPATTSPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEIQHFRMSDDVHSLGKVTSDLAKRRKLNSGGGLSEEL
GSARRSGEVTLTKGDPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEE
EEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTL
SPNHAGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVL
CETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGT
AAPAPPPLSQDVPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQE
SERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRT
PLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEV
IRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELR
NKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETS
TMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRL
QLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNII
PVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLP
ELGSLPPVNT
```

300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE

A0A024RZ38 **A0A024RZ38_HYPJR** (1108 aa)
Uncharacterized protein. *Hypocrea jecorina (strain ATCC 56765 / BCRC 32924 / NRRL 11460 / Rut C-30) (Trichoderma reesei)*

```
MNGSAYAGLNPYSQKQGSQLPRDLLIKSSGKAASNLFPHNKDGTQIVNSGITPSSVNAYKTSRFHSTANSSPWKVINYQI
PVPIGDCSAHFLVDINSNKVRRAFLMDGGTNAGTYVAWVQILKALRFIDLQLGNDWKFDSWVVTHWDADHYSGVKDLLLN
EGIKFTRCSGAGNYVTRGMSGSFASLYFAEDAWLCCGAWDVEAMFVRGDGFLRHFVRQDNLHLWGSLSMTIPARPVGTEA
KSLLRCIWGEKLIGLDLFTRSYQYHSGTGEEYEYTEHLFEFERRLESDHHAVAAKNTPRFCVVGANGYGIGQSTPFKKEK
PSKNETSILALLYWKRQNLCSYYTGGDGNPGVFKEIVRPWLDKTWPDCDVEMVKLDHHGSTRENLGGSHLSKTKFKSESE
EENQQSKSKSKSRKEEQEGPRTDSETIRLIIKDLKPRKVLVTPGTLHGHPTWDVIIFLRAYFEELSGARGNPSAMIQGLF
TTRAVYWLIKGEVSLKDINQNHLLGEAFEKRGRSVTGGGFNKMIAEDEQASNDADQGGPDNDEDDNSSDSDYDIFFGRAR
DLQERQEAQGILQEARGKFNDFLSEGEKAARRGQKHGKGKTKLVRYKFWLGEDAKKRNYTALTKAAKKTKEDYDEEQRQE
ARDELGHLKQDARRLDRMTPKKLEALRAVLQNYATDEHDQSSTPDDAVEVRLRRELCDAITEVAEAADDTQQEGLEDFRT
ICWQPLPVSERDDPHFIIRFEFNGRRQDTLVQVFDDSGQFRYVKTSSQAHNGSGQHEDVKAASLTPESGQADGPVELVKQ
SEAKPMGLLVEDDQNPWVKYAYGECAIATMLSIDSIETPVKPTLGARGPKNMVFQYYEKREADTKENIGELINLAQLGNK
RKNSSCTTSTTQYGRRSEMRADVEVAVKTFTKRRGNLKKPVRGILIAEGEEEEGEEEEEEEEEEEEEEEEEEEEEEEEG
LKKSTRRRSKAGKRKGSLKRADRERGKAEKRERNRSTDKNDSEGLLRKRAARAPCGNSASVKKVIVTQEFKGPVSKSKAT
KQRKLKATKTENNRKEAQLVTSESDTESRRISEKIQEKKKTQTETENRTKRESKSQKAGKKTNSKVSY
```

935 - 954:	EEEEEEEEEEEEEEEEEEEE
936 - 955:	EEEEEEEEEEEEEEEEEEEE
937 - 956:	EEEEEEEEEEEEEEEEEEEE
938 - 957:	EEEEEEEEEEEEEEEEEEEE
939 - 958:	EEEEEEEEEEEEEEEEEEEE
940 - 959:	EEEEEEEEEEEEEEEEEEEE

A0A024UYH6 **A0A024UYH6_PLAFA** (5937 aa)
Uncharacterized protein. *Plasmodium falciparum Vietnam Oak-Knoll (FVO)*

```
MIYKGYMKNITFLVSFLIFLRSINANISITNFTYTNQKGDIKVEFFQTDYIAIFKLPFGGSHEQIFEISDDYIITNDKET
NNCNIPNNNFGFVYSKSNSQNKFLIVQREYTTIYIKDKNNNCSLISKVEPSLYSFQTIEYKKEKIKLGTTTKCDEKMVEK
LKIYIDLLNDMNLSEDKVCNQIIASSFIQNIEIIDCTVYIGSIFLRNNLNREEYYICIKKEHNNNKMKNNISLLINTIDL
NNTLIMNTFYCNMERDICSIIINSIYFNNIPNITDDTLVLKAQCNIDSNPLINIDHVLREGYYTFHFRNPKIYFLQICII
DNLKKYRMLGKIYFLKAYEPIICFIGTPCVIKSFTVKENVQYVQNNIDNETFIFTNKKCDNENVNENMNMIETDYDMKEL
ENHQHFYLFSKNPLTDEKYLCTSNNKKFLLLFNIVLIKLPEYNIHYSIINNVVINYSTLFFEYNNYLGPYVKYECSDKSI
VPDEYNNFNNNKDNNFLLKNEELNFTIKFKAIIMRLCLKQNNYYYDIGKIYIENFINYKKISSLKDFIFNADVSLHADDI
NTKLLKFAIKEDHNCHSDQGFFVQSKDNFRADKKPFYKNIFINHTTVYESINQIILDKDIYYICMCSLHEKCYDNNNLID
YNVYTNISIQNEIQPLQNKKKFICKIFADCSFTINFENEYNNTSDIWVAKKGQSCNSKDIQVGIHVSHQNVKEINKEKIN
VTKVNFKIYYLISHIHYSYLFNKDIFICGNYRNQHFIVHIKSDFFLLYYALPFEEEINIKNVTQTNVATNTYEAQEKNIN
IQSFENVKQKFKRLFIYSYRDDAKSNLYKTMNINQDENQISNTIKFEIPNDHPTKYNEIYFINECHYDQGVIIYDHKSES
NNIAINNDNNNNNNNHIIKSKELYWARKKRIYNKKLKKKENKNEIINIYNCSNEIMNNHTLTSILIFDGPLKPLDIYCYM
```

```
ELDCIHKENFSILNFDYSLFVEISDTQRIIIHIKESEGNNKEKLNKAEKIYFNDSKRTTELILSIPKHISKGLEPGPYKI
IYTRKFKQFIHELYVGTFHFIGAPSQKYHLIRENEENIIIHGYFKNIENERIHILKHQNTCVLTNKDKNKKLLKSSEIEY
ILNEIKTNIQNCTYLDDTKLLCKNDLPVEGKFILCWCYNILNDQNNLCHNLNIYRPKITEVSSLLYSIDPILEISKSSLT
NFLNYNIGDFFFIIDDDCKNIKNIKLKSKLNDEQNILDIYKHLQYPKKYDLCICIVQHNIPCDKEENFKNFYIKLNEQIY
FTMEMGSIDEFNNKDKFIKDFTFSTDYLDQLKLNIVPVFVFLPGPVEYKEYVCFAGIPCNATIKIKRSAQTRLSTGNKQI
IGEKKDVANPYTGSYGNRNKANIKKGEEKKEQKRNDKKEGEIGHKKEGEIGHKKEDELGDKKEDELGDKKEDELGDKKED
NNEDQNQDNKQDKIENMNKDINKDKEIKTKETNIEEEEEVEEEEVEEEEEEEEEEEEEEEEEEEEEQEEEEEEKEEKEEEE
EEEEQEEQFDHNEHEVKGADKNKDKNFNQNKGESQNVNPNTQQNQYDEQIISEEEQDNIENSLLGKHQYIYYTLNDTKEC
KNEYETVYKSNASSIYVSQEINYLHHEFIDGVYNLKIDIVPTDITKRYEICASFYEDDKYFYNIGNIIFYGIFNESNTLD
IISGVPFSFEINQFYSKYDLFIRLIYEKHGDSKTCRLYNNNFENVFLEGTIERTIVQHDKKVLDNYITNYKWKDVTIILD
TDNNNYMTSYQNVDGSYNLYVCSCYELTEGHCQSGNYFSTQVMKFYVHTVELKEPKMNSLMHFLKPFTLKLETTKILNGS
IKVIPIDIISDLSKLCLELNLKNIYLKYQAEINEYEQTYNITINFLSQGFIICWCGKDNCKDHEYLTKVAFFRLNSPNFI
DVHTDLNGNFSFHFLNQFVNINDRVRFVGQASSCLDDENVDLFNNHIVIKNVQNKKGKTSNGGNTKKEQQKNNNKINSNN
NEEDENDNENKNERKDEDDNYESYSIDWEQIIEIFGKPRNIFKGINQNWTWVSENYKMKTSNEKYIKICYCFHFYYKNCK
DTKNFLYIGLVHNHIWDSKTTIMQNELDTNYEISNMIYFNKDSIKFVAINSFNDLNRNVCDNINYEKNIIMPFFSGYNKF
HNTTINQKNILNILKTYYHNEFIFILCYNTEYYKKKTNYLLTTKDMTELNDFTTYYNEEINTYNIIQSSFSYHSDIKDIS
TTNENIEKYEHMQLLLQNRGNTPNIFENYFYQKDVYKKNNMSIYNMNLYNMSPYVVYNNNKKKITNIQVKNRLKIILTKM
YHMTSVDINEVIYYKGKGELLTDLNLQNIFILPKQKKVILCCYNDDYIEVIINDDNKIGMKKSNKIQELIDILKKYHPNF
ERNKKKQNDILEQFNNINDILFKYDYIRDVNKNQIYYDTGFFRNNIYIQLINQPFDLKIYGSNIQKKKNKDYILYIIEFH
NICYNNMNKNGFFLEHKRYNEMENYIHFLQISMNKINNYKLCLYDKERDIYSNVGILNITDYFVIKESSFFDNEDIGNIK
KKNMETDSYNYNNDNNYDGNYDNNYDNNYDQNNNKYYIKNYNQDVIKNVCLIMDNNTNQIIVIKGKGSFYFNLQIEKGIF
IEKKGQKLNELFPDIKNHEPISCKNKKKNTIILTKTHIFFYTNNNDISFSTKHNLPFPYDIDFDDQYIYVNDLYLNKIAR
IQILSNKDNKTPIPIINNKQRSKRSIINHGHESQQNIQKTHQTYDHFTPLHKVEKKEILQNNNIVQLKENEFPITNLKNI
EYSKNNIPNQKISSKDDIYKMSDFQAFINKYANLITTNSFRLYNYFEKKKYYGTLNYFIKRVWFNKVGPSREENYSTESK
IEQNDKNNNNNNNNNNINNNYNYNYNDLHNNNHNIILNSNNYNNNNQSSRHQNFIYSYHVSLDGKKKQSENLLTHSLNNF
IQFFQNKKNSILKKEKEKRKNIPSYNIMYKNINHITNTLNKRKQQELTSSIIKKRTKRNVQEKRMSQSAYNELVLASIKK
YTNKVEPAHFVNNKLDYLNYITNLKSPLNISVQNNILYILDSIKNTFFSYNLINKEIKELEKYDFNDHPLILKNPLHFSI
YNGIITEYTEHKNNLAFVTQIDSNEIKVIDLNSSKKYKIIKAIKLRKGYKHNHINYVIGIKQKLLIITSQSQNIDHYKNI
IYHYHFNSFDQYFSISFNYTFAKNYNANDNLYITPDIDKYSDNIIYFCFLNSNNKCTNIDELTKLSISHETGIITGKLNY
FGTFSLKIFAKTYFQYKINTYSNLYSYCGISQEYNKTKSTCESCPIGTFWNSEKLLCENCQKYIENTSTLKNGSKLKTDC
LCSPGYEYSDKSSKCEKCKPGYYKKSVGNFICIKGCPINEKSITYGAKSYGEMDCKCIEGYYRKKDKCVLCLSNYYCPGN
ELIKPCDKNKISKEGVIHKNDCICKENYIKDNKNNNCVYCASIAKILGKPIYCSLCDPIYFHEDIYKNIFLLPNNIHNYG
LINNIYNYDEDLSLQGNIMKYAYFHKTTNIERNFTHYINIKNIYHTFNNNINNYDYLTNSKFAIEIDIPEPKKCIFCDSG
YYIKKKKCISCTTKYCEGFNHNPKACPKNSVVNKMKASSIFDCSCKRGYGILNERRNAYSNTITCQICPQNFFKHIISDD
SCFPCPLYTYTLNQGATSILQCLPKKGYFIYMFKSINIDYLRYKFDINTENRIYNYFENNNKIFDEDVYNFFLNKQYSKF
FYNTENKTNTNNNHNNNNNNNHNHNNHNNNHNNHNNNNNNKYTKDNHFDNQVGNINKHTNNLQIKITENIYNIQYLEHLG
FIKKTSLFYIYMILLRNIEERYNFNMDKMLKITCHINLHLKKNPHFTITYKKNLQECIDSCKTNIYCTGIEFSRKRVEYT
QIILKNNKKIILGYFKCKQFYFQNIYDYSSYNLDSYLNEHIENQINIKSTLTYTNFIMRNKPDIIYTCSIDRDPKYLLYK
NYKLVECVIGKFCPGNNTPYMISCPINSTTIIPASEDVNKCLCLKGYSYVGVTSYRCSLCDRGSYKNSVGNNKCDNCPLT
FSTTHRGSTNIKDCSCTSGNYLTFDTLGNFIRTENMQHKNISDQYFVIPIKQESQPENEIKDDNKNINIYNANNINNHDI
VYKTKMIKINLHKENDNHNDYMNNILKQTIGLCKPCTLENHYCEGGLESDITFNNKLIKGKFHTLPKKCPRGLGIPNIIK
ERNSINNCLCIHGKVQRTTENKNVECFPCPPNTFKENEYDNSCSGACPPFSTTFVGSSYENQCFCKNNYYLVSTDDENDT
NGNSINNNKNIYNNNNIYNNNNNNNNNNNNNFNNKSDVKKKSCKICPIGAICNRGFNIYIYLKLLNDRSYNNINVIDHET
PFPKYGYYAVYREKTNPTKSWDTLDDSAILNYVYPYHKLLLFIQKNIQKGNYFFLEKGNKFFLNDDFVEKMNEKSKYEEE
NANKFVTKSEIIHNVNTNNLKGKHNTLNNNNNNNINKSSSFLNQNNYNNDIIQLSSYENNPFKNLSSTSEVSSNNNVISF
IQNNDKTNNSTNDNNIENLVDIFNKYVQEAKELQIQNRKFERIPDIHPCTIPNRCLGTLINLCSDGSTGYQCNNCSKNYD
MSYFKSKCKKCQNLFYEILHFILLKLLYYIIVIFICSLNGNILNKLHVSGILMRIWLNCSFTFIAYGFFIPNMNSFISKY
WYLYKTAFSYHMKIFAYYLRVQCLLNSLNINLSYNQMWYIQKYMNICTPIFDSIFITILLFAVIHIYKFFFYKKNIDIFE
QLLCTIPELNTLYKKNCIDNIHKVKNKKFANKVESFEENENQNKEKKNKKNIKRKNKAKNKHNNDNNDNNDDNDNNNDNN
NDNNKININSKDEHINHFEKCSSITTILNNLELNNEEKNKESKKKKIFDIKKKTSIENIKENETNHLWNDTHNNVKNKES
NINTTNISNNINYELKYIKNKEWYNIFLNKTIQYIYKEKKIFGLWHFIFTKNDNWFKNMGTFLNDTLPCYVLIMILSIPY
ILLELVQLTYCTPIKYKTQKTYFYLTYLITQKCSLSSKLFITGLIVTITMFALYIFLWILLLYLYSKRKRLNLFDLLTTN
LLSGFRKGKGIFELIFLLKHILIVLLICFNIYYGFYYIVFLTLILITFAILEILSNPYDKRSFNILNKSLNIGNVLNIFF
PLIIWGSFYWTYENFFIFPIFVIYAYHIYMFYHIVKEFTLSIHFIKTENIVNIQTIGYDPENIKNKNYKIYYKVMNKIKY
FLNKNQKKNISNINENKDKHLNKNNNSKDHVKFEPIENIIKRYNLKLNKGILKDANNNNNNNNIKNMSDQVEDNKKDILF
IKKNVLPVNVHNVASIWYDEQNEDLLFQMPYQNKFCLNMNNEANENNDQINDLTKDKTSEEENNNDHVNDPTKDQTNDEK
KKNKNKKNKNNNNNNNENNCHSNDNSNNNNNKEVHKNDDNINHNNINNHNKSSNISTTNKKNYFNKFSDYIIDKRNKKSI
KYFITSLMEVIEKFLDSSTHGFIYENWFDFTIRFAFVYISWIKKCNKKNNIMLPMNIQQLHIHMDLFIFTPIFPKNNSTC
INEQNIQNYSKKKKIYNKINMYDEKIETGELLEKHNSFENTEIKISRSFGSHNYMPNIKNRKNNYDKKEDITSINDINVD
IIKQDDQKEDSNINHLINEHNQKEPSQHIYNINDKNIMDYNIDENISKNNEKEKHIKIPPKNISITQKEYYNNNDIFNYS
LDIFSSEMFNEKMFHSIISLFELYMAIKTLKLMNPHIFNKLYQMYNKKIITFDTSVMFYINKLRDDIKSEIEQIDKEINT
GDTTEKERIQNYYYYKEELFKRKKLEEELLSKIKSLEECIEVNKRSQSLRNMLLTKKKKNNNLNNENLEEHINYIFSHLH
NEGTYKLNHSQNMDKKN
```

1486 - 1505:	EEEEEEEEEEEEEEEEEEEE

A0A024UYK2 **A0A024UYK2_PLAFA** (365 aa)
Transmission-blocking target antigen S230 (Fragment). *Plasmodium falciparum Vietnam Oak-Knoll (FVO)*

```
MKKIITLKNLFLIILVYIFSEKKDLRCNVIKGNNIKDDEDKRFHLFYYSHNLFKTPETKEKKNKKECFYKNGGIYNLSKE
IRMRKDTSVKIKQRTCPFHKEGSSFEMGSKNITCFYPIVGKKERKTLDTIIIKKNVTNDHVVSSDMHSNVQEKNMILIRN
IDKENKNDIQNVEEKIQRDTYENKDYESDDKLIEWFDDNTNEENFLLTFLKRCLMKIFSSPKRKKTVVQKKHKSNFFINS
SLKYIYMYLTPSDSFNLVRRNRNLDEEDMSPRDNFVIDDEEEEEEEEEEEEEEEEEEEEEEEEEEYDDYVYEESGDETEE
QLQEEHQEEVGAESSEESFNDEDEDSVEARDGDMIRVDEYYEDQD
```

280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE

A0A024UYQ9 **A0A024UYQ9_PLAFA** (764 aa)
Uncharacterized protein. *Plasmodium falciparum Vietnam Oak-Knoll (FVO)*

```
MIKIIIGVIGYYILYSSYHIYENIKSPIFNDGNVIKNNEGDKNEQLVIPKEGKKRNSINEEEEEYINKPFKNVLKKDDII
DYHLYFSCEEDIDINKHMQDKYLEKDERFISVYKILNGKYSWNNNVDLLDEKRKKNSFFFFFEKVHPSFDISIPKELIDQ
RKDIYLHILTYVNKELYRYGSRTVVITKRKEKTTTRGKKKFLWKSLIDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEKKYQHGNYEKGGSYKVHKNISNNKPNNKNPNDKRDIKHNNNNNNNKMKKDNFIKSNQNSLNIHKKKKKRKHKDFLFYI
PKKIRFGPVIEYNDFHISKLGFFSNMHVDKDTNTYLLPIYINNDLTPDDEYRMIKMKNSDDMMKKKRSSEKNDPYYKENV
RNDNNNNNNNNNIKNNYLEIYDLSKRTYEMRNERNKKIYEKNSSINNNVHKLEHELMDYIINIEYVPINYNYYNLLNMLK
FNVSYVKKKYNFISFDMDSITTFLCCHITCSMIIYILCIIYIIMEITYLLFDIKMWKRWNNLYTFTYNNDIVMNITLLFF
ILLYLRNIDYGRVIMIYYIMKMMVLIFKIIYNYDICILNDYPYICINKKSLKEMNKEMIMDEEFEKKIKKKVNIFMIFSI
ILIFIYNYFYTKYDSYYSYVIHTLGFSSYLYKFILMLPQIITNIYTRTVQRMSFPFFLFLLVNVLINDLFIIFLRMPKVH
KYYLFADDFILFLFIIQYCIYKKENKIFGAREKLVLLKSAKKNK
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209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE

A0A024V456 **A0A024V456_PLAFA** (1956 aa)
Uncharacterized protein. *Plasmodium falciparum Vietnam Oak-Knoll (FVO)*

```
MNVCKMKVQQKKNLKDCNLKSKNTILTSFEKKKNEKDENNLLKFSKLIDNKNKVVNSKLLKNDNYKFNERKESLTRCSTN
ESLKLKNIKTLTKDFDYNNNNNNNINNNNDYNNNNNNNNNNNNNNNNNNNNNNKNNNNNNNGHSKLFFKKNDKDIESKVR
EEDGKKSEKKNNDLINNKNEFKVNNKLILKSKEFKSNNNNNNNICKLNNIDDKNKKQQMDTYSPKENEEDNSNNMKKSSS
LKNIKKNQINEMEIISNSVEENHDTHSKGDKENNGVSTKNVKRMNTMSKEINHKNNNLKKHVSKSNSLELKKGKKGEKSK
DKLSNNVSGKKGMNKEKEVVQSSSVRRNSSRYSIDYGRRDSSRRGSVKQEKGKERRGSKNVSKKVSNSKYTRKKSKRIKE
ESDESDDDDEEEEEEDDEEEEEEEEEEEEEEEEEEEEEEDNDNSDNNDESDEVYTNRSRRSTRCSIVKRKSSLCIGKKNS
KIIKKSTSKTKNNKKKKGSVIKLVKKKEKLSKKGILKKTNKKTKGKLRKNSKLYHRKKNIKNEKDGIDEEDIDEEDIEEE
EEPSYFDEYNLSYEERKKDLEEKEKKKEIKEKYIKQIKLPKYADDESIIFINNPNYVMVLLFLTVYKDVLKMNWNFKDIE
EMFQNKETTEFGRNFILKLFFFLGRYFNSKSIFMYKYISRIFEDKEESLSRVVNFHELFPVLETKKEIKNSGVGSKRKKD
KRGKKMKIHQKEDELLYDEEVIGNEDVHIFEEEEDNEHSNDDEDEEEEDNEHSNDDEDEEEEDNEHSNDDEEKEDVHYND
EEEKKSDLNNDSTKNTVIKEEKDGLHISEGSHNLVNIVNDSMKREESCKNGHIGDNERSGDINTNDDKNNADNNDDVDGE
KIVDSKNNIENKLDNTVEGKHDINSTEGIIKSENVDDEKGLLTNKLFLEWDDLSVISKLRIIRMLLNLVLCESNNLKKML
GDEKLNYNNGYLGKINNEKYWFIFNDTINIEYKLYLEREEEGSFIFICDDDDMLYTIGYNFLRNSDTKFMGEALIERYNK
VCRERRNRSRMLKQQKKLLCADINLNDPLLGTKKRQHKQVEYFNFDNNEKMRRKKSDMNNNNPYSVPPTKSYQKNDRSFR
LAARNAQKGSVDDLEAWKLNEGSLGIENQGATSGNYNIANDGTNMTETNNINDNHNNDNNNNNDGVVNADGNNIYGPNNN
NVIGSDGNVNNANNTTTNNNNNNNLGTVKIPLKRGRKKKSEKKKRGRKKKILSVDGIGEIANNLSALNVDENRRKSMPNI
GRGRRGTYTKRNTKPSVSIKYGTRSHSINKYENDVMSFNEYSLNPGLSMDDFYKNMVMDPKFFHANMNMNNYMNGGFNMP
NNNNSMMNMRNGSKMGNMNNIGGYNFPYMCTPPPMYNQYYMYNGNNMYLPNGGPNNNMNMSNANNGASVVMGGNVVSNQN
TVKDVKAENMHMAKNSIMENRNSIIVNNMNNMNNINMNSMPHKNSFMGNDGINNMNSMNNNNNNNNVNNNNNNVSNNNNN
NVSNNNNNNVNFMDNMGNNNNNNNNNNNPMNKYNNYMMNRNVLNNMGGTNPLYNNMYNMKFPYMNNDMMNYNYNINSFQN
MNYDKMNKSMFKRYPNFMGGYPYNNMNPYNNFNAFNMNYQQNDQMNQLPNMQGGYKSKLMNDNLSNYQSFNNNNVKQNHH
DNNNNDNNNNKNNSEGGNKNMDDSNKNNDINKNDILDSTKLTEQPVGGVVPNNDCITRGEDNHRIDLKGDIAEALVGNNN
EKMNSSDHNLNSLKNLPNINNTYNMDHMSHMRNSVSASSIGMINPGHMNSSHSGSIMNKDKFRDLQLNSNNNNNNNNNN
YVKVNPFDHPMKNMNPNLMDDKYPKDNNNMMMMMMNSVYNMMGSDHFHMNNSHMMDPMGSPKMNDNMYNHNNMNFENTNT
NHNNHNNHNNHNNLNNLNNLNNHNNHNNRIQDKLPE
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418 - 437:	EEEEEEEEEEEEEEEEEEEE
419 - 438:	EEEEEEEEEEEEEEEEEEEE
420 - 439:	EEEEEEEEEEEEEEEEEEEE

A0A024VGZ0 **A0A024VGZ0_PLAFA** (3091 aa)
Transmission-blocking target antigen S230. *Plasmodium falciparum FCH/4*

```
MKKIITLKNLFLIILVYIFSEKKDLRCNVIKGNNIKDDEDKRFHLFYYSHNLFKTPETKEKKNKKECFYKNGGIYNLSKE
IRMRKDTSVKIKQRTCPFHKEGSSFEMGSKNITCFYPIVGKKERKTLDTIIIKKNVTNDHVVSSDMHSNVQEKNMILIRN
IDKENKNDIQNVEEKIQRDTYENKDYESDDKLIEWFDDNTNEENFLLTFLKRCLMKIFSSPKRKKTVVQKKHKSNFFINS
SLKYIYMYLTPSDSFNLVRRNRNLDEEDMSPRDNFVIDDEEEEEEEEEEEEEEEEEEEEEEEEYDDYVYEESGDETEEQ
LQEEHQEEVGAESSEESFNDEDEDSVEARDGDMIRVDEYYEDQDGDTYDSTIKNEDVDEEVGEEVGEEVGEEVGEEEGEY
VDEKERQGEIYPFGDEEEKDEGGESFTYEKSEVDKTDLFKFIEGGEGDDVYKVDGSKVLLDDDTISRVSKKHTARDGEYG
EYGEAVEDGENVIKIIRSVLQSGALPSVGVDELDKIDLSYETTESGDTAVSEDSYDKYASNNTNKEYVCDFTDQLKPTES
GPKVKKCEVKVNEPLIKVKIICPLKGSVEKLYDNIEYVPKKSPYVVLTKEETKLKEKLLSKLIYGLLISPTVNEKENNFK
EGVIEFTLPPVVHKATVFYFICDNSKTEDDNKKGNRGIVEVYVEPYGNKINGCAFLDEDEEEEKYGNQIEEDEHNEKIKM
KTFFTQNIYKKNNIYPCYMKLYSGDIGGILFPKNIKSTTCFEEMIPYNKEIKWNKENKSLGNLVNNSVVYNKEMNAKYFN
VQYVHIPTSYKDTLNLFCSIILKEEESNLISTSYLVYVSINEELNFSLFDFYESFVPIKKTIQVAQKNVNNKEHDYTCDF
TDKLDKTVPSTANGKKLFICRKHLKEFDTFTLKCNVNKTQYPNIEIFPKTLKDKKEVLKLDLDIQYQMFSKFFKFNTQNA
KYLNLYPYYLIFPFNHIGKKELKNNPTYKNHKDVKYFEQSSVLSPLSSADSLGKLLNFLDTQETVCLTEKIRYLNLSINE
LGSDNNTFSVTFQVPPYIDIKEPFYFMFGCNNNKGEGNIGIVELLISKQEEKIKGCNFHESKLDYFNENISSDTHECTLH
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```
AYENDIIGFNCLETTYPNEVEVEVEDAEISLQPENCFNNVYKGLNSVDITTILKNAQTYNINNKKTPTFLKIPPYNLLED
VEISCKCTIEQVVKKIKVIITKNDTVLLKREVQSESTLDDKIYKCEHENFINPRVNKTFDENVEYTCNIKIENFFNYIQI
FCPAKDLGIYKNIQMYYDIVKPTRVPQFKKFNNEELHKLIPNSEMLHKTKEMLILYNEEKVDLLHFYVFLPIYIKDIYEF
NIVCDNSKTMWKNQLGGKVIYHITVSKREQKVKGCSFDNEHAHMFSYNKTNVKNCIIDAKPKDLIGFVCPSGTLKLTNCF
KDAIVHTNLTNINGILYLKNNLANFTYKHQFNYMEIPALMDNDISFKCICVDLKKKKYNVKSPLGPKVLRALYKKLNIKF
DNYVTGTDQNKYLMTYMDLHLSHKRNYLKELFHDLGKKKPADTDANPESIIESLSINESNESGPFPTGDVDAEHLILEGY
DTWESLYDEQLEEVIYNDIESLELKDIEQYVLQVNLKAPKLMMSAQIHNNRHVCDFSKNNLIVPESLKKKEELGGNPVNI
HCYALLKPLDTLYVKCPTSKDNYEAAKVNISENDNEYELQVISLIEKRFHNFETLESKKPGNGDVVVHNGVVDTGPVLDN
STFEKYFKNIKIKPDKFFEKVINEYDDTEEEKDLESILPGAIVSPMKVLKKKDPFTSYAAFVVPPIVPKDLHFKVECNNT
EYKDENQYISGYNGIIHIDISNSNRKINGCDFSTNNSSILTSSVKLVNGETKNCEININNNEVFGIICDNETNLDPEKCF
HEIYSKDNKTVKKFREVIPNIDIFSLHNSNKKKVAYAKVPLDYINKLLFSCSCKTSHTNTIGTMKVTLNKDEKEEEDFKT
AQGIKHNNVHLCNFFDNPELTFDNNKIVLCKIDAELFSEVIIQLPIFGTKNVEEGVQNEEYKKFSLKPSLVFDDNNNDIK
VIGKEKNEVSISLALKGVYGNRIFTFDKNGKKGEGISFFIPPIKQDTDLKFIINETIDNSNIKQRGLIYIFVRKNVSENS
FKLCDFTTGSTSLMELNSQVKEKKCTVKIKKGDIFGLKCPKGFAIFPQACFSNVLLEYYKSDYEDSEHINYYIHKDKKYN
LKPKDVIELMDENFRELQNIQQYTGISNITDVLHFKNFNLGNLPLNFKNHYSTAYAKVPDTFNSIINFSCNCYNPEKHVY
GTMQVESDNRNFDNIKKNENVIKNFLLPNIEKYALLLDDEERQKKKKQQQEEEQQEQILKDQDDRLSRHDDYNKNHTYIL
YDSNEHICDYEKNESLISTLPNDTKKIQKSICKINAKALDVVTIKCPHTKNFTPKDYFPNSSLITNDKKIVITFDKKNFV
TYIDPTKKTFSLKDIYIQSFYGVSLDHLNQIKKIHEEWDDVHLFYPPHNVLHNVVLNNHIVNLSSALEGVLFMKSKVTGD
ETATKKNTTLPTDGVSSILIPPYVKEDITFHLFCGKSTTKKPNKKNTSLALIHIHISSNRNIIHGCDFLYLENQTNDAIS
NNNNNSYSIFTHNKNTENNLICDISLIPKTVIGIKCPNKKLNPQTCFDEVYYVKQEDVPSKTITADKYNTFSKDKIGNIL
KNAISINNPDEKDNTYTYLILPEKFEEELIDTKKVLACTCDNKYIIHMKIEKSTMDKIKIDEKKTIGKDICKYDVTTKVA
TCEIIDTIDSSVLKEHHTVHYSITLLRWDKLIIKYPTNEKTHFENFFVNPFNLKDKVLYNYNKPINIEHILPGAITTDIY
DTRTKIKQYILRIPPYVHKDIHFSLEFNNSLSLTKQNQNIIYGNVAKIFIHINQGYKEIHGCDFTGKYSHLFTYSKKPLP
NDDDICNVTIGNNTFSGFACLSHFELKPNNCFSSVYDYNEANKVKKLFDLSTKVELDHIKQNTSGYTLSYIIFNKESTKL
KFSCTCSSNYSNYTIRITFDPNYIIPEPQSRAIIKYVDLQDKNFAKYLRKL
```

280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE

A0A024VJE2 **A0A024VJE2_PLAFA** (796 aa)
Uncharacterized protein. *Plasmodium falciparum FCH/4*

```
MIKIIIGVIGYYILYSSYHIYENIKSPIFNDGNVIKNNEGDKNEQLVIPKEGKKRNSINEEEEEYINKPFKNVLKKDDII
DYHLYFSCEEDIDINKHMQDKYLEKDERFISVYKILNGKYSWNNNVDLLDEKRKKNSFFFLFEKVHPSFDISIPKELIDQ
RKDIYLHILTYVNKELYRYGSRTVVITKRKEKTTTRGKKKFLWKSLIDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKKYQHGNYEKGGSYKVHKNISNNKPNNKNPNDKRDIKHNNNNNNNKMKK
DNFIKSNQNSLNIHKKKKKKRKPKDFLFYIPKKIRFGPVIEYNDFHISKLGFFSNMHVDKDTNTYLLPIYINNDLTPDDEY
RMIKMKNSDDMMKKKLKKKRSSEKNDPYYKENVRNDNNNNNNNNIKNNYLEIYDLSKRTYEMRNERNKKIYEKNSSINNN
VHKLEHELMDYIINIEYVPINYNYYNLLNMLKFNVSYVKKKYNFISFDMDSITTFLCCHITCSMIIYILCIIYIIMEITY
LLFDIKMWKRWNNLYTFTYNNDIVMNITLLFFILLYLRNIDYGRVIMIYYIMKMMVLIFKIIYNYDICILNDYPYICINK
KSLKEMNKEMIMDEEFEKKIKKKVNIFMIFSIILIFIYNYFYTKYDSYYSYVIHTLGFSSYLYKFILMLPQIITNIYTRT
VQRMSFPFFLFLLVNVLINDLFIIFLRMPKVHKYYLFADDFILFLFIIQYCIYKKENKIFGAREKLVLLKNAKKNK
```

209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEEE
225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE

231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE
239 - 258:	EEEEEEEEEEEEEEEEEEEE
240 - 259:	EEEEEEEEEEEEEEEEEEEE
241 - 260:	EEEEEEEEEEEEEEEEEEEE
242 - 261:	EEEEEEEEEEEEEEEEEEEE
243 - 262:	EEEEEEEEEEEEEEEEEEEE
244 - 263:	EEEEEEEEEEEEEEEEEEEE
245 - 264:	EEEEEEEEEEEEEEEEEEEE
246 - 265:	EEEEEEEEEEEEEEEEEEEE
247 - 266:	EEEEEEEEEEEEEEEEEEEE
248 - 267:	EEEEEEEEEEEEEEEEEEEE
249 - 268:	EEEEEEEEEEEEEEEEEEEE
250 - 269:	EEEEEEEEEEEEEEEEEEEE
251 - 270:	EEEEEEEEEEEEEEEEEEEE
252 - 271:	EEEEEEEEEEEEEEEEEEEE

A0A024VT79 **A0A024VT79_PLAFA** (515 aa)
Uncharacterized protein. *Plasmodium falciparum FCH/4*

```
MHLTNKLTKNISFFYHVPLFQKRKLTTFALRKKYIWKNNTHTKKNDEKKIMTCSGDFIEKKKKNYEWEIERKEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEQDEECSENDIEVMNKEVACNINNDIKIKENNKINVDDDISVCDEYKFLFERPKHFAHI
DDEPIIRRPGCIIDIKTLLRNNWSFPAVGFNSKLEIPIYKFEADENDDNIKYISVPNDIFGLPIRSDILHKCYYFYRTAL
AGYTERMQLYKWEWPGSTKKYRSQKKSGKARMNWRKTCGRYLGVKNHPIRPFDQKTNINRKFLWKGMKILLSAKFAQDQI
KVVDNFLIKSHKTKYTVKYLRNILGKNCNSALLVHEGKTDVNDNFLWACANIASVKRENVEGVNIYNLLKYRYVVFTYKA
LKNIIYELKIYPYKMKWLPTYATPNNTQAPIPEKVKNWNFLWLEKKKRNNFSKFDKETLKKRIQEWKWSSDIKGALKVKK
HDPYKNFILTKFQCNDPVPEYIKYEYLFNFVFFTR
```

73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE

A0A024VVE3 **A0A024VVE3_PLAFA** (539 aa)
Uncharacterized protein. *Plasmodium falciparum FCH/4*

```
MRVCTRLLQIGAKMHLTLYEIAKISTRKNIDEESILEHLVKDSITQAYQMMDYTSLMSTNRLGYILDLAEIKMNKKKKNS
KIKTVEINDDKIINQLYEKNQGNLFFNEKGETTGGEGSLKSPPSIKKDNDIIKSNIYNKNVSNNNLIKDVDDMISINSSS
NTTNSIKNVSLINESYKNIYSNNVIKNNNSDFFNKNIENNIDLMNITNQVNNINLCLNIKKEDNETNGEENDMSLKQNNL
KHTHLNSRSDFSKECENTTESKNITMKLKKENFSNNSPDNLLDKPLDTLLNEPLDHFLGKPLNKFVDKPLDNMLENISGE
VSDMSNISNNLSNVSDKIKVDTSEYKDEALFCNSPNDDTKVKKKKKKKDSDLDGYPKDQKNYTNCDDGDKINSDDNGINK
ENEMINQVKNNLNDDEEEEEEEEEEEEEEEEEEEEEEENDDYDVTFKKPSGTIKRISENTGTAYRSMEMNKINSIWMIRDK
NNKIINVKWENKIFEKLFFETFENYIKKYINDYHRDWRNYPYNGSKITTTKHAYLNNIK
```

416 - 435:	EEEEEEEEEEEEEEEEEEEE
417 - 436:	EEEEEEEEEEEEEEEEEEEE
418 - 437:	EEEEEEEEEEEEEEEEEEEE

A0A024VWF3 **A0A024VWF3_PLAFA** (346 aa)
Transmission-blocking target antigen S230 (Fragment). *Plasmodium falciparum Tanzania (2000708)*

```
MKKIITLKNLFLIILVYIFSEKKDLRCNVIKGNNIKDDEDKRFHLFYYSHNLFKTPETKEKKNKKECFYKNGGIYNLSKE
IRMRKDTSVKIKQRTCPFHKEGSSFEMGSKNITCFYPIVGKKERKTLDTIIIKKNVTNDHVVSSDMHSNVQEKNMILIRN
IDKENKNDIQNVEEKIQRDTYENKDYESDDKLIEWFDDNTNEENFLLTFLKRCLMKIFSSPKRKKTVVQKKHKSNFFINS
SLKYIYMYLTPSDSFNLVRRNRNLDEEDMSPRDNFVIDDEEEEEEEEEEEEEEEEEEEEEEEEEYDDYVYEESGDETEE
QLQEEHQEEVGAESSEESFNDEDEDS
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280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE

A0A024W3M9 **A0A024W3M9_PLAFA** (1991 aa)
Uncharacterized protein. *Plasmodium falciparum Tanzania (2000708)*

```
MNVCKMKVQQKKNLKDCNLKSKNTILTSFEKKKNEKDENNLLKFSKLIDNKNKVVNSKLLKNDNYKFNERKESLTRCSTN
ESLKLKNIKTLTKDFDYNNNNNINNNNDYNNNNNNNNNNNNNNNNNNNNNNNNNKNNNNNGHSKLVFKKNDKDIESKVREEDG
KKSEKKNNDLINNKNEFKVNNKLILKSKEFKSNNNNNNNICKLNNIDDKNKKQQMDTYSPKENEEDNSNNMKKSSSLKNI
KKNQINEMEIISNSVEENHDTHSKGDKENNGVSTKNVKRMNTMSKEINHKNNNLKKHVSKSNSLELKKGKKGEKSKDKLS
NNVSGKKGMNKEKEVVQSSSVRRNSSRYSIDYGRRDSSRRGSVKQEKGKERRGSKNVSKKVSNSKYTRKKSKRIKEESDE
SDDDDEEEEEEDDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDNDNSDNNDESDEVYTNRS
RRSTRCSIVKRKSSLCIGKKNSKIIKKSTSKTKNNKKKKGSVIKLVKKKEKLSKKGILKKTNKKTKGKLRKNSKLYHRKK
NIKNEKDGIDEEDIDEEDIEEEEEPSYFDEYNLSYEERKKDLEEKEKKKEIKEKYIKQIKLPKYADDESIIFINNPNYVM
VLLFLTVYKDVLKMNWNFKDIEEMFQNKETTEFGRNFILKLFFFLGRYFNSKSIFMYKYISRIFEDKEESLSRVVNFHEL
FPVLETKKEIKNSGVGSKRKKDKRGKKMKIHQKEDELLYDEEVIGNEDVHIFEEEEDNEHSNDDEDEEEEDNEEDNEHSN
DDEDEEEEDNEHSNDDEEKEDVHYNHEEEKKSDLNNDSTKNTVIKEEKDGLHISEGSHNLVNIVVNDSMKREESCKNGHI
GDNERSGDINTNDDKNNADNNDDVDGEKIVDSKNNIENKLDNTVEGKHDINSTEGIIKSENVDDEKGLLTNKLFIEWDDL
SVISKLRIIRMLLNLVLCESNNLKKMLGDEKLNYNNGYLGKINNEKYWFIFNDTINIEYKLYLEREEEGSFIFICDDDDM
LYTIGYNFLRNSDTKFMGEALIERYNKVCRERRNRSRMLKQQKKLLCADINLNDPLLGTKKRQHKQVEYFNFDNNEKMRR
KKSDMNNNNPYSVPPTKSYQKNDRSFRLAARNAQKGSVDDLEAWKLNEGSLGIENQGATSGNYNIANDGTNMTETNNIND
NHNNDNNNNNNDGVVNADGNNIYGPNNNNVIGSDGNVNNANNTTTNNNNNNNNNLGTVKIPLKRGRKKKSEKKKRGRKKK
ILSVDGIGEIANNLSALNVDENRRKSMPNIGRGRRGTYTKRNTKPSVSIKYGTRSHSINKYKNDVMSFNEYSLNPGLSMD
DFYKNMVMDPKFFHANMNMNNYMNGGFNMPNNNNSMMNMRNGSKMGNMNNIGGYNFPYMCTPPPMYNQYYMYNGNNMYLP
NGGPNNNMNMSNANNGASVVMGGNVVSNQNTVKDVKAENMHMAKNSIMENRNSIIVNNMNNMNNINMNSMPHKNSFMGND
GINNMNSMNNNNNNNNNVNNNNNNVSNNNNNNNVSNNNNNNVNFMDNMGNNNNNNNNNNPMNKYNNYMMNRNVLNNMGG
TNPLYNNMYNMKFPYMNNDMMNYNYNINSFQNMNYDKMNKSMFKRYPNFMGGYPYNNMNPYNNFNAFNMNYQQNDQMNQL
PNMQGGYKSKLMNDNLSNYQSFNNNNVKQNHHDNNNNDNNNNKNNSEGGNKNMDDSNKNNDINKNDILDSTKLTEQPVGD
VVPNNDCITRGEDNHRIDLKGDIAEALVGNNNEKMNSSDHNLNSLKNLPNINNTYNMDHMSHMRNSVSASSIGMINPGHM
NSSHSGSIMNKDKFRDLQLNSNNNNNNNNNNNYVKVNPFDHPMKNMNPNLMDDKYPKDNNNMMMMMMNSVYNMMGSDHFH
MNNSHMMDPMGSPKMNDNMYNHNNMNFENTNTNHNNHNNHNNHNNHNNLNNLNNLNNHNNHNNRIQDKLPE
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414 - 433:	EEEEEEEEEEEEEEEEEEEE
415 - 434:	EEEEEEEEEEEEEEEEEEEE
416 - 435:	EEEEEEEEEEEEEEEEEEEE
417 - 436:	EEEEEEEEEEEEEEEEEEEE
418 - 437:	EEEEEEEEEEEEEEEEEEEE
419 - 438:	EEEEEEEEEEEEEEEEEEEE
420 - 439:	EEEEEEEEEEEEEEEEEEEE
421 - 440:	EEEEEEEEEEEEEEEEEEEE
422 - 441:	EEEEEEEEEEEEEEEEEEEE
423 - 442:	EEEEEEEEEEEEEEEEEEEE
424 - 443:	EEEEEEEEEEEEEEEEEEEE
425 - 444:	EEEEEEEEEEEEEEEEEEEE
426 - 445:	EEEEEEEEEEEEEEEEEEEE
427 - 446:	EEEEEEEEEEEEEEEEEEEE
428 - 447:	EEEEEEEEEEEEEEEEEEEE
429 - 448:	EEEEEEEEEEEEEEEEEEEE
430 - 449:	EEEEEEEEEEEEEEEEEEEE
431 - 450:	EEEEEEEEEEEEEEEEEEEE
432 - 451:	EEEEEEEEEEEEEEEEEEEE
433 - 452:	EEEEEEEEEEEEEEEEEEEE
434 - 453:	EEEEEEEEEEEEEEEEEEEE
435 - 454:	EEEEEEEEEEEEEEEEEEEE

436 - 455:	EEEEEEEEEEEEEEEEEEEE
437 - 456:	EEEEEEEEEEEEEEEEEEEE
438 - 457:	EEEEEEEEEEEEEEEEEEEE
439 - 458:	EEEEEEEEEEEEEEEEEEEE
440 - 459:	EEEEEEEEEEEEEEEEEEEE
441 - 460:	EEEEEEEEEEEEEEEEEEEE
442 - 461:	EEEEEEEEEEEEEEEEEEEE

A0A024WGR9 **A0A024WGR9_PLAFA** (5916 aa)
Uncharacterized protein. *Plasmodium falciparum MaliPS096_E11*

```
MIYKGYMKNITFLVSFLIFLRSINANISITNFTYTNQKGDIKVEFFQTDYIAIFKLPFGGSHEQIFEISDDYIITNDKET
NNCNIPNNNFGFVYSKSNSQNKFLIVQREYTTIYIKDKNNNCSLISKVEPSLYSFQTIEYKKEKIKLGTTTKCDEKMVEK
LKIYIDLLNDMNLSEDKVCNQIIASSFIQNIEIIDCTVYIGSIFLRNNLNREEYYICIKKEDNNNKMKNNISLLINTIDL
NNTLIMNTFYCNMERDICSIIINSIYFNNIPNITDDTLVLKAQCNIDSNPLINIDHVLREGYYTFHFRNPKIYFLQICII
DNLKKYRMLGKIYFLKAYEPIICFIGTPCVIKSFTVKENVQYVQNNIDNETFIFTNKKCDNENVNENMNMIETDYDMKEL
ENHQHFYLFSKNPLTDEKYLCTSNNKKFLLLFNIVLIKLPEYNIHYSIINNVVINYSTLFFEYNNYLGPYVKYECSDKSI
VPDEYNNFNNNKDNNFLLKNEELNFTIKFKAIIMRLCLKQNNYYYDIGKIYIENFINYKKISSLKDFIFNADVSLHADDI
NTKLLKFAIKEDHNCHSDQGFFVQSKDNFRADKKPFYKNIFINHTTVYESINQIILDKDIYYICMCSLHEKCYDNNNLID
YNVYTNISIQNEIQPLQNKKKFICKIFADCSFTINFENEYNNTSDIWVAKKGQSCNSKDIQVGIHVSHQNVKEINKEKIN
VTKVNFKIYYLISHIHYSYLFNKDIFICGNYRNQHFIVHIKSDFFLLYYALPFEEEINIKNVTQTNVATNTYEAQEKNIN
IQSFENVKQKFKRLFIYSYRDDAKSNLYKTMNINQDENQISNTIKFEIPNDHPTKYNEIYFINECHYDQGVIIYDHKRES
NNIAINNDNNNNNNNHIIKSKELYWARKKRIYNKKLKKKENKNEIININYNCSNEIMNNHTLTSILIFDGPLKPLDIYCYM
ELDCIHKENFSILNFDYSLFVEISDTQRIIIHIKESEGNNKEKLNKAEKIYFNDSKRTTELILSIPKHISKGLEPGPYKI
IYTRKFKQFIHELYVGTFHFIGAPSQKYHLIRENQENIIIHGYFKNIENERIHILKHQNTCVLTNKDKNKKLLKSSEIEY
ILNEIKTNIQNCTYLDDTKLLCKNDLPVEGKFILCWCYNILNDQNNLCHNLNIYRPKITEVSSLLYSIDPILEISKSSLT
NFLNYNIGDFFFIIDDDCKNIKNIKLKSKLNDEQNILDIYKHLQYPKKYDLCICIVQHNIPCDKEENFKNFYIKLNEQIY
FTMEMGSIDEFNNKDKFIKDFTFSTDYLDQLKLNIVPVFVFLPGPVEYKEYVCFAGIPCNATIKIKRSAQTRLITGNKQI
IGEKKDVANPYTGSYGNRNKANIKKGEEKKEQKRNDKKEGEIGHKKEGEIGHKKEDELGDKKEDELGDKKEDELGDKKED
NNEDQNQDNKQDKIENMNKDINKDKEIKTKETNIEEEEEVEEEEVEEEEEEEEEEEEEEEEEEEEEEEKEEQFDHNEHEVK
GADKNKDKNFNQNKGESQNVNPNTQQNQYDEQIISEEEQDNIENSLLGKHQYIYYTLNDTKECKNEYETVYKSNASSIYV
SQEINYLHHEFIDGVYNLKIDIVPTDITKRYEICASFYEDDKYFYNIGNIIFYGIFNESNTLDIISGVPFSFEINQFYSK
YDLFIRLIYEKHGDSKTCRLYNNNFENVFLEGTIERTIVQHDKKVLDNYITNYKWKDVTIILDTDNNNYMTSYQNVDGSY
NLYVCSCYELTEGHCQSGNYFSTQVMKFYVHTVELKEPKMNSLMHFLKPFTLKLETTKILNGSIKVIPIDIISDLSKLCL
ELNLKNIYLKYQAEINEYEQTYNITINFLSQGFIICWCGKDNCKDHEYLTKVAFFRLNSPNFIDVHTDLNGNFSFHFLNQ
FVNINDRVRFVGQASSCLDDENVDLFNNHIVIKNVQNKKGKTSNGGNTKKEQQKNNNKINSNNNEEDENDNENKNERKDE
DDNYESYSIDWEQIIEIFGKPRNIFKGINQNWTWVSENYKMKTSNEKYIKICYCFHFYYKNCKDTKNFLYIGLVHNHIWD
SKTTIMQNELDTNYEISNMIYFNKDSIKFVAINSFNDLNRNVCDNINYEKNIIMPFFSGYNKFHNTTINQKNILNILKTY
YHNEFIFILCYNTEYYKKKTNYLLTTKDMTELNDFTTYYNEEINTYNIIQSSFSYHSDIKDISTTNENIEKYEHMQLLLQ
NRGNTPNIFENYFYQKDVYKKNNMSIYNMNLYNMSPYVVYNNNKKKITNIQVKNRLKIILTKMYHMTSVDINEVIYYKGK
GELLTDLNLQNIFILPKQKKVILCCYNDDYIEVIINDDNKIGMKKSNKIQELIDILKKYHPNFERNKKKQNDILEQFNNI
NDILFKYDYIRDVNKNQIYYDTGFFRNNIYIQLINQPFDLKIYGSNIQKKKNKDYILYIIEFHNICYNNMNKNGFFLEHK
RYNEMENYIHFLQISMNKINNYKLCLYDKERDIYSNVGILNITDYFVIKESSFFDNEDIGNIKKKNMETDSYNYNNDNNY
DGNYDNNYDNNYDQNNNKYYIKNYNQDVIKNVCLIMDNNTNQIIVIKGKGSFYFNLQIEKGIFIEKKGQKLNELFPDIKN
HEPISCKNKKKNTIILTKTHIFFYTNNNDISFSTKHNLPFPYDIDFDDQYIYVNDLYLNKIARIQILSNKDNKTPIPIIN
NKQRSKRSIINHGHESQQNIQKTHQTYDHFTPLHKVEKKEILQNNNIVQLKENEFPITNLKNIEYSKNNIPNQKISSKDD
IYKMSDFQAFINKYANLITTNSFRLYNYFEKKKYYGTLNYFIKRVWFNKVGPSREENYSTESKIEQNDKNNNNNNNNNIN
NNYNYNYNDLHNNNHNIILNSNNYNNNNQSSRHQNFIYSYHVSLDGKKKQSENLLTHSLNNFIQFFQNKKNSILKKEKEK
RKNIPSYNIMYKNINHITNTLNKRKQQELTSSIIKKRTKRNVQEKRMSQSAYNELVLASIKKYTNKVEPAHFVNNKLDYL
NYITNLKSPLNISVQNNILYILDSIKNTFFSYNIINKEIKELEKYDFNDHPLILKNPLHFSIYNGIITEYTEHKNNLAFV
TQIDSNEIKVIDLNSSKKYKIIKAIKLRKGYKHNHINYVIGIKQKLLIITSQSQNIDHYKNIIYHYHFNSFDQYFSISFN
YTFAKNYNANDNLYITPDIDKYSDNIIYFCFLNSNNKCTNIDELTKLSISHETGIITGKLNYFGTFSLKIFAKTYFQYKI
NTYSNLYSYCGISQEYNKTKSTCESCPIGTFWNSEKLLCENCQKYIENTSTLKNGSKLKTDCLCSPGYEYSDKSSKCEKC
KPGYYKKSVGNFICIKGCPINEKSITYGAKSYAEMDCKCIEGYYRKEDKCVLCLSNYYCPGNELIKPCDKNKISKEGVIH
KNDCICKENYIKDNKNNNCVYCASIAKILGKPIYCSLCDPIYFHEDIYKNIFLLPNNIHNYGLINNIYNYDEDLSLQGNI
MKYAYFHKTTNIERNFTHYINIKNIYHTFNNNINNYDYLTNSKFAIEIDIPEPKKCIFCDSGYYIKKKKCISCTTKYCEG
FNHNPKACPKNSVVNKMKASSIFDCSCKRGYGILNERRNAYSNTITCQICPQNFFKHIISDDSCFPCPLYTYTLNQGATS
ILQCLPKKGYFIYMFKSINIDYLRYKFDINTENRIYNYFENNNKIFDEDVYNFFLNKQYSKFFYNTENKTNTNNNNNNNN
NNNHNHNNHNNNHNHNNNNNNNKYTKDNHFDNQVGNINKHTNNLQIKITENIYNIQYLEHLGFIKKTSLFYIYMILLRNI
EERYNFNMDKMLKITCHINLHLKKNPHFTITYKKNLQECIDSCKTNIYCTGIEFSRKRVEYTQIILKNNKKIILGYFKCK
QFYFQNIYDYSSYNLDSYLNEHIENQINIKSTLTYTNFIMRNKPDIIYTCSIDRDPKYLLYKNYKLVECVIGKFCPGNNT
PYMISCPINSTTIIPASEDVNKCLCLKGYSYVGVTSYRCSLCDRGSYKNSVGNNKCDNCPLTFSTTHRGSTNIKDCSCTS
GNYLTFDTLGNFIRTENMQHKNISDQYFVIPIKQESQPENEIKDDNKNINIYNANNINNHDIVYKTKMIKINLHKENDNH
NDYMNNILKQTIGLCKPCTLENHYCEGGLESDITFNNKLIKGKFHTLPKKCPRGLGIPNIIKERNSINNCLCIHGKVQRT
TENKNVECFPCPPNTFKENEYDNSCSGACPPFSTTFVGSSYENQCFCKNNYYLVSTDDENDTNGNSINNNKNIYNNNNIY
NNNNNNNNNNNNNNFNNKSDVKKKSCKICPIGAICNRGFNIYIYLKLLNDRSYNNINVIDHETPFPKYGYYAVYREKTNPT
KSWDTLDDSAILNYVYPYHKLLLFIQKNIQKGNYFFLEKGNKFFLNDDFVEKMNEKSKYEEENANKFVTKSEIIHNVNTN
NLKGKHNTLNNNNNNNINKSSSFLNQNNYNNDIIQLSSYENNPFKNLSSTSEVSSNNNVISFIQNNDKTNNSTNDNNIEN
LVDIFNKYVQEAKELQIQNRKFERIPDIHPCTIPNRCLGTLINLCSDGSTGYQCNNCSKNYDMSYFKSKCKKCQNLFYEI
LHFILLKLLYYIIVIFICSLNGNILNKLHVSGILMRIWLNCSFTFIAYGFFIPNMNSFISKYWYLYKTAFSYHMKIFAYY
LRVQCLLNSLNINLSYNQMWYIQKYMNICTPIFDSIFITILLFAVIHIYKFFFYKKNIDIFEQLLCTIPELNTLYKKNCI
DNIHKVKNKKFANKVESFEENENQNKEKKNKKNIKRKNKAKNKHNNDNNDNNDDNDNNNDNNKININSKDEHINHFEKCS
SITTILNNLELNNEEKNKESKKKKIFDIKKKTSIENIKENETNHLWNDTHNNVKNKESNINTTNISNNINYELKYIKNKE
WYNIFLNKTIQYIYKEKKIFGLWHFIFTKNDNWFKNMGTFLNDTLPCYVLIMILSIPYILLELVQLTYCTPIKYKTQKTY
FYLTYLITQKCSLSSKLFITGLIVTITMFALYIFLWILLLYLYSKRKRLNLFDLLTTNLLSGFRKGKGIFELIFLLKHIL
IVLLICFNIYYGLYYIVFLTLILITFAILEILSNPYDKRSFNILNKSLNIGNVLNIFFPLIIWGSFYWTYENFFIFPIFV
IYAYHIYMFYHIVKEFTLSIHFIKTENIVNIQTIGYDPENIKNKNYKIYYKVMNKIKYFLNKNQKKNISNINENKDKHLN
KNNNSKDHVKFEPIENIIKRYNLKLNKGILKDANNNNNNNNIKNMSDQVEDNKKDILFIKKNVLPVNVHNVASIWYDEQN
EDLLFQMPYQNKFCLNMNNEANENNDQINDLTKDKTSEEENNNDHVNDPTKDQTNDEKKKNKNKKNKNNNENNNNENNCH
SNDNSNNNNNKEVHKNDDNINHNNINNHNKSSNISTTNKKNYFNKFSDYIIDKRNKKSIKYFITSLMEVIEKFLDSSTHG
FIYENWFDFTIRFAFVYISWIKKCNKKNNIMLPMNIQQLHIHMDLFIFTPIFPKNNSTCINEQNIQNYSKKKKIYNKINM
YDEKIETGELLEKHNSFENTEIKISRSFGSHNYMPNIKNRKNNYDKKEDITSINDINVDIIKQDDQKEDSNINHLINEHN
QKEPSQHIYNINDKNIMDYNIDENISKNNEKEKHIKIPPKNISITQKEYYNNNDIFNYSLDIFSSEMFNEKMFHSIISLF
ELYMAIKTLKLMNTHIFNKLYQMYNKKIITFDTSVMFYINKLRDDIKSEIEQIDKEINTGDTTEKERIQNYYYYKEELFK
RKKLEEELLSKIKSLEECIEVNKRSQSLRNMLLTKKKKNNNLNNENLEEHINYIFSHLHNEGTYKLNHSQNMDKKN
```

1486 - 1505:	EEEEEEEEEEEEEEEEEEEE
1487 - 1506:	EEEEEEEEEEEEEEEEEEEE

1488 - 1507:	EEEEEEEEEEEEEEEEEEEE

A0A024WXW3 **A0A024WXW3_PLAFA** (3091 aa)
Transmission-blocking target antigen S230. *Plasmodium falciparum MaliPS096_E11*

```
MKKIITLKNLFLIILVYIFSEKKDLRCNVIKGNNIKDDEDKRFHLFYYSHNLFKTPETKEKKNKKECFYKNGGIYNLSKE
IRMRKDTSVKIKQRTCPFHKEGSSFEMGSKNITCFYPIVGKKERKTLDTIIIKKNVTNDHVVSSDMHSNVQEKNMILIRN
IDKENKNDIQNVEEKIQRDTYENKDYESDDKLIEWFDDNTNEENFLLTFLKRCLMKIFSSPKRKKTVVQKKHKSNFFINS
SLKYIYMYLTPSDSFNLVRRNRNLDEEDMSPRDNFVIDDEEEEEEEEEEEEEEEEEEEEEEEEYDDYVYEESGDETEEQ
LQEEHQEEVGAESSEESFNDEDEDSVEARDGDMIRVDEYYEDQDGDTYDSTIKNEDVDEEVGEEADEEVGGEEVGEEEGE
YVDEKERQGEIYPFGDEEEKDEGGESFTYEKSEVDKTDLFKFIEGGEGDDVYKVDGSKVLLDDDTISRVSKKHTARDGEY
GEYGEAVEDGENVIKIIRSVLQSGALPSVGVDELDKIDLSYETTESGDTAVSEDSYDKYASNNTNKEYVCDFTDQLKPTE
SGPKVKKCEVKVNEPLIKVKIICPLKGSVEKLYDNIEYVPKKSPYVVLTKEETKLKENLLSKLIYGLLISPTVNEKENNF
KEGVIEFTLPPVVHKATVFYFICDNSKTEDDNKKGNRGIVEVYVEPYGNKINGCAFLDEDEEEEKYGNQIEEDEHNEKIK
MKTFFTQNIYKKNNIYPCYMKLYSGDIGGILFPKNIKSTTCFEEMIPYNKEIKWNKENKSLGNLVNNSVVYNKEMNAKYF
NVQYVHIPTSYKDTLNLFCSIILKEEESNLISTSYLVYVSINEELNFSLFDFYESFVPIKKTIQVAQKNVNNKEHDYTCD
FTDKLDKTVPSTANGKKLFICRKHLKEFDTFTLKCNVNKTQYPNIEIFPKTLKDKKEVLKLDLDIQYQMFSKFFKFNTQN
AKYLNLYPYYLIFPFNHIGKKELKNNPTYKNHKDVKYFEQSSVLSPLSSADSLGKLLNFLDTQETVCLTEKIRYLNLSIN
ELGSDNNTFSVTFQVPPYIDIKEPFYFMFGCNNNKGEGNIGIVELLISKQEEKIKGCNFHESKLDYFNENISSDTHECTL
HAYENDIIGFNCLETTYPNEVEVEVEDAEISLQPENCFNNVYKGLNSVDITTILKNAQTYNINNKKTPTFLKIPPYNLLE
DVEISCKCTIEQVVKKIKVIITKNDTVLLKREVQSESTLDDKIYKCEHENFINPRVNKTFDENVEYTCNIKIENFFNYIQ
IFCPAKDLGIYKNIQMYYDIVKPTRVPQFKKFNNEELHKLIPNSEMLHKTKEMLILYNEEKVDLLHFYVFLPIYIKDIYE
FNIVCDNSKTMWKNQLGGKVIYHITVSKREQKVKGCSFDNEHAHMFSYNKTNVKNCIIDAKPKDLIGFVCPSGTLKLTNC
FKDAIVHTNLTNINGILYLKNNLANFTYKHQFNYMEIPALMDNDISFKCICVDLKKKKYNVKSPLGPKVLRALYKKLNIK
FDNYVTGTDQNKYLMTYMDLHLSHKRNYLKELFHDLGKKKPADTDANPESIIESLSINESNESGPFPTGDVDAEHLILEG
YDTWESLYDEQLEEVIYNDIESLELKDIEQYVLQVNLKAPKLMLSAQIHNNRHVCDFSKNNLIVPESLKKKEELGGNPVN
IHCYALLKPLDTLYVKCPTSKDNYEAAKVNISENDNEYELQVISLIEKRFHNFETLESKKPGNGDVVVHNGVVDTGPVLD
NSTFEKYFKNIKIKPDKFFEKVINENDDTEEEKDLESILPGAIVSPMKVLKKKDPFTSYAAFVVPPIVPKDLHFKVECNN
TEYKDENQYISGYNGIIHIDISNSNRKINGCDFSTNNSSILTSSVELVNGETKNCEININNNEVFGIICDNETNLDPEKC
FHEIYSKDNKTVKKFREVIPNIDIFSLHNSNKKKVAYAKVPLDYINKLLFSCSCKTSHTNTIGTMKVTLNKDEKEEEDFK
TAQGIKHNNVHLCNFFDNPELTFDNNKIVLCKIDAELFSEVIIQLPIFGTKNVEEGVQNEEYKKFSLKPSLVFDDNNNDI
KVIGKEKNEVSISLALKGVYGNRIFTFDKNGKKGEGISFFIPPIKQDTDLKFIINETIDNSNIKQRGLIYIFVRKNVSEN
SFKLCDFTTGSTSLMELNSQVKEKKCTVKIKKGDIFGLKCPKGFAIFPQACFSNVLLEYYKSDYEDSEHINYYIHKDKKY
NLKPKDVIELMDENFRELQNIQQYTGISNITDVLHFKNFNLGNLPLNFKNHYSTAYAKVPDTFNSIINFSCNCYNPEKHV
YGTMQVESDNRNFDNIKKNENVIKNFLLPNIEKYALLLDDEERQKKKKQQQEEQEEQILKDQDDRLSRHDDYNKNHTYIL
YDSNEHICDYEKNESLISTLPNDTKKIQKSICKINAKALDVVTIKCPHTKNFTPKDYFPNSSLITNDKKIVITFDKKNFV
TYIDPTKKTFSLKDIYIQSFYGVSLDHLNQIKKIHEEWDDVHLFYPPHNVLHNVVLNNHIVNLSSALEGVLFMKSKVTGD
ETATKKNTTLPTDGVSSILIPPYVKEDITFHLFCGKSTTKKPNKKNTSLALIHIHISSNRNIIHGCDFLYLENQTNDAIS
NNNNNSYSIFTHNKNTENNLICDISLIPKTVIGIKCPNKKLNPQTCFDEVYYVKQEDVPSKTITADKYNTFSKDKIGNIL
KNAISINNPDEKDNTYTYLILPEKFEEELIDTKKVLACTCDNKYIIHMKIEKSTMDKIKIDEKKTIGKDICKYDVTTKVA
TCEIIDTIDSSVLKEHHTVHYSITLLRWDKLIIKYPTNEKTHFENFFVNPFNLKDKVLYNYNKPINIEHILPGAITTDIY
DTRTKIKQYILRIPPYVHKDIHFSLEFNNSLSLTKQNQNIIYGNVAKIFIHINQGYKEIHGCDFTGKYSHLFTYSKKPLP
NDDDICNVTIGNNTFSGFACLSHFELKPNNCFSSVYDYNEANKVKKLFDLSTKVELDHIKQNTSGYTLSYIIFNKESTKL
KFSCTCSSNYSNYTIRITFDPNYIIPEPQSRAIIKYVDLQDKNFAKYLRKL
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280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE

A0A024X0P9 **A0A024X0P9_PLAFC** (5921 aa)
Uncharacterized protein. *Plasmodium falciparum (isolate Camp / Malaysia)*

```
MIYKGYMKNITFLVSFLIFLRSINANISITNFTYTNQKGDIKVEFFQTDYIAIFKLPFGGSHEQIFEISDDYIITNDKET
NNCNIPNNNFGFVYSKSNSQNKFLIVQREYTTIYIKDKNNNCSLISKVEPSLYSFQTIEYKKEKIKLGTTTKCDEKMVEK
LKIYIDLLNDMNLSEDKVCNQIIASSFIQNIEIIDCTVYIGSIFLRNNLNREEYYICIKKEDNNNKMKNNISLLINTIDL
NNTLIMNTFYCNMERDICSIIINSIYFNNIPNITDDTLVLKAQCNIDSNPLINIDHVLREGYYTFHFRNPKIYFLQICII
DNLKKYRMLGKIYFLKAYEPIICFIGTPCVIKSFTVKENVQYVQNNIDNETFIFTNKKCDNENVNENMNMIETDYDMKEL
ENHQHFYLFSKNPLTDEKYLCTSNNKKFLLLFNIVLIKLPEYNIHYSIINNVVINYSTLFFEYNNYLGPYVKYECSDKSI
VPDEYNNFNNNKDNNFLLKNEELNFTIKFKAIIMRLCLKQNNYYYDIGKIYIENFINYKKISSLKDFIFNADVSLHADDI
NTKLLKFAIKEDHNCHSDQGFFVQSKDNFRADKKPFYKNIFINHTTVYESINQIILDKDIYYICMCSLHEKCYDNNNLID
YNVYTNISIQNEIQPLQNKKKFICKIFADCSFTINFENEYNNTSDIWVAKKGQSCNSKDIQVGIHVSHQNVKEINKEKIN
VTKVNFKIYYLISHIHYSYLFNKDIFICGNYRNQHFIVHIKSDFFLLYYALPFEEEINIKNVTQTNVATNTYEAQEKNIN
IQSFENVKQKFKRLFIYSYRDDAKSNLYKTMNINQDENQISNTIKFEIPNDHPTKYNEIYFINECHYDQGVIIYDHKRES
NNIAINNDNNNNNNNHIIKSKELYWARKKRIYNKKLKKKENKNEIINIYNCSNEIMNNHTLTSILIFDGPLKPLDIYCYM
ELDCIHKENFSILNFDYSLFVEISDTQRIIIHIKESEGNNKEKLNKAEKIYFNDSKRTTELILSIPKHISKGLEPGPYKI
IYTRKFKQFIHELYVGTFHFIGAPSQKYHLIRENEENIIIHGYFKNIENERIHILKHQNTCVLTNKDKNKKLLKSSEIEY
ILNEIKTNIQNCTYLDDTKLLCKNDLPVEGKFILCWCYNILNDQNNLCHNLNIYRPKITEVSSLLYSIDPILEISKSSLT
NFLNYNIGDFFFIIDDDCKNIKNIKLKSKLNDEQNILDIYKHLQYPKKYDLCICIVQHNIPCDKEENFKNFYIKLNEQIY
FTMEMGSIDEFNNKDKFIKDFTFSTDYLDQLKLNIVPVFVFLPGPVEYKEYVCFAGIPCNATIKIKRSAQTRLSTGNKQI
IGEKKDVANPYTGSYGNRNKANIKKGEEKKEQKRNDKKEGEIGHKKEGEIGHKKEDELGDKKEDELGDKKEDNNEDQNQD
NKQDKIENMNKDINKDKEIKTKETNIEEEEEVEEEEVEEEEEEEEEEEEEEEEEEEEEKEEKEEEQEEQEEQFDHNEHEVK
GADKNKDKNFNQNKGESQNVNPNTQQNQYDEQIISEEEQDNIENSLLGKHQYIYYTLNDTKECKNEYETVYKSNASSIYV
SQEINYLHHEFIDGVYNLKIDIVPTDITKRYEICASFYEDDKYFYNIGNIIFYGIFNESNTLDIISGVPFSFEINQFYSK
YDLFIRLIYEKHGDSKTCRLYNNNFENVFLEGTIERTIVQHDKKVLDNYITNYKWKDVTIILDTDNNNYMTSYQNVDGSY
NLYVCSCYELTEGHCQSGNYFSTQVMKFYVHTVELKEPKMNSLMHFLKPFTLKLETTKILNGSIKVIPIDIISDLSKLCL
ELNLKNIYLKYQAEINEYEQTYNITINFLSQGFIICWCGKDNCKDHEYLTKVAFFRLNSPNFIDVHTDLNGNFSFHFLNQ
FVNINDRVRFVGQASSCLDDENVDLFNNHIVIKNVQNKKGKTSNGGNTKKEQQKNNNKINSNNNEEDENDNENKNERKDE
DDNYESYSIDWEQIIEIFGKPRNIFKGINQNWTWVSENYKMKTSNEKYIKICYCFHFYYKNCKDTKNFLYIGLVHNHIWD
SKTTIMQNELDTNYEISNMIYFNKDSIKFVAINSFNDLNRNVCDNINYEKNIIMPFFSGYNKFHNTTINQKNILNILKTY
YHNEFIFILCYNTEYYKKKTNYLLTTKDMIELNDFTTYYNEEINTYNIIQSSFSYHSDIKDISTTNENIEKYEHMQLLLQ
NRGNTPNIFENYFYQKDVYKKNNMSIYNMNLYNMSPYVVYNNNKKKITNIQVKNRLKIILTKMYHMTSVDINEVIYYKGK
GELLTDLNLQNIFILPKQKKVILCCYNDDYIEVIINDDNKIGMKKSNKIQELIDILKKYHPNFERNKKKQNDILEQFNNI
NDILFKYDYIRDVNKNQIYYDTGFFRNNIYIQLINQPFDLKIYGSNIQKKKNKDYILYIIEFHNICYNNMNKNGFFLEHK
RYNEMENYIHFLQISMNKINNYKLCLYDKERDIYSNVGILNITDYFVIKESSFFDNEDIGNIKKKNMETDSYNYNNDNNY
DGNYDNNYDNNYDNNYDQNNNKYYIKNYNQDVIKNVCLIMDNNTNQIIVIKGKGSFYFNLQIEKGIFIEKKGQKLNELFP
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DIKNHEPISCKNKKKNTIILTKTHIFFYTNNNDISFSTKHNLPFPYDIDFDDQYIYVNDLYLNKIARIQILSNKDNKTPI
PIINNKQRSKRSIINHGHESQQNIQKTHQTYDHFTPLHKVEKKEILQNNNIVQLKENEFPITNLKNIEYSKNNIPNQKIS
SKDDIYKMSDFQAFINKYANLITTNSFRLYNYFEKKKYYGTLNYFIKRVWFNKVGPSREENYSTESKIEQNDKNNNNNNN
NNINNNYNYNYNDLHNNNHNIILNSNNYNNNNQSSRHQNFIYSYHVSLDGKKKQSENLLTHSLNNFIQFFQNKKNSILKK
EKEKRKNIPSYNIMYKNINHITNTLNKRKQQELTSSIIKKRTKRNVQEKRMSQSAYNELVLASIKKYTNKVEPAHFVNNK
LDYLNYITNLKSPLNISVQNNILYILDSIKNTFFSYNLINKEIKELEKYDFNDHPLILKNPLHFSIYNGIITEYTEHKNN
LAFVTQIDSNEIKVIDLNSSKKYKIIKAIKLRKGYKHNHINYVIGIKQKLLIITSQSQNIDHYKNIIYHYHFNSFDQYFS
ISFNYTFAKNYNANDNLYITPDIDKYSDNIIYFCFLNSNNKCTNIDELTKLSISHETGIITGKLNYFGTFSLKIFAKTYF
QYKINTYSNLYSYCGISQEYNKTKSTCESCPIGTFWNSEKLLCENCQKYIENTSTLKNGSKLKTDCLCSPGYEYSDKSSK
CEKCKPGYYKKSVGNFICIKGCPINEKSITYGAKSYGEMDCKCIEGYYRKEDKCVLCLSNYYCPGNELIKPCDKNKISKE
GVIHKNDCICKENYIKDNKNNNCVYCASIAKILGKPIYCSLCDPIYFHEDIYKNIFLLPNNIHNYGLINNIYNYDEDLSL
QGNIMKYAYFHKTTNIERNFTHYINIKNIYHTFNNNINNYDYLTNSKFAIEIDIPEPKKCIFCDSGYYIKKKKCISCTTK
YCEGFNHNPKACPKNSVVNKMKASSIFDCSCKRGYGILNERRNAYSNTITCQICPQNFFKHIISDDSCFPCPLYTYTLNQ
GATSILQCLPKKGYFIYMFKSINIDYLRYKFDINTENRIYNYFENNNKIFDEDVYNFFLNKQYSKFFYNTENKTNTNNNH
NNNNNNNHNHNNHNNNHNNHNNNNNNNKYTKDNHFDNQVGNINKHTNNLQIKITENIYNIQYLEHLGFIKKTSLFYIYMIL
LRNIEERYNFNMDKMLKITCHINLHLKKNPHFTITYKKNLQECIDSCKTNIYCTGIEFSRKRVEYTQIILKNNKKIILGY
FKCKQFYFQNIYDYSSYNLDSYLNEHIENQINIKSTLTYTNFIMRNKPDIIYTCSIDRDPKYLLYKNYKLVECVIGKFCP
GNNTPYMISCPINSTTIIPASEDVNKCLCLKGYSYVGVTSYRCSLCDRGSYKNSVGNNKCDNCPLTFSTTHRGSTNIKDC
SCTSGNYLTFDTLGNFIRTENMQHKNISDQYFVIPIKQESQPENEIKDDNKNINIYNANNINNHDIVYKTKMIKINLHKE
NDNHNDYMNNILKQTIGLCKPCTLENHYCEGGLESDITFNNKLIKGKFHTLPKKCPRGLGIPNIIKERNSINNCLCIHGK
VQRTTENKNVECFPCPPNTFKENEYDNSCSGACPPFSTTFVGSSYENQCFCKNNYYLVSTDDENDTNGNSINNNKNIYNN
NNIYNNNNNNNNNNNNNFNNKSDVKKKSCKICPIGAICNRGFNIYIYLKLLNDRSYNNINVIDHETPFPKYGYYAVYREK
TNPTKSWDTLDDSAILNYVYPYHKLLLFIQKNIQKGNYFFLEKGNKFFLNDDFVEKMNEKSKYEEENTNKFVTKSEIIHN
VNTNNLKGKHNTLNNNNNNNINKSSSFLNQNNYNNDIIQLSSYENNPFKNLSSTSEVSSNNNVISFIQNNDKTNNSTNDN
NIENLVDIFNKYVQEAKELQIQNRKFERIPDIHPCTIPNRCLGTLINLCSDGSTGYQCNNCSKNYDMSYFKSKCKKCQNL
FYEILHFILLKLLYYIIVIFICSLNGNILNKLHVSGILMRIWLNCSFTFIAYGFFIPNMNSFISKYWYLYKTAFSYHMKI
FAYYLRVQCLLNSLNINLSYNQMWYIQKYMNICTPIFDSIFITILLFAVIHIYKFFFYKKNIDIFEQLLCTIPELNTLYK
KNCIDNIHKVKNKKFANKVESFEENENQNKEKKNKKNIKRKNKAKNKHNNDNNDNNDDNDNNNDNNNDNNKININSKDEH
INHFEKCSSITTILNNLELNNEEKNKESKKKKIFDIKKKTSIENIKENETNHLWNDTHNNVKNKESNINTTNISNNINYE
LKYIKNKEWYNIFLNKTIQYIYKEKKIFGLWHFIFTKNDNWFKNMGTFLNDTLPCYVLIMILSIPYILLELVQLTYCTPI
KYKTQKTYFYLTYLITQKCSLSSKLFITGLIVTITMFALYIFLWILLLYLYSKRKRLNLFDLLTTNLLSGFRKGKGIFEL
IFLLKHILIVLLICFNIYYGFYYIVFLTLILITFAILEILSNPYDKRSFNILNKSLNIGNVLNIFFPLIIWGSFYWTYEN
FFIFPIFVIYAYHIYMFYHIVKEFTLSIHFIKTENIVNIQTIGYDPENIKNKNYKIYYKVMNKIKYFLNKNQKKNISNIN
ENKDKHLNKNNNSKDHVKFEPIENIIKRYNLKLNKGILKDANNNNNNNNIKNMSDQVEDNKKDILFIKKNVLPVNVHNVA
SIWYDEQNEDLLFQMPYQNKFCLNMNNEANENNDQINDLTKDKTSEEENNNDHVNDPTKDQTNDEKKKNKNKKNKNNNNN
ENNCHSNDNSNNNNNKEVHKNDDNINHNNINNHNKSSNISTTNKKNYFNKFSDYIIDKRNKKSIKYFITSLMEVIEKFLD
SSTHGFIYENWFDFTIRFAFVYISWIKKCNKKNNIMLPMNIQQLHIHMDLFIFTPIFPKNNSTCINEQNIQNYSKKKKIY
NKINMYDEKIETGELLEKHNSFENTEIKISRSFGSHNYMPNIKNRKNNYDKKEDITSINDINVDIIKQDDQKEDSNINHL
INEHNQKEPSQHIYNINDKNIMDYNIDENISKNNEKEKHIKIPPKNISITQKEYYNNNDIFNYSLDIFSSEMFNEKMFHS
IISLFELYMAIKTLKLMNPHIFNKLYQMYNKKIITFDTSVMFYINKLRDDIKSEIEQIDKEINTGDTTEKERIQNYYYYK
EELFKRKKLEEELLSKIKSLEECIEVNKRSQSLRNMLLTKKKKNNNLNNENLEEHINYIFSHLHNEGTYKLNHSQNMDKK
N
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1478 - 1497:	EEEEEEEEEEEEEEEEEEEE

A0A024X2T2 **A0A024X2T2_PLAFC** (383 aa)
Casein kinase II subunit beta (CK II beta). *Plasmodium falciparum (isolate Camp / Malaysia)*

```
MEFVSNDESADDIIQDESNEGEVELTDADFYDLTVINDKIDEEIIEDDEEEADNDDQENDNVQEVYNIDDEDNDIHNDKL
LLDQQRDNDVNEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEDDDDDDDDDDDDDDDDDDDDYDDDDEYDEDDFNEATVSWI
EWFCQLKQNLFLVEVDEDFIRDEFNLIGLQTKVPHFKKLLKIILDEDDDDDDDDDDDYDDEDDEINRDSEEMYKNKDMHE
QNAACLYGLIHSRFILTSKGLALMREKYKSGIYGTCPSIYCENAKLLPTAISEIPKFLSPLLYCPRCCETYYPSKNSLLN
QLDGCYFGTSFASFFALSFNIASDKKKVYYTPQICGFTINRNIRETLYMDVNKDNTESSEECQ
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92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE

A0A024X589 **A0A024X589_PLAFC** (779 aa)
Uncharacterized protein. *Plasmodium falciparum (isolate Camp / Malaysia)*

```
MIKIIIGVIGYYILYSSYHIYENIKSPIFNDGNVIKNNEGDKNEQLVIPKEGKKRNSINEEEEEYINKPFKNVLKKDDII
DYHLYFSCEEDIDINKHMQDKYLEKDERFISVYKILNGKYSWNNNVDLLDEKRKKNSFFFFFEKVHPSFDISIPKELIDQ
RKDIYLHILTYVNKELYRYGSRTVVITKRKEKTTTRGKKKFLWKSLIDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEKKYQHGNYEKGGSYKVHKNISNNKPNNKNPNDKRDIKHNNNNNNNKMKKDNFIKSNQNSLNIHKK
EKKRKHKDFLFYIPKKIRFGPVIEYNDFHISKLGFFSNMHVDKDTNTYLLPIYINNDLTPDDEYRMIKMKNSDDMMKKKL
KKKRSSEKNDPYYKENVRNDNNNNNNNNIKNNYLEIYDLSKRTYEMRNERNKKIYEKNSSINNNVHKLEHELMDYIINIEY
VPINYNYYNLLNMLKFNVSYVKKKYNFISFDMDSITTFLCCHITCSMIIYILCIIYIIMEITYLLFDIKMWKRWNNLYTF
TYNNDIVMNITLLFFILLYLRNIDYGRVIMIYYIMKMMVLIFKIIYNYDICILNDYPYICINKKSLKEMNKEMIMDEEFE
KKIKKKVNIFMIFSIILIFIYNYFYTKYDSYYSYVIHTLGFSSYLYKFILMLPQIITNIYTRTVQRMSFPFFLFLLVNVL
INDLFIIFLRMPKVHKYYLFADDFILFLFIIQYCIYKKENKIFGAREKLVLLKNAKKNK
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209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE

213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEEE
225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE

A0A024XE76 **A0A024XE76_PLAFC** (3068 aa)
Transmission-blocking target antigen S230. *Plasmodium falciparum (isolate Camp / Malaysia)*

```
MKKIITLKNLFLIILVYIFSEKKDLRCNVIKGNNIKDDEDKRFHLFYYSHNLFKTPETKEKKNKKECFYKNGGIYNLSKE
IRMRKDTSVKIKQRTCPFHKEGSSFEMGSKNITCFYPIVGKKERKTLDTIIIKKNVTNDHVVSSDMHSNVQEKNMILIRN
IDKENKNDIQNVEEKIQRDTYENKDYESDDKLIEWFDDNTNEENFLLTFLKRCLMKIFSSPKRKKTVVQKKHKSNFFINS
SLKYIYMYLTPSDSFNLVRRNRNLDEEDMSPRDNFVIDDEEEEEEEEEEEEEEEEEEEEEEEEYDDYVYEESGDETEEQ
LQEEHQEEVGAESSEESFNDEDEDSVEARDGDMIRVDEYYEDQDGDTYDSTIKNEDVDEEVDEKERQGEIYPFGDEEEKD
EGGESFTYEKSEVDKTDLFKFIEGGEGDDVYKVDGSKVLLDDDTISRVSKKHTARDGEYGEAVEDGENVIKIIRSVLQSG
ALPSVGVDELDKIDLSYETTESGDTAVSEDSYDKYASNNTNKEYVCDFTDQLKPTESSPKVKKCEVKVNEPLIKVKIICP
LKGSVEKLYDNIEYVPKKSPYVVLTKEETKLKEKLLSKLIYGLLISPTVNEKENNFKEGVIEFTLPPVVHKATVFYFICD
NSKTEDDNKKGNRGIVEVYVEPYGNKINGCAFLDEDEEEEKYGNQIEEDEHNEKIKMKTFFTQNIYKKNNIYPCYMKLYS
GDIGGILFPKNIKSTTCFEEMIPYNKEIKWNKENKSLGNLVNNSVVYNKEMNAKYFNVQYVHIPTSYKDTLNLFCSIILK
EEESNLISTSYLVYVSINEELNFSLFDFYESFVPIKKTIQVAQKNVNNKEHDYTCDFTDKLDKTVPSTANGKKLFICRKH
LKEFDTFTLKCNVNKTQYPNIEIFPKTLKDKKEVLKLDLDIQYQMFSKFFKFNTQNAKYLNLYPYYLIFPFNHIGKKELK
NNPTYKNHKDVKYFEQSSVLSPLSSADSLGKLLNFLDTQETVCLTEKIRYLNLSINELGSDNNTFSVTFQVPPYIDIKEP
FYFMFGCNNNKGEGNIGIVELLISKQEEKIKGCNFHESKLDYFNKNISSDTDECTLHAYENDIIGFNCLETTYPNEVEVE
VEDAEISLEPENCFNNVYKGLYSVDITTILKNAQTYNINNKKTPTFLKIPPYNLLEDVEISCKCTIKQVVKKIKVIITKN
DTVLLKREVQSESTLDDKIYKCEHENFINPRVNKTFDENVEYTCNIKIENFFNYIQIFCPAKDLGIYKNIQMYYDIVKPT
RVPQFKKFNNEELHKLIPNSEMLHKTKEMLILYNEEKVDLLHFYVFLPIYIKDIYEFNIVCDNSKTMWKNQLGGKVIYHI
TVSKREQKVKGCSFDNEHAHMFSYNKTNVKNCIIDAKPKDLIGFVCPSGTLKLTNCFKDAIVHTNLTNINGILYLKNNLA
NFTYKHQFNYMEIPALMDNDISFKCICVDLKKKKYNVKSPLGPKVLRALYKKLNIKFDKYVTGTDQNKYLMTYMDLHLSH
KRNYLKELFHDLGKKKPADTDANPESIIESLSINESNESGPFPTGDVDAEHLILEGYDTWESLYDEQLEEVIYNDIKSLE
LKDIEQYVLQVNLKAPKLMMSAQIHNNRHVCDFSKNNLIVPESLKKKEELGGNPVNIHCYALLKPLDTLYVKCPTSKDNY
EAAKVNISENDNEYELQVISLIEKRFHNFETLESKKPGNGDVVVHNGVVDTGPILDNSTFEKYFKNIKIKPDKFFEKVIN
ENDDTEEEKDLESILPGAIVSPMKVLKKKDPFTSYAAFVVPPIVPKDLHFKVECNNTEYKDENQYISGYNGIIHIDISNS
NRKINGCDFSTNNSSILTSSVELVNGETKNCEININNNEVFGIICDNETNLDPEKCFHEIYSKDNKTVKKFREVIPNIDI
FSLHNSNKKKVAYAKVPLDYINKLLFSCSCKTSHTNTIGTMKVTLNKDEKEEEDFKTAQGIKHNNVHLCNFFDNPELTFD
NNKIVLCKIDAELFSEVIIQLPIFGTKNVEEGVQNEEYKKFSLKPSLVFDDNNNDIKVIGKEKNEVSISLALKGVYGNRI
FTFDKNGKKGEGISFFIPPIKQDTDLKFIINETIDNSNIKQRGLIYIFVRKNVSENSFKLCDFTTGSTSLMELNSQVKEK
KCTVKIKKGDIFGLKCPKGFAIFPQACFSNVLLEYYKSDYEDSEHINYYIHKDKKYNLKPKDVIELMDENFRELQNIQQY
TGISNITDVLHFKNFNLGNLPLNFKNHYSTAYAKVPDTFNSIINFSCNCYNPEKHVYGTMQVESDNRNFDNIKKNENVIK
NFLLPNIEKYALLLDDEERQKKKKQQQEEEQQEQILKDQDDRLSRHDDYNKNHTYILYDSNEHICDYEKNESLISTLPND
TKKIQKSICKINAKALDVVTIKCPHTKNFTPKDYFPNSSLITNDKKIVITFDKKNFVTYIDPTKKTFSLKDIYIQSFYGV
SLDHLNQIKKIHEEWDDVHLFYPPHNVLHNVVLNNHIVNLSSALEGVLFMKSKVTGDETATKKNTTLPTDGVSSILIPPY
VKEDITFHLFCGKSTTKKPNKKNTSLALIHIHISSNRNIIHGCDFLYLENQTNDAISNNNNNSYSIFTHNKNTENNLICD
ISLIPKTVIGIKCPNKKLNPQTCFDEVYYVKQEDVPSKTITADKYNTFSKDKIGNILKNAISINNPDEKDNTYTYLILPE
KFEEELIDTKKVLACTCDNKYIIHMKIEKSTMDKIKIDEKKTIGKDICKYDVTTKVATCEIIDTIDSSVLKEHHTVHYSI
TLSRWDKLIIKYPTNEKTHFENFFVNPFNLKDKVLYNYNKPINIEHILPGAITTDIYDTRTKIKQYILRIPPYVHKDIHF
SLEFNNSLSLTKQNQNIIYGNVAKIFIHINQGYKEIHGCDFTGKYSHLFTYSKKPLPNDDDICNVTIGNNTFSGFACLSH
FELKPNNCFSSVYDYNEANKVKKLFDLSTKVELDHIKQNTSGYTLSYIIFNKESTKLKFSCTCSSNYSNYTIRITFDPNY
IIPEPQSRAIIKYVDLQDKNFAKYLRKL
```

280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE

284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE

A0A026VX20 **A0A026VX20_OOCBI** (2572 aa)
Uncharacterized protein. *Ooceraea biroi (Clonal raider ant) (Cerapachys biroi)*

```
MDARRKKETDVLDLDGEETQLFKQKIRQLAECDEIVSAEIINVVGEITKDVEMAEDNVPSSDEFDEDLEEEYRNLNVMLD
LPNDTYSLTEIKPELPTCVKYGVRSGLTHLNMPRFSPLSRGYQGSAIAIAAFATTTVHKSRGWNEAVIDQIIEDGDTFYC
ESYKDMNTGDRRTMTILDLKKNFLVQKKFNVTIKIDDPAYAGKFRSHDPTELHLAKALELFFERYDAGILTSPVLNIAIW
RDAKYYNIFDGQARQENGVSAADQVSGTAKLFLVRDLTEVLFIILEKSGVQNEPFVIHAIAVVCVEAVSPDDPEEAARTP
GRPQRRPSGYRIRRKHRAVVQGSYHLNHPALPKTLRNKGHLVIAIAALVYSRLIGANKWTTALLDLIFNHSNIYLIDLVR
VLGKKLDDAFELRLEDLMSDIILGVYSAKVKVDANVIPGHAQKRGKLDMDTGLCEFFETQEIGILEVKKIFYAVWKHGNV
YYFLDPFACDDEGFRIRYNDTEQTTIDSARYAACVTMNRTVKEVVETVLENTGTKDRDPFLIHGLKVLYVKTGMTLRGGP
FEKVIYREKGTNRRPRAPSPPMPIDTTIAKPIDTTPRARPESRRFADVSTQFPDIMQNAEEYMMTDDEPVTFLFAREQVK
REKRADEEEEEEYEDIKKEENEGEMEETLMDKDIDDEQMETDEKAQQKAPVNFITGYRMINAHRLLLRGTKNCLSEEYRA
RSRGRQGLIAALTTLAYRRLKDPTRWRNIDVDQIVDVSNKAYEQVITWIEQGRPEIKEAKAMEEELGEEEEEEEEEEEE
IEEEEEEEEEEEVVARKLAVAPSHLDVSHLPPRLKLAEYDALFRTKPNVINGEADPLANLAEALERYFERYPELLLENKR
LTYAIWREDGKFFLFNPYGSDSEGWRLRDHPASFAVTDGLNELVDLLHGVLEYNDSSFALHFVTLDAIQPGKYASPVEIV
IPDEQTIKIFRTKFLPITDDDLLKLEEKKPDIVVEKIEEPAEEIEEEEEEEEEEEEEEEEEEEEEEAEEEEEEEAKEKKFK
ELEKPLVDPLLEVEERMQPDAPHRLNLALLTSTVTIEEPTETELNGLHEEVVMEKMKYDHPPPYVMPPKRTLLILLKAKQ
ASKSIPSLVSRFSIDSRLEVKKRDGLVIDLPALAAIVSLPQDAKPSKMIKLSLRKYLYSRLPPIRIIPLRAIDESYIQDE
ETDKVLDEKCLERGKSEEKYATLAELPVLPCLHRTELIPVGPIIKTPVVVTKHLTCLDERKRKSVSKNEKKVLAFKKNLC
DAEKLLFKLIFPKFHLDLQLPEEKDDGGKINEKKMIISVKDSDKKIYPLSPEDVGFKVVDDNTEIIRGNWSLTDRSRVES
SHFKPCYFSAILCILAKIARDADRFHSNTLNQLILLSNKINQRIGKLRYKEYRTFYNVDILDTNYNIVLKEIVRADPETV
PSDQLDTVIKKFFERNQTGILVLTNCAYAFWTTDDKYYLFDPYPCDEKGNTNEEGYCCLMRFRELKPMLDRIKENAGETT
RKPFRLYIMSITHVEIKRRKRRQRKAVKRPTKIAEESVHSKEMQDVMTLPSAKSESSLIESVEWVTSDPELDPHRDVTSR
GFTPMRHYSASMLEIAVLENYITTPTLAPFKESLKPDHDRGKTTVERMETLDRTFRNYTSVAIPIDLCVMAWSLIHDPAS
WSERTFRGLFEASVDYALDSVLASEDTSVGDMTDALLPEFEIANYAFRAVFAPLHFGTLYATEGWNLAMTLCKIFETKIY
TGAIIVCHYAHVGVTKKGNNYFAWWTVTGTKNLRMITSRNMSEFLKLIVKEIDAPQKTGFVVRAITISYARKLAPDWSDI
EGLHEPMAPTTSLAKIHRKESETRDIEAIFKPIESTPKPIFIHGTVALRDRDSLLEPRAKRCYFVALLAVVVKRDIVQSP
LPAIIDKILEVAESLYREFSEPKFHVEHILRNVPLMNRFFDLRDCASSLVTLTTNPRTGRNDFLMKVKKCLKCHFKMYTS
GILHFTNCCYGFWYSRSTNCYYYLDPYQCDARGRKTLSDGNACLCIFSSVCQMVKHMCLNQHEGTTGFFLHRIHVDSIDT
PASEKFQEDPMWVYLDYHWNFTHSIVRARKKRKVSDRSASSQIDRFWHNYVVEVTGLIYSIWGTIGAYDCRFGDRAGKNR
TAICVAVLAIQNLCHPSRWSPAILDSAVICGDTYYTESLRSLARECSQPTNRFGLRSSLRLFPHVWTVDFGTSVCGVLYD
DRNRLTLTAALKLAFEEARNIIVECNNITLAVSAAKNAYYVADPCWIGPPLFVKDRGAIYTLCCRNVYALVYAITKMINT
NQRLGVRVTPVLFTFDREDSREEPEPCPATAKILSRSLRRDPGRIDDPGMRIPGATAVPDESSYPQYLQRLARAVTGTGS
QLEECQLSSRHTEPALNPENVNNTLVSAKWRLNLGQARPPKRPRPPLDLVWLKDDSTEFVDSATDLFEPRHSQVSITDLT
ACDYYPKPMDFASNIPAPGIEFLECASERSFIREQSRTEFDKRAAEMSQDPYKSHPHRPPVIVIQKADEATENAELSEAT
TTDATEFTDSEF
```

1005 - 1024:	EEEEEEEEEEEEEEEEEEEE
1006 - 1025:	EEEEEEEEEEEEEEEEEEEE

A0A026W0N7 **A0A026W0N7_OOCBI** (401 aa)
Troponin T. *Ooceraea biroi (Clonal raider ant) (Cerapachys biroi)*

```
MEFWGISRDLPESELNRPDLKRVTFVFAPAFFRESGENPEFMKRQEQKRSDLDEQLKEYIAEWRKQRVKEEEELKRLKEK
QAKRKVTRADEEKRLAQKKKEEEERRQREIEEKKQRDIEEKRRRLEESEKKRQAMMQAMKDQSKAAKGPNFTITKKDALS
GNLTSAQLERNKTKEQLEEEKKISLSIRIKPLEIDGLSIEKLRTKATELWEAIVKLETEKYDLEERQKRQDYDLKELKER
QKQQLRHKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGLTDQQKETMEKLWAEQKQQFMGRQKTKL
PKWFGERPGKKPGDPESPEGEEDVKAVADEDLEEPQFDEEEEEEGGEKEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEE
E
```

372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE
379 - 398:	EEEEEEEEEEEEEEEEEEEE
380 - 399:	EEEEEEEEEEEEEEEEEEEE
381 - 400:	EEEEEEEEEEEEEEEEEEEE
382 - 401:	EEEEEEEEEEEEEEEEEEEE

A0A026W5I1 **A0A026W5I1_OOCBI** (605 aa)
Dynein heavy chain-like protein. *Ooceraea biroi (Clonal raider ant) (Cerapachys biroi)*

```
MAEITEFGTRKTIFILAIVAGCFAVLWPKIFYPMLTASVTPHHPTSDSSVCCDVIFDSDVTAVDIMQEMCQNILRHHPID
PRVRDALKLSKLTPQSASLCREEVLARCGIDLSSFLAERERLGKTYKQVLEEIRSFNSSLCLKMNFGIPLSQLGTPHLIR
YHILMPHSTIQQERPTPPHAGGMHPAMRERGRAIPSSHIVPKITDRSDHIVPKMRPPLGGAGHVVPPPKGNGTMGIIMPL
YTIGIVLFFLYTIVKVLKKTSDSEIISEYPGAAAEKEFRKMVFSPEALTTAMTGGTMQYSREKSPQKTAAPTIEELKDLD
GAPQSNGLAGVDRGSKEDTGGQESHSREGEEIDVAEHSPTVKVMGMEMTASCESGQKCSRPTTPIIPTPSSNVEREKTPP
KPIYLEGALPPQCELLVTDSETQAEKSEDDDDAPVVLSGKMTLSLISLDQIPATSEEEIAVTMETNSLNDATEEKVVGLT
RILRRPSDDADSEKVERKTPVVSDSEEDYDEEAQEEDDEEKKEKTIYYNGKTKEDEKEEEEEDEEEVEEIEVEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEDKEEIEMEEEEEKEARRLQRPYK
```

553 - 572:	EEEEEEEEEEEEEEEEEEEE
554 - 573:	EEEEEEEEEEEEEEEEEEEE
555 - 574:	EEEEEEEEEEEEEEEEEEEE
556 - 575:	EEEEEEEEEEEEEEEEEEEE
557 - 576:	EEEEEEEEEEEEEEEEEEEE
558 - 577:	EEEEEEEEEEEEEEEEEEEE
559 - 578:	EEEEEEEEEEEEEEEEEEEE
560 - 579:	EEEEEEEEEEEEEEEEEEEE
561 - 580:	EEEEEEEEEEEEEEEEEEEE
562 - 581:	EEEEEEEEEEEEEEEEEEEE
563 - 582:	EEEEEEEEEEEEEEEEEEEE

A0A026W6K6 **A0A026W6K6_OOCBI** (3892 aa)
Remodeling and spacing factor. *Ooceraea biroi (Clonal raider ant) (Cerapachys biroi)*

```
MASDNEASCASDPNFAVICSFLGCFGKSCGIIYPDMARLQEMLENTQEVSQELINLHIKLLRKTRKTVSPEKWERALVKF
CHTYSNQDGWELERFGYKKARIAVKLRLLKILLETQFDLNQKFKNEVNKLAADELRVEPLGRDKSGLAYWCQLDEECNIR
VYREDLDEENWELVAKDREGVANLINTLSNGEAGAIPINEDSNSLEISEKPIIDTGQVTTSPSLEDEENGVQENGVHTDE
MKEEEEEEQEEEEEEEEEEEEEEEEEEEEEEEEEDITNDESSKQITEEDDSQEMVQTPSTESRYTNASSLLPATHTKTL
KVDAIPEDTCHKEAGNETSASLTSETKSPVTHNALAITGVAKTEESMPLKSIETPVITSSPLKLVNIAELKQPEEKSVSA
VTPIDVPLNAAKKHGASDETADPSAKPLPDKLPGKNTLSFSSADSTPIGHSKLSVKPIDQLAANLVRIQSEKLEKPTAPK
SLEKIAESLARSSGMLGSMVNGSEDDRLPQDFCARNQSEKSATLRGHRGIDLSTSPRSWESANEQDRPMDFSGIDLSSRK
LGKTVDLPSPGYRAQPDFQHREMDLSTKKVSKPEVPNLPYDARSVMMRNHAMVADLSKRQMPFTAYEMSSTPYHNAARLP
AKDEHRLPSYTVLPDPSKITALRINTASLKRPLEGDDAQQDMLKRIRADVIPIRGSMDKRPMMGGGNWREEVGEAIEEPM
MMVQGEGSGSDCDAVNPGVGEAVEEPTIFFHGEGSGAECETGNPGDDTSTDNKESNESKTEPDSATATLPQNKVLSEDET
VSASTVLSNKPPVKLNRNYPQSNVSVNDNCQIVDSIQEKPKFKPTLGVQIIPESTTGPVKKLSRWDVGKPEEKVDCDNSI
ISNEEDISLKRTTDDDNEREDTKQTPLITDALTTKLGYEDTVGENQDIKIEESSVNAESATNEGSAKSQVSDVSLERTNT
MEEERCSKLQEPMQCVSSVSTCQADTSQIPESCTMNPEPTVPITDMQSAKSDSDSVVSRESNVSGAVDDECKPAAASPPR
FFFGPNCVAYTSKCDELESQSEHDLATSASDKTVDTVQYECVSSSKPADGTIYPCQTGDFDLAQTNNNSLKASPFASESD
SALRGNGSEDAEKIEEPNKDTQWNQRALTVDSSRETNDTAEDNVTNSSIAQIEMDTKETVCTEKEMKEDVSLEVDTSSTS
ETATENENVNDESVTEEEPIKISSISESSVVQPEESGSVEPPQCDRSDLEKPVNTVNQESFSPERIGAITSHVLDDKKNE
DEISLADDCKNDCQVASNSDMFEDDQERKESVTHSTSSSFVQNVQVEHRTGLEEFGDRDDDSSKLLDSTDAVECASYHRE
TSTPPKNDLDSAGESCDKQSDKNDNFSEIDGQEDHSTDTDNEKMKGLTGSDADSVCVNYDKNSERTDALSDMGMQDDGSG
DSEEIKEKGLNDAQINDAVFDIDSSTHLAESSVVTSSETAQDGDNLVPTVSSSENICVQYSSSRESEPEQMDDEKTENRS
SSADNLSTSDILPAVVPEMNTFEPSESPIVEATRETNSSNLVQSTSEYADDVSENPSSCVDQDSNEEMVIDDRVSESNES
SKETEEATCEQEQQPEENANQVTTKFAEERKEEVEEAPAVTATEQESLMNYESESNDDDGSDDVFEPDLTQVSDSKDDDV
AIQEREMDKSMHENSAKEENLVKEAEVNITDLTCDVPHEQPPAQHEVDECPETKINEASNEKSTVVEQEDVKITAQEYTD
ETQIKPTCNNIECLSNEPTMPLNTDRFQEETSDIRDIFINDQSEASEVSDATTPLADPVAEGTMESLLSKNSEIITGDNE
KGEEHPNNLIDNTKTAEETENVKMRTEKTECLISKSVGDRLNEDDASNREKSSFARDNLELNAIGGQATDAEDTFSAREQ
HTDEKLNVSFDAEDTARQRDTSEHASEELPVPCKRLKEDLAEYDSKDTKWNVKSQLHEESLTKLPWKEEFMDVNIPIHQA
VCPPESNVMPSKLDSVLTEDKSQCKTESASLETVPSDTLYYANSVYTKIENVNNLDSSNDQNESLNTNVNISKITDNSSK
SSPLNTSDESAFLVQETISEIGTIKSDAKKEASKRLIDASDVEDIPPLKSKPQSPYVETVETLEKKTPEDTASTDVQATK
SLDTFHEIENFKSQLKDETKTAVICTTQLFQNDFDMVNDTASTAATSVEDSTKKESLEIQSVEMKPEAVLSDDSSGADNE
SGLNLDPAEDADPLACGNDDPLKIADIAENDASKISIRVKSVSEMVYEGWKLDSTTEAPKISRKRRNSAHESNSEDGIAK
EDEEMMGGKRMKLRAKRMPDKELRKSVEENREMAVSSEDEATKCGSDNVTEHPNKDGSDDPSIMQSMVIDKKIRGRPRGR
RRRGFRGGGRPNRPKLTDLQRDQISEVSSGVHPDGAPNDSGTTSMTQKTRKKRKMVLGLEIGRDISLEAQSAPKQDETPV
RQSRRIAQLKIKEQADRRRIEEETMRELEEKKESEKKKRKKQKPESEDEIILYPKEIEKENKSKKKRRKRKKKKMLAKFN
EANPWQSSSGSSSDEENENEDEEEEEEEIESEGSLLFKSDHEFSPESDLEKDQESEPLRRARTAQKAQSDVEEAEDEYAC
QKCGKADHPEWILLCDSCDKGWHCSCLRPALMLIPEGDWFCPPCQHNLLVIKLGETLKTFDQVSKRHENEVLRKKRLAFV
GISLDNVLHKGEPQRGSRGSKASSQESNNDSSDSSSSASSSETSSSEESEPVYQLRERRCANTYKFNEYDDMINAAIQDE
VEAVQGAGNQGRGKDIATIVNAEKEEAQAEALKMTQLEEDKDDVESKPEKESDDEYKIENDDMDNEEMEEEQSTARKLLA
RKKHRKLNSLDISSEDDPESDEDFKGTSSEEDDFDDHHISSSDDSSLADVKRRRRKSDLRPVRRSTRARMTRAYDEDFIN
DDSEESDRPKRKKSRSLWGDSDSEDSDNSWRQRKKKSRTIPASRVRTIPKPKGKKKKKRKRIIESDNQSENDEEYELKID
GHQLQDVHNQFTELLNVDKQENLENNAGENNVEIKDEGGLQEVASAEMTIQQSQEGVMPIQKIKKDIVPKPKKAIRRKII
YGGLPDENRQKEDEILSRRTRGRKINYREEMASDSEEELKKALMMRKTGESEDEFVVNEADDMNDEGDKDSDSGDVYIPK
KNALKFKNKSPKAKKPRNSKSPAAKRKSLSDDVPKQRKKPGPKPGSKNRARKQKLKDDGDGDMIGAVMDNPIGDITTKID
ENLTDNVGLTGTTMSVASSFTGDVPEGSLTGLGAAELADLDDEQLEQMMMDEEYGRRQLELAAIEIAKKKKKEEREAKKL
EKARLKALEILAAERQRDPNAPEGTDSEAPKKKKRGRRSKAEIIAEQMRRDGAPNLGIAPAAVGGVVGIGGSGVGGIGTP
TNGAGNMHNMNSAALSAGLTPEIERNVEGGHMSLMTGPDAQLFNPDGMPVRPKRRGRGKGKKTLALEAARAAEAAKVVVD
VNLIAGMGTDSNPELKQNDIPNVLPTPGSSTSGSAPSTPPASAVPTPGPPSTQPSNVQPVYPSLPPGGQQSSVITRMLQS
QPVSSSPQSFTAAAAAMGHKYFGGPNTGGQIMGGPRTGYEMQPRARIPSPYRQAGQSSMPPHFAAVRSGTPPMRMRVPGP
QMYHTPHHPMDPSPSGGGPISINNRDRSSPLTPGGPAMIPPSAGSPLAKGGPTPPPPPPYVRGGPPMARFTENPMGPRHQ
MPPFTNASPVNHNMQQPSPPPNRPPGNFSPYHPPPPPNYHYGAYPPPPPMTTADDAAAYQGSPYPSEHFSSPADSQPPIQ
APPPPQAPPPPPQQQQQQQQQQSHPGDEEGTGEFGGLVSYFSSQREDDLDS
```

250 - 269:	EEEEEEEEEEEEEEEEEEEE
251 - 270:	EEEEEEEEEEEEEEEEEEEE
252 - 271:	EEEEEEEEEEEEEEEEEEEE
253 - 272:	EEEEEEEEEEEEEEEEEEEE
254 - 273:	EEEEEEEEEEEEEEEEEEEE
255 - 274:	EEEEEEEEEEEEEEEEEEEE
256 - 275:	EEEEEEEEEEEEEEEEEEEE

A0A034VQR2 **A0A034VQR2_BACDO** (224 aa)
Troponin T, skeletal muscle. *Bactrocera dorsalis (Oriental fruit fly) (Dacus dorsalis)*

```
MERNKTKEQLEEEKKISLSFRIKPLAIEGFNESKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRH
KALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWEEIGKEVNEKIWNEKKDQYSGRQKSKLPKWFGER
PGKKAGEPETPEGEEDAKADEDIVEDEEEVEEEVVEEEDEEAEEEEEEEEEEEEEEEEEEEEE
```

203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE

A0A034VQR8 **A0A034VQR8_BACDO** (384 aa)
Troponin T, skeletal muscle. *Bactrocera dorsalis (Oriental fruit fly) (Dacus dorsalis)*

```
MSDEEEYTSEEEEEVVEETKEKKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYINEWRKQRAKEEDELKKLKEKQAKR
KISRAEEEQKMAQRKKEEEERRVREVEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKEAGLGLSSAA
MERNKTKEQLEEEKKISLSFRIKPLAIEGFNESKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRH
KALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWEEIGKEVNEKIWNEKKDQYSGRQKSKLPKWFGER
PGKKAGEPETPEGEEDAKADEDIVEDEEEVEEEVVEEEDEEAEEEEEEEEEEEEEEEEEEEEE
```

363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE

A0A034VT59 **A0A034VT59_BACDO** (362 aa)
Troponin T, skeletal muscle. *Bactrocera dorsalis (Oriental fruit fly) (Dacus dorsalis)*

```
MSDEEEYTGEGDPEFIKRQDQKRSDLDEQLKEYINEWRKQRAKEEDELKKLKEKQAKRKISRAEEEQKMAQRKKEEEERR
VREVEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKEAGLGLSSAAMERNKTKEQLEEEKKISLSFRI
KPLAIEGFNESKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQV
ASKYERRVDTRSYDDKKKLFEGGYNTLFKEALEKRWQERQERFTSRTKSKLPKWFGERPGKKAGEPETPEGEEDAKADED
IVEDEEEVEEEVVEEEDEEAEEEEEEEEEEEEEEEEEEEEE
```

341 - 360:	EEEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEEE

A0A034VT65 **A0A034VT65_BACDO** (224 aa)
Troponin T, skeletal muscle. *Bactrocera dorsalis (Oriental fruit fly) (Dacus dorsalis)*

```
MERNKTKEQLEEEKKISLSFRIKPLAIEGFNESKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRH
KALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYNTLFKEALEKRWQERQERFTSRTKSKLPKWFGER
PGKKAGEPETPEGEEDAKADEDIVEDEEEVEEEVVEEEDEEAEEEEEEEEEEEEEEEEEEEEE
```

203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE

A0A034VU76 **A0A034VU76_BACDO** (384 aa)
Troponin T, skeletal muscle. *Bactrocera dorsalis (Oriental fruit fly) (Dacus dorsalis)*

```
MSDEEEYTSEEEEEVVEETKEKKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYINEWRKQRAKEEDELKKLKEKQAKR
KISRAEEEQKMAQRKKEEEERRVREVEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKEAGLGLSSAA
MERNKTKEQLEEEKKISLSFRIKPLAIEGFNESKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRH
KALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYNTLFKEALEKRWQERQERFTSRTKSKLPKWFGER
PGKKAGEPETPEGEEDAKADEDIVEDEEEVEEEVVEEEDEEAEEEEEEEEEEEEEEEEEEEEE
```

363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE

A0A034VVU1 **A0A034VVU1_BACDO** (362 aa)
Troponin T, skeletal muscle. *Bactrocera dorsalis (Oriental fruit fly) (Dacus dorsalis)*

```
MSDEEEYTGEGDPEFIKRQDQKRSDLDEQLKEYINEWRKQRAKEEDELKKLKEKQAKRKISRAEEEQKMAQRKKEEEERR
VREVEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKEAGLGLSSAAMERNKTKEQLEEEKKISLSFRI
KPLAIEGFNESKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQV
ASKYERRVDTRSYDDKKKLFEGGWEEIGKEVNEKIWNEKKDQYSGRQKSKLPKWFGERPGKKAGEPETPEGEEDAKADED
IVEDEEEVEEEVVEEEDEEAEEEEEEEEEEEEEEEEEEEEE
```

341 - 360:	EEEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEEE

A0A044TLI4 **A0A044TLI4_ONCVO** (179 aa)
Uncharacterized protein. *Onchocerca volvulus*

```
MNISSTLCETSSQHGHLEQKEEEEEEEEEEEEEEEEEEEEEEEEQEGWGHWILLLARFSATCNCNCNTTCYTNIFRSMSYK
SIKHMSPNDRHASCMPQGLFPHCYLFAYLQSSNLHLTTFHNFISSSSPTTNRHLFLLQLIPSLTLTLFYSVYHFLNSGKT
IPKIASIYKFLPYSVHMQT
```

21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE

A0A059BNF1 **A0A059BNF1_EUCGR** (1315 aa)
NB-ARC domain-containing protein. *Eucalyptus grandis (Flooded gum)*

```
MLDAWTDDAIVDGRSDTFGLVGEYMSTLKRKLEELSNRVADLDEQWRSKSKRIKAWSMDRAFREGKSFFAQQVGRVDNLS
KEVEEILGHCSFQKGLATHAAGCRKSSPLVTTELVGEKGEETIEEICDYLMEEEMVILGIYGMGGVGKTAILMHVHNRVL
ENPAFNDVFWVTIPREFSICELQDEIANAVGLDTLSKDRDAKRRASILNRHLKKKRAVLILDGLWMHFNYEDVGIPVEKG
GIKLALTTRSLDVCHKMLCQKQIEIRPLHRQDDYWDLFLKNLCFGRDLPLEVKKVASSILDKCGGLPLGIIEIATYMRGV
EEVREWEDLLQKLEKSMIELNVLKKLKLSYMNLGNLQVQQCFLHLILCFGEYKAEIIEKVLIESFIDEGLLSGIATRHEL
HDKGNIILDKIKKACLGVDIDGEYLLVHPLIRDMVLQIVTSTTHMVKANMRLKEIPDEEFWTNHLEKVFLQGNDIKEIPD
CISPNCPKLTRLSLNDNMALEAIHKSFFKHLKGLKVLDLSQTEIMELPDTISHLVSLEALLLRGCKELRHIPSIRKLGSL
RKLDLNGCAMLEEVPEGMEMLAKLSYLDLHGTKIEMLSEGMLGKLVNLQYLVIEKLMAEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEIKLTKVEGFYCFVSNVETFNAYVRFLEQDNSLPYKLWLNGSQYNSFRDKHERYIIIKSCHSIAARVDGEI
GGDGHALLPKNVQALKVGQCNAVTSLCEVGPLENLEELTLEEWKKLEELGAVHFPRLRRLNIIWCTELKHFLKEGHELRC
LQWFKIEGSEELEGINIAAPFLYNIEVYRCPKMKWVEIIGGLPPIGATCRLTNIEIEGCNNLKRVLMTHDMFLHIPLLRE
VFVKDCMGVEAIIGTIPSMTQPSILNLIHLNLQNLPELKSICEATVSYLSIRCMNITECPKLKRLPLLGCGPRTSDIINI
DGLTWQSLEWDQSPFQPSLLHLARHYGVSNWHDQRICECIESCDAITARVDGQIGGDGCNLLPRNVQVLEVGGGSRVTSL
SEVGPLENLEELTINQWEQLEELGAIYFPQLQELNIKWCSKLKRLSVEGRGLPHLHWFTIRGSEELEGINLAAPNLNFME
VRCCPKMKRVVEWDWLTTHLPNLKSISIIYCKKLEKIIGGPLPISATFHLTKIEIIACNNMKGVLLTHDMLLHIPFLEYI
TVERCEGIEVIIGTAPNMMQPSFPKLISLNLWGLPELKRMCDRLESCDHIQYIEILNCLKLKRIPLRMRALDNGLLSPPP
SLEQILIDVKTWQALEWDHPLARVSLEPFIEFGDC
```

619 - 638:	EEEEEEEEEEEEEEEEEEEE
620 - 639:	EEEEEEEEEEEEEEEEEEEE
621 - 640:	EEEEEEEEEEEEEEEEEEEE
622 - 641:	EEEEEEEEEEEEEEEEEEEE
623 - 642:	EEEEEEEEEEEEEEEEEEEE
624 - 643:	EEEEEEEEEEEEEEEEEEEE
625 - 644:	EEEEEEEEEEEEEEEEEEEE
626 - 645:	EEEEEEEEEEEEEEEEEEEE
627 - 646:	EEEEEEEEEEEEEEEEEEEE
628 - 647:	EEEEEEEEEEEEEEEEEEEE
629 - 648:	EEEEEEEEEEEEEEEEEEEE
630 - 649:	EEEEEEEEEEEEEEEEEEEE
631 - 650:	EEEEEEEEEEEEEEEEEEEE

A0A059CKQ1 **A0A059CKQ1_EUCGR** (592 aa)
PBPe domain-containing protein (Fragment). *Eucalyptus grandis (Flooded gum)*

```
DPSSRTILRVKFTGLSGEIQLKNGQLQQPLAFEIVNVFGRVKRIGFWTQFNGITTGLNRSTVAVQSPSVREMGSIGWPGS
SLAIPKFQRIIPKADKRLRIGVPIKVGFKELVGMELDPVTNATMVTGFCIDVFKAAIDMLPYEVKFDFIPFTNSNILMAA
SYYDDLIYQVYRQQYDAAVGDITIIANRSLYVDFTIPFTETGVAMIVPIETSRSTNMWIFIQPLTVELWLVIGTFFVFTG
CVLWTIEHNDNDEFKGPLAQQIGIAIWYSFSTLVFAQREKLITNLSKVVVIVWLFVVLILTSSYTAKLSSMLTVHQLQSM
PKDESIGFPFNSPADQTFLINLPFRKHSFYPLKKAEDYANALRDGSQKGGVLAIIDEIPYVKLFLSKYSAQYTMVEPSHY
STKGFGFAFPKGSPLVPDISAAIAKMRGEGTLYLISQNWFQNHSLYANQDSETKVARLDLYSFRGLFLITGITSSVAAIA
SCKYMKKESTTSHQQHEVADKPVEEKFSPGWFLPSKNLRDQSKMKFPCILYHKERKKEEEEEEEEEEEEEEEEEEEEEE
ESLQVQSSGVKAVTISEMANQLEQSKVCQSYI
```

538 - 557:	EEEEEEEEEEEEEEEEEEEE
539 - 558:	EEEEEEEEEEEEEEEEEEEE
540 - 559:	EEEEEEEEEEEEEEEEEEEE
541 - 560:	EEEEEEEEEEEEEEEEEEEE
542 - 561:	EEEEEEEEEEEEEEEEEEEE

A0A059WCM8 **A0A059WCM8_PLAFA** (181 aa)
Pfs230 (Fragment). *Plasmodium falciparum*

```
RDNFVIDDEEEEEEEEEEEEEEEEEEEEEEEEEEYDDYVYEESGDETEEQLQEEHQEEVGAESSEESFNDEDEDSVEARDG
DMIRVDEYYEDQDGDTYDSTIKNEDVDEEVGEEVGEEVGEEVGEEVGEEVDEEVGEEVGEEEGEEVGEEEGE
EEGEEVGEEEGEYVDEKERQG
```

9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE

A0A059WCN2 **A0A059WCN2_PLAFA** (190 aa)
Pfs230 (Fragment). *Plasmodium falciparum*

```
RDNFVIDDEEEEEEEEEEEEEEEEEEEEEEEEEEYDDYVYEESGDETEEQLQEEHQEEVGAESSEESFNDEDEDSVEARD
GDMIRVDEYYEDQDGDTYDSTIKNEDVDEDADEEVGEEVGEEVGEEVGEEVGEEVGEEVGEEVGEEVGEEEGEEVG
EGVGEEVGEEEGEEVGEEEGEYVDEKERQG
```

9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE

A0A059WHM4 **A0A059WHM4_PLAFA** (170 aa)
Pfs230 (Fragment). *Plasmodium falciparum*

```
RDNFVIDDEEEEEEEEEEEEEEEEEEEEEEEEEEYDDYVYEESGDETEEQLQEEHQEEVGAESSEESFNDEDEDSVEARD
GDMIRVDEYYEDQDGDTYDSTIKNEDVDEEVGEEVGEEVGEEVGEEVGEEEGEEVGEGVGEEVREEEGEEVGEEEG
EYVDEKERQG
```

9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE

A0A059WHM8 **A0A059WHM8_PLAFA** (182 aa)
Pfs230 (Fragment). *Plasmodium falciparum*

```
RDNFVIDDEEEEEEEEEEEEEEEEEEEEEEEEEEYDDYVYEESGDETEEQLQEEHQEEVGAESSEESFNDEDEDSVEARD
GDMIRVDEYYEDQDGDTYDSSLKNEDVDEHADAEVGEEVGEEVGAEVGEEVGEEVGEEVGEEEGEEVGEGVGEELR
EDEGEEVGEEEGEYVDEKERQG
```

9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE

A0A059WIK5 **A0A059WIK5_PLAFA** (179 aa)
Pfs230 (Fragment). *Plasmodium falciparum*

```
RDNFVIDDEEEEEEEEEEEEEEEEEEEEEEEEEYDDYVYEESGDETEEQLQEEHQEEVGAESSEESFNDEDEDSVEARDGDM
IRVDEYYEDQDGDTYDSTIKNEDVDEEVGEEVGEEVGEEVGEEVGEEVGEEVDEEVGEEVGEEEGEEVGEEEGEEE
GEEVGEEEGEYVDEKERQG
```

9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE

A0A059WIL0 **A0A059WIL0_PLAFA** (189 aa)
Pfs230 (Fragment). *Plasmodium falciparum*

```
RDNFVIDDEEEEEEEEEEEEEEEEEEEEEEEEEYDDYVYEESGDETEEQLQEEHQEEVGAESSEESFNDEDEDSVEARDG
DMIRVDEYYEDQDGDTYDSTIKNEDVDEDADEEVGEELGEEVGEEVGEEVGEEVGEEVGEEVGEEEGEDVGE
GVGEEVGQEEGEEVGEEEGEYVDEKERQG
```

9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE

A0A059WNB1 **A0A059WNB1_PLAFA** (178 aa)
Pfs230 (Fragment). *Plasmodium falciparum*

```
RDNFVIDDEEEEEEEEEEEEEEEEEEEEEEEEEEEYDDYVYEESGDETEEQLQEEHQEEVGAESSEESFNDEDEDSVEARD
GDMIRVDEYYEDQDGDTYDSTIKNEDADEDADEEVGEEVGEEVGEEVGEEVDEEVGEEVGDEEGEGVGEELGEEEG
EEVGEEEGEYVDEKERQG
```

9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE

A0A059WNB7 **A0A059WNB7_PLAFA** (186 aa)
Pfs230 (Fragment). *Plasmodium falciparum*

```
RDNFVIDDEEEEEEEEEEEEEEEEEEEEEEEEEEEYDDYVYEESGDETEEQLQEEHQEEVGAESSEESFNDEDEDSVEARD
GDMIRVDEYYEDQDGDTYDSTIKNEDVDEDADEEVGEEVGEEVGEEVGEEVGEEVGEEVGEEEGEEVGEGVG
EEVGEEEGEEVGEEEGEYVDEKERQG
```

9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE

A0A059WNF8 **A0A059WNF8_PLAFA** (177 aa)
Pfs230 (Fragment). *Plasmodium falciparum*

```
RDNFVIDDEEEEEEEEEEEEEEEEEEEEEEEEEYDDYVYEESGDETEEQLQEEHQEEVGAESSEESFNDEDEDSVEARDG
DMIRVDEYYEDQDGDTYDSTIKNEDVDEDADEEVGEEVGEEVGEEVGEEVGEEVGEEEGEEVGEGVGEEVGEEEGE
EVGEEEGEYVDEKERQG
```

9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE

11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE

A0A059WNG3 **A0A059WNG3_PLAFA** (185 aa)
Pfs230 (Fragment). *Plasmodium falciparum*

```
RDNFVIDDEEEEEEEEEEEEEEEEEEEEEEEEEEEYDDYVYEESGDETEEQLQEEHQEEVGAESSEESFNDEDEDSVEARDG
DMIRVDEYYEDQDGDTYDSTIKNEDVDEDADEEVGEDADEEVGEEVGEEVGEEVGEEVGEEVGEEEGEEVGEGVGE
EVGEEEGEEVGEEEGEYVDEKERQG
```

9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE

A0A060CY72 **A0A060CY72_9GAMA** (443 aa)
Putative immediate early protein. *Bovine gammaherpesvirus 6*

```
MPILTRRNCPGGAKCRKKHAGLGSSSRSRSRSKSRSRSRSRSRAGSRGGSRGRGSRGGSRGRGSRGGSRGRGSRGGSRGR
GSRGGSRGRGSRGGSRGGSRGRGRPSALGRRRSHGPSRGDMYDEPPSKKPRYGDPENMSLLGGGWPSPQPSPQPSPQPSP
QPSPQPSPQPSPQPSPQPSPQPSPQPSPQPSPQPSPQPSPQPSPQPFEEEEEKEEEKEEEKEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDGVQSENGPPSDPGEGPSTGPHRPSVRSRPTRKHRGP
KHHPEAEKLKNKYGLRNVCPWGPDKTKATCSLTFSSLSKDCLYKAQCAIKTLCPGVPCTTISYPCGPGPRNCCVFTLYGT
EESDMKRIQEAVVASNVTNVRAGCIWVSFSLLCPPLPLQAPME
```

222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEEE
225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE
239 - 258:	EEEEEEEEEEEEEEEEEEEE
240 - 259:	EEEEEEEEEEEEEEEEEEEE
241 - 260:	EEEEEEEEEEEEEEEEEEEE
242 - 261:	EEEEEEEEEEEEEEEEEEEE
243 - 262:	EEEEEEEEEEEEEEEEEEEE
244 - 263:	EEEEEEEEEEEEEEEEEEEE
245 - 264:	EEEEEEEEEEEEEEEEEEEE
246 - 265:	EEEEEEEEEEEEEEEEEEEE
247 - 266:	EEEEEEEEEEEEEEEEEEEE
248 - 267:	EEEEEEEEEEEEEEEEEEEE
249 - 268:	EEEEEEEEEEEEEEEEEEEE
250 - 269:	EEEEEEEEEEEEEEEEEEEE

251 - 270:	EEEEEEEEEEEEEEEEEEEE
252 - 271:	EEEEEEEEEEEEEEEEEEEE
253 - 272:	EEEEEEEEEEEEEEEEEEEE
254 - 273:	EEEEEEEEEEEEEEEEEEEE
255 - 274:	EEEEEEEEEEEEEEEEEEEE
256 - 275:	EEEEEEEEEEEEEEEEEEEE
257 - 276:	EEEEEEEEEEEEEEEEEEEE
258 - 277:	EEEEEEEEEEEEEEEEEEEE
259 - 278:	EEEEEEEEEEEEEEEEEEEE
260 - 279:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE
262 - 281:	EEEEEEEEEEEEEEEEEEEE
263 - 282:	EEEEEEEEEEEEEEEEEEEE
264 - 283:	EEEEEEEEEEEEEEEEEEEE

A0A060RN34 **A0A060RN34_PLARE** (3075 aa)
Transmission-blocking target antigen s230. *Plasmodium reichenowi*

```
MKKIITLKNLFLIILVYIFIEKKDLRCNVIKGNNIKDDEDKRLHLFYYSHNLFKTPERKEKKNKKEYVSKNGDIYNLSKE
ITMRKDTSVKIKQRTCPFHKEGSSFEMGSKNITCFYPIVGKKERKTLDTIIIKKNVTNDHFVSSNMHSNVQEKNMILIRN
IDKENKNDIQNVEEKIQRDTYENEDYESDDKLIEWFDDNTNEENFLLTFLKRCLMKIFPSPKKKKTVVQKKHKSNFFINS
SLKYIYMYLTPSDSFNLVRRNRNLDEEDMSPRDNFVIDDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEYDDYVYEESR
DETEEPLQEEQHEEVAAESSEESFNDEEEDYVETQDGDMIRVDEYYEDQDSDTYDSTIKNEDADEEVGEEEGEYVDTYED
EKESQSEIYRVGDEEEKDEGGESVTYEKSDIDKTDLFKFIEGGEGDDVYKVDSSKLLLDDDTISRVSKKHAVRDGEEGED
VEEGEDEESVIKIIRSVLQSGALPSVGVDEVDKIDLSYETTESGDTAVSEDSYDKYASNNTNKEYVCDFTDQLKPTESSP
KVKKCELKVNEPLIKVKIICPLKGSVEKLYDNIEYAPKKSPYVVLTKEETKLKENLLSKLIYGLLISPTVNEKENNFKEG
VIEFTLPPVVQKTTVFYFICDNSKTEDDSKKGNRGIVEVHVEPYGNKINGCAFLDEDEEEEEKYGDQVVEDEHNEKIKMK
TFFTQNIYKKNIIYPCYMKLYSGDVGGIMFPKNIKSTTCFEEMIPYNKEIKWNKEKKSLTNLVNNSVIYNKEMNAKYFNV
QYVHIPTSYKDTLNLFCTIILKDEESNLNSNSYLVYVSINEELNFSLLDFYESFVPIKKTIQVAQKNGNNKEHDYTCDFT
DKLDKTIPSTVDGKKLFICRKHLKEFDTFTLKCNVNKIQYPNMEIFPKTLKDKKEVLKLDLDIQYNMFSKFYKFNTENSK
YLNLYPYYLIFPFNHIGKKELKNNPTYKNHKDVKYFEQSSILSPLSSSDSLGKLLNFLDTQETVCLTEKIRYLNLTINEL
ESDNNTFSVTFQVPPYIDIKEPFYFMFGCNNNKGEGNIGIVELLISKQEEKIKGCNFHKSKLDYFSKNISSDTDECTLHA
YENDIIGFNCLETTHSNEAESDDGTEISLQPENCFNNVYKGLNSVDITTILKNAQTYNINNKKTPTFLKIPQYNLLEDVE
ISCKCTIDHVVKKIKVIITKSDTVLLKREVQSESTLDDKIYKCEHENFINPRVNKTFDQNVEYTCNIKIENFFNYIQIFC
PAKDLGIYKNIQMYYDTIKPTRVPQFKKFNNEELHKLIPNSEMLHKTKEMLILYNEEKVDLLHFYVFLPIYIKDIYEFNI
VCDNSKSTWKNQLGGKVIYHITVSRREQKVKGCSFNDEHAHMFSDNKTNVKNCIIDAKPKDIIGFVCPSGTLKLTNCFKD
AIIHSNLTNINHILYLKNNLANFTYKHQFNYMEIPTLMDNDISFKCICVDLKKKKYNIKSPLGPKVLRALYKKLNIKFDK
YVTGTDQNTYLMTYMDLYLSHKRNYLNELFNDLDKKKPAETDSNPESIIESLSINESNESGPFPTGDVDAEHLILEGYDT
WESLYDEQLEEIIYNDIESLELKDIEQYVLQVNLKAPKLMMSAKINKNKHVCDFSRNNLIVPESLKKKEELGSNPVSIHC
YALLKPLDILYVKCPTSKDNYEAAKANISESDNEYELQVISLIEKKFHNFEVLDSKNPGNGDVAHNGAVDSGPVLDNSTF
EKYFKNIKIKPDKFFEKIIIKTDDTEEEKDFESILPGVIVSPMKILKKKDPFTSYAALVVPPIVPKDLHLKVECNNTEYK
DENQYISGYNGIIHIDISNSDKKINGCDFSTNNSSILTSSVELVNGETKNCEININNNEIFGIICDNETNLDPEKCFHEI
YDKDNINVKKFREVIPNIDIFSLHNSNKKKVAYAKIPLDYINKLSFSCSCKTSHTNTIGTMKVTLNKDEKEEEDFKTAQG
IKHNNVHLCNFFDNPELTFDNNKIVLCKIDAELFSEVIIQLPIFGTKKVEGVQDEQYKKFSLKPSLVFDDNDNDIRVIGK
EKNEVSISSALKGVYGNRIFTFDKNGKKGEGISFFIPPTKVDTDLKIIINETIDNSNIKQRGLIYIFVRKNVSENSFKLC
DFTTGSTSLMELNSQVKEKKCSVKIKKGDIFGLKCPKGFAIFPQACFSNVLLEYYKSDYADSQHINYYIHKDKKYNLKPK
DVIELMDENFRELQNIQQYTGISNITDMLHFKNFNLGNLPLNFKNHYSTAYAKVPDTFNSIITFSCHCYNPEKHVYGTMQ
VESDNRNIDNINKNENIIKNFLLPNIEKYALLLDDEEREKKQKNLKDQDDTLTTHDDDFNKNHIYMLYDSNEHICDYEKN
ESLISTLPNDTKKIQKSICKINAKALDVVTIKCPHTKNFTPKDYFSNSSLTTNDKKIVISFDKKNFVTYIDPTKKTFSLK
DIYIQSFYGVTLDHLNQIKKIQEEWDDVHLFYPPHNVLHNVVLNNHIVKLSSALEGVLYMKSKVTTDETSTKKNTTLPSD
GVSSILIPPYVKEDMTFHIFCGKSTTKKPNKNNTSLALIHIHISANRNIIHGCDFLYLEKHTNDSINNNSYSIFTHNKNT
ENNLICDISLIPKTVIGIKCPNKKLSPQTCFDEVYYVKEDDVPSKTITADKYNTFSKDKIENILKNAISINNPDQNDNTY
TYLILPEIFEEELIDIKKVLACTCDNKYIIHMRIEKSTMDKIKIDEKKTIGKDICKYDVATKVATCEIIETIDSSTLKEH
HTVHYSITLSRWDKLIIKYPTNEKTHFEKFFVNPFNLKDKVLYNYNKPINIEHILPGAITTDIYDTRTKIKQYILRIPPY
VHKDIHFSLEFNNSLSLTKQNQNIIYGNVAKIFIHINQGYKEIHGCDFTGKYSHLFTYSKKPLPNDQDICNVTIGNNTFS
GFACLSHFELKPNNCFSSIYDHNEANKVKKLFDLSTNVELDHIKQNTSGYTLSYIIFNKESTKLKFSCTCSSNYSNYTIQ
ITFDPNYITPEPQSRAIIKYVDLKDKNFAKYLRKP
```

280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE
287 - 306:	EEEEEEEEEEEEEEEEEEEE
288 - 307:	EEEEEEEEEEEEEEEEEEEE
289 - 308:	EEEEEEEEEEEEEEEEEEEE
290 - 309:	EEEEEEEEEEEEEEEEEEEE
291 - 310:	EEEEEEEEEEEEEEEEEEEE

A0A060RXX6 **A0A060RXX6_PLARE** (380 aa)

Casein kinase II subunit beta (CK II beta). *Plasmodium reichenowi*

```
MEFVSNDESADDIIQDESNEGEVELTDADFYDLTVINDKIDEEIIEDDEEEADMDDQENDNVQEVYNIDDDDNDIHNDKL
LLDQQRDNDVNEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEDDDDDDDDDDDDDDDDDYDDEYDEDDFNEATVSWIEWF
CQLKQNLFLVEVDEDFIRDEFNLIGLQTKVPHFKKLLKIILDEDDDDDDDDDDDYDDDDDEINRDSEEMYKNKDMHEQNA
ACLYGLIHSRFILTSKGLALMREKYKSGIYGTCPSIYCENAKLLPTAISEIPKFLSPLLYCPRCCETYYPSKNSLLNQLD
GSYFGTSFASFFALSFNIASDKKKVYYTPQICGFTINRNIRETLYMDVNKDHTESSEEYQ
```

92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE

A0A060S1W6 **A0A060S1W6_PLARE** (2002 aa)
Uncharacterized protein. *Plasmodium reichenowi*

```
MNVCKMKVQQKKNLKDCNLKSKNTILTSFEKKKNEKDENNLLKFAKLIDNKNKVVNSKFLKNDNYKCNERKESLTRCSTN
ESLKLKNMKTLTKDFDYNNNNDDYNNNNDDYNNNNDDYNNNNDDYNNNINNNNNNNNNNNNNNNNGHSKLVFKKKSKDIE
STVIEEDEKKSEKKTNDLINNKNEFKVNNKLILKSKEFKSNNNNNNNNNNNNNNNNNNNICKLKNVDDKNKKQQMDTYSPK
ENEEDNSNNMKKNSCLKNIKKNQINEKEIIPNTVEEKHDTHSKGDKEHNGVSTKNVKRMNTMSKEINHKNNNILKKNLSK
SNSLELKKGKKGDKLKDKLINNLSGKKGMNKEKEVVQSSSAKRSSSRYSIDYGRRDSSRRGSAKQEKGKERRASKNVSKK
VSKSKYTRKKSKRIKEESDESDDDDDEEEEDDDDDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEED
NENNNSDNNDESDEVYTNRSRRSTRCSIVKRKSSLCIGKKNSKIIKKSTSKTKNNKKKKGSVIKLEKKKEKLSKKGILKK
KNKKTKGKLRKNSKVYHRKKNIKNEKVGIDEEDIEEEIEEEEEPSYFDEYNLSIEERKKDLEEKEKKKEIKEKYIKQIKL
PKYADDESIIFINNPNYVMVLLFLTVYKDVLKMNWNFKDIEEMFQNKETTEFGRNFILKLFFFLGRYFNSKSIFMYKYIS
RIFEDKEESLSRVVNFHELFPVLETKKEIKNSGVGSKRKKDKRGKKMKIHQKEDELLYDEEVIGNEDVNIFEEEEEDDEE
EDDDEEDNEHSNDDEDEEEEDNEHYNDDEEKEDVNYKDEEEKKSDMNNDSTKNTVIKEEKDGLHISESNHNLVNSVNDSM
KREESCKNGHVVDNERSADFKINDDKNNEDNNDDDDGGDKIVDSKNNIENKLDKSVEGMKDINSTEGIIKNENVDDEKGL
TNKLFLEWDDLSVISKLRIIRMLLNLVLCESNNLKKMLGDEKLNYNNGYLGKINNEKYWFIFNDTINIEYKLYLEREEEG
SFIFICDDDDMLYTIGYNFLRNSDTKFMGEALIERYNKVCRERRNRSRMLKQQKKLLCSDINLNDPLLGTKKRQPKQVEY
FNFNNNEKIRRKKSDINNNNNPYSVPLTKSYQKNDRSFRLAARNAQKGSVDDLEAWKLNEGLLGIENEGGISGNYNIEND
GNNMVETNNINDNNNDNNKKNNNNNNNNNNNVVVKADGNNIYGPNNNNVIGSDGNMNNGNNTTTTNNNNNNNNLGTVKVP
LKRGRKKKSEKKKRGRKKKILSVDGIGDVGNNLSSLNVDENRRKSMPNIGRGRRGTYTKRNTKPSVSIKYGTRSNSINKY
ENDVMSFNEYSLNPGLSMDDFYKNMVMDAKFFHGNMSMNNYMNGGFNMPNNNNSMMNMRNGSKMGNINNLGGYNFPYMCT
PPPPMYNQYYMYNGNNMYLPNGGAINNMNMSNTNNSASVGIGGNVVSNQNTVKDVKAENMNMAKNSIMENRNSISVNSMN
NINMNNMSHKNSFLGNDGINNMNSMMNNNNNNNNNNNVSNNNNNNNNNNNVNFMDNMGNNNNSNNNSNNSNNPMNKYNNY
MMNRNALNNMGGTNPMYNNMYNMKFPYMNNDMMNYNYNINTFQNMNYDKMNKSMFKRYPNFMGGYPYNNMNPYNNFNAFN
MNYQQNDQMNQLPNMQGAYKSKLMNDNLSNYQSFNNNNIKQNHHDNNNNNNNDNNNNNINKNNSECGNKNVDDSNKNNDI
NKNDILDSTKFTEQAVGGVALNNDCTTRGEDNHRIDLKGDVVEALVGNNNEKMNSSDHNLNSLKNLQNINSTYNMDHMSH
MRNSVSGSSIGMINPGHMNSSHSGSIMNKDKFRDLQLNNNNNNNNNNNNNNNNNNNYVKVNPFDHPMKNMNQNLMDDKYP
KDNNMMMMMMNSVYNIMGSDHFHMNNSHMMDPMGSPKMNDNMYNHNNMNFENTNTNHNNHNNHNNHNNHNNHNNRIQDKL
PE
```

436 - 455:	EEEEEEEEEEEEEEEEEEEE
437 - 456:	EEEEEEEEEEEEEEEEEEEE
438 - 457:	EEEEEEEEEEEEEEEEEEEE
439 - 458:	EEEEEEEEEEEEEEEEEEEE
440 - 459:	EEEEEEEEEEEEEEEEEEEE
441 - 460:	EEEEEEEEEEEEEEEEEEEE
442 - 461:	EEEEEEEEEEEEEEEEEEEE
443 - 462:	EEEEEEEEEEEEEEEEEEEE
444 - 463:	EEEEEEEEEEEEEEEEEEEE
445 - 464:	EEEEEEEEEEEEEEEEEEEE
446 - 465:	EEEEEEEEEEEEEEEEEEEE
447 - 466:	EEEEEEEEEEEEEEEEEEEE
448 - 467:	EEEEEEEEEEEEEEEEEEEE
449 - 468:	EEEEEEEEEEEEEEEEEEEE
450 - 469:	EEEEEEEEEEEEEEEEEEEE
451 - 470:	EEEEEEEEEEEEEEEEEEEE
452 - 471:	EEEEEEEEEEEEEEEEEEEE
453 - 472:	EEEEEEEEEEEEEEEEEEEE
454 - 473:	EEEEEEEEEEEEEEEEEEEE

455 - 474:	EEEEEEEEEEEEEEEEEEEE
456 - 475:	EEEEEEEEEEEEEEEEEEEE
457 - 476:	EEEEEEEEEEEEEEEEEEEE
458 - 477:	EEEEEEEEEEEEEEEEEEEE
459 - 478:	EEEEEEEEEEEEEEEEEEEE
460 - 479:	EEEEEEEEEEEEEEEEEEEE

A0A060YHK3 **A0A060YHK3_ONCMY** (212 aa)
Uncharacterized protein. *Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri)*

```
MGVCWMTDTPIKQTFQHSTEEEEEEEEEEEEEEEEEEEEEEEEENLEDSGETRSRLLESLRRNPALVKEFRPILEETLEER
LEKMGLRKGTKGISKKTFKSLSTLVSGQRHQMSRQKADLLELRESLARELTRRVHALQRSQGITVPNLPRQVTIPSTTPQ
SHKKRSPSREKSPKSRQTPVKVKVSLRKKKAPRPQQTPSTHRKKNRYAHSIY
```

20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE

A0A061AV76 **A0A061AV76_CYBFA** (1813 aa)
CYFA0S02e03994g1_1. *Cyberlindnera fabianii (Yeast) (Hansenula fabianii)*

```
MELIQGLMAQQKTQSAEEIIPTLCDRLAHARLASDKRAAILTLKGFARQYRESVISNGLRALISTLREFAVDTDIIKASL
ETILVLFIRGESEEDQTRAWISQQSRTQNGKYPSPLLMKQEDETSAFDHFSLWIADEITQSEEKISVIVSLLENNDFYVR
LYTLQLLEALVAMRPNKTKDSLLNAPLGIPALISVLDDLHDPVKNEAVLLLMAVANDNSNIQKLVAFGDTFDKLFEIIHE
EGDIRGSIVVQDCLTLLTNLLKYNVSNQKLFLETYCLPKLAFLIAEPLEDDDILWNDQRLQNIIIALEIIGLFVIEGNES
TLKNQNSLHNAGIFVTVLRLAFSPSTDNKIRPHALRTVAVLMSNNPDIQQTFSEIDVPYIDPSLPKQLQRFKDPVPAVVA
LLNWCLFVNSVHVFDIRITALDVLTAYFEGNNDNKLAFLQDQISDFYNEDRDDEVEDAEEEEEEEEEEEEEEEEEEEKE
EAKTVVPEQNGSRTDIPHTSDDSNGSETNPATNDSAGTNGTTSALEMKETPIANIFQALLEYDPELKLNPYKVWFSAVIL
INLIQHNDDLKALVRGVHTGDEDAGEEKISAIQAMSGLLVTTLTNQYQRVSVGYLQLLIVLLYEDFESVDDFLGDVSNVK
SLLQYLAQPSSDGIVHGLMTVLIGVAFEFSSQSSPLSRVDFHSLIVKMLGKDSYGFKVLQFREDEAFANFSEDDILKLTW
DETGLPKVYFVRTVVSLIKDNYYRIKNTLNQDPELESNGRISYEKFEELNDHYHQLQKTHSEYMEKSTTTHKEITANLEK
TTADLSKITEAHDSTQKELDALRVTHAELEAKFESTSTALANLEKLHADLTDSSDKQSKDIESTTQQLATKETLIINLKQ
ELKQVQEQKKKAENDVSKMSRDLFQLNTKKEELERTVKKLEKDVQKNVKHQEKLEQSLKQKEAEASDLKTRLGEAMKELK
TAESTKTTLQRSIDEHKSKGSENKMLIDQMTEKLRSIATTCNELASAKAALEEESATLKATSSRELELYKSKVADLEASS
KDLQSLTDKLSADKDQLESTLQATKSEHVSAIQKLEGENQELQKNISDLKAELETSKDLSGKHEEQINSLTTQLKSTKDE
LSGLKEAHSISVKETADSHHKALSAVQKELSSHKETHKSKIGELQTRIAELTKAEEAATKELDSHKNDIAQAKKDLEKKN
SKLESLEKQLGERKTEIEVLKSSNAALETKLKDSDEKSKNKLSELQQTVDQLTKTKTDLETELDELALELESKESESKNE
IRNLSEKIKSVEEEKKSLSSTLEIISQRIETKDMESQSLNKSLKAKTSEIEEVTKSKNALETEKKSMEQSLEKSQEQVET
LQVEIGTLQENLETTTEKLSKSEAALKAANQRLEDQKKSWSEKVTVLEREIKTLKESIEKKNTEFEKERTLLSENSSSTT
KEYSEKVTKLEEELQKLQTSSGTKTEELEKAKQNLEETIADLRSGNESLTSDLKSKDAKVTELKTNIKELEKKIKDLERK
HIEALKDTANVATLEANLKEKDGTIQGLKSDLKEKEDEAKDLKKKLDTSVGVIEKLERDAERLEKEAESETTKSSSIKAT
LEAKVKTLETELSSLKKQNAKLTADIDGASSKSVTEIEQKQNEIEELKKRASTTEADLKTAKASLIKAEESENASKKKLL
EVMESAKSEKESMQTEISTLKKSVEESEKLTKDIEAVKEKNANLSRDLESAKSSSTDIDKFKKENDELKQKLEDFKKTMV
ARSELDDLMLVLDDLDDKKKKYKEKVKSLGGDVSSDEEDEEDDDDDDDDSDEE
```

459 - 478:	EEEEEEEEEEEEEEEEEEEE

A0A061B023 **A0A061B023_RHOTO** (1298 aa)
RHTO0S05e02102g1_1. *Rhodosporidium toruloides (Yeast) (Rhodotorula gracilis)*

```
MSAVSNAQASKPFLSAADDLITRLLLDYSIFGEDRLGRATGKIEDRRELRMNDGEVETARQLVQRIRQGTITVNDALEEF
LALSPVRSFCSRWEEDDGPLIFANHAKRYILALRPESGIAFHETDRYKNPRNGPRGKKRASLPATTSRRDPETFIEVGVF
ATRNFKKGEVVNLRGGIADLTEEEDDEVRDSGGRRDFSVLWSERKNCFCLLLGPARFVNHDCRNNVEFQLVGANMTFKVL
EDIKKDEEIFTHYGEHYFEKDNAACLCATCEQLEQGAFTSTKKKAAAPIAPRAAAPPTPPTAPSRRSGRAATVAAPNYSE
DDPPSGSGHNVLAKRSLRDRGLARSSSLSSLSKATPTASPRSVRPPSSRVVPVRNAPSPAEALRGKPRAVIQPKLPPPPG
YASDYVWDWRNRVARYVGPSYSKADVPALKRKGLSRSASAPSSLSALGKRRREATDSPAPSPKGKSRLRDDEDSPRPKRQ
RSLLVKLKQVRLGERSSTRIAGGSISARERTFAKLQKALGKSEGDEDSDLSELEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEVADAEPEDSPLTDVEESEGEKTDEEDDAVQEQLLSPANGAAVRHESVASSTAPSDGSSVPSVLPEASSSADTPAT
TASSAISLTLDASAIAAPRPESVEAGITTSTPAEELLSPPLPGLSDADEEDDRIVLCPVPSPPKANAADRPRLPLASPSQ
GFYTSAASTSSNGASSTSAGPDFRYGRTPADGGGRGADPAGVGDLGGGGGGGIGGSGGDDGEDGRPPKPSLPADKMEVDE
IEEEQDEAKPLTAASGKGKAAAPTGEVLAANSPYHAPVAAAALPETTEDPADVAAALLLLAALPCGPSALAPLSTGSTPP
QMETASDASASSSNAGASTSRMRLDDPPATKRKKRESEEAKPAIHPSLNPRSTRRHSKLPEQEPVAPSSPPAAVRRAKRS
DATSQTVEGPSASTPTSRRTRSQPLPGKLEDVLSAPETLAATGGFDWAKGRYISKHEALRNPSANPGPPPRSTRTPSPSP
PPQRKTSSRQAAAPARPRSAARSTPAPVVGPPRLTSPIVAPDGVRATRKSFPMEGVKLAEIVYSREARLAAGGWDPSVGK
YVSAAAGANTPEPAEPGSSYSAARARQQTPTLAPALTSSHGESRIHSSGRQVAPPDGKRSTRKSFPMEGVKLADLVYSED
ALRAAGGGWDPVLEKYVRTTSRPGVVAPEASTSQARLPSVSLPSTTDGKRSTRASLPLADVKVADLVHSPAARHALGGWD
PLTKRYTPAGSRKTAAAE
```

534 - 553:	EEEEEEEEEEEEEEEEEEEE
535 - 554:	EEEEEEEEEEEEEEEEEEEE
536 - 555:	EEEEEEEEEEEEEEEEEEEE
537 - 556:	EEEEEEEEEEEEEEEEEEEE
538 - 557:	EEEEEEEEEEEEEEEEEEEE

539 - 558:	EEEEEEEEEEEEEEEEEEEE
540 - 559:	EEEEEEEEEEEEEEEEEEEE
541 - 560:	EEEEEEEEEEEEEEEEEEEE
542 - 561:	EEEEEEEEEEEEEEEEEEEE
543 - 562:	EEEEEEEEEEEEEEEEEEEE
544 - 563:	EEEEEEEEEEEEEEEEEEEE
545 - 564:	EEEEEEEEEEEEEEEEEEEE
546 - 565:	EEEEEEEEEEEEEEEEEEEE

A0A061B0T0 **A0A061B0T0_RHOTO** (523 aa)
RHTO0S08e01596g1_1. *Rhodosporidium toruloides (Yeast) (Rhodotorula gracilis)*

```
MPATLPRLPVELLRRILDEVTRGEDAAEPEDLGRIVARVCSEWKDVGQELAFRRPVFLGYYRSGAVPALIRHLHAFPHLA
NYVREIVLGSQLEAEKCTTESLRQLFQICQGVTHVDWSFKSPDLLDATFPHLPFANLISLAVSRAGLWDPSPLLAVLPKC
MRLRRFQLNTSLESSFFPPKAPSPEPTAPPQPLRSLSLYRFLSLFDPASLTSLRVSCQSPNVVGVAEWIARCVNLLSLDL
RLATGLNTGRSCHIETYTRMLRSLRRLESLCLSDNLYDLDAHGDRTRRQALLSGFLAALPDTLVELVLGFEIPLGACYEI
LAAFLETRLIASPLLRVEFWTTLRKEGFVNVTATKQVLLIEDYDSDDEDDEERDYVWISHEWEEAGRADAKDLADELANV
LRILPDESIVAGRRWCMSFDNTEGTCSWCMSGDAGWWVLGSEEARRYELEEPGGQAEDSESEWESEDESEEEEESEEEEE
ADEEEEEEEEEEEEEEEEEEEXXXXXXXGGGGVASQKQCKGG
```

483 - 502:	EEEEEEEEEEEEEEEEEEEE

A0A061G2R5 **A0A061G2R5_THECC** (323 aa)
Coiled-coil domain-containing protein 97 isoform 1. *Theobroma cacao (Cacao) (Cocoa)*

```
MERKVRIEAIESITERLSCLENLYFPRALQSSASDPSHRKSILHDLLSRDVPVFLERYGSELTSDELLEFDALNDDYEVN
WHLKHLRSKMSPSSEELKSRSVTVKNRRRAYLNKLICDGQYFSEDAMREREPYLHHEYLGKFQDLSGRSMAKPGERWSET
LMRRCEEARLVAKIREEQQRLGVAQKDWVGNETNQQEEEEEEEEEEEEEEEEEEEEEEEEEEDENEMKKENGGEHGNEM
LLDHPGNDRGATSATMGEDEEAPSAEEMQDRMDQFTYIMQQKFLSGEDREHLDYTKIDDDETLDDHWLREANHDAEEKYF
AED
```

197 - 216:	EEEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE

A0A061HU09 **A0A061HU09_CRIGR** (890 aa)
Uncharacterized protein (Fragment). *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MLRFEASDMECLLSHVKERLNEDLTMSQRGSSLRFSFDSVKYEELELIAEQTGLPLSESEKIDGLNKRRKQVQDTARKIV
RKTLKLSMRRKNADLLPTVPPVISGEQRRAKKLIQDILFQTELLRGSEQTREKKKREAKEVKKPLGDKALMQKRQMYWKM
YWEQEKRKEKAEQAEPKEGPSEEASETPPREAQKVSQTPTVPARRTTVAARRTTVPARRITVPKRRITVPKRRITVPKRR
TTVPKRRTTVPARRTTVPEKDTTVPEKDTTVPEKDITVPEKDVTVPEKDTTVPEKDTTKYERKLSHGLSGTPGRMSQLEK
TSWRDDICQLLTSRIASSHPDMIRDLGEELADLADAVLTNEPSWALFNELCPWRRASGMVPSELGKVDKKAIKEEVPGTA
TDEEVSLSKIKEMVIDFLESYLILEIERLKASGKQKGETVEDREEVISLEEEEERTHDKETPAAPGKLLTTGDEKQLRKE
KRRKQITDEKEPTHPEETLMQAKEIYNALQNMLAKAKLRQEEKLRGEKQATVSEEGRADLEKKEQVWQKTMEALNESMRA
KQQKRHRERRKGEEEEELAKEEQEEQEGERIRPQEEKKWSWPSERTEEEEEDYDYWVLDRFLSSSEDEERSDEETEDEES
EETWKKERLADQEDTEEGKEADRLVRGEGDQQELEGLAQDGESLEPGEKEWPTWKRGRKKGAQKETRMTQKERRELWEKE
KMRLAKKQRGEEEEEEEEEEEEEEEEEEEEDEETRKQKEAAKEEKKERAEKARLANIIRKLFPKVEEMLQRARPRQREQL
VLVKGMAQEKGRHEMKKETEVVKDEKAPERRKRIRKKEKERLQSEKEEGQFQEEKEEQEEEEEEEEEKKEKEKKEKKEKK
EKKEKKKKEK
```

731 - 750:	EEEEEEEEEEEEEEEEEEEE

A0A061HU43 **A0A061HU43_CRIGR** (591 aa)
Retrotransposon gag domain-containing protein 4. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MSEAAGNLNSLRLANVALREELNALRGENAHLGLQLGRALAEVNSLRGNVSSYISWQVPIVPVLAEENFELLINEDDPTP
EEEVPFLCWPPPRTDPEYVSDDLLINVVQDYSNPDGSLDPPLSPSLSQSELHSPASKEPPLQALLPPLERPDIEPFSGDP
VYLAEFLMQLETFIANHEDHFPGGAERVAFLISFFTGEARDWAISVTQEGSSLHANFPRFLDEIRKEFCGPIPSRVAKKA
IRKLKQGDCTLGSYADAFQFLAQFLSWDDCRLQNQFLKGLSDFFRKELLWSTEMADLDELILECVEIEKKVRASKAAPLT
GIQNSVYHFVQVPNEDENEGVECYSEDEGEEAGRHRLYLMDQRKHMNVFSQELREEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEDKEEEEMRKEEEEREEEEEEEEEDEYEDEEEEEEEEEEEEEEDKEEEEMRKNDDGDGNKYEEEDEIVVRVL
ESEEEQGREEIQHVYVHDCMHVHLHALAAHHHCLHGELVEMEEPVFVDTSTQTISSGIGYHAENYLGLSPSTHSSRQRNQ
NQVPLLEGIPDTNAPFYSSPPLIHHAGLAAF
```

375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE
379 - 398:	EEEEEEEEEEEEEEEEEEEE
380 - 399:	EEEEEEEEEEEEEEEEEEEE
381 - 400:	EEEEEEEEEEEEEEEEEEEE
382 - 401:	EEEEEEEEEEEEEEEEEEEE
383 - 402:	EEEEEEEEEEEEEEEEEEEE
384 - 403:	EEEEEEEEEEEEEEEEEEEE
385 - 404:	EEEEEEEEEEEEEEEEEEEE
386 - 405:	EEEEEEEEEEEEEEEEEEEE
387 - 406:	EEEEEEEEEEEEEEEEEEEE
388 - 407:	EEEEEEEEEEEEEEEEEEEE
389 - 408:	EEEEEEEEEEEEEEEEEEEE
390 - 409:	EEEEEEEEEEEEEEEEEEEE

A0A061HUM9 **A0A061HUM9_CRIGR** (566 aa)
Retrotransposon gag domain-containing protein 4. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MSEAAGNLNSLRLANVALREELNALRGENAHLGLQLGRALAEVNSLRGNVSSYISWQVPIVPVLAEENFELLINEDDPTP
EEEVPFLCWPPPRTDPEYVSDDLLINVVQDYSNPDGSLDPPLSPSLSQSELHSPASKEPPLQALLPPLERPDIEPFSGDP
VYLAEFLMQLETFIANHEDHFPGGAERVAFLISFFTGEARDWAISVTQEGSSLHANFPRFLDEIRKEFCGPIPSRVAKKA
IRKLKQGDCTLGSYADAFQFLAQFLSWDDCRLQNQFLKGLSDFFRKELLWSTEMADLDELILECVEIEKKVRASKAAPLT
GIQNSVYHFVQVPNEDENEGVECYSEDEGEEAGRHRLYLMDQRKHMNVFSQELREEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEDKEEEEMRKEEEEREEEEEEEEEDEYEDEEEEEEEEEEEEEEDKEEEEMRKNDDGDGNKYEEEDEIVVRVL
ESEEEQGREEIQHVREFQKGKHHSSKLWSLSADVNMLVMLSVCLWRSAKGRCTVPHIPETSLAQALPDPVVLLTLNTCSL
SQGEYA
```

375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE
379 - 398:	EEEEEEEEEEEEEEEEEEEE
380 - 399:	EEEEEEEEEEEEEEEEEEEE
381 - 400:	EEEEEEEEEEEEEEEEEEEE
382 - 401:	EEEEEEEEEEEEEEEEEEEE
383 - 402:	EEEEEEEEEEEEEEEEEEEE
384 - 403:	EEEEEEEEEEEEEEEEEEEE
385 - 404:	EEEEEEEEEEEEEEEEEEEE
386 - 405:	EEEEEEEEEEEEEEEEEEEE
387 - 406:	EEEEEEEEEEEEEEEEEEEE
388 - 407:	EEEEEEEEEEEEEEEEEEEE
389 - 408:	EEEEEEEEEEEEEEEEEEEE
390 - 409:	EEEEEEEEEEEEEEEEEEEE

A0A061HV23 **A0A061HV23_CRIGR** (499 aa)
Putative disks large-like isoform 1. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MHKHQHCCKCPECYEVTRLAALRRLEPPGYGDWQVPDPYGPSGGNGASSSYGGYSSQTLPSQAGATPTPRTKAKLIPTGR
DVGPVPPKPVPGKSTPKLNGSGPSWWPECTCTNRDWYEQANPAPLLVSPEALEPSLSVNGSDGMFKYEEIVLERGNSGLG
FSIAGGIDNPHVPDDPGIFITKIIPGGAAAMDGRLGIAGGIGNQHIPGDNSIYITKIIEGGAAQKDGRLQIGDRLLAVNN
TNLQDVRHEEAVASLKNTSDMVYLKVAKPGSLHLNDMYAPPDYASTFTALADNHISHNSSLGYLGTVESKVTTYPAPPQV
PPTRYSPIPRHMLAEEDFTREPRKIILHKGSTGLGFNIVGGEDGEGIFVSFILAGGPADLSGELRRGDRILSVNGVNLRN
ATHEQAAAALKRAGQSVTIVAQYRPEGLCSEILSPKLKKKEEGEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEERRRRKKKK
```

447 - 466:	EEEEEEEEEEEEEEEEEEEE
448 - 467:	EEEEEEEEEEEEEEEEEEEE
449 - 468:	EEEEEEEEEEEEEEEEEEEE
450 - 469:	EEEEEEEEEEEEEEEEEEEE

451 - 470:	EEEEEEEEEEEEEEEEEEEE
452 - 471:	EEEEEEEEEEEEEEEEEEEE
453 - 472:	EEEEEEEEEEEEEEEEEEEE
454 - 473:	EEEEEEEEEEEEEEEEEEEE
455 - 474:	EEEEEEEEEEEEEEEEEEEE
456 - 475:	EEEEEEEEEEEEEEEEEEEE
457 - 476:	EEEEEEEEEEEEEEEEEEEE
458 - 477:	EEEEEEEEEEEEEEEEEEEE
459 - 478:	EEEEEEEEEEEEEEEEEEEE
460 - 479:	EEEEEEEEEEEEEEEEEEEE
461 - 480:	EEEEEEEEEEEEEEEEEEEE
462 - 481:	EEEEEEEEEEEEEEEEEEEE
463 - 482:	EEEEEEEEEEEEEEEEEEEE
464 - 483:	EEEEEEEEEEEEEEEEEEEE
465 - 484:	EEEEEEEEEEEEEEEEEEEE
466 - 485:	EEEEEEEEEEEEEEEEEEEE
467 - 486:	EEEEEEEEEEEEEEEEEEEE
468 - 487:	EEEEEEEEEEEEEEEEEEEE
469 - 488:	EEEEEEEEEEEEEEEEEEEE
470 - 489:	EEEEEEEEEEEEEEEEEEEE
471 - 490:	EEEEEEEEEEEEEEEEEEEE
472 - 491:	EEEEEEEEEEEEEEEEEEEE

A0A061HVW5 **A0A061HVW5_CRIGR** (95 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MASLKAFKELNLAVSKRKKEEEEEEKEEEEEKGEEEEKEEEEEEKKREEEEEEEEEEEEEEEEEEEEEEEEEDNDGND
NNTVSLSAFQRKVFR
```

48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE

A0A061HWA8 **A0A061HWA8_CRIGR** (575 aa)
TANK-binding kinase 1-binding protein 1. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MAAVEVFGKPEVWGGDEAKQSRQVLGCASAGTAGPIHRSLWVLEGALPCHCSFLDPVYQLSPESTLEVHLGPFPTPTSSD
SRGRMPPAEGEGGGPVWAEALTMESMFEDDISILTQEALGPSEVWLDGPGDSSLGGDMCSASHFALITAYGDIKERLGGL
ERENATLRRRLKVYEIKYPLITDFGEEHGFPLCEIKDGSLLELEKVSLQQRFNQFQHELQKNKEQEEQLGEMIQAYEKLC
VEKNDLETELGEMRALVETHLRQICGLEQQLQQQQGLRDAAFPSLSPPPAPATPCPDLDLHYLALRGGPALGHAGWPGPT
SVSVSELERRQLEEALEAAQGEARGAQLREEQLQAECERLQGELKQLQETRAQDLASNQSECDMAWVKRVGDDQVNLALA
YTELTEELGRLRELSSLQGRILRTLLQEQARNADISECQEPGWDITEEDNLNPMSLVSSRTVRTTRETLSQKSNSNESEE
EEEEEEKEEEEEEEEEEEEEEEEEEEEEEEEKEEEEEKEEEEEKEEEEEEEEDVEEEEEKEEEEEEEEEEEEEEEEEEE
EEEEEEERGPLLISG
```

488 - 507:	EEEEEEEEEEEEEEEEEEEE
489 - 508:	EEEEEEEEEEEEEEEEEEEE
490 - 509:	EEEEEEEEEEEEEEEEEEEE
491 - 510:	EEEEEEEEEEEEEEEEEEEE
492 - 511:	EEEEEEEEEEEEEEEEEEEE
541 - 560:	EEEEEEEEEEEEEEEEEEEE
542 - 561:	EEEEEEEEEEEEEEEEEEEE
543 - 562:	EEEEEEEEEEEEEEEEEEEE
544 - 563:	EEEEEEEEEEEEEEEEEEEE

545 - 564:	EEEEEEEEEEEEEEEEEEEE
546 - 565:	EEEEEEEEEEEEEEEEEEEE
547 - 566:	EEEEEEEEEEEEEEEEEEEE
548 - 567:	EEEEEEEEEEEEEEEEEEEE

A0A061HWW3 **A0A061HWW3_CRIGR** (299 aa)
Transposase, L1 containing protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MPGICSPDLSSPVGSGTPRHSQGPGNSAASIHKKRTDIRVLELFASTRREPWSHSHQERKRILLHPPEERVRRGQCKRTF
NNRKPNMTPPETKNHTSARPEHHNADEAEENDLKNIFMKMIEDLKEDMRKSLKEMEERTNKKIQDINKSLRETGQDLKTE
IETIKKAQSEGFLELEKLGKRSGTTDVSIISRIQEMEERISGSEDTLGEKDSSTKENLKSNKSLTQNIQEIWDTVKRPNL
RIIGIEEGEEIQLKEEEEEEEEEEEEEEEEEEEEEEADILQTSGTLAPLGTSDYQSNGEK
```

255 - 274:	EEEEEEEEEEEEEEEEEEEE
256 - 275:	EEEEEEEEEEEEEEEEEEEE

A0A061HXS0 **A0A061HXS0_CRIGR** (146 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MEEDMGRRQNKNNLNNTKTNMTPSESRESTSARLERHNTEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEREGEEGEEGE
GGEGGEEGEGGEEREEEEKEEEEEKEGEYEPVCKNYFMKKIESLKEEIRKSLKEIEEKTKKKSRNK
```

40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE

A0A061HXW3 **A0A061HXW3_CRIGR** (513 aa)
Peroxisomal membrane protein 4. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MSDGRLSLWIQRRGGAPCASGLCSRSPGLSVRVQPGSSTEFSDAMASPPQLQALLQAVNTLLRKRRYHAVLALLKGFRNG
AVYGVKIRAPHALVMTFLFRSGSLQEKLQAILKATYTHSRNLACFVFIYKSLCALQSHVQGETHQMHSFLAAFIGGLLVF
RKNNNINSQINMYLTSRVLFALCRLGVEKGYIPKLSWDPFPLHTAVIWGLVLWLFEYHRPTLQPSLQSSMTYLYEDSNVW
HDISDFLIFNKSRPSKSRLEEEEEEEEEEEEEEEEEEEEEEEEVYCKMHIPELIKILNWTGDVAEASFGAFGTLRIVAR
ILNSAVSWVLSRAHLPEGGTEAQTGKDLDPSLVAYYVKRRLDLETDHQYLAGSSGPFRGRGRHPGKGVKSPGEKSRYETS
LNLTTKRFLELLSRSADGVVDLNWAAEVLKVQKRRIYDITNVLEGIQLIAKKSKNHIQWLGSRTMVGISKRLEGLTRDLQ
QLQESEQHLDRLMHICTTQLQLLSEDSDSQRYP
```

260 - 279:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE
262 - 281:	EEEEEEEEEEEEEEEEEEEE
263 - 282:	EEEEEEEEEEEEEEEEEEEE
264 - 283:	EEEEEEEEEEEEEEEEEEEE
265 - 284:	EEEEEEEEEEEEEEEEEEEE

A0A061HY50 **A0A061HY50_CRIGR** (66 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MLKRQVVMGKGKVYRKSYYSCGKMLNNEEEEEEEEEEEEEEKEEEEEEEEEEEEEEEEEEEEEEK
```

43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE

A0A061HYP9 **A0A061HYP9_CRIGR** (100 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MDISAGKLLAEWNRAEQERDFYIHVGGNHPPLEYRYRYSLTSNSQDTFPFTAIEEEEEEEEEEEEEEEEEEEEEEEEE
EEEGEREREGGGTLTKSKQQ
```

54 - 73:	EEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEE

A0A061HYR8 **A0A061HYR8_CRIGR** (298 aa)
Ankyrin repeat domain-containing protein 60. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MTVRELKEELDLMVGIPFNLQRLHFLDQGGSCPTPSRTPLLPWVPKKHLTTQGILMDDAILKFYDVIPGAVISLCIWHYD
GWTELVLAAVEGDPSKLSCLGVSEDTFYRTANSQHFKGANCLGKSPLGRTPLHVVAAMGRMDCIRPLLEHSANIHDRDAK
GETPVTIARRLNRSNFERKMFLLYWMIKVLKQNKLEEEEEEEEEEEEEEEEEEEEASMMPQDFLDVPVIHWLVGSWKYSA
MFAVNLTETEIKPIHPGKGSALLGPLSPVWRDTRITFFPRSEVKLGELALFFHVGPGY
```

196 - 215:	EEEEEEEEEEEEEEEEEEE

A0A061HYV2 **A0A061HYV2_CRIGR** (152 aa)
MOSC domain-containing protein 2 (EC 1.-.-.-). *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MVVKEDGHMITAHQEPCLVLVSITMENNYLMLEAPCMDPMVLPIKMPSSNEIHDCRLFGLDIKGRDCGDEVAQWFTNYLK
MQPYRAWFNLIPACSILDCIHVFLKEEEEEEEEEEEEEEEEEEEEEEEKEEEEEEEEEEEATLNTEFVYNE
```

106 - 125:	EEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEE

A0A061HZD4 **A0A061HZD4_CRIGR** (674 aa)
Solute carrier family 15 member 5. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MLLLKGAQNACAMHDWKDHFPVNTPLPAEQSRKDNNNSELGVVWILTRLHQSTTDLLQGRGSWFGYRWRKQRAVKRIPYM
YKTKQMKKGGGGGGGGGGGGEGGGGGGGGGGEEEEEEEEEEEEEEEEEEEEEAINLRVGVGACLLLVELCEKLTFFEVAC
NMIPFCTVKLGYFNHQAAILNLCFIGASVFTPTFVGWLADNYFGRNKLVYMSLALHFLGTALLSVLAFPLEDFYGGSYPV
VNNVAMEERAGLFHTALLTLCLGTGGIRAVVCPLDAYGLQEEESKKPKSFFNWASWSMNLNAAAVFLGISCIQHSGAGAI
VALLPSLSLVTALAALYMRHCNLIYQPEKHCSLLTVAGVLLKALKRHCLSYCHLGQDGASWSDRAVQKHGGCHSELQEED
TELVFSTLLPLFSFQLVYRMCLMQIPSGYYLQTMNSNRNLDGFLLPIALMNALSILPLLILVPFMDYFSHRLLPSKKVEP
FLSACIIAGNGCAALSVAIAGFLEIHRKLTPEQSPSGKAFSVSSLACGSLVPQYVLLGVSEALVNPAVSMVIHRFIPSTF
RGTSMTFLSLFQGFACFLGALLVELVYLISKGNWFPNTLNKGNLEGFFFVLASLTLLNILGFWRASRRYCNLNHFNAQSI
SGGNRETLLWEKSLKFYGSTQETSSSIDLWETAL
```

113 - 132:	EEEEEEEEEEEEEEEEEEE

A0A061HZI8 **A0A061HZI8_CRIGR** (67 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MRVRKWDKKTGREEEEEEEVEEEEEEEEEEEEEEEEEEEEEEEEKERGDRWFKPGTNLRYACPSLL
```

21 - 40:	EEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEE

26 - 45:	EEEEEEEEEEEEEEEEEEEE

A0A061HZM7 **A0A061HZM7_CRIGR** (158 aa)
Centromere protein Cenp-B, dimerization domain containing protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MDMEGLKEEEEEEEEEEEEEEEEEEEEEEEEEERFTAIGRESLVWFEASSFWYTIKAGLTGTPLAYPEALDMKDHSVQVLHQ
ITARTSSTILKRYGESGQPCLVPDFRGITLSFSPFSLMLAVGLVYIAFIMFRYVPVLLFSPHLYHERMLDFDKGFFSV
```

8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE

A0A061I137 **A0A061I137_CRIGR** (69 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MKKRENEEEEEEEEEEEEEEEEEEEEEEEEEEEEKRRKQYYNLPALGVFSGVLKKILLDLPFESVLKLMR
```

7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE

A0A061I1T2 **A0A061I1T2_CRIGR** (743 aa)
Lactotransferrin (EC 3.4.21.-). *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MRRGQEEEEEEEEEEEEEEEEEEEEEEEEDDDDDDDNSTSLDQRQEQRPGLFSRSPKTIGMRLLIPALLFLEALGLCLARR
AAVRWCAVSRFEAQKCSRWQKAMKGVDVQPLSCVKRSSTSQCIKAIVTNKADAMTLDGGKMFDAGMPPYKLRPMAAEVYG
TKEQPRTHYYAVAVVKKSSNFHLNQLQGLRSCHTGLGRSAGWNVPIGILRPFLNWDGPPASLEEAVSKFFSMSCVPGANK
DRFPNLCSLCAGTGANKCASSREEPYSGYAGAFKCLRDNAGDVAFTRGSTILEELPDKAERDQYKLLCPDNTWKSVEEYK
ECHLAQVPSHAVVARSVRGKEDAIWELLSQAQEKFGKNKASEFQLFASPSGQKDLLFKDSAIGFLRVPPKVDVGLYLTFN
YITSILNLRKSEQDVAATRARVMWCAVGSEEKHKCDQWSRVSNGTVTCTSFPTTEDCITSIMKGDADAMSLDGGYIYTAG
KCGLFPVLAENQKSPQNTGSDCVDRPAEGYFAVAAVRKQDTGFRWSSVRGKKSCHTAVGRTAGWNIPVGLLVNQTRSCKF
DEFFSQSCAPGADPKSNLCALCIGDERGENKCAANSNERYHGYTGALRCLAEKAGDVAFLKDSTVLQNTDGKNTHEWARN
LRLEDFELLCLDDTRKPVTEAKNCHLAIAPNHAVVSRMDKVEYIQKVMINQQKHFGNTGSRFEKKSVPECPTFCFPQHCW
KPVPSLPSENTEQMAAPSQEASA
```

6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE

A0A061I364 **A0A061I364_CRIGR** (98 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MKSGLESDGGEMAVRHLTPPDYEMKNGSDGHGNSMQSKGRSDVTKWFFDLHMHTHKEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEVKL
```

57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE

66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE

A0A061I387 **A0A061I387_CRIGR** (145 aa)
Nucleoplasmin containing protein (Fragment). *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
VHQSKVSSFLSLPALWTCALLEWDPGSGLEMLSKHHQQITVENLTSIQTLLGHRKAHCPCFEEAHEMGSLLGDFLSPKIC
AVLRAPGYHGCVISVFNWPIDPLLISILWSEWKITKSEEEEEEEEEEEEEEEEEEEEEEAAAAC
```

118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE

A0A061I5C6 **A0A061I5C6_CRIGR** (93 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MYIELVYIQIEHYIQEEEEEEEEEEEEEEEEEEEEGRRRRRKKKKKEEEEEEERRRKKKKKKKKKEEEEEEEEEEEEEEEE
EEEEEGKKLIQIK
```

65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE

A0A061I5N0 **A0A061I5N0_CRIGR** (893 aa)
Kinesin-like protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MKRHKNGNKQYFTKMGTRKKVQAFVRVKPTDDFAHDMIKYGDDNKSIDIHLKKDTRRGVVNNQQTDWSFKLDGVLHDATQ
DLVYETVAKDAVSQALDGYNAPFTSRVLDGAKHAEDTRVVHEVIFLNVTQTYFEMFAGTIMCYGQTGAGKTYTMTGATEN
YKHRGILPRALQQVFRMIEERPTHAITVRVSYLEIYNENLFDLLSTLPYVGPSVSPMTIVENPQGVFIKGLSVHLTSQEE
DAFSLLFEGETNRIIASHTMNKNSSRSHCIFTIYVEAHSRTLSDEKYITSKINLVDLAGSERLGKTGSEGRVLKEATYIN
KSLSFLEQAIIALGDQKRDHIPFRQCKLTHALKDSLEEEEEEEEEEEEEEEEEEEEGLLSSLKFASRMKLVTTEPAINE
KYDAERMVKNLEKELALLKQELAIHDSLNGPCCSCLGSGSCCLFNTCSSSFKSNRTLVNYDPMDEIQIAEINSQVRRYLE
GTLDEIDAGLMDAEGHLVGEPDGQSFGLGVAPFSIKPGKKIKSKKTGKEQISTSARKEGASSPGSGKDLDVGPSVSKTQL
IPSSKDGDIKDMLSRDRETSSIEPLPSDSPKEESRPIRPSTPPPKPVAFEDFKNERGSEINRIFKENKSILNERRKRASE
TTQRINAIKQEIDVTKEALNFQKSLREKQGQYENKGLMIIDEEEFLLILKLKDLKKQYRNEYQELRDLRAEIQYCQRLVD
QCRNRLLMGIPVGKVGRLLEVKGGRRARPRINSEVFSDLLTEGPELSQGLQVCGFQGSEGGRWGAVSLTLVEFDIWYNES
FVIPEEIQTALKIGSSIRPGMVPVSRIVSLGEDDQDRFSQLQQTVLPEGPDSISFYNAKVKTEQKVTWVAHVYEGGGPRD
FITRTPRITNPIG
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE

A0A061I5R6 **A0A061I5R6_CRIGR** (1088 aa)
FERM domain-containing protein 4A isoform 1. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MGKFALPQLCTAKSAAGYLGPVGAGGGHLNWLQLDRRVLEHDFPKKSGPVVLYFCVRYAPKCSLNPLTSSISAPNTHAVQ
WQPVIPITDAPGPPPPSTSQIQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEELCGREAFELKFYIES
ISYLKDNATIELFFLNAKSCIYKELIDVDSEVVFELASYILQEAKGDFSSNEVVRSDLKKLPALPTQALKEHPSLAYCED
RVIEYYKKLNGQTRGQAIVNYMSIVESLPTYGVHYYAVKDKQGIPWWLGLSYKGIFQYDYHDKVKPRKRLSEACDSCFSR
ASVTRRTFGHSGIAVHTWYACPALIKSIWAMAISQHQFYLDRKQSKSKIHAARSLSEIAIDLTETGTLKTSKLANMGSKG
KIISGSSGSLLSSGSQESDSSQSAKKDMLAALKSRQEALEETLRQRLEELKRLCLREAELTGKLPVEYPLDPGEEPPIVR
RRIGTAFKLDEQKILPKGEEAELERLEREFAIQSQITEAARRLASDPNVSKKLKKQRKTSYLNALKKLQEIENAINENRI
KSGKKPTQRASLVIDDGNIASEDSSLSDALVLEDEDSQVTSTISPLQSPHKGLPPRPPSSHNRPPPPQSLEGLRQMHYHR
TDYDKSPLKPKMWSESSLDEPYEKVKKRSSHSHSSSHKRFPSTGSCTEAGVSSSLQNSPIRGLPHWNSQSSMPSTPDLRV
RSPHYVHSTRSVDISPTRLHSLALHFRHRSSSLESQGKLLGSENDTGSPDFYTPRTRSSNGSDPMDDCSSCTSHSSSEHY
YPAQMNANYSTLAEDSPSKARQRQRQRQRAAGALGSASSGSMPNLAARSGAAGAGGGGVYLHSQSQPSSQYRIKEYPLYI
EGSATPVVVRSLESDQEGHYSVKAQFKTSNSYTAGGLFKESWRGGGDEGDAGRLTPSRSQILRTPSLGRDGTHDKGSGRA
AVSDELRQWYQRSTASHKEHSRLSHTSSTSSDSGSQYSTSSQSTFVAHSRVTRMPQMCKATSAALPQSQRSSTPSSEIGA
TPPSSPHHILTWQTGSYSDSCFLDSSLYPELADVQWYGQEKAKPGTLV
```

103 - 122:	EEEEEEEEEEEEEEEEEEEE

104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE

A0A061I5Y8 **A0A061I5Y8_CRIGR** (2052 aa)
Liprin-beta-2. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MPGARDALCHQALQLLAELCARGALEHDSCQDFIYHLRDRARPRLRDPDISVSLLTLVVTACGLALFGVSLFVSWKLCWV
PWRERGLFSGSKDNQEPLNCTDTETNEQENSEDFLDPPTPCPDSSMKISHTSPDIPLSTQPGGQENCAHAIRVQRQVTEP
TPSARPNSIRRQLNLSNPDFNIHQLQRQEQLTGIGKIKPELYKQRSLDNDDGRRSNSKACGKLNFILKYDCDLEQLIVKI
HKAVNLPAKDFSGTSDPYVKIYLLPDRKTKHQTKVHRKTLNPVFDEVFLFPVPYNDLEARKLHFSVYDFDRFSRHDLIGQ
VVVDHFFDLADFPRECILWKDIEYVTNQDALTLSVKKLLTDQATMLLSNVFLEDCCSMVKLYSVFSVGRLKYDRKYLPLV
LRKAVYRVGPLIDNVDLGELMFSLCYLPTAGRLTITIIKARNLKAMDITGASDPYVKVSLMCDGRRLKKRKTSTKRNTLN
PVYNEAIVFDVPPESIDQIHLSIAVMDYDRVGHNEVIGVCHVGNEAERLGRDHWSEMLSYPRKPIAHWHSLMESPPYSIL
KLHKLYGNLKDFGSAWQSNGYQVLKNRLSMHLKLSTWCAQHLMNARMMVAHRGACLLVLLLAAFLPPPQHAQDPAMVHYI
YQRFQVLEQGLEKCTQTTRAYIQDFQEFSKNISIMLGKCQTHTSEYKSAVNNLALRVERAQREIDYLEYLREADICIESE
EKTLAEKVLQEAEEEKKIRTLLNASCDNMLMSIKSLKIVKKTMDTDGSWMKDAGGNSAKVYLLIGSRNNTVWEFANLRAF
MEDSTKPGPRKLILPLSWQGSGQVIYKSFLFFHNQGTSNEIIKYNLQKKTVEDRMLLPGGAGRAPIYQHSLSTYIDLAVD
EHGLWAIHSGPGIQGHLVVTKIDPDTLGVEHSWETPCRNQDAEASFLLCGVLYVVYSFGGQGPHRITCVYDPLGTVREEH
LPNLFFPRRPRSHSMIHYNPRDKQLYAWNEGNQIIYKLQTKKRLPLEYVQIFIVAKPELRVQVPAVLTHLFARVLMFCSH
VNPLATPVILDYQGLKEEEEEEEEEEEEEEEEEEEEEEEEGKEKKRLCPVEICQHSSGGTYLSSSNTEGQQGPKYGFVA
LGGLWFGEKGLSIWQEETKQTKGAMASDASHVLEAALEQMDGIIAGTKTVADISDGTCEPGLSPPSSCMNSIPVLHLIED
LRLALEMLALPQEREALLSQIPGPTAAYIKEWFEDSLSQVNHHSAASNETYQERLARLEGDKESLILQVSVLTDQVEAQG
EKIRDLEVCLEGHQVKLNAAEEMLQQELLSRTSLETQKLDLMTEVSELKLKLVGMEKEQREQEEKQKKAEELLQELKHLK
IKVEELENERNQYEWELKATKAEVAQLQEQVALKDAEIERLHSQLSRSAALHSDHTERDQEIHRLKMGMETLLVANEDKD
RRIEELTGLLNKYLRVKEIVKATQGPSERTISINEDEMEGSFRKWNPTNKNPEEVLKQEVSPRGSSPTPGPPPLPQKSLE
TRAQKKLSCSLEDLRHDSGDKCVDGNQLSLVGEPKDSSFLAEQKYPTLPGKLSGAMPNGEAAKSPTASPQPDPSGSSLLK
LRETESGWEDTVLTNELSSTSSGTESSPQSPLTPDGKRSPKGIKKFWGKIRRTQSGNFNTDAPGMAEFRRGGLRATAGPR
LSRTRDTKGQKCDANAPFAQWSTERVCAWLEDFGLAQYVIFARQWVASGHTLLTATPQDMEKELGIKHPLHRKKLVLAVK
AINAKQEEKSALLDHIWVTRWLDDIGLPQYKDQFHESRVDGRMLQYLTVNDLLFLKVTSQLHHLSIKCAIHVLHVNKFNP
HCLHRRPADESNLSPSEVVQWSNHRVMEWLRSVDLAEYAPNLRGSGVHGGLIILEPRFTGDTLAMLLNIPPQKTLLRRHL
TTKFNALIGPEAEQEKRDKMASPAYSPLTTTAKVRPRKLGFSHFGNMRKKKFDESTDYICPMEPGDAANDSHRVYGVYRG
QSPLDNHELDGLDQMAPSEGTVTQIGLLSQDIHRLTTLLSEDQLLNDSPGCP
```

1057 - 1076:	EEEEEEEEEEEEEEEEEEEE
1058 - 1077:	EEEEEEEEEEEEEEEEEEEE
1059 - 1078:	EEEEEEEEEEEEEEEEEEEE
1060 - 1079:	EEEEEEEEEEEEEEEEEEEE
1061 - 1080:	EEEEEEEEEEEEEEEEEEEE
1062 - 1081:	EEEEEEEEEEEEEEEEEEEE

A0A061I622 **A0A061I622_CRIGR** (1173 aa)
Rho family-interacting cell polarization regulator 2. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MQFLDPEEFLVDEEDDVFGEEEEEEEEEEEEEEEEEEEEEEEEEEEEDNEGQGREGHLGTEVKLAVINDSDIRARTGSGLN
LEWQDHTILFVGLPTRLPEIMLVGSQSFSPGGPNGIIRSQSFAGFSGLQERRSRQLILAIMSSHVLTFGDMTHQRCNSFI
ENASALKKPQAKLKKMHNLGHKNNNTPKEPQPKRVEEVYRALKNGLDEYLEFHQTELDKLTAQLKDMKRNSRLGVLYDLD
KQIKTIERYMRRLEFHISKVDELYEAYCIQRRLQDGASKMKQAFAASPASKAARESLSEINRSYKEYTENMCTIEAELES
LLGEFSIKMKGLAGFARLCPGDQYEIFMKYGRQRWKLKGKIEVNGKQSWDGEETVFLPLIVGLISIKVTELKGLATHILV
```

```
GSVTCETKELFAARPQVLAVDINDLGTIKLNLEITWYPFDVEDTTPSSGPGNKTAALQRRMSMYSQGTPETPTFKDHSFF
RWLRLSVLSALRDTFFATLHHNHSVGDLPSLSLNPKALLEFYSNLPDDIFESGKATEEKRPLSLSFSDLQDGDCVFTSSS
ATSPSSSHSAHPEITITPAELTHGSLSSQNEGTEDSSSASSRNSLGEDHEPKSHTKSDTVEARKPGVSAGSRAESLFLEN
SVAEALLQESDEASELKPVELDTFEGNITKQLVKRLTSAEGPIVTEKLFFEGSVGSESEAGRSFLDGSLEDAFNGLFLAL
DPHKEQYKEFQDLNQEVTHLDDVLKCKPVGSRSRSSSLSLTVESALESFDFLNTSDFDEEEDGDEACHGGGGADSVFSDT
ETEKTGYRSVHPEARGHLSEALTEDTGVGTSVAGSPLPLTTGNESLDITIVKHLQYCTQLIQQIVFSSKIPFVARSLLEK
LSRQVLVMEKLAAVSDENLGNITSVVEAIPEFHKKLSLLSFWTKCCSPVGVYHSSADRVIKQLEASFARTINKEFPGLAE
PVFRTLVSQILDRSEPLLPSSLSSEVITVFQYYSFFTSHGVSDLETYLSQLARQVAMVQTLQSLRDEKLLQTMSDFTPSN
LPAQQEVLRTLALLLTRDDNEVSEAVTLYLAAASKNEHFREKALLYYCEALTKTNLQLQKAACLALKSLEATESIKMLVT
LCQSDTEEIRNVASETLLSLGEDGRLAYEQLDKFPRDCVKVGGRHGTEVATAF
```

20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE

A0A061I6S5 **A0A061I6S5_CRIGR** (148 aa)
Uncharacterized protein (Fragment). *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
ESEVIQEERLKTVIYLYDEVKVMKNEGRSSGALIQVLVMREILLCHKVLTQGVGFDSWQWEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEERGGGGKGRRRKGEEKEGEREGRSRRNMSNEYDTDNAETYRFLS
```

61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE

A0A061I6V1 **A0A061I6V1_CRIGR** (806 aa)
Kinesin-like protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MKRHKNGNKQYFTKMGTRKKVQAFVRVKPTDDFAHDMIKYGDDNKSIDIHLKKDTRRGVVNNQQTDWSFKLDGVLHDATQ
DLVYETVAKDAVSQALDGYNGTIMCYGQTGAGKTYTMTGATENYKHRGILPRALQQVFRMIEERPTHAITVRVSYLEIYN
ENLFDLLSTLPYVGPSVSPMTIVENPQGVFIKGLSVHLTSQEEDAFSLLFEGETNRIIASHTMNKNSSRSHCIFTIYVEA
HSRTLSDEKYITSKINLVDLAGSERLGKTGSEGRVLKEATYINKSLSFLEQAIIALGDQKRDHIPFRQCKLTHALKDSLE
EEEEEEEEEEEEEEEEEEEEGLLSSLKFASRMKLVTTEPAINEKYDAERMVKNLEKELALLKQELAIHDSLSNRTLVNYD
PMDEIQIAEINSQVRRYLEGTLDEIDIINLRQIQEVFNQFKVVLSQQEQEVEAALRRKYTLIDKNDFAAISAVQKAGLMD
AEGHLVGEPDGQSFGLGVAPFSIKPGKKIKSKKTGKEQISTSARKEGASSPGSGKDLDVGPSVSKTQLIPSSKDGDIKDM
```

```
LSRDRETSSIEPLPSDSPKEESRPIRPSTPPPKPVAFEDFKNERGSEINRIFKENKSILNERRKRASETTQRINAIKQEI
DVTKEALNFQKSLREKQGQYENKGLMIIDEEEFLLILKLKDLKKQYRNEYQELRDLRAEIQYCQRLVDQCRNRLLMEFDI
WYNESFVIPEEIQTALKIGSSIRPGMVPVSRIVSLGEDDQDRFSQLQQTVLPEGPDSISFYNAKVKTEQKHSYMKTMIGL
PQSHRK
```

320 - 339:	EEEEEEEEEEEEEEEEEEEE
321 - 340:	EEEEEEEEEEEEEEEEEEEE

A0A061I6W6 **A0A061I6W6_CRIGR** (723 aa)
Kelch-like protein 24 (Fragment). *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
PWDPINVCFNFKTTFLHSYFCEVLTTVKDIAMTPPENTNSLLIQQLLAILFFKMNKARQEGGKEEEEEEEEEEEEEEEEE
EEEEEPPSPSTIPQPPPPPWCKVECCISGPKLSFLKKNLVSFYVHECFDGILNREDLGVRDSPATKRKVFEMDPKSLTGH
EYFDFSSGSSHAENILQIFNEFRDSRLFTDVIICVEGKEFPCHRAVLSACSSYFRAMFCNDHRESREMLVEINGILAEAM
ECFLQYVYTGKVKITTENVQYLFETSSLFQISVLRDACAKFLEEQLDPCNCLGIQRFADTHSLKTLFTKCKTFALQTFED
VSQHEEFLELDKDELIDYICSDELVIGKEEMVFEAVMRWVYRAVDLRRPLLHELLTHVRLPLLHPNYFVQTVEVDQLIQN
SPECYQLLHEARRYHILGNEMMSPRTRPRRSTGYSEVIVVVGGCERVGGFNLPYTECYDPVTGEWKSLAKLPEFTKSEYA
VCALRNDILVSGGRINSRDVWIYNSQLNIWIRVASLNKGRWRHKMAVLLGKVYVVGGYDGQNRLSSVECYDSFSNRWTEV
APLKEAVSSPAVTSCIGKLFVIGGGPDDNTCSDKVQSYDPETNSWLLRAAIPIAKRCITAVSLNNLIYVAGGLTKAVYCY
DPVEDYWMHVQNTFSRQENCGMSVCNGKIYILGGRRENGEATDTILCYDPATSIITGVAAMPRPVSYHGCVTIHRYNEKC
FKL
```

64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE

A0A061I6Y3 **A0A061I6Y3_CRIGR** (1077 aa)
FERM domain-containing protein 4A isoform 2. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MGKFALPQLCTAKSAAGYLGPVGAGGGHLNWLQLDRRVLEHDFPKKSGPVVLYFCVRYAPKCSLNPLTSSISAPNTHAVQ
WQPVIPITDAPGPPPPSTSQIQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEELCGREAFELKFYIES
ISYLKDNATIELFFLNAKSCIYKELIDVDSEVVFELASYILQEAKGDFSSNEVVRSDLKKLPALPTQALKEHPSLAYCED
RVIEYYKKLNGQTRGQAIVNYMSIVESLPTYGVHYYAVKDKQGIPWWLGLSYKGIFQYDYHDKVKPRKRLSEACDSCFSR
ASVTRRTFGHSGIAVHTWYACPALIKSIWAMAISQHQFYLDRKQSKSKIHAARSLSEIAIDLTETGTLKTSKLANMGSKG
KIISGSSGSLLSSGSQESDSSQSAKKDMLAALKSRQEALEETLRQRLEELKRLCLREAELTGKLPVEYPLDPGEEPPIVR
RRIGTAFKLDEQKILPKGEEAELERLEREFAIQSQITEAARRLASDPNVSKKLKKQRKTSYLNALKKLQEIENAINENRI
KSGKKPTQRASLVIDDGNIASEDSSLSDALVLEDEDSQVTSTISPLQSPHKGLPPRPPSSHNRPPPPQSLEGLRQMHYHR
TDYDKSPLKPKMWSESSLDEPYEKVKKRSSHSHSSSHKRFPSTGSCTEAGVSSSLQNSPIRGLPHWNSQSSMPSTPDLRV
RSPHYVHSTRSVDISPTRLHSLALHFRHRSSSLESQGKLLGSENDTGSPDFYTPRTRSSNGSDPMDDCSSCTSHSSSEHY
YPAQMNANYSTLAEDSPSKARQRQRQRQRAAGALGSASSGSMPNLAARSGAAGAGGGGVYLHSQSQPSSQYRIKEYPLYI
EGSATPVVVRSLESDQEGHYSVKAQFKTSNSYTAGGLFKESWRGGGDEGDAGRLTPSRSQILRTPSLGRDGTHDKGSGRA
AVSDELRQWYQRSTASHKEHSRLSHTSSTSSDSGSQYSTSSQSTFVAHSRVTRMPQMCKATSAALPQSQRSSTPSSEIGA
TPPSSPHHILTWQTGEATENSPIMDGSESPTHQSTDE
```

103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE

126 - 145:	EEEEEEEEEEEEEEEEEEEE

A0A061I798 **A0A061I798_CRIGR** (1345 aa)
Rho family-interacting cell polarization regulator 2. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MQFLDPEEFLVDEEDDVFGEEEEEEEEEEEEEEEEEEEEEEEEEEDNEGQGREGHLGTEVKLAVINDSDIRARCNSFIE
NASALKKPQAKLKKMHNLGHKNNNTPKEPQPKRVEEVYRALKNGLDEYLEFHQTELDKLTAQLKDMKRNSRLGVLYDLDK
QIKTIERYMRRLEFHISKVDELYEAYCIQRRLQDGASKMKQAFAASPASKAARESLSEINRSYKEYTENMCTIEAELESL
LGEFSIKMKGLAGFARLCPGDQYEIFMKYGRQRWKLKGKIEVNGKQSWDGEETVFLPLIVGLISIKVTELKGLATHILVG
SVTCETKELFAARPQVLAVDINDLGTIKLNLEITWYPFDVEDTTPSSGPGNKTAALQRRMSMYSQGTPETPTFKDHSFFR
WLRLSVLSALRDTFFATLHHNHSVGDLPSLSLNPKALLEFYIQQQKQFLMVCFPLPAYTHISNKSPALKSFHLNCLLSCL
EMNCAKHIMLYLSLQSNLPDDIFESGKATEEKRPLSLSFSDLQDGDCVFTSSSATSPSSSHSAHPEITITPAELTHGSLS
SQNEGTEDSSSASSRNSLGEDHEPKSHTKSDTVEARKPGVSAGSRAESLFLENSVAEALLQESDEASELKPVELDTFEGN
ITKQLVKRLTSAEGPIVTEKLFFEGSVGSESEAGRSFLDGSLEDAFNGLFLALDPHKEQYKEFQDLNQEVTHLDDVLKCK
PVGSRSRSSSLSLTVESALESFDFLNTSDFDEEEDGDEACHGGGGADSVFSDTETEKTGYRSVHPEARGHLSEALTEDTG
VGTSVAGSPLPLTTGNESLDITIVKHLQYCTQLIQQIVFSSKIPFVARSLLEKLSRQVLVMEKLAAVSDENLGNITSVVE
AIPEFHKKLSLLSFWTKCCSPVGVYHSSADRVIKQLEASFARTINKEFPGLAEPVFRTLVSQILDRSEPLLPSSLSSEVI
TVFQYYSFFTSHGVSDLETYLSQLARQVAMVQTLQSLRDEKLLQTMSDFTPSNLPAQQEVLRTLALLLTRDDNEVSEAVT
LYLAAASKNEHFREKALLYYCEALTKTNLQLQKAACLALKSLEATESIKMLVTLCQSDTEEIRNVASETLLSLGEDGRLA
YEQRICKKTRQGYRKLLTYLRGLWKTFKTHFKPQEEEQALSTADCIFHKEKIEELGKTLKNIHLSLEKRAMAAQKIGLLA
FTGGVVAANFASEYMKEVAFIMQTEKVMSPKTKILLLQSVACWCYLNPASQKRARQLQFIPIFITFFDTPFHSTIKSEVN
SHRLVQFWTCYALSSMTCNNLSIIRELRSYGTLKYHLQILAMENWVGWSENFAEVLYFLLGFHRN
```

20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE

A0A061I7Q4 **A0A061I7Q4_CRIGR** (301 aa)
Heterogeneous nuclear ribonucleoprotein H2 isoform 2. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MMLGPEGGEGYVVKLCGLLWSGSIEDVQNFLSNCTIHDGVSGVHFIYTSEGRQSGEAFVELQSENDVKLALKKKKDRESM
GHRYIEVFKSHRTKMDWVLKHSGSNRANSANDGFVRLPGLPFGCTKEEIVQFFSGLEIVPNGITLPVDPEGKITGEAFIQ
IASQELAEKALGKHKERIGQSAGYGSYEEYSGLGDGYGFTTDLFGRDLSYSFSGMYDHRYGDSEFTGQSTTESRAPRTIA
SRRERQFFLYGMHANDEKEEEEEEEEEEEEEEEEEEEEEEEELEPVRSSVGSLSMRTQRKL
```

259 - 278:	EEEEEEEEEEEEEEEEEEEE
260 - 279:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE
262 - 281:	EEEEEEEEEEEEEEEEEEEE
263 - 282:	EEEEEEEEEEEEEEEEEEEE

A0A061I823 **A0A061I823_CRIGR** (116 aa)
Uncharacterized protein (Fragment). *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
PLSQTTISNQVPNLGFCKNFFHLPPVTGIFCAAANISTQVDLLPLLLVFKPKERKKKKKKKKKKKKKKKKKKKKKKKKK
REEEEEEEEEEEEEEEEEEEEAERCERRLGKMFLKI
```

82 - 101:	EEEEEEEEEEEEEEEEEEEE

A0A061I989 **A0A061I989_CRIGR** (1010 aa)
Intersectin-1 isoform 1. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MLGGILNDKVPNNFALITGAFLNAFPTHSFVPGDGKGRREEEEEEEEEEEEEEEEEEEEEEEEDDDLMLESWKGSAYLSS
DVHRCKRNRTMAQFPTPFGGSLDIWAITVEERAKHDQQFHSLKPISGFITGDQARNFFFQSGLPQPVLAQIWALADMNND
GRMDQVEFSIAMKLIKLKLQGYQLPSALPPVMKQQPVAISNAPAFATLPKSSSFSRSGPGSQLNTKLQKAQSFDVASAPP
AAEWAVPQSSRLKYRQLFNSHDKTMSGHLTGPQARTILMQSSLPQTQLASIWNLSDIDQDGKLTAEEFILAMHLIDVAMS
GQPLPPVLPPEYIPPSFRRVRSGSGMSVISSSSVDQRLPEEPASEDEQQLEKKLPVTFEDKKRENFERGNLELEKRRQAL
LEQQRKEQERLAQLERAEQERKERERQEQERKRQLELEKQLEKQRELERQREEDRRKEIERRENDKKHQLEGKLQDIRCR
LTTQRQDLESTNKSRELRIAEITHLQQQLQESQQMLGRLIPEKQILNDQLKQVQQNSLHRDSLLTLKRALEAKELARQQL
RDQLDEVERETRSKLQEIDVFNNQLKELREIHSKQQLQKQKSIEAERLRQKEQERKSLELEKQKEETQRRVQERDKQWLE
HVPREEHPRPRKPHEEDKLKREDSIRKKEGEERAKPQVQDKLNRLFHPHQDSAKPAVQAPWSATEKGPLTISAQENVKVV
YYRALYPFESRSHDEITIQPGDVVMVDESQTGEPGWLGGELKGKTGWFPANYAEKIPENEVPTPAKPVTDLTSAPIPKLA
LRETPAPLPVTSSEPSTTPNNWADFSSTWPASTSEKPETDNWDAWAAQPSLTVPSAGQLRQRSAFTPATATGSSPSPVLG
QGEKVEGLQAQALYPWRAKKDNHLNFNKNDVITVLEQQDMWWFGEVQGHKGWFPKSYVKLISGPVRKATSIDTGPTESPA
SLKRVSSPAAKPAVPGEASEALKQEQCVLALKGQLTCEVFSYHQHQLAVE
```

40 - 59:	EEEEEEEEEEEEEEEEEEEE

41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE

A0A061I9A3 **A0A061I9A3_CRIGR** (155 aa)
Armadillo-like helical containing protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MRARTVSIIALQFLRLHAVQYFSKCIFMTKKRKEEKKKKKKEEEEEEEEEKEKKKKKKKKKKKKXEEEEEEEEEEEEEE
EEEEEEEEEEEEARMQKKCGFGILPVNVLLFSPDVCLSSQSMLDVQVLSALLILSLAGNYSKRGLKTLFLKDIRS
```

67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE

A0A061I9M3 **A0A061I9M3_CRIGR** (86 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MNLIKRGENKIEEEEEEEEGEGEGGGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEIIQRSREKRRDG
HSSTHL
```

27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE

A0A061I9M8 **A0A061I9M8_CRIGR** (1252 aa)
Rho family-interacting cell polarization regulator 2. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MQFLDPEEFLVDEEDDVFGEEEEEEEEEEEEEEEEEEEEEEEEEEEDNEGQGREGHLGTEVKLAVINDSDIRARTGSGLN
LEWQDHTILFVGTGEMTQWLRAHFALAEDPSSIFSIHIWPVTTTYNSISSSSNTSDLNGHLHSKVSEAFHGPHDQDLVSH
LTLYTCGCRQAQCFCANLPDSHHGLPSILQDCQPDSQKSCWWDLNPSRLEGPMASSGASPSRALAACRKGDPGKCNSFIE
NASALKKPQAKLKKMHNLGHKNNNTPKEPQPKRVEEVYRALKNGLDEYLEFHQTELDKLTAQLKDMKRNSRLGVLYDLDK
QIKTIERYMRRLEFHISKVDELYEAYCIQRRLQDGASKMKQAFAASPASKAARESLSEINRSYKEYTENMCTIEAELESL
LGEFSIKMKGLAGFARLCPGDQYEIFMKYGRQRWKLKGKIEVNGKQSWDGEETVFLPLIVGLISIKVTELKGLATHILVG
SVTCETKELFAARPQVLAVDINDLGTIKLNLEITWYPFDVEDTTPSSGPGNKTAALQRRMSMYSQGTPETPTFKDHSFFR
WLRLSVLSALRDTFFATLHHNHSVGDLPSLSLNPKALLEFYSNLPDDIFESGKATEEKRPLSLSFSDLQDGDCVFTSSSA
TSPSSSHSAHPEITITPAELTHGSLSSQNEGTEDSSSASSRNSLGEDHEPKSHTKSDTVEARKPGVSAGSRAESLFLENS
```

```
VAEALLQESDEASELKPVELDTFEGNITKQLVKRLTSAEGPIVTEKLFFEGSVGSESEAGRSFLDGSLEDAFNGLFLALD
PHKEQYKEFQDLNQEVTHLDDVLKCKPVGSRSRSSSLSLTVESALESFDFLNTSDFDEEEDGDEACHGGGGADSVFSDTE
TEKTGYRSVHPEARGHLSEALTEDTGVGTSVAGSPLPLTTGNESLDITIVKHLQYCTQLIQQIVFSSKIPFVARSLLEKL
SRQVLVMEKLAAVSDENLGNITSVVEAIPEFHKKLSLLSFWTKCCSPVGVYHSSADRVIKQLEASFARTINKEFPGLAEP
VFRTLVSQILDRSEPLLPSSLSSEVITVFQYYSFFTSHGVSDLETYLSQLARQVAMVQTLQSLRDEKLLQTMSDFTPSNL
PAQQEVLRTLALLLTRDDNEVSEAVTLYLAAASKNEHFREKALLYYCEALTKTNLQLQKAACLALKSLEATESIKMLVTL
CQSDTEEIRNVASETLLSLGEDGRLAYEQLDKFPRDCVKVGGRHGTEVATAF
```

20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE

A0A061I9P6 **A0A061I9P6_CRIGR** (238 aa)
Centromere protein N-like protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MWSSEEEEEEEEEEEEEEEEEEEEEEEEEEGGDTQVHRHRKLWNVFEMSKEPGEDVDLFDMKWFQCSFKKILQRALRNALKV
ASKHHQIVQMDLRSRHLDSLKAIVFREYDQTFESHNSTVPLQEGNLGLDMNLDSNIIHENLEEKERIHRVTQETFGAHPQ
PQLEFAQYKLETKFKSGISGGILADRKEPLRCLIKFSSPHLLEALKSLAPAGIADAPLSPLLTCIANKKMNYFKIRDK
```

5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE

A0A061I9W9 **A0A061I9W9_CRIGR** (144 aa)
Putative polypeptide N-acetylgalactosaminyltransferase-like protein 3 (EC 2.4.1.41). *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MASLRRVKVLLVLNLIAVAGFVIFLAKCRPIAVRSGDAFHEIRPRAEVANLSTHSASPIQDAVLKRLSLLEDIVYRQLNE
EEEEEEEEEEEEEEEEEEEEKYGLSTLEMYQSPDDEGTDSNTNSHKGDNREHLLNTCLMYQSLH
```

80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE

A0A061IA04 **A0A061IA04_CRIGR** (467 aa)
Metal transporter CNNM1 (Fragment). *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
DNRKKQRVPHRERRRHDFSLFKLSDSEIRVKISPQLLLATHRFMATEVEPFKSLYLSEKILLRLLKHPNVIQELKFDERN
KKAPEHYLYQRSRPVDYFVLLLQGKVEVEVGKEGLRFENGAFTYYGVPAIMTTACSVPVSVSRTFAFSRGDSLAGSPVNR
SPSRCSGLNRSESPNRERSDFGGSNTQLYSSSNNLYTPDYSVHILSDVQFVKITRQQYQNALTACHMDSSPQSPDMEAFT
DGDSTKAPTTRGTPQTPKDDQVLTLLSNRTSLPCSRSDGLRSPGEVVYLRMEEMAFPQEEMTNFEEHKTQQFSLSPAAVP
TSDKYSVLCSGIKMQLCTRQWWFTPLIPAVKEAESGRYCEFKDSQGFTQRNPFWKNQKEKEEEEEEEMMMMMMMMMKKRR
RRRKEEEEEEEEEEEEEEEEEEEEEEEEEEEERELASSIAPTGLQSRQSLWNFPCILGSLHLRCRVPLP
```

405 - 424:	EEEEEEEEEEEEEEEEEEEE
406 - 425:	EEEEEEEEEEEEEEEEEEEE
407 - 426:	EEEEEEEEEEEEEEEEEEEE
408 - 427:	EEEEEEEEEEEEEEEEEEEE
409 - 428:	EEEEEEEEEEEEEEEEEEEE
410 - 429:	EEEEEEEEEEEEEEEEEEEE
411 - 430:	EEEEEEEEEEEEEEEEEEEE

A0A061IA27 **A0A061IA27_CRIGR** (81 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MYEYAPYRVPGQPLKQYRETLSQEEEEEEEEEEEEEEEEEEEEEEEKKKKKKKKKKKKKKKKKKKKKKKKKKNCSQTAVT
H
```

24 - 43:	EEEEEEEEEEEEEEEEEEEE

25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE

A0A061IA81 **A0A061IA81_CRIGR** (95 aa)
Uncharacterized protein (Fragment). *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
LEVALLPGHRQCPGVLDPTAEFGSEGGEGRGGGRKAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEVILQGWLSR
```

37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE

A0A061IAH4 **A0A061IAH4_CRIGR** (586 aa)
Cytochrome-b5 reductase (EC 1.6.2.2). *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MNEFFFHEVSLKQKQTHVCGGTIISSQWVITAAHCMANRKVALTLNVTAGEHNLSQAEPGEQTLAIETIIIHPQFSTRKP
MNYDIALLKMVGTFQFGPFVRPVCLPEPGEHFKAGFVCTTAGWGRLAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEINI
LPKRQNTCIQLLMMEGLSIFTSEQLCVWTLLVPEDMHILLSLSHLDAESCYHNYLAMYSLEDRLVGKFCGESLPSSILVG
SSSIRLRFISDATDYATGFSLTYKALKPNYLPDSGCKSLTILFEEGTIHSLHYPEDYSDMASCTWIFQAPSHFLIKDHSL
LLAFGVIRATVILFALKKMSLKEKDCITLQDPEAKYPLPLIEKEQINHNTRRFRFGLPSQDHVLGLPVGNYVHFLAQIKD
ELVIRAYTPVSSDDDKGFVDFIIKIYFKDVHPTYPEGGKMTQYLENMKIGDTILFRGPTGRLFYHNPGITPMLQLIRHIT
KNSNDGTRMSLLFANQTEEDILLRKELEEVTTTHRHQFNLWYTLDWPPDGWKYSSGFVTADMIKEHLPAPGEDTLILLCG
PPPMIQEAVRPSLEQLGYTKDMIFTY
```

128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE

133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE

A0A061IAJ9 **A0A061IAJ9_CRIGR** (1092 aa)
Rho family-interacting cell polarization regulator 2. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MQFLDPEEFLVDEEDDVFGEEEEEEEEEEEEEEEEEEEEEEEEEEEDNEGQGREGHLGTEVKLAVINDSDIRARCNSFIE
NASALKKPQAKLKKMHNLGHKNNNTPKEPQPKRVEEVYRALKNGLDEYLEFHQTELDKLTAQLKDMKRNSRLGVLYDLDK
QIKTIERYMRRLEFHISKVDELYEAYCIQRRLQDGASKMKQAFAASPASKAARESLSEINRSYKEYTENMCTIEAELESL
LGEFSIKMKGLAGFARLCPGDQYEIFMKYGRQRWKLKGKIEVNGKQSWDGEETVFLPLIVGLISIKVTELKGLATHILVG
SVTCETKELFAARPQVLAVDINDLGTIKLNLEITWYPFDVEDTTPSSGPGNKTAALQRRMSMYSQGTPETPTFKDHSFFR
WLRLSVLSALRDTFFATLHHNHSVGDLPSLSLNPKALLEFYSNLPDDIFESGKATEEKRPLSLSFSDLQDGDCVFTSSSA
TSPSSSHSAHPEITITPAELTHGSLSSQNEGTEDSSSASSRNSLGEDHEPKSHTKSDTVEARKPGVSAGSRAESLFLENS
VAEALLQESDEASELKPVELDTFEGNITKQLVKRLTSAEGPIVTEKLFFEGSVGSESEAGRSFLDGSLEDAFNGLFLALD
PHKEQYKEFQDLNQEVTHLDDVLKCKPVGSRSRSSSLSLTVESALESFDFLNTSDFDEEEDGDEACHGGGGADSVFSDTE
TEKTGYRSVHPEARGHLSEALTEDTGVGTSVAGSPLPLTTGNESLDITIVKHLQYCTQLIQQIVFSSKIPFVARSLLEKL
SRQVLVMEKLAAVSDENLGNITSVVEAIPEFHKKLSLLSFWTKCCSPVGVYHSSADRVIKQLEASFARTINKEFPGLAEP
VFRTLVSQILDRSEPLLPSSLSSEVITVFQYYSFFTSHGVSDLETYLSQLARQVAMVQTLQSLRDEKLLQTMSDFTPSNL
PAQQEVLRTLALLLTRDDNEVSEAVTLYLAAASKNEHFREKALLYYCEALTKTNLQLQKAACLALKSLEATESIKMLVTL
CQSDTEEIRNVASETLLSLGEDGRLAYEQLDKFPRDCVKVGGRHGTEVATAF
```

20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE

A0A061IAM5 **A0A061IAM5_CRIGR** (77 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MNLQLQRFWSELQTASKATEKPCLEKQNKTKQKQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAG
```

35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE

A0A061IAP5 **A0A061IAP5_CRIGR** (185 aa)
Putative caiB/baiF CoA-transferase family protein C7orf10 like protein (EC 2.-.-.-). *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MQSGFYDCKHLPVFSLMEHRGRGGPAVRYSKFKMSEAKPPPLLGQHTKHILKEVLRYDDRAIGELLGSGVIEQHETNLCN
IDIIGMDEDSGFARVQSHAELISHVLAVIPELEQKEKPEKPSDVPVISISSGFKTHPYLEGYVFIQEEEEEEEEEEEEE
EEEEEEEEEEEEEEKKNMALNYGR
```

147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE

A0A061IAS4 **A0A061IAS4_CRIGR** (177 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MDKQLTRKQTQGDAFFEFSISTRTKPSKTKIVNPSENLIKHGLIHFVGGQRSTHPEEPKGKSTKQTSRTRKKKKKKEEEE
EEEEEEEKKKRRKKKKRRKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEENLIVEAAVFGNQKSHHVVLAYLATRGNPPVSAF
QALGLQRRFIVPGSATL
```

100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE

A0A061IB14 **A0A061IB14_CRIGR** (107 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MDAPCSPDMFTAAYFQFNFYKQRGGEEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEPDNRKQTIAHARKIKLYRHN
CTTHITLDEIISNRYRIPLYEVLFRTI
```

35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE

A0A061IC00 **A0A061IC00_CRIGR** (73 aa)
Uncharacterized protein (Fragment). *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
EEKHTKVFFFYYSPFHNLLYKEGGGGGGGGGGEEEEEEEEKKKKKKKEEEEEEEEEEEEEEEEEEEEEARPLN
```

48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE

A0A061IC42 **A0A061IC42_CRIGR** (134 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MLGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGRKKLRLGNGWLALYNQGETTQGVVLPTVGDDDDDDDDDDDDDDNDN
DSNDDEEDDNDEDRVGDGNEDNDGVRDDDEDNYVNGYDGDEVGGDDDDGMGMVM
```

4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE

A0A061IC77 **A0A061IC77_CRIGR** (185 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MSKGKALSSPDAALEQAAPQRSHRGKAEHQAVLQAISPLLFNRPFLEQRICGSWWAPPRGDRNESVCEMYSEQNPERERM
ICHTITQLGHFLLLVTEDPLLKTCRIQRYYSRGWTQELLFLVNSSARRHSNAEEEEEEEEEEEEEEEEEEEEEEEGEEG
EKGEEGEKGRRRNETMKLLVQFEAT
```

133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE

A0A061ICC8 **A0A061ICC8_CRIGR** (848 aa)
Kinesin-like protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MKRHKNGNKQYFTKMGTRKKVQAFVRVKPTDDFAHDMIKYGDDNKSIDIHLKKDTRRGVVNNQQTDWSFKLDGVLHDATQ
DLVYETVAKDAVSQALDGYNGTIMCYGQTGAGKTYTMTGATENYKHRGILPRALQQVFRMIEERPTHAITVRVSYLEIYN
ENLFDLLSTLPYVGPSVSPMTIVENPQGVFIKGLSVHLTSQEEDAFSLLFEGETNRIIASHTMNKNSSRSHCIFTIYVEA
HSRTLSDEKYITSKINLVDLAGSERLGKTGSEGRVLKEATYINKSLSFLEQAIIALGDQKRDHIPFRQCKLTHALKDSLG
EDVFGPQRGGSVSWGGLGLAQEEEEEEEEEEEEEEEEEEEEGLLSSLKFASRMKLVTTEPAINEKYDAERMVKNLEKELA
LLKQELAIHDSLSNRTLVNYDPMDEIQIAEINSQVRRYLEGTLDEIDIINLRQIQEVFNQFKVVLSQQEQEVEAALRRKY
TLIDKNDFAAISAVQKRDRSLDLLASQPGIVFNVWNQAGLMDAEGHLVGEPDGQSFGLGVAPFSIKPGKKIKSKKTGKEQ
ISTSARKEGASSPGSGKDLDVGPSVSKTQLIPSSKDGDIKDMLSRDRETSSIEPLPSDSPKEESRPIRPSTPPPKPVAFE
DFKNERGSEINRIFKENKSILNERRKRASETTQRINAIKQEIDVTKEALNFQKSLREKQGQYENKGLMIIDEEEFLLILK
LKDLKKQYRNEYQELRDLRAEIQYCQRLVDQCRNRLLMEFDIWYNESFVIPEEIQTALKIGSSIRPGMVPVSRIVSLGED
DQDRFSQLQQTVLPEGPDSISFYNAKVKTEQKHSYMKTMIGLPQSHRK
```

342 - 361:	EEEEEEEEEEEEEEEEEEEE

A0A061ICM5 **A0A061ICM5_CRIGR** (1951 aa)
Liprin-beta-2. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MPGARDALCHQALQLLAELCARGALEHDSCQDFIYHLRDRARPRLRDPDISVSLLTLVVTACGLALFGVSLFVSWKLCWV
PWRERGLFSGSKDNQEPLNCTDTETNEQENSEDFLDPPTPCPDSSMKISHTSPDIPLSTQPGGQENCAHAIRVQRQVTEP
TPSARPNSIRRQLNLSNPDFNIHQLQRQEQLTGIGKIKPELYKQRSLDNDDGRRSNSKACGKLNFILKYDCDLEQLIVKI
HKAVNLPAKDFSGTSDPYVKIYLLPDRKTKHQTKVHRKTLNPVFDEVFLFPVPYNDLEARKLHFSVYDFDRFSRHDLIGQ
VVVDHFFDLADFPRECILWKDIEYVTNDNVDLGELMFSLCYLPTAGRLTITIIKARNLKAMDITGASDPYVKVSLMCDGR
RLKKRKTSTKRNTLNPVYNEAIVFDVPPESIDQIHLSIAVMDYDRVGHNEVIGVCHVGNEAERLGRDHWSEMLSYPRKPI
AHWHSLMESPPYSILKLHKLYGNLKDFGSAWQSNGYQVLKNRLSMHLKLSTWCAQHLMNARMMVAHRGACLLVLLLAAFL
PPPQHAQDPAMVHYIYQRFQVLEQGLEKCTQTTRAYIQDFQEFSKNISIMLGKCQTHTSEYKSAVNNLALRVERAQREID
YLEYLREADICIESEEKTLAEKVLQEAEEEKKIRTLLNASCDNMLMSIKSLKIVKKTMDTDGSWMKDAGGNSAKVYLLIG
SRNNTVWEFANLRAFMEDSTKPGPRKLILPLSWQGSGQVIYKSFLFFHNQGTSNEIIKYNLQKKTVEDRMLLPGGAGRAP
IYQHSLSTYIDLAVDEHGLWAIHSGPGIQGHLVVTKIDPDTLGVEHSWETPCRNQDAEASFLLCGVLYVVYSFGGQGPHR
ITCVYDPLGTVREEHLPNLFFPRRPRSHSMIHYNPRDKQLYAWNEGNQIIYKLQTKKRLPLEYVQIFIVAKPELRVQVPA
VLTHLFARVLMFCSHVNPLATPVILDYQGLKEEEEEEEEEEEEEEEEEEEEEEEEEGKEKKRLCPVEICQHSSQEETKQT
KGAMASDASHVLEAALEQMDGIIAGTKTVADISDGTCEPGLSPPSSCMNSIPVLHLIEDLRLALEMLALPQEREALLSQI
PGPTAAYIKEWFEDSLSQVNHHSAASNETYQERLARLEGDKESLILQVSVLTDQVEAQGEKIRDLEVCLEGHQVKLNAAE
EMLQQELLSRTSLETQKLDLMTEVSELKLKLVGMEKEQREQEEKQKKAEELLQELKHLKIKVEELENERNQYEWELKATK
AEVAQLQEQVALKDAEIERLHSQLSRSAALHSDHTERDQEIHRLKMGMETLLVANEDKDRRIEELTGLLNKYLRVKEIVK
ATQGPSERTISINEDEMEGSFRKWNPTNKNPEEVLKQEVSPRGSSPTPGPPPLPQKSLETRAQKKLSCSLEDLRHDSGDK
CVDGNQLSLVGEPKDSSFLAEQKYPTLPGKLSGAMPNGEAAKSPTASPQPDPSGSSLLKLRETESGWEDTVLTNELSSTS
SGTESSPQSPLTPDGKRSPKGIKKFWGKIRRTQSGNFNTDAPGMAEFRRGGLRATAGPRLSRTRDTKGQKCDANAPFAQW
STERVCAWLEDFGLAQYVIFARQWVASGHTLLTATPQDMEKELGIKHPLHRKKLVLAVKAINAKQEEKSALLDHIWVTRW
LDDIGLPQYKDQFHESRVDGRMLQYLTVNDLLFLKVTSQLHHLSIKCAIHVLHVNKFNPHCLHRRPADESNLSPSEVVQW
SNHRVMEWLRSVDLAEYAPNLRGSGVHGGLIILEPRFTGDTLAMLLNIPPQKTLLRRHLTTKFNALIGPEAEQEKRDKMA
SPAYSPLTTTAKVRPRKLGFSHFGNMRKKKFDESTDYICPMEPGDAANDSHRVYGVYRGQSPLDNHELDGLDQMAPSEGT
VTQIGLLSQDIHRLTTLLSEDQLLNDSPGCP
```

992 - 1011:	EEEEEEEEEEEEEEEEEEEE

993 - 1012:	EEEEEEEEEEEEEEEEEEEE
994 - 1013:	EEEEEEEEEEEEEEEEEEEE
995 - 1014:	EEEEEEEEEEEEEEEEEEEE
996 - 1015:	EEEEEEEEEEEEEEEEEEEE
997 - 1016:	EEEEEEEEEEEEEEEEEEEE

A0A061IDD1 **A0A061IDD1_CRIGR** (113 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MPAFHGLPLWIALSIHGGFNGHQGFPRGGEGEEEDKEEEVVEEEKKKEDDDTRRRRRKKRLGGGEERKEEEKEKGEKKKG
GGRGEEEEEEEEEEEEEEEEEEEEEEEEGRRRRR
```

85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE

A0A061IEC5 **A0A061IEC5_CRIGR** (89 aa)
Uncharacterized protein (Fragment). *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
LKKEDDKEEEEEEEDKEEKEEKEEEEKRRRRGKKKEEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEVFVLREASEISQ
LLPGTISGI
```

42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE

A0A061IEF2 **A0A061IEF2_CRIGR** (87 aa)
Krueppel-like factor 1-like protein (Fragment). *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
QIKKSAKEEEEEEEEEEEEEEEEEEEEEEGGEKPYACSWDGCEWRFARSDELTRHYRKHTGHRPFCCRLCPRAFARSDHLA
LHMKRHL
```

8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE

A0A061IES4 **A0A061IES4_CRIGR** (103 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MATEQQSVPYSVFKCILSQEMGTDAEALHPQPDRKEELIFKRRERTKKKGGGKGEGGGGGGGGGGGGGGEEEEEEEEE
EEEEEEEEEEEEEEENNDKKTFVD
```

72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE

A0A061IEW7 **A0A061IEW7_CRIGR** (177 aa)
RNA polymerase I, subunit RPA34.5 containing protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MPPTPPLIPTPFHFSEQLLDEGSRMAYKVVINLIMGGRHLSYWLYWLPEEVPHLNHGTQNIFSPANSGPAFGFDRLVIIN
SLHCMSVLRIQVEGRHILYQKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEXKRKKKKKKKKKKKKKKKKKKKKKKKK
KKKSHRMAFNTVPNVPF
```

102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE

104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE

A0A061IFW7 **A0A061IFW7_CRIGR** (147 aa)
U7 snRNA-associated Sm-like protein LSm10-like protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MKKWLRKELRALAVLANDPEEEEEEEEEEEEEEEEEEEEEEEEEGDEGLQGQITTVDLQDESSARGRIDNVDAFMNIRLA
NVTYTDRWGHQVELDDLFVTGRNVRYVHIPDDVNITATIEQQLQIIHRVRNFGGKGQGRREFPSKKL
```

20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE

A0A061IGA2 **A0A061IGA2_CRIGR** (131 aa)
Nucleoplasmin containing protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MPYPALLKPGQHRTQQFASVSTYSCVCDALGHWALPSSFSEKNSLFTVPQNTQRQNPNPDPHLPVARLPYETGMVTLQEN
DRALLNCIPKASFRPIPETEEEEEEEEEEEEEEEEEEEEEEEETQLAGKRR
```

100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE

A0A061IGG2 **A0A061IGG2_CRIGR** (79 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MIKKQRKCCFSEFVEAFFCKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKTNTQASNNKSIQEYQPQGPSREDWESS
```

22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE

A0A061IH27 **A0A061IH27_CRIGR** (72 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MGEVVGAEQSPDSSYSQELQQDRGLSVAKGILNELGIYNLYLKSGKEEEEEEEEEEEEEEEEEEEEEEEENA
```

47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE

A0A061IH63 **A0A061IH63_CRIGR** (100 aa)
Uncharacterized protein (Fragment). *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
YGQRVIQDAFSSTSKVHVIPDGRNGDTARKYWTKGKLKPNKEQETGWPSDRGTGKKEKEEAEEEEEEEEEEEEEEEEEEE
EEEEEEEGNEMIPNDILLYS
```

62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE

A0A061IHE1 **A0A061IHE1_CRIGR** (74 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MSAPSCNGEYKRQVTRYRHERKRTHGFMREREREREREREEEEEEEEEEEEEEEEEEEEEEEEEEEEKKKGGKHL
```

40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE

A0A061IHE5 **A0A061IHE5_CRIGR** (107 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MKEEKKKKEKNKEKRTRQKGETNPGKEVRQTPASQTQEAVKNEFEASHGNLTRVASSLKEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEKEEEEEEEEEEEEELGLGI
```

60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE

A0A061IHS4 **A0A061IHS4_CRIGR** (228 aa)
RR_TM4-6 domain-containing protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MALGFPVLCNFARTAVVKSSVSSHAKLPSLQVIFTLVARRRYIVALVGFCQLDTLPDLSVKRESQLRNCFYQNVMWQKSK
PKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEMHMLQRKKKKGGEVSLQADIKTVCVRLGQW
ILSIDAAPVFHNSGMYGCSGEKYWKKPSKGFFHVTGPFLAAIGPGARSRHQSSSESMMTLEVEQFSLM
```

83 - 102:	EEEEEEEEEEEEEEEEEEEE

84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE

A0A061IHW0 **A0A061IHW0_CRIGR** (508 aa)
Myelin-oligodendrocyte glycoprotein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MKMTSSWNFSLSSCLLSLLLLLQMPSSCAGQFRVIGPGHPIRALVGDEAELPCRISPGKNATGMEVGWYRPPFSRVVHLY
RNGKDQDAEQAPEYRGRTELLKDSIAEGKAILRIRNVRFSDEGGFTCFFRDHSYQEEAAMELKVEDPFYWINPGVLVLIA
LLPALLLQISVGLVFLFLQHRLRGKLRAEVENLHRTFDPHFLRVPCWKITLFVIVPVLGPLVALVICYNWLHRRLAGHFL
EELKEEEEEEEEEEEEEEEEEEEEEEEEEGHVRGGGSGSHCPPPPGFHSLQFFATIVSQPGVREPSFIFVGFVDDTQFLC
YNNQGKSQRMEPRAMWVRQMGPSYWERQTQIVKDIAKNSLVNLREAMGVYNHSEDDPPKAYVTHHPRPEGDSILRCWALG
FYPSDITLIWQLDEEDQTQDMDLIETRPAGDGTFQKWAAMVVPSGEEQRYTCHVQHEALTQPLVLKWDPPKPTTPIMGII
AALIFLGVVFTGAVAAIVMRKRRVNIRN
```

245 - 264:	EEEEEEEEEEEEEEEEEEEE
246 - 265:	EEEEEEEEEEEEEEEEEEEE
247 - 266:	EEEEEEEEEEEEEEEEEEEE
248 - 267:	EEEEEEEEEEEEEEEEEEEE
249 - 268:	EEEEEEEEEEEEEEEEEEEE
250 - 269:	EEEEEEEEEEEEEEEEEEEE

A0A061II36 **A0A061II36_CRIGR** (79 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MNVLSVIAPDTIYMYSSYSLKGGGDEGYTTPMASDCGQKDEYNTRRHPEEEEEEEEEEEEEEEEEEEEEEEEEEEENEI
```

49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE

55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE

A0A061IIS9 **A0A061IIS9_CRIGR** (466 aa)
PI-PLC X domain-containing protein 3. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MISKLNIMEAGRILIGRKKLKKEEKAKEEEEERKKERRRRRRRRRKEEEEEEEEEEEEEEEEEEEEEEEEEEEATSAASPS
GITITSNTWEWKVGRVKCKGANIIGTDAECGDQRSGKQTGTMASSQGKNELKFADWMATLPESIHSIPLTNLAIPDSQEG
STVENHLCFVLALSDAIGPGSHDSFSFYIDEASPVGPEQPETVQNFVSVFGTVAKKLMRKWLATQTMSFTGQLGAGIRYF
DLRISTKPRDPDNELYFAHGLFSAKVNEGLEEINAFLTDHHKEVVFLDFNHFYGMQKYHHEKLVQMLKDIYGNKMCPAIF
AQEVSLKYLWEKDYQVLVFYHSPVALEVPFLWPGQMMPAPWANTTDPEKLIQFLQASITERRKKGSFFISQVVLTPKAST
VVKGVASGLRETITERALPAMMQWVRTQKPGESGINIVTADFVELGDFISTVIKLNYVFDEGEADT
```

47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE

A0A061IIV0 **A0A061IIV0_CRIGR** (97 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MQKLHSNSEKNLTKEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGICGILSLFWTSGKEEEKKMNKMKEEEEEEE
EEEEEEEEEEEEEEDF
```

18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE

A0A061IIW0 **A0A061IIW0_CRIGR** (600 aa)
Patr class I histocompatibility antigen. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MKMTSSWNFSLSSCLLSLLLLLQMPSSCAGQFRVIGPGHPIRALVGDEAELPCRISPGKNATGMEVGWYRPPFSRVVHLY
RNGKDQDAEQAPEYRGRTELLKDSIAEGKAILRIRNVRFSDEGGFTCFFRDHSYQEEAAMELKVEDPFYWINPGVLVLIA
LLPALLLQISVGLVFLFLQHRLRGKLRAEVENLHRTFDPHFLRVPCWKITLFVIVPVLGPLVALVICYNWLHRRLAGHFL
EELKEEEEEEEEEEEEEEEEEEEEEEEEEGHVRGGGSGSHCPPPPGFHSLQFFATIVSQPGVREPSFIFVGFVDDTQFLC
YNNQGKSQRMEPRAMWVRQMGPSYWERQTQIVKDIAKNSLVNLREAMGVYNHSEDGSHVFQCVSGCDVGPKGVFLRGYEQ
HAYDGRDYLALNQDLRSWTAGDSAAQITLRKWEEAGVTEQRRSYLKGECVESLRTYLDIGKETLLGADPPKAYVTHHPRP
EGDSILRCWALGFYPSDITLIWQLDEEDQTQDMDLIETRPAGDGTFQKWAAMVVPSGEEQRYTCHVQHEALTQPLVLKWD
PPKPTTPIMGIIAALIFLGVVFTGAVAAIVMRKRRVNIRN
```

245 - 264:	EEEEEEEEEEEEEEEEEEEE
246 - 265:	EEEEEEEEEEEEEEEEEEEE
247 - 266:	EEEEEEEEEEEEEEEEEEEE
248 - 267:	EEEEEEEEEEEEEEEEEEEE
249 - 268:	EEEEEEEEEEEEEEEEEEEE

250 - 269:	EEEEEEEEEEEEEEEEEEE

A0A061IJD5 **A0A061IJD5_CRIGR** (207 aa)
AAA domain protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MQESLPLLVGMGPRYPSGRYKQFQYSDVCPLLMDGGGTVTRALAVSGFVGSHCQVRICPLHTSYTYTYTYTYTYTYTYTY
TYTYTCTYTYTYTYTSILKCFTNVSLQHSQGFRSLFEALEYITTKPYANSLKPSAHMYLDERINLEEEKAEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEDNKSRTTSYVFAKLKFR
```

151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE

A0A061IJI4 **A0A061IJI4_CRIGR** (917 aa)
Histone-lysine N-methyltransferase EHMT1 (EC 2.1.1.43). *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MKGNTRQPPVPEKRPPEVQHFRMSDDMHSLGKVTSDAAKRRKLNSGSLSEVEALAEPLSEEEEEEEEEEEEEEEEEEEE
EEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRTKEPRGVNGVGSTGPSEYMEVPLGSLELPSEGTLS
PNHAGVSNDTSSLETERGFDELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLC
EAHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKAYLRTFSHSARMRGHGEPRRPPCDPLTDTIDSSGPSLTLP
NGSCLSAVGLPPGPGREALEKALVIQESERRKKLRFHPRQLYVSVKQGELQKVILMLLDNLDPNVQNDQQSKRTPLHAAA
QKGFVEICHVLLQAGANINAVDKQQRTPLMEAVVHNRLEVARYMVQLGGCVYSKEEDGSTCLHHAAKMGNLEMVSLLLST
GQVDVNAQDSGGWTPIIWAAEHKHIDVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDT
PLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAVRTEKIICRDVARGYENV
PIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCADDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPL
IFECNQACSCWRSCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKD
GEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSE
KCKHSAEAIALEQSRLARLDPHPELLPELSALPPINT
```

60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE

A0A061IJK1 **A0A061IJK1_CRIGR** (189 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MNCPELRASLATYWQEGEQPEEEALVPKPLSAFVSPLRSIDKNGKKKQEENEEEERKEEEEEEEEEEEEEEEEEEEEEE
EEKKKKQKKEEERRKKKKKKKKKKKKKKKKKKKKKKKKHASLNHTSHTTGLPDSPQDPIELKEMVLGNDTIRIAMTQGCFG
ISQRSFSEDPVTMVCQKPETLNQTNDSLQ
```

58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE

62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE

A0A061IKE6 **A0A061IKE6_CRIGR** (804 aa)
Peroxisomal carnitine O-octanoyltransferase isoform 2 (EC 2.3.1.137). *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MWLFKKEEGEEEEEKEEEERRRRRKKKKKKEEEEEEEEEEEEEEEEEEEEEEVNVGPLLLVPVNCHCWKMQKSAKNKVFHT
FKSQRVAPASVSGRLIALSRSPWFQIRIVQAPGSPEHFHLGLLFFYCDYIMENQLAKSIEERTFQYQGSLPSLPVPSLKE
SLKKYLESGWWCSMQSPALDILLMSFMSYQRTWYLLAVCKLANSKRDLCLSVSSRILDVRRGYLEQPDLMLKPFANEEEY
KKTEEIVQKFENGVGEKLHQKLLERAKGKRNWLEEWWLNVAYLDVRIPSQLYVNFVGPSPHFEHCWPAMEGTQLERGSII
LWHNLNYWQLLRREKLPVHKSGNTPLDMNQFRMLFSTCKIPGIARDSIMNHFRTESEGHCPTHIAVLCRGRAFVFDVVHE
GCLITPPELLRQLTYIYKKCSSEPVGAGVAALTSEERTRWAKAREYLIGLDPENLTLLEKIQTSLFVYSMEDTSPHVTSE
DYSEIFEMLLAGDPAVRWGDKSYNLISFANGLFGCCCDHAPFDAMVMVNIAHYVDERVLETEGRWKGSEKVRDIPLPEEL
VFTVDEKVLNDIYQAKAQHLKGASDLQIAAYTFTSFGKKVTKKEALHPDTFIQLALQLAYYRLHGRPGCCYETAMTRYFY
HGRTETVRSCTVEAISWCQSMQNPSTSLLERHQKMLQAFEKHNKMMKECSNGKGFDRHLLGLLLIAKEEGLPVPELFEDP
LFSRSGGGGNFILSTSLVGYLRVQGVVVPMVHNGYGFFYHIRDDRFVVACSAWRSCPETDSKKLVQMTFHAFHDMLQLMN
TAHL
```

31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE

A0A061IKK8 **A0A061IKK8_CRIGR** (117 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MYPNSAHLPSPPLSLQHAPPTKENKSKRRIKKNEREVEEDEEDEEKEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEEG
EGEEETKIQAVMFHTQISSSVIDSMKIQMRLFLLVFF
```

47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE

A0A061IKN7 **A0A061IKN7_CRIGR** (173 aa)
Centromere protein Cenp-B, dimerization domain containing protein (Fragment). *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
EEEEEEEEEEEEEEEEEEEEEEEEIGSIRMGEKSSYQGRVKRNKVHTLTISVHNGIYIQILHTRKQEEESATQTKGIGSA
WQENMTADGRHGSLTQKLSAYILSPKHKADDYDDEDYDDGNDDDDEDDVLHLDGTFGSLQFHEDTGKEAKTENKIKDSDS
SAVHLEHLFLLAN
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE

A0A061IL15 **A0A061IL15_CRIGR** (68 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MCLGLCCPVVCFQTSWVPVQKSPIGLKHRTKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDRKDEHSS
```

32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE

40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE

A0A061IL30 **A0A061IL30_CRIGR** (326 aa)
Single-strand selective monofunctional uracil DNA glycosylase-like protein (EC 3.2.2.-). *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MAVSQAFLPGPTHEPTGPLMEPLPCTRSLAEGFLEEELRLNAELRQLQFPEPVGVIYNPVDYAWEPHSNYVTRYCQGPKE
VLFLGMNPGPFGMAQTGVPFGEVNVVRDWLGVGGSVRTPPQEHPKRPVLGLECTQSEVSGARFWGLFRALCGQPHVFFRH
CFVHNLCPLLFLAPSGRNLTPAELPAKQREQLLMICDAALCRQVQLLGVRLVVGVGRLAEQRARRALAGLSPEVQVEGLL
HPSPRSPQANKGWEAAARERLQELGLLPLLTKKPCLKKTKQKQTSKNEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKE
EEEGRG
```

288 - 307:	EEEEEEEEEEEEEEEEEEEE
289 - 308:	EEEEEEEEEEEEEEEEEEEE
290 - 309:	EEEEEEEEEEEEEEEEEEEE
291 - 310:	EEEEEEEEEEEEEEEEEEEE
292 - 311:	EEEEEEEEEEEEEEEEEEEE
293 - 312:	EEEEEEEEEEEEEEEEEEEE
294 - 313:	EEEEEEEEEEEEEEEEEEEE
295 - 314:	EEEEEEEEEEEEEEEEEEEE
296 - 315:	EEEEEEEEEEEEEEEEEEEE
297 - 316:	EEEEEEEEEEEEEEEEEEEE
298 - 317:	EEEEEEEEEEEEEEEEEEEE
299 - 318:	EEEEEEEEEEEEEEEEEEEE

A0A061IL32 **A0A061IL32_CRIGR** (70 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MHGSRRNHSEQGEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEKQEEQEQEEESSYSRSCSVAF
```

15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE

A0A061ILJ9 **A0A061ILJ9_CRIGR** (714 aa)
Peroxisomal carnitine O-octanoyltransferase isoform 1 (EC 2.3.1.137). *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MWLFKKEEGEEEEEKEEEERRRRRKKKKKKEEEEEEEEEEEEEEEEEEEEEVNVGPLLLVPVNCHCWKMQKSAKNKVFHT
FKSQRVAPASVSGRLIALSRSPWFQIRIVQAPGSPEHFHLGLLFFYCDYIMENQLAKSIEERTFQYQGSLPSLPVPSLKE
SLKKYLESVKPFANEEEYKKTEEIVQKFENGVGEKLHQKLLERAKGKRNWLEEWWLNVAYLDVRIPSQLYVNFVGPSPHF
EHCWPAMEGTQLERGSIILWHNLNYWQLLRREKLPVHKSGNTPLDMNQFRMLFSTCKIPGIARDSIMNHFRTESEGHCPT
HIAVLCRGRAFVFDVVHEGCLITPPELLRQLTYIYKKCSSEPVGAGVAALTSEERTRWAKAREYLIGLDPENLTLLEKIQ
TSLFVYSMEDTSPHVTSEDYSEIFEMLLAGDPAVRWGDKSYNLISFANGLFGCCCDGSEKVRDIPLPEELVFTVDEKVLN
DIYQAKAQHLKGASDLQIAAYTFTSFGKKVTKKEALHPDTFIQLALQLAYYRLHGRPGCCYETAMTRYFYHGRTETVRSC
TVEAISWCQSMQNPSTSLLERHQKMLQAFEKHNKMMKECSNGKGFDRHLLGLLLIAKEEGLPVPELFEDPLFSRSGGGGN
FILSTSLVGYLRVQGVVVPMVHNGYGFFYHIRDDRFVVACSAWRSCPETDSKKLVQMTFHAFHDMLQLMNTAHL
```

31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE

A0A061IM00 **A0A061IM00_CRIGR** (883 aa)
Histone-lysine N-methyltransferase EHMT1 (EC 2.1.1.43). *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MKGNTRQPPVPEKRPPEVQHFRMSDDMHSLGKVTSDAAKRRKLNSGSLSEVEALAEPLSEEEEEEEEEEEEEEEEEEEE
EEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRTKEPRGVSNDTSSLETERGFDELPLCSCRMEAPKI
DRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCEAHRARMVKHHCCPGCGYFCTAGTFLECHPDFRV
AHRFHKAYLRTFSHSARMRGHGEPRRPPCDPLTDTIDSSGPSLTLPNGSCLSAVGLPPGPGREALEKALVIQESERRKKL
RFHPRQLYVSVKQGELQKVILMLLDNLDPNVQNDQQSKRTPLHAAAQKGFVEICHVLLQAGANINAVDKQQRTPLMEAVV
HNRLEVARYMVQLGGCVYSKEEDGSTCLHHAAKMGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIDVIRMLLTR
GADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTA
WDLTPERSDVWFALQLNRKLRLGVGNRAVRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRN
ITHLQHCTCADDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRSCKNRVVQSGIKVRLQLYRTAK
MGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFML
HQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELSALPP
INT
```

60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE

A0A061IM04 **A0A061IM04_CRIGR** (130 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MNTVTEEDMLVLSPGLQHLCVPPCLFKGEEKKRRRRKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDDDDDDDD
DDDDDDDDDDLAQHGLGSSSGKALKCCKCTARLFTALQTNAMTRIFNLVQ
```

39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE

A0A061IM47 **A0A061IM47_CRIGR** (114 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MNAKDTLGCVETEKKRLYLRLKDDLFSFRTFLRQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEASFVRWRKCSGEG
SMLAKDRISSPVLSMRHFRTRFVHSTSGASIYIT
```

35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE

A0A061IM61 **A0A061IM61_CRIGR** (68 aa)
Uncharacterized protein (Fragment). *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
RWNCTAIEVAQISKNEEEEEGEGGEGEGEEEEEEEEEEEEEEEEEEEEQQQQQQQQQQTKHGMCLYLL
```

29 - 48:	EEEEEEEEEEEEEEEEEEEE

A0A061IM68 **A0A061IM68_CRIGR** (139 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MDPCAHQSYWRVSYLDLPAPTLTTMVILEEEEEEEEEEEEEEEEEEEEEEEEEEGVGRGDEGKGGGRTVGGRGGGGGDEG
QLCDFLFLTITNNAAMNITEQNTLLYECEYFGTVDSQLMVEEQINYLLSLFKTTNPENV
```

29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE

A0A061IMF7 **A0A061IMF7_CRIGR** (165 aa)
Pre-mRNA-splicing factor SLU7. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MNRSWKQPLAYLGRQMEAGLPLGAWCSEPAATELGLARSPLASGDQSRAEEEKEEEEEEEEEEEEEEEEEEEEEEEE
EEEGHKADPMKLELLYKSFKVKDFKEQQKEKYGGHEHLDAPPAELLLAQTEDYVEYSAWGSHERPGAGCVLLQISKVISS
NKMFL
```

54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE

A0A061IMS4 **A0A061IMS4_CRIGR** (640 aa)
Chromaffin granule amine transporter. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MDGRKRVVLGAPQRLLKEGRESRQLVLVVVFVALLLDNMLLTVVVPIVPTFLYATEFRDVNSSLHRGPSVRSQQAVTSPD
FSTIFSFFDNTTTTAEAHVLFHVAWTNGTIPPPVTEAGSAPKNSCLQGIEFLEEENIRVGVLFASKALMQLLVNPFVGPL
TNRIGYHIPMFAGFMIMFLSTLKRGEGGGGGGGGGGGGGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEELSTGLVTNYLDFPGTEALHNVTFSSGTIKVPVFAFSGTYALLFVARTLQGIGSSFSSVAGLGMLASVYTDNH
ERGRAMGIALGGLALGLLVGAPFGSVMYEFVGKSSPFLILAFLALLDGALQLCILWPSKVSSENAMGTPLLTLLKDPYIL
VAAGSICLANMGVAILEPTLPIWMMQTMCSPEWQLGLAFLPASVAYLIGTNLFGVLANKMGRGTMRNSSFGSFQVPLAHN
IFGLIGPNAGLGFAIGMVDSSLMPIMGYLVDLRHTSVYGSVYAIADVAFCIGFAIGPSTGGAVVQVIGFPWLMVVIGVIN
IIYAPLCCFLQNPPAKEEKLAILSQECPMETQMYASRKPTKEFPLGDNSDDPGSSVSTPGQFQTGADWVFDNHSSVTAGT
```

201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE
208 - 227:	EEEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE

211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEEE
225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE

A0A061INA2 **A0A061INA2_CRIGR** (205 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MMALSMFRCFFVVMKHHDQKQVGKEGVYLAYSSASQFITEIGGGCLKKTKEEEEEEEEEEEEEEEEEEEEDLRWNHPSIR
SSVVSAAEVICVYCKGKDVTVVKDGYGKKERAGEASSKHVAVFTVEEVTVLGTSQVLASSAFLCTCLKDWLTDSCQDVLP
AEPEAVPASSQVPLPQVPPKEHSSVSACSLLLLCYQLWGLQCAQL
```

51 - 70:	EEEEEEEEEEEEEEEEEEEE

A0A061INH4 **A0A061INH4_CRIGR** (742 aa)
Peroxisomal carnitine O-octanoyltransferase isoform 1 (EC 2.3.1.137). *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MWLFKKEEGEEEEEKEEEERRRRRKKKKKKEEEEEEEEEEEEEEEEEEEEEVNVGPLLLVPVNCHCWKMQKSAKNKVFHT
FKSQRVAPASVSGRLIALSRSPWFQIRIVQAPGSPEHFHLGLLFFYCDYIMENQLAKSIEERTFQYQGSLPSLPVPSLKE
SLKKYLESVKPFANEEEYKKTEEIVQKFENGVGEKLHQKLLERAKGKRNWLEEWWLNVAYLDVRIPSQLYVNFVGPSPHF
EHCWPAMEGTQLERGSIILWHNLNYWQLLRREKLPVHKSGNTPLDMNQFRMLFSTCKIPGIARDSIMNHFRTESEGHCPT
HIAVLCRGRAFVFDVVHEGCLITPPELLRQLTYIYKKCSSEPVGAGVAALTSEERTRWAKAREYLIGLDPENLTLLEKIQ
TSLFVYSMEDTSPHVTSEDYSEIFEMLLAGDPAVRWGDKSYNLISFANGLFGCCCDHAPFDAMVMVNIAHYVDERVLETE
GRWKGSEKVRDIPLPEELVFTVDEKVLNDIYQAKAQHLKGASDLQIAAYTFTSFGKKVTKKEALHPDTFIQLALQLAYYR
LHGRPGCCYETAMTRYFYHGRTETVRSCTVEAISWCQSMQNPSTSLLERHQKMLQAFEKHNKMMKECSNGKGFDRHLLGL
LLIAKEEGLPVPELFEDPLFSRSGGGGNFILSTSLVGYLRVQGVVVPMVHNGYGFFYHIRDDRFVVACSAWRSCPETDSK
KLVQMTFHAFHDMLQLMNTAHL
```

31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE

A0A061INU7 **A0A061INU7_CRIGR** (645 aa)
Chromaffin granule amine transporter. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MDGRKRVVLGAPQRLLKEGRESRQLVLVVVFVALLLDNMLLTVVVPIVPTFLYATEFRDVNSSLHRGPSVRSQQAVTSPD
FSTIFSFFDNTTTTAEAHVLFHVAWTNGTIPPPVTEAGSAPKNSCLQGIEFLEEENIRVGVLFASKALMQLLVNPFVGPL
TNRIGYHIPMFAGFMIMFLSTLKRGEGGGGGGGGGGGGGGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEELSTGLVTNYLDFPGTEALHNVTFSSGTIKVPVFAFSGTYALLFVARTLQGIGSSFSSVAGLGMLASVYTDNH
ERGRAMGIALGGLALGLLVGAPFGSVMYEFVGKSSPFLILAFLALLDGALQLCILWPSKVSSENAMGTPLLTLLKDPYIL
VAAGSICLANMGVAILEPTLPIWMMQTMCSPEWQLGLAFLPASVAYLIGTNLFGVLANKMGRWLCALVGMVAVGISLLCV
PLAHNIFGLIGPNAGLGFAIGMVDSSLMPIMGYLVDLRHTSVYGSVYAIADVAFCIGFAIGPSTGGAVVQVIGFPWLMVV
IGVINIIYAPLCCFLQNPPAKEEKLAILSQECPMETQMYASRKPTKEFPLGDNSDDPGSSVSTPGQFQTGADWVFDNHSS
VTAGT
```

201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE

206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE
208 - 227:	EEEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEEE
225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE

A0A061IPH7 **A0A061IPH7_CRIGR** (2363 aa)
Sperm-associated antigen 17. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MKKKKKKKKKKKKKKKKKKKKKKKKKSVFFVLVLLLIPLPYRDRHRQEAVTTLVKFFKAETLEEKKKKKKKKKKKKKKKK
KKKKKKKKKLPPLCPFTWAVTRRHGRRKKKEEEEEEEEEEEEEEEEEEEEEEEEEEENDWKASIAFVVGNRIEDFLLI
EALGMAVQYPQRKLFSLVSWQDILQQIDEIQSLAAAVSSKKGKKPPNGGLPLYYEVLMAARVIMDSGEKLTLPLIGKLLK
FQLLQIKLKDQQRQENEKKMVEDRAKSEKDKGKVKSPKEKKSGSAKAGKGKGKDQPEAAAAVKKSTQLKRRGDDDDIKAY
IDDEPDDGAQHYIIVVGFNNPQLLAIMTELGISIASVIKISSENYEPLQTYLEAVRQQQEAILQPEEIEAEELKTQRSIK
ELENFWKYLEPILNNEKPETNLFDVARLHYTVNMAYFPSDWSDHEMMLDLGTEIFENVACLMYDSLDWKRQHQHYLESMH
LINVPQVVSEKTMLEAMPIPEPPPPTAPAPGKKKPQYEEPQAPPGKLAFIITTDVDMRYYNDLLNPIPEEFISVPLILHC
MLEQVVATEEDLIPPSLVEPRPRADGLDFRIAAHIVSILPSLCLSEKEKKNLQEIFLAEGESESKALPKGPLLLNYHDAH
SHKKYALKDQKNFDPVQIEQEMQSKLPLWEFLQFPLPPPWNSTKRLATIHELMHFCTNEVLSWNEVERAFKVFTFESLKL
SEVDEAGQLKPAEVVSQADAENINIPWDNPARFAKHIRQQCMHRANIQKAKPVADIGNKDRILFINQNLSRSEAEEYPDP
NEPDVNSVRPSTSDTRRPLDAGNRELSEKETSGSMWPQSESLEQTMDSEIKDEAATKDDSPEKKPKKIVVEANLEDIKKT
QQRSLTDWSFTEHFQPKVLLQVLQEAHQQYRCVDSYYHTQDNSLLLVFHNPMNTQRLHCEYWNIALHSNVGFRNYLELIA
KSIQDWITEEEAKYQEAKMAEELNRTKIELELKASTSKISSSKSVSLKKSKSNKIVSKTEMPEQEKEKEKEKIPFILEGS
LKAWKEEQERLAEEERLKEEKKAEKKAEKKGKDAGKKKGKDKVENLIEETKILKKKSSSKEKAKEDPVKIPETIEESFPL
PEPETVYPFRGYNMGDVPVKITGKNYYLYPSDGGQIEVEKTMFERGPTFIKVKVKKDKHNFIIHLKDPKEIVKKDKEEDY
SSEEEEEEERVKQNNEKKTTQVVNEAVSKFGSFSATLENGICLSISYYGANGMAPEVTDPELETIMNIPSALIATVIPTI
VTVPQGKVKPKVKGKEKPKESLKEEEHPKEEEKKNYVPEEAEPEIVIQEPSYVPTFQNLNVSCPNGLLLTFIGQESTDHP
IVDEEPTWDLMIRQSYPQRVKHYEFYKAVMPPMEQEASRVVTSQGTVIKYMLDGSTQVLFADGAVSSSPDSGPVYTSPDL
STSPHNGDLVDSASQPKSETAPSEIVITKKGKGHKNQTSVAHKNETHDTLPGVVPTVPTTIETHTGTWFTTTPDGNRIGT
KGLEKIEHLKPYLSFQATDPINGTVMTTREDKVIIVEKKDGTRIVDHADGTRITTFYQVYEDHIIPPDGEETTEGPGTVT
RQVKCMRIESSHYATIITNCEDSSCCATFGDGTSIIAKPQGSYQVLPPNTGCLYIDRDCSATYCHESSSNIYHPFQKREQ
LRASRYIMKHTSEVICEVLDPEGNTFQVMADGSVSTMLPKRKLEDDANVQTEGYDSLSSTHLEKNHMQIYGEHVPRFFVI
YTDGSGMELLRDSDIEEYLSLAYGESTTVVLQEPVQEHPGALSITVLRPFHEASPWLMKKELNTIVPRNLQSRSWETFPS
VEKKTPGPPFGTQIWKGLCIGSKQLTNAPAPILKGPRVLQMRQFIQHEVIKSEVKLRLQISLKDYINHILKKEDELQEMT
VKDSRTEEERGNAADLLKLVMSFPKMEETTKSHVTEVAAHLTDLFKQSMDLTPKYSPDSFAKEFFEKKWRTTSSAKSWKE
KLEKQSMSCGFSFKYNYLKNLSKNLPPFPKKNETTTKPDVSDPDSDSTLTADVEQEAKNTPPLPKQEVAENMKKPASQSD
AENVTKSIKRSPSQNTPENLVQYTQESDTQSKTETITKSPKESANQKCIIKLKKSTKKSTSQNQIENLKYTKESASQNQV
ENVTRPPTEEPDFFMPIKIPTQSLLQDVTGQARKEKVRLPHYLMSSKPKCQPLAKVEDCVGGKVNTSSIASAVIHNTNAA
PFGFHLLPPSVKFGVLKEGQTYATTVKLKNVGVNFCRFRVKQPSPSTGLKVTYKPGPVAAGLHAELKIELFAMALEDDVL
TSSNYDNRPKNFPQGKENPTVYKTSTISSSALGVFTSRKATRR
```

111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE

119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE

A0A061IPY3 **A0A061IPY3_CRIGR** (93 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MKLSKPSTPEKLLQHAHPTPRNQNWGAPTEDSERLQKTGKSKPPNIQKYLQNLIVFIKEEEEEEEEEEEEEEEEEEEEE
ETRAESVSPSVSS
```

59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE

A0A061IQ09 **A0A061IQ09_CRIGR** (112 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MLANHVIIYIITKGYIKKLFLDLKKTNKEEEEEEEEEEEEEEEEEEEEEEEENNLFYLRSVKYPTTGSWPSRQCQALAVSHD
MDLIGWPLSKVLYYLYPSTFWRLDKFCLTTLA
```

29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE

A0A061IQ93 **A0A061IQ93_CRIGR** (160 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MPTQIDSKNLVIVLRERERETDRERERERERERERERERERDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEGSHGVIVIPFQQDVILRKQHPLFLLLALRGSIHLHSVVFSCLGLDMKDLRDLVMEKTKQNKKQVNIEKDDG
```

43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE

70 - 89:	EEEEEEEEEEEEEEEEEEEE

A0A061IQA9 **A0A061IQA9_CRIGR** (211 aa)
Survival motor neuron containing protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MNSVWKEYNLMYQEITSFSSNKGVVVVVEEGGGDKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDKLPISAGIQRK
VEGELGPGGKTSRTILKRYGASGPSYLVNDFRGILISSPFSLMLAVGLLYIVFIMFRLVGKSRKKLCLLFPMTPPKPSVA
ENIPTPQHYFLQLQELLYQEDQIAGSQKREFIFMPDQPLKSQLNQKGLIRL
```

36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE

A0A061IQP0 **A0A061IQP0_CRIGR** (2177 aa)
Sperm-associated antigen 17. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MGKMSMSEVQEHSLAEEEKKKKKKKKKKKKKKKKKKKKKKKKKKLPPLCPFTWAVTRRHGRRKKKEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEDAGMFVALLIDVTKYPMKNDWKASIAFVVGNRIEDFLLIEALGMAVQYPQRKLFSLVSWQDILQQID
EIQSLAAAVSSKKGKKPPNGGLPLYYEVLMAARVIMDSGEKLTLPLIGKLLKFQLLQIKLKDQQRQENEKKMVEDRAKSE
KDKGKVKSPKEKKSGSAKAGKGKGKDQPEAAAAVKKSTQLKRRGDDDDIKAYIDDEPDDGAQHYIIVVGFNNPQLLAIMT
ELGISIASVIKISSENYEPLQTYLEAVRQQQEAILQPEEIEAEELKTQRSIKELENFWKYLEPILNNEKPETNLFDVARL
HYTVNMAYFPSDWSDHEMMLDLGTEIFENVACLMYDSLDWKRQHQHYLESMHLINVPQVVSEKTMLEAMPIPEVGMSSSI
CMAFIITTDVDMRYYNDLLNPIPEEFISVPLILHCMLEQVVATEEDLIPPSLVEPRPRADGLDFRIAAHIVSILPSLCLS
EKEKKNLQEIFLAEGESESKALPKGPLLLNYHDAHSHKKYALKDQKNFDPVQIEQEMQSKLPLWEFLQFPLPPPWNSTKR
LATIHELMHFCTNEVLSWNEVERAFKVFTFESLKLSEVDEAGQLKPAEVVSQADAENINIPWDNPARFAKHIRQQCMHRA
NIQKAKPVADIGNKDRILFINQNLSRSEAEEYPDPNEPDVNSVRPSTSDTRRPLDAGNRELSEKETSGSMWPQSESLEQT
MDSEIKDEAATKDDSPEKVLQEAHQQYRCVDSYYHTQDNSLLLVFHNPMNTQRLHCEYWNIALHSNVGFRNYLELIAKSI
QDWITEEEAKYQEAKMAEELNRTKIELELKASTSKISSSKSVSLKKSKSNKIVSKTEMPEQEKEKEKEKIPFILEGSLKA
WKEEQERLAEEERLKEEKKAEKKAEKKGKDAGKKKGKDKVENLIEETKILKKKSSSKEKAKEDPVKIPETIEESFPLPEP
ETVYPFRGYNMGDVPVKITGKNYYLYPSDGGQIEVEKTMFERGPTFIKVKVKKDKHNFIIHLKDPKEIVKKDKEEDYSSE
EEEEEERVKQNNEKKTTQVVNEAVSKFGSFSATLENGICLSISYYGANGMAPEVTDPELETIMNIPSALIATVIPTIVTV
PQGKVKPKVKGKEKPKESLKEEEHPKEEEKKNYVPEEAEPEIVIQEPSYVPTFQNLNVSCPNGLLLTFIGQESTDHPIVD
EEPTWDLMIRQSYPQRVKHYEFYKAVMPPMEQEASRVVTSQGTVIKYMLDGSTQVLFADGAVSSSPDSGPVYTSPDLSTS
PHNGDLVDSASQPKSETAPSEIVITKKGKGHKNQTSVAHKNETHDTLPGVVPTVPTTIETHTGTWFTTTPDGNRIGTKGL
EKIEHLKPYLSFQATDPINGTVMTTREDKVIIVEKKDGTRIVDHADGTRITTFYQVYEDHIIPPDGEETTEGPGTVTRQV
KCMRIESSHYATIITNCEDSSCCATFGDGTSIIAKPQGSYQVLPPNTGCLYIDRDCSATYCHESSSNIYHPFQKREQLRA
SRYIMKHTSEVICEVLDPEGNTFQVMADGSVSTMLPKRKLEDDANVQTEGYDSLSSTHLEKNHMQIYGEHVPRFFVIYTD
GSGMELLRDSDIEEYLSLAYGESTTVVLQEPVQEHPGALSITVLRPFHEASPWLMKKELNTIVPRNLQSRSWETFPSVEK
KTPGPPFGTQIWKGLCIGSKQLTNAPAPILKGPRVLQMRQFIQHEVIKSEVKLRLQISLKDYINHILKKEDELQEMTVKD
SRTEEERGNAADLLKLVMYNYLKNLSKNLPPFPKKNETTTKPDVSDPDSDSTLTADVEQEAKNTPPLPKQEVAENMKKPA
SQSDAENVTKSIKRSPSQNTPENLVQYTQESDTQSKTETITKSPKESANQKCIIKLKKSTKKSTSQNQIENLKYTKESAS
QNQVENVTRPPTEEPDFFMPIKIPTQSLLQDVTGQARKEKVRLPHYLMSSKPKCQPLAKVEDCVGGKVNTSSIASAVIHN
TNAAPFGFHLLPPSVKFGVLKEGQTYATTVKLKNVGVNFCSMQTHIKSEAAWLHALSPQSAVILWLHDLAASIHINTDSY
AARHTPAKHGPGPIGNL
```

65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE

A0A061IR90 **A0A061IR90_CRIGR** (173 aa)
MIF4-like, type 1/2/3 containing protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MVKADQHSDYRRDEMFPDDHTFSEVWVPSSHFIGEDCTAIICFLKDTRTLGNLSAAYGTAILTCSNGCRGGTIVTVLEDH
LSQPAPSSWAELYAQLPDTPSDDNVQDSSHKSANVSSLNDEHRRRRRKEEEEEEKEEEEEEEEEEEEEEEEEEEEEEEE
ERLKQIRLQVMWK
```

136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE

A0A061IRG3 **A0A061IRG3_CRIGR** (72 aa)
Uncharacterized protein (Fragment). *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
LLTMFNTVALEEEEEEEEEEEEEEEEEEEEEEEEEEEEAAMVWGDSQFVLKGRVVGGSEKESVQVNGPQPPDG
```

11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE

A0A063BY57 **A0A063BY57_USTVR** (61 aa)
Uncharacterized protein. *Ustilaginoidea virens (Rice false smut fungus) (Villosiclava virens)*

```
MATSRKQSTRPAVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEECHYSG
```

14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE

A0A063CDH2 **A0A063CDH2_USTVR** (60 aa)
Uncharacterized protein. *Ustilaginoidea virens (Rice false smut fungus) (Villosiclava virens)*

```
MQPFLVTAFKTKEPDASAAAAEEEEEEEEEEEEEEEEEEEEEEEERGGGRKKRKREISPVD
```

22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE

A0A066WZ74 **A0A066WZ74_COLSU** (348 aa)
Uncharacterized protein. *Colletotrichum sublineola (Sorghum anthracnose fungus)*

```
MPVRVQHMLVIHCVFHKGPQSEPGLVAVYLAFAAAGVRLGVAEGVLLRDEDKELLEEEEEEEEEEEEEEEEEEEEEELL
DEEEEDDELEDDGDAVLDEDVVLDLEDDVAAELEENKVPKILFKRPAEDEEDVVADVGEDVAVKDEAEDAPKSWLERPTE
DEEDVPGVVDDVAVEDEADAVTDDEEEPDPKNEVDVVPCEDDEAGEVLRSWFNRSIEDEVDVDPAVEEVEEVAAPEDEAD
EADEVPRIWFKRAIEDEVDDVPEVEVDVAPGEEDEADEVPRSWFNRAVEAELDEVPGVEADVAVDEELDVAAEDEADETP
MDWTKMAIEDEVEVAPADVDAEDWSAGV
```

56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE

A0A066XDW6 **A0A066XDW6_COLSU** (1372 aa)
ANK_REP_REGION domain-containing protein. *Colletotrichum sublineola (Sorghum anthracnose fungus)*

```
MTRRCGSSHIVSAIRVGGPGFLKALIGRARENLAVAEQELMSSTSSEVCELWNGHEVVRCMGSAPIKEFICLLPGSGAKT
LDNQIEVRVKPFEEVLNRQLHEIGETQFLIKSLKIKPLRELLHKTLSLNSSTGRAEDKEKAPGSDSVKPSTSAIIVTQNP
HSYAPNITLNSHDLKSRAKLRSSAALGIIIQLGLVAYAAYSVYHPTLSFPKDGKPVAQYAFFCHAIGTLFLVLGMLVCAH
VVESSTEETELRPEDDFEARLVWLQQTKTVNDQSFESSAIYAKTKRTTITTSQRRRDATKFLGLSSPPPGQPSVPAVHPA
SDEAPAMSLEVKTIIGTIFSLCGYIVQFIGLRGLHWSPSIAQLGAILFMTGVRAWVRRHLADPPSSRQTMSGHELDWFAT
TFADVQNAPWREDKGTKPDAKIWRIGRLEAHVEEFKEVSESNESDPNAAGCTAHRVVTIRTDLARLAKWQGRTSTEAISL
ARSIEATMNLLFHDRKERHLTWSLSTPEKGLVQFNLDRKNGKWTAYSDELEAALSLWVFSADNDENSQMYERRPQSSSAH
MLLSDAYKRDDSWLRVEGSPAKPGLRVLGSYEEKLHRDLSWWMPSDSADVLRLKMFEDSDEKTKRLEMRSHRIVGSVDSR
PVPEQLRNKTNQYGVMELGEFYITIPLFGGKEEEEEEEEEEEEEQEEEEEEEEEEEEEEEEEEEEEEEEQRRSVNGSESN
ADQGTHEGADSGKDLLAVEVNGPLKLLYAQDIFSSFFWAAANSLQRPLAGLPKIATTTDEAWQSFSLHHDGLSELAQSIQ
STGLGSLGEVYLSMIPSLSATGKLPQASTIVDLARRHAEPHEKLQRWEEAGDVYVWLYRVAKTFPPKSRLNSQATAILLE
LLRQVDEAMTVRKAEQKGDAWYMMDRRDNTFDQQEKLKRTLEDLLRLFAEQKRPLDIAFEINLDFGASYNYPEEFGLTTM
HRWLLNNRNVVDSRGDVNAEDVLGWTPLHLAVQLSRGWKIQSLLQSDRTNVNSRTLLGWTPLHYACNRKQSDDTYITSDH
TNIISQLLKNGADIDAQGRDGIAPIHCAARMGYLQAVMLLTEGGANIDSLDALRRTPLLWAVFYGHQETVEYLWSCANKT
LRDSNGRTALHLAVLLEHKNMAEWLIENGADVQARDRGEWTPLHQAAWSGQQMIVQLLCNKDLGAVNVTDEDGFTPLHWA
AGNGQKEVVKWLVEEAKADVDAQDGRGRTPLHRAAENGHEEVVKWLVEEAKANVNALDDWRETPLFKAVEKGRVNVVKFL
LGKNPNLETRNMFGFTPLEEAAFKGQEAVAELLFQAGARYIKNKNGKGVLFWAGMYGGQGKKAKKIAFAKLLEKYQPTPE
GADDGDRSGDGV
```

686 - 705:	EEEEEEEEEEEEEEEEEEEE
687 - 706:	EEEEEEEEEEEEEEEEEEEE
688 - 707:	EEEEEEEEEEEEEEEEEEEE
689 - 708:	EEEEEEEEEEEEEEEEEEEE
690 - 709:	EEEEEEEEEEEEEEEEEEEE

A0A066XLU3 **A0A066XLU3_COLSU** (363 aa)
Uncharacterized protein. *Colletotrichum sublineola (Sorghum anthracnose fungus)*

```
MDEASMLFTKPWAAAQLTHYGIKFPAKAAKGRLLDMIGRAVDLGKMTADDLNQCVSVPKAVVQMQQDEAEKRRIDESFAK
CTTPGQKAACDLRRFMEHHFLTEGKPDQEKALMPLALYGFKKQSALKALVDLVPGLHTRTAGSFMTLCIGWDIPSLMVLA
SQVDSQAVHAKKNRRHVSQQVKGDGKKLLHLVLQEGGRPRRTRTRGLFILDICASKDGLLVAAHDFGLFEGAMILSLSEE
KLKLLDELEGKEDSVEDSYDYGYYDSDDDNCKDKGPSLAEVVAYGKHKANKHGWMRTSAGGDEEEEEEEEEEEEEEEEE
EEEEADAVVLPSGLQGLERAGKKPEPWNSFSSAAYEYARSARR
```

303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE

A0A067JB11 **A0A067JB11_JATCU** (913 aa)
C3H1-type domain-containing protein. *Jatropha curcas (Barbados nut)*

```
MPPPSSAATRSDHDDDDHAPSSSDPPVKISDSKLDNDKQHEVEVEEVEEQEEDVNDNDDGSEEEEAEEEEYEEIEVEEEE
EIEEEIEVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
SALDSSKEPNEKRNDVSQDMEFQGNDRQQIQSCSPLGKSDLGIQ
SNSLVEDSFCNLKFSGSSNEQLTLREESHVNDEDSKCLKSREHLIAAGANGSQESVVKDDAHALMIKKNAKVMSEPHSDG
KAHLCNSEDMAAETTSSSSIVGHVSNAFATKDCSDMNANGILDSKVKPMEISSEDGKERTTTRLVNSDIRTRSLSFSAEF
```

```
KDQNKRPAVICDFFAKGWCIRGSSCRFLHIKSEADNAKKQLEEDATAAIFSKGDQFNEGLRNIMEKSKLPDFPDLKATPN
GNCAAISCHFSSERILALENGENRMLHQLEDEHKFSSLKRKELSHDVNPDTQQFPSSKDDLGISSSLKDVGTENFRHNCT
TTDYGSYTSLTNKYNSPSFQNNFPPENRASSSGSAVTSINYRGVNPSSYLSSLDNLRYIRDKYVNGSSFDGSFSSSGMFP
SHLISAWTGPSFSFSSSLNTSPLGSQKLLDSDRDFRASRSSSLLHSASPLSGPERENLPMNIASRDPLNFAEHKAKVSSN
DWEPSVPFRPSFFITHTISSSPGSQYDPLHDSIDLPTAGYKIPFKFSFVSHRMPSLDTLHQPAHGNSSVSRSLGPEHNAD
KSTLSFHSRFHENVSAKNCYTTGTDMLATGTVVGETCVVDAQKGTTPNEENASSTGERRDIPDMSKVDADHDSSPRHQND
GPRHKKDSKVDKVKQKREMVVDQKIEGESRAVRHFRAALVDFVKELLKPTWREGHLSKDAHNTIVKKAVEKVLSTLQLHQ
IPTTMESIKQYLSSSQPKIAKLVEGYCTKYGKS
```

89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE

A0A067JG76 **A0A067JG76_JATCU** (426 aa)
Uncharacterized protein. *Jatropha curcas (Barbados nut)*

```
MVISPPKLDRRNWREGDTRKAKKSRLKVSSPAVSTENGENRLKIALHGVALLLTQEESIESLLAGCVHRKRRESPENSFA
RCHATSNAIPSRFKLCFRKTRLQMASSHCALQFRAMARRLWWPEAGDRRRGREENGAPARSPLPPRFRPLPGENDGWRSI
PLMPPVTLLVLLHIDRSSFFPCDAVASSDSESVRFPVRLNGFQRLLWLSSLCEENDRASVGSTASYYLRSLEEKGGGNPV
VSIQSRSSSAHNRRPPCGLRSNLDCPIRNLFVPDWSYARRKCRIRLTAALESDGGAIWWLTTRRSCSRLATTQRGGGASG
GALRFSLSCCLRAIRTEGGDRRAWRRQAATRSGGEVVVARGSAALPLSRQERRPKENENERRKEQERKEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEDWGGE
```

389 - 408:	EEEEEEEEEEEEEEEEEEEE
390 - 409:	EEEEEEEEEEEEEEEEEEEE
391 - 410:	EEEEEEEEEEEEEEEEEEEE
392 - 411:	EEEEEEEEEEEEEEEEEEEE
393 - 412:	EEEEEEEEEEEEEEEEEEEE
394 - 413:	EEEEEEEEEEEEEEEEEEEE
395 - 414:	EEEEEEEEEEEEEEEEEEEE
396 - 415:	EEEEEEEEEEEEEEEEEEEE
397 - 416:	EEEEEEEEEEEEEEEEEEEE
398 - 417:	EEEEEEEEEEEEEEEEEEEE
399 - 418:	EEEEEEEEEEEEEEEEEEEE
400 - 419:	EEEEEEEEEEEEEEEEEEEE
401 - 420:	EEEEEEEEEEEEEEEEEEEE
402 - 421:	EEEEEEEEEEEEEEEEEEEE

A0A067JZ34 **A0A067JZ34_JATCU** (107 aa)
Uncharacterized protein. *Jatropha curcas (Barbados nut)*

```
MTELQGLVAGGRLAARAGWRTFLLELLGRDTGTNTEKKKGKERKERKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEE
```

48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE

59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE

A0A067JZU2 **A0A067JZU2_JATCU** (177 aa)
Uncharacterized protein. *Jatropha curcas (Barbados nut)*

```
MRGYPVVSIQSRSSSAHNRRPPCGLQSNLDYQGLLCAARSGRGWSAAAGVTRRGVVLARDGSARVGGGAIRFCQHWSRKR
REEKERKRKKRKERKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERRWQWWRGGAAGGVAEM
VREREGDERGDKKKEGF
```

97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE

114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE

A0A067K5N6 **A0A067K5N6_JATCU** (130 aa)
Uncharacterized protein. *Jatropha curcas (Barbados nut)*

```
MQVQGRRKGKERKKERKGKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEERKGKEGGGDGVAGDREAQKKKKWGRGVRCARNRKKKKF
```

20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE

56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE

A0A067KCY9 **A0A067KCY9_JATCU** (263 aa)
Uncharacterized protein. *Jatropha curcas (Barbados nut)*

```
MAISKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAEKKKKERRLEKGKGKLEEV
EKEEKKEKLEEEKKEETGKEKEAATEVEIELEKGLEEEKEKDKARTEEKKKSVDSKKDIEKEEAVEVEEASDANTKKLEL
SDEEKETEVDAKKESEVLTAQRSREAMMGKLEKELIEEHNKELDEAIKQKKPKQVKHIAGKHKVHGRNPPLHPFSKRSES
PTETSPAQNLISFKRLRTDSKPL
```

6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE

34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE

A0A067KE69 **A0A067KE69_JATCU** (124 aa)
Uncharacterized protein. *Jatropha curcas (Barbados nut)*

```
MAVALVVLRGGRRHRKNMEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERRGWRWHWWC
YAVVEGVGKIWVRKVRHTLEIEEEENSRWSGSNRFDLIRFGPNL
```

19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE

A0A067KK54 **A0A067KK54_JATCU** (194 aa)
Uncharacterized protein. *Jatropha curcas (Barbados nut)*

```
MNNCPYTIWPANLAGSGPQLSSTGFELTSKASLTLTTMPPWSGRFWARTGCTTDPSGKQKGLWWRDELEEGQAVTQAQLQ
GRRKGKKERKKKERKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEGKREEVARWGSGGRQTGGAERVRMSV
```

96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE

148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE

A0A067KMD6 **A0A067KMD6_JATCU** (112 aa)
Uncharacterized protein. *Jatropha curcas (Barbados nut)*

```
MCTRGANPPYLADRRDRPGRGLTVARGGAAGVAGKKKGKERKKKERKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEERRGGRAVVAVTVVDWRWRRKW
```

49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE

A0A067KRR5 **A0A067KRR5_JATCU** (155 aa)
Uncharacterized protein. *Jatropha curcas (Barbados nut)*

```
MNIKFTFVTLWRRLQSFSRISCFLVPERFGEKGERRGGAVRDGGGATGCGSHLCCCWLRSTQAQSQQERRREEEEKGKKE
RKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGGGAAVMVRSREVQRWKEKKGKGIF
```

84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE

100 - 119:	EEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEE

A0A067KVG3 **A0A067KVG3_JATCU** (420 aa)
Uncharacterized protein. *Jatropha curcas (Barbados nut)*

```
MHEKSGGNTLRPGRTLVFCILALMDRWMDTTHAFHLPFGEMTITPIDFATITGLLFGGRSMVFDDRMRTLDRPSLRASLR
VAIGMEPTILIIESGMRAFVLTVRRCLGTAALSYLYYDMDLCVREAHLKVNYKQVIELLVHVPPPTEFDPFAEVEELDGA
QGTVPVQLGSGSLKLKDEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAEKKKKERRLEKGK
GKLEEVEKEEKKEKLEKEKKEETGKEKEAAAEVEIESEKGLEEEKEKDEVGTEEKKEFVDSRKETEKEEVVEVEEASDAD
TEKLKLSEEEKETKVEAKKELQFLTAQRSRETMLGKLEKELIEEHNKELDEAIKQGKAVITHNQSLIESLERMKNVNERR
LATLKVKSTPYTSTSEKPKK
```

181 - 200:	EEEEEEEEEEEEEEEEEEE
182 - 201:	EEEEEEEEEEEEEEEEEEE
183 - 202:	EEEEEEEEEEEEEEEEEEE
184 - 203:	EEEEEEEEEEEEEEEEEEE
185 - 204:	EEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEE
190 - 209:	EEEEEEEEEEEEEEEEEEE
191 - 210:	EEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEE
194 - 213:	EEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEE
196 - 215:	EEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEE

A0A067LS37 **A0A067LS37_9AGAM** (1918 aa)
Uncharacterized protein. *Botryobasidium botryosum FD-172 SS1*

```
MDKGGSSPEFHGEDRGRAIPSLASSATIAGPSCLQGREFQQTRQAPHINRVSRWRQSSLSSSQESKREKALALTREDLLV
DFHDEAVELLRQEKDATGEPRSCRIYQESLELASESLSPESQKYYEPEAEKKRKEPKDFEDKLAADAIYDVGSSPSPNQP
LKCTFGLPKRDAPMAGHSPPSQPVPIPRIPTAKVMIRAIDMLPLGADGQFAAHKVDGFDYEKNAGIPFVDYNVKTQVLDE
EQRKKHDVAESAETGEIDSWDTGAKFGAFKAMENTDAAMYYGHIEASDQAEEPFFEFIFEKRAHAKASALSERGMGEGGS
SEGEEVADMDLEGSDGGELIDIDLDESDRGEGGGDNEQRRGGRGRKGRTGSEVKARNQQEGGQVRILAPAPAPTLKEASK
EIEKARVFPNSHSARRHRPGLLAASKATGWQTPLDPSTLLDVSQPGLRGLKRTRGQAGDSLPPSPRKQARKIVPEIRLQP
```

```
SLVPAAPPVHPPSPIMFSEEEEESGEDDDCGRAQLEKRIALRARVNRSGDDEDDDGDEQRMDALDATRSCFTAMTSFDPF
EEEEEEEEEEEEEEEEEEEEGAGTDTQRMGTGPGITYPRPTITKPSAAFEEVGEEEEEEEEDAGTDEQRAGSGSSTCCTT
YLCPTVMNGTDEQRMDSGFSTTYPRRTATEPSAPFEENAGADEQRMDRGSDATHPHSNTAMPPTSSSNSPTDVERPSEIN
EHNQCIDDPCARRFGLSVNLYHRILLCVNAGDKCPRVVTPWGLKEHLKSHGISMPQSEVDNLVQLHAIRTGSTYFPTLET
GSVQGLPVMDGNQCPMGCSFYWHKSGSTSRRHILSEHNNDVTLLAGCPHPVQKLYGPTGRYIGVKAALDPSPRAPLSPTD
LVLQRFEQFMRDNEVPDPAREDTSLYLRKSGLLEWSEDKPEPYRIKLQELAKQPGRRDPLFAVMEAASAYIEEALNYCNT
ETRLIRQHLGSLVPTPTVRRMFDRLKPETVATRKRLLGQFIVFCLKLHDANLEPYPCEWLEGQATYMERIHKNLGDSSAL
ISAIHGLAYSTLAAQGAVPTSPTLQTIATMYARPTGAPKFSWKENNEFLFEGKRCTLGGVQCMTKDLRDKLLDSFADVTA
HVCLDKFFPLPKGMSDDPSNNKPGVCFASLPENDLEGRITEFLAEVCKVGGHFFDESGRPKVVECQEWVRGNRWFRELMQ
ANIFFDGGPPKRGGDLGYLLMLNTAGLRRSAFWDDERIILKGGRHKTYWEAGDEDGAVRALDQQLSAIVGFTIIYLRRMD
AIISQAALGLKAEDVHRCHSELFYASGKELTTSTLSETLGHFSGEHLGYRFTTSHFRHIIIGLSNRYILPIMKREKVFAD
LLNRQASHTSLVASKFYARTAYQDDKNLVSELCMREISNVWHKYSPKFYTACQQVQQPWWLAGDPLLPPDVVPETPERLQ
GRYQHAIPSSAPPSPTPAQRLPPAHRSPKKENAAVDYADGLDAQQLPSIPWGIAAARGILLAKFPRAMRESELLDVDLIF
VRNLQQHKVVLHYQIRVSMGLNALPLQAPTYSLWVQMLDIWDENLEAQPNNPSISPLFHVASWQGAKDGQTPPGLVYRKY
CFVPRGDALKYIWELWAHTPESKITTYAFEKWTLPRYGVYASREIVLITQAKYDAVASTELRRECMKFPYRLRPRPHTPS
PVRARSSEQYQAVEKFPRPPPANTGTIVIDDDSDGATPPAKSAMEPSTTPRTRKPSGAATPLARKPGPNGLGCHRLRRLC
QIFTAAPATFLSLLQTDNIPSLFGTHRANQNLSWMQSRQRTRLAPAATTSLCRSPLVTLRLRRPTSQQLGLPALARPQPP
ATCTPRAAEGSAIPAVHRPIHLHKLAPRRSRRRRGAYGKSELPNMPKTRPRETPCIETTKYGPKPISPARRTAGPRGP
```

561 - 580:	EEEEEEEEEEEEEEEEEEEE

A0A067NE28 **A0A067NE28_PLEOS** (415 aa)
Uncharacterized protein. *Pleurotus ostreatus PC15*

```
MSTSDNVNTSRFKFRLQSPTPILSTSFRKLQPKDSAPSGLNTSKDKGKGREKDRDKDKDGSLVCQATRNTIHQVLLTYCL
GEDGLEAIADILAQMYELMHEKDFTVFATSTLENKMSKAERKKTKPLHLVAIMLAELKDGTDPVAPSVFVPSSISQKSSG
GRKVTVEEVDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEGDSSAKNETSTQSPLKPPSGRHGLGARPPVSVHMKIE
GLSAPLANKPLEKPGRSSPEPLSTSPLSTVNAEVRSRHRGVDWKAVTSDHTTPIRKHRIRFVTVYCHELHKVKTLPSPGV
LVPAVWTSMNGDILILYNVRSAQAIKGADSHRVWYFEDGWKNITKVWNEGLDEAHIAHPDQVGMCDYFLTKNAGKPSWIQ
SASQRAKIRRNTSKE
```

171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE
180 - 199:	EEEEEEEEEEEEEEEEEEEE
181 - 200:	EEEEEEEEEEEEEEEEEEEE
182 - 201:	EEEEEEEEEEEEEEEEEEEE

A0A067NGV6 **A0A067NGV6_PLEOS** (150 aa)
Uncharacterized protein. *Pleurotus ostreatus PC15*

```
MREIVDMTREVVDITVCFVVEAGEGRGVRVVRLGVEEREERTIDDDGSEVGDGGGDVSDGDVVEVYDDEKEEEELDIDVE
EEEEEEEEEEEEEEEEEEEEEEEEEGEDDELEDGAEVELVSDNELDELLELIDDDDDDADNDDEDEIALE
```

80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE

A0A067NL38 **A0A067NL38_PLEOS** (226 aa)
Uncharacterized protein. *Pleurotus ostreatus PC15*

```
MATCGTEGGTTRTRAYQYTVTASMRTEPANTQQDPSLPASQPPSLPDMWEGATERCVRRRDGGMEGWREGEGGQGQGQTG
VVSGKRRSRGMSGRVYGCTGVRVYGACVRYAEEEEEEEEEEEEEEEEEEEEEEEERAHALAGETGVDVNVGRQRQRQLQRQR
HIFKRSNVQISNFKCDGDVEMLSAWAEARGLRSGGTRNEGRAVLREERKRAAQRRRARQESARRTY
```

112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE

A0A067NNA8 **A0A067NNA8_PLEOS** (224 aa)
Uncharacterized protein. *Pleurotus ostreatus PC15*

```
MIGFTLTGRGRVGILSENVLARKIDPLLGAGDHEVSRKPQDRFEIIIENLCTLWRARFGGQTRQDRTGQNGGLDKRNINK
RNKHWNTEDWRGPSGDRDAVTTSEIGRENANTDRLANCGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEG
GKERTKKGRGERGGGLSDGARDEGAACIVYRVSSSVSVMPMGIANCESRIEGKRREDADHPHAE
```

120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE

A0A067S4E5 **A0A067S4E5_GALM3** (1313 aa)
Uncharacterized protein. *Galerina marginata (strain CBS 339.88)*

```
MSTNASSSSQPLSQAPAPATAAYSPRANSLLLAAFPWDTDSLTEPVLADVFQGSSTLDKLLKHFGNSMDMFEKRFGAHRI
TGDSGLRQLLRIEGPDMETGEPAASNTVVAYKKGKKPVKVNNDLAILVCSYRVLDVAAWLLGRQSMVLVPQHPKLPLPKL
SLRRLSLVNDCQSILLDARANFRSQDTLQTPYATNNIHLSTLKFLCNVEANSGSLQTLWNLQLAAMHLRHLLTMEYTPDS
YSIPDVPNDLNDLFFPSEEVSSSLTPAEKAIFTKLTEDYKHAGFRLSLQIALLVSPIMLLSDLKLCSFSWDKAEMIGFSK
ALGNQKPEIIKRIERMIWLTLFGIAEGSSQPYLAMQYLATELPWSDIENMTDSEIEWFKPDQNLKTALPSTSEVTIVGPI
SESWPMASVLRPLLPGLIASASQQGPRGNPDGEEDGESGSAGAGSGSGSGSGAGSGSGAGAGSGSGLGSGSGSGAASGSG
LGAPAPEPEDTTGDAPADQSAPGTQDPLEEQETDGNEPVAPGDPPALNTEDLGRKLRERGEKRPLPVPEPIVKKNPKKNP
KRNTQSKGKGKANPKLLTYSPLPLFNVEEDQKTYVPQDEIEMSFPDAKLDVVTNPPERVKMYDEVKAADVNDAVLYDAFG
RPTVVHPTFHKKSDAQNFYGLLKAVESCYVNGKPRHTQKGVYSNFLIMDEKAYKELEPEAVQDLVRYRQLVLTDCEMSSI
EFTPRSLSNICSLTSSLCIHDHSVVSKNPNDCHHTGNLQQILDCIDQGDKGKILNVLDIPNSTSPLPTTGYSSELIAWNA
TGADLFCHRQTEHFPYSDMSWYLIGLSGALHLGHIDSDGQGTVIEVRNQDGAKFWMKATRKELLKKNDDPEVDRAAALLE
LANINMFLQFSLEVPNLDHWILEGILLTHKTRLVMGPDCPHWVYTPFHTICSGGHYIASSTIHDTMIGLIHAFMLDNFIS
NTNHTPTRILLCRLASLYYEGLVKQRYNKHEIAHAHVFDFENFSSVVDLMSFCNLIILINVLDFKTYMYNQDITVNNVKE
LSAERLAAIEAFDFNAVHPKDRLRYQHARGQAYALIDWLFKSVDIIDKKTNQTVKNPRTSLWVPYIAQQASALLLYRKKA
DKAKFKGAPGSTAATLNRQILLCFEGTFLEDPVNAAMESEHEVFTFLEPLRYDVTRLTGLKAPLLLREPFDWGETAADKK
FHLGNAQGWALSSEDIEEAYLTARDLEPEEEEPVVPVVQEQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEPEVAVRPSKRRKTQVIPSPSASPPVSSEV
```

1242 - 1261:	EEEEEEEEEEEEEEEEEEEE
1243 - 1262:	EEEEEEEEEEEEEEEEEEEE
1244 - 1263:	EEEEEEEEEEEEEEEEEEEE
1245 - 1264:	EEEEEEEEEEEEEEEEEEEE
1246 - 1265:	EEEEEEEEEEEEEEEEEEEE
1247 - 1266:	EEEEEEEEEEEEEEEEEEEE
1248 - 1267:	EEEEEEEEEEEEEEEEEEEE
1249 - 1268:	EEEEEEEEEEEEEEEEEEEE
1250 - 1269:	EEEEEEEEEEEEEEEEEEEE
1251 - 1270:	EEEEEEEEEEEEEEEEEEEE
1252 - 1271:	EEEEEEEEEEEEEEEEEEEE
1253 - 1272:	EEEEEEEEEEEEEEEEEEEE
1254 - 1273:	EEEEEEEEEEEEEEEEEEEE

1255 - 1274:	EEEEEEEEEEEEEEEEEEEE
1256 - 1275:	EEEEEEEEEEEEEEEEEEEE
1257 - 1276:	EEEEEEEEEEEEEEEEEEEE
1258 - 1277:	EEEEEEEEEEEEEEEEEEEE
1259 - 1278:	EEEEEEEEEEEEEEEEEEEE
1260 - 1279:	EEEEEEEEEEEEEEEEEEEE
1261 - 1280:	EEEEEEEEEEEEEEEEEEEE
1262 - 1281:	EEEEEEEEEEEEEEEEEEEE
1263 - 1282:	EEEEEEEEEEEEEEEEEEEE
1264 - 1283:	EEEEEEEEEEEEEEEEEEEE
1265 - 1284:	EEEEEEEEEEEEEEEEEEEE

A0A067SES7 **A0A067SES7_GALM3** (101 aa)
Uncharacterized protein (Fragment). *Galerina marginata (strain CBS 339.88)*

```
LDDEQEEDDDEDDDEDVNVDDEDNTEDDTDDDDTNNDDDEKEEEEEEEEEEEEEEEEEEKEKKKEKKKKQPEVEEEDEEE
EEEEEEEEEEEEEEEEEDIS
```

78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE

A0A067SH90 **A0A067SH90_GALM3** (148 aa)
Uncharacterized protein. *Galerina marginata (strain CBS 339.88)*

```
MHWGETAGDRKYHRGSLLDWKLSQEEFDKAYSAVLEAYEEDQQDGDTEEEEEEEEEEEEEEEEEEEEEEEEEEEKEEKEE
KEEEEEEEEEREKEKEKEEEEEEEEEEEEEEEEEEEEEEEVQNAAARPSKRRKISHAKILQSPLLSSSV
```

48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE

A0A068ABU4 **A0A068ABU4_9GAMA** (1277 aa)
Orf73. *Alcelaphine gammaherpesvirus 2*

```
MVLLRSGRGTGDPSPSDNEPLAKRLRSTCSGGPECQFRSPPRKHPGKRKRNDEKCEKNESRKKKTKKPKTPLEGEGPGGP
PGPEEGEGPRGPPGPEEGEGPRGPPGPEEGEGPGGPPGPEEGEGPGGPPGPEEGEGPGGPPGPEEGEGPGGPPGPEEGEG
PRGPPGPEEGEGPRGPPGPEEGEGPRGPPGPEEGEGPGGPPGPEEGEGPRGPPGPEEGEGPGGPPGPEEGEGPGGPPGPE
EGEGPGGPPGPEEGEGPGGPPGPEEGEGPGGPPGPEEGEGPGGPPGPEEGEGPGGPPGPEEGEGPGGPPGPEEGEGPRGP
PGPEEGEGPRGPPGPEEGEGPRGPPGPEEGEGPGGPPGPEEGEGPRGPPGPEEGEGPGGPPGPEEGEGPGGPPGPEEGEG
PGGPPGPEEGEGPGGPPGPEEGEGPGGPPGPEEGEGPGGPPGPEEGEGPGGPPGPEEGEGPRGPPGPEEGEGPRGPPGPE
EGEGPRGPPGPEEGEGPGGPPGPEEGEGPRGPPGPEEGEGPGGPPGPEEGEGPGGPPGPEEGEGPRGPPGPEEGEGPGGP
PGPEEGEGPRGPPGPEEGEGPGGPPGPEEGEGPGGPPGPEEGEGPQGPPGPEEGEGPGGLDVIDGPREAVGEEEEEEEEE
EEEEEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEELLK
TLLTKMSLCTNTDEDSDDSLKRSCRRVCLGLKPSSSSSSSSDGGEGGNPTDRWPSDVILISSDDGGEGGDKTDEGPCDVI
LISSGGEGEGEEGEGEGEEGGGEGEEGGGEGEEGGGEGEEGGGEGEEGGGEGEEGGGEGEEGGGEGEEGGGEGEEGGGEG
EEGGGEGEEGGGEGEEGGGEGEEGGGEGEEGGGEGEEGGGEGEEGGGEGEEGGGEGEEGGGEGEEGGGEGEEGGGEGEEG
GGEGEEGGGEGEEGGGEGEEGGGEGGSDEDEKPLVRFCGGYYDLTVSTSHSDSGSNFGCDPLGLLGEDIDDSNGSPGPPT
LSPQGGDPGNNDNDPNLGPPILSPQGSPNESGYGQSGPSGGESSDGGPSGTDGPPDDPTPDSEPPGLSPPGNPGDSDGSE
NGDPRDPPYCPVGSSSSSSSNEDEEDDDPGEGTSGGRGRRPPKHFPQTVRARRGTLGLDPLYDPTRAGATLSLHISSHTK
DPLVRLSRMLRQLYPESPCTNICFVCGIFLFIIYGNDDDEAQRLISFINHEQQSNPQQGRVNVSMASHLTPVPFPSS
```

649 - 668:	EEEEEEEEEEEEEEEEEEEE
650 - 669:	EEEEEEEEEEEEEEEEEEEE
651 - 670:	EEEEEEEEEEEEEEEEEEEE
652 - 671:	EEEEEEEEEEEEEEEEEEEE
653 - 672:	EEEEEEEEEEEEEEEEEEEE

654 - 673:	EEEEEEEEEEEEEEEEEEEE
655 - 674:	EEEEEEEEEEEEEEEEEEEE
656 - 675:	EEEEEEEEEEEEEEEEEEEE
657 - 676:	EEEEEEEEEEEEEEEEEEEE
658 - 677:	EEEEEEEEEEEEEEEEEEEE
659 - 678:	EEEEEEEEEEEEEEEEEEEE
660 - 679:	EEEEEEEEEEEEEEEEEEEE
661 - 680:	EEEEEEEEEEEEEEEEEEEE
662 - 681:	EEEEEEEEEEEEEEEEEEEE
663 - 682:	EEEEEEEEEEEEEEEEEEEE
664 - 683:	EEEEEEEEEEEEEEEEEEEE
665 - 684:	EEEEEEEEEEEEEEEEEEEE
666 - 685:	EEEEEEEEEEEEEEEEEEEE
667 - 686:	EEEEEEEEEEEEEEEEEEEE
668 - 687:	EEEEEEEEEEEEEEEEEEEE
669 - 688:	EEEEEEEEEEEEEEEEEEEE
670 - 689:	EEEEEEEEEEEEEEEEEEEE
671 - 690:	EEEEEEEEEEEEEEEEEEEE
672 - 691:	EEEEEEEEEEEEEEEEEEEE
673 - 692:	EEEEEEEEEEEEEEEEEEEE
674 - 693:	EEEEEEEEEEEEEEEEEEEE
675 - 694:	EEEEEEEEEEEEEEEEEEEE
676 - 695:	EEEEEEEEEEEEEEEEEEEE
677 - 696:	EEEEEEEEEEEEEEEEEEEE
678 - 697:	EEEEEEEEEEEEEEEEEEEE
679 - 698:	EEEEEEEEEEEEEEEEEEEE
680 - 699:	EEEEEEEEEEEEEEEEEEEE
681 - 700:	EEEEEEEEEEEEEEEEEEEE
682 - 701:	EEEEEEEEEEEEEEEEEEEE
683 - 702:	EEEEEEEEEEEEEEEEEEEE
684 - 703:	EEEEEEEEEEEEEEEEEEEE
685 - 704:	EEEEEEEEEEEEEEEEEEEE
686 - 705:	EEEEEEEEEEEEEEEEEEEE
687 - 706:	EEEEEEEEEEEEEEEEEEEE
688 - 707:	EEEEEEEEEEEEEEEEEEEE
689 - 708:	EEEEEEEEEEEEEEEEEEEE
690 - 709:	EEEEEEEEEEEEEEEEEEEE
691 - 710:	EEEEEEEEEEEEEEEEEEEE
692 - 711:	EEEEEEEEEEEEEEEEEEEE
693 - 712:	EEEEEEEEEEEEEEEEEEEE
694 - 713:	EEEEEEEEEEEEEEEEEEEE
695 - 714:	EEEEEEEEEEEEEEEEEEEE
696 - 715:	EEEEEEEEEEEEEEEEEEEE
697 - 716:	EEEEEEEEEEEEEEEEEEEE
698 - 717:	EEEEEEEEEEEEEEEEEEEE

A0A068WIY2 **A0A068WIY2_ECHGR** (172 aa)
Uncharacterized protein. *Echinococcus granulosus (Hydatid tapeworm)*

```
MLYDIFKATHEKAEDKEEEEEKKKKKKKEGEASAEELLSPEELLNKVEQDFFETIDEERRKRERDNSERSRRLESLNGAG
DEGEEEEEEEEEEEEEEEEEEEEGGEDEATADEQDGNEEGEDSEGEEEDEEDIEGEARRIEGEGLAVGATDGAETSDRA
PPEENEVIGKGG
```

84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE

A0A068WNX2 **A0A068WNX2_ECHGR** (112 aa)
Pfam-B_19522 and Nop14 domain containing protein. *Echinococcus granulosus (Hydatid tapeworm)*

```
MGGTKGKREDNEDDCHVGKRQKRLEEREEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEECILRLL
NRDSSLRRKNSGQLTHTDKFGRKVQAPTFQHR
```

31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE

A0A068WV54 **A0A068WV54_ECHGR** (157 aa)
Nucleoplasmin and Pfam-B_368 and Ribosomal_60s domain containing protein. *Echinococcus granulosus (Hydatid tapeworm)*

```
MLVCEKKYGETGKDTDINMGTEKYFLLVTINPGYKIILGKCLCPSHTTLPTLKLLQLTATRVGCTELSMLLQLCRLLCFN
IYADVLRRHVTTEDVVNVITARLRCDSPHNCGIGGGGGGGGGGGGGGGGGGEEEEEEEEEEEEEEEEEEEEEEESW
```

133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE

A0A068Y225 **A0A068Y225_ECHMU** (83 aa)
Uncharacterized protein. *Echinococcus multilocularis (Fox tapeworm)*

```
MLHEHDDVSKMLTRNVTTEDVVNVITARLRCDSPHNCGIGGSGGSGGGGGGGGGGGGGGGEEEEEEEEEEEEEEEEEEE
EES
```

62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE

A0A068Y2X5 **A0A068Y2X5_ECHMU** (150 aa)
Uncharacterized protein. *Echinococcus multilocularis (Fox tapeworm)*

```
MLLCEKKYGEKGKDTEKYFLLVTINPGYKVILGKCLCPSHTTLPTLKLLEFTETRVGCTELSMLLQLCRLLCFNIYADVL
TRNVTTEDVVNVITARLRCDSPHNCGIGGSGGSGGGGGGGGGGGGEEEEEEEEEEEEEEEEEEEEEEES
```

127 - 146:	EEEEEEEEEEEEEEEEEEEE

128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE

A0A068Y6F5 **A0A068Y6F5_ECHMU** (172 aa)
Uncharacterized protein. *Echinococcus multilocularis (Fox tapeworm)*

```
MLYDIFEATHEKAEDKEEEEEKKKKKKKEGKASAEELLSPEELLNKVEQDFFETIDEERRKRERNNSERSRRLESLNGAG
DEGEEEEEEEEEEEEEEEEEEEEEGGEDEATAGEQDGHEEGEDSEGEEGDEEDIEEEARRIEGEGLGVGATDSAETSDRA
PPEENEVIGKGG
```

84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE

A0A068Y770 **A0A068Y770_ECHMU** (76 aa)
Uncharacterized protein. *Echinococcus multilocularis (Fox tapeworm)*

```
MQLYVTTELKWPHCANANVYLEVEDDDDDDKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGYASLCAVQIATS
```

32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE

A0A068Y9H4 **A0A068Y9H4_ECHMU** (365 aa)
Calmodulin. *Echinococcus multilocularis (Fox tapeworm)*

```
MPGSPSEESLEELREVFALFDRDHNGYMSLSELKTMMKQFNRACTTDEAKEIFSNLDKNHDGRIDFREFVSLMQPLLDES
KSGDFYFRIAFAFFDKNDDGSITTMELKQLLHNLHLKLTDNEVEEMILEADLDRNGIISYEEFKNMMDNDQHNPQRVILF
QRDAVDSSVNALLHVGVSPEGEGKSTTCSSPSRDPDPDTSLNSSPSLRHESRPSRGPPTSVPTCHIYCSTGQTASCVIDK
CEWEVMAKCHLGWMRRMKKKKKKKKKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGRGGSNALTH
GIELRLATVAASASKAVSHHEPLAQSTRQSASQPASQSFCLAAYR
```

268 - 287:	EEEEEEEEEEEEEEEEEEEE
269 - 288:	EEEEEEEEEEEEEEEEEEEE
270 - 289:	EEEEEEEEEEEEEEEEEEEE
271 - 290:	EEEEEEEEEEEEEEEEEEEE
272 - 291:	EEEEEEEEEEEEEEEEEEEE
273 - 292:	EEEEEEEEEEEEEEEEEEEE
274 - 293:	EEEEEEEEEEEEEEEEEEEE
275 - 294:	EEEEEEEEEEEEEEEEEEEE
276 - 295:	EEEEEEEEEEEEEEEEEEEE
277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE

285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE
287 - 306:	EEEEEEEEEEEEEEEEEEEE
288 - 307:	EEEEEEEEEEEEEEEEEEEE
289 - 308:	EEEEEEEEEEEEEEEEEEEE
290 - 309:	EEEEEEEEEEEEEEEEEEEE
291 - 310:	EEEEEEEEEEEEEEEEEEEE

A0A068YIK2 **A0A068YIK2_ECHMU** (86 aa)
Uncharacterized protein. *Echinococcus multilocularis (Fox tapeworm)*

```
MEVRKCCSKFNSVQILVVTTVTRKRQKKMMTEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEALM
```

32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE

A0A072NW58 **A0A072NW58_9EURO** (555 aa)
PHD domain-containing protein. *Exophiala aquamarina CBS 119918*

```
MDTDLETSSTSDEELGSSRRYEILVDRLNQFLEKYPEFAEDEDEDEETPWCYCKQGDLGTVSVRCDAPGCQIRWYHKDCL
PYKDQLLVDEFDLWICPNCLMHQLVDLIKEQRSIAGTSDQGDSTDEIMKQEIDMAMVDARLRRSGRWIFKDSIKKTARHP
RSGKPRMQSDAQPFHPHQGARSLIAAGTAPTITPEVPRQPGNPVPGTWGASLSVQAKLTMSVSNLDSLQRSARIWTSEDT
QVTVTTDEMLFVEYKHDCWIPEATDDLDNCPRFLLKCASACDGNDAIEVPLDLLLAFSLNIQQMTREISAKPAPRRLLGT
IHLTHVDMAVLISALRFLKGEALSILLPGTNTSLTVGQKLVIIQYTHLAHSLSIQPLQNAAMHALCASILRRPQDWSDTW
AVADLLNEITTEGNPARRVLFDGPKCLLPNKDRKQLPCGVVARNIICMNRRVKAIWKPRATIPAEYAEDEDSMDVDSDDD
DEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVGNMHEDEGEEQEFEQAVDDIDEDEDEDEYEGDDEETEDDIER
```

482 - 501:	EEEEEEEEEEEEEEEEEEEE
483 - 502:	EEEEEEEEEEEEEEEEEEEE
484 - 503:	EEEEEEEEEEEEEEEEEEEE
485 - 504:	EEEEEEEEEEEEEEEEEEEE
486 - 505:	EEEEEEEEEEEEEEEEEEEE
487 - 506:	EEEEEEEEEEEEEEEEEEEE
488 - 507:	EEEEEEEEEEEEEEEEEEEE
489 - 508:	EEEEEEEEEEEEEEEEEEEE
490 - 509:	EEEEEEEEEEEEEEEEEEEE
491 - 510:	EEEEEEEEEEEEEEEEEEEE
492 - 511:	EEEEEEEEEEEEEEEEEEEE
493 - 512:	EEEEEEEEEEEEEEEEEEEE

A0A072P9I0 **A0A072P9I0_9EURO** (758 aa)
U3 small nucleolar ribonucleoprotein protein MPP10. *Exophiala aquamarina CBS 119918*

```
MALPSSLLSSLSSDCHHFLQPTFNLHHQTLSTIKTLLDPLAFDIAGAQTLRRDENRRKRKRGDTGHEDTPLPLQLRQIYT
DGLAIRQIWEQARRILDAASDEVAKNIVAQAAQDEPIVNAIATENRPTDEQEEKEEEDGLDEEALDEWEDEKEIEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEYDDDDDGDGIGIDDNDTGQDTEDSDHQDSSSKAKDANPGTYLQDPNNLNDGFFSID
DFNKQTQFLEQQDARGDDDNPSDEDEVDWDADPLTMAFYKPKDHEGTKGKGKHEEEADSSDDGPTFGDADLSAIGSDEEI
LDPDDDLDQGLAGIDNTNDIRYADFFAPPPKKPSRSNRMRALPKTQPKPRIANQTDSDAENDISRAMADVRRDLLGSEDE
ASDDDLSGSDLDKPSMKNLSTHEKQRLQIAAEIRRLEAANIAKKDWTVSGEARGADRPVNSLLEEDLEFERVGKPVLVDT
AETTEEIEQLIKRRILAREFDEVIRRHPDALGDASTTRRGRVELDDNKPTAGLGEIYEQEHLKSTDPGYVDQRSAATKKA
QQEISRIWKEVSSQLDLLSNLNFKPRRAQAEIKTVEDKPTISMEDARPVGAGGEDSMLAPQEIYRPGEDQKRKGAGGDDN
DIVVRKGGSSAARDEMTREEKLRRRRREKERIKKANQMQGTTDAAHLQKNRVERPGRKPKDAEKEDILTQLRKGNVKVID
KKGELQDLAGKKTRRKKSASGGRDTDVAANGGAGNLKL
```

155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE

A0A072U9D5 **A0A072U9D5_MEDTR** (86 aa)
Uncharacterized protein. *Medicago truncatula (Barrel medic) (Medicago tribuloides)*

```
MIQDKKNKREEEGGGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGKRGRGKLTFLSLRSIGRTLEVKVVHHVRKHLVIFF
GYAVAP
```

16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE

A0A072UAB8 **A0A072UAB8_MEDTR** (89 aa)
Uncharacterized protein. *Medicago truncatula (Barrel medic) (Medicago tribuloides)*

```
MATLVVRLFEHYEDYITRLIQQSQDKKSLLTHVHCRHRREEEEEEEEEEEEEEEEEEEEEEEHKIKVDLFIENNCHLLFQ
EQKMVLQTR
```

40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE

[A0A072UD73](https://prosite.expasy.org) **A0A072UD73_MEDTR** (105 aa)
Uncharacterized protein. *Medicago truncatula (Barrel medic) (Medicago tribuloides)*

```
MNGGGGGGGGGGGGGGGGGGGGGGGGGGGGGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEVHCCV
```

32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE

75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE

A0A072UYK0 **A0A072UYK0_MEDTR** (105 aa)
Uncharacterized protein. *Medicago truncatula (Barrel medic) (Medicago tribuloides)*

```
MKNEYQWFLRGFLRQYKLEEEEEEEEEEEEEEEEEEEEEGGGGGGGGGGGGGGGGGGGGGGGGGGEGEGEEEGEGEGEG
EEEEERGGGGGEMEVKWIQGYHNCG
```

19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE

A0A072VAZ3 **A0A072VAZ3_MEDTR** (442 aa)
Uncharacterized protein. *Medicago truncatula (Barrel medic) (Medicago tribuloides)*

```
MFAHFIPTHFQYNCNQNNQAILHLHQLKLRLRLILHLTNGDIPNKILKKKKKKKKKKKKKKKKKKKKKKKEKEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGMLG
```

73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE

104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE

156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE
180 - 199:	EEEEEEEEEEEEEEEEEEEE
181 - 200:	EEEEEEEEEEEEEEEEEEEE
182 - 201:	EEEEEEEEEEEEEEEEEEEE
183 - 202:	EEEEEEEEEEEEEEEEEEEE
184 - 203:	EEEEEEEEEEEEEEEEEEEE
185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE
190 - 209:	EEEEEEEEEEEEEEEEEEEE
191 - 210:	EEEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE
194 - 213:	EEEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEEE
196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE

208 - 227:	EEEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEEE
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220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE
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232 - 251:	EEEEEEEEEEEEEEEEEEEE
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234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE
239 - 258:	EEEEEEEEEEEEEEEEEEEE
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242 - 261:	EEEEEEEEEEEEEEEEEEEE
243 - 262:	EEEEEEEEEEEEEEEEEEEE
244 - 263:	EEEEEEEEEEEEEEEEEEEE
245 - 264:	EEEEEEEEEEEEEEEEEEEE
246 - 265:	EEEEEEEEEEEEEEEEEEEE
247 - 266:	EEEEEEEEEEEEEEEEEEEE
248 - 267:	EEEEEEEEEEEEEEEEEEEE
249 - 268:	EEEEEEEEEEEEEEEEEEEE
250 - 269:	EEEEEEEEEEEEEEEEEEEE
251 - 270:	EEEEEEEEEEEEEEEEEEEE
252 - 271:	EEEEEEEEEEEEEEEEEEEE
253 - 272:	EEEEEEEEEEEEEEEEEEEE
254 - 273:	EEEEEEEEEEEEEEEEEEEE
255 - 274:	EEEEEEEEEEEEEEEEEEEE
256 - 275:	EEEEEEEEEEEEEEEEEEEE
257 - 276:	EEEEEEEEEEEEEEEEEEEE
258 - 277:	EEEEEEEEEEEEEEEEEEEE
259 - 278:	EEEEEEEEEEEEEEEEEEEE

260 - 279:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE
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263 - 282:	EEEEEEEEEEEEEEEEEEEE
264 - 283:	EEEEEEEEEEEEEEEEEEEE
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267 - 286:	EEEEEEEEEEEEEEEEEEEE
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312 - 331:	EEEEEEEEEEEEEEEEEEEE
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370 - 389:	EEEEEEEEEEEEEEEEEEEE
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381 - 400:	EEEEEEEEEEEEEEEEEEEE
382 - 401:	EEEEEEEEEEEEEEEEEEEE
383 - 402:	EEEEEEEEEEEEEEEEEEEE
384 - 403:	EEEEEEEEEEEEEEEEEEEE
385 - 404:	EEEEEEEEEEEEEEEEEEEE
386 - 405:	EEEEEEEEEEEEEEEEEEEE
387 - 406:	EEEEEEEEEEEEEEEEEEEE
388 - 407:	EEEEEEEEEEEEEEEEEEEE
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391 - 410:	EEEEEEEEEEEEEEEEEEEE
392 - 411:	EEEEEEEEEEEEEEEEEEEE
393 - 412:	EEEEEEEEEEEEEEEEEEEE
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396 - 415:	EEEEEEEEEEEEEEEEEEEE
397 - 416:	EEEEEEEEEEEEEEEEEEEE
398 - 417:	EEEEEEEEEEEEEEEEEEEE
399 - 418:	EEEEEEEEEEEEEEEEEEEE
400 - 419:	EEEEEEEEEEEEEEEEEEEE
401 - 420:	EEEEEEEEEEEEEEEEEEEE
402 - 421:	EEEEEEEEEEEEEEEEEEEE
403 - 422:	EEEEEEEEEEEEEEEEEEEE
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405 - 424:	EEEEEEEEEEEEEEEEEEEE
406 - 425:	EEEEEEEEEEEEEEEEEEEE
407 - 426:	EEEEEEEEEEEEEEEEEEEE
408 - 427:	EEEEEEEEEEEEEEEEEEEE
409 - 428:	EEEEEEEEEEEEEEEEEEEE
410 - 429:	EEEEEEEEEEEEEEEEEEEE
411 - 430:	EEEEEEEEEEEEEEEEEEEE
412 - 431:	EEEEEEEEEEEEEEEEEEEE
413 - 432:	EEEEEEEEEEEEEEEEEEEE
414 - 433:	EEEEEEEEEEEEEEEEEEEE
415 - 434:	EEEEEEEEEEEEEEEEEEEE

416 - 435:	EEEEEEEEEEEEEEEEEEEE
417 - 436:	EEEEEEEEEEEEEEEEEEEE
418 - 437:	EEEEEEEEEEEEEEEEEEEE
419 - 438:	EEEEEEEEEEEEEEEEEEEE

A0A072VBE1 **A0A072VBE1_MEDTR** (248 aa)
Uncharacterized protein. *Medicago truncatula (Barrel medic) (Medicago tribuloides)*

```
MLYCGSMTEAQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKRRLT
ILGQKHNA
```

12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE

54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE

106 - 125:	EEEEEEEEEEEEEEEEEEEE
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108 - 127:	EEEEEEEEEEEEEEEEEEEE
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118 - 137:	EEEEEEEEEEEEEEEEEEEE
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123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
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144 - 163:	EEEEEEEEEEEEEEEEEEEE
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146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE

158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE
180 - 199:	EEEEEEEEEEEEEEEEEEEE
181 - 200:	EEEEEEEEEEEEEEEEEEEE
182 - 201:	EEEEEEEEEEEEEEEEEEEE
183 - 202:	EEEEEEEEEEEEEEEEEEEE
184 - 203:	EEEEEEEEEEEEEEEEEEEE
185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE
190 - 209:	EEEEEEEEEEEEEEEEEEEE
191 - 210:	EEEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE
194 - 213:	EEEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEEE
196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE
208 - 227:	EEEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEEE

210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE

A0A072VEF8 **A0A072VEF8_MEDTR** (891 aa)
Zinc finger C-x8-C-x5-C-x3-H type protein. *Medicago truncatula (Barrel medic) (Medicago tribuloides)*

```
MPNSDSSVEDDPSLQEEEEDEVDDDEEEEFEEVEVEEEEEDQEEEEEIEEVEQEEEEQEEVEEEEEEEEIEEEEEDEVEE
EEEEVEKEEVETVVVEEEEEEEEEEEEEEEEEEEEEEEEEEAIESEHIKETIKVEEEEKEEEEEEEEEEEEEEEEEKEEE
EEEEEEEEEEEEEEEMEDEEKQEKIVVEEKDKDKDEVPNSLPDADKHSKEVEEEEEKEENEEAIDMEVEEEQETVVEKDKE
KDEVPDSLPDADKRSKDSSQHMELDVKEENLGSVSHVPDNPEVIRPSHYMEENDAMSKASVSLHEELTLKNEDYPLKQKV
ESPPKPSENLISAEDGKNQGLNVDVENPGHLQRKASEGCSEPDCNSKASLSDVMDIDSRATKPSSDTGKDVVTGIILRDN
FVEDADGDQNSKEKVMQSEMESTVDVKQKPSRTRIHSPSAEIKDGNKRPAIICAFFAKGWCIRGSSCSFLHVKDSVNNTD
QGAEGDVVTAHQKRELKLEKGVKENEEEASPSWHPSHEKEKFLMRDSLFPENKSAFNTSNNYFSSNLSSYSSRAEEMIAI
RNQHMYRGYTSTKDFSSPLGASALDSHAHKSSFSSDREDFHLVGSSRVAPHANGYTLKTRSNWEPSVPFRPSFFITSMNV
SSPRDLYDPLRNSIEIPNIGDGSLKASLLIRGSSVQASSQVRTYDDSAAVGKQMSDVNDDKSSVSSHHKFYENEPNRSSV
PRGKDCLATKAEITSGTCANYQNGDIGVGQYAFGVEDRIETLKKRTEHDARHHSDESEHKKNRVAKDNKFHEMEVDFQTD
GSVLKETKTLKIFHAVLVDLVKELLKPFWHEGRLSKDAHILIVKKSVDKVISTLEPRQIPTTEDTAKQYVSLCRPKIAKL
VHGYVNKHGKS
```

96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE

A0A073HZK8 **A0A073HZK8_9SPIT** (66 aa)
Uncharacterized protein. *Oxytricha trifallax*

```
MYFNNFMIAKDDDEEEQEEEEEEEEEEEEEEEEEEEEEEEEEEEEAEQEDKEEEEEKEEKEQIDDDQ
```

18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE

A0A074X5M8 **A0A074X5M8_AURPU** (318 aa)
Uncharacterized protein. *Aureobasidium pullulans EXF-150*

```
MAPAQIYQRMSEFVNAIKISNSANMALPHGYYIRYEDVQANYNVRMDYHPTKQALVALGLTLSYFDLCMHLFDVFNGGIA
LQALVLANCEFRANTFSHITSVTLSRLSINNVSLYQTPVLLDPTKPWPKIPGYWHNVLPILAHQGAIEECELKDLRDGFT
LTSPEHWAGLNLRCRGKETIKLALMNLAAGWRDAAIFMRHPVNAMDEELEAPRDEHVAVELAAADEEEEEEEEEEEEEEE
EEEEEEEEEEERSVPTKSDHSCKKCRKDKKGCDKTIPICGRASSWRIGVELHYRTSSAPSVKASRGLRATQAIQEKVQ
```

226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE

A0A074X613 **A0A074X613_9PEZI** (684 aa)
Uncharacterized protein. *Aureobasidium namibiae CBS 147.97*

```
MASGGSEGGDDDSKPPGEDKSGLSDGDWRANAHEGEGGQGSVNSWVNVDSNQKIIDRIAITDSWSTEDTEEPERYRGIYE
ELVRKGMSMSDAIFGGSSRIPFYKEAYVQGLLTPESRATETGTVRMRGYRRGNANDPRRVPGSIHWRIYMDHCYAGDLWK
LIDFHAMDGTPIPESFIWYAMECLASALVQMETCARARPYAREQKDETIVLLDIKPTNVLLDMAGQSGRYPVYPRLRISD
FGSAHITYKDDPENMYNRLEMTVTPEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGALPAPHNLGNLGAYKVTKASDED
GDEGATHHHDLDDSKSAEEKGGLPAPHNLGNLGAYAITKASDGDGDEGDEGDEGEGDGDEEDGDEVSIHHQDLDESSSEE
DENMHVEVPDMVPYDEMDVWEESVEHGKLYVGAGNEGAGKEDSGDNEFGDKEARNEGDKDGEDESEQEEDGEEEFTPWYS
WTNVWQLGRTIEVMMRTEEVDDCDWDDPDSDKESKIQTDPPDHPNDPDFLYSEDLIDLVWPTPTELLDMINSISPVHNER
MDAWGTEDWVQEQYDDMGPLTEDHKRFMKASIQRRAAAGRLWFLDDFEDRNLATRYRELDLDIPEECELKWQPEKFRHRV
GQMFGAEESESESESESTERSKNNKRPRTNKAITITPPKKKQKI
```

266 - 285:	EEEEEEEEEEEEEEEEEEEE
267 - 286:	EEEEEEEEEEEEEEEEEEEE
268 - 287:	EEEEEEEEEEEEEEEEEEEE
269 - 288:	EEEEEEEEEEEEEEEEEEEE
270 - 289:	EEEEEEEEEEEEEEEEEEEE
271 - 290:	EEEEEEEEEEEEEEEEEEEE
272 - 291:	EEEEEEEEEEEEEEEEEEEE
273 - 292:	EEEEEEEEEEEEEEEEEEEE
274 - 293:	EEEEEEEEEEEEEEEEEEEE
275 - 294:	EEEEEEEEEEEEEEEEEEEE
276 - 295:	EEEEEEEEEEEEEEEEEEEE
277 - 296:	EEEEEEEEEEEEEEEEEEEE

A0A074XIB3 **A0A074XIB3_AURPU** (1202 aa)
Uncharacterized protein. *Aureobasidium pullulans EXF-150*

```
MEPNSKICETEIAQVSTQKPIKWDDRVLRSFYELMSREMLSKHIRPSPTALADLWSTHQWPREPSQQVQKVVCKILRWFV
RHTPDFVTEEQVDEHSGEYVSYWPETALEWVTSDTWVGNFKGFSVSEDDRRVTRKEKERYISETKATTACSAVITGLHDL
VELDSPTNTQGELDVDFEDEQHRPQSGNQAQPGTLPPAEQQCHPVKPEQWCQYPPDQSREQQQHQAWSPSSLLQHSPSAQ
QNHQDHSQVPRHYNRCQTQNYDSPEPSCDGHIDPQQSYLTHAPQHSCSQSLGESYLPRSRPQEHDARQYLLTQSLHRRLA
PLPRFDDAHPEQHYHPPPAPIGITRLHQHNNPQRLGYDHQQSSMRQQQSHAPSARKEERCFNEANYTAAPQPRGLPSKLL
GQGVGSSYDLFTPLLEQDSAYISKTEGHVRVASKLSGYSPRAPDFERANDRPRASRSAPTSWRLTNPLQQSWPPASAKFE
GDLQSSCRVDTQPPRRPSRPFSGGTADERCFRMNEGGQSRQIQADEDRSEVLRRANSLYQEGDVDDRLAAVALTLGCLLS
RDRDRADKRKSWLFTRRDEWTDRFVRHRDRSYAPTLPLIISHHFQRVLTSMVLYFFRSRPPRLVIQTLNMFFSQDQDDHS
LAKRLQDHIHYIEDDLRELHHEMVALGISEIEQRGLKKLIRKLYITIDWLEGEQKKDSLEQSLNKDDIQQLRNLFWSVQQ
KLDESTKLQTQTLNRLDSFGQRLEEMQARYHEDQTHMEEKMQDAIDAALRIHSATFLSYMSERLHEFEQRSEACTQSQVQ
KLVSKHRFNGRRWRCPSPTKLSRQLESQRSLLSELQDLGEESDSTQTNDGESLSISTTPATEPTIDSSMTDSHQQRSDRV
KRHKKYVVSPKHQSKTFTTRDLDRGPMVLPNQSAPIAPDSSSLKRMPQNLSNHSPNYIPQLLSTSALPIATKHLPSSARS
GEPLPGPYLRKPFQVRTAVSDSANTDQKGAYASKRPLSNNNNTWSCRAPDVLHQKSQCFSSPGISRARGLVMKGTPDVTK
FHNTFSTMKSHTFITTPSAIDKYPQISAETPCQQIYKHQGRQNAIITDHTNREKIQASSSRLSTPQQSKEQRDSLPDWTI
HHGSASNSALLHSAAQGSSNKATELQSNVSPEEEEEEEEEEEEEEEEEEEEEEEDPPVETASESFQPVPETQCATVEPD
YI
```

1152 - 1171:	EEEEEEEEEEEEEEEEEEEE
1153 - 1172:	EEEEEEEEEEEEEEEEEEEE
1154 - 1173:	EEEEEEEEEEEEEEEEEEEE
1155 - 1174:	EEEEEEEEEEEEEEEEEEEE
1156 - 1175:	EEEEEEEEEEEEEEEEEEEE

A0A074YRG7 **A0A074YRG7_AURSE** (482 aa)
Bromo domain-containing protein. *Aureobasidium subglaciale (strain EXF-2481) (Aureobasidium pullulans var. subglaciale)*

```
MVAGLEFCAEFLDKYYDLYQAGKADFIEPFLNKVSNDDAADYETLIPRPMWLARMAYRLIKNRYANVEVFVADFKLMILN
CRKYNKESRFAGHENGRFLKSASQFENDFLSECSKKNILIAPFLQDHDDNDDNDDDDDPSKPRTTRSSTRQAGTPGQGTS
MAGGRLSTLRRTTGAKRPRTQTERGALGEPSTKRARKSGPVDDEVEEEEEGEGEGEEEEEEGEGEGEGEGEGEGEEEEEE
EEEEEEEEEEEEEEEEEAQVTAPPKRKSMSLSIRLTVSPSKGNEGPTPQPTLSDAVVASEGGRQDAEEDVVNEQSTERAH
TDDSPKHDEDDVNDVEEEEDEDNEVEHANQIHELVGDLRNTMEGEFQEFARHQYQLMLRTEATRDVYDKTSREIWKSKCR
ARIINEAGPGSEVSIRAMMKQTWTEADKEQLMAILQKEAESRAECFDVWSKLDNHAVQTQIDLQIPPFDQTKCLTPVREA
KD
```

235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE

A0A077Y2A7 **A0A077Y2A7_9APIC** (969 aa)
Phosphatidylinositol 3-and 4-kinase, putative. *Plasmodium yoelii*

```
MGSNSIAISQQMYFSTHNALRINEENDVISTLFYEINGHRHISLLIFPFYDVQMLKRLLIKKLDLPDIKVNDILIFYKGI
KLPNYRIISTYLDNSNRVDNVKKKKKKKVNKLYWAIKDPNPNASIRVIDNKSYPPFFENILNDIKLAFKKNIAPKLTMDG
TGGTYLLFNSKKKVCSVFKPADEEAFSPFNPRGYEGKIYQEGFRAGVLSGEGASREIAAYILDNTYNNFSNVPCTIMVEA
CNPHFNNKSNLKYIYNENTLKWKCGSLQEFIDSRESVGNYDHKQFSIRDVHKIGILDIRVMNLDRNDGNILVSPIKSLKD
```

```
CCNQFLYRNNKRFSTNDEDILKRIITIDQKPSRYSLIPIDHGLIMPHIMDVAEIDLVWFGWPQTKIPFDNEVLEVIFSFD
PDKDADKIRNKLLIREDCIRTMRVCTRLLQIGAWMHLNLHEIAKISTRKNIDEESILERLVRDSIIQAYQMMDYTSLMST
NRLGYILDLAEIKINKKKKNSKNKTIELIDSNKTKDENSNDIKKNTISQKEEENYETNNNTTYAKSKSLDIKKIENSFTI
VSFKDIRDNKSSSSFTLVNNNTNQNGNNSYDDKLETYNINMNDQKGGECNSTYKTLIQHRSGSKESGNKFIHTKINNISN
REHARGYYSLSKDNNIEVRNDNIEVRNDNIEVRNDNIEVRNDNIEMRNDSINDQNKEKNISETNSFSNKSEYTFVTATSN
SKKDDNINKSSNDVEQNSDGSKNLGGSSENFVGNVDEENGAKVEKKMKKKKKKKKKIKSDEKVESYQSDKKESSFNISDD
NDQNVENVENSNNSKNERNVENEKNEKNTIEHNQQNLNSYQDKEEEEEEEEEEEEEEEEEEEEEEEEDDENYVRFKKTTGT
MKRISENTGTAYRNIEMNKINSVWMIKDKNNKTINVKWENKIFEKLFFETFENYVKKYINDYHPNWREYQYNGSKVVNTK
HSYLSSVKQ
```

844 - 863:	EEEEEEEEEEEEEEEEEEEE
845 - 864:	EEEEEEEEEEEEEEEEEEEE
846 - 865:	EEEEEEEEEEEEEEEEEEEE
847 - 866:	EEEEEEEEEEEEEEEEEEEE

A0A077Y949 **A0A077Y949_9APIC** (2584 aa)
Kelch domain-containing protein, putative. *Plasmodium yoelii*

```
MNKNFNISNYNLDLIKCLQNESGIYFILDPTKAIHDKKHSDVYDIFIPENSDGVTLHVQKVNNEYKCIGVSITKRGIDIN
TGTRIFNTKIADWLEQLFNFNKTLGNNNNANNNENEDGNNSTENRTNNLNGKNNWSNMERNGPNNHGFGTIVNNKNTSIN
ANPINNIGSNNNNDQGNASGDDKDANDIDGNDHLENSDDNNNSIINNGNNNKYNNNYNNVRHNLSNNQTGAPITNLIKNS
KGGYDNFENNDNYNNAINMTNKTKNNKNPINQGNCNLNVNSNLSTHIIPSSNLSSSQSKKQNQHTKQIRLNQMNNSHKSH
LMQYHNSNYDDKNSKLYNNVNSSNTVINKHISSENSGAPHGSASNNNDAVKINKIGCNTRQKNAPHILHNSNNNRDGNNN
SCKGQQPYNENLGYRPTLFNLLEVLSNHNITTPDQRVCIRGIVTDFLNNELPHGKIYAYIGAVVGHDILHDIIKKLEKDP
NRNAVPDASGLARIEASFGLSKSSYDFMNHNSTNSSMNNIPNVLFNNRNLNSALLNNHIYSNILSNVANNNNNNNIGDNM
GHSGMLNADSEKIGNNKTANDINNMMMKYGDNDKSGGSYNNNMLNINKKKALNMLNMRYMDNNNNNNSNNNNNMTDMGNL
GMGNMNNTDNGYMNQMNIDLANLENLNNAKNSGLSMHDYLYASKNLHNANPLNRNNNIVEDEEELMKVIKKNIETYKMNN
IKNILISSVFGRIKWLKIMNESPHAYLYGHSIVKYGNKLYMFGGTNNKHKKVPFNHTLTFSLIYYNYKLLPLSGNYPDER
DGHTTHLVSLKSGLSVFLFGGANNNIYYNDIYILDMETRKWSKRIVNGKLPLPRHQHCSLVYPAKSEHLRGEKLNLTEGV
IIYGGKCLYNNNNIVNLNDMWIFLFQANMWVRINYLGDQIPIGRYGMNLIWSDTNTLCLFGGECLQSDKNYKTRKLLDDM
WTFRLNTPLLINNTEDIGADVKYLSYENTVNTQSEVHKHQKGTKTDSHLNNSNGNNGISTHDNNNNNDNYYGQTDNINDK
NGINENDNKMGNNNESQAVDNKGGIENNNSNNNNSNNNNNNNNSNNSNNNNSSNNSSNTNLINKIKIAGEWKREIYEGNI
GSRSNYSSIFITQRHQDFKGAEPKTIEKLMLLCSGITYDNKLKIVSSDEIYVYFFSQKRWYLLKGKLYNEEYMYSARQRH
VGCFFESKNVLGRSNRNPVPCIFIHGGFKKNSVFGDAWLLSLTGENPLRLYEYDTCREKISTTQMPLYYFRDTHSISLLY
TFCTLQKWLFGAFANLVDNSVYAINPAENVFIKYELTPEHDGMISIQDDGEGLDFNAMNRILRMYGNYKNYDNNSFYNNN
NNNNIKKHSLPNNDDSDGYEIDNYDENDENDENEQAHNEETNNNNEPNNNENNNSDQNNNQCDNNNNNAAFDKTGNNNTE
SNQTQPNAENDTKSEKGPDGENNNNLSGSNCEGIIKKENETRNKNGVIGKKKCTWNDSFYYKKKNQHYFYNDISNSIFDI
KYGVGFKTAFARIASSCAIMSRTINTIGIGLLSLELMNHCDAKELATPLCMWKLPNKELINRNIANKSEHRHHQKLLMSY
TPFNSPSLLAEQINILGTYSGTRLLYWNFRDDMDFIIFNPTNNNIYLSSSPLSIDELKNKNKKQKNTQGEGSNFSSKYQG
VKDIKFPNRIIKRKGVFEEDGNLKKLKTDVENSDEQVEKNEDIIADDKNEENIKKEHDNISNSSKNNIILDNNNNNNDDN
NNNDGDENTTNCNEKLKYEDELKYNNNNYFKKRMNLFEYNSHLTPNISKEKYNMNQIFPLWDHPKDSIDYCLSTYLYWLY
LRRSTNIFLQNTLLIPTCMRREKDMNQNKNNNDNNKGKKKGTKSTKLRNKKINKQNDEKIANTEENNGEKIPNTSETVLE
NNNSFVKSELIQEKNDDNNHVDAQNEANVNNEKGENISEQNQNTEINNNGIKNENVCTNKVEGEKEENNNLEDGKKNNNC
ENDTNGGLTKLEKQKLEEALEYGISQNVQPQNSANKNGTDDEEEEDEEDEEEEEEEEEEEEEEEEEEEEEEEEEKEKEKEEV
SKNNEDNGNINETNNDVENEKAEVEGEINQVDEGGVVKTETQNEMETENNVEDGNETNKKNKKENKNKVGKTIDDTNEDS
IASRRKRRKKKDDLSADTTANDKKNGEIEKMKKENYVNVYMENFKIKDEYYINNPSKYTLYHFLRRKLYKMVESHYLFTP
ADHTYGSFIMMGFLNDNNNTSIEVNRVCETGILLYYKNRLIKRLDAPFIDTPYNLFLSKYPPNPSLYEGNLYKYALTVIV
NVPNWLKPSVSKQEFVHENNHAFLVFKKKLVTLIKHYLSICEDVVKLNKWRESRDMKLKKYLEKIQNQSVKSRNDSDYEN
DDDNNNNSKNKNFNIIYNNDEEGDNYMNDQNDGNKKKKEEINYSGKNKTPYTNDSEPILHKNKKTKTNNNDDSNKRDHNP
TSENESANNDNENNQENDVLEGEKEQEDDEYDQEAENRPNFQDEKDEHEENEEEAEEEEEEEEEEDPDDEEYNAEMDDQK
NRSVEQETEEEMIEEDEEYEPEDE
```

2050 - 2069:	EEEEEEEEEEEEEEEEEEEE
2051 - 2070:	EEEEEEEEEEEEEEEEEEEE
2052 - 2071:	EEEEEEEEEEEEEEEEEEEE
2053 - 2072:	EEEEEEEEEEEEEEEEEEEE

A0A077Z0P2 **A0A077Z0P2_TRITR** (68 aa)
Uncharacterized protein. *Trichuris trichiura (Whipworm) (Trichocephalus trichiurus)*

```
MPTFFEEEEEEEEEEEEEEEEEEEEEESLDCENIVLYFTCNINFCSSQHLWILTGPVIKLMVGLRRSTK
```

6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE

A0A077Z880 **A0A077Z880_TRITR** (113 aa)
Uncharacterized protein. *Trichuris trichiura (Whipworm) (Trichocephalus trichiurus)*

```
MVMADPDNLILLGCIVAMPYDEALTTSLKLDGHKFMTRGWLKLHKMKPKYLNDYVHLKEDVLCSLCPKIVKIVPEVLINR
KVRQFTIYSFLNLEEEEEEEEEEEEEEEEEEEE
```

94 - 113:	EEEEEEEEEEEEEEEEEEEE

A0A078FTT8 **A0A078FTT8_BRANA** (546 aa)
BnaC04g02840D protein. *Brassica napus (Rape)*

```
MGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEESSNSMCILPELLEEIFIRLPLKSILRFRTVS
```

KHCRSLLESRRFSEKRMSLQKNRRILAAYNCDCGDRPRLLTESRFEGDEEIVYLHCLASRPSLSCDGLLCFPEQDWIIVL
NPSTRQLRRFPSGLNHKCRFGFGLWSSFSPGNWAIGFGRDKVTGSFKVVRLCFSFREIGQEEPVLECGVLDVQTGVWSKL
SPPPHVVNPGSKSVCVNGSIYWLHVDVYVEKHYKILALDLHKQEFKKFPVPPTRATKESRLVNLEERLAFVKTNVLPIWR
VEIWSTDTYQKRWSKTFSIHLKLDVVSWPKRRRWFTPVAVSKQGNLVFYDNQNKLFKYYPRTNETRCLSLDTCVISPYVE
NLVSLPLKPSHPYPHVSVETRMSRCRLFSRESSSWIFKALQRNEFRILEILFTSLVVAGYICSPRK

3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE

52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
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74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
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93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE

104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE

A0A078GA25 **A0A078GA25_BRANA** (314 aa)
BnaA08g12610D protein. *Brassica napus (Rape)*

```
MEEGTSSGSRRTRSQVAPDWTLKDCLILVNEIAAVESDCSNALSSFQKWTMISDNCNALDVHRNFNQCRRKWDSLVSDYS
QIKKWESQERGGGHSYWSLSVEKRRKLNLPGNVDNELFQAINAVVMIQENKDGSEPDSDSDPEAQEDFDVVDVTAELGSK
RSRQRTMVVMKENPPHKRKTEEERRRKNIQEQRAKATHQKNKTMEVKKKPVVEISTDEEEEEEEEEEEEEEEEEEEETMS
IEEEVKALEAKLGEKADMIHAIVGRNLAKGSETEDDVGIEDKLKFVKQQGDELIACLSEIVNTLDRLREVPQEI
```

218 - 237:	EEEEEEEEEEEEEEEEEEEE

A0A078I0H8 **A0A078I0H8_BRANA** (460 aa)
BnaA02g29820D protein. *Brassica napus (Rape)*

```
MASRHHHACSQSHNHHNQIPLVPTSPHCCTHSNHPSPPPPDTLLHLLASYLQTHQQETHFPNQTCSCNQNNVPRQQHDQV
ILSCLLRKIDALESSLNKFAPFHDQRRDRHSTVRDSAARVIQTHFRSYLVRRSISFRHLKELAVIKSSFLSLKSSVSGKP
IFPYKVVSRKATDLLLQLDSIQGRVDPMIRSSKRSLSRDLVRFLQYVDDCVVRRYAADVSFVGSHSKRPQGFGVVEERRG
EELDSTTDDSEEVSIDKRKSGSSKFRTGANVVKPTVRKTMVLDKNRTVYQDESVDSSEEETLVVTRDNERKHHGLKTRKM
VLVKEGGGKSRVVKTVRFDEDGNVYKVYGDTPEASSISEEGDDSTSGSNDGNGDKKGNEVEEIKYVPKEKEGFEEEEEEE
EEEEEEEEEEEEETQSEKEVSSSEGSERDATGSNEHKKRQIQVQKGNLMVSPPLPLKMEP
```

394 - 413:	EEEEEEEEEEEEEEEEEEEE

A0A078J0U6 **A0A078J0U6_BRANA** (622 aa)
BnaC04g55130D protein. *Brassica napus (Rape)*

```
MASPNPYTKHPSPPRTTAAATPPSVSPASGGFFSKSILLGMFLLALPLFPSQAPDFVGETVLTKLWELIHLLFVGIAVAY
GLFSRRNVEESNVESRMSCVDESSLSYVSRILQVSSVFDEEEEEEMNKSEYGEINQVQAWNSRYLQGRSKVVVARPAYGL
DGHVVHQSLGLPVRSLRSALEEEESLADDDDEVMAAAPSSPWHSSPEMMAMGDDGTRFTSRSSVSSSSSSQTSFESNDQK
NRYSPSRSVSGDSLISNVEEKSLQGSSRPSPSPPPSPELVRDDTHRRVLHSRHYSDGFLLEEDVRQEGFEDELEGSKDRG
GFSKKDPGSKSLKLTAESSLNKSPRSYPPDLISSPVDHSTARRRYLQQNSDGHLFEKGLESDHNKMSVKKVRSHDSLEFQ
PRNDKASRRAIRSSSRGGSDTLVVKDNKRNSEDDDDSEDYDNTRNKDLPGDNKEVISNSPRSEPQSWRGSSKVSSRGKSV
RTIRSDSSDDRAESHGRTKPRRQWQQELAIVLHQEKHSETLTTSEPEDDDVMEESEAEQPEVTLEEEEEEEEEEEEEEEE
EEEEEVVAWESQSNASNEHYEVDRKADEFIAKFREQIRLQKLHSCEQRRGGGTGVIRNRHFR
```

545 - 564:	EEEEEEEEEEEEEEEEEEEE
546 - 565:	EEEEEEEEEEEEEEEEEEEE

A0A078K2Q4 **A0A078K2Q4_BRANA** (180 aa)
BnaAnng39850D protein (Fragment). *Brassica napus (Rape)*

```
YEEEEEEEEEEEEEEEEEEEEEEEEEGFNETYTVYDEVDQRRRSIFFSNFLRSQRLSHITNFFKVRKDSGKKGTEDFRKGE
DFRVRLAINLNGNSLGCGIIEFETADRAKKALLYESSRLNIISDVVEMSPYPIRPKYKYNRAEKLWNKFNLPPEIPPVVK
RKYSQLSERRSEKKTFSDDD
```

2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE

A0A084G1U3 **A0A084G1U3_PSEDA** (849 aa)
Uncharacterized protein. *Pseudallescheria apiosperma (Scedosporium apiospermum)*

```
MPLTGKVALITGGTKNLGAEIARQLAGQGAHLALHYNSQGSKIDGDKLKAELQKSSPKSKVALYQGDLTTKAAVDGLFAA
VLKDFGGLDIVVNTVGKVLKKPITEISEAEYDEMFAVNSKAAFFILQAGAKNVSDGGKLITIVTSLLAAFTGFYTSYAGS
KAPVEHFTRGVAKELQSRKISVNAIAPGPMDTPFFYPQESEEAVAYHKSQGMGGRLTEVEDIAPIVKFLCTEGQWITGQT
IFANGGYTTRSTGLSTPTRFSHHPKTKSQTRLNIKTIEDRRMTLKRKASISTTDVSASPLPPSKRVRAEGQDMESGHNSR
RQEDAESSNSFGQPYSVVFSAVIKGGGVETRPDGSSASKDGEKEEEEEREEEDEDEEEEEEEEEEEEEEEEEEEEEDINP
WADEFPEGQGVWEQKQKEREEEEAAARKEEEESEEEEEEEEEEEEDSDDDDGEERPTIAPWIQRVLDSTPSPESEWAQEG
PSEPESESESEAESEAESDVELESEDNRLPSDSDSNFTSDSGDDKPNTGFYGELVDFGFLLGVARKRKLIVCERLKSGGY
PAKQGWQIVDWLQQRGNIRKLHYGIKFVSPPRSPPGRNKQEREIRDEGQWAPAVLDRIANATNRNRFYHTLKTRLAQSNS
VTWAWIINIMSREAVTLEVYGPPKQDFIRDVEYHYFDKVDPEDGWGMMTTRPARLRRYLHEEIMEMKNFLELQISVFSAI
TLVPGSDRFQLLDVAPLEGLHRLYVNTWDNDSHLFEPIEAGDGVIGYAGQVLTPIGSPPPTDIRWPPKFLDLDLASEDES
```

```
DLSYATGSESDDTEGTSTGPTPDSPDAGNTDDSLMRSARPDESDSDMSG
```

376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE

[A0A085LKL0](https://prosite.expasy.org/) **A0A085LKL0_9BILA** (622 aa)
Uncharacterized protein. *Trichuris suis (pig whipworm)*

```
MKRDSMQGEILNVEEEEQEEGEEQEEGEEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEQEEEQEEEEEEEEEEEEEEEQEEEQ
EEEEEEEEEEEEEEEQEEEQEEEEEEEEEEEEEEEQEEEQEEEEEEEEEEEEEEEQEEEQ
EEEEEEEEEEEEEEEQEEEQEEEEEEEEEEEEEEEQEEEQEEEEEEEEEEEEEEEQEEEQ
EEEEEEEEEEEEEEEQEEEQEEEEEEEEEEEEEEEQEEEQEEEEEEEEEEEEEEEQEEEQ
EEEEEEEEEEEEEEEQEEEQEEEEEEEEEEEEEEEQEEEQEEEEEEEEEEEEEEEQEEEQ
EEEEEEEEEEEEEEEQEEEQEEEEEEEEEEEEEEEQEEEQEEEEEEEEEEEEEEEQEEEQ
EEEEEEEEEEEEEEEQEEEQEEEEEEEEEEEEEEEQEEERRGGEESFKVWQDALLTYVNQNS
```

34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
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48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
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61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
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69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE

74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
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80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE

A0A085LKL2 **A0A085LKL2_9BILA** (141 aa)
Uncharacterized protein (Fragment). *Trichuris suis (pig whipworm)*

```
ACYGQSPVVQGGEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGRREEEEEEEEEEEEEEEEEEEEEEEEE
ERRRRRRRRTRRRRRRTRRRRRTRRTRRRRRTRRRRRTRRRRRRRTFENKRSSYRTTHAFL
```

16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE

20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE

A0A085LKN3 **A0A085LKN3_9BILA** (100 aa)
BZIP domain-containing protein (Fragment). *Trichuris suis (pig whipworm)*

```
EEEQEETTRAGRRRTGRTRRRRRRRRRRRRRRRRRRRRRRTRRRRRRRRKEEEEEEEEEEEEEEEEEEEEEEEEEEEEGE
EEEEEEEDEEEEEEGEEEHL
```

50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE

A0A085LLC7 **A0A085LLC7_9BILA** (190 aa)
Uncharacterized protein. *Trichuris suis (pig whipworm)*

```
MALRKFDPSNLFREAFGNHLFSEFHGVHSPISESTIRKHTTQEQEEEQQEEQKEDEEQQQKAEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEELKTKDLLTGQRMFFQNACYGLSPVVQRGKKKKKKKKNNNKNKKHKKKNKNKTKKNKKINKN
KNKKKKKNKKEKNKEKNEKKTKKNEKTKEK
```

63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE

73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE

A0A085LLY4 **A0A085LLY4_9BILA** (358 aa)
Uncharacterized protein. *Trichuris suis (pig whipworm)*

```
MERDSIQGEILKVVWCKIQDTITTSPAHASTRQYNPVKQHGTYRTYRFTYLQDVPVPGPGTTSPAHTNTRQYNPVKQHGT
YRTYRFTYLQDVPDEEEQEEGEEEEEEEQEQEQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEQEEEQEEEEEEEEEEEEEEEEQEEEQEEEEEEEEEEEEEEEQEEEQEEEEEEEEEEE
EEEEQEEEQEEEEEEEEEEEEEEEQEEEQEEEEEEEEEEEEEEEQEEEQEEEEEEEEEEEEEEEQEEEQEEEEEEEEEEE
EEEEQEEEQEEEEEEEEEEEEEEEQEEEQEEEEEEEEE
```

114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE

152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE

A0A085LMG5 **A0A085LMG5_9BILA** (103 aa)
Uncharacterized protein. *Trichuris suis (pig whipworm)*

```
MDTKMKRSDMTWKALEHEAKKSCKKKKKKEELEEEEEEEEEEEEEEEEEEEEEEEEEEESAKKNKKNKRKTNKKNKNKK
KENNKNNTSKNKKNQKKKNRKKN
```

33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE

A0A085LNU4 **A0A085LNU4_9BILA** (137 aa)
Uncharacterized protein. *Trichuris suis (pig whipworm)*

```
MDTKMKRSDMTWKTLEHEAKKSCKKKKNKKKNKNKKKENKKKNKKKKKEEEEEEEEEEEEEEEEEEEEEEEEKKEEEEEE
EEEEEEEEEEEEEEEEEKKKKENKNKKKNKNKKKNNKKNTSKNKKNQKKKNKKKN
```

49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE

A0A085LP05 **A0A085LP05_9BILA** (138 aa)
Uncharacterized protein. *Trichuris suis (pig whipworm)*

```
MDLKFGELLKKSPKLRVLARTMSRSLMPWMYGTTSVGRPSCRELCLGEEEQQEKQKKKKKKKKKKKKKKEEEKKKKKKKK
KKKKKKKKKKKKKKKKKKKKEEEEEEEEEEEEEEEEEEEEEEEGGGGWPLREGEKGLRR
```

100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE

103 - 122:	EEEEEEEEEEEEEEEEEEE

A0A085LQL3 **A0A085LQL3_9BILA** (139 aa)
Uncharacterized protein. *Trichuris suis (pig whipworm)*

```
MHAVDTAYIYAFGSLLEPSSAKVLKSRSVRLSSGRYADSGEAKTKEEQEQEEEQEEEQQEEGEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEQSAKKNKKNKRKTNKKNKNKKKENNKENTGKNKKNQKKKNKKKI
```

63 - 82:	EEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEE

A0A085LR43 **A0A085LR43_9BILA** (140 aa)
Uncharacterized protein. *Trichuris suis (pig whipworm)*

```
MHERLPTFHLLREGQEGDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEQEEEEEE
EEMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMVNRNVNLKT
```

19 - 38:	EEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEE

46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE

A0A085LS79 **A0A085LS79_9BILA** (190 aa)
Uncharacterized protein. *Trichuris suis (pig whipworm)*

```
MTCASTKSNSREKKKKKKKKKKKKKKKKKKKKKKKNKKKKKKKKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEERRLTYLRNFAQS
```

43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE

82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE

134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE

A0A085LUE9 **A0A085LUE9_9BILA** (255 aa)
Uncharacterized protein. *Trichuris suis (pig whipworm)*

```
MSSFVTVLSQRRQWKKCKGIYEKEISVDYVFTITVYNILSSIGQVTIPTDRVVCCTSKKKKKKKKKKKKKKKKKKKKKKK
KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKNKKKKEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEAH
```

147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE

167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE
180 - 199:	EEEEEEEEEEEEEEEEEEEE
181 - 200:	EEEEEEEEEEEEEEEEEEEE
182 - 201:	EEEEEEEEEEEEEEEEEEEE
183 - 202:	EEEEEEEEEEEEEEEEEEEE
184 - 203:	EEEEEEEEEEEEEEEEEEEE
185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE
190 - 209:	EEEEEEEEEEEEEEEEEEEE
191 - 210:	EEEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE
194 - 213:	EEEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEEE
196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE
208 - 227:	EEEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEEE

219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEEE
225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE

A0A085LW28 **A0A085LW28_9BILA** (542 aa)
Uncharacterized protein. *Trichuris suis (pig whipworm)*

```
MAGVRCLCRCPFLVPVLNVVVGWLSVSIVFLGSDSSSLPQMWRIGEKQLIHEGKGVKKKKKKKKKKKKKKKKKKKKKKKK
EEEEEEEEEEEEEEEEEEEEEEEEEEKKKEEEEEEEEEEEEEEEEEEEEEEEQEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEQEEEDALVVLYEEDLFDAPTGQIEPEQCAACSATADAANARSIATLCGNDDVLPRDLVVAEPPFSRSCLALISMLKN
PTRDHHWSEDPTSEKIQRLGRTLNVSVCYTWGSNLRSLLRSDKARVLSEEHPGVVYEVKCSCSATYIGETGFSLTHRFSQ
HMRHLARYTGAKQDPESGGSATTRSRGRTSSVPLTVAMERALATSAVAEQAAHCSGSLQTRVICKESHLPRRRIKEVFFI
QHNECINQDNGKEICALWTSLIQEKQSTRTTNLRQRSEQEEETGNDINTGHQPYQRFTGLTL
```

81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE

151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE
180 - 199:	EEEEEEEEEEEEEEEEEEEE
181 - 200:	EEEEEEEEEEEEEEEEEEEE
182 - 201:	EEEEEEEEEEEEEEEEEEEE
183 - 202:	EEEEEEEEEEEEEEEEEEEE
184 - 203:	EEEEEEEEEEEEEEEEEEEE
185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE
190 - 209:	EEEEEEEEEEEEEEEEEEEE
191 - 210:	EEEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE
194 - 213:	EEEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEEE
196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE

203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE
208 - 227:	EEEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEEE

A0A085LXK2 **A0A085LXK2_9BILA** (219 aa)
Uncharacterized protein. *Trichuris suis (pig whipworm)*

```
MSGSHADPEVELSRRCRVVPPCRFSGHAPTDGFCLRSLGCRCSYLWHKHFSISDECNKTDIDIWLGCDSEDAGFQILNGD
EIVATVSNSHGEPEEGEEEEEEEEEEEEEEEEEEEEEEEEEFYDDEMLENVCPLHEKAYQCLEVVLQWFEMQEECDSKRM
QRLKSIRDLTANKRTTALKQTSITNFFQICVNYWFYIDDKVLHNMNSCRIPSKNRADRK
```

97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE

A0A085LXX0 **A0A085LXX0_9BILA** (310 aa)
Uncharacterized protein. *Trichuris suis (pig whipworm)*

```
MCRTGAQKVSESAHRTVHSLHERHSVKCGKTFVTVTVGCGQTLAPVKFLLDTGSSVSILSESSFLLHSDSVGVEPRSKQV
RTYCDDPVRVLGCFRVEIVHKTKRKTANLLLCPSETSLLGVDAIDALKIGIRCSQLVAPIASRMDSPEVRHLRNQNVARK
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEQEEEEKKKKKKKKNKNKNKNKKKNKKKNKKKNKKGKEQKKNKKKRRTRKRTKQEE
```

161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE

173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE
180 - 199:	EEEEEEEEEEEEEEEEEEEE
181 - 200:	EEEEEEEEEEEEEEEEEEEE
182 - 201:	EEEEEEEEEEEEEEEEEEEE
183 - 202:	EEEEEEEEEEEEEEEEEEEE
184 - 203:	EEEEEEEEEEEEEEEEEEEE
185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE
190 - 209:	EEEEEEEEEEEEEEEEEEEE
191 - 210:	EEEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE
194 - 213:	EEEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEEE
196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE

A0A085M606 **A0A085M606_9BILA** (65 aa)
Uncharacterized protein (Fragment). *Trichuris suis (pig whipworm)*

DRSTLRTLREGGGGGEEEEEEEEEEEEEEEEEEEEEQEEEEEEEEEEQEEEEEQQQQQQRQEEHL

16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE

A0A085M6L3 **A0A085M6L3_9BILA** (74 aa)
Uncharacterized protein. *Trichuris suis (pig whipworm)*

MECSSSIIYEMEKVFTLTKVYVAHSGTKIEEEEEEGEEEEEEEEEEGEEEEEEEEEEEEEEEEEEEKRHYFKK

48 - 67:	EEEEEEEEEEEEEEEEEEEE

A0A085M9Q1 **A0A085M9Q1_9BILA** (124 aa)
Uncharacterized protein. *Trichuris suis (pig whipworm)*

```
MSKVGQALLARELRRDFAGPLHSYDDATVREGTDVHHIAIATKDIIQQVVGESCHMQHIHEPLPHQIITCSGPWSARFEK
KKKKKKKKKKKKKKKKKKKKKKEEEEEEEEEEEEEEEEEEEEGVH
```

102 - 121:	EEEEEEEEEEEEEEEEEEEE

A0A085M9Q3 **A0A085M9Q3_9BILA** (107 aa)
Uncharacterized protein. *Trichuris suis (pig whipworm)*

```
MDTKLRKVMQKEEEQEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEQSTKKKQEEQKENKNKKKN
KNKKKKNNEKNTSRNKKNQKKKNKKKN
```

19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE

A0A085MGJ8 **A0A085MGJ8_9BILA** (242 aa)
Uncharacterized protein. *Trichuris suis (pig whipworm)*

```
MTPWKMASWIGTESATEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDPPAINWPEGRPINSVTKQGVWREAQLR
SL
```

17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE

28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE

80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE

132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE
180 - 199:	EEEEEEEEEEEEEEEEEEEE
181 - 200:	EEEEEEEEEEEEEEEEEEEE
182 - 201:	EEEEEEEEEEEEEEEEEEEE
183 - 202:	EEEEEEEEEEEEEEEEEEEE

184 - 203:	EEEEEEEEEEEEEEEEEEEE
185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE
190 - 209:	EEEEEEEEEEEEEEEEEEEE
191 - 210:	EEEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE

A0A085MR46 **A0A085MR46_9BILA** (160 aa)
Uncharacterized protein. *Trichuris suis (pig whipworm)*

```
MDTKLRKVMQKEEEQEEREEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEESTKKKQEEQKENKNKKKNKNKKKKNNKKNTSKNKKNQKKKNKKKNQKKKNKKKKKKNWNDKEEITMN
```

19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE

56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE

A0A085MR48 **A0A085MR48_9BILA** (75 aa)
Uncharacterized protein. *Trichuris suis (pig whipworm)*

MGINGEDVEVALAFREEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGVH

16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE

45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE

A0A085MS36 **A0A085MS36_9BILA** (300 aa)
Uncharacterized protein. *Trichuris suis (pig whipworm)*

```
MTSLYLRRTSGSQNVCVKIFLYKRHGHSDAAEIRQNEAPVLHFDAKSLRNGAASNRYDQAQAYRNRVVFWGERARMNSAE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEDIARKRFSRIFEFRRPKLLFSFCWVKILFLWCIATD
```

80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE

117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE

169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE
180 - 199:	EEEEEEEEEEEEEEEEEEEE
181 - 200:	EEEEEEEEEEEEEEEEEEEE
182 - 201:	EEEEEEEEEEEEEEEEEEEE
183 - 202:	EEEEEEEEEEEEEEEEEEEE
184 - 203:	EEEEEEEEEEEEEEEEEEEE
185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE
190 - 209:	EEEEEEEEEEEEEEEEEEEE
191 - 210:	EEEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE
194 - 213:	EEEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEEE
196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE
208 - 227:	EEEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE

221 - 240:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEEE
225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE
239 - 258:	EEEEEEEEEEEEEEEEEEEE
240 - 259:	EEEEEEEEEEEEEEEEEEEE
241 - 260:	EEEEEEEEEEEEEEEEEEEE
242 - 261:	EEEEEEEEEEEEEEEEEEEE
243 - 262:	EEEEEEEEEEEEEEEEEEEE
244 - 263:	EEEEEEEEEEEEEEEEEEEE
245 - 264:	EEEEEEEEEEEEEEEEEEEE

A0A085MW86 **A0A085MW86_9BILA** (122 aa)
Uncharacterized protein. *Trichuris suis (pig whipworm)*

```
MEWTQKNKTRRTRRSKNKGRTRTRRRTRGRTKEEEEEEEEEEEEEEEEEEEEEEQSTKKKQEEQKENKNKKKNKNKKKKN
NKKNTSKNKKNQKKKNKKKNQKKKNKKKKKKNWNDKEEITMN
```

33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE

A0A085MY57 **A0A085MY57_9BILA** (644 aa)
Uncharacterized protein. *Trichuris suis (pig whipworm)*

```
MLAERYDFNFEWGEMETKHLLRLTVQQCWLKDTTLISRGHVYLEQAWRKFQRAYGEVYARRIREARQLGITSFFKPSASK
KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
KKKKKKKKKKKKKKKKKKKKKKKKEEEEKKKKKKKKKKKKKKKKKKKKKKKKKKEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERRRGGWGVNRA
ANNL
```

535 - 554:	EEEEEEEEEEEEEEEEEEEE
536 - 555:	EEEEEEEEEEEEEEEEEEEE
537 - 556:	EEEEEEEEEEEEEEEEEEEE
538 - 557:	EEEEEEEEEEEEEEEEEEEE
539 - 558:	EEEEEEEEEEEEEEEEEEEE
540 - 559:	EEEEEEEEEEEEEEEEEEEE
541 - 560:	EEEEEEEEEEEEEEEEEEEE
542 - 561:	EEEEEEEEEEEEEEEEEEEE
543 - 562:	EEEEEEEEEEEEEEEEEEEE
544 - 563:	EEEEEEEEEEEEEEEEEEEE

545 - 564:	EEEEEEEEEEEEEEEEEEEE
546 - 565:	EEEEEEEEEEEEEEEEEEEE
547 - 566:	EEEEEEEEEEEEEEEEEEEE
548 - 567:	EEEEEEEEEEEEEEEEEEEE
549 - 568:	EEEEEEEEEEEEEEEEEEEE
550 - 569:	EEEEEEEEEEEEEEEEEEEE
551 - 570:	EEEEEEEEEEEEEEEEEEEE
552 - 571:	EEEEEEEEEEEEEEEEEEEE
553 - 572:	EEEEEEEEEEEEEEEEEEEE
554 - 573:	EEEEEEEEEEEEEEEEEEEE
555 - 574:	EEEEEEEEEEEEEEEEEEEE
556 - 575:	EEEEEEEEEEEEEEEEEEEE
557 - 576:	EEEEEEEEEEEEEEEEEEEE
558 - 577:	EEEEEEEEEEEEEEEEEEEE
559 - 578:	EEEEEEEEEEEEEEEEEEEE
560 - 579:	EEEEEEEEEEEEEEEEEEEE
561 - 580:	EEEEEEEEEEEEEEEEEEEE
562 - 581:	EEEEEEEEEEEEEEEEEEEE
563 - 582:	EEEEEEEEEEEEEEEEEEEE
564 - 583:	EEEEEEEEEEEEEEEEEEEE
565 - 584:	EEEEEEEEEEEEEEEEEEEE
566 - 585:	EEEEEEEEEEEEEEEEEEEE
567 - 586:	EEEEEEEEEEEEEEEEEEEE
568 - 587:	EEEEEEEEEEEEEEEEEEEE
569 - 588:	EEEEEEEEEEEEEEEEEEEE
570 - 589:	EEEEEEEEEEEEEEEEEEEE
571 - 590:	EEEEEEEEEEEEEEEEEEEE
572 - 591:	EEEEEEEEEEEEEEEEEEEE
573 - 592:	EEEEEEEEEEEEEEEEEEEE
574 - 593:	EEEEEEEEEEEEEEEEEEEE
575 - 594:	EEEEEEEEEEEEEEEEEEEE
576 - 595:	EEEEEEEEEEEEEEEEEEEE
577 - 596:	EEEEEEEEEEEEEEEEEEEE
578 - 597:	EEEEEEEEEEEEEEEEEEEE
579 - 598:	EEEEEEEEEEEEEEEEEEEE
580 - 599:	EEEEEEEEEEEEEEEEEEEE
581 - 600:	EEEEEEEEEEEEEEEEEEEE
582 - 601:	EEEEEEEEEEEEEEEEEEEE
583 - 602:	EEEEEEEEEEEEEEEEEEEE
584 - 603:	EEEEEEEEEEEEEEEEEEEE
585 - 604:	EEEEEEEEEEEEEEEEEEEE
586 - 605:	EEEEEEEEEEEEEEEEEEEE
587 - 606:	EEEEEEEEEEEEEEEEEEEE
588 - 607:	EEEEEEEEEEEEEEEEEEEE
589 - 608:	EEEEEEEEEEEEEEEEEEEE
590 - 609:	EEEEEEEEEEEEEEEEEEEE
591 - 610:	EEEEEEEEEEEEEEEEEEEE
592 - 611:	EEEEEEEEEEEEEEEEEEEE
593 - 612:	EEEEEEEEEEEEEEEEEEEE
594 - 613:	EEEEEEEEEEEEEEEEEEEE
595 - 614:	EEEEEEEEEEEEEEEEEEEE
596 - 615:	EEEEEEEEEEEEEEEEEEEE

597 - 616:	EEEEEEEEEEEEEEEEEEEE
598 - 617:	EEEEEEEEEEEEEEEEEEEE
599 - 618:	EEEEEEEEEEEEEEEEEEEE
600 - 619:	EEEEEEEEEEEEEEEEEEEE
601 - 620:	EEEEEEEEEEEEEEEEEEEE
602 - 621:	EEEEEEEEEEEEEEEEEEEE
603 - 622:	EEEEEEEEEEEEEEEEEEEE
604 - 623:	EEEEEEEEEEEEEEEEEEEE
605 - 624:	EEEEEEEEEEEEEEEEEEEE
606 - 625:	EEEEEEEEEEEEEEEEEEEE
607 - 626:	EEEEEEEEEEEEEEEEEEEE
608 - 627:	EEEEEEEEEEEEEEEEEEEE
609 - 628:	EEEEEEEEEEEEEEEEEEEE
610 - 629:	EEEEEEEEEEEEEEEEEEEE

A0A085N2T4 **A0A085N2T4_9BILA** (116 aa)
Uncharacterized protein. *Trichuris suis (pig whipworm)*

```
MDPLASWIGTESATREEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEQSTKKKQEEQKENKNKKKNKNKKKKNNKKNTS
KNKKNQKKKNKKKNQKKKNKKKKKKNWNDKEEITMN
```

16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE

A0A085N2Z5 **A0A085N2Z5_9BILA** (118 aa)
Uncharacterized protein (Fragment). *Trichuris suis (pig whipworm)*

```
DRSTLRTLREGGGGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGV
```

15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE

29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
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40 - 59:	EEEEEEEEEEEEEEEEEEEE
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43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
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60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
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63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
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77 - 96:	EEEEEEEEEEEEEEEEEEEE
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81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
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85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE

A0A085N3D7 **A0A085N3D7_9BILA** (221 aa)
Uncharacterized protein. *Trichuris suis (pig whipworm)*

```
MYSICKGIDVWRKKYQWIMYSPSLSITFCHLLGSRVLHIEEEEEEEEEEEEEEEEEEEEEEKKKKEEEEEEEEEEEEEEEE
EEEEEEEEEEKKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEQSTKKKQEEQKENKNKKKNKNKKKNNKKNTSKNKKNQKKKNKKKNQNISALV
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40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE

115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
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141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE

A0A085NC27 **A0A085NC27_9BILA** (234 aa)
Uncharacterized protein. *Trichuris suis (pig whipworm)*

```
MEDDDDDGDDDDDGDDDGDDDGDDDDDDDDDDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEELYDDETINKTI
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33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE

45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
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81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
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91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE

97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
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113 - 132:	EEEEEEEEEEEEEEEEEEEE
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117 - 136:	EEEEEEEEEEEEEEEEEEEE
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123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
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143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE

149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
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161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
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168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
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171 - 190:	EEEEEEEEEEEEEEEEEEEE
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173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE
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181 - 200:	EEEEEEEEEEEEEEEEEEEE
182 - 201:	EEEEEEEEEEEEEEEEEEEE
183 - 202:	EEEEEEEEEEEEEEEEEEEE
184 - 203:	EEEEEEEEEEEEEEEEEEEE
185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE
190 - 209:	EEEEEEEEEEEEEEEEEEEE
191 - 210:	EEEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE
194 - 213:	EEEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEEE
196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE

201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE

A0A085NCA5 **A0A085NCA5_9BILA** (251 aa)
Uncharacterized protein. *Trichuris suis (pig whipworm)*

```
MIIHSEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDKPVGQ
EEQMMALFFIV
```

6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE

48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
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63 - 82:	EEEEEEEEEEEEEEEEEEEE
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146 - 165:	EEEEEEEEEEEEEEEEEEEE
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148 - 167:	EEEEEEEEEEEEEEEEEEEE
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152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
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158 - 177:	EEEEEEEEEEEEEEEEEEEE
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161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
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167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
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173 - 192:	EEEEEEEEEEEEEEEEEEEE
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176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE
180 - 199:	EEEEEEEEEEEEEEEEEEEE
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200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE

204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE
208 - 227:	EEEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE

A0A085NTV3 **A0A085NTV3_9BILA** (604 aa)
Protein kinase domain-containing protein. *Trichuris suis (pig whipworm)*

```
MVLSQCDSPYVTKYYGSYLKGSKLWIIMEYLGGGSALDLMKPGRLEEMHIAVIIREILKGLDYLHSERKIHRDIKAANVL
LSEQGDVKLADFGVAGQLTDTIRKRITFVGTPFWMAPEVIKQASYDAKADVWSLGITAIELAKGEPPHADLHPMRVLFLI
PKNPPPQLMGTYSKPFKDFVEACLNKDPENRPTARELLKHPFVRKAKKNNVLTELIERYKQWKIHMGPGSDSDQEDNEAE
HNEEGFGEWEYPTVRRPTGMDLTNDGTVKMKKNITISESNLDDINATVRVKPSSSQNDQIPAIGTLSLSAGTSTSGQNNG
IADESKLSLDNGVGPTKIHVVMEALPSDEAAILRPNSSADHSGCFSKQPLSQTDRRDNMKHRRRRILDNTVLPFLESELK
KRSMENKPYRALAQLKRALLATEDACPGFSEHFFTELLRLVASPSSNGISQSQFQSGVEKLRGYSTTGILQSRPHEEAHE
INEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
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483 - 502:	EEEEEEEEEEEEEEEEEEEE
484 - 503:	EEEEEEEEEEEEEEEEEEEE
485 - 504:	EEEEEEEEEEEEEEEEEEEE
486 - 505:	EEEEEEEEEEEEEEEEEEEE
487 - 506:	EEEEEEEEEEEEEEEEEEEE
488 - 507:	EEEEEEEEEEEEEEEEEEEE
489 - 508:	EEEEEEEEEEEEEEEEEEEE
490 - 509:	EEEEEEEEEEEEEEEEEEEE
491 - 510:	EEEEEEEEEEEEEEEEEEEE
492 - 511:	EEEEEEEEEEEEEEEEEEEE
493 - 512:	EEEEEEEEEEEEEEEEEEEE
494 - 513:	EEEEEEEEEEEEEEEEEEEE
495 - 514:	EEEEEEEEEEEEEEEEEEEE
496 - 515:	EEEEEEEEEEEEEEEEEEEE
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498 - 517:	EEEEEEEEEEEEEEEEEEEE
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532 - 551:	EEEEEEEEEEEEEEEEEEEE
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535 - 554:	EEEEEEEEEEEEEEEEEEEE
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537 - 556:	EEEEEEEEEEEEEEEEEEEE
538 - 557:	EEEEEEEEEEEEEEEEEEEE
539 - 558:	EEEEEEEEEEEEEEEEEEEE
540 - 559:	EEEEEEEEEEEEEEEEEEEE
541 - 560:	EEEEEEEEEEEEEEEEEEEE
542 - 561:	EEEEEEEEEEEEEEEEEEEE
543 - 562:	EEEEEEEEEEEEEEEEEEEE
544 - 563:	EEEEEEEEEEEEEEEEEEEE
545 - 564:	EEEEEEEEEEEEEEEEEEEE
546 - 565:	EEEEEEEEEEEEEEEEEEEE
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554 - 573:	EEEEEEEEEEEEEEEEEEEE
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559 - 578:	EEEEEEEEEEEEEEEEEEEE
560 - 579:	EEEEEEEEEEEEEEEEEEEE
561 - 580:	EEEEEEEEEEEEEEEEEEEE
562 - 581:	EEEEEEEEEEEEEEEEEEEE
563 - 582:	EEEEEEEEEEEEEEEEEEEE
564 - 583:	EEEEEEEEEEEEEEEEEEEE
565 - 584:	EEEEEEEEEEEEEEEEEEEE
566 - 585:	EEEEEEEEEEEEEEEEEEEE

567 - 586:	EEEEEEEEEEEEEEEEEEEE
568 - 587:	EEEEEEEEEEEEEEEEEEEE
569 - 588:	EEEEEEEEEEEEEEEEEEEE
570 - 589:	EEEEEEEEEEEEEEEEEEEE
571 - 590:	EEEEEEEEEEEEEEEEEEEE
572 - 591:	EEEEEEEEEEEEEEEEEEEE
573 - 592:	EEEEEEEEEEEEEEEEEEEE
574 - 593:	EEEEEEEEEEEEEEEEEEEE
575 - 594:	EEEEEEEEEEEEEEEEEEEE
576 - 595:	EEEEEEEEEEEEEEEEEEEE
577 - 596:	EEEEEEEEEEEEEEEEEEEE
578 - 597:	EEEEEEEEEEEEEEEEEEEE
579 - 598:	EEEEEEEEEEEEEEEEEEEE
580 - 599:	EEEEEEEEEEEEEEEEEEEE
581 - 600:	EEEEEEEEEEEEEEEEEEEE
582 - 601:	EEEEEEEEEEEEEEEEEEEE
583 - 602:	EEEEEEEEEEEEEEEEEEEE
584 - 603:	EEEEEEEEEEEEEEEEEEEE
585 - 604:	EEEEEEEEEEEEEEEEEEEE

A0A086J7H9 **A0A086J7H9_TOXGO** (1826 aa)
Ribonuclease type III Dicer. *Toxoplasma gondii p89*

```
MQLCRSRDLAHVCLTDVAALEGGVAVAERTGSLPQVLACSLFSDKLLRLDQVLRDSFGRAQAQAQAQTKAQAQTQTQRRE
GSVADDKRGSGPDKRAGRPGDEEERRTEDGGEATRSGLRIKASSTGDRECSPSPKKSGVRTPVPSFSSSPSCVSPSALSF
APSSMSLSSRFPAASRSPASPDVAFGGVPKCGLVFCRRRVDAWLVCEFLTARRLVFVDWICSSSLASQGASWLFGIGKAS
QGRSSCLDRLRAMHTVWGKLEKKTQKLNAQKHRPSTTPQSHSPSLASSLSSSLASSLSSSLASSASSSASSSASSSLSSS
ASSSASWGDGGKGVWRLMRRLGWGAPLQLLVSTSVLEEGIDVPACNLVVQMDMPSSLVRFVQAKGRARKKPAEFVVLCPD
SGPCGASWPDASLPFSSSFPSSSSFFPFSSSLQSQTPDCTASSPSLLLSLQSVSSLAVSSSSLSAPFSVSLRSRTGEAPT
TPAFAAQGFSAAGGAACYLQAVSPSVNFELARLQLCEAKVAALAADVEATERFGLLGPFRCMRKVCSLDDLLLTHTGAMV
HSSFAPALLREIVDACTAGKTDERTERGADERGEEGRWAEDTEDEGREERERGNAELRTGREKALGTCCSNAPSSSSLSS
SGMRRVSDLCETRRQRTPSALRLLSTQDGKWILSVPSLQGFRSSPLPPFSIEFSPTGSAPTRASAAAGVLAVRVLRRLVQ
EGVVDSFLRCRDRDSVEKDLRDEKERRRRENCGGVGAVDLLWRELPACLLPPRSWRNARRASGDRHGDSEETLHTSAKTR
EEAARAEEAVSGSNEERRRSRDHKEGTIKGDAGAQEVEENAEEGRKEEEGDQLKRLPSGTGKKDKTSTSNAKSETHREKT
RTPAPPPGVTRLFLHRVWCTPLTAREAALERLWEPNEKQRRRRRRVLKKLAESRGFLPSPLYESGGFCGLWRIFADAEAP
LQAADLALDGASRRRQEKAKEKEQIEPDAGDGEGDEDGLWWTGNRRQREACFEKREREGGDGKRDQCKEDEKCRAEKEEE
EEEEEEEEEEEEEEEEEKKWSWQEEEKNRQRREILELIRSRIDAVVEGRRGPDSVLQPLCLLLAHPIPATVAFHALHPE
ASEKAALHRGRRPRTGRTSFSLRASKAEKASNAWTELEADEEGEEGVEEGDEEGDEEGEEEEGEEDGEEEGDEEDVPGLM
RVEVEKPAKTMFIDLPTEYVEKVLLRFTHIHLFRLLQLSNFSPNGTCNSLLLTVLQFLSALPFRRFPFRTVPSSSSLSSS
ASASASASCLGGDGEPRSRFVSLPLPACASASRLLPSHALSLFALPPSLFSLLSLLSLAAEEAEESTESTLHSQSPPSSP
RSSSPRSSSPRSSSLSSSSPSTSAEQLKRQMVEACSSLAKAGVVDLQRVMFPFFVLAPLSPLDAKSVDLDFIHRLASLRL
FLRSGQRRSSGFLEAGACPPSLMLQHDRRLLRGAVESLHCLPSLSAVARLFCAGNSARKLDYEGGRSLQKAERRSARKEQ
NEGDAAEENGAFNWPRSLLGTLPSSDRESESAKDTKEKRTPGSEKGERREADGERREEDGEKGATKEDGLFSKEEQFFRR
LQSYKGSIFSRGGDAANAWTTEEQKLLTFFQQRNENALSVKEALREEGMEIFYHLRSRGFEPVALRMTHQFGRSFRFYRL
QTIHRNVRRCVYDYLTPRNVVINSDAGFTLGTLCRVYLSRFKQRLAEPHPDSQQGPQGNCFLVQGVKRRQEISWMPAILY
QLEVQGKHCDLVRRLRQEMRPFLFTAEENISPPLVPSEQCKRWKRPQQESQSAAEREKTRRSRKYV
```

1038 - 1057:	EEEEEEEEEEEEEEEEEEEE
1039 - 1058:	EEEEEEEEEEEEEEEEEEEE

A0A086JE25 **A0A086JE25_TOXGO** (3578 aa)
Tyrosine kinase-like (TKL) protein (EC 2.7.11.25). *Toxoplasma gondii GAB2-2007-GAL-DOM2*

```
MGGGVGRAPRAGRGASVSDSEALSLPALLPPLSPLSSPSPALGDSACFPFIGLEPLKPPAGGRGSPASPVRSLSSILIVS
SASAAAFVRSASSSFASSLSSRASSSSAPVPVYIHPVSGTVHPYPAQPAPPPPTHLVLAVPASASYAPPASSSSSSFLEG
LSVGFSGVSGRPSARATAQEKPDASFFAALQTSVVQLLKRSRSIRSVVLRGDGDWLEVLREALQNHVSVSSVSLEAVTNL
SEKELTSGYARLLSGLSKCTSISIRGCGLTSRGLKSLLRSLGKQSDFVEHLQEIDLAHNDLDDEAAAVLLSLFSSSSPRR
LASLRLDANPCSLSALEPLLALLASCDGASSEEESGLNLLSLGGLTNVSESTLSSLSLFSSLSSLSLSRCRSDSPHTLRL
LPSLASSLTAASLTSKFAFLSTLTHLDLSHVPSLLSDDDVALLVEILFPRESLPRLQTRGGRDERGKSPACTRKPQTAKG
RDRSVSAVSSVSSLLSLSLAGDGLTGGCLRALALGLLSPSCRLQHLDLSRNSFGKKPSIDGDAGSDSHAPERKDKDKRRA
KGRPGARKRPEEKEEEVLPIEPLVDALQQGYEEAPHAPCGLRFLSLAFCELSLEAMQQLAAALLTNGENLVFLDLRGNLR
SAEGPDGGEEQRKGDRRDELRLARCAFDTVAGMCGLQVLLLEEETKKRRQETEETEETEETQETGRKRQKRGTRQPKGRR
RDKATEEANEEEGTVEEGEDEEDEEEDDEKHGEEGTRGVRGGRAVEIERRRCGGKGGRGRRSEKSESKKRKAEMAEEDSG
RSSVRTRRQRKDDEEEEEEEEEEEEEEEEEEEEEEDDEEEEEDDEEDESFDELDAMEAEQKADESSEDEGGEDGEEKEEDE
DEEEEEEDETTRTSLRKRGRHSGMRSEKEQESMSKATEPRQRTMESENGGKTTPRRGRPTRRTSADSSRRKKSKKDESEE
EEEEEDEEEEEEEEEEEEDDDDEEYEEGESVTGRKGRRRRHPQRGRDQVVSAHVRKRRKTTAEEKEAGEERLEKREQVDE
QVEENLKNNAVLPSPSPQKEGRRRRTVCAVPSARASRPRKTRADPEDETSFPETAGDQESCMLSGQTSASPSLPLRSRQK
SRWIEEDSVSGPLPHPRASRPSSFFVAETGRIGVGGAQPRRSCSALMSTTSVDLEGGGELFGNRERGPPRRRQSASFLAA
PAAPAIVVHQVSPAPGAGERPRKKESLAVNKKSEATFSSSVVSAATPVDTPFLMYFDMKREYPATSALRDPEANGDLRPG
EEDALPRGGVYVQPSAGAPSEAREALGRVRVREEEARRVESSRGFAVLPPVPAAPEEQRDIRVFLNRAGIHLLNLFFPRD
SHSYVGKTPLQPLLRSYPQELLLGLKYILSSHYLPLLSFPDVYTLQELSLSPHLSPPLQLLLSIIFEELARTNLTYKYQQ
YGELGFDENLCHPGKVLFDGGPGCQAIHAAEFRVFWMRRHGRRLGRRRPGWGSRAQLAVGSRADDAPVAPFQSPPPPLPL
ASPQASGLERERLFSGKKFERRDPRDAFSGACTLDGLDHDSPPGASPCTSPKQAEFPPPTPQFVETPDRVRGLAGLFEGS
PRSAFSAAENGDHSTSLSTVFDLLEPARLHPLAASFDGDTFGSAGPEKGLLKISGKAPENGRPLQCTCGRDEAERRRQLP
GERPSKPPLREKKPLDAETKKNSADGSRTADGAPTPELSEVPTGQPPPLPNAEKSGAELFATPAPFRWMKKALGAVRSQG
ISGLKKETVPRNLDFYFRLNRRASDDAAQLQAKADSAKRGETSTARAESAGDLNAAGPPAAGEEFQGLSDAGKDETDVAS
```

```
KNRETPGGGVSRSSVDSRSLSERRDSEVSVSAPADDRDSQDEVVAVSRPSALTGRGGLYSAVSSPALSASDFAEELSENE
ARPVVLRTNGHRPEVRPAEPRREEEGDTFGPPAWAPKGEAPGSEEGKATRDDEEKAGREKAPVPRCASTPQDRFVVSWDD
DEWLGSIECFLDDLSLCPSAASTRACSFESSSTHGASCPLASRGAPHTRSLPADFVLHPPLLPPSLSPSAPPSSVSLSAV
SAPLVPASPCVGGAGVQTPGPCSCREVIVVDVQSDAQLRKRIWDVQTLFTGSELSVHRKIELLRRMVLRSIKSAATGYGE
QKDEVKRLAAEHDGFVYLGDVNYGFSRHMALLFKVLCDASQIPCRVMRAGLLGEETVGDNGDTSTRNPELGGGAPGEGEK
RLAGPRARRDGLERQERRRREEEEFVYNVVLVKDATKSELEQLIPIIWTQNAAAGLWRRHLSPGVEKGARGEDRERKRGR
HSSLTDFLASGVVRLNPPTLSSIPLPRRLRALQRRLAVSSASFSSCGQERSSERSRCVERDLETETGRGATAGNERCGDT
AGDLGGDRELPPLGRARSPRPFDYFKHGWVDRRRETSHCCCCASRSLPSLEAETGGDRAETRGDNGRDNRVGRDSAPGGD
VTSRNERSEKTEKENWGTKPSEDGPLHRQHADLDRLLLAASGASAFCGCGGAPASVAATELDLDAFFDFREKLGKGSFGE
VWRVRIKSEGRAVGAARRKPRERKRSREEQDAGVREENAVSEEEERGKEVHSGEERAEAPWRRETDEDGEADEAGERGEA
DEACRGDSGEPAEPEYALKLVPKSEENLPEAEIMRSYSHPRVVPFLGVFEGFQMLEDRSKKKVKNTSLCFLMDIADQSLE
SLLEEHEKANTCLDVEFILTILLDTARGMNYLHSPSATKPHLLHRDLKPANILLKDGRAMVTDFGVARVAEVSFEHEMTQ
GPGTEGYIAPEQRTAAYDRPADVWAFGVVCARLLGLREWKKLSDPQHRVALSDFALKDAFLINLCLACLERRPLMRPTFH
QIVQRLIDKIFRLEFERILRTPYRNCLPLLHAENPLVFSSPASLPVGRGDTPSRAVETVDVRRLGEKSGAITPFRSPSLC
PSQLAPPARPVPSRLSRSLLEAPFSAGGENVEALASRTEKVSPKARPEEGVCSGRPASACTHRSGNDEAAAPASSLSTGG
EEEVFFSGEESEATSQAKNAEAKGEPQLGPVADPEVTEDQEEEGFFSRLRLRTMKRSRPLLLSSSEVSPASSEREDAAEE
CDGAVEPDTNAKEKKLETKSESNEKSQEKREEVDPVDGVVTPHRLSPSDKKEPKEPSLLKKSGASPLQKKQGSPASKKKV
WKTPTSFVSLRTPDKVAANSSSSSSSSSSSSSSSSSSSSSSSSSSSSSASSSPSSPSSAASASLSPTGGSRRRAASPQREREER
RRPGRTSPKLTPRGREEERRLSPTEKDDRGQSLSRGRSVSRGRCLGKEGEKIRTKERNVEKTPTQTPNHRRGSPSPSLST
SPLSRFDEAGVQDAEEGVLRHPSSRGPRSKISENPRISACSPSSPFSPCPSPSSASSPSASSPSAFSSLSASVLKNRVGS
VDAQRSLGERKGLLLSSSASVGSETRDARRSPEGVSAVSSEGSASLSGAPRVLASRQADSSSDSLVEKEISHAPNCASSA
FPPPARVAGLAAPFAAKPATQTAPIRKGDSFSDAYKVSGATEQLASGGNEGRGSGSLS
```

814 - 833:	EEEEEEEEEEEEEEEEEEEE
815 - 834:	EEEEEEEEEEEEEEEEEEEE

A0A086JFM5 **A0A086JFM5_TOXGO** (130 aa)
Uncharacterized protein (Fragment). *Toxoplasma gondii FOU*

```
ALNPVEASTSRSKWASAASSRTGKSEKEEEEEEEEEEEEEEEEEEEEEEEEEEVEEDLEGRSTWRGRSWRQSKKPPDGHER
KSEEKLPRRRLAGSEVTGESSRERLNARREENSGENSSPNGFRSWLALRC
```

28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE

A0A086JHK4 **A0A086JHK4_TOXGO** (1245 aa)
MI domain-containing protein. *Toxoplasma gondii GAB2-2007-GAL-DOM2*

```
MRGRRPSQQRKKAASLGASSLLSSLPSSLPSSLFSRGDSVGRRLGKRRGIEEEGGKRKRARGGRSARHNFPEVDQQGGSD
LDELPSSEADPREAQQDGEGSFGHEQELAETLKKSKRAVLERKRRRHEERRQKKQIHRKQQQLWKLERQKALLERQLDMQ
KAAISGVRVNQGTGSGVRTPCGPEADSEDEEEDVSPRREKKTPSSLSSSLSSSLSSLDVRGSVLSALSAKDKKHTVSGEV
LLLSGVSSRSTEEHRKAEERRLALDAAGRQLDAELAFLESKLGIGKDSSKAGEKKKKKLAQELLDDGFDEDLQTLLDDIL
GGKAENRKRKTKTDYDHDEGEMEGEETQEGAHEELGRVEAEEDEEDEEEEDDEEDEEDDEEENEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEDEGDEEDEEEGEDLKLKTEQYSTCASASAGKYLPPHLRNRAQRELSNEAEFDGDNPGRNST
RQHGAAPASEASDKANFVASKLPLSCLEKARQTATDAGRGLTQRLRGSLNRVSEGNVEVILQQISQEVKAALTQVLSGAL
PVPATSPALTPRDVRGLRREQEISFFQEVNCIIVRLLMQSMVESKFSTASLVATQTALCCGLSCLLDASLCSQLLAALGE
AFRKFFPLALAQADRRTETGEPVGLYVRHTLMALCFLFDFNVVQPAVFLGLLQRLSGKVATTKEKGEAKNGERNEPLVEF
QVECLLMVLRLGGGKLRNDNPVLFKEAWNFLMTRVKGGEGEREVQVHSGREERPFEEQTREEQRARLARVSTSFSGALRQ
RQEGEQPATTGRLHYLARELEELKNNKGNTIHLASKASQEAMRRWLQTSPLLAQSPLRQCAGEGKSVLVGVSSWQEVEDG
VVSVSPSSHRPPVSPHKSVRVEKEKQSCLGDTGSEKALLDLAAKLRLHSEEQKKIFLAIMSAESPNDAVKRLLQLVPRTN
KKKNFVTTAVAVLLHISLQQSAFNPFYALVIARLCARCSCASWGRLEAEAEQPPLLGPLGSGRASVNQRRARGPCACLLP
PDKEGKVFRRVTQRGLAAQNSAAHGFPLRRLLHLARLEAFLIRIGVVELRVTRFVSFEGEKGQADAHMGLSGKLGVFLKE
LCTELLCSPAFASVPLPGPSTASPLLPFLSLSALPDVREAFLLVLEDVLLPEARKNACSENGKGAKESVNAACMPGRQGK
CVRAKGAMCTPACGIRKDVISRVIWFMKKQERYEEEDPNTFAFDA
```

384 - 403:	EEEEEEEEEEEEEEEEEEEE
385 - 404:	EEEEEEEEEEEEEEEEEEEE
386 - 405:	EEEEEEEEEEEEEEEEEEEE
387 - 406:	EEEEEEEEEEEEEEEEEEEE
388 - 407:	EEEEEEEEEEEEEEEEEEEE
389 - 408:	EEEEEEEEEEEEEEEEEEEE
390 - 409:	EEEEEEEEEEEEEEEEEEEE
391 - 410:	EEEEEEEEEEEEEEEEEEEE
392 - 411:	EEEEEEEEEEEEEEEEEEEE
393 - 412:	EEEEEEEEEEEEEEEEEEEE
394 - 413:	EEEEEEEEEEEEEEEEEEEE
395 - 414:	EEEEEEEEEEEEEEEEEEEE
396 - 415:	EEEEEEEEEEEEEEEEEEEE
397 - 416:	EEEEEEEEEEEEEEEEEEEE

398 - 417:	EEEEEEEEEEEEEEEEEEEE
399 - 418:	EEEEEEEEEEEEEEEEEEEE
400 - 419:	EEEEEEEEEEEEEEEEEEEE

A0A086JJR3 **A0A086JJR3_TOXGO** (133 aa)
Uncharacterized protein (Fragment). *Toxoplasma gondii FOU*

```
EEEEEEEEEEEEEEEEEEEEEEEEEVRGLAYVSRRRIVILLLRTAFVSRRGKTKTKGCKVPRQASDEETEGRRSSFSTQAR
PSGIRRASRGNWSRNEASRPQKNATQTKSKSRRAWTARKKEIEVCLLFARWND
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE

A0A086JKE2 **A0A086JKE2_TOXGO** (941 aa)
Uncharacterized protein (Fragment). *Toxoplasma gondii FOU*

```
MRGRRPSQQRKKAASLGASSLLSSLPSSLPSSLFSRGDSVGRRLGKRRGIEEEGGKRKRARGGRSARHNFPEVDQQGGSD
LDELPSSEADPREAQQDGEGSFGHEQELAETLKKSKRAVLERKRRRHEERRQKKQIHRKQQQLWKLERQKALLERQLDMQ
KAAISGIRVNQGTGSGVRTPCGPEADSEDEEEDVSPRREKKTPSSLSSSLSSSLSSLDVRGSVLSALSAKDKKHTASGEV
LLLSGVSSRSTEEQRKAEERRLALDAAGRQLDAELAFLESKLGIGKDSSKAGEKKKKKLAQELLDDGFDEDLQTLLDDIL
GGKAENRKRKTKTDYDHDEGEMEGEETQEGAHEELGRVEAEEDEEDEEEEDDEEDEEDDEEENEEEEEDEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEKEEEEEEEEDEGDEEDEEEGEDLKLKTEHYSTCASASAGKYLPPHLRNRAQRDLS
NEAEFDGDNPGRNSTRQHGAAPASEASDKANFVASKLPLSCLEKARQTATDAGRGLTQRLRGSLNRVSEGNVEVILQQIS
QEVKAALTQVLSGALPVPATSPALTPRDVRGLRREQEMSFFQEVNCIIVRLLMQSMVESKFSTASLVATQTALCCGLSCL
LDASLCSQLLAALGEAFRKFFPLALAQADRRTETGEPVGLYVRHTLMALCFLFDFNVVQPAVFLGLLQRLSGKVATTKEK
GGAKNGERNEPLVEFQVECLLMVLRLGGGKLRNDNPVLFKEAWNFLMTRVKGGEGEREVQVHSGREERPFEEQTREEQRA
RLARVSTSFSGALRQRQEGEQPATTGRLHYLARELEELKNNKGNTIHLASKASQEAMRRWLQTSPLLAQSPLRQCAGEGK
SVLVGVSSWQEVEDGVVSVSPSSHRPPVSPHKSVRVEEEKQSCLGDTGSEKALLDLAAKLR
```

390 - 409:	EEEEEEEEEEEEEEEEEEEE
391 - 410:	EEEEEEEEEEEEEEEEEEEE
392 - 411:	EEEEEEEEEEEEEEEEEEEE
393 - 412:	EEEEEEEEEEEEEEEEEEEE
394 - 413:	EEEEEEEEEEEEEEEEEEEE
395 - 414:	EEEEEEEEEEEEEEEEEEEE
396 - 415:	EEEEEEEEEEEEEEEEEEEE
397 - 416:	EEEEEEEEEEEEEEEEEEEE
398 - 417:	EEEEEEEEEEEEEEEEEEEE
399 - 418:	EEEEEEEEEEEEEEEEEEEE
400 - 419:	EEEEEEEEEEEEEEEEEEEE
401 - 420:	EEEEEEEEEEEEEEEEEEEE
402 - 421:	EEEEEEEEEEEEEEEEEEEE
403 - 422:	EEEEEEEEEEEEEEEEEEEE
404 - 423:	EEEEEEEEEEEEEEEEEEEE
405 - 424:	EEEEEEEEEEEEEEEEEEEE
406 - 425:	EEEEEEEEEEEEEEEEEEEE

A0A086JNG8 **A0A086JNG8_TOXGO** (784 aa)
Utp14. *Toxoplasma gondii p89*

```
MTLPKQRVRLHLFHPGASPAASQRELARPVTCGLSVGCLALRPRRLHARRASCWEVMCRAKGSFLFAAFRGSPASVECVS
GDSRRPDLLRFPTRTTRGARLRRRRQCLAGETGDGLLGVERPARTNAFSAAQTGFTHSLLRRLKVSASVSYALSGGAQRT
RIEGRQVAARQQLLSRGKKEPGERRSFSGVWTARENALQASFLRHPQLSLSPSDSVSAPSFDFSAFQVSLAFSPFLTQIL
LASMALERRTARRVPPRSQKEQEELTPWLTAGPQADDNEEEENEEEEKEEEEDEEEEEEEEEKEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEGEANASKARVLKQRGKAMISAQKKSRDKDASDALSICRLMKDLVSDSWDGLPEEEEAEEEED
EEEAEEEEDEEESEEEEAEEEEEGEEGGEEEGLPSKLLKSLQRGQRTEEEEVDPFEGVSEHSLSLLKSEGDRRRVAASSQ
ADSGEEGGDAGTRQVDAQLDAASADALSFSSLLTSLSTTTSRSGLRKQLESLARPRAASAAASSVRGSDETAVDADVVQE
PLGPTQQKALLRSAAYAEAKETAKKWTRVVQRNQQAVQLQLGVSTARSRGGDGRGEAPTEVRSLSHALSDFKANDAFEDA
LLAAVNADGVSDQKLKASGGLGPADAIKRQAEQRQVARLKFLLFTEQRRARRLKRIKSKLSRKKRKQAERREEEKIMEKL
EVGNPALAEELRKKFEEKRAKMRLLRQQNARAKWAALAARFGGRDVQQEISRQMQTRVYVKLST
```

304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE

306 - 325:	EEEEEEEEEEEEEEEEEEEE
307 - 326:	EEEEEEEEEEEEEEEEEEEE
308 - 327:	EEEEEEEEEEEEEEEEEEEE
309 - 328:	EEEEEEEEEEEEEEEEEEEE
310 - 329:	EEEEEEEEEEEEEEEEEEEE
311 - 330:	EEEEEEEEEEEEEEEEEEEE
312 - 331:	EEEEEEEEEEEEEEEEEEEE
313 - 332:	EEEEEEEEEEEEEEEEEEEE
314 - 333:	EEEEEEEEEEEEEEEEEEEE
315 - 334:	EEEEEEEEEEEEEEEEEEEE
316 - 335:	EEEEEEEEEEEEEEEEEEEE
317 - 336:	EEEEEEEEEEEEEEEEEEEE
318 - 337:	EEEEEEEEEEEEEEEEEEEE
319 - 338:	EEEEEEEEEEEEEEEEEEEE

A0A086JSW4 **A0A086JSW4_TOXGO** (3578 aa)
Tyrosine kinase-like (TKL) protein (EC 2.7.11.25). *Toxoplasma gondii FOU*

```
MGGGVGRAPRAGRGASVSDSEALSLPALLPPLSPLSSPSPALGDSACFPFIGLEPLKPPAGGRGSPASPVRSLSSILIVS
SASAAAFVRSASSSFASSLSSRASSSSAPVPVYIHPVSGTVHPYPAQPAPPPPTHLVLAVPASASYAPPASSSSSSFLEG
LSVGFSGVSGRPSARATAQEKPDASFFAALQTSVVQLLKRSRSIRSVVLRGDGDWLEVLREALQNHVSVSSVSLEAVTNL
SEKELTSGYARLLSGLSKCTSISIRGCGLTSRGLKSLLRSLGKQSDFVEHLQEIDLAHNDLDDEAAAVLLSLFSSSSPRR
LASLRLDANPCSLSALEPLLALLASCDGASSEEESGLNLLSLGGLTNVSESTLSSLSLFSSLSSLSLSRCRSDSPHTLRL
LPSLASSLTAASLTSKFAFLSTLTHLDLSHVPSLLSDDDVALLVEILFPRESLPRLQTRGGRDERGKSPACTRKPQTAKG
RDRSVSAVSSVSSLLSLSLAGDGLTGGCLRALALGLLSPSCRLQHLDLSRNSFGKKPSIDGDAGSDSHAPERKDKDKRRA
KGRPGARKRPEEKEEEVLPIEPLVDALQQGYEEAPHAPCGLRFLSLAFCELSLEAMQQLAAALLTNGENLVFLDLRGNLR
SAEGPDGGEEQRKGDRRDELRLARCAFDTVAGMCGLQVLLLEEETKKRRQETEETEETEETQETGRKRQKRGTRQPKGRR
RDKATEEANEEEGTVEEGEDEEDEEEDDEKHGEEGTRGVRGGRAVEIERRRCGGKGGRGRRSEKSESKKRKAEMAEEDSG
RSSVRTRRQRKDDEEEEEEEEEEEEEEEEEEEEEEDDEEEEEDDEEDESFDELDAMEAEQKADESSEDEGGEDGEEKEEDE
DEEEEEEDETTRTSLRKRGRHSGMRSEKEQESMSKATEPRQRTMESENGGKTTPRRGRPTRRTSADSSRRKKSKKDESEE
EEEEEDEEEEEEEEEEEEEDDDDEEYEEGESVTGRKGRRRRHPQRGRDQVVSAHVRKRRKTTAEEKEAGEERLEKREQVDE
QVEENLKNNAVLPSPSPQKEGRRRRTVCAVPSARASRPRKTRADPEDETSFPETAGDQESCMLSGQTSASPSLPLRSRQK
SRWIEEDSVSGPLPHPRASRPSSFFVAETGRIGVGGAQPRRSCSALMSTTSVDLEGGGELFGNRERGPPRRRQSASFLAA
PAAPAIVVHQVSPAPGAGERPRKKESLAVNKKSEATFSSSVVSAATPVDTPFLMYFDMKREYPATSALRDPEANGDLRPG
EEDALPRGGVYVQPSAGAPSEAREALGRVRVREEEARRVESSRGFAVLPPVPAAPEEQRDIRVFLNRAGIHLLNLFFPRD
SHSYVGKTPLQPLLRSYPQELLLGLKYILSSHYLPLLSFPDVYTLQELSLSPHLSPPLQLLLSIIFEELARTNLTYKYQQ
YGELGFDENLCHPGKVLFDGGPGCQAIHAAEFRVFWMRRHGRRLGRRRPGWGSRAQLAVGSRADDAPVAPFQSPPPPLPL
ASPQASGLERERLFSGKKFERRDPRDAFSGACTLDGLDHDSPPGASPCTSPKQAEFPPPTPQFVETPDRVRGLAGLFEGS
PRSAFSAAENGDHSTSLSTVFDLLEPARLHPLAASFDGDTFGSAGPEKGLLKISGKAPENGRPLQCTCGRDEAERRRQLP
GERPSKPPLREKKPLDAETKKNSADGSRTADGAPTPELSEVPTGQPPPLPNAEKSGAELFATPAPFRWMKKALGAVRSQG
ISGLKKETVPRNLDFYFRLNRRASDDAAQLQAKADSAKRGETSTARAESAGDLNAAGPPAAGEEFQGLSDAGKDETDVAS
KNRETPGGGVSRSSVDSRSLSERRDSEVSVSAPADDRDSQDEVVAVSRPSALTGRGGLYSAVSSPALSASDFAEELSENE
ARPVVLRTNGHRPEVRPAEPRREEEGDTFGPPAWAPKGEAPGSEEGKATRDDEEKAGREKAPVPRCASTPQDRFVVSWDD
DEWLGSIECFLDDLSLCPSAASTRACSFESSSTHGASCPLASRGAPHTRSLPADFVLHPPLLPPSLSPSAPPSSVSLSAV
SAPLVPASPCVGGAGVQTPGPCSCREVIVVDVQSDAQLRKRIWDVQTLFTGSELSVHRKIELLRRMVLRSIKSAATGYGE
QKDEVKRLAAEHDGFVYLGDVNYGFSRHMALLFKVLCDASQIPCRVMRAGLLGEETVGDNGDTSTRNPELGGGAPGEGEK
RLAGPRARRDGLERQERRRREEEFVYNVVLVKDATKSELEQLIPIIWTQNAAAGLWRRHLSPGVEKGARGEDRERKRGR
HSSLTDFLASGVVRLNPPTLSSIPLPRRLRALQRRLAVSSASFSSCGQERSSERSRCVERDLETETGRGATAGNERCGDT
AGDLGGDRELPPLGRARSPRPFDYFKHGWVDRRRETSHCCCCASRSLPSLEAETGGDRAETRGDNGRDNRVGRDSAPGGD
VTSRNERSEKTEKENWGTKPSEDGPLHRQHADLDRLLLAASGASAFCGCGGAPASVAATELDLDAFFDFREKLGKGSFGE
VWRVRIKSEGRAVGAARRKPRERKRSREEQDAGVREENAVSEEEERGKEVHSGEERAEAPWRRETDEDGEADEAGERGEA
DEACRGDSGEPAEPEYALKLVPKSEENLPEAEIMRSYSHPRVVPFLGVFEGFQMLEDRSKKKVKNTSLCFLMDIADQSLE
SLLEEHEKANTCLDVEFILTILLDTARGMNYLHSPSATKPHLLHRDLKPANILLKDGRAMVTDFGVARVAEVSFEHEMTQ
GPGTEGYIAPEQRTAAYDRPADVWAFGVVCARLLGLREWKKLSDPQHRVALSDFALKDAFLINLCLACLERRPLMRPTFH
QIVQRLIDKIFRLEFERILRTPYRNCLPLLHAENPLVFSSPASLPVGRGDTPSRAVETVDVRRLGEKSGAITPFRSPSLC
PSQLAPPARPVPSRLSRSLLEAPFSAGGENVEALASRTEKVSPKARPEEGVCSGRPASACTHRSGNDEAAAPASSLSTGG
EEEVFFSGEESEATSQAKNAEAKGEPQLGPVADPEVTEDQEEEGFFSRLRLRTMKRSRPLLLSSSEVSPASSEREDAAEE
CDGAVEPDTNAKEKKLETKSESNEKSQEKREEVDPVDGVVTPHRLSPSDKKEPKEPSLLKKSGASPLQKKQGSPASKKKV
WKTPTSFVSLRTPDKVAANSSSSSSSSSSSSSSSSSSSSSSSSSSASSSPSSPSSAASASLSPTGGSRRRAASPQREREER
RRPGRTSPKLTPRGREEERRLSPTEKDDRGQSLSRGRSVSRGRCLGKEGEKIRTKERNVEKTPTQTPNHRRGSPSPSLST
SPLSRFDEAGVQDAEEGVLRHPSSRGPRSKISENPRISACSPSSPFSPCPSPSSASSPSASSPSAFSSLSASVLKNRVGS
VDAQRSLGERKGLLLSSSASVGSETRDARRSPEGVSAVSSEGSASLSGAPRVLASRQADSSSDSLVEKEISHAPNCASSA
FPPPARVAGLAAPFAAKPATQTAPIRKGDSFSDAYKVSGATEQLASGGNEGRGSGSLS
```

814 - 833:	EEEEEEEEEEEEEEEEEEEE
815 - 834:	EEEEEEEEEEEEEEEEEEEE

A0A086JUR0 **A0A086JUR0_TOXGO** (733 aa)
WD domain, G-beta repeat-containing protein (Fragment). *Toxoplasma gondii GAB2-2007-GAL-DOM2*

```
EDSASRAAPAFPRSLVALVGERQPWVLRLDGPAGEGHPVGYQAAACAAELSEGHQGEPSRFSEAHAAPAVCCDVSRKGCW
VLSGASDGSLAVWHAATGRCLAQVPPGHHGGAINAVAFQQKEWLRPSPLFKKSMREGVLAASGRKEKKESSDLSVPLCAC
DCRGINASTPHALLFAAASSGDHAVKVWKAEISPSFLSGKVRGDDEPGASGKKKKTADTGHSQILVTSLASVVAHRKEIN
DVKISPNDALLCTVSQDKTGKLFSFPSLVYVGELRGHSRSIFACAFPKREKIVATASADSTVKLWNVDTCACIKTFQIWC
LDVCGPAMVTGGSGGQLCLWEDVTNLVRHKAELAQQRETQQLAALKLLAAEGRGDEVFSLLLRLRRRAGMREFLENQCGK
ILLQAFQRGLELQRRIAFYSGQPLARSGSDQDASASTFGRLSAFLESLEEERVAAREDEDDRRGGQESKAELGASKKRKG
EKKVKGEETEAGARGRPDAPLRSAWLRDLNGDLSLPQLLKKMKKKDVATLLEFAAAWNTNSHTSWLAQGLVRLLLEARGE
DIFEGAEKAGRNVSDVENVISSFCAYTARHDRRLTALIEKTFLLDLLQGCESGDTRDLGDRWSGETRREPHREKTLDPRD
ATTFTRLCLYGDESEQTEMSQGKKTKNEPKRDSDERSTQEEEEEEEGEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEAEEEEEADA
```

690 - 709:	EEEEEEEEEEEEEEEEEEEE
691 - 710:	EEEEEEEEEEEEEEEEEEEE
692 - 711:	EEEEEEEEEEEEEEEEEEEE
693 - 712:	EEEEEEEEEEEEEEEEEEEE
694 - 713:	EEEEEEEEEEEEEEEEEEEE
695 - 714:	EEEEEEEEEEEEEEEEEEEE
696 - 715:	EEEEEEEEEEEEEEEEEEEE
697 - 716:	EEEEEEEEEEEEEEEEEEEE
698 - 717:	EEEEEEEEEEEEEEEEEEEE
699 - 718:	EEEEEEEEEEEEEEEEEEEE
700 - 719:	EEEEEEEEEEEEEEEEEEEE
701 - 720:	EEEEEEEEEEEEEEEEEEEE
702 - 721:	EEEEEEEEEEEEEEEEEEEE
703 - 722:	EEEEEEEEEEEEEEEEEEEE
704 - 723:	EEEEEEEEEEEEEEEEEEEE
705 - 724:	EEEEEEEEEEEEEEEEEEEE

A0A086JXG8 **A0A086JXG8_TOXGO** (536 aa)
Utp14 (Fragment). *Toxoplasma gondii FOU*

```
MALERRTARRVPPRSQKEQEELTPWLTAGPQADDNEEEEKEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEGEANASKARVLKQRGKAMISAQKKSRDKDASDALSICRLMKDLVSDSWDGLPEEEESEEEEAEEEE
EGEEGGEEEGLPSKLLKSLQRGQRTEEEEVDPFEGVSEHSLSLLKSKGDRRRAAASSQADSGEEGGDAGTRQVDAQLDAA
SADALSFSSLLTSLSTTTSRSGLRKQLESLARPRAASAAASSVRGSDETAVDADVVQEPLGPTQQKALLRSAAYAEAKET
AKKWTRVVQRNQQAVQLQLGVSTARSRGGDGRGEAPTEVRSLSHALSDFKANDAFEDALLAAVNADGVSDQKLKASGGLG
PADAIKRQAEQRQVARLKFLLFTEQRRARRLKRIKSKLSRKKRKQAERREEEKIMEKLEVGNPALAEELRKKFEEKRAKM
RLLRQQNARAKWAALAARFGGRDVQQEISRQMQREADERRTVERLARRRPGSSDGS
```

46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE

66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE

A0A086JXY0 **A0A086JXY0_TOXGO** (997 aa)
Uncharacterized protein. *Toxoplasma gondii p89*

```
MRGRRPSQQRKKAASLGASSLLSSLPSSLPSSLPSSLFSRGDSVGRQLGKRRGIEEEGGKRKRARGGRSARHNFPEVDQQ
GGSDLDELPSSEADPREAQQDGEGSFGHEQELAETLKKSKRAVLERKRRRHEERRQKKQIHRKQQQLWKLERQKALLERQ
LDMQKAAISGIRVNQGTGSGVRTPCGPEADSEDEEEDVSPRREKKTPSSLSSSLSSSLSSLDVRGSVLSALSAKDKKHTA
SGEVLLLSGVSSRSTEEQRKAEERRLALDAAGRQLDAELAFLESKLGIGKDSSKAGEKKKKKLAQELLDDGFDEDLQTLL
DDILGGKAENRKRKTKTDYDHDEGEMEGEETQEGAHEELGRVEAEEDEEDEEEEDDEEDEEDDEEENEEEEEDEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEEEEEEEEDEGDEEDEEEGEDLKLKTEHYSTCASASAGKYLPPHLR
NRAQRDLSNEAEFDGDNPGRNSTRKHGAAPASEASDKANFVASKLPLSCLEKARQTATDAGRGLTQRLRGSLNRVSEGNV
EVILQQISQEVKAALTQVLSGALPVPATSPALTPRDVRGLRREQEISFFQEVNCIIVRLLMQSMVESKFSTASLVATQTA
LCCGLSCLLDASLCSQLLAALGEAFRKFFPLALAQADRRTETGEPVGLYVRHTLMALCFLFDFNVVQPAVFLGLLQRLSG
KVATTKEKGEAKNGERNEPLVEFQVECLLMVLRLGGGKLRNDNPVLFKEAWNFLMTRVKGGEGEREVQVHSGREERPFEE
QTREEQRARLARVSTSFSGALRQRQEGEQPATTGRLHYLARELEELKNNKGNTIHLASKASQEAMRRWLQTSPLLAQSPL
RQCAGEGKSVLVGVSSWQEVEDGVVSVSPSSHRPPVSPHKSVRVEEEKQSCLGDTGSEKALLDLAAKLRSANIQRLLFSI
HLPSENRILCSPPCLESHFHMALCASFRTPLSSFIFA
```

394 - 413:	EEEEEEEEEEEEEEEEEEEE
395 - 414:	EEEEEEEEEEEEEEEEEEEE
396 - 415:	EEEEEEEEEEEEEEEEEEEE
397 - 416:	EEEEEEEEEEEEEEEEEEEE
398 - 417:	EEEEEEEEEEEEEEEEEEEE
399 - 418:	EEEEEEEEEEEEEEEEEEEE
400 - 419:	EEEEEEEEEEEEEEEEEEEE
401 - 420:	EEEEEEEEEEEEEEEEEEEE
402 - 421:	EEEEEEEEEEEEEEEEEEEE
403 - 422:	EEEEEEEEEEEEEEEEEEEE
404 - 423:	EEEEEEEEEEEEEEEEEEEE
405 - 424:	EEEEEEEEEEEEEEEEEEEE
406 - 425:	EEEEEEEEEEEEEEEEEEEE
407 - 426:	EEEEEEEEEEEEEEEEEEEE
408 - 427:	EEEEEEEEEEEEEEEEEEEE
409 - 428:	EEEEEEEEEEEEEEEEEEEE
410 - 429:	EEEEEEEEEEEEEEEEEEEE
411 - 430:	EEEEEEEEEEEEEEEEEEEE
412 - 431:	EEEEEEEEEEEEEEEEEEEE
413 - 432:	EEEEEEEEEEEEEEEEEEEE
414 - 433:	EEEEEEEEEEEEEEEEEEEE

A0A086K1I2 **A0A086K1I2_TOXGO** (541 aa)
Utp14. *Toxoplasma gondii GAB2-2007-GAL-DOM2*

```
MALERRTARRVPPRSQKEQEELTPWLTAGPQADDNEEEENEEEEKEEEEDEEEEEEEEEKEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEGEANASKARVLKQRGKAMISAQKKSRDKDASDALSICRLMKDLVSDSWDGLPEEEEAEEEEDEEE
AEEEEDEEESEEEEAEEEEEGEEGGEEEGLPSKLLKSLQRGQRTEEEEVDPFEGVSEHSLSLLKSEGDRRRVAASSQADS
GEEGGDAGTRQVDAQLDAASADALSFSSLLTSLSTTTSRSGLRKQLESLARPRAASAAASSVRGSDETAVDADVVQEPLG
PTQQKALLRSAAYAEAKETAKKWTRVVQRNQQAVQLQLGVSTARSRGGDGRGEAPTEVRSLSHALSDFKANDAFEDALLA
AVNADGVSDQKLKASGGLGPADAIKRQAEQRQVARLKFLLFTEQRRARRLKRIKSKLSRKKRKQAERREEEKIMEKLEVG
NPALAEELRKKFEEKRAKMRLLRQQNARAKWAALAARFGGRDVQQEISRQMQTRVYVKLST
```

61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE

63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE

A0A086K325 **A0A086K325_TOXGO** (1778 aa)
Ribonuclease type III Dicer (Fragment). *Toxoplasma gondii GAB2-2007-GAL-DOM2*

```
MRRLWQHLAPLTKQRAQRNWENFRRHLLHVQSELGFWSVWRLKEKVEADLEAWQARLGAATEERSRAQTRRSRRDCEGAE
CEESEKEDETDNSGRGKESQKRVRFAGENQRTKAGRSEEGNRTRGDRDRIKSTLAEIPFWISFPFRRPLSSDLDLQHGSS
LSSSSLSSSSLSSLDPVGGQPVERLLRRLFFGFFFLFSKALSTACSHSSLQLTMQLCRSRDLAHVCLADVAALEGGVAGA
ERTGSLPQVLACSLFSDKLLRLDQVLRDSFGRAQAQAQTQTQRREGSVADDKRGSGPDKRAGRPGDEEERRTEDGGEATR
SGLRIKASSKGDRECSPSPKKSGVRTPVPSFSSSPSCVSPSALSSAPSSMSLSSRFPAASRSPASPDVAFGGVPKCGLVF
CRRRVDAWLVCEFLTARRLVFVDWICSSSLASQGASWLFGIGKASQGRSSCLDRLRAMHTVWGKLEKKTQKLNAQKHRPS
TTPQSHSPSLASSLSSSLSSSLSSSASSSASSSASSSLSSSLSSSLSSSASSSASWGDGGKGDGKWILSVPSLHGFRSSP
LPPFSIEFSPTGSAPTRASAAAGVLAVRVLRRLVQEGVVDSFLRCRDRDSVEKDLRDEKERRRRENCGGVGAVDLLWREL
PACLLPPRSWRTASRASGDRHGDSEETLHTSAKTREEAARAEEAVSGSNEERRRSRDHKEGTTEEDAGAQEVEENAEEGR
KEEEGDQLKRLPSGTGKKDKTSTSNAKSETHREKTRTPAPPPGVTRLFLHRVWCTPLTAREAALERLWEPNEKQRRRRRR
VLKKLAESRGFLPSPLYESGGFCGLWRIFADAEAPLQAADLALDGASRWRQEKAKEKEQIEPDAGDGEGDEDGLWWTGNR
RQREACFEKREREGGDGKHDQCKENEKCRAEKEEEEEEEEEEEEEEEEEEEEEEEKKWSWQEEEKNRQRREILELIRSRI
DAVVEGRRGPDSVLQPLCLLLAHPIPATVAFHALHPEASEKAALHRGRRPRTGRTSFSLRASKAEKASNAWTELEADEEG
EEGDEEGEEEGEEGEEEGEEEGEEDGEEEGDEEDVPGLMRVEVEKPEKTMFIDLPTEYVEKVLLRFTHIHLFRLLQLSNF
SPNGTCNSLLLTVLQFLSALPFRRFPFRTVPSSSSLSSSASASASASCLGGDGEPRSRFVSLPLPACASASRLLPSHALS
LFALPPSLFSLLSLLSLAAEEAEESTESTLHSQSPPSSPRSSSPRSSSPRSSSLSSSSPSTSAEQLKRQMVEACSSLAKA
GVVDLQRVMFPFFVLAPLSPLDAKSVDLDFIHRLASLRLFLRSGQRRSSGFLEAGACPPSLMLQHDRRLLRGAVESLHCL
PSLSAVARLFCPGNSARKLDYEGGRSLQKAERRSARKEQNEGDAAEENGAFNWPRSLLGTLPSSDRESESAKDTKEKRTP
GSEKGERGEADGERREEDGEKGATKEDGLFSKEEQFFRRLQSYKGSIFSRGDDAANAWTTEEQKLLTFFQQRNENALSVK
EALREEGMEIFYHLRSRVFEPVALRMTHQFGRSFRFYRLQTIHRNLTPRNVVINSDAGFTLGTLCRVYLSRFKQRLAEPH
PDSQQGPQGNCFLVQGVKRRQEISWMPAILYQLEVQGKHCDLVRRLRQEMRPFLFTAEENISPPLELDFRLVSRALTAPQ
SRQVGAVDAAGVDWHGQRLEFLGDAVLKFVVSYYLFFHVHEGKPAEPRADAERKETEKEETGLESGEPGDAEAAEEVEEQ
GEEPESKETGGEREEREE
```

913 - 932:	EEEEEEEEEEEEEEEEEEEE
914 - 933:	EEEEEEEEEEEEEEEEEEEE
915 - 934:	EEEEEEEEEEEEEEEEEEEE
916 - 935:	EEEEEEEEEEEEEEEEEEEE

A0A086K3X0 **A0A086K3X0_TOXGO** (2800 aa)
Transporter, major facilitator family protein. *Toxoplasma gondii GAB2-2007-GAL-DOM2*

```
METSENPNAAERARVDTAATPHHDDPLAGISQASPLFPLPSDDLSLSLTSCPPGADPENPSGFTTYSQSPSPGEPDTSGQ
YPSSTGDAVLSSPASLLSPLIDRVSPAFCLSTPSPETAATSTLRPRNSGDFLSVISSPVHSPPASPVSSVSIVSCSRDLP
SALTPSCFMSGVPREEKDGRRLVVLGLHLTSPRCLDGARRVEVHCAAQASKERNKDEVCMRNDGADQRNCENDSRKETAR
KRGKGRACRRKAESADGAQQDRTPEKEIHDEKLEKRETLGSEVENHSDSEDSTPGPEAGEGGTVTVTREPSDEEEEEEDE
DENDEERDEDENDEEADESIGSKRREFESRRRWKTRMFALLLMIQMTLNIDNGVVPAVLADLGREFQATASEQGLVGALP
HIGMLVFCPFCARCLEAVGPQRLLLVSLLLNAAAVVFFAVSSSCFSLFLSRFLIGFSQTAFVVYAPVWVDKFAPHKLLTV
WMGFTHSAVVVGVVVGYLFAGFLRQSKHNWRGALLLQVVLLLSLILVLAFSDSVHVDVWADAESSAANASHYRAAAVPPL
QEGNETEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEGEEEEEGTGQVCREECEFRD
KAEDVEARQEVRRTLQQKKEKTTDLWGRAELQGEASTGALEAREAIKGRSGEVSESRRDEKEDREVPHAVVVEKGDGDDE
ARKKGEEEGSECERKTEIRPSGQRETRHFENQMMSALPPSPPVSSPRLSCLVRYTPDPPHESLHAESSVHSSHRKRTLFR
AFSSAGFVVAPVSSSSQPTSFRPSSSASRLSPQCPFCVCSGASFCSSSSTSRVVSLTQTDASSCSVALSASSNGASSSSS
SSSSSSVLPSNAAASSFPCKASSSLCRTKFFLAAPRSLSLHRLPPSAFPLSCSASSSSAAFLCPFLSCFPPPSVPRTCMR
LPDKMPRGSQTVPPCGKAEDLLKNEWFSSSEKETLPGAPERSECPPGSHRSFPAAEWSVTSSFPWIATTVAACSASRASL
TLDEPHRRAGGEESLNGTTRSDLENAQQTSSPRSVANAVVSRSEEAEIMASVRNGNERSAAVAQESTVRTAEAGRGGSVE
KRTEGPRQAPREEAARLEKTRPLRGTASQTQEKQVSSTQASFSRSASLPFGSWRRRLEGRARPPRFASCGENGRAEERQR
TTKKRRERDAILAALAHAYYSEGRPDEVEATCRGGEGIRGRSAEARSSQKTEERRVRARATEGGSVDRAKARKGRCRLGE
TLERGEKEEEKRVQTEEMFCSKAGDSETIPAQSGAAKERRKQVEERLPDLQSVSVKNDQKGPLDSLLDARRQLSRPVKLV
SGERDSERHDTLPCSIRNPAPARLLRRSTSASASVSSAPFSASRTSLGTRNEAKGRLHVLRPAAKSLPRAHIVFIRPASG
QTDTSQAENEKADGRDAVDRPETPESSCSALHALQSACKRRKREDMRCVVAVHTTPSSHSELVFNAFLRGTKLLLFTPPI
GLMLSSSAAAPRAGSQEAHRSGSRKRASEATQEGGGQEEDARGDKRGTGMAERPRRRTQRSRQEQAPAAREDEAKVGGKD
AKEAGQKEREEALEEGEQRQRQRGRAGERTRATVGDSGAQKRTARAEESERLRLSPGRLASGYRKQTTSGRHESSARAES
RTCEEATEGETGRDKREKETQRRRVERGFIEVGRDRRVGDGGSVETDAFGESEGRQVPRLKQMRGFPSWCYSLLRLPSER
LHDPACCPYRSRGDGKDCRHRAVVKRATETSSRNRGRESKRRNESETERDDSDDERLGLAHAFVPAPRLATGSFFPPQSV
ARAAELRQGHSHAQQLLSDTAPAFSQAGAPPCSPALFPKTPSAEIREEPTMLFEGSRQLQSLHVVDLSCQTSHLSSSASG
VRHIFPRLPASPSAAATKAEAAPSSHMSSPSSSSQSSSPISASSSSPVSHSSSLGWPPPTSSSGGSLNAFCRAPRVAAGA
RDGVREGRTRVEDEAERRGQAEWEAQPKTQRIGEGTRGQGDEEERRSIPGLCPAHTPLLVAVHEEAAVATAAVFAAPVWA
EESPASGKEKVKKCPWATDIEQAKVRKTENHEDENRSEDNAGTSGGRSHIHTLAVVSLRQRPQAEDKSKRKAEAGATRKG
KPAKEKEEATLPEKNRERRRERRGDGDGQIRCGSPRTVFSPCKRLSEESRREEREEDEAPSNQPRGRDGRAAEVEGIEGD
NPTADNRLQEEFFVHTVCVDLPALHVLDGGAKAGDQEAGREYSKDGRSEEGERAYKSGGERMKTVVVTSHLEKTTDVIFI
```

```
ARKEITGQNLEVQSPSGVAVVGVELQATAGDDAECKPASHEDDDPGTRDEEARKEEETADEGVKGDASTQSARGQHERRN
HEVANGGKILGIEWKVKGCPTGQEAIEATRACEEVEDNRQQEAYSGHGDEDDTSDLKQAHKRNFWNLKQWRKKRGVSREG
REPRRQTHADGPAEKGKRPQKQLETKDADEGDQEKTRDNTVEKQQDEASTLCSSREEDDEDSRVAGTWKKRTLGRLLTNP
LYVCLTLALSSLFFEVTAIQFWATRYFDEELHADTATVLVSFSVTAATAPAVGILVGAVLMDWLGGYRETPEKRRRALFC
LLGLSLTCVLLGVFAAYCSLSFWPSLASIWFILFFGGGILPIASGLLLATVDEELRTKASGAATLFYTLLGYTAGTFLPG
VISDSIGTKGGMQMILLWSLSGFAFLLLATAFASRILNTKGAEGGEEVEAGEEAEKNRKSLEARGRPRRERRARRGTDSV
```

567 - 586:	EEEEEEEEEEEEEEEEEEEE
568 - 587:	EEEEEEEEEEEEEEEEEEEE
569 - 588:	EEEEEEEEEEEEEEEEEEEE
570 - 589:	EEEEEEEEEEEEEEEEEEEE
571 - 590:	EEEEEEEEEEEEEEEEEEEE
572 - 591:	EEEEEEEEEEEEEEEEEEEE
573 - 592:	EEEEEEEEEEEEEEEEEEEE
574 - 593:	EEEEEEEEEEEEEEEEEEEE
575 - 594:	EEEEEEEEEEEEEEEEEEEE
576 - 595:	EEEEEEEEEEEEEEEEEEEE
577 - 596:	EEEEEEEEEEEEEEEEEEEE
578 - 597:	EEEEEEEEEEEEEEEEEEEE
579 - 598:	EEEEEEEEEEEEEEEEEEEE
580 - 599:	EEEEEEEEEEEEEEEEEEEE
581 - 600:	EEEEEEEEEEEEEEEEEEEE
582 - 601:	EEEEEEEEEEEEEEEEEEEE
583 - 602:	EEEEEEEEEEEEEEEEEEEE
584 - 603:	EEEEEEEEEEEEEEEEEEEE
585 - 604:	EEEEEEEEEEEEEEEEEEEE
586 - 605:	EEEEEEEEEEEEEEEEEEEE
587 - 606:	EEEEEEEEEEEEEEEEEEEE
588 - 607:	EEEEEEEEEEEEEEEEEEEE
589 - 608:	EEEEEEEEEEEEEEEEEEEE
590 - 609:	EEEEEEEEEEEEEEEEEEEE
591 - 610:	EEEEEEEEEEEEEEEEEEEE
592 - 611:	EEEEEEEEEEEEEEEEEEEE
593 - 612:	EEEEEEEEEEEEEEEEEEEE
594 - 613:	EEEEEEEEEEEEEEEEEEEE
595 - 614:	EEEEEEEEEEEEEEEEEEEE
596 - 615:	EEEEEEEEEEEEEEEEEEEE

A0A086KBS9 **A0A086KBS9_TOXGO** (373 aa)
WD domain, G-beta repeat-containing protein (Fragment). *Toxoplasma gondii p89*

```
LAQQRETQQLAALKLLAAEGRGDEVFSLLLRLRRRAGMREFLENQCGKILLQAFQRGLELQRRIALYSGQPLARSGSDQD
ASASTFGRLSAFLESLEEERVAAREDEDDRRGGQESKAELGASKKRKGEKKVKGEETEAGARGRPDAPLRSAWLRDLNGD
LSLPQLLKKMKKKDVATLLEFAAAWNTNSHTSWLAQGLVRLLLEARGEDIFEGAEKAGRNVSDVENMISSFCAYTARHDR
RLTALIEKTFLLDLLQGCESGDTRDLGDRWSGETRREPRREKTLDPRDATTFTRLCLYGDESEQTEMSQGKKTKNEPKRD
SDERSTQEEEEEEEEEGEGEEEEEEEEEEEEEEEEEEEEEEEEEPEEEEEADA
```

340 - 359:	EEEEEEEEEEEEEEEEEEEE
341 - 360:	EEEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEEE
344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE

A0A086KD89 **A0A086KD89_TOXGO** (1414 aa)
Putative DNA mismatch repair protein MSH6-1 (EC 3.4.21.72) (Fragment). *Toxoplasma gondii GAB2-2007-GAL-DOM2*

```
ASVGDSTAARSSSGNEEDPGSEDVRKLKRLRRRLALSDDEEKMETPPSIRRRRQAEQTKKVEKEAARRAKPEEEEEEEED
EEEEEESEPSAFSDESYEDESEEESEDDSEDEEEEEEEEEEEEEEEEEEEEEEEEEVRGKKRPAPKKEKRVEEGSQTTWTTA
ASSASSSSRAKLKDLVYSASSEKPGTTSSLTPPPVTSPPSSSPPAAPEPTSSSSSLSSSLSSSSVSSSSVSSSSVSSSSV
SSSSRLPCSTGRKATDAVDEAELRRRLLASPAAQNCHYFRHYIEDFYMYHRQFSFPPWADPARMRDISGRRAIDCGEDYD
```

```
FSSLWIPSPDSQLARAHARPHMTPGMAQYWEIKKEHFDKLILFKIGKFYELVYGDACAAHRILDLKWMGGGGADAKPHCG
FPEQNLHFQARQLVQAGYKVVVVEQMETPKELEKRNSQAAAGAKDKAVRREVCEVYSAGTVRHADMLGQAARYLLVLYFG
EEDEEVDVDTEVATEKQVAADRRGADIMAADRRETGERASTGAGDRGDPEVQQSLDAEEKATVGMDSSTRDARDTSEKRR
ELKPGFAACLVDVSTCRVSLVRLSDDPTAAWPSLRLLLAQTLPVEVVYSPTNIPASVLKLLKFLPSPPQLSPLTSFPDLL
GAHTEVDRYITSRLDALTSKSNASSSSSSSSASSPASRSSSLSSSSSSSPAQSLELCRTLCDRWPSLHCAVGGLCVYLRE
CRLDASVLPLCQFESFRPRDASVLVLDAHALRQLEILQTQDGCAKQALLGYLDRTVTAFGHRLLRRWLVAPLRNVAELTR
RLDAVDWLCNSPESVADIRKALQACPDIERLSAKICAQGLQGERRAVYFDHFHQKLLADFFALLDAFLSVESLAKRLAQR
LATSHGQEGAEEREAAEEREGEEGRGGRLLDLCADREHGGLFPPLGELVASLKSKVAINADGHKIPAKGVLAAYDDTVTE
MQEVQQKLENLLDDLRSSWKMKSLQFVHSKFKYEVECPDTVSKELLRTHECDITSSRKGFFRFRTPEICELVAELEDLEQ
KQKDMFYPFFSILFNAFYSHFTHTFGRAIQVAAELDCLQSLATVVATHPGHSGQMCRPTIVEAREDAPPILALKNCRHPV
AETLMDNFVPNDVYLNCGPHESKRTLLITGPNMGGKSTLLRQAALCVVMAQVGCFVPADSCTLSPVDRIFTRLGAEDSIL
QGASTFLVELKDISELMTYGTRHSLAVIDELGRGTSTFDGTAIALASLEHITDNLQCRCLFATHYHLLCYEMQGHPHVVN
VHMKAAINEEQQSLAFLYKLTKGVCPKSHGIHVARLAGIDPRILECAEEKSLRLQQEVVRQQRHWRLLGVAKTLEAADPA
TLQSLFARKESVLEDLIQEEEAEAGEEETKAGEEEAKAGEEEAVPNEREVEMEG
```

112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE

A0A086KDI5 **A0A086KDI5_TOXGO** (1785 aa)
IgA-specific metalloendopeptidase (EC 3.4.24.13) (Fragment). *Toxoplasma gondii p89*

```
MTSARTREGLVGAEAPLGEGEEDLQDSIACSVPRAPTNSFEEGYEVECVDECPYIKFQHASKLPLSPLLFDASSSPAPLP
ERLLAARCTDSLCLLHCCGVLLLPGLDSILAVDATEAACGSPISRGRLPLHASKEGETKDAFPSLLLLSPDARFLAVAVD
CQVKLVQLGGCGGPSCSKSAGEASREGNAEARLGGQQGGDSCISEKTQVLSLAGFASPVKDISWIWPSGDRTETWCEGDT
RGDAERLIGLAVLTESGEAFILSPRGAQAFPLPAHGLAIHALPRRSPAAAKSEGAGPGGLAPLTAVVSCCAPASLWLVGL
QETALLPEGSGQGESLYDFGHRRPDVSRETAKEEKRKGRRKIRVEGLADIPGYEDEAQALHKGRGRFVGVHCLGASLDSA
AGESPLPLALAWFVPDADLSTGEDDWEKPELESDSAEPRLDPLRQAPASAEDCGDSWSCFILFGFLARRPYTPSDARALR
GDIGEAESADEKEELVFRIYAASRNEMFLRSVAASTVCRFRWIPQWHCLWVFSNACTQVICFALPHSFSRNGDPLPSPRS
SSFLGSGEVPWRCFTMPEGRALETADEDAFPQGLALFFNFKESMFREHSTTDTPPLEHPPVFFLLQSDGQVCVHLADCCE
CYVDDAGIGKEKRLLPRLEWTPVSPPSSFLLTSWTEPRRRACGEQPATPVPKVSPPALSPSSSSLASPLFASLQQGKPTP
SLFGTLSTNAASAPLFSSSSGTSLFPSSASSASSLFTPAKSEEEARKTGWVVPTTHLKVTSASSPANDPSASNGASASNN
LSALDGSSPRPLSSSRKDCVDQARPAAKETREEAPTRRLPAKSSSRDPQRRGHCLHCGAVDVGDRRGGREAERRRREKKL
RRRVEAKNASLRQAAAAANEVIEATLQAARGTKAEPAREKNAKKRILLTEEQSEVKALLDEFEEKKHAFCSFSRFLPSSL
FRPLLLSARCFENALRHEERRDVLLESSPVSSSASSSSSSSSSSSASSSSSSSSSSPGSLFVSRCGEKDAPVDCGAEQEK
STAALLPAAAAGLARTGRLADKLKDEQRNVRTKQETETEVVETLQEAQQHLVAWRSCLEAVRDQLLLRMQFAEKKSENLT
ERNGEQTDAAGREEGRGDREADGREEKRERQAERGNNVTEEDVIACMQKIQSESGARRNLFEALQTLLPADAEHAQLNTD
THTKCVLTHLESGLLRAERRLLLLLQRFRFYTSFQTRFPSSLDPESGSSVRRLAASGWPGSWKINSGLSSLSSYGDKGVS
SLPLAHGKDSDRDARTKRGSVHTPDTACGRGRPGGCYGLRFEWLEEDEFPDKREESVVDSHRRVSSTTHPVSEGTPGARP
SLAFSLSASPPSAFHLSLFGSPGGARDSRIACSQGPGGSVKDGGLAGSRSGAASGDFLLDMHAEHRAAGLVAELEAAVSE
FLSSVRQLEIDLAKLEWKATDLQSPARQSPSSSSSTSSFAASLSLLSSSVFGEPLPPSGPSGLPDVVGAEKPAKDGEQRF
PVSSLREQRERFDERRKLRRQLLEVWRATTSTDPQQEGEEETETDADEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EDESDAFEVLEDSSSVSYDEESDEWEPVGSASPENPQTPPRQSVVSRRLGASLRSGRRTSRSKQRAKFAPLSGDEDSSEN
ACSSSPSSPDDVSPRRRGAELSDSEGAPEDGASRSNSHDESASLPVCGVPGETHSISHSSLFSIKPEDVTQPPQSASFQF
ASSLPPRRASGLGHTLFSFASNSSS
```

1568 - 1587:	EEEEEEEEEEEEEEEEEEEE
1569 - 1588:	EEEEEEEEEEEEEEEEEEEE
1570 - 1589:	EEEEEEEEEEEEEEEEEEEE

A0A086KFB2 **A0A086KFB2_TOXGO** (3005 aa)
Ribonuclease type III Dicer. *Toxoplasma gondii FOU*

```
MCEEDEKEEESSRRRGDGERETLEERSWWTETPADAWEESGEGRSDGDEVEDVEREQGPQGQQSTHPAEQNRGGDERRLG
EERLARDEREEAGTLLQIEFEEETRGRTREEGSDRDPRRRGAERKTESKCEQETKSPHVAYCWWQAGARESGKRGHRVLK
TCDAVLPLEEETYSDRDTRGQLQAWPYQYRVYRRATLENTVVALPTGTGKTLVAAMVVHTWLANVFVADKLVIFLAPTTQ
LARQQHRAISTVLSLLRDPAGAEASRGRLAVRLPGVLEKERRTRGRVASRDDDDGERAYFRSVLRVDWSHPKYWAAFYSA
LSEYKAALLDLQRLPAAPPAAFDLRRFHTGRLLAPYRFVDSQRAALLRESFAEPSSEEANVQAASLEDSEGERSGNREGE
REEDENEQDVSEVEHQAVCWPRVFVMTPDKFRNLACRGLLRIDRIGLLIFDEAHTVGRPLRSLGAYATILRVFLHLCQEE
AKPRILGLTASPVPDGKLGFFDLESELKRAMRSLETIFQARIVKADTESAPGIRDWSQGQPDAQRQGEQQRGVMGVRLTA
AGSREIREAVEEESERSAANEARGNARRGSGETRQDHLGGDKPLRTMETTEGDEETFTGCALKTVRYQLAPSPFYYDHEL
LILDRLTTPRVEAGRQQWRVAAWQPPPGTLRGSREPTGGVPAVSNGDREQRKDRLPRREGTERGDPPTRSTSRKPNGTKE
RETEEEELEEKKAKEKEAKAKNGQVNRDGLEGKRSEGREDAVRWNGSEVAAFRHFVEREARGRHTYFSLLLQEVLEICST
FFYVEVTRLKEEREANEERHHPHETTPAEEARQETMHRILKTDCGSPCASHPSPSFSSFPSCSPPLSSSPAAPPLASSFS
CSSASAAFSASALCSSAAPSRVPASLRSSFLAEVWGAADARLNVRVMRRLWQHLAPLTKQRAQRNWENFRRHLLHVQSEL
GFWSVWRLKEKVEADLEAWQARLGAATEERSRAQTRRSRRDCEGAECEESEKEDETDNSGRGKESQKRVRFAGENQRTKA
GRSEEGNRTRGDRDRIKSTLAEIPFWISFPFRRPLSSDLDLQHGSSLSSSSLSSSSLSSLDPVGGQPVERLLRRLFFGFF
FLFSKALSTACSHSSLQLTMQLCRSRDLAHVCLADVAALEGGVAGAERTGSLPQVLACSLFSDKLLRLDQVLRDSFGRAQ
AQAQTQTQRREGSVADDKRGSGPDKRAGRPGDEEERRTEDGGEATRSGLRIKASSKGDRECSPSPKKSGVRTPVPSFSSS
PSCVSPSALSSAPSSMSLSSRFPAASRSPASPDVAFGGVPKCGLVFCRRRVDAWLVCEFLTARRLVFVDWICSSSLASQG
ASWLFGIGKASQGRSSCLDRLRAMHTVWGKLEKKTQKLNAQKHRPSTTPQSHSPSLASSLSSSLSSSLSSSASSSASSSA
SSSLSSSLSSSLSSSASSSASWGDGGKGVWRLMRRLGWGAPLQLLVSTSVLEEGIDVPACNLVVQMDMPSSLVRFVQAKG
RARKKPAEFVVLCPDSGPCGASWPDASLPFSSSFSSSSSFFPFSSSLQPQTPDCTVSSPSLLLSLQSVSSLAVSSSSLSA
PLSVSLRSRTGEAPTTPAFAAQGFSAAGGAACYLQAVSPSVNFELARLQLCEAKVAALAADVEATERFGLLGPFRCMRKV
CSLDDLLLTHTGAMVHSSFAPALLREIVDACTAGKTDERIERGADERGEEGRWAEDTEDEGREERERGNAELRTGREKAL
GTCCSNAPFSSSLSSSGMRRVSDLCEARRQRRPSALRLLSTQDGKWILSVPSLHGFRSSPLPPFSIEFSPTGSAPTRASA
AAGVLAVRVLRRLVQEGVVDSFLRCRDRDSVEKDLRDEKERRRRENCGGVGAVDLLWRELPACLLPPRSWRTASRASGDR
HGDSEETLHTSAKTREEAARAEEAVSGSNEERRRSRDHKEGTTEEDAGAQEVEENAEEGRKEEEGDQLKRLPSGTGKKDK
TSTSNAKSETHREKTRTPAPPPGVTRLFLHRVWCTPLTAREAALERLWEPNEKQRRRRRRVLKKLAESRGFLPSPLYESG
GFCGLWRIFADAEAPLQAADLALDGASRWRQEKAKEKEQIEPDAGDGEGDEDGLWWTGNRRQREACFEKREREGGDGKHD
QCKENEKCRAEKEEEEEEEEEEEEEEEEEEEEEEEEEKKWSWQEEEKNRQRREILELIRSRIDAVVEGRRGPDSVLQPLCLL
LAHPIPATVAFHALHPEASEKAALHRGRRPRTGRTSFSLRASKAEKASNAWTELEADEEGEEGDEEGEEEGEEGEEEGEE
EGEEDGEEEGDEEDVPGLMRVEVEKPEKTMFIDLPTEYVEKVLLRFTHIHLFRLLQLSNFSPNGTCNSLLLTVLQFLSAL
PFRRFPFRTVPSSSSLSSSASASASASCLGGDGEPRSRFVSLPLPACASASRLLPSHALSLFALPPSLFSLLSLLSLAAE
EAEESTESTLHSQSPPSSPRSSSPRSSSLSSSSPSTSAEQLKRQMVEACSSLAKAGVVDLQRVMFPFFVLAPLSP
LDAKSVDLDFIHRLASLRLFLRSGQRRSSGFLEAGACPPSLMLQHDRRLLRGAVESLHCLPSLSAVARLFCPGNSARKLD
```

```
YEGGRSLQKAERRSARKEQNEGDAAEENGAFNWPRSLLGTLPSSDRESESAKDTKEKRTPGSEKGERGEADGERREEDGE
KGATKEDGLFSKEEQFFRRLQSYKGSIFSRGDDAANAWTTEEQKLLTFFQQRNENALSVKEALREEGMEIFYHLRSRVFE
PVALRMTHQFGRSFRFYRLQTIHRNLTPRNVVINSDAGFTLGTLCRVYLSRFKQRLAEPHPDSQQGPQGNCFLVQGVKRR
QGARQLFSRERVVDGDEFAGLHAPQFAHLLPISEPMFQASACNIGRTVARKWGKRERADERAERGEYRNSLRHVVERQGR
EAACRFTQEKDRHKTNGLEAGKFRGCPRFSTSWRYRANTATSSVG
```

2173 - 2192:	EEEEEEEEEEEEEEEEEEEE
2174 - 2193:	EEEEEEEEEEEEEEEEEEEE
2175 - 2194:	EEEEEEEEEEEEEEEEEEEE
2176 - 2195:	EEEEEEEEEEEEEEEEEEEE

A0A086KJ34 **A0A086KJ34_TOXGO** (337 aa)
WD domain, G-beta repeat-containing protein. *Toxoplasma gondii FOU*

```
MREFLENQCGKILLQAFQRGLELQRRIALYSGQPLARSGSDQDASASTFGRLSAFLESLEEERVAAREDEDDRRGGQESK
AELGASKKRKGEKKVKGEETEAGARGRPDAPLRSAWLRDLNGDLSLPQLLKKMKKKDVATLLEFAAAWNTNSHTSWLAQG
LVRLLLEARGEDIFEGAEKAGRNVSDVENMISSFCAYTARHDRRLTALIEKTFLLDLLQGCESGDTRDLGDRWSGETRRE
PHREKTLDPRDATTFTRLCLYGDESEQTEMSQGKKTKNEPKRDSDERSTQEEEEEGEGEEEEEEEEEEEEEEEEEEEEE
EEEAEEEEAEEEEEADA
```

299 - 318:	EEEEEEEEEEEEEEEEEEEE
300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE

A0A086KLF7 **A0A086KLF7_TOXGO** (2706 aa)
IgA-specific metalloendopeptidase (EC 3.4.24.13). *Toxoplasma gondii GAB2-2007-GAL-DOM2*

```
MTSARTREGLVGAEAPLGEGEEDLQDSIACSVPRAPTNSFEEEYEVECVDECPYIKFQHASKLPLSPLLFDASSSPAPLP
ERLLAARCTDSLCLLHCCGVLLLPGLDSILAVDATEAACGSPISRGRLPLHASKEGETKDAFPSLLLLSPDARFLAVAVD
CQVKLVQLGGCGGPSCSKSAGEASREGNAEARLGGQQGGDSCISEKTQVLSLAGFASPVKDISWIWPSGDRTETWCEGDT
RGDAERLIGLAVLTESGEAFILSPRGAQAFPLPAHGLAIHALPRRSPAAAKSEGAGPGGLAPLTAVVSCCAPASLWLVGL
QETALLPEGSGQGESLYDFGHRRPDVSRETAKEEKRKGRRKIRVEGLADIPGYEDEAQALHKGRGRFVGVHCLGASLDSA
AGESPLPLALAWFVPDADLSTGEDDWEKPELESDSAEPRLDPLRQAPASAEDCGDSWSCFILFGFLARRPYTPSDARALR
GDIGEAESADEKEELVFRIYAASRNEMFLRSVAASTVCRFRWIPQWHCLWVFSNACTQVICFALPHSFSRNGDPLPSPRS
SSFLGSGEVPWRCFTMPEGRALETADEDAFPQGLALFFNFKESMFREHSTTDTPPLEHPPVFFLLQSDGQVCVHLADCCE
CYVDDAGIGKEKRLLPRLEWTPVSPPSSFLLTSWTEPRRRACGEQPATPVPKVSPPALSPSSSSLASPLFASLQQGKPTP
SLFGTPSTNAASAPLFSSSSGTSLFPSSASSASSLFTPAKSEEEARKTGWVVPTTHLKVTSASSPANDPSASNGASASNN
LSALDGSSPRPLSSSRKDCVDQARPAAKETREEAPTRRLPAKSSSRDPQRRGHCVHCGAVDVGDRRGGREAERRRREKKL
RRRVEAKNASLRQAAAAANEVIEATLQAARGTKAEPAREKNAKKRILLTEEQSEVKALLDEFEEKKHAFCSFSRFLPSSL
FRPLLLSARCFENALRHEERRDVLLESSPVSSSASSSSSSSSSSSASSSSSSSSSSPGSLFVSRCGEKDAPVDCGAEQEK
STAALLPAAAAGLARTGRLADKLKDEQRNVRTKQETETEVVETLQEAQQHLVAWRSCLEAVRDQLLLRMQFAEKKSENPT
ERNGEQTDAAGREEGRGDREADGREEKRERQAERGNSVTEEDVIACMQKIQSESGARRNLFEALQTLLPADAEHAQLNTD
THTKCVLTHLESGLLRAERRLLLLLQRFRFYTSFQTRFPSSLDPESGSPVRRPAASGWPGSWKINSGLSSLSSYGDKGVS
SLPLAHGKDSDRDARTKRGSVHTPDTACGRGRPGGCYGLRFEWLEEDEFPDKREESVVDSHRRVSSTTHPVSEGTPGARP
SLAFSLSASPPSAFHLSLFGSPGGARDSRIACSQGPGGSVKDGGLAGSRSGAASGDFLLDMHAEHRAAGLVAELEAAVSE
FLSSVRQLEIDLAKLEWKATDLQSPARQSPSSSSSTSSFAASLSLLSSSVFGEPLPPSGPSGLPDVVGAEKPAKDGEQRF
PVSSLREQRERFDERRKLRRQLLEVWRATTSTDPQQEGEEETETDADEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EDESDAFEVLEDSSSVSYDEESDEWEPVGSASPENPQTPPRQSVVSRRLGASLRSGRRTSRSKQRAKFAPLSGDEDSSEN
ACSSSPSSPDDVSPRRRGAELSDSEGAPEDGASRSNSHDESASLPVCGVPGETHSISHSSLFSIKPEDVTQPPQSASFQF
ASSLPPRRASGLGHTLFSFASNSSSLPPDPTKPSSSTSAPLPPDPTKPSSSTSAPLPPDPTKSSSSTSAPLPPDPTKPSL
STSAPLPPDPTKPSSSTSAPLPPDPTKPSSSTSAPLPPDPTKPSSSTSAPLPPDPTKPSSSTSAPLPPDPTKPSSSTSAP
LPPDPTKPSSSTSAPLPPDPTKPSLSTSAPLPPDPTKPSSSTSAPLPPDPTKPSSSTSAPLPPDPTKPSLSTSAPLPPDP
TKPSSSTSAPLPPDPTKPSLFTSAPLPPDPTKPSLSTSAPLPPDPTKPSLSTSAPLPPDPTKPSSSTAAPLPADPTKPSS
STSAPLPPDPTKPSSSTSAPLPPDPTKPSSSTSAPLPPDPTKPSSSTSAPLPPDPTKPSLSTSAPLPPDPTKPSSSISAP
LPPDPTKPSSSTSAPLPPDPTKPSSSTSAPLPPDPTKPSSSTSAPRPPEPLDPGAVGREKGEEETGEGERIVSDSGEKVA
EVSPDLSETSLSSGSSSYAQARELSQPELQTSEEKAGDAEKKAEAGEDKPKIASSLLGVTSLGASNAAPPASSPFGGSTT
SPFAAVGPQAGSPFSSQAPSFGSVSSQTAGSFFTGTFDTKPSAGGSSLFGGSKLDLKSLSESLAAPPPMTSGFAGNSFLS
GGLFGSSPAFSASAQPGEKLAGGANSGAQVGGGLLGLSTQQPSFASPFSAAFGSNASPFSGVTAAPFGGIGAGGDAAAAA
PSVSFRDVAVDDLSIGQRQTYSFGMADNSSNLSSVNLGGSSLGNSGPTPERTGFANLAGNGSGGFAAFSTVTAPTGGGFA
ALAAQNSTGSGFFSSSFSSSSSSFASSSSSFASSSSSFPSSSSSFASSSSSFASSPFSFTPAGASGAAAAPSAFPAGGAF
PSSAVSSFSGFGASTAPGTGFGSTGASPSGFAAFASQGPAASSAGRAAAPAGGSLWSRPRTSNPLN
```

1568 - 1587:	EEEEEEEEEEEEEEEEEEEE
1569 - 1588:	EEEEEEEEEEEEEEEEEEEE
1570 - 1589:	EEEEEEEEEEEEEEEEEEEE

A0A086KZY6 **A0A086KZY6_TOXGO** (253 aa)
Uncharacterized protein. *Toxoplasma gondii p89*

```
MCAKEALPTSVGGSSCSRRPSVSALCLLGPIANAFSLPAACSFLPSPGTPPPSRLALASVPTSPAQRPASWALPFLLRSR
LQEGTRRSRRRRKDRKRRRCWTEASSVERSITHRDVRGEKWREDCGAETTQDPKTEAQEEEEEEEEEEEEEEEEEEEEE
EEEEGEEEEEEEEEGEEEEEEEEAEEGEEAEEEAEEGEEAEEEAEEGEEEEEEEEDEEEGEEEEEEEEEGEETDAGGHTDV
TEEDEDTDVGLWE
```

139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE

A0A086L5K1 **A0A086L5K1_TOXGO** (1789 aa)
IgA-specific metalloendopeptidase (EC 3.4.24.13) (Fragment). *Toxoplasma gondii FOU*

```
MTSARTREGLVGAEAPLGEGEEDLQDSIACSVPRAPTNSFEEEYEVECVDECPYIKFQHASKLPLSPLLFDASSSPAPLP
ERLLAARCTDSLCLLHCCGVLLLPGLDSILAVDATEAACGSPISRGRLPLHASKEGETKDAFPSLLLLSPDARFLAVAVD
CQVKLVQLGGCGGPSCSKSAGEASREGNAEARLGGQQGGDSCISEKTQVLSLAGFASPVKDISWIWPSGDRTETWCEGDT
RGDAERLIGLAVLTESGEAFILSPRGAQAFPLPAHGLAIHALPRRSPAAAKSEGAGPGGLAPLTAVVSCCAPASLWLVGL
QETALLPEGSGQGESLYDFGHRRPDVSRETAKEEKRKGRRKIRVEGLADIPGYEDEAQALHKGRGRFVGVHCLGASLDSA
AGESPLPLALAWFVPDADLSTGEDDWEKPELESDSAEPRLDPLRQAPASAEDCGDSWSCFILFGFLARRPYTPSDARALR
GDIGEAESADEKEELVFRIYAASRNEMFLRSVAASTVCRFRWIPQWHCLWVFSNACTQVICFALPHSFSRNGDPLPSPRS
SSFLGSGEVPWRCFTMPEGRALETADEDAFPQGLALFFNFKESMFREHSTTDTPPLEHPPVFFLLQSDGQVCVHLADCCE
CYVDDAGIGKEKRLLPRLEWTPVSPPSSFLLTSWTEPRRRACGEQPATPVPKVSPPALSPSSSSLASPLFASLQQGKPTP
SLFGTPSTNAASAPLFSSSSGTSLFPSSASSASSLFTPAKSEEEARKTGWVVPTTHLKVTSASSPANDPSASNGASASNN
LSALDGSSPRPLSSSRKDCVDQARPAAKETREEAPTRRLPAKSSSRDPQRRGHCVHCGAVDVGDRRGGREAERRRREKKL
RRRVEAKNASLRQAAAAANEVIEATLQAARGTKAEPAREKNAKKRILLTEEQSEVKALLDEFEEKKHAFCSFSRFLPSSL
FRPLLLSARCFENALRHEERRDVLLESSPVSSSASSSSSSSSSSASSSSSSSSSSPGSLFVSRCGEKDAPVDCGAEQEK
STAALLPAAAAGLARTGRLADKLKDEQRNVRTKQETETEVVETLQEAQQHLVAWRSCLEAVRDQLLLRMQFAEKKSENPT
ERNGEQTDAAGREEGRGDREADGREEKRERQAERGNSVTEEDVIACMQKIQSESGARRNLFEALQTLLPADAEHAQLNTD
THTKCVLTHLESGLLRAERRLLLLLQRFRFYTSFQTRFPSSLDPESGSPVRRPAASGWPGSWKINSGLSSLSSYGDKGVS
SLPLAHGKDSDRDARTKRGSVHTPDTACGRGRPGGCYGLRFEWLEEDEFPDKREESVVDSHRRVSSTTHPVSEGTPGARP
SLAFSLSASPPSAFHLSLFGSPGGARDSRIACSQGPGGSVKDGGLAGSRSGAASGDFLLDMHAEHRAAGLVAELEAAVSE
FLSSVRQLEIDLAKLEWKATDLQSPARQSPSSSSSTSSFAASLSLLSSSVFGEPLPPSGPSGLPDVVGAEKPAKDGEQRF
PVSSLREQRERFDERRKLRRQLLEVWRATTSTDPQQEGEEETETDADEEEEEEEEEEEEEEEEEEEEEEDEEEEDEEEEE
EDESDAFEVLEDSSSVSYDEESDEWEPVGSASPENPQTPPRQSVVSRRLGASLRSGRRTSRSKQRAKFAPLSGDEDSSEN
ACSSSPSSPDDVSPRRRGAELSDSEGAPEDGASRSNSHDESASLPVCGVPGETHSISHSSLFSIKPEDVTQPPQSASFQF
ASSLPPRRASGLGHTLFSFASNSSSLPPD
```

1568 - 1587:	EEEEEEEEEEEEEEEEEEEE
1569 - 1588:	EEEEEEEEEEEEEEEEEEEE
1570 - 1589:	EEEEEEEEEEEEEEEEEEEE

A0A086L7E5 **A0A086L7E5_TOXGO** (770 aa)
Transporter, major facilitator family protein (Fragment). *Toxoplasma gondii p89*

```
METSENPNAAERARVDTAATPHHDDPLLGISQASPLFPLPSDDLSLSLTSCPPGAAPEIPSGFTAYSQSPSPGEPNTSGQ
YPSSTGDAVLSSPASLLSPLINRVSPAFCLSTPSPETAATSTLRPRNSGDFLSVISSPVHSPPASPVSSVSIVSCSRDLP
SALTPSCFMSGVPREEKGGRRLVVLGLHLTSPRCLDRARRVEVNCAAQASKEGNKDEVCMRNDGADQRNCENDGRKETAR
KRGKGRACRSKAESADGAQQDRTPEKEIYDEKLEKRETLGSEVENHSDSEDSTPGPEGEDDGRGTQQARATCSKCNGETH
VPQFSQQSPRRLFSRWTQHRERKTTVRRTGANARWSFFLPSRKKKQGESRGSRHNRRLTAGLEDESRQKSESENWETDGE
RELEDMRPFTASNDSSRLRGCLRACSPADLLSAGEGGTVTVTREPSDEEEEEEDEDENDEERDEDENDEERDEDENDEEG
DEDEHDEEADESIGSKRREFESRKRWKTRMFALLLMIQMTLNIDNGVVPAVLADLGREFQATASEQGLVGALPHIGMLVF
CPFCARCLEAVGPQRLLLVSLLLNAAAVVFFAVSSSCFSLFLSRFLIGFSQTAFVVYAPVWVDKFAPHKLLTVWMGLTHS
AVVVGVVVGYLFAGFLRQSKHNWRGALLLQVVLLLSLILVLAFSDSVHVDVWADAESSAANASHYRAAAVPPLQEGNETE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

720 - 739:	EEEEEEEEEEEEEEEEEEEE
721 - 740:	EEEEEEEEEEEEEEEEEEEE
722 - 741:	EEEEEEEEEEEEEEEEEEEE
723 - 742:	EEEEEEEEEEEEEEEEEEEE
724 - 743:	EEEEEEEEEEEEEEEEEEEE
725 - 744:	EEEEEEEEEEEEEEEEEEEE
726 - 745:	EEEEEEEEEEEEEEEEEEEE
727 - 746:	EEEEEEEEEEEEEEEEEEEE
728 - 747:	EEEEEEEEEEEEEEEEEEEE
729 - 748:	EEEEEEEEEEEEEEEEEEEE
730 - 749:	EEEEEEEEEEEEEEEEEEEE
731 - 750:	EEEEEEEEEEEEEEEEEEEE
732 - 751:	EEEEEEEEEEEEEEEEEEEE
733 - 752:	EEEEEEEEEEEEEEEEEEEE
734 - 753:	EEEEEEEEEEEEEEEEEEEE
735 - 754:	EEEEEEEEEEEEEEEEEEEE

736 - 755:	EEEEEEEEEEEEEEEEEEEE
737 - 756:	EEEEEEEEEEEEEEEEEEEE
738 - 757:	EEEEEEEEEEEEEEEEEEEE
739 - 758:	EEEEEEEEEEEEEEEEEEEE
740 - 759:	EEEEEEEEEEEEEEEEEEEE
741 - 760:	EEEEEEEEEEEEEEEEEEEE
742 - 761:	EEEEEEEEEEEEEEEEEEEE
743 - 762:	EEEEEEEEEEEEEEEEEEEE
744 - 763:	EEEEEEEEEEEEEEEEEEEE
745 - 764:	EEEEEEEEEEEEEEEEEEEE
746 - 765:	EEEEEEEEEEEEEEEEEEEE
747 - 766:	EEEEEEEEEEEEEEEEEEEE
748 - 767:	EEEEEEEEEEEEEEEEEEEE
749 - 768:	EEEEEEEEEEEEEEEEEEEE
750 - 769:	EEEEEEEEEEEEEEEEEEEE
751 - 770:	EEEEEEEEEEEEEEEEEEEE

A0A086L7F3 **A0A086L7F3_TOXGO** (2174 aa)
Transporter, major facilitator family protein (Fragment). *Toxoplasma gondii p89*

```
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEEEEGEEEEGEEEEEGTGQVCREECEFRDKAEDVEARQEVRRT
LQQKKEKTTDLWGRAELQGEASTGALEAREAIKGRSGEVSESRRDEKEDREVPHAVVVEKGDGDDEARKKGEEEGSECER
KTELRPSGQRETRHFENQMMSALPPSPPVSSPRLSCLVRYTPDPPHESLHAESSVHSSHRKRTLFRAFSSAGFVVAPVSS
SSQPTSFRPSSSASRLSPQCPLCVCSGASFCSSSSTSRVVSLTQTDASSCSVALSASSNGASSSSSSSSSSSVLPSNAAA
SSFPCKASSSLCPTKFFLAAPRSLSLHRLPPSAFPLSCSASSSSAAFLYPFLSCFPPPSVPRTCMRLPDKTPRGSQTVPP
CGKAEDLLKNEWFSSSEKETLPGAPERSECPPGSHRSFPAAEWSVTSSFPWIATTVAACSASRASLTLDEPHRRAGGEES
LNGTTRSDLENAQQTSSPRSVANAVVSRSEEAEIMASVRNGNERSAAVAQESTVRTAEAGRGGSVEKRTEGPRQAPREEA
ARLEKTRPLRGTASQTQEKQVSSTQASFSRSASLPFGSWRRRLEGRARPPRFASCGENGRAEERQRTTKKRRERDAILAA
LAHAYYSEGRPDEVEATCRGGEGVRGRSAEARSSQKTEERRVRARATEGGSVDRAKARKGRRRLGETLERGEKEEEKRVQ
TEEMFCSKAGDSETIPAQSEAAKERRKQVEERLPDLQSVSVKNDQKGPLDSLLDARRQLSRPVKPVSGELDSERHDTLPC
SIRNPAPARLLRRSTSASASVSSAPFSASLTSLGTRNEAKGRLHVLRPAAKSLPRAHIVFIRPASGQTDTSQAENEKADG
RDAVDRPETPESSCSALHALQSACKRRKRDDMRCVVAVHTTPSSHSELVFNAFLRGTKLLLFTPPIGLMLSSSAAAPRAG
SQEANRSGSRKRASEWTQEGGGQEEDARGDKRGTGMAERPRRRTQRSRQEQAPAAREDEAKVGGKDAKEAGQKEREEALE
EGEQRQRQRGRAGERTRATVGDSGAQKRTARAEESERLRLSPGRLASGYRKQTTSGRHESSARAESRTCEEATEGETGRD
KREKETQRRRVERGFIEVGRDRHVGDVGSVETDAFGESEGRQVPRLKQMRGFPSWCYSLLRLPSERLHDPACCPYRSRGD
GKDCRHRAVVKRATETSSRNRGRESKRRNESETERDDSDDERLGLAHAFVPAPRLATGSFFPPQSVARAAELRQGHSHAQ
QLLSDTAPAFSQAGAPPCSPALFPKTPSAEIREEPTMLFEGSRQLQSLHVVDLSCQTSHLSSSASGVRHIFPRLPASPSA
AATKAEAALSSHMSSPSSSSQSSSPISASSSSPVSHSSSLGWPPPTSSSGGSLNAFCRAPRVAAGARGGVREGRTRVGDE
TERRGQAEWEAQPKTQGIGEGTRGQGDEEERRSIPGLCPAHTPLLVAVHEEAAVATAAVFAAPVWVEESPASGKEKVKKC
PWATDIEQAKVRKTENHEDENRSEDNAGTSGGRSHTHTLAVVSLRQRPQAEDKSKRKTEAGATRKGKPAKEKEEATLPEK
NTERRRERLGDGDGQIPCGSPRTVFSPCKRLSEESRREEREEDEAQSNQPRGRDGRAAEVEGIEGDNPTADNRLQEEFFI
HTVCVDLPALHVLDGGAKAGDQEAGREHSKDGRSEEGERAYKSGGERMKTVVVTSHLEKTTDVIFIARKEITDQNLEVQS
PSGVAVVGVELQATAGDDAECKPASHEDDDPGTRDEEARKEEEAADEGVKGDASTQSARGLHERRNREVANGGKILGIEW
KVKGCPTGQEAIEATRACEEVGDNRQQEAYSGHGDEDDTSDLKQAHKRNFWNLKQWRKKRGVSREGREPRRQTHADGPAE
KGKRPQKQLETKDADEGDQEKTRDNTVEKQQDEASTLCSSREEDDEDSRVAGTWKKRTLGRLLTNPLYVCLTLALSSLFF
EVTAIQFWATRYFDEELHADTATVLVSFSVTAATAPAVGILVGAVLMDWLGGYRETPEKRRRALFCLLGLSLTCVLLGVF
AAYCSLSFWPSLASIWFILFFGGGILPIASGLLLATVDEELRTKASGAATLFYTLLGYTAGTFLPGVISDSIGTKGGMQV
RRCNDTGACSLPRS
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE

A0A086L9U8 **A0A086L9U8_TOXGO** (1414 aa)
Putative DNA mismatch repair protein MSH6-1 (EC 3.4.21.72) (Fragment). *Toxoplasma gondii FOU*

```
ASVGDSTAARSSSGNEEDPGSEDVRKLKRLRRRLALSDDEEKMETPPSIRRRRQAEQTKKVEKEAARRAKPEEEEEEEED
EEEEEESEPSAFSDESYEDESEEESEDDSEDEEEEEEEEEEEEEEEEEEEEEEEVRGKKRPAPKKEKRVEEGSQTTWTTA
ASSASSSSRAKLKDLVYSASSEKPGTTSSLTPPPVTSPPSSSPPAAPEPTSSSSSLSSSLSSSSVSSSSVSSSSVSSSSV
SSSSRLPCSTGRKATDAVDEAELRRRLLASPAAQNCHYFRHYIEDFYMYHRQFSFPPWADPARMRDISGRRAIDCGEDYD
FSSLWIPSPDSQLARAHARPHMTPGMAQYWEIKKEHFDKLILFKIGKFYELVYGDACAAHRILDLKWMGGGGADAKPHCG
FPEQNLHFQARQLVQAGYKVVVVEQMETPKELEKRNSQAAAGAKDKAVRREVCEVYSAGTVRHADMLGQAARYLLVLYFG
EEDEEVDVDTEVATEKQVAADRRGADIMAADRRETGERASTGAGDRGDPEVQQSLDAEEKATVGMDSSTRDARDTSEKRR
ELKPGFAACLVDVSTCRVSLVRLSDDPTAAWPSLRLLLAQTLPVEVVYSPTNIPASVLKLLKFLPSPPQLSPLTSFPDLL
GAHTEVDRYITSRLDALTSKSNASSSSSSSSASSPASRSSSLSSSSSSSPAQSLELCRTLCDRWPSLHCAVGGLCVYLRE
CRLDASVLPLCQFESFRPRDASVLVLDAHALRQLEILQTQDGCAKQALLGYLDRTVTAFGHRLLRRWLVAPLRNVAELTR
RLDAVDWLCNSPESVADIRKALQACPDIERLSAKICAQGLQGERRAVYFDHFHQKLLADFFALLDAFLSVESLAKRLAQR
LATSHGQEGAEEREAAEEREGEEGRGGRLLDLCADREHGGLFPPLGELVASLKSKVAINADGHKIPAKGVLAAYDDTVTE
MQEVQQKLENLLDDLRSSWKMKSLQFVHSKFKYEVECPDTVSKELLRTHECDITSSRKGFFRFRTPEICELVAELEDLEQ
KQKDMFYPFFSILFNAFYSHFTHTFGRAIQVAAELDCLQSLATVVATHPGHSGQMCRPTIVEAREDAPPILALKNCRHPV
AETLMDNFVPNDVYLNCGPHESKRTLLITGPNMGGKSTLLRQAALCVVMAQVGCFVPADSCTLSPVDRIFTRLGAEDSIL
QGASTFLVELKDISELMTYGTRHSLAVIDELGRGTSTFDGTAIALASLEHITDNLQCRCLFATHYHLLCYEMQGHPHVVN
VHMKAAINEEQQSLAFLYKLTKGVCPKSHGIHVARLAGIDPRILECAEEKSLRLQQEVVRQQRHWRLLGVAKTLEAADPA
TLQSLFARKESVLEDLIQEEEAEAGEEETKAGEEEAKAGEEEAVPNEREVEMEG
```

112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE

A0A086LDB3 **A0A086LDB3_TOXGO** (2935 aa)
Transporter, major facilitator family protein. *Toxoplasma gondii FOU*

```
METSENPNAAERARVDTAATPHHDDPLAGISQASPLFPLPSDDLSLSLTSCPPGADPENPSGFTTYSQSPSPGEPDTSGQ
YPSSTGDAVLSSPASLLSPLIDRVSPAFCLSTPSPETAATSTLRPRNSGDFLSVISSPVHSPPASPVSSVSIVSCSRDLP
SALTPSCFMSGVPREEKDGRRLVVLGLHLTSPRCLDGARRVEVHCAAQASKERNKDEVCMRNDGADQRNCENDSRKETAR
KRGKGRACRRKAESADGAQQDRTPEKEIHDEKLEKRETLGSEVENHSDSEDSTPGPEGEDDGRGTQQARATCSKCNGETH
VPQFNQQSPRRLFSRWTQHRERKTTVRRTGANARWSFFLPSRKKKQGESRGSRHNRRLTAGLEDESRQKSESENWETDGE
RELEDMRPFTASNDSSRLRGCLRACSPADLLSAGEGGTVTVTREPSDEEEEEEDEDENDEERDEDENDEEADESIGSKRR
EFESRRRWKTRMFALLLMIQMTLNIDNGVVPAVLADLGREFQATASEQGLVGALPHIGMLVFCPFCARCLEAVGPQRLLL
VSLLLNAAAVVFFAVSSSCFSLFLSRFLIGFSQTAFVVYAPVWVDKFAPHKLLTVWMGFTHSAVVVGVVVGYLFAGFLRQ
SKHNWRGALLLQVVLLLSLILVLAFSDSVHVDVWADAESSAANASHYRAAAVPPLQEGNETEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEGEEEEEGTGQVCREECEFRDKAEDVEARQEVRRTLQQKKEKTTDL
WGRAELQGEASTGALEAREAIKGRSGEVSESRRDEKEDREVPHAVVVEKGDGDDEARKKGEEEGSECERKTEIRPSGQRE
TRHFENQMMSALPPSPPVSSPRLSCLVRYTPDPPHESLHAESSVHSSHRKRTLFRAFSSAGFVVAPVSSSSQPTSFRPSS
SASRLSPQCPFCVCSGASFCSSSSTSRVVSLTQTDASSCSVALSASSNGASSSSSSSSSSSVLPSNAAASSFPCKASSSL
CRTKFFLAAPRSLSLHRLPPSAFPLSCSASSSSAAFLCPFLSCFPPPSVPRTCMRLPDKMPRGSQTVPPCGKAEDLLKNE
WFSSSEKETLPGAPERSECPPGSHRSFPAAEWSVTSSFPWIATTVAACSASRASLTLDEPHRRAGGEESLNGTTRSDLEN
AQQTSSPRSVANAVVSRSEEAEIMASVRNGNERSAAVAQESTVRTAEAGRGGSVEKRTEGPRQAPREEAARLEKTRPLRG
TASQTQEKQVSSTQASFSRSASLPFGSWRRRLEGRARPPRFASCGENGRAEERQRTTKKRRERDAILAALAHAYYSEGRP
DEVEATCRGGEGIRGRSAEARSSQKTEERRVRARATEGGSVDRAKARKGRCRLGETLERGEKEEEKRVQTEEMFCSKAGD
SETIPAQSGAAKERRKQVEERLPDLQSVSVKNDQKGPLDSLLDARRQLSRPVKLVSGERDSERHDTLPCSIRNPAPARLL
RRSTSASASVSSAPFSASRTSLGTRNEAKGRLHVLRPAAKSLPRAHIVFIRPASGQTDTSQAENEKADGRDAVDRPETPE
SSCSALHALQSACKRRKREDMRCVVAVHTTPSSHSELVFNAFLRGTKLLLFTPPIGLMLSSSAAAPRAGSQEAHRSGSRK
RASEATQEGGGQEEDARGDKRGTGMAERPRRRTQRSRQEQAPAAREDEAKVGGKDAKEAGQKEREEALEEGEQRQRQRGR
AGERTRATVGDSGAQKRTARAEESERLRLSPGRLASGYRKQTTSGRHESSARAESRTCEEATEGETGRDKREKETQRRRV
ERGFIEVGRDRRVGDGGSVETDAFGESEGRQVPRLKQMRGFPSWCYSLLRLPSERLHDPACCPYRSRGDGKDCRHRAVVK
RATETSSRNRGRESKRRNESETERDDSDDERLGLAHAFVPAPRLATGSFFPPQSVARAAELRQGHSHAQQLLSDTAPAFS
QAGAPPCSPALFPKTPSAEIREEPTMLFEGSRQLQSLHVVDLSCQTSHLSSSASGVRHIFPRLPASPSAAATKAEAAPSS
HMSSPSSSSQSSSPISASSSSPVSHSSSLGWPPPTSSSGGSLNAFCRAPRVAAGARDGVREGRTRVEDEAERRGQAEWEA
QPKTQRIGEGTRGQGDEEERRSIPGLCPAHTPLLVAVHEEAAVATAAVFAAPVWAEESPASGKEKVKKCPWATDIEQAKV
RKTENHEDENRSEDNAGTSGGRSHIHTLAVVSLRQRPQAEDKSKRKAEAGATRKGKPAKEKEEATLPEKNRERRRERRGD
GDGQIRCGSPRTVFSPCKRLSEESRREEREEDEAPSNQPRGRDGRAAEVEGIEGDNPTADNRLQEEFFVHTVCVDLPALH
VLDGGAKAGDQEAGREYSKDGRSEEGERAYKSGGERMKTVVVTSHLEKTTDVIFIARKEITGQNLEVQSPSGVAVVGVEL
QATAGDDAECKPASHEDDDPGTRDEEARKEEETADEGVKGDASTQSARGQHERRNHEVANGGKILGIEWKVKGCPTGQEA
IEATRACEEVEDNRQQEAYSGHGDEDDTSDLKQAHKRNFWNLKQWRKKRGVSREGREPRRQTHADGPAEKGKRPQKQLET
KDADEGDQEKTRDNTVEKQQDEASTLCSSREEDDEDSRVAGTWKKRTLGRLLTNPLYVCLTLALSSLFFEVTAIQFWATR
YFDEELHADTATVLVSFSVTAATAPAVGILVGAVLMDWLGGYRETPEKRRRALFCLLGLSLTCVLLGVFAAYCSLSFWPS
LASIWFILFFGGGILPIASGLLLATVDEELRTKASGAATLFYTLLGYTAGTFLPGVISDSIGTKGGMQMILLWSLSGFAF
LLLATAFASRILNTKGAEGGEEVEAGEEAEKNRKSLEARGRPRRERRARRGTDSV
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702 - 721:	EEEEEEEEEEEEEEEEEEEE
703 - 722:	EEEEEEEEEEEEEEEEEEEE
704 - 723:	EEEEEEEEEEEEEEEEEEEE
705 - 724:	EEEEEEEEEEEEEEEEEEEE
706 - 725:	EEEEEEEEEEEEEEEEEEEE
707 - 726:	EEEEEEEEEEEEEEEEEEEE
708 - 727:	EEEEEEEEEEEEEEEEEEEE
709 - 728:	EEEEEEEEEEEEEEEEEEEE
710 - 729:	EEEEEEEEEEEEEEEEEEEE
711 - 730:	EEEEEEEEEEEEEEEEEEEE
712 - 731:	EEEEEEEEEEEEEEEEEEEE
713 - 732:	EEEEEEEEEEEEEEEEEEEE
714 - 733:	EEEEEEEEEEEEEEEEEEEE
715 - 734:	EEEEEEEEEEEEEEEEEEEE

716 - 735:	EEEEEEEEEEEEEEEEEEEE
717 - 736:	EEEEEEEEEEEEEEEEEEEE
718 - 737:	EEEEEEEEEEEEEEEEEEEE
719 - 738:	EEEEEEEEEEEEEEEEEEEE
720 - 739:	EEEEEEEEEEEEEEEEEEEE
721 - 740:	EEEEEEEEEEEEEEEEEEEE
722 - 741:	EEEEEEEEEEEEEEEEEEEE
723 - 742:	EEEEEEEEEEEEEEEEEEEE
724 - 743:	EEEEEEEEEEEEEEEEEEEE
725 - 744:	EEEEEEEEEEEEEEEEEEEE
726 - 745:	EEEEEEEEEEEEEEEEEEEE
727 - 746:	EEEEEEEEEEEEEEEEEEEE
728 - 747:	EEEEEEEEEEEEEEEEEEEE
729 - 748:	EEEEEEEEEEEEEEEEEEEE
730 - 749:	EEEEEEEEEEEEEEEEEEEE
731 - 750:	EEEEEEEEEEEEEEEEEEEE

A0A086LDD0 **A0A086LDD0_TOXGO** (153 aa)
Uncharacterized protein. *Toxoplasma gondii FOU*

```
MEKMENREKREGEEGEEEEGEEGEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEELFVVWTSLGK
FRGSREEKEQDAGGDAELRTNPRQKGGSSSVENREKNRMQWSDGETQRYPGRRQEGKEETSGETGENAAIVFA
```

29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE

A0A086LKI3 **A0A086LKI3_TOXGO** (135 aa)
Uncharacterized protein (Fragment). *Toxoplasma gondii RUB*

```
EEEEEEEEEEEEEEEEEEEEEEEEEEEVRGLAYVSRRRIVILLLRTAFVSRRGKTKTKGCKVPRQASDEETEGRRSSFSTQ
ARPSGIRRASRGNWSRNEASRPQKNATQTKSKSRRAWTARKKEIEVCLLFARWND
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE

A0A086LQH0 **A0A086LQH0_TOXGO** (3136 aa)
Ribonuclease type III Dicer. *Toxoplasma gondii RUB*

```
MQSAGRCSPPRGGATRGNSDILSSSRFHPSDRPPREPSPCSPVDSSAFSCSSSSSALFPSRQFALHSAEESGPAEAGRPG
HHAFLPHSAERRARLLPLLLQALAPSAASLLLREEVCAREKTTDPETRDATLQREGDRTVKLANPPVVACGSSSLCSSSL
SSSSSLSSSSLSSSSSLSSSSLSSSLSSSSSLSSSSSLSSSSFSSSSLSSVPCSCRSPFVSFASSPEFSALRDALFAQVH
QLGEEEKAAHRGCLSLLLASRTSASASVACCGFSGGSATVLSPYDSQNVLPFQEQYAGGRGAAGVDDRAAARRREEATVL
RAVRAFGARTSAPLSETRAGRGEEDGRHSETGMCEEEGKEEEGKEEESSRRRGDGARETLEERSWWTETPADAWEESGEG
RSDGDEVEDVEREQGPQGQQSTHPAEQNRGGDERRLGEERLVRDEREEAGTLLQIEFEEKTRGRTREEGSDRDPRRRGAE
RKTESKCEQETKSPHVAYCWWQAGARESGKRSHRVLKTCDAVLPLEEETYSDRDTRGQLQAWPYQYRVYRRATLENTVVA
LPTGTGKTLVAAMVVHTWLANVFVADKLVIFLAPTTQLARQQHRAISAVLSLLRDPAGAEASRGRLAVRLPGVLEKERRT
RGRVASRDDDDGERAYFRSVLRVDWSHPKYWAAFYSALSEYKAALLDLQRLPAAPPAAFDLRRFHTGRLLAPYRFVDSQR
AALLRESFAEPSSEEANTQAASLEDSEGERSGNREGEREEDENEQDVSEVEHQAVCWPRVFVMTPDKFRNLACRGLLRID
RIGLLIFDEAHTVGRPLRSLGAYATILRVFLHFCQEEAKPRILGLTASPVPDGKLGFFDLESELKRAMRSLETIFQARIV
KADTESAPGFRNWSQGQPDAQRQGEQQRGVMGVRLTAAESREIREAVEEESERSAANEARKNARRGNGETRQDHLGGDKP
LRTMETTEGDEETFTGCAVKTVRYQLAPSPFYYDHELLILDRLTTPRVEAGRQQWRVAAWQPPPGTLRGSREPTGGVPAV
SNGDREQRKDRLPRREGTERGDPPTRSTSTKPTGTKERETEEEELEEKNAKEKEAKAKNGQVNCDGLEGKRSEGREDAVR
WNGSEVAAFRHFVEREARGRHANFSLLLQEVFDICSTFFYVEVTRLKEGREANEERHHPHETTPAEEARQETMHRILKTD
CGSPCASHPSPSFSSFPSCSPPLSSSPAAPPLASSFSCSSASAAFSASALCSSAAPSRVPASLRSSFLAEVWGAADARLN
VRVMRRLWQHLAPLTKQRAQRNWENFRRHLLHVQSELGFWSVWRLKEKVEADLEAWQARLGAATEERSRAQTRRSRRDCE
GAECEESEKEDETDNSGRGKESQKRVRFAGENQRTKAGRSEEGNRTRGDRDRIKSTLAEIPLWISFPFRRPLSSDLDLQY
GSSLSSSSLSSLDPVGGQPVERLLRRLFFGFFFLFSKALSTACSHSSLQLTMQLCRSRDLAHVCLADVAALEGGVSGAER
TGSLPQVLACSLFSDKLLRLDQVLRDSFGRAQAQAQTQRREGSVADDKRGSGPDKRAGRPGDEEERRTEDGGEATRSGLR
IKASSKGDRECSPSPKKSGVRTPVPSFSSSPSCVSPSALSSAPSSMSLSSRFPAASRSPASPDVAFGGVPKCGLVFCRRR
VDAWLVCEFLTARRLVFVDWICSSSLASQGASWLFGIGKASQGRSSCLDRLRAMHTVWGKLEKKTQKLNEQKHRPSTTPQ
SHSSSLASSASSSASSSASWGDGGKGVWRLMRRLGWGAPLQLLVSTSVLEEGIDVPACNLVVQMDMPSSLVRFVQAKGRA
RKKPAEFVVLCPDSGPCGASWPDASLPFSSSFPSSSSFFPFSSSLQSQTPDCTVSSPSLLLSLQSVSSLAVSLSSLSAPF
SVSLRSRTGEAPTTPAFAAQGFSAAGGAACYLQAVSPSVNFELARLQLCEAKVAALAADVEATERFGLLGPFRCMRKVCS
LDDLLLTHTGAMVHSSFAPALLREIVDACTAGKTDERTERGADERGEEGRWAEDTEDEGREERERGNAELRTGREKALGT
CCSNAPSSSSLSSSGMRRVSDLCEAQRQRTPSALRLLSTQDGKWILSVPSLQGFRSSPLPPFSIEFSPTGSVPTRASAAA
GVLAVRVLRRLVQEGVVDSFLRCRDRDSVEKDLRDEKERRRRENCGGVGAVDLLWRELPACLLPPRSWRNARRASGDRHG
DSEETLHTSAKTREEAARAEEAVSGSNEERRRSRDHKEGTIEGDAGAQEVEENAEEGRKEEEGDQLKRLPSGTGKKDETS
TSNAKSETHGEKTRTPAPPPGVTRLFLHRVWCTPLTAREAALERLWEPNEKQRRRRRRVLKKLAESRGFLPSPLYESGGF
CGLWRIFADAEAPLQAADLALDGASRWRQEKAKEKEQIEPDAGDGEGDEDGLWWTGNRRQREACFEKRREGGDGKRDQC
KEDEKCRAEKEEEEEEEEEEEEEEEEEEEEEEEKKWSWQEEEKNRQRREILELIRSRIDAVVEGRRGPDSVLQPLCLLLAHPI
PATVAFHALHPEASEKAALHRGRRPRTGRTSFSLRASKAEKASNAWTELEADEEGEEGVEEGEEGEDEDGEEEEDEEDVP
GLMRVEVEKPAKTMFIDLPTEYVEKVLLRFTHIHLFRLLQLSNFSPNGTCNSLLLTVLQFLSALPFRRFPFRTVPSSSSL
SSSASASASASCLGGDGEPRSRFVSLPLPACASASRLLPSHALSLFALPPSLFSLLSLLSLAAEEAEESTESTLHSQSPP
SSPRSSSPRSSSPRSSSPRSSSLSSSSPSTSAEQLKRQMVEACSSLAKAGVVDLQRVMFPFFVLAPLSPLDAKSVDLDFI
HRLASLRLFLRSGQRRSSGFLEAGACPPSLMLQHDRRLLRGAVESLHCLPSLSAVARLFCAGNSARKLDYEGGRSLQKAE
RRSARKEQNEGDAAEENGAFNWPRSLLGTLPSSDRESESAKDTKEKRTPGSEKGERGEADGERREEDGEKGATKEDGLFS
KEEQFFRRLQSYKGSIFSRGDDAANAWTTEEQKLLTFFQQRNENALSVKEALREEGMEIFYHLRSRGFEPVALRMTHQFG
RSFRFYRLQTIHRNVS
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2491 - 2510:	EEEEEEEEEEEEEEEEEEEE

A0A086LWF2 **A0A086LWF2_TOXGO** (1894 aa)
IgA-specific metalloendopeptidase (EC 3.4.24.13) (Fragment). *Toxoplasma gondii RUB*

```
MTSARTREGLVGAEAPLGEGEEDLQDSIACSVPRAPTNSFEEGYEVECVDECPYIKFQHASKLPLSPLLFDASSSPAPLP
ERLLAARCTDSLCLLHCCGVLLLPGLDSILAVDATEAACGSPISRGRLPLHASKEGETKDAFPSLLLLSPDARFLAVAVD
CQVKLVQLGGCGGPSCSKSAGEASREGNAEARLGGQQGGDSCISEKTQVLSLAGFASPVKDISWIWPSGDRTETWCEGDT
RGDAERLIGLAVLTESGEAFILSPRGAQAFPLPAHGLAIHALPRRSPAAAKSEGAGPGGLAPLTAVVSCCAPASLWLVGL
QETALLPEGSGQGESLYDFGHRRPDVSRETAKEEKRKGRRKIRVEGLADIPGYEDEAQALHKGRGRFVGVHCLGASLDSA
AGESPLPLALAWFVPDADLSTGEDDWEKPELESDSAEPRLDPLRQAPASAEDCGDSWSCFILFGFLARRPYTPSDARALR
GDIGEAESADEKEELVFRIYAASRNEMFLRSVAASTVCRFRWIPQWHCLWVFSNACTQVICFALPHSFSRNGDPLPSPRS
SSFLGSGEVPWRCFTMPEGRALETADEDAFPQGLALFFNFKESMFREHSTTDTPPLEHPPVFFLLQSDGQVCVHLADCCE
CYVDDAGIGKEKRLLPRLEWTPVSPPSSFLLTSWTEPRRRACGEQPATPVPKVSPPALSPSSSSLASPLFASLQQGKPTP
SLFGTPSTNAASAPLFSSSSGTSLFPSSASSASSLFTPAKSEEEARKTGWVVPTTHLKVTSASSPANDPSASNGASASNN
LSALDGSSPRPLSSSRKDCVDQARPAAKETREEAPTRRLPAKSSSRDPQRRGHCVHCGAVDVGDRRGGREAERRRREKKL
RRRVEAKNASLRQAAAAANEVIEATLQAARGTKAEPAREKNAKKRILLTEEQSEVKALLDEFEEKKHAFCSFSRFLPSSL
FRPLLLSARCFENALRHEERRDVLLESSPVSSSASSSSSSSSSSSASSSSSSSSSSPGSLFVSRCGEKDAPVDCGAEQEK
STAALLPAAAAGLARTGRLADKLKDEQRNVRTKQETETEVVETLQEAQQHLVAWRSCLEAVRDQLLLRMQFAEKKSENPT
ERNGEQTDAAGREEGRGDREADGREEKRERQAERGNSVTEEDVIACMQKIQSESGARRNLFEALQTLLPADAEHAQLNTD
THTKCVLTHLESGLLRAERRLLLLLQRFRFYTSFQTRFPSSLDPESGSPVRRPAASGWPGSWKINSGLSSLSSYGDKGVS
SLPLAHGKDSDRDARTKRGSVHTPDTACGRGRPGGCYGLRFEWLEEDEFPDKREESVVDSHRRVSSTTHPVSEGTPGARP
SLAFSLSASPPSAFHLSLFGSPGGARDSRIACSQGPGGSVKDGGLAGSRSGAASGDFLLDMHAEHRAAGLVAELEAAVSE
FLSSVRQLEIDLAKLEWKATDLQSPARQSPSSSSSTSSFAASLSLLSSSVFGEPLPPSGPSGLPDVVGAEKPAKDGEQRF
PVSSLREQRERFDERRKLRRQLLEVWRATTSTDPQQEGEEETETDADEEEEEEEEEEEEEEEEEEEEEEEEDEEEDEEEEE
EDESDAFEVLEDSSSVSYDEESDEWEPVGSASPENPQTPPRQSVVSRRLGASLRSGRRTSRSKQRAKFAPLSGDEDSSEN
ACSSSPSSPDDVSPRRRGAELSDSEGAPEDGASRSNSHDESASLPVCGVPGETHSISHSSLFSIKPEDVTQPPQSASFQF
ASSLPPRRASGLGHTLFSFASNSSSLPPDPTKPSSSTSAPLPPDPTKPSSSTSAPLPPDPTKSSSSTSAPLPPDPTKPSS
STSAPLPPDPTKPSLSTSAPLPPDPTKPSLSTSAPLPPDPTKPSSSTSAPLPPD
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1568 - 1587:	EEEEEEEEEEEEEEEEEEEE
1569 - 1588:	EEEEEEEEEEEEEEEEEEEE
1570 - 1589:	EEEEEEEEEEEEEEEEEEEE

A0A086LXK0 **A0A086LXK0_TOXGO** (2696 aa)
Transporter, major facilitator family protein. *Toxoplasma gondii RUB*

```
METSENPNAAERARVDTAATPHHDDPLAGISQASPLFPLPSDDLSLSLTSCPPGADPEIPSGFTAYSQSPSPGEPDTSGQ
YPSSTGDAVLSSPASLLPPLINRVSPAFCLSTPSPETAATSTLRPRNSGDFLSVISSPVHSPPASPVSSVSIVSCSRDLR
SALTPSCFMSGVPREEKGGRRLVVLGLHLTSPRCLDRARRVEVNCAAQASKEGNKDEVCMRNDGADQRNCENDGRKETAR
KRGKGRACRSKAESADGAQQDRTPEKEIHDEKLEKRETLGSEVENHSDSEDSTPGPEGEDDGRGTQQARATCSKCNGETH
VPQFSQQSPRRLFSRWKQHKERKTTVRRTGANARWSFFLPSRKKKQGESRGSRHNRRLTAGLEDESRQKSESENWETDGE
RELEDMRPFTASNDSSRLRGCLRACSPADLLSAGEGGTLTVTREPSDEEEEEEDEDENDEERDEDEHDEERDEDENDEEA
DDSIGSKRREFESRKRWKTRMFALLLMIQMTLNIDNGVVPAVLADLGREFQATASEQGLVGALPHIGMLVFCPFCARCLE
AVGPQRLLLVSLLLNAAAVVFFAVSSSCFSLFLSRFLIGFSQTAFVVYAPVWVDKFAPHKLLTVWMGLTHSAVVVGVVVG
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YLFAGFLRQSKHNWRGALLLQVVLLLSLILVLAFSDSVHVDVWADAESSAANASHYRAAAVPPLQEGNETEEEEEEEEEE
EEEEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEGTGQVCREECEFRDKAED
VEARQEVRRTLQQKKEKTTDLWGRAELQGEASTGALEAREAIKGRNGEVSESRRDEKEDREVPHAVVVEKGDGDDEARKK
GEEEGSECERKTELRPSGQREKRHFENQMMNKMPRGSQTVPPCGKAEDLLKNEWFSSSEKETLPGAPERSECPPGSHRSF
PAAEWSVTSSFPWIATTVAACSASRASLTLDEPHRRAGGEESLNGTTRSDLENAQQTSSPRSVANAVVSRSEEAEIMASV
RNGNERSAAVAQESTVRTAEAGRGGSVEKRTEGPRQAPREEAARLEKTRPLRGTASQTQEKQVSSTQASFSRSASLPFGS
WRRRLEGRARPPRFASCGENGRAEERQRTTKKRRERDAILAALAHAYYSEGRPDEVEATCRGGEGIRGRSAEARSSQKTE
ERRVRARATEGGSVDRAKARKGRCRLGETLERGEKEEEKRVQTEEMFCSKAGDSETIPAQSGAAKERRKQVEERLPDLQS
VSVKNDQKGPLDSLLDARRQLSRPVKLVSGERDSERHDTLPCSIRNPAPARLLRRSTSASASVSSAPFSASRTSLGTRNE
AKGRLHVLRPAAKSLPRAHIVFIRPASGQTDTSQAENEKADGRDAVDRPETPESSCSALHALQSACKRRKREDMRCVVAV
HTTPSSHSELVFNAFLRGTKLLLFTPPIGLMLSSSAAAPRAGSQEAHRSGSRKRASEATQEGGGQEEDARGDKRGTGMAE
RPRRRTQRSRQEQAPAAREDEAKVGGKDAKEAGQKEREEALEEGEQRQRQRGRAGERTRATVGDSGAQKRTARAEESERL
RLSPGRLASGYRKQTTSGRHESSARAESRTCEEATEGETGRDKREKETQRRRVERGFIEVGRDRRVGDGGSVETDAFGES
EGRQVPRLKQMRGFPSWCYSLLRLPSERLHDPACCPYRSRGDGKDCRHRAVVKRATETSSRNRGRESKRRNESETERDDS
DDERLGLAHAFVPAPRLATGSFFPPQSVARAAELRQGHSHAQQLLSDTAPAFSQAGAPPCSPALLPKTPSAEIREEPTML
FEGSRQLQSLHVVDLSCQTSHLSSSASGVRHIFPRLPASPSAAATKAEAALSSHMSSPSSSSQSSSPRSASSSSPVSHSS
SLGWPPPTSSSGGSLNAFCRAPRVAAGARDGVREGRTRVGDETERRGQAEWEAQPKTQGIGEGTRGQGDEEERRSIPGLC
PAHTPLLAAVHEEAAVATAAVFAAPMWTEESPASGKEKVKKCPWATDIEQAKVRKTENHEDENRSEDNAGTSGGRSHTHT
LAVVSLRQRPQAEDKSKRKAEAGATRKGKPAKEKEEATLPEKNRERRRERRGDGDGQIRCGSPRTVFSPCKRLSEESLRE
EREEDEAQSNQPRGRDGCAAEVEGIEGDNPTADNRLQEEFFVHTVCVDLPALHVLDGGAKAGDQEAGREYSKDGRSEEGE
RAYKSGGERMKTVVVTSHLEKTTDVIFIARKEITDQNLEVQSPSGVAVVGVELQATAGDDAECKPASHEDDDPGTRDEEA
RKEEETADEGVKGDASTQSARGQHERRNHEVANGGKILGIEWKVKGCPTGQEAIEATRACEEVEDNRQQEAYSGHGDEDD
TSDLKQAHKRNFWNLKQWRKKRGVSREGREPRRQTHADGPAEKGKRPQKQLETKDADEGDQEKTRDNTVEKQQDEASTLC
SSREEDDEDSRVAGTWKTRTLGRLLTNPLYVCLTLALSSLFFEVTAIQFWATRYFDEELHADTATVLVSFSVTAATAPAV
GILVGAVLMDWLGGYRETPEKRRRALFCLLGLSLTCVLLGVFAAYCSLSFWPSLASIWFILFFGGGILPIASGLLLATVD
EELRTKASGAATLFYTLLGYTAGTFLPGVISDSIGTKGGMQVRRCNDTGACSLPRS

729 - 748:	EEEEEEEEEEEEEEEEEEEE
730 - 749:	EEEEEEEEEEEEEEEEEEEE
731 - 750:	EEEEEEEEEEEEEEEEEEEE
732 - 751:	EEEEEEEEEEEEEEEEEEEE
733 - 752:	EEEEEEEEEEEEEEEEEEEE
734 - 753:	EEEEEEEEEEEEEEEEEEEE
735 - 754:	EEEEEEEEEEEEEEEEEEEE
736 - 755:	EEEEEEEEEEEEEEEEEEEE
757 - 776:	EEEEEEEEEEEEEEEEEEEE
758 - 777:	EEEEEEEEEEEEEEEEEEEE
759 - 778:	EEEEEEEEEEEEEEEEEEEE
760 - 779:	EEEEEEEEEEEEEEEEEEEE
761 - 780:	EEEEEEEEEEEEEEEEEEEE
762 - 781:	EEEEEEEEEEEEEEEEEEEE
763 - 782:	EEEEEEEEEEEEEEEEEEEE

A0A086M087 **A0A086M087_TOXGO** (711 aa)
WD domain, G-beta repeat-containing protein. *Toxoplasma gondii RUB*

MVRKSPERFAREHAVLVQYPSAGQGMLSATVARPLSLCWISPSFKLRPSPLFKKSMREGVLAASGRKEKKESSDLSVPLC
ACDCRGINASTPHALLFAAASSGDHAVKVWKAEISPSFLSGKVRGDDEPGASGKKKKTTDTGHPQILVTSLASVVAHRKE
INDVKISPNDALLCTVSQDKTGKLFSFPSLVYVGELRGHSRSIFACAFPKREKIVATASADSTVKLWNVDTCACIKTFQS
TVGGGVLALGFLSRDTQLVTGTSEGFLQLWNCRTAECVGSLPSVHEENKASVSAGGRGAQIIWCLDVCGPAMVTGGSGGQ
LCLWEDVTNLVRHKAELAQQRETQQLAALKLLAAEGRGDEVFSLLLRLRRRAGMREFLENQCGKILLQAFQRGLELQRRI
ALYSGQPLARSGSDQDASASTFGRLSAFLESLEEERVAAREDEDDRRGGQESKAELGASKKRKGEKKVKGEETEAGVRGR
PDAPLRSAWLRDLNGDLSLPQLLRKMKKKDVATLLEFAAAWNTNSHTSWLAQGLVRLLLEARGEDIFEGAEKAGRNVSDV
ENVISSFCAYTARHDRRLTALIEKTFLLDLLQGCESGETRDLGDRWSGETRREPHREKTLDPRDATTFTRLCLYGDESEQ
TEMSQGKKTKNEPKRDSDERSTQEEEEEEEEGEGEEEAEEEEEEEEEEEEEEEEEEEEEEEEEEAEEEEEADA

679 - 698:	EEEEEEEEEEEEEEEEEEEE
680 - 699:	EEEEEEEEEEEEEEEEEEEE
681 - 700:	EEEEEEEEEEEEEEEEEEEE
682 - 701:	EEEEEEEEEEEEEEEEEEEE
683 - 702:	EEEEEEEEEEEEEEEEEEEE

A0A086M0M1 **A0A086M0M1_TOXGO** (852 aa)
Uncharacterized protein (Fragment). *Toxoplasma gondii RUB*

```
MRGRRPSQQRKKAASLGASSLLSSLPSSLPSSLFSRGDSVGRRLGKRRGIEEEGGKRKRARGGRSARHNFPEVDQQGGSD
LDELPSSEADPREAQQDGEGSFGHEQELAETLKRSKRAVLERKRRRHEERRQKKQIHRKQQQLWKLERQKALLERQLDMQ
KAAISGIRVNQGTGSGVRTPCGPEADPEDEEEDVSPRREKKTPSSLSSSLSSSLSSLDVRGSVLSALSAKDKKHTASGEV
LLLSGVSSRSTEEQRKAEERRLALDAAGRQLDAELAFLESKLGIGKDSSKAGEKKKKKLAQELLDDGFDEDLQTLLDDIL
GGKAENRKRKTKTDYDHDEGEMEGEETQEGAHEELGRVEAEEDEEDEEEEDDEEDEEDDEEENEEEEEDEEEDEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEDEGDEEDEGDEEDEEDGEDLKLKTEHYSTCASASAGKYLPPHLRNRAQRDLSNEAEFD
GDNPGRNSTRQHGAAPASEASDKANFVASKLPLSCLEKARQTATDAGRGLTQRLRGSLNRVSEGNVEVILQQISQEVKAA
LTQVLSGALPVPATSPALTPRDVRGLRREQEISFFQEVNCIIVRLLMQSMVESKFSTASLVATQTALCCGLSCLLDASLC
SQLLAALGEAFRKFFPLALAQADRRTETGEPVGLYVRHTLMALCFLFDFNVVQPAVFLGLLQRLSGKVATTKEKGGAKNG
ERNEPLVEFQVECLLMVLRLGGGKLRNDNPVLFKEAWNFLMTRVKGGEGEREVQVHSGREERPFEEQTREEQRARLARVS
TSFSGALRQRQEGEQPATTGRLHYLARELEELKNNKGNTIHLASKASQEAMR
```

394 - 413:	EEEEEEEEEEEEEEEEEEEE
395 - 414:	EEEEEEEEEEEEEEEEEEEE
396 - 415:	EEEEEEEEEEEEEEEEEEEE
397 - 416:	EEEEEEEEEEEEEEEEEEEE
398 - 417:	EEEEEEEEEEEEEEEEEEEE
399 - 418:	EEEEEEEEEEEEEEEEEEEE
400 - 419:	EEEEEEEEEEEEEEEEEEEE
401 - 420:	EEEEEEEEEEEEEEEEEEEE
402 - 421:	EEEEEEEEEEEEEEEEEEEE
403 - 422:	EEEEEEEEEEEEEEEEEEEE

A0A086M1L7 **A0A086M1L7_TOXGO** (1274 aa)
Putative DNA mismatch repair protein MSH6-1 (EC 3.4.21.72) (Fragment). *Toxoplasma gondii RUB*

```
ASVGDSTAARSSSGNEEDPGSEDVRKLKRLRRRLALSDDEEKMETPPSIRRRRQAEQTKKIEKEAARRAKPEEEEEEEEA
EEEEEEESEPSAFSDESYEDESEEESEDDSEDEEEEEEEEEEEEEEEEEEEEEEEENCHYFRHYIEDFYMYHRQFSFPPWAD
PARMRDISGRRAIDCGEDYDFSSLWIPSPDSQLARAHARPHMTPGMAQYWEIKKEHFDKLILFKIGKFYELVYGDACAAH
RILDLKWMGGGGADAKPHCGFPEQNLHFQARQLVQAGYKVVVVEQMETPKELEKRNSQAAAGAKDKAVRREVCEVYSAGT
VRHADMLGQAARYLLVLYFGEEDEEVDVDTEVATEKQVAADRRGADIMAADRHETGERASTGAGDRGDPEVQQSLDAAEK
ATLGMDSSTRDARDTSEKRRELKPGFAACLVDVSTCRVSLVRLSDDPTAAWPSLRLLLAQTLPVEVVYSPTNIPASVLKL
LKFLPSPPQLSPLTSFPDLLGAHTEVDRYITSRLDALTSKSNASSSSSSSSASSPASQSSSLSSSSSSSPAQSLELCRTL
CDRWPSLHCAVGGLCVYLRECRLDASVLPLCQFESFRPRDASVLVLDAHALRQLEILQTQDGCAKQALLGYLDRTVTAFG
HRLLRRWLVAPLRNVAELTRRLDAVDWLCNSPESVADIRKALQACPDIERLSAKICAQGLQGERRAVYFDHFHQKLLADF
FALLDAFLSVESLAKRLAQRLATCHGQEAAEEREAAEEREGEEGRGGRLLDLCADREHGGLFPPLGELVASLKSKVAINA
DGHKIPAKGVLAAYDDTVTEMQEVQQKLENLLDDLRSSWKMKSLQFVHSKFKYEVECPDTVSKELLRTHECDITSSRKGF
FRFRTPEICELVAELEDLEQKQKDTFYPFFSILFNAFYSHFTHTFGRAIQVAAELDCLQSLATVVATHPGHSGQMCRPTI
VEAREDAPPILALKNCRHPVAETLMDNFVPNDVYLNCGPHESKRTLLITGPNMGGKSTLLRQAALCVVMAQVGCFVPADS
CTLSPVDRIFTRLGAEDSILQGASTFLVELKDISELMTYGTRHSLAVIDELGRGTSTFDGTAIALASLEHITDNLQCRCL
FATHYHLLCYEMQGHPHVVNVHMKAAINEEQQSLAFLYKLTKGVCPKSHGIHVARLAGIDPRILECAEEKSLRLQQEVVR
QQRHWRLLGVAKTLEAADPATLQSLFARKESVLEDLIQEEEAEAGEEEAKAGEEEAKAGEEEAVPNEREVEMEG
```

112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE

A0A086PJF0 **A0A086PJF0_TOXGO** (953 aa)
Utp14 (Fragment). *Toxoplasma gondii VAND*

```
MTLPKQRVRLHLFHPGASPATSQRELARPVTCGLSVGCLALRPRRLHARRASCWEVSLAFSPFLTQILLASMALERRTAR
RAPPRSQKEQEELTPWLTAGPQADDNEEEEKEEEEEKEEEDEEEEEEEEEEEEEEDDEEEEEEEEEEEEEEEEEEEEEEE
EGEANASKARVLKQRGKAMISAQKKSRDKDASDALSICRLMKDLVSDSWDGLPEEEEAEEEESEEEESEEEEAEEEEAEE
EEEGEEGGEEEGLPSKLLKSLQRGQRTEEEEVDPFEGVSEHSLSLLKSKGDRRRAAASSQPDSGEEGGDAGTREVDAQLD
AASADALSFSSLLTSLSTTTSRSGLRKQLESLARPRAASAAASSSVRGSDETAVDADVVQEPLGPTQQKALLRSAAYAEA
KETAKKWTRVVQRNQQAVQLQLGVSTARSRGGDGRGEAPTEVRSLSHALSDFKANDAFEDALLAAVNADGVSDQKLKASG
GLGPADAIKRQAEQRQVARLKFLLFTEQRRARRLKRIKSKLSRKKRKQAERREEEKIMEKLEVGNPALAEELRKKFEEKR
AKMRLLRQQNARAKWAALAARFGGRDVQQEISRQMQREADERRTVERLARRRPGSSDASESESAESAESAESEEEQSAGD
KARLLRTLSRETADLQEALPDKGLLALPFMRRGLEKRRERNRQEIERLRRHGESEEDSEGADEALEAGRKPSGDEDASDL
ESTLDETEAREARDAVAEAEVERRPTQTGRRKRAVDLDPKAVEAAEQELEGKFQFFELNEADGSETQASPKDAGKAGAGE
QRAFASSAAARAFFQAELEKEEKRREEAATKRSREAHATAWAQAERSGGSERERQRELERSAEAANPWLRPQKKRKVSTA
GTQVEETAQQLQKLLNDEESSASEAEGARPASNLRGKTEREAQRELIQQAFVCDEDAEEEFIQEQEEENKKEE
```

140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE

A0A086PPG7 **A0A086PPG7_TOXGO** (125 aa)
Uncharacterized protein (Fragment). *Toxoplasma gondii VAND*

```
EEEEEEEEEEEEEEEEEEEEEEEEEQCWSAVDEEGEAGESGCREEERKVKGERDPSAEDVRRIGSSRTSETNWFSEAAGD
SKKRAVRGTDQQRERDIVEPGVARITADDSGDAWVIAKSASVEYE
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE

A0A086PXI9 **A0A086PXI9_TOXGO** (1427 aa)
Putative DNA mismatch repair protein MSH6-1 (EC 3.4.21.72) (Fragment). *Toxoplasma gondii MAS*

```
ASVGDSTAARSSSGNEEDPGSEDVRKLKRLRRRLALSDDEEKMETPPSIRRRRQAEQTKKIEKEAARRAKPEEEEEEEED
EEEEEESEPSAFSDESYEDESEEESEDDSDEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVRGKKRPAPKKEKRVEEGSQT
TWTTASSSASSSSRAKLKDLVYSASSEKPGTTSSLTPPPVTSPPSSSPPAAPEPTSSSSSLSSSLSSSSLSSSSVSSSSV
SSSSVSSSSVSSSSRLPCSTGRKATDAVDEAELRRRLLASPAAQNCHYFRHYIEDFYMYHRQFSFPPWADPARMRDISGR
RAIDCGEDYDFSSLWIPSPDSQLARAHARPHMTPGMAQYWEIKKEHFDKLILFKIGKFYELVYGDACAAHRILDLKWMGG
GGADAKPHCGFPEQNLHFQARQLVQAGYKVVVVEQMETPKELEKRNSQAAAGAKDKAVRREVCEVYSAGTVRHADMLGQA
ARYLLVLYFGEEDEEVDVDTEVATEKQVAAGRRGADIMAADRRETGERASTEAGDRGDPEMRQSLDAAEKATVGMDSSTR
DARDTSEKRRELKPGFAACLVDVSTCRVSLVRLSDDPTAAWPSLRLLLAQTVPVEVVYSPTNIPASVLKLLKFLPSPPQL
SPLTSFPDLLGAHTEVDRYITSRLDALTSKSNASSSSSSSSSSSSSSPASGSSSLSSSSSSSPAQSLELCRTLCDRWPSL
HCAVGGLCVYLRECRLDASVLPLCQFESFRPRDASVLVLDAHALRQLEILQTQDGCAKQALLGYLDRTVTAFGHRLLRRW
LVAPLRNVAELTRRLDAVDWLCNSPESVADIRKALQACPDIERLSAKICAQGLQGERRAVYFDHFHQKLLADFFALLDAF
LSVESLAKRLAQRLATSHGQEGAEEREAAEEREGEEGRGGRLLDLCADREHGGLFPPLGELVASLKSKVAINADGHKIPA
KGVLAAYDDTVTEMQEVQQKLENLLDDLRSSWKMKSLQFVHSKFKYEVECPDTVSKELLRTHECDITSSRKGFFRFRTPE
ICELVAELEDLEQKQKDTFYPFFSILFNAFYSHFTHTFGRAIQVAAELDCLQSLATVVATHPGHSGQMCRPTIVEAREDA
PPILALKNCRHPVAETLMDNFVPNDVYLNCGPHESKRTLLITGPNMGGKSTLLRQAALCVVMAQVGCFVPADSCTLSPVD
RIFTRLGAEDSILQGASTFLVELKDISELMTYGTRHSLAVIDELGRGTSTFDGTAIALASLEHITDNLQCRCLFATHYHL
LCYEMQGHPHVVNVHMKAAINEEQQSLAFLYKLTKGVCPKSHGIHVARLAGIDPRILECAEEKSLRLQQEVVRQQRHWRL
LGVAKTLEAADPATLQSLFARKESVLEDLIQEEEAEAGEEEAKAGEEEAKAGEEEAVPNEREVEMEG
```

112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE

A0A086Q4A8 **A0A086Q4A8_TOXGO** (1252 aa)
MI domain-containing protein. *Toxoplasma gondii VAND*

```
MRGRRPSQQRKKAASLGASSLLSSLPSSLPSSLFSRGDSVGRRLGKRRGIEEEGGKRKRARGGRSARHNFPEVDQEGGSD
LDELPSSEADPREAQQDGEGSFGHEQELAETLKKSKRAVLERKRRRHEERRQKKQIHRKQQQLWKLERQKALLERQLDMQ
KAAISGIRVNQGTGSGVRTPCGPEADSEDEEEDVSPRREKKTPSSLSSSLSSSLSSLDVRGSVLSALSAKDKKHTVSGDV
LLLSGVSSRSTEEHRKAEERRLALDAAGRQLDAELAFLESKLGIGKDSSKAGEKKKKKLAQELLDDGFDEDLQTLLDDIL
GGKAENRKRKIKTDYDHDEGEMEGEETQEGAHEELGRVEAEEDEEDEDDEEEENEEGEEDEEEEEEEEEEEEEEDEEEEE
EEEEEEEEEEEEEEEEEEEEDEGDEEDEGDEEDEEEGEDLKLKTEQYSTCASASAGKYLPPHLRNRAQRDLSNEAEFDGD
NPGRNSTRQHGAAPASEASDKANFVASKLPLSCLEKARQTATDAGRGLTQRLRGSLNRVSEGNVEVILQQISQEVKAALT
QVLSGALPVPATSPALTPRDVRGLRREQEISFFQEVNCIIVRLLMQSMVESKFSTASLVATQTALCCGLSCLLDASLCSQ
LLAALGEAFRKFFPLALAQADRRTETGEPVGLYVRHTLMALCFLFDFNVVQPAVFLGLLQRLSGKVATTKEKGEAKNGER
NEPLVEFQVECLLMVLRLGGGKLRNDNPVLFKEAWNFLMTRVKGGEGEREVQVHSGREERPFEEQTREEQRARLARVSTS
FSGALRQRQEGEQPATTGRLHYLARELEELKNNKGNTIHLASKASQEAMRRWLQTSPLLAQSPLRQCAGEGKSVLVGVSS
WQEVEDGVVSVSPSSHRPPVSPHKSVRVEEEKQSCLGDTGSEKALLDLAAKLRLHSEEQKKIFLAIMSAESPNDAVKRLL
QLVPRTNKKKNFVTTAVAVLLHISLQQSAFNPFYALVIARLCARCSCASWGRLEAEAEQPPLLGPLGSGRASVNQRRARG
PCACLLPPDKEGKVFRRVTQRGLAAQNSAAHGFPLRRLLHLARLEAFLIRIGVVELRVTRFVSFEGEKGQADAHMGLSGK
LGVFLKELCTELLCSPAFASVPLPGPSTASPLLPFLSLSALPDVREAFLLVLEDVLLPEARKNACSENGKGAKESVNAAC
MPGRQGKCVRVEGAMCTPACGIRKDVISRVIWFMKKQERYEEEDPNTFAFDA
```

395 - 414:	EEEEEEEEEEEEEEEEEEEE
396 - 415:	EEEEEEEEEEEEEEEEEEEE
397 - 416:	EEEEEEEEEEEEEEEEEEEE
398 - 417:	EEEEEEEEEEEEEEEEEEEE
399 - 418:	EEEEEEEEEEEEEEEEEEEE
400 - 419:	EEEEEEEEEEEEEEEEEEEE
401 - 420:	EEEEEEEEEEEEEEEEEEEE

A0A086Q531 **A0A086Q531_TOXGO** (723 aa)

WD domain, G-beta repeat-containing protein (Fragment). *Toxoplasma gondii VAND*

```
EDSASQAAPAFPRSLVALVGERQPWVLRLDGPAGEGHPVGYQAAACAAELSEGHQGEPSRFSEAHAAPAVCCDVSRKGCW
VLSGASDGSLAVWHAATGRCLAQVPPGHHGGAINAVAFQQKEWLRPSPLFKKSMREGVLAASGRKEKKESSDLSVPLCAC
DCRGINASTPHALLFAAASSGDHAVKVWKAEISPSFLSGKVRGDDEPGASGKKKKTADTGHPQILVTSLASVVAHRKEIN
DVKISPNDALLCTVSQDKTGKLFSFPSLVYVGELRGHSRSIFACAFPKREKIVATASADSTVKLWNVDTCACIKTFQIWC
LDVCGPAMVTGGSGGQLCLWEDVTNLVRHKAELAQQRETQQLAALKLLAAEGRGDEVFSLLLRLRRRAGMREFLENQCGK
ILLQAFQRGLELQRRIALYSGQPLARSGSDQDASASTFGRLSAFLESLEEERVAAREDEDDRRGGQESKAELGASKKRKG
EKKVKGEETEAGARGRPDAPLRSAWLRDLNGDLSLPQLLRKMKKKDVATLLEFAAAWNTNSHTSWLAQGLVRLLLEARGE
DIFEGAEKAGRNVSDVENMISSFCAYTARHDRRLTALIEKTFLLDLLQGCESGDTRDLGDRWSGETRREPHREKTLDPRD
ATTFTRLCLYGDESEQTEMSQGKKTKNEPKRDSDERSTQEEEEEEDGEGEEDEEEEEAEEEEEEEEEEEEEEEEEEEEE
ADA
```

699 - 718:	EEEEEEEEEEEEEEEEEEEE
700 - 719:	EEEEEEEEEEEEEEEEEEEE
701 - 720:	EEEEEEEEEEEEEEEEEEEE

A0A086Q619 **A0A086Q619_TOXGO** (135 aa)
Uncharacterized protein (Fragment). *Toxoplasma gondii VAND*

```
EEEEEEEEEEEEEEEEEEEEEEEEEEVRGLAYVSRRRIVILLLRTAFVSRRGKTKTKGCKVPRQASDEETEGRRSSFSTQ
ARPSGIRRASRGNWSRNEASRPQKNATQTKSKSRRAWTARKKEIEVCLLFARWND
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE

A0A086Q951 **A0A086Q951_TOXGO** (1420 aa)
Putative DNA mismatch repair protein MSH6-1 (EC 3.4.21.72) (Fragment). *Toxoplasma gondii VAND*

```
ASVGDSTAARSSSGNEEDPGSEDVRKLKRLRRRLALSDDEEKMETPPSIRRRRQAEQTKKIEKEAARRAKPEEEEEEEED
EEEEEESEPSAFSDESYEDESEEESEDDSEDEEEEEEEEEEEEEEEEEEEEEEEEVRGKKRPAPKKEKRVEEGSQTTWTTA
ASSASSSSRAKLKDLVYSASSEKPGTTSSLTPPPVTSPPSSSPPAAPEPTSSSSSLSSSSVSSSSLSSSSVSSSSVSSSS
VSSSSVSSSSRLPCSTGRKATDAVDEAELRRRLLASPAAQNCHYFRHYIEDFYMYHRQFSFPPWADPARMRDISGRRAID
CGEDYDFSSLWIPSPDSQLARAHARPHMTPGMAQYWEIKKEHFDKLILFKIGKFYELVYGDACAAHRILDLKWMGGGGAD
AKPHCGFPEQNLHFQARQLVQAGYKVVVVEQMETPKELEKRNSQAAAGAKDKAVRREVCEVYSAGTVRHADMLGQAARYL
LVLYFGEEDEEVDVDTEVATEKQVAADRRGADIMAADRRETGERASTGAGDRGDPEVQQSLDAEEKATVGMDSSTRDARD
TSEKRRELKPGFAACLVDVSTCRVSLVRLSDDPTAAWPSLRLLLAQTLPVEVVYSPTNIPASVLKLLKFLPSPPQLSPLT
SFPDLLGAHTEVDRYITSRLDALTSKSNASSSSSSSSSSSPASRSSSLSSSSSSSPAQSLELCRTLCDRWPSLHCAVGGL
CVYLRECRLDASVLPLCQFESFRPRDASVLVLDAHALRQLEILQTQDGCAKQALLGYLDRTVTAFGHRLLRRWLVAPLRN
VAELTRRLDAVDWLCNSPESVADIRKALQACPDIERLSAKICAQGLQGERRAVYFDHFHQKLLADFFALLDAFLSVESLA
KRLAQRLATSHGQEAAEEREAAEEREGEEGRGGRLLDLCADREHGGLFPPLGELVASLKSKVAINADGHKIPAKGVLAAY
DDTVTEMQEVQQKLENLLDDLRSSWKMKSLQFVHSKFKYEVECPDTVSKELLRTHECDITSSRKGFFRFRTPEICELVAE
LEDLEQKQKDTFYPFFSILFNAFYSHFTHTFGRAIQVAAELDCLQSLATVVATHPGHSGQMCRPTIVEAREDAPPILALK
NCRHPVAETLMDNFVPNDVYLNCGPHESKRTLLITGPNMGGKSTLLRQAALCVVMAQVGCFVPADSCTLSPVDRIFTRLG
AEDSILQGASTFLVELKDISELMTYGTRHSLAVIDELGRGTSTFDGTAIALASLEHITDNLQCRCLFATHYHLLCYEMQG
HPHVVNVHMKAAINEEQQSLAFLYKLTKGVCPKSHGIHVARLAGIDPRILECAEEKSLRLQQEVVRQQRHWRLLGVAKTL
EAADPATLQSLFARKESVLEDLIQEEEAEAGEEEAKAGEEEAKAGEEEAVPNERDVEMEG
```

112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE

A0A086QB89 **A0A086QB89_TOXGO** (1778 aa)
IgA-specific metalloendopeptidase (EC 3.4.24.13) (Fragment). *Toxoplasma gondii MAS*

```
MTSARTREGLVGAEAPLGEGEEDLQDSVACSVPRAPTNSFEEGYEVECVDECPYIKFQHASKLPLSPLLFDASSSPAPLP
ERLLAARCTDSLCLLHCCGVLLLPGLDSILAVDATEAACGSPISRGRLPLHASKEGETKDAFPSLLLLSPDARFLAVAVD
CQVKLVQLGGCGGPSCSKSAGEASREGNAEARLGGQQGGDSCISEKTQVLSLAGFASPVKDISWIWPSGDRTETWCEGDT
RGDAERLIGLAVLTESGEAFILSPRGAQAFPLPAHGLAIHALPRRSPAAAKSEGAGPGGLAPLTAVVSCCAPASLWLVGL
QETALLPEGSGQGESLYDFGHRRPDVSRETAKEEKRKGRRKIRVEGLADIPGYEDEAQALHKGRGRFVGVHCLGASLDSA
AGESPLPLALAWFVPDADLSTGEDDWEKPELESDSAEPRLDPLRQAPASAEDCGDSWSCFILFGFLARRPYTPSDARALR
GDIGEAESADEKEELVFRIYAASRNEMFLRSVAASTVCRFRWIPQWHCLWVFSNACTQVICFALPHSFSRNGDPLPSPRS
SSFLGSGEVPWRCFTMPEGRALETADEDAFPQGLALFFNFKESMFREHSTTDTPPLEHPPVFFLLQSDGQVCVHLADCCE
CYVDDAGIGKEKRLLPRLEWTPVSPPSSFLLTSWTETRRRACGEQPATPVPKVSPPALSPSSSSLASPLFASLQQGKPTP
SLFGTPSTNAASAPLFSSSSGTSLFPSSASSASSLFTPAKSEEEARKTGWVVPTTHLKVTSASSPANDPSASNGASASNN
LSALDGSSPRPLSSSRKDCVDQARPAAKETREEAPTRRLPAKSSSRDPQRRGHCLHCGAVDVGDRRGGREAERRRREKKL
RRRVEAKNASLRQAAAAANEVIEATLQAARGTKAEPAREKNAKKRILLTEEQSEVKALLDEFEEKKHAFCSFSRFLPSSL
FRPLLLSARCFENALRHEERRDVLLESSPVSSSASSSSSSSSSSSPGSLFVSRCGEKDAPVDCGAEQEKSTAALLPAAAAG
LARTGRLADKLKDEQRNVRTKQETETEVVETLQEAQQHLVAWRSCLEAVRDQLLLRMQFAEKKSENPTERNGEQTDAAGR
EEGRGDREADGREEKRERQAERGNSVTEEDVIACMQKIQSESGARRNLFEALQTLLPADAEHAQLNTDTHTKCVLTHLES
GLLRAERRLLLLLQRFRFYTSFQTRFPSSLDPESGSPVRRPAASGWPGSWKINSGLSSLSSYGDKGVSSLPLAHGKDSDR
DARTKRGSVHTPDTACGRGRPGGCYGLRFEWLEEDEFPDKREESVVDSHRRVSSTTHPVSEGTPGARPSLAFSLSASPPS
```

```
AFHLSLFGSPGGARDSRIACSQGPGGSVKDGGLAGSRSGAASGDFLLDMHAEHRAAGLVAELEAAVSEFLSSVRQLEIDL
AKLEWKATDLQSPARQSPSSSSSTSSFAASLSLLSSSVFGEPLPPSGPSGLPDVVGAEKPAKDGEQRFPVSSLREQRERF
DERRKLRRQLLEVWRATTSTDPQQEGEEETETDADEEEEEEEEEEEEEEEEEEEEEEDEEEEDEEEEEEDESDAFEVLED
SSSVTYDEESDEWEPVGSASPENTQTPPRQSVVSRRLGASLRSGRRTSRSKQRAKFAPLSGDEDSSENACSSSPSSPDDV
SPRRPGAELSDSEGAPENGASRSNSHDESASLPVCGVPGETHSISHSSVFSIKPEDVTQPPQSASFQFASSLAPRRASGL
GHTLFSFESNSSSLPPDP
```

1556 - 1575:	EEEEEEEEEEEEEEEEEEEE
1557 - 1576:	EEEEEEEEEEEEEEEEEEEE
1558 - 1577:	EEEEEEEEEEEEEEEEEEEE

A0A086QKA8 **A0A086QKA8_TOXGO** (1803 aa)
IgA-specific metalloendopeptidase (EC 3.4.24.13) (Fragment). *Toxoplasma gondii VAND*

```
MTSARTREGLVGAEAPLGEGEEDLQDSIACSVPRAPTDSFEEGYEVECVDECPYIKFQHASKLPLSPLLFDASSSPAPLP
ERLLAARCTDSLCLLHCCGVLLLPGLDSILAVDATEAACGSPISRGRLPLHASKEGETKDAFPSLLLLSPDARFLAVAVD
CQVKLVQLGGCGGPSCSKSAGEASREGNAEARLGGQQGGDSCISEKTQVLSLAGFASPVKDISWIWPSGDRTETWCEGDT
RGDAERLIGLAVLTESGEAFILSPRGAQAFPLPAHGLAIHALPRRSPAAAKSEGAGPGGLAPLTAVVSCCAPASLWLVGL
EETALLPEGSGQGESLYDFGHRRPDVSRETAKEEKRKGRRKIRVEGLADIPGYEDEAQALHKGRGRFVGVHCLGASLDSA
AGESPLPLALAWFVPDADLSTGEDDWEKPELESDSAEPRLDPLRQAPASAEDCGDSWSCFILFGFLARRPYTPSDARALR
GDIGEAESADEKEELVFRIYAASRNEMFLRSVAASTVCRFRWIPQWHCLWVFSNACTQVICFALPHSFSRNGDPLPSPRS
SSFLGSGEVPWRCFTMPEGRALETADEDAFPQGLALFFNFKESMFREHSTTDTPPLEHPPVFFLLQSDGQVCVHLADCCE
CYVDDAGIGKEKRLLPRLEWTPVSPPSSFLLTSWTETRRRACGEQPATPVPKVSPPALSPSSSSLASPLFASLQQGKPTP
SLFGTPSTNAASAPLFSSSSGTSLFPSSASSASSLFTPAKSEEEARKTGWVVPTTHLKVTSASSPANDPSASNGASASNN
LSALDGSSPRPLSSSRKDCVDQARPAAKETREEAPTRRLPAKSSSRDPQRRGHCVHCGAVDVGDRRGGREAERRRREKKL
RRRVEAKNASLRQAAAAANEVIEATLQAARGTKAEPAREKNAKKRILLTEEQSEVKALLDEFEEKKHAFCSFSRFLPSSL
FRPLLLSARCFENALRHEERRDVLLESSPVSSSASSSSSSSSSSSASSSSSSSSSSPGSLFVSRCGEKDAPVDCGAEQEK
STAALLPAAAAGLARTGRLADKLKDEQRNVRTKQETETEVVETLQEAQQHLVAWRSCLEAVRDQLLLRMQFAEKKSENPT
ERNGEQTDAAGREEGRGDREADGREEKRERQAERGNSVTEEDVIACMQKIQSESGARRNLFEALQTLLPADAEHAQLNTD
THTKCVLTHLESGLLRAERRLLLLLQRFRFYTSFQTRFPSSLDPESGSPVRRPAASGWPGSWKINSGLSSLSSYGDKGVS
SLPLAHGKDSDRDARTKRGSVHTPDTACGRGRPGGCYGLRFEWLEEDEFPDKREESVVDSHRRVSSTTHPVSEGTPGARP
SLAFSLSASPPSAFHLSLFGSPGGARDSRIACSQGPGGSVKDGGLAGSRSGAASGDFLLDMHAEHRAAGLVAELEAAVSE
FLSSVRQLEIDLAKLEWKATDLQSPARQSPSSSSSTSSFAASLSLLSSSVFGEPLPPSGPSGLPDVVGAEKPAKDGEQRF
PVSSLREQRERFDERRKLRRQLLEVWRATTSTDPQQEGEEETETDADEEEEEEEEEEEEEEEEEEEEEEDEEEEDEEEEE
EDESDAFEVLEDSSSVSYDEESDEWEPVGSASPENPQTPPRQSVVSRRLGASLRSGRRTSRSKQRAKFAPLSGDEDSSEN
ACSSSPSSPDDVSPRRRGAELSDSEGAPEDGASRSNSHDESASLPVCGVPGETHSISHSSLFSIKPEDVTQPPQSASFQF
ASSLPPRRASGLGHTLFSFASNSSSLPPDPTKPSSSTSAPLPP
```

1568 - 1587:	EEEEEEEEEEEEEEEEEEEE
1569 - 1588:	EEEEEEEEEEEEEEEEEEEE
1570 - 1589:	EEEEEEEEEEEEEEEEEEEE

A0A086QME4 **A0A086QME4_TOXGO** (4102 aa)
Ribonuclease type III Dicer. *Toxoplasma gondii MAS*

```
MQSAGRCSPPRGGATRGNSDISSSSRFHPSDRPPREPSPCSPVDSSAFSCSSSSSALFPSRQFALHSAEESGPAEAGRPG
HHAFLPHSAERRARLLPLLLQALAPSAASLLLREEVCAREKTTDPETRDATLQREGDRTVKLANPPVVACGSSSLCSSSL
SSSSLSSSSSLSSSSLSSSLSSSSSSLSSSSLSSSSSLSSSSFSSSSLSSVPCSCRSPFVSFASSPEFSALRDALFAQVH
QLGEEEKAAHRGCLSLLLASRTSASASVACCGFSGGSATVLSPYDSQNVLPFQEQYAGGRGAAGVDDRAEARRREEATVL
RAVRAFGGRTSAPLSETRAGRGEEDGRHSETGMCEEEGKEEEGKEEESSRRRGDGARETLEERSWWTETPADAWEESGEG
RSDGDEVKDIEREQGPQGQQSTHPAEQNRGGDERRLGEERLPRDEREEAGTLLQIEFEEETRGRTREEGSDRDPRRRGAE
RKTESKCEQETKSPHVAYCWWQAGARESGKRGHRVLKTCDAVLPLEEETYSDRDTRGQLQAWPYQYRVYRRATLENTVVA
LPTGTGKTLVAAMVVHTWLANVFVADKLVIFLAPTTQLARQQHRAISTVLSLLRDPAGAEASRGRLAVRLPGVLEKERNA
RGRVASRDDDDGERAYFRSVLRVDWSHPKYWAAFYSALSEYKAALLDLQRLPAAPPAAFDLRRFHTGRLLAPYRFVDSQR
AALLRESFAEPSSEEANAQAASLEDSEGERSGNREGEREEDENEQDVSEVEHQAVCWPRVFVMTPDKFRNLACRGLLRID
RIGLLIFDEAHTVGRPLRSLGAYATILRVFLHFCQEEAKPRILGLTASPVPDGKLGFFDLESELKRAMRSLETIFQARIV
KADTESAPGIRNWSQGQPDAQRQGEQQRGVMGVRLTAAGSREIREAVEEESERSAANEARKNARRGNGETRQDHLGGDKP
LRTMEATEGDEETFTGCALKTVRYQLAPSPFYYDHELLILDRLTTPRVEAGRQQWRVAAWQPPPGTLRGSREPTGGVSAV
SNGDREQRKDRLPRREGTERGDPPTRSTSTKPPGTKERETEEEELDEKKAKEKEAKAKNGQVNCDGLEGKRSEGREDAVR
WNGSEVSAFRHFVEREARGRHTNFSLLLQEVFDICSTFFYMEVTRLKEGREANEERHHPHETTPAEEARQETMHRILKTD
CGSPCASHPSPSFSSFPSCSPPLSSSPAAPPLAPSFSCSSASAAFSASALCSSAAPSRVPASLRSSFLAEVWGAADARLN
VRVMRRLWQHLAPLTKQRAQRNWENFRRHLLHVQSELGFWSVWRLKEKVEADLEAWQARLGAATEERSRAQTRRSRRDCE
GAECEESEKEDETDNSGRGKESQKRVRFAGENQRTKAGRSEEGNRTRGDRDRIKSTLAEIPLWISFPFRRPLSSDLDFQH
GSSLSSSSLSSLDPVGGQPVERLLRRLFFGFFFLFSKALSTACSHSSLQLTMQLCRSRDLAHVCLADVAAIEGGVAGAER
TGSLLQVLACSLFSDKLLRLDQVLRDSFGRAQAQAQTQRREGSVADEKRGSGPDKRAGRPGDEEEGRTEDGGEATRSGLR
IKGSSKGDRECSPSPKKSGVRTPVPSFSSSPSCVSPSALSSAPSSMSLSSRFPAASRSPASPDVAFGGVPKCGLVFCRRR
VDAWLVCEFLTARRLVFVDWICSSSLASQGASWLFGIGKASQGRSSCLDRLRAMHTVWGKLEKKTQKLNAQKHRPSTTPQ
SHSPSLASSLSSSLPSSLSSSLASSASSSLSSSLSSSLSSSLSSSASSSASWGDGGKGVWRLMRRLGWGAPLQLLVSTSV
LEEGIDVPACNLVVQMDMPSSLVRFVQAKGRARKKPAEFVVLCPDSGPCGASWPDASLPFSSSFSSSSSFFPFSSSLQSQ
TPDCTVSSPSLLLSLQSVSSLAVSSSSLPAPLSVSLRSRTGEAPTTPAFAAQGFSAAGGAACYLQAVSPSVNFELARLQL
CEAKVAALAADVEATERFGLLGPFRCMRKVCSLDDLLLTHTGAMVHSAFAPALLREIVDACTAGKTAERTERGADERGEE
GRWAEDTEDEGREERERGNAELRTGREKALGTCCSNAPFSSSLSSSGMRRVSDLCETRRQRTPSALRLLSTQDGKWILSV
PSLQGFRSSPLPPFSIEFSPTGSAPTRASAAAGVLAVRVLRRLVQEGVVDSFLRCRDRDSVEKDLRDEKERRRRENCGGV
GAVDLLWRELPACLLPPRSWRNARRASGDRHGDSEETLHTSAKTREEAARAEEAVSGSNEERRRSRDHKEGTIEGDAGAQ
EVEENAEEGRKEEEGDQLKRLPSGTGKKDETSTSNAKSETHREKTRTPAPPPGITRLFLHRVWCTPLTAREAALERLWEP
NEKQRRRRRRVLKKLAESRGFLPSPLYESGGFCGLWRIFADAEAPLQAADLALDGASRRRQEKAKETEQIEPDAGDGEGD
EDGLWWTGNRRQREACFEKREREGGDGKHDQCKEDEKCRAEKEEEEEEEEEEEEEEEEEEEEEEEEEEKKWSWQEEEKNR
QRREILELIRSRIDAVVEGRRGPDSVLQPLCLLLAHPIPATVAFHALHPEASEKAALHRGRRPRTGRTSFSLRASKAEKA
SNAWTELEADEEGEEGDEEGDEEEGEEEGEEEEGEEEDGEEEDGEEDVPGLMRVEVEKPAKTMFIDLPTEYVEKVLLRFT
HIHLFRLLQLSNFSPNGTCNSLLLTVLQFLSALPFRRFPFRTVPSSSSLSSSASASASASCLGGDGEPRSRFVSLPLPAC
ASASRLLPSHALSLFALPPSLFSLLSLLSLAVEEAEESTESTLHSQSPPSSPRSSSPRSSSLSSSSPSTSAEQLKRQMVE
ACSSLAKAGVVDLQRVMFPFFVLAPLSPLDAKSVDLDFIHRLASLRLFLRSGQRRSSGFLEAGACPPSLMLQHDRRLLRG
AVESLHCLPSLSAVARLFCAGNSARKLDYEGGRSLQKAERRSARKEQNEGDAAEEKGAFNWPRSLLGTLPSSDRESESAK
DTKEKRTPGSEKGERGEADGERREEDGEKGATKEDGLFSKEEQFFRRLQSYKGSIFSRGGDAANAWTTEEQKLLTFFQQR
NENALSVKEALRAEGMEIFYHLRSRGFEPVALRMTHQFGRSFRFYRLQTIHRNLTPRNVVINSDAGFTLGTLCRVYLSRF
KQRLAEPHPDSQQGPRGNCFLVQGVKRRQGARQLFSRERVVDGDEFAGLHAPQFAHLLPISEPMFQEISWMPAILYQLEV
QGKHCDLVRRLRQEMRPFLFTAEENISPPLELDFRLVSRALTAPQSRQVGAVDAAGVDWHGQRLEFLGDAVLKFVVSCYL
FFHVHEGKPAESRADAERKETEKEETGLESGEPGDAEAAEEVEEQVEEPESKETGGEREEREEGEEEEARWKFLFSLLT
```

```
QEEAGRFFGGVDEGVLSRLRQHYVANDYLRFAMRRFRLQAYLVNFPFVSHKKSLLDLREQPVSEKAQADVIEALLGAVYL
SNADSALFGAQPGKRSGGKETTGKTEDREATEKRGGTEENEREGERREKEREGRGRDVGENVSKKETEGRVDKRQAVHRR
PREMRHRGLDKETTEEREEQAVVGSSSGCMAAAAFFDAYLLLPSAVNNAVLLFDEEVEREKGRRETGERDNKLKEREESE
EDRLSHEGVALAPDGAGEQREVPDRQEKETLEHWKALLVDCLEEALRRRDRGVSVSDLGEDRHKEENAFPCSAKDINRDA
WMLLPDRLAKQTEDLRALARLPHMSETFLLLSRATNRQRTPHNGLSHDDEETEEEEDETEEEEEDGTEEEGDETEEEEED
ETEEEEEDEIEEDESGVWREEPSRREVEASQRVWMSKIFSRYDTDGGRGDLDRVMAVDSVQLIYRGPRQSLLSSLQEGKK
RANLETSGDRDHLRRCLLLLSETVRGCASNASVLRMWSSTGNATREERRAQKVGEKGRVEKKKKTERTQNEEEEQKEQSL
HRKEGNAGGTAKAQTNRRTEGSPSCVSSTSFASSLSSSSSSLSSPSSSLSSSSSSSSPPASSSLSSFCGRREREFPLKGL
LTAARNRDVVSARVFRAPCSLL
```

2523 - 2542:	EEEEEEEEEEEEEEEEEEEE
2524 - 2543:	EEEEEEEEEEEEEEEEEEEE
2525 - 2544:	EEEEEEEEEEEEEEEEEEEE
2526 - 2545:	EEEEEEEEEEEEEEEEEEEE
2527 - 2546:	EEEEEEEEEEEEEEEEEEEE
2528 - 2547:	EEEEEEEEEEEEEEEEEEEE
2529 - 2548:	EEEEEEEEEEEEEEEEEEEE

A0A086STZ3 **A0A086STZ3_ACRC1** (203 aa)
Cupin_5 domain-containing protein. *Acremonium chrysogenum (strain ATCC 11550 / CBS 779.69 / DSM 880 / JCM 23072 / IMI 49137)*

```
MPTPPTNSTLASTLASPTAAAAAAEIISLLNLEPYSEKGYLHETFRDPITTGTGSNRSASTAIYYLLEGRAGYSLWHKVV
DAAEVWHYYASAPLTLELVYEEEEGEEGEEEEEEEEEEEEEEEEEEEESGRGKKEEEIRLGVDLRAGERPQGVVPRGVW
QRARCLGEWTLVGTTVAPGFEPSGFVLMPEGWQPGDPEPAKAE
```

109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE

A0A087FZH2 **A0A087FZH2_ARAAL** (503 aa)
eIF2A domain-containing protein. *Arabis alpina (Alpine rock-cress)*

```
MELLEIRRNKYKKLNSYISLGVINDLQWSPLGSYLLSVRGGDAFLSGFKQSYYPNLQRYHHQDHEVKLADFSPGEKYLVT
YSSPKLPKKSIPSELQIFDVRTAIPMVGAMMGEYDEGFAKVSWPLIRWAQGKDDKYFATLGKNSISVYETNTFNLLSEKK
NPMEVEDVVDMCWSPTESIFAVLNVCGKVALVEIPSMVELHNEQLPDDVDVVNGKMYWQSNGEYLAVKFDRYVFILSGIR
DRDIQIEVLEVNKKIHAFAWEPTGHRFALIIHRSHSSPIISFYSMQKPGSLGKVSEIATFNDKEVDTLLWSPRGNDIVLA
GLKGSGILKFFDIEKRVMNKREHPKATAAAWDPTGRYLASAYTISPDMEKGFKYGFNTLLLGDHINGVNIETNPVYTRAT
NVLNIWSLEGDKLYSKSILKEYPLLQLNWRPYGGEIVDNETLNSQLKQMEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEDYSKEIESARAAMVVILEG
```

450 - 469:	EEEEEEEEEEEEEEEEEEEE
451 - 470:	EEEEEEEEEEEEEEEEEEEE
452 - 471:	EEEEEEEEEEEEEEEEEEEE
453 - 472:	EEEEEEEEEEEEEEEEEEEE
454 - 473:	EEEEEEEEEEEEEEEEEEEE
455 - 474:	EEEEEEEEEEEEEEEEEEEE
456 - 475:	EEEEEEEEEEEEEEEEEEEE
457 - 476:	EEEEEEEEEEEEEEEEEEEE
458 - 477:	EEEEEEEEEEEEEEEEEEEE
459 - 478:	EEEEEEEEEEEEEEEEEEEE
460 - 479:	EEEEEEEEEEEEEEEEEEEE
461 - 480:	EEEEEEEEEEEEEEEEEEEE
462 - 481:	EEEEEEEEEEEEEEEEEEEE
463 - 482:	EEEEEEEEEEEEEEEEEEEE
464 - 483:	EEEEEEEEEEEEEEEEEEEE
465 - 484:	EEEEEEEEEEEEEEEEEEEE

A0A087G4Q2 **A0A087G4Q2_ARAAL** (179 aa)
Uncharacterized protein. *Arabis alpina (Alpine rock-cress)*

```
MHRRFLNLTINTGRARRFPAVRASSSNGAGDSPTTPVPPSQSPAYVPPSPPPSQSPVSVPPSPPPSPFSVFFPTYSKMKE
EEEKEKEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEEEEEEEEEEEEEGEEEEAAEEAEEEEAEEKREF
REYWEQEREMNKHIYYAMK
```

89 - 108:	EEEEEEEEEEEEEEEEEEEE

90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE

A0A087H2X3 **A0A087H2X3_ARAAL** (196 aa)
Uncharacterized protein. *Arabis alpina (Alpine rock-cress)*

```
MSVAILSFDHCLCRYLVHHHLVHRLRLVHRRPPLPSTFTIIHHFFRSRDKEIEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEKEEEEREKRG
```

53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE

84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE

136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE

A0A087QVI5 **A0A087QVI5_APTFO** (164 aa)
Protein FAM163A. *Aptenodytes forsteri (Emperor penguin)*

```
MTAGTVVITGGILATVILLCIIAVLCYCRLQEEEEEEEEEEEEEEEEEEEEEEPDLATHSHLGTCNACNSRMVDGQGSPA
PPPSELNQHGAHNYCPTCSPYGSPFYIRTADMVRNGGERVTYTPACYKEMGPPINMATLQSYPVSRHSLLRESFPNPRAI
STEV
```

32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE

A0A087R877 **A0A087R877_APTFO** (842 aa)
B-cell lymphoma/leukemia 11A. *Aptenodytes forsteri (Emperor penguin)*

```
MSRRKQGKPQHLSKREFSPEPLEAILTDDEPEHGTLGAPEGDHDLLTCGQCQMNFPLGDILIFIEHKRKQCNGSLCLEKA
VDKPPSPSPSELKKASNPVEVGIQVTPEDDDCLSTSSRGICPKQEHIAGKLKQGEVFASSFPFQLQRSMFAVVNCCVCLS
VLLAVTADVLNTLPSVSGKDEPSSYTCTTCKQPFNSAWFLLQHAQNTHGLRIYLESEHGSPLTPRVGIPTGLGAECPSQP
PLHGIHIADNNPFNLLRIPGSVSREASGLGEGRFPPTPPLFSPPPRHHLDPHRIERLGAEEMALATHHPSAFDRVLRLNP
MAMEPPAMDFSRRLRELAGNTSSPPLSPSRPSPMQRLLQPFQPGSKPPFLATPPLPPLQSAPPPSQPPMKSKSCEFCGKT
FKFQSNLVVHRRSHTGEKPYKCNLCDHACTQASKLKRHMKTHMHKSSPMTVKSDDGLSTASSPEPGTSDLVGSASSALKS
VVAKFKSENDPNMIPENGDEEEEEEEEEEEEEEEEEEEEEEEEEEEGMSLEAARHHENNSRAGEEGRSMPDVMQGMVLS
SMQHFSEAFHQVLGEKHKRGHLPEPEAHRDTCDEDSVAGESDRIDEGAVNGRGCSPGESASGGLSKKLLLGSPSSLSPFS
KRIKLEKEFDLPAAAMPNTENVYSQWLAGYAASRQLKDPFLSFGDSRQSPFASSSEHSSENGSLRFSTPPGELDGGISGR
SGTGSGGSTPHISGPGPGRPSSKEGRRSDTCEYCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQSSKLTRHMKTHG
QVGKDVYKCEICKMPFSVYSTLEKHMKKWHSDRVLNNEIKTE
```

500 - 519:	EEEEEEEEEEEEEEEEEEEE
501 - 520:	EEEEEEEEEEEEEEEEEEEE

502 - 521:	EEEEEEEEEEEEEEEEEEEE
503 - 522:	EEEEEEEEEEEEEEEEEEEE
504 - 523:	EEEEEEEEEEEEEEEEEEEE
505 - 524:	EEEEEEEEEEEEEEEEEEEE
506 - 525:	EEEEEEEEEEEEEEEEEEEE
507 - 526:	EEEEEEEEEEEEEEEEEEEE
508 - 527:	EEEEEEEEEEEEEEEEEEEE

A0A087RJ47 **A0A087RJ47_APTFO** (876 aa)
Beta-1,4-N-acetylgalactosaminyltransferase (EC 2.4.1.244) (Fragment). *Aptenodytes forsteri (Emperor penguin)*

```
SSASLVPQYKGKANLHVFEDWCGGAVRHLRKNLHFPLFPHTRTTVKKLAVSPKWKNYGLRIFGYIHPFKDGDFQFSVASD
DNSEFWLSSDESPSNSRLAAFVGKLGTEWTAPGEFTKFSSQVSKPLRLMSSRRYYFELLHKQDDRGSDHVEVGWRVFLPS
LKFEVIDSSYISLYTDESSLKMNHVEHIPQTLASHSGSYLWEAQQDEHGADMLKSDPRDTFFLTPAIEASRVENVLVPCA
YSPTYVVKDFPIARYQGLQFVYLSFVYPNDFTRLTHMETENKCFYRESPLYLENQNPWGIYVRLYSLDFLEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGVDSPEPTDPPSEAKEKSFGP
VAEAKGKETLPVTGDYGDDLDYYSFRRKQGQARDEASMPGQPGRWSTTAATTDYNSSEVTHSEGTRVTSFLKMSETTASQ
QEEGRGQEEEEEEEEEVSDYSYETGELQQSWLEDSINWQRTFSVSSVDFELLRSDWNDLRCNVSGNLQLSESEVVDVVAQ
YMEKLNEKNGGIYTLLRIVNVEKRRDTARGNRYLLELELAERGQRTVRLSEYVYVLLHQGKQDDSAEANPEGPALGATEP
QPSTWSILYGRPVLCRPLRLSWKQDVMVHFVVPVKNQARWVQQFISDMARLYGATKDANFNVILVDFDSDDMDVEKALQD
ARLPRYQYLRRTGNFERSAGLQAGVDTVEDGHSIVFLCDLHIHFPPNILDSIRKHCVEGKLAYAPIVMRLSCGSSPREPN
GYWEVNGFGLFGIYKSDFDRVGGMNTEEFRDRWGGEDWELLDRVLQSGLEVERLRLRKLYHYYHSKRGMWNTRSKK
```

311 - 330:	EEEEEEEEEEEEEEEEEEEE
312 - 331:	EEEEEEEEEEEEEEEEEEEE
313 - 332:	EEEEEEEEEEEEEEEEEEEE
314 - 333:	EEEEEEEEEEEEEEEEEEEE
315 - 334:	EEEEEEEEEEEEEEEEEEEE
316 - 335:	EEEEEEEEEEEEEEEEEEEE
317 - 336:	EEEEEEEEEEEEEEEEEEEE
318 - 337:	EEEEEEEEEEEEEEEEEEEE
319 - 338:	EEEEEEEEEEEEEEEEEEEE
320 - 339:	EEEEEEEEEEEEEEEEEEEE
321 - 340:	EEEEEEEEEEEEEEEEEEEE
322 - 341:	EEEEEEEEEEEEEEEEEEEE
323 - 342:	EEEEEEEEEEEEEEEEEEEE
324 - 343:	EEEEEEEEEEEEEEEEEEEE
325 - 344:	EEEEEEEEEEEEEEEEEEEE
326 - 345:	EEEEEEEEEEEEEEEEEEEE
327 - 346:	EEEEEEEEEEEEEEEEEEEE
328 - 347:	EEEEEEEEEEEEEEEEEEEE
329 - 348:	EEEEEEEEEEEEEEEEEEEE
330 - 349:	EEEEEEEEEEEEEEEEEEEE
331 - 350:	EEEEEEEEEEEEEEEEEEEE
332 - 351:	EEEEEEEEEEEEEEEEEEEE
333 - 352:	EEEEEEEEEEEEEEEEEEEE
334 - 353:	EEEEEEEEEEEEEEEEEEEE
335 - 354:	EEEEEEEEEEEEEEEEEEEE
336 - 355:	EEEEEEEEEEEEEEEEEEEE
337 - 356:	EEEEEEEEEEEEEEEEEEEE
338 - 357:	EEEEEEEEEEEEEEEEEEEE
339 - 358:	EEEEEEEEEEEEEEEEEEEE
340 - 359:	EEEEEEEEEEEEEEEEEEEE
341 - 360:	EEEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEEE
344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE

346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE

A0A087TX68 **A0A087TX68_STEMI** (236 aa)
Uncharacterized protein (Fragment). *Stegodyphus mimosarum (African social velvet spider)*

```
MEEDSTPSESPTPCKIRRRDDVWPPKSPSVRYLPRTGFSPTIMREGGQGKKFIWPPPKEGQEHHLNDVDQLPHGNVGQVW
NPEANALGNRPPPFAPRTAPTKRCTDDIWPPRGSEYQPGHKPSPRPVKTVGRFEDYIKCRSGPSVPPTYRTPPGTQHIQV
TELEGEYIHETKTTTTVMTNSTATRNIVNRPPAQTAPVARRVEVEEEEEEEEEEEEEEEEEEEEEEEEEEEESEEE
```

205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE
208 - 227:	EEEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE

A0A087VJB5 **A0A087VJB5_BALRE** (302 aa)
Bone sialoprotein 2 (Bone sialoprotein II) (Cell-binding sialoprotein) (Integrin-binding sialoprotein). *Balearica regulorum gibbericeps (East African grey crowned-crane)*

```
MRTALVFACLVGMACTFSVKSWLRQSKLDDSEENAVFKNRHRYYLYRYAYVHPLQRRYQGSDSSEEEGDGSEEEEEGGLP
RAGMAVTLCLPTMAGFICWWQAGHPAGAAPGDSQGALKGGRNSAAGKGGDSENEDSDENEEEEEEEEEVSENENGINGTS
TNTTKGEDGPHGNGTAVAEEGTGMAGEEEEEEEEEEEEEEEEEEEEESEATTIASTTSEEGLSQATTTGDGGPTDTTTAG
EQWEYEVTAGGRGRGDEGTTDGSYGEQDEYTRGDSYRAYEDEYGYYKGHGYDVYGQDYYYSQ
```

187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE

A0A087VZI1 **A0A087VZI1_ECHMU** (320 aa)
Uncharacterized protein. *Echinococcus multilocularis (Fox tapeworm)*

```
MKVEEEEESVGFEQSAEIYPFTHPLGQHVSGAEAASSCGSGASTLSLSDAPRILIAFVNLHVSATLLKSSPTETTDDDII
TTSLPRFEYVFACSPLLFPECQFICLHSSPTLSRTEEEEEEEEEEEEEEEEEEEEEFPSIALFFYYCGKVHIRNNAIRVM
CLLRDEVSQGSRPQVTCVETDHEARDSVSHVESCRVVTHLCLGVVLPDLEVEEAATLKVVVAWNWRCCYQDSAEKDDENE
DKVDTFCLMPFLLSDLHVGMFYDCVKPSISEHSISFGHQFFTFQKKKKKKKEEEEEEEEEDEEPFLATLQMYRIGVGCVE
```

116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE

A0A087W0F0 **A0A087W0F0_ECHMU** (112 aa)
Uncharacterized protein. *Echinococcus multilocularis (Fox tapeworm)*

```
MGGTKGKREDNEDDYHVGKRRKRLEEREEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEECILRLL
NWDSSLRRKNSGQLTHTDKFGRKVQAPTFQQR
```

31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE

A0A087W0P0 **A0A087W0P0_ECHMU** (212 aa)
Uncharacterized protein. *Echinococcus multilocularis (Fox tapeworm)*

```
MNTRGCRRKMWCCGALNMKRLEEREEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEECILRWVEVANPNAVTCPQ
MLVGFVGVLWTKLPPLECVSTLDGCGHMRMGFIVGNAIFMMSGSASTNDVCFGMALCLHSILSMRLLLLPDACGVVAGIV
EVRKKAARKYLLCTGNAAFKGGCGSPTFAVEFCLSYALLSNRIDMVQLSDMA
```

28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE

A0A088RHQ6 **A0A088RHQ6_9TRYP** (1338 aa)
Phophatase-like protein. *Leishmania panamensis*

```
MPTRPQQQQHLRQPPLKQLPQMREDGGIGGDHDDSQASSPFSCGTSSWSLRASASAMAAVNDSPDDGGGAEMTSTGGSD
DGDDSGGNGRVAALLNSKNSQQRQRQSCRHSRVSPCVKSTRKAAGSDPVCISSLESGLGRAAAAAVLSTTSLVRPLQAPV
TSTSAVAKDRVAYYSPPSSNLRPANACISAAGSPRDTCASRILSDSKGIEAGTLSNKNNHSGSPRAAAHAVMPGSEPSSQ
AGRISNHSGGGSVGAFAIHDSVDGDAWRTEDCCTPETALRLDGEGGTGAHTSPPSPATAAANTMPLTYAAVASSLHGKRL
PQSRIGFSQWRKRVCCGSASLPSTIGSTSTTPGITSATTANTTVAESTAHASLEDSLKNSVPSISPSLTIPSVVTTANPS
```

```
RATDKSTPTSSPYLGGDGEASFPNSDEHFSTNEGPQHPSATLMMPPLPQSVHRHQPTHLILQLPNAPLSQQQHNGPDSEE
EEEEEEEEEEEEEEEEEEDITYPDFPCTAVAPRAAATASELSSSAKLPAKSRCAVTESAAPSLLLPVSEGTPVTRVRTPG
APMAAQQLLRIQRPLITPSPMAFTPTASAAARVAAGKGMHRATSTAPSFNAAQILPGLFLGSYAEATDTATLAEHGVSLV
INCAFDCPVTSVMANNNHHVRYVQFPLRDHSDEVIAPFFAPVTRIIHDQLHRRQVHQQCMARRTAASAPSADANNTEEHQ
AQDCMLWAWTDEGENVWAVPPSPVTPSMSVDGQQSFENRRETPPTPPSLPGLGERLGEGVECRRTTTSFSVPALSSSPLT
IVDPRDCGGVLVCCRMGVSRSATFIIAYLILYGCTLAPLDDTASLFASFLERERRIIEEAGGVTSFTDDDSGGVPTTTST
ATAISGRGSGSTNRPALAFPSLSLPQSPPSSASANTPFASRGSPKANGSQSFLQRHFSTNSPWIRRRSSTIPVSSPLSFG
GNCSGGGYAAGPLTTPLSGNPSAMSQQQQQQQRLRMASPPTPIEFASRMCQPCYLMHLRERRLQQAAQRRMLISGQPQQR
LREQSDEEHQMRRHMPARELGKEYGRRGDIADGSNFGGSSSTTTINSCDDLRPEEQQYHYSRCVVSVLPSSAPVASHRSA
RGSCRMTLLEAAYADERTQDEDGVDEMTPPQQKSEAMWTPRRGGARMANEQRLENRSAGSATTTPRVASTATQHRNAFST
CKVCVAAEEAAATTLGSSAVASMRRGHSKNVYGTPLLPGEQQHALSRCSYAPHSLQTPMNGSIHGDLNTSMNTLLGFSFA
SSDGGSPGAFGSVPPVMTYRDAFDAVKRQKADVNPNIGFVLALRELASGGDFSFSMSF
```

479 - 498:	EEEEEEEEEEEEEEEEEEEE

A0A090M8D4 **A0A090M8D4_OSTTA** (392 aa)
DEK, C-terminal. *Ostreococcus tauri*

```
MDAVRAPSDAMGDGSDGRGRGKRARKAVETFVVDVAPARASKIEIGRGKGTKLSEIPNVAFRLSKISRKEDILKFIYRVL
YKGTPRQLTVKRDIGEFSGWTFESDGERAVKEDLLMRAYKETLHEILDLFEVPRGSGAEAKKESQVARLMAFLDAPKASG
KKSLAEAAEKKKKAKDRQRTTKSATSAKKDAASGGGLAKHVALIKKLRAENAALKKKIVELTGKEEAEEDGDDEEEEEQE
EEEEEEEEEEEEEEEEEEESEDEEDSDEEFTAKNPAPKKPKPTPAPAKEAPKSSDAPKPAPPTPKSAPVEPTQPKPLEQT
PQPEQAAQQPTKPAPSAEDLASAIRTMLASADMSEVSMKTIRKDMEAKFGISFADRKEEIKTVVTSFIENQA
```

240 - 259:	EEEEEEEEEEEEEEEEEEEE

A0A090XAN9 **A0A090XAN9_IXORI** (388 aa)
Putative troponin t skeletal muscle. *Ixodes ricinus (Common tick) (Acarus ricinus)*

```
MTEAEMLMEEKLRKKKEEEEEMWAEYLEQRKKQRAKEEEELRKLKERQAKRKLQRAEQESKMNEYKRKQEEQRIREMEEK
KHREAEAKRKRLEEAEKKRQAMQAAKEKREQEPVKPNFVISKREGDETGFGTGKLRLGQVRQRSCTPAARWARPRSRWRR
IRRPSLSFRVKPLEIEGLTVEQLRDMAKKLWEKVVALESDKYDLEERQKRQDYDLKELAERQRQINRSRALKKGLDPEAL
QGKHPPKIQVSSKYERRLDRRSFEDKRELYDGGLEAMTDAEMEKMWEDRMNAFKEQCRGQLPKWDPENPKNKQVSHIRRL
EEEDDEEELVPVFEPPKPEPPKPAAPPPKPAQQQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE

A0A091CIU3 **A0A091CIU3_FUKDA** (71 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MKHKGREEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDKYSSPADIQVREVSDTTVFTWQPTN
```

7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE

16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE

A0A091CK95 **A0A091CK95_FUKDA** (255 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MTENMQEFSGEDMIYEKGYGFQNVTIVHRRNAAAPGERVSSRCLNAPSSREPDRPVGHPGGRSAARAGTAAGSRCSWGAR
AGYRPQAAVQVLMDFKVQRRGCTGDGDPRRCLLLRGAKLTQQKATASLLVNFPLLSFGKRGDKGGVEAFSVQLHLTEGIP
GCVASRRARREEGRGRRQRVREEEEEEEEEEEEEEEEEEEEEERGRVEEEEEEEEEEEEEEEEGEEEEEEEEEEEEEEGE
EEEEEEEWNRKEKKR
```

182 - 201:	EEEEEEEEEEEEEEEEEEEE
183 - 202:	EEEEEEEEEEEEEEEEEEEE
184 - 203:	EEEEEEEEEEEEEEEEEEEE

A0A091CKE9 **A0A091CKE9_FUKDA** (86 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MAQLPEAKNQTGGTNPTSRDAREEEEEKEEEEEEEEEEEEEEEEEEEEEEEEEERGRRRNGIKKRREKTISLVYPTSVGT
GFLKVT
```

29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE

A0A091CKQ5 **A0A091CKQ5_FUKDA** (131 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MCLRLSKMNPPNVPTDLDKQLKCSVNAQINPVIAGEQFKFAMSLEDEFSSSSSNISVNKGRIKQLKKKKKKKKKKKKKKK
KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKEEEEEEEEEEEEEEEEEEEEECKQ
```

109 - 128:	EEEEEEEEEEEEEEEEEEEE

A0A091CKT6 **A0A091CKT6_FUKDA** (133 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MKKKVKKANKEEEEEEEEEEEEEEEEKEGGGGGGGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEERRGRSPLPNRKNNGIDRLYFLKCISVHGAFD
```

35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE

43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE

A0A091CM08 **A0A091CM08_FUKDA** (120 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MQVMDGVTMQASAGNGNGLKTRTFSHLGKVNGDEETTGASAQRNHGVQKEEEGGEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVSERL
```

55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE

61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE

A0A091CM59 **A0A091CM59_FUKDA** (167 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MGRNPLPGSAGLIPALDVLQKCPGPSLEQSGEYWHSCSGASTAFTPHALGPPGCAGTGSILQRRKKKKKKEEEEEEEEVE
EEEEEEEEEKEEEEEEEEEEEEEEEEEEEEEEEEEGERERERKKERKKERKEGRKEGRKEGRKEATRRKKGKERKEGKR
QETKHRI
```

91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE

A0A091CML5 **A0A091CML5_FUKDA** (114 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MLPPPVAAAGPSLATGEGEGEKKEEEEEEEEEEEEEEEEEEEEEEKGIILMLKFPGRIQYGVKTAFRIGDDAGDRQPQTP
```

```
LMSKTRSPVERVGLASPNDSFHFGIKCMHDPRVL
```

24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE

A0A091CMM0 **A0A091CMM0_FUKDA** (130 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MSSFIVQVGWADICTDPALSSRFCIAGYSGNKGEGEEKGGGEGGRSRSRRRKEEEEEEEEEEEEKEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEDGKRRWRMGRTGRSLNEEEELDRLREEDLAI
```

66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE

A0A091CMY0 **A0A091CMY0_FUKDA** (84 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MATIRSSHLCPPTALMSTSRHEIKDEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
TVKH
```

32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE

54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE

A0A091CN41 **A0A091CN41_FUKDA** (170 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MEETSLFLTPAESIRKTFLLVVLLNSNSLTEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
KKKKKFLTTF
```

31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE

70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE

122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE

A0A091CN61 **A0A091CN61_FUKDA** (100 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MKKRKKKEEEEEQEEEEQEEKEQEEQEDEKKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGRRRRRRRRKKKKKKKKK
KKKRRRRRRRRRRKKKKKTA
```

33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE

A0A091CQI2 **A0A091CQI2_FUKDA** (200 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MDLAWSRLKNENDSAQWWSELGFQARLYIGLILRGFLKILALKQKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVVQDLSSRSQQKHWCFVEKDNKGRFWGLHNGTVGNLDNLAS
GIISTSGGADKRLQLEHCSQRLSPRNYICHFGKDPSPARF
```

47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE

57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE

A0A091CQX4 **A0A091CQX4_FUKDA** (1488 aa)
Zinc finger protein 827. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MYSRSNLFKAHFVITSKGVSDESLSQQEFLGAAGAVYLEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKRRRR
KRKKKEWHSDRAKDVSRQEEAEAELSEGEHWYGNSSETPSEASYGEVQENYKLSLEDRIREQSTSPDTSLGSATPSSHTL
ELVALDSDVLRDSLQCQDHLSPGVSSLCEDDPPGSNKPLSSNLRRLLEAGSLKLDATATANGRVESPVNAGSNLSFSPPS
HHAQQLSVLARKLAEKQEQSDQYTPSNRFIWNQGKWLQSSTTTCGLSPDSAILKLKAAANAVLQDKSLTRTEETMRFESF
SSPFSSQSASSTLAALSKKVSERSLTPGQEHPPPASSFLSLASMTSSAALLKEVAARAAGNLLAEKSSLLPEDPLPPPSE
KKPEKVTPPPPPPPPPPPPPPPQSLELLLLPVPKGRVSKPSNSGCGVFNSLRVHHLIAFPPRQRDTIEWKIKLEMERSAL
IPGLPLTKEQKAFPTPPQFRFLTSSEEESGKPFQCPICGLVIKRKSYWKRHMVIHTGLKSHQCPLCPFRCARKDNLKSHM
KVHQHQDRGETFQCQLCPFTSSRHFSLKLHMRCHQHFLRTEAKVKEEIPDPEVKGSPHLSDSGCLGQQREGGGTELVGTV
MTSNTPERTSQGGAGVSPLLVKEEPKEDNGLPTSFTLNAADRPANHTKLKDPSEYVASSAAALFSQDISVKMASDFLMKL
SAANQKEPMNLNFKVKEEPREEEALSTTLPRSSYVFSPEPEVAAPSISEDSLKPQEGKASVLRRDMSVKAASELLMKLSA
ESYKETQMLKIKEEPMEVDIQDSHVSMSPSRNVGYSTLIGREKTEPLQKMPEGRIPPERNLFSQDISVKMASELLFQLSE
```

```
KVSKEHNHTKENTIRTTTSPFFSEDTFRQSPFTSNSKDLLPSESVLHGRISTPETEKIVLEAGNGLPSWKFNDQLFPCDV
CGKVFGRQQTLSRHLSLHTEERKYKCHLCPYAAKCRANLNQHLTVHSVKLVSTDTEDIVSAVTSEGSDGKKHPYYYSCHV
CGFETELNVQFVSHMSLHVDKEQWMFSICCTACDFVTMEEAEMKAHIGTKHTGEDRKTPSESNSPSSSSLSALSDSANSK
DDSDSSQKNKGGNNLLVISVLPGSQPSVNSEEKPEKGFECVFCNFVCKTKNMFERHLQIHLITRMFECDVCHKFMKTPEQ
LLEHKKCHTVPTGGLKCPFCIYSTNRPAAMECHLKTHYKMEYKCRICQTVKANQLELETHTREHRLGNHYKCDQCGYLSK
TANKLIEHVRVHTGERPFHCDQCSYSCKRKDNLNLHKKLKHAPRQTFSCEECLFKTTHPFVFSRHVKKHQSGDCPEEDKK
GLCPAPKEPAGPRAPLLVVGSSRNLLSPLSVMSASQALQTVALSAAHGCGSEPNLALKALAFNGAPLRFDKYRNSDFAHL
IPLTMLYPKNHLDLTFHPPRPQTAPPSIPSPKHSFLAYLGLRERAETV
```

39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE

A0A091CRA0 **A0A091CRA0_FUKDA** (86 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MVAPRFFLACAPTPGVRAAASVWGLCACADGIGGLWLGLRALTEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGRRRR
RGRRKT
```

44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE

A0A091CRA4 **A0A091CRA4_FUKDA** (89 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MLDSPPEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKKKIVKHIAYLQHRGPSGELGLERIMELLHHSNGVSLR
VFRSELPKE
```

7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE

12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE

A0A091CRB6 **A0A091CRB6_FUKDA** (117 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MRTKTCHVKEQDPNDEGDCTVSLKSTNKLNEKKNKPYCEMILLSIKDHEEEEDDEEDDEEEEDDDEEEEEDEEKEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEIWMTQST
```

75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE

A0A091CRE4 **A0A091CRE4_FUKDA** (84 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MHQRSQLFKGTWQRKKKRGEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDESLSNESNR
HLIY
```

23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE

36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE

A0A091CRI9 **A0A091CRI9_FUKDA** (68 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MRNVDKVVKEEEEEEEEKEEEEGGEEEEEEEEEEEEEEEEEEEEEEEEEQEQEEEEEEEEEEEEEDD
```

25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE

A0A091CRN7 **A0A091CRN7_FUKDA** (156 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MGRRLVVPYLDYFMEFGYWNNSSGYIMDDITNGGDIYEISLKEKKKEEEQEQEEEEEEEEEEEEEEEEEEEEEEEEEK
EEEEEEEEEEEEEEEEEKEEEEEEEEEEEEEEEGGGGGRGRRRRRRRRRRRRRKGGGRRKEKKIYNLCLNFEIVS
```

53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE

A0A091CRQ7 **A0A091CRQ7_FUKDA** (181 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MSAAGGGNVGRTGKVPEEEEKEEEEEEEVRRDEEQQISRPGDLSVNHSNSKQNNREEEEEKEGKRKRKRKKNKKKRRRRR
RGRGRRRRGGGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKNTERVADPMGKDKPGNREKLTTLNPF
LREIRRNSAPTRSKVNIMKRR
```

92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE

97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE

A0A091CT05 **A0A091CT05_FUKDA** (117 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MLVWWQVMQCGYSMGFKIGHVMSGVHFWQVPINSIKKKREEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEE
EEEEEEEEEEEEEEEDLAIREWRGKSGSRENSVNAP
```

40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE

A0A091CT20 **A0A091CT20_FUKDA** (1165 aa)
Histone-lysine N-methyltransferase EHMT2. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MGALLLEEPRGAPERVPGSLGDTPHGEETLPKAKPDSLEPTGPSSPASVTVTVGDEGADTPVGAAPILGDDAENLEGEGS
RVLLGHATKSFPSSPSKGGACASRAKMSMTGAGKSPPSVQSLAMRLLNLPGAQGPAAVGPEPTPATTVSPEGQPKVHRAR
KTMAKPGNGQPPVLEKRPPEVQHFRMSDDVHSLGKVASDVAKRRKLNPGGGLSEELGSTRGSGGVTLDKGDPRSLEEWET
VVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKA
KKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGPSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEE
LPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNTAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCT
AGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGGTPPAGTAAPAPPPLAQDAPGRADTSQPS
SGPSLTLPSGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSK
RTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLE
MVGLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIDVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLH
AVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRD
VARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQE
FNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSY
LFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKY
```

FTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNT

276 - 295:	EEEEEEEEEEEEEEEEEEE
277 - 296:	EEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEE

A0A091CT61 **A0A091CT61_FUKDA** (122 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

MNAPVGLAGDSREQRRQFQVMRVPIPASHTMSLGISQSGDETVEQGRGVPRVRYRKERNEEGKEEKEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEENNKKNGPLQGMSLLSLVNIVGSSM

67 - 86:	EEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEE

A0A091CTF5 **A0A091CTF5_FUKDA** (177 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

MPAAVAHELLDSRAKFLSFTCVGSHGNGFINDANFLQSREIYLKINSMKSFVVLRIRIEKKKEELGGVEEKGEEGEGEGE
EEEEEEEEEEEEEEEEEEEEEEEEEEEERRRRRRTRRRRQRRGRGRAGGGGQGEKRGRRKRSRNYRKKRTVNSNKILIEN
ELSTVLVAKANLKHLDK

80 - 99:	EEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEE

A0A091CTP9 **A0A091CTP9_FUKDA** (416 aa)
Olfactory receptor 8H2. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

MPDFILMGLTDSAETQLVLSVLFLLIYLITVLGNSGMILIIRLDPQLHTPMYFFLTHLSFLDLNYSSVITPKTLQNLLTS
TKSISFLGCFTQMFFFIVFVAAEGFILSSMAYDRYVAICRPLHYPVIMSPRLCWSLLSGCYVMGFAYSTVIEISMTRLHF
CNSNVIQHFFCDTSPILALSCSNTYEAEITIFICAGSNLLLSLSTISASYLSILSTILKINSTAGKKKAFSTCASHLLGV
TIFYSSTIFTYLKPKTSYSLGRDQVASVFYTIVIPMLNPLIYSLRNKEVKNAALRVLKKGEEGGRKEEEGGGRRKEEGGR
RKEEGGRKRKRKRKRKKKRKRKKKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEKR

346 - 365:	EEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEE

348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE
379 - 398:	EEEEEEEEEEEEEEEEEEEE
380 - 399:	EEEEEEEEEEEEEEEEEEEE
381 - 400:	EEEEEEEEEEEEEEEEEEEE
382 - 401:	EEEEEEEEEEEEEEEEEEEE
383 - 402:	EEEEEEEEEEEEEEEEEEEE
384 - 403:	EEEEEEEEEEEEEEEEEEEE
385 - 404:	EEEEEEEEEEEEEEEEEEEE
386 - 405:	EEEEEEEEEEEEEEEEEEEE
387 - 406:	EEEEEEEEEEEEEEEEEEEE
388 - 407:	EEEEEEEEEEEEEEEEEEEE
389 - 408:	EEEEEEEEEEEEEEEEEEEE
390 - 409:	EEEEEEEEEEEEEEEEEEEE
391 - 410:	EEEEEEEEEEEEEEEEEEEE
392 - 411:	EEEEEEEEEEEEEEEEEEEE
393 - 412:	EEEEEEEEEEEEEEEEEEEE
394 - 413:	EEEEEEEEEEEEEEEEEEEE
395 - 414:	EEEEEEEEEEEEEEEEEEEE

A0A091CUP6 **A0A091CUP6_FUKDA** (115 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MVTSSAPVTPGLAPTSIKKRSIILTWLKEALPLTFSTPQLHPTLKKERKKERKKERKKERKKERKKERKKERKKRRRRRR
RRKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKS
```

84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE

A0A091CW24 **A0A091CW24_FUKDA** (272 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MQDKQMMALDEAVEPRRRRKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
VEEEERKKKRKKKCPLQGMSLLLQVDNVGSSM
```

21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE

56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE

108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
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117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE

160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE
180 - 199:	EEEEEEEEEEEEEEEEEEEE
181 - 200:	EEEEEEEEEEEEEEEEEEEE
182 - 201:	EEEEEEEEEEEEEEEEEEEE
183 - 202:	EEEEEEEEEEEEEEEEEEEE
184 - 203:	EEEEEEEEEEEEEEEEEEEE
185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE
190 - 209:	EEEEEEEEEEEEEEEEEEEE
191 - 210:	EEEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE
194 - 213:	EEEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEEE
196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE
208 - 227:	EEEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEEE

A0A091CWD9 **A0A091CWD9_FUKDA** (76 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

MKKKKRKRRRRREEEEEEEEEEEEEEEEEEEEEVEEEEEEEEEEEEEEEEEEEEEEEEEEEEQKLKLRATAFQNITS

13 - 32:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE

A0A091CXN0 **A0A091CXN0_FUKDA** (413 aa)
Cyclic nucleotide-gated cation channel beta-3. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

MRDVIGAATANQNDFRVCMDHTVAYMNTYSIPQSVQSRIRAWFEYIWYSQRMLDESDLLENLPTTMQLALAVDMNFSIIS
KVDLFKGEIGKEMYIIKQGEIQVLGGPDGSQVLVTLKAGAVFGEFSLLATGGGNRRTTDVVAHGFVKLLTLDKKTLQEIL
VHYPDSEKLLMKKARDTKMFKALLGDRGKVDLGRLLKLKREQTTQSLYIMRPCLKESKTKNEEEEEERKKKKEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGSKYYKPFTFKRLKFTFLFLTCNTVMIFGLALTNACSPKDSLSLIIQ
YQFLITASSRKKSGNSKGERDKRKEDEDKGRGPAEKTLATSKDEASSITTQEKPQSSRRAVLPSENSRQSLIISMAPSTE
TEKEVLTRTQRKV

233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE
239 - 258:	EEEEEEEEEEEEEEEEEEEE
240 - 259:	EEEEEEEEEEEEEEEEEEEE
241 - 260:	EEEEEEEEEEEEEEEEEEEE
242 - 261:	EEEEEEEEEEEEEEEEEEEE
243 - 262:	EEEEEEEEEEEEEEEEEEEE
244 - 263:	EEEEEEEEEEEEEEEEEEEE
245 - 264:	EEEEEEEEEEEEEEEEEEEE
246 - 265:	EEEEEEEEEEEEEEEEEEEE
247 - 266:	EEEEEEEEEEEEEEEEEEEE
248 - 267:	EEEEEEEEEEEEEEEEEEEE
249 - 268:	EEEEEEEEEEEEEEEEEEEE
250 - 269:	EEEEEEEEEEEEEEEEEEEE
251 - 270:	EEEEEEEEEEEEEEEEEEEE
252 - 271:	EEEEEEEEEEEEEEEEEEEE
253 - 272:	EEEEEEEEEEEEEEEEEEEE
254 - 273:	EEEEEEEEEEEEEEEEEEEE

A0A091CY06 **A0A091CY06_FUKDA** (59 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

MEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDDDVACRLKTEFMAFQWS

2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE

8 - 27:	EEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEE

A0A091CYI3 **A0A091CYI3_FUKDA** (317 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MDSKFSPCNESISPGFEVPRRPSRKELQKCETTLHSSTFPSVKRLCEPEWFGYRKKKEEEEKEEEEEEKEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

70 - 89:	EEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEE

102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
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118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
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121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
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136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
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148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE

154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
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158 - 177:	EEEEEEEEEEEEEEEEEEEE
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169 - 188:	EEEEEEEEEEEEEEEEEEEE
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172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
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178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE
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181 - 200:	EEEEEEEEEEEEEEEEEEEE
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183 - 202:	EEEEEEEEEEEEEEEEEEEE
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187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE
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191 - 210:	EEEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE
194 - 213:	EEEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEEE
196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE

206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE
208 - 227:	EEEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEEE
225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE
239 - 258:	EEEEEEEEEEEEEEEEEEEE
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241 - 260:	EEEEEEEEEEEEEEEEEEEE
242 - 261:	EEEEEEEEEEEEEEEEEEEE
243 - 262:	EEEEEEEEEEEEEEEEEEEE
244 - 263:	EEEEEEEEEEEEEEEEEEEE
245 - 264:	EEEEEEEEEEEEEEEEEEEE
246 - 265:	EEEEEEEEEEEEEEEEEEEE
247 - 266:	EEEEEEEEEEEEEEEEEEEE
248 - 267:	EEEEEEEEEEEEEEEEEEEE
249 - 268:	EEEEEEEEEEEEEEEEEEEE
250 - 269:	EEEEEEEEEEEEEEEEEEEE
251 - 270:	EEEEEEEEEEEEEEEEEEEE
252 - 271:	EEEEEEEEEEEEEEEEEEEE
253 - 272:	EEEEEEEEEEEEEEEEEEEE
254 - 273:	EEEEEEEEEEEEEEEEEEEE
255 - 274:	EEEEEEEEEEEEEEEEEEEE
256 - 275:	EEEEEEEEEEEEEEEEEEEE
257 - 276:	EEEEEEEEEEEEEEEEEEEE

258 - 277:	EEEEEEEEEEEEEEEEEEEE
259 - 278:	EEEEEEEEEEEEEEEEEEEE
260 - 279:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE
262 - 281:	EEEEEEEEEEEEEEEEEEEE
263 - 282:	EEEEEEEEEEEEEEEEEEEE
264 - 283:	EEEEEEEEEEEEEEEEEEEE
265 - 284:	EEEEEEEEEEEEEEEEEEEE
266 - 285:	EEEEEEEEEEEEEEEEEEEE
267 - 286:	EEEEEEEEEEEEEEEEEEEE
268 - 287:	EEEEEEEEEEEEEEEEEEEE
269 - 288:	EEEEEEEEEEEEEEEEEEEE
270 - 289:	EEEEEEEEEEEEEEEEEEEE
271 - 290:	EEEEEEEEEEEEEEEEEEEE
272 - 291:	EEEEEEEEEEEEEEEEEEEE
273 - 292:	EEEEEEEEEEEEEEEEEEEE
274 - 293:	EEEEEEEEEEEEEEEEEEEE
275 - 294:	EEEEEEEEEEEEEEEEEEEE
276 - 295:	EEEEEEEEEEEEEEEEEEEE
277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE

A0A091CYS1 **A0A091CYS1_FUKDA** (93 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MKKRKKEEEEEEEEEEEEEEEEEEEEEENRRGERKKKKRCPLQGALDCAEESPDSRMSWKFSSLLETDNICTVLDEVLNWER
EHRRQAESFSVEI
```

7 - 26:	EEEEEEEEEEEEEEEEEEEE

A0A091CYS2 **A0A091CYS2_FUKDA** (229 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MLFISRTGVRREDPQPVFMCTTAKKEQEKPPCMAELLHCSLLKGLHSPAPWFPRSQKRLTEDGIPLPMHPFPYNVIQDGL
DALSWATPEKTQTPQVLDRSHLLKQVFEDKISRYFLVDPEKQFMDLRDLEWRYFKGLAKWKHTTVVSFVDIKYNSEKRFV
KRRDMSDVISVPLIQEEEEEEEEEEEEEEEEEEEEEEEEEEEEVASRDKGVLTVCQNGLHGSPAYKLH
```

176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE
180 - 199:	EEEEEEEEEEEEEEEEEEEE
181 - 200:	EEEEEEEEEEEEEEEEEEEE
182 - 201:	EEEEEEEEEEEEEEEEEEEE
183 - 202:	EEEEEEEEEEEEEEEEEEEE
184 - 203:	EEEEEEEEEEEEEEEEEEEE
185 - 204:	EEEEEEEEEEEEEEEEEEEE

A0A091CZ65 **A0A091CZ65_FUKDA** (546 aa)
DNA polymerase delta subunit 3. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MPFGYQLPTDAPTGDWKKKDKEEGEDGEGEEEEVEEEEERTRRKRKKKKKEEEKKEEEEEEEEEEEEEEEGEKEEEEEEE
EEEEEEEEEEEEEEEEEEEVTYKWLSYTLGVHVNQAKQMLYDYVERKRKENSGAQLHVTYLVSGSFIQNGHTCHKVAVVR
EDKLEAVKSKLAVTASIHVYSIQKAMLKDSGPLFNTDYDILKSNLQNCSKFSAIQCAAAIPRVPAESSSSRKFEQPNLQA
SNETPASNELTTNGHGPPPSKQVSHQPKGIMGMFASKTATKTQDTNKEPKTEAKEITNVSSAGSKAPGKGNTMSNFFGKA
AMNKLKVNLDSEQAVKEEKIVEQPPVSVTEPKLATPADLKKSSKKAEPVKMQQMEKKCNRVKRIELTDDETKETGNVKKK
```

```
RRRIKLPQSDSSEDEVIPDSPGTYEAESPSLPPPISSPPDPVRKTEPEPPSFKNSSGENKRKRKRVLKSKTFMDMEGCIV
TEKFFESESCTDSEEELTIKTSSGHRSPAMTVKKEPKEERKGPKKGTAALGKANRQVSITGFFQRK
```

74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE

A0A091CZM8 **A0A091CZM8_FUKDA** (126 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MVRQNSWNAMATAREEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERERERKRERGSLQKKTEDGEESVWALAGV
SACGVTAAHLPVHRNEWYTTAPCGLPGHLCSLGYSQVDQPLMLGIG
```

19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE

A0A091D092 **A0A091D092_FUKDA** (748 aa)
Disintegrin and metalloproteinase domain-containing protein 1b. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MLLLGIVLLPSIHGHLGPGHYSSYEIVIPKSLTVKGTEDPAEKTSYTLLMQGRKQRVHLKVRRDYFVHDFPVYSYHNGIL
GQEIPSISHDCHYEGYIEGVPGSFVSVNTCSGLRGILIKEQTSYVIEPILSSKRFEHALYSVAQQAPVSCSISPRDSQAV
STSQQQESRKPHDLQALSYLWSRTKYVEMFVVVNNQRFQMWGSDVNETVQRVVDVVALANVFTRGINTEVVLAGMEIWTE
GDLTEVPGDLQVTLRNFNSWRQGELLPRVRHDVAHMIVGHHPGGTWGQAFLSGACTSGFAAAVEAFHHEDALLFAALMVH
QLGHNLGIQHDHSACVCKGRHFCLMHETVTKESGFSNCSSDYLYRFLHEHKGACLFNKPRCKSRGRRDANCGNGEVEAPE
ECDCGSACDGDPCCEPTCKLKENAQCSRGLCCSKCKMLMRGHVCRQSIGPCDLPEYCDGVSAKCPADSYMQDGTPCHEQF
FCLKAQCTDPSIQCKNFFGFGSISAPEECYTSFNSKGDLFGSCGHSGNPVTYVSCSADNIKCGNLVCTGVSLLPLIKPLS
ALIQRPHENNWCWSTGTFQPDSSSAQNVLYGTPCANNKACVQAECTDFTLDTVNCSDSEMCNENGVCNNLGNCHCQDGFA
PPDCKTEGSGGSLDSGPPDKPSFVNPPTKAIEEESASKLPLIALILLGLLLLVLIICVCCCKRRAAAAAPLEKTAEEAEV
EEEEEEEEEEEEEEEEEEEEEEEEEDED
```

721 - 740:	EEEEEEEEEEEEEEEEEEEE
722 - 741:	EEEEEEEEEEEEEEEEEEEE
723 - 742:	EEEEEEEEEEEEEEEEEEEE
724 - 743:	EEEEEEEEEEEEEEEEEEEE
725 - 744:	EEEEEEEEEEEEEEEEEEEE
726 - 745:	EEEEEEEEEEEEEEEEEEEE

A0A091D0K5 **A0A091D0K5_FUKDA** (109 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MPDLDIPKDPTSLARGPPVLGHREKAPRNERPQRRTAAPGLAGGVGVYWEKRGFKEEEEAEEESEEVGAGAGAGAEEEEE
EEEEEEEEEEEEEEEEEEEEEEEERRRYQ
```

76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE

78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE

A0A091D2Y5 **A0A091D2Y5_FUKDA** (68 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MAHFSSQTCPLWDPGQFSQPFLFIQLDIREEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDKEEEESL
```

30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE

A0A091D3S2 **A0A091D3S2_FUKDA** (513 aa)
39S ribosomal protein L24, mitochondrial. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MWCAEPADGRALSTWPGLPHFSAPTVFTACCPGFSGSWVMAQPWIDEMPEATVKSTANKYQVFFFGTHETAFLGPKDLFP
YEESKEKFGKPNKRKGFSEGLWEIENNPTVKASGYQSSQKKSCSEEPEPEPEATEGDSDKKGNAEGSSDEEGKLVIDEPA
KEKNEKGPLKRRAGDLLEDSPKRPKEAEDPEGEKEAATLEGERPIPTEGEKNSTPSEPISSRGPPPEEEEEEEEEEEEE
EEEEEEATKEDAEAPGIRDHERAPVGPLAGSFRWIRSSHLLGILVALAMRLSALLALASKVTLPPYHRYGMSRPGSLADK
RKNRPWIRRRPVLVEPISDEDWHLFCGDVVEILEGKDAGKQGRVVQVIRQRNWVVLEGLNTHFRYVGRTKDFRGTMIPSE
APLLHNHVKLVDPVDRQAPGAVVRGKPTEIEWRFTEAGERVRVSTRSGRIIPKPEFPRADGIIPETWIDGPKDTSVEDAL
ERTYVPRLKTLEEEVMEAMGIQETRRYKKVYWY
```

227 - 246:	EEEEEEEEEEEEEEEEEEEE

A0A091D5I7 **A0A091D5I7_FUKDA** (152 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MTLTGTQDTEAATTVQLTTLTKEDFQSCSRKRPEQWDECVQRQTRQATTECCVGQAAGRVNPSPHPDRQKSKCIHVYASW
QLKRSDNQQNRISTTYTCAPVNQEEEEEEEEEEEEEEEEEEEEEEEEKEEEEEEEEEEQEEEEEEEEEEWRS
```

104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE

A0A091D5J7 **A0A091D5J7_FUKDA** (112 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MLVLGPALGTGDSKELNIVPNKEGERERRRSRKKEEEGEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEGKGEGEEEEEDD
EEEQEQEEEEEEEEEEEEEEEGGGGGGGRRYP
```

42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE

45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE

A0A091D5L8 **A0A091D5L8_FUKDA** (155 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MQVAHGLKQLPALPGALEYKTISEQLGSPAAAACRLLGVFGDSQGFCTRADWAAAEERRKRKKKKRKKKKKKKKKKKKKK
KKKKKNEEKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERIQ
```

91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE

133 - 152:	EEEEEEEEEEEEEEEEEEEE

A0A091D645 **A0A091D645_FUKDA** (2526 aa)
ATP-dependent helicase ATRX (EC 3.6.4.12) (Transcriptional regulator ATRX) (Fragment). *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
SESKLNTLVQKLHDFLAHSSEESEETSSPPRLAMNQSTDKIGGSGNNSDMMENNKEEGTSSSEKSKSSGSSRSKRKPSIV
TKYIESDDEKLLDETVNEDASNENSENDITMQSLPKGTVIVQPEPVLNEDKDDFKGPEFRSRSKMKTENLKKRGEDGLHG
IVSCTACGQQVNHFQKDSIYRHPSLQVLICKNCFKYYMSDDISRDSDGMDEQCRWCAEGGNLICCDFCHNAFCKKCILRN
LGRKELSTIMDENNQWYCYICHPEPLLDLVTACNSVFENLEQLLQQNKKKIKVDIEKSSKVCDHAPRFSPKKSSSNCNGE
EKKYDDSCSGSVTYSYSALIVPKEMIKKAKKLIETTANMNSSYVKFLKQATDNSEISSSIKLRQLKAFKSVLADIKKAHL
ALEEDLNSEIRALDIVNKEKNTKEHKVVDAKPEVKVRKGEKPCALERKDISKSEAKLSRKQVESQHTDQSVPIEEQRANK
STSGEHKKSDRKEEPQYEPANTSEDLDMDIVSVPSSVPEDIFENLETAMEVQCSANCQGDSSSASDQELENSSVKLNTPS
KDNRGGIKSKTTAKVTKELYVKLTPVSLSNSPVKGADCQEDPQEKDGSKSSGLHSKSEKCGLVQENSDNELLVENEIPLP
LEESDLRRSPRVKTTPLRRQAETNPATSNSDEESNEILKEKQKLSVPMRKNDKRNSDRAIDNPKPNKLPKSKLSEIVDQN
SDSDEMLAILKEVSRMNHSSSSDTDINETHKNHKTLCDLKTQPGKDDKGKRKRKSSTSGSDFDIKERKSAKSSIISKKIR
QNQSESSNYDSELEKEIKSMSKIGATRTTKKRFPNKKDYDSSEDEKHSKKEVDNQGQKNLKTVQEGSSDDAERTLESESF
SLVESTVNKDKTIKELRDQFSKKHQPSTSPDGADKSSGKESLNSPEDKKVADSKEKSKHLRTKTCKKIQSGLFHVTEKFS
KKEQSDESSEDDKKNKRGSEEKGKKTDSKKKVIKIEQQYESSSDGTEKLPEGEEICHFPKDIKQSKSNSTDREKRGKKIK
DKMSKKKDDLSDNVGKLSGKGDSCDSSEDRKSKNRTSSREKKRCGFPEKSSRKRQDCSSSDTEKYSMKEDGCDSSDRRLK
RIELRERRNLNSKRNAKDIQSGSSSSDVEESSEDNKKQKKQRTSAKKKSVIVKEKKRNSLRTSIKRKQADIISSSSDIGD
DRNSVGEGSSDEQKIKPVTESLVLSSHTGFCQSSGDEALSKSVPVTVDDDDDDNDPENRIAKKMLLEEIKANLSSDEDGS
SDDESEEGKKRGEKQNEENPGDEEGKNPVNSESDSDSEESKKPRYRHRLLRHKLTVSDGESGEEKRTKPKEQKEVKGRNR
RKVSSEDSEDSDFQETGVSEEVSDSEDEQRPRTRSAKKAELEENQRSYKQKKKRRRIKVQEDSSSENKSNSEEEKEEEEE
EEEEEEEEEEEEEEEEEDENDDSKSPGKGRKKIRKILKDDKLRTETQNALKEEEERRKRIAERERERERERKLREVIEIEDAS
PTKCPITTKLVLDEDEETKEPLVQVHRNMVIKLKPHQVDGVQFMWDCCCESVKKTKKSPGSGCILAHCMGLGKTLQVVSF
LHTVLLCDKLDFSTALVVCPLNTALNWMNEFEKWQEGLRDDEKLEVSELATVKRPQERSYMLQRWQEDGGVMIIGYEMYR
NLAQGRNVKSRKLKEIFNKALVDPGPDFVVCDEGHILKNEASAVSKAMNSIRSRRRIILTGTPLQNNLIEYHCMVNFIKE
NLLGSIKEFRNRFINPIQNGQCADSTMVDVRVMKKRAHILYEMLAGCVQRKDYTALTKFLPPKHEYVLAVRMTSIQCKLY
QYYLDHLTGVGNSSEGGRGKAGAKLFQDFQMLSRIWTHPWCLQLDYISKENKGYFDEDSMDEFIASDSDETSMSLSSDDY
TKKKKTKGKKGKKDSSSSGSGSDNDVEVIKVWNSRSRGGGEGNVDETGNNPSVSLKLEESKATSSSDPSSPAPDWYKDFV
TDADAEVLEHSGKMVLLFEILRMAEEIGDKVLVFSQSLISLDLIEDFLELASREKTEDKDKPLIYKGEGKWLRNIDYYRL
DGSTTAQSRKKWAEEFNDETNVRGRLFIISTKAGSLGINLVAANRVIIFDASWNPSYDIQSIFRVYRFGQTKPVYVYRFL
AQGTMEDKIYDRQVTKQSLSFRVVDQQQVERHFTMNELTELYTFEPDLLDDPNSEKKKKRDTPMLPKSKNKLAKHQRGSN
FLATHPWYVPAKYAAMLQRSVLRWVKEDTILAELLQIHKEHIVGYHEHDSLLDHKEEEELTEEERKAAWAEYEAEKKGLT
MRFNIPTGTNLPPVTFSSQTPYIPFNLGALSAMSNQQLEDLINQGREKVVEATNSVTAVRIQPLEDIISAVWKENMNLSE
AQVQALALSRQATQELDVKRREAIYNDVLTKQQMLISCVQRILMNRRLQQQYNQQQQQQMTYQQATLGHLMMPKPPNLIM
NPSNYQQIDMRGMYQSVAGGMQPPPLQRAPPPMRSKNPGPSQGKSM
```

1436 - 1455:	EEEEEEEEEEEEEEEEEEEE
1437 - 1456:	EEEEEEEEEEEEEEEEEEEE
1438 - 1457:	EEEEEEEEEEEEEEEEEEEE

A0A091D8C9 **A0A091D8C9_FUKDA** (184 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MRGSLLGSDIAAPSDQGKASANWSFWNWRTPLRLLERKCEEHSSAPSAAADRWRKIYRSQAERESQRQLREEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEDEAILGALLLLT
```

71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE

92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE

144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE

A0A091D934 **A0A091D934_FUKDA** (67 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MTELQRRRKKKKKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKRDERQKQGKCVS
```

15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE

A0A091D946 **A0A091D946_FUKDA** (172 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MRYSRRILDLQIAVSTKTSEKSKKEKDMCSHTYKVEQNMDSKRKRKRKRKKKKKKKKKKKKKEEEEERRKKKEERRKKKE
EEGRKKKEERRRRRRKKKKEERRKKKEERRKKKEEEEEEEEEEEEEEEEEEEEEKTKAEHQQNRGGYQYDTASHVLAKP
NLAIFLTLISTG
```

114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE

A0A091D962 **A0A091D962_FUKDA** (140 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MRDKEEPRLMSGSNFPICGCEIKDFLKRSKFEGSSTDSAASSFPYGFAPSSAVSTKPLPFDWIIRISSAQEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEKRRRRSFKDMPPGDSPLLETYLLTVHSTMNRLMYR
```

71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE

73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE

A0A091D970 **A0A091D970_FUKDA** (288 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MVLVGGLGLSDLPLPERCLRRRNLPNIQRRPEDRWIGVGYENGTREGGHAQEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEVDQVMDGVGREEMARGVYKE
```

52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE

84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE

136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE
180 - 199:	EEEEEEEEEEEEEEEEEEEE
181 - 200:	EEEEEEEEEEEEEEEEEEEE
182 - 201:	EEEEEEEEEEEEEEEEEEEE
183 - 202:	EEEEEEEEEEEEEEEEEEEE
184 - 203:	EEEEEEEEEEEEEEEEEEEE
185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE

188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE
190 - 209:	EEEEEEEEEEEEEEEEEEEE
191 - 210:	EEEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE
194 - 213:	EEEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEEE
196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE
208 - 227:	EEEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEEE
225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE
239 - 258:	EEEEEEEEEEEEEEEEEEEE

240 - 259:	EEEEEEEEEEEEEEEEEEEE
241 - 260:	EEEEEEEEEEEEEEEEEEEE
242 - 261:	EEEEEEEEEEEEEEEEEEEE
243 - 262:	EEEEEEEEEEEEEEEEEEEE
244 - 263:	EEEEEEEEEEEEEEEEEEEE
245 - 264:	EEEEEEEEEEEEEEEEEEEE
246 - 265:	EEEEEEEEEEEEEEEEEEEE
247 - 266:	EEEEEEEEEEEEEEEEEEEE
248 - 267:	EEEEEEEEEEEEEEEEEEEE
249 - 268:	EEEEEEEEEEEEEEEEEEEE

A0A091D986 **A0A091D986_FUKDA** (85 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MPVWGGGLTSHSTNYYGNQIREEQERGERRWRRKKEEERRKKKKRKEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAE
EGEEK
```

49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE

A0A091D9Q9 **A0A091D9Q9_FUKDA** (325 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MSRENLTDQNEMKQPQTFGTMRAWHTATACQMPMTPYSSEGPYGAADGPLRLYQIKNKVLKSKKIFLKEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAALCSPVMLR
RINLL
```

69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE

88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE

140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE
180 - 199:	EEEEEEEEEEEEEEEEEEEE
181 - 200:	EEEEEEEEEEEEEEEEEEEE
182 - 201:	EEEEEEEEEEEEEEEEEEEE
183 - 202:	EEEEEEEEEEEEEEEEEEEE
184 - 203:	EEEEEEEEEEEEEEEEEEEE
185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE
190 - 209:	EEEEEEEEEEEEEEEEEEEE
191 - 210:	EEEEEEEEEEEEEEEEEEEE

192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE
194 - 213:	EEEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEEE
196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE
208 - 227:	EEEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEEE
225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE
239 - 258:	EEEEEEEEEEEEEEEEEEEE
240 - 259:	EEEEEEEEEEEEEEEEEEEE
241 - 260:	EEEEEEEEEEEEEEEEEEEE
242 - 261:	EEEEEEEEEEEEEEEEEEEE
243 - 262:	EEEEEEEEEEEEEEEEEEEE

244 - 263:	EEEEEEEEEEEEEEEEEEEE
245 - 264:	EEEEEEEEEEEEEEEEEEEE
246 - 265:	EEEEEEEEEEEEEEEEEEEE
247 - 266:	EEEEEEEEEEEEEEEEEEEE
248 - 267:	EEEEEEEEEEEEEEEEEEEE
249 - 268:	EEEEEEEEEEEEEEEEEEEE
250 - 269:	EEEEEEEEEEEEEEEEEEEE
251 - 270:	EEEEEEEEEEEEEEEEEEEE
252 - 271:	EEEEEEEEEEEEEEEEEEEE
253 - 272:	EEEEEEEEEEEEEEEEEEEE
254 - 273:	EEEEEEEEEEEEEEEEEEEE
255 - 274:	EEEEEEEEEEEEEEEEEEEE
256 - 275:	EEEEEEEEEEEEEEEEEEEE
257 - 276:	EEEEEEEEEEEEEEEEEEEE
258 - 277:	EEEEEEEEEEEEEEEEEEEE
259 - 278:	EEEEEEEEEEEEEEEEEEEE
260 - 279:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE
262 - 281:	EEEEEEEEEEEEEEEEEEEE
263 - 282:	EEEEEEEEEEEEEEEEEEEE
264 - 283:	EEEEEEEEEEEEEEEEEEEE
265 - 284:	EEEEEEEEEEEEEEEEEEEE
266 - 285:	EEEEEEEEEEEEEEEEEEEE
267 - 286:	EEEEEEEEEEEEEEEEEEEE
268 - 287:	EEEEEEEEEEEEEEEEEEEE
269 - 288:	EEEEEEEEEEEEEEEEEEEE
270 - 289:	EEEEEEEEEEEEEEEEEEEE
271 - 290:	EEEEEEEEEEEEEEEEEEEE
272 - 291:	EEEEEEEEEEEEEEEEEEEE
273 - 292:	EEEEEEEEEEEEEEEEEEEE
274 - 293:	EEEEEEEEEEEEEEEEEEEE
275 - 294:	EEEEEEEEEEEEEEEEEEEE
276 - 295:	EEEEEEEEEEEEEEEEEEEE
277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE
287 - 306:	EEEEEEEEEEEEEEEEEEEE
288 - 307:	EEEEEEEEEEEEEEEEEEEE
289 - 308:	EEEEEEEEEEEEEEEEEEEE
290 - 309:	EEEEEEEEEEEEEEEEEEEE
291 - 310:	EEEEEEEEEEEEEEEEEEEE

A0A091D9W8 **A0A091D9W8_FUKDA** (124 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MRGVGEEGGAEGDEEEEEEEEEEEEEQEEEKKEEEEEVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEEEE
EEEEEEKKKEEEEEEEEEEEEEGRGGGGGDGEGEREGEKNSPTH
```

40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE

A0A091DA10 **A0A091DA10_FUKDA** (232 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MVGVFPRLKWALGHASLVPRRDWPDSPGAVSLPYPGIGRSRVPQLCSTEPALEGCLPCQTGDSGFLTLAQERSLVWQRVP
GLWGVLKTKRASGGSSPCLKKKKKKEKEKEKEKREEKKKKKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEGGGGGGGGGGGGTAEKTSQALGLVSSWQNGSGLRQYQGRWFLWQNPAHLQILVPVFLK
```

123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE

153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE

A0A091DA86 **A0A091DA86_FUKDA** (157 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MRLAKEGTGKIAWGEYENQTLRECTLFALDFHYFKATSAVSEDPERGVGADREPGQRLLWHRFSVVEIFHRRTRMAGQDL
PIVAVVKREEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEGEEGEEGEEGEEGEEGEEGEEEEKEEGVFNISRT
```

89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE

A0A091DAA7 **A0A091DAA7_FUKDA** (88 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MTSPSALPLRPFTCPPHMQQQFPEEPWPRVMGQAETKKKEERRKKKEERRKKKEEEEEEEEEEEEEEEEEEEEEEEEES
VLGHHPFS
```

54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE

A0A091DAI9 **A0A091DAI9_FUKDA** (1388 aa)
Collagen alpha-1(II) chain. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MVRLGAPQMLVLLTLLVAAVLRCQGQDAIENRSCLQDGESYNDKDVWKPEPCRICVCDSGFILCDDIICEDTKDCLNPEI
PFGECCPICPADRATASGRPPGPKGQKGEPGDIKDIVGPKGPPGPQGPAGEQGPRGDRGDKGAKGAPGPRGRDGEPGTPG
NPGPPGPPGPPGTPGLGGNFAAQMAGGFDEKAGGAQMGVMQGPMVRKTAVLCSQNDKEVVLSRAREPDNLCFVDSCLQQR
FLGPMGPRGPPGPAGAPGPQGFQGNPGEPGEPGVSGPLGPRGPPGPPGKPGDDGEAGKPGKSGERGPPGPQGYPGLDGAK
GEAGATGVKGPRGLPGERGRTGPAGAAVRNQQSQMASFRVHKLISLDPQDKSLRVPEATMGSRAQLGLRVPLVRLVVLAS
LVLLVLRVRPAPLEPVVPKALKVPEVNRVTLGPLGLLVLLETLEQMASLEPKDLPVLLGLLVLLASLGPVVLLVLKVQQV
LWVQKGAPGNRGFPGQDGLAGPKGAPGERGPSGLAGPKGANGDIGRPGEPGLPGARGLTGRPGDAGPQGKVGPSGIPGED
GRPGPPGPQGARGQPGVMGFPGPKGANGEPGKAGEKGLAGAPGLRGLPGKDGETGAAGPPGPAGLPGEAGAPGLVGSRGE
RGFPGERGSPGTQGLQGPRGLPGTPGTDGPKGASGPAGPPGAQGPPGLQGMPGERGAAGIAGPKGDRGDVGEKGPEGAPG
KDGGRGLTGPIGPPGPAGANGEKGEVGPPGPAGSAGARGAPGERGEIGPPGPAGFAGPPGADGQPGAKGEQGVAGHKGDA
GAPGLQGPSGAPGPQGPTGVTGPKGARGAQGPPGNPGPPGPPGPSGKDGPKGARGDSGPAGRAGDPGLQGPAGPPGEKGD
PGDDGPSGADGPPGPQGLAGQRGIVGLPGQRGERGFPGLPGPSVNLDEREALALMGPRAEMAQLESRVIAGRLVLWVLPE
PLGLLALLAPLAQLASKETEEKLVHKAPWDLQDQLEPEESRQLRVTDRNPLGCLRVEREEEEEEEEEEEEEEEEEEEEEE
ERGWEGHTPAFHLPRVLLETKVLQGPPGPVGPSGKDGANGIPGPIGPPGPRGRSGETGPAGPPGNPGPPGPPGPPGPGID
MSAFAGLGQREKGPDPLQYMRADQAAGTLRQHDVEVDATLKSLNNQIENIRSPEGSRKNPARTCRDLKLCHPEWKSGDYW
IDPNQGCTLDAMKVFCNMETGETCVYPSPANVPKKNWWSSKTKEKKHIWFGETINGGFHFSYGDDNLAPNTANIQMTFLR
LLSTEGFQNITYHCKNSIAYLDEVAGNLKKALLLQGSNDVEIRAEGNSRFTYTALKDGCTKHTGKWGKTVIEYRSQKTSR
LPIIDIAPMDIGGPEQEFGVEIGPVCFL
```

1019 - 1038:	EEEEEEEEEEEEEEEEEEEE
1020 - 1039:	EEEEEEEEEEEEEEEEEEEE
1021 - 1040:	EEEEEEEEEEEEEEEEEEEE
1022 - 1041:	EEEEEEEEEEEEEEEEEEEE

A0A091DBS7 **A0A091DBS7_FUKDA** (190 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MDNLKKEKERQFQETIESKRREKDRQEERKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEGGGGEG
EGEGEEEEEEEKKKRKKKKKKKEEEKKKTKKKKEEEEKKKKKKKKRRRRRKRKKKKKKKKKKKKKKKKKKRKRKRKRKR
```

KRKRKRKRKKKKNLGWNSPAEVDTGPGASG

32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE

A0A091DBZ1 **A0A091DBZ1_FUKDA** (346 aa)
Phosphatidate phosphatase PPAPDC1A. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

MSKLSTLISPRIVMWSKCRVNRARLLSEFKEELATEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEGEEEEEGERIRRRRGRGRGRGRRKKSSIIAGKVIRARKENLLSSEASDHFAVWQKTRSGFLVTERCIPHQGVALLDEQ
PGNCKRKNEDDRRRVCMNLMAQPRPDFFYRCFPDGVMNSEMHCTGDPDLVSEGRKSFPSIHSSFAFSGLGFTTFYLAGKL
HCFTETGRGKSWRLCAAILPLYCAMMIALSRMCDYKHHWQDSFVGGVIGLIFAYICYRQHYPPLANTACHKPYVSLRMPT
SMKKEEMPTADSAPTLPLEGITEGPV

36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE

58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE

A0A091DC12 **A0A091DC12_FUKDA** (86 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MKVFKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDRERSREGGKGRGGQEGEGEGEGEEIFISKETK
NVFHIN
```

6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE

A0A091DC67 **A0A091DC67_FUKDA** (200 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MKVASNWSSVRIRAKTIVILASLNVDMQFRLVVREMKDDVIPEAISKGELRPDYKELDLLTATSKTGPETRGTKEKEEEE
EEGKQEEEEKVVEEEVEKERKRKKRRNGKKRRKRKKKKERRKIRKKRTGRERGSKGVGEEREEEEEEEEEEEEEEEEEE
EEKEEAEEEEVLEVVVVVVVVVVVRAQKRVQALEGRCTMI
```

143 - 162:	EEEEEEEEEEEEEEEEEEEE

A0A091DCA0 **A0A091DCA0_FUKDA** (119 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MKKKKKKKKKKKKKKKKKKKKKKKKKRKRKRKRKRKKGGGGEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEGRERKRRKVKKSGASFRISSLNLMELTDKI
```

44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE

50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE

A0A091DCA7 **A0A091DCA7_FUKDA** (307 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MATPHSLTPTYDQGFPRLEQNQTRKVAREIIKEQLIEDESRGSSSTLKDLELLRKGVDGTFATPAATSLCAICLKASKDE
RWTEISSNPAVIDSPDASASRAQLPGLLGESEGLLLGNRGDSKNRHRPPPGPGSPPTAYGWTIGVLSLLTSAYHENCWRG
RRTPYPPSNAAAAAAPQPTHMEKKKSKNRKEEKEEKERERQRERERERERKKRRRKRRRRKRRRRRRKKKKKKKKKKKKK
KKKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEQQQQQEEEQEEEEDDEEEAFGFICSR
```

245 - 264:	EEEEEEEEEEEEEEEEEEEE
246 - 265:	EEEEEEEEEEEEEEEEEEEE
247 - 266:	EEEEEEEEEEEEEEEEEEEE
248 - 267:	EEEEEEEEEEEEEEEEEEEE
249 - 268:	EEEEEEEEEEEEEEEEEEEE
250 - 269:	EEEEEEEEEEEEEEEEEEEE
251 - 270:	EEEEEEEEEEEEEEEEEEEE
252 - 271:	EEEEEEEEEEEEEEEEEEEE
253 - 272:	EEEEEEEEEEEEEEEEEEEE
254 - 273:	EEEEEEEEEEEEEEEEEEEE
255 - 274:	EEEEEEEEEEEEEEEEEEEE
256 - 275:	EEEEEEEEEEEEEEEEEEEE
257 - 276:	EEEEEEEEEEEEEEEEEEEE
258 - 277:	EEEEEEEEEEEEEEEEEEEE
259 - 278:	EEEEEEEEEEEEEEEEEEEE
260 - 279:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE
262 - 281:	EEEEEEEEEEEEEEEEEEEE

A0A091DCQ2 **A0A091DCQ2_FUKDA** (454 aa)
Guanine nucleotide-binding protein subunit alpha-15. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MLRGGGESRAEVDVTEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERKRRRRRSAPA
MARSLAWSCCPWCLTEEEKTAARIDQEINKILLEQKKQDRGELKLLLLGPGESGKSTFIKQMRIIHGAGYSEEDRKGFRP
LVYQNIFASMQAMIEAMERLQIPFGRSDSKHHASLVMSQDPYKVTTFQKRYAVAMQSLWQDAGIRACYERRREFHLLDSA
IYYLSHLERITEECYIPTAQDVLRSRMPTTGINEYCFSVQKTNLRIVDVGGQKSERKKWIHCFENVIALIYLASLSEYDQ
CLEENNQENRMKESLALFGTILELPWFKSTSVILFLNKTDILEEKIVASHLATYFPSFQGPKQDAEAAKKFILDMYTGMY
TGCVDGLEGSKKGPRSRRLFSHYTCATDTQNIRKVFKDVRDSVLARYLDEINLL
```

16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE

A0A091DD00 **A0A091DD00_FUKDA** (148 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MRSEGREVRDLINTLRSRAAEQELNTGASVPKPVMLALTLVDRLINQPPSCIGSMVDLACEPFFTRCGLYFHRGSRAFSV
TQKKGRRKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGRKKMMMTINKKKDEKQNVV
```

89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE

101 - 120:	EEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEE

A0A091DD57 **A0A091DD57_FUKDA** (263 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MEKTSNSLDFSLPPLKTDMCHHLPPLANINQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEELKGIFLYLK
```

32 - 51:	EEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEE

69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE

121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE

173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE
180 - 199:	EEEEEEEEEEEEEEEEEEEE
181 - 200:	EEEEEEEEEEEEEEEEEEEE
182 - 201:	EEEEEEEEEEEEEEEEEEEE
183 - 202:	EEEEEEEEEEEEEEEEEEEE
184 - 203:	EEEEEEEEEEEEEEEEEEEE
185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE
190 - 209:	EEEEEEEEEEEEEEEEEEEE
191 - 210:	EEEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE
194 - 213:	EEEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEEE
196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE
208 - 227:	EEEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEEE

225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE

A0A091DDL7 **A0A091DDL7_FUKDA** (76 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MVVAPSIQKFSVVESQGLHLSASVKEEEEEEEEEEEEEEEEEEEEEEEEEESKQMRELKKKVGVPLERKLMINQRCK
```

26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE

A0A091DDT6 **A0A091DDT6_FUKDA** (135 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MEGRISHAEIPSLLQLDQVDQRRRGGGGGGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEGRRRRRRPVETRSHSEVVRQLPDILS
```

32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE

57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE

A0A091DE86 **A0A091DE86_FUKDA** (121 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MLTQVAGRVSGHHAHQHCERPGQEDCKFNLSLRDLMSKKEKEERRKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEERGRGRGEEEEEEEEEEEEEEEKKTLRKDGQNVI
```

47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE

60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE

A0A091DEP4 **A0A091DEP4_FUKDA** (88 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MRRTRLLLDHGSSVHPRSGVNTILGEDGTGGGRGPSVMSWEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEK
EEEEEEKE
```

41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE

A0A091DEP6 **A0A091DEP6_FUKDA** (172 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MWRAIEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAKA
SLVGVLPVGKLF
```

6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE

17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE

69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE

121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE

A0A091DF52 **A0A091DF52_FUKDA** (72 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MKKKGGEEEEEEEEEEEEEEGEGEGEGEGEGEGEGEGEGEGEGEGEEEEEEEEEEEEEEEEEEEEEERIKNQIE
```

45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE

A0A091DF71 **A0A091DF71_FUKDA** (766 aa)
Sodium/nucleoside cotransporter. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MKGEEERACGLASSGQQVSGQLSFAGHTGRRWTRKADILDKSQAEPTRICQDAGLQEEGEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEAAAARSRRGKLCLVLPWGKGQRSKGSEPEAQKRCSSPVSSLVLARFLDRAAVRYLPSKVTWAGIPG
ASVFPKYFSHNSVYYIQDLGSQGVSRIAQAGQHSGPCRMPAPRLLLLSQLPLLIVLQDESSDFLVGGAGMTWTAYTAYFL
AACILDFHRALALFVITCLVVFVLAHHFLQKFFGKKLSRCLKPLKHSRLQVWMKWVIAGVSLVGLVLWLALDTAQRPEQL
ISFAGICMFLLILFACSKHHSAIFLDYTVAGSSFVFGDTLVKEAFAFQSLPIIIFFGCVMSILYYLGLVQWVVQKIAWFL
QITMGTTATETLAVAGNIFVGMTEAPLLIRPYLADMTLSEIHAVMTGGFATIAGSVLGAFISFGIDAPSLISASVMAAPS
ALALSKLVYPEVEESKFKSKEGLKLQRGKERNILEAASSGATDAIGLVANIAASLIAYLAVLAFINAVLSWMGELVDIPG
LTFQVICSYVLRPMVFMMGVDWADCAIVAEIVGIKFFTNEFVAYQQLSQYKSKRLSGVEEWSEGEKQWISVKAEIIATFS
LCGFANLSSIGITLGGLTSMVPQRKNDLSRVVVRALFTGACVSLISACMAGILYVPRGAEADCVSFLNASFTNRTYESYV
CCQELFQSTSLNGTNSLSFSGPWENKEFSATALVNCCEFYTNAVCA
```

60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE

A0A091DF77 **A0A091DF77_FUKDA** (735 aa)

Leukotriene-B(4) omega-hydroxylase 2. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MGLMIPIVTLWHPDIAMCFLSALGAHVEPVENKFEDKRKRVFIEKRRRQKKEEEDDEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEERRGGRRLLVELLLGQRFSSLGRRLMKQKVAENHGLSGMRHHGTWKTNNLAKRRRRR
ALGIKKRLKGKLEITEKVEKPKTTQMKHSEMLLVVVVVVIGACLHKHRMTQLSLSWLGLGSVTASPWLIGLLVGAAWLLA
QILTWMYALYEKSHRLRCFPQPPKRNWLVGHLGLIQSSEGGLLYTQGLARTYRDVCCWWVGPCHAVVRIFHPSCIKPVLF
APAAIALKDVVFYSFLRPWLGDGLLLSAGDKWSRHRRMLTPAFHFNILKPYVKIFTDSTKVMHAKWQRLISQGSARLDMF
ELISLMTLDSLQKCVFSFESNCQEKPSKYIAAILELSALVAKRHQQLLLHPDFLYHLTCDGHRFRTACRLVHDFTDAVIQ
ERRCSLPNQGIDDFLKAKARSKTLDFIDVLLLSKDENGRELSDEDVRAEADTFMFAGHDTTASGLSWVLYNLARHPEYQE
RCRQEVRELLRGREPEEIEWEDLAQLPFLTMCIKESLRLHPPVSVVSRCCTQDVVLPDGRVIPKGVICLISIFGTHHNPA
VWPDPEVYDPFRFDPENSKDRSPLAFIPFSAGPRNCIGQTFAMAEMKVVLALTLLRFRVLPDATEPRRKPELILRAEGGL
WLRVEPLSEQAAPLT
```

57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE

A0A091DFP7 **A0A091DFP7_FUKDA** (238 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MEGGAGLHEHFRDTLELASATLPPGGGGRGGGGGRGGGGKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEER
```

41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE

52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE

104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE

156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
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164 - 183:	EEEEEEEEEEEEEEEEEEEE
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167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
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177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE
180 - 199:	EEEEEEEEEEEEEEEEEEEE
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183 - 202:	EEEEEEEEEEEEEEEEEEEE
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190 - 209:	EEEEEEEEEEEEEEEEEEEE
191 - 210:	EEEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE
194 - 213:	EEEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEEE
196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE

208 - 227:	EEEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEEE

A0A091DFQ5 **A0A091DFQ5_FUKDA** (85 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MPLQVQGLAQSGGLRVGGGAQRCPCGYPPGVGGAAMAAPIREEEEEEEEEEEEEEEEEEEEEVEEEEEEESRRRKKGEREE
KSGTP
```

42 - 61:	EEEEEEEEEEEEEEEEEEEE

A0A091DGG6 **A0A091DGG6_FUKDA** (1202 aa)
Myelin transcription factor 1. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MKHLGPNPITKSYEIDEKVNSMMFGPPFSALVGTARENNQMEMSLESDDKRARTRSKALRGPPETTGADLRDCRLLLSVA
TGITVSVLGTEKSNFWATDLANCPTPGCTGSGHVRGKYSRHRSLQSCPLAKKRKLEGAEAEHLVSKRKSHPLKLALDEGY
GMDSDGSEDGEVKDASVSDESEGTLDEAEAEMSGQEEIHRPEPAEGRSPIKSHFGSNPIGSSTGSSKSSYSSYQGIIATS
LLNLGQIAEETLVGEDSGRVAKLGPSIVHLLQEEATEGATSDEGEKDLFIQPEDAEEVIEVTSERSQEPCSQSMEDVARE
SSSKLKGVLDHEEEEEEEEEEEEEEEEEEEEEEDEEEEEGGGVGEEEEEEEGEEGEEVEEEEEAAPKVLFEEDASHTSAQ
KASEPHCPEPSSLKPEYSVIVEVRSDDDKDEDMHSQKSTVTDESEMYDMMTRGNLGLLEQAIALKAEQVRTVCETGCPPA
EQGQLGPGEPGKVVKPLDTMRKSCYSKDPSRAEKREIKCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRIPPEILAMHENV
LKCPTPGCTGQGHVNSNRNTHRSLSGCPIAAAEKLAKSHEKQQPQMGDPSKNSSNSDRILRPMCFVKQLEVPPYGSYRPS
VAPATPRANLAKELEKFSKVTFDYASFDAQVFGKRMLAPKIQTSETSPKAFQCFDYSHDAEAAHMAATAILNLSTRCWEM
PENLSTKPQDLPSKSVDIEVDENGTLDLSMNKHRKRENALPSSSSCSSSPGIKSPDVSQRQSNTSAPSSSITSPQSSQAS
RQDEWDRPLDYTKPSRLREEEPEESEPAAHSFASSEADDQEVSEENFEERKYPGEVTLTNFKLKFLSKDIKKELLTCPTP
GCDGSGHITGNYASHRSLSGCPLADKSLRNLMAAHSADLKCPTPGCDGSGHITGNYASHRSLSGCPRAKKSGLKVAPTKD
DKEDPELMKCPVPGCVGLGHISGKYASHRSASGCPLAARRQKEGSLNGSSFSWKSMKSEGPTCPTPGCDGSGHANGSFLT
HRSLSGCPRATFAGKKGKLSGDEVLSSKFKTSDVLENDEEIKQLNQEIRDLNESNSEMEAAMVQLQSQISSMEKNLKNIE
EENKLIEEQNEALFLELSGLSQALIQSLANIRLPHMEPICEQNFDAYVSTLTDMYSNRDCYQNPENKGLLETIKQAVRGI
QV
```

332 - 351:	EEEEEEEEEEEEEEEEEEEE
333 - 352:	EEEEEEEEEEEEEEEEEEEE
334 - 353:	EEEEEEEEEEEEEEEEEEEE

A0A091DGK3 **A0A091DGK3_FUKDA** (159 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MVAYLLGFSAALCQRSRLTRGPQAAAGLHCCSSLYLEKKEKEKEKEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVEEEEEEEEEEERTKREIYAGTKKNFRGKLKSKDKLKRHNTT
```

48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE

62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE

A0A091DH18 **A0A091DH18_FUKDA** (751 aa)
Leucine-rich repeat and fibronectin type-III domain-containing protein 5. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MEKFLFYLFFIGIAVRAQICPKRCVCQILSPNLATLCAKKGLLFVPPNIDRRTVELRLADNFVTNIKRKDFANMTSLVDL
TLSRNTISFITPHAFADLRNLRALHLNSNRLTKITNDMFSGLSNLHHLILNNNQLTLISSTAFDDVFALEELDLSYNNLE
TIPWDAVEKMVSLHTLSLDHNMIDNIPKGTFSHLHKMTRLDVTSNKLQKLPPDPLFQRAQVLATSGIISPSTFALSFGGN
PLHCNCELLWLRRLSREDDLETCASPVLLTGRYFWSIPEEEFLCEPPLITRHTHEMRVLEGQRAILRCKARGDPEPAIHW
ISPEGKLISNATRSLVYDNGTLDIVITTVKDTGAFTCIASNPAGEATQTVDLHIIKLPHLLNSTNHIHEPDPGSSDISTS
TKSGSNASSSNGDTKMSQDKIVVTEATSSTALLKFNFQRNIPGIRMFQIQYNGTYDDTLVYRMIPPTSKSFLVNNLAAGT
MYDLCVLAIYDDGITSLTATRVVGCIQFTTEQDYVRCHFMQSQFLGGTMIIIIGGIIVASVLVFIIILMIRYKVCNNNGQ
HKVTKVSNVYSQTNGAQMQGCSITLPQSMSKQAVGHEESTQCCKVASDNVTQSSETCSSQDSSTTTSALPPTWTSSTPVS
QKQKRKTSAKPSAEPQSEAVTNVESQNTNRNNSTALQLAGQPPDSVTEGPASKRAHTKPIRTLYHQERKEEEEKEEGEGE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEDP
```

720 - 739:	EEEEEEEEEEEEEEEEEEEE
721 - 740:	EEEEEEEEEEEEEEEEEEEE
722 - 741:	EEEEEEEEEEEEEEEEEEEE
723 - 742:	EEEEEEEEEEEEEEEEEEEE

724 - 743:	EEEEEEEEEEEEEEEEEEEE
725 - 744:	EEEEEEEEEEEEEEEEEEEE
726 - 745:	EEEEEEEEEEEEEEEEEEEE
727 - 746:	EEEEEEEEEEEEEEEEEEEE
728 - 747:	EEEEEEEEEEEEEEEEEEEE
729 - 748:	EEEEEEEEEEEEEEEEEEEE
730 - 749:	EEEEEEEEEEEEEEEEEEEE

A0A091DHF0 **A0A091DHF0_FUKDA** (92 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MNQEASGKPIRSQEKEKANGVKKEEEEEERRKKKEERRKKKKDEEDEEEEEEEEEEEEEEEEEEEEEEEEEEQEQEQEE
EEEEEEEEEEER
```

47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE

A0A091DIV6 **A0A091DIV6_FUKDA** (140 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MQEGGREPFHLGEMEYFIEEVYVTEYAFKQWVILVLILKESVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKKSRGLR
SSEGLQEHGDDRVKEHRANRIHPLFPHSSSGVSLSNAGQFCKIPSKEKGGGWTRGENMFD
```

43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE

A0A091DJ30 **A0A091DJ30_FUKDA** (49 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MSVLTRRALGVFQSIWHKQSEEEEEEEEEEEEEEEEEEEEEEKKKEEGT
```

21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE

A0A091DJB2 **A0A091DJB2_FUKDA** (314 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MGERQTEREKKKKKRGGGRGGGGGEEKEEQEEEEGAEELEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKKNRKRENI
```

41 - 60:	EEEEEEEEEEEEEEEEEEEE

42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE

94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
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117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
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122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE

146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
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190 - 209:	EEEEEEEEEEEEEEEEEEEE
191 - 210:	EEEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE
194 - 213:	EEEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEEE
196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE

198 - 217:	EEEEEEEEEEEEEEEEEEEE
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200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE
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209 - 228:	EEEEEEEEEEEEEEEEEEEE
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212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEEE
225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE
239 - 258:	EEEEEEEEEEEEEEEEEEEE
240 - 259:	EEEEEEEEEEEEEEEEEEEE
241 - 260:	EEEEEEEEEEEEEEEEEEEE
242 - 261:	EEEEEEEEEEEEEEEEEEEE
243 - 262:	EEEEEEEEEEEEEEEEEEEE
244 - 263:	EEEEEEEEEEEEEEEEEEEE
245 - 264:	EEEEEEEEEEEEEEEEEEEE
246 - 265:	EEEEEEEEEEEEEEEEEEEE
247 - 266:	EEEEEEEEEEEEEEEEEEEE
248 - 267:	EEEEEEEEEEEEEEEEEEEE
249 - 268:	EEEEEEEEEEEEEEEEEEEE

250 - 269:	EEEEEEEEEEEEEEEEEEEE
251 - 270:	EEEEEEEEEEEEEEEEEEEE
252 - 271:	EEEEEEEEEEEEEEEEEEEE
253 - 272:	EEEEEEEEEEEEEEEEEEEE
254 - 273:	EEEEEEEEEEEEEEEEEEEE
255 - 274:	EEEEEEEEEEEEEEEEEEEE
256 - 275:	EEEEEEEEEEEEEEEEEEEE
257 - 276:	EEEEEEEEEEEEEEEEEEEE
258 - 277:	EEEEEEEEEEEEEEEEEEEE
259 - 278:	EEEEEEEEEEEEEEEEEEEE
260 - 279:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE
262 - 281:	EEEEEEEEEEEEEEEEEEEE
263 - 282:	EEEEEEEEEEEEEEEEEEEE
264 - 283:	EEEEEEEEEEEEEEEEEEEE
265 - 284:	EEEEEEEEEEEEEEEEEEEE
266 - 285:	EEEEEEEEEEEEEEEEEEEE
267 - 286:	EEEEEEEEEEEEEEEEEEEE
268 - 287:	EEEEEEEEEEEEEEEEEEEE
269 - 288:	EEEEEEEEEEEEEEEEEEEE
270 - 289:	EEEEEEEEEEEEEEEEEEEE
271 - 290:	EEEEEEEEEEEEEEEEEEEE
272 - 291:	EEEEEEEEEEEEEEEEEEEE
273 - 292:	EEEEEEEEEEEEEEEEEEEE
274 - 293:	EEEEEEEEEEEEEEEEEEEE
275 - 294:	EEEEEEEEEEEEEEEEEEEE
276 - 295:	EEEEEEEEEEEEEEEEEEEE
277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE

A0A091DJC5 **A0A091DJC5_FUKDA** (87 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MGGKSASGSVQVHHLSWGDGMTTFENEEEQEEEEEEEEEEEEEEEEEEEEEEQEEQEEEEVEEEEGEEEEEEEEEGEK
ELLLQSA
```

31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE

A0A091DK39 **A0A091DK39_FUKDA** (71 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MQTGSCGKRYNLEAVAAPLRHPRQALTPKAKGWLPSNPQEEEEEEEEEEEEEEEEEEEEEEEEEEEEESL
```

40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE

A0A091DKH4 **A0A091DKH4_FUKDA** (122 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MHTERCDWRFYSRSGSRERDRERGGRRRRRRRRRRRKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEGEEEEEERERRTKKGRSFY
```

39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE

75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE

A0A091DKM7 **A0A091DKM7_FUKDA** (72 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MKTEAHWKSEENLCNKGTQTTMKKKEEEEEEEEEEEEEEEEEEEEKEEEEEEEEEEEEEEEEEEEEEEEEER
```

26 - 45:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE

A0A091DKZ2 **A0A091DKZ2_FUKDA** (122 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MGAPQTCESLDPMQSVQDDSPPVKEEEEEQEEEEEEEEEVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKKKKKKKKKRR
RRRRRRRRKKKRNQQLIGKFSTGNANPQSPVGFSELKTVTVW
```

41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE

A0A091DLD5 **A0A091DLD5_FUKDA** (99 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MMIREQKKKEKAMKSKSDTKIVHKLLKSKEDSECKKKLSEEEEEEEEEEEEEEEEEEEEEEEKKKKKKKKKKRHSYVSCG
EQKTNPQLFSPLFWKMMVK
```

40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE

A0A091DMB1 **A0A091DMB1_FUKDA** (120 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MASSSSPNTSKKITFPHGEDDVDFDCCPVGLHIPRGKSVMWLYFMALDWSMFNSTVHIINLGTIVALSLSTKKEEEEEEE
EEEEEEEEEEKKEEEEEEEEEEEEEEEEEEEEEEEEEEEESWP
```

93 - 112:	EEEEEEEEEEEEEEEEEEEE

94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE

A0A091DMQ7 **A0A091DMQ7_FUKDA** (133 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MRRGGREEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEMEERKEIREEKRSGVFLYQMLQEMHVHVIHNSNVTLWQKV
```

7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE

49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE

A0A091DP46 **A0A091DP46_FUKDA** (121 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MTILISTLKDEERIGLKKRKKRRKEGGGGGEEEEEEEEEEEAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAANTTMGLGS
```

43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE

64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE

A0A091DP83 **A0A091DP83_FUKDA** (235 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MEVCLEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGRRRKNTLGELNAHHYLQK
```

6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE

24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE

76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE

128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE

180 - 199:	EEEEEEEEEEEEEEEEEEEE
181 - 200:	EEEEEEEEEEEEEEEEEEEE
182 - 201:	EEEEEEEEEEEEEEEEEEEE
183 - 202:	EEEEEEEEEEEEEEEEEEEE
184 - 203:	EEEEEEEEEEEEEEEEEEEE
185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE
190 - 209:	EEEEEEEEEEEEEEEEEEEE
191 - 210:	EEEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE
194 - 213:	EEEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEEE
196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE

A0A091DPI4 **A0A091DPI4_FUKDA** (82 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MSGDAKEHLDAKELPSPGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVEEEEEEEEWGRNKCLR
KN
```

19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE

A0A091DRH7 **A0A091DRH7_FUKDA** (193 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MPEQQHKQRKQHSTFPCLPIFQFSTPPHCKTQLHASYSARDTVMQFVSSPPPTQGQDAHGRRAVSKREMTHPVEILFMNV
```

```
SSGLSSPYMQRIRREVLIVNSLTVLFAGSEEGKKFKEDQRDKKHVRNLYLHTKMPLFRNATFEGEEEEEEEEEEEEEEEE
EEEEEDEEEEEEEEEEEEEEEEEGEEANIVLEN
```

145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE

A0A091DS60 **A0A091DS60_FUKDA** (95 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MVHSSPHSVTRTPSQVEGLQSYKWLQELHQEYMVQECEKDSPLLEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEENRSSH
```

45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE

A0A091DSC6 **A0A091DSC6_FUKDA** (167 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MTRKSLLSAMKTLSSSCSSKNEFVLEEQSSRNDTVEREKKKKKKKKKKKQKKKKEEEEEEEEEEEEQEEEEEEEEEEEE
EEEEEEEEEQEEQERREQRKKDIYSLDNCQGNSEDSFSLKIEMEASLEQILRFPSPVPAKNEVTQQQTPAPYALCSKGCS
LATNVHK
```

69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE

A0A091DSD2 **A0A091DSD2_FUKDA** (94 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MGYTLVHKAECELFEEGKKKKKKKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EETRKRNEIQRKEL
```

26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE

29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE

A0A091DSY6 **A0A091DSY6_FUKDA** (68 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

MHTFSQKSTDFGKKQKDMIFEEEEEEEEEEEEEEEEEEEEEEEEEEEEEENIYILKNAEIYAFCFFYLK

21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE

A0A091DU49 **A0A091DU49_FUKDA** (157 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MAFELLNKLQLKHHNEKLLSSECISPVVEKCGYTCVYFKIEDSRQQDKAKEEEEEEEEGGGGGGEGEGEGGGEGGEGEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERRRGERREEEEEKGKKKEKKNNSINTKQNHK
```

78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE

A0A091DUA9 **A0A091DUA9_FUKDA** (211 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MNKSKQKEEEQGEGGEEEKGGGKGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEERKRKRKKKRRKKKKRRRRRMRKRRKRKKQ
```

25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE

39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE

91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE

143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE

A0A091DUE8 **A0A091DUE8_FUKDA** (184 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MGGCTWSECEKMGAVLPNVSITQELSFLLQVLESHLKLLIMVDLRSILAFYKDEEEANGTGFDVPLHLDSAPAMGSLPVG
VRLTLKVQISSLLLLSLFCLCTGHICIPQWLHILVAQWLHILVADGLAVLTQGREALKSYLACEEEEEEEEEEEEEEEEE
EEEEEEEEEEEERTLKMSCENMQK
```

144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE

A0A091DUK6 **A0A091DUK6_FUKDA** (146 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MSSGETGPSSDWVDLIIGPTFLEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKKKNTHTH
THKKKDGNVHTQEAALEHASQLRCMRELPDSCLEFQLLRLTSMGRLWWNPRVLTSSKPPRDADVLS
```

23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE

33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE

A0A091DV52 **A0A091DV52_FUKDA** (68 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MWVLSMPVLHVCVIKLEDLHLCPGRLLKEEEEEEEEEEEEEEEEEEEEEEEEEEEKEVHSRYEGIIFT
```

29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE

A0A091DW17 **A0A091DW17_FUKDA** (107 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MEHADEVEFLGLQSDLGWPRVTSVEAVSKKTWRGGRKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEQEEEEEEEEEEEE
EEEEEQEIFLKFWQKLDKGITKVHQYL
```

38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE

A0A091DWM7 **A0A091DWM7_FUKDA** (77 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

MEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEFQRVASAVGEPKVISQSLSKEMIFECEVKKNRSQSYENLRKLHARL

2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE

A0A091DX35 **A0A091DX35_FUKDA** (88 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

MRGVEQGQEKKRSQKIGGLCHQGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVMLMDPFECCEKLGELK
LSFHTPEA

24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE

A0A091DXC6 **A0A091DXC6_FUKDA** (103 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

MARATTALCCQLEPWCSSWYGELCEESTEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEESVESLYETQDSEKAWDRES

29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE

37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE

A0A091DY88 **A0A091DY88_FUKDA** (105 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MSLGEETVSPSFLDQAVVQKFSGTKGGVTILGLPGTEDWGMRRRRGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEGEEEVEEKCSTLDGSAEPYG
```

47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE

65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE

A0A091DYN5 **A0A091DYN5_FUKDA** (130 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MSPFPGGRSNKVAEPGDSGEVVWKQKDAAGQMQGRQEYYLGIEVIQKLKTRARQAVRSKKKEERRKEEEEKKNKKEEEKE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERRGRGGRRGRRRGRRRNN
```

80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE

A0A091DYP0 **A0A091DYP0_FUKDA** (306 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MPWAESKALFADLSCAIISVWPGWEDKYVSLSTKLGELQLIETAAIVQEHSDIRASGQVGPKSAEPQKSHSGNLKIQQAG
GDSKGLSSNLQEIFISVCVQCSLTYITQTEGGGEEEEGKKQEKEEEEEEERKKIEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVKEEERKGRKGIGKGEGEGEEEEEEELWIYQLF
```

135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE

160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE
180 - 199:	EEEEEEEEEEEEEEEEEEEE
181 - 200:	EEEEEEEEEEEEEEEEEEEE
182 - 201:	EEEEEEEEEEEEEEEEEEEE
183 - 202:	EEEEEEEEEEEEEEEEEEEE
184 - 203:	EEEEEEEEEEEEEEEEEEEE
185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE
190 - 209:	EEEEEEEEEEEEEEEEEEEE
191 - 210:	EEEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE
194 - 213:	EEEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEEE
196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE
208 - 227:	EEEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE

212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEEE
225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE
239 - 258:	EEEEEEEEEEEEEEEEEEEE
240 - 259:	EEEEEEEEEEEEEEEEEEEE
241 - 260:	EEEEEEEEEEEEEEEEEEEE
242 - 261:	EEEEEEEEEEEEEEEEEEEE
243 - 262:	EEEEEEEEEEEEEEEEEEEE
244 - 263:	EEEEEEEEEEEEEEEEEEEE
245 - 264:	EEEEEEEEEEEEEEEEEEEE
246 - 265:	EEEEEEEEEEEEEEEEEEEE
247 - 266:	EEEEEEEEEEEEEEEEEEEE
248 - 267:	EEEEEEEEEEEEEEEEEEEE
249 - 268:	EEEEEEEEEEEEEEEEEEEE
250 - 269:	EEEEEEEEEEEEEEEEEEEE
251 - 270:	EEEEEEEEEEEEEEEEEEEE
252 - 271:	EEEEEEEEEEEEEEEEEEEE
253 - 272:	EEEEEEEEEEEEEEEEEEEE
254 - 273:	EEEEEEEEEEEEEEEEEEEE

A0A091DYR2 **A0A091DYR2_FUKDA** (473 aa)
Doublesex-and mab-3-related transcription factor C1. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MWEEKLRFQEETHLTRHLLKNSKRSRERIYDKQGKERDIIIGTALCWRKTRRAGQLKKKKKKKKKKKKKKKKKKKKKRR
RRRRKEEEKKKKRRRRRKEEEEKKKKKKKKKKRRRRRKEEERRRRRKEEEERRRKKKKKKKKKKKKKKKKKKKEEEEEE
EEEEEEEEEEEEEEEEKGQRQTHRLRYAWVLLWFLCGKQQPLGASPTNHRCGPPISLMRRPRDQELESSSTCGLIHGNSA
SQKRKGTGLRNEQRRALPALSALKREQRAQLRKHLAQSLIRPMADIPISHTPMKKLAVDTEVLTEKENAVPQPEACPCAA
PQEESPKGPLLLHWPLGPSSLPCTPTTPEQQLAVSLSGESQGHPALPSMCSSVILDPCATPDPLELQPQLPDASAEASVS
AFLEWERKLEAAKALLALKNSSSAPPPDALPLHQPCSPLAPETEESSFPAPPYDPAERTPLEWLLDICAALFP
```

154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE

156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE

A0A091E0D9 **A0A091E0D9_FUKDA** (143 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MIAVYTGKTDLNPVNTKMKIVKLQIDVTGKMENKEEEAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKKTKKKKR
RRRRRKEDEEEEGEEEEEEEEEEEEEEEEEEEEEEEEGEEEEEEEEEEEEEEEEEEEEEDCIVVEK
```

39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE

A0A091E0L3 **A0A091E0L3_FUKDA** (80 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MGTQASVRGLTHSIKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEEDEEEEEKRIYPVHLWILKRNIIA
```

16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE

A0A091E3L1 **A0A091E3L1_FUKDA** (173 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MKGKKRKEGGGEGGGEEEGEEEGEGGGGTEEEEEEEEEEEEEEEEEEEDTDADEDEEEDKDEEEEKKEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEADTEADEDEEEDKDKEEEEEEEEEEEEEEEEKKKGRRLKRRRKISRNQEGTDSKIR
NQREVGDSDHNAK
```

68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE

A0A091E3W0 **A0A091E3W0_FUKDA** (112 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MNHLQSKAVLRKRIFHKEEEEEEEEGKGEMKKKEKEEKEKRRRRRRRKRKRKKKKKKKKKKKKKKKKKKREEEEEEEEEE
EEEEEEEEEEEEEISLGLSVRVPRDKKKKHSN
```

71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE

A0A091E474 **A0A091E474_FUKDA** (130 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MGVGLLESLLYIPVAEQTMETLYIQIMKRYVLEDLSGTKGTEDPHNRLRRRKGRRGRKGEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERRRRSRKLLMQRFTKGG
```

60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE

76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE

A0A091E4J4 **A0A091E4J4_FUKDA** (174 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MEVETAQSWTGMVGRRRRGEEEEEEEEEEEEEEEEEEEEEGEGGEEEEEEGRKKKKKKEEEEEEEEEEEEEEEEEGEGGEE
EEEEGRKKKKKKEEEEEEEEEEEEEEEEEEEEEEKKKRRKEEKKKRRRKKKKNPPQGQWTSDCERRHRLLQTLHCCEWEREAQ
LGPKGASPVLREQV
```

20 - 39:	EEEEEEEEEEEEEEEEEEEE

A0A091E4N3 **A0A091E4N3_FUKDA** (1844 aa)
WD repeat-containing protein 87. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MKSRSEDMVEKRTFLMTERLPPIQSMVHTGSFHILVVYCGDMLLRLFGDHFRAFKPLGTVPCRFNVTCLCYDPEMKMLLS
GIRGSVVTWVIDQSGKGLQIAHMFSMPGNELVQHIMLNGPNGSLLALCETVVRALERQGQGRLGEVKKFTSTCSGSSITC
CFTSLDQGFLYAGNKAGEIQVWNLSHNKALHSFKAHSALVVCIRSRSEANTLLTAGKEGLMKEWNLTSGNLLRRLELGEE
LYRLQFIDDTIFFCQTTYTFSLHSLPCFYNLFHVCGSAPQHVHRVCRGENWYRILCITEDGLLRFVSPITGALLLLTWPF
SILDQAVDWAYHPGKEELFVATGSTDVLVLDTTRCPCPAKYLLCTSPNSQDFVYCLAYGHFHLGRGIEGLIFSGHQSGII
RVLSQHSCARIEKFVHFGAVLALSTLSAGLLSGQENSLLCSYGMDDYIHLSEAVLDGTKVQLQPLSSILSSCHLKQLVLL
PNAVGAITDSNCLRLWKFHDVMSYESQGGSKFIETLPLHQCTITSFDVCLSLSLFVTAGSDGSVRIWDFHGRLIAMLDSS
LHFGPVCFANDRGDLLVTFNQGLYLLQLTYWDGLNPYEILRCYFGYGREWTLAPDCYIPNSVIRARLWPEGSPIHLQCNL
HSPQRELNWATSQPFFFWHSRVRNLSEAQEYEEKDESFLALRKSKDGTYNVLIDAANRSWLGRKMSEIAISSLIKTILNI
MIHASPMKFQCCIGALGQIFASYQVLPSLRSETAHRLLDDTTNANPLIRELAWEGLKRLGMVTHLFALPLTQGLMDKDER
VRNKALTIMPEIGIHSRTSLLNLIQRQETFQELQQQMVGEESLDRLLGMRPTDLQILFTQVQQRLNENLTLSKEDKKPHF
SLYVSRASVSRSPSIQPATEEVEVKHSKGQRRGRAGGRKHKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEELVTEEQ
RQIQEEQTKIRKQRKVAQNKRQQAKEEKRLAEEEEKLAQEERKLAQEEKKLAQEYVKLSLKDEKMDQEKSMFAKKEEKLA
QREEVLSHKAEQLAHKRKKLAKKLEKTAQEEEKLAKKEEKTIEVQMLLAKKGETLKQKEQRLEWEENDLAQELEELERNM
EDLALKEVELDQEEERLAEEKEELAQEEKILVWREETLAKKEKALAQEEELLVQEEEKLAQDKEKNPREARRLAQKRQKL
IEKKEKLAQEREKLVQNKKEFTQKKERLAQKEENLAQKRKNLAQEEEKLAQRKKYLHHVKEELLQERARLAQVKQKMGTY
KETLDQVEEKLKQEKEIVLKKKEKLDAIEKKLVQAGGILAKNQEKVAQEKMELSLEKKAVFQGRNLLRDELDIAKKETSL
NMEMKMLAQKKIRLAEVMEILSKEGTQETSRKTKLTKQEIDVMKKKLSLEEKIIKYKDRILATEEKDVAKGKLEFTTEQR
VYAKEERKLAKVISKLVKEKKDIFKEPTKKSSVMKVLQKLVSDERKITQEEIKMTKIKRSLIVKESRLSKEQSRLDINEL
NFSEQCGGPAVTTLTCLSRGGHGRAPTEQESELATDEEKLAREQRKLAKKMRNITNQEEKMTGEESRLAKEQREVIQAVE
EEEKIEEEEKIPFFKQKWRKKEQPKEIDTLKGKFYINVYERESEENTSKEIESLLEKVEQDSLSDEEVEEEEDEEEEEEE
EEEEEDEEEQEEEEAAQEEEKKKMEVKEGEMKVEKEEEKEEEEEEEQEEEEAAQEEEKKKMEVKEGEMKVEKEEEKKMEV
QEEEEEEKKEEKEKKRMEKEEKKEKEEKRKKKKKVEEEDEGPKKEEKSMGEEELENLSETEEERSSIEEDKEKDIFKEEK
LFKL
```

922 - 941:	EEEEEEEEEEEEEEEEEEEE
923 - 942:	EEEEEEEEEEEEEEEEEEEE
924 - 943:	EEEEEEEEEEEEEEEEEEEE
925 - 944:	EEEEEEEEEEEEEEEEEEEE
926 - 945:	EEEEEEEEEEEEEEEEEEEE
927 - 946:	EEEEEEEEEEEEEEEEEEEE
928 - 947:	EEEEEEEEEEEEEEEEEEEE
929 - 948:	EEEEEEEEEEEEEEEEEEEE
930 - 949:	EEEEEEEEEEEEEEEEEEEE
931 - 950:	EEEEEEEEEEEEEEEEEEEE

932 - 951:	EEEEEEEEEEEEEEEEEEE
933 - 952:	EEEEEEEEEEEEEEEEEEE
934 - 953:	EEEEEEEEEEEEEEEEEEE
935 - 954:	EEEEEEEEEEEEEEEEEEE

A0A091E5I4 **A0A091E5I4_FUKDA** (311 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MEATSAEIPVYDFEVQESHRRHFQQFLKNTDFHLANGDSQVAEENLRDTVERDGHITYVHDKEVNGEIMFREITLKRKKK
RRRKKEEEEEEEEEEEEEEEEEEEEEGGGGGREKKKNKKEERRRRRRRGRKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKMKKSLENGKERKRLEGGE
```

86 - 105:	EEEEEEEEEEEEEEEEEEE

A0A091E5J7 **A0A091E5J7_FUKDA** (148 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MEGVKGGQEFREEMRTKILHVKAQGPNDECNCTAYLKSANKLNKKEGEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEQEEEEEEEEEGEEEEGKIGDLQENGGVVFKSSASVRFGI
```

53 - 72:	EEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEE

89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE

A0A091E6W6 **A0A091E6W6_FUKDA** (1402 aa)
Serine/threonine-protein kinase Nek1. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MEKYVRLQKIGEGSFGKAILVKSTEDGRQYVIKEINISGMSSKEREESRREVAVLANMKHPSIVQYRESFEEDGSLYIVM
DYCEGGDLFKRINAQKGVLFQEDQFEAGNMKNLVLKIISGSFPPVSLHYSYDLRSLLSQLFKRNPRDRPSVNSILEKGFI
AKRIEKFLSPQLFAEEFCLKTFSKCGAQPMPVKRPASGQSLASVVPAQKITKPAAKYGVPLTYKKLGDKKLPEKKPLLKH
KQAHQTPVKKVNPGEERRKMFEEAPRKKRSECIEKEKKQRYQISLLKAEQMKRQEKERLERINRAREQGWRNVLSAGGSG
EAKAPFFGIGGAVAPSSCSSRGQYEHYHAIFDQMQQQRAEDNEVKWKGEIHGHGLPEREILPGVRPGFPNGAAGHHHFPD
ADAIRKTLKRLKAVSKQANANRHKGLLAVERAKQVEEFLQRKQEAMQNKARAEGHMGILQNLAAMYGGRPSSSRGGKPRN
KEEEVYLARLRQIRLQNFNERQQIKAKLRGEKKEADSCEGQQGTEEADLRRKKIESIKAQTNSRAAILKEQLERKRKEAY
EREKKVWEEHLVAKGVKSSDVSPPSGQHETGGSPSKQQMRSVISVTSALKEVCMDKSLIDSQETSEEMQKANSAISSKRE
ILRRLNENLKAQEDEKGKQHPCDTCKIIVPEDAKENEKEKPVSSDRKKWEIGGQLVIPLDELTLDTSFSAIEKNTVGEVI
KLDPSGSPRKVWGKSSTDSVLKILGEAELQLHTELLESTTVRSEFSPEGEKCKPLIVEEKLQCISQEIKSSTTVDSSAET
KSPKFSETSPQASLEPKGNMEEPDDLETEVLQEPSRKNKDESLPCIVTDVWVSEEKETKETELEDRVAIRQDEVSEDESL
RNVDRLSEVTTEHGLDDSQNSKYDIDKSIQPEPFFQKVVHSEHLNIVSQVHSIQCSPEESIPLRSHSDSPPQYKNKNSLL
IGLSTGLFDANNPKASILLRTCSLPDLSKLFRSLMDVPTVGDVHQDNLEIDEIEDEQIKEGPSDSEDIVFEEADTDLQEL
RASMEQLLREQPGEEYSEEEESALKSSDVEQTANGTDLADEEDNPSSESALNEEWHSDNSDGEATSECEYDSVFNHLEEL
RLHLEQEIGFEKFFEVYEKIKAIHEDEDENIEICSAVVQNILGNEHQHLYAKILHLVMADGAYQEVPNTQKSDHTGINQL
QTTLHPDCELSELTALGSHFLFWDKKVTGTAAVKYFKGKVEIRLRGVSKGTSLSSGEAKDLQWPVSADLLVAVTMWGPYL
CTYLHFPLDHQHPKKEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDHLVHHLEDSGHERELPGCLTASRPIR
ATGWPPVTETHCAVRHGPGNARGVLSLAQERQQVSSFHIPLS
```

1298 - 1317:	EEEEEEEEEEEEEEEEEEEE
1299 - 1318:	EEEEEEEEEEEEEEEEEEEE
1300 - 1319:	EEEEEEEEEEEEEEEEEEEE
1301 - 1320:	EEEEEEEEEEEEEEEEEEEE
1302 - 1321:	EEEEEEEEEEEEEEEEEEEE
1303 - 1322:	EEEEEEEEEEEEEEEEEEEE
1304 - 1323:	EEEEEEEEEEEEEEEEEEEE
1305 - 1324:	EEEEEEEEEEEEEEEEEEEE
1306 - 1325:	EEEEEEEEEEEEEEEEEEEE
1307 - 1326:	EEEEEEEEEEEEEEEEEEEE
1308 - 1327:	EEEEEEEEEEEEEEEEEEEE
1309 - 1328:	EEEEEEEEEEEEEEEEEEEE
1310 - 1329:	EEEEEEEEEEEEEEEEEEEE
1311 - 1330:	EEEEEEEEEEEEEEEEEEEE
1312 - 1331:	EEEEEEEEEEEEEEEEEEEE
1313 - 1332:	EEEEEEEEEEEEEEEEEEEE
1314 - 1333:	EEEEEEEEEEEEEEEEEEEE

A0A091E775 **A0A091E775_FUKDA** (147 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MTDKGPPGKELHKCPSNSQRITLIPLISVWKPQLEAYMDNRNWGTRPPAKGPPRQQLQRRPSERGEEEKKKEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEERILSHCNHWTIPSQFFCSIVVPFWDIDIRNIIYNKLFIFV
```

72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE

86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE

A0A091E7H4 **A0A091E7H4_FUKDA** (68 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MEMTLLLFLDMLCLSHCSIWSLLEERKKKKEEEEEEEEEEEEEEEEEEEEEEEEEEEELPLRLNLSLS
```

31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE

A0A091EAF7 **A0A091EAF7_FUKDA** (68 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MLLLLSSHHPKVSSGGRGGEKEGGGGGGGGGGGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEIK
```

35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE

A0A091ECJ8 **A0A091ECJ8_FUKDA** (1076 aa)
Adenylate cyclase (EC 4.6.1.1). *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MRLEAELGDQETRELLELRGNLADIGLSAEAGPGILSVSSMASRVKNLDTKGELENSPELRGEQTVECVTRGTSEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERIKAGLSGVTQILFVEVKVGWGYQFSLLAVGFGLVVATSHLLVTATL
VPAKRPRLWRTLGANALLFVGVNMFGVFVRIVTERSQRKAFLQARGCIEDRLRLEDENEKQERLLMSLLPRNVAMEMKED
FLKPPERIFHKIYIQRHDNVSILFADIVGFTGLASQCTAQELVKLLNELFGKFDELATENHCRRIKILGDCYYCVSGLTQ
PKADHAHCCVEMGLDMIDTITSVAEATEVDLNMRVGLHTGRVLCGVLGLRKWQYDVWSNDVTLANVMEAAGLPGKVHITK
TTLACLNGDYEVEPGHGHERNSFLKTHNIETFFIVPSHRRKIFPGLILSDIKPAKRMRFKTVCYLLVQLMHCRKMFKAEI
PFSNVMTCEDDDKRRALRTASEKLRNRSSFSANVVYTTPGTRVNRYISRLLEARQPELEMADLNFFTLKYKHVERERKYH
QLQDEYFTSAVVLALILAALFGLIYLLVIPQSVAVLLLLVFCICFLVACVLYLHITRVQCFPGCLTIQIRTVLCVFIVVL
IYSVAQGCVVGCLPWAWSSKSNSSLVVLAAGGRRTVLPALPCESAHHALLCCLVGTLPLAIFLRVSSLPKMILLSGLTTS
YILVLELSGYTKAGGGALSGRSYEPIMAILLFSCTLALHARQVDVRLRLDYLWAAQARWAEEERDDMERVKLDNKRILFN
LLPAHVAQHFLMSNPRNMDLYYQSYSQVGVMFASIPNFNDFYIELDGNNMGVECLRLLNEIIADFDELMEKDFYKDLEKI
KTIGSTYMAAVGLAPTAGSRAKKSISSHLCTLADFAIEMFDVLDEINYQSYNDFVLRVGINVGPVVAGVIGARRPQYDIW
GNTVNVASRMDSTGVQGRIQVTEEVHRLLRKCPYQFVCRGKVSVKGKGEMLTYFLEGRTDGNGVHARPMHLERRMCSYGG
AGGQARRPPLCPAARARLPPAPPGPYLPSTAAGKEA
```

75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE

81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE

A0A091EIS5 **A0A091EIS5_FUKDA** (78 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MAVSGSTCERAWVPEPGGEAAVPLLQAALSLCSPYLAHEGKEEEEEEEEEEEEEEEEEEEEEEEEEEQEKEEEEAPWC
```

42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE

A0A091ELA5 **A0A091ELA5_FUKDA** (84 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MCLSDNIYSEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERRRKKKKKKKKKKKKKKKKKKRKKKKRRKKMENNFTLNSGPK
SSRL
```

10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE

A0A091ELW3 **A0A091ELW3_FUKDA** (148 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MVPLQAREATSNLRPRDTEDQEMGKIRHTYLSYSRVSKHRGQALGSRDANQPTTLIMDKVSAPGEKKIITEFSSKSDSFV
TERRRRRRRGGEEEEEEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERRRRRNKNKYF
```

105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE

110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE

A0A091EPF9 **A0A091EPF9_FUKDA** (177 aa)
Uncharacterized protein. *Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)*

```
MWEEEQDSGEADHAQPLGTQKQRPCWRHQARESLVVKIHFKDNGRWLDCMKISAMEPAKTDNAGEEIKISRFLSFSLKNK
KSEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGMFSYYLYFNLTQSTRMADKAGAMERPPGFYTTSEPEEAKHW
LWLEACSSQFSLLFPTL
```

83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE

A0A091FKV3 **A0A091FKV3_9AVES** (699 aa)
X-linked retinitis pigmentosa GTPase regulator (Fragment). *Cuculus canorus (common cuckoo)*

```
VLESGAIFTFGKSKFAEDVPSKFWFKNDKPVHISCGDEHTAIVTGNGKLYVFGSNNWGQLGLGSKNTVSKPTCVKALKPE
KTKLAVCGRNHTLVYTEKGNVYAAGGNSEGQLGLGDTEERTTFHLISFFTSQHKIKQLAAGSYTSAAVTEDGQLFVWGDN
SEGQIGLADEACVSVPCQVDVGKPVSYVSCGYYHSALITGDGELYTFGEPDNGKLGLLPEQLKNNRVPQPVLGIMEKVNK
VACGGEHTVVLTETDVYTFGLGQYGQLGHGTFIFETSVPKSVKHLRRHKICNITCGENHTAVIAENGLMFTFGDGRHGKL
GLGEESFTNQFDPTLCYNFLSFTVLLVACGGCHMLVFAAPRPKGSEEVLLEDLSENDFNATISKISGESLLTNTLQLTSA
RMRRRREKSPEQFVRMARSLPPLGESFLKSSLPVTSNTSPLWFSTTSLPKAESRKDRDHGKGKNHQKDELSEDSAEDSD
SENNDRNLGDTTDILNMTHAMKLNPSDQSLKLSPLQKQKRVEEEGEGAEEGEGEEGVEAEEEEEEEEGEEEEEEEEEEE
EEEEEEVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGGEEEKGEGEGEEEGEGEGEKEEGEEGPQGEGEEEKRDVGE
EDKEDKREEEEVEEEEKAKGKRKNDSSKLPQTKSKTRKPEKTESTALPNSSKQKIKSKQ
```

568 - 587:	EEEEEEEEEEEEEEEEEEEE
569 - 588:	EEEEEEEEEEEEEEEEEEEE
570 - 589:	EEEEEEEEEEEEEEEEEEEE
571 - 590:	EEEEEEEEEEEEEEEEEEEE
572 - 591:	EEEEEEEEEEEEEEEEEEEE
573 - 592:	EEEEEEEEEEEEEEEEEEEE
574 - 593:	EEEEEEEEEEEEEEEEEEEE
575 - 594:	EEEEEEEEEEEEEEEEEEEE
576 - 595:	EEEEEEEEEEEEEEEEEEEE
577 - 596:	EEEEEEEEEEEEEEEEEEEE
578 - 597:	EEEEEEEEEEEEEEEEEEEE
579 - 598:	EEEEEEEEEEEEEEEEEEEE

580 - 599:	EEEEEEEEEEEEEEEEEEEE

A0A091GH78 **A0A091GH78_9AVES** (457 aa)
Isthmin-2 (Fragment). *Cuculus canorus (common cuckoo)*

```
QVSASSNPHSAGNEELSPSGKARGLRRTGQAGPRRHRRRGMAQQAARSPVVPHPSSTGREESLPFMLDLQSLPGLANVDL
SAQNPNIQVTIEVVDDPQAEMEMDLLKETSNDWSVTSSEWLSHKDLFWPLFWEYTDPPEEEEEEEEEEEEEEEEEEEDD
NLDVGDGEEEEEEEDYTAEYEEEESMLSGVGGDWDQQWPAQKNWIFKEKYSYDYEDEEEWSPWSPCSITCGSGNQKRTRS
CGYACTATESRTCDLPRCPGAEREMVFPTEETPFKSDNTTELFNSEVDSCEKWLNCKSDFLTKYLSKVLTDLPSCPCSYP
LEAVYSAVNLRDEQQGKNFRWRDASGPKERLDIYKPTARFCLRSMLSLDSTTLAAQHCCYDEHTRLITRGKGAGVPNLIS
TEFSPELHYKVDMLPWILCKGDWSRYHAIRPPNNGRRCADNPAEEEYLSQLQEAKEY
```

139 - 158:	EEEEEEEEEEEEEEEEEEEE

A0A091GTS6 **A0A091GTS6_9AVES** (1118 aa)
Myelin transcription factor 1. *Cuculus canorus (common cuckoo)*

```
MSLENDDKRARTRSKSIRVPTELIGQEVSCPTPGCNGSGHIRGKYARHRSLQSCPLAKKRKLQDAEAEHLVSKRKSHPLK
LALDEGYNVDSDGSEEAEVKEESGSDESEGTLEEDEAEAVEQEEIRSPEPAEERSPTKSTHYGQTTATSTSGPSKANYSS
YQEIIANSLLNLGQIAEETLAIEGQLPEAELQVSKPPPNVVHLVHEDAGEELVEEECDKEIIIQTEDAEEVIEVTSERSS
ELCPEHRDDANCEESCKLQKAEAEEEDDEDDEEDEEEEEEEEEEEEEEEEEEEEEEEDEEEEEMAPEVICEEAPCTSQDTQ
KSHCEGQFSPKPEYSVIVEVRSDDDKDDDARSQKSAVTDESEMYDMMTRGNLGLLEQAIALKAEQVKIVREPSRLPGEHV
KHFQVDEKQSKPLDSIRKSYYGKDPSRPEKREIKCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRIPPEILAMHENVLKCP
TPGCTGQGHVNSNRNTHRSLSGCPIAAAEKLAKSHEKQQTQSGDPSKTSSNSDRILRPMCFVKQLEIPQYGSYRPNMVPA
TPRANLAKELEKYSKVTFDYASFDAQVFGKRMLAPKIQTSETSPKAFKCFDYSHDAEAAHMAATAILNLSTRCWEMPENL
STKQQETPSKSMDIEVDENGTLDLSMNKHRKRESTLPSSSSCSSSPSMKSPDVSQRQNSTSATSSTMTSPQSSQTSRQDE
WDGPIDYTKPNRQREEEPEESEPAAHSFASSEADEQEVSEENFEERKYPGEVTLTNFKLKFLSKDIKKELLTCPTPGCDG
SGHITGNYASHRSLSGCPLADKSLRNLMAAHSADLKCPTPGCDGSGHITGNYASHRSLSGCPRAKKSGIKITPTKDDKED
PELMKCPVPGCVGLGHISGKYASHRSASGCPLAARRQKEGSLNGSSFSWKSLKNEGPTCPTPGCDGSGHANGSFLTHRSL
SGCPRAPFAGKKGKLSGDEILNTKFKTSDVLENDEEIKQLNKEISDLNESNSEMEAAMVKLQSQISTMEKNLKNIEEENK
IIEEQNEALFLELSGLSQALIQSLANIRLPHMEPISEQNFDAYVNTLTDMYTNQECYQNPENKDLLESIKQAVKGIQV
```

275 - 294:	EEEEEEEEEEEEEEEEEEEE
276 - 295:	EEEEEEEEEEEEEEEEEEEE
277 - 296:	EEEEEEEEEEEEEEEEEEEE

A0A091H788 **A0A091H788_BUCRH** (307 aa)
Bone sialoprotein 2 (Bone sialoprotein II) (Cell-binding sialoprotein) (Integrin-binding sialoprotein). *Buceros rhinoceros silvestris*

```
MRTVLIFACLVGMACAYSVKSWLQRAKSDDSEENAVFKNRHRYYLYRYVYVHPPQRRYQGSDSSEEEGDGSEEEEEGGLC
PCLPHAAQYWKATTSQHPTNAVLYSLRQGKGCQGLQKGSGNNAAGKGGDSENEDSDENEEEEEEEEEVAENENGINGTST
NTTEGADGPYGNGTKVAEEGTGVAEEEEEEEEEEEEEEEEEEEEETEVTTIASTTSEEGLSQATTMGDGGPTDATTAGEQ
WEYEVTAGGHSRGDESTTDGSYVEQDEYARGDSYRAYEDDYRAYEDEYGYYKGHGYDVYGQDYYYSQ
```

185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE

A0A091ICF3 **A0A091ICF3_CALAN** (309 aa)
Bone sialoprotein 2 (Bone sialoprotein II) (Cell-binding sialoprotein) (Integrin-binding sialoprotein). *Calypte anna (Anna's hummingbird) (Archilochus anna)*

```
MRTALVFACLVGMACAFSVKSWLRRAKSDDSEENAVFKNRHRYYLYRYVYVHPPQMRYQGSDSSEEKGDGSDEEEEGGGV
LRCAHTCPMPRGTKKLKPPEIQLMLCYFPLCQGKDCQGLLNGSRKSAAGKGDDSENEDSDENEEEEEEEEEEEVAEHENG
VNGTSTNTTEGADGPHSNDTVVAEEGTGRAEEEEEEEEEEEEEEEEEEEEEEEETEATTVASTTNEEGLSQATTVGDGEP
TYATTVGEQWEYEVTAGHHGRGDEGTTDGSYVEQDEYARGDSYRAYEDEYGYYKGHGYDVYGQDYYYNQ
```

191 - 210:	EEEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE
194 - 213:	EEEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEEE

A0A091JB80 **A0A091JB80_EGRGA** (251 aa)
Bone sialoprotein 2 (Bone sialoprotein II) (Cell-binding sialoprotein) (Integrin-binding sialoprotein) (Fragment). *Egretta garzetta (Little egret)*

```
VFKNRHRYYLYRYAYVHPPQRRYQGSDSSEEEGDGSEEEEEGGVIVTSRHPTNAALFSPCQGKGCQGSPNGGRNSAAGKG
GESENEDSDEEEEEEEEEEVAENENGINGTSTNTTEGADGPHGNGTSVPKEGTGAAEEEEEEEEEEEEEEEEEEEETEAT
TIASTTGEEGLSQATTTGDGGPTDATTAGEQWEYEVTVGSHGRGDEGTTDSSYGEQDEYARGDSYRAYEDEYGYYKGHGY
DVYGQDYYYSQ
```

137 - 156:	EEEEEEEEEEEEEEEEEEEE

A0A091K645 **A0A091K645_COLST** (293 aa)
Bone sialoprotein 2 (Bone sialoprotein II) (Cell-binding sialoprotein) (Integrin-binding sialoprotein). *Colius striatus (Speckled mousebird)*

```
MRIALVFACLVGMTCAFSVKSWLWRAKSDDSEENTVFKNRHPYYLYRYVYMHPPQQQYQESDSSEEEGDGSEEEEEGGGL
PRVRMAVALCLPTMAGFICPWQGTSPSSTGTGNRAASKGDDSENEDSNENEQEEEEEEEEEVAENENGVNGTSTNTTEGA
DGSHSNGTAVAEEGTGVAEEEEEEEEEEEEEEEEEEEEEIEATTAASTTGEEGLSQATTTDDGGPMDATTTGEQWEYEVTA
RAHSRGDEGTTDGSYTEQDEYARGDSYRAYEDEYGYYKGHGYDVYGQDYYYSQ
```

179 - 198:	EEEEEEEEEEEEEEEEEEEE

A0A091P6Z1 **A0A091P6Z1_APAVI** (1132 aa)
Myelin transcription factor 1. *Apaloderma vittatum (Bar-tailed trogon)*

```
MSLENDDKRARTRSKSIRVPTELIGQEVSCPTPGCNGSGHIRGKYARHRSLQSCPLAKKRKLQDAEAEHLVSKRKSHPLK
LALDEGYNVDSDGSEEAEAKEESGSDESEGTLEEDEGEAVEQEETRSPEPAEERSPAKSTHYGQNTATSTSGPSKANYSS
YQEIIANSLLNLGQIAEETLAIEGQLPEAELQVPKPPSNVVHLVHEDAGEELVEEECDKDIIIQTEDAEEVIEVTSERSS
ELCPEHRDDANCEESCKLEKAEAEEEEEEEEEEEEDEDDEEEEEEEEEEEEEEEEEEEEEEEEMAPEVICEEAPHTSQDTQ
KSHCEGQFSPKPEYSVIVEVRSDDDKDDDARSQKSAVTDESEMYDMMTRGNLGLLEQAIALKAEQVKIVREPSRLPGEHV
KHFQVDEKQNKPLDSIRKSYYGKDPSRPEKREIKCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRIPPEILAMHENVLKCP
TPGCTGQGHVNSNRNTHRSLSGCPIAAAEKLAKSHEKQQTQSADPSKTSSNSDRILRPMCFVKQLEIPQYGSYRPNMVPA
TPRANLAKELEKYSKVTFDYASFDAQVFGKRMLAPKIQTSETSPKAFKCFDYSHDAEAAHMAATAILNLSTRCWEMPENL
STKPQEAPGSCWQLLTLGIFPTFQSMDIEVDENGTLDLSMNKHRKRESTFPSSSSCSSSPSVKSPDVSQRQNSTSATSST
MTSPQSSQTSRQDEWDGPIDYTKPNRQREEEPEESEPAAHSFASSEADEQEVSEENFEERKYPGEVTLTNFKLKFLSKDI
KKELLTCPTPGCDGSGHITGNYASHRSLSGCPLADKSLRNLMAAHSADLKCPTPGCDGSGHITGNYASHRSLSGCPRAKK
SGIKITPTKDDKEDPELMKCPVPGCVGLGHISGKYASHRSASGCPLAARRQKEGSLNGSSFSWKSLKNEGPTCPTPGCDG
SGHANGSFLTHRSLSGCPRATFAGKKGKLSGDEILNTKFKTSDVLENDEEIKQLNKEISELNESNSEMEAAMVKLQSQIS
TMEKNLKNIEEENKIIEEQNEALFLELSGLSQALIQSLANIRLPHMEPISEQNFDAYVNTLTDMYTNQECYQNPENKDLL
ESIKQAVKGIQV
```

280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE

A0A091PG61 **A0A091PG61_HALAL** (257 aa)
Bone sialoprotein 2 (Bone sialoprotein II) (Cell-binding sialoprotein) (Integrin-binding sialoprotein) (Fragment). *Haliaeetus albicilla (White-tailed sea-eagle) (Falco albicilla)*

```
VFKNRHRYYLYRYVYVHPLQQRYQGTDSSEEEGDGSEEEEEGGVSMANQQPAKQIWEFGNFLWGKSCQGPLKGGRSSTAG
KGGDSENEDSDENEEEEEEEEVTENENGINGTSTNTTEKADGPHGNGTAVAEESTGTAEEEEEEEEEEEEEEEEEEEEE
EETEVTTITSTTGEDGLSQATTMGDGGPTDATTVGEQWEYEVTAADHRRGEEGTTDGSYRDQDEYTRGDSYRAYEDEYGY
YKGHGYDVYGQDYYYSQ
```

139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE

A0A091QCD7 **A0A091QCD7_MERNU** (555 aa)
Serine/threonine-protein kinase RIO1 (EC 2.7.11.1) (Fragment). *Merops nubicus (Northern carmine bee-eater)*

```
SELTQETEAAHEDELTESCPSCMCKEAHAEEGDGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDWDWDDEMGRLTRR
HNSAGGCNPQANRQAPNSAKMSTPTDKALRKFEHKINLDKLNFDDCVINRVTEKSRQKEADMYRVKDKSDRATVEQVLDP
RTRMILFKMLTRGVISEINGCISTGKEANVYHASTANGENRAIKIYKTSILMFKDRDKYVSGEFRFRHGYCKGNPRKMVK
TWAEKEMRNLIRLNTAQIPCPEPIMLRSHVLLMGFIGKGDRPAPLLKNAQLSDSKVRELYLQVIHYMRRMYQDARLVHAD
LSEFNMLYHGGALHIIDVSQAVEHDHPHALEFLRKDCANVNDFFQKRNVAVMTVRELFEFITDPSITSENIDDYLSKAME
IAAKRTEEERSSQDKVDEEVFKKAYIPRTLTEVKNYERDVDIMMKLKEEDILYQTVTGLRKDLSGVQKIPALLEKKADES
ETDSDDDDDDGGSSEDSDSGCKESIHPKDKPPEVTIDKKERKKMVKEAQREKRKTKVPKHMKKRKEKTAKMKKGK
```

35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE

42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE

A0A091SEC0 **A0A091SEC0_NESNO** (303 aa)
Bone sialoprotein 2 (Bone sialoprotein II) (Cell-binding sialoprotein) (Integrin-binding sialoprotein). *Nestor notabilis (Kea)*

```
MRTALVFACLVGIACTFSVKSWLRRAKLDDSEENAVFKNRHRYYLYRYAYLHSPQQRYQGSDSSEEEGDGSDEEEEEVGV
STANQQPAKQIREFGDFLWFHGHPIGAAPGDSKGGLGGDLACPQQVWGVDSENEDSDENEEEEEEEEIAENENGVNGTST
NTTEGADGPHGNGTTVAEEGTGAAEEEEEEEEEEEEEEEEEEEEEEEEETEATTIASTTNEEGLSQATTTGHAAPTDATTA
GEQWEYEVTVGGHGWGDEGTTDGSYGEQDEYARGDSYRAYENEYGYYKGHGYDVYGQDYYYSQ
```

185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE

A0A091T6Z8 **A0A091T6Z8_PHALP** (1115 aa)
Myelin transcription factor 1. *Phaethon lepturus (White-tailed tropicbird)*

```
MSLENDDKRARTRSKSIRVPTELIGQEVSCPTPGCNGSGHIRGKYARHRSLQSCPLAKKRKLQDAEAEHLVSKRKSHPLK
LALDEGYNVDSDGSEEAEAKEESGSDESEGTLEEDEAEAVEQEETRSPQPAEERSPAKSTHYGQNTATSTSGPSKANYSS
YQEIIANSLLNLGQIAEETLAIEGQLPEAELQVSKPASNVVHLVHEDAGEELVEEECDKEIIIQTEDAEEVIEVTSERSS
ELCPEHRDDANCEESCKLQKAEAEEEDEEDEEEDEDEEEEEEEEEEEEEEEEEEEEEEEEEMAPEVICEEAPHTSQDTQKSH
CEGQFSPKPEYSVIVEVRSDDDKDDDARSQKSAVTDESEMYDMMTRGNLGLLEQAIALKAEQVKIVREPSRLPGEHVKHF
QVDEKQSKPLDSIRKSYYGKDPSRPEKREIKCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRIPPEILAMHENVLKCPTPG
CTGQGHVNSNRNTHRSLSGCPIAAAEKLAKSHEKQQTQSGDPSKTSSNSDRILRPMCFVKQLEIPQYGSYRPNMVPATPR
ANLAKELEKYSKVTFDYASFDAQVFGKRMLAPKIQTSETSPKAFKCFDYSHDAEAAHMAATAILNLSTRCWEMPENLSTK
QQEAPGKPMDIEVDENGTLDLSMNKHRKRESTFPSSSSCSSSPSMKSPDVSQRQNSTSATSSTMTSPQSSQTSRQDEWDG
PIDYTKPNRQREEEPEESEPAAHSFASSEADEQEVSEENFEERKYPGEVTLTNFKLKFLSKDIKKELLTCPTPGCDGSGH
ITGNYASHRSLSGCPLADKSLRNLMAAHSADLKCPTPGCDGSGHITGNYASHRSLSGCPRAKKSGIKITPTKDDKEDPEL
MKCPVPGCVGLGHISGKYASHRSASGCPLAARRQKEGSLNGSSFSWKSLKNEGPTCPTPGCDGSGHANGSFLTHRSLSGC
PRATFAGKKGKLSGDEILNTKFKTSDVLENDEEIKQLNKEISELNESNSEMEAAMVKLQSQISTMEKNLKNIEEENKIIE
EQNEALFLELSGLSQALIQSLANIRLPHMEPISEQNFDAYVNTLTDMYTNQECYQNPENKDLLESIKQAVKGIQV
```

277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE

A0A091TSV5 **A0A091TSV5_PHORB** (277 aa)
Isthmin-2 (Fragment). *Phoenicopterus ruber ruber*

```
DLQSLPGLANVDLSAQNPNIQVTIEVVDDPQAEMEMDLLKETSNDWSLTSSEWLSHKDLFWPLFWEYTDPAEEEEEEEEE
EEEDDNLDVGDRDEEEEEEEEEEEEEEEEEEEEEEEDYTAEYEEEESMLSGVGGDWDQRWPGQKNWIFKEKYNYDYEDEEEW
SPWSPCSITCGSGNQKRTRSCGYACTATESRTCDLPHCPGAEAEMVFPTEETPFKSDNTTELFNSEVDSCEKWLNCKSDF
LTKYLSKVLTDLPSCPCSYPLEAVYSAVNLQDERQGK
```

94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE

A0A091VNY6 **A0A091VNY6_NIPNI** (289 aa)
Bone sialoprotein 2 (Bone sialoprotein II) (Cell-binding sialoprotein) (Integrin-binding sialoprotein). *Nipponia nippon (Crested ibis) (Ibis nippon)*

```
MRTALVFACLVGMACSFSVKSWLQRAKSDDSEENAVFKNRHRYYLYRYAYVHPPQRWYQGSDSSEEEGDGSEEEEEGGVT
AASQHPTNAVLFSSCQGKGCQGPLKGGRNSAAGKGGDSENEDSDENEEEEEEEEVAENENGINGTSTNTTKGADAPHGNG
TAAAEEGTGAAEEEEEEEEEEEEEEEEEEEEEEEEETEATTVISTTGEEGLSQATTIGDGGPTDATTAGEQWEYEVTAGGHG
RGDEGTTDGSYGEQDEYARGDSYRAYEDEYGYYKGHGYDMYGQDYYYSQ
```

172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE

A0A091VW73 **A0A091VW73_NIPNI** (1117 aa)
Myelin transcription factor 1. *Nipponia nippon (Crested ibis) (Ibis nippon)*

```
MSLENDDKRARTRSKSIRVPTELIGQEVSCPTPGCNGSGHIRGKYARHRSLQSCPLAKKRKLQDAEAEHLVSKRKSHPLK
LALDEGYNVDSDGSEEAEAKEESGSDESEGTLEEDEAEAVEQEETRSPELAEERSPAKSTHYGQNTATSTSGPSKANYSS
YQEIIANSLLNLGQIAEETLAIEGQLPEAELQVSKPPSNVVHLVHEDAGEELVEEECDKEIIIQTEDAEEVIEVTSERSS
ELCPEHRDDANCEESCKLQKAEAEEEDEEDEEEDEDEEEEEEEEEEEEEEEEEEEEEEEEEMAPEVICEEAPHTSQDTQK
SHCEGQFSPKPEYSVIVEVRSDDDKDDDARSQKSAVTDESEMYDMMTRGNLGLLEQAIALKAEQVKIVREPSRLPGEHVK
HFQVDEKQSKPLDSIRKSYYGKDPSRPEKREIKCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRIPPEILAMHENVLKCPT
PGCTGQGHVNSNRNTHRSLSGCPIAAAEKLAKSHEKQQTQSGDPSKTSSNSDRILRPMCFVKQLEIPQYGSYRPNMVPAT
PRANLAKELEKYSKVTFDYASFDAQVFGKRMLAPKIQTSETSPKAFKCFDYSHDAEAAHMAATAILNLSTRCWEMPENLS
TKQQEAPSKSMDIEVDENGTLDLSMNKHRKRESTFPSSSSCSSSPSMKSPDVSQRQNSTSATSSTMTSPQSSQTSRQDEW
DGPIDYTKPNRQREEEPEESEPAAHSFASSEADEQEVSEENFEERKYPGEVTLTNFKLKFLSKDIKKELLTCPTPGCDGS
GHITGNYASHRSLSGCPLADKSLRNLMAAHSADLKCPTPGCDGSGHITGNYASHRSLSGCPRAKKSGIKITPTKDDKEDP
ELMKCPVPGCVGLGHISGKYASHRSASGCPLAARRQKEGSLNGSSFSWKSLKNEGPTCPTPGCDGSGHANGSFLTHRSLS
GCPRATFAGKKGKLSGDEILNTKFKTSDVLENDEEIKQLNKEISELNESNSEMEAAMVKLQSQISTMEKNLKNIEEENKI
IEEQNEALFLELSGLSQALIQSLANIRLPHMEPISEQNFDAYVNTLTDMYTNQECYQNPENKDLLESIKQAVKGIQV
```

277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE

A0A091VYW2 **A0A091VYW2_OPIHO** (294 aa)
Bone sialoprotein 2 (Bone sialoprotein II) (Cell-binding sialoprotein) (Integrin-binding sialoprotein). *Opisthocomus hoazin (Hoatzin) (Phasianus hoazin)*

```
MRTALVFACLVGMACAFSVKSWLRQAKSDDSEENAVFKNRHRYYLYRYTYVYPPQRRYQGSDSSEEEGDGSEEEKEDEGG
VIATSLCSTNAVLFPPCQGKGCQGPWKGGRNSAVVKGGDSEDEDSDENEEEEEEEEVVENENGVNGTRTNTTEGADGPHG
NGTMVAEEGTGAAEEEEEEEEEEEEEEEEEEEEEEEEEETEATTVASTTSEEGLSQATTTEDGGPTDTTTAGEQWEYEVT
AGGHGRGDEGTTDGNYGEQDEYARGDSYRAYEDEYGYYKGHGYDVYGQDYYYSQ
```

174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE
180 - 199:	EEEEEEEEEEEEEEEEEEEE

A0A091W5P8 **A0A091W5P8_OPIHO** (1118 aa)
Myelin transcription factor 1. *Opisthocomus hoazin (Hoatzin) (Phasianus hoazin)*

```
MSLENDDKRARTRSKAIRVPTELIGQEVSCPTPGCNGSGHIRGKYARHRSLQSCPLAKKRKLQDAEAEHLVSKRKSHPLK
LALDEGYNVDSDGSEEAEVKEESGSDESEGTLEEDEAEAVEQEETRSPEPAEERSPAKSTHYGQNTSTSTSGPSKANYSS
YQEIIANSLLNLGQIAEETLAIEGQLPEAELQVSKPPSNVVHLVHEDTGEELVEEECDKEIIIQTEDAEEVIEVTSERSS
ELCPEHRDDANCEESCKLEKAEAEEEDEEDEEEDEDEEEEEEEEEEEEEEEEEEEEEEEEEEMAPEVICEEAPHTSQDTQ
KSHCEGQFSPKPEYSVIVEVRSDDDKDDDARSQKSAVTDESEMYDMMTRGNLGLLEQAIALKAEQVKIVREPSRLPGEHV
KHFQVDEKQSKPLDSVRKSYYGKDPSRPEKREIKCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRIPPEILAMHENVLKCP
TPGCTGQGHVNSNRNTHRSLSGCPIAAAEKLAKSHEKQQTQSGDPSKTSSNSDRILRPMCFVKQLEIPQYGSYRPNMVPA
TPRANLAKELEKYSKVTFDYASFDAQVFGKRMLAPKIQTSETSPKAFKCFDYSHDAEAAHIPATAILNLSTRCWEMPENL
STKQQEAPGKSMDIEVDENGTLDLSMNKHRKRESTFPSSSSCSSSPSMKSPDVSQRQNSTSATSSTMTSPQSSQTSRQDE
WDGPIDYTKPNRQREEEPEESEPAAHSFASSEADEQEVSEENFEERKYPGEVTLTNFKLKFLSKDIKKELLTCPTPGCDG
SGHITGNYASHRSLSGCPLADKSLRNLMAAHSADLKCPTPGCDGSGHITGNYASHRSLSGCPRAKKSGIKITPTKDDKED
PELMKCPVPGCVGLGHISGKYASHRSASGCPLAARRQKEGSLNGSSFSWKSLKNEGPTCPTPGCDGSGHANGSFLTHRSL
SGCPRATFAGKKGKLSGDEILNTKFKTSDVLENDEEIKQLNKEISELNESNSEMEAAMVKLQSQISTMEKNLKNIEEENK
IIEEQNEALFLELSGLSQALIQSLANIRLPHMEPISEQNFDAYVNTLTDMYTNQECYQNPENKDLLESIKQAVKGIQV
```

277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE

A0A093EEF8 **A0A093EEF8_TAUER** (306 aa)
Bone sialoprotein 2 (Bone sialoprotein II) (Cell-binding sialoprotein) (Integrin-binding sialoprotein). *Tauraco erythrolophus (Red-crested turaco)*

```
MRSALLFACLLGMACAFSVKSWLRRAKSDDSEENAVFKNRHRYYLYRYVYMHPPQRRYQGSDSSEEEGDGSEEEEEGGGC
APPMLLTTSPLLCLSLQEPSHAGTQAVGHPAGTAPGDSQGGLGGDIASPQQVWGDSENEDSDENEEEEEEEEEEVAENEN
GVNGTSTNTTEGADGPHGNGTVAAEEGTGAAEEEEEEEEEEEEEEEEEEEEEETEATTVASTTGEEGLSQATTIGDGGPT
DATTAAEQWEYEVTARGHGDEGTTDGSYGEQDEYARGDSYRAYEDEYSYYKGHGYDVYGQDYYYSQ
```

192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE
194 - 213:	EEEEEEEEEEEEEEEEEEEE

A0A093EQV0 **A0A093EQV0_9AVES** (195 aa)
Bone sialoprotein 2 (Bone sialoprotein II) (Cell-binding sialoprotein) (Integrin-binding sialoprotein) (Fragment). *Pterocles gutturalis (yellow-throated sandgrouse)*

```
CQGPQNGGRNGAAGKGGDSENEDSDENEEEEEEEEEEEEEEVAENENGINGTSTNTTEGTDGAHGNGTTAVEEEGTGAAEE
EEEEEEEEEEEEEEEEEEEETEATTVASTTGEEGLSQATTVADGGPTDATTIAEQWEYEVTAGGHARGDEGTTDGSYGEQ
DEYARGDSYRAYEDEYGYYKGHGYDVYGQDYYYSQ
```

79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE

A0A093IJ94 **A0A093IJ94_FULGA** (262 aa)
Bone sialoprotein 2 (Bone sialoprotein II) (Cell-binding sialoprotein) (Integrin-binding sialoprotein) (Fragment). *Fulmarus glacialis (Northern fulmar)*

```
VFKNRHRYYLYRYAYVYPPQQRYQGSDSSEEEGDGSEEEQEGGGLPRAGMAVTPRLPTSAGFICWWQAGYPAGAAPGDSQ
GRLGGDVASPQQVWGDSENEDSDENEEEEEEEEEEEVAENENGINGTSTNATEGADGPHGTEEEEEEEEEEEEEEEEEEE
EEEEEEETEATTVASTTGKEELSQVTTTGDRGPTDATTAGEQWEYEVTAGGRGRGDEGTTDGSYGEQDEYARGDSYQAYE
DEFGYYKGHGYDVYGQDYYYSQ
```

142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE

A0A093LS13 **A0A093LS13_EURHL** (289 aa)
Bone sialoprotein 2 (Bone sialoprotein II) (Cell-binding sialoprotein) (Integrin-binding sialoprotein). *Eurypyga helias (Sunbittern)*

```
MRTALLFICLLGMACAFSVKSWLRRTKSDDSEENAVFKNRHRYYLYRYAYVHPPQRRYQGSDSSEEEGEGSEEEEGGVTP
ESSDLLTNAALSSPCQGKGCQGPLKGDRYSAVGKGGDSENEDSDENEEEEKEEEEEVAENENGVNGTSTNTTEGADGPHG
NGTAVAEEGTGAAEEEEEEEEEEEEEEEEEEEEEETEATTIASTTGEEGLSQATTTGDVGPTDATTAAEQWEYEVTVGGHG
RGDEGTTDGSYGEQDEYARGDSYRTYEDEYGYYKGHGYDVYGQDYYYSQ
```

174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE

A0A093QCE8 **A0A093QCE8_9PASS** (306 aa)
Bone sialoprotein 2 (Bone sialoprotein II) (Cell-binding sialoprotein) (Integrin-binding sialoprotein). *Manacus vitellinus (golden-collared manakin)*

```
MRTVLVFVCLVGMACAFSVKSWLRRAKLDDSEENAVFKNRHRHYLYRYIYVYPPQRRYQGSDSSEEEGDGSEEEEEGGVS
MANQQLAKQIREIGNFLWFSGHPAGAAPGDCQGTLKGVRHGTASKGEDSENEDSDENEEEEEEEEEVDENENGINGTSTN
TTEGADGPHGNGTAVAEEGTGAAEEEEEEEEEEEEEEEEEEEEEEEETEATTIASTTDEEGLTQATTVGDGGPTDATTDA
TTVGELWDYDVTARDHSRGDEGTTAGGYEEQDEYARGDSYRAYEDEYGYYKGHGYDVYGQDYYYSQ
```

184 - 203:	EEEEEEEEEEEEEEEEEEEE
185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE

A0A093RF06 **A0A093RF06_PYGAD** (291 aa)
Bone sialoprotein 2 (Bone sialoprotein II) (Cell-binding sialoprotein) (Integrin-binding sialoprotein). *Pygoscelis adeliae (Adelie penguin)*

```
MRTALVFACLVGMACAFSVKSWLRRAKSDDLEENGVFKNRHRYYLYRYAYVHPPQRQYQGSDSSEEEGDGSEEEGGVSTA
NQQPAKQIRELGNFLWFCTGHPAGAAPGDSQDGLEGDVASPQQVWNSAAGKGGDSENEDSDENEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEETEATKATTITSTTGEEGLSQATTTGDGGPTDATTAGEQWEYEVTARG
RSRGDEGTTEGSYGEQDEYARGDSYQAYEDEYGYYKGHGYDVYGQDYYYSQ
```

144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE

A0A093VAY4 **A0A093VAY4_TALMA** (694 aa)
Dynein heavy chain-like protein. *Talaromyces marneffei PM1*

```
MGSVIQRLISISKDLDTARNEVAKQDVQHQYDAERLQKKIRTLEGQRGCDQKRIKKLQSELADLRHYKKATNPGAQDEEE
GEEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGDDGSDDRIIEVKLQKLKDTYDPANITALAWPEGHLDVPI
VSSIQRLKDSYNDLYKETAALVKIMSSLRAQVKHHKRRAEQWQRWCAGLSAQNMAPPIAQVVRQQNDAPSTPASARTQIM
GHNVPNSSVVASTASNSSPIPPVLSREVSGTHSESNDGDQSRIIRVKDEPLSTGPLEGSSLGQEIFPAASEDLDEVGDAV
TTPRSRRFAVFEDGVYRLQQEGPITTPSFQSGERRAFQPKDTNQINHFRTPQESAFKRRKTCDSGASAISTVAEDGEDQN
YIPSVMKVATIENNTPSKGPVRHPNAHRRLDDLLAARPQRQSPALDRPAIRSPVQSAIPVPCPGHQTPSVSVNQTPSSNG
PTKTITNYMKATGKRAAAKRKFQLETNANTNSEEDWEAIVESVPFRELPVDCLNLSHFKPNPGRNQGLDYAFKDVVRGSE
RKCLPGCMRADCCGDKFRAMVRATGIKYDAEKHRALLEEHLGDRKSTLQQMSEQTLNGLLIEAKATQLANQFGKHRHAYE
RARSPPGFWRTDMPSTQELAKDRIEADRMERVKILERVAEAMRPDGLWKFADEI
```

88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE

94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE

A0A093XHK4 **A0A093XHK4_9PEZI** (388 aa)
NADAR domain-containing protein. *Pseudogymnoascus sp. VKM F-3808*

```
MPPIFFWRDTNPPFAFLSQDSRTPFHDNDTETVWPSAEHYMLSEMAMLFAAPDVAARIAHTASVDEVRELACGVDAFDEK
IWEEDRYGIVEEATYHKFAHSLVQDRDLKAELLGTGEDELVLASPLDGIWGIGYEAGEAVGKRDTWGTNLLGKALMMARA
WIRMEEIGSATWEKGGAFDVTAEQRRHDMPMEVQTYEASKGYISPSDHKYWDTEREEGLAAEYYDKTREFGPPGGYPDHA
AGGPEQTEGTKAIEGGAPEPSSSDALAVIGAVGAGELALREARGGSYGVDEEENSDDELRKEVIDNLFQRKPEEIEDSSS
DESEDEKPPEPDSSSDEEDEPESEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDAGSDSDGDSD
```

344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE

A0A093Y5H3 **A0A093Y5H3_9PEZI** (98 aa)
Uncharacterized protein. *Pseudogymnoascus sp. VKM F-3557*

```
MCKRIILIFPCGCRKSSTVKTCGYVGQQGHRIVDTGRIKRRSRDCNECFATEECGSEDWEGEEEEEEEEEEEEEEEEEE
EEDEDAWEGEEEEEGEEA
```

62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE

A0A093YAU6 **A0A093YAU6_9PEZI** (1211 aa)
CobW C-terminal domain-containing protein. *Pseudogymnoascus sp. VKM F-3557*

```
MPSKRSSSSRRQQQQDPQPAAKKHKNNSSKYSKKQDTVMMPISITGEKIATFKTLPITLLSGFLGSGKTTLLQYILHSKD
HGLRIAIIVNDMAAVNVDANLIRSSMSSSNPASQQKLVAMQNGCICCTLRGDFVLELARLAKDGQYDYVLIESTGISEPQ
QVAESFTKEFSLAIVEAEREDGEGETTWSKEEKGILGKLAENGGLNSIAKIDTTVTVVDAFRFFEEFETVELLHQRFASE
VETPEDERTVTDLMIDQIEFADVIIVNKIDMVDDKVLIRIRGLIKTLNPGCKILETALRASKQSENPFGAVSLDVKEIIA
TGLYSEETSIKSSGWLKSVHDMSIIDSHGRKVLAPKPETEEYGINSFVYRSRRPFHPARLYELVHDKFVILEPQNEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEDENSEHELISSSSSATAEGEHFESLQQQDSPISTPPATLNSPTITAATTTTSPSTSFTE
DANKLTQYPDIPLEQRLTNKKAHPLFSRLLRSKGFIWLATRPKLSGDWSQAGAMLTFSPGLQWFTTLPEDEWPLPAGDAG
KEVKNVIKKDFEGEWGDRRQEVVLIGEGLDVDRLTACLDSCLLSVEEMQEWEGVMRMDCDEEKREDMLNDLFEDGWEEWD
DPQSMMNGDEEGHVHGPAWYVDLNCLIESRLRLLLTMGPIPYNTLQEWKQHVLSMSDPFIARIPKIELHVHIEGTLTPEL
RWELGQRNGILIKSDRLQRTFYSLEQLKEMYNLLEPRSIKGANQVSAFFDAYYGGMEVLQTEEDFYDLAMHYFVKAASMQ
VRYCEPFFDPQAHTRRGVKFQTFMRGFRRAQTDSERDLNVKSQWIMCILRDLPLTSAMEHYEAALPYKEMIVGIGLDSNE
YDRPPLLFEALYQRARADGFKITSHCDVTQKDTHEHIRQVAESIGGTGADRCDHGLDAAECPDLVALIKQKGLGMTLCPW
AYVRHHTEADLFQHIRTLFDSDIKINISSDSPVYVEGNWITHNLLLLRFKCKFTDDEIAKVERNSVEVCWATEDVKRCIL
KEIDSFCVSPI
```

396 - 415:	EEEEEEEEEEEEEEEEEEEE
397 - 416:	EEEEEEEEEEEEEEEEEEEE

398 - 417:	EEEEEEEEEEEEEEEEEEEE
399 - 418:	EEEEEEEEEEEEEEEEEEEE
400 - 419:	EEEEEEEEEEEEEEEEEEEE
401 - 420:	EEEEEEEEEEEEEEEEEEEE
402 - 421:	EEEEEEEEEEEEEEEEEEEE
403 - 422:	EEEEEEEEEEEEEEEEEEEE
404 - 423:	EEEEEEEEEEEEEEEEEEEE
405 - 424:	EEEEEEEEEEEEEEEEEEEE
406 - 425:	EEEEEEEEEEEEEEEEEEEE
407 - 426:	EEEEEEEEEEEEEEEEEEEE
408 - 427:	EEEEEEEEEEEEEEEEEEEE
409 - 428:	EEEEEEEEEEEEEEEEEEEE
410 - 429:	EEEEEEEEEEEEEEEEEEEE
411 - 430:	EEEEEEEEEEEEEEEEEEEE
412 - 431:	EEEEEEEEEEEEEEEEEEEE
413 - 432:	EEEEEEEEEEEEEEEEEEEE
414 - 433:	EEEEEEEEEEEEEEEEEEEE
415 - 434:	EEEEEEEEEEEEEEEEEEEE
416 - 435:	EEEEEEEEEEEEEEEEEEEE
417 - 436:	EEEEEEEEEEEEEEEEEEEE
418 - 437:	EEEEEEEEEEEEEEEEEEEE
419 - 438:	EEEEEEEEEEEEEEEEEEEE
420 - 439:	EEEEEEEEEEEEEEEEEEEE
421 - 440:	EEEEEEEEEEEEEEEEEEEE
422 - 441:	EEEEEEEEEEEEEEEEEEEE
423 - 442:	EEEEEEEEEEEEEEEEEEEE
424 - 443:	EEEEEEEEEEEEEEEEEEEE
425 - 444:	EEEEEEEEEEEEEEEEEEEE
426 - 445:	EEEEEEEEEEEEEEEEEEEE
427 - 446:	EEEEEEEEEEEEEEEEEEEE
428 - 447:	EEEEEEEEEEEEEEEEEEEE
429 - 448:	EEEEEEEEEEEEEEEEEEEE
430 - 449:	EEEEEEEEEEEEEEEEEEEE
431 - 450:	EEEEEEEEEEEEEEEEEEEE
432 - 451:	EEEEEEEEEEEEEEEEEEEE
433 - 452:	EEEEEEEEEEEEEEEEEEEE
434 - 453:	EEEEEEEEEEEEEEEEEEEE
435 - 454:	EEEEEEEEEEEEEEEEEEEE
436 - 455:	EEEEEEEEEEEEEEEEEEEE
437 - 456:	EEEEEEEEEEEEEEEEEEEE
438 - 457:	EEEEEEEEEEEEEEEEEEEE
439 - 458:	EEEEEEEEEEEEEEEEEEEE
440 - 459:	EEEEEEEEEEEEEEEEEEEE
441 - 460:	EEEEEEEEEEEEEEEEEEEE
442 - 461:	EEEEEEEEEEEEEEEEEEEE
443 - 462:	EEEEEEEEEEEEEEEEEEEE
444 - 463:	EEEEEEEEEEEEEEEEEEEE
445 - 464:	EEEEEEEEEEEEEEEEEEEE
446 - 465:	EEEEEEEEEEEEEEEEEEEE
447 - 466:	EEEEEEEEEEEEEEEEEEEE
448 - 467:	EEEEEEEEEEEEEEEEEEEE
449 - 468:	EEEEEEEEEEEEEEEEEEEE

450 - 469:	EEEEEEEEEEEEEEEEEEEE
451 - 470:	EEEEEEEEEEEEEEEEEEEE
452 - 471:	EEEEEEEEEEEEEEEEEEEE
453 - 472:	EEEEEEEEEEEEEEEEEEEE
454 - 473:	EEEEEEEEEEEEEEEEEEEE
455 - 474:	EEEEEEEEEEEEEEEEEEEE
456 - 475:	EEEEEEEEEEEEEEEEEEEE
457 - 476:	EEEEEEEEEEEEEEEEEEEE
458 - 477:	EEEEEEEEEEEEEEEEEEEE
459 - 478:	EEEEEEEEEEEEEEEEEEEE
460 - 479:	EEEEEEEEEEEEEEEEEEEE
461 - 480:	EEEEEEEEEEEEEEEEEEEE
462 - 481:	EEEEEEEEEEEEEEEEEEEE
463 - 482:	EEEEEEEEEEEEEEEEEEEE
464 - 483:	EEEEEEEEEEEEEEEEEEEE
465 - 484:	EEEEEEEEEEEEEEEEEEEE
466 - 485:	EEEEEEEEEEEEEEEEEEEE
467 - 486:	EEEEEEEEEEEEEEEEEEEE
468 - 487:	EEEEEEEEEEEEEEEEEEEE
469 - 488:	EEEEEEEEEEEEEEEEEEEE
470 - 489:	EEEEEEEEEEEEEEEEEEEE
471 - 490:	EEEEEEEEEEEEEEEEEEEE
472 - 491:	EEEEEEEEEEEEEEEEEEEE
473 - 492:	EEEEEEEEEEEEEEEEEEEE
474 - 493:	EEEEEEEEEEEEEEEEEEEE
475 - 494:	EEEEEEEEEEEEEEEEEEEE
476 - 495:	EEEEEEEEEEEEEEEEEEEE
477 - 496:	EEEEEEEEEEEEEEEEEEEE
478 - 497:	EEEEEEEEEEEEEEEEEEEE
479 - 498:	EEEEEEEEEEEEEEEEEEEE
480 - 499:	EEEEEEEEEEEEEEEEEEEE
481 - 500:	EEEEEEEEEEEEEEEEEEEE
482 - 501:	EEEEEEEEEEEEEEEEEEEE
483 - 502:	EEEEEEEEEEEEEEEEEEEE
484 - 503:	EEEEEEEEEEEEEEEEEEEE
485 - 504:	EEEEEEEEEEEEEEEEEEEE
486 - 505:	EEEEEEEEEEEEEEEEEEEE
487 - 506:	EEEEEEEEEEEEEEEEEEEE
488 - 507:	EEEEEEEEEEEEEEEEEEEE
489 - 508:	EEEEEEEEEEEEEEEEEEEE
490 - 509:	EEEEEEEEEEEEEEEEEEEE
491 - 510:	EEEEEEEEEEEEEEEEEEEE
492 - 511:	EEEEEEEEEEEEEEEEEEEE
493 - 512:	EEEEEEEEEEEEEEEEEEEE
494 - 513:	EEEEEEEEEEEEEEEEEEEE
495 - 514:	EEEEEEEEEEEEEEEEEEEE
496 - 515:	EEEEEEEEEEEEEEEEEEEE
497 - 516:	EEEEEEEEEEEEEEEEEEEE
498 - 517:	EEEEEEEEEEEEEEEEEEEE
499 - 518:	EEEEEEEEEEEEEEEEEEEE
500 - 519:	EEEEEEEEEEEEEEEEEEEE
501 - 520:	EEEEEEEEEEEEEEEEEEEE

502 - 521:	EEEEEEEEEEEEEEEEEEEE
503 - 522:	EEEEEEEEEEEEEEEEEEEE
504 - 523:	EEEEEEEEEEEEEEEEEEEE
505 - 524:	EEEEEEEEEEEEEEEEEEEE
506 - 525:	EEEEEEEEEEEEEEEEEEEE
507 - 526:	EEEEEEEEEEEEEEEEEEEE
508 - 527:	EEEEEEEEEEEEEEEEEEEE
509 - 528:	EEEEEEEEEEEEEEEEEEEE
510 - 529:	EEEEEEEEEEEEEEEEEEEE
511 - 530:	EEEEEEEEEEEEEEEEEEEE
512 - 531:	EEEEEEEEEEEEEEEEEEEE
513 - 532:	EEEEEEEEEEEEEEEEEEEE
514 - 533:	EEEEEEEEEEEEEEEEEEEE
515 - 534:	EEEEEEEEEEEEEEEEEEEE
516 - 535:	EEEEEEEEEEEEEEEEEEEE
517 - 536:	EEEEEEEEEEEEEEEEEEEE
518 - 537:	EEEEEEEEEEEEEEEEEEEE
519 - 538:	EEEEEEEEEEEEEEEEEEEE
520 - 539:	EEEEEEEEEEEEEEEEEEEE
521 - 540:	EEEEEEEEEEEEEEEEEEEE
522 - 541:	EEEEEEEEEEEEEEEEEEEE
523 - 542:	EEEEEEEEEEEEEEEEEEEE
524 - 543:	EEEEEEEEEEEEEEEEEEEE
525 - 544:	EEEEEEEEEEEEEEEEEEEE
526 - 545:	EEEEEEEEEEEEEEEEEEEE
527 - 546:	EEEEEEEEEEEEEEEEEEEE
528 - 547:	EEEEEEEEEEEEEEEEEEEE
529 - 548:	EEEEEEEEEEEEEEEEEEEE
530 - 549:	EEEEEEEEEEEEEEEEEEEE
531 - 550:	EEEEEEEEEEEEEEEEEEEE
532 - 551:	EEEEEEEEEEEEEEEEEEEE
533 - 552:	EEEEEEEEEEEEEEEEEEEE
534 - 553:	EEEEEEEEEEEEEEEEEEEE
535 - 554:	EEEEEEEEEEEEEEEEEEEE
536 - 555:	EEEEEEEEEEEEEEEEEEEE
537 - 556:	EEEEEEEEEEEEEEEEEEEE
538 - 557:	EEEEEEEEEEEEEEEEEEEE
539 - 558:	EEEEEEEEEEEEEEEEEEEE
540 - 559:	EEEEEEEEEEEEEEEEEEEE
541 - 560:	EEEEEEEEEEEEEEEEEEEE
542 - 561:	EEEEEEEEEEEEEEEEEEEE
543 - 562:	EEEEEEEEEEEEEEEEEEEE
544 - 563:	EEEEEEEEEEEEEEEEEEEE
545 - 564:	EEEEEEEEEEEEEEEEEEEE
546 - 565:	EEEEEEEEEEEEEEEEEEEE
547 - 566:	EEEEEEEEEEEEEEEEEEEE
548 - 567:	EEEEEEEEEEEEEEEEEEEE
549 - 568:	EEEEEEEEEEEEEEEEEEEE
550 - 569:	EEEEEEEEEEEEEEEEEEEE
551 - 570:	EEEEEEEEEEEEEEEEEEEE
552 - 571:	EEEEEEEEEEEEEEEEEEEE
553 - 572:	EEEEEEEEEEEEEEEEEEEE

554 - 573:	EEEEEEEEEEEEEEEEEEEE
555 - 574:	EEEEEEEEEEEEEEEEEEEE
556 - 575:	EEEEEEEEEEEEEEEEEEEE
557 - 576:	EEEEEEEEEEEEEEEEEEEE
558 - 577:	EEEEEEEEEEEEEEEEEEEE
559 - 578:	EEEEEEEEEEEEEEEEEEEE
560 - 579:	EEEEEEEEEEEEEEEEEEEE
561 - 580:	EEEEEEEEEEEEEEEEEEEE
562 - 581:	EEEEEEEEEEEEEEEEEEEE

A0A093YDS9 **A0A093YDS9_9PEZI** (571 aa)
Uncharacterized protein. *Pseudogymnoascus sp. VKM F-3808*

```
MSLSDAIAKRAQRLLERKSLDDQLPALKPRSKERERIIVEKKISDLDKEIQKDDSEIKKLEIEDAEKQKKLAEKAAAEEV
AKKAAEEEAAKKAAEEEAAKKAAEENAAEDADNENPQMTEEEKAAKKAADEEAAKKAADEEAAKKAADEAAKKAAEDKA
AREPPSDNENDDIISRLRKGQPISKLKKPISISVEALLSPKQHVVGHKNGFGKPVIILDNTFPYARICRIRRDIAHDKSS
PNIMLQRRGGELKPNSVEKWGVDDLSAVKMIAIDVPLDYASSPVNLVKLIPKMTGTEKDAFKANNETIPRQPDVQLYCEW
KEPLILDTGKEVYSSWESRATCRLIWKKNADAYLLYVAKCIEEWYQKVSGGQYADEPMPTIEIFRAGRSMSPGTEATPTP
KNTPRQTPEPKVTLVPFRMKPPQGTGNKSPSILSSDDDEETEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEETEQELRE
KRLREIEDQYRAKHKISSKARLTSKQEKTIKKTFTSTYGAFEETEQELREKQIRGIEDQYRAKHKISPKAKLTLKQEKAI
KKKLTSTYGVI
```

446 - 465:	EEEEEEEEEEEEEEEEEEEE
447 - 466:	EEEEEEEEEEEEEEEEEEEE
448 - 467:	EEEEEEEEEEEEEEEEEEEE
449 - 468:	EEEEEEEEEEEEEEEEEEEE
450 - 469:	EEEEEEEEEEEEEEEEEEEE
451 - 470:	EEEEEEEEEEEEEEEEEEEE
452 - 471:	EEEEEEEEEEEEEEEEEEEE
453 - 472:	EEEEEEEEEEEEEEEEEEEE
454 - 473:	EEEEEEEEEEEEEEEEEEEE

A0A093YGH6 **A0A093YGH6_9PEZI** (551 aa)
Protein-ribulosamine 3-kinase (EC 2.7.1.172). *Pseudogymnoascus sp. VKM F-3808*

```
MSHAEILEILGNIPNVHSGDGIDPVDAASTEPSLDPETLQILRNIPNVHSGDGINPVDATSTEPSLDPETLKILRNIPNV
RSGDGLDLVDAASKEPFPVLEVPEIQESISNIRIGDAQRKLETTPSEPFPLPQTTGAYTVDSSVVAAFPIPGTKVLHALS
YGESLWGKTAKIIAQLPSGATENYFLKVVTLGETGRHMCEGEFESLSAIYAVSPGFVPKPYAWGKYDTTATDNKDIYFLL
AEFRDVGEQPADPVKLAARLADMHQRSTSPTGKFGFHISTCHAKIAQAVNTWEDSWCTLYSNHLGHVMDLAKPVLQWAEF
DIVCKLTLEKVVPRLLLPLQADGRVLKPSLIHGDCWDGNTATDMNTGEAFVFDVCSFYGHNEYDTGNWRAPRHRLSKLAY
IKNYKKCFPVSEPEEDWDARNLLYSLTFNIGNTIYIPGSSQRQVVYDDMTTLCGMFCPDNLKQELTALRISQNKAGHLAN
SIDVASGYGEETEEEEEEEEEEEEEEEEEEEEEEDDEVEGKESMKPYQTRVQVDVKESIEPYQAPVQVEAV
```

493 - 512:	EEEEEEEEEEEEEEEEEEEE
494 - 513:	EEEEEEEEEEEEEEEEEEEE
495 - 514:	EEEEEEEEEEEEEEEEEEEE

A0A093ZJI6 **A0A093ZJI6_9PEZI** (391 aa)
NADAR domain-containing protein. *Pseudogymnoascus sp. VKM F-3557*

```
MPPIFFWRDTNPPFAFLSQDSRTPFHDNDTETVWPSAEHYMLSEMAMLFAAPDVAARIAHTPSVDEVRELACGVDAFDEK
IWEEDRYGIVEEATYHKFAHSLVQDRDLKAELLGTGEDELVLASPLDGIWGIGYEAGEAVGKRDTWGTNLLGKALMMARA
WIRMEETGSATWEKGGAFDVTAEQRRHDMPMEVQTYEASKGYISPSDHKYWDTEREEGLAAEYYDKTREFGPPGGYPDHA
AGVPEQTEGTKAIEGGAAEPSSSDALAVIGAVGAGELALREARGGSYGVEEEEENSDDELRKEVIENLFRKKPEEIEDSS
SDESEDEKPPEPDSSSDEEEEPESESEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDAGSDSDGDSD
```

347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE

355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE

A0A094A3B2 **A0A094A3B2_9PEZI** (1262 aa)
WD_REPEATS_REGION domain-containing protein (Fragment). *Pseudogymnoascus sp. VKM F-3808*

```
MATIASLSPETLAHILSYIPRDHDNLMVRLARIRDGGPIKPTSELPPYATVCKTWQWHIEQRTFREINLPSSELEYFSKL
LIGHRRAALREVKYQVILPEYDDAACAVVETEEDKKANDVAFNTAIADLFELMKGWEEEDEKELSRTGAREGLVPLSLEM
SQIYSPSDAKKRNSGLLREQQLAVERGERSDLFEGRHCDSWLRLGPLDGVPELKRVTKYVVSPSYPRPVEAESMARLAKK
FPALETLNLEIMERSEDIEVRRRDRYDFALALFPLSSLPLTSFSLCAETLSPRYQFQDPPSVLLPDSETDHFSLALYAIS
LIPSLKTIDLTGPIMISPQLFQAPAVLDSAFASVASKTPQWPSLTTYSANFSTVRPAGSWYFVRHPDNPVPPGFVAPLEP
EPNSDRGTEMFRTYPDDEAIDELLAAAGEAKYNMPALQMMSLTASLSLEHSENAEFEAVWFKAGQKNYLDHRLTEQPVEV
GNETFIRGDHVYWWTGKGGDWRPKREVERVWVGEGNQQWFKGYPQEEEGEEEEEEEEEEEEEEEEEEEEEDEEEEEEE
GGDVDMEAIYQENEDAKSELTLSSDFEDTEVPSEVESYSDNIKSLASVSSDGSSTDSDCSNEIPARRSKNERKSPKKRIK
KLSPSLSPSPSSSPPLSSCPSPKSGRESPTTANSLSPALPRPISDANKRTQESARLRRCFTVTNEASKNPVKRETLLTMQ
LQGDQLVVSLSSTAMLEKVCHLYNDTRVAPVAQDPTTEVEPGISAEIYRIVRRINFGMATTALGRLREAHTMSTGSKEAR
AIAAIKFDLACVSEESTYEAMKELQATDAARYSRIIGPFDSMRREGLKVLLYTGLMGSPAALMVWPWTAVHSATGFTLHR
QTGVFIQAVVSFILGSGDFIYIKALINHISTWFEGWVLGKIRAVEAIDQLGEYLREYNKGMLPKHETVGARLVRDYGPKY
GTISDIIAIFTNIPRLAQETYSAVGTADPISLAISDMETLDSHEQLSERAIEAALLTTRFASRVMAARASGYGSLYEPRE
YEDGMAMDIDLEADIILCSVHTGASAQYVQLANGPDDGISGLSWSPVSRHLAVASWDGKVRIYDMTQKRSGEGRALIDFG
GPALRQEQNLIGHLNVEGWPKGCRRWRRQGCSTSRSRSKRRAPAASRSTRCAHLIGALLHSALLKRAHDRDGVLGQDRQV
LGPEAADCSCVCGVPGASVFHGYEGRFARHRHSRSTHQCHQTRQPNRIPPVSPEPSIAPDPR
```

530 - 549:	EEEEEEEEEEEEEEEEEEEE
531 - 550:	EEEEEEEEEEEEEEEEEEEE
532 - 551:	EEEEEEEEEEEEEEEEEEEE
533 - 552:	EEEEEEEEEEEEEEEEEEEE

A0A094BYG5 **A0A094BYG5_9PEZI** (523 aa)
Uncharacterized protein (Fragment). *Pseudogymnoascus sp. VKM F-4246*

```
SPYELPRSPDLTVGHNEVLASNHIAGYLKYFRNVLGLHCIATVSEDTLWFHLARLVSEAGNPFITREEWSIFLRVCNEIQ
QMISWDEETGLVCALRTGWEPVGHAAVPLPLPRCPEVTLPLEQLTEILELMRRYFLRAIPEAMDVNAVTWHDAAHVFYHF
DYIVGERGLSVATFSALCLKYFSACWTTGPEGCLQWNAPDHFLSMINTIHNYVTALSETADIGTVLPFDHLRNTINTAFD
DMATVEAGAPVLAYPRASVVTENNQTNIVFTYREDLPQSRLIRVISDDQLTAIYIFVHRYWEDPSTKRTVWPKELREVYN
NYQQDPSLRVAHPRAFLTTFAQPYGYCWIRDDRRIEFAPAPPQKTTLGPASAGVLGGQGGPQPQGGGQPQGGLFNQGGNG
IPVLTQPPQLPPQQQQQGGPQPQGGLFPQWEDEIPNLMRPPQQPPQQPPQQQQQGGPQPRTGLFPQGGNGILDRNSNSS
TTGSSNTEAVNLKQEEEEEEEEEEEEEEEEEEEEEEGGMGFRI
```

495 - 514:	EEEEEEEEEEEEEEEEEEEE
496 - 515:	EEEEEEEEEEEEEEEEEEEE
497 - 516:	EEEEEEEEEEEEEEEEEEEE

A0A094C8M0 **A0A094C8M0_9PEZI** (449 aa)
NADAR domain-containing protein. *Pseudogymnoascus sp. VKM F-3775*

```
MPPIFFWRDTNPSFAFLSQDSRAPFHDNETETVWPSAEHYMLSEMAMLFAAPEIAARIAHEPDVEDIRALARGVEAFDEK
IWEEDRYGIVEEATYHKFAHSMVRDRDLKAELLATGEDELVLASPLDGIWGIGYEAGEAVGNRATWGMNLLGKALMMVRA
WIRMEDIGSAPWAKGGAFDVTAEERRKDLPLEVQTYESSKGYISPSDHKYWDTERGEGLAAEYYDTTREFGPPGGYPDHP
PGEPEESGGTRAIEGAPEPSSSDALAVIGAVGAGALALREARGGSYGVDEEEEENSDDELRREVIDNLFRKKPEEEEEEL
NDSDDDTPPEPESDSEPEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAEICDAAFIRRRRRRRRRRRRRRRRRRRRRRR
RRRRRRRNQNPNPNPKQKTTIQIQIQIEISIKGDELRYEYGTSARGYDD
```

338 - 357:	EEEEEEEEEEEEEEEEEEEE
339 - 358:	EEEEEEEEEEEEEEEEEEEE
340 - 359:	EEEEEEEEEEEEEEEEEEEE
341 - 360:	EEEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEEE
344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE

A0A094CKF3 **A0A094CKF3_9PEZI** (1027 aa)
Uncharacterized protein. *Pseudogymnoascus sp. VKM F-4516 (FW-969)*

```
MATIASLSPETLAHILSYIPRDHDNLMVRLARIRDGGPIKPTSELPPYATVCKTWQWHIEQRTFREINLPSSELEYFSKL
LTGHRRAALREVKYQVILPEYDDAACAVVETEEDKKANDVAFNTAIADLFELMKGWEEEDEKELSRTGAREGLVPLSLEM
SQIYSPSDAKKRNSGLLREQQLAVERGERSDLFEGRHCDSWLRLGPLDGVPELKRVTKYVVSPSYPRPVEAESMARLAKK
FPALETLNLEIMERSEDVEVRRRDRYDFALALLSLSSLSLTSFSLCAETLSPRYQFQDPPSVLLSDSEIDHFSLALYAIS
LIPTLKTIDLTGPIMISPQLFQAPAVLDSAFASVTSKTPQWPSLTSYSVNFSTVRPSGSWYFVRHPDNPVPPGFVAPLEP
EPNSDRGTEMFRTYPDDEAIDELLAAAGEAKYNMPALQMMSLTASLSLEHSENAEFEAVWFKAAQKNYLDHRLTEQPVEV
GNETRREEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGDVDMEAIYRENEDTKSELVLSSDSEDVEVPSEVEP
DSDDIESLATVSSDESSDSGYSDEEIPARRPPKDKGRKKDMRSPKKRIKKQSSPSPSPSPSSSPPLSSCPSLKSGKESPT
TAKSLSPALPHPISDANKRMQESARLRRYFTVINEASKNPVKRETLLAMQLQGDQLVESLSSTAMLENVRHLLYNDTRVA
PVAQDPATEVEPGISAEIYRIVRRINFGMATTALGRLREAHTSLDIIQVFNTEIKKRKPLLPVSTGSKEVRAIAAIKFDL
ACVSEESTYEAMKELQATDAARYSRIIGPFDRMRREGLKVLLYTGLMGPPAALMVWPWTAVHSATGFTLHRQTGVFIQAV
VSFILASSDFIYIKALINHISTWFEGWVLGKIWAVEAIDQLGEFLREYNKGMLPKHETVGARLVRDYGPKYGTISDIIAI
FTNIPRPAQETYSAVGTADPISLAISDMETLDSHEQLSERAIHHTLHQQGDGCPRVWIREPIRPKGI
```

487 - 506:	EEEEEEEEEEEEEEEEEEEE
488 - 507:	EEEEEEEEEEEEEEEEEEEE
489 - 508:	EEEEEEEEEEEEEEEEEEEE
490 - 509:	EEEEEEEEEEEEEEEEEEEE
491 - 510:	EEEEEEEEEEEEEEEEEEEE
492 - 511:	EEEEEEEEEEEEEEEEEEEE
493 - 512:	EEEEEEEEEEEEEEEEEEEE
494 - 513:	EEEEEEEEEEEEEEEEEEEE
495 - 514:	EEEEEEEEEEEEEEEEEEEE
496 - 515:	EEEEEEEEEEEEEEEEEEEE
497 - 516:	EEEEEEEEEEEEEEEEEEEE
498 - 517:	EEEEEEEEEEEEEEEEEEEE
499 - 518:	EEEEEEEEEEEEEEEEEEEE
500 - 519:	EEEEEEEEEEEEEEEEEEEE
501 - 520:	EEEEEEEEEEEEEEEEEEEE
502 - 521:	EEEEEEEEEEEEEEEEEEEE
503 - 522:	EEEEEEEEEEEEEEEEEEEE
504 - 523:	EEEEEEEEEEEEEEEEEEEE
505 - 524:	EEEEEEEEEEEEEEEEEEEE

A0A094DLC3 **A0A094DLC3_9PEZI** (386 aa)
NADAR domain-containing protein. *Pseudogymnoascus sp. VKM F-4516 (FW-969)*

```
MPPIFFWRDTNPPFAFLSQDSRTPFHDNDTETVWPSAEHYMLSEMAMLFAAPDVAARIAHTPSVDEVRELACGVDAFDEK
IWEEDRYGIVEEATYHKFAHSLVQDRDLKAELLGTGEDELVLASPLDGIWGIGYEAGEAVGKRDTWGTNLLGKALMMARA
WIRMEETGSATWEKGGAFDVTAEQRRHDMPMEVQTYEASKGYISPSDHKYWDTEREEGFAAEYYDKTREFGPPGGYPDHA
AGGPEQTEGTKAIEGGAPEPSSSDALAVIGAVGAGELALREARGGSYGVEEEEENSDDELRKEVIENLFRKKPEEIEDSS
SDESEDEKPPEPDSSSDEEEEPESESEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDAGSDSDGDSD
```

347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE

A0A094E1L4 **A0A094E1L4_9PEZI** (410 aa)
NADAR domain-containing protein. *Pseudogymnoascus sp. VKM F-103*

```
MPPIFFWRDTNPSFAFLSQDSHAPFHDNETETVWPTTEHYMLSEMAMLFAAPDIAARIAHEPHVEDIRALARGVDNFDEK
IWEEDRYGIVEEATYHKFAHSLVRERDLKAALLATGEDELVLASPLDGIWGIGYEAGEAVGQRETWGTNLLGKALMMVRA
WIRMEETGSASWEKGGAFDVTAEQRRVDMPLEVQTYEASKGYISPSDHMYWDTERGEGLAAEYYDKTREFGPPGGYPDHG
VPEEQTEGSRAIEGAPDASGSDNALAVLGALGAGGLVLHEARGGSYGVEEEEEENSDDELRKEVIENLFRKKPEEEEEEL
HDSEDEKTPEPESEEEPEEEEEEEPEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEPESESESEEEEEVAEEEAEEED
AGSDSDGDSD
```

346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE

A0A094FA00 **A0A094FA00_9PEZI** (419 aa)
NADAR domain-containing protein. *Pseudogymnoascus sp. VKM F-4518 (FW-2643)*

```
MPPIFFWRDTNPSFAFLSQDSRAPFHDNETETVWPTTEHYMLSEMAMLFAAPDVAARIAHEPSIDDIRALACGVEAFDEK
IWEEDRYGIVEEATYHKFAHSLVRDRDLRAELLGTGEDELVFASPLDGIWGIGYEAGEAVGKRKTWGHNLLGKALMMVRA
WIRMEDIGSATWVKGGAFDVTAEQRRHDLPLEVQTYEASKGYISPSDHKYWDTEREDGLAAEYYDKTREFGPPGGYPDQA
AGGPEQSEGTRAIEGSAPEASSSDNALAVIGGLGAGALVLQEARGGSYGADEEEEENSDDELRKEVIDNLFRKKPEEEEE
ELNDSEDEKTPEPEPESDSEPEEEEEQPESESESEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEPESESEDEEE
EEDADSGSGSGSGSDGDSD
```

355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE

A0A094FPU2 **A0A094FPU2_9PEZI** (1182 aa)
CobW C-terminal domain-containing protein. *Pseudogymnoascus sp. VKM F-4516 (FW-969)*

```
MPSKRSSSSRRQQQQDPQPAAKKHKNNSSKYSKKQDTAMMPISITGEKMANFKTLPITLLSGFLGSGKTTLLQYILHSKD
HGLRIAIIVNDMAAVNVDANLIRSSMSSSNPASQQKLVAMQNGCICCTLRGDFVLELARLAKDRQYDYVLIESTGISEPQ
QVAESFTKEFSLAIVEAEREDGEGETTWSKEEKGILGKLAENGGLNSIAKIDTTVTVVDAFRFFEEFETIELLHQRFASE
VETPEDERTVTDLMIDQIEFADVIIVNKIDMVDDKVLIRIRGLIKTLNPGCKILETALRASKQSENPFGAVSLDVKEIIA
TGLYSEETSIKSSGWLKSVHDMSIIDSHGRKVLAPKPETEEYGINSFVYRSRRPFHPARLYELVHDKFVILEPQNQEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDENSEHEL
ISSSSLATAEGEHFESLQQQDSPISTPPATLNSPTITAATTTTSPSTSFTEDANKLTQYPDIPLEQRLTNKKAHPLFSRL
LRSKGFIWLATRPKLSGDWSQAGAMLTFSPGLQWFTTLPEDEWPLPAGDAGKEVKNVIKKDFEGEWGDRRQEVVLIGEGL
DVDRLTACLDSCLLTVEEMQEWEGVMRMDCDEEKREDMLNDLFADGWEEWDDPQSMMNGDEEGHVHGPAWYVDLNCLIES
RLRLLLTMGPIPYNTLQEWKQHVLSMSDPFIARIPKIELHVHIEGTLTPELRWELGQRNGILIKSDRLQRTFYSLEQLKE
MYNLLEPRSIKGANQVSAFFDAYYGGMEVLQTEEDFYDLAMHYFVKAASMQVRYCEPFFDPQAHTRRGVKFQTFMRGFRR
AQTDSERDLNVKSQWIMCILRDLPLESAMEHYEAALPYKEMIVGIGLDSNEYDRPPLLFEALYQRARADGFKITSHCDVA
QKDTHEHIRQVAESVGGTGADRCDHGLDAAECPDLVALIRQKGLGMTLCPWAYVRHHTEADLFQHIRTLFDADIKINISS
DSPVYVEGNWITHNLLLLRFKCKFTDDEIAKVERNSVEVCWATEDVKRCILKEIDSFCVSPI
```

397 - 416:	EEEEEEEEEEEEEEEEEEEE
398 - 417:	EEEEEEEEEEEEEEEEEEEE
399 - 418:	EEEEEEEEEEEEEEEEEEEE
400 - 419:	EEEEEEEEEEEEEEEEEEEE

401 - 420:	EEEEEEEEEEEEEEEEEEEE
402 - 421:	EEEEEEEEEEEEEEEEEEEE
403 - 422:	EEEEEEEEEEEEEEEEEEEE
404 - 423:	EEEEEEEEEEEEEEEEEEEE
405 - 424:	EEEEEEEEEEEEEEEEEEEE
406 - 425:	EEEEEEEEEEEEEEEEEEEE
407 - 426:	EEEEEEEEEEEEEEEEEEEE
408 - 427:	EEEEEEEEEEEEEEEEEEEE
409 - 428:	EEEEEEEEEEEEEEEEEEEE
410 - 429:	EEEEEEEEEEEEEEEEEEEE
411 - 430:	EEEEEEEEEEEEEEEEEEEE
412 - 431:	EEEEEEEEEEEEEEEEEEEE
413 - 432:	EEEEEEEEEEEEEEEEEEEE
414 - 433:	EEEEEEEEEEEEEEEEEEEE
415 - 434:	EEEEEEEEEEEEEEEEEEEE
416 - 435:	EEEEEEEEEEEEEEEEEEEE
417 - 436:	EEEEEEEEEEEEEEEEEEEE
418 - 437:	EEEEEEEEEEEEEEEEEEEE
419 - 438:	EEEEEEEEEEEEEEEEEEEE
420 - 439:	EEEEEEEEEEEEEEEEEEEE
421 - 440:	EEEEEEEEEEEEEEEEEEEE
422 - 441:	EEEEEEEEEEEEEEEEEEEE
423 - 442:	EEEEEEEEEEEEEEEEEEEE
424 - 443:	EEEEEEEEEEEEEEEEEEEE
425 - 444:	EEEEEEEEEEEEEEEEEEEE
426 - 445:	EEEEEEEEEEEEEEEEEEEE
427 - 446:	EEEEEEEEEEEEEEEEEEEE
428 - 447:	EEEEEEEEEEEEEEEEEEEE
429 - 448:	EEEEEEEEEEEEEEEEEEEE
430 - 449:	EEEEEEEEEEEEEEEEEEEE
431 - 450:	EEEEEEEEEEEEEEEEEEEE
432 - 451:	EEEEEEEEEEEEEEEEEEEE
433 - 452:	EEEEEEEEEEEEEEEEEEEE
434 - 453:	EEEEEEEEEEEEEEEEEEEE
435 - 454:	EEEEEEEEEEEEEEEEEEEE
436 - 455:	EEEEEEEEEEEEEEEEEEEE
437 - 456:	EEEEEEEEEEEEEEEEEEEE
438 - 457:	EEEEEEEEEEEEEEEEEEEE
439 - 458:	EEEEEEEEEEEEEEEEEEEE
440 - 459:	EEEEEEEEEEEEEEEEEEEE
441 - 460:	EEEEEEEEEEEEEEEEEEEE
442 - 461:	EEEEEEEEEEEEEEEEEEEE
443 - 462:	EEEEEEEEEEEEEEEEEEEE
444 - 463:	EEEEEEEEEEEEEEEEEEEE
445 - 464:	EEEEEEEEEEEEEEEEEEEE
446 - 465:	EEEEEEEEEEEEEEEEEEEE
447 - 466:	EEEEEEEEEEEEEEEEEEEE
448 - 467:	EEEEEEEEEEEEEEEEEEEE
449 - 468:	EEEEEEEEEEEEEEEEEEEE
450 - 469:	EEEEEEEEEEEEEEEEEEEE
451 - 470:	EEEEEEEEEEEEEEEEEEEE
452 - 471:	EEEEEEEEEEEEEEEEEEEE

453 - 472:	EEEEEEEEEEEEEEEEEEEE
454 - 473:	EEEEEEEEEEEEEEEEEEEE
455 - 474:	EEEEEEEEEEEEEEEEEEEE
456 - 475:	EEEEEEEEEEEEEEEEEEEE
457 - 476:	EEEEEEEEEEEEEEEEEEEE
458 - 477:	EEEEEEEEEEEEEEEEEEEE
459 - 478:	EEEEEEEEEEEEEEEEEEEE
460 - 479:	EEEEEEEEEEEEEEEEEEEE
461 - 480:	EEEEEEEEEEEEEEEEEEEE
462 - 481:	EEEEEEEEEEEEEEEEEEEE
463 - 482:	EEEEEEEEEEEEEEEEEEEE
464 - 483:	EEEEEEEEEEEEEEEEEEEE
465 - 484:	EEEEEEEEEEEEEEEEEEEE
466 - 485:	EEEEEEEEEEEEEEEEEEEE
467 - 486:	EEEEEEEEEEEEEEEEEEEE
468 - 487:	EEEEEEEEEEEEEEEEEEEE
469 - 488:	EEEEEEEEEEEEEEEEEEEE
470 - 489:	EEEEEEEEEEEEEEEEEEEE
471 - 490:	EEEEEEEEEEEEEEEEEEEE
472 - 491:	EEEEEEEEEEEEEEEEEEEE
473 - 492:	EEEEEEEEEEEEEEEEEEEE
474 - 493:	EEEEEEEEEEEEEEEEEEEE
475 - 494:	EEEEEEEEEEEEEEEEEEEE
476 - 495:	EEEEEEEEEEEEEEEEEEEE
477 - 496:	EEEEEEEEEEEEEEEEEEEE
478 - 497:	EEEEEEEEEEEEEEEEEEEE
479 - 498:	EEEEEEEEEEEEEEEEEEEE
480 - 499:	EEEEEEEEEEEEEEEEEEEE
481 - 500:	EEEEEEEEEEEEEEEEEEEE
482 - 501:	EEEEEEEEEEEEEEEEEEEE
483 - 502:	EEEEEEEEEEEEEEEEEEEE
484 - 503:	EEEEEEEEEEEEEEEEEEEE
485 - 504:	EEEEEEEEEEEEEEEEEEEE
486 - 505:	EEEEEEEEEEEEEEEEEEEE
487 - 506:	EEEEEEEEEEEEEEEEEEEE
488 - 507:	EEEEEEEEEEEEEEEEEEEE
489 - 508:	EEEEEEEEEEEEEEEEEEEE
490 - 509:	EEEEEEEEEEEEEEEEEEEE
491 - 510:	EEEEEEEEEEEEEEEEEEEE
492 - 511:	EEEEEEEEEEEEEEEEEEEE
493 - 512:	EEEEEEEEEEEEEEEEEEEE
494 - 513:	EEEEEEEEEEEEEEEEEEEE
495 - 514:	EEEEEEEEEEEEEEEEEEEE
496 - 515:	EEEEEEEEEEEEEEEEEEEE
497 - 516:	EEEEEEEEEEEEEEEEEEEE
498 - 517:	EEEEEEEEEEEEEEEEEEEE
499 - 518:	EEEEEEEEEEEEEEEEEEEE
500 - 519:	EEEEEEEEEEEEEEEEEEEE
501 - 520:	EEEEEEEEEEEEEEEEEEEE
502 - 521:	EEEEEEEEEEEEEEEEEEEE
503 - 522:	EEEEEEEEEEEEEEEEEEEE
504 - 523:	EEEEEEEEEEEEEEEEEEEE

505 - 524:	EEEEEEEEEEEEEEEEEEE
506 - 525:	EEEEEEEEEEEEEEEEEEE
507 - 526:	EEEEEEEEEEEEEEEEEEE
508 - 527:	EEEEEEEEEEEEEEEEEEE
509 - 528:	EEEEEEEEEEEEEEEEEEE
510 - 529:	EEEEEEEEEEEEEEEEEEE
511 - 530:	EEEEEEEEEEEEEEEEEEE
512 - 531:	EEEEEEEEEEEEEEEEEEE
513 - 532:	EEEEEEEEEEEEEEEEEEE
514 - 533:	EEEEEEEEEEEEEEEEEEE
515 - 534:	EEEEEEEEEEEEEEEEEEE
516 - 535:	EEEEEEEEEEEEEEEEEEE
517 - 536:	EEEEEEEEEEEEEEEEEEE
518 - 537:	EEEEEEEEEEEEEEEEEEE
519 - 538:	EEEEEEEEEEEEEEEEEEE
520 - 539:	EEEEEEEEEEEEEEEEEEE
521 - 540:	EEEEEEEEEEEEEEEEEEE
522 - 541:	EEEEEEEEEEEEEEEEEEE
523 - 542:	EEEEEEEEEEEEEEEEEEE
524 - 543:	EEEEEEEEEEEEEEEEEEE
525 - 544:	EEEEEEEEEEEEEEEEEEE
526 - 545:	EEEEEEEEEEEEEEEEEEE
527 - 546:	EEEEEEEEEEEEEEEEEEE
528 - 547:	EEEEEEEEEEEEEEEEEEE
529 - 548:	EEEEEEEEEEEEEEEEEEE
530 - 549:	EEEEEEEEEEEEEEEEEEE
531 - 550:	EEEEEEEEEEEEEEEEEEE
532 - 551:	EEEEEEEEEEEEEEEEEEE
533 - 552:	EEEEEEEEEEEEEEEEEEE

A0A094IB65 **A0A094IB65_9PEZI** (407 aa)
NADAR domain-containing protein. *Pseudogymnoascus sp. VKM F-4520 (FW-2644)*

```
MPPIFFWRDTNPSFAFLSQDSRAPFHDNETETVWPTTEHYMLSEMAMLFAAPDVAARIAHEPSIDDIRALACGVDAFDEK
IWEEDRYGIVEEATYHKFAHSLVRDRDLRAELLGTGEDELVLASPLDGIWGIGYEAGEAVGKRETWGQNLLGKALMMVRA
WIRMEDIGSATWVKGGAFDVTAEQRRHDLPLEVQTYEASKGYISPSDHKYWDTEREDGLAAEYYDKTREFGPPGGYPDQA
AGGPEQSEGTRAIEGNAPEASSSDKALAVIGGLGAGALVLQEARGGSYGVEEEEEEENSDDELRKEVIENLFKKKPEEEE
EKLDDSEDEKTPEPESDSEPEEEEEQPESESEEEEEEEEEEEEEEEEEEEEEEEEEEEEERESESEDEGEEEDADSDTGS
DSDGDSD
```

352 - 371:	EEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEE

A0A094K487 **A0A094K487_9PEZI** (411 aa)
NADAR domain-containing protein. *Pseudogymnoascus sp. VKM F-4519 (FW-2642)*

```
MPPIFFWRDTNPSFAFLSQDSHAPFHDNETETVWPTTEHYMLSEMAMLFAAPDIAARIAHEPHVEDIRALARGVDNFDEK
IWEEDRYGIVEEATYHKFAHSLVRERDLKAALLATGEDELVLASPLDGIWGIGYEAGEAVGQRETWGTNLLGKALMMVRA
WIRMEETGSASWEKGGAFDVTAEQRRVDMPLEVQTYEASKGYISPSDHMYWDTERGEGLAAEYYDKTREFGPPGGYPDHE
VPEAQEQSEGSRAIEGAPEASGSDNALAVLGALGAGGLVLHEARGGSYGVEEEEEEENSDDELRKEVIENLFRKKPEEEE
EELHDSEDEKTPEPESEEEPEEEPEEEEEPEEEEEEEEEEEEEEEEEEEEEEEEEEEEEPESDSDSEEEEEEAEEEAEEE
DAGSDSDGDSD
```

351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE

A0A094KH15 **A0A094KH15_PODCR** (835 aa)
Myelin transcription factor 1 (Fragment). *Podiceps cristatus (Great crested grebe)*

```
MSLENDDKRARTRSKSIRVPTELIGQEVSCPTPGCNGSGHIRGKYARHRSLQSCPLAKKRKLQDAEAEHLVSKRKSHPLK
LALDEGYNVDSDGSEEAEVKEESGSDESEGTLEEDEAEAVEQEETHSPEPAEERSPAKSTHYGQNTATSTSGPSKANYSS
YQEIIANSLLNLGQIAEETLAIEGQLPEAELQVSKPPSNVVHLVHEDAGEELVEEECDKEIIIQTEDAEEVIEVTSERSS
ELCPEHRDDANCEESCKLQKAEAEEEDEEEEEEDEEEEEEEEEEEEEEEEEEEEEEDEEEEEMAPEVICEEAPHTSQDTQK
SHCEGQFSPKPEYSVIVEVRSDDDKDDDARSQKSAVTDESEMYDMMTRGNLGLLEQAIALKAEQVKIVREPSRLPGEHVK
HFQVDEKQSKPLESIRKSYYGKDPSRPEKREIKCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRIPPEILAMHENVLKCPT
PGCTGQGHVNSNRNTHRSLSGCPIAAAEKLAKSHEKQQTQPGDPSKTSSNSDRILRPMCFVKQLEIPQYGSYRPNMVPAT
PRANLAKELEKYSKVTFDYASFDAQVFGKRMLAPKIQTSETSPKAFKCFDYSHDAEAAHMAATAILNLSTRCWEMPENLS
TKQQEAPGKSMDIEVDENGTLDLSMNKHRKRESTFPSSSSCSSSPSMKSPDVSQRPNSTSATSSTMTSPQSSQTSRQDEW
DGPIDYTKPNRQREEEPEESEPAARSFASSEADEQEVSEENFEERKYPGEVTLTNFKLKFLSKDIKKELLTCPTPGCDGS
GHITGNYASHRSLSGCPLADKSLRNLMAAHSADLK
```

275 - 294:	EEEEEEEEEEEEEEEEEEEE
276 - 295:	EEEEEEEEEEEEEEEEEEEE

A0A094MEG8 **A0A094MEG8_ANTCR** (301 aa)
Bone sialoprotein 2 (Bone sialoprotein II) (Cell-binding sialoprotein) (Integrin-binding sialoprotein). *Antrostomus carolinensis (Chuck-will's-widow) (Caprimulgus carolinensis)*

```
MRTVLLFACLVGMSCAFSVKSWLRRAKSDDSEENAVFKNRHRYYLYRYAYLHPPQRWYQGSDSSEEEGDGSEEEEEAGLC
PCLPHATWHQKAATSSHPAVVFYLYQGKGCQEPLKGGRNSAAGKGSDSENEDSDENEEEEEEEEEEEVAENENGINGTST
NTTEGTDGPHGNGTAVAEEHAGVAEEEEEEEEEEEEEEEEEEEEEETEVTTIISTTSEDGLSQATTMGDGGLTDATTAGE
QWEYEVTAGDHGRGDEGTTADSYGEQEEYARGDSYRAYEDEYGYYKGHGYDVYGQDYYYSQ
```

185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE

A0A095CEL6 **A0A095CEL6_CRYGR** (779 aa)
Telomere replication protein EST3. *Cryptococcus gattii serotype B (strain R265) (Filobasidiella gattii) (Cryptococcus bacillisporus)*

```
MAEDIRSWITKALIDHDTAHGANFRVPVNCKHYCQLLKFYTYRDDKNPRAQIEGSIGDRTHCVKVIFDIEETDRFELPDP
DTGYKHSLTSQLRSIFQIKQFHIRIAPPSSSAGAKIPLVAFYVTKWDVVSGNHDEPVYWLDTCKVGEGNNDEKIREVLQK
WWFGESNSESSQNRSSQKILSQDNIPDMSIITTRPKVENDVAYHRTSVALGDIISIEEAKASRVGEWDPRFALAWLERNQ
DTVLNTYAQYRNYSSNNIETIDSSQRFQGKTVSNQPSGNGHPPKSQPVDVASRDSGTPRLFNKRSPSSSSQSHHASSPTF
LRVSPSKRQLLRKKIIDPLNSPSSPATSMSPGSIDEELLSQYEREERRKRSGKSKGIKGDGDKEMEQRSPSPSPLSQSSS
VFHSSPTIATPRGLEGELIQTDRPSPELSSAQNATISNARDKWKRPRESMNSRRQSRVVILDEDEDIDEGPLIKKGSKRK
LILSSPEPPSQVIEKRDSSDDEENVAETSSSPTTQGGTRGDAEHTVTELQDLMPRTKEVTRPIKTLSSSSVLNEIGTDQR
AVEEGDQVEDKGERKRRNGLNDEEEIMEQEEEEGEEEEEGEEEEEEEEEEEEEEEEEEEEEEGEEEEEGEEEEEEEEEEE
EEEEEEEEEEVEEEEEEETEKDKKIEEKEEGERLQTDKKGKGTQYERSTRMDLLGMEKKKEKREPQTSFPVPEGETENFQ
RKRKNRTEDPTSSQQVPKFGGFKLDMTLREGGLDGACVLQMLEWAREKRQEIAKRAKKP
```

601 - 620:	EEEEEEEEEEEEEEEEEEEE
602 - 621:	EEEEEEEEEEEEEEEEEEEE
603 - 622:	EEEEEEEEEEEEEEEEEEEE
630 - 649:	EEEEEEEEEEEEEEEEEEEE

631 - 650:	EEEEEEEEEEEEEEEEEEEE

A0A096MLF1 **A0A096MLF1_PAPAN** (736 aa)
YTH domain containing 1. *Papio anubis (Olive baboon)*

```
MAADIREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSN
NKRIVSTKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEE
EEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSA
SESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVIL
IFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQE
IELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQ
RPGYLKDPRYQEVDSFTNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQ
AHPPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERER
LCDRDRDRGERGRYRR
```

230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE

A0A096MTJ9 **A0A096MTJ9_PAPAN** (735 aa)
YTH domain containing 1. *Papio anubis (Olive baboon)*

```
LKSDSDKEDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSNN
KRIVSTKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVDR
RASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEE
EEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSAS
ESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVILI
FSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEI
ELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQR
PGYLKDPRYQEVDSFTNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQA
HPPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERL
CDRDRDRGERGRYRR
```

229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE

A0A096NH96 **A0A096NH96_PAPAN** (1266 aa)
Euchromatic histone lysine methyltransferase 2. *Papio anubis (Olive baboon)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGA
LLLEKETRGASERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDESENLEGDGDLH
GGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGPEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEELGSARRSEVTLAKGDPGSLEEWET
VVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAKK
KWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEELP
LCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAG
TFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGAAAPAPPPLSQDAPGRADTSQPSAR
MRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQ
KVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVTNHLEVARYMVQRGGCV
YSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHW
ASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLN
RKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGESCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSN
CLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFI
CEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDI
RTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE

A0A096NIC3 **A0A096NIC3_PAPAN** (1431 aa)
Tau tubulin kinase 1. *Papio anubis (Olive baboon)*

```
MSGLVLMLAARCIVGSSPLRRCRRRRPRRIGAGPGRDGPGRKAAAAAAAGGSGSPNAALSRPRPAPAPGDAPPRAAASTA
AAAAAAAGTEQVDGPLRAGPADTPPSGWRMQCLAAALKDETNMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEA
MDLLTRENVALKVESAQQPKQVLKMEVAVLKKLQGKDHVCRFIGCGRNEKFNYVVMQLQGRNLADLRRSQPRGTFTLSTT
LRLGKQILESIEAIHSVGFLHRDIKPSNFAMGRLPSTYRKCYMLDFGLARQYTNTTGDVRPPRNVAGFRGTVRYASVNAH
KNREMGRHDDLWSLFYMLVEFAVGQLPWRKIKDKEQVGMIKEKYEHRMLLKHMPSEFHLFLDHIASLDYFTKPDYQLIMS
VFENSMKERGIAENEAFDWEKAGTDALLSTSTSTPPQQNTRQTAAMFGVVNVTPVPGDLLRENTEDVLQGEHLSDQENAP
PILPGRPSEGLGPSPHLVPHPGGPEAEVWEETDVNRNKLRINIGKSPCVEEEQSRGMGVPSSPVRAPPDSPTTPVRSLRY
RRVNSPESERLSTADGRVELPERRSRMDLPGSPSRQACSSQPAQMLSVDTGHADRQASGRMDVSASVEQEALSNAFRSVP
LAEEEDFDSKEWVIIDKETELKDFPPGAEPSTSGTTDEEPEELRPLPEESEERRRLGAEPTVRPRGRSMQVLAEEDLQHL
PPQPLPPQLSQADGRSETSQPPTPGSPSHSPLHSGPRPRRRESDPTGPQRQVFSVAPPFEVNGLPRAVPLSLPYQDFKRD
LSDYRERARLLNRVRRVGFSHMLLTTPQVPLSPVQPQANGKEEEEEEEEEDEEEEEEDEEDEEEEEEEEEEEEEEEEEEE
EAAAAVALGEVLGPCSGSSSEGSERSTDRSQEGAPSTLLADDQKESRGRASMADGDLEPEEGSKTLVLVSPGDMKKSPVT
AELAPDPDLGTLAALTPQHERPQPTGSQLDVSEPGTLSSVLKSEPKPPGPGAGPGAGTVTTGAGGVAVTSSPFTKVERTF
VHIAEKTHLNVMSSSGQALRPEEFSTGGELGLELASDGGTVEEGAPAPLENGLALSGLNRAEIEGCALSGPPGETPSAMA
TNSLPNGPALADSPAPVSPLEPSPEKVATISPRHHAMPGSRPRSRIPILLSEEDTGSEPSGSLSAKERWSKRARLQQDLA
```

```
RLVMEKRQGRLLLRLASGASSSSSEEQRRASETLSGTGSEEDTPASEPAVALPRKAGRAAATRSRIPRPIGLRMPMPAAA
QQLPSKSHGAAPASDTAITSRLQLQTPPGSATAADLRPKQPPGRGLGPGRAQAGARPPAPRSPGLPTSTSAARNASASPR
SQSLSRRESPSPSHQARPGVPPPRGVPSARAQPDGTPSPGGSKKGPRGKLQAQRATTKGRAGGAEGRAGAR
```

862 - 881:	EEEEEEEEEEEEEEEEEEEE

A0A096NKA3 **A0A096NKA3_PAPAN** (619 aa)
Ran GTPase activating protein 1. *Papio anubis (Olive baboon)*

```
MGLPRRPPVICGLYSRVAPAAPPPSRPTPTGGPGWRRCPWNRCESMHLTSETIEFAIPFAGFVSALWSLAAKDVIKEIED
FDSLEALRLEGNTVGVEAARVIAKALEKKSELKRCHWSDMFTGRLRTEIPPALISLGEGLITAGAQLVELDLSDNAFGPD
GVQGFEALLKSSACFTLHELKLNNCGMGIGGGKILAAALTECHRKSSAQGKPLALKVFVAGRNRLENDGATALAEAFRVI
GTLEEVHMPQNGINHPGVTALAQAFAVNPLLRVINLNDNTFTEKGAVAMAETLKTLRQVEVINFGDCLVRSKGAVAIADA
IRGGLPKLKELNLSFCEIKRDAALAVAEAMADKTELEKLDLNGNTLGEEGCEQLQEVLEGFNMAKVLASLSDDEDEEEEE
GEEEEEAEEEEEEEEEEEEEEEEEEEEEPQQGGQGEKSATPSQKILDPNTGEPAPVLSSPPPADVSTFLAFPSPEKLLR
LGPKSSMLIAQQTDTSDPEKVVSAFLKVSSVFKDEATVRTAVQDAVDALMKKAFSSSSFNSSAFLTRLLAHMGLLKSEDK
VKAIANLYGPLMALNHMVQQDYFPKALAPLLLAFITKPNSALESCSFARHSLLQTLYKV
```

408 - 427:	EEEEEEEEEEEEEEEEEEEE
409 - 428:	EEEEEEEEEEEEEEEEEEEE
410 - 429:	EEEEEEEEEEEEEEEEEEEE

A0A096NKA4 **A0A096NKA4_PAPAN** (556 aa)
Ran GTPase activating protein 1. *Papio anubis (Olive baboon)*

```
MSQGSSHAKDVIKEIEDFDSLEALRLEGNTVGVEAARVIAKALEKKSELKRCHWSDMFTGRLRTEIPPALISLGEGLITA
GAQLVELDLSDNAFGPDGVQGFEALLKSSACFTLHELKLNNCGMGIGGGKILAAALTECHRKSSAQGKPLALKVFVAGRN
RLENDGATALAEAFRVIGTLEEVHMPQNGINHPGVTALAQAFAVNPLLRVINLNDNTFTEKGAVAMAETLKTLRQVEVIN
FGDCLVRSKGAVAIADAIRGGLPKLKELNLSFCEIKRDAALAVAEAMADKTELEKLDLNGNTLGEEGCEQLQEVLEGFNM
AKVLASLSDDEDEEEEEGEEEEAEEEEEEEEEEEEEEEEEEEEPQQGGQGEKSATPSQKILDPNTGEPAPVLSSPPP
ADVSTFLAFPSPEKLLRLGPKSSMLIAQQTDTSDPEKVVSAFLKVSSVFKDEATVRTAVQDAVDALMKKAFSSSSFNSSA
FLTRLLAHMGLLKSEDKVKAIANLYGPLMALNHMVQQDYFPKALAPLLLAFITKPNSALESCSFARHSLLQTLYKV
```

345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE

A0A096NME2 **A0A096NME2_PAPAN** (1093 aa)
Solute carrier family 24 member 1. *Papio anubis (Olive baboon)*

```
MGKLIRMGPQDRRLLRTKRLPWSRLLFLLGMLIISSTYQHLRGPRGLSSLWAAVSSHQPVKLASRDLPSEEMMMVSSNPP
KPSSEMGGEMLVPQASVGSDEATLSMTVENIPDIPKRTAKMIPTTTKNNYSPTAAGTERRKEDTPTSSRTLTYYTSTSSR
QIVKKYTPTPTGEMKSYSPTQVREKVKYTPSPRGRRVGTYASSTFMTTETSHAITPRTTVKDSDITTTYKILETNSLKRI
MEETTPTTLKGMVDSTPTFLTHEVETNVLTSPRSIVEKNNLSPPRRVESNSSAHPWGLVGKNNLKTPQGTVLTHTPATSE
GQVTISTMTGSNPSETKAFTAAWSVRNPSPRTSVSAIETAPTTVWRLAKKPYIAPSTSTTPTVRAKLTTQVHHCVVVKPT
PAMPTTPSPSLTTALLPEELSPSPSVLPPILPDLPPKGEYPPDLFSVEERRQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLIMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKQIEAWVKEQLSRRPAAKVMALGDLSKPGDGAIAVDE
LQDNKKLKLPSLLTRGSSSTSLHNSTIRSTIYQLMLHSLDPLREVCLAEEKEEESLNQEARAQPQAKSESKPEDEEPAKL
PAVTVTPAPAPDIKGDQKENPGGQEDVAEAESTGEMTGEEGETAGEGETEEKSGGETQPEGEGETGTQGKGEEREKENEA
EGKGDNEGEGEGEIHAEDGEMKGIEGETESQELSAENHGEAKSDEKGVEDGGGSDGGDNEEEEEEEEEEEEEEEEEEEEE
EEEEEGNEEPLSLHWPETRQKQAIYLFLLPIVFPLWLTVPDVRRQESRKFFVFTFLGSIVWIAMFSYLMVWWAHQVGETI
GISEEIMGLTILAAGTSIPDLITSVIVARKGLGDMAVSSSVGSNIFDITVGLPVPWLLFCLINGLQPVPVSSNGLFCAIV
LLFLMLLFVISSIASCKWRMNKILGFTMFLLYFVFLIISVMLEDRIISCPVSV
```

860 - 879:	EEEEEEEEEEEEEEEEEEEE
861 - 880:	EEEEEEEEEEEEEEEEEEEE
862 - 881:	EEEEEEEEEEEEEEEEEEEE
863 - 882:	EEEEEEEEEEEEEEEEEEEE
864 - 883:	EEEEEEEEEEEEEEEEEEEE
865 - 884:	EEEEEEEEEEEEEEEEEEEE
866 - 885:	EEEEEEEEEEEEEEEEEEEE

A0A096P2G2 **A0A096P2G2_PAPAN** (1180 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Papio anubis (Olive baboon)*

```
MLLPSLSPRVQPAFIQCAGPQPPPHAHSPVGGRRGVFASSRHATTGARGKMAAAVLSGPSAGSAAGVPGGTGGLSAVNSG
PRLRLLLLESVSGLLQPRTGSAVAPVHPPNRSAPHLPGLMCLLRLHGSVGGAQNLSALGALVSLSNARLSSIKTRFEGLC
LLSLLVGESPTELFQQHCVSWLRSIQQVLQTQDPPATMELAVAVLRDLLRYAAQLPALFRDISMNHLPGLLTSLLGLRPE
CEQSALEGMKACMTYFPRACGSLKGKLASFFLSRVDALSPQLQQLACECYSRLPSLGAGFSQGLKHTESWEQELHSLLAS
LHTLLGALYEGAETAPVQNEGPGVEMLLSSEDGDAHILLRLRQRFSGLARCLGLMLSSEFGAPVSVPVQEILDFICRTLS
VSSKNISLHGDGPLRLLLLPSIHLEALDLLSALILACGSRLLRFGILISRLLPQVLNSWSIGRDSLSPGQERPYSTVRTK
VYAVLELWVQVCGASAGMLQGGASGEALLTHLLSDISPPADALKLRSPRGSPDGSLQTGKPSAPKKLKLDVGEAMAPPSH
RKGDSNANSDVCAAALKGLSRTILMCGPLIKEETHRRLHDLVLPLVMGVQQGEVLGSSPYTSSRCRRELYCLLLALLLAP
```

```
SPRCPPPLACALQAFSLGQREDSLEVSSFCSEALVTCAALTHPRVPPLQPMGPTCPTPAPVPPPEAPSPFRAPPFHPPGP
MPSVGPMPSAGPMPSAGPMPSAGPVPSARPGPPTTANHLGLSVSGLVSVPPRLLPGPENHRAGSNEDPILAPSGTPPPAI
PPDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDSVVIVPEGLPPLPPPPPSGATPPPIAPTGPPTASPPVPAKEEPE
ELPAAPGPLPPPPPPPPPVPGPVTLPPPQLVPEGTPGGGGPPALEEDLTVININSSDEEEEEEEEEEEEEEEEEEEEEDF
EEEEEDEEEYFEEEEEEEEEFEEEFEEEEGELEEEEEEEDEEEEEELEEVEELEFGTAGGEVEEGGPPPPTLPPALPPPE
SPPKVPPEPEPEPGLLLEVEEPGAEEEHGADTAPTLAPEVLPSQGEVEREEGSPSAGPPPQELVEEEPSAPPTLLEEGTE
DGGDRVQPPPETPAEEEMETETEAEALQEKEQDDTAAMLADFIDCPPDDEKPPPPTEPDS
```

938 - 957:	EEEEEEEEEEEEEEEEEEEE
939 - 958:	EEEEEEEEEEEEEEEEEEEE

A0A096P999 **A0A096P999_OSTTA** (767 aa)
Protein SDA1. *Ostreococcus tauri*

```
MSKAAMDLLTLRDRCKRDPEGYGEEAAMQTRRYEALRALFAMKPSREHAEFGELVSFISHVSGVYPELTRGFAEGVVDLL
ERHAGGLDASTRRALVSALILMRNKGSIGVEVTLPLFFKLFRVKDKSLRVMMFKHIVSDAKAANKKRTNDKYNRTVQSFL
YAAIKDENETTAKKALAVLTDMYRRNIWTDAKSVNLVVEACKHPSQKILVAALKFFEGQDEAAEAAAAEGDESDSESDPA
ARENDIKCRTSGGVSKTDVFKAYKTGVASSKKKKQKKLKRTIKSMQRKERNAENAVDARFAALQLINDPQALAELLFHKL
QIGHMSYDTKMLCIMMMCRIIGMHQLIMLNVYPFLQRYIQPSQLEVTRLLAAAATACHELVPPDALEPLLRQLVNQFIHD
RARPEVAAVGLNAVREICARCPLVMNEDLLQDLAQYKKAKDKPVSNAARGLIALFRELAPGLLEKKDRGKGVDMSRTLKA
YGETEVVDRIEGVDLLQRDLLKRKREEEEEAYSEDDDEENDEEDEEEEEEEEEEEEEEEEEEEEEEEEEEDEFETGKRE
REDIEIDPDAPPPKIRKNGKLSLSELKRRHKALVQKRKEEEEEEARAEREEEEEELGGPIEQERILTSEDFKRIKALQTE
KQLDAALKRAGANKSATVASDNIRLMMRRADRATDRRVNPDALAATGIKRAHDKAARLATVLAGREDNEYGSSTVRKQKK
TGGSSNAEKSKRKNLPLAARIHAATRRRNAPKINGKQQRGRKVWKNK
```

525 - 544:	EEEEEEEEEEEEEEEEEEEE
526 - 545:	EEEEEEEEEEEEEEEEEEEE
527 - 546:	EEEEEEEEEEEEEEEEEEEE
528 - 547:	EEEEEEEEEEEEEEEEEEEE
529 - 548:	EEEEEEEEEEEEEEEEEEEE
530 - 549:	EEEEEEEEEEEEEEEEEEEE
531 - 550:	EEEEEEEEEEEEEEEEEEEE
532 - 551:	EEEEEEEEEEEEEEEEEEEE

A0A098KX92 **A0A098KX92_CRIGR** (83 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MQNETRELVKEDVSDVATVDVRFTAVPKKKKKKKKKKKKKKKKKKKKEEEEEEEEEEEEEEEEEEEEEEEPIVGVFKKQL
SEE
```

48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE

A0A099P181 **A0A099P181_PICKU** (622 aa)
Uncharacterized protein. *Pichia kudriavzevii (Yeast) (Issatchenkia orientalis)*

```
MATTVNGEQLLEWFQDPANKSYFNHELLTIKKSPISNGIGVFALRSQAPVPKELDDDESNLLLRVHKSMVLSAQTCAISN
LIYEEKLGAMYGLVLAFIYERQLGERSPWFTYIETINYKNSKGDLIVPLCLYADKEKAILKGTEVEFMGGLDPQDLKSHF
EVSQKFANKVHKEAGLPIPSVLKDNSQFEEFAAITMAVASRAFEIDNYIELGLVPGADLFNHDPFGNEHVHFVAMGDVCP
FCGKDDGCGHEDFGPPDSEGEYEEEGWEDVENYDEDEAMDGSEEYQESDDKSKEEEPGDDFSKLEEFDGSCKSETPTYES
DEEVEELEEITMDYVAKIERELKEEEEREKAEEEEERDSDMDSEEEFELKELYLNPDECCDIVLERKIFKNKEVFNTYGE
LPNSVLLVKYGFAVEDNPYDSICLGPQIVEYRKSHQELEERIDWWGCMGWLLLREQERADEEDAQRDERGGSDADSEEGD
DGRNEEEEEEEEEEEEEEEEEEEESWLFNCRIEHPGRANAQLVAVSKLFTMSTAEFEKMIGDEECDGSTIKELLVNSKAT
MESKKLLRSWIDGRLSSTGDGKTRSGEMKRHLKKADPLSVRTMLIVATLNEKKLLEKALKTL
```

485 - 504:	EEEEEEEEEEEEEEEEEEEE

A0A099P6H8 **A0A099P6H8_PICKU** (1464 aa)
Uncharacterized protein (Fragment). *Pichia kudriavzevii (Yeast) (Issatchenkia orientalis)*

```
MDGAERENRQEISTNENKEKLIVRLSRRNTLIEQATRRHYENNPNVIFVYEEEEVLDTPEYWATIARRANIPVEEDDVEE
VPSLVDEGDSKCYDNPRELYEKLLARQQAYKKLSTEAEDEYYANIEYEYQLKKNRKRKSDEKIQTERQSSLRGSKDAEPS
VNTSAENNAEKPDDVDSDVSLVILSEHDDVNDKVGHQEEIAEGRCTGNYDLETGSNRIADGDGFEVEELYEEEKSSLLDD
EIIDIHETLNPEGDYENFSDNYDMGMNVRAEEDINLTHKIIPGIQEVGYTYFEETVTTSEACETDGTNLSEEISEKNEET
EEGAGSEADYVVKNDKATEVNNFVSLDSDSDSYGKFGNNNSMSNEGLNEQGLSEELSEEELSEEELSEEELSEEELSEER
LSEERLSEERLSEERLSEEELSEKESSEEESSEEESNEEGSNRKRLSEEEEEELIVRLSRRNTLIEQATRRHYENNPNVI
FVYEEEEVLDTPEYWATIARRANIPVEEDDVEEVPSLVDEGDSKCYDNPRELYEKLLARQQAYKKLSTEAEDEYYAKIEY
EYQLKKNRKRKSDEKDSDRESKIDNFMKLFNYQQSSLRGSKDAEQSVNTSAENNAEKPDDVDSDVSLVILSEHDDVNDKV
GHQEEIAEGRCMGNYDLETGSNRIANGDGFEVEELYEEEKSSLLDDVEDVRNYNNEEIIDIHETLNPEGDYENFSDNYDM
GMNVRAEEDINLTHKIIPGIQEVGYTYFEETVTTSEACETDGTNLSEEISEKNEETEEGAGSEADYVVKNDKATEVNNFV
SLDSDSDSYGKFGNNNSMSNEGLNEQGLSEEESSEESSKEELSEEESSKEELSEEELSEEELSEERLSEERLSEERLSEE
RLSEEGLSEERLSEERLSQVKKKSQVKKKKGEEEEEEEEEEEEEEEEEEEEEEEEEEEGNKLNRKNNYLANDARQANTEQ
```

```
PLEEEVVEIQRNEIEPRNQAGIQENHVFSEDASLDDSLLGNNTETIQVYPESDTKISSIDETTFHSAIGNASIEGSTPQE
VLEPSHRHVIFKPMTPPRPPTPEAPQLFIGLSELLSASLDIQSKQSAGHDVDPELVETTSKLIEKTSNVIGEISDTELER
IISGPSTVDREQKIDAEEEDKVESEAEYTEHMVVIDEPQIKVTRDKQSTPLPENYITKKAASVLDNLASESFSVLSESSM
LANTKNEGADNCVNEEDYINSLITETLNDTNRTNLVAASGESLSDQKDEDGMEDNVTDNKEETFNNNDDEEIIDHKSTDT
DELEDSVTHDVTSFIHVTNNAIQSNVEPNAEVDDNFTIGSDTSETGKLRNEATLASNDHLRNEHEATESLTASFQEECSN
ASNLEKEEKKVKKRAFDEVGDISNNFDSTGEFPRLKRRQFSIFNPFSWFGKTTFKNVENKNIFEFSNGEKIESNKLFQNE
SIGEGVDGVAEDNCSYSTQEKEKE
```

912 - 931:	EEEEEEEEEEEEEEEEEEEE
913 - 932:	EEEEEEEEEEEEEEEEEEEE
914 - 933:	EEEEEEEEEEEEEEEEEEEE
915 - 934:	EEEEEEEEEEEEEEEEEEEE
916 - 935:	EEEEEEEEEEEEEEEEEEEE
917 - 936:	EEEEEEEEEEEEEEEEEEEE
918 - 937:	EEEEEEEEEEEEEEEEEEEE
919 - 938:	EEEEEEEEEEEEEEEEEEEE

A0A099P8X1 **A0A099P8X1_PICKU** (190 aa)
Uncharacterized protein. *Pichia kudriavzevii (Yeast) (Issatchenkia orientalis)*

```
MDVVYRKPHFEGKVSAAAGGRKGDDLQISSDSEWVLFGSKYPNEGTRTRTRVSASADVGAEADVYVATTLRQSSDHEESI
LSSRSVGSGSVNARELDGGYVISDFDEHLSTESDWRYKYDGEDGSYDYDYDGDDAHDEDNDSLLDDVRTQMDEIVRSMGE
EEEEEEEEEEEEEEEEEEEEEEERNLMKHQ
```

160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE

A0A099ZEC7 **A0A099ZEC7_TINGU** (1338 aa)
Tau-tubulin kinase 1 (Fragment). *Tinamus guttatus (White-throated tinamou)*

```
QINGSFKLGATKILSGWQMQCLAAVIKDEPNMSGGGEQVDILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTRENVAL
KVESAQQPKQVLKMEVAVLKKLQGKDHVCRFIGCGRNEKFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESI
EAIHSVGFLHRDIKPSNFAMGRLPSTYRKCYMLDFGLARQYTNTTGEVRPPRNVAGFRGTVRYASVNAHKNREMGRHDDL
WSLFYMLVEFAVGQLPWRKIKDKEQVGMIKEKYEHRMLLKHMPSEFHLFLDHIASLDYFTKPDYQLIMSVFENSMKERGI
TENEAFDWEKAGTDILLSTSTSTPPQQNTRQTAAMFGVVNVTPVPGDLLRENTEDVLQGEHLSDQENAPPILSGRPTEGL
GQAPNTAFNEAEVWEETDVNRNKLRISISKTQCMVEEEQRNGVCPSSPVRVPPESPTAQARSLRYRRVNSPESERLSTAD
GKADLHERRSRMDLPGSPSRLVCSSQPAQMLSIDTGQADRQASGRMDVSASVEHEALSNAFRSVPLAEEEDFDSKEWVII
DKETELKDFHPGAEPSTSGTTDEEPEELRPIEEGEERRRLGADLAVRPKMHDGRSRGMQPVTEEDSSHRHEGPSQTVSDS
KHEQQTGSPAHSPLHSAPATRQRRRESEPTGPQRQAYSLKSFEMNGLPKAVPLSLPYQDFKKDLSDYWEKPKAPQRIKKV
DFSNVVLTAPCKPLESHLKMNGKEEEEEEEEEEEEEEEEEEEEVGDEIDMHSGSSSDLSQKSTERSQECAPSTLLADDQK
GSKGRASTADGDLELEEGSKTLVLFSPGDLKKSPVTTDLAPEVDLGTLAALTPQSERPQPMGSQLDVSEPGTLSSVLKSE
PKPPMAVATTSSPFTKVERTFVHIAEKTHLNVMSSSGQLMRHEDYCPPGPFEEIIIEEEMEENLVLVENGSIHSGLEGAE
TESCALSANPIEITSETAGIAKPPEEKLELSDKVAPLLDLEEPGKTIPREHELKKTKPITEHLKQAEIPLDAPQQGPRRP
LGSRYRSRIPILFSEEDTGSDLSTSLSAKDRLYKRAKHPDLARLVMEKRQNRLLRLASGASSSASSSDERRRASETLSAT
GSEEDTHDSDDSIQRKAGKEKAALLGKAEKHISTKSRIPRPITPMKSPLETMRSEGSVPVSVPVLCSSLQDGAAAYRLQA
QRPAGSIPNDSRPAQMQSRLPSSPSSTAPPPRSGSRRPPCAPPRSPILPSRNPSATPRSQLPSRKESPSPCRQRKPGTGI
QRVPPSPRPQPQAQALGPTGDSLPSPGVTKKGQRGKKQTQSPATKGKQASPESKAAAR
```

744 - 763:	EEEEEEEEEEEEEEEEEEEE

A0A099ZME4 **A0A099ZME4_TINGU** (707 aa)
X-linked retinitis pigmentosa GTPase regulator (Fragment). *Tinamus guttatus (White-throated tinamou)*

```
VLESGAVFTFGKSSFAENIPSKFWFKNDKPVHISCGDEHTAIVTGNGKLYMFGSNNWGQLGLGSKNTVSKPTCVKALKPE
KTKLAACGRNHTLVYTEKGNVYAAGGNSEGQLGLGDTEERTTFHLISFFTNQHKIKQLAAGSYTSAAITEDGQLFMWGDN
SEGQIGLANEASVCVPCQVVVGKPVSSVSCGYYHSALITGDGELYTFGEPENGKLGLLPEQLKNSRVPQPVPGIMEKVNK
VACGGGHTVVLTERDVYTFGLGQYGQLGHGTFIFETSVPKSVEHLRRHKILSIACGENHTAVIAENGLMFTFGDGRHGKL
GLGEENFVNQFKPILCSNFLRFTVLLVACGGCHMLVFAAPRPKGSEEILIEDVQNCLTATTSGMSIVSSATGTLQKTLSA
RMRRRAKERSPEQFLRMIQTLPPLGGNFLKSSLHVTSNTSLPYFSATDLPEVKPMELDHETEKNHQKDKPREGSEEDSDD
ESNHRNLGDTSDILNVTHVMKLNPSDQSLKLSPIQKQKVLEEEGNEEQKEEEEGEEEEEGEEEEEEGEEEEEGEEEEEE
EEEEEEEEEEEEEEEEEEEEGDEEEGEEEEGEEEGEEEEGEEEEEGEEEEGEEEEEEGEEEEEDEEEEKEDEEEEKKEEE
EEEEKKGEEEEEEEEEEEKSKHKKQVASNKLTQKKSQNSRKPKTESTAVPNSAKQKMKSKHCVANGL
```

555 - 574:	EEEEEEEEEEEEEEEEEEEE
556 - 575:	EEEEEEEEEEEEEEEEEEEE
557 - 576:	EEEEEEEEEEEEEEEEEEEE
558 - 577:	EEEEEEEEEEEEEEEEEEEE
559 - 578:	EEEEEEEEEEEEEEEEEEEE

560 - 579:	EEEEEEEEEEEEEEEEEEEE
561 - 580:	EEEEEEEEEEEEEEEEEEEE

A0A0A0HRR6 **A0A0A0HRR6_PARBD** (374 aa)
Repressor of RNA polymerase III transcription MAF1. *Paracoccidioides brasiliensis (strain Pb18)*

```
MKVRRSNPRGYVPSWSFLPLSEFEDVAGALNFDTEDCHVVGGCDLYTTKAAGGDKKLYKNIENALESQYESLLRLSASLS
QPNASQAAQSLNLSRSSPFGPLSEHSSRRTFAYLIATLNASHPDYDFSHLLRPSDFQCEKSLRCVMNVIDTALFNLRPRM
TRDVTPQTSTTTFGLRPSSSTMHSWGPRMWKIIDNQMSLRECAIFCYSPEEDPYDGEEGSIWSLNYFFFNKTRKRVCYLY
LRGISILNHLPDGSTTPSLVDMRDGDDGFSTPDYGARKRVKYWLGDPVSGASAEEEEDQQEEEEEEEEEEEEEEEEEEE
DEVEETPQASSRPVRPVVDEFDNYLLSDEEVQSKSRSKSSMCAVSDEIADSMEV
```

301 - 320:	EEEEEEEEEEEEEEEEEEEE

A0A0A0K7G2 **A0A0A0K7G2_CUCSA** (61 aa)
Uncharacterized protein. *Cucumis sativus (Cucumber)*

```
MEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERRHKKRV
```

2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE

A0A0A0K867 **A0A0A0K867_CUCSA** (69 aa)
Uncharacterized protein. *Cucumis sativus (Cucumber)*

MSSSYLKSSGRKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEESRHG

13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE

A0A0A0KAV3 **A0A0A0KAV3_CUCSA** (953 aa)
Chloride channel protein. *Cucumis sativus (Cucumber)*

MIISIMGAFDSMGLKLNNAPHYPCLSSLPSAFFCSNFSTLNFSSSISGLHDLSIPISNGLENCAVGNRSYDSLLGLHFSL
RPKRTASCFRPISALPGSGESESPISVSSNAGFSIKQSEQEEYDDDDAEEEEEGEEEEEGEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGIPFGTGSSTIISSCFVGLLTGIGVVLF
NNAVHEIRDFSWDGIPNRGASWLREMPIEDIWKRVILVPASGGFLVSFLNLLRDATDVKVDQPQGDDPSTKFGVPISISN
KLKAALQPFLKAIAASVTLGTGNSLGPEGPSVDIGTSVGKGISTVFEMNSRTKLSLIAAGSAAGISSGFNAAVAGCFFAI
ESVLWPSPADSTFSLTNTTSMVILSAVIASVVSQVGLGVEPAFKVPVYDFRSPSELPLYLLLGVLCGLVSLSFSKCTSYL
LATVDKFHKEFGAPRAMFPILGGFTIGLIALAYPEILYWGFENVDLLLESRPFVKPLSAELLAQLVVIKILATSLCRASG
LVGGYYAPSLFIGAATGMAYGKFIGIALSEPNSVLDFSIFEVASPQAYGLVGMAATLAGVCQVPLTAVLLLFELTQDYRI
VLPLLGAVGVSSWITSGQKRKRSSQQTKKLSPGKSPSTQQSTAYDSNANNQSSNYAEDGQTNYPNDLCEIESSLCAYESD
SETVELERKISVSEAMTTKYITILMGTCLVEAVNLMLAEKQSCALIVDEGNILIGILELEDIQKLSKNAKSRNEQLKDFV
VSEICSLDEKMCRVPWTATPSMDILTAKMIMKNLGVTQVPVVRDQMGYVVGVLDWECIDLTCRILATRESLGR

141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE

145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
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254 - 273:	EEEEEEEEEEEEEEEEEEEE
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257 - 276:	EEEEEEEEEEEEEEEEEEEE
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266 - 285:	EEEEEEEEEEEEEEEEEEEE
267 - 286:	EEEEEEEEEEEEEEEEEEEE
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271 - 290:	EEEEEEEEEEEEEEEEEEEE
272 - 291:	EEEEEEEEEEEEEEEEEEEE
273 - 292:	EEEEEEEEEEEEEEEEEEEE

A0A0A0KB23 **A0A0A0KB23_CUCSA** (566 aa)
DUF4005 domain-containing protein. *Cucumis sativus (Cucumber)*

```
MGKATRWLKGLLGIKKDKDPSSNSNSNSNSTTLPADNRKDKKRWSFAKSTRDSAQTLPPPLESAWFRSSYISDSDREQNK
HAIAVAAATAAAADAAVAAAQAAVAVVRLTSQGRGRASHYITGRDRWAAVKIQTVFRGYLARKALRALKGLVKLQAVVRG
FLVRKRAAATLHSMQALFRAQTAVRTQRARRSFNKENRFNPDIRPRKSSERFDETRSELFHSKRLSVASSYETCMNSLDE
SPKIVEIDTYRTRSRSRRYISTLSECGGDDIAFQSSPIPCSNRPRVVVDCHNNNVLRDFEWCLMGEDCKFPTAHSTPRLS
NNSFVSANVPVTPSKSVCGDSFYRPYINYCPNYMANTQSFKAKLRSQSAPKQRPEPGSKKKLSLNEIMAARNSLSSVRMQ
RPNNQMLQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDEEE
ETSYGF
```

409 - 428:	EEEEEEEEEEEEEEEEEEEE
410 - 429:	EEEEEEEEEEEEEEEEEEEE
411 - 430:	EEEEEEEEEEEEEEEEEEEE
412 - 431:	EEEEEEEEEEEEEEEEEEEE
413 - 432:	EEEEEEEEEEEEEEEEEEEE
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415 - 434:	EEEEEEEEEEEEEEEEEEEE
416 - 435:	EEEEEEEEEEEEEEEEEEEE
417 - 436:	EEEEEEEEEEEEEEEEEEEE
418 - 437:	EEEEEEEEEEEEEEEEEEEE
419 - 438:	EEEEEEEEEEEEEEEEEEEE
420 - 439:	EEEEEEEEEEEEEEEEEEEE
421 - 440:	EEEEEEEEEEEEEEEEEEEE
422 - 441:	EEEEEEEEEEEEEEEEEEEE
423 - 442:	EEEEEEEEEEEEEEEEEEEE
424 - 443:	EEEEEEEEEEEEEEEEEEEE
425 - 444:	EEEEEEEEEEEEEEEEEEEE
426 - 445:	EEEEEEEEEEEEEEEEEEEE
427 - 446:	EEEEEEEEEEEEEEEEEEEE

428 - 447:	EEEEEEEEEEEEEEEEEEEE
429 - 448:	EEEEEEEEEEEEEEEEEEEE
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431 - 450:	EEEEEEEEEEEEEEEEEEEE
432 - 451:	EEEEEEEEEEEEEEEEEEEE
433 - 452:	EEEEEEEEEEEEEEEEEEEE
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461 - 480:	EEEEEEEEEEEEEEEEEEEE
462 - 481:	EEEEEEEEEEEEEEEEEEEE
463 - 482:	EEEEEEEEEEEEEEEEEEEE
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465 - 484:	EEEEEEEEEEEEEEEEEEEE
466 - 485:	EEEEEEEEEEEEEEEEEEEE
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528 - 547:	EEEEEEEEEEEEEEEEEEEE
529 - 548:	EEEEEEEEEEEEEEEEEEEE
530 - 549:	EEEEEEEEEEEEEEEEEEEE
531 - 550:	EEEEEEEEEEEEEEEEEEEE

532 - 551:	EEEEEEEEEEEEEEEEEEEE
533 - 552:	EEEEEEEEEEEEEEEEEEEE
534 - 553:	EEEEEEEEEEEEEEEEEEEE
535 - 554:	EEEEEEEEEEEEEEEEEEEE
536 - 555:	EEEEEEEEEEEEEEEEEEEE

A0A0A0KD43 **A0A0A0KD43_CUCSA** (180 aa)
Uncharacterized protein. *Cucumis sativus (Cucumber)*

```
MKKVKLQKRERERERERERGHIEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEVCK
```

23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
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31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
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35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
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41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
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55 - 74:	EEEEEEEEEEEEEEEEEEEE
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57 - 76:	EEEEEEEEEEEEEEEEEEEE
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61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE

65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
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80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
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86 - 105:	EEEEEEEEEEEEEEEEEEEE
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91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
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100 - 119:	EEEEEEEEEEEEEEEEEEEE
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103 - 122:	EEEEEEEEEEEEEEEEEEEE
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105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
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117 - 136:	EEEEEEEEEEEEEEEEEEEE
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157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE

A0A0A0KFG5 **A0A0A0KFG5_CUCSA** (743 aa)
Protein kinase domain-containing protein. *Cucumis sativus (Cucumber)*

```
MAKPTSFLLQFTLLVCFTAIHGRAEITSSSCDAYVSYFTKSSQFFDLHSISKLFGVKALKIAKASNLESDKTPLFDGQLL
FIPVTCNSTTNGNNSFFFSNTTYKINQGDTFYLVSTSFFEHLCDSDIVVKMNPSLNPNNLSVGVEAVFPLFCKCPSKENL
EQGIQFFITYVWQLTDVVSGVRSIFNVSKDANLEDVKGVKLTNFVAGEALFIPLSKLPLLSQSPPQRKKIKHLVIVVGGV
ALGVGFLLVAYVFFIYKKMKLPIWGNSIKMKMKQNGQLLPLPPPPVVSDYLGRPILYDYKVIMDATMSFNEGFKIGKSVY
KAIINGQISVIKEAKPDSTEELMILQKVNHINLVKLVGFSSDDKENFYLVYEFAENGSLDKWLYSSSEASSSNLTWSQRL
NIALDVANGLQYMHDHTQPSIVHQDIKTSCILLDLRFRAKISNLAKARPAVDSLSTKVDVFAFGVVVLKLLSGKKALKCT
VNGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEVGNLCKEIRDVLDNEEGREDKLRDWMDSKLKDCYPIEGALSLAVMARACTQDEPLSRPSMAEIVFNLCVLAESSPEKV
EKSWVSLLEADEIGHSHSPIRAR
```

484 - 503:	EEEEEEEEEEEEEEEEEEEE

485 - 504:	EEEEEEEEEEEEEEEEEEEE
486 - 505:	EEEEEEEEEEEEEEEEEEEE
487 - 506:	EEEEEEEEEEEEEEEEEEEE
488 - 507:	EEEEEEEEEEEEEEEEEEEE
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537 - 556:	EEEEEEEEEEEEEEEEEEEE
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542 - 561:	EEEEEEEEEEEEEEEEEEEE
543 - 562:	EEEEEEEEEEEEEEEEEEEE
544 - 563:	EEEEEEEEEEEEEEEEEEEE
545 - 564:	EEEEEEEEEEEEEEEEEEEE
546 - 565:	EEEEEEEEEEEEEEEEEEEE
547 - 566:	EEEEEEEEEEEEEEEEEEEE
548 - 567:	EEEEEEEEEEEEEEEEEEEE
549 - 568:	EEEEEEEEEEEEEEEEEEEE
550 - 569:	EEEEEEEEEEEEEEEEEEEE
551 - 570:	EEEEEEEEEEEEEEEEEEEE
552 - 571:	EEEEEEEEEEEEEEEEEEEE
553 - 572:	EEEEEEEEEEEEEEEEEEEE
554 - 573:	EEEEEEEEEEEEEEEEEEEE
555 - 574:	EEEEEEEEEEEEEEEEEEEE
556 - 575:	EEEEEEEEEEEEEEEEEEEE
557 - 576:	EEEEEEEEEEEEEEEEEEEE
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561 - 580:	EEEEEEEEEEEEEEEEEEEE
562 - 581:	EEEEEEEEEEEEEEEEEEEE
563 - 582:	EEEEEEEEEEEEEEEEEEEE
564 - 583:	EEEEEEEEEEEEEEEEEEEE
565 - 584:	EEEEEEEEEEEEEEEEEEEE
566 - 585:	EEEEEEEEEEEEEEEEEEEE
567 - 586:	EEEEEEEEEEEEEEEEEEEE
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570 - 589:	EEEEEEEEEEEEEEEEEEEE
571 - 590:	EEEEEEEEEEEEEEEEEEEE
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573 - 592:	EEEEEEEEEEEEEEEEEEEE
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578 - 597:	EEEEEEEEEEEEEEEEEEEE
579 - 598:	EEEEEEEEEEEEEEEEEEEE
580 - 599:	EEEEEEEEEEEEEEEEEEEE
581 - 600:	EEEEEEEEEEEEEEEEEEEE
582 - 601:	EEEEEEEEEEEEEEEEEEEE
583 - 602:	EEEEEEEEEEEEEEEEEEEE
584 - 603:	EEEEEEEEEEEEEEEEEEEE
585 - 604:	EEEEEEEEEEEEEEEEEEEE
586 - 605:	EEEEEEEEEEEEEEEEEEEE
587 - 606:	EEEEEEEEEEEEEEEEEEEE
588 - 607:	EEEEEEEEEEEEEEEEEEEE

589 - 608:	EEEEEEEEEEEEEEEEEEEE
590 - 609:	EEEEEEEEEEEEEEEEEEEE
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592 - 611:	EEEEEEEEEEEEEEEEEEEE
593 - 612:	EEEEEEEEEEEEEEEEEEEE
594 - 613:	EEEEEEEEEEEEEEEEEEEE
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596 - 615:	EEEEEEEEEEEEEEEEEEEE
597 - 616:	EEEEEEEEEEEEEEEEEEEE
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599 - 618:	EEEEEEEEEEEEEEEEEEEE
600 - 619:	EEEEEEEEEEEEEEEEEEEE
601 - 620:	EEEEEEEEEEEEEEEEEEEE
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603 - 622:	EEEEEEEEEEEEEEEEEEEE
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610 - 629:	EEEEEEEEEEEEEEEEEEEE
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613 - 632:	EEEEEEEEEEEEEEEEEEEE
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617 - 636:	EEEEEEEEEEEEEEEEEEEE
618 - 637:	EEEEEEEEEEEEEEEEEEEE
619 - 638:	EEEEEEEEEEEEEEEEEEEE
620 - 639:	EEEEEEEEEEEEEEEEEEEE
621 - 640:	EEEEEEEEEEEEEEEEEEEE
622 - 641:	EEEEEEEEEEEEEEEEEEEE
623 - 642:	EEEEEEEEEEEEEEEEEEEE

A0A0A0KG68 **A0A0A0KG68_CUCSA** (479 aa)
Uncharacterized protein. *Cucumis sativus (Cucumber)*

```
MSNFKSNLSLTTTDLDMNQDQMDTNHNEFHQCSFPRQQGNPTSLSPLPFKKTPDPENHHPIHPFHSISQHSFPFLTPPSS
VSSPASTRPLFPFALEPSQFKTDPLAPMVHQPPSLLPHHNQFVAPPLASTQNGFGYPPYFMGEFASFQQQQQKQQQHHQF
LQYWNESLDLNSKAGFRPQAFKLRGENARLNFPELLLNKDKEAEEEEEEASQASAPQQDVDNNNHDNDIELESNNEGVTE
ENRQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGI
SKTQEMVWREMAEAWLNAMPAGWGPGSPVWDDLDTTNNLLLQPQLQFVNPIQQQSFDLTSASPSSSSCPMKPFFLKDED
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245 - 264:	EEEEEEEEEEEEEEEEEEEE
246 - 265:	EEEEEEEEEEEEEEEEEEEE
247 - 266:	EEEEEEEEEEEEEEEEEEEE
248 - 267:	EEEEEEEEEEEEEEEEEEEE
249 - 268:	EEEEEEEEEEEEEEEEEEEE
250 - 269:	EEEEEEEEEEEEEEEEEEEE
251 - 270:	EEEEEEEEEEEEEEEEEEEE
252 - 271:	EEEEEEEEEEEEEEEEEEEE
253 - 272:	EEEEEEEEEEEEEEEEEEEE
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255 - 274:	EEEEEEEEEEEEEEEEEEEE
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291 - 310:	EEEEEEEEEEEEEEEEEEEE
292 - 311:	EEEEEEEEEEEEEEEEEEEE
293 - 312:	EEEEEEEEEEEEEEEEEEEE
294 - 313:	EEEEEEEEEEEEEEEEEEEE
295 - 314:	EEEEEEEEEEEEEEEEEEEE
296 - 315:	EEEEEEEEEEEEEEEEEEEE
297 - 316:	EEEEEEEEEEEEEEEEEEEE
298 - 317:	EEEEEEEEEEEEEEEEEEEE
299 - 318:	EEEEEEEEEEEEEEEEEEEE
300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE
306 - 325:	EEEEEEEEEEEEEEEEEEEE

307 - 326:	EEEEEEEEEEEEEEEEEEEE
308 - 327:	EEEEEEEEEEEEEEEEEEEE
309 - 328:	EEEEEEEEEEEEEEEEEEEE
310 - 329:	EEEEEEEEEEEEEEEEEEEE
311 - 330:	EEEEEEEEEEEEEEEEEEEE
312 - 331:	EEEEEEEEEEEEEEEEEEEE
313 - 332:	EEEEEEEEEEEEEEEEEEEE
314 - 333:	EEEEEEEEEEEEEEEEEEEE
315 - 334:	EEEEEEEEEEEEEEEEEEEE
316 - 335:	EEEEEEEEEEEEEEEEEEEE
317 - 336:	EEEEEEEEEEEEEEEEEEEE
318 - 337:	EEEEEEEEEEEEEEEEEEEE
319 - 338:	EEEEEEEEEEEEEEEEEEEE
320 - 339:	EEEEEEEEEEEEEEEEEEEE
321 - 340:	EEEEEEEEEEEEEEEEEEEE
322 - 341:	EEEEEEEEEEEEEEEEEEEE
323 - 342:	EEEEEEEEEEEEEEEEEEEE
324 - 343:	EEEEEEEEEEEEEEEEEEEE
325 - 344:	EEEEEEEEEEEEEEEEEEEE
326 - 345:	EEEEEEEEEEEEEEEEEEEE
327 - 346:	EEEEEEEEEEEEEEEEEEEE
328 - 347:	EEEEEEEEEEEEEEEEEEEE
329 - 348:	EEEEEEEEEEEEEEEEEEEE
330 - 349:	EEEEEEEEEEEEEEEEEEEE
331 - 350:	EEEEEEEEEEEEEEEEEEEE
332 - 351:	EEEEEEEEEEEEEEEEEEEE
333 - 352:	EEEEEEEEEEEEEEEEEEEE
334 - 353:	EEEEEEEEEEEEEEEEEEEE
335 - 354:	EEEEEEEEEEEEEEEEEEEE
336 - 355:	EEEEEEEEEEEEEEEEEEEE
337 - 356:	EEEEEEEEEEEEEEEEEEEE
338 - 357:	EEEEEEEEEEEEEEEEEEEE
339 - 358:	EEEEEEEEEEEEEEEEEEEE
340 - 359:	EEEEEEEEEEEEEEEEEEEE
341 - 360:	EEEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEEE
344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE

359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE
379 - 398:	EEEEEEEEEEEEEEEEEEEE

A0A0A0KKH3 **A0A0A0KKH3_CUCSA** (102 aa)
Uncharacterized protein. *Cucumis sativus (Cucumber)*

```
MMNLDSELWSAKRLKTKRSEFLFLKKKFLRGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEGKLMSNETRSYGNLI
```

32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE

58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE

A0A0A0KZ57 **A0A0A0KZ57_CUCSA** (196 aa)
Uncharacterized protein. *Cucumis sativus (Cucumber)*

```
MKAGTSNNQKALDSRDMVNRGGVELIRNCDLPPPQKVFKSGMEEKMELLKALRLSQTRAREAERKAAKLMEERDCISRAF
EDEARMVFCYRQSLKLLELRVFKLQKQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
SDKNGGNGGMKWVWALAICLSVVGVGFLLGYTCNPS
```

108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE

A0A0A0L172 **A0A0A0L172_CUCSA** (103 aa)

Uncharacterized protein. *Cucumis sativus (Cucumber)*

```
MGEMRSVDGVLKRSMKNKEIYVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEKPAKTEYLNKKGDNALF
```

23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE

A0A0A0L2E8 **A0A0A0L2E8_CUCSA** (99 aa)
Uncharacterized protein. *Cucumis sativus (Cucumber)*

```
MTFYKLKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEKERLRYGKGKLSLSSVG
```

8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE

56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE

A0A0A0L3Q8 **A0A0A0L3Q8_CUCSA** (631 aa)
Uncharacterized protein. *Cucumis sativus (Cucumber)*

```
MTRLFRSKSCGHVRVSEFKPPPPPPSSYYDSDDEEEEEEEEEEEDDDYYGDGVGIKVNENGFGLVLRNSVCDSDEEKQEG
ATRQSNNGNQFPILDILVTALRKSLVTCSVEPDDVSSMDISSPVNVRHVSHVTFDRFNGFLGLPTEFEPEVPTRVPSASA
SVFGVSAKSMQCSFDDRGNSVPTILLMMQKRLYSEGGLKAEGIFRINAENSQEEFVRNELNSGVVPRGIDVHCLAGLIKA
WLRELPTGVLDTLTPEQVMHCNTEEDCTQLVKLLPPMEAAILDWAINLMADVVQHEKYNKMNARNIAMVFAPNMTQMADP
LTALIHAVQVMNLLKTLILKILQEREESEARQPSCLDSPNAKINMKSSNKTIGKSANQPPSSAIDDVKCTSFDRADYTSG
GKFESFEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEQYHSASGRSTPVRYGVGALQQSGYETSDWLSLRKGVRKICRHPVFQLSKSSKKSRSFGVVSCKY
```

410 - 429:	EEEEEEEEEEEEEEEEEEEE
411 - 430:	EEEEEEEEEEEEEEEEEEEE
412 - 431:	EEEEEEEEEEEEEEEEEEEE
413 - 432:	EEEEEEEEEEEEEEEEEEEE
414 - 433:	EEEEEEEEEEEEEEEEEEEE
415 - 434:	EEEEEEEEEEEEEEEEEEEE
416 - 435:	EEEEEEEEEEEEEEEEEEEE
417 - 436:	EEEEEEEEEEEEEEEEEEEE
418 - 437:	EEEEEEEEEEEEEEEEEEEE
419 - 438:	EEEEEEEEEEEEEEEEEEEE
420 - 439:	EEEEEEEEEEEEEEEEEEEE
421 - 440:	EEEEEEEEEEEEEEEEEEEE
422 - 441:	EEEEEEEEEEEEEEEEEEEE
423 - 442:	EEEEEEEEEEEEEEEEEEEE
424 - 443:	EEEEEEEEEEEEEEEEEEEE
425 - 444:	EEEEEEEEEEEEEEEEEEEE
426 - 445:	EEEEEEEEEEEEEEEEEEEE
427 - 446:	EEEEEEEEEEEEEEEEEEEE
428 - 447:	EEEEEEEEEEEEEEEEEEEE
429 - 448:	EEEEEEEEEEEEEEEEEEEE
430 - 449:	EEEEEEEEEEEEEEEEEEEE
431 - 450:	EEEEEEEEEEEEEEEEEEEE
432 - 451:	EEEEEEEEEEEEEEEEEEEE
433 - 452:	EEEEEEEEEEEEEEEEEEEE
434 - 453:	EEEEEEEEEEEEEEEEEEEE
435 - 454:	EEEEEEEEEEEEEEEEEEEE
436 - 455:	EEEEEEEEEEEEEEEEEEEE
437 - 456:	EEEEEEEEEEEEEEEEEEEE
438 - 457:	EEEEEEEEEEEEEEEEEEEE
439 - 458:	EEEEEEEEEEEEEEEEEEEE
440 - 459:	EEEEEEEEEEEEEEEEEEEE
441 - 460:	EEEEEEEEEEEEEEEEEEEE
442 - 461:	EEEEEEEEEEEEEEEEEEEE
443 - 462:	EEEEEEEEEEEEEEEEEEEE
444 - 463:	EEEEEEEEEEEEEEEEEEEE
445 - 464:	EEEEEEEEEEEEEEEEEEEE

446 - 465:	EEEEEEEEEEEEEEEEEEEE
447 - 466:	EEEEEEEEEEEEEEEEEEEE
448 - 467:	EEEEEEEEEEEEEEEEEEEE
449 - 468:	EEEEEEEEEEEEEEEEEEEE
450 - 469:	EEEEEEEEEEEEEEEEEEEE
451 - 470:	EEEEEEEEEEEEEEEEEEEE
452 - 471:	EEEEEEEEEEEEEEEEEEEE
453 - 472:	EEEEEEEEEEEEEEEEEEEE
454 - 473:	EEEEEEEEEEEEEEEEEEEE
455 - 474:	EEEEEEEEEEEEEEEEEEEE
456 - 475:	EEEEEEEEEEEEEEEEEEEE
457 - 476:	EEEEEEEEEEEEEEEEEEEE
458 - 477:	EEEEEEEEEEEEEEEEEEEE
459 - 478:	EEEEEEEEEEEEEEEEEEEE
460 - 479:	EEEEEEEEEEEEEEEEEEEE
461 - 480:	EEEEEEEEEEEEEEEEEEEE
462 - 481:	EEEEEEEEEEEEEEEEEEEE
463 - 482:	EEEEEEEEEEEEEEEEEEEE
464 - 483:	EEEEEEEEEEEEEEEEEEEE
465 - 484:	EEEEEEEEEEEEEEEEEEEE
466 - 485:	EEEEEEEEEEEEEEEEEEEE
467 - 486:	EEEEEEEEEEEEEEEEEEEE
468 - 487:	EEEEEEEEEEEEEEEEEEEE
469 - 488:	EEEEEEEEEEEEEEEEEEEE
470 - 489:	EEEEEEEEEEEEEEEEEEEE
471 - 490:	EEEEEEEEEEEEEEEEEEEE
472 - 491:	EEEEEEEEEEEEEEEEEEEE
473 - 492:	EEEEEEEEEEEEEEEEEEEE
474 - 493:	EEEEEEEEEEEEEEEEEEEE
475 - 494:	EEEEEEEEEEEEEEEEEEEE
476 - 495:	EEEEEEEEEEEEEEEEEEEE
477 - 496:	EEEEEEEEEEEEEEEEEEEE
478 - 497:	EEEEEEEEEEEEEEEEEEEE
479 - 498:	EEEEEEEEEEEEEEEEEEEE
480 - 499:	EEEEEEEEEEEEEEEEEEEE
481 - 500:	EEEEEEEEEEEEEEEEEEEE
482 - 501:	EEEEEEEEEEEEEEEEEEEE
483 - 502:	EEEEEEEEEEEEEEEEEEEE
484 - 503:	EEEEEEEEEEEEEEEEEEEE
485 - 504:	EEEEEEEEEEEEEEEEEEEE
486 - 505:	EEEEEEEEEEEEEEEEEEEE
487 - 506:	EEEEEEEEEEEEEEEEEEEE
488 - 507:	EEEEEEEEEEEEEEEEEEEE
489 - 508:	EEEEEEEEEEEEEEEEEEEE
490 - 509:	EEEEEEEEEEEEEEEEEEEE
491 - 510:	EEEEEEEEEEEEEEEEEEEE
492 - 511:	EEEEEEEEEEEEEEEEEEEE
493 - 512:	EEEEEEEEEEEEEEEEEEEE
494 - 513:	EEEEEEEEEEEEEEEEEEEE
495 - 514:	EEEEEEEEEEEEEEEEEEEE
496 - 515:	EEEEEEEEEEEEEEEEEEEE
497 - 516:	EEEEEEEEEEEEEEEEEEEE

498 - 517:	EEEEEEEEEEEEEEEEEEEE
499 - 518:	EEEEEEEEEEEEEEEEEEEE
500 - 519:	EEEEEEEEEEEEEEEEEEEE
501 - 520:	EEEEEEEEEEEEEEEEEEEE
502 - 521:	EEEEEEEEEEEEEEEEEEEE
503 - 522:	EEEEEEEEEEEEEEEEEEEE
504 - 523:	EEEEEEEEEEEEEEEEEEEE
505 - 524:	EEEEEEEEEEEEEEEEEEEE
506 - 525:	EEEEEEEEEEEEEEEEEEEE
507 - 526:	EEEEEEEEEEEEEEEEEEEE
508 - 527:	EEEEEEEEEEEEEEEEEEEE
509 - 528:	EEEEEEEEEEEEEEEEEEEE
510 - 529:	EEEEEEEEEEEEEEEEEEEE
511 - 530:	EEEEEEEEEEEEEEEEEEEE
512 - 531:	EEEEEEEEEEEEEEEEEEEE
513 - 532:	EEEEEEEEEEEEEEEEEEEE
514 - 533:	EEEEEEEEEEEEEEEEEEEE
515 - 534:	EEEEEEEEEEEEEEEEEEEE
516 - 535:	EEEEEEEEEEEEEEEEEEEE
517 - 536:	EEEEEEEEEEEEEEEEEEEE
518 - 537:	EEEEEEEEEEEEEEEEEEEE
519 - 538:	EEEEEEEEEEEEEEEEEEEE
520 - 539:	EEEEEEEEEEEEEEEEEEEE
521 - 540:	EEEEEEEEEEEEEEEEEEEE
522 - 541:	EEEEEEEEEEEEEEEEEEEE
523 - 542:	EEEEEEEEEEEEEEEEEEEE
524 - 543:	EEEEEEEEEEEEEEEEEEEE
525 - 544:	EEEEEEEEEEEEEEEEEEEE
526 - 545:	EEEEEEEEEEEEEEEEEEEE
527 - 546:	EEEEEEEEEEEEEEEEEEEE
528 - 547:	EEEEEEEEEEEEEEEEEEEE
529 - 548:	EEEEEEEEEEEEEEEEEEEE
530 - 549:	EEEEEEEEEEEEEEEEEEEE
531 - 550:	EEEEEEEEEEEEEEEEEEEE
532 - 551:	EEEEEEEEEEEEEEEEEEEE
533 - 552:	EEEEEEEEEEEEEEEEEEEE
534 - 553:	EEEEEEEEEEEEEEEEEEEE
535 - 554:	EEEEEEEEEEEEEEEEEEEE
536 - 555:	EEEEEEEEEEEEEEEEEEEE
537 - 556:	EEEEEEEEEEEEEEEEEEEE
538 - 557:	EEEEEEEEEEEEEEEEEEEE
539 - 558:	EEEEEEEEEEEEEEEEEEEE
540 - 559:	EEEEEEEEEEEEEEEEEEEE
541 - 560:	EEEEEEEEEEEEEEEEEEEE
542 - 561:	EEEEEEEEEEEEEEEEEEEE
543 - 562:	EEEEEEEEEEEEEEEEEEEE
544 - 563:	EEEEEEEEEEEEEEEEEEEE
545 - 564:	EEEEEEEEEEEEEEEEEEEE
546 - 565:	EEEEEEEEEEEEEEEEEEEE
547 - 566:	EEEEEEEEEEEEEEEEEEEE
548 - 567:	EEEEEEEEEEEEEEEEEEEE

A0A0A0L4R0 **A0A0A0L4R0_CUCSA** (237 aa)
Uncharacterized protein. *Cucumis sativus (Cucumber)*

```
MSKTRTSFPHQSLFDFCSFKTKIEDKDEEPERKISKQAALGSSANKAKCKSKSKQPESRKQIWQQRFTAEPEQHLSGNST
SKASSPEAPANPKRRNAESVEEKRKKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE

156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE
180 - 199:	EEEEEEEEEEEEEEEEEEEE
181 - 200:	EEEEEEEEEEEEEEEEEEEE
182 - 201:	EEEEEEEEEEEEEEEEEEEE
183 - 202:	EEEEEEEEEEEEEEEEEEEE
184 - 203:	EEEEEEEEEEEEEEEEEEEE
185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE
190 - 209:	EEEEEEEEEEEEEEEEEEEE
191 - 210:	EEEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE
194 - 213:	EEEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEEE
196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE

208 - 227:	EEEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEEE

A0A0A0L508 **A0A0A0L508_CUCSA** (115 aa)
Uncharacterized protein. *Cucumis sativus (Cucumber)*

```
MKKKLSLSSSSSLYALTAAVYRWGPRSQVGEGVVRKVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEERIGGDVEK
```

38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE

74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE

A0A0A0L5C7 **A0A0A0L5C7_CUCSA** (489 aa)
Uncharacterized protein. *Cucumis sativus (Cucumber)*

```
METAETAGAKGLSCEAMDCLSERLSLQEDLYFPRALQSTASNPSQRKAILLDLLSRDVAVFLERYGSQLTSNELHEFDAL
KDDYEINWHLKHLRSIKNPTSDELHTRSVIVKNRRRAYLNKLIYDGQYFSEDAMREREPFLHHEYVGKFQDPSGRGMARP
GERWSETLMRRSEEAMLVAKIRGEQRRLGVAERDLVGNNVNQGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
TRAMDDQHEMPATENSEAAEGGSNHVATLSEADMQDQMDQFTYIMHQKFLLGEDNEHLDYSKIDNDETLDDHWMREANDD
AEEKYFDED
```

204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE
208 - 227:	EEEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEEE
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232 - 251:	EEEEEEEEEEEEEEEEEEEE

233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
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353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE

A0A0A0L6F9 **A0A0A0L6F9_CUCSA** (480 aa)
Uncharacterized protein. *Cucumis sativus (Cucumber)*

```
MLTFAMSIGTDRILTESISPNWLNSLAKAFFFTFNGKFPTNTVLKSLLSSSNPSFVTNISEGSSNAFLFFPTTFPPEPST
SSSATSDTPYFLASYSLSISEPKTVPFFLLLSFNPPCDSKPLSPSSSTLSNSRSRDFFFSFFLDFLISDEVLTPSVESKS
IPTLLSLPFFLLISAGGGGTESEAFLRKGLSVEKIETGGFSTPALPKRVSKTLKEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDDDEI
```

215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE
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225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
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242 - 261:	EEEEEEEEEEEEEEEEEEEE
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342 - 361:	EEEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEEE
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358 - 377:	EEEEEEEEEEEEEEEEEEEE
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372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
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379 - 398:	EEEEEEEEEEEEEEEEEEEE
380 - 399:	EEEEEEEEEEEEEEEEEEEE
381 - 400:	EEEEEEEEEEEEEEEEEEEE
382 - 401:	EEEEEEEEEEEEEEEEEEEE
383 - 402:	EEEEEEEEEEEEEEEEEEEE
384 - 403:	EEEEEEEEEEEEEEEEEEEE
385 - 404:	EEEEEEEEEEEEEEEEEEEE
386 - 405:	EEEEEEEEEEEEEEEEEEEE
387 - 406:	EEEEEEEEEEEEEEEEEEEE
388 - 407:	EEEEEEEEEEEEEEEEEEEE
389 - 408:	EEEEEEEEEEEEEEEEEEEE
390 - 409:	EEEEEEEEEEEEEEEEEEEE
391 - 410:	EEEEEEEEEEEEEEEEEEEE
392 - 411:	EEEEEEEEEEEEEEEEEEEE
393 - 412:	EEEEEEEEEEEEEEEEEEEE
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396 - 415:	EEEEEEEEEEEEEEEEEEEE
397 - 416:	EEEEEEEEEEEEEEEEEEEE

398 - 417:	EEEEEEEEEEEEEEEEEEEE
399 - 418:	EEEEEEEEEEEEEEEEEEEE
400 - 419:	EEEEEEEEEEEEEEEEEEEE
401 - 420:	EEEEEEEEEEEEEEEEEEEE
402 - 421:	EEEEEEEEEEEEEEEEEEEE
403 - 422:	EEEEEEEEEEEEEEEEEEEE
404 - 423:	EEEEEEEEEEEEEEEEEEEE
405 - 424:	EEEEEEEEEEEEEEEEEEEE
406 - 425:	EEEEEEEEEEEEEEEEEEEE
407 - 426:	EEEEEEEEEEEEEEEEEEEE
408 - 427:	EEEEEEEEEEEEEEEEEEEE
409 - 428:	EEEEEEEEEEEEEEEEEEEE
410 - 429:	EEEEEEEEEEEEEEEEEEEE
411 - 430:	EEEEEEEEEEEEEEEEEEEE
412 - 431:	EEEEEEEEEEEEEEEEEEEE
413 - 432:	EEEEEEEEEEEEEEEEEEEE
414 - 433:	EEEEEEEEEEEEEEEEEEEE
415 - 434:	EEEEEEEEEEEEEEEEEEEE
416 - 435:	EEEEEEEEEEEEEEEEEEEE
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418 - 437:	EEEEEEEEEEEEEEEEEEEE
419 - 438:	EEEEEEEEEEEEEEEEEEEE
420 - 439:	EEEEEEEEEEEEEEEEEEEE
421 - 440:	EEEEEEEEEEEEEEEEEEEE
422 - 441:	EEEEEEEEEEEEEEEEEEEE
423 - 442:	EEEEEEEEEEEEEEEEEEEE
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426 - 445:	EEEEEEEEEEEEEEEEEEEE
427 - 446:	EEEEEEEEEEEEEEEEEEEE
428 - 447:	EEEEEEEEEEEEEEEEEEEE
429 - 448:	EEEEEEEEEEEEEEEEEEEE
430 - 449:	EEEEEEEEEEEEEEEEEEEE
431 - 450:	EEEEEEEEEEEEEEEEEEEE
432 - 451:	EEEEEEEEEEEEEEEEEEEE
433 - 452:	EEEEEEEEEEEEEEEEEEEE
434 - 453:	EEEEEEEEEEEEEEEEEEEE
435 - 454:	EEEEEEEEEEEEEEEEEEEE
436 - 455:	EEEEEEEEEEEEEEEEEEEE
437 - 456:	EEEEEEEEEEEEEEEEEEEE
438 - 457:	EEEEEEEEEEEEEEEEEEEE
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440 - 459:	EEEEEEEEEEEEEEEEEEEE
441 - 460:	EEEEEEEEEEEEEEEEEEEE
442 - 461:	EEEEEEEEEEEEEEEEEEEE
443 - 462:	EEEEEEEEEEEEEEEEEEEE
444 - 463:	EEEEEEEEEEEEEEEEEEEE
445 - 464:	EEEEEEEEEEEEEEEEEEEE
446 - 465:	EEEEEEEEEEEEEEEEEEEE
447 - 466:	EEEEEEEEEEEEEEEEEEEE
448 - 467:	EEEEEEEEEEEEEEEEEEEE
449 - 468:	EEEEEEEEEEEEEEEEEEEE

450 - 469:	EEEEEEEEEEEEEEEEEEE
451 - 470:	EEEEEEEEEEEEEEEEEEE
452 - 471:	EEEEEEEEEEEEEEEEEEE
453 - 472:	EEEEEEEEEEEEEEEEEEE
454 - 473:	EEEEEEEEEEEEEEEEEEE
455 - 474:	EEEEEEEEEEEEEEEEEEE

A0A0A0L6Q6 **A0A0A0L6Q6_CUCSA** (284 aa)
RWP-RK domain-containing protein. *Cucumis sativus (Cucumber)*

```
MDSNPQTFHNIPQFDFEWLHEDLFPFHNELDELPPLDKDEFLDVNSSGSLLSFHLVDNNVLEFESEFLSREMDEIERKGL
PSSTWKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEKRLRLMRNNN
GNKRRKRSFVLGLEEIKKYYHIPISEAAKEMNVGLTVLKRRCRQLNIMRWPHRKLKSYNSLIQNVKEMGLTNEVKGLEEQ
KRLLVESPNMDLTHTTKRLRQACFKDKYRKNRRLRSNNIASLHH
```

87 - 106:	EEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEE

127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE

A0A0A0L7B9 **A0A0A0L7B9_CUCSA** (113 aa)
Uncharacterized protein. *Cucumis sativus (Cucumber)*

```
MGGRNRREKKEPSESVARRRRKRKRKRKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEGKLCGQLEMKGREY
```

29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE

73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE

A0A0A0L7Y0 **A0A0A0L7Y0_CUCSA** (118 aa)
Uncharacterized protein. *Cucumis sativus (Cucumber)*

```
MKRTKTTDGNLKRTEQSHERLRLKKSRMNEALINLEDEEGEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDGSKALRLVRAFEER
```

41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE

80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE

A0A0A0L8B3 **A0A0A0L8B3_CUCSA** (208 aa)
Uncharacterized protein. *Cucumis sativus (Cucumber)*

```
MENRKWGVREKWKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEERGGCFVEGSGKVVMGKTNERERIRA
```

14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE

56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
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59 - 78:	EEEEEEEEEEEEEEEEEEEE
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62 - 81:	EEEEEEEEEEEEEEEEEEEE
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65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
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71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
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81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE

108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE

160 - 179:	EEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEE

A0A0A0L8D6 **A0A0A0L8D6_CUCSA** (124 aa)
Uncharacterized protein. *Cucumis sativus (Cucumber)*

```
MALAESPLILSAATSCARAAISAVVKVPSQIRDFFLGCRISDTHLPQLLLHSEFQLFDSAIVDSQKRRKEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

70 - 89:	EEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEE

A0A0A0L9H9 **A0A0A0L9H9_CUCSA** (1944 aa)
PHD-type domain-containing protein. *Cucumis sativus (Cucumber)*

```
MLHICFLGLCNWTNYRILQSLRACRLIISLGPRWCFQFLFLIFVMRLSSGSVAPSLNQSGNRSGPRLKKKHKRLDAICEK
EYSRNHGDVNENVSGLGTLEADPGLRRSSRVRRAPVLLDASPIPRKKRRIVQGNGTLGVRTSANTLPLFSDDLKDETEGN
WRSRLRSSSRNLGIRVDKGARASRKRKLFDEIVDVKVRNGGMRIDLDEEKGRMEFGESLVGRSNRTRRRFGVINDPIKIE
EEVKSPRIKDDCCKKDMLVIDIDDEEEGEGEGEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEVEGKEVVT
AKDERGDGVLPLENEMDEENVKVVDDVTPQVVEKLDKETSSSLHVDEACRADHNEELANAVENANNGEIRLEESKQLNEG
VNETQDVAAAVVSTNEVVGGRSCNEKAVDMGKFTEKSREHGDDLNLKKFTDSSRGMLGKARIKEGRRCGLCGGGIDGKPP
```

```
KKTAQDSGESGNEACSGSSASEEPNYDKWDGFGDEPGWLGRLLGPINDRYGIAGIWVHQHCAVWSPEVYFAGLGCLKNVR
AALCRGRALKCTRCGRPGATIGCRVDRCPRTYHLPCARANGCIFDHRKFLIACTDHRHIFQPHGNQYLARIKRLKAKKMK
LEIKKQSNDAWRRDIEAEEKWLENCGEDEEFLKRESKRLHRDLVRIAPVYIGGSNSEGENLFHGWESVAGLQGVIQCMKE
VVFLPLLYPELFDRFGITPPRGVLLHGYPGTGKTHVVRALIGSCARGDKRIAYFARKGADCLGKYVGDAERQLRLLFQVA
EKCQPSIIFFDEIDGLAPCRTRQQDQTHNSVVSTLLALLDGLKSRGSVVVIGATNRPEAVDPALRRPGRFDREIYFPLPS
VEDRAAILSLHTQKWPKPIDGPLLQWIARRTAGFAGADLQALCTQAAMSALKRNFPLKEVLSASGEQVSRVNRPPLPSIL
VEERDWLEALLYSPPPCSRREAGMAANDVPSSPLPFHLIPCLLQPLSTLLVSLYLDERITLPTNLLKAATLIKSVIVSAL
DGKKIVTSCWWSHVHDFVQDADIANEIEIKLQGSGVLVEDSTFGSSGVLNVDTSNESSKFENLGHCGGRPSTMVEHSSFT
LGNKSGFRILIAGNPRSGPRHLASCLIHCYIQHVEVRKVDIATISQEGHGDLVQGISQILLNCSSMGSCLVFMPRIDLWA
IETQSQTSEECGLYLNEDQYLEDGTIVNDDDQLGERENRCYSDQSKSTERTGLQDECLSSASYAWSSFVEQVESLSTPLM
ILATSEVPFLLLPQEIRQFFRNDLSMCRPTTSEHSVPRFSVQIDGVFDHDMVINQSAAELSRDIVKLLVHLIHQKSHTRT
LTCTKYQIPVIQDENNAENQQIDKETASEHNGEMKSPDVSSLRIAPLPGSRTMKVKSNLISVISTFGHQILRYPHFAELC
WVTSKLKEGPYADVSGPWKGWPFNSCIIRPMSTLEKGTSSSSLSNGKSKEISGLVRGLIAVGLSAIRGAYTSLRKVSLDV
RLVLELLVEQINAKINSGKERYQYFRLLSQVAYLEDVVNSWAFTLQSLEHDSRTIETSKNLTSGGSEIHCEKNEPIISNK
GSLANEIPEVSCQEPVEEEIVRIDSLVDGNLNHSSSKDTTIVSEEHGERNFGIGNLVSDETYNNAAAVDDQLIDNIPLKH
GEATILQPDSLDNERNDTSVKTPLDFGTESIVDLDHHHQNSSVLCSDEIPSGTKPCSTSNGGCSALENGCKRDNSQLDTN
DLEVNVHSSQSRSGHSTNSALICSVQCCTGCLNVLYNMSKNILRNELESDQNDWTIEDVHDVVVALSVDLLAAVRRAFLD
EKNGTLFDDRQMGGNGRFKSLDSRTCDCKSSKDMVFKGVECICHLSEKVSPSHSEMGIDPNFIFRDGVLVSVDPEKNVLF
HCKVETLCLCSLTELIVMAKKPLN
```

275 - 294:	EEEEEEEEEEEEEEEEEEEE
276 - 295:	EEEEEEEEEEEEEEEEEEEE
277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE
287 - 306:	EEEEEEEEEEEEEEEEEEEE
288 - 307:	EEEEEEEEEEEEEEEEEEEE
289 - 308:	EEEEEEEEEEEEEEEEEEEE

A0A0A0LAX4 **A0A0A0LAX4_CUCSA** (572 aa)
Glutaredoxin domain-containing protein. *Cucumis sativus (Cucumber)*

```
MWGQISKRRGERIIPQKQKKKKVPFEIFDRWDPFAQFSNEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEASMGCVSSKLYQKDLQRDIIVNNGGEYLNHVVSLTSSTYGVLNLDADQKSKELVSEPTKKSPPREEP
EVINAWELMDGLEEGVPIANRGKKSPKPRVFLRGLADFDRRSPLKFFNQIGTPKKAMKSGGKENRGRANGVGRLDYSPKE
ILKVNNSSKVSPKSALKLTVPVKSTPISARRQSFGSDSGLLSARRRSLSPLFDPELVASYEKQLTEEGEQIKRIVSETPK
SRAARHFQESETALKKFEELCPPGGETSVVIYTTTLRGIRKTFEDCNKVRSIVESYGIHVVERDVSMDSGFKEELRALMG
SKEVKVPAVFVKGRLIGGAAEVLKMEEEGKLGVLFEGIPTAAGSGCEGCGGMRFVMCLDCNGSCKVLDQTKKKTTKCGEC
NENGLIRCPICS
```

40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE

58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE

110 - 129:	EEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEE

A0A0A0LCM0 **A0A0A0LCM0_CUCSA** (195 aa)
Uncharacterized protein. *Cucumis sativus (Cucumber)*

```
MRRTETNPNQEKQRKEEGKSETEQKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEETQKRRRERKINSGVVEL
```

26 - 45:	EEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEE

28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE

80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE

132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE

A0A0A0LED9 **A0A0A0LED9_CUCSA** (146 aa)
Uncharacterized protein. *Cucumis sativus (Cucumber)*

```
MIGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGG
```

4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE

23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE

75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE

A0A0A0LF92 **A0A0A0LF92_CUCSA** (180 aa)
Uncharacterized protein. *Cucumis sativus (Cucumber)*

```
MAGQKQLNEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEE
```

11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE

59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE

111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE

A0A0A0LJD7 **A0A0A0LJD7_CUCSA** (93 aa)
Uncharacterized protein. *Cucumis sativus (Cucumber)*

```
MKHSWEEKINKCKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEKERIKKKRACT
```

14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE

62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE

A0A0A0LMZ2 **A0A0A0LMZ2_CUCSA** (526 aa)
Uncharacterized protein. *Cucumis sativus (Cucumber)*

```
MSSRRRPLQTCGVSFLAVAHSTCSRAQNLDGRLGSITRKMVWIAKLMNPLIFLLKYQSLLVLCFIDDRLLAIANTLEKIF
PPSKLVFDKIDVLLHLIETFPSKFDDAVDKIPCFNQEVLLLDWTVTHVISLLNFMITILMNWGRDVAREKEILVDMNYKE
SCNGSKSIDKSKCCSEGIVSSLSEIQRTSMNEKMKSNPMKGSYAEILKMGTKGVLKDDEGCKENEKKGTRDEINEKEDCK
KDEKGNSNRVEKGIEVMEDKESYKKDENNEIHNAKMEESVGKAKGNEEIRDDQSHKRIINNEEKSKEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGVMD
NESEKGNKGSKENAEDEILELFESAWLMKPTIKGKGNVMQRSSSLF
```

307 - 326:	EEEEEEEEEEEEEEEEEEEE
308 - 327:	EEEEEEEEEEEEEEEEEEEE
309 - 328:	EEEEEEEEEEEEEEEEEEEE
310 - 329:	EEEEEEEEEEEEEEEEEEEE
311 - 330:	EEEEEEEEEEEEEEEEEEEE
312 - 331:	EEEEEEEEEEEEEEEEEEEE
313 - 332:	EEEEEEEEEEEEEEEEEEEE
314 - 333:	EEEEEEEEEEEEEEEEEEEE
315 - 334:	EEEEEEEEEEEEEEEEEEEE
316 - 335:	EEEEEEEEEEEEEEEEEEEE
317 - 336:	EEEEEEEEEEEEEEEEEEEE
318 - 337:	EEEEEEEEEEEEEEEEEEEE
319 - 338:	EEEEEEEEEEEEEEEEEEEE
320 - 339:	EEEEEEEEEEEEEEEEEEEE
321 - 340:	EEEEEEEEEEEEEEEEEEEE
322 - 341:	EEEEEEEEEEEEEEEEEEEE
323 - 342:	EEEEEEEEEEEEEEEEEEEE
324 - 343:	EEEEEEEEEEEEEEEEEEEE
325 - 344:	EEEEEEEEEEEEEEEEEEEE
326 - 345:	EEEEEEEEEEEEEEEEEEEE
327 - 346:	EEEEEEEEEEEEEEEEEEEE
328 - 347:	EEEEEEEEEEEEEEEEEEEE
329 - 348:	EEEEEEEEEEEEEEEEEEEE
330 - 349:	EEEEEEEEEEEEEEEEEEEE
331 - 350:	EEEEEEEEEEEEEEEEEEEE
332 - 351:	EEEEEEEEEEEEEEEEEEEE
333 - 352:	EEEEEEEEEEEEEEEEEEEE
334 - 353:	EEEEEEEEEEEEEEEEEEEE
335 - 354:	EEEEEEEEEEEEEEEEEEEE
336 - 355:	EEEEEEEEEEEEEEEEEEEE
337 - 356:	EEEEEEEEEEEEEEEEEEEE
338 - 357:	EEEEEEEEEEEEEEEEEEEE
339 - 358:	EEEEEEEEEEEEEEEEEEEE
340 - 359:	EEEEEEEEEEEEEEEEEEEE
341 - 360:	EEEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEEE
344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE

349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE
379 - 398:	EEEEEEEEEEEEEEEEEEEE
380 - 399:	EEEEEEEEEEEEEEEEEEEE
381 - 400:	EEEEEEEEEEEEEEEEEEEE
382 - 401:	EEEEEEEEEEEEEEEEEEEE
383 - 402:	EEEEEEEEEEEEEEEEEEEE
384 - 403:	EEEEEEEEEEEEEEEEEEEE
385 - 404:	EEEEEEEEEEEEEEEEEEEE
386 - 405:	EEEEEEEEEEEEEEEEEEEE
387 - 406:	EEEEEEEEEEEEEEEEEEEE
388 - 407:	EEEEEEEEEEEEEEEEEEEE
389 - 408:	EEEEEEEEEEEEEEEEEEEE
390 - 409:	EEEEEEEEEEEEEEEEEEEE
391 - 410:	EEEEEEEEEEEEEEEEEEEE
392 - 411:	EEEEEEEEEEEEEEEEEEEE
393 - 412:	EEEEEEEEEEEEEEEEEEEE
394 - 413:	EEEEEEEEEEEEEEEEEEEE
395 - 414:	EEEEEEEEEEEEEEEEEEEE
396 - 415:	EEEEEEEEEEEEEEEEEEEE
397 - 416:	EEEEEEEEEEEEEEEEEEEE
398 - 417:	EEEEEEEEEEEEEEEEEEEE
399 - 418:	EEEEEEEEEEEEEEEEEEEE
400 - 419:	EEEEEEEEEEEEEEEEEEEE

401 - 420:	EEEEEEEEEEEEEEEEEEEE
402 - 421:	EEEEEEEEEEEEEEEEEEEE
403 - 422:	EEEEEEEEEEEEEEEEEEEE
404 - 423:	EEEEEEEEEEEEEEEEEEEE
405 - 424:	EEEEEEEEEEEEEEEEEEEE
406 - 425:	EEEEEEEEEEEEEEEEEEEE
407 - 426:	EEEEEEEEEEEEEEEEEEEE
408 - 427:	EEEEEEEEEEEEEEEEEEEE
409 - 428:	EEEEEEEEEEEEEEEEEEEE
410 - 429:	EEEEEEEEEEEEEEEEEEEE
411 - 430:	EEEEEEEEEEEEEEEEEEEE
412 - 431:	EEEEEEEEEEEEEEEEEEEE
413 - 432:	EEEEEEEEEEEEEEEEEEEE
414 - 433:	EEEEEEEEEEEEEEEEEEEE
415 - 434:	EEEEEEEEEEEEEEEEEEEE
416 - 435:	EEEEEEEEEEEEEEEEEEEE
417 - 436:	EEEEEEEEEEEEEEEEEEEE
418 - 437:	EEEEEEEEEEEEEEEEEEEE
419 - 438:	EEEEEEEEEEEEEEEEEEEE
420 - 439:	EEEEEEEEEEEEEEEEEEEE
421 - 440:	EEEEEEEEEEEEEEEEEEEE
422 - 441:	EEEEEEEEEEEEEEEEEEEE
423 - 442:	EEEEEEEEEEEEEEEEEEEE
424 - 443:	EEEEEEEEEEEEEEEEEEEE
425 - 444:	EEEEEEEEEEEEEEEEEEEE
426 - 445:	EEEEEEEEEEEEEEEEEEEE
427 - 446:	EEEEEEEEEEEEEEEEEEEE
428 - 447:	EEEEEEEEEEEEEEEEEEEE
429 - 448:	EEEEEEEEEEEEEEEEEEEE
430 - 449:	EEEEEEEEEEEEEEEEEEEE
431 - 450:	EEEEEEEEEEEEEEEEEEEE
432 - 451:	EEEEEEEEEEEEEEEEEEEE
433 - 452:	EEEEEEEEEEEEEEEEEEEE
434 - 453:	EEEEEEEEEEEEEEEEEEEE
435 - 454:	EEEEEEEEEEEEEEEEEEEE
436 - 455:	EEEEEEEEEEEEEEEEEEEE
437 - 456:	EEEEEEEEEEEEEEEEEEEE
438 - 457:	EEEEEEEEEEEEEEEEEEEE
439 - 458:	EEEEEEEEEEEEEEEEEEEE
440 - 459:	EEEEEEEEEEEEEEEEEEEE
441 - 460:	EEEEEEEEEEEEEEEEEEEE
442 - 461:	EEEEEEEEEEEEEEEEEEEE
443 - 462:	EEEEEEEEEEEEEEEEEEEE
444 - 463:	EEEEEEEEEEEEEEEEEEEE
445 - 464:	EEEEEEEEEEEEEEEEEEEE
446 - 465:	EEEEEEEEEEEEEEEEEEEE
447 - 466:	EEEEEEEEEEEEEEEEEEEE
448 - 467:	EEEEEEEEEEEEEEEEEEEE
449 - 468:	EEEEEEEEEEEEEEEEEEEE
450 - 469:	EEEEEEEEEEEEEEEEEEEE
451 - 470:	EEEEEEEEEEEEEEEEEEEE
452 - 471:	EEEEEEEEEEEEEEEEEEEE

453 - 472:	EEEEEEEEEEEEEEEEEEEE
454 - 473:	EEEEEEEEEEEEEEEEEEEE
455 - 474:	EEEEEEEEEEEEEEEEEEEE
456 - 475:	EEEEEEEEEEEEEEEEEEEE
457 - 476:	EEEEEEEEEEEEEEEEEEEE

A0A0A0LT02 **A0A0A0LT02_CUCSA** (99 aa)
Uncharacterized protein. *Cucumis sativus (Cucumber)*

```
MNSEYNNQWYMYILCMEYLIVLSFSESSLFLSMNLRGEMKRGCEKISLKVDGDKSLFYNLVGFEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEE
```

64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE

A0A0A0LX81 **A0A0A0LX81_CUCSA** (346 aa)
Uncharacterized protein. *Cucumis sativus (Cucumber)*

```
MGDLTDSHTPSSANSRQVPIREDCWSEDATSTLIDAWGRRFLDLNRGNLRQKDWQDVADSVNSLHGLTKKTHRTDVQCKN
RIDTVKKKYKTERARVSASHGNFVSSWPFYARLDELIGPTVSMKKPSSPPLALPLPFRKTPPPSAAASSAIVAVSQKRPA
VAMEDVSFRRNYSAAAAAAAAVALSEEEEEEEEEEEEEEEEEEEEERVSDDDEAEGEGMSRLARAIKRFGEVYERVEAEK
VRQMVELEKQRMQFAKDLELQRMHMFMETQVQLERIKRGKKSTPSGLENLFSRFNVASSMTMFGLGMFGEDVSKLAKANN
PFRTPCREVGQTANLRRAILSSTTKN
```

186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE

A0A0A0LXL5 **A0A0A0LXL5_CUCSA** (105 aa)
Uncharacterized protein. *Cucumis sativus (Cucumber)*

```
MTLFGCKNERMDALLSQLFEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERAVVGIWSS
IAWLVGMTILISILSQYIVATIEVT
```

20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE

31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE

A0A0A0LZ46 **A0A0A0LZ46_CUCSA** (100 aa)
Uncharacterized protein. *Cucumis sativus (Cucumber)*

```
MWVTAEEVHGFEEEEEEDGDGGDDDDDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEGYNGVL
```

28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE

53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE

A0A0A1V9Z9 **A0A0A1V9Z9_9HYPO** (1150 aa)
Sad1/UNC-like domain protein. *Metarhizium robertsii*

```
MPPRPVRRRPTRFSVREPETPSNANPLTFQKPNLPPLQGTPSSRRQYSYGAEVEPMPSRPGHGLSRSQARDIGSAVRNVL
TAPGVNDEDEEQDEDEREQTQKPQKPKNAQPEPDELAGGQLSRPPHLPSYLSGPSNTALATRSLLSLRNARPDGSDGDDT
RSFGIESEFYGDATISSTPRALPPQRPELRDELSGDSVSANETPSRSTMNKPPAIIGENEQVDLVRQPQNAYKGPAKSTV
GPSPLRAPPRRPPQQSARQPRFEQQEEEEEEEEEEEEEEEEEEEEEEEEGEEEHEDEEEENELDTNATDKEREGSEEDDL
IRRQEPRPILQTNTPVPGRSQQAPRENVQRTRIGGPSPAPPHPRPIPRLLPPNTTRGTLGPTESTRPDKMRRTQLLTGAP
LEPRQRSNREHRGPNFEENSSEDGRWLDRATATTTSLFAQAKFLVNSSPFSLGRRYPTDESERDAAIQRDITEAEAEVAR
ERLREEEEAAYQRSYQRWLWLKSFVPFIGREQTHTELDGAAARANNRWSTFALIRFLNPMTYVRAIGWLIHAVLDWIMEL
VYFIIPAGVWDQLSSVFGFLPHILAGALAFVAAFALATQLAGSTDSSWAPNAIEATLRTFDDLRYRISDLIPTVTWPKRD
RWVDLDDLWEDDDSSRDKLQHFLNRMEEEFLTLKRSGKIHDASLRKLENILPSIVHMELKDGRPVISEEFWHALRDLIHG
DGGFLAFDKVGSEYVVSSDRQWSAITSRLLRDPAFTTKLNLTALGLEDRLSRKMATFWDKWVKDNDDKIAHLLGTAVDRI
KSAGSQREFEDRLNKIVSEQLSQREEKEGQNGKFVSREEFLRHLRNEIASLSSQLRAELDDLRPQMERLVQQTVDLATKD
LTHSMSRADITALVNNLIGKALADVNLEAMALGKIHNHWDTELRNQVNYFAVGSGAKVDPRLTSATWDPRGAAIAPHQYK
HGWRGSEAFPPIAALEPWQEEGDCWCAARSVNHRGNPHGATLSVQLHHSIIPQHIVVEHILPGATTQPGARPKSIEVWAE
ILDSEARERVLDFGSVYLPDDKSDWNYTPPDFPAQFAKIAQFVYEGTELHEGVHVHRLNSELLALGAHTDRVIVRAVSNH
GAENHTCFYRVRLYGFNVELDRDEGGNSYY
```

266 - 285:	EEEEEEEEEEEEEEEEEEEE
267 - 286:	EEEEEEEEEEEEEEEEEEEE
268 - 287:	EEEEEEEEEEEEEEEEEEEE
269 - 288:	EEEEEEEEEEEEEEEEEEEE
270 - 289:	EEEEEEEEEEEEEEEEEEEE

A0A0A1WQT7 **A0A0A1WQT7_ZEUCU** (378 aa)
Troponin T, skeletal muscle. *Zeugodacus cucurbitae (Melon fruit fly) (Bactrocera cucurbitae)*

```
MSDEEEYTSEEEEEVVEETKEGEGDPEFIKRQDQKRSDLDEQLKEYINEWRKQRAKEEDELKKLKEKQAKRKISRAEEEQ
KMAQRKKEEEERRVREVEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKEAGLGLSSAAMERNKTKEQ
LEEEKKISLSFRIKPLAIEGFNDSKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDP
EALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWEEIGKEVNEKIWNEKKDQYVGRQKSKLPKWFGERPGKKSGEPE
TPEGEEDAKADEDIIEDEEEVEEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE

352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE

A0A0A1WSE0 **A0A0A1WSE0_ZEUCU** (227 aa)
Troponin T, skeletal muscle. *Zeugodacus cucurbitae (Melon fruit fly) (Bactrocera cucurbitae)*

```
MERNKTKEQLEEEKKISLSFRIKPLAIEGFNDSKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRH
KALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWEEIGKEVNEKIWNEKKDQYVGRQKSKLPKWFGER
PGKKSGEPETPEGEEDAKADEDIIEDEEEVEEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE
208 - 227:	EEEEEEEEEEEEEEEEEEEE

A0A0A2VBI0 **A0A0A2VBI0_BEABA** (3642 aa)
HC-toxin synthetase. *Beauveria bassiana D1-5*

```
MANAKAPVDWSSGMDEQNNAGCDNGWRFIVVTCPPLDGICDGDEVETMDMLRLAWGIVLGMYTGASDISFGCIRRESASN
ESPVKEWVHRMVIDRSTPVMELLKQSSSSKLHQNGGLEDVASQKISFGGCDTVLMLDVDSGGAAKVLRRPDMTNVNIVLV
VDGTTMSLGYRISKLGSLQARSMAAAMGRIISTLIDRPLTPMRDFDMCDDKDMNILAEWNNVETTWKEQCVHDLFAKQVA
DCADNVAVDAWDGQLTYRELDRLSSNLAEHLMDLGVKPETFVALCFEKSKWLVVSILAVIKAGAAYVVIEPYYPLARMTD
ICTQLEIDIMLASPDLLHLANKLSNQAVVVEPGVEYLDHGQGARKQRKRTTPSNPRNALYVVFSSGSTGKPKGIVVEHAA
FVSWGTTLRQSLCLGSHSRVLQFSSFAFLIAHRDVLLTLMFGGCVCVPSESQRLNHLETFITDHGVNWANLTPSVAALLN
PEMATGLQTLLLTSEPMSLSSLTTWDGKVKLLFAYGQGESVSLCCVNTSPTAGSDRKNVGHRVGRKVWLVDPDNHDKLVP
VGAIGELVIQGPILARGYLDSERTALVFLDDAPWLQKLQPGYSGRLYKTGDLAQFADDGSVRYISRKDNSVKLYGQRLDL
DEVVRHIENCLTEMSDTAVSNVVVDLFPVPHSNDVKLTAFLGFDSTSPDTSNTLLLGPLDQASVYLREFRSRLADVVPRY
MIPALVVPVSRIPLNLSGKIDRRQLRDMLSLMTDAELASCMESNVSHEAPCTAQERQLRTLWSQVLHTAESSIGRLDDFF
RRGGDSLAAMKLVSLAQAAGFALRFGDVFAHPRLSSQAHLVDSAAPRRAQDDYCCAPFGLITESRKQIILAVAAEKYELS
ESQVEDIYPTTPMQEGLIALNDLRPGSYVSQRVYKIANDVSLCNLEAAWKSTMDANPPLRTRLVRCSDNGSTYQLVVRNQ
MAIDMNNDLNDYLTKDAAKPMNLGTPLVRISITCNAQKAPRFCVVTMHHCIYDAWSTSLLLRQVRDAYHGSIPSPQTFRQ
FVNYVQQASHDSAEYWKAELADIHAEPFPALPSQSHSPRTTESEMLSTQLPRSGASTANTTLATCIQLAWAVTVASYTGI
NDVVFGLTVSGRASPVPRIDKMAGPTIATFPLRVQLQSNASIREELQALQNRVLSTIPFEHFGLQNISRLGDDAAKACKF
QSLLVIQQNEFLPKENREILIPTAGLVVRPTWDTYALSILCSPAAVDGNIQFEAVYDAAVVPKAQTRRILQVFANILKQT
VSSPDMVMADMNGISTEDMQQIQAWNNSVSPTVMKCIHDMIHDHVVSRPEATAIDAWDGQLTYKDLDEQSSLLSGILAGH
GLLRQETFVPLCLKKSKWVAVAILAVIKAGGAFILLDTSHPAERLAWICKNAQAPIILCAKDTAGLAAQLGCKLVIQVDA
SNNTQEKALSALSTGVHHQPSSRRQTRPGNAVCAIYTSGSTGAPKGVVIEHSALATQISSLGPLYDLNHQSRIFQFASHA
FDVAVSDYLFGLATGACICVPQEADSRDNLAGAMRGCRANWAFLTPSVARTLNPYNVPNLRVLVTGGESARAADFRIWSG
ALRLLYVYGPAECSIYSTVQTVSQPTANPVNVGRGVTGACWLVEANNPEKLVAIGAVGELLVEGPLVGRCYLGDESLSSS
SFIPYPKWLRALRGGHSVNRLYRTGDMLRYSPIGDGSLEFVGRKDNQVKLHGQRMELAEIEHHVAQSFPMATDSIVEMIT
PLGSTDQKILAAFIWDATTTSSSSSSSSAGKHSVQSLGTLDEPSLFAGPDEAFKSRISSAEAKLRKTLPRFMIPSLWIPL
ARFPLSPNGKANRRLIQGQACLLSRQELGIYQSCFGPFNKRLTRPPSTESEGRIHQLVADVLGLSGTDVGMNDNFFQLGG
DSIKAMIMSTRAADMDLRLAAADILAYPRLCDMAAEVAVSASVNKKPCSSFEQRAPPPPFSLLPPEHNHDELLQEISEQC
KVDKDCIEDVYPCTPLQEGLFALTIKQPSAYVLRFTLQLTQDVDVDRFKMAWDMVMAANPILRTRIVCATSLGGSLVQAV
MCNKASYEQPIDTTSRYTVGLGKPLLNIQLWPPDKDVDRCKAVVTIHHALYDGVSLRLLLKQLSAAYYQRQETTRTWPFN
CFIQYCLSQPPDDQVKRFWAAELADAAGSVFTTAAPIMMDSYFLQSPLHAESRVSLAMSDAQSNVPLSAALKLAWGVVVS
SFTGQGDAVFGTVVSGRMANVKGIDRMAGPTIATVPFRIRHAPAMTIQQALDDVQSHSVEMIRFEQTGLQRIRQLGFADA
CRFQSLLMIQFAEEENIPASPLYTLVQDKSADTFHTYPLTMECSPSSGGSVHLRATFDSDVMPAKLVSRLLTQYSLALVH
ITAKPWEPLSSIPLQCPEDATRVWAWNEIVPRRKDTCVHEIISGNLAKRRNSSAVCASDGELTYQELEDKSARLAGHLTS
LGVGPGKMVPLCFEKSKWAIVATLAVLKAGGAFVPLDTSQAAGRRETILACVRAEVILTSAKYATTLASTDRLVFSVCDA
SLKELQLPLVTPALHGLGSSAAYVLFTSGSTGKPKGVVVDHGALSTSCLSHGSEMGFNEKTRALQFTSYTFDISLMEIFT
TLLYGGCICIPSDADRFNNLELSASSMQVNTVSLTASVARLVEPDRMRSLETIIFVGEDATDDDFKKWRHLPHIFNAYGP
TECTIFCSINKVQFNSNSSSNIGKAVGSVCWVVSPQDHCRLVPIGAVGELLVEGPVLARGYLNDSEKTLASFMEDPPWLV
QGIAGYAGRRGRLYKTGDLVRYNEDGSLTYCGRKDTQVKIRGHRVELGEVECQIRDCIAGVNHAVVMAIPPDGPNAVPVL
TTFLCFDDDDDDDDDDDDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEESSKEIHCRTVSIPTSTREALADRLPAYMMPSIFLAVGRFPLNTSGKLDRSRLRDIFSSHFRGQRVKGNVTLQGLQQQ
QQNRQPQQEQKVELQHGQPTAAGASSLAASSSPFRDCANETERRIRVAWATVLGIRSDMIGIDDNFYDIGGDSIRIISLM
RLIQNEFDVWLGQSLVNSRNTTISKIADYVDNNNRFDVGGSTFDLEEKMGDALSSNWAAATSQPWFSPTKSVRAPAIIFL
TGGTGFLGTQILHRLLISDVVARVVALVRATSAAHGLERLRQSAVTAGWWKAEYEARITVWTGDLQLAQLGLSGSQWAQL
SGTATVDNVTAVIHNGAVVNWHMDYDSLQSANVSATIELLKATALSRSSPRFVFVSGGVMADLDASPGNTVVAEQLSRSN
```

GYSQSKFVAETIVRRFVSQLPSSQNRFSVIKPGMIIGTAERGVANVDDFIWRVVATASRLQLFPLDAKESWVPVSDAAFV
ALQTVAQILSDDISPYVNIATTFGLGSFDFWQQVNSELNCACEPVSWSVWVERAFEDINRGGQEHPLWPVQDVLRGRNAR
GISVSSPLSPPDKQVLCKAVRANVRHLGRVGFLGKPEQSNTV

2900 - 2919:	EEEEEEEEEEEEEEEEEEEE
2901 - 2920:	EEEEEEEEEEEEEEEEEEEE
2902 - 2921:	EEEEEEEEEEEEEEEEEEEE
2903 - 2922:	EEEEEEEEEEEEEEEEEEEE
2904 - 2923:	EEEEEEEEEEEEEEEEEEEE
2905 - 2924:	EEEEEEEEEEEEEEEEEEEE
2906 - 2925:	EEEEEEEEEEEEEEEEEEEE
2907 - 2926:	EEEEEEEEEEEEEEEEEEEE
2908 - 2927:	EEEEEEEEEEEEEEEEEEEE
2909 - 2928:	EEEEEEEEEEEEEEEEEEEE
2910 - 2929:	EEEEEEEEEEEEEEEEEEEE
2911 - 2930:	EEEEEEEEEEEEEEEEEEEE
2912 - 2931:	EEEEEEEEEEEEEEEEEEEE
2913 - 2932:	EEEEEEEEEEEEEEEEEEEE
2914 - 2933:	EEEEEEEEEEEEEEEEEEEE
2915 - 2934:	EEEEEEEEEEEEEEEEEEEE
2916 - 2935:	EEEEEEEEEEEEEEEEEEEE
2917 - 2936:	EEEEEEEEEEEEEEEEEEEE
2918 - 2937:	EEEEEEEEEEEEEEEEEEEE
2919 - 2938:	EEEEEEEEEEEEEEEEEEEE
2920 - 2939:	EEEEEEEEEEEEEEEEEEEE
2921 - 2940:	EEEEEEEEEEEEEEEEEEEE
2922 - 2941:	EEEEEEEEEEEEEEEEEEEE
2923 - 2942:	EEEEEEEEEEEEEEEEEEEE
2924 - 2943:	EEEEEEEEEEEEEEEEEEEE
2925 - 2944:	EEEEEEEEEEEEEEEEEEEE
2926 - 2945:	EEEEEEEEEEEEEEEEEEEE
2927 - 2946:	EEEEEEEEEEEEEEEEEEEE
2928 - 2947:	EEEEEEEEEEEEEEEEEEEE
2929 - 2948:	EEEEEEEEEEEEEEEEEEEE
2930 - 2949:	EEEEEEEEEEEEEEEEEEEE
2931 - 2950:	EEEEEEEEEEEEEEEEEEEE
2932 - 2951:	EEEEEEEEEEEEEEEEEEEE
2933 - 2952:	EEEEEEEEEEEEEEEEEEEE
2934 - 2953:	EEEEEEEEEEEEEEEEEEEE
2935 - 2954:	EEEEEEEEEEEEEEEEEEEE
2936 - 2955:	EEEEEEEEEEEEEEEEEEEE
2937 - 2956:	EEEEEEEEEEEEEEEEEEEE
2938 - 2957:	EEEEEEEEEEEEEEEEEEEE
2939 - 2958:	EEEEEEEEEEEEEEEEEEEE
2940 - 2959:	EEEEEEEEEEEEEEEEEEEE
2941 - 2960:	EEEEEEEEEEEEEEEEEEEE
2942 - 2961:	EEEEEEEEEEEEEEEEEEEE
2943 - 2962:	EEEEEEEEEEEEEEEEEEEE
2944 - 2963:	EEEEEEEEEEEEEEEEEEEE
2945 - 2964:	EEEEEEEEEEEEEEEEEEEE
2946 - 2965:	EEEEEEEEEEEEEEEEEEEE
2947 - 2966:	EEEEEEEEEEEEEEEEEEEE
2948 - 2967:	EEEEEEEEEEEEEEEEEEEE
2949 - 2968:	EEEEEEEEEEEEEEEEEEEE

2950 - 2969:	EEEEEEEEEEEEEEEEEEEE
2951 - 2970:	EEEEEEEEEEEEEEEEEEEE
2952 - 2971:	EEEEEEEEEEEEEEEEEEEE
2953 - 2972:	EEEEEEEEEEEEEEEEEEEE
2954 - 2973:	EEEEEEEEEEEEEEEEEEEE
2955 - 2974:	EEEEEEEEEEEEEEEEEEEE
2956 - 2975:	EEEEEEEEEEEEEEEEEEEE
2957 - 2976:	EEEEEEEEEEEEEEEEEEEE
2958 - 2977:	EEEEEEEEEEEEEEEEEEEE
2959 - 2978:	EEEEEEEEEEEEEEEEEEEE
2960 - 2979:	EEEEEEEEEEEEEEEEEEEE
2961 - 2980:	EEEEEEEEEEEEEEEEEEEE
2962 - 2981:	EEEEEEEEEEEEEEEEEEEE
2963 - 2982:	EEEEEEEEEEEEEEEEEEEE
2964 - 2983:	EEEEEEEEEEEEEEEEEEEE
2965 - 2984:	EEEEEEEEEEEEEEEEEEEE
2966 - 2985:	EEEEEEEEEEEEEEEEEEEE
2967 - 2986:	EEEEEEEEEEEEEEEEEEEE
2968 - 2987:	EEEEEEEEEEEEEEEEEEEE
2969 - 2988:	EEEEEEEEEEEEEEEEEEEE
2970 - 2989:	EEEEEEEEEEEEEEEEEEEE
2971 - 2990:	EEEEEEEEEEEEEEEEEEEE
2972 - 2991:	EEEEEEEEEEEEEEEEEEEE
2973 - 2992:	EEEEEEEEEEEEEEEEEEEE
2974 - 2993:	EEEEEEEEEEEEEEEEEEEE
2975 - 2994:	EEEEEEEEEEEEEEEEEEEE
2976 - 2995:	EEEEEEEEEEEEEEEEEEEE
2977 - 2996:	EEEEEEEEEEEEEEEEEEEE
2978 - 2997:	EEEEEEEEEEEEEEEEEEEE
2979 - 2998:	EEEEEEEEEEEEEEEEEEEE
2980 - 2999:	EEEEEEEEEEEEEEEEEEEE
2981 - 3000:	EEEEEEEEEEEEEEEEEEEE
2982 - 3001:	EEEEEEEEEEEEEEEEEEEE
2983 - 3002:	EEEEEEEEEEEEEEEEEEEE
2984 - 3003:	EEEEEEEEEEEEEEEEEEEE
2985 - 3004:	EEEEEEEEEEEEEEEEEEEE
2986 - 3005:	EEEEEEEEEEEEEEEEEEEE
2987 - 3006:	EEEEEEEEEEEEEEEEEEEE
2988 - 3007:	EEEEEEEEEEEEEEEEEEEE
2989 - 3008:	EEEEEEEEEEEEEEEEEEEE
2990 - 3009:	EEEEEEEEEEEEEEEEEEEE
2991 - 3010:	EEEEEEEEEEEEEEEEEEEE
2992 - 3011:	EEEEEEEEEEEEEEEEEEEE
2993 - 3012:	EEEEEEEEEEEEEEEEEEEE
2994 - 3013:	EEEEEEEEEEEEEEEEEEEE
2995 - 3014:	EEEEEEEEEEEEEEEEEEEE
2996 - 3015:	EEEEEEEEEEEEEEEEEEEE
2997 - 3016:	EEEEEEEEEEEEEEEEEEEE
2998 - 3017:	EEEEEEEEEEEEEEEEEEEE
2999 - 3018:	EEEEEEEEEEEEEEEEEEEE
3000 - 3019:	EEEEEEEEEEEEEEEEEEEE
3001 - 3020:	EEEEEEEEEEEEEEEEEEEE

3002 - 3021:	EEEEEEEEEEEEEEEEEEEE
3003 - 3022:	EEEEEEEEEEEEEEEEEEEE
3004 - 3023:	EEEEEEEEEEEEEEEEEEEE
3005 - 3024:	EEEEEEEEEEEEEEEEEEEE
3006 - 3025:	EEEEEEEEEEEEEEEEEEEE
3007 - 3026:	EEEEEEEEEEEEEEEEEEEE
3008 - 3027:	EEEEEEEEEEEEEEEEEEEE
3009 - 3028:	EEEEEEEEEEEEEEEEEEEE
3010 - 3029:	EEEEEEEEEEEEEEEEEEEE
3011 - 3030:	EEEEEEEEEEEEEEEEEEEE
3012 - 3031:	EEEEEEEEEEEEEEEEEEEE
3013 - 3032:	EEEEEEEEEEEEEEEEEEEE
3014 - 3033:	EEEEEEEEEEEEEEEEEEEE
3015 - 3034:	EEEEEEEEEEEEEEEEEEEE
3016 - 3035:	EEEEEEEEEEEEEEEEEEEE
3017 - 3036:	EEEEEEEEEEEEEEEEEEEE
3018 - 3037:	EEEEEEEEEEEEEEEEEEEE
3019 - 3038:	EEEEEEEEEEEEEEEEEEEE
3020 - 3039:	EEEEEEEEEEEEEEEEEEEE
3021 - 3040:	EEEEEEEEEEEEEEEEEEEE
3022 - 3041:	EEEEEEEEEEEEEEEEEEEE
3023 - 3042:	EEEEEEEEEEEEEEEEEEEE
3024 - 3043:	EEEEEEEEEEEEEEEEEEEE

A0A0A2VWZ8 **A0A0A2VWZ8_BEABA** (590 aa)
Uncharacterized protein. *Beauveria bassiana D1-5*

```
MPSMAVFSGNRRVVLLPALLFLFLFTLLAVDESLKPGRFSRIVTSRPTTSPQSRPKSRVSSFHYLVPASSPNIKLCYNII
SAAVNRYPAALLLGWKGKGEMDAAETHLAKLRAIQQYLQNLSADNDDDLVLIVDGYDIIMQLPVEIMIERYFTIQRDSDA
RLAERFNMSVSALHDKGFRNTIFWGPDKICWPIDWSAPRCWAVPASHLDAHTFGPNQGDGGMATNDPKWLNSGTVIGPVG
DLRTYINVTMAEIARTYDANFENRESDQYYLANVWGRQEYHRSKEVLALRSDVDDKAAAKLEGSDEFKLPDPLAFPGEPT
EFHISIEYESALFQTKAGYEWYFGHMKFDQPGYTARMDVDMFEQGTSFVPYSIPMPAAVYAALTRIYEAAVKPSSAARQA
VSEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAAPHRSRREATATSSRSRLPASEWLRSASLGVNYVTRHIYGLWH
CTGGKEFIDGEYKAMWFFPYVASLLRANALASRAGDQLTSAEMDGRAWLPQLQYPVEDSRNPLAGGEYGGAFTDYEGEEF
LSFGQLCGEWQDTLFSGEMDAVAAREEGRS
```

403 - 422:	EEEEEEEEEEEEEEEEEEEE
404 - 423:	EEEEEEEEEEEEEEEEEEEE
405 - 424:	EEEEEEEEEEEEEEEEEEEE
406 - 425:	EEEEEEEEEEEEEEEEEEEE
407 - 426:	EEEEEEEEEEEEEEEEEEEE
408 - 427:	EEEEEEEEEEEEEEEEEEEE
409 - 428:	EEEEEEEEEEEEEEEEEEEE
410 - 429:	EEEEEEEEEEEEEEEEEEEE
411 - 430:	EEEEEEEEEEEEEEEEEEEE
412 - 431:	EEEEEEEEEEEEEEEEEEEE
413 - 432:	EEEEEEEEEEEEEEEEEEEE
414 - 433:	EEEEEEEEEEEEEEEEEEEE
415 - 434:	EEEEEEEEEEEEEEEEEEEE
416 - 435:	EEEEEEEEEEEEEEEEEEEE
417 - 436:	EEEEEEEEEEEEEEEEEEEE

A0A0A6YWS6 **A0A0A6YWS6_MOUSE** (640 aa)
UTP25 small subunit processome component. *Mus musculus (Mouse)*

```
MGKRRNRGRSQMLSTMTKKQKKHLRDFGEEHPFYDRVSKKEAKPQICQLPESSDSSHSESESESEQEHVSGYHRLLATLK
NVSEEEEEEEEEEEEEEEEEEEEEDDSAVGDAEMNEEAGSEDGSVGEAAVSEAAEEAAETQEHMSLADNSKEKDGEEPPG
VSQKSSEEFTDVKHESLFSLETNFLEEDSGGSCSQRPSQDPFQQHVNKELKEKEIQAAASSPPATQQLKWPVLGHLVFSS
KFQKTETFKPPKDIDLKLLHLQKPLESTWAKTNSQFLSGPQKSNSSFTPLQKELFLIMNSYRDLFYPERTALKNGEEVRH
VYCLHAINHVLKANAQVLANNSRRRSQKLGVGEDDDFRDQGLTRPKVLIVVPFREAALRVVQLFISLLEGDSKKKIIVSN
KKRFQGEYGSDPEERPPNLKRPEDYEAVFVGNIDDHFRIGVAILQRSIRLYAPFYSSDILIASPLGLRTIIGGEGEKKRD
```

```
FDFLSSVELLIIDQADIYLMQNWEHVLHLMNHMNLLPLDSHGVDFSRVRMWSLNNWSKYYRQTLLFGALQDAQINSVFNK
HCINAQGQVAVRNVPMTGSISHVLVQLPHVFQRMEAQDLSSVIDARFCLSTGMLSCLTHSSMSPPTLTLCVSEITSRKKS
```

84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE

A0A0A9VJC7 **A0A0A9VJC7_ARUDO** (187 aa)
KELP. *Arundo donax (Giant reed) (Donax arundinaceus)*

```
MDEEMKRKVKETVLEILRGSDMEFVTEYKVRAAAADRLGIDLSVPDRKLFVRGVVESYLRSLPSEEEQQQQDGASEEGKD
KQEEEEEEEEEEEEEEEEEEEEEKGGRKREYDDLGDLILCRLSSKRRVTLSEFKGRTLVSIREFYLKDGKEMPTSKGISM
TVEQWEAFRNAVPAIEDAIKKVGEASD
```

83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE

A0A0A9VM86 **A0A0A9VM86_ARUDO** (188 aa)
KELP. *Arundo donax (Giant reed) (Donax arundinaceus)*

```
MDEEMKRKVKETVLEILRGSDMEFVTEYKVRAAAADRLGIDLSVPDRKLFVRGVVESYLRSLPSEEEQQQQQDGASEEGK
DKQEEEEEEEEEEEEEEEEEEEEEKGGRKREYDDLGDLILCRLSSKRRVTLSEFKGRTLVSIREFYLKDGKEMPTSKGIS
MTVEQWEAFRNAVPAIEDAIKKVGEASD
```

84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE

A0A0B0DL35 **A0A0B0DL35_NEUCS** (1100 aa)
Repressor/activator protein 1 homolog (Telomeric repeat-binding factor 2-interacting protein 1). *Neurospora crassa*

```
MPSAGIVYEGALANQTPDGNNNQNQSEGTLFKGLKFWISLKVPARQSLVESVKAQGGKKVELEKNADILIADHAKKNYAP
AGSLSWKYITDSIDEGQLADRDLYTIDHATAKGVRPGGSATSTKSTRTPYTPQDDNLLIHWVLEKERSGAYIRGNQIYMD
LAEKYPRHTWQSWKDRFKKQYDHQHRHGLAELLPQNYQPPPPAPPPSQVPAPVRKEENVRPGTPPATTTTVHTPAPDRSQ
AVSAPATGRVTFTQEDDQHLIGYLKQMKRQGESLQGNLIYKVFAEQHPRHSWQSWRNRWVETLEATTNLDEEDPAAAPNP
PEPSLPRPTPRATVHPQVKATPQSADQAAPKRRISAALHRTRQDVPAKSWSSPMGPVKAAMTSSAHKHSPPRSTPSRLEE
INKRARLVHGEKKKIKSASIIQRAWRSYQARKQDPERQSLIMFQALAQGALVRWACAPAFESQSQQYSEDEGSVDLGHPL
EEAVSVPTQTPREQFYVYLKRYNEAIEANPVTWVTIGGKAVDMWDLWTAVTEQDVPANARDWQEIAELLDFDWIAEPDVP
NQLQTAFQEHLAEFENYYKEFQEAQSFELNQGTDEDSEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEESEEVDNDKIEAE
EEEDDANEAQDTTLRQDPNTTEFRSSPPIPIIGALKSSGALKRNSDQIMTSPLDRMTSKRPRYDVEDEVPESPPKRWQSP
LPPILEATSRPELAADAALINKDNEDDADDDMPILGDDGEDYGVDEYREEDEDPFITQPQQPWQPTVEEASSLRSSSALR
SQELSSAQKKSAPQPSSTTQAQYISSDSDSDSSDDAFGPPINSPRPPPEQRSSPIPISVPRPSIEIPTARRQLPPRDTAP
ASRSPPPRFRIPPDPYAADDEGSSNLRPAPQRQTSRQAQPQASSHAPPQPSASRSSLAASAGHQDRHQNPHPQSTAPPKP
PPHTGLDLGDGIASEDPEAIINRYLARGYKKRHCVRGMRVTAHDPYLAGRAIDALECGGGLPDNVPGIWTEIDDEGLRLL
ERWERRIKKGKKMDEEAKEVEKRLLEKHGRKRMKLRMDFLKGLDVLDKSTRRRDDARYLA
```

598 - 617:	EEEEEEEEEEEEEEEEEEEE
599 - 618:	EEEEEEEEEEEEEEEEEEEE
600 - 619:	EEEEEEEEEEEEEEEEEEEE
601 - 620:	EEEEEEEEEEEEEEEEEEEE
602 - 621:	EEEEEEEEEEEEEEEEEEEE
603 - 622:	EEEEEEEEEEEEEEEEEEEE
604 - 623:	EEEEEEEEEEEEEEEEEEEE
605 - 624:	EEEEEEEEEEEEEEEEEEEE
606 - 625:	EEEEEEEEEEEEEEEEEEEE
607 - 626:	EEEEEEEEEEEEEEEEEEEE
608 - 627:	EEEEEEEEEEEEEEEEEEEE
609 - 628:	EEEEEEEEEEEEEEEEEEEE

A0A0B0DVR6 **A0A0B0DVR6_NEUCS** (229 aa)
Uncharacterized protein. *Neurospora crassa*

```
MGACPLTYESSLLCVLQATKPMAWSTRYLRYSTQNVDGQKEKSKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERTGKQD
VFPTTLPSRWNLPYPRMAYKTVIEPLLHECGVGFSYDRWYIHLYLEGQNDTGKKQDGQPIAVPASSRGLHPTTRLSSQGP
EGEKACYLSNGRGARAYGIMHLVRIHYIDVHTFPEQVKCKSANPVMTMKSLRRSLTIVHFVGYTSCSGR
```

45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE

48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE

A0A0B0ED22 **A0A0B0ED22_NEUCS** (765 aa)
Amidase signature enzyme. *Neurospora crassa*

```
MSVPNLITCEVDGIQYLLHPQVLGSTEAPIKADQVIPVLLLTEEELNGTPDQIGQLLQYYVETDDVCSPSFTDILVEKPS
KNGNISLFTERKDDSSCSSKATYRLHKTILHTSNTDNPEAQDDDNLPSGPYFLSGPNVHQAYRLYPDTQDAFVYGMIPND
VHNPSGFQAVSFLASDSMSKTIPVPSRHYTRLTPRGQKRPSPIRGKRITLTDGLSLLGTQTTLSCKAYVDTYPPATETDA
YVQRLLEEGAVLVGKTKTSQLRIGSSMWPETHFPANPRAARKRNVFDCNGTAVGSASALAGYSWLEFAVGGNVDSAVRES
GKRCGLYGLRRSLTAEHDKPSPGPNDSVGIFCRSLHDLSLIAECTFPPLTALAKESSRYNINKILYLDYAKDQKLEHAMD
VFVNALERHLNVARTTVNLDEEWEKYRVKSGINFSLRKTARFLYDLSHYHEYAKFRKDYQAKFHSSRGLVDLEAQVLWSS
ARDHVKRQRKLQDQVNTFRDWFEQHILATETDTATCGTTGDTIIVIPDIDFHHYHIIGFFGRVLAMEDMLSPQTTTPQLS
VPFTQNPGERLGDEQTYSPVVASVIGPRMTDTSLITLITEALKASGLPTSVQPGPLCFPLPSSSSADATTTTTATAAADA
TAAADSDDDKNNDGKKKAEPTAAELQGSTRATKLHLHEMWLYSEQEKEEEEEEEEEEEEEEEEEEEEEEEDDDDDDDD
DDEKKATVTSELEKKRLKSDGNSWDGKALAESSLNIKVDLRALRE
```

688 - 707:	EEEEEEEEEEEEEEEEEEEE
689 - 708:	EEEEEEEEEEEEEEEEEEEE
690 - 709:	EEEEEEEEEEEEEEEEEEEE
691 - 710:	EEEEEEEEEEEEEEEEEEEE
692 - 711:	EEEEEEEEEEEEEEEEEEEE
693 - 712:	EEEEEEEEEEEEEEEEEEEE

A0A0B1P4Y7 **A0A0B1P4Y7_UNCNE** (1496 aa)
Putative 3-dehydroshikimate dehydratase. *Uncinula necator (Grape powdery mildew)*

```
MATPVRNLISPSCLSHIPIDQLSPSLELTASLSIKAVVTLTWPYSSATDSISFLFSEPDFRKRNSRGQVRVEFSGNSGKN
VVKAGVSSGDLVVLSLEGVEWIRDDSSSVFPGRGIEFKLRFTDKILLQFQRDGSKELQEVRVDHLLEEDLSLDSNRIDSE
TKFASQCTPGSLSGKLDQSDLGKIFIGNNLYSSPAFLKRARTSYGSLFDSDLDTFIEADGTVQGKGRKKSRLSLTWGYRS
PSPYLEEKEDKGDVSVEVLENIPNQVKPFMVDEGVQTNEHGFSEILNLTLPVAEPIDKANKDTSVSTMDEGIQTTRFSNL
GPTESVHKNLLISPHNSPVPSENLKQYPKSSMAEQYSIYGNSGSVNTQVQVKRIPPSPIFCIDDDKNKLNDSERNPIVQE
KEKLQNFPTYSIPAEVETSHFTQHLTTIKGEGTSDLSSYSPLYSKNTIKIQPNSSQPIKSALEPQDVEKITKQNIGVEEI
GVIDANLNSVLGKHNEVPTKSLNASRVVESEHDMTVSSTDNKFSGDNFGSEYRSNLVELSYSSPRSAIPKSESERLTLSA
NLIEEDENYESLSIKTCQSLSYNKISLESNDETRTLPSISENNLSSPFYQGSENEVLEEQSYMYQSFTGNEYKDNEKSYK
YCSQIEKENNSEKNALLSGTFEEFRRERDNDPLSENEIYHMNNELPKYIDLISSDDEEGTSAPVKIISDRISSSSVFRNS
KISKDSKDKEYEKDADAIMKLQEIKDLMDVEDLKIREKVQEIKDEQGPGVMKVMTDSEDLEDVEAQKLKDEEELKDVEDT
EEEEELEDMEDVEEVGDMEGVEGVEGVEAQKIKDEEELKDVEDVEGVEVVEDMEEVEDAEGVKVVEDMEEVEDVEGVEAQ
KIKDEEELKDMEDTEEEEELEDMKDVEDMEDVEGVKVVEDMEEVEDVEGVEAQKIKDEEELKDMEDTEEEEELEDMEDVE
EVGDMEGVEGVEAQKIKDEEELKDVXVEGVEAQKIKDEEELEDVEDVKNVKNVEVVEEELDKENMEDMEGVKDLEDVEAQ
KLKDVEELKDLEDTEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDVEDVEEEDDVDDVDDVNHMDDKEDVEEMKEVQEIKD
VEEEQDKDNVDAEEKEELTLCEDQVETTRRFQKEDSRLCISTEKQHNLGKVHFQQFETQDPSIVYEKKLNKTTPMSQAFK
FDELSTKEILIVHKESPMSRDISSKDISQANVKQNDWSFDNRKIFTGKEASDQVIASPEKYIPESPEEKSSTNVSHHSEH
IYWSTKLSTSSKSPEPDSIVRNSSIKSQQRGIGHDASFEIALSSLGSPSKKQLLPLVDKNIIFAQKLQTELSEYTPLKIL
SQHLNKKLDVLGIVASSPTIPKRVKGGPRDYVVTFDITDPSIEPVSFTQIQIFRPYQDALPVVEIGDGIILRNFQVLMNK
KNCRLKSMKQEGSGWIVVKRNGEVQVKGPPVEYSKAEIEYISELQTWFSELDTITQ
```

1055 - 1074:	EEEEEEEEEEEEEEEEEEEE
1056 - 1075:	EEEEEEEEEEEEEEEEEEEE
1057 - 1076:	EEEEEEEEEEEEEEEEEEEE
1058 - 1077:	EEEEEEEEEEEEEEEEEEEE
1059 - 1078:	EEEEEEEEEEEEEEEEEEEE
1060 - 1079:	EEEEEEEEEEEEEEEEEEEE
1061 - 1080:	EEEEEEEEEEEEEEEEEEEE
1062 - 1081:	EEEEEEEEEEEEEEEEEEEE
1063 - 1082:	EEEEEEEEEEEEEEEEEEEE
1064 - 1083:	EEEEEEEEEEEEEEEEEEEE

A0A0B1PCI5 **A0A0B1PCI5_UNCNE** (646 aa)
Uncharacterized protein. *Uncinula necator (Grape powdery mildew)*

```
MVSSTDKDLFTCNGCGDDIGSERARILCNICVDFNLCSNCYVLNYASKTHKKSHSTSVFRTSGYVNSENSNALTLLQTEN
SGGNLRKPSQENERKYSEIPTANWGALWNVMKAPLTKKDKRASKSTGKPESGTSLEARNKNDSLSPLSRVPEPLSSLSVS
TKSQVTPVYPGPTYFRPDKWEPFFESDNTPSSIFVGLMSSIFNTLDEKGTGYLKPEEFSFFLEIQGYPLSANIWKMAWQK
```

```
AAGGSSKDVADLELGLYFAEREIPFTLAARPIELETSGGNSPEKPLNSKTKKKNSKDVNKNMPLLSRQGFIDLSASEYLK
DPSMAYQYIMNALHELKVWKELGDLPRSVLPIFPMNNQVQDQEEEEEEEEEEEEEEEEEEEEDSDISILIPNSKENESSE
SENENHQLNENQELILLNIDKEGTKSESSNINTSENEPLTPVSIDKSVATPIVENTGNQGLTAQHLRISADEPMTSLFIG
KPGFSLSDGDRMDQKSAFQHRNNSENESMSPTFVKKSELTLTGEDKKNQKSSFQHLKTSVKEPLSPRFVVKFQDNSCEPT
VNLNTKIIDPKNMKSSRLLQNKHKLVVKTDFPNQWLSTASALSARSPQRRKVEMLVEAYEFVRANSICLDERPVFKSASI
YKNTST
```

363 - 382:	EEEEEEEEEEEEEEEEEEEE

A0A0B1PCV1 **A0A0B1PCV1_UNCNE** (168 aa)
Uncharacterized protein. *Uncinula necator (Grape powdery mildew)*

```
MMKNCLIQARGNGGESTQKRVTRIVRQTNANGRKLDMRRSADKQARGGAIGQCGRQSKKTGGRRTKKESGHSSVRGAAEE
RFCEERMKEYRKWLAAENEALIPTNYNLEGQGRQEEEEEEEEEEEEEEEEEEEEEEEEEEKKKTNGDVLSPYCDKSTHIF
QSRTLPEG
```

115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE

A0A0B2SPX8 **A0A0B2SPX8_GLYSO** (233 aa)
Uncharacterized protein. *Glycine soja (Wild soybean)*

```
MKKILVSIKFLLCLSLLCVLFLSFPLLLQSLKPSLMQFFSYMVEKSYMFLLCNGLLLVLIAINSAPINASSPPTTERAAV
AVHIEEKSSQLESKEPDIAVAAPIAGEETESPHKEEKILVRVEQDNVLSDTQEEEEKEEEKEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEGNVLVIIDEDKHDTEELNKKCEDFIKRMKATFSSNNLELRAVDSFYFDNQKLPVAVN
```

142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE

A0A0B5EKS1 **A0A0B5EKS1_9SPER** (1119 aa)
DNA-directed RNA polymerase subunit beta (RNAP subunit beta) (EC 2.7.7.6) (RNA polymerase subunit beta) (Transcriptase subunit beta). *Callitropsis vietnamensis*

```
MRLEENKGIFTIPQFGKIQLEGFFRFINQGLIEEINNFSKIESSNKKIKIILFGSEYKLTEPFIKERDAVYMSLTYNCQL
YVPARLIKKTKKTCEIQDQILYLGDIPLMNSKGTFVITGNYRVVVNQIVRSPGIYYTWERKPSGNIIWIGTIISDWGGRS
RLELNKKKEKIWIRIKKKKISVLLFLLAMGLNSEDIFNYKNVKAFFQYSKEYYTYKYDWYGGKRKAILKLYKKLYISDEN
EEEGEEEGEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEELDFESIYEKVTTFFRTKCLLGKIGRRNLNKKLSLDIPENEIL
LLPHDILAAVDYLIKVQFGAGTPDDIDHLQNRYIRSVADLLQEQLRLALYDFREAVEKTILPVSINAKKRITLIKLETFI
SLTDTFHNFFGLHPLSQFLDQTNPLAEIVHSRKVSSLGPGGLTSRTSTFRTRDIHPSHYGRICPITTSEGINVGLIGSLS
IYATLGHYGSLQSPFYRLSERSNKDHMVYLLPGEDEYYRIAIGNSLALNQGVPEEQLTAARFQQEFLFFAWDQIHFRSIF
PSQYFSVGVCLIPFIEHNDANRALMGSNMQRQALPLVQPEKCIVGTGLEGQVALDSGSVAIAKQGGKIKYIDGENIIITS
SVARDNIETELILYQRSNSDTCMHQKPRVRQGEYVKRGQIIADSAATAGGELSLGKNILVAYMPWEGYNFEDAILISERL
VYEDIFTSFQIVRYEIGVYFTDQGPEVITREIPHLNAYLLRHLDENGIVMIGSWIETGDILVGKLILEAEEDSLINTPEG
KLLQALFDIKAPTGKENCFRVPKGVKGRVIDVRCFQEFEEEEDDYLGDIIEKVHVYILQKRKIQVGDKVAGRHGNKGIIS
KILPRQDMPYLQNGTPVDMVLNPLGVPSRMNVGQIFECLLGLAGKLMNKHYRLPPFDERYEREASRKLVFSELYKASEQT
ANPWVFETDNPGKHRLIDGRTGKVFEQPVTIGIAYISKLCHQVDDKIHARSRGPYALVTQQPLKGKSSRGGQRVGEMEVW
ALEGFGVAYILHEILTLKSDHMDTREKIFGAIFNGEPMPKPTTFTESFRLLSRELRSLALELNHTILSEIDFQIDKKEV
```

253 - 272:	EEEEEEEEEEEEEEEEEEEE
254 - 273:	EEEEEEEEEEEEEEEEEEEE
255 - 274:	EEEEEEEEEEEEEEEEEEEE
256 - 275:	EEEEEEEEEEEEEEEEEEEE
257 - 276:	EEEEEEEEEEEEEEEEEEEE
258 - 277:	EEEEEEEEEEEEEEEEEEEE
259 - 278:	EEEEEEEEEEEEEEEEEEEE

A0A0B7F849 **A0A0B7F849_THACB** (988 aa)
NAD-dependent histone deacetylase HST4. *Thanatephorus cucumeris (strain AG1-IB / isolate 7/3/14) (Lettuce bottom rot fungus) (Rhizoctonia solani)*

```
MVKKRVQSKKSPARRPTVAKKAPRYPPKLKSPEPKSPELPYSIEDALKNRVLTKFNKSINKDLNDTKWQRETYQLIPENV
EEPEDLDEDSRILRVLNDFSFWYARYPRGITKGDGKKKPVLPTPPLPGAGEKWSGFCLRGVTASLNGPARYLAMAGEFEV
EWPTLESVPLELKKGEIEDIALLSDPAFRDGKKSIVVFTKRFVYFLLTPDRAFEKHWKSVIPYWEQYMEVGSLYIDELKY
TDPRRKWWHGRQSFLAFRSWKRASLNAESALIGEPDKSRDGPKPEEEEEEEEEEEKDEEEEEEEEEEEEEEEEEEEKDE
EEDIGDGGNEGEGEARAKSRQGEGPSKRAVSGRGPPSRLAATHLSVTGSSKRKASADSSSGRTVRPRPESIASQPGSPTS
EKEQEETLPPPPATASQTPTSFGVSAISIQDVAGSQILQKAHGEAEEILRGNTLEEFFRMDGWRDEGNSSMGHEYLDFNI
DYEPADVSPLSNLNFPLPEMLAQSVLADIDDSAQASDPRVGDSTGSELAPDIFQRHARPLRLNIHHIKISHHLHIAPDNN
SMSNARRLNLLTSLDDSGRKSAQSVLTGVVNSRCMILCGAGISVQAQIPDSRSAEGLMSPLKLNILGQEVSSKDLFTNSE
APGGKRLLALNFLMTTLRQHARVTELTDFHRLIHAMLDTNRAVRCLTRNFDGLETRDRPDLSNKVMELHGRNDTLTCLGG
HAQTDHGTAADYDHLFLEGTEVPCPSCVGILAQERSSSNRKLRKTGTIHHLRPAVYLDERFVPSMNDVDSRSELLDLAGT
CQVLLIAGTSVSTPHIYQLFLELADRIHASDGVVVFINTKDMSKGRIGHSVDFYLQLDLQLCARFMMHTIHQQKKLDVQL
GKDIWLELSDRDLPGTTSNALEPLSITTCCYCAHPMVDVLLPCKLCNRYFCFDSPGLKLGRMCVSLDKFTTPPLAPFEER
VKNFVCPECYAHEEGKIYPVFNLLMSIV
```

298 - 317:	EEEEEEEEEEEEEEEEEEEE

A0A0B7N565 **A0A0B7N565_9FUNG** (258 aa)
Uncharacterized protein. *Parasitella parasitica*

```
MRFNSISLGLVATLVLAVSVRANAVGGVGKDTVDNATGDVTDKVGDGKVGNTVSGLTDDIGTGNGDLVGTLIGNLKRSAR
LSRRKLSRRAEESDIEGAGGDAEKENIAGEETEAAKEDTVEEGAVEGSAETQAPAAPAAPASDIESSASANQGEEEEEEE
EEEEEEEEEEEEEGVTKRSEKDEDEXXXXEEDEEEEDEDEEDEEEGKRKRSEIDEEEKDEEEKDEKEVEKDEEEKDEEEP
EENEIEADELGDEESQAH
```

154 - 173:	EEEEEEEEEEEEEEEEEEEE

A0A0B7NH41 **A0A0B7NH41_9FUNG** (645 aa)
WD_REPEATS_REGION domain-containing protein. *Parasitella parasitica*

```
MPGAINALSISQDSNSVVVAGREILKIYDIRNPDIRESLNLRAGSQSNLNYASNDVKWGNNEREIKEHSRAVNRVSFQPN
NGNLLISASQDGTVKCWKWDIRNPRVNHDRKVSTHNGACFTLAHNGPCFTLDWHPNGNYIATGGRDMTIKVWGLTSDERK
PLYTIKTMSSVSRIQWRPNHPNEIASCALLTDNRVHIWDVRRPSVPKYIFERHSSAPSDKWFIRQHIKGAYRPVEEMKRN
AMSWNVQGDVAFNIDKSSRELFVDESKVLNPLAEPSRNSKRLGLKSALEEVVKSRAFANSLHANRTQANQYAPPQSSGIV
HMPLFDFEAFSIFAVNYVISGEDVAVACDVNSKLAWNMGRHRTSQTWAIIGMFYSDEALEADFLDESTHEDMANVNIEDG
QDFNSVDQDSSGIYTHEEEDEYEEEEEEEEEEEEEEEEEEEDKLESSEGDVESLNTSHSSCLQHSSSLFNLKVPWKHEP
VVMELLEYYTDQGDIQMCVTLYLVLEKYLNIDHERVADWFSAYIDMLRRFKLWSAATAIIKACKIQSIRELNENATTVNI
ACNTCFKLVNGTTSGSWACDKCHRLLNPCSLCHQTVRGLYVWCQGCNHGGHLSHMREWFEAEKLCPTGCGHTCVLQPLLS
HEEQA
```

423 - 442:	EEEEEEEEEEEEEEEEEEEE

A0A0B8RPG6 **A0A0B8RPG6_BOIIR** (582 aa)
Ran GTPase-activating protein 1-like. *Boiga irregularis (Brown tree snake)*

```
MASEDITKLAESLAKTQVGGGQLSFKGKSLKLNTAEDAEDVIKEIEEFDGLEALRLEGNTVGVEAAKVIAKALEKKSQLK
RCHWSDMFTGRLRSEIPSALISLGEALISAGCQLVELDLSDNAFGPDGVRGFEALLKSPTCFTLQELKLNNCGMGIGGGK
ILAGALKECHRKSTAQGKPLALKVFMAGRNRLENDGATALAEAFTVIGTMEEVHMPQNGINHPGITALAEAFAVNPLLRV
INLNDNTFTEKGAMAMAETLKKLRQVETINFGDCLVRSKGAVAIAEAVSEGLHKLKELNLSFCEIKLDAGLVVVEAIEDK
SELEKLELNGNCFGEEGCEQLQEILEGFNMGEILSSLSEDDGEDDEEEEEEEEEEEEEEEEEEEEEEEEEEPLQVQERGQ
GEQEPLIPKKILEEHDSTPLSSPLPPVDVGTFLAFPSPEKLLRLGPKCSTLIIQQTDTSDTEKVVTVFLKISSVFKDETV
VKTAVCETTDALMREAFSSANFNSDAFITSLLIHMGLLKSEEKIRAVPSLYGPLMTLNHMVQQDYFPKSLVPILLAFVTK
PNRALDPCSFARHLLLQTLHQL
```

366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE

A0A0C2ET71 **A0A0C2ET71_9PEZI** (116 aa)
Uncharacterized protein. *Sporothrix brasiliensis 5110*

```
MRRVRLFNFSIQEALYSQLPQHLPDQDAERQPEPEQGQEQEPEQEQEQEQEQEQEEEEEEEEEEEEEEEEEEEEQEHEA
DRRRSQPLTPSFAATAVSPASLPPSPNDFWCDSRQK
```

55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE

A0A0C2FI21 **A0A0C2FI21_9PEZI** (102 aa)
Uncharacterized protein. *Sporothrix brasiliensis 5110*

```
MRALASSMGITRVLLRRRLAKLRSTIIQREEERCAATTMGTEAAIESGKEEEEEEEEEEEEEEEEEEEEEEEGGEEGRRGG
GGRRRRRRRRRRRKRGVGQRGE
```

50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE

A0A0C2WRK2 **A0A0C2WRK2_9AGAM** (1146 aa)
Uncharacterized protein. *Serendipita vermifera MAFF 305830*

```
MSINQRRAAQTTSSRPATPASGQSHHSTGMHSASSSSPGGLLDPPQGIAFADFVKQWGDPHVARWLADNRCAQHAPAFRD
NDIRGDIILELDMDTLKEIGITSVGDRTRIRSAVKELRRLCSGINPQPQAAPRVLVNGASSDLRMSRTNGLKLKNETPQQ
QDPIDSSPAAVRNSRGRPPPLQIDNVREKDLPQIQRLDSARLAGTPTPRPQPTTTSRTGPPSRNAPPPTPSAASAARMTP
RLTVPTSSSSSRIRTPTSESPHPPPFTNDPLPPAPSPVSPWVSNSGQRGLPSNPAPGNLGGGSFATRATSPLPAGRSRLQ
SQTAGLSHQRQGSGTNRSHGSGSSHPYSSSSSTLAPAPIPSHILSPVNETFMSMSGSPPNGYTVGKGPFGKGGQSQGAVR
EEELRKKLIKFHMGSVSRVFEVKELEDGTDLLERALRKFGVPMHDHQHEMDGSLSVGGWGVFMGPDPDAPPISENELFAL
FHAPDHPGRENLHIRQIATGKRSKALERIFGETPPSLHAPTSPIEESLNALTANRNLNKKLNRASTISVLSGLGVPLGSP
PTSPGGTKSATGGSFGKLRNFFGHRPPSELITTHLPEYFPFADKKVLKKTARNSMMRQSIKQGVIGPGSAGIWVPPRSAS
RFSTSTMGSGRSIRHSVAPSSGTLIGMASPRSSQEDKRRAAVTIPRVSIEADDSDSMRLTLVDEEPSPAIDSSPFAHQQK
ELPQIQPLKFAQDTFSPNPSDQLTVGGTSRAAKRASKITELKPSNPIPEEAESMITVENVTTGIEHAIEEKRNRDSFLPG
MKRLSTASVVSAAVAKRESLQPKEVPVDEAEDEYEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEDDTPAKVTSNAGTRSI
KWIRGALIGSGSFGNVYLGMDAQRGLLMAVKQVELKGSSYSEERKRSMLTALEREIELLKTLQHENIVQYLDSAIDDNNL
NIFLEYVPGGSVASLLKNYGAFEESLAANWVRQIVRGLEYLHGQTIIHRDIKGANILVDNKGGIKISDFGISKKVEEGFP
RANRVSLQGSVFWMAPEVVKQTSYTSKADIWSVGCLIIEMLTGQHPFPEFSQMQAIFKLGSGTAKPVIPSDITPIATEFL
QKTFELDYTARPSATELMNHAWIAES
```

838 - 857:	EEEEEEEEEEEEEEEEEEEE
839 - 858:	EEEEEEEEEEEEEEEEEEEE
840 - 859:	EEEEEEEEEEEEEEEEEEEE
841 - 860:	EEEEEEEEEEEEEEEEEEEE
842 - 861:	EEEEEEEEEEEEEEEEEEEE
843 - 862:	EEEEEEEEEEEEEEEEEEEE
844 - 863:	EEEEEEEEEEEEEEEEEEEE
845 - 864:	EEEEEEEEEEEEEEEEEEEE

A0A0C3AQM5 **A0A0C3AQM5_9AGAM** (1525 aa)
Uncharacterized protein. *Serendipita vermifera MAFF 305830*

```
MPQPSESAYMFWTNAFDTYTFGTETFKLCPGLGPVDSAFEFGFKDATDQEREAAKAFILQQVKPLSEDGKVDKLWNAKSL
PTVKVLNNIYYYLQNRIHFHANLDRSLQKRNDHAYYFLSQAKKKGEKLPTPSIFIKDIVKMNLLHTELFGKEGWEKSREG
NDIAIPRLWNATKAVYTAHWARARDSFKKRGETLENELKVLKAAHEVFMDPKQMITVQQLKHYGNKLESSLERAKFIYDD
AAIAQVNQYKAEVQLVVDALKLGSSGIEELRSHGITRLTKKDLEAVVQKMKDHHYDLFSPRWTKILSPEADQDENSAVEV
IPGATSGALQDLFNGSPKKAIGMDEEQKMSTADLCQALGIPKGGGIPGLLLAAYKDGQASLRAQVPNAADRRNMQEKAHL
AHTSGHTPQNWRPQNPMWHQLCGTHRLLRHLAESKKSNGGMLIADDVGLGKTLQVISFILMVARMIQLQKQNESWPPVHK
KYGGRDHYIYDGQQFSDQKCHILVVPNGLAAQWAEEIERFAGAALEVYTFKGKPEEVVDWFDTLSTSSHFQMSSVPIYRR
LIILTRSTLRRLSEQQVKATPADHKGLSNGLVASFQDKTTKAGSIWHQGFNTMTLDEIHDYRTGGQDFNGAKQLRDQTMV
VIGLSATPMYTRPQDLANIGRLLRIPGLMSASSDEDDMDAARDQRRWSFLQMLLDKYKSLSDPQADALIKARNGVIKRIL
GVRGYLGKNMYRRTRESPPEMGQRYLIPGLKPVWFQEIHLVPHPDELALMDMISKEEYQLAKDKKKEKDNLISLEADESE
EEEEEEFQNPALQVPSAAKTAAKDIKISSFYLRNRQGALNPVLTWSLVKETTAPPLYTGKNDFYQRASTKEAALIAVIKH
HMKQDHQQANPVTKITLGEDGKWDKEWEHRTTPEPIFNDGKPTKVMVFCDLVTHIPYLASALKAFKIKYLELTGNMTPAK
RAEVVEDFKNGDATVIICSNVAITGINLASANILVFMASSFLYGEGIILKNAIVQTQVWSKQAEDQIVGRTWRPPQEKQV
IVYKLLLEGTTDNILKNIAEMKACLLDSFIEGVESGVKDVVEKIQPVIRDITESVPPPKGTKSRPGKNAKAVEAANPPPP
EPETTNVSARDAVEPPASKKQTEASKKSKKGKQPRTKPAPLSKAIITDSDDEMPVDTEPSNVPPKVSKSKGGKQQSSKKA
MKEPIKYTSKQIQEFKRLEISAHKEQLRFGTGMAKVMAEAEVYNNTPLRKKVKKPVKGSTNTQMDVDADLDAVPGGTSPL
SQKSSLVEPANEEASNPEGTALDQAPTSDDGSGPQADGMDHEVSSPDAAAVAPAPSLSGTEDLEASEEVAAVANPSEEEE
EDEDEEEEEEEEEEEEEEEEEEEEDDKSYGKVIPSETASEVASNDLAEAESSDAEEDMGGAAIRSSLPNDSEESEVGNDL
ESQTQGANHAESDDDDEDYVPVTRGAKGKRRAKSRTPESENGQPTLLNPLRHNAQGMESRSQPAPKRRKLEFHPNMSKAG
TRDTQ
```

1365 - 1384:	EEEEEEEEEEEEEEEEEEEE

A0A0C3GE91 **A0A0C3GE91_PILCF** (207 aa)

PP28 domain-containing protein. *Piloderma croceum (strain F 1598)*

```
MARGRGGKFKTKRGGGRNFSKNLVIDENGTAVSTDKRWAPRKEGSEEDSDDEEEEEEEEEEEEEEEEEEEEVAQVAGGSN
EPELTRAERRELKKKQAPKQKGSGDEEDDEDLINTNHVEKKLNIADLGKDRQLSRREREQKEKQEAKDRYWKLHVQGKTD
QAKADLGRLAKIRAEREEAQAKRKAEAEAKAAEIEAKKKAAASGKRV
```

52 - 71:	EEEEEEEEEEEEEEEEEEEE

A0A0C4EQK4 **A0A0C4EQK4_PUCT1** (730 aa)
Uncharacterized protein. *Puccinia triticina (isolate 1-1 / race 1 (BBBD)) (Brown leaf rust fungus)*

```
MNRPLPFTHPDLTFEPKKDLQQYTYAFQQGQEQGEYDEEDGSQEDDEGEEEGDGEEDEGEEEVAEVEDGINEGEEEEEDE
EEEEEEEEEEEEEEEEEEEEEVEERGPSTLPDPAAHQMTFALVQKPMTVRQRKELEKIARQQERQRKKELKEREKAERLA
KREQEKLARIAKKEQLLLQSKAAKKAKATLDGDQRAWSIGRPMKTTGSSSQLLTTRKIKVDSRIETVRRLITHAENGELH
IHPSGAALDPSGNTRWCETKVHQGVTYLVEDDELTLPSDPKGDTKVTPEGVLLGDGRHVVDDYYEDAALASGANSGEIAL
ADGSEPQDRAASNSAPGQPGDPSALPDMPESTTRLPCQSAFRLALNRVNPSAAGSASLGLKTIFGGDGKAPSIAIPNDSK
ERRRRMASHLTAKNWMIHYCRAISEMNRHLRGIRNERMVPFPKYPSIARLAADPSTNGAIGTLANNAVEEEMEWREVEVE
MRLNTDGKIMEPGEEMDTKEEPDDDDDNNSNAGGPSASAPEPAQVFSRITNPLPPSSIITIYGVKNSSTSQEQTNTGEGT
PGQGGGGADSSRVGGSGLHPARARSPHKRPFKLRGKKSQNDWWTTTTRVLEQRPKQPVMGLLDVHTGQPHVRQDTQSTMA
IWETADDLDDWTRCNKRQKLNGSQIDPQAGYDPSLLESRTIMNGPGIGRPGLSSVNDTILIETIFDDELTRPKYELLPGM
WDFRSIDPQA
```

80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE

A0A0C4F6Q6 **A0A0C4F6Q6_PUCT1** (769 aa)
Uncharacterized protein. *Puccinia triticina (isolate 1-1 / race 1 (BBBD)) (Brown leaf rust fungus)*

```
MNRPLPFTHPDLQQYTYAFQQGQEQGEYDEEDGSQEDDEGEEEGDGEEDEGEEEVAEVEDGINEGEEEEEDEEEEEEEEE
EEEEEEEEEEEEEVEERGPSTLPDPAAHQMTFALVQKPMTVRQRKELEKIARQQERQRKKELKEREKAERLAKREQEKLA
RIAKKEQLLLQSKAAKKAKATLDGDQRAWSIGRPMKTTGSSSQLLTTRKIKVDSRIETVRRLITHAENGELHIHPSGAAL
DPSGNTRWCETKVHQGVTYLVEDDELTLPSDPKGDTKVTPEGVLLGGRQYKIPTFTSKDRANHNKHFVLSIDAARAAGYR
DSLYFFRRNPLIQKLPHVVDDYYEDAALASGANSGEIALADGSEPQDRAASNSAPGQPGDPSALPDMPESTTRLPCQSAF
RLALNRVNPSAAGSASLGLKTIFGGDGKAPSIAIPNDSKERRRRMASHLTAKNWMIHYCRAISEMNRHLRGIRNERMVPF
PKYPSIARLAADPSTNGAIGTLANNAVEEEMEWREVEVEMRLNTDGKIMEPGEEMDTKEEPDDDDDNNSNAGGPSASAPE
PAQVFSRITNPLPPSSIITIYGVKNSSTSQEQTNTGEGTPGQGGGGADSSRVGGSGLHPARARSPHKRPFKLRGKKSQND
WWTTTTRVLEQRPKQPVMGLLDVHTGQPHVRQDTQSTMAIWETADDLDDWTRCNKRQKLNGSQIDPQAGYDPSLLESRTI
MNGPGIGRPGLSSVNDTILIETIFDDELTRPKYELLPGMWDFRSIDPQA
```

72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE

A0A0C7NBP5 **A0A0C7NBP5_9SACH** (1036 aa)
LALA0S09e03136g1_1. *Lachancea lanzarotensis*

```
MDGKGLDLSNLKHKVASKMKENKKSSKSSKKDSGKDTKKSDTSKSVPKQDSKEKIAEKEAIRREALALGASEKDLTLISG
LSDDDDLSEQEFESSKQSSDKKFDDDFKQFLKTAGIDAAVPPQDAEEEEREEEEEEEEEEEEEEEEEEEEEEGSDSESIP
ELVKDAEPQLIEGPELSDDEKSSSDEEGPFLNQDSDAETAEEKKEDKDLISQTHLVTSDNLLVPADAVWYEIPLDPQANL
QNEPLPADKIETLYQRAKQALEADNTLYFDEFTKNSSQRKFMSQILSDGTLNDKISALTLLIQESPLHNTKSLDTLISYC
GKKSRNSALQSLNALKDLLLNGLLPDRKLRYFKNQNLSMMLNKRTLAIFYFEDYLKTLFFQVLQVIERLSHDPIIHVRMQ
VLSHIFDLLTAKPEQEFNLLRLGVNKLGDIDNKVSSKTSFQLLKLEQAHPNMKSIVLDATVDVALRPSADYHTTYYSVLT
LNQTILKRSEDKIANQLIKTYFTLFEKFLLSTDSENAEGGDHAPKNKQASYENKRKKNFKRGKKGGKSVKNDRTDKEVVD
EKNSKLFSAILTGLNRALPFSNMPASVYEAHLDTLFQITHSSNFNTAVQALVLIHQVTLKAELNNDRYYRTLYESLLDAR
LVTSSKQGIYMNLLYKSLKHDKHVARVEAFVKRILQVCSSWLNVGALAGMLFLLLQLTKAVPQIKNLFTNTPADAEYASE
EEKDAGTDSSKQLAYDSGKRDPKYANADHSSAWEMRHFLNHFHPTVQTYAEAFLTNSEDVTKPDLGLYTLAHFLDRFVYR
NAKQKPSTRGSSIMQPLGGSHTGSLIVRASDTRATGLDAVPANTQDWLAKKADQVSPDERFFHQYFSTKQSAIKRADKEK
GAGQSNEFDEGSELDEDDVWDALVKSRPDVEDDSDDDEDMMSMSEDDEEEEAAEEAEEAEEAEEADDDVFYSFADESNAN
VKKRGRDDDSVSDDESDDEALAQAFQSDSESESEAEQAAAAATTTASEDGGPMSRKKLKALPVFASMDDYASYLSD
```

131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE

A0A0C9PT57 **A0A0C9PT57_9HYME** (140 aa)
Up protein (Fragment). *Fopius arisanus*

```
KGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWEEIGKEVNEKIWNEKKDQYSGRQKSKLPKWFGERPGKK
AGEPETPEGEEDAKADEDIVEDEEEVEEEVVEEEDEEAEEEEEEEEEEEEEEEEEEEEE
```

119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE

A0A0C9UMM7 **A0A0C9UMM7_SPHS4** (316 aa)
Unplaced genomic scaffold SPHSTscaffold_291, whole genome shotgun sequence. *Sphaerobolus stellatus (strain SS14)*

```
MDIPGIKLTNKDREHLSPNCSDVLTILQEVMPAWDIPHNPQHLVKPTLSQLQFWVGPLVPLDSLVINLLIKWTHQYMFTM
NEVFLKDKDQNNYPVLGSWKDILTFWTVSNICNLVHAPAFKPHKAYWSGLPHGPKHTSFKDRFSSFFPGPTIIFGSNSYW
NIFKDNGYISEYHDLLKTLNDQEKLAFSDHMQFAFGLLECLPDRGLAAKSQAWRYDKIKGGPCFIVNATSYKILGVGAKK
QVSGQRHPKAVSNHKRIQALLLADKENVSLDEALKQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGYDSATFL
```

277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE
287 - 306:	EEEEEEEEEEEEEEEEEEEE
288 - 307:	EEEEEEEEEEEEEEEEEEEE
289 - 308:	EEEEEEEEEEEEEEEEEEEE

A0A0C9UMV0 **A0A0C9UMV0_SPHS4** (235 aa)
Unplaced genomic scaffold SPHSTscaffold_106, whole genome shotgun sequence. *Sphaerobolus stellatus (strain SS14)*

```
MTDLVLPAYMLAWKTSGEVDHMEDVPAGDSRRTIQGFQADKKFNQPALMFSFDDPNEEEEDHLSKVARYWKARNQEWTQC
ESRYRELLDAEEAAASWKRSEEATWALKKAQEEEKAKEKEREKEKGKEKEKRGRLGVQRAKRRKRGCPGVQKSKRDVHLE
SEEEEEEEEEEEEEEEEEEEEEEEEEEEEEHNDKLQSCLYCMKKKIPCMPQSGKKEGSEKVTEAMQELTKLERC
```

162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE

A0A0C9VMF6 **A0A0C9VMF6_SPHS4** (678 aa)
Unplaced genomic scaffold SPHSTscaffold_51, whole genome shotgun sequence. *Sphaerobolus stellatus (strain SS14)*

```
MGRPYRGSRLATFYSSLDSETTSNDGSSEAALSSISSAFQLQEYISALVRMDPHDVERIVKVPGKIGGGGVGSKDKAVVE
RETEGDVEGKEGVDEACWIYEQLRKLAQDLTYPLIVSLQQECSRETCKEMKAGEWLYLCVAHGSAGAMEHCCAIDYILHT
VDSATALLNSPRAFPSRLSIPSSSHRHFPSLARRLGRIFAHAYYHHRALFSTAEAETSLYARFLALSRRFELVPEEFLVI
PPLEGPHEGEKDIPRNLPAKNAESKPITLLTRSGPPSSAATLAASSSGSTEEETSAQSKSPRLGNRSRTDTMYLSSGTNY
AAESATQRRVPSPLAATLAREEEAELEAEIQPQAQVAEEKDVQESTIPIEVPKDVRADEEHEDVHESEEHEEEIDLADPP
PGLFERDFAFQERGGKKEVEGEVNEDVKDKEGGSDAHVVEDKSANDAKDGVDDVLGEQEQATGQVRADVKEAKQEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEETAEEPPKAEEPKAEEPNAEEPKAEEAKPEETQVEAE
PPIEKKEVAEQSVQPTPTPEATVTTETPSEDDAPSDSDMLKKDVEPAEETASAPAPATSKAEETTTTISATKEEEKETST
PPPASESTIASEPQVETETEAKSESDPPKEPEEKKEES
```

475 - 494:	EEEEEEEEEEEEEEEEEEEE
476 - 495:	EEEEEEEEEEEEEEEEEEEE
477 - 496:	EEEEEEEEEEEEEEEEEEEE
478 - 497:	EEEEEEEEEEEEEEEEEEEE
479 - 498:	EEEEEEEEEEEEEEEEEEEE
480 - 499:	EEEEEEEEEEEEEEEEEEEE
481 - 500:	EEEEEEEEEEEEEEEEEEEE
482 - 501:	EEEEEEEEEEEEEEEEEEEE

483 - 502:	EEEEEEEEEEEEEEEEEEEE
484 - 503:	EEEEEEEEEEEEEEEEEEEE
485 - 504:	EEEEEEEEEEEEEEEEEEEE
486 - 505:	EEEEEEEEEEEEEEEEEEEE
487 - 506:	EEEEEEEEEEEEEEEEEEEE
488 - 507:	EEEEEEEEEEEEEEEEEEEE
489 - 508:	EEEEEEEEEEEEEEEEEEEE
490 - 509:	EEEEEEEEEEEEEEEEEEEE
491 - 510:	EEEEEEEEEEEEEEEEEEEE
492 - 511:	EEEEEEEEEEEEEEEEEEEE
493 - 512:	EEEEEEEEEEEEEEEEEEEE
494 - 513:	EEEEEEEEEEEEEEEEEEEE
495 - 514:	EEEEEEEEEEEEEEEEEEEE
496 - 515:	EEEEEEEEEEEEEEEEEEEE
497 - 516:	EEEEEEEEEEEEEEEEEEEE
498 - 517:	EEEEEEEEEEEEEEEEEEEE
499 - 518:	EEEEEEEEEEEEEEEEEEEE
500 - 519:	EEEEEEEEEEEEEEEEEEEE
501 - 520:	EEEEEEEEEEEEEEEEEEEE
502 - 521:	EEEEEEEEEEEEEEEEEEEE
503 - 522:	EEEEEEEEEEEEEEEEEEEE
504 - 523:	EEEEEEEEEEEEEEEEEEEE
505 - 524:	EEEEEEEEEEEEEEEEEEEE

A0A0C9VUY8 **A0A0C9VUY8_9AGAM** (392 aa)
Unplaced genomic scaffold scaffold_25, whole genome shotgun sequence. *Hydnomerulius pinastri MD-312*

```
MSSTCVTDLHAHNSDNETLLHIAVERGRVDVVDFLLSKNVQVPSDILFSAFHSSQGKPRECQPEIIRALVNHGADLHARN
SDGKTPLHLAVEGGWIVVVECILSKNIQLPSDILFAAFRATSHQAKIVFLLVDYGANLDACGPADGKTPLHIAVEEGLIS
VVKALLAQTVQVPSHILFAVPSARENKKELTCILLDHGADTNAPGSNGRTLLQAAAASVDIPMVEHLLATKINLPFDILL
TAMSATPHRPKIVRLLVEHGADVYASNSNGMTPLHIAVARGHLASVEYLLLHIRVDQLPSDILRTALRANAHQEEIVRML
VNLGANVHWHGLTQNDIEDIRLAMSYEDSGESEDGGLYSEEEEEEEEEEEEEEEEEEEEFVDALDILHASQA
```

360 - 379:	EEEEEEEEEEEEEEEEEEEE

A0A0C9W7C7 **A0A0C9W7C7_9AGAM** (1534 aa)
Unplaced genomic scaffold scaffold_78, whole genome shotgun sequence. *Hydnomerulius pinastri MD-312*

```
MSAPPKPNCPVKYNPSKRITKTVITKLIEKGSYVDKKLQTLCMIDVSQTSSMTVAHAPEKYQDILKIISYQCDVYRHTIK
LLLEADTSADIDGAVQMLARVLQYLDEVRSSYMSSARNTKAEDKDWFCATLEYHLWLDATQDGYQEDARAKLKEVMNVSF
ESVVARQKPCVLDYIDLDEYYKRLSVGIDLCGRNVKMRRSASEIPEAARQWAKYLIEDLEDTPKEGGKKGRRNVKGKGKA
TPKGRKKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
RGRGRGRGRGKEEEREKEEDEEEEEEAAVNTKEEEKVVVAKGKGTGKGKGKGKGKGKGKVEEVVRRSQPSTAKAKGKGKG
KGKAWESDGETEIEEEEEEEEDEEDEELDDITSFSIEVEDQQEGSSSKRKGDKPRAKHRRRPLSPVLLHWERRFSSLQNI
ISLLIREHFDLNLDDIVDTSDIEKLAMTTDSDLIEGVLNFLHSLIPLDGDDPKSISGMFSLLAERLRDLRGDSAMVVYSE
GEEPQYHDEEGAQGGEVGTHAGNEEGRNDEGDNGGGERRSKSRDERGRRGDDGGDGAETGSGDKRDGRGEGREGKGDGGN
SGADRIREEVVDIFACSGGPEVQIGDMTSGIHQMEITTGLKRKRTSSAGSTRSKLLNKLQDGSASVTSTSTSKKVKGAEL
PTSAVVENPLGGVVEDVEDSGVGPSIVINPFNAAFINMAQAQDYTGTVDPTSSDENQQGNLEKPKPAPKGRGRPKKAPRG
RGKAKASAFQRRTTTAEPVYERVVVHASPKKRTQVFKAPVAQDTTGPSDSIDLGAVQTWIEQTADHMKNAVKARNLSPTK
MMHQIGTYIADDVPSSDIRDWYENPHIKGDLITLVQALSALEADFGLPPDWKRALERLSDVRAMVNEAQKECSVQAEELG
TVEEHILWVINTQRDNNATALDAQLTALEDHEYKSARNKVLIHLAHLTNTKKLQKIHLRSFKLHLQMASRELAKALLQKH
APGPTQPPARRRSKPFPATKKKSKKQKPNAQAVVATTVSLRPMDDTDMDIDHDVHEDEQSDGIEQSDENQRIRDILRQGF
NAKAHRHEMPASLPPPSTLITPARCDTCADVGTIWTCTVEDCNTKLCIQQDGPGCIRIFDRHTTKETFMCPRCMCARRLP
MPYKVESYVQAHLFLQRSENAMWAAFLTWGRDRTYGEDIISRSLAEHFGNTAEDLHIVKRAIRKGNNQPKVLIPNINWMA
RAQHQNDVLVGFSPQLRVLLSYLGEPFLEAMAKIEASIKEGYTIIRGLTILSCGPTVRNHQSFARLHALVNESVFDFVFA
FGGQSTIDHIVVPALMRFVENVYIYCMDPWTGLLQSFGEDRHALDSTPVALIWAEYEPIENERLKRKDVNTRVLALSNPL
RRPWGIEFWRCKRCHRGMQYLKFNLCGKRHFGDEWGRNKLRYNCSGCGHEERGIARPEWITVIKGRRDLVSLPWPLTPEQ
LSAFGVQDAQPLYH
```

249 - 268:	EEEEEEEEEEEEEEEEEEEE
250 - 269:	EEEEEEEEEEEEEEEEEEEE
251 - 270:	EEEEEEEEEEEEEEEEEEEE
252 - 271:	EEEEEEEEEEEEEEEEEEEE
253 - 272:	EEEEEEEEEEEEEEEEEEEE
254 - 273:	EEEEEEEEEEEEEEEEEEEE
255 - 274:	EEEEEEEEEEEEEEEEEEEE

256 - 275:	EEEEEEEEEEEEEEEEEEEE
257 - 276:	EEEEEEEEEEEEEEEEEEEE
258 - 277:	EEEEEEEEEEEEEEEEEEEE
259 - 278:	EEEEEEEEEEEEEEEEEEEE
260 - 279:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE
262 - 281:	EEEEEEEEEEEEEEEEEEEE

A0A0C9XAW7 **A0A0C9XAW7_9AGAR** (1068 aa)
Stress response protein NST1. *Laccaria amethystina LaAM-08-1*

```
MAYPAQQQQQQQQPRSARAASKAPLPYQHQQQQQQHRNPSPSSKGKPSPNKIWSTSTTEERERIKDFWLGLGEEERRNLV
KIEKDTVLRKMKEQQKHSCSCAVCGRKRNAIEEELEVLYDAYYEELEQYANYQQRYVSSGGTIPPPPGPGPFPGSVELDK
NGAVVHPSPKQRSKKSVVPPVLNGRKPPHTHPPPPPREGEFEDEDPEEDEYEEEDEYEEEEEEEEEEEEEEEEEEEEQQ
QQQPQRRAANGRKPVAAARRAPPTQQKPTPPTAPSPNGTVPSKAGRDGLFNIGSSLTATGPGNILTVADDLLKNDGQKFL
EMMEQLAERRMQREEEAAADVEDDSEEESDRDPNDESDDNDEDEDEEVSDEDDEDDEEDEDEEVMTEEQKMEEGKKMFSI
FAARMFEQRVLQAYREKVAQERQLQLLRELEDEDKLSKEREAKKQTQNQKKKDKKKQQKQAKEEERAAKAAEKAAEDAAL
KARQVAQEEENRKKKREEDRVKREASRKAAEEEKARKEEERRKRALEEREREQERERKKKEKEERTRAERKEREERERNAR
IAKEKEERERVERQKKEEREKRAAKQKEEERAEKEAREKQAAAMQKAAAVSPNGKGPSRMNAASSSSSSISSLSTPVKGN
AAASGSAPPLQRSPNTSGHGASSSSNGPSSSKKAVNKATPVITPPVSTPANPTAPPRQQQQHASRVQQQQHQNQPQPLSM
APTPISTTLLPPPPQSAPGMMFAQGSLGGMIPPLAMSPRPGSFAPPVPYPFSAQNMQHQQRGFNGGPHPTPPFDHPYPRG
MPLGVLPQHHPPPIQPPPPQSAPSPIGPPPKAKTPLPLSVPPSISAPGPSMLLAPGQGRRGSVPILGGSSGDVGGPSGPG
PITRPIIAPIARPGTGEGASSSSITNNAPGTTSSGSGSPIRRSPSPKGMLLGSSALAADDDEVVSPTTSRRATAPIGIGI
GLGLGVGAVGQGWGPASPRTALGMGEQIPLRGAGGGPWGPPPGFGRGHMHQQVGQQQVPTGNLWGTPPPPNNSEWHPPGT
FFPPHTPAAYMVGHNPSTATATQHTSGN
```

218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE

A0A0D0C6R3 **A0A0D0C6R3_9AGAR** (1131 aa)
Unplaced genomic scaffold GYMLUscaffold_15, whole genome shotgun sequence. *Gymnopus luxurians FD-317 M1*

```
MFLFSRSHSRSRQPTPETNNYSDSPPSGDPESLVENGDLSERPISHSPAGMSRDSEGYPSWLPKRPPPPAPASTFASSTG
GHEPIPPPTPSPMLGGRKPTPRSVRIVSLEQHEAEKARVPTDHTRVPSNHRIWSRATGSAFTPTAFSLDPYNPRLPQPRF
RSRGANLDVLQNPSSLARLYFYLSYIFLFAHIPLQTFFDFNAVFILIQVSKFPNPQGPGVPGSGRNWALGAAAYVASWLA
WILVVCIMYELVYSFIRRWRTKRPAIYPIYLSASAFTFASLTSYSNFCFLQHLRYAAFFGQHGGIRDGLAETFWFYSQNL
PTVALLLPRAGLSLALLFSFSSPVPGDITLTDAGVSVRDATFFRGNGALTDYARGVLIANAAWTAWKILVLFTSWVGLWV
VSGQGCAGLCGPRYRWEEEDAEKTITSIYSVDNLSDSEQPLPWSWKENTRMRILDAYDFCSVTARPGSGRWGHAKKPSDM
SDLLGTAYPLPVPESSKGFEGMDRLMAAVGLPGDSHIHQPRRGILSDDLFTQPEAGPSGFKGNYEVPSDFAAVIPKVVQR
ASRDKDLASPSAPLMKLPYPFTAPGAAQMSSEDERIPFPPSPSVPSFKESSSGTKSRSRTHGTTEEDNEEEEEEEEEEE
EEEEEEEEETPNTSSEDPSSSSGRGSNSMSSLGHPVSSRYPFQFRQPTRGTSFSSGVPSHATPPSNGHSIASRFSQGTRS
TGNRESTDSHSPRSHYTTSGSDAPSPMSMSGLPMPPRHPQTYQGRGRARAGTVPVPSVPSSPSIDFPRRARARTRTSDPY
NASSPEPAIWSSDVERDEDAADESHIEDSIMEQPEPEGSQEAAEGEDVVGLLSPSRGPSPRTSLTALRHRASAISSHHRR
SFGAGSGSGSRSGSNSRTNSHSGSSSGSRSRAGSISVAMTVRSRAQSLMQNVGSASRSSLELVQGAIRSRANSSMARLEE
DSPYYSDRTHSRSGSGSDGVLSSQENYTFGQPLRTQWQSQAERVEEEVSPATGSFSTSSPTAGPEVHDTSSQQPLTATSE
AAPPSPHPSESTMHQELRSEPSGLTIPGAGRQTESVSAYSSHPDISTAAASFVTAPATVEGSTTDESGRTPPSWGGITHM
VDRSDGTWRPA
```

629 - 648:	EEEEEEEEEEEEEEEEEEEE
630 - 649:	EEEEEEEEEEEEEEEEEEEE

A0A0D0CNA3 **A0A0D0CNA3_9AGAR** (101 aa)
Unplaced genomic scaffold GYMLUscaffold_47, whole genome shotgun sequence. *Gymnopus luxurians FD-317 M1*

```
MAHYKQASSIAKLVAKHYLGFAKPTFKVFEANLFGPGIDYRSPGESFLLGDRLEQLAGHTLQKKTDDSNDDDHSDDEEEE
EEEEEEEEEEEEEEEEEEEEM
```

77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE

A0A0D0DKB2 **A0A0D0DKB2_9AGAM** (1163 aa)
Unplaced genomic scaffold scaffold_850, whole genome shotgun sequence. *Paxillus rubicundulus Ve08.2h10*

```
MAAAHPPSTPHSTSSSSAPTPPLLSSVTSSAKVASAGDHIYKGKYTNRSWQQLPPELVRTIATHYLLDVAGLSYCPLTWD
AKELWHPRIVYTTFRDANALEKLMQVTPTWAAALEIHLFWDKACAVLDPHDVLANFRYVRPQPLPSGAGGATPAHPQQTY
RITPYHHFRQMTTRSCFVCRINSPFSSVGLAAAKRTHNVPNLGTIALCRDHRKTMFCGLCLREAPPAECDPQFDIHGNTM
RFTPYHQPYAPAGNLNIGIGAYNPYANAINPALMVCCAENEDDETWPGIDTTCRACRSESLWQRISISLRDREAVGGPRF
IPSSSRSSPAKDRQVITTVSRYPPAKYASVDWETRQTVDAFIELGEGSISEVIAVAREKFWLRSQTKMPELMEQAVAATR
WAGEGMGVDFTPHTPVINQHRQEANSHHLESSGGVDMSQETDVGIDVADTYSTSPSPPSPRSAQRSRSPSPRSVYSSEYE
GSEEEEDPELLSLTEDASGVRELAISDWARTRILDGHWCSPADQWYGYAWPAGGGVRDAGEETESEPDPNEELREGCTVR
RTTRVEAVHPCPLTISSSSPSFSLPSSPTSEMDDMHPRSSTVRAQVPPSFALCEQAYRAYQKQLRLILLPPMNNLVRKFV
```

```
IEYSSGIAGDPAVRAARMELEEVLAELRAPGVWFDGVDWAAGGLVSNGERERQRRREGEREREEDSASSASSRSDGSHTT
SPVLSTTTLQTTPSPPPAHNDDKDKKTNSIGNTSTVKAGQRSPPVVIPIPVSPVLESPRLIHPVPYVPVTLAHMAQFSLE
AFKIVWREACAPLFHCRCTICERAMIHASAAAGHAVPSQAQPQSAPLVVSQPPQRPQQAQQPQPQPTEIALEEVRVVSRE
HPLAEEEEEVAEEELYEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEQSEDDFSSLDDGGDAVTHRHPAVD
NAHTVTPRKRSSGDLEADSIVSAGEEVGVPRVGTPPKRARTGAHIMPSHGLNTPATKTTENGGTPNSRSKRLEREGSILS
SMLEVSPPRQRKRSSEELELSGGSSSPSSSDGTDQHIGSLQKRLRVESSSPGMKNTATATPRAMFASPPSSATVTSVSPS
EEEDKGESGGYVDVGLSEGDISTLKTGLVNGGELDGLYVFEET
```

897 - 916:	EEEEEEEEEEEEEEEEEEEE
898 - 917:	EEEEEEEEEEEEEEEEEEEE
899 - 918:	EEEEEEEEEEEEEEEEEEEE
900 - 919:	EEEEEEEEEEEEEEEEEEEE
901 - 920:	EEEEEEEEEEEEEEEEEEEE
902 - 921:	EEEEEEEEEEEEEEEEEEEE
903 - 922:	EEEEEEEEEEEEEEEEEEEE
904 - 923:	EEEEEEEEEEEEEEEEEEEE
905 - 924:	EEEEEEEEEEEEEEEEEEEE
906 - 925:	EEEEEEEEEEEEEEEEEEEE
907 - 926:	EEEEEEEEEEEEEEEEEEEE
908 - 927:	EEEEEEEEEEEEEEEEEEEE
909 - 928:	EEEEEEEEEEEEEEEEEEEE
910 - 929:	EEEEEEEEEEEEEEEEEEEE
911 - 930:	EEEEEEEEEEEEEEEEEEEE
912 - 931:	EEEEEEEEEEEEEEEEEEEE
913 - 932:	EEEEEEEEEEEEEEEEEEEE
914 - 933:	EEEEEEEEEEEEEEEEEEEE
915 - 934:	EEEEEEEEEEEEEEEEEEEE
916 - 935:	EEEEEEEEEEEEEEEEEEEE
917 - 936:	EEEEEEEEEEEEEEEEEEEE

A0A0D0DXT7 **A0A0D0DXT7_9AGAM** (507 aa)
Non-specific serine/threonine protein kinase (EC 2.7.11.1). *Paxillus rubicundulus Ve08.2h10*

```
MKLDATDLRYITSDEFRVLTAVEIGSKNHEVVPTPLIVQISGLRNGGVNKIIGSLAKRNLVAKVQNSKYDGYRLTYGGYD
YLAMRALSKRDSMYSVGNQIGVGKEADVYIVADGEGNEMVLKLHRLGRISFRAIKEKRDYLGKRKSASWMYMSRLAAQKE
WAFMKILHEHDFPVPRPVDQARHCILMEAIDAYPLRQITDIPSPGKLYSTLMDIIVRFARAGLIHGDYNEFNILIRRESG
EPVVIDFPQMVSTSHENAEWYFNRDVECIRTFFRRRFNYESALYPRFKAIKPGHEKEGERFQLDVMVAASGFTKKDQKVL
EEYMERAEGEGPGEGDDDITTEEEEEEEEEEEEEEEEEEEEGEEEGEGEEKEEEEGHVRQGMDQEGGTDDYHTKLCGQAL
AEEGEMCSRSLHGGSAPPSRPSTPLSQLSRSPPRSRSPSPDTLAKMTAALSLRSSDVRERVATDLAKHARQQKKYHTKRG
AQRVGRPQGSKAKQDQRVKLDRGGMWD
```

342 - 361:	EEEEEEEEEEEEEEEEEEEE

A0A0D0E1Y0 **A0A0D0E1Y0_9AGAM** (1370 aa)
Vacuolar import and degradation protein 21. *Paxillus rubicundulus Ve08.2h10*

```
MLSESIESLVAERVAELEAIAQRKNELIREVRHMMRREHQAGSVLSLDTINDGNEDEDEDERLREFLDTSDLHKNPESGM
VSSLPRSKLFIPSSLLPSKDIVEETEKQGPAEVDSPMSEPPASPARIKSPMSEEGAKELEPNTLTDSSEVADSPAPSWST
PSRKRPREDDEAEAEEAEEEEEEETGEEEEEEEEEEEEEEEEEEEEEEEEEQSEEEVPLDVQACVHSSSRSPSRPVSSS
ARRSPSVSRRSSPCQSQFMLSQSPQRVSVGPEVSETHEMGTSGAMEDVLKSSPVLMHPPSSPIFVQREPNHDTVASSIVA
VSPSPEPLGQRPMVIRTAVDIGTIHPSLLIPTPTSPAPALPDFSFEEPEAEGIEEASQENSPGIKRHHFNPAYNLPPLKA
LPPDYLRKGRSSKQKKKDKDRADNKGGREEWAPIGFVKWGALVRANPIHKKVSRAAKCLSTKDWGVAMTELRLMRTLERV
ESLENVAKWSYRQPKKQRNLGGMIKTHWDYLLDEMKWMRVDFREERKWKHVLAFNLSTAVLEWHEAKNREERIQLGICMH
WKRPRTSTAASTHSQPQPHDMDVDGASVEPGEKESAYSDRESGDEDDDGEVEQRDVIDPLEVRNELQEALERRGSRSGSG
SGESGESSQRQSMGPEGSVKPKVEDVEDSSALKNESGGGAGDAMDVDGEGELGQGAGGGTTKTEVIDLVALKLNSNDPVL
GLLASSEPPINNHPVPGSSKHVPKSNLYAPLREKLAYSGDKKLFVDNDDVDLVKALSDLTTEDSTPPFPSFAPTHNASDL
SDLFPDLQLLGIPDPAPFGSGSKKKSDKKSEREDSRRVDDSGYTKMAPMGKFMLCKPTLLGPLQPAKRWKKGRWFPPEEP
AVTEVEASSNKISEEHLSELFDGVKPQLIGGTIVPHPPKDNKKRLEHAWSAAEDVLLKSLVDKYPSNWTLVAESFNSARV
TISIDRRTTWECFERWNLKFGSAMATGRLTGVGGHVDASPPAGADGTPPPATPSSSQPVQMTTRGVKRLASINVTQNQVG
GALSSDMMKRRRHTLMYETIRKAAKRREAAQKAASVNQRKPPNIHDTHGQYSKMPKLTPAELSRMKAEKESREQQDMLTR
RRQEDMARQQLLRTQGPSQVAAAVAAQHQPQQPQQASSAPRLASQPAQTVPQIRAPPVPQVNISQQRIPTPIAATGAARM
LPQQMLQVQAAQARANAITAQSQAHAQFQAQTQAQAHSTPQLTANSLPASAHLSPPYQSRAATSSPGVGVTQQASPPRNV
VTPSNAGISATSPRPPSAQAQPQQSIQAAQIAGNAIPRPAGSIPAHYFPVVPTAPHFTQDQMDKALMFSNPMQRTSMAQA
QQGAQYPSQS
```

187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE
190 - 209:	EEEEEEEEEEEEEEEEEEEE

191 - 210:	EEEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE

A0A0D0T502 **A0A0D0T502_9TREE** (1260 aa)
Unplaced genomic scaffold supercont1.6, whole genome shotgun sequence. *Cryptococcus gattii VGII Ram5*

```
MSGFTPALGLHHTHSSSVLPTISNVTEPNPPTSSQPHQLAAYSCLYTISPNYASKITNESSCSSSTTHYGFKYVRPSTSP
LLKPPKGKSFSAYLGDWGSQELFTFLDIHKCGQYLAIFQKNDINGKILLDLDAAALKSMGIDKISERVRLIGGIKDLRRR
VTDESIRAPFTLCRCSPERTLLPILPSHSNVLLDRWDCSSSTSCLGKRQITFRPPPLDLRGHMPPRLSNHSSQSIASIDT
HDIHTTNPKIGAYVQQYPLDQPQSVSTNRSDSLTLRAPPSRNIGRRSPSPRHVEGCESQTDSFTTLNVASDQQVLSSTVN
SLTLREDCHLQREEGLPLFLKVPHFRNTFTSSHKTLLSGRSDLAGGDTTSHQPSGPAIAEEDNHRRCRIPDIITSIKGTS
QEDLNHPFAVKSSKSQSGMLTGVCDMVHGPMADGTKPKGKASVPLTGISSPSAVNANSAALSLADLRRQLVKFINTEDDT
IRTVNVMHVTSGVEILERALKKFGKWGTGMHSGPDVYSDDDANGTLEIDGWGVYTESTPDESSKPLSESSLLQKCTFHRE
ETAIPDKGLFLHKKKRWQKRKNIHDFFGETPPPLMSPTLPTLFTGPRLGLVQNKSQPASESALSSSTRLSTSTNKGPNRA
STISVMSGLGVPITCTLPSPQGNGLRLTGQVNSHKKKSMYNFFGHRPPSELISNHLADYFPSAKKSDVEKARHSLLRLSG
GTSAYQESWIDEGDDAPDYWSKPGSSQPPLLPPFEPSRDTLSDSLQAYASTAIHLSRPKRNTALRRRRDSDSSSRSHMSV
LMQTRLNRDHSDTASLLTVDEITAEVEHRRTSAVLKENCIEETKGSPAFERDMLPKYEERKGLLHAVCSDSNSNVADGQS
YRGNSDLDPEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEEEEEDEENEQGKAFTSTGSKRIIKWIKGALIGAGSF
GSVYLGMDAQSGLLMAVKQVELSAGSAKNEDRKRSMLSALEREIELLKELQHENIVHYLGENSPLMETIWTLTPYQDSSV
DTNHLNIFLEYVPGGSVAALLNNYGAFEEALVRNFVRQILTGLNYLHMRGIVHRDIKGANILVDNKGGIKISDFGISKKV
ENSLITGLRTNRPSLQGSVFWMAPEVVKQTSYSPKADIWSVGCLVVEMLTGTHPWADLTQMQAIFRIGSLARPAPPSDIS
VQADEFLRKTFEIEHTKRPTAAQLLKHPFIGSPRLRATSSNFINGAIVSEKMKVQIVEEM
```

893 - 912:	EEEEEEEEEEEEEEEEEEEE
894 - 913:	EEEEEEEEEEEEEEEEEEEE
895 - 914:	EEEEEEEEEEEEEEEEEEEE
896 - 915:	EEEEEEEEEEEEEEEEEEEE
897 - 916:	EEEEEEEEEEEEEEEEEEEE
898 - 917:	EEEEEEEEEEEEEEEEEEEE
899 - 918:	EEEEEEEEEEEEEEEEEEEE
900 - 919:	EEEEEEEEEEEEEEEEEEEE
901 - 920:	EEEEEEEEEEEEEEEEEEEE
902 - 921:	EEEEEEEEEEEEEEEEEEEE

A0A0D0TU55 **A0A0D0TU55_9TREE** (733 aa)
Telomere replication protein EST3. *Cryptococcus gattii VGII Ram5*

```
MAEDIRSWITKALIDHDTAHGANFRVPVNCKHYCQLLKFYTYRDDKNPRAQIEGSIGDRTHCVKVIFDIEETDRFELPDP
DTGYKHSLTSQLRSIFQIKQFHIRIAPPSSSAGAKIPLVAFYVTKWDVVSGNHDEPVYWLDTCKVGEGNNDEKIREVLQK
WWFGESNSESSQNRSSQKILSQDNIPDMSIITARPKVENDVAYHRTSVALGDIISIEEAKASRVGEWDPRFALAWLERNQ
DTVLNTYAQYRNYSSNNIETIDSSQRFQGKTVSNQPSGNGHPPKSQPVDVASRDSGTPRLFNKRSPSSSSQSHHASSPTF
LRVSPSKRQLLRKKIIDPLNSPSSPATSMSPGSIDEELLSQYEREERRKRSGKSKGIKGDGDKEMEQRSPSPSPLSQSSS
VFHSSPTIATPRGLEGELIQTDRPSPELSSAQNATISNARDKWKRPRESMNSRRQSRVVILDEDEDIDEGPLIKKGSKRK
LILSSPEPPSQVIEKRDSSDDEENVAETSSSPTTQGGTRGDAEHTVTELQDLMPRTKEVTRPIKTLSSSSVLNEIEEEEE
EEEEEEEEEEEEEEEEEEEGEEEEEEEEEEEEEEEEEEEEEEEEVEEEEEEETEKDKKIEEKEEGERLQTDKKGKGTQYE
RSTRMDLLGMEKKKEKREPQTSFPVPEGETENFQRKRKNRTEDPTSSQQVPKFGGFKLDMTLREGGLDGACVLQMLEWAR
EKRQEIAKRAKKP
```

556 - 575:	EEEEEEEEEEEEEEEEEEEE
557 - 576:	EEEEEEEEEEEEEEEEEEEE
558 - 577:	EEEEEEEEEEEEEEEEEEEE
559 - 578:	EEEEEEEEEEEEEEEEEEEE
560 - 579:	EEEEEEEEEEEEEEEEEEEE
581 - 600:	EEEEEEEEEEEEEEEEEEEE
582 - 601:	EEEEEEEEEEEEEEEEEEEE
583 - 602:	EEEEEEEEEEEEEEEEEEEE
584 - 603:	EEEEEEEEEEEEEEEEEEEE
585 - 604:	EEEEEEEEEEEEEEEEEEEE

A0A0D0WHV6 **A0A0D0WHV6_9TREE** (4238 aa)
Unplaced genomic scaffold supercont1.2, whole genome shotgun sequence. *Cryptococcus gattii EJB2*

```
MLPPQRIRPPGPYNRFPPAEVHAWLDGLQQKIANGIHPPESPLSSPSPVQQQEQDEQDVFGDVAQLHDTRGTQGNLVGSV
WTEEEAREEQEQPGQAVAGFLDQNPDEQQEEDEEEGHEQEEEGGFRGYPDNAQYSAYPYDKEEQDELYEDHGDFDPGYGV
FPEEDNQAYVESDGDAYAGAYASGSEDEGEDEQQWQQQEEEEEERSESPTKQEDDGDESDGIEYIGQSNSPQPPQPAPQS
QPQSQPQALPPFPLQTNLYPPLPDAPTPYADPGAPLATASPAVPPLGGGRALTVEQDAMQIDPSLLQDGYQIDTGFLQDL
VHHVSQGMPPPPQEGDEENEEDEDVVYYEEEEEDEVEDEEEEEDGVYDEDFIMSGDEREQPRNVQQYSEEEEEEEDEEEE
DELVDEPSFEEQASPVKVQPTTIREVIEIGSSSEEEESGEESEVERREAVGRDEEEVEYEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
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2756 - 2775:	EEEEEEEEEEEEEEEEEEEE
2757 - 2776:	EEEEEEEEEEEEEEEEEEEE
2758 - 2777:	EEEEEEEEEEEEEEEEEEEE
2759 - 2778:	EEEEEEEEEEEEEEEEEEEE
2760 - 2779:	EEEEEEEEEEEEEEEEEEEE
2761 - 2780:	EEEEEEEEEEEEEEEEEEEE
2762 - 2781:	EEEEEEEEEEEEEEEEEEEE
2763 - 2782:	EEEEEEEEEEEEEEEEEEEE
2764 - 2783:	EEEEEEEEEEEEEEEEEEEE
2765 - 2784:	EEEEEEEEEEEEEEEEEEEE
2766 - 2785:	EEEEEEEEEEEEEEEEEEEE
2767 - 2786:	EEEEEEEEEEEEEEEEEEEE
2768 - 2787:	EEEEEEEEEEEEEEEEEEEE
2769 - 2788:	EEEEEEEEEEEEEEEEEEEE
2770 - 2789:	EEEEEEEEEEEEEEEEEEEE
2771 - 2790:	EEEEEEEEEEEEEEEEEEEE
2772 - 2791:	EEEEEEEEEEEEEEEEEEEE
2773 - 2792:	EEEEEEEEEEEEEEEEEEEE
2774 - 2793:	EEEEEEEEEEEEEEEEEEEE

2775 - 2794:	EEEEEEEEEEEEEEEEEEEE
2776 - 2795:	EEEEEEEEEEEEEEEEEEEE
2777 - 2796:	EEEEEEEEEEEEEEEEEEEE
2778 - 2797:	EEEEEEEEEEEEEEEEEEEE
2779 - 2798:	EEEEEEEEEEEEEEEEEEEE
2780 - 2799:	EEEEEEEEEEEEEEEEEEEE
2781 - 2800:	EEEEEEEEEEEEEEEEEEEE
2782 - 2801:	EEEEEEEEEEEEEEEEEEEE
2783 - 2802:	EEEEEEEEEEEEEEEEEEEE
2784 - 2803:	EEEEEEEEEEEEEEEEEEEE
2785 - 2804:	EEEEEEEEEEEEEEEEEEEE
2786 - 2805:	EEEEEEEEEEEEEEEEEEEE
2787 - 2806:	EEEEEEEEEEEEEEEEEEEE
2788 - 2807:	EEEEEEEEEEEEEEEEEEEE
2789 - 2808:	EEEEEEEEEEEEEEEEEEEE
2790 - 2809:	EEEEEEEEEEEEEEEEEEEE
2791 - 2810:	EEEEEEEEEEEEEEEEEEEE
2792 - 2811:	EEEEEEEEEEEEEEEEEEEE
2793 - 2812:	EEEEEEEEEEEEEEEEEEEE
2794 - 2813:	EEEEEEEEEEEEEEEEEEEE
2795 - 2814:	EEEEEEEEEEEEEEEEEEEE
2796 - 2815:	EEEEEEEEEEEEEEEEEEEE
2797 - 2816:	EEEEEEEEEEEEEEEEEEEE
2798 - 2817:	EEEEEEEEEEEEEEEEEEEE
2799 - 2818:	EEEEEEEEEEEEEEEEEEEE
2800 - 2819:	EEEEEEEEEEEEEEEEEEEE
2801 - 2820:	EEEEEEEEEEEEEEEEEEEE
2802 - 2821:	EEEEEEEEEEEEEEEEEEEE
2803 - 2822:	EEEEEEEEEEEEEEEEEEEE
2804 - 2823:	EEEEEEEEEEEEEEEEEEEE
2805 - 2824:	EEEEEEEEEEEEEEEEEEEE
2806 - 2825:	EEEEEEEEEEEEEEEEEEEE
2807 - 2826:	EEEEEEEEEEEEEEEEEEEE
2808 - 2827:	EEEEEEEEEEEEEEEEEEEE
2809 - 2828:	EEEEEEEEEEEEEEEEEEEE
2810 - 2829:	EEEEEEEEEEEEEEEEEEEE
2811 - 2830:	EEEEEEEEEEEEEEEEEEEE
2812 - 2831:	EEEEEEEEEEEEEEEEEEEE
2813 - 2832:	EEEEEEEEEEEEEEEEEEEE
2814 - 2833:	EEEEEEEEEEEEEEEEEEEE
2815 - 2834:	EEEEEEEEEEEEEEEEEEEE
2816 - 2835:	EEEEEEEEEEEEEEEEEEEE
2817 - 2836:	EEEEEEEEEEEEEEEEEEEE
2818 - 2837:	EEEEEEEEEEEEEEEEEEEE
2819 - 2838:	EEEEEEEEEEEEEEEEEEEE
2820 - 2839:	EEEEEEEEEEEEEEEEEEEE
2821 - 2840:	EEEEEEEEEEEEEEEEEEEE
2822 - 2841:	EEEEEEEEEEEEEEEEEEEE
2823 - 2842:	EEEEEEEEEEEEEEEEEEEE
2824 - 2843:	EEEEEEEEEEEEEEEEEEEE
2825 - 2844:	EEEEEEEEEEEEEEEEEEEE
2826 - 2845:	EEEEEEEEEEEEEEEEEEEE

2827 - 2846:	EEEEEEEEEEEEEEEEEEEE
2828 - 2847:	EEEEEEEEEEEEEEEEEEEE
2829 - 2848:	EEEEEEEEEEEEEEEEEEEE
2830 - 2849:	EEEEEEEEEEEEEEEEEEEE
2831 - 2850:	EEEEEEEEEEEEEEEEEEEE
2832 - 2851:	EEEEEEEEEEEEEEEEEEEE
2833 - 2852:	EEEEEEEEEEEEEEEEEEEE
2834 - 2853:	EEEEEEEEEEEEEEEEEEEE
2835 - 2854:	EEEEEEEEEEEEEEEEEEEE
2836 - 2855:	EEEEEEEEEEEEEEEEEEEE
2837 - 2856:	EEEEEEEEEEEEEEEEEEEE
2838 - 2857:	EEEEEEEEEEEEEEEEEEEE
2839 - 2858:	EEEEEEEEEEEEEEEEEEEE
2840 - 2859:	EEEEEEEEEEEEEEEEEEEE
2841 - 2860:	EEEEEEEEEEEEEEEEEEEE
2842 - 2861:	EEEEEEEEEEEEEEEEEEEE
2843 - 2862:	EEEEEEEEEEEEEEEEEEEE
2844 - 2863:	EEEEEEEEEEEEEEEEEEEE
2845 - 2864:	EEEEEEEEEEEEEEEEEEEE
2846 - 2865:	EEEEEEEEEEEEEEEEEEEE
2847 - 2866:	EEEEEEEEEEEEEEEEEEEE
2848 - 2867:	EEEEEEEEEEEEEEEEEEEE
2849 - 2868:	EEEEEEEEEEEEEEEEEEEE
2850 - 2869:	EEEEEEEEEEEEEEEEEEEE
2851 - 2870:	EEEEEEEEEEEEEEEEEEEE
2852 - 2871:	EEEEEEEEEEEEEEEEEEEE
2853 - 2872:	EEEEEEEEEEEEEEEEEEEE
2854 - 2873:	EEEEEEEEEEEEEEEEEEEE
2855 - 2874:	EEEEEEEEEEEEEEEEEEEE
2856 - 2875:	EEEEEEEEEEEEEEEEEEEE
2857 - 2876:	EEEEEEEEEEEEEEEEEEEE
2858 - 2877:	EEEEEEEEEEEEEEEEEEEE
2859 - 2878:	EEEEEEEEEEEEEEEEEEEE
2860 - 2879:	EEEEEEEEEEEEEEEEEEEE
2861 - 2880:	EEEEEEEEEEEEEEEEEEEE
2862 - 2881:	EEEEEEEEEEEEEEEEEEEE
2863 - 2882:	EEEEEEEEEEEEEEEEEEEE
2864 - 2883:	EEEEEEEEEEEEEEEEEEEE
2865 - 2884:	EEEEEEEEEEEEEEEEEEEE
2866 - 2885:	EEEEEEEEEEEEEEEEEEEE
2867 - 2886:	EEEEEEEEEEEEEEEEEEEE
2868 - 2887:	EEEEEEEEEEEEEEEEEEEE
2869 - 2888:	EEEEEEEEEEEEEEEEEEEE
2870 - 2889:	EEEEEEEEEEEEEEEEEEEE
2871 - 2890:	EEEEEEEEEEEEEEEEEEEE
2872 - 2891:	EEEEEEEEEEEEEEEEEEEE
2873 - 2892:	EEEEEEEEEEEEEEEEEEEE
2874 - 2893:	EEEEEEEEEEEEEEEEEEEE
2875 - 2894:	EEEEEEEEEEEEEEEEEEEE
2876 - 2895:	EEEEEEEEEEEEEEEEEEEE
2877 - 2896:	EEEEEEEEEEEEEEEEEEEE
2878 - 2897:	EEEEEEEEEEEEEEEEEEEE

2879 - 2898:	EEEEEEEEEEEEEEEEEEEE
2880 - 2899:	EEEEEEEEEEEEEEEEEEEE
2881 - 2900:	EEEEEEEEEEEEEEEEEEEE
2882 - 2901:	EEEEEEEEEEEEEEEEEEEE
2883 - 2902:	EEEEEEEEEEEEEEEEEEEE
2884 - 2903:	EEEEEEEEEEEEEEEEEEEE
2885 - 2904:	EEEEEEEEEEEEEEEEEEEE
2886 - 2905:	EEEEEEEEEEEEEEEEEEEE
2887 - 2906:	EEEEEEEEEEEEEEEEEEEE
2888 - 2907:	EEEEEEEEEEEEEEEEEEEE
2889 - 2908:	EEEEEEEEEEEEEEEEEEEE

A0A0D0XJZ5 **A0A0D0XJZ5_9TREE** (794 aa)
Unplaced genomic scaffold supercont2.10, whole genome shotgun sequence. *Cryptococcus gattii VGIV IND107*

```
MADDIRSWITKALIDHDIKHGPNFRVPVNCKHYCQLLKFYTYRDDKNPRAQIEGSIGDRTHCVKVIFDIEETDKFELPDP
DTGYKHSLTSQLRSIFQIKQFQIRIAPPPPSAGSKIPLVAFYVTKWDVVSGNHDEPVYWLDTCKIGEGNNDGKIREVLKK
WWFGESNSESSQNRSSQKIPSQDNIPDMSITTAGPRVKNDVTYHRTSVALGDIISIEEAKASRVGEWDPRFALAWLERNQ
DTVLNTYAQYRNYLSNNIETIDSSQRFQGKTVSNEPSGNGHPPKSQPVDVVSRDSGTPRLFNKRSPSSSSQSHQASSPAF
RRVSPSKRQLLRKKIIDPLNFPSSPATSMSPGSTDEELLSQYEREERRRRGESKGIKGDGDKELEQRSPSSSQLSQSSLV
FHSSPTMATPRRLEGELSQTDHPSPDLSSAQNATISNTRDKWKRPRESMSSRRQSRVVILDEDEDIDEGPLIKKGSKRKL
ILSSPEPPSQVIEIRDSSDDEENVAETSSSPTTQGGTRGDAEHTVTALQDLMPRTKEVTRPIKTPSSSSVLNGIGADQRA
VEDGDEVEDKGERKRENGLNDEEEIMEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEEEEEEEEEEKEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEVEEEGKEEIEKDRKIEEKEEGEKLQTGKKGKGTQDERSTRMDLWGMEKEKEKREP
QTSLPVPEGETEHFRRKRKNRTEDRTSSQHVPKFGGFKLDMTLREGGLDEACVLQMLEWAREKRQEIAKRAKKP
```

592 - 611:	EEEEEEEEEEEEEEEEEEEE
593 - 612:	EEEEEEEEEEEEEEEEEEEE
594 - 613:	EEEEEEEEEEEEEEEEEEEE
595 - 614:	EEEEEEEEEEEEEEEEEEEE
596 - 615:	EEEEEEEEEEEEEEEEEEEE
597 - 616:	EEEEEEEEEEEEEEEEEEEE
598 - 617:	EEEEEEEEEEEEEEEEEEEE
599 - 618:	EEEEEEEEEEEEEEEEEEEE
600 - 619:	EEEEEEEEEEEEEEEEEEEE
632 - 651:	EEEEEEEEEEEEEEEEEEEE
633 - 652:	EEEEEEEEEEEEEEEEEEEE
634 - 653:	EEEEEEEEEEEEEEEEEEEE
635 - 654:	EEEEEEEEEEEEEEEEEEEE
636 - 655:	EEEEEEEEEEEEEEEEEEEE
637 - 656:	EEEEEEEEEEEEEEEEEEEE
638 - 657:	EEEEEEEEEEEEEEEEEEEE
639 - 658:	EEEEEEEEEEEEEEEEEEEE
640 - 659:	EEEEEEEEEEEEEEEEEEEE
641 - 660:	EEEEEEEEEEEEEEEEEEEE
642 - 661:	EEEEEEEEEEEEEEEEEEEE
643 - 662:	EEEEEEEEEEEEEEEEEEEE
644 - 663:	EEEEEEEEEEEEEEEEEEEE
645 - 664:	EEEEEEEEEEEEEEEEEEEE
646 - 665:	EEEEEEEEEEEEEEEEEEEE

A0A0D0Y5J4 **A0A0D0Y5J4_9TREE** (772 aa)
Telomere replication protein EST3. *Cryptococcus gattii EJB2*

```
MADDIRSWITKALIDHDKAHGANFRVPVNCKHYCQLLKFYTYRDHRNPRAQIEGSIGDRTHCVKAIFDIEETDKFELPDP
DTGYKHSLTSQLRSIFQIKQFQIRIAPPPPWAGAKIPLVAFYVTKWDVVSGNHDEPVYWLDTCKVGEGNNDGKIREVLQK
WWFGESNSEASQNRSSQKIPSQDNIPDMSITTARPRVKNDVAYHRRTVALGDIISIEEAKASRVGEWDPRFALAWLERNQ
DTVLNTYAQYRNYSSNNIETIDSPQRFQNKTVLNEPSGNGHPPKSQPVDVVRGDSESPHLFNKRSPSSSPQSHHASSPTS
LRVSPSKRQLLRKKIIDPLNFPSSPATSMSRGSTDEELLSQYEREERRKRGESKGIKGDGDKELEQRSPSSSQLSQSSLV
FHSSPTMATPRRLEGELSQTDRPSPELSSAQNATISNARDKWKRSRESMNSRRQSRVVILDEDEDIGEGPLIKKGSKRKL
ILSSPEPASQVIEIRDSSDDEENVAEISSSLTTQGGARDDDEHTVKALQDLMPRTKEVARPIKTPSSSSVLNEIGADQRA
VEDGDEMEDKGERKRGNGLKDEEEIMEGEEEEEEEEEEEEEEEEEEEKEKEKEEEEEEEEEEEEEEEEEEEEEEEEEKEE
EEEEEKEEEEEEIEKDKKIEEKEEGERWKTGKKGKGTQDERSTRMDLLGTEKEKEKREPQTSLVPEGETENFRRKRKNRT
EDPTSSQHVPKFGGFKLDMTLREGGLDEACVLQMLEWAREKRQEIAKRAKKP
```

613 - 632:	EEEEEEEEEEEEEEEEEEEE
614 - 633:	EEEEEEEEEEEEEEEEEEEE
615 - 634:	EEEEEEEEEEEEEEEEEEEE
616 - 635:	EEEEEEEEEEEEEEEEEEEE
617 - 636:	EEEEEEEEEEEEEEEEEEEE
618 - 637:	EEEEEEEEEEEEEEEEEEEE

A0A0D0YGL4 **A0A0D0YGL4_9TREE** (1600 aa)
Unplaced genomic scaffold supercont1.20, whole genome shotgun sequence. *Cryptococcus gattii EJB2*

```
MTPKRKGGKLAKSQSTTTEELSKKPGRPRKAHEFFDVTGASTFNVDPRAATALVKASQDKRSIDFGSVSDDYAPRRKMSR
QKKGRHLIRSSLIGPTVLTMTILDRVGILANVAGDCLLTLLTNGYPPRNRRDSAVDEGKRAWDGLYALKQSYIFSPYSPP
FPLPEDVLSSLSPTISASLRQNPLALNRAVYLSNLATFVWLILRPDEAGDIMGPLDVDEGNDKRVTRSRQGVDTEKEAIK
GRVRRRNALMVAAWKKYWTAIIPRGQHGKEIALRLWLDLVTQIEISYRLQTITSSTESDFLPQIDDVLHDDMFSISSISR
FGLPSDQDTSGDEGDEEMEDHKLYLHDLWGDLSVEREEELPKLELEEARAAYPWDDFQRGMLRFVKDEILGENGEESLLT
PGRRGVLASTQTRTTQTRGESELDSEREESEESPELSQEVAQAPNSPPRPFTDSPTRENSNPGDSPIDFDLLEEIARELA
AEEPNKVDAFPPLTRGSSGNGTGDGSNSRNSPESSSTWAINESTSIPVPSRPSSSRPLSHENQSPKQTTTEKGTGKERSP
LNLFGKKVKMDGFEWNKRQEGAERIAWESQSQSQLSTPRAARQFQEEIQEITITQEQVEKTQEEIESTAYDASDLLPDAR
QFRFTNPRSNLRPDEANEDEGYLEEDVLLDLRQLDRVQQAVGAEEEGYKVDIMLDPRQLKARPSGELVAKQETEDGEEGY
EEDERVLTDPGQFTRTTRSQTRAFQQKETEKATAGASTRAQKAETQIVEEEERDDEHDYNELLGSLKESPTSGQPEQQAQ
TPAGDEDLFFNPNPNFPFDDLPRQAEMDDYDVEDVARAERQAELEAENAYEGTNGDYVVKNTSAERREMSEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEHSPKGKRPYSSAFAAISSSEDEADRQRIFSRHQKSFETMSSQKRST
QPQFLGTSLFSPPTSPDRFPPNRQASAGPGPSTTRNRHAAAQPSSSARSLSFENDESPFQKEDGYVSTTVIDEGDPFLVD
EDGSPLTPSEEYTLPDDRSRQFSFFKSNLYGRTSDKGSRYVRLSGPRRWTKEEELLLWRTVQRLPATQVYPLRVVWYLHG
DGGLLSEKLRWFSVQHMKDKMRTTVMRRLRSGELVEGNARAWAPLGSKEKENWDEEEWDRMNDRALLATQLERQEFEKRK
EAARLREEERRKEEKRRIEEEKKKEREEKKRKLQDEKARLKEDKRKWAEEQKRKREEEKRRKEEEKQKKKKEREKKAK
TKKGTGRQCRESEDERSEESEENENEEQQDEPQEEVDELESRADGSVGSESTTSPPPPKRRTNRASASNINPKRNTKKGS
KIQKGAGAEPSGKSVAAVTRSSSQTNAKGPSSQSRRLMMEAWKSHAAANSEEDDDQENDEFENEDEQTASHLPARPAPFK
TTAARKATNQPVKQNQGAVTARAARKTTSNADGSTGRPINSAYVSSGLSASDLMKQSARKRTQFDEGDLTTEKEGKMDRG
SESEVDELQEELELKSNPELEVLPPESNEEMAEEEGIHPPLGQGTHAMMARSVRSDSSAHATHVPGTQYTDLLSNEAERR
```

871 - 890:	EEEEEEEEEEEEEEEEEEEE
872 - 891:	EEEEEEEEEEEEEEEEEEEE
873 - 892:	EEEEEEEEEEEEEEEEEEEE
874 - 893:	EEEEEEEEEEEEEEEEEEEE
875 - 894:	EEEEEEEEEEEEEEEEEEEE
876 - 895:	EEEEEEEEEEEEEEEEEEEE
877 - 896:	EEEEEEEEEEEEEEEEEEEE
878 - 897:	EEEEEEEEEEEEEEEEEEEE
879 - 898:	EEEEEEEEEEEEEEEEEEEE
880 - 899:	EEEEEEEEEEEEEEEEEEEE
881 - 900:	EEEEEEEEEEEEEEEEEEEE
882 - 901:	EEEEEEEEEEEEEEEEEEEE
883 - 902:	EEEEEEEEEEEEEEEEEEEE
884 - 903:	EEEEEEEEEEEEEEEEEEEE
885 - 904:	EEEEEEEEEEEEEEEEEEEE
886 - 905:	EEEEEEEEEEEEEEEEEEEE
887 - 906:	EEEEEEEEEEEEEEEEEEEE
888 - 907:	EEEEEEEEEEEEEEEEEEEE
889 - 908:	EEEEEEEEEEEEEEEEEEEE
890 - 909:	EEEEEEEEEEEEEEEEEEEE
891 - 910:	EEEEEEEEEEEEEEEEEEEE
892 - 911:	EEEEEEEEEEEEEEEEEEEE
893 - 912:	EEEEEEEEEEEEEEEEEEEE

894 - 913:	EEEEEEEEEEEEEEEEEEEE
895 - 914:	EEEEEEEEEEEEEEEEEEEE

A0A0D0YVH4 **A0A0D0YVH4_9TREE** (1604 aa)
Unplaced genomic scaffold supercont2.6, whole genome shotgun sequence. *Cryptococcus gattii VGIV IND107*

```
MPPKRKGGKLAKSQSTTTEELSKKPGRPRKAREFFDVTGASTSNVDPRAATALVKASQDDRSVDFGPVSDDYAPRRKMSR
QKNGRHLIRSSLIGPSVLTMTILDRVEILANVAGDCLLTLLTNGYPPRNRRDSAVDEGKRAWDGLYALKQSYIFSPYSPP
FPLSEDVLSSLSPTTSASLRQNPLALNRAVYLSNLATFVWLILRPDEAGDIMGPLDVDEGNDKRVTRSRQGIDTEKEAIK
GRVRRRNALMVAAWKKYWTAIIPRGQHRKEIALRLWLDLVTQIEISYRLQTITSSTESDFLPQIDDVLHDDMFSISSISR
FGLPFDQDTSGDEGDEEMEDHKLYLHDLWGDLSVEREEELPKLELEEARAAYPWDDFQRGMLRFVKDEILGESGEESLLT
PGRRGVLAGTQTRTTQTRGRSELDNERQESEESPKLSQEVAQAPNSPPRPFTDWPARKNSSPGDGPIDFDLLEEIARELA
AEEPNKVDAVFPLTHGGSGNGTGDGSNSRNSPETSSTWAINESTSTPVPSRPSSSRPLSHENQSLKQTTTEKGKGKERGP
LNLLGKKAKRDGFEWNKRQERAERIAWESQSQSQASTPRASRQFQEEIQKITITQEQVEETQEEIESTAYDASDLLPDAR
QFRFTNPRSNLRPDEANEDEGYLEEDVLLDLRQLDRVQQAVGAEEEGYEVDIMLNSRQLKARPSGELVAKQETKNGEEGY
EEDGKVLTDPGQFTRTTRSQGRAFQQKETERATAGASTRAQKAETQIVEEEEQDDEHDYNELLGSLKESPTSGQPEQQAQ
IPAGDEDFVFHPNPDFPFDDLRRQAEMDDYDVEDVARAERQAELEAENAYEGTNDDYVVKDTSAEGRGMSEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEHSPKGKRAYSSAFAAISSSEDEADRQRILSRRQKSFETM
SSQKRSTQPQFLGTSLFSPTSPDRFSPNRQASAGPGPSTTRNRHAAAQPSSSARSVSFENDESPFQKEDGNVSTTVVVEG
DPFLVDEDGSPLTPSEEYTLPDDRNRQFSFFKSNLYGRTSDKGSRYVRLSGPRRWTKEEELLLWRTVQRVPATQVYPLRV
VWYLHGDGGRFSEKLRWFSVQHMKDKMRTTVMRRLRSGELVEGNARAWAPLGSKEKENWDEEEWDRMDDRALLAIQLERQ
EFEKRKEAARLREEAREKRKEEKRRIEEEKKKEREEKKRKLQDEKARLKEDKRKWAEEQKRKREEEKRRKEEEKQKKKEE
REKKAKTKKGTGRQYRESEDERSEESEESENEEQQDEPQEEVDELESRADGSVGSESTASPPPPKRRTNRASASNINPKR
NTKKGSKVQKGAGAEPFGKSAAVTRSSSQTNAKGLSSQSKRLMMEAWKSHVAANSEEDDDQENDEFENEDEQTASHLPAR
SAPFKATAARKTTSQPVKQNQGAVTARAARKTTSNADGSTSRPINSAYVSSGLSASDTTKQSATKRTQFDEGDLTTEKGG
KMDQGSESEVDELQEELELESNSELEVLPAELNEEMADEEGIHPPLGQGTHAMMARSVRSDPSAQATHVSGAQYTGDAEQ
AEWR
```

871 - 890:	EEEEEEEEEEEEEEEEEEEE
872 - 891:	EEEEEEEEEEEEEEEEEEEE
873 - 892:	EEEEEEEEEEEEEEEEEEEE
874 - 893:	EEEEEEEEEEEEEEEEEEEE
875 - 894:	EEEEEEEEEEEEEEEEEEEE
876 - 895:	EEEEEEEEEEEEEEEEEEEE
877 - 896:	EEEEEEEEEEEEEEEEEEEE
878 - 897:	EEEEEEEEEEEEEEEEEEEE
879 - 898:	EEEEEEEEEEEEEEEEEEEE
880 - 899:	EEEEEEEEEEEEEEEEEEEE
881 - 900:	EEEEEEEEEEEEEEEEEEEE
882 - 901:	EEEEEEEEEEEEEEEEEEEE
883 - 902:	EEEEEEEEEEEEEEEEEEEE
884 - 903:	EEEEEEEEEEEEEEEEEEEE
885 - 904:	EEEEEEEEEEEEEEEEEEEE
886 - 905:	EEEEEEEEEEEEEEEEEEEE
887 - 906:	EEEEEEEEEEEEEEEEEEEE
888 - 907:	EEEEEEEEEEEEEEEEEEEE
889 - 908:	EEEEEEEEEEEEEEEEEEEE
890 - 909:	EEEEEEEEEEEEEEEEEEEE
891 - 910:	EEEEEEEEEEEEEEEEEEEE
892 - 911:	EEEEEEEEEEEEEEEEEEEE
893 - 912:	EEEEEEEEEEEEEEEEEEEE
894 - 913:	EEEEEEEEEEEEEEEEEEEE
895 - 914:	EEEEEEEEEEEEEEEEEEEE
896 - 915:	EEEEEEEEEEEEEEEEEEEE
897 - 916:	EEEEEEEEEEEEEEEEEEEE
898 - 917:	EEEEEEEEEEEEEEEEEEEE
899 - 918:	EEEEEEEEEEEEEEEEEEEE
900 - 919:	EEEEEEEEEEEEEEEEEEEE
901 - 920:	EEEEEEEEEEEEEEEEEEEE
902 - 921:	EEEEEEEEEEEEEEEEEEEE

A0A0D1DRI2 **A0A0D1DRI2_USTMA** (491 aa)
Uncharacterized protein. *Ustilago maydis (strain 521 / FGSC 9021) (Corn smut fungus)*

```
MADVSSSRASGSKRKALAASAAAASGPKSKKSRSVSEEDASIPLGRALASTEKRIRDGAVRSLQAYLSTNGAHTIPALEL
QKLWKGLFYCFWMSDKPLIQQRLANDLAQLVLVHPATSSTTQDGVSERAIAGLKFLEAFWDTIVAEWSGLDKHRIDKFYL
LVRRFVAAGFRLLAEEKWPSEAVKDFGRILGKSEGGVLSTNDPRVPDSLTYHLSDIYLDELEKVLETHAESEEAKEEEAQ
EEDDLPLVPTLELLMPFVDALATAKSKAMYDRIWSNVLEPLLDDTLRASARDEEDVDLDLTSNDEEESIDEDAEEEPGDE
TANGTEFHSFADESTVTAQDDESEPSIPDSSDSDSEDEGENDVRFPLLLALSSVPAPKIDEDAKDDDEHLDDTHIDVALV
LRKAIFQALFTAASRKDATEARRRLLYQLWRNEQDRLNDLNDGGDEEQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEENDEEEE
```

449 - 468:	EEEEEEEEEEEEEEEEEEEE
450 - 469:	EEEEEEEEEEEEEEEEEEEE
451 - 470:	EEEEEEEEEEEEEEEEEEEE
452 - 471:	EEEEEEEEEEEEEEEEEEEE
453 - 472:	EEEEEEEEEEEEEEEEEEEE
454 - 473:	EEEEEEEEEEEEEEEEEEEE
455 - 474:	EEEEEEEEEEEEEEEEEEEE
456 - 475:	EEEEEEEEEEEEEEEEEEEE
457 - 476:	EEEEEEEEEEEEEEEEEEEE
458 - 477:	EEEEEEEEEEEEEEEEEEEE
459 - 478:	EEEEEEEEEEEEEEEEEEEE
460 - 479:	EEEEEEEEEEEEEEEEEEEE
461 - 480:	EEEEEEEEEEEEEEEEEEEE
462 - 481:	EEEEEEEEEEEEEEEEEEEE
463 - 482:	EEEEEEEEEEEEEEEEEEEE
464 - 483:	EEEEEEEEEEEEEEEEEEEE
465 - 484:	EEEEEEEEEEEEEEEEEEEE
466 - 485:	EEEEEEEEEEEEEEEEEEEE

A0A0D1YYD1 **A0A0D1YYD1_9EURO** (618 aa)
Amidase domain-containing protein. *Exophiala spinifera*

```
MAASTWETIATEAQKSLLASIPPKWRLPGPVNAGITDVRSIPRTCGLLTEKQLEITEQTASELLPKLRNGTLLSVEVTEA
FCARAAIAHQCVNCLTAFFSEEAMARARELDDILSKTGKPVGPLHGLPVGIKDIFHMKGKRLTMGYVAWHDNECTTDASV
VQILRNAGAVFFVRTAMPQTGMFLETWSNLWGRTKNPFNTNFSAGGSSGGDGALVAMRGAPFCPSTDIGGSIRAPGTFNG
LYAIRPTAERTAKRGMGTAAPGQISIKVSCGPNCHSMSDLKLVTEILLTHHGLPFEATAVSMPWKQIEAKQGKLSFGLMT
TDDCVTPHPPIARALQETAAKLRSAGHEVLEFKPPFDCWEIAHATWQLWFQTGARETIDLVKSSGEPIYPTFQWYLDFFR
IKPLTVPELFKLNTKLAECRYDFTRAWHETSARTSTSRPIDALIAPCAPSASFPHGHPVWWGYFSLWNLLDYPSVVMPLK
NMRVDPEKDVKDTNYTPKDNVFDRMNWEIYDPELWKNQPLTIQIVKPQFMDEELISVAETIDGICNADAYIYEDEEDEDE
EDEDEEDEDEEDEDEEDEDEEDEDEEEEEEEEEEEEEEEEEEEEEEEENRWLQSVYDS
```

585 - 604:	EEEEEEEEEEEEEEEEEEEE
586 - 605:	EEEEEEEEEEEEEEEEEEEE
587 - 606:	EEEEEEEEEEEEEEEEEEEE
588 - 607:	EEEEEEEEEEEEEEEEEEEE
589 - 608:	EEEEEEEEEEEEEEEEEEEE

A0A0D1Z3E1 **A0A0D1Z3E1_9EURO** (226 aa)
Uncharacterized protein. *Cladophialophora immunda*

```
MPESPSELNFDSPDLRYGSVMDNNMPDTGERPLALGGPGASFGSGSSVGSARHSRSQPGPNVAQTLTAGLESAIKEDEAR
YRQLSEPNHISEISPWLRKSAFHQYLAGLEAKLVTISHTTPRLDNDNPRLYELVWSIERVLQKAYELVPNLLYVDTWVEV
LTTALGISAKLVELRLREDREITSNTKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDTHLVSEP
```

188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE
190 - 209:	EEEEEEEEEEEEEEEEEEEE
191 - 210:	EEEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE
194 - 213:	EEEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEEE
196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE

198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE

A0A0D2C578 **A0A0D2C578_9EURO** (198 aa)
Uncharacterized protein. *Cladophialophora immunda*

```
MAEWTKRLWKVKGSAEESGPSFLETNIGTSRIDALSRAQQQQRSSFNLSNDDDNVPDPTAISAAKQRSLGAKKKQIEALD
SQTVERVLTWLHCRYYQDPDPVPQAVGNPDETGSGTHTEAEEEEEEEEEEEEEEEEEEEEEEEETEDNQPVGQRNEGVD
ETPVAAGEFDDAPAPIDLVVEPEDRVVLYTARFSYLEP
```

121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE

A0A0D2D7G6 **A0A0D2D7G6_9EURO** (501 aa)
Uncharacterized protein. *Cladophialophora immunda*

```
MNASDTTLVRGWVSQPNGRGTFDLVLSCAVTVFLCSWSSIWVNVPRSDHSKRELFWDKWHMVCLSMLGPEFIFMLALGQY
VRAYDSMKLFHDQGYKSWTIKHGFYANMGGFVFQPSGWKSFPVDAKQVLYLVKRGYIPYPDINEAAIKDKNKSDRLARFV
TSCQIIWFILNVIARATQHLAVTTLEITTIGFIFCTLGVNICWREKPMDVSTVTVLHSEHTIDQILLEGPRAAAQPYRLT
PLDFASREEWNATKLWQYKVNILRRLGVVRQRPRVRPVQNLSSFGFPKPLSRAASAVTLAVALGYAAIFMAAWNLEFPSV
AERLLWLACTSLTTAVTLAVGVIEVVLPAPGDPHQDEEESLHTAVAAGGGGGGGGGGGGEEEEEEEEEEEEEEEEEEEE
EEEEEEEEAGEAQKSHQPSVDGRRRSPRGLLARLADKHFNNSPDKDPALEVPLMSMLFTQPICALYTVCRLYVLLEDIIG
LRALPASTFKTVDWTVYWPHI
```

381 - 400:	EEEEEEEEEEEEEEEEEEEE
382 - 401:	EEEEEEEEEEEEEEEEEEEE
383 - 402:	EEEEEEEEEEEEEEEEEEEE
384 - 403:	EEEEEEEEEEEEEEEEEEEE
385 - 404:	EEEEEEEEEEEEEEEEEEEE
386 - 405:	EEEEEEEEEEEEEEEEEEEE
387 - 406:	EEEEEEEEEEEEEEEEEEEE
388 - 407:	EEEEEEEEEEEEEEEEEEEE
389 - 408:	EEEEEEEEEEEEEEEEEEEE

A0A0D2ES98 **A0A0D2ES98_9EURO** (1306 aa)
Histone acetyltransferase (EC 2.3.1.48). *Exophiala xenobiotica*

```
MPPLVSEELDDASSLDQESVTLETTAEAGTKEEAAEPLVGSDTAGAKDGRMTTNDDEEEKEQEIDSSHTPNPDDNALGEQ
LQRSAEEEQSEDGEAESAIAPHPGVKKDNFTKDVDADADADAEADEDEDADADAETDADADADAEANEEADQQGGSGDED
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEDVPDDNESQKSEQLVEESVQSPSEPGEEVAEETPAAEAKLQCMFCKQGP
NAEAGEVESLLSCSDCDGRAHLRCARGDDAVKDEDYSDWQCPNCVKQHPLSESPKEQTVRSKNSAPRLVRDLLPVTRGVQ
KPGSHSIFAQPLIQEGEDGGRSLRKRKSLTVEPPPTEKRRRKATPRALEAMTADSKAETERAIAHSTRRSSLKITKPTAR
ILQHRPFQKAPPHKFILAFRLDQSKIEEILSNPPRPGKRRGGREKKKVPKIAPPIFQPPVPKFPALPTHNLIFPSAFTDR
DAEPNAKPYGGILSEADADTSRSLPQLKDREIFEIARKEAEEERRKTSAAAEAEINVDKEGTAKPNRTVSGPPTKIKCIQ
FGKFVIDTFYAAPYPEEYSHESRLFICEYCLKYLPSEFVAYRHKLKCPAKHPPGDEIYRDGTLSVWEVDGRKKTEYCQCL
CLMAKMFLGSKTLYYDVEPFLFYILTEYDEFGYHFVGYFSKEKRPASQNNVSCILVMPIHQRKGYAMFLIDFSYLLTRIE
GKDGSPEKPLSDMGLTAYRSYWDLTVSRHLLAIGLKPFSTKALMARTGMTADDVIHSLERLYAFVRDPVTKTYAVRYDKK
LYERIVHEFESKKHRQLRPENLVWTPYIMGRSDQAALDGQPLHTMAPRDDEDEDEGDKDNPVSEAISKAGNSATDAVVEA
TEPGHLSPKSRTKRTTAMSQPPSAAAAEESVDVKDSSLVNEHGTVAPGPPPTEALNGTVSTQVTQPEVKVNGLELVNGDD
KSNDDTIVVSTNVDAESKGKNVEGGGEGNKEKADEAQPQEPEPALTGYALAYRTLNIPPSRFQIDPPIPPAMLRQRSTKK
RSLATAFGRPKPNGGLTDTSSAVAVRSSPRNAGVNGGGTVTRSRGASLSFDKVDRDKDKDKDKDKFSVPNTPVRRSGRRS
GLANINTIENTIEVASPKPSPLSRRNQATAASVGAGTVAGPRGGEGADDHDADAPADEDADVDAEADEDEDEQDPGKGKA
KASVKDEDAEAEAEAEAEAEAESSDSSGGDEADEEEEDASVAAEGDESDDVDDDDDDDEDAEIPEDEESDTTEDDDADDE
VDLPDDDDDEDAEVDEDDEDDDDEDD
```

161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE

169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE

A0A0D2EUF9 **A0A0D2EUF9_9EURO** (400 aa)
Sodium/potassium/calcium exchanger 1. *Exophiala xenobiotica*

```
MAQSTSQATHGTTAPRMTPDKNKAALHTAKVMNGGNPLFSQALVTSDFPHKNEWDNDNLPDILFYLVPPKSIHNTEKLQR
ISDNGQPVLNDKGRRIRDFEILPRHISVAVEGWLLETWRRLDTRITYNDIRDRMVADPTYGNGVGLVIPSANSLQNQCRR
DCRALLNNWAEHDKRGAEPTRTDVETIEKLTSYNVACNTVLDVVTLWPQTDQEMHRLRKVKLVRDSNGRLRMEPSVVTTD
NWMQTTYALDHFKSGLGAGNAEYVPLNEARLAAWELLLVLQERADIHGVQHWSKLTKTCLPTSWFERTADKAVPNDTYDG
GCQICTWRSEEEGVAGVNGDAKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEANEGPAYEALTWHIYTPDNFPFL
```

343 - 362:	EEEEEEEEEEEEEEEEEEEE
344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE

A0A0D2EVE3 **A0A0D2EVE3_9EURO** (108 aa)
Uncharacterized protein. *Exophiala xenobiotica*

```
MLLPPNSRLHHDLGLKFLAPTSLVFSPKCYLRAFGHVRPRVEYYVVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EVTSIKSLYKAIPTALFLRSYATPAQST
```

47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE

A0A0D2FTR2 **A0A0D2FTR2_XYLBA** (163 aa)
Unplaced genomic scaffold supercont1.15, whole genome shotgun sequence. *Cladophialophora bantiana CBS 173.52*

```
MDDTHEVVRRTQKTVIDTSGTVMDTRGAIIGPETLLLQLRGSYLTCRRLVGDIRASASNLRKSNVQITEITFDRCKGWKD
GTRESRLRCVRYFGLLDKICITGTRTEQGQVQHQQQHQQHQQQQGGEEEEEEEEEEEEEEEEEEEEEEELVVVVAMGV
GGN
```

127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE

A0A0D2GI83 **A0A0D2GI83_XYLBA** (92 aa)
Unplaced genomic scaffold supercont1.2, whole genome shotgun sequence. *Cladophialophora bantiana CBS 173.52*

```
MNVTVERAYEWRKGQVHSWRGARTKVEEEEEEEEEEEEEEEEEEEEEGEDEEDIEQDHERRGGQRRLSRTRNGTYLLTLS
SDIHLFPRFAQD
```

27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE

A0A0D2GRF6 **A0A0D2GRF6_9EURO** (2134 aa)
Unplaced genomic scaffold supercont1.8, whole genome shotgun sequence. *Fonsecaea pedrosoi CBS 271.37*

```
MSDSEPEDRELQELLEWLAPLTYHGQQAGFAQKRHPGSLQWFLNSEPYQKWVHAKPHPPNPEEQAQDLRTLFCPGPAGAG
KTILASTVVEDLSCRFAPGSSASKIGIAYIYCVFHLYEEQSPENLLLLLLHQLSPPRLLPLRQTCHEVFARPDGGPPSLA
NIAATLERAVRTYDRVFFVVDALDECAVDHRTRLLEEIFKLQANNPIHLLATSDLDPEIASRFVNTASLEIRADQDDLRS
FLERCIMDQLPAFLGDMPDLRQEITETIARVADGRFLLAMLHIHSLAGKPSPEAIRAALSGVVATLDTTSIDEYNAAYDA
VMERIERQSLDQSDLAKRALSYVLCATRPLTVTELRHALAVEASDTELERASMPQIDAIIAVCTGLIVVIGREPWGSDRS
NSEAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEELDEEVDETAKVQLVHRTTYDYLQRTCERWLPAREKQ
IATACMAYLSLRYFRSGSCRSDDDVRRRLQTYPLYCYAALGWGYHARVAFSKFPDMVNMDFGLLSSKPHIESAFQVFFMA
KHKVPWSEFPHFMAGIHLAAHFGITNLVYALIPSDSRRGRADFSINARDGHGCTALAWAAHEGHDEAVQALVNAANVDLD
ARDGEGQTPVLRATQRCHITIIERLLSGGANPNLKDFSRTSPLSYAAKEGHTAIADLLVRHGADVNAATTESSIGLHTPL
SLAVMHGHDEIARLLLAQLGIQASAKVKPRSMGDREYTSLEFAVKGNLHRVVELFLSHADVSGEHEVLLHAAAEEGDERV
VQWLLEMDVDVNTQSEHGDTPLHGAVRMQHDGVAVLLLSPAGVLPNLSNDDGDTAALLAARWGRVQVLQLMLAKGADGGA
RNKKGRTPLADAAEKGYLSVVELLLATDGVAADPQDHEGRTPLSLAVSPATRMRFDDARGRRAVVRCLLDSDRVDINSRD
TQGRTPLAFAAGMYNAMPMVGLLLGYEELDVNTMDEQGRTPLASAVRWSLDGTARLLLKRGADPTLGGYDEGESLLSCAV
KNSASDIVRTILSSGGADPGQRDRDGHTPLCHAAARGDVEILDKLLTVGGLDANAHCEHGQTPLHHAARSSKDTDQVVAF
LLAQTNIAVDTQDEEGRTPLHHAVLHGDEAVVSSLPGAENVCLNCKDREGRTPLSLAVSSGRLSIVEKLLSLDGVIADAK
DNTGRTPLSWAVGQRLWPSHEVVKRLIQRDDVNPNAEDDKGWTPLLWAVQGEGGSSLIEVILKEGAGRVDIDHGDREGNT
PLSLALKDQNEVVARQLRAAGARLKSGAESIGESVQRGSHVLTQGVSIDGEDEEQRQRTDTANAKGDRHAFEDTSDEGNH
QGSTKFGPSYESSPDRYRRRRRRWMKMNWFDDDSGSGGDSDSNWSGTDPEIYDRLSDDEAGARCSRRTRPPTPREVHIEL
GVQAEEHHVGDEGPLCHQCKTIDLNALFSQQPQGGFTVIADLGEIDESWKSRRCAMCRLIAAVCPSLMGYRPAKYELCAY
SSSATWLSGANVVAQRHFQSDWVDTIVLGLESGHWTAYSALKRAWRAKGSQMGIDPSEILPFGFIGRVGSNDPNQLRSLT
LHGLKRRRIDFSKARSWIACCVEHHGKRCNANTHRRIPHARFIDCKTRTVVDQGGDSEAHRFVALSYVWGPSPKTKGLVD
HHCVENAERVVEDAIHVTLELGYRYLWVDRHCITNEDQEMRKEQLLHMNGVYESAEVTIVAAAGRNSSFGLPGVSRAQLG
RPYGRVQGHALTAVPCEPREQVEESVWWTRGWTFQEGMLSRRRLIFTEHELSYECKGMVAREAVELPIDVHRLAATRYPM
HEHMRVFPRRRHDARTGGDGEYIWSCIGEYTRRRLTLDADILNAFLGILQVFSERKSPVYHLCGVPLVREKSANDKDKSR
IPTLLEAFAVGLCWYWLMPVPRRKGFPSWSWTGWKGRRHPLHGQSRSSIAFQPGHSIEVSMVPRDVSSRTVSWADFEAMS
PAEKASLPQDYRLRITASTTQISLFPQHAYDDDWGAILYSGDDAFQGRLSLSKDPKQDVEFCRRLVEERWDAIVLGNLRT
YREHLVLLLVDKLDTETVREAEGLWERVGVITLVHNKLQDFAPGAFRKGTFLIE
```

405 - 424:	EEEEEEEEEEEEEEEEEEEE
406 - 425:	EEEEEEEEEEEEEEEEEEEE
407 - 426:	EEEEEEEEEEEEEEEEEEEE
408 - 427:	EEEEEEEEEEEEEEEEEEEE
409 - 428:	EEEEEEEEEEEEEEEEEEEE
410 - 429:	EEEEEEEEEEEEEEEEEEEE
411 - 430:	EEEEEEEEEEEEEEEEEEEE
412 - 431:	EEEEEEEEEEEEEEEEEEEE
413 - 432:	EEEEEEEEEEEEEEEEEEEE
414 - 433:	EEEEEEEEEEEEEEEEEEEE
415 - 434:	EEEEEEEEEEEEEEEEEEEE
416 - 435:	EEEEEEEEEEEEEEEEEEEE
417 - 436:	EEEEEEEEEEEEEEEEEEEE
418 - 437:	EEEEEEEEEEEEEEEEEEEE
419 - 438:	EEEEEEEEEEEEEEEEEEEE
420 - 439:	EEEEEEEEEEEEEEEEEEEE
421 - 440:	EEEEEEEEEEEEEEEEEEEE
422 - 441:	EEEEEEEEEEEEEEEEEEEE
423 - 442:	EEEEEEEEEEEEEEEEEEEE
424 - 443:	EEEEEEEEEEEEEEEEEEEE
425 - 444:	EEEEEEEEEEEEEEEEEEEE

A0A0D2HJM3 **A0A0D2HJM3_XYLBA** (384 aa)
Unplaced genomic scaffold supercont1.13, whole genome shotgun sequence. *Cladophialophora bantiana CBS 173.52*

```
MDAYQQYNCSLPEATSNPALSATVSYYFVRPNKVVKPSSRNSSPRTLGRRKTMTAASTSSRTRSVVDHLRSSTQWQQHSD
TPRSRPVSWHPNSLEALNFTFNSVPNEQDLSTWNIATAQVNGLVTPISYPSMSEPQLPEPFTPLDELPVQDPSLVLEGQP
FPEEQMWLSQGQVKPEPNFLPLYSQQPFPQPLWGLNQAVMAPNVTTAPPSPDCRPLQNLGLDTLSLDTNHSTSQVDSEEL
IGMGLYDSPAEVQSSCLLFSGSAGSGRKGLKLEESFEPVEREEEEEEEEEEEEEEEEEEEEENDTEDAEEDETGQPGVQQE
DEEDDDDDSVWGYSGTAEYESRSIADHLTFGMQAQPDSLAIKYLSTLRQLNSAYYPSGHSYGWA
```

282 - 301:	EEEEEEEEEEEEEEEEEEEE

A0A0D2SVB3 **A0A0D2SVB3_GOSRA** (1008 aa)
RING-type domain-containing protein. *Gossypium raimondii (New World cotton)*

```
MASSQLEIVPSSPFGCVLRDHNRKERCRDSNVSSVQTVFDKNFNDLVRDHINGCISLSSPKSPQNHNNVASWVSAEQGNA
NANANANANRHNLPSFSNKNHHNKKKGDPSPINPKQSPVLDRWVTRQSQDVAVSTIDKQVNEAAEQVLAPSHSNPVSPPP
PPPPMASSSTTKNAQTRSENASVTHNLAASSLVQIWEARLNRSNSINSYQNQSMDSNTSRTSSGVSSNENNASPMEESST
SEPFEEKMENRTNNVDSLIELESPSDRTAAGEAASSSSSSCSKTFDAGEIERVRIVDIIKKLKNCREDADDHEHTGSHSQ
CKEPKHCSKPNESLRRCFSLVINSPLIRGRQAFQDFLVRIERDKKRELDSLVKRQAVSKFPQRGRVQSMLRLKSLQRCLT
IQDKCRPQLNRSQGSTIMHLREKFSTGAEQGMTAQNVSATPRYICKDKSSTCKPPQREDTHCQKGQQSSSPVVSLTTNKN
GDVKEQAKPPSDAVQQKTSLEAKSPESPKIAKETKPLEGPSENDVAKKEDLSSQQLILGSQETAETVTQNEVAKAEQEKD
QHQLILDSQETMETTTTTTTSVVSSIENEIVEEDIGDQQHICVDPQSQDIVDNTSTSCINDRNENEVTEEEEDHYQQYFD
ETDDYDWFSNISRPRSYWEGLRQAWYEEVLNTTSNNEEIRQLLERGRVSTLLGSDFRDTMDRLMTSRVQMQADEAESQQE
VDDKEGIICRGRVSTLFDSDFLEKMNRLMTSRVQMQADVAESQQEVEDKEGMVQPVSYEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEYDDEEERSLSSRQCQEVNNYFNNSSPSIQMPSPSAMMTRSWSFQDDNETSNDERGASLYSPPPQPSQAERYQ
DARQSASSINRPSLEMELICDLRGHIEQLHSEISELRKSVMTCMDMQMKWQHYSLNREVHSVEGEGKNSADRTPWKRRCC
ICYEMQVDSLLYRCGHMCTCLKCGNELQWRSGKCPICRAPILDVVPAK
```

779 - 798:	EEEEEEEEEEEEEEEEEEEE
780 - 799:	EEEEEEEEEEEEEEEEEEEE
781 - 800:	EEEEEEEEEEEEEEEEEEEE
782 - 801:	EEEEEEEEEEEEEEEEEEEE
783 - 802:	EEEEEEEEEEEEEEEEEEEE
784 - 803:	EEEEEEEEEEEEEEEEEEEE
785 - 804:	EEEEEEEEEEEEEEEEEEEE
786 - 805:	EEEEEEEEEEEEEEEEEEEE
787 - 806:	EEEEEEEEEEEEEEEEEEEE
788 - 807:	EEEEEEEEEEEEEEEEEEEE
789 - 808:	EEEEEEEEEEEEEEEEEEEE

A0A0D2TZI8 **A0A0D2TZI8_GOSRA** (67 aa)
Uncharacterized protein (Fragment). *Gossypium raimondii (New World cotton)*

```
RSKFDLNKEEEEEEGEEEEEEEEEEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE

48 - 67:	EEEEEEEEEEEEEEEEEEEE

A0A0D3ATX2 **A0A0D3ATX2_BRAOL** (178 aa)
Uncharacterized protein. *Brassica oleracea var. oleracea*

```
MCKDKREHKVLSLLQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEYANNWR
NMIASNMWTEAVGNGTQR
```

16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE

62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE

114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE

A0A0D3B1P1 **A0A0D3B1P1_BRAOL** (415 aa)
Chromo domain-containing protein. *Brassica oleracea var. oleracea*

```
MTDTPLDSSTQNMEGAGVKNDAGEADTAVETVGGSGDEGGRGETIPGKIGDDRRTEDVEEKEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EGKEDGPKVAEEFYEVEAIRHKRVHKGEVQYLIKWKGWPETDNTWEPLENLQSLSASIDAFEKRLKKADKKRKSQYGGSN
SQSKKKKQQKRLTSTSHDASERTDPTLNELKGQVTNSDGSGSSQEGEAAIGSEGDNARTNDLLKGKRKEKSGVRGVKRRK
PSIVKKYMIPDETTTSNNQTITATDQNETPNLDIVRIIKPVEVITSITNNVQDSLVTFSVQRADGEEVTVDNKFLRAHNH
HLLLDFYEQHITYKS
```

62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE

85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE

137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE

A0A0D3B640 **A0A0D3B640_BRAOL** (296 aa)
Uncharacterized protein. *Brassica oleracea var. oleracea*

```
KPVDYAAIFAVNRRRHGVLLDEAASRFGAFEHPIQRLPSGSRVYAQPESLLGGNYRHGGLIVVMRVGTVRLEERNYLGLG
EEKMVLYGVCYLLGLLRWLLRGEEEEEEEEEEEEEEEEEEEEEEEEEEDEMATEMATEISGRRRRKRADMGGNDGLASE
TPTQQQVFVLDTSSWLEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAEEEEAEEKKKKKKKKPLSFSKDI
```

103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE
180 - 199:	EEEEEEEEEEEEEEEEEEEE
181 - 200:	EEEEEEEEEEEEEEEEEEEE
182 - 201:	EEEEEEEEEEEEEEEEEEEE
183 - 202:	EEEEEEEEEEEEEEEEEEEE
184 - 203:	EEEEEEEEEEEEEEEEEEEE
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197 - 216:	EEEEEEEEEEEEEEEEEEEE
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204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE
208 - 227:	EEEEEEEEEEEEEEEEEEEE

209 - 228:	EEEEEEEEEEEEEEEEEEEE
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238 - 257:	EEEEEEEEEEEEEEEEEEEE
239 - 258:	EEEEEEEEEEEEEEEEEEEE
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242 - 261:	EEEEEEEEEEEEEEEEEEEE
243 - 262:	EEEEEEEEEEEEEEEEEEEE
244 - 263:	EEEEEEEEEEEEEEEEEEEE
245 - 264:	EEEEEEEEEEEEEEEEEEEE
246 - 265:	EEEEEEEEEEEEEEEEEEEE
247 - 266:	EEEEEEEEEEEEEEEEEEEE
248 - 267:	EEEEEEEEEEEEEEEEEEEE
249 - 268:	EEEEEEEEEEEEEEEEEEEE
250 - 269:	EEEEEEEEEEEEEEEEEEEE
251 - 270:	EEEEEEEEEEEEEEEEEEEE
252 - 271:	EEEEEEEEEEEEEEEEEEEE
253 - 272:	EEEEEEEEEEEEEEEEEEEE

A0A0D3BNV7 **A0A0D3BNV7_BRAOL** (393 aa)
Uncharacterized protein. *Brassica oleracea var. oleracea*

```
MAVDDDPNNSNTVVKCICSDKKVVEVDRKTWELFNKMVPKEGFHRIREPVEMYFVRSTAFKKILTYCVRISDGTCSERWM
YDELLHSESLIGLFHLVGTADFLNFESLDAFILHYVEDKSEEEISYMVRNEELKSLLKIIKFARFYLKNPDKLFSAVLPL
VKKSQEEFSQMIVNKDLPSLIKLIKVAEYIGYENVRKAARNHILSKSKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDDTLMNQIPIDEATNQVPIYDGSKKVSA
```

209 - 228:	EEEEEEEEEEEEEEEEEEEE

210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
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262 - 281:	EEEEEEEEEEEEEEEEEEEE
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264 - 283:	EEEEEEEEEEEEEEEEEEEE
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267 - 286:	EEEEEEEEEEEEEEEEEEEE
268 - 287:	EEEEEEEEEEEEEEEEEEEE
269 - 288:	EEEEEEEEEEEEEEEEEEEE
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273 - 292:	EEEEEEEEEEEEEEEEEEEE
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279 - 298:	EEEEEEEEEEEEEEEEEEEE
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281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE
287 - 306:	EEEEEEEEEEEEEEEEEEEE
288 - 307:	EEEEEEEEEEEEEEEEEEEE
289 - 308:	EEEEEEEEEEEEEEEEEEEE
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312 - 331:	EEEEEEEEEEEEEEEEEEEE
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320 - 339:	EEEEEEEEEEEEEEEEEEEE
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322 - 341:	EEEEEEEEEEEEEEEEEEEE
323 - 342:	EEEEEEEEEEEEEEEEEEEE
324 - 343:	EEEEEEEEEEEEEEEEEEEE
325 - 344:	EEEEEEEEEEEEEEEEEEEE
326 - 345:	EEEEEEEEEEEEEEEEEEEE
327 - 346:	EEEEEEEEEEEEEEEEEEEE
328 - 347:	EEEEEEEEEEEEEEEEEEEE
329 - 348:	EEEEEEEEEEEEEEEEEEEE
330 - 349:	EEEEEEEEEEEEEEEEEEEE
331 - 350:	EEEEEEEEEEEEEEEEEEEE
332 - 351:	EEEEEEEEEEEEEEEEEEEE
333 - 352:	EEEEEEEEEEEEEEEEEEEE
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335 - 354:	EEEEEEEEEEEEEEEEEEEE
336 - 355:	EEEEEEEEEEEEEEEEEEEE
337 - 356:	EEEEEEEEEEEEEEEEEEEE
338 - 357:	EEEEEEEEEEEEEEEEEEEE
339 - 358:	EEEEEEEEEEEEEEEEEEEE
340 - 359:	EEEEEEEEEEEEEEEEEEEE
341 - 360:	EEEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEEE
344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE

A0A0D3BPJ0 **A0A0D3BPJ0_BRAOL** (524 aa)
F-box domain-containing protein. *Brassica oleracea var. oleracea*

```
MGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEESSNSMCILPELLEEIFIRLPLKSILRFRTVSKHCRSLLESRRFSEKRMSLQKNRR
ILAAYNCDCGDRPRLLTESRFEGDEEIVYLHCLASRPSLSCDGLLCFPEQDWIIVLNPSTRQLRRFPSGLNHKCRFGFGL
WSSFSPEKWAIGFGRDKVTGSFKVVRLCFSFREIGQEEPVLECGVLDVQTGVWSKLSPPPHVVNPGSKSVCVNGSIYWLN
FEVGEYCKLLALDLHKQEFNRIPLPATGLGATKETLIVNFEEHLAYVNTSKLPEWRLDIWSMDNTDQKQWSKTFSIRLEL
KVVAWRRKNRWFTPVAVSKQGNLVFCDNQKRLFKYYPGTNEIRCLSLDTYVISPYSENLVSLPLKPSHQYPHLSVETRMS
RCRLFSKESSSSWIFQALRRNEFSILEIVFTSLVVAGYICLPRM
```

3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE

15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
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41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
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58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE

67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE

A0A0D3BV32 **A0A0D3BV32_BRAOL** (133 aa)
Uncharacterized protein. *Brassica oleracea var. oleracea*

```
MYKLSFVLALICKRNWLRGFEVMCDSEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVNQV
```

27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE

54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
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57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
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61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
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81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
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91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE

106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE

A0A0D3BV36 **A0A0D3BV36_BRAOL** (266 aa)
Dimer_Tnp_hAT domain-containing protein. *Brassica oleracea var. oleracea*

```
CNVLSISIKTVSSESSFCVGSRVISKYRSRLLPSNVLALICKRNWLRGFEVMCKFSDFLLIFILKCDSEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEVNQV
```

69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
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101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE

110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
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237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE
239 - 258:	EEEEEEEEEEEEEEEEEEEE
240 - 259:	EEEEEEEEEEEEEEEEEEEE
241 - 260:	EEEEEEEEEEEEEEEEEEEE
242 - 261:	EEEEEEEEEEEEEEEEEEEE
243 - 262:	EEEEEEEEEEEEEEEEEEEE

A0A0D3BZ22 **A0A0D3BZ22_BRAOL** (288 aa)
Dimer_Tnp_hAT domain-containing protein. *Brassica oleracea var. oleracea*

```
MVDVRVLERQETGTLHPSLSRSIIPASAGIQSKLSPTRTEQFKYKEGGKQVFAESEFGDFKSTTASTSETTLVNSMPVGY
GEFYAFFSQNAGTRKSALDVYLAEPVLDMAVFKTLDVLRYWRNNATRFKELSRMACDVLSIPITTVSSESSFSAGSCVLS
KYRSRLLPSNVQALICGRNWLHGFEVTSDSEDDDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEGEVEEESGRKKRRK
```

195 - 214:	EEEEEEEEEEEEEEEEEEEE
196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE
208 - 227:	EEEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE

211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE
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230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE
239 - 258:	EEEEEEEEEEEEEEEEEEEE
240 - 259:	EEEEEEEEEEEEEEEEEEEE
241 - 260:	EEEEEEEEEEEEEEEEEEEE
242 - 261:	EEEEEEEEEEEEEEEEEEEE
243 - 262:	EEEEEEEEEEEEEEEEEEEE
244 - 263:	EEEEEEEEEEEEEEEEEEEE
245 - 264:	EEEEEEEEEEEEEEEEEEEE
246 - 265:	EEEEEEEEEEEEEEEEEEEE
247 - 266:	EEEEEEEEEEEEEEEEEEEE
248 - 267:	EEEEEEEEEEEEEEEEEEEE
249 - 268:	EEEEEEEEEEEEEEEEEEEE
250 - 269:	EEEEEEEEEEEEEEEEEEEE
251 - 270:	EEEEEEEEEEEEEEEEEEEE
252 - 271:	EEEEEEEEEEEEEEEEEEEE
253 - 272:	EEEEEEEEEEEEEEEEEEEE

A0A0D3BZH7 **A0A0D3BZH7_BRAOL** (591 aa)
Uncharacterized protein. *Brassica oleracea var. oleracea*

```
MSVACGLECVFCVGFSRWGWKRCTHVGSDDSATWAAATPEEFEPIPRICRVILAVYEPDLRNPKVSPSIGKFDLNPDWVI
KRVTYEKTQGRSPPYIVYVDHDHREIVLAIRGLNLAKESDYKILLNNKLGQKMLVGGYVHHGLLESAVWVLNQESETLRG
LWEENGREYDLVFAGHSLGSGVAALMAVLVVNTPAMIGGLPRSKIRCFALAPARCMSLNLAVKYADVIFSVILQDDFLPR
TATPLEDIFKSIFCLPCLLFLVCLRDTFIPEGRKLRDPRRLYAPGRIYHIVERKFCRCGRFPPEVRTAIPVDGRFEHIVL
SSNATSDHAILWIERESEKALQEMREKSAETVVTKAPKEKRMERLNTLEKEHKDALERAVSLNIPHAVSAAEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEECNNAEASEPKS
KKKSWDEVVEKLFHRSNSGELVLNENVNIKG
```

392 - 411:	EEEEEEEEEEEEEEEEEEEE

393 - 412:	EEEEEEEEEEEEEEEEEEEE
394 - 413:	EEEEEEEEEEEEEEEEEEEE
395 - 414:	EEEEEEEEEEEEEEEEEEEE
396 - 415:	EEEEEEEEEEEEEEEEEEEE
397 - 416:	EEEEEEEEEEEEEEEEEEEE
398 - 417:	EEEEEEEEEEEEEEEEEEEE
399 - 418:	EEEEEEEEEEEEEEEEEEEE
400 - 419:	EEEEEEEEEEEEEEEEEEEE
401 - 420:	EEEEEEEEEEEEEEEEEEEE
402 - 421:	EEEEEEEEEEEEEEEEEEEE
403 - 422:	EEEEEEEEEEEEEEEEEEEE
404 - 423:	EEEEEEEEEEEEEEEEEEEE
405 - 424:	EEEEEEEEEEEEEEEEEEEE
406 - 425:	EEEEEEEEEEEEEEEEEEEE
407 - 426:	EEEEEEEEEEEEEEEEEEEE
408 - 427:	EEEEEEEEEEEEEEEEEEEE
409 - 428:	EEEEEEEEEEEEEEEEEEEE
410 - 429:	EEEEEEEEEEEEEEEEEEEE
411 - 430:	EEEEEEEEEEEEEEEEEEEE
412 - 431:	EEEEEEEEEEEEEEEEEEEE
413 - 432:	EEEEEEEEEEEEEEEEEEEE
414 - 433:	EEEEEEEEEEEEEEEEEEEE
415 - 434:	EEEEEEEEEEEEEEEEEEEE
416 - 435:	EEEEEEEEEEEEEEEEEEEE
417 - 436:	EEEEEEEEEEEEEEEEEEEE
418 - 437:	EEEEEEEEEEEEEEEEEEEE
419 - 438:	EEEEEEEEEEEEEEEEEEEE
420 - 439:	EEEEEEEEEEEEEEEEEEEE
421 - 440:	EEEEEEEEEEEEEEEEEEEE
422 - 441:	EEEEEEEEEEEEEEEEEEEE
423 - 442:	EEEEEEEEEEEEEEEEEEEE
424 - 443:	EEEEEEEEEEEEEEEEEEEE
425 - 444:	EEEEEEEEEEEEEEEEEEEE
426 - 445:	EEEEEEEEEEEEEEEEEEEE
427 - 446:	EEEEEEEEEEEEEEEEEEEE
428 - 447:	EEEEEEEEEEEEEEEEEEEE
429 - 448:	EEEEEEEEEEEEEEEEEEEE
430 - 449:	EEEEEEEEEEEEEEEEEEEE
431 - 450:	EEEEEEEEEEEEEEEEEEEE
432 - 451:	EEEEEEEEEEEEEEEEEEEE
433 - 452:	EEEEEEEEEEEEEEEEEEEE
434 - 453:	EEEEEEEEEEEEEEEEEEEE
435 - 454:	EEEEEEEEEEEEEEEEEEEE
436 - 455:	EEEEEEEEEEEEEEEEEEEE
437 - 456:	EEEEEEEEEEEEEEEEEEEE
438 - 457:	EEEEEEEEEEEEEEEEEEEE
439 - 458:	EEEEEEEEEEEEEEEEEEEE
440 - 459:	EEEEEEEEEEEEEEEEEEEE
441 - 460:	EEEEEEEEEEEEEEEEEEEE
442 - 461:	EEEEEEEEEEEEEEEEEEEE
443 - 462:	EEEEEEEEEEEEEEEEEEEE
444 - 463:	EEEEEEEEEEEEEEEEEEEE

445 - 464:	EEEEEEEEEEEEEEEEEEEE
446 - 465:	EEEEEEEEEEEEEEEEEEEE
447 - 466:	EEEEEEEEEEEEEEEEEEEE
448 - 467:	EEEEEEEEEEEEEEEEEEEE
449 - 468:	EEEEEEEEEEEEEEEEEEEE
450 - 469:	EEEEEEEEEEEEEEEEEEEE
451 - 470:	EEEEEEEEEEEEEEEEEEEE
452 - 471:	EEEEEEEEEEEEEEEEEEEE
453 - 472:	EEEEEEEEEEEEEEEEEEEE
454 - 473:	EEEEEEEEEEEEEEEEEEEE
455 - 474:	EEEEEEEEEEEEEEEEEEEE
456 - 475:	EEEEEEEEEEEEEEEEEEEE
457 - 476:	EEEEEEEEEEEEEEEEEEEE
458 - 477:	EEEEEEEEEEEEEEEEEEEE
459 - 478:	EEEEEEEEEEEEEEEEEEEE
460 - 479:	EEEEEEEEEEEEEEEEEEEE
461 - 480:	EEEEEEEEEEEEEEEEEEEE
462 - 481:	EEEEEEEEEEEEEEEEEEEE
463 - 482:	EEEEEEEEEEEEEEEEEEEE
464 - 483:	EEEEEEEEEEEEEEEEEEEE
465 - 484:	EEEEEEEEEEEEEEEEEEEE
466 - 485:	EEEEEEEEEEEEEEEEEEEE
467 - 486:	EEEEEEEEEEEEEEEEEEEE
468 - 487:	EEEEEEEEEEEEEEEEEEEE
469 - 488:	EEEEEEEEEEEEEEEEEEEE
470 - 489:	EEEEEEEEEEEEEEEEEEEE
471 - 490:	EEEEEEEEEEEEEEEEEEEE
472 - 491:	EEEEEEEEEEEEEEEEEEEE
473 - 492:	EEEEEEEEEEEEEEEEEEEE
474 - 493:	EEEEEEEEEEEEEEEEEEEE
475 - 494:	EEEEEEEEEEEEEEEEEEEE
476 - 495:	EEEEEEEEEEEEEEEEEEEE
477 - 496:	EEEEEEEEEEEEEEEEEEEE
478 - 497:	EEEEEEEEEEEEEEEEEEEE
479 - 498:	EEEEEEEEEEEEEEEEEEEE
480 - 499:	EEEEEEEEEEEEEEEEEEEE
481 - 500:	EEEEEEEEEEEEEEEEEEEE
482 - 501:	EEEEEEEEEEEEEEEEEEEE
483 - 502:	EEEEEEEEEEEEEEEEEEEE
484 - 503:	EEEEEEEEEEEEEEEEEEEE
485 - 504:	EEEEEEEEEEEEEEEEEEEE
486 - 505:	EEEEEEEEEEEEEEEEEEEE
487 - 506:	EEEEEEEEEEEEEEEEEEEE
488 - 507:	EEEEEEEEEEEEEEEEEEEE
489 - 508:	EEEEEEEEEEEEEEEEEEEE
490 - 509:	EEEEEEEEEEEEEEEEEEEE
491 - 510:	EEEEEEEEEEEEEEEEEEEE
492 - 511:	EEEEEEEEEEEEEEEEEEEE
493 - 512:	EEEEEEEEEEEEEEEEEEEE
494 - 513:	EEEEEEEEEEEEEEEEEEEE
495 - 514:	EEEEEEEEEEEEEEEEEEEE
496 - 515:	EEEEEEEEEEEEEEEEEEEE

497 - 516:	EEEEEEEEEEEEEEEEEEEE
498 - 517:	EEEEEEEEEEEEEEEEEEEE
499 - 518:	EEEEEEEEEEEEEEEEEEEE
500 - 519:	EEEEEEEEEEEEEEEEEEEE
501 - 520:	EEEEEEEEEEEEEEEEEEEE
502 - 521:	EEEEEEEEEEEEEEEEEEEE
503 - 522:	EEEEEEEEEEEEEEEEEEEE
504 - 523:	EEEEEEEEEEEEEEEEEEEE
505 - 524:	EEEEEEEEEEEEEEEEEEEE
506 - 525:	EEEEEEEEEEEEEEEEEEEE
507 - 526:	EEEEEEEEEEEEEEEEEEEE
508 - 527:	EEEEEEEEEEEEEEEEEEEE
509 - 528:	EEEEEEEEEEEEEEEEEEEE
510 - 529:	EEEEEEEEEEEEEEEEEEEE
511 - 530:	EEEEEEEEEEEEEEEEEEEE
512 - 531:	EEEEEEEEEEEEEEEEEEEE
513 - 532:	EEEEEEEEEEEEEEEEEEEE
514 - 533:	EEEEEEEEEEEEEEEEEEEE
515 - 534:	EEEEEEEEEEEEEEEEEEEE
516 - 535:	EEEEEEEEEEEEEEEEEEEE
517 - 536:	EEEEEEEEEEEEEEEEEEEE
518 - 537:	EEEEEEEEEEEEEEEEEEEE
519 - 538:	EEEEEEEEEEEEEEEEEEEE
520 - 539:	EEEEEEEEEEEEEEEEEEEE
521 - 540:	EEEEEEEEEEEEEEEEEEEE
522 - 541:	EEEEEEEEEEEEEEEEEEEE
523 - 542:	EEEEEEEEEEEEEEEEEEEE
524 - 543:	EEEEEEEEEEEEEEEEEEEE
525 - 544:	EEEEEEEEEEEEEEEEEEEE
526 - 545:	EEEEEEEEEEEEEEEEEEEE
527 - 546:	EEEEEEEEEEEEEEEEEEEE
528 - 547:	EEEEEEEEEEEEEEEEEEEE
529 - 548:	EEEEEEEEEEEEEEEEEEEE
530 - 549:	EEEEEEEEEEEEEEEEEEEE

[A0A0D3CGZ1](#) **A0A0D3CGZ1_BRAOL** (127 aa)
Uncharacterized protein. *Brassica oleracea var. oleracea*

```
MLCRVSNESEIEESRIIKELHLSWHFSGGGGGGAEQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE

50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE

102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE

A0A0D3CZJ3 **A0A0D3CZJ3_BRAOL** (99 aa)
Uncharacterized protein. *Brassica oleracea var. oleracea*

```
MGQLTKLETVSKQNTIIAEFVRSEAETAVAETNGDDDDDDDDDDDDDYDDDYERMSVVGTCWTYMQGVEDLDGSEEEEEE
EEEEEEEEEEEEEEEEEE
```

75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE

A0A0D3DGR7 **A0A0D3DGR7_BRAOL** (183 aa)
Uncharacterized protein. *Brassica oleracea var. oleracea*

```
MFLNLRKVKNKRELINKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEMFIK
```

18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE

46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE

98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE

150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE

A0A0D3DW04 **A0A0D3DW04_BRAOL** (650 aa)
RING-type E3 ubiquitin transferase (EC 2.3.2.27). *Brassica oleracea var. oleracea*

```
MDRGEIQLPCDADDVCMRCKSKIPSEECLTCSTCVTPWHVSCLRSPPATLASTQSWECPDCSGDVDPAPAPASGLNPSNS
SLVAAIRAIEADASLNEAQKAKKRQQLVSGKAVEEEEKEEQQSDDFLVSLRKNVSCSICLHLPERPVTTPCGHNFCLKCF
QKWVAGKRKPTCGTCRASIPKKMKDNPRINSVLVSAIRLAMVSKSTTVSTAKTYQFIRNVDRPEKAFTTERAKKTGKANA
CSGRIYVTVPSDHFGPILAGNDPDRNQGVLVGESWEDRQECRQWGAHFPHVAGIGGQSSYGAQSVALSGGYKDDEDHGEW
FLYTGSGGRDLTGNKRTNKDQAFDQQFTKSNAALRISCKMGYPVRVVRSHKEKRSAYAPAEKSVRYDGVYRIEKCWRKVG
IQGKRVCRYLFVRVDNEPAPWTSDEHGDRPRPLPSIPELKKATDMFVRTESPSWDFDESDGRWKWMKSPPASRKAIAALD
PAARKAMKGGGNKRDKFLKEFGCQICRKVMSSPVTTPCAHNFCKECLTGKFAGITQVRQRSRGGRTLRAQKNVMKCPCCP
NDISDFLQNPQVNRELMDVIEEVKKKKELEERQDEGNSENSAEGENTGSEEEEEEEEEEEEEEEEEEEEEESDVHVSEDE
PAAKKIKLSA
```

610 - 629:	EEEEEEEEEEEEEEEEEEEE
611 - 630:	EEEEEEEEEEEEEEEEEEEE
612 - 631:	EEEEEEEEEEEEEEEEEEEE

A0A0D3E9D7 **A0A0D3E9D7_BRAOL** (178 aa)
Uncharacterized protein. *Brassica oleracea var. oleracea*

```
MARLLPQTVTVKTSLHYCISPARASMMASDGTTPPTVMYDDSKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEE
```

44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
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65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE

68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE

120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE

A0A0D3ECK2 **A0A0D3ECK2_BRAOL** (1285 aa)
Uncharacterized protein. *Brassica oleracea var. oleracea*

```
MGIDVKETCAIIWKVIGFSMSTSIKFMRNHPILSLVSMFLLALYILLPSLLFFLIYSSPVLACVVVYAREKLGLRFSGSS
SGPENCEGEKKGGRCHLRQQRSVRRNARMRVEEWDSQTSDEEKDKVILTSLYNDLLGRTPQFEESPKAIETNVVEEEKDK
AFAEEDSRMSSQDLGYLNVEEEPMVCNCEVNEEKHDDKEETISNVNEHGISEVERNKRLESLIARRRTRRLFKLALDQHN
KLQAEETTSPTQNNNLHITVPRNNNNNSFEKRRSYQSGLQVPGSAPSVMLQARSPFDIPYDPQEERPNLTGDSFDQEFSF
FNPNDMFLCRHESFCSFAHFSPEHAQCMNSPVPASDISTTRKLLDLDNEYMDHNEQNIPCYVKPVTTKDDKSGKNGDVEV
NHETDTSEEDDDTSSCSEESEAELNRFNKAELREAISHSMDKFPGFLVNQARNDIPSPLPRGLLAPRLDDNNMFYARRGA
SSHNRTFSIASDMQVEVSELGSPPTTVDWLDDWSNGGESYTYDTDIDREIIRGEESRKRVSQQCESRSGTGTKEDDNGLV
TKPYQKCLSDEHLGTADEMSLLDRRSQTRENFEMRPSRSSDVPKSRSYGKLDGLLFHTSVSLSSITEEPETILDSVDARN
TENMNGLTKELTDQIFPTSTDSSMKNLVDEEVVDVQQLEHDDLCGPPKIMDSNIIDHQQKDQTLNIIQGEHDTEENAKPK
EYAASQSVLDASLTSPYVESFEIEIREEEPDLDNSTKEVTQQREDEALQGDLMSSPKLQESVVMEENGQELVKNSDENVK
PMEQEETHDVLDAFLIHPCTQLSEEYGNAKNDSDVILIQVQDGNNSTLDDSTDQQFSKEGESSGLLKDLHAESTQESNNI
VNIEEESIGSEDAPNSQPWTQQQGTCSSQKPEHDDIISQDIAKDLEYENTKPMEYEADQSVLDSSLDTPCVDSFKREMKE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDNFTKAVTEQTEDK
ALQGDLTSSHFLTNLQESEVMEENDPKLVKTSDKSAKLVEQEKTHDVLEASSSPPYTQLVEDYENAKNDCDVTLLKVQDG
NHSTLDESTDQKFSNSGLLKDLHAEPTQEYNNIVNVKGELIGLEDAHDSQGSQPWTQQNGTDSSELISPRTLEITQRPEH
DVSQDIAKDKVATEAKDSTDTEKNDEENLKHEHVIEEDVEKELLTLQSLHHNTGLTAREDDEESKKVVEAVHNSETKTSK
TETDP
```

960 - 979:	EEEEEEEEEEEEEEEEEEEE
961 - 980:	EEEEEEEEEEEEEEEEEEEE
962 - 981:	EEEEEEEEEEEEEEEEEEEE
963 - 982:	EEEEEEEEEEEEEEEEEEEE
964 - 983:	EEEEEEEEEEEEEEEEEEEE
965 - 984:	EEEEEEEEEEEEEEEEEEEE
966 - 985:	EEEEEEEEEEEEEEEEEEEE
967 - 986:	EEEEEEEEEEEEEEEEEEEE
968 - 987:	EEEEEEEEEEEEEEEEEEEE
969 - 988:	EEEEEEEEEEEEEEEEEEEE
970 - 989:	EEEEEEEEEEEEEEEEEEEE
971 - 990:	EEEEEEEEEEEEEEEEEEEE
972 - 991:	EEEEEEEEEEEEEEEEEEEE
973 - 992:	EEEEEEEEEEEEEEEEEEEE
974 - 993:	EEEEEEEEEEEEEEEEEEEE
975 - 994:	EEEEEEEEEEEEEEEEEEEE
976 - 995:	EEEEEEEEEEEEEEEEEEEE
977 - 996:	EEEEEEEEEEEEEEEEEEEE
978 - 997:	EEEEEEEEEEEEEEEEEEEE
979 - 998:	EEEEEEEEEEEEEEEEEEEE
980 - 999:	EEEEEEEEEEEEEEEEEEEE
981 - 1000:	EEEEEEEEEEEEEEEEEEEE
982 - 1001:	EEEEEEEEEEEEEEEEEEEE
983 - 1002:	EEEEEEEEEEEEEEEEEEEE
984 - 1003:	EEEEEEEEEEEEEEEEEEEE
985 - 1004:	EEEEEEEEEEEEEEEEEEEE
986 - 1005:	EEEEEEEEEEEEEEEEEEEE
1007 - 1026:	EEEEEEEEEEEEEEEEEEEE

A0A0D3EEG9 **A0A0D3EEG9_BRAOL** (429 aa)
Uncharacterized protein. *Brassica oleracea var. oleracea*

```
MHPRCVQLHPLPPLHLLHPLVFHDEIGALSKKEGPWPIINKEDELQKKTQHLRDQNLRENRFIESNDLVWYFFSPYESTN
KRPRRTTRSGFWKVTGVDRKIKDKGTLDLLFPRESSPVRVSPNFILSNPPPPLGRHSLLPRLAVRSAVTSVRSFNPFPSL
RNTKVFLFALFLAKRRGSLEVGTMMNAFLGLNSRSKAIVTKGLTLRNRFWVKSLTVFSCLLQMSESILKAARSNDPDLVT
KKTNSDLTHILFLLLWCKAGLFSASVSSLLLRSLDSSQFICSRGSFLFLYIRHIRSFPWWQTITVVVVVTELVVMTIEGV
REQWRRFGGGGGGGAEQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

338 - 357:	EEEEEEEEEEEEEEEEEEEE
339 - 358:	EEEEEEEEEEEEEEEEEEEE
340 - 359:	EEEEEEEEEEEEEEEEEEEE
341 - 360:	EEEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEEE
344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE

355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE
379 - 398:	EEEEEEEEEEEEEEEEEEEE
380 - 399:	EEEEEEEEEEEEEEEEEEEE
381 - 400:	EEEEEEEEEEEEEEEEEEEE
382 - 401:	EEEEEEEEEEEEEEEEEEEE
383 - 402:	EEEEEEEEEEEEEEEEEEEE
384 - 403:	EEEEEEEEEEEEEEEEEEEE
385 - 404:	EEEEEEEEEEEEEEEEEEEE
386 - 405:	EEEEEEEEEEEEEEEEEEEE
387 - 406:	EEEEEEEEEEEEEEEEEEEE
388 - 407:	EEEEEEEEEEEEEEEEEEEE
389 - 408:	EEEEEEEEEEEEEEEEEEEE
390 - 409:	EEEEEEEEEEEEEEEEEEEE
391 - 410:	EEEEEEEEEEEEEEEEEEEE
392 - 411:	EEEEEEEEEEEEEEEEEEEE
393 - 412:	EEEEEEEEEEEEEEEEEEEE
394 - 413:	EEEEEEEEEEEEEEEEEEEE
395 - 414:	EEEEEEEEEEEEEEEEEEEE
396 - 415:	EEEEEEEEEEEEEEEEEEEE
397 - 416:	EEEEEEEEEEEEEEEEEEEE
398 - 417:	EEEEEEEEEEEEEEEEEEEE
399 - 418:	EEEEEEEEEEEEEEEEEEEE
400 - 419:	EEEEEEEEEEEEEEEEEEEE
401 - 420:	EEEEEEEEEEEEEEEEEEEE
402 - 421:	EEEEEEEEEEEEEEEEEEEE
403 - 422:	EEEEEEEEEEEEEEEEEEEE
404 - 423:	EEEEEEEEEEEEEEEEEEEE
405 - 424:	EEEEEEEEEEEEEEEEEEEE
406 - 425:	EEEEEEEEEEEEEEEEEEEE

407 - 426:	EEEEEEEEEEEEEEEEEEEE
408 - 427:	EEEEEEEEEEEEEEEEEEEE
409 - 428:	EEEEEEEEEEEEEEEEEEEE
410 - 429:	EEEEEEEEEEEEEEEEEEEE

A0A0D3EGT7 **A0A0D3EGT7_BRAOL** (372 aa)
Protein kinase domain-containing protein. *Brassica oleracea var. oleracea*

```
MDKYEVVKDLGTGNFGVARLLRHKETKELVAMKYIERGRKIDENVAREIINHRSLKHPNIIRFKEVILTPTHLAIVMEYA
SGGELFERICTAGRFSEAEARYFFQQLICGVDYCHSLQICHRDLKLENTLLDGSPAPLLKICDFGYSKSSILHSRPKSTV
GTPAYIAPEVLSRREYDGKHADVWSCGVTLYVMLVGAYPFEDPNDPKNFRKTIQRIMAIQYKIPDYVHISQECKHLLSRI
FVTNPAKRITLKEIKNHPWYLKNLPKELLESAQAVYYKRDNTSYSLQSVEDIMKIVGEARNPASSSSVSKSLGSGVEEEE
DVEAEVEEEEEEEEEEEEEEEEEEEEEDEYEKHVKEAHSSIQEPHEALKEKK
```

327 - 346:	EEEEEEEEEEEEEEEEEEEE
328 - 347:	EEEEEEEEEEEEEEEEEEEE

A0A0D3G7A9 **A0A0D3G7A9_9ORYZ** (1302 aa)
Uncharacterized protein. *Oryza barthii*

```
MAPPLYLLLLLPLLACADEVPDRYAVLRAPQGPGASAAAKEYLDPTFPLPAPPPAAPSCTVPVLSYSFGDTYGAAPAKAS
YAPPAGCPAPWSLVVLTFSASCAGDQYDRVAAVWLDGAELLRTTTAEPTPEGVRWTVRKDVTRYSALLRSPPGGVLSVML
ENVVNDKYTGVYSVNVSLEFHGTPPYLSDAASSSPAGVASNDPKEPMLPESYFQPADLIVPISDVAGNGKGGFWFRIQNA
SDSHSRLVTIPSSTYRAVLEVFVSPHSNDEYWYSNPPDIYIRENNLTTRRGNAAYREVVVSVDHRFVGSFVPFPVIYTGG
INPLFWQPVAALGAFDLPTYDVELTPFLGLLVDSNAHEIGLSVFDGIAEWLVDANLHLWLDPSTSDVHAALGAYQTPRLK
ISRHYSTRLLEGRFKIKAKRKSSFSGWVKSSFGNFTTEVEAELKATSLVEFTGDGRNKTVSLEAKQETKTLIRAGDTRKV
IGRVEREAKYPLSLFAETEDGENGTSVVTVSLTHGLSVETEVETKALESKEKLDDAQAAQGWMVLLDHDVLNGSVTTTQA
YRFSDDEREYERAIDVVDGAVLSDNVTESFSALAAAAADARRRRFHAGIAALIRFRPHRRDQDYCFSSEGEGKVSTGDDL
LDALVEVFPQLNFLTLVEVCMEYKNDIDGAADYIIHNVLPSIPDNNDAHANEDSHMKRPASVDNDADSVQSYLANKYTAE
QEEEVEEEEEEEEEEEEEEEEEEEDEDDDEEEEDEDDDEEEDEDDEEEDRLMEENSDCLVAIDLNSKPGTSAFDDDLVT
HDDGLPAMNIQSSYPVRLELLDNAIADEIDEKVTLMSNVTAINQMLEDIKLKEEKTKQAVLEATQAGNDIFVKVEELKEM
TMLSTEENDKVVAGEVFAEQSILASEAHGLQARLSNISEERNNYALIIDEMRHTLQNRFAEAEVETVAAEKKKVERETLA
EKMLNEQELILDATKERSKMLEQQVRENAKLRELLMDRGQVVDALQGEMLGIFDKISQLQLRVDKQLPEPLLSSMSSSVN
SADNIAQLQCRVDGPQHSVDDSLQLASPRLSSSFKSTDSTAQAHCRVDEPQISVDESLLPVDECEQLQLISPRLSSSVMS
AQSQYRVDELLPVDEVLQLASSSLSSSLKSGDNIAQLLGVLDVHLPVDELLELPSLILSSSVKLSDSIAQFQQKADADEM
LQSSSLASSEKPATFKNWSSASDTITQFQQRANADESLPLPSSSLASSEKPATFKSTWSSAAESNSVFSGDEEIDDASFH
DSIDLDDSWDLVDDEAIYMCAN
```

726 - 745:	EEEEEEEEEEEEEEEEEEEE

A0A0D3GSY4 **A0A0D3GSY4_9ORYZ** (505 aa)
NPH3 domain-containing protein. *Oryza barthii*

```
MEMEMSRSWQELGVVDTIYEDDHEEEEEEEEEEEEEEEEEEEEEEECFDSLTMSSSPAATSRSCSPPPAAEEFAMPAALRN
AVREWSRANGPCKPDVIVRVQEHCFALHRDPITSQSSYLKRRLSECSDVAVDLPAGLTVDAFVDAVASCYGAEAALSPGS
LAAAWAAADWLELRGEDGLARRAEDYFFQEVATDHGRAAATLASSGGADGRWLDDVAALPVEEFEVAVEAMRARFAHDHD
LMYTIVDHYLQDLETNNLNLNHRGKLTEEEKSRVCYNVNCTKLSHHLFMHLVQNPRLPLRFVVQAMLVEQLHSHHSMLLS
GGHHHHAGAAGAPSSAAPPASLLKSSLSGAFGACGGFAATAAAAGDAASSMTLGDILQRDAVLRQSAHIRASMQATTQRI
DSLERELAGLRTRLRRSEQAAAAAATASAAIDRAGLKSRLVLGFKNLFGRRPVTAAAAAPPTSGERAAARVSVNDKAMST
DAPELDADADADELTRPHRRNLSIV
```

24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE

A0A0D3GSY5 **A0A0D3GSY5_9ORYZ** (496 aa)
NPH3 domain-containing protein. *Oryza barthii*

```
MEMEMSRSWQELGVVDTIYEDDHEEEEEEEEEEEEEEEEEEEEEEECFDSLTMSSSPAATSRSCSPPPAAEEFAMPAALRN
AVREWSRANGPCKPDVIVRVQEHCFALHRDPITSQSSYLKRRLSECSDVAVDLPAGLTVDAFVDAVASCYGAEAALSPGS
LAAAWAAADWLELRGEDGLARRAEDYFFQEVATDHGRAAATLASSGGADGRWLDDVAALPVEEFEVAVEAMRARFAHDHD
LMYTIVDHYLQNHRGKLTEEEKSRVCYNVNCTKLSHHLFMHLVQNPRLPLRFVVQAMLVEQLHSHHSMLLSGGHHHHAGA
AGAPSSAAPPASLLKSSLSGAFGACGGFAATAAAAGDAASSMTLGDILQRDAVLRQSAHIRASMQATTQRIDSLERELAG
LRTRLRRSEQAAAAAATASAAIDRAGLKSRLVLGFKNLFGRRPVTAAAAAPPTSGERAAARVSVNDKAMSTDAPELDADA
DADELTRPHRRNLSIV
```

24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE

A0A0D9QHR0 **A0A0D9QHR0_PLAFR** (379 aa)
Casein kinase II subunit beta (CK II beta). *Plasmodium fragile*

```
MDEEGVSNNDSSNDVLDEENCEEGRDFSDISFGHREEEEGGLHVGSVDGHSGDGGDDGDGGHAGLDVEDVDGQGADAPGQ
```

```
EKDAEGGGNQEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDDEDDDEDDDDDDDYDDDEYDEDDFNEATVSWIEWFCQL
KQNIFLVEVDEDFIRDEFNLIGLQTKVPHFKKLLKIILDEDDDDDDDDEEEDDYDEEDDEINRGSDELYKNKDIYEQNAA
CLYGLIHSRFILTSKGLALMREKYKSSIYGTCPSIYCDNAKLLPTAISEVPKFLSPLLYCPRCCETFYPHKNSLINQLDG
AYFGTSFASFFALSFNIQSDKKRIYYTPQICGFTINRDIRETLYLDMNKDNSESSEEYS
```

94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE

A0A0D9QYX5 **A0A0D9QYX5_CHLSB** (728 aa)
YTH domain-containing protein. *Chlorocebus sabaeus (Green monkey) (Cercopithecus sabaeus)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSN
NKRIVSTKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKPCVRKRDPERRAKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEE
EEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSA
SESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVIL
IFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQE
IELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQ
RPGYLKDPRYQEVDRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQAHPPYSGH
HPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDR
GERGRYRR
```

230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE

A0A0D9R0J7 **A0A0D9R0J7_CHLSB** (586 aa)
RanGAP1_C domain-containing protein. *Chlorocebus sabaeus (Green monkey) (Cercopithecus sabaeus)*

```
MASEDIAKLAETLAKTQVAGGQLSFKGKSLKLNTAEDAKDVIKEIEDFDSLEALRLEGNTVGVEAARVIAKALEKKSELK
RCHWSDMFTGRLRTEIPPALISLGEGLITAGAQLVELDLSDNAFGPDGVQGFEALLKSSACFTLHELKLNNCGMGIGGGK
ILAAALTECHRKSSAQGKPLALKVFVAGRNRLENDGATALAEAFRVIGTLEEVHMPQNGINHPGVTALAQAFAVNPLLRV
INLNDNTFTEKGAVAMAETLKTLRQVEVINFGDCLVRSKGAVAIADAIRGGLPKLKELNLSFCEIKRDAALAVAEAMADK
TELEKLDLNGNTLGEEGCEQLQEVLEGFNMAKVLASLSDDEDEEEEEGEEEEEAEEEEEEEEEEEEEEEEEEEEEPQQG
GQGEKSATPSQKILDPNTGEPAPMLSSPPPADVSTFLAFPSPEKLLRLGPKSSMLIAQQTDTSDPEKVVFAFLKVSSVFK
DEATVRTAVQDAVDALMKKAFSSSSFNSSAFLTRLLAHMGLLKSEDKVKAIANLYGPLMALNHMVQQDYFPKALAPLLLA
FITKPNSALESCSFARHSLLQTLYKV
```

375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE

A0A0D9R911 **A0A0D9R911_CHLSB** (1197 aa)
Uncharacterized protein. *Chlorocebus sabaeus (Green monkey) (Cercopithecus sabaeus)*

```
SQGEAPAEMGALLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDE
SENLEGDGDLHGGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGPEPPPATT
SPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEELGSARRSEVTLAK
GDPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDR
SGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSS
LETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHC
CPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGAAAPAPPPLSQDAP
GRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQ
LYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEV
ARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTL
TDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPE
RSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGESCPEDYKYISENCETSTMNIDRNITHLQH
CTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVR
ALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRF
PRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

287 - 306:	EEEEEEEEEEEEEEEEEEEE
288 - 307:	EEEEEEEEEEEEEEEEEEEE
289 - 308:	EEEEEEEEEEEEEEEEEEEE
290 - 309:	EEEEEEEEEEEEEEEEEEEE
291 - 310:	EEEEEEEEEEEEEEEEEEEE

A0A0D9RGX3 **A0A0D9RGX3_CHLSB** (1325 aa)
Tau tubulin kinase 1. *Chlorocebus sabaeus (Green monkey) (Cercopithecus sabaeus)*

```
MQCLAAALKDETNMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTRENVALKVESAQQPKQVLKMEVAV
LKKLQGKDHVCRFIGCGRNEKFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESIEAIHSVGFLHRDIKPSNF
AMGRLPSTYRKCYMLDFGLARQYTNTTGDVRPPRNVAGFRGTVRYASVNAHKNREMGRHDDLWSLFYMLVEFAVGQLPWR
KIKDKEQVGMIKEKYEHRMLLKHMPSEFHLFLDHIASLDYFTKPDYQLIMSVFENSMKERGIAENEAFDWEKAGTDALLS
TSTSTPPQQNTRQTAAMFGVVNVTPVPGDLLRENTEDVLQGEHLSDQENAPPILPGRPSEGLGPSPHLVPHPGGPEAEVW
EETDVNRNKLRINIGKSPCVEEEQSRGMGVPSSPVRAPPDSPTTPVRSLRYRRVNSPESERLSTADGRVELPERRSRMDL
PGSPSRQACSSQPAQMLSVDTGHADRQASGRMDVSASVEQEALSNAFRSVPLAEEEDFDSKEWVIIDKETELKDFPPGAE
PSTSGTTDEEPEELRPLPEEGEERRRLGAEPTVRPRGRSMQVLAEEDLQHLPPQPLPPQLSQADGRSETSQPPTPGSPSH
SPLHSGPRPRRRESDPTGPQRQVFSVAPPFEVNGLPRAVPLSLPYQDFKRDLSDYRERARLLNRVRRVGFSHMLLTTPQV
PLSPVQPQANGKEEEEEEEEEEDEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAAAAVALGEVLGPRSGSSSEGSERS
TDRSQEGAPSTLLADDQKESRGRASMADGDLEPEEGSKTLVLVSPGDMKKSPVTAELAPDPDLGTLAALTPQHERPQPTG
SQLDVSEPGTLSSVLKSEPKPPGPGAGPGAGTVTTGAGGVAVTSSPFTKVERTFVHIAEKTHLNVMSSSGQALRPEEFST
GGELGLELASDGGTVEEGAPAPLENGLALSGLNGAEIEGCALSGPPGETPSAMATNSLPNGPALADSPAPVSPLEPSPEK
VATISPRHRAMPGSRPRSRIPILLSEEDTGSEPSGSLSAKERWSKRARLQQDLARLVMEKRQGRLLLRLASGASSSSSEE
QRRASETLSGTGSEEDTPASEPAAALPRKAGRAAATRSRIPRPIGLRMSVPAAAQQLPSRSHGAAPASDTAITSRLQLQT
PPRSATAADLRPKQPPGRGLGPGRAQAGARPPAPRSPGLPTSTSAARNASASPRSQSLSRRESPSPSHQARSGVPPPRGV
PSARAQPDGTPSPGGSKKGPRGKLQAQRATTKGRAGGAEGRAGAR
```

751 - 770:	EEEEEEEEEEEEEEEEEEEE
752 - 771:	EEEEEEEEEEEEEEEEEEEE
753 - 772:	EEEEEEEEEEEEEEEEEEEE
754 - 773:	EEEEEEEEEEEEEEEEEEEE
755 - 774:	EEEEEEEEEEEEEEEEEEEE
756 - 775:	EEEEEEEEEEEEEEEEEEEE

A0A0D9RKM4 **A0A0D9RKM4_CHLSB** (1196 aa)
Solute carrier family 24 member 1. *Chlorocebus sabaeus (Green monkey) (Cercopithecus sabaeus)*

```
MGKLIRMGPQDRRLLRTKRLPWSRLLFLLGMLIISSTYQHLRRPRGLSSLWAAVSSHQPVKLASRDLPSEEMMMVSSNPP
KPSSEMGGEMLVPQASVGSDEATLSMTVENIPDIPKRTAKMIPTTTKNNYSPTAAGTERRREDTPTSSRTLTYYTSTSSR
QIVKKYTPTATGEMKSYSPTQVREKVTYTPSPRGRRVVTYASSTFMTTETSHAITPRTTVKDSDITTTYKILETNSLKRI
MEETTPTTPKGMVDSTPTFLTHEVETNVLTSPRSIVEKNNLSPPRRVESNSSAHPWGLVGKNNLKTPQGTVLTHTPATSE
GQVTISTMTGSNPSETKAFTAAWSVRNPSPRTSVSAIETAPTTVWRLEKKPYTAPSTSTTPTVRAKLTTQVHHCVVVKPT
PATPTTPSPSLTTALLPEELSPSPSVLPPILPDLPPKGEYPPDLFSVEERRQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLIMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKQIEAWVKEQLSRRPAAKVMALGDLSKPGDGAIAMDE
LQDNKKLKLPSLLTRGSSSTSLHNSTIRSTIYQLMLHSLDPLREVRLAEEKEEDSLNQEARAQPQAKSESKPEEEEPAKL
PAVTVTPAPAPDIKGDQKENPGGQVGTQPLHRQNWRGLAEVAPLHSSLGDRGDCLQKKKKKKGEREKESEVPKMTEAASG
GEFYTPGNDHIKAGQPLGRGLSFQIHSEKHANKENGGVSEGKQSEEDVAEAESTGEMTGEEGETAGEGETEEKSGGETQP
EGEGETGTQGKGEEREKENEAEGKGDNEGEGEGEIHAEDGEMKGIEGETESQELSAENHGEAKSDEKGVEDGGGSDGGDN
EEEEEEEEEEEEEEEEEEEEEEEEEEEEGNEEPLSLHWPETRQKQAIYLFLLPIVFPLWLTVPDVRRQESRKFFVFTFLG
SIMWIAMFSYLMVWWAHQVGETIGISEEIMGLTILAAGTSIPDLITSVIVARKGLGDMAVSSSVGSNIFDITVGLPVPWL
LFCLINGLQPVPVSSNGLFCAIVLLFLMLLFVISSIASCKWRMNKILGFTMFLLYFVFLIISVMLEDRIISCPVSV
```

961 - 980:	EEEEEEEEEEEEEEEEEEEE
962 - 981:	EEEEEEEEEEEEEEEEEEEE
963 - 982:	EEEEEEEEEEEEEEEEEEEE
964 - 983:	EEEEEEEEEEEEEEEEEEEE
965 - 984:	EEEEEEEEEEEEEEEEEEEE
966 - 985:	EEEEEEEEEEEEEEEEEEEE
967 - 986:	EEEEEEEEEEEEEEEEEEEE
968 - 987:	EEEEEEEEEEEEEEEEEEEE
969 - 988:	EEEEEEEEEEEEEEEEEEEE

A0A0D9RKY8 **A0A0D9RKY8_CHLSB** (1222 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Chlorocebus sabaeus (Green monkey) (Cercopithecus sabaeus)*

```
MKIVRTLAPFVRTTCTLNITGPPRTRSPAITPGTQHPGASACRLLSPRMLLPSLSPRVQPAFTQCAGPQPPPHAHSSVGR
RRGVFASSRHATTGARGKMAAAVLSGPSAGSAAGVPGGTGGLSAVNSGPRLRLLLLESVSGLLQPRTGSAVAPVHPPNRS
APHLPGLMCLLRLHGSVGGAQNLSALGALVSLSNARLSSIKTRFEGLCLLSLLVGESPTELFQQHCVSWLRSIQQVLQTQ
DPPATMELAVAVLRDLLRYAAQLPALFRDISMNHLPGLLTSLLGLRPECEQSALEGMKACMTYFPRACGSLKGKLASFFL
SRVDALSPQLQQLACECYSRLPSLGAGFSQGLKHTESWEQELHSLLASLHTLLGALYEGAETAPVQNEGPGVEMLLSSED
GDAHVLLRLRQRFSGLARCLGLMLSSEFGAPVSVPVQEILDFICRTLSVSSKNISLHGDGPLRLLLLPSIHLEALDLLSA
LILACGSRLLRFGILISRLLPQVLNSWSIGRDSLSPGQERPYSTVRTKVYAVLELWVQVCGASAGMLQGGASGEALLTHL
LSDISPPADALKLRSPRGSPDGSLQTGKPSAPKKLKLDVGEAMAPPSHRKGDSNANSDVCAAALRGLSRTILMCGPLIKE
ETHRRLHDLVLPLVMGVQQGEVLGSSPYTSSRCRRELYCLLLALLLAPSPRCPPPLACALQAFSLGQREDSLEVSSFCAE
ALVTCAALTHPRVPPLQPMGPTCPTPAPVPPPEAPSPFRAPPFHPPGPMPSAGPMPSAGPMPSAGPVPSARPGPPTTANH
LGLSVSGLVSVPPRLLPGPENHRAGSNEDPILAPSGTPPPAIPPDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDSV
VIVPEGLPPLPPPPPSGATPPPIAPTGPPTASPPVPAKEEPEELPAAPGPLPPPPPPPPPVPGPVTLPPPQLVPEGTPGG
GGPPALEEDLTVININSSDEEEEEEEEEEEEEEEEEEEEEDFEEEEEDEEEYFEEEEEEEEEFEEEFEEEEGELEEEEEE
EDEEEEEELEEVEELEFGAAGGEVEEGGPPPPTLPPALPPPESPPKVQPEPEPEPGLLLEVEEPGAEEEHGADTAPTLAP
EVLPSQGEVEREEGSPSAGPPPQELVEEEPSAPPTLLEEGTEDGGDRVQPPPETPAEEEMETETEAETLQEKEQDDTAAM
LADFIDCPPDDEKPPPPTEPDS
```

980 - 999:	EEEEEEEEEEEEEEEEEEEE
981 - 1000:	EEEEEEEEEEEEEEEEEEEE

A0A0D9VJ71 **A0A0D9VJ71_9ORYZ** (493 aa)
Uncharacterized protein. *Leersia perrieri*

```
MAGFDNETDLVGVEYDDDMGDFIVYSDDDVVLGDEQKEEQKEFDELEEEEEEEEEEEEEEEEEEEEEPPPVGQVEILTLR
EKLKADIRRKNQAQQGAAAGRASSSSSVQPPIKDRFGSFFGPSRPSLARRVIEEGCSSIFKEKQNVPSSKNSGSLTSKAQ
QLTKEHKQKPKFVSEEKKKVDALRQNRDYSCLFKDDTDTLQPTEERSGNMSALPLKSDENASTHSTGKNSNVYTTLTEPS
KDIGLEGAPSVQSSAGSLGKKPNTKRMIASAKNGSNLPATKKIKRLQSSADGQKVQQAMQGKKPNGLLPGKKHLGSSESQ
REQNNGQQSLQCGKTKPSSIKSHHSGQKVSAQSHERSRIALKQLAHSSKPKPPRPISSSAVHNDHGKARRVVKRKSNDGC
DEEGVDYSSIIRGMFNYNPEKFAGRDEDDRNMEANYASIQMEERRSAKLARKEDDEQLRLIMEEERRENQERKRKKLAQK
GWGQTLNAAEDFS
```

47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE

A0A0D9VJ72 **A0A0D9VJ72_9ORYZ** (480 aa)
Uncharacterized protein. *Leersia perrieri*

```
MAGFDNETDLVGVEYDDDMGDFIVYSDDDVVLGDEQKEEQKEFDELEEEEEEEEEEEEEEEEEEEEEPPPVGQVEILTLR
EKLKADIRRKNQAQQGAAAGRASSSSSVQPPIKDRFGSFFGPSRPSLARRVIEEGCSSIFKEKQNVPSSKNSGSLTSKAQ
QLTKEHKQKPKFVSEEKKKVDALRQNRDYSCLFKDDTDTLQPTEERSGNMSALPLKSDENASTHSTGKNSNVYTTLTEPS
KDIGLEGAPSVQSSAGSLGKKPNTKRMIASAKNGSNLPATKKIKRLQSSADGQKVQQAMQGKKPNGLLPGKKHLGSSESQ
REQNNGQQSLQCGKTKPSSIKSHHSGQKVSAQSHERSRIALKQLAHSSKPKPPRPISSSAVHNDHGKARRVVKRKSNDGC
DEEGVDYSSIIRGMFNYNPEKFAGRDEDDRNMEANYASIQMEERRSAKLARKEDDEQLRLIMEEERRENQERKRKKLAQK
```

47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE

A0A0D9X356 **A0A0D9X356_9ORYZ** (998 aa)
F-box domain-containing protein. *Leersia perrieri*

```
MVAQVLESSSNKPLVIILKRSEEGDEYENEAPTLMNPFSDDDDDSASFLQQKQKELQTVINKGKQQQCLDCLQGEWLLML
DNATKQCSLVSSTSSPNFITTISMPPLETPLEPLGRCALSSSSPLSPDCTVMFATLFDNYLAYTRPREDDDWWQLDDVDV
EFVGDIVSCKGKMYVPIVMVDASTYHPDIERRGIPKPSRIHSMMQQRLLDMDHHRLDADDYTWQKVESIGGDNCVVLSDA
TKAGIRPDCVYVLYTRCRDGVRFYTIRMDDRTTSFRLLPPPTTPSISIVSHHLDDDLQVQEEEEEEEEEEEEEEEEEEE
EEEEEEEECCWPALPIDMVEEIVSKISFIDYFRLRQVCKGWSSSMVKPIKYADRYPAYPMLMTICSNSNGVYKLFDPIVE
QEYTINKLESQDYFQMLLFSRHDDGWVLVTRGDKYMYATNPFSGEIEIPAGGNEFDGICLSATPTSPDCIAFSVSKERNP
NSNGVYVMLWRAGDRQWTTERIEHHTPFRTAYCNPVFYNDEFYCLGTRGGLAVFNPKNMTWNVVLDKPEPILMNIGADDP
MPGDMYCHLLEFMGDLFTVFRPHNEWGNQHVQARLMAWTKLDRLDDAVLFVDNWNATMIPAPRDAVRNRIYLPKFGGCNH
AGDANKSAFYDLESRKSQSMRVGQAAFIFVSHKAALAAVGAPDNLVHIITGFAETGQALVSSVDKIFFVGSPGVGRMVIQ
VAARAALQSSGQNCAGAERFYVHKDIYSTFVSQVVKIVKSISVGPPLSGRYDMGAICMIEHSEKLQSLVNDAIDKGAEIA
GRGSFGNLGEDAVDQFFPPTVLVNVNHTMKIMQEEAFGPILPIMKFSSDEEVVKLANDSKYGLGCAVFSGNQKRAIKIAS
QLHCGVAAINDFASSYMCQSLPFGGVKDSGFGRFAGVEGLRACCLVKAVVEDRWWPYVKTMIPKPIQYPVSEHGFEFQEL
LVETLYGLSVWDRLRSLVNLLKMISEQNSHANTRKKSR
```

301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE
306 - 325:	EEEEEEEEEEEEEEEEEEEE
307 - 326:	EEEEEEEEEEEEEEEEEEEE
308 - 327:	EEEEEEEEEEEEEEEEEEEE
309 - 328:	EEEEEEEEEEEEEEEEEEEE

A0A0D9X357 **A0A0D9X357_9ORYZ** (897 aa)
F-box domain-containing protein. *Leersia perrieri*

```
MVAQVLESSSNKPLVIILKRSEEGDEYENEAPTLMNPFSDDDDDSASFLQQKQKELQTVINKGKQQQCLDCLQGEWLLML
DNATKQCSLVSSTSSPNFITTISMPPLETPLEPLGRCALSSSSPLSPDCTVMFATLFDNYLAYTRPREDDDWWQLDDVDV
EFVGDIVSCKGKMYVPIVMVDASTYHPDIERRGIPKPSRIHSMMQQRLLDMDHHRLDADDYTWQKVESIGGDNCVVLSDA
TKAGIRPDCVYVLYTRCRDGVRFYTIRMDDRTTSFRLLPPPTTPSISIVSHHLDDDLQVQEEEEEEEEEEEEEEEEEEE
EEEEEEEECCWPALPIDMVEEIVSKISFIDYFRLRQVCKGWSSSMVKPIKYADRYPAYPMLMTICSNSNGVYKLFDPIVE
QEYTINKLESQDYFQMLLFSRHDDGWVLVTRGDKYMYATNPFSGEIEIPAGGNEFDGICLSATPTSPDCIAFSVSKERNP
NSNGVYVMLWRAGDRQWTTERIEHHTPFRTAYCNPVFYNDEFYCLGTRGGLAVFNPKNMTWNVVLDKPEPILMNIGADDP
MPGDMYCHLLEFMGDLFTVFRPHNEWGNQHVQARLMAWTKLDRLDDAVLFVDNWNATMIPAPRDAVRNRIYLPKFGGCNH
AGDANKSAFYDLESRKSQSMRVGQAAFIFVSHKAALAAVGAPDNLVHIITGFAETGQALVSSVDKIFFVGSPGVGRMVIQ
VAARAALQSSGQNCAGAERFYVHKDIYSTFVSQVVKIVKSISVGPPLSGRYDMGAICMIEHSEKLQSLVNDGIDKGAEIA
GRGSFGNLGEDTVDQFFPPTVLVNVNHTMKIMQEQSLPFGGVKDSGFGRFAGVEGLRACCLAKAVVEDRWWPYVKTMIPK
TIQYYKIATSRVDAIAS
```

301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE
306 - 325:	EEEEEEEEEEEEEEEEEEEE
307 - 326:	EEEEEEEEEEEEEEEEEEEE
308 - 327:	EEEEEEEEEEEEEEEEEEEE
309 - 328:	EEEEEEEEEEEEEEEEEEEE

A0A0D9ZHL5 **A0A0D9ZHL5_9ORYZ** (728 aa)
DUF4220 domain-containing protein. *Oryza glumipatula*

```
MGISSALDWWDDWKLRILVLGSNTIQLFLFIYGGVRWHRISLWFRLCIWLAYIGGDSLAIYTLATLFNRHKHEAPAVSEL
EVLWAPILLIHLSGQDMIASYSIQDNYLWWRQVVTLVSQVTVAMYVFCLAWSGEKIVLKAAVLLFIVGILKFCAKPWALK
RAIIRSIARHPPSVLRRKKLIGSGGGQLVDYWRSCTTGFIPTVTMFVVSRELRERPQPNDETEAVEQGERREGGQFHENL
ERSTVKTAIEPVVEQQKKEEEEEEEEEEEEEEEEEEEEEEEEEDLINLNEYVERAKEIMNRQGQLSKPTLRRLQSVLQPE
LFMADAFVTYSKRLKILQFLMAINTNYSYRVIRAGLFDVYIRLYTRVRVTIMPIASWLRLLSILLATTAAGLYTRSHKDM
YNKHDITVTYILFFSTALLELISLVTLCPLFFPLARWYIKQTPSMDRIFEAVKHHVIFYGWSKYIKSAASYRRFNCMRGQ
LAMKKFLPGSAKDHPAASKHLLVVGNSLSIPFDESVLLWHIATEIWFHHQTRTSNDDNTSLDSAVPLGLEISRYMMYLFT
SQPEMLMPGTRSHLFANACDDITFMAKYSDIAGHSITLAQAAQQLAKGILHTARHRWVYGDCVGPLIPKACELADALIFF
MEELLDHSTLEKMVRDVWVEMLCYTASRCGGGYLHAVSLGSGIEPLTLVWFSQCYLGMETMADRLQRPVPEPEKEEEKTQ
GAQDSNKE
```

259 - 278:	EEEEEEEEEEEEEEEEEEEE
260 - 279:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE
262 - 281:	EEEEEEEEEEEEEEEEEEEE
263 - 282:	EEEEEEEEEEEEEEEEEEEE
264 - 283:	EEEEEEEEEEEEEEEEEEEE

A0A0D9ZYT0 **A0A0D9ZYT0_9ORYZ** (1296 aa)
Uncharacterized protein. *Oryza glumipatula*

```
MAPPLYLLLLLPLLACADEVPDRYAVLRAPQGPGASAAAKEYLDPTFPLPAPPPAAPSCTVPVLSYSFGDTYGAAPAKAS
YAPPAGCPAPWSLVVLTFSASCAGDQYDRVAAVWLDGAELLRTTTAEPTPEGVRWTVRKDVTRYSALLRSPPGGVLSVML
ENVVNDKYTGVYSVNVSLEFHGTPPYLSDAASSSPAGVASNDPKELMLPESYFQPADLIVPISDVAGNGKGGFWFRIQNA
SDSHSRLVTIPSSTYRAVLEVFVSPHSNDEYWYSNPPDIYIRENNLTTRRGNAAYREVVVSVDHRFVGSFVPFPVIYTGG
INPLFWQPVAALGAFDLPTYDVELTPFLGLLVDSNAHEIGLSVFDGIAEWLVDANLHLWLDPSTSDVHAALGAYQTPRLK
ISRHYSTRLLEGRFKIKAKRKSSFSGWVKSSFGNFTTEVEAELKATSLVEFTGDGRNKTVSLEAKQETKTLIRAGDTRKV
IGRVEREAKYPLSLFAETEDGENGTSVVTVSLTHGLSVEAEVETKALESKEKLDDAQAAQGWMVLLDHDVLNGSVTTTQA
YRFSDDEREYERAIDVVDGAVLSDNVTESFSALAAAAADARRRRFHAGIAALIRFRPHRRDQDYCFSSEGEGKVSTGDDL
LDALVEVFPQLNFLTLVEVCMEYKNDIDGAADYIIHNVLPSIPDNNDAHANEDSHMKRPASVDNDADSVQSYLANKYTAE
QEEEEEEEEEEEEEEEEEEEEEEEEEEDEDDDEEEDEDDEEDRLMEENSDCLVAIDLNSKPGTSAFDDDLVTHDNGLPA
MNIQSSYPVRLELLDNAIADEIDKKITLMSNVTAINQMLEDIKLKEEKTKQAVLEATQAGNDIFVKVEELKEMTMLSTEE
NDKVVAGEVFAEQSILASEAHGLQARLSNISEERNNYALIIDEMRHTLQNRFAEAEVETVAAEKKKVERETLAEKMLNEQ
ELILDATKERSKMLEQQVRENAKLRELLMDRGQVVDALQGEMLGIFDKISQLQLRVDKQLPEPLLSSMSSSVNSADNIAQ
LQCRVDDPQHSVDDSLQLASPRLSSSFKSTDSTAQAHCRVDEPQISVDESLLPVDECEQLQLISPRLSSSVMSAQSQYRV
DEPLLPVDEVLQLASSSLSSSLKSGDNIAQLLGVLDVHLPVDDLLQLPSLILSSSVKSSDSIAQFQQKADADEMLQSSSL
ASSEKPATFKNWSSASDTITQFQQRANADESLPLPSSSLASSEKPATFKSTWSSAAESNSVFSGDEEIDDASFHDSIDLD
DSWDLVDDEAIYMCAN
```

722 - 741:	EEEEEEEEEEEEEEEEEEEE
723 - 742:	EEEEEEEEEEEEEEEEEEEE
724 - 743:	EEEEEEEEEEEEEEEEEEEE
725 - 744:	EEEEEEEEEEEEEEEEEEEE
726 - 745:	EEEEEEEEEEEEEEEEEEEE
727 - 746:	EEEEEEEEEEEEEEEEEEEE
728 - 747:	EEEEEEEEEEEEEEEEEEEE
729 - 748:	EEEEEEEEEEEEEEEEEEEE

A0A0E0L261 **A0A0E0L261_ORYPU** (1270 aa)
Uncharacterized protein. *Oryza punctata (Red rice)*

```
MAPPLYLLLLFLPLLAVPACPDEVPDRYAFRRAPQGPGASAAAKEYLDPTFPLPPPPPAAPSCTVPVLSYSFGDTYGAAP
AKASYAPPAGCPAPWSLVVLTFSASCAGDQYDRVAAVWLDGAELLRTTTAEPTPEGVRWTVRKDVTRYSALLRSPPGGVL
SVMLENVVNDKYTGVYSVNVSLEFHGTPPYLSDAASSSSTSPAGVGNNDPEEPMLPESYFQPADLIIPISDVTGNGKGGF
WFRIQNASDSHSRLVTIPSSSYRAVLEVFVSPHSNDEYWYSNPPDIYIRENNLTTRRGNAAYREVVVSVDHRFVGSFVPF
PVIYTGGINPLFWQPVAALGAFDLPTYDVELTPFLGLLVDSNAHEIGLSVVDGIAEWLVDANLHLWLDPSTSDVHAALGS
YQTPRLKISRHYSTRLLEGRFKIKAKRKSSFSGWVKSSFGNFTTEVETELKATSLVEFTGDGQNKTVSLEAKQETKALIR
AADTRKVIGKVEREAKYPLSLFAETEDGENGTSVVTVSLTHGLNVETEIETKAFESKEKLDDEQTAVGWMVVMDHDVVNG
```

```
SVTTTQAYRFSDEDREYERTIDVVDGAVLSDNVTESFSALAAAADGRAGIAALKGGYLGLSWELSCLVSSIATENSGEIR
QFEEFLCAGFVSKGIDVSQDYCFSSEGKGKMSTGDDLLDALVEVFPQLNFLTLVEVCMEYKNDIDGAADYIIHNVLPSIL
DDNDVNANEDSHLRGPASVDNDVDSVQSDIANKYTAEEQEEKEDEDEDEEEEEEEEEEEEEEEEEEEEEEEEEDRFMEEN
SDCLVAIDLNSKPETSAFDDDLVTHDDGLPALTIQSSCPVRLESLDNAIADEIDKKVTLMSNVTEITQMLEDIKLKEEKT
KQAVLEATQAGNDIFVKVAGEVFAEQSILASEAHGLQARLSNISEDRKNYALIIDEMRHTLQNRFAAAEVETIAAEKKKV
ERKTLAEKMLNEQELILDATKERSKMLEQQVRENAKLRELLMDRGQVVDALQGEMLGIFDKISQLQLRVDKQLPEPLLSS
MSCSVNSADNIAQLQCRVDDPQHSVDDSLQLASPRLSSSFKSTDSTAQAHCRVDEPQISVDESLLPIDECEQLQLVSPRL
SSSVMSAQSQGRVDEPLLPVDEVLQLASSSSSSSLKSGDNIAQLLGVLDVHLPVDESLQLPSLSLSSSVKSSDNIAQFQQ
KADTDESLQSSSLASSEKPATFKSSWSSAAESNSVFSGDEEIDDASFHDNIDLDDSWDLVDDEAVYMCAN
```

769 - 788:	EEEEEEEEEEEEEEEEEEEE
770 - 789:	EEEEEEEEEEEEEEEEEEEE
771 - 790:	EEEEEEEEEEEEEEEEEEEE
772 - 791:	EEEEEEEEEEEEEEEEEEEE
773 - 792:	EEEEEEEEEEEEEEEEEEEE
774 - 793:	EEEEEEEEEEEEEEEEEEEE

A0A0E0MMK7 **A0A0E0MMK7_ORYPU** (479 aa)
F-box domain-containing protein. *Oryza punctata (Red rice)*

```
MDGDGDDRWGDVPTDVLWEILRRLPEISGRRRVRLVCRRWLDVVDEIEPEVQRRRAKPLPFFKNGCYEHPSAFFLDDLAG
ECDVRSLFPEDVDDDRDISDRYNEDDMVGSCNGLLCFWIDRHYSGGCGVFVINPVTGETLHIPSPPPETLATSRSSRAGT
LSFGYHPTTGKYKIVHFPSNGGLVDDVSLGNTTSTAASSSSSSASRHGGHGGGVVNVLTLGDDTGGGGAWWRAVEAPPWT
LCSAWGVVSVDGATYWVNNGREIMSFDLEHERVAAVAPLPAMSKCRLPVSMAKKDACCQLTDVGGRLGVSIAIHRRNSIC
IEVWILEGRGDKQSWSQWGTIQGLQPSQKIGRPYFAYGKCVLTNIYRQVFDDRLNNIVYRHLPCSLKGGSILSRAIEGMP
VAKFKTRELRMFSYIETREPLNIYKEEEEESSSSSLEEEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEAVVF
```

447 - 466:	EEEEEEEEEEEEEEEEEEEE
448 - 467:	EEEEEEEEEEEEEEEEEEEE
449 - 468:	EEEEEEEEEEEEEEEEEEEE
450 - 469:	EEEEEEEEEEEEEEEEEEEE
451 - 470:	EEEEEEEEEEEEEEEEEEEE
452 - 471:	EEEEEEEEEEEEEEEEEEEE
453 - 472:	EEEEEEEEEEEEEEEEEEEE
454 - 473:	EEEEEEEEEEEEEEEEEEEE
455 - 474:	EEEEEEEEEEEEEEEEEEEE
456 - 475:	EEEEEEEEEEEEEEEEEEEE

A0A0F0IF04 **A0A0F0IF04_ASPPU** (168 aa)
Ubiquinol-cytochrome C reductase hinge protein. *Aspergillus parasiticus (strain ATCC 56775 / NRRL 5862 / SRRC 143 / SU-1)*

```
MGISDFFSDIISSFSLPEAQAEAPAENVEQPSSQETETEEKPAMTEESTSEETAEKTEESAEETPEEPAEEEPEQEEEEE
EEEEEEEEEEEEEEEEPEDIKPQLEEECANSAQCAPYKHHFDECVERVTQQQEDADYKGPKEDCVEEFFHLAHCASECAA
PKLWKSLK
```

76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE

A0A0F2LWH9 **A0A0F2LWH9_SPOSC** (842 aa)
Nucleolar complex protein 2. *Sporothrix schenckii 1099-18*

```
MAVAKKNAKATRKFEKKHLKGVLEKRKASAKIKQRNILQEKKKAKRSQDAAFYKGAASATGANGETVGSGPRSKRPDAKV
SEMSVDDFFQGGFQILDKEEGGKGKGKAKGKDKAEKADTKAQLGKRKRNGAAAAGEDDSASASGGSDSENEPEYDAVAPS
DDSDEDDNLDLDAADIGMTKEAMEALAEKDPEFYKFLKENDPEALDFDEDADLSGLGGGDDEDEDDEDDEDDEDAKRPRK
KQKAAKAAAPRDNELTRPMIAKWEASMAESFSLRAARQAVLAFRCAAHLNEDADEAASLSQRFAIKSPNVFHDILVVALK
HVPLVLQHHIPVKESSTHRVYVQTESKKFKALSALIRSFASSVLHLLSTLSDDGTLKLTLSALTPLLPYLLSFRKVLKQL
VKSVVGFWAQPASSQTTRITAFLVLRRLVVIGDKGVRESVLKATYQGLVQGSRATNSNTIAGINLMKNSAAELWGLDPAI
GYTTAFASIRQLAIHLRNSIVHNQNNAFRNVYNWQYVHSLDFWSCVLAEHCSPTATAAAGSGGGDDSQLKLLVYPLVQVT
LGAMRLIPTAAYFPLRFQLFRSLLRVSRATGTYIPLAPVLLEVLNSADMKKAAKISTEKQLDFAVAYKAPKSLLHTTVYQ
TAVGEQVVELLSEYFALWATSIAFPEFALPVVIMLKRWIKDARKRGGKNGRQLNNKVVSGLVLVVQKLEANAAFIEAKRA
HVTFAPRDRTQVDAFLKDFDWQKTPVGAFVVAQRKASAERQRVLEETRKQEDARRQEEKKQLQAARLDEDNGEEEEEEEE
EEEEEEEEEEEEEEEEDEDEEEIELESDDEDIESDDDEEEDE
```

793 - 812:	EEEEEEEEEEEEEEEEEEEE
794 - 813:	EEEEEEEEEEEEEEEEEEEE
795 - 814:	EEEEEEEEEEEEEEEEEEEE
796 - 815:	EEEEEEEEEEEEEEEEEEEE
797 - 816:	EEEEEEEEEEEEEEEEEEEE

A0A0F4GGF3 **A0A0F4GGF3_9PEZI** (650 aa)
Uncharacterized protein. *Zymoseptoria brevis*

```
MSRKSVSSTSPPPNMTRPSPPLHSYSSPSPACPISSSSSSAPKLVSSTNSLPPWNFPFGPSTKYHNREKTRPRHARYQSA
YTPRGPVLSTEKRAHRRAAHSSVSIPRYSPTSPSSRSSPLSRFPSYNSTKMSAAKMSINPATPAKHLYRRSSDFQDSPFS
DYFSEDGRSVYTTCASDETKQLLVRMNRLQSQLMRDQSGDRHKAIAVVARKLGEMEEELSKLNDNATSNLDDSAVFIDEP
VEGRKSTTEPAVSSTPSTPSRKSSATGRTHVSKPSMNDSVMEATQTFTYEQIKAERDSLAVRLQGLSEGLNTVQGELTQR
YAEVRRLNNFHNEERERYEQHVEKLQSENEGLRSDLGFEYSELLYLKLQMKSLEVDIDNIPDEDIDPRHATIADLRRARA
KRARRNRILSEMDRWRTDWQDVSTRFKRRRNRYGVPTSPIVEFEGHEFAAEWHLETVREARGHATCLTIKRIEGPPVREL
TALREEIVDPDALRLAEAKVFKGYIDQGAQTEMSAADYMHVNFDEAETESFFDHEYPALDELEDIDCDVAVESRRDFTTG
AIGEDDEAEAEESEEEEEEEEEEEEEEEEEEEEEEEEEEDIHPQPKEPTGSAPLPLTPTTLPPNSSRSAWQELWASLASLS
GLPDDDEEDF
```

574 - 593:	EEEEEEEEEEEEEEEEEEEE
575 - 594:	EEEEEEEEEEEEEEEEEEEE
576 - 595:	EEEEEEEEEEEEEEEEEEEE
577 - 596:	EEEEEEEEEEEEEEEEEEEE
578 - 597:	EEEEEEEEEEEEEEEEEEEE
579 - 598:	EEEEEEEEEEEEEEEEEEEE

A0A0F7SPH4 **A0A0F7SPH4_PHARH** (318 aa)
Uncharacterized protein. *Phaffia rhodozyma (Yeast) (Xanthophyllomyces dendrorhous)*

```
MMTTKTFATNSMDASVPVNPADATSQSSRSKEHWQTPIGDSWKQRQRRIRPRPSRHAASVNHPPDDFRTPLPSQHGLKLQ
LNDTEEEEEKEDEEEMSVSSVSHRLPAYRPELGVTQYLEEPRRLSSSSRIDWVDQEPPDELNENDEEEEEEEEEEEEEEE
EEEEEEEEEESEIKGDSPYAPMNRLLYTLHQQRYPQTPSTSPTAAITVPTSPCSSPLFAPPTPNLRPTYRPHPLSKQTSS
VSSLQPTIRANSSSEVELIVGAGSLSRQKVADQEVIEGRTIKDNGEREREEVERRYEVANRLLGGLVLGRRRGREEVE
```

146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE

A0A0F7SQ34 **A0A0F7SQ34_PHARH** (558 aa)
WD40 repeat-containing protein. *Phaffia rhodozyma (Yeast) (Xanthophyllomyces dendrorhous)*

```
MAPKRKAPVSTSSSSKPKPKGGPKSKPEGYWPKKNKQPAVKKARVEVEYEDSASSLKKSGKFGSSGPKKASQPVKPKSAA
PSSVTKPKKSEKKLTFAKDIPYKSPFADESEIAQDDDEEPTESAKTTAPKVKKPKAPLPTGPRTFQIVAGSYEKLLYGLS
GLLPEPTAEGEQQAEHDYTMKPVFIFPAHQACVKTVAASEGGKWLATGSSDEMVKIWDLRRRKEVGGLMNHNGTITSLYF
PSRSHLLTTSEDSTLSLFRTRDWTLLRSFKGHVGRVNSVTVHPSGKLALTVGKDRVLRMWDLMKGKPGGGVKIGKEGEIV
RFAPSGDQFAILSVSTLDVYTKEMKLVQTIENPKRFHDFQFLDVKQGEKTRELLVAAVEQGYVRVYEKFESKESKQLEAA
KDEEEEEDVEDQWKEVARLGGHTNRVKSLAVLYPLLSTVSSDGFINLYNLSNLPNVPTSNGSDVPTILPVGKYDTNGTRL
TCLTMAEGVRLSSGGGEGEVVDSETESESEDELEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEDEDEEEMEEE
```

514 - 533:	EEEEEEEEEEEEEEEEEEEE
515 - 534:	EEEEEEEEEEEEEEEEEEEE
516 - 535:	EEEEEEEEEEEEEEEEEEEE
517 - 536:	EEEEEEEEEEEEEEEEEEEE
518 - 537:	EEEEEEEEEEEEEEEEEEEE
519 - 538:	EEEEEEEEEEEEEEEEEEEE
520 - 539:	EEEEEEEEEEEEEEEEEEEE
521 - 540:	EEEEEEEEEEEEEEEEEEEE
522 - 541:	EEEEEEEEEEEEEEEEEEEE
523 - 542:	EEEEEEEEEEEEEEEEEEEE

A0A0F7SQM9 **A0A0F7SQM9_PHARH** (1176 aa)
DUF1708 domain-containing protein. *Phaffia rhodozyma (Yeast) (Xanthophyllomyces dendrorhous)*

```
MLSLFTLSPNRRKQSRSYKGRRGVVGGAGGAGGNSSDEKSSLSGKSSQAGSFNSSESDQALLLSRKTRGRQTIPATPSPP
SRRRLTGGPNSTALPLSPPGSETKKPSTFDARPTDLDEASELEWRFASTSIPLVDTGRKTIKWGLMSERNDVILGLEDLG
ILVQTICAELSKRGLETPLLFSSLAVNLSCQKIKSLVRTYVASVQSAFDWTIPRPTPQEDTWAREISLSGERELAWVLRW
ALARVLQIRERNEEKRGLADLDQYAEWRKSERAADHPQTHIFAFAAKLGTLVQPIFVDLLTLFSKLVAHSHLSGCTPPVI
GGLFGPLVFGLPVTLTLVDTQKHFVKSALATEHLLLSFIRSQSFASLQKNLPLPPRLQSWAKNYPATIVSDQVWLSGDPR
KDGRSVRSELVRKDVRAYSVELFRTAESWVGELERASDGYEVCGAWVRDVVAPVKTKAGSVASNRGPRFASDYRKRLNIP
NTTLPSYRVGSHGSLCALAAGEADDDDDDDGWDKDEGGAGWETLAEKKWGFFAQDGFDFIGENHERSLDLNKPEDPVSGK
LQFDLTESSRAAKMAEKRASITWNDFSNTGFPDSGITLSDPLNLFLPIQKEITNWPEHREQVYQRLKSSQKNLPAFDYDV
RPRVCEPVTMEEAFVDAWADLLFSAGWMNRVDPTARECNWAIVQYKTISRKEGPTKPDTLYVVFEEIVPIEYQRQLVAPP
PRKQINFNLFNPRRSKQKRAGKDPVRIRRERERERERERERPEPEPEPNRELGRDEKSDPAVWQDRSTRQHLVFHRSYSTH
```

```
LDDRTNLPRSHSSTAIDRSELRPEPGIRPRGVHGSRSEPSLVNIRKGLVKSNQGVTGNPGKDEKDEKDDDAPRKTRAAAM
TREAVVRDRIDRYMQEFRETKDTTNPVRSPAESCTGIARPIVRDLSEPPEPGPKLVGSVYSLTPVVRVTTESGESVSVGP
TGRSIDTTGMVRSGTGSAQKELLRVGESGGDGGDGGGRGRRGEDERTKAGVEPLRIFPRPDVRAESHRLTTDPACDLDEA
RNDLAPLGAPLLVRSGQASGGGGRQEVVPLQRPVVAEVMPLAVGVSMYLGEVVRPTRPREEPSGERRTTDGARSWSNGDE
RIIRVLRDLFVPVSSYVHGQPLHNLLEEEEEEEEEEEEEEEEEEEEEEEEEEEW
```

1147 - 1166:	EEEEEEEEEEEEEEEEEEEE
1148 - 1167:	EEEEEEEEEEEEEEEEEEEE
1149 - 1168:	EEEEEEEEEEEEEEEEEEEE
1150 - 1169:	EEEEEEEEEEEEEEEEEEEE
1151 - 1170:	EEEEEEEEEEEEEEEEEEEE
1152 - 1171:	EEEEEEEEEEEEEEEEEEEE
1153 - 1172:	EEEEEEEEEEEEEEEEEEEE
1154 - 1173:	EEEEEEEEEEEEEEEEEEEE
1155 - 1174:	EEEEEEEEEEEEEEEEEEEE
1156 - 1175:	EEEEEEEEEEEEEEEEEEEE

A0A0F7SXD6 **A0A0F7SXD6_PHARH** (1727 aa)
Uncharacterized protein. *Phaffia rhodozyma (Yeast) (Xanthophyllomyces dendrorhous)*

```
MSRWDLNPYDEPEEEFDHWISDLQSTITRALNPIRKPLYPNPEPTISILTPKIAPLVPRDSSECEDGDVNMEENLQVDDL
QVMIGEKERDKEDLAVGSKFEQIDVSESSLEKHASDQDESDENDQDSEASKQTYSDENESESEGEDSDFEHDDQAFPPFP
THLQAPSSVRSTPKFNSARDVFFRSQDTPIVPSFTVDQNEDGEDVIELEDSDEDAHLESEPEGEQATWYAKGGMVKIGGL
SNLNRGSEEDDELSREDDEEDEDEDDEENSEDREQEEESLEDSEEDDDEEEEEEEEEEEEEEEEEEEEEEEEGDHESSE
GSDIEEPSALQTHSTYRPRRLSPPGSLPEPAASVPSDISRDELGSVSQVVSTSAPPSLPQDPIEDVEEYEEEDSEDTDEL
GDHDVFCSKDDNDANQAINIETFEDESDELIEGESVVDEDENENENENENGQGTSQEEIFIDPDLSSFVPLGLPMDLMTT
EPLRLSSDPSYKLAFASTASSPSSVNHFNFFTSNSKEVTPLLSSASSPGLSSTSLPKGSVNNGVDIQGPGVDLDTDQLSR
PLRYGLEPDGIEVIDRDGDLVEWHPGNRDTYMLEREDPDDHGSVDTDKENEDEGDLNEVEMSVVHDAFDDIDSDGEEDES
RKQDKSSEEELGVDIREIEHDAEDEKEKILLPVKEIRDATSVYLPKTEGLAEAFDFASTSSYAEQMPSTANILEQFTLSK
EEFSANENTNHSEKPSPIRSPVPKEDEFEREHELAIQPRPVVSHSADSTDHCFAESIEAEEINQEQRQVEEPESFSSTDK
TKADKDVEESDLSSKNIEEERGLDGEGVDDLETRHDTVQPQTKSMKTPSNHSSGDLSAIFVSTPTVEPASADIDPVDEFE
REHEQAVQPHPHTSLLAESISSAGSEATSPELLSEAEPQFDEFEEEHQAAMQPHTHPHPRPEIQSPAEQESTSLPTSPLN
DETLSSAVDLTPTEKVSREVEAEAMAEKGADSEDTMATEGSADATRSEAKDDAVMNLVDTNLNSMSSTSSLEQIQHADDD
MGKGEAPSSPESQSFSTNDSSFLPIDPHTTHVAFDMEEDELDEDPIPDDYVFGAEPTKSSIFTTEENAVDNSRSDTESAM
ATGSSGEADFISIETDEESRTLHPEINESPEAFVMSSPQIRDRPLTKLVQINPPTDSFPPSSPQSARQVTAPISGVEHDD
DNSKATPIRLSGVTRPGLWNDSIPLRFVSSQDQADKTLSKSGRLQDRTEDATSSKIQPTLSPPSSPPHSPEKTTIPAYVE
PSTPMTPTLESDADEQSISSPQPSNSTTDERILLEESNILNDEPMGLEQSDAFSPSIASPPRHSLPSTSNSTPTAQARQL
SFHQHSSTRQQSRPTPAGPVPKIVSDTTTPSRSQQVQPKFSSPVTRSQCKYHVLTIPSPESDRVSRFIVPSCSMSNAQDM
AKEHARITGEATIEENQRRQPLIGEGKPTVSEEIEQSLTRIVGIDLVKEGHVFFLDTISQQDDEASGVASATDSSASTDR
ASSLDEQTEAVAISDSGSSRIEESPVDEQVVDHPLSSQRKSPANVSANPMSSNFTNKSEQPVSEESGTESLQEKLISEDE
GDGKHKEDDEGLEGRLASAEEADENEKSGEDSIADDAPLETSFVQAKRKRSLGFTGDETDNAKEAETTATAAAGEVPEDE
VDSGEGGRVKRVRLESDEPRNQTADPKGVSSPSSKPKTGFLRSLFKR
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289 - 308:	EEEEEEEEEEEEEEEEEEEE
290 - 309:	EEEEEEEEEEEEEEEEEEEE
291 - 310:	EEEEEEEEEEEEEEEEEEEE
292 - 311:	EEEEEEEEEEEEEEEEEEEE
293 - 312:	EEEEEEEEEEEEEEEEEEEE
294 - 313:	EEEEEEEEEEEEEEEEEEEE

A0A0F7UC91 **A0A0F7UC91_NEOCL** (1606 aa)
DNA excision repair protein, putative. *Neospora caninum (strain Liverpool)*

```
MAPTNDACTDKQSDSLNSGRANPAFHAGHENWEAERSAAEAGDLSGLNIEHPSQRAWPQKQHTPASGGVASSPLAPCAAG
MASKDREKNSRPYSKECQSADTHAVDSNRREGATVALSAPGGSIVSTAQSKEASPLPHGKEGDGIPLFAAASSLESVANE
SGSVLDSSLSLSLFQRLGVRAVSASAVEERVQEELQQQEATLKKQRQKNRSLASTSSSSGASSSPSCPELISRSNAPSAE
RTSSSDARGQDDVFRAEQTVQGQNAACSSGYGVEDRSGTGLDELVRGFASRLEPAVGDKLTESCGERETETEFSRNRLLP
LPRNAASDALRLKTGGGVEPPFRECMRKEDNRTHSEDRPSTREAEGDTEKDKERAVDFGCSVERTGSEGPYREGHEEEKE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEDEEEQADLDEDDCWTPETETTERRRGLQTSRSGPRTSEQPSHRPSGR
AALKRKREGDSQCPTGHDSADQALGSGAPRGYLPRSVCVGAGELATKRRFNPRGASGRGDATGASPGRQAAVASDSALEE
KGDSTFEQVGAPASSEPSEDPPGEPPRQRLPGDLSSLSLSRSPASSPHRSLHNAFVDDSSLQVYRRRIAVFEANARDSDG
AACREDILISAEAEERLPGESDGGGDRDGPSRLFAQSFLRVPKYIWENLYPHQQTGVRWLWQLLKQGVGGIVGDEMGLGK
TIQAVAFLAALHHSGVMKDLWDFQRQAITRAALAASLPLDAAQAAANVSSQHPSSRKGGNGGVIVVCPATVLHQWTKEFH
LWYPPLRVCLFHHKSVNLLEKAARGAEESNGILLTTYETFRMHLRLLLRHVWKMIILDEGQKIRNPHAAITLAVKQLPTP
HRLILSATPIQNNLQEFWSLLDFAAPGRLGTLPVFLEQIAEPITMGGYANASRERVETAYRCACLLRKVALPLILRRSKK
EMQEFLRLPNKAEEVLLCHMTPEQYALYVDFLAAQKARFSRNHYHPNDSFASPYEASEETLEKRERCRMLFTLSVLRKIA
NHPDLLLVHNDVRPEDYGNPERSGKLIVLREILRVWKAEGRRVLLFAQTVQMLDILQTFLENCDTSLPSSSPSAAPSPSG
DSSLPSVKRENEEGKKSGRKTAGSKDRGFSFLRLDGGVPVASRHAIVDRFQRDSSIFALLLTTRVGGVGLNLTAADRVVI
FDPDWNPMTDMQARERSWRIGQSKDVCIYRLLTSGSMEEKVYHRQVFKFFLSQKVLQDPRQRKFFKRNDLQEMLEPPPPP
PGFSASTALGDAGASSNYRDWLRGGIRCERRAAEKAFKREREEEATEKKKKARKARGERADVEDETWHAFQRAAAESGAQ
GEGDFGEDLARENNLILKTLLDAKGIKTSLTQDDVERPLLDAAIVDRQSRDIAKAAMRALRDSQLERMSHGIHVPTWTGK
RGRAGIPAAARRAQASSSRPSSSLSSFNSSSSSPGLAASILAGLRKLQQTLKPSRERSPDSRSVTVSRDPEGRRGRRGER
DDSVTLTFEEKKLAEELLHFFLSRSDTDFAVTTGELLEVFAPRVPAFRRKVFRAILKELCEMARSNDATQKPSYWILRPE
FRPQTS
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400 - 419:	EEEEEEEEEEEEEEEEEEEE

401 - 420:	EEEEEEEEEEEEEEEEEEEE
402 - 421:	EEEEEEEEEEEEEEEEEEEE
403 - 422:	EEEEEEEEEEEEEEEEEEEE
404 - 423:	EEEEEEEEEEEEEEEEEEEE
405 - 424:	EEEEEEEEEEEEEEEEEEEE
406 - 425:	EEEEEEEEEEEEEEEEEEEE
407 - 426:	EEEEEEEEEEEEEEEEEEEE
408 - 427:	EEEEEEEEEEEEEEEEEEEE
409 - 428:	EEEEEEEEEEEEEEEEEEEE
410 - 429:	EEEEEEEEEEEEEEEEEEEE
411 - 430:	EEEEEEEEEEEEEEEEEEEE

A0A0F7UZK5 **A0A0F7UZK5_TOXGV** (3098 aa)
Transporter, major facilitator family domain containing protein. *Toxoplasma gondii (strain ATCC 50861 / VEG)*

```
MRRDPLRHIPSVPVKEGATDKLLGHRMSLAAEEGLERGENEETDNVKGKEGHCGSRIETKTPQNQPLSRGGRDTSAPQTK
SGEDLEKTTDRELHSKTTGKESRVEHDRQMETSENPNAAERARVDTAATPHHDDPLLGISQASPLFPLPSDDLSLSLTSC
PPGAAPEIPSGFTAYSQSPSPGEPNTSGQYPSSTGDAVLSSPASLLSPLINRVSPAFCLSTPSPETAATSTLRPRNSGDF
LSVISSPVHSPPASPVSSVSIVSCSRDLPSALTPSCFMSGVPREEKGGRRLVVLGLHLTSPRCLDRARRVEVNCAAQASK
EGNKDEVCMRNDGADQRNCENDGRKETARKRGKGRACRSKAESADGAQQDRTPEKEIYDEKLEKRETLGSEVENHSDSED
STPGPEGEDDGRGTQQARATCSKCNGETHVPQFSQQSPRRLFSRWTQHRERKTTVRRTGANARWSFFLPSRKKKQGESRG
SRHNRRLTAGLEDESRQKSESENWETDGERELEDMRPFTASNDSSRLRGCLRACSPADLLSAGEGGTVTVTREPSDEEEE
EEDEDENDEERDEDENDEERDEDENDEEGDEDEHDEEADESIGSKRREFESRKRWKTRMFALLLMIQMTLNIDNGVVPAV
LADLGREFQATASEQGLVGALPHIGMLVFCPFCARCLEAVGPQRLLLVSLLLNAAAVVFFAVSSSCFSLFLSRFLIGFSQ
TAFVVYAPVWVDKFAPHKLLTVWMGLTHSAVVVGVVVGYLFAGFLRQSKHNWRGALLLQVVLLLSLILVLAFSDSVHVDV
WADAESSAANASHYRAAAVPPLQEGNETEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEDEEEEEEGEEEEGEEEEEGTGQVCREECEFRDKAEDVEARQEVRRTLQQKKEKT
TDLWGRAELQGEASTGALEAREAIKGRSGEVSESRRDEKEDREVPHAVVVEKGDGDDEARKKGEEEGSECERKTELRPSG
QRETRHFENQMMSALPPSPPVSSPRLSCLVRYTPDPPHESLHAESSVHSSHRKRTLFRAFSSAGFVVAPVSSSSQPTSFR
PSSSASRLSPQCPLCVCSGASFCSSSSTSRVVSLTQTDASSCSVALSASSNGASSSSSSSSSSSVLPSNAAASSFPCKAS
SSLCPTKFFLAAPRSLSLHRLPPSAFPLSCSASSSSAAFLYPFLSCFPPPSVPRTCMRLPDKTPRGSQTVPPCGKAEDLL
KNEWFSSSEKETLPGAPERSECPPGSHRSFPAAEWSVTSSFPWIATTVAACSASRASLTLDEPHRRAGGEESLNGTTRSD
LENAQQTSSPRSVANAVVSRSEEAEIMASVRNGNERSAAVAQESTVRTAEAGRGGSVEKRTEGPRQAPREEAARLEKTRP
LRGTASQTQEKQVSSTQASFSRSASLPFGSWRRRLEGRARPPRFASCGENGRAEERQRTTKKRRERDAILAALAHAYYSE
GRPDEVEATCRGGEGVRGRSAEARSSQKTEERRVRARATEGGSVDRAKARKGRRRLGETLERGEKEEEKRVQTEEMFCSK
AGDSETIPAQSEAAKERRKQVEERLPDLQSVSVKNDQKGPLDSLLDARRQLSRPVKPVSGELDSERHDTLPCSIRNPAPA
RLLRRSTSASASVSSAPFSASLTSLGTRNEAKGRLHVLRPAAKSLPRAHIVFIRPASGQTDTSQAENEKADGRDAVDRPE
TPESSCSALHALQSACKRRKRDDMRCVVAVHTTPSSHSELVFNAFLRGTKLLLFTPPIGLMLSSSAAAPRAGSQEANRSG
SRKRASEWTQEGGGQEEDARGDKRGTGMAERPRRRTQRSRQEQAPAAREDEAKVGGKDAKEAGQKEREEALEEGEQRQRQ
RGRAGERTRATVGDSGAQKRTARAEESERLRLSPGRLASGYRKQTTSGRHESSARAESRTCEEATEGETGRDKREKETQR
RRVERGFIEVGRDRHVGDVGSVETDAFGESEGRQVPRLKQMRGFPSWCYSLLRLPSERLHDPACCPYRSRGDGKDCRHRA
VVKRATETSSRNRGRESKRRNESETERDDSDDERLGLAHAFVPAPRLATGSFFPPQSVARAAELRQGHSHAQQLLSDTAP
AFSQAGAPPCSPALFPKTPSAEIREEPTMLFEGSRQLQSLHVVDLSCQTSHLSSSASGVRHIFPRLPASPSAAATKAEAA
LSSHMSSPSSSSQSSSPISASSSSPVSHSSSLGWPPPTSSSGGSLNAFCRAPRVAAGARGGVREGRTRVGDETERRGQAE
WEAQPKTQGIGEGTRGQGDEEERRSIPGLCPAHTPLLVAVHEEAAVATAAVFAAPVWVEESPASGKEKVKKCPWATDIEQ
AKVRKTENHEDENRSEDNAGTSGGRSHTHTLAVVSLRQRPQAEDKSKRKTEAGATRKGKPAKEKEEATLPEKNTERRRER
LGDGDGQIPCGSPRTVFSPCKRLSEESRREEREEDEAQSNQPRGRDGRAAEVEGIEGDNPTADNRLQEEFFIHTVCVDLP
ALHVLDGGAKAGDQEAGREHSKDGRSEEGERAYKSGGERMKTVVVTSHLEKTTDVIFIARKEITDQNLEVQSPSGVAVVG
VELQATAGDDAECKPASHEDDDPGTRDEEARKEEEAADEGVKGDASTQSARGLHERRNREVANGGKILGIEWKVKGCPTG
QEAIEATRACEEVGDNRQQEAYSGHGDEDDTSDLKQAHKRNFWNLKQWRKKRGVSREGREPRRQTHADGPAEKGKRPQKQ
LETKDADEGDQEKTRDNTVEKQQDEASTLCSSREEDDEDSRVAGTWKKRTLGRLLTNPLYVCLTLALSSLFFEVTAIQFW
ATRYFDEELHADTATVLVSFSVTAATAPAVGILVGAVLMDWLGGYRETPEKRRRALFCLLGLSLTCVLLGVFAAYCSLSF
WPSLASIWFILFFGGGILPIASGLLLATVDEELRTKASGAATLFYTLLGYTAGTFLPGVISDSIGTKGGMQMILLWSLSG
FAFLLLATAFASRILNTKGAEGGEEVEAGEEAEKNRKSLEARGRPRRERRARRGTDSV
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829 - 848:	EEEEEEEEEEEEEEEEEEEE
830 - 849:	EEEEEEEEEEEEEEEEEEEE
831 - 850:	EEEEEEEEEEEEEEEEEEEE
832 - 851:	EEEEEEEEEEEEEEEEEEEE
833 - 852:	EEEEEEEEEEEEEEEEEEEE
834 - 853:	EEEEEEEEEEEEEEEEEEEE
835 - 854:	EEEEEEEEEEEEEEEEEEEE
836 - 855:	EEEEEEEEEEEEEEEEEEEE
837 - 856:	EEEEEEEEEEEEEEEEEEEE
838 - 857:	EEEEEEEEEEEEEEEEEEEE
839 - 858:	EEEEEEEEEEEEEEEEEEEE
840 - 859:	EEEEEEEEEEEEEEEEEEEE
841 - 860:	EEEEEEEEEEEEEEEEEEEE
842 - 861:	EEEEEEEEEEEEEEEEEEEE
843 - 862:	EEEEEEEEEEEEEEEEEEEE
844 - 863:	EEEEEEEEEEEEEEEEEEEE
845 - 864:	EEEEEEEEEEEEEEEEEEEE

846 - 865:	EEEEEEEEEEEEEEEEEEEE
847 - 866:	EEEEEEEEEEEEEEEEEEEE
848 - 867:	EEEEEEEEEEEEEEEEEEEE
849 - 868:	EEEEEEEEEEEEEEEEEEEE
850 - 869:	EEEEEEEEEEEEEEEEEEEE
851 - 870:	EEEEEEEEEEEEEEEEEEEE
852 - 871:	EEEEEEEEEEEEEEEEEEEE
853 - 872:	EEEEEEEEEEEEEEEEEEEE
854 - 873:	EEEEEEEEEEEEEEEEEEEE
855 - 874:	EEEEEEEEEEEEEEEEEEEE
856 - 875:	EEEEEEEEEEEEEEEEEEEE
857 - 876:	EEEEEEEEEEEEEEEEEEEE
858 - 877:	EEEEEEEEEEEEEEEEEEEE
859 - 878:	EEEEEEEEEEEEEEEEEEEE
860 - 879:	EEEEEEEEEEEEEEEEEEEE
861 - 880:	EEEEEEEEEEEEEEEEEEEE
862 - 881:	EEEEEEEEEEEEEEEEEEEE
863 - 882:	EEEEEEEEEEEEEEEEEEEE
864 - 883:	EEEEEEEEEEEEEEEEEEEE
865 - 884:	EEEEEEEEEEEEEEEEEEEE
866 - 885:	EEEEEEEEEEEEEEEEEEEE
867 - 886:	EEEEEEEEEEEEEEEEEEEE
868 - 887:	EEEEEEEEEEEEEEEEEEEE
869 - 888:	EEEEEEEEEEEEEEEEEEEE
870 - 889:	EEEEEEEEEEEEEEEEEEEE
871 - 890:	EEEEEEEEEEEEEEEEEEEE
872 - 891:	EEEEEEEEEEEEEEEEEEEE
873 - 892:	EEEEEEEEEEEEEEEEEEEE
874 - 893:	EEEEEEEEEEEEEEEEEEEE
875 - 894:	EEEEEEEEEEEEEEEEEEEE
876 - 895:	EEEEEEEEEEEEEEEEEEEE
877 - 896:	EEEEEEEEEEEEEEEEEEEE
878 - 897:	EEEEEEEEEEEEEEEEEEEE
879 - 898:	EEEEEEEEEEEEEEEEEEEE
880 - 899:	EEEEEEEEEEEEEEEEEEEE
881 - 900:	EEEEEEEEEEEEEEEEEEEE
882 - 901:	EEEEEEEEEEEEEEEEEEEE
883 - 902:	EEEEEEEEEEEEEEEEEEEE
884 - 903:	EEEEEEEEEEEEEEEEEEEE
885 - 904:	EEEEEEEEEEEEEEEEEEEE
886 - 905:	EEEEEEEEEEEEEEEEEEEE
887 - 906:	EEEEEEEEEEEEEEEEEEEE

A0A0F7UZN5 **A0A0F7UZN5_TOXGV** (4027 aa)
Helicase, putative. *Toxoplasma gondii (strain ATCC 50861 / VEG)*

```
MQSAGRCSPPRGGATRGNSDISSSSRFHPSDRPPREPSPCSPVDSSAFSCSSSSSALFPSRQFALHSAEESGPAEAGRPG
HHAFLPHSAERRARLLPLLLQALAPSAASLLLREEVSAREKTTDPETRDATLQREGDRTVKLANPPVVACGSSSLSSSSL
SSSSSSLSSSSLSSSSSSLSSSSLSSSSLSSSSSLSSVTCLCRSPFVSFASSPEFSALRDALFAQVHQLGEEEKAAHRGC
MSLLLASRTSASASVACCGFSGGSATVLSPYDSQNVLPFQEQYAGGRGAAGVDDRAAARRREEATVLRAVRMFGARTSAP
LSETRAGRGEEDGRHSETGMCEEDEKEEEESSRRRGDGARETLEERSWWTETPADAWEESGEGRSDGDEVEDVEREQGPQ
GQQSTHPAEQNRGGDERRLGEERLVRDEREEAGTLLQIEFEEETRGRTREEGSDRDPRRRGAERKTESKCEQETKSPHVA
YCWWQAGARESGKRGHRVLKTCDAVLPLEEETYSDRDMRGQLQAWPYQYRVYRRATLENTVVALPTGTGKTLVAAMVVHT
WLANVFVADKLVIFLAPTTQLARQQHRAISTVLSLLRDPAGAEASRGRLAVRLPGVLEKERSARGRVASRDDDDGERAYF
RSVLRVDWSHPKYWGAFYSALSEYKAALLDLQRLPAAPPAAFDLRRFHTGRLLAPYRFADSQRAALLRESFAEPSSEEAN
AQAASLEDSEGERSGNREGEREEDENEQDVSEVEHQAVCWPRVFVMTPDKFRNLACRGLLRIDRIGLLIFDEAHTVGRPL
RSLGAYATILRVFLHLCQEEAKPRILGLTASPVPDGKLGFFDLESELKRAMRSLETIFQARIVKADTESAPGIRDWSQGQ
PDAQRQGEQQRGVMGVRLTAAGGREIREAVEEESERSAANEARGNARRGSGETRQDHLGGDKPLRTMETTEGNEETFTGC
ALKTVRYQLAPSPFYYDHELLILDRLTTPRVEAGRQQWRVAAWQPPPGTLRGSREPTGGVPAVSNGDREQRKDRLPRREG
TERGDSPMRSTSTKPTGTKERETEEEELDEKNAKEKEAKAKNGQVNCDGLEGKRSEGREDAVRWNGSEVAAFRHFVEREA
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RGRHTNFSLLLQEVLDICSTFFYLEVTRLKEGREANEERHHPHETTPAEEARQETMHRILKTDCGSPCASHPSPSFSSFP
SCSPPLSSSPAAPPLAPSFSCSSASAAFSASALCSSAAPSRVPASLRSSFLAEVWGAADARLNVRVMRRLWQHLAPLTKQ
RAQRNWENFRRHLLHVQSELGFWSVWRLKEKVEADLEAWQARLGAATEERSRAQTRRSRRDCEGAECEESEKEDETDNSG
RGKESQKRVRFAGENQRTKAGRSEEGNRTRGDRDRIKSTLAEIPLWISFPFRRPLSSDLDFQHGSSLSSSSLSSLDPVGG
QPVERLLRRLFFGFFFLFSKALSTACSHSSLQLTMQLCRSRDLAHVCLADVAALEGGVAGAERTGSLPQVLACSLFSDKL
LRLDQVLRDSFGRAQAQAQTQTQRREGSVADDKRGSGPDKRAGRPGDEEERRTEDGGEATRSGLRIKASSKGDRECSPSP
KKSGVRTPVPSFSSSPSCVSPSALSSAPSSMSLSSRFPAASRSPASPDVAFGGVPKCGLVFCRRRVDAWLVCEFLTARRL
VFVDWICSSSLASQGASWLFGIGKASQGRSSCLDRLRAMHTVWGKLEKKTQKLNAQKHRPSTTPQSHSPSLASSLSSSLA
SSASSSASSSASSSLSSSLASSASSSLSSSLSSSASWGDGGKGVWRLMRRLGWGAPLQLLVSTSVLEEGIDVPACNLVVQ
MDMPSSLVRFVQAKGRARKKPAEFVVLCPDSGPCGASWPDASLPFSSSFPSSSSFFPFSSSLQSQTPDCTVSSPSLLLSL
QSVSSLAVSSSSLSAPLSVSLRSRTGEAPTTPAFAAQGFSAAGGAACYLQAVSPSVNFELARLQLCEAKVAALAADVEAT
ERFGLLGPFRCMRKVCSLDDLLLTHTGAMVHSAFAPALLREIVDACTAGKTDERTERGADERGEEGRWAEDTEDEGREER
ERGNAELRTGREKALGTCCSNAPSSSSLSSSGMRRVSDLCETRRQRTPSALRLLSTQDGKWILSVPSLQGFRSSPLPPFS
IEFSPTGSAPTRASAAAGVLAVRVLRRLVQEGVVDSFLRCRDRDSVEKDLRDEKERRRRENCGGVGAVDLLWRELPACLL
PPRSWRNARRASGDRHGDSEETLHTSAKTREEAARAEEAVSGSNEERRRSRDHKEGTTEGDAGAQEVEENAEEGRKEEEG
DQLKRLPSGTGKKDETSTSNAKSETHREKTRTVWCTPLTAREAALERLWEPNEKQRRRRRRVLKKLAESRGFLPSPLYES
GGFCGLWRIFADAEAPLQAADLALDGASRWRQEKAKEKEQIEPDAGDGEGDEDGLWWTGNRRQREACFEKRERREGGDGKH
DQCKEDEKCGAEKEEEEEEEEEEEEEEEEEEEEEEEEKKWSWQEEEKNRQRREILELIRSRIDAVVEGRRGPDSVLQPLCLL
LAHPIPATVAFHALHPEASEKAALHRGRRPRTGRTSFSLRASKAEKASNAWTELEADQEGEEGVEEGDEEEGEEEGEEEG
EEDGEEEGDEEDVPGLMRVEVEKPAKTMFIDLPTEYVEKVLLRFTHIHLFRLLQLSNFSPNGTCNSLLLTVLQFLSALPF
RRFPFRTVPSSSSLSSSASASASASCLGGDGEPRSRFVSLPLPACASASRLLPSHALSLFALPPSLFSLLSLLSLAAEEA
EESTESTLHSQSPPSSPRSSSPRSSSPRSSSLSSSSPSTSAEQLKRQMVEACSSLAKAGVVDLQRVMFPFFVLAPLSPLD
AKSVDLDFIHRLASLRLFLRSGQRRSSGFLEAGACPPSLMLQHDRRLLRGAVESLHCLPSLSAVARLFCLGNSARKLDYE
GGRSLQKAERRSARKEQNKGDAAEENGAFNWPRSLLGTLPSSDRESESAKDTKEKRTPGSEKGERREADGERREEDGEKG
ATKEDGLFSKEEQFFRRLQSYKGSIFSRGDDAANAWTTEEQKLLTFFQQRNENALSVKEALREEGMEIFYHLRSRGFEPV
ALRMTHQFGRSFRFYRLQTIHRNLTPRNVVINSDAGFTLGTLCRVYLSRFKQRLAEPHPDSQQGPQGNCFLVQGVKRRQE
ISWMPAILYQLEVQGKHCDLVRRLRQEMRPFLFTAEENISPPLELDFRLVSRALTAPQSRQVGAVDAAGVDWHGQRLEFL
GDAVLKFVVSCYLFFHVHEGKPAEPRAVAERKETEKEETGLESGEPGDAEAAEEVEEQGEEPESKETGGEREEREEEGER
EEEEGEEEEARWKFLFSLLTQEEAGRFFGGVDEGVLSRLRQHYVANDYLRFAMRRFRLQAYLVNFPFVSHKKSLLDLREQ
PVSEKAQADVIEALLGAVYLSNADSALFGAQPGKRSGGKETTGKTEDREATEKRGGTEENEREGERREKEREGRGRDVGE
NVSKKETEGRVDKRQAVHRRPREMRHRGLDKETTEEREEQAVVGSSSGCMAAAAFFDAYLLLPSAVNNAVLLFDEEVERE
KGRREPGERDNKLKEREESEEDRLSHEGVALAPDGAGKQREVPDRQEKETLEHWKALLVDCLEEALCRRDRGVSVSDLGE
DRHKEENAFPCSAKDINRDAWMLLPDRLAKQTEDLRALARLPHMSETFLLLSRATNRQRTPHNGLSHDDEEAEEEEDETE
EEEDETEEEEEEDETEEEEDEIEEDESGVWREEPSRRDVEASQRVWMSKIFSRYDTDGGRGDLDRVMAVDSVQLIYRGPR
QSLLSSLQEGKKRANLETSGDRDHLRRCLLLLSETVRGCASNASVLRMWSSAGNATREERRAQKVGEKGRVEKKKKTERT
QNEEEEQNEQSLHRKEGNAGGTGKAQTNRRTEGSLSCVSSTSFASSLSSPSSSLSSSSSSSSPPASSSLSSFCGRREREF
PLKGLLTAARNRDVVSARVFRAPCSLL

2494 - 2513:	EEEEEEEEEEEEEEEEEEEE
2495 - 2514:	EEEEEEEEEEEEEEEEEEEE
2496 - 2515:	EEEEEEEEEEEEEEEEEEEE

A0A0F7V3H7 **A0A0F7V3H7_TOXGV** (1412 aa)
WD-40 repeat protein, putative. *Toxoplasma gondii (strain ATCC 50861 / VEG)*

MAELSTTWQPRLLLQSFCGNSATVSSVSLSTPQAVSSPEREETQVLFSLSGGSLFAVALDAAARSADETNEAEASTEASG
VVPTPDEEGQVTAPAFLRSPFAAPQQLVDEEVEEGLAAFAACDLSLPSASSPSSATHKDGFLVTAGASTGLVRCFRVYVQ
PKRQEATPEEDDDAAEASRGLQLLRAMQQRKGKGKEDEPSSPFVLNGENGSGAWLRMEELVKWKSSSAVARLIALSPPFE
APFLLSKGRKALCRCLAIGCADGAVECHLLIFFEGRKKSESEQDGRLTQLQVVQRCFVDRLSGEAVSALKFHPSRLLLAF
GGERGSLRLVDLCAFVLSSLCVAAGRPAPSTPRATVHPLADHMSAINSLCFAAGEDARQSRAAGMLVSAGGDRLLNFWNL
NSLSENAGDLEATAAELSQRRDKQKKERSKAETDLAPAFQLPTSELVTAMVYVHPSAPGVAREPRAGDKQEPAGVLVVGG
EQGTLFVFSLQQRKFIRSIDLPTRSAASVAASLASPSQSPQKQLEDFNAVVRSLALLPRRGSPHLLAVQESGAAACLPLA
LFFSSAKGKPELALKPTFFIGRMDGILGIKFLPEPPACACPCCSARRASALGEAQLSGRGKRKRGDVQEEDSASRAAPAF
PRSLVALVGERQPWVLRLDGPAGEGHPVGYQAAACAAELSEGHQGEPSRFSEAHAAPAVCCDVSRKGCWVLSGASDGSLA
VWHAATGRCLAQVPPGHHGGAINAVAFQQKEWLRPSPLFKKSMREGVLAASGRKEKKESSDLSVPLCACDCRGINASTPH
ALLFAAASSGDHAVKVWKAEISPSFLSGKVRGDDEPGASGKKKKTADTGHPQILVTSLASVVAHRKEINDVKISPNDALL
CTVSQDKTGKLFSFPSLVYVGELRGHSRSIFACAFPKREKIVATASADSTVKLWNVDTCACIKTFQSTVGGGVLALGFLS
RDTQLVTGTSEGFLQLWNCRTAECVGSLPSVHEENKASIWCLDVCGPAMVTGGSGGQLCLWEDVTNLVRHKAELAQQRET
QQLAALKLLAAEGRGDEVFSLLLRLRRRAGMREFLENQCGKILLQAFQRGLELQRRIALYSGQPLARSGSDQDASASTFG
RLSAFLESLEEERVAAREDEDDRRGGQESKAELGASKKRKGEKKVKGEETEAGARGRPDAPLRSAWLRDLNGDLSLPQLL
KKMKKKDVATLLEFAAAWNTNSHTSWLAQGLVRLLLEARGEDIFEGAEKAGRNVSDVENMISSFCAYTARHDRRLTALIE
KTFLLDLLQGCESGDTRDLGDRWSGETRREPHREKTLDPRDATTFTRLCLYGDESEQTEMSQGKKTKNEPKRDSDERSTQ
EEEEEGEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAEEEEAEEEEEADA

1369 - 1388:	EEEEEEEEEEEEEEEEEEEE
1370 - 1389:	EEEEEEEEEEEEEEEEEEEE
1371 - 1390:	EEEEEEEEEEEEEEEEEEEE
1372 - 1391:	EEEEEEEEEEEEEEEEEEEE
1373 - 1392:	EEEEEEEEEEEEEEEEEEEE
1374 - 1393:	EEEEEEEEEEEEEEEEEEEE
1375 - 1394:	EEEEEEEEEEEEEEEEEEEE
1376 - 1395:	EEEEEEEEEEEEEEEEEEEE
1377 - 1396:	EEEEEEEEEEEEEEEEEEEE
1378 - 1397:	EEEEEEEEEEEEEEEEEEEE
1379 - 1398:	EEEEEEEEEEEEEEEEEEEE

A0A0F7V8L3 **A0A0F7V8L3_TOXGV** (2732 aa)
IgA-specific metalloendopeptidase. *Toxoplasma gondii (strain ATCC 50861 / VEG)*

MTSARTREGLVGAEAPLGEGEEDLQDSIACSVPRAPTNSFEEGYEVECVDECPYIKFQHASKLPLSPLLFDASSSPAPLP
ERLLAARCTDSLCLLHCCGVLLLPGLDSILAVDATEAACGSPISRGRLPLHASKEGETKDAFPSLLLLSPDARFLAVAVD

```
CQVKLVQLGGCGGPSCSKSAGEASREGNAEARLGGQQGGDSCISEKTQVLSLAGFASPVKDISWIWPSGDRTETWCEGDT
RGDAERLIGLAVLTESGEAFILSPRGAQAFPLPAHGLAIHALPRRSPAAAKSEGAGPGGLAPLTAVVSCCAPASLWLVGL
QETALLPEGSGQGESLYDFGHRRPDVSRETAKEEKRKGRRKIRVEGLADIPGYEDEAQALHKGRGRFVGVHCLGASLDSA
AGESPLPLALAWFVPDADLSTGEDDWEKPELESDSAEPRLDPLRQAPASAEDCGDSWSCFILFGFLARRPYTPSDARALR
GDIGEAESADEKEELVFRIYAASRNEMFLRSVAASTVCRFRWIPQWHCLWVFSNACTQVICFALPHSFSRNGDPLPSPRS
SSFLGSGEVPWRCFTMPEGRALETADEDAFPQGLALFFNFKESMFREHSTTDTPPLEHPPVFFLLQSDGQVCVHLADCCE
CYVDDAGIGKEKRLLPRLEWTPVSPPSSFLLTSWTEPRRRACGEQPATPVPKVSPPALSPSSSSLASPLFASLQQGKPTP
SLFGTPSTNAASAPLFSSSSGTSLFPSSASSASSLFTPAKSEEEARKTGWVVPTTHLKVTSASSPANDPSASNGASASNN
LSALDGSSPRPLSSSRKDCVDQARPAAKETREEAPTRRLPAKSSSRDPQRRGHCVHCGAVDVGDRRGGREAERRRREKKL
RRRVEAKNASLRQAAAAANEVIEATLQAARGTKAEPAREKNAKKRILLTEEQSEVKALLDEFEEKKHAFCSFSRFLPSSL
FRPLLLSARCFENALRHEERRDVLLESSPVSSSASSSSSSSASSSSSSSSSSPGSLFVSRCGEKDAPVDCGAEQEKSTAA
LLPAAAAGLARTGRLADKLKDEQRNVRTKQETETEVVETLQEAQQHLVAWRSCLEAVRDQLLLRMQFAEKKSENPTERNG
EQTDAAGREEGRGDREADGREEKRERQAERGNSVTEEDVIACMQKIQSESGARRNLFEALQTLLPADAEHAQLNTDTHTK
CVLTHLESGLLRAERRLLLLLQRFRFYTSFQTRFPSSLDPESGSPVRRPAASGWPGSWKINSGLSSLSSYGDKGVSSLPL
AHGKDSDRDARTKRGSVHTPDTACGRGRPGGCYGLRFEWLEEDEFPDKREESAVDSHRRVSSTTHPVSEGTPGARPSLAF
SLSASPPSAFHLSLFGSPGGARDSRIACSQGPGGSVKDGGLAGSRSGAASGDFLLDMHAEHRAAGLVAELEAAVSEFLSS
VRQLEIDLAKLEWKATDLQSPARQSPSSSSSTSSFAASLSLLSSSVFGEPLPPSGPSGLPDVVGAEKPAKDGEQRFPVSS
LREQRERFDERRKLRRQLLEVWRATTSTDPQQEGEEETETDADEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDES
DAFEVLEDSSSVSYDEESDEWEPVGSASPENPQTPPRQSVVSRRLGASLRSGRRTSRSKQRAKFAPLSGDEDSSENACSS
SPSSPDDVSPRRRGAELSDSEGAPEDGASRSNSHDESASLPVCGVPGETHSISHSSLFSIKPEDVTQPPQSASFQFASSL
PPRRASGLGHTLFSFASNSSSLPPDPTKPSSSTSAPLPPDPTKPSSSTSAPLPPDPTKPSLSTSAPLPPDPTKPSLSTPA
PLPPDPTKPSLSTSAPLPPDPTKPSLSTSAPLPPDPTKPSSSTSAPLPPDPTKPSSSTSAPLPPDPTKPSSSTSAPLPPD
PTKPSSSTSAPLPPDPTKPSLSTSAPLPPDPTKPSSSTSAPLPPDPTKPSLSTSAPLPPDPTKPSSSTSAPLPPDPTKPS
SSTSAPLPPDPTKPSLSTSAPLPPDPTKPSSSTSAPLPPDPTKPSLFTSAPLPPDPTKPSLSTSAPLPPDPTKPSLSTSA
PLPPDPTKPSSSTAAPLPADPTKPSSSTSAPLPPDPTKPSSSTSAPLPPDPTKPSSSTSAPLPPDPTKPSSSTSAPLPPD
PTKPSLSTSAPLPPDPTKPSSSISAPLPPDPTKPSSSTSAPLPPDPTKPSSSTSAPLPPDPTKPSSSTSAPRPPEPLDPG
AVGREKGEEETGEGERIVSDSGEKVAEVSPDLSEISLSSGSSSYAQARELSQPELQTSEEKAGDAEKKAEAGEDKPKIAS
SLLGVTSLGASNAAPPASSPFGGSTTSPFAAVGPQAGSPFSSQAPSFGSVSSQTAGSFFTGTFDTKPSAGGSSLFGGSKL
DLKSLSESLAAPPPMTSGFAGNSFLSGGLFGSSPAFSASAQPGEKLAGGANSGAQVGGGLLGLSTQQPSFASPFSAAFGS
NASPFSGVTAAPFGGIGAGGDAAAAAPSVSFRDVAVDDLSIGQRQTYSFGMADNSSNLSSVNLGGSSLGNSGPTPERTGF
ANLAGNGSGGFAAFSTVTAPTGGGFAALAAQNSTGSGFFSSSFSSSSSSFASSSSSFASSSSSFPSSSSSFASSSSSFAS
SPFSFTPAGASGAAAAPSAFPAGGAFPSSAVSSFSGFGASTAPGTGFGSTGASPSGFAAFASQGPAASSAGRAAAPAGGS
LWSRPRTSNPLN
```

1564 - 1583:	EEEEEEEEEEEEEEEEEEEE
1565 - 1584:	EEEEEEEEEEEEEEEEEEEE
1566 - 1585:	EEEEEEEEEEEEEEEEEEEE

A0A0F7V9X2 **A0A0F7V9X2_TOXGV** (1261 aa)
Uncharacterized protein. *Toxoplasma gondii (strain ATCC 50861 / VEG)*

```
MRGRRPSQQRKKAASLGASSLLSSLPSSLPSSLFSRGDSVGRQLGKRRGIEEEGGKRKRARGGRSARHNFPEVDQQGGSD
LDELPSSEADPREAQQDGEGSFGHEQELAETLKKSKRAVLERKRRRHEERRQKKQIHRKQQQLWKLERQKALLERQLDMQ
KAAISGIRVNQGTGSGVRTPCGPEADSEDEEEDVSPRREKKTPSSLSSSLSSSLSSLDVRGSVLSALSAKDKKHTASGDV
LLLSGVSSRSTEEHRKAEERRLALDAAGRQLDAELAFLESKLGIGKDSSKAGEKKKKKLAQELLDDGFDKDLQTLLDDIL
GGKAENRKRKTKTDYDHDEGEMEGEETQEGAHEELGRVEAEEDEEDEEEEDDEKDEEDDEEENEEEDEEEEEEEEEDEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEANEGDEEDEGDEEDEEEGEDLKLKREHYSTCASASAGKYLPP
HLRNRAQRDLSNEAEFDGDNPGRNSTRQRGAAPASEASDKANFVASKLPLSCLEKARQRATDAGRGLTQRLRGSLNRVSE
GNVEVILQQISQEVKAALTQVLSGALPVPATSPALTPRDVRGLRREQEISFFQEVNCIIVRLLMQSMVESKFSTASLVAT
QTALCCGLSCLLDASLCSQLLAALGEAFRKFFPLALAQADRRTETGEPVGLYVRHTLMALCFLFDFNVVQPAVFLGLLQR
LSGKVATTKEKGEAKNGERNEPLVEFQVECLLMVLRLGGGKLRNDNPVLFKEAWNFLMTRVKGGEGEREVQVHSGREERP
FEEQTREEQRARLARVSTSFSGALRQRQEGEQPATTGRLHYLARELEELKNNKGNTIHLASKASQEAMRRWLQTSPLLAQ
SPLRQCAGEGKSVLVGVSSWQEVEDGVVSVSPSSHRPPVSPHKSVRVEEEKQSCLGDTGSEKALLDLAAKLRLHSEEQKK
IFLAIMSAESPNDAVKRLLQLVTTAVAVLLHISLQQSAFNPFYALVIARLCARCSCASWGRLEAEAEQPPLLGPLGSGRA
SGNQRRARGPCACLLPPDKEGKVFRRVTQRGLAAQNSAAHGFPLRRLLHLARLEAFLIRIGVVELRVTRFVSFEGEKGQA
DAHMGLSGKLGVFLKELCTELLCSPAFASVPLPGPSTASPLLPFLSLSALPDVREAFLLVLEDVLLPEARKNASGENGKG
AKESVNAACMPGRQGKCVRAKGAMCTPACGIRKDVISRVIWFMKKQERYEEEDPNTFAFDA
```

398 - 417:	EEEEEEEEEEEEEEEEEEEE
399 - 418:	EEEEEEEEEEEEEEEEEEEE
400 - 419:	EEEEEEEEEEEEEEEEEEEE
401 - 420:	EEEEEEEEEEEEEEEEEEEE
402 - 421:	EEEEEEEEEEEEEEEEEEEE
403 - 422:	EEEEEEEEEEEEEEEEEEEE
404 - 423:	EEEEEEEEEEEEEEEEEEEE
405 - 424:	EEEEEEEEEEEEEEEEEEEE
406 - 425:	EEEEEEEEEEEEEEEEEEEE
407 - 426:	EEEEEEEEEEEEEEEEEEEE
408 - 427:	EEEEEEEEEEEEEEEEEEEE
409 - 428:	EEEEEEEEEEEEEEEEEEEE
410 - 429:	EEEEEEEEEEEEEEEEEEEE
411 - 430:	EEEEEEEEEEEEEEEEEEEE
412 - 431:	EEEEEEEEEEEEEEEEEEEE
413 - 432:	EEEEEEEEEEEEEEEEEEEE
414 - 433:	EEEEEEEEEEEEEEEEEEEE
415 - 434:	EEEEEEEEEEEEEEEEEEEE

416 - 435:	EEEEEEEEEEEEEEEEEEEE
417 - 436:	EEEEEEEEEEEEEEEEEEEE
418 - 437:	EEEEEEEEEEEEEEEEEEEE
419 - 438:	EEEEEEEEEEEEEEEEEEEE

A0A0F7YZQ4 **A0A0F7YZQ4_MICFL** (585 aa)
Ran GTPase-activating protein 1-like protein. *Micrurus fulvius (Eastern coral snake) (Coluber fulvius)*

```
MASEDITKLAESLAKTQVGGGLLSFKGKSLKLNTAEDAEDVIKEIEEFDGLEALRLEGNTVGVEAAKVIAKALEKKSQLK
RCHWSDMFTGRLRSEIPPALISLGEALISAGCQLVELDLSDNAFGPDGVSGFAALLKSPTCFTLQELKLNNCGMGIGGGK
ILAGALKECHRKSTAQGKPLALKVLMAGRNRLENDGATALAEAFTVIGTLEDVHMPQNGINHPGITALAKAFAVNPLLRV
INLNDNTFTEKGAVAMAETLKKLRQVEIINFGDCLVRSEGAVVIAEAVSEGLHKLKELNLAFCEIKIDAALIVVAATEDK
SELEKLDLNGNCFGEEGCEQLQDILEGFNMGEVLGSLSDDDGENSEDDEEEEEEEEEEEEEEEEEEEEEEEEEPLQVQE
RGQGEQEPLTPKKILEEHDSTPLSSPLPPVDVGTFLAFPSAEKLLRLGPKCSTLIMQQTDTSDTEKVVTVFLKISSVFKD
ETVVKTAVCETTDALMREAFSSANFNSDAFITSLLIHMGLLKSEDKIRAVPSLYGPLMTLNHMVQQDYFPKSLAPILLAF
VTKPNRALDSCSFARHSLLQTLHQL
```

369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE

A0A0F7Z621 **A0A0F7Z621_MICFL** (418 aa)
Ras-related GTP-binding protein. *Micrurus fulvius (Eastern coral snake) (Coluber fulvius)*

```
MSEVPGKLKEQQENEGAEKKAEEEEEEEEEEEEEEEEEEEEEEEIVGLADYGDESESFSDGDHEKSGDGAYFNDPFNTEVK
PRILLMGLRRSGKSSIQKVVFHKMSPNETLFLESTNKICREDVSNSSFVNFQIWDFPGQIDFFDPTFDYEMIFRGTGALI
FVIDSQDDYMEALARLHLTVTRAYKVNPDINFEIFIHKVDGLSDDHKIETQRDIHQRANDDLADAGLEKIHLSFYLTSIY
DHSIFEAFSKVVQKLIPQLPTLENLLNIFVSNSGIEKAFLFDVVSKIYIATDSTPVDMQTYELSCDMIDVVIDISSIYGL
KKDGAGTPYDKESTAIIKLNNATVLYLKEVTKFLALVCFVREESFERKGLIDYNFHCFRKAIHEVFEVRMKAVKTQKNQN
QVQKNKRATHNGTPRMPL
```

22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE

A0A0F7ZBH4 **A0A0F7ZBH4_CROAD** (586 aa)
Ran GTPase-activating protein 1-like protein. *Crotalus adamanteus (Eastern diamondback rattlesnake)*

```
MASEDITKLAESLAKTQVGGGQLSFKGKSLKLNTAEDAEEVIKEIEEFDGLEALRLEGNTVGVEAAKVIAKALENKSQLK
RCHWSDMFTGRLRSEIPPALISLGEALISAGCQLVELDLSDNAFGPDGVRGFEALLKSPTCFTLQELKLNNCGMGIGGGK
ILAGALKECHRKSTARSKPLALKVFMAGRNRLENDGATALAEAFAVIGTLEEVHMPQNGITHPGITALAEAFAVNPLLRV
INLNDNTFTEKGAVAMAETLKKLRQVETINFGDCLVRSKGAVAIAEAVSEGLHKLKELNLSFCEIKLDAALIIAEATEDK
SLLEKLDLNGNYFGGEGCEQLQEILESFNMADVLGSLSDDDGENGEEEEEEEEEEEEEEEEEEEEEEDEEEEEPLQVQE
RGQGEQEPLTPKKILKEHDSTPLSSPSLPPVDVGTFLAFPSPEKLLRLGPKCSTLITQQTDTSDTEKVVTVFLKISSVFK
DETVVKTAVTETTDALMREAFSSANFNSDAFITSLLIHMGLLKSEEKIRAVPSLYGPLMTLNHVVQQDYFPKSLVPILLA
FVTKPNRALDSCSFARHLLLQTLHQL
```

366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE

A0A0F8AH20 **A0A0F8AH20_LARCR** (1003 aa)
Brefeldin A-inhibited guanine nucleotide-exchange protein 3. *Larimichthys crocea (Large yellow croaker) (Pseudosciaena crocea)*

```
MVMVWSQLRMRVEVSVCDGVQVEELKCSSSSEEAQTAPRLMLSGALDSSAPKRPRASAACFSLRRSHSCGSQTAVWGPAG
VTSGLPQGQTVERWRKGGGEARAEEEEEEEEEEEEEEEEEEEEEEKSTSCVSSFFFAGGAAGGRGGGTGCGVREEKKHE
LKKKKKKKKRRKRRKRRKRRKRRREDAVTVTTPLKRHRPARRRPRSLPVSPPVSPPVCLPVSPPVCLVGARMEEILRKLQ
KDASGHKHKAIRDGCVYACETLESQDGSVKISASQLRENVLCIVTENRWCVFPEALLAPLKCLNTDELSSHWFYCRRLTH
TLFYTLCVCVCVCVCVCVCVCVCVCVCVFFQVCIETYVSSCHQRSINTAVRATLSQILGDLTLQLRHRQEGADGDEVT
APPLHRRDISPTSQALCDDVVTVLTVFCEKLESVDSGHQLLQLLYLESILSMLSSCPPTMHLSRGFTDLVWKQLCPSLVA
IMGNPVNDKTIASHHGYMGAPDRERLSDRLSLGISQDVDSSGGGVSDQGRGSGCSSSAPARIAPVVRTVCYIAAELVRLV
SCVESMKPVLQSLYHRILLYPPPQHRTEAIRIMKEILGSPQRLYDLAGPCVVEPEIRKRSFSKRKSHLDLLKLVMDGMTE
ACMKGGIEACYSSVSCACALLGALDELSQGRGIQPEQARLLLRRLEDLKDGTESTRESMEINEADFRWQRHILSSEQAPY
DPTSSTGATTGATERSPDISISITTETGQTTLDLEAGELGLGHTTPEECGGEDARLPSPSCCGVQERTKDEPSLEPEKVV
QQVEKGGGAVQVEGRGEKQRAAGGGGGGERGGVVPPDVVQRSHGLVYPDITNFLSVESRTRSHHGGGSRYSESNFSMEEQ
DLSRTEFDSCDQYSMAAEKDSGRSDVSDIGSDNVSLADEEQQTPRDCPGHRSLRTAALSLKLLRNQEADQQSARLFVQSL
```

AALLPRLLGLATTMDVDLSLQNFSSTFCSGLQAGEGGGRAGRG

104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE

A0A0F8AIU4 **A0A0F8AIU4_LARCR** (1794 aa)
Putative transporter SVOPL. *Larimichthys crocea (Large yellow croaker) (Pseudosciaena crocea)*

MRTDVKETWMGDGLKTQLVSAIHLQEVELQEKPADKKQGSKNNITADETFTVEEAVETIGFGRFHILLFVIMGSSNIVEA
MEIMLLAVVSPEIRCEWKLDDWQVALVSTMVFLGFMVCGVFGGYIADRYGRWKVVFGGFVWSAYFSLLTSFAPSYGWFIF
LRSMVGCGVAGVSQGFVLKTEFIPEKHRAFLLPLASIFWMIGSMLIILLGMLVVPTLGWRWMIRISVTPSIILIFLFKFI
PESARYNVSAGNIQAAVATLEKIAKMNRASLPPGRLVEPAVNERGSWRILLSPSFRRTSLLLWYSWFVASFIYYGSVLSS
SELLEKNLLCVTDADREHRVKHQHEDGLCYCIPFALSDYQTLLISCLGEVALIPINICLLNVFGRKMSLTVLQLLSAILF
MILNICTTMLGFTVLLFLLRSLVSMNFNVVYIYTAEVYPTAARSLGMGFCTSFSRIGGMIAPFIAQVLMSKSVIEALSPF
AVACVICAVGNFLLPIETKGRALLVTPFPWCPAAFGIAMGDELYPECRAQQLFDEFVSSLTCRAALWSFSQLCEHLQLDR
TAAERPLYQLIKHRLNYWKANALWAKLDRRAAQEEYQRARVCSNTTCVIIGAGPCGLRTAVELSFMGARVVLLEKRDSFS
RNNVLHLWPFTIHDLRGLGAKKFYGKFCAGSIDHISIRQLQLVLLKVALLLGVEVHVNVEFKNLVEPPKDQHRHRGAMAE
GRHPAIDSSFLTLLHPAPSGQVSGAVASSSSMQVSGCHDFSHLSSKSSLKVGWRMEVSPKSHPVSQLQFDVIIGADGRRN
TLSGFRRKEFRGKLAIAITANFKNRNSTAEAKVEEISGVAFIFNQRFFQELRQETGIDLENIVYYKDDTHYFVMTAKKQS
LLEKGVIKQDFADTELLLSRGNVDQNALQTYACEAAAFSTNHQLPSLDFAMNHYGQPDVAMFDFTCMYASENAAMVRQRH
GHQLLVTLVGDSLLESSGCFFCQKRVYLMERLCAEGFFFHRSCFQCFQCSSTLRLAAYAFNQDTGRFYCLQHADCRLNVT
AARKRTPASDGASRKTSTVSLASAPSSADSLVSADRRRSSGVSMMAAVTLERIEFENWQSSTRVEEELLEEPEEVSEETL
TRFNLDHRSSSESSQPCHVTSEDARASCKETLQLHLRDEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEQEEEEEEEEEDKEEEEEEVEGEEGSSEVESSDEGEYSPQDM
ERQSGLWLLLEEETEEELSSVAGSDITHRGTPVDSSVACITSSTPSSKTPPFTASFVTTPDSDTAPPTQLTPVVVMETAV
AGSGFFDDVTPELPQKNPLMQVTGTSDEEAATSEGVRRRRHRGAHSLPPCLFLSPLQDGGEALLQVKGLREAPPPVLVDM
EGGGARALWRAVFSGNRKQKKKKWGRTIPPGADRVKEDAANQRRATGVSLTESGLNSTTLLQRRLHLDLFDLTSQIQRVT
IKEDQNQDQDQPLYVPHALAFKRAYAIKKRSLKAKIPIQDSDGQSSCSTEVVGILAQPKEPSSLSVKETMFQRDEDKDED
LDTKITRRVQRAARQKAKQEQLKRLHKAQMIQRQLQHVEEKQRQLEEKGVKVERALRGEADYWGESNDDDEVHLTGLGKA
DDPALMQRWFQLVQQKNSLVRYESELMILARELELEDRQSRLQQELRERMAVDDHLKEEWELVEERLILEEMLEVVEQRD
SLVSLLEEQRQQERQEDQDLEQVMMTQGLGLTWT

1161 - 1180:	EEEEEEEEEEEEEEEEEEEE
1162 - 1181:	EEEEEEEEEEEEEEEEEEEE
1163 - 1182:	EEEEEEEEEEEEEEEEEEEE
1164 - 1183:	EEEEEEEEEEEEEEEEEEEE
1165 - 1184:	EEEEEEEEEEEEEEEEEEEE
1166 - 1185:	EEEEEEEEEEEEEEEEEEEE
1167 - 1186:	EEEEEEEEEEEEEEEEEEEE
1168 - 1187:	EEEEEEEEEEEEEEEEEEEE
1169 - 1188:	EEEEEEEEEEEEEEEEEEEE
1170 - 1189:	EEEEEEEEEEEEEEEEEEEE
1171 - 1190:	EEEEEEEEEEEEEEEEEEEE
1172 - 1191:	EEEEEEEEEEEEEEEEEEEE
1173 - 1192:	EEEEEEEEEEEEEEEEEEEE
1174 - 1193:	EEEEEEEEEEEEEEEEEEEE
1175 - 1194:	EEEEEEEEEEEEEEEEEEEE
1176 - 1195:	EEEEEEEEEEEEEEEEEEEE
1177 - 1196:	EEEEEEEEEEEEEEEEEEEE
1178 - 1197:	EEEEEEEEEEEEEEEEEEEE
1179 - 1198:	EEEEEEEEEEEEEEEEEEEE
1180 - 1199:	EEEEEEEEEEEEEEEEEEEE
1181 - 1200:	EEEEEEEEEEEEEEEEEEEE
1182 - 1201:	EEEEEEEEEEEEEEEEEEEE
1183 - 1202:	EEEEEEEEEEEEEEEEEEEE
1184 - 1203:	EEEEEEEEEEEEEEEEEEEE
1185 - 1204:	EEEEEEEEEEEEEEEEEEEE
1186 - 1205:	EEEEEEEEEEEEEEEEEEEE
1187 - 1206:	EEEEEEEEEEEEEEEEEEEE
1188 - 1207:	EEEEEEEEEEEEEEEEEEEE
1189 - 1208:	EEEEEEEEEEEEEEEEEEEE
1190 - 1209:	EEEEEEEEEEEEEEEEEEEE

1191 - 1210:	EEEEEEEEEEEEEEEEEEEE
1192 - 1211:	EEEEEEEEEEEEEEEEEEEE
1193 - 1212:	EEEEEEEEEEEEEEEEEEEE
1194 - 1213:	EEEEEEEEEEEEEEEEEEEE
1195 - 1214:	EEEEEEEEEEEEEEEEEEEE
1196 - 1215:	EEEEEEEEEEEEEEEEEEEE
1197 - 1216:	EEEEEEEEEEEEEEEEEEEE
1198 - 1217:	EEEEEEEEEEEEEEEEEEEE
1199 - 1218:	EEEEEEEEEEEEEEEEEEEE
1200 - 1219:	EEEEEEEEEEEEEEEEEEEE
1201 - 1220:	EEEEEEEEEEEEEEEEEEEE
1202 - 1221:	EEEEEEEEEEEEEEEEEEEE
1203 - 1222:	EEEEEEEEEEEEEEEEEEEE
1204 - 1223:	EEEEEEEEEEEEEEEEEEEE
1205 - 1224:	EEEEEEEEEEEEEEEEEEEE
1206 - 1225:	EEEEEEEEEEEEEEEEEEEE
1207 - 1226:	EEEEEEEEEEEEEEEEEEEE
1208 - 1227:	EEEEEEEEEEEEEEEEEEEE
1209 - 1228:	EEEEEEEEEEEEEEEEEEEE
1210 - 1229:	EEEEEEEEEEEEEEEEEEEE
1211 - 1230:	EEEEEEEEEEEEEEEEEEEE
1212 - 1231:	EEEEEEEEEEEEEEEEEEEE
1213 - 1232:	EEEEEEEEEEEEEEEEEEEE
1214 - 1233:	EEEEEEEEEEEEEEEEEEEE
1215 - 1234:	EEEEEEEEEEEEEEEEEEEE
1216 - 1235:	EEEEEEEEEEEEEEEEEEEE
1217 - 1236:	EEEEEEEEEEEEEEEEEEEE
1218 - 1237:	EEEEEEEEEEEEEEEEEEEE
1219 - 1238:	EEEEEEEEEEEEEEEEEEEE
1220 - 1239:	EEEEEEEEEEEEEEEEEEEE

A0A0F8AJS3 **A0A0F8AJS3_LARCR** (2484 aa)
Histone-lysine N-methyltransferase, H3 lysine-36 and H4 lysine-20 specific. *Larimichthys crocea (Large yellow croaker) (Pseudosciaena crocea)*

```
MSGPYTGPGRETHQSSCPLTPGRDLSTHSCSSRHHDHTRIGLTMSAATSSLKHASVYGFTQREHSSSSSSSSSSSSSSS
SSSSSSSYSPLRRLQHLTSMVSQPDLVLPIRESGERSWEWGMNRKERRKDSWVDCTSSGYSGTQNTSREESFGKSSAGQK
QPVVQTRSRDAPAANRSDPAVSEKKTEGCFSGPPSPAFSLDSNSPFANGFLHFESSLFEDDDNDEERETVSPVEEVLQDK
PERTGDVLQSTSGDLNSDPKDALLSSAKVVTRSQSSGQRRRYWDGSDDEWESDTELFLLEDSPLRHSVIAKRFQNSWKSS
VAEAESVLPDRPKMTSSISSSINDALHDSSTAERVNKAHPTFPPSTSPTLPETSHLTNGSILSPVISSPITTPAKPSTLK
KSSGKNKPSKSSRDLNSKHPKKMLRNSPDQSNRDNGECPYSDLDSVPKILCPKALERQPKLVPTKPSVTVVKEAKKQPEI
QSGLWFSKSGKDRRPKTTSPMPDRTLFSKVPCKKKTASVVSKKTLVPGASSSSGGPSDLSGLSDKHKTLLPAEATLSPEQ
TGHLKCKNTLVANRYFSSSGSPPDQSGLSDKQKSMVSVETGVPSDKCGYSKGRQTVSNTTDNVTGIVCDQLGSSDVKKAL
ESSITLKFSDQSRFSESVMNRTEHDMKVFVIDRISDQAEEKESHKTLASTLNVDTTDPLVRLEKQTSLVSKCRLPFVKLI
RKDIKGRKFLNSSVTISPSDKPEHTKNEKIPDTNMTAKQSDCMDRKAGVLIDKTVSSESIKVSVKKLKASGGTGILRLSS
ESSQSKTIVDANVAKVSDELSSPEAERIPVLKVNASNVTSSSSNQSDQSEGKKTSASNVTSMSSDQLGSSEQKATPEERT
VFNTTTPPSPQHGNLACKNAHVPESPSSEKSKKVVHKTKQVLDKVNKVVLQEQPAHLPASNRLMTRALEAMQKVEKKKRE
KARKVAEQKDLLKSYRKSEDHVCHSARNSTWNPESKRDHCTKTKSLESHCKDNGEYDRDTVSSCSTPPISESVDFEADVK
SEDEDLSISSTPPMDFIPLTSKVKAKKEDHSSDRSSPSSPFSFMNAFKNVQEVSFQSVTNEGDGKPISFKADTNYKFSTF
LMMLKDLHDTRREREGTPLELEIGPPSAHVKAEPLVMPGEATPAGQDQQLDHINKNSSPDKIKVARNEGSTSQTSKRPYNR
RGSSTGVKKKTSRKVPCRPARSGPGFPGLESLPSVDSSSRVESRVQSMLGLQTSNWERQAGSGDGVIGEEEEERWSRVNE
NLQNMVPLDQRGCNTTLCLEQPNGLVGDSTENNASLMRNAGEGDNAPTAHKRIRKPSKRLIEWTEEYDQIFSTRKKTKKP
LQLIGKATQPITPVSEPLGSDKDTHDHPSLDLLPEIQTPPPEEIAATTPTELQIPSTENSSPQDAPVLSIDTLTPPPEAD
PSLSDGLVKDTGNAPVLGRKRKRKPTQKILEYCLEAEASTGPKKKVKTLKNNSNPASQSDSAPPSLKSKNRHLAVSSSTP
TNTEISTCTPPPPIQTDRPPSSPASPTPAPAPPEPAQVDTASADVDPTQAEDSKTQEAKKDRAESEGDPSSLDHSFSSMK
DDLSLCDDPLVPSRKIIGDRGGPASMKENICQVCEKTGELLLCEGQCCGAFHLPCISLAEAPKGKFVCPECKSGIHTCFV
CKKRSEDVRRCMIPVCGKFYHGECIANFAPTAPVNRGFRCSIHVCLTCFIANPNSSSISKGRLVRCVRCPVAYHATDLCM
AAGCVVLSNNSIICPNHFTPRRGVKNHEHVNVSWCFVCTEGGSLLCCESCPAAFHRECLNMEMPKGSWYCNDCKAGKKPR
YKDILWVKVGRYRWWPAEVSHPKTIPENIQRMRHDVGEFPVHFFGSNDYLWTYQARVFPYMDVDANSKEKMGKGVDATYK
KALEEAAVRFRELQAEKELRQLQEDRKNDRKPPPYKHIKVNRPIGKVQIFTADLSEIPRCNCKATDESPCGMDSECINRM
LLYECHPQVCPAGERCLNQAFTKRQYSQVEIFRTLSRGWGLRCVHDIKKGQFVSEYVGEVIDEEECRSRIRHAQENDICN
FYMLTLDKDRIIDAGPKGNEARFMNHCCQPNCETQKWTVSGDTRVGLFALVDVPAGTELTFNYNLECLGNGKTVCKCGAS
NCSGFLGVRPKNNPPSEDKGRKLKRRGHGKRKNKVVVTKEREDECFSCGDGGQMVSCKRPGCPKVYHADCLNLTKRPAGR
WECPWHQCDICGKDAASFCEMCPSSYCSQHREGLLFISKLDGKLCCSEHDPCGPEPLEPGEIREYTPEPRALTSGLGMAV
IPSAASNTTTSVNPTTRRVQEVSAGAGMCASESIPAFSIPVPITIPVTAPPASPPPSSTDTPSSPHVFDVPHYSPISSYE
EERDEEEELLEEVEDDSVEEGEVGRQKSDSHEEDGEAVMEEIGVEYLDEEDEDDEEEDEEEDEEEEEEEEEEEEEEEEE
EEEE
```

2463 - 2482:	EEEEEEEEEEEEEEEEEEEE

2464 - 2483:	EEEEEEEEEEEEEEEEEEEE
2465 - 2484:	EEEEEEEEEEEEEEEEEEEE

A0A0F8AK05 **A0A0F8AK05_LARCR** (560 aa)
Leiomodin-2. *Larimichthys crocea (Large yellow croaker) (Pseudosciaena crocea)*

```
MSCFGYRRELSKYEDVDEDELLASLSPEELAELEKELVDIDPDANVPIGLRQRDQTDKTPTGTFSREALMKYWENETRRL
LEDEICGGSPKPDEERDEECVTEENSGAEDEKDVENEKEQTQEKQKEEEEEEEEEEEEEEEEEEEEEAVTEEEEDEEEEE
EEEEEDNKLKPEPSKDSGVLTSQGDAPMLLKPQRVEPMRLTPPPPPVDPNTTGNPTVVDDALQRVLSNDSELTEVNLNNI
DDISQETLIRFTEALRCNTHVRVFSLANTRADDPVALAIAKMLRENSSIVSLNIESNYVTGKGVMALVQALPGNNTLTEL
RFHNQRHMCGGQVEMEMVKILRENYTLIKLGYQFNLPGPRMSMTGILTRNQDRQRQKRLQEQRQQQQQQGAPEGAVNPRT
TVLKGTPRSSPYSSPWSSPKLPRSDLAKKQTPPAPPPPPPPPPPPPPPPPPPPQREKKPTRMIAEVIKAHEAGSRKAT
KVTKGKKSKKAKSKETGNDETSGILKELKNALRPVSVEKRGEEGSRPSTPMRSAHDQLMESIRSSSTRSLRRVPVPHHLR
```

127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE

A0A0F8APD4 **A0A0F8APD4_LARCR** (1218 aa)
Myelin transcription factor 1. *Larimichthys crocea (Large yellow croaker) (Pseudosciaena crocea)*

```
MSQDTTETRTRTRSKGIRVSTELAGQEMKQELSSSCPTPGCDGKGHVSGRYSRHRSVLGCPIVKKRKLEEAESEENQSAP
KRRNQPAKQSADEGFAADSDAAEEEEEEEEEEEEEDLKEKKKNKTKNRQEAIKPDCSLVATEDPETSICPVAEDVKNESI
ITSETEHECESEKSEEVKPEVLSDDHQREETETKDEEEGQLVAKDESSEQPEGETEVVTELKETKGEEEEEAEEEEKEEG
EQQENIVQERDVERQTISQENSDHLYSSGDYNHQAKESTEEQSKREEREEEEEEEEEEEEEEEEEEEEEEDEGEEREVHQ
EIDTLYTLSPHTQGSEAEVSLREEKVSTPMTEEDNEEQDEEREEEEEEEEEDKRQGKEAGEVVVEEEEEDRDSSKASPTTV
VIEVRSEEDDDEDEEEDEEEEEEEEEEEEEEEDEEEEDEEEEEEDVEEQDRVSEGSGITDDSENWDMTRGNLGLLEQAIALK
AEEVQGGQEAQSSPDYHPYSTSSKSSEPAAAARRTGHYSKEKKEVKCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRIPPE
ILAMHENVLKCPTPGCTGQGHVNSNRNTHRSLSGCPIAAAAKLNKSQDKQVHLQASSSESSSNSDRVLRPMCFVKQLEIP
QYGSFRPNTVTTTPRANLAKELEKYSKVSFDYASFDVQVFGKRMLIPKTPSSTETSPKAFKSKSFPKASSPSHSVSGGFS
KSASSSSGYDYSQDAEAAHMAATAILNLSTRCWERPETISTKPREACTKESDIEVDENGTLDLSMKKTKREGMPPPEASS
SSSSSSQQIGATLSQGHTQSEWEGPLDFTKPSGVKEEDHEEVEYTAPSYTSSDGEEEDQENLEDRKYPGEVTTSSFKVKF
QPKDSKKEILVCPTPGCDGSGHITGNYASHRSLSGCPLADKSLRTLMAAHTAELKCPTPGCDGSGHITGNYASHRSLSGC
PRAKKGGVKSTPTKDDKEDSELLRCPVPGCDSLGHISGKYATHRSAYGCPLAARRQKEGLLNGTPFSWKAFKTEGPTCPT
PGCDGSGHANGSFLTHRSLSGCPRASANKKRAKFPGDEYITAKFRASDVLDNDEDIKQLNKEINELSESNSEMEADMMNL
HTQISSMEKNLKNMEEENKQIEERNEALFLELSGLSQALIRSLANIRLPTMKEPLSEQNFDSYVETLTHMFTNKDCYQNP
ENRALLESINQAVKGIEV
```

289 - 308:	EEEEEEEEEEEEEEEEEEEE
290 - 309:	EEEEEEEEEEEEEEEEEEEE
291 - 310:	EEEEEEEEEEEEEEEEEEEE

A0A0F8AQM7 **A0A0F8AQM7_LARCR** (70 aa)
Uncharacterized protein. *Larimichthys crocea (Large yellow croaker) (Pseudosciaena crocea)*

```
MLHQSLEEEESQETGSDRDRPVIITPSDQTGLNRSELDLTGLVKRDPSEEEEEEEEEEEEEEEEEEEEGS
```

49 - 68:	EEEEEEEEEEEEEEEEEEEE

A0A0F8B1U3 **A0A0F8B1U3_LARCR** (898 aa)
B-cell lymphoma/leukemia 11A. *Larimichthys crocea (Large yellow croaker) (Pseudosciaena crocea)*

```
MNAANRSRTDNNSVGIKGGGPSQGHYRRANDGWKERGGEGRGGKEEPTTYTCTTCKQSYGSAWFLLQHAQNTHGFRIYLE
SEHGSPLTPRMGGPSSLGGGADCPSQPPLHGLHLPPDASPFNLLRIPGSGSGGRDSVGIGGGVGSGGAVGKEEPTTYTCT
TCKQSYGSAWFLLQHAQNTHGFRIYLESEHGSPLTPRMGGPSSLGGGADCPSQPPLHGLHLPPDASPFNLLRIPGSGSGG
RDSVGIGGGVGSGGAVGGGHHQRFPPTPPLFSPPPRNHLDPHHLSPEELALAAHHPSAFDRVLRLNPPLPLDPPPTMDFS
RRLRELAGNTSGSTPPLSPSRPSPMQRLLQPFQTGGGNGSTGGAGGSKPPYLATPPPLPGSMQSPVGSQTTPTTPLPPAG
APPSSTTPLKSKCCEFCGKAFKFQSNLIVHRRSHTGEKPYKCHLCDHACTQASKLKRHMKTHMHKSSSPNTGKSEDGLST
ASSPEPGTSEHLGSASNALKSVVAKLKSENNRMLRENGEEEEEEEEEEEEEEEEEEEEEEEGEEEEEEEEQNGERAVRRN
NNSYHFGLNLEAARQHENNGGIGSRLGAVAEEGSIPRSLPEVMQGMGLAASMQHFSEALNAHKRNAMAQENHLHHHLNRD
HHHNREMCDGESVLETDRGEEGSVSTVNGRGASPNESASVGLSKKLLLGSPSPLSPFSKRIKLEKEFDLPTPTIPNTENV
YSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRFSTPPGELDGGMSGRSGTGSGGSTPHLGGPGRPGSKD
GRRSDTCEYCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQSSKLTRHMKTHGQVGKDVYKCEICQMPFSVYSTLEK
HMKKWHSDRPLSTEIKSE
```

519 - 538:	EEEEEEEEEEEEEEEEEEEE
520 - 539:	EEEEEEEEEEEEEEEEEEEE
521 - 540:	EEEEEEEEEEEEEEEEEEEE
522 - 541:	EEEEEEEEEEEEEEEEEEEE

A0A0F8BJL1 **A0A0F8BJL1_LARCR** (468 aa)
Uncharacterized protein. *Larimichthys crocea (Large yellow croaker) (Pseudosciaena crocea)*

```
MASLGFLLLSSALIHAAQFLPVARGGGRGLDESVGGVRRQRRDLRNLLPYEEQMMSYPASQGGGGLNDLYYQSDDWRGRG
LDQALQRLVERDQRREQEEEQRAAYLAVLLRLLSEAESVGLVSPGDVEVVEEEEDEEDDQGPQGDFQSPDYDETGRGLNM
GRPPSAWWGPVEPQLAQALLDRVEPQLAQTLLERARLQQAGRVSSGLNRDQDALRRLVARLLSSIGPNDATVISGRQARS
```

```
DLSVAASKPINSAHRRTRRSLDDMAPPPSPSNDPPLLRVKRLEEDDDEEERLRPPAAGLQRMKRIDTMATIAMEELNHAT
HGIHERVRGGEEEEEEEKKEEEEEEKKEEEEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEFILTECLSGNDGVATG
AALSVAMTMPFSPLSSDEEQQRMLGNNRHLYPGAEDEEEEEEEEEEEKEEEEEEEEEDEEEEEEEEE
```

360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE

A0A0F8CY58 **A0A0F8CY58_LARCR** (1393 aa)
X-linked retinitis pigmentosa GTPase regulator. *Larimichthys crocea (Large yellow croaker) (Pseudosciaena crocea)*

```
MAGETEDEIPESGAVFTFGKSKFADNVPSKFWLKNDTPLKIACGDEHTALITENGKLFMFGSNNWGQLGLGSKVTVNKPT
CVKALKSEKVQLVACGRNHTLICTAQGKVFASGGNSEGQLGLGDCEERTAFQRIDVFDSHGPIKMLAAGSNTSAALTESG
KLFMWGDNTEGQIGLGKESHASTPQEVSVGRPISWVSCGYYHSALVTVDGALYTFGERDSGKLGLGTDQLQRHRVPQLVK
SIKEPVIQVACGGGHTLALTEDDVFTFGLGQFGQLGHGTFSFESRLPRPVEHFKKGRVCQVACGENHSAVITDGGLLYTF
GDGRHGKLGLGEENFTNQFKPTLCPRFLKYNVQAATCGGCHMVVLARPRDESCNDVSLEEDDVTEDYLEKPYVELLGGTA
DSSTLQRSLSARVRRREREKSPDQFGTMFRTLPAMMPGYLHPPLPISSQTIPPRLPPPELTHRKVLNGTHQHRSAGSNQQ
GQTGGETDSVVESLTDADSVKGLGDTTDFLNMTHVMKMDPGDKSLTLSPVQKRKGKHGKTDKGQKENQKKERRLLKQSSF
SSTSTSQKSDAVSPRRALPTELLRGRDARSLASESPPRQKTTKQNKENLIMAVEELQRKPGKNQPPSVGDIRKAASKQRL
KPAAGKGQLIEVGRKLSDSPETRKEESESAVAKVKKAQPQPAKNKPIVVQSHHARGHAGSPGFHLSDASNEESLSSPRLL
SEVKKGSKEKTDFNKKSKNEKNQKEAQSKKETSDLGLLAGAASLAAGSVLMHEVVSRSRFSSASSPSPSESSRGVLKESV
TKSRSEESESYAADFSKKSAVSINIIPAPESSEARTSQDEEETSQDESEEESKEQTDSASVKYDEEEEDEDEDRQRTSAD
VSEEEEEEDVSHSLGKVTEEDEDDTDSDTLKPDDEPETDVGSKDEEEEEEGEEEEEESGTAGSGSEDETEEKESKGSDVS
EEEEEEEEEEESNEGSSHETDSRGGESENEEEGEEEEGDLESEGEEEEGESESLKSSEQSKESETEEGEEEEEEEEEEQS
SAEEEEDESSEEEESENEEESEEEDEEVEEEEEEESAEAEEEIDSEGEEEEEGEEAEEEEVENKNEEEEAEEEEEEEEEE
EEEEEEEEEEEVVKKKKAAEVKRQNTKNRRKPGSQMWSKGEEEGEEEEDNVDEEEEEEEEEEEEDNDTSAETEGPSSSFD
DSTEKPTEETQSPKPEELKEESIPDGEQKAAEITEQPDTTGQEKKDDGTKPANGTTESNSKSQSGANKKRESDPEVHDRM
EEYQNGSEGSFNSEETDGIVKECIESVVAGDDYSQSQVNKWTASIVERCLTQLVKQGKPYKYIVTCAVMQKTGAGLHTAN
SCYWDTAMDGSCTVRWENRTMYCVVSVFAVAIA
```

1111 - 1130:	EEEEEEEEEEEEEEEEEEEE
1112 - 1131:	EEEEEEEEEEEEEEEEEEEE

A0A0F8D0A3 **A0A0F8D0A3_LARCR** (1651 aa)
UPF0606 protein. *Larimichthys crocea (Large yellow croaker) (Pseudosciaena crocea)*

```
MAGLVSSVGWLVMFKALMHARSQRAVFLGMTVLVTVIAADSPVADESHSNILDVNQLSPSSAPLENKPTHDINMLPNPEE
ILAPGYNVPFIAPLPTLPPSEPTEVSPEDFYPTNTMEFDWGSGDYLETMSFLNSDEDDYSLVTKVPSDSYDLEEYTENYD
TSFPSRVGIYPSSLHPLHTSPSPSLMTAYSTIVPLKTISPSFISPTIHYILEPTPTSNSDISDASDIDWPDTFTIQPTDV
LLPDMNSLEYYTTQLTRENSSSDTGAEHRGNVTVVSISTTDITPTSSIANDTKLTEDESSSDLSGFEPPDELTTVVPTED
SPQLVNASEPFLDPSILPTHFFDLSSSTWSSQVSTTDLGVPTITVGLDSTALTEDQMIVSTTPFLPDVVMSSSSLTDVHW
FVTESFQQSTIQATSVFPATIPFSPVPTEPAANTTTTEVTPQDFTFTSEQTPNITLIPTEPPSNVTLLLPDVLGDQGVTE
DGIDISATMTLIPTSSEANTVSAVPTTTTAATTSHQATSRTTAATEASTSVSIISTTSEKTTVTTTTTTTISRQYLCNLD
RPAYLVKIGFPSGATVGYAKSQVRDILKGEFNKSVELQVVDPPPKFVFRVVSGPVVYTAISVINALRRSGRRFLSVSPNW
AIPDNKYQIHTVLQFVPGHIDVRFCNFSESIEKGLTMAFAEMRRRSKESTNFTVHIVNITMAAPKYQEQRLVRQPVDITF
TVRSSRGYLMGSEVSNALMKLTMVEFSYYMGFPVLQIAEPFHYPELNTSHVLRSSWVRTVLLGVLDQKVGERTFQASMER
RVAMLLGEAMGFVRRVKRATTIGNSSVQVVSASRLVGVDHPLEIVYFVEGPSGQRVPAAQAANLLNNMDVQRAAIILGYR
VQGILAQPVEKVATSPTDAENTNMWIVIGVVIPLLVVIVIISILYWKLCRTDKLEFQPDAMTSIQQRQKSTASFRESRTS
LPQTLPPFKKDIDYSEEEYEEEEEEYEEEEEEEEEKEIKTGKKPVALPKSKQSMSSEEEEEEDEEEEEEEEEEEEEEEE
EEEEEEEEEEEDKDEAKKGIKQEEQRRQGQSKAMIMKTGETKKEDRTKVLTKGKRATQELQAPSVKGFDFAKLHLGQQSK
DDVMVIQEPVPPGPGPGPLPVSIKDGFSPSENGEIPTPISKNSASSIKTSRSGRRRGRISPSDGDSVVSDRSSERESTEE
NLRAHTTPSDSKQTRPPPMNGTNEQLSSASIFEHVDRMSRAADASRRLPNKVQLIAMQPMPVPPLHSPPVNGKLSPDSNQ
INKEIQVALRHKSEIEHHRNKIRLRAKRKGHYDFPTMDDMTSGHADQKDQDRIYQKAQIQIDKILDPDAQMSSIFVGSKK
SGRGRRSPKQRMKEQLNGGMMEADKDHLITEDSDAAYRKCPGVNNVAYVSDPDQGPGSPHRSPSPTDDVFLGPTSSPPGH
APPPPPYMPPQPSIEEARQQMHSLLDDAFALVSPTSQGSTAGITLPGVNTNPPASSPPGRGPRPWGPSYPPPSSFPSRFT
ELGMSPPSVQGLTPSRVNGYPAGVRAAPGHNGGIGWNHYHDDNFSRTEPEKDAYLDCPDYSPPSIFQTPRSGIREPSAPP
VHLDNPVGYLSAPPPLVTSPPTHSSASLIKAIREELLRLSQKQAAVPSYHS
```

1024 - 1043:	EEEEEEEEEEEEEEEEEEEE
1025 - 1044:	EEEEEEEEEEEEEEEEEEEE
1026 - 1045:	EEEEEEEEEEEEEEEEEEEE
1027 - 1046:	EEEEEEEEEEEEEEEEEEEE
1028 - 1047:	EEEEEEEEEEEEEEEEEEEE
1029 - 1048:	EEEEEEEEEEEEEEEEEEEE
1030 - 1049:	EEEEEEEEEEEEEEEEEEEE
1031 - 1050:	EEEEEEEEEEEEEEEEEEEE
1032 - 1051:	EEEEEEEEEEEEEEEEEEEE

A0A0F8D1H4 **A0A0F8D1H4_LARCR** (1822 aa)
Bromodomain and WD repeat-containing protein 3. *Larimichthys crocea (Large yellow croaker) (Pseudosciaena crocea)*

```
MWDIGRPVAELYYLIARFLQSGPCKKAAQILVEELEEYELVPERWSWDGKKYKRTFQDWMILNQHIPADYLLRVCQRIGP
```

```
LIEKEIPPSVPGVQTLMGLGRQSLLRTTKSCSHKVCSGSAVAALHRGRPPEPPVSSGDPPNIVSIMGARQTIGTARFSQA
MPSSSYQHMKIHKRILGHLSSVYCIAFDRTGRRIFTGSDDCLIKIWATDDGRLLATLRGHSAEICDMAVCYENTLLASAS
CDKTIRVWCLRTCAPITVLQAHGASITSIQFCPAVKGTTRYLGSTGADGMVCFWKWHSISMKFNDQPVKFIERSRPGVQV
STSSFSSGGMFMATGGTDHMIRVYYLGAETPMKVSEMDAHTDKVVVVQFSNNSDSLRFVSGSRDGTARIWHYQQQEWKSV
TLDIAARLPGSTVANGDDKTKLVVTMVAWDRADRTIITAVSNYLLKVWSTTTGQLLHVLSGHDDEVFVLEAHPFDSRIML
SAGHDGNIYMWDLTKGAKIRNFFNMIEGQGHGAIYDCKFSADGQHFACTDSHGHVLIFGFGCSRPYEKIPDQMFFHTDYR
PLIRDSNNYVLDEQTQQAPHLMPPPFLVDVDGNPHPPHYQRLVPGRENCKEDQLVPQLGYMANSDGELVEQVLGQQTAEN
RESMLDNLIRQLQNEQDERQNVEEEADGAEADDAAGMVPSSPAAGPRRSGQVDGVWQMQHNALRSQVATERDLLAWSRRV
LVNEVPQGIFRVLEDCRQAKGDMECSLYNAERKKKPVTCTPKSEALTSRLRSLRPTKKKQQRHAYQTRSAQVRRPGTRSR
NQSNRRNSDSQAESDSDGEAAEQAEQSEASSDGEARWQSESSSSDASSEYSDWTADAGINLQPPKRSSRRPVQPQGYSSS
EEEEGDDKAKETKKKENEKRKKPKETKQKATSSLAGLDAEEWLPPSWIMETIPRRSPFVPQMGDELIYFKQGHQAYVRAV
RRAKAYSINPQKQPWNRLNLRDQESVKVVGIKYEVGPPTLCCLKLAFLDSVSGKMTNDSFSLKYHDMPDVIDFLVLQQFY
NEAKEHNWQPGMRFRSIIDDAWWFGSVEDQEPLQLEYPDSLFQCYAVKWDNGEREKMSPWDMEPIPEEAALPEQVGDGVE
VAEEELKALLYTPQEGEWGAHTRDEDCERVIHGIDQLLTLEVAKAFALPVNLRDYPLYCTAVAYPTDLSTIRKRLENRFY
RRISALMWEVRYIEHNARTFNEPQSPIVATAKVVTDVLLHFIGDQSCTDITDLYYKLRCEISSGGEEAEAELDVDSDTPG
TSTGHRGSNLKRGVVLDVKAWRGQCRELLRRMIASPDSEPFRQPVDLFEYPDYRDIIDTPMDLGTVSETLVEGNYVNPME
FAKDVRLIFSNSKAYTPNKKSQIYTMTLSLSAFFEKNIISIISDHKSALQNERRARQRLSYRDRLHNGGSSPPNSPSPSS
KGKHKSGKVSKPKKSRTSTKNRSQRPYQAQHSSSVAEEEDIQPSSPGSGTSSESGKRNEGPHRVTRSQATPVKKSGHRNA
HLSNGSRQQHRQEAPQSEKEEEASGSNSSSSGSSSSSSSSSSSSDSENSSDSEMEKYVEGGDHDYSKAPCLSVRLSGKG
KLAVLGKRRHDGGEEEAQRPKRARVQLPIVPVLQVKVEEEEGDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEQQQPL
DVRHEKEEGEVEGEEGEVEGEEGEVEGEEDEEEEEEPEEEEEPEEEEEEPEEEEEPEEEEEEEEEEPAAAAPAASSARGS
HCKSRRVSTRNQGRRTVLYRDESEDDGHGSKEDPLNLGRSRSGRVRRMTEKARVSHLMGWSH
```

1644 - 1663:	EEEEEEEEEEEEEEEEEEEE
1645 - 1664:	EEEEEEEEEEEEEEEEEEEE
1646 - 1665:	EEEEEEEEEEEEEEEEEEEE
1647 - 1666:	EEEEEEEEEEEEEEEEEEEE
1648 - 1667:	EEEEEEEEEEEEEEEEEEEE
1649 - 1668:	EEEEEEEEEEEEEEEEEEEE
1650 - 1669:	EEEEEEEEEEEEEEEEEEEE
1651 - 1670:	EEEEEEEEEEEEEEEEEEEE
1652 - 1671:	EEEEEEEEEEEEEEEEEEEE
1653 - 1672:	EEEEEEEEEEEEEEEEEEEE
1654 - 1673:	EEEEEEEEEEEEEEEEEEEE
1655 - 1674:	EEEEEEEEEEEEEEEEEEEE
1656 - 1675:	EEEEEEEEEEEEEEEEEEEE

A0A0F8V636 **A0A0F8V636_9EURO** (1509 aa)
Uncharacterized protein. *Aspergillus rambellii*

```
MAFSIAPSNPAGGIPAELGAELPDVCAEEVGFKGVSGDSNVQLLPTPWPTDALPAPTCTLLAVAATKGIVVGAGPNSLSI
ASSESVRAAISSSAGAEQVKTKPFQPQATISLPARSTHIAFASGDTALVLATENGPQLSVFQTTALLQPNAQPALSIPTN
GATFRAVAPNPAPAEDSHSSSLVALVTTGGELLIADLKAGSLVSGPNGNILKTGVSSVCWSNKGKQLVAGLVDGTAYQMA
PDGVQKDLIPCPSDLEEPCHVSSIAWLENDIFLTVYTPNAAEDDMGNTLPSSYYIITRRKQAPFLIQKLPELAAPWGFKR
APAYQFIARLRDYKPHLKDALIISSTASADVGLITRSDQPLASDDGAAAAVGLFVTTEVNDDTKKASIPLMDSGDETSVI
GLGIDLSSSELVISPIQGEDIPESSTPLPNLFLLNHEGILSSWWFIYSESIRQKTPYSGLASVASQQQPAPQPQLQPVQQ
QPAALPTFGQSGFGSSTGLGAPSFGSSGFGRPSAAPAFGSPSSLGSTQTPGFGKPSFGAPAFGAPSQIGPSFGSSSALGQ
GGSPFGKTAFGQPSTTGKGLANPFGTAGQTSGGGFGSFASTGGFAGLAASKPSGESPFSKVTGGSPFSKPSEPSVFGSQS
ATQSAFGTQQTTETKSPFGLGSGGFVLGSTFKGDGTAVNDGPKPEKSSGLFSLGALDEMVSTPDKESPPTEAMDDMDDSS
APQQNTPEPKAQAPSLFGVPSKPAPSGSSSLFGSFGSQAQAPQPFSSAPSSKSPFSILGNAAAEKQTLSPPSPPSEKTAV
ASPPLTQAKLPEPETTPAISLPEPPLPPDSTSKTVYGPGDTSASSNVSKCSVEDAPLPPDFEAAPKFSESDSEPPLPPDF
TTAPAAGGEPPLPPDFTTAPKLSGADSEPPLPPDFTSKPKEKLKPAEEAPLPPDFMTQKPSTLTKGAPPVPDGSDADESE
KGFNEEEEEEEEEEEEEEEEEEEEEEEESDFEDSGEDITHDLGEPESDGPSPETSFGAEISDKSSAGGLFDRISQPNQPGR
QQPRQLFGEISKPFFPQAVQTREPPRSPSPVRPLRAQQNVLKQESYTSVSTPHKPGSALAARKASLSEIAKRDGPLRPEP
IHAVQRPRPQPIVQTQDETLSDDEDERLRADLSRSLEPVPTLDPFLPHQDYTGQATKPGIPGQIERLYRDINSMVDTLGI
NSRSLASFLLYQQGSANPNWMSLLQSDHPADILDEKLLLREIEELGHAVTLLVGSLEEQRVQGVEEKLEKCRELLSKDIL
TLRSQCASIRKTLDAHTDAAAIVSARLSAEQANLQQDLRSLSAEIQGRLADLESAVSLLRAKIADAPRADGSRQSTKRPT
VEAVTSTIATMMNMVESKSSDIDVLEVQLKKLGIDTSASPVSREGSPFTTPRKGLGKLPSTPGSCGSVDVPVSSYHTPDS
SARGLNFRASINGSAKVSRLRTVENMSGLEGKSRSTQWMAKMQRKQHMVESLKKAIGEKQSKVRSMDDL
```

965 - 984:	EEEEEEEEEEEEEEEEEEEE
966 - 985:	EEEEEEEEEEEEEEEEEEEE
967 - 986:	EEEEEEEEEEEEEEEEEEEE
968 - 987:	EEEEEEEEEEEEEEEEEEEE

A0A0F8WDJ8 **A0A0F8WDJ8_9EURO** (248 aa)
Uncharacterized protein. *Aspergillus rambellii*

```
MSSTNTGALAAQFLDLTTVSGHQSANMVELSVLPALREPVLRAPGANINNLNTTRAVNREAVMMQVTGLERLGANACSYC
QRGFGPFSSCVMSPGRFSNTCANCHWNSSGSRCSHRMDVKEEEEEEEEEEEEEEEEEEEEEEEEEEEARGPPRRYATLSA
SRMHRLFITAATSFDAMRAGFAAMARAVAMAADEFADDGGYAAPSNRGGNPNSLYRMILGEEDEEEEKEKEKEKEKEEEE
EEWEGFSD
```

121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE

123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE

A0A0F8WUR3 **A0A0F8WUR3_9EURO** (789 aa)
Ribosome assembly protein. *Aspergillus rambellii*

```
MAGSQKKSTKKFEKKHLKDVLERRKAAAKIKQRNHLKEKRKADSAKLRAGNEDVSEENSEQEKKQNTFAEMNVDDFFSGG
FDIADAAAEKSNKAKKKNVTPKIGKRKRSDPQEDEDESSAASSGGEEDGVQSADEEDADSQASDLDAFEAHKDQLEALKQ
KDPEFYKYLKENDAELLDFGDLAEVDELSEAEAEEEPAKKKKKKAAKEEEEEEATNMLTVAMVKKWQKLMEDQNSIRAMR
QIVLAFRAAAYLNDADVQEQKYSISDSNVYHQVLVTALGNVPRVLSHHLPVKQTASGKVKLSLDSKKFKTLTPLIKSHTS
SVHQLLVNLSDEQTLKLTLSSIEPMLPYLLQFRKLLKVLIKTVVGIWADVSTTEATRIVAFLLLRRLMVIGDAGLKEAVL
KASYEGVVKGSRNTTVHTLSGVNLMKNSAAELWGIDQNVSYTAGFNFIRQLAMHLRSSITNTSKESYKTIYNWQYVHSLD
FWSRVLSQHCDGLVEAKVGKQSALRPLIYPVVQITIGAMRLIPTAQYFPLRFQLTRSLLRVSRATGTYIPLASALLEVLN
SSEMRKAPKSSTLKPLDFNTAIRAPKSYLRSRVYQDGVGEQVAELLSEFFVLWTKHIAFPELSVPVVVSLKRWLKQVSSR
SGGNKNTKINQMILLLVQKVETNARWIEERRLSVSYAPRNRTEVETFLKDVDWETTPFGAFVKSQRKLREEKAAILEQGR
REEEKRRAEEKEGDEDMLMDDVASENDISEEEEDEGSDEEGSSEEEEEEEEEEEEEEEEEEEEMEEEED
```

764 - 783:	EEEEEEEEEEEEEEEEEEEE

A0A0F8X913 **A0A0F8X913_9EURO** (631 aa)
RNA helicase (EC 3.6.4.13). *Aspergillus rambellii*

```
MPIPVDTAKSISKKRKRKHGGNGNARGAIDENASDVEVSAPKLVGEKDGVSGEMASKKKSKKQKDIELAKKVVTEEAQKK
RKVSHSSNEEDVSKENGDEEEEEEEEEEEEEEEEEEEEEEEEEEADEEIVTDLPSVEAVSLPQTDGGPKKFTELNLSEKTLQ
GIKEMGFETMTEIQQRTIPPLLAGRDVLGAAKTGSGKTLAFLIPAIEMLSALRFKPRNGTGVLVVSPTRELALQIFGVAR
ELLSAHSQTYGIVIGGANRRAEAEKLAKGVNLLIATPGRLLDHLQNTPGFVFKNLKTLVIDEADRILEVGFEDEMRQIVK
ILPSEERQTMLFSATQTTKVEDLARISLRPGPLYINVDHKKEHSTVEGLEQGYVICEADKRFLLLFSFLKRNLKKKIIVF
FSSCNCVKYHAELLNYIDLPVLDLHGKQKQQKRTNTFFEFCNAKQGVLICTDVAARGLDIPAVDWIIQFDPPDDTRDYVH
RVGRTARGVNGKGRSLMFLQPSEVGFLKYLKEARVPVVEFEFPASKIVNVQSQLEKLIGQNYYLNKSAKEGYRSYLQAYA
SHSLRSVFDVHKLDLVKVAKGFGFSTPPRIDIQLGSSLSRDKKQQQQGRRTYGSQPKNNKGLKFKRRHDDD
```

99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE

A0A0F9PYQ5 **A0A0F9PYQ5_9ZZZZ** (610 aa)
SBP_bac_5 domain-containing protein. *marine sediment metagenome*

```
MKRKFLWSGLSFLLVAALVLASCGDGVGEQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEPVVGAPQYGGTLTPWSSHQFF
DPPGPAVAHGNWASLYWLDYIQEGLIIGDTETYGVRGTGEYRFQTSDYLPTAYTTGHLAESWELSLEKLVWHIRPGIMWQ
GTNAVKTVMENREFTADDVVQDIIAYMESPWKGRFVGFIDIDDPASSVYATDRYTVVIEFEKYTPALWKFFTYDVRAKIS
PPEMIAAGADKWENQVGTGPFVFEEYVTGSHMSWVKNPDYWKTMTINGVEYQMPFVDRVVAPILPDVATQMAALQTGKID
FFTYAPLGYWDVLDGVKGLQMTDQMHGGGAIIWMRSDQPPFDDVKVRQAVRIGTDQMEFVKMAKAEGLPLDWWPSNPGNP
AVYVPLEERPADIQLLYDYNPELAMEMLADAGYPEGFATRFLVTNTPTDLDIAALLKFQWAKIGIDIEIDGVDSATYVAA
KYPYPTPTYDGLVSDGAPVGDPFFVATQYLYSLVGSFNYSQYSSPELNALTDTAVYETDPAERALLLKEMNLMIDRDSPA
IPLQYFPNRNYWWPWAKNYNGEAAVINVGRNSSITMRIWIDQELKADMGY
```

31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE

A0A0F9VIR2 **A0A0F9VIR2_9ZZZZ** (156 aa)
Uncharacterized protein. *marine sediment metagenome*

```
MIQLLMVLIVVIGFIVMASLFFVRGFVDEVLSEESDEQDPGPPIKECEEEEKEEEEEEEEEEEEEEEEEEEEEEIP
KHDWSVEGDPFILIAKGKSIKEIRELVQEYEVSAKNLEASGMSNQRQGYIVSASTDFSASIRFKSRVDKLKKIIAA
```

53 - 72:	EEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEE

A0A0G2E1F8 **A0A0G2E1F8_9EURO** (72 aa)
Uncharacterized protein. *Phaeomoniella chlamydospora*

```
MNPNARLNPNSHELLILPEARVAAFVEEEEEEEEEEEEEEEEEEEEEEEEDVDDELDDPEFVSEIPVSAPLV
```

27 - 46:	EEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEE

A0A0G2GPT2 **A0A0G2GPT2_9EURO** (178 aa)
Uncharacterized protein. *Phaeomoniella chlamydospora*

```
MLPKKKWCDFLTEIPEDKEEKEEEMIKKEEEEEEEEEEEEEEEEEEEEEEEEEEDDDEDEDEDEEAEQVEEGEAEREMHG
GGGGGDNMEMEIEQPLNSQFNITDAHVDLQVFILTQLQQLNEKFDTVLENQQRLDTIQTESIRLLIEENRKTLQYLRHIS
MWTTFIKDALNKMLDVVT
```

29 - 48:	EEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEE

A0A0G2JIR1 **A0A0G2JIR1_HUMAN** (1233 aa)
Histone-lysine N-methyltransferase EHMT2. *Homo sapiens (Human)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGA
LLLEKETRGATERVHGSLGDTPRSEETLPKANPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDESENLEGDGDLR
GGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGSEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEIQHFRMSDDVHSLGKVTSDLAKRRKLNSGGGLSEELGSARRSGEVTLTKGDPGSLEEWE
TVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAK
KKWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELS
GCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCG
EDASEAQEVTIPRGDGVTPPAGTAAPAPPPLSQDVPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGC
LSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGS
VEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVD
VNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHI
AARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPC
VNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFEC
NQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVY
CIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKH
SAEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

357 - 376:	EEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEE

A0A0G2JIS2 **A0A0G2JIS2_HUMAN** (1176 aa)
Histone-lysine N-methyltransferase EHMT2. *Homo sapiens (Human)*

```
MAAAAGAAAAAAAEGEAPAEMGALLLEKETRGATERVHGSLGDTPRSEETLPKANPDSLEPAGPSSPASVTVTVGDEGAD
TPVGATPLIGDESENLEGDGDLRGGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGA
AAAGSEPPPATTSPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEIQHFRMSDDVHSLGKVTSDLAKRRKLNSGGGLSEEL
GSARRSGEVTLTKGDPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEE
EEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAPK
IDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFR
VAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLSQDVPGRADTSQPSARMRGHGEPRRP
PCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNL
DPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTC
LHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIA
EVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNR
AIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRC
WYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISD
AEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDY
GDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE

A0A0G2JK64 **A0A0G2JK64_HUMAN** (1267 aa)
Histone-lysine N-methyltransferase EHMT2. *Homo sapiens (Human)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGA
LLLEKETRGATERVHGSLGDTPRSEETLPKANPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDESENLEGDGDLR
GGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGSEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEIQHFRMSDDVHSLGKVTSDLAKRRKLNSGGGLSEELGSARRSGEVTLTKGDPGSLEEWE
TVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAK
KKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEEL
PLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTA
GTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLSQDVPGRADTSQPSA
RMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGEL
QKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGC
VYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLH
WASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQL
NRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSS
NCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTF
ICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRD
IRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE

A0A0G2JRN8 **A0A0G2JRN8_HUMAN** (922 aa)
Histone-lysine N-methyltransferase EHMT2 (Fragment). *Homo sapiens (Human)*

```
SEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAK
EPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMA
TESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLN
GMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLSQDVPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGP
SLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTP
LHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVS
LLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVN
YHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVAR
GYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNK
IEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFD
LDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTC
QCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE

A0A0G2JRR0 **A0A0G2JRR0_HUMAN** (888 aa)
Histone-lysine N-methyltransferase EHMT2 (Fragment). *Homo sapiens (Human)*

```
SEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAK
EPRGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCE
THRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAA
PAPPPLSQDVPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESE
RRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPL
MEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIR
MLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNK
EGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTM
NIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQL
YRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPV
RVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPEL
GSLPPVNT
```

12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE

A0A0G2JTA5 **A0A0G2JTA5_RAT** (1172 aa)
Euchromatic histone lysine methyltransferase 2. *Rattus norvegicus (Rat)*

```
MAAAAGAAAAAAAEGEAPAEMGALLLEKEPRGAAERVHGSLGDTSHSEETLPKANPDSLEPTGPSSPASVTVTVGDEGAD
TPVGATPLIGEEPENLEGDGGRILLGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAATAG
PEPPPATTAGQEGQPKVHRARKTMSKPSNGQPPVPEKRPPEVQHFRMSDDMHLGKVTSDVAKRRKLTSGSLSEDLGSAGG
SGEVILEKGEPRPLEEWETVVGDDFSLYYDAYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEED
EESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAPKIDRI
SERAGHKCMATESVDGELLGCNAAILKRETMRPSSRVALMVLCEAHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHR
FHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGGTPPVGTVAPAPPPLAHDAPGRADTSQPSARMRGHGEPRRPPCDP
LADTIDSSGPSLTLPNGGCLSAVGLPPGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNF
QSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQLGGCVYSKEEDGSTCLHHA
AKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIDVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLL
NAQCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAVRT
EKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDK
DGRLLQEFNKIEPPLIFECNQACSCWRSCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEAD
VREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRF
WDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPDLSSLPPINT
```

295 - 314:	EEEEEEEEEEEEEEEEEEEE
296 - 315:	EEEEEEEEEEEEEEEEEEEE
297 - 316:	EEEEEEEEEEEEEEEEEEEE
298 - 317:	EEEEEEEEEEEEEEEEEEEE
299 - 318:	EEEEEEEEEEEEEEEEEEEE
300 - 319:	EEEEEEEEEEEEEEEEEEEE

A0A0G2JX51 **A0A0G2JX51_RAT** (68 aa)
Uncharacterized protein. *Rattus norvegicus (Rat)*

```
EEEEEEDKEEEEEEEEEEEEEEEEEEEEEEEIKTKQNKTKTLNLKIFQTIGNKNKMVNLSRLPSKENCK
```

9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE

A0A0G2JZM5 **A0A0G2JZM5_RAT** (1206 aa)
Euchromatic histone lysine methyltransferase 2. *Rattus norvegicus (Rat)*

```
MAAAAGAAAAAAAEGEAPAEMGALLLEKEPRGAAERVHGSLGDTSHSEETLPKANPDSLEPTGPSSPASVTVTVGDEGAD
TPVGATPLIGEEPENLEGDGGRILLGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAATAG
PEPPPATTAGQEGQPKVHRARKTMSKPSNGQPPVPEKRPPEVQHFRMSDDMHLGKVTSDVAKRRKLTSGSLSEDLGSAGG
SGEVILEKGEPRPLEEWETVVGDDFSLYYDAYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEED
EESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNH
AGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELLGCNAAILKRETMRPSSRVALMVLCEAH
RARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGGTPPVGTVAPA
PPPLAHDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPPGPGREALEKALVIQESERR
KKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLME
AVVNNHLEVARYMVQLGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIDVIRML
LTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNAQCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEG
DTAWDLTPERSDVWFALQLNRKLRLGVGNRAVRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNI
DRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRSCKNRVVQSGIKVRLQLYR
TAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRV
FMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPDLSS
LPPINT
```

295 - 314:	EEEEEEEEEEEEEEEEEEEE

296 - 315:	EEEEEEEEEEEEEEEEEEEE
297 - 316:	EEEEEEEEEEEEEEEEEEEE
298 - 317:	EEEEEEEEEEEEEEEEEEEE
299 - 318:	EEEEEEEEEEEEEEEEEEEE
300 - 319:	EEEEEEEEEEEEEEEEEEEE

A0A0G2K877 **A0A0G2K877_RAT** (219 aa)
LRRGT00112-like. *Rattus norvegicus (Rat)*

```
MRKTLIKGKPFIGAGLQFRGWSLALYDFTFKDQRPIKSTALNGFPYRDWGNDPECPMGLEFRSCTWTVSPFQAVKERGGG
VGGGGGGGGGEEEEEEEEEEEEEEEEEEEEEEEEEDDEETTIGVWMVSELLALMPPTMMDCSPCGTSHFFPAPLAFLTL
FGYTNAAAQCTPAMVITKGIGDQRKSPLKDLPLSYNGSHGGRCAFFNKTDALNMALCLS
```

92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE

A0A0G2K8H1 **A0A0G2K8H1_RAT** (1229 aa)
Euchromatic histone lysine methyltransferase 2. *Rattus norvegicus (Rat)*

```
MRGLPRGRGLMRARGRGRAAPTGGRGRGRGGAHRGRGRPRSLLSLPRAQASWAPQLPAGLTGPPVPCLPSQGEAPAEMGA
LLLEKEPRGAAERVHGSLGDTSHSEETLPKANPDSLEPTGPSSPASVTVTVGDEGADTPVGATPLIGEEPENLEGDGGRI
LLGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAATAGPEPPPATTAGQEGQPKVHRARKT
MSKPSNGQPPVPEKRPPEVQHFRMSDDMHLGKVTSDVAKRRKLTSGSLSEDLGSAGGSGEVILEKGEPRPLEEWETVVGD
DFSLYYDAYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAKKKWR
KDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELLGCNA
AILKRETMRPSSRVALMVLCEAHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDAS
EAQEVTIPRGDGGTPPVGTVAPAPPPLAHDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAV
GLPPGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEIC
HVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQLGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQ
DSGGWTPIIWAAEHKHIDVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNAQCDLHAVNYHGDTPLHIAARE
SYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAVRTEKIICRDVARGYENVPIPCVNGV
DGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQAC
SCWRSCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDA
RYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEA
IALEQSRLARLDPHPELLPDLSSLPPINT
```

352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE

A0A0G2K9A5 **A0A0G2K9A5_RAT** (94 aa)
Uncharacterized protein. *Rattus norvegicus (Rat)*

```
CTAWGCRKLGEEEEQEEEEQEEEEQEEEGGKGRGRGGGGGGGGGGGGGGGEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEENYGNLKGET
```

53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE

65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE

A0A0G4F131 **A0A0G4F131_9ALVE** (560 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MSVFLEVLPQNLTVKKWDVDVSYRIIVQNHKYEGYTVKKGDNFIFNETNLDRGWPDMITLDELTRAQGFLGPSNELTLRA
EVQVISEEFPPENVETPEDGSELKIRKKNKKTDKKIPPKFESAHEIEFVLEDFPYNFASMPMGHYVKSPTKRVGGNVDFS
LLIYPSGEVKEDAGAMTVFLEAKVPKRWVRWEVETEYQIELVNFNDEGLSVERWDRFTFRKKRDTFGWGEFIRKGNLTRE
KGFLGPSDEAIVRARVNVLSEVVKKRRWYWTDVLFCLLICFLGCWFLWHVSCVLLRRWRRAEAAAAAGRRAIQEVAQTRS
QLSRERQKAKKREAAQQAQSQSVPSTTGSPLLDSGSTEEEDEKKEEEEERRPTCTTISEDSSARSRFSIFCWVSRLKSFK
IFVYAAKKEDRESGSLSEEGTNASSSVREMEGSSASEEEEEEEEEQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEGEQEQEEEEEEEEEESCASCGVPDQQLDRTLKRCMRCLAVKYCLKECQTKHWRAHRPYCHPIVEEEHN
```

447 - 466:	EEEEEEEEEEEEEEEEEEEE
448 - 467:	EEEEEEEEEEEEEEEEEEEE
449 - 468:	EEEEEEEEEEEEEEEEEEEE
450 - 469:	EEEEEEEEEEEEEEEEEEEE
451 - 470:	EEEEEEEEEEEEEEEEEEEE
452 - 471:	EEEEEEEEEEEEEEEEEEEE
453 - 472:	EEEEEEEEEEEEEEEEEEEE
454 - 473:	EEEEEEEEEEEEEEEEEEEE
455 - 474:	EEEEEEEEEEEEEEEEEEEE
456 - 475:	EEEEEEEEEEEEEEEEEEEE
457 - 476:	EEEEEEEEEEEEEEEEEEEE
458 - 477:	EEEEEEEEEEEEEEEEEEEE
459 - 478:	EEEEEEEEEEEEEEEEEEEE
460 - 479:	EEEEEEEEEEEEEEEEEEEE
461 - 480:	EEEEEEEEEEEEEEEEEEEE
462 - 481:	EEEEEEEEEEEEEEEEEEEE
463 - 482:	EEEEEEEEEEEEEEEEEEEE
464 - 483:	EEEEEEEEEEEEEEEEEEEE
465 - 484:	EEEEEEEEEEEEEEEEEEEE
466 - 485:	EEEEEEEEEEEEEEEEEEEE
467 - 486:	EEEEEEEEEEEEEEEEEEEE
468 - 487:	EEEEEEEEEEEEEEEEEEEE
469 - 488:	EEEEEEEEEEEEEEEEEEEE
470 - 489:	EEEEEEEEEEEEEEEEEEEE
471 - 490:	EEEEEEEEEEEEEEEEEEEE
472 - 491:	EEEEEEEEEEEEEEEEEEEE
473 - 492:	EEEEEEEEEEEEEEEEEEEE
474 - 493:	EEEEEEEEEEEEEEEEEEEE

A0A0G4F7S4 **A0A0G4F7S4_9ALVE** (95 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MLPLLEEEDEEEEEKEKEEEGKGSFLEKIEGGDGLRTQSGIDVKAEGREEEDEEEEEEEEEEEEEEEKEKEEEEEEEEE
EEEEEEEEEEEGKED
```

72 - 91:	EEEEEEEEEEEEEEEEEEEE

A0A0G4F9E0 **A0A0G4F9E0_9ALVE** (101 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MAAGESAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGAEVEELAEEEDEESQPPPSPSLLRSLSPGLG
PWGRRALGGGGGVSSRVLWRF
```

8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE

11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE

A0A0G4FBE3 **A0A0G4FBE3_9ALVE** (141 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MLPLLEEEDEEEEEKEKEEEGKGSFLKKIKGGDGLRTQSGIDVKAEGREEEDEKEEEEEEEEEEEEEEEEEEEEEEEE
EEEEKEEEEKEEEEEEEEEEEEEEEEEEEEEEKEEEEEKKEEEEEEEEEEEEEEEEEKED
```

55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE

A0A0G4FCL6 **A0A0G4FCL6_9ALVE** (205 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MSSSVIRRGVRVGRPSLGIASSAAAWGVFPGGCLAFRISATWWSSICFLLTLRTLPKYFPPPSLALAVTTTTFPSCGGLL
GGGSWPMAVGKSAAEEEEEEEEEEEEEEEEEEEEELQEEEEEEEEEEEEEEEEEEEEDEEEEEEEEEEEEEGEEEEELA
GEEDKGSEPPPSPSLLRALSPGPGPRGRGALGGGGGVSSGVLWRF
```

95 - 114:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE

A0A0G4FWC1 **A0A0G4FWC1_9ALVE** (92 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MAAGKSAAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEEELAEEEDEGSEPPPSPSLLRALSPGLGPRGGGALGG
```

GGGVSNGVLWGF

9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE

A0A0G4G2U9 **A0A0G4G2U9_VITBC** (172 aa)
Uncharacterized protein. *Vitrella brassicaformis (strain CCMP3155)*

MVRHWVMLGLVALVCLLSINTVVCEGGDLPGESVAEVHQDALDPLALDDEAEDAPENKPTDGTSLDAMSDEQKEVLSELS
EDYEAQVGNTLPVLAQPKPSIKQRRLRGRGLRDEEEEEEEEGEEEEEEEEEEEEEEEEEEEEGGAAGGGEGGGGGGGTG
GGGPAILRSGGP

123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE

A0A0G4G4U3 **A0A0G4G4U3_9ALVE** (89 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

MAAGESAVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGAEVGELAEEEDKGFEPPPSPSLLRSLSPGPGPQGGGALGGGRG
VFNRLLWGF

9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE

A0A0G4G6B3 **A0A0G4G6B3_9ALVE** (113 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

MDSLLPFTITFRTPVAEEEDEEEEEKEKEEEGKGSFLEKIEGEDGLKTQSGIDVKAEGREEEDEEEEEEEEEEEEEEEE
EEEEEKEEEEEEEEEEEEEEEEEEEEEEGKED

64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE

A0A0G4G6F3 **A0A0G4G6F3_9ALVE** (227 aa)
Uncharacterized protein (Fragment). *Chromera velia CCMP2878*

```
EEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEEEEGEEEEEEEEEEEEEEEKEEEGSIRWPGLSPPSPPCLLPPS
FLPLQGPAEEEEKKRADEEEEEEEEAGAAAAAAAAEKEEEEEEEEEEEEEEEAEEEEEEEEEEEEEEEEEEEEEEEKEE
GEEVGAAAAEEEKEREEEEEAAAAAAAEEEEEEEEDEEEVEGEGEGEEEEEEEEEEEEAKREKFLKGF
```

7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE

A0A0G4G7E4 **A0A0G4G7E4_9ALVE** (85 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MALEWSGAAEAELFEELPPPAGVSCGGSWPIAAGKSAAAEEEEEEEEEEEEEEEEEEEEEEEEEKEEELAEEEDEGSEPPP
SPLLL
```

40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE

A0A0G4G7J1 **A0A0G4G7J1_9ALVE** (109 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MDSLLPFTVTFRTPVAEEEDEEEEKKKEEEGKGSFLEKIEGGDGLRTQSGIDVKAEGREEEGEEEEEEEEEEEEKEEEE
EEEEKEEEEEEEEEEEEEEEEEEEEGKED
```

86 - 105:	EEEEEEEEEEEEEEEEEEEE

A0A0G4G9U4 **A0A0G4G9U4_9ALVE** (181 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MFRAHISTPLSFLFCLLFLFVTGEDKKEKEEEEDEEEEKEKEKEEEEEEDEDEDEDEDKDKDKDEEEDEEEEEEEEEEEA
EEEEAEEEKKEEEEEEEEEEEEEKEEEEEEEEKEEEEEEEEKEEEEIGGEEEEEEEEEEEEEEEEEEEEISRRSGLFPPL
PPCPFPPSFFPPPVPEKEEQK
```

130 - 149:	EEEEEEEEEEEEEEEEEEEE

A0A0G4GAB7 **A0A0G4GAB7_9ALVE** (122 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MDSLLPFTVTFRTPVAEEEDEEEEEKEKEEEGKGSFLEKIEGGDGLRTQSGIDVKAEGREEEDEEEEEEEEEEEEEEEE
EEEEEGEEEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEGKED
```

64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE

95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE

A0A0G4GAF1 **A0A0G4GAF1_9ALVE** (115 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MDSLLPFTVTFRTPVIEEEDEEEEEKEKEEEGKGSFLEKIEGGDGLRTQSGIDVKAEGQEEADEEEEEEEEEEEEEEEE
EKEKEEEEEEEEEEEEEEEEEEEEEEEEEEEKQD
```

85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE

A0A0G4GC22 **A0A0G4GC22_9ALVE** (201 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MTASWPSGSLAPPNWSCLKNSRPLLVSPVGCQLGTGFCISPVPPHRWSSICFLLTLRTLPNFPSPPSLAPAVTTTTSPSC
GGLSGEGSWPMAAGENVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEEEKEEEEEEEEEQEGVEVEDLAEEED
KGSEPPPSPSLLRSLSPGPGPQGGGALSSGGEGFSGVLWGF
```

98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE

A0A0G4GEA5 **A0A0G4GEA5_9ALVE** (146 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MDSLLPFTVTFRMPVAEEKDEEEEEEKEKEEERKGSFLEKIEGEDGLRTQSGIDVKAEGREEEDKEEEEEEEEEEEEQEE
EEEEEEEEEEEEEKEEEEEEEEEEEEEEEEEEEEKEEKEEEEEEEEGEKEEEEEEEEEEEEKED
```

95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE

A0A0G4GEQ4 **A0A0G4GEQ4_9ALVE** (126 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MDSLFPFTVMFRTPVAEEEDEEEEEKEKEEEGKGSFLEKIEGGDGLRTQSGIDVKAEGREKEDEEEEEEEEEEEEEEEEE
EEEEEKEEEKEEKEEEKEEEEEEKEEEEEEEEEEKEEEEEEEGKED
```

64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE

A0A0G4GH64 **A0A0G4GH64_9ALVE** (1592 aa)
GPS domain-containing protein. *Chromera velia CCMP2878*

```
MGQHRWLPSFQSLCVLLLSTFFYIPLCRAQGSQHDPGASVLTGILAEARTARNHHDTKEACRKVSKGMKLIHQAVRTAQG
SEETESDYVSAASLRLYPEIPLEFFNRNSPGEGLSELGVTELKKGLGGGLLLYREVVWDAQTDADLRFPEVGDQTDEEDG
LFDDLIDAVTSLQRCWSPVGRTIVTALEAELLELPSVLSSFQAVTSTLDSLHFLVKRGRRPVALQAMTFLQSLVDTTGDL
MSFLVDGFFSEISQVPLVLEAPEDATRTSSSFSFSGSSWHFGGRGSFGSSQHRGGGRGGGVPKCKVSSEDATVTSLDPAE
ALATAQVLREVGEALDGLRGVAGQLLLQGMGVNSILIEAHGGGVKFDGSVSDPSVLSVGASLVRPGQDREERLGVKTPDL
SAYVQSAFSRQAGGAGGCTELPLISMSFSPLNLHSFASEWGETGLRFGCGGLAVPSVSVRLTLCSEPVEVHGLEEGFEFS
PPPFPSFLLDNLPNGSDGGGNLECSTWDDSLGAWRNRGCDSVYTHRGGSRNKKKKHGHTYQPHHSQSTDEALQPFSCSCN
RFGDFALAFVTEQGEAAATTTTTTTTSITTTTIHRTTTTTTTTTKKKQQHHTQKPKPKKKHQTASHSHTHTNHTAAAHPT
FSHQAQIPSAADHQHTIHPSPSHPPTTTIDGPHSNHGVAPSTHPTSHLTTTPKKPHQPPHHASTTPAPTPARTDPVIPSA
ADSPVTAPADSSPPLGYVPIHSEAGEGEGDRTKQPNGKQKDKEQTTTSGKKVEGQTQLAHSSSHLSTGKKTRQVALVWLA
GLLVTILLITLAMCTCIVSVDKPARAAVRRLLARQFISQGCVIDCARPPTRSAKLLKLRHSFRSVLYTSLTSPEGEDVGG
GADTDRGGGNPGGGKGGAQGDGSRHTQQSYNGMSQSAGHCQLQIMEEDNGEGRKVWDWLDKEEGEGEGEEEEDLERIERQ
GSKGGGRNNDFLTGGEGGGGGKGIGIEVTKGKDFGDRPSLASNFSSKASAILPAPSPNPGGGQGNAKASNPEKYLSLPSL
WSILPLSLPGPSSRDSDGVGGPGGCREGGVWAQTDIECPPTPPLQSAGQVDTEAKPMTDEQAHEFRLLAVGKHDAPFPDI
PEELKPQTVAPIVIPPSASKDGEEGPVIKARPMTSCDDVNKFLNSDSESEREKDGQGRGRIGVGVSRRMEKEREGGGAVR
GLGDRRKAMTLSTEIGDLVSEGEGEGEGSSDEGVFKGRGREPQTSSTNTGKQTSFNSVIRSPAENPRRPEVTLLGRPSGG
GGPEGILPSPSPSPLSEGTPDADPHSPRSRASSMSDGENFRAKLAAAREQLDRFTSKRAAGTDAKSSEERCEGVSEGRAA
ALAGQRRSLMESPEGGEPETGRESDAWWLQRFFAAASGAKKTFTFVSSPLASSSSPSSSGRGSSFSLSLPSVLKLWSLAF
RCNQPLWSVFSAPHFLPRRTWRGVALLVGVTARVSALFWLTLLVGMRGGSWGSVWDFLVVEGRTGGAEAEAYAEAEAEEE
EEKEIQAEEKEEEEEEEEEEEEEEEEEEEEEEKEEEEEEEEEEDEEEGEEEEEEEDDTATGGGGRSEGEPA
```

1531 - 1550:	EEEEEEEEEEEEEEEEEEEE
1532 - 1551:	EEEEEEEEEEEEEEEEEEEE
1533 - 1552:	EEEEEEEEEEEEEEEEEEEE
1534 - 1553:	EEEEEEEEEEEEEEEEEEEE

A0A0G4GH91 **A0A0G4GH91_9ALVE** (91 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MAMGKSAAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEQEEEEEEEEDITEEEDEGSEPPPSPSLLRALSPGPGPRGRGALGGG
GGVSSGVLWGF
```

9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE

A0A0G4GJV0 **A0A0G4GJV0_9ALVE** (214 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MGEDKKEKEEEENEEEEEEEEKEEEEEEKEEEEEEEEEEGDEEDEEEEEEEEEEEEEEEEEEEEEEEEKEEEKEEEEEEE
EEGDGEEEEEKKEEEEIGGGEEEEEEEEEEEEEEKEGEEEEEEEEEISRRSGLFPPLPPYPFPPSFFPPPVPEKEKQKQRDS
EEKEKQEEDAEEVVKLQGDGTGRGQQGKEARTEQEREEHTHKHILACICSSFKL
```

45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE

A0A0G4GKY8 **A0A0G4GKY8_9ALVE** (81 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MAAGESAEEEEEEEEEEEEEEEEEEEEEEEEEEDEEEEEEEEEEEEEEEGAEVEELAEEEDEGSELPPSPSLLQSLSPGPG
P
```

8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE

A0A0G4GN53 **A0A0G4GN53_9ALVE** (660 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MLVKEERWSELKPEISLVGPSLVEVKITVGGRRVHVFGLYLPGSWSVYRDSRVPDLLKDVFGGVPLEADKVVMGDFNAHS
GSLVPKNLLWSRADLFLPPRDSGGVDGRGENDEGSEEPDRPSFVRTSQCSKDVDRSGRDFIQIRSDTNLVPLNGLMGEAG
GELSFVFPGECTHYSRQSSMSTPTSLIDYVLTDPSTIQRVSDWEVDFDGIASPDRTTVSFSFSPPLAEPEFEDALLPHQN
LSDCPPLFCSNRIAPVSDEEIAPLAAAVRSFAEDQWPGFWAYHEQIEPFKEPPAPPPPPVSPHPQPGLTSEGGDDRAYLH
RLVEEWWHMLVGPIKQTGDKGPGPEGRRSKREAWFDSECKALQKEVREADERWKLVRDGNGRGIEFDRLQRLLRKTRTNQ
KRKKRRNKKRKKKKRRKKRKTRKNRRKERRRKKKRKKKRRRKKKKRKKRIEEEEEEEEEEEEEEEEEEEEEEEEEDEEEE
EEGEEEEEEEEEEEEEEEEEEEEEEKEKEEEEEEEEEKEEEEEEEEEEEEEEEEEEEEEEEDKDEEKEEEEEEEEEKEEE
EEKKEEEEEEEEEEDKEEEEEEELTAMVSLLVFFSSPPSLSPFLLAAAASAGPTSCLPRQRRKRSPCRRRGSKRSCGTSV
QNYQLIPTVLIQSDKRVSSK
```

450 - 469:	EEEEEEEEEEEEEEEEEEEE
451 - 470:	EEEEEEEEEEEEEEEEEEEE
452 - 471:	EEEEEEEEEEEEEEEEEEEE
453 - 472:	EEEEEEEEEEEEEEEEEEEE
454 - 473:	EEEEEEEEEEEEEEEEEEEE
455 - 474:	EEEEEEEEEEEEEEEEEEEE
456 - 475:	EEEEEEEEEEEEEEEEEEEE
484 - 503:	EEEEEEEEEEEEEEEEEEEE
485 - 504:	EEEEEEEEEEEEEEEEEEEE
486 - 505:	EEEEEEEEEEEEEEEEEEEE
519 - 538:	EEEEEEEEEEEEEEEEEEEE
520 - 539:	EEEEEEEEEEEEEEEEEEEE
521 - 540:	EEEEEEEEEEEEEEEEEEEE
522 - 541:	EEEEEEEEEEEEEEEEEEEE

A0A0G4GQA5 **A0A0G4GQA5_9ALVE** (103 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MDSLLPFTVMFHTPVAEKKDEEEEEKGKKEEEKGLFLEKIEGGDGLRTQSGIDMKAEGWEEEDKEEEEEEEEEEEEEEEE
EEEEDEEEEEEEEEEEEEEEE
```

65 - 84:	EEEEEEEEEEEEEEEEEEEE

A0A0G4GRR4 **A0A0G4GRR4_9ALVE** (133 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MWRLDPSQKEKEEEEKEEEEEEEEEAAAAAAAAVEKEEEEEEEEEKEEEEEEEEEEEEEEEEEEEEAGAAAAKEKKGKEEE
EEEEEAAAAAEEEEEEEEEEDEEEAEGEGEGEEEEEEEEEEEEEAKGEEFLKRF
```

46 - 65:	EEEEEEEEEEEEEEEEEEEE

A0A0G4GSK6 **A0A0G4GSK6_9ALVE** (426 aa)
WD_REPEATS_REGION domain-containing protein (Fragment). *Chromera velia CCMP2878*

```
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAEEEEEEEEEEEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEERKXXRGRGGRRGRGRGRRGRRGRGRRRRKKTRKRNDEYYLATRAKTGDALVFDYSKHSLYDHDDECKP
KLRLKGPDEEGWGLGWSPHRHGYMIASSKDQRVYMWDIKGSTTEASKGDRGADHVLPLTILHSPQKKPIDDCHFSATDPN
TIGSVSVDSILCLWDIRQDNRKPIAFTECHKGKACNSLAFSPFISTLIATGGEDQVVNLWDLRKLSAPMHVLEGHRGEVL
RVNFAPFNESIIASSGTDRKLNVWDLSRVGMELIDGEPEDGPPELLFVHGGHTKQVTDFSWNPMDGQEWTVASVADDNML
QIWSPAEQIVIEGSDETDAAMEEDLE
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE

2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE

A0A0G4GVK2 **A0A0G4GVK2_9ALVE** (103 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MLPLLEEEDEEEEEKEKEEEGKGSFLEKIEGGDGLRTQSGIDVKAEGREEEDKEEEEEEEEEEEEEEEEEEEEKEEEEE
EEKEEEEKEEEEEEEEEEEKED
```

54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE

A0A0G4GWE6 **A0A0G4GWE6_9ALVE** (119 aa)
TFIIS central domain-containing protein. *Chromera velia CCMP2878*

```
MAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEEEEEEEEEEEEEEEEEEEEEEKEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEELLQALSPGPGPRGGGALSGGGGVSSGVL
```

3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE

5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE

A0A0G4GXZ5 **A0A0G4GXZ5_9ALVE** (98 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MAVGESAAEEEEEEEEEEEEEEEGEEEEEEEEEEEEEEEEEEEEEEGAEVEELAEEEDEGSEPPPSLSLLRSLSLGPGPRG
GGALSSGGGVSSGVLWGF
```

24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE

A0A0G4GYG8 **A0A0G4GYG8_9ALVE** (997 aa)
MFS domain-containing protein. *Chromera velia CCMP2878*

```
MSSERRSPRHVAVLEELEVGGRGDSPLPNGLQEAVRSPSFSPHESECESRPRVLGKQTGSPPLGSSASSGSAMRGKGRTK
TFKGGGTGPAFSRLDDGGEDPRGGHDGDGVLALQMEQQQRPQGGGGTEMKLTFAVILAIGVACMTELLLGYDIGIMAGAM
LFVKKDFELSAEQVEVAVGVLNFVATVGALLGGRLSDALGRRAVIGFAAVSFFAGAAMLAAAWNYSFFVAGRIVMGFGRP
PPVFVGPRSALSDNCSGFTSLSVPLPRFLSPPPFTILSSFSTRKHRSASCIXMAGAMLFVKKDFELSAEQVEVAVGVLNF
VATVGALLGGRLSDALGRRAVIGFAAVSFFAGAAMLAAAWNYSFFVAGRIVMGFGVGAGLTVPPMYVAEVTPAKHRGALS
SLGEFFINVGILAGYVAAFCLRSLPQGIEWRVMLGVGTVPPVMILAGLLFLPESPRWLALAGRHEEALRSLERLTGSSAQ
AQEMLEGVGHSLNSPEVADAIEEEDDDDDDETDLPTVNSGARGGAVSNGIGEPSESPAVITPHTRTVLSGSASSSSQEGR
RFRCWGLCKGRGVKVKLKFCKFKLGSKWKALVCPKSAGMRRRVAAAMGVALFVQLTGIEPVTYYATTILEEAGFREENGD
VFLASVVMGSLKLAAVGVAIVFVDRAGRRPLLFLSFSVQSAALFLFAWLSVGDSPGYLRLSAICLFVIGFSLGAGPLVYT
LPSELLPLRLRGIGVGLAMFLSRLVSSITSVTYLSLTDALGPVGVFSLFGVICLGALLFSATMVPETKGTSLEDIEDAAS
TVGGSHEYGDPGLGRSPPDSARGPPVYIQTMMESELERSRGFEEEEEKEEEEEEKEEEEEEEEEEEEEEEKEEGEEEEEE
KEEEEEEEEEEEEEEEEEEEGEEEEEEEEEEGSIRWPGLSPPSPPCPLPPSFFPLPGLVEEEEKKRADEEEEEKEEEEE
EEEKEEEDEEEAEGEGEGEEEEEEEEEEEEDEEEEEE
```

882 - 901:	EEEEEEEEEEEEEEEEEEEE

A0A0G4GYT8 **A0A0G4GYT8_9ALVE** (68 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MKAEGREEENEEEEEEEEEEKEEEEEEEEEEEEEEEEEEEEEKEKEEEEEEEKEEEEEEEKEEKED
```

23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE

A0A0G4GZM2 **A0A0G4GZM2_9ALVE** (77 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MNRRKSPPPQEPIADFVALGLLFTSTSRGVGDGFARKDLEIGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEPLWA
```

43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE

A0A0G4H7D3 **A0A0G4H7D3_9ALVE** (150 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MEEALRDIRAEVANRIYSDLRPLSLAEVKGPCDCFMALWWSGAAEAEWSSICFLLTLRTLPKYFPPPSFAPAVTTTTSPS
CGGLSGRGSWSIAAGKSAAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVEEEEDPKRRRRGQKWRN
```

100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE

A0A0G4H7Z1 **A0A0G4H7Z1_9ALVE** (96 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MNFCISVLQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGAEVEELAEEEDEGSAPPPSPSLLRALSPGPGPRGGE
ALSGGGGVSCGVLWGF
```

10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE

18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE

A0A0G4H919 **A0A0G4H919_9ALVE** (249 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MHVFNGSIRLGWGRGLAGWPPSFPAQPDKSRAALFPLIPPPLPSFPPLPAAEEEEEEEEEEEEEEKEEEKEEAREEEEEE
EQEEEEEEGEEEEEEEEEEEEEEEEEEEEEGEEEDFLKKKKKKKKKKKKKKKKKKKKKKKGPSGGLASPPPPLPIRCLPR
SFPCQVRRKRKKRKEQTKKKKKKKKKKKKKKKKKKRKKKKKMKRKRKEKRREKKKKKKKKKKKKKQREKNFQKDSDICPVF
LENSSSKPF
```

90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE

A0A0G4H992 **A0A0G4H992_9ALVE** (260 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MTSVTFIHSQMLGASGRFPSALLSTSTGQKRSKSREEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEEGE
EEGEEEGEEEGEEEGEEEGEEEGEEEGEEEGEEEGEEEGEEEGEEEEEEEEEEEEEEEEEEERKQKKQRKKDVVCVPACLWT
RVAEIVLGTLLFGGAYANVISQFVLKTDVLDPEFAKVLLRTAAGLTLLLLFIVTPANIFMWTHGARLPKDGPEIPSSVHP
IRGALQIVLTTMMTEIVRAT
```

36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE

A0A0G4HAM1 **A0A0G4HAM1_9ALVE** (1396 aa)
Ephrin_rec_like domain-containing protein. *Chromera velia CCMP2878*

```
MEGLLRKFVFALLGAFWFLSISTEALRRDVWDPVRREAHKRQLEEQQEADRKAGRRLQSTSVTYPKIQKCFSDTERASYQ
TQGYISKAAVGSLNIDWEYGEQITTDIDGNNKTGFKLALPEFSWISQTYMTHIATILAEEVMGFNVTQVVAWDTIPALET
ISGCPVSEANNYICTQAVNKNNPDIHVWLEVFPSTVESYTFAVTPNTEDVGPAGYTGGVVWFTSPDLLCNATWYTYWDTT
SGSPSDRELFTNLTALSSAFQPSVSAPYQTCDSTANGTVFGLSRLWLCQQDPADSTSDYRLMRHDSNGYKECFTSGSDCD
TYTSENDCQTVADENNGALDTGTAISCGTTNPYTWCSYLYDPLYCWFDGTYSWTITKTCLTELAAGNQCVPMISFLSRPP
WLELGEVARAGSPIAYGSSAYTTMTTYTLDANSPYKLVHLWPWPSNEHGQQGIELARVYLPDDAEPTKEIASKYVWPKLR
TLAPRLYWMIRQLAATGTEIRDLVEKTGQEGSKAYTAFEMACNWVKGNAQFWFPWTEHVCPQGYFVNKTAGACEACPQGT
FNANETARACTNCTEGTYNARDGQSECTACELGYYRTVDNPNRTECVLCPKGTYADTLGSAICKQCPAGKTTENEGSSAL
SDCKCGDGLFYSYKRQICRECIEGMICNTTTDDLPVLEPGYWMPLVHVKELFDEALVFKCPVAPLCPGGSADPDLQEDKP
MCYERRIGISCFSCIRGYFKSGVECGKCNPVSSLPLLLTLVLALIGCFLVYKYLNNARTSAAMASIRMSLAASQILAFVQ
RLAIVVTLNVGWPPALQGVVGVLKIFVFDTEILRAGCTFSQEPFNAYMSQLGFPVILTGYFIILYCLMWVAFKFKIRKAP
WDIDLTINSIGFAFQVVYTSVCIATLAAFQCVEQPCGYSNLIPFPTVLCPSQAYTQLLPLGVLAVVGYLIGIMGWFIYVV
TIAPNQMHKEGFRKRYRFLMARFRAPVWFWGVVNMIRSLLMAVTGVIEREDGLLQIAMIAIIVLMHSSLILYFMPWKDPY
NNWLDIIINLGLLYVLLISTKFATATERAEIFLGYSVMFAIGFIVVVAAISVLSALREQTKKGKIQLTERRERMAWAIKQ
AMIVLTQMSVTEWSQALGQATAHDQKVIEDFLKLCFHEVDPRLGAIFSTGKLIARARLNYGTEAQLLTRARAQGTNPFAD
MNDIEGGAGESEDDWGDDIYGLPIKSAPDMSDLGKKKLGTETDPPPARFAFGDDDLDSSDGEEENKGRRASAYRAEETHK
NLRDFADIRGNAQEEEEEEEEEEEEGGEEEEEEEEEEEEEEEEEEEEEEEEEPSPVEKKEEPKEAKKEEIKETKKEEETETK
KEEPKREEPKKPEPEEDEESDVLNDLPSIPDLSDDD
```

1308 - 1327:	EEEEEEEEEEEEEEEEEEEE
1309 - 1328:	EEEEEEEEEEEEEEEEEEEE
1310 - 1329:	EEEEEEEEEEEEEEEEEEEE
1311 - 1330:	EEEEEEEEEEEEEEEEEEEE

A0A0G4HCY4 **A0A0G4HCY4_9ALVE** (563 aa)
CAF1C_H4-bd domain-containing protein. *Chromera velia CCMP2878*

```
MPSIFEQHLKAKEDAKKERKPEDSLMDENVDDVEEDKLIMEDYKIWKKNTPFLYDFVLNNGLEWPSLTVDWINRKRTRQG
ADWNAFRLILGTHTSENYQNHVIIGEVRIPELTKETNVRKFETHAEFKNQRPELKGHMQKKPMEKEEYPRFEIICKMLHE
GEINREEKKKKKKKEEEKEENLEKEGEFGEGRRIWRRKENLEKEKLEKEKEGEFGEGEGRRIWRRRRKENLEKEKEGEEE
EREGEEKEGEEEEEKEEKEGEEKEEKEEKEGEEKEGEEEEGEEEEEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAEEEEEEEEEKRRGRGTAQHCPQDEYYLATRAKTGDG
LSA
```

291 - 310:	EEEEEEEEEEEEEEEEEEEE
292 - 311:	EEEEEEEEEEEEEEEEEEEE
293 - 312:	EEEEEEEEEEEEEEEEEEEE
294 - 313:	EEEEEEEEEEEEEEEEEEEE
295 - 314:	EEEEEEEEEEEEEEEEEEEE
296 - 315:	EEEEEEEEEEEEEEEEEEEE
297 - 316:	EEEEEEEEEEEEEEEEEEEE
298 - 317:	EEEEEEEEEEEEEEEEEEEE
299 - 318:	EEEEEEEEEEEEEEEEEEEE
300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE
325 - 344:	EEEEEEEEEEEEEEEEEEEE
326 - 345:	EEEEEEEEEEEEEEEEEEEE
327 - 346:	EEEEEEEEEEEEEEEEEEEE
328 - 347:	EEEEEEEEEEEEEEEEEEEE
329 - 348:	EEEEEEEEEEEEEEEEEEEE
330 - 349:	EEEEEEEEEEEEEEEEEEEE
331 - 350:	EEEEEEEEEEEEEEEEEEEE
332 - 351:	EEEEEEEEEEEEEEEEEEEE
333 - 352:	EEEEEEEEEEEEEEEEEEEE
334 - 353:	EEEEEEEEEEEEEEEEEEEE
335 - 354:	EEEEEEEEEEEEEEEEEEEE
336 - 355:	EEEEEEEEEEEEEEEEEEEE
337 - 356:	EEEEEEEEEEEEEEEEEEEE

338 - 357:	EEEEEEEEEEEEEEEEEEEE
339 - 358:	EEEEEEEEEEEEEEEEEEEE
340 - 359:	EEEEEEEEEEEEEEEEEEEE
341 - 360:	EEEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEEE
344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE
379 - 398:	EEEEEEEEEEEEEEEEEEEE
380 - 399:	EEEEEEEEEEEEEEEEEEEE
381 - 400:	EEEEEEEEEEEEEEEEEEEE
382 - 401:	EEEEEEEEEEEEEEEEEEEE
383 - 402:	EEEEEEEEEEEEEEEEEEEE
384 - 403:	EEEEEEEEEEEEEEEEEEEE
385 - 404:	EEEEEEEEEEEEEEEEEEEE
386 - 405:	EEEEEEEEEEEEEEEEEEEE
387 - 406:	EEEEEEEEEEEEEEEEEEEE
388 - 407:	EEEEEEEEEEEEEEEEEEEE
389 - 408:	EEEEEEEEEEEEEEEEEEEE

390 - 409:	EEEEEEEEEEEEEEEEEEEE
391 - 410:	EEEEEEEEEEEEEEEEEEEE
392 - 411:	EEEEEEEEEEEEEEEEEEEE
393 - 412:	EEEEEEEEEEEEEEEEEEEE
394 - 413:	EEEEEEEEEEEEEEEEEEEE
395 - 414:	EEEEEEEEEEEEEEEEEEEE
396 - 415:	EEEEEEEEEEEEEEEEEEEE
397 - 416:	EEEEEEEEEEEEEEEEEEEE
398 - 417:	EEEEEEEEEEEEEEEEEEEE
399 - 418:	EEEEEEEEEEEEEEEEEEEE
400 - 419:	EEEEEEEEEEEEEEEEEEEE
401 - 420:	EEEEEEEEEEEEEEEEEEEE
402 - 421:	EEEEEEEEEEEEEEEEEEEE
403 - 422:	EEEEEEEEEEEEEEEEEEEE
404 - 423:	EEEEEEEEEEEEEEEEEEEE
405 - 424:	EEEEEEEEEEEEEEEEEEEE
406 - 425:	EEEEEEEEEEEEEEEEEEEE
407 - 426:	EEEEEEEEEEEEEEEEEEEE
408 - 427:	EEEEEEEEEEEEEEEEEEEE
409 - 428:	EEEEEEEEEEEEEEEEEEEE
410 - 429:	EEEEEEEEEEEEEEEEEEEE
411 - 430:	EEEEEEEEEEEEEEEEEEEE
412 - 431:	EEEEEEEEEEEEEEEEEEEE
413 - 432:	EEEEEEEEEEEEEEEEEEEE
414 - 433:	EEEEEEEEEEEEEEEEEEEE
415 - 434:	EEEEEEEEEEEEEEEEEEEE
416 - 435:	EEEEEEEEEEEEEEEEEEEE
417 - 436:	EEEEEEEEEEEEEEEEEEEE
418 - 437:	EEEEEEEEEEEEEEEEEEEE
419 - 438:	EEEEEEEEEEEEEEEEEEEE
420 - 439:	EEEEEEEEEEEEEEEEEEEE
421 - 440:	EEEEEEEEEEEEEEEEEEEE
422 - 441:	EEEEEEEEEEEEEEEEEEEE
423 - 442:	EEEEEEEEEEEEEEEEEEEE
424 - 443:	EEEEEEEEEEEEEEEEEEEE
425 - 444:	EEEEEEEEEEEEEEEEEEEE
426 - 445:	EEEEEEEEEEEEEEEEEEEE
427 - 446:	EEEEEEEEEEEEEEEEEEEE
428 - 447:	EEEEEEEEEEEEEEEEEEEE
429 - 448:	EEEEEEEEEEEEEEEEEEEE
430 - 449:	EEEEEEEEEEEEEEEEEEEE
431 - 450:	EEEEEEEEEEEEEEEEEEEE
432 - 451:	EEEEEEEEEEEEEEEEEEEE
433 - 452:	EEEEEEEEEEEEEEEEEEEE
434 - 453:	EEEEEEEEEEEEEEEEEEEE
435 - 454:	EEEEEEEEEEEEEEEEEEEE
436 - 455:	EEEEEEEEEEEEEEEEEEEE
437 - 456:	EEEEEEEEEEEEEEEEEEEE
438 - 457:	EEEEEEEEEEEEEEEEEEEE
439 - 458:	EEEEEEEEEEEEEEEEEEEE
440 - 459:	EEEEEEEEEEEEEEEEEEEE
441 - 460:	EEEEEEEEEEEEEEEEEEEE

442 - 461:	EEEEEEEEEEEEEEEEEEEE
443 - 462:	EEEEEEEEEEEEEEEEEEEE
444 - 463:	EEEEEEEEEEEEEEEEEEEE
445 - 464:	EEEEEEEEEEEEEEEEEEEE
446 - 465:	EEEEEEEEEEEEEEEEEEEE
447 - 466:	EEEEEEEEEEEEEEEEEEEE
448 - 467:	EEEEEEEEEEEEEEEEEEEE
449 - 468:	EEEEEEEEEEEEEEEEEEEE
450 - 469:	EEEEEEEEEEEEEEEEEEEE
451 - 470:	EEEEEEEEEEEEEEEEEEEE
452 - 471:	EEEEEEEEEEEEEEEEEEEE
453 - 472:	EEEEEEEEEEEEEEEEEEEE
454 - 473:	EEEEEEEEEEEEEEEEEEEE
455 - 474:	EEEEEEEEEEEEEEEEEEEE
456 - 475:	EEEEEEEEEEEEEEEEEEEE
457 - 476:	EEEEEEEEEEEEEEEEEEEE
458 - 477:	EEEEEEEEEEEEEEEEEEEE
459 - 478:	EEEEEEEEEEEEEEEEEEEE
460 - 479:	EEEEEEEEEEEEEEEEEEEE
461 - 480:	EEEEEEEEEEEEEEEEEEEE
462 - 481:	EEEEEEEEEEEEEEEEEEEE
463 - 482:	EEEEEEEEEEEEEEEEEEEE
464 - 483:	EEEEEEEEEEEEEEEEEEEE
465 - 484:	EEEEEEEEEEEEEEEEEEEE
466 - 485:	EEEEEEEEEEEEEEEEEEEE
467 - 486:	EEEEEEEEEEEEEEEEEEEE
468 - 487:	EEEEEEEEEEEEEEEEEEEE
469 - 488:	EEEEEEEEEEEEEEEEEEEE
470 - 489:	EEEEEEEEEEEEEEEEEEEE
471 - 490:	EEEEEEEEEEEEEEEEEEEE
472 - 491:	EEEEEEEEEEEEEEEEEEEE
473 - 492:	EEEEEEEEEEEEEEEEEEEE
474 - 493:	EEEEEEEEEEEEEEEEEEEE
475 - 494:	EEEEEEEEEEEEEEEEEEEE
476 - 495:	EEEEEEEEEEEEEEEEEEEE
477 - 496:	EEEEEEEEEEEEEEEEEEEE
478 - 497:	EEEEEEEEEEEEEEEEEEEE
479 - 498:	EEEEEEEEEEEEEEEEEEEE
480 - 499:	EEEEEEEEEEEEEEEEEEEE
481 - 500:	EEEEEEEEEEEEEEEEEEEE
482 - 501:	EEEEEEEEEEEEEEEEEEEE
483 - 502:	EEEEEEEEEEEEEEEEEEEE
484 - 503:	EEEEEEEEEEEEEEEEEEEE
485 - 504:	EEEEEEEEEEEEEEEEEEEE
486 - 505:	EEEEEEEEEEEEEEEEEEEE
487 - 506:	EEEEEEEEEEEEEEEEEEEE
488 - 507:	EEEEEEEEEEEEEEEEEEEE
489 - 508:	EEEEEEEEEEEEEEEEEEEE
490 - 509:	EEEEEEEEEEEEEEEEEEEE
491 - 510:	EEEEEEEEEEEEEEEEEEEE
492 - 511:	EEEEEEEEEEEEEEEEEEEE
493 - 512:	EEEEEEEEEEEEEEEEEEEE

494 - 513:	EEEEEEEEEEEEEEEEEEEE
495 - 514:	EEEEEEEEEEEEEEEEEEEE
496 - 515:	EEEEEEEEEEEEEEEEEEEE
497 - 516:	EEEEEEEEEEEEEEEEEEEE
498 - 517:	EEEEEEEEEEEEEEEEEEEE
499 - 518:	EEEEEEEEEEEEEEEEEEEE
500 - 519:	EEEEEEEEEEEEEEEEEEEE
501 - 520:	EEEEEEEEEEEEEEEEEEEE
502 - 521:	EEEEEEEEEEEEEEEEEEEE
503 - 522:	EEEEEEEEEEEEEEEEEEEE
504 - 523:	EEEEEEEEEEEEEEEEEEEE

A0A0G4HEN8 **A0A0G4HEN8_9ALVE** (125 aa)
Uncharacterized protein (Fragment). *Chromera velia CCMP2878*

```
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEELA
EEEDEGSEPPPSPSLLRALSLGPGPRGRGALSGGRGVSSGVLWGF
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE

37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE

A0A0G4HEQ6 **A0A0G4HEQ6_9ALVE** (1646 aa)
SET domain-containing protein. *Chromera velia CCMP2878*

```
MNICVLEDKEVFPAHHIMYGGQHWYYYPQYNWGIDGSLPQAGQGSGHFSSPNAQQWYHQQYPSTYQNEDSFPSHAPIPGQ
GSSVLPSPGSFPPQQAYNQSTSQYQNTLRFSSIPTPEQLRSFFSSQNAASQSQGHPGAPLRGPVSGLTDKDTQRSLCTAW
GEKSSFNFREPHPSALTSASMPGLIQSQPPQQQQENHLLFGQGLPGHFFPPPIPPAAFPPEPPGMVEISPTSSINVSMEP
VVEETPQTRTSLTPSSADISMQPVLVVNPQIKTLFTPSCTDISMEPVGEETPQTKSTQQTEEDGEGGGSRGGGGAEPPAA
ATAETAAAASSFFFPAMQRNREAGGVAAGDDRHTGGVEGVGLDQSDSLGVEHVGEGGGDRDSLSGMEKECGMQQTSLVAQ
PPPLIRPAASAETLGSVSVPLPQQERVGVQTETGVVARRPVEEKKVKNENYRLPGVVYHKRQKLWESFVVLNGDLSGPLL
EVSMYFDTSLYGHDEAFQLAKACRLDMDTMREEGVREADPILQKLRPKYPRKPPLCAGNKTEERQQQQTDAPSDTPTTPA
SPAAAPPGEGLEEAVRRAAPATHTGGKPKRRQSGVEGVSWDPKNCQWVAKVFVDGRISLDKFPVSAYGEELALQAAIRYR
EVHVMGAQQKKGKGGGNQMGKGEDALVPVGCRPKRNNKKEKKEGEETGELKGVGWHPQKEAYQAHVSLPLGSANIAFRVA
HYGQKNALKQAKACRKEMERLKRKGWKDHKAMVQHLRKTKFPLQKKRPKPLQQGGGESEGEGMEEGAELDQTGGGDPSPS
AASAAAAASARGSSGKRGTAAPSAGGRKGTSEVVEGVSWDPRLSSWVAKGRLDGRVTLERFPVSVFGDAGALEAAHNFRK
LMVEGEKSSMGSDAPQVRKRAERAVEEREGEEEEEEEEEGEVGSRKSGVKGVTWMGYGQNAWRASVTLDGRNVYLQFPSF
SYGDEKALEKAKECRAEMEKMREEGWTDHETFRKEIRRQFPAVLGQKKGGVSDEEEEEEEEEEEEEEEEEEEGPRESGMT
GVVWIGGKKREWRAGVTIHYKNVYRHFPGLTLGDKVALQKAKECRAEMEKMREEGWTDVQKFRREIRKRFPIDSELLEGG
ESEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGGARKSGVTGVTWNTQLQAWYAVFSKGSKNYAVVFPTRTLGFK
EALERAIKCRKESERMKAQGRTDYKTMKEELRAKFLEGVGGLQLTSQQQPRKPMQSAGGRGGKMEGRETNKGPSAVNRRG
KTQTESSPDESDSESEGKGKGGLTLRTAAPNVPPQAADRKRKLTVALALPNPKQRKASKKQEKEEEKESEGFKNCTFATP
CETCRKNDAFLFSSFSSSSPSSCSPSSASSSASASFPPVESGAGEGEVAMIQKEGVETPKTTKGAEAEKSSLFASTVEKR
KMLIGGLNPHRLPECYSDKKTSRDERADKFLRVRAESQFTTPVAKTIEYLHTRWCKPVIIGGKAVAVVGDGVKVSNSTLG
PDVGLGLFATREFEEGDFVTEFVGPRGDRDAAMRQKKSGLHSHIVALLKNTLCLMGFKHVVPGLGGAHFANDGHISVNGK
PPRGVNAMLYWHFDKDLADTRVFLKATKRIEPGQEIFTSYGETYWK
```

1129 - 1148:	EEEEEEEEEEEEEEEEEEEE
1130 - 1149:	EEEEEEEEEEEEEEEEEEEE
1131 - 1150:	EEEEEEEEEEEEEEEEEEEE
1132 - 1151:	EEEEEEEEEEEEEEEEEEEE
1133 - 1152:	EEEEEEEEEEEEEEEEEEEE
1134 - 1153:	EEEEEEEEEEEEEEEEEEEE
1135 - 1154:	EEEEEEEEEEEEEEEEEEEE
1136 - 1155:	EEEEEEEEEEEEEEEEEEEE
1137 - 1156:	EEEEEEEEEEEEEEEEEEEE
1138 - 1157:	EEEEEEEEEEEEEEEEEEEE

A0A0G4HET2 **A0A0G4HET2_9ALVE** (80 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MAAGESAEEEEEEEEEEEEEEEEEEEEEEEEEEEELAEEEDEGSEPPPSPSLLRALSLGPGPRGGGALGGGGEVSSGVLWGF
```

8 - 27:	EEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEE

A0A0G4HEW8 **A0A0G4HEW8_9ALVE** (76 aa)
Uncharacterized protein (Fragment). *Chromera velia CCMP2878*

EEEEEEEEEEEEEEEEEEEEEEEEEEEEELAEEEDEGSELSPSPSLLRALSPGPGPRGGGALGGGGGVSSGVLWGF

1 - 20:	EEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEE

A0A0G4HH66 **A0A0G4HH66_9ALVE** (188 aa)
MYND-type domain-containing protein (Fragment). *Chromera velia CCMP2878*

VEGQVGVCGKGSSCSSCLACAKKLGGRFIRRNTGPAERGRVSGRGVGGERERERGNFEYIRKRKAEEEKDSHSEGEIETD
SEKETESESESEEEEEEEEKEEEEKEEEEEEEEEEEEEEEEEEEEEEEEKRKEEKEEESCTACGVPAHQCNLKACLGCRA
VKYCTREYQKRHWRDHQKGCRSLMAAAD

106 - 125:	EEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEE

A0A0G4HHF4 **A0A0G4HHF4_9ALVE** (112 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

MDSLLPFTIMFHTPVAEEEDEEGEEKEEEGKSLFLEKIEGGDGLTTQSGIDVKVEGREEEDEEEEEEEEEEEEEEEEEE
EKKKKEKEEEEEEEEEEEEEEEEEEEEEGKED

62 - 81:	EEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEE

A0A0G4HHT4 **A0A0G4HHT4_9ALVE** (306 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

MLTSILTCCSEFPDGWGEVGAESCWWLPGSPLPPPVFVPHLEHTATEGHARTHPHPQQLGAEMATPCISLVTGQPLVLKE
VTPSMLAKKRNSHRRATGTPQLQQQAQQLRDGEESGEAGVKQQTNEETDEKEEEESILNPAVPQKIVLGRDKEEEEEEEE
EEEEEEEEKEEEEEEEEEKEEEEEEEEEEEEEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEREGF
TRPGEEEEEKRAGEEEKDEKEEEEEEEEEEEEEEEEEEKEEEEEKEEEEEEEEEEEEEEEEEEEEED

196 - 215:	EEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEE

201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE
208 - 227:	EEEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE

A0A0G4HKU0 **A0A0G4HKU0_9ALVE** (201 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MGENKKEKEEEEDEEEEEEEEKEEEEEEDEDEDEDEDEDEDEDEDEDEDEDEDEEEEEEEEEEEEEEEKEEEEEAEEEEEKQE
EEEEEEEEEEEEKEEKEEKEEKEEEEEDKEEEGIGGGEEEEEEEEEEEEEEEEEEEEEEKEEEEEEEEEEISRRFGLFPPL
PPCSFPPSFFPPPVPGKEEQKARDSEEKEKQEEDAEEVVKL
```

118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE

A0A0G4HM35 **A0A0G4HM35_9ALVE** (28 aa)
Uncharacterized protein (Fragment). *Chromera velia CCMP2878*

```
EEEEEEEEEEEEEEEEEEEEEEEEWRF
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE

A0A0G4HQ38 **A0A0G4HQ38_9ALVE** (228 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MAVRKSTAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEELAEEEDEGSEPPPSPSLL
RALSPGPGPRGGGALGGGGGVSSGVVGGFGGSGGWKGAASGVSLRLSRVCGCVCVYAGMGFFGGAAAGWKGAASGFSEEH
VGDWVEDMLRKGGGVAVCVSAGWGEVLIGVGLGRSPGSRLSVCRAGSYSGGALWMVVLGGGRRRWGCV
```

9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE

21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE

A0A0G4HQV0 **A0A0G4HQV0_9ALVE** (92 aa)
Uncharacterized protein (Fragment). *Chromera velia CCMP2878*

```
VAEGRTGGAEAEAYAEAEAEEQEEKETEAEEEEEEEEEDEEEKEEEEEEEEEEEEEEEEEEEEEDEEEGEEEEEEEEEDD
DTATGGGGRSEN
```

44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE

A0A0G4HQV1 **A0A0G4HQV1_9ALVE** (212 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MTVSQHLTTQTLERTSKGTLSFQQELEQETAETRQRKKKKKKNEEEEEEEEEEEEEEEEEEEEEGEEEEEEEKEEEQEKEE
EEEEEEEEEKEEEGSIRWPGLSPPSPPCPLPTSFLPLQGPAEEEEKKRADKEEEEEEEEEAGAAAAAVAAEKEEEEEEEE
EEAVAAAAVEEEEEEEEEDEEEAEGEGEGEKDEEEEEEEEEEAKGEKFPKGF
```

44 - 63:	EEEEEEEEEEEEEEEEEEEE

A0A0G4HRC2 **A0A0G4HRC2_9ALVE** (283 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MSAPFVSSAKSGLCTKLSVLPLTFRAHISTPLSFLFCLLFLFVTGEDKKEKEEEEDEEEEEEEEKEKEEKEEEEDEDEDE
DEDEDEDEDEDEDEKEEEEEEEEEAEEEAEEEEEEEEEEEEKEEEEEEKEEEEEKEEEEDEDEDEDEDEDEDEDEDEDEDE
KEEEEEEEAEEEAEEEEEEKEEEEEEEKEEEEEKEEEEEEEKEEEGIGGGEEEEEEEEEEEEEEEEEEEEEISRRFGLFP
PLPPCSFPPSFFPPPVPGKEEQKLRDSEEKEKQEEDAEEVVKL
```

211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE

A0A0G4HTY5 **A0A0G4HTY5_9ALVE** (245 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MKYADDEGEGEVINVDKEKRLQVVQMLVENDVNEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKREKEEEKEEEEEEE
KEEEEEEEEKEEEGSIWWPGLSPPSPPCLLPPSFLPLQGPAEEEEKKRADKEEEEEGEAAAAAAAAAEKEEKEEEEEEEE
EKAEEEEEEKEEEEEKEEEEEEEAGAAAAEEEKEREEEEEATAEEEEEEEEEEEDEKEAEGEGEGEEEEEEEEEEAKGEE
FPKRF
```

34 - 53:	EEEEEEEEEEEEEEEEEEEE

35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE

A0A0G4HU64 **A0A0G4HU64_9ALVE** (317 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MAAGKSAAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEES
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEEEEEEEEEEEEEEEEEELAEEEDEGFEPLSSLLLLRALSRVRGP
GVGERLAVEGGCLVEYCGGSNMFLHRGGRLGCLLELGEGRCDHLCCMVSLAGHISTRCTFPPTYGMHSIRLPSPLASSGV
GGMGFFGGTAAGWKGAASGFSEEHVGDWVEGMLREGGGFAVCASVGWGEVLIGVGLGRSPESRLSVRRAGSCSGGAL
```

9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE

43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE

A0A0G4HUC0 **A0A0G4HUC0_9ALVE** (112 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MLRTLLKYFPPPSLTPAVTTTTSPSRGGLSDGGSWPMAVGESAEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEGAEVEELAEEEDEESEPPPSPSLL
```

48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE

62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE

A0A0G4HUG7 **A0A0G4HUG7_9ALVE** (221 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MSAPFVSSAKSGLCTKFSVLPLTFRAHISTPLSFLFCLLFLFITGEDKKEKEEEEDEEEEEEEEEGKDEDEDEDEDEDED
EDEDEDEEEEEGEEEEEEEKEEAEEVEEEEEEEEEEEEEEEEEEEEKEEEEKKKEEEKEEEEEEEKEEEGIGGGEEEE
EEEEEEEEEISRRSGLFPPLPPCSFPPSFFPPPEPGKEEQKPRDSEEKEKQEEDAEEVVEL
```

107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE

A0A0G4HVA0 **A0A0G4HVA0_9ALVE** (122 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MDSLLPFTVTFRTPVTEEKDDEEEKKEKEEEGKGSFLEKIEGGDGLRTQSGIDVKAEGQEEEGEGEEEEEEEEEEEEEEE
EEEEEEEEKEEEEEEEEEEEEEEEKEEEEEKKEEEEEEKED
```

66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE

A0A0G4HWA2 **A0A0G4HWA2_9ALVE** (292 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MTASWPSGGLVPPKRSCLKNSRPLLVSPVGCQPGTGFCVSPFPPHRWSSICFLLMLRTLPKYFPPPSLAPAVTTTTFPSR
GGLSGGGSWPMAAGKSAAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEL
AEEEDEGSEPPPSPSLLRALSPGLGPWGGGALGGGGGVSCGVMGLFGGAVAGWMGAASGFSEEHVGDWVEGMLRERGGFA
VCASVGWGEVLIGVGLGRSPGSRLSVCRVGSCSGRVLWMVVLGGGRRRWGCV
```

99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE

119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE

A0A0G4HXE3 **A0A0G4HXE3_9ALVE** (392 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MHRIAGVTMKSADRCFARVAGPVWVIPFGSSSEMQLQHAFSACQGSSSSLRFSALGCDKEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEKEEEEEEEEKEKEEEEEEEDEDEEEEEEEEKEKEEEEEEEEEEEEEEEEEEEEEEEEEEKVREGFTRWP
GLPXKKKKKKKKKKKKKGEAKHSSHSSSFFVLCSEGQLQHAFSACQGSSSSLRFSALGCDKEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEKEEEEEEEEKEEEEEEEEEEEEKEEKEEKEEEEEEDEKEEEEEEKEKEEEEEEEEEEE
EEEEEEEEEEEEEEEKMGHEEYSYFWSKQKNLGRKKWEKRSEGLEEVQVEEVALQENEEEDLERRESQERKR
```

60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEEE
225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE

227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE
239 - 258:	EEEEEEEEEEEEEEEEEEEE
240 - 259:	EEEEEEEEEEEEEEEEEEEE
241 - 260:	EEEEEEEEEEEEEEEEEEEE
242 - 261:	EEEEEEEEEEEEEEEEEEEE
243 - 262:	EEEEEEEEEEEEEEEEEEEE
310 - 329:	EEEEEEEEEEEEEEEEEEEE
311 - 330:	EEEEEEEEEEEEEEEEEEEE
312 - 331:	EEEEEEEEEEEEEEEEEEEE
313 - 332:	EEEEEEEEEEEEEEEEEEEE
314 - 333:	EEEEEEEEEEEEEEEEEEEE
315 - 334:	EEEEEEEEEEEEEEEEEEEE
316 - 335:	EEEEEEEEEEEEEEEEEEEE

A0A0G4HY15 **A0A0G4HY15_9ALVE** (256 aa)
MYND-type domain-containing protein. *Chromera velia CCMP2878*

```
MLFLINFEVLTKQNAVELIEDVPKGRRKEVLSRLLSRHPPSRIDPLVETYKKGLRCLEMRAKWLPPLGKDQQEDTIGPAK
ALAKLLSEVLKRSLDDPVEDMKLLKECSVCGRKDSAFLRCSGCGVAAYCGRAHQKQHWQTHKQECGKLKKASEVRLDDLI
SGKLSRAQMGGEEEEETESAIKFSVLPLTFNAHTSTPFCFLFRFFLDTRKKEEEEEGEEEEAEEEKEEEEEEEEEEEEEE
EEEEEEEEEEEEEEE
```

227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE

A0A0G4I0S3 **A0A0G4I0S3_9ALVE** (106 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MDSLLPFTVTFRTPVAEEEDEEEEEKEKEEEGKGSFLEKIEGGDGLRTQSGIDVKTEGREEKDEEEEEEEEEEEEEKEEE
EEEEEEEEEEEEEEEEEEEEEEGKED
```

78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE

A0A0G4I484 **A0A0G4I484_9ALVE** (98 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MAAGKSAAEEEEEEEEEEEEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEPAEEEDEGSEPPPSPSLLRALSSGPGPRG
GGALGGGGGVFSGVLWGF
```

25 - 44:	EEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEE

A0A0G4I4I3 **A0A0G4I4I3_9ALVE** (95 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MAAAGKSAAEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEEEKEEEEEEELAEEEDEGSESPPSPSLLRALSPGPGPWGGGA
LGGGGGVSSGVLWGF
```

10 - 29:	EEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEE

A0A0G4I5Z5 **A0A0G4I5Z5_9ALVE** (107 aa)
Uncharacterized protein (Fragment). *Chromera velia CCMP2878*

```
EEEEEGEEEEEEEEEEEEEEEEEEEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEELAEEEDEGSEPSPSPSLLRA
LSLGPGPRGGGALGGGRGVSSGVLWGF
```

7 - 26:	EEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEE

A0A0G4I6E3 **A0A0G4I6E3_9ALVE** (538 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MTLGKDGAVTPNADPLVFVACYNQFDNLAHQPRGYPATDTLWVYRLHRKSATLTLLTKTSAISNPAFIRFHPQKNILYTC
TEDITKDNEIVAFSVSPTTGELVKLGSVSAEGKSTCYLTIAADQRHMLFVNYWDSVIGTIPVSPTGLLGPVKHKRAPATP
VVARDIADHLNNRQSEPHAHAIVLDPYVNRVAYVPDLGEDDIKQYVYDEATGQLRYTCTISCGPKEGKPHGPRYLEFHPT
MNTVYVVNELSSTVSVFEFDMAAADSLTEGSNVQTLRFIQNISTIPTAYPRKSNTCGRIAVDPKGLHVFVSNRGHDSIAV
FRIDDDSSSCGEGGKLSIVSYCHTRGRTPRHFQFDPLGEFVLCANQDTNSITLFKFDQESSELSFTGESYNVPSPNFVCV
ETMKTGVRSRREAPRIHKALAEQDTVIAPTHGHSHHGGLAQVAEGHTGGAEAETYAEAEAEEEEEKETEGEEEEEEEEEE
EEEEEEEEEEEEEEEKEEEEEEEEEEEEDEEEGEEEEEEEEDDDTATGGGGRLEGEPA
```

471 - 490:	EEEEEEEEEEEEEEEEEEEE
472 - 491:	EEEEEEEEEEEEEEEEEEEE
473 - 492:	EEEEEEEEEEEEEEEEEEEE
474 - 493:	EEEEEEEEEEEEEEEEEEEE
475 - 494:	EEEEEEEEEEEEEEEEEEEE
476 - 495:	EEEEEEEEEEEEEEEEEEEE

A0A0G4I8E6 **A0A0G4I8E6_9ALVE** (108 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MPCVSGCSYGHGGALRFSQHHNVYLVSEGHTGGAEAEAHIEAEAEEEEKKETEAEEEEEEEEEEEEEEEEEEEEEEEEE
EEEGEEEEEEEDDDTITGGGGRSEEEPA
```

55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE

A0A0G4I8R9 **A0A0G4I8R9_9ALVE** (186 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MHTFNRSIRLEWGRGPAGWPPSFLAQPDKSRAALFPLIPPPLPSFPPLPAAEEEEEEEEEEEEEEEEEEEEEKEEEEGEE
EEEGEQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKKEEKEEEEDKEEVEGEEKEEEEREGEGEEEEEEEEEEEEEEEEK
EEEGSIRWPGLSPPSPPCLLPPSFLP
```

52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE

A0A0G4ICI3 **A0A0G4ICI3_9ALVE** (155 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MDSLLLFTVMFRTPVAEEKDEKEEEKEKEEEGKGSFLEKIEGEDGLRTQSGIDVKAEGWEKKDEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEKEEEEEEKEEEKEEEEEKEEEEKEEEKEEEEEEEEEEDNIFNIFQIISYISLTYFLIFL
```

64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE

A0A0G4IDH9 **A0A0G4IDH9_9ALVE** (967 aa)
Uncharacterized protein. *Chromera velia CCMP2878*

```
MILDELRASIRSIGDLALVLEEKVAVIEAQWKRRDVDSSHAVPAAASSSAALSEAEAEKALTDEKDWLSVFSMTQIVKAS
KKAMHAAVDAFVSRHYRIDLGSLLKMEVANVIRSFKAVEASTVHDVMVSGDRIRDIELLAELGIDEKGISNGKSLLMHAS
KMGREACARVLLENGASIQAPEGTTRRVDPLLLAVSNRHFRLAQKLVQAGANVHAKMPGNLKTVLALACDRMEPGEGNGD
EGQHEAPADGGGPQPAAEANGGDGQQEDVEANEGQEEEEEEEEEEEEEEEEEEEEEEEEDGEANEGQQEEEGEEEEEANE
EQGEDGDENGEETEEGGEQMNDDADENALPPQVPVNVNEEHENGNGDAGAAGAGEGVGEEVPQDPNEEMDQAAVEFVKAL
IEKGVDPNETWDGEKALDRAYKNKDWKLATVLVEKGADPEVNVGSTSQTATPLMRALMAEQWQLARLLISKGARVDVQTR
VGKYTALHYAAGTANDGLSFSWSTQSPSVDSEGARASQAERLEMVRLLIDKGASVDHVPAFFTPLRVACMRRDLAVASLL
LDRGADIEFKGQSDTTPLTDAMTSGFLDVVDFLLSRGADMNATEKSNSNLHLAARNRFSEGAKRLLEKGADPTVQNSRGD
TPLMCAVRGGNLGFVEDAFLSSRVDVNGPGRRKRTVLHLAVEMNQTTTAEWLILRGANMNAKDSRGETPLHLSVSKGLEE
MCRLLVAFGSKVTLTNEDGDGPLHEAAFQGNRTLARFLIEHGAEVDGVNKRGETALHLAAGEGHADLLREFVVSLRANSE
VAAKDGSSALLHACGAGRGSAVEALLDVGADVKAVDNRGNSALHKAALDGRLDVVKILCERGCPVNAVNKNLDSPLHTAV
LLGNVDLARFLLEAGADVRAVNEKGETPLHTAVSRGWLLVLESTELLLSKGADIQAKNKSGDTVVALASKRFGKGPVFEF
LLSRGGS
```

276 - 295:	EEEEEEEEEEEEEEEEEEEE
277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE

A0A0G4M1L3 **A0A0G4M1L3_9PEZI** (698 aa)
Uncharacterized protein. *Verticillium longisporum*

```
MHFKAIILLLSASASLAAAQSVDPAVPSVAPEVAPGEGVGEVPVLAPEPAVPVPGGNDEEGVPAVEVPAPEVPAGDVAAP
EVPAAPEAPIAPEVPAAPEVPAAPEAPLAPEIPEAPEAPIAPEVPAEQPVADLPDADQDGIPDGAETGGQGAELRPLPGL
QETVGELRPLPGTGGEQIEEVQPPEGAEPVQSALPVSSALPVSSALPVESSAPAESSLPAASSAPIPSEAPVESALPLES
AAPVEGVSPLQPIAPADPLQPSDSASSIVESAIPTLAPLLPGSVAPSVDPASSIPPVSESAVPSLPLDITDPPAPSAASS
DLLLPTESSELVVPSASSALLEPSAPLSLVESAIPSPPLAAPLVPSAPAAPLVPVAPVESLPVIPTNATLPQVPQVQTPE
PIPALPVGGALPSAPPSAVIGNGTAPVAPPAAPVPGDAEEVQGPSGGETGLEPLPGTDDSGSGELQDRPAGDEGAADEEQ
DGGEADEEGDEEDSGSGSNEESDSDSDSESDSDEDSSSEEESGDDEEAGDGEEAGDEEEESGDGEDEEEEEEEEEEEEEE
EEEEEEESSGEAGDNADEGDEEEEDSGSGAGSGSGSGTQPSALLAPTGLAPNRTATLPGTLLVATSSFGAGLTMQTSLRL
ATGVSAEVTAPSNGGLEAVTTGANGGTLNAEDDQGAGVRVGVTGFAGMVVMAAVVFVL
```

547 - 566:	EEEEEEEEEEEEEEEEEEEE
548 - 567:	EEEEEEEEEEEEEEEEEEEE

A0A0H1BRC4 **A0A0H1BRC4_9EURO** (393 aa)
Uncharacterized protein. *Blastomyces silverae*

```
MATQQINPKRQQELQAQYQNYKTTLQQLAQKIGDIEQETEEHKLVIDTLEPLPGDRKCFRLINGVLVERTVKDVIPPLKT
NSDGLKQVLDELLKQYKAKQDELDGWKVGGGGRREEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGPFHLFFARGH
```

115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE

119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
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162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
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165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE

171 - 190:	EEEEEEEEEEEEEEEEEEEE
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221 - 240:	EEEEEEEEEEEEEEEEEEEE
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223 - 242:	EEEEEEEEEEEEEEEEEEEE
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327 - 346:	EEEEEEEEEEEEEEEEEEEE
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343 - 362:	EEEEEEEEEEEEEEEEEEEE
344 - 363:	EEEEEEEEEEEEEEEEEEEE
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348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE

A0A0H5C2L0 **A0A0H5C2L0_CYBJN** (1342 aa)
SED4 protein. *Cyberlindnera jadinii (strain ATCC 18201 / CBS 1600 / BCRC 20928 / JCM 3617 / NBRC 0987 / NRRL Y-1542) (Torula yeast) (Candida utilis)*

```
MKFNTAEYDIGYPVFDAKFLNDKTLLVTGGGHSEPGATVNRLTALTIQFEKKKKIKKFRELKLSEEDDIPYVLDAANNLI
FLGANESAEAIRAGHNHNLRKFVYRNDHLVYLTSASLEPIATPLQYQKLITLSEDGVMAATATSKLPTVIHILSTEKVFE
KYEIETNNEVKDMDFSPDGKMLTYITPTTLEIISSVTGKSLMRKTDFQGTLSKVKFQDNNNVLVTYSLPESSGVGISRLS
IRKKLKVVKDRVITKKIKGITTIDINVKNGVIALAGNENSVILLKSQSLKTIKIVPNVHGLSITKVCFTPNGKFLATVSA
AKTIKVLEIPDKLGIETHRIYYFFLRLFQLALFCVFASGAWFLYYATGSNDNELLEYFTLIQKTQTTQSSITSSIAPVLT
STAPEHIYEDEIAESVAAVSIESTVTLTSEPGPKTLIGDSTVKKRKKKKTKTKNIKKTKSASSQSDVNIDTSEKSIPVEP
ITSTVLVTSEPTALTKTESTTTTSDVDTLSSSFEKSSIASHSVVQANPEGETKRKTKVTEPSVEVETSSSNSPDKLSGSH
VVEKNEPTLSTASLDDVVLEHTSLDDTDEILIMREEQQLSDDSTYVDQEEKTEEDKTAEDEKEAEKDGEEAEEDEGQEEQ
EDSEGRDKDTITSETEEEPDEEPETVISVGTEKGVTREPEGTSDHTEVQTEKYTEEDVSAVEHSQEEESEVKLESDVEEE
SQEELRATTETTTKKEIDGKGEEKEEEEETEEEEEEEEEEEEEEEEEEEEEEEEEEEEEETEEEEEEDEDEEDDEGE
EEVNKAVTKNEETYPSEETTRERSTDTNLSNEENTHSTSLDVHPEDTQVGGTRGSFEFDNEEEAPVDLSNVGNNQQQEED
DDDWRKYQTHIAFESMSRKAPETTAVDSEVLGSQEEITDGEHESSTGKPGALDASVGHEHAPAEVNDEFSKETDLALSAT
QPHIDVTDHESLEEDEQEDNENGEEDEEDEEDDEDEEDDEDDEDEGDEEDEDEEEEEDEDEDEDEDDHHTDADSSVLTKL
QEPSSPESSALNEAYSHASVDIEISNTTLPTDKVTDPVFESPLAKSLDGKLSDVSFKKDTTGEDVPMGTADVTELNSTHS
NSVSSSQFEYQELSDIAIEPQEADQSAFDISTEIVEGSFASSITEDNINTQSLQQTSSEEEIASEEFKTDYEQSSELSLV
DSSFGDLEVDTTEEDSIMETVETMIAEGSGTPSSYAGFDSSDVKSTEQGSISDNSETDSAENSLVSTSMSTGSLLTETIQ
TTTSSSFVLESTHQDATDGNELMTESDNVESNVSPSPHEEETTDETYSEVNKDEKVTVHDEL
```

751 - 770:	EEEEEEEEEEEEEEEEEEEE
752 - 771:	EEEEEEEEEEEEEEEEEEEE

753 - 772:	EEEEEEEEEEEEEEEEEEEE
754 - 773:	EEEEEEEEEEEEEEEEEEEE
755 - 774:	EEEEEEEEEEEEEEEEEEEE
756 - 775:	EEEEEEEEEEEEEEEEEEEE
757 - 776:	EEEEEEEEEEEEEEEEEEEE
758 - 777:	EEEEEEEEEEEEEEEEEEEE
759 - 778:	EEEEEEEEEEEEEEEEEEEE
760 - 779:	EEEEEEEEEEEEEEEEEEEE
761 - 780:	EEEEEEEEEEEEEEEEEEEE
762 - 781:	EEEEEEEEEEEEEEEEEEEE
763 - 782:	EEEEEEEEEEEEEEEEEEEE
764 - 783:	EEEEEEEEEEEEEEEEEEEE

A0A0J5PDV8 **A0A0J5PDV8_ASPFM** (812 aa)
Diphthamide synthase (EC 6.3.1.14) (Diphthamide synthetase) (Diphthine--ammonia ligase). *Aspergillus fumigatus Z5*

```
MSPPTQTPPATPGLNVIALISGGKDSLYSILHCIRNGHKVVALANLYPSTSRQAASTAAKDSHEDLKKEEGTEDEEEEEE
EEEEEEEEEEEEEEEEEDIDSFMYQTIGHSVIPLYEAALGIPLYRAPITGDAVDTSRIYRHNAADQMAEGSESANEENKQ
HRQDETESLVPLLRRIKAAHPEANAVSAGAILSTYQRTRIENVASRLGLVPLAWLWQYPVLPAPVERSALSAESSLLGDA
GLLEDMAACGCEARIIKVASGGLDERFLWGNVSSADGALRRRIVNGMRRFAAPGDLRGAVLGEGGEYESLALDGPGFLWR
SRIEVCETEVRTGEGGVGYVWLKGARCVPKTATEGDTITPESVRRPMLLDEAFARVLADVRSASGSYGGEVLAKSISAGG
IKCDPRQLRNGRIWHICNITAPEAGTEAAEQMKGIVEEIRTILQSSSNIPRGTEDIVFATVLLRSMADFASMNGSYVSLF
KKPNPPARATVACGDELPEGVNVMVSFIVDLGDRDARQGLHVQSRSYWAPANIGPYSQAMSIPLRGAEHIVYIAGQIPLE
PASMQMVCDSAPTEERSWLSDYSLRAVLSLQHMWRIGVTMHVDWWLGAVAFITGAENIAAKAQVAWHIWETMNRKRDDES
IDEEESSFDVWDIKYGRRTEEQTPKATVSASIPNFEVLRSSGVTPPFLAVQVEELPRASDIEWQGLGYRCDGLELNAEET
DQGRITRTVTEQKAGYTIIEIDMEKPESDLKSALQRILAAHTVTSALTHAVIYTTKAFPLMTWPGEVVPCKSVWGRKGRR
LAAGIIFQSLES
```

75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE

A0A0J5PJY2 **A0A0J5PJY2_ASPFM** (788 aa)
Ribosome assembly protein Noc2, putative. *Aspergillus fumigatus Z5*

```
MAGSQKKSTKKFEKKHLKDVLERRKANAKIKQRIHLKEKRRADNARGRENGDVEEESPEERKKQNAFAEMNVDDFFAGGF
EIADADTDKGKSRRKDVTPKIGKRKRSEEQKEEDEEASSVASSEEEEDGGVSDDDAASQASSAPDDFEAHKNQLQALKDK
DPEFYKYLKENDSELLDFGEHGDLTEVLELSEDEAEEGPAKKKKKAAKDEGEEAADNTLTIAMVKKWQKLMEEQNSIRAM
RQAVLAFRCAAYINEAETQEQKYSISDPDVYHQVLVTALGTVPKVLAHHLPVKETASGKVRVSLDSKKFKTLTPLIKSHT
SSVHQLLVNLSDASTLKLTLSSIEPMLPYLLQFRKLLKVLIKTIVGIWADVSTTEATRITGFLLLRKLMVIGDSGLKETV
LKASYEGVVKGSRNTTVHTLSGVNLMKNSAAELWGIDQNISYTTGFSFIRQLAMHLRSSITNASKESYKTIYNWQYTHSL
DFWSRVLSQHCDGLVEAKAGKQSALRPLIYPVVQITLGAMRLIPTATYFPLRFQLTRALLRLSRATGTYVPLAPALLEVL
NAAEMRKPPKSSTLKQLDFSTAIRAPKSYLRTRIYQDGVGEQVAELLSEFFVLWTKHIAFPELSVPIVVALKRWLKQVGS
RTTGNKNAKVNQAILLLVQKVEANARWIEEKRLNVTYTPRNRAEVESFLKDVDWESTPLGAFVKTQRKLREEKAAILEQG
RREEEKRRAAEKKADEDEMMEDAPSDDDGSEASSGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEFEEE
```

756 - 775:	EEEEEEEEEEEEEEEEEEEE
757 - 776:	EEEEEEEEEEEEEEEEEEEE
758 - 777:	EEEEEEEEEEEEEEEEEEEE
759 - 778:	EEEEEEEEEEEEEEEEEEEE
760 - 779:	EEEEEEEEEEEEEEEEEEEE
761 - 780:	EEEEEEEEEEEEEEEEEEEE
762 - 781:	EEEEEEEEEEEEEEEEEEEE
763 - 782:	EEEEEEEEEEEEEEEEEEEE
764 - 783:	EEEEEEEEEEEEEEEEEEEE
765 - 784:	EEEEEEEEEEEEEEEEEEEE

A0A0J5PTY6 **A0A0J5PTY6_ASPFM** (161 aa)
Conserved glutamic acid-rich protein. *Aspergillus fumigatus Z5*

```
MSTRKRKQEAEEEEELQALPSDESEEEEEYEDSEVGESEEEGSEEEEEFEEDEGEGEEEEEEEEEPSKDKAPPSKRRKTA
PEGEAKENGNGREEEEEEEEEEEEEEEEEEEEEEEEDGEGEPEDEEPADTAKTSTPAAAATKAKGSAGPAEAEVEVGEENE
K
```

93 - 112:	EEEEEEEEEEEEEEEEEEEE

94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE

A0A0J7JYJ7 **A0A0J7JYJ7_LASNI** (110 aa)
Uncharacterized protein. *Lasius niger (Black garden ant)*

```
MFRWKKKRREEEEERKKKRRKRGKKKKQRKIGEEEEEEEEEEEEGEEGEEEEEEEEERREEREEKKKKQRKIGEGEEEEE
EEEEEEEEEEEEEEEEKKKERKKGRNKEK
```

76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE

A0A0J7KWK2 **A0A0J7KWK2_LASNI** (1186 aa)
[Histone H4]-N-methyl-L-lysine(20) N-methyltransferase (EC 2.1.1.362). *Lasius niger (Black garden ant)*

```
MVVDCLSIQTSATAVRKQERRLGGTVNAKMQPNSGGGGCGMTPKELSDNDDLATSLVLDPYLGFTTHKMNIRYRPLKANK
DELRKIICEFIQSQNYEKTYKKLMGGDWGARLPHTKSKQQQINLENHIKRYLRVFDKDSGFAIEPCYRYSLEGQKGAKIC
ATRKWLKHEKISCLVGCIAELSEKEEAALLHPGKNDFSVMFSCRKNCAQLWLGPAAYINHDCRANCKFVATGRDTACVKV
LRDIEVGEEITCFYGEDFFGDGYRLRETDNRINRTKHRQQPLNRNKQQADTALTERNAVLVGNAAVAPQSLSMKELRRKG
LTKYDAELLIAQGCRFSDINQQQPAINNGENVLQTRPHPSAVTTSVTRSLRNKQMCKFDSNIDDGSALKNTQSLRTSRLH
KRTESKKGKISMKSVSVCLDNSVAKDAEVANISHRKEDSDRVPEESLYSRLQKHLVTEIDRDFYVEDSRRRTATEESSTE
GACPLRLTKMEDESNVSDDLMEDERGIPNLTAEVEPDTVNIINSSNYKKGHYSTNACDSIRLNSAPQIHVQQRLHTAELI
PDDTNCRSRDYRRSSSPVRDKEGENDPYNTENCLNKLSKSRSKRFSSTDDCKALNEDSSCEDDDSPPSIEEKKALRQADF
RHNDVLYESSSRSDDECCDINSAKVIVVQKYAMEKDMESEDCESPIVVDATADRNRTDSVEFCGLNSEEVIEMKTSIGNV
LKCYSSTVPSQEEEEEEEEEEQEEEEEEEEEEEEEEEEEEEEEEVEEEEEEGEEEEEEEEEEGEEKEEEEEEDSVMKS
DGYITNVDTDVRSEVTTLRAIEIDSRVHIRGENNAVDFNNVQIGTEYNNDLTGHRNLQDNHDPSSIKRSTSRRKDHALEI
ASSRSSRKSQKRLSSSKSKFGVWTEDAQDDGVEGKSHGKTGKSKNKSTKSQRRDRQRSATAEIGEADDDSGIQGDIYEFS
EKESNLEDIGILSIIRRGKHESRHASSSTSPVSEMQCNDEYSKAEPPVLIPEEPWPPIDSTARSEHGTDSNNGVQSGENC
DVEESLERLTVYENNGSARKSSSNPSSECQWQTSNPSDCRVWPVTPEKPSRGLKLTLRMKRSCPLLEDNVESGTSGLSED
SYEPEYEVLRVEGLERRKRRKKHKSRDRERRHKKSRELNLDPPPPPMKRLRLILGNETRTIDLTHS
```

743 - 762:	EEEEEEEEEEEEEEEEEEEE
744 - 763:	EEEEEEEEEEEEEEEEEEEE
745 - 764:	EEEEEEEEEEEEEEEEEEEE
746 - 765:	EEEEEEEEEEEEEEEEEEEE
747 - 766:	EEEEEEEEEEEEEEEEEEEE

A0A0J7KWL1 **A0A0J7KWL1_LASNI** (213 aa)
Troponin t (Fragment). *Lasius niger (Black garden ant)*

```
LKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGPSNFVTERSLRSPKEKRQYGGR
VFPDESSRCVRITPSMPFCPLVFQGLTDQQKEFMEKQWTQQKEQFLGRQKTKLPKWFGERPGKKPGDPESPEGEEDVKAA
VDDDLEEPQFEEEEEEEEGGEKEEVEEEEEEEEEEEEEEEEEEEEEEEEEE
```

186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE
190 - 209:	EEEEEEEEEEEEEEEEEEEE
191 - 210:	EEEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE
194 - 213:	EEEEEEEEEEEEEEEEEEEE

A0A0J7L421 **A0A0J7L421_LASNI** (360 aa)
Dynein heavy chain-like protein. *Lasius niger (Black garden ant)*

```
MRPPLGGAGHVVPAPKGNGTMGIIMPLYTIGIVLFFLYTIVKVLKKNSDSEIISEYPGAAAEKEFRKMVFSPEALATAMT
GETLHYPREKSPYRTAPTIEELKDLPESHSRDGEELDAVEQSPTVKVMGMEMTASCESGQKCSRPTTPIIPIPSNVEREQ
TPPKPIYLEGALPQQCELLVTDSETQAEKSEDDDDAPVVLSGKMTLSLISLDQIPADSENEAGSGNEKESLKTNAEIENV
LNKELKLWQRKEKEKKEEEEKEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVWEWDMEKE
DEAECEEKVKEKKAGEDKDDEEHWKHKVENLKRNRETNQD
```

266 - 285:	EEEEEEEEEEEEEEEEEEEE
267 - 286:	EEEEEEEEEEEEEEEEEEEE

268 - 287:	EEEEEEEEEEEEEEEEEEEE
269 - 288:	EEEEEEEEEEEEEEEEEEEE
270 - 289:	EEEEEEEEEEEEEEEEEEEE
271 - 290:	EEEEEEEEEEEEEEEEEEEE
272 - 291:	EEEEEEEEEEEEEEEEEEEE
273 - 292:	EEEEEEEEEEEEEEEEEEEE
274 - 293:	EEEEEEEEEEEEEEEEEEEE
275 - 294:	EEEEEEEEEEEEEEEEEEEE
276 - 295:	EEEEEEEEEEEEEEEEEEEE
277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE
287 - 306:	EEEEEEEEEEEEEEEEEEEE
288 - 307:	EEEEEEEEEEEEEEEEEEEE
289 - 308:	EEEEEEEEEEEEEEEEEEEE
290 - 309:	EEEEEEEEEEEEEEEEEEEE
291 - 310:	EEEEEEEEEEEEEEEEEEEE
292 - 311:	EEEEEEEEEEEEEEEEEEEE

A0A0J7L865 **A0A0J7L865_LASNI** (125 aa)
Uncharacterized protein. *Lasius niger (Black garden ant)*

```
MNEEEMAAMVVRRKRATVVAATATRREEKKRRGKRKSRGEEEEEEEEEEEEEEEEEEEEEEEEWLTGWPQHKLEVNQTYR
SYRSLPLPPTELLPVTSLYLDFVLRLSFPFFLSLLSDALCVDRIE
```

40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE

A0A0J8DZ79 **A0A0J8DZ79_BETVV** (504 aa)
Uncharacterized protein. *Beta vulgaris subsp. vulgaris (Beet)*

```
MTDCHSSNVARNRSFEIQVEDTVGDERLPRGRDRPSAAVCLFGGSKGPVIQENLDRPVTAGQAAVVPPRGQSQEGRPGKC
RPPRQEMTKPLSKGKQPAVSELRRKMDWKLVVRPGDNIPPSGQKMETDAREYLEAKRAAALQRLASGSTPYMKDPPLRIP
SRTERRSQRPSAVQPMQEKTILQPMLCRRQALANTSSNPVLKEYRWEHIPTEGHAGALKINWPTPFSARSWKIPKEREEE
EDEEDEEEEDQEEEEEEQEEEEEEEEEERKKRRKKRRKKRRKRRRKRRKKKKRKKKRKKRKKRRKKRRKKRRKKRRKKK
KKRKKKKKKKKRKKKKRRKRKRKRRKRRKKEEEEEEEEEEEEEEEEEEEEEDVDDDDNDDDDAPPSSNPTSDDDDKDEDEDDA
DDDDDDDDAPPSSDHTSDDDDKDEDDDEDDDDDDDDGDDDDKDEDEDDDDDDAPPSSDPTSDDDSSDPIVGDDDEDGITQ
ETAFEEDSDNDKPRSTWDTVDFLA
```

348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE

A0A0J9S8G6 **A0A0J9S8G6_PLAVI** (378 aa)
Casein kinase II subunit beta (CK II beta). *Plasmodium vivax India VII*

```
MDEEGLSNNESSNDVVDEENLEEERGLSDASFGHREEEEGGLHGGSGEGGDCEDGLDGCDCDHGVDGGLDVEDLEGQAAD
APGEEKDAEGGGNEEEEEEEEEEEEEEEEEEEEEEEEEEDDDEDDDDEDDDDDDYDDDEYDEDDFNEATVSWIEWFCQLK
QNIFLVEVDEDFIRDEFNLIGLQTKVPHFKKLLKIILDEDDDDDDDDDEEDDYDEEDDEINRGSDELYKNKDIYEQNAAC
LYGLIHSRFILTSKGLALMREKYKSSIYGTCPSIYCDNAKLLPTAISEVPKFLSPLLYCPRCCESFYPHKNSLLNQLDGS
YFGTSFASFFALSFNIQSDKKRIYYTPQICGFTINRDIRETLYVGMNKDNSESSEEYS
```

94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE

A0A0J9SG09 **A0A0J9SG09_PLAVI** (1119 aa)
Histone acetyltransferase (EC 2.3.1.48). *Plasmodium vivax India VII*

```
MKPKCSHKLSLASAEESKNEEIDREYYSCIKNCATDLQNLSLNFFPSINTYTCIPKINAINSITFHPCISSRDYFNNTYS
FKPLFTHHFFSDSEQVIGFDSLKIDFYYTCDNYEVFMKLSGSISDQYENSNYIMLMLLQNLYITTPYPGGFIETEEEFLR
ILRRNEGKTKASGAKQSAALTQEQIYKPPGFIIYEKRLSDDIYLQIRKCGFSSKYFKLESVSNADEEEEEEEEEEEEEE
EEEEEGEKPGEKPGEKLEANLGGTDGSVYQNGFADMVQNENTPSKDQPCSPPKTDRSKHKRGSSVKETKSEHRKSSKGGE
INSSCINQNDNHNIKRGLPNEPCEDDSKGEGNEAATPKYVIHDDNCGSSTTSNEFNKEILRKKRDSKTSLVGSCTRSNEE
SLSSKEKIKKEKKTKEPPTHPVVDGADCGNDNSPVELKKAKKNFTKHVTERDMSKLYRQYLRVVRAKRRNSLAARGDSLK
EKTPARRKLERQKCSGGSARGGAAVPVEENAAGNAAETAAETRGSSPKKGGSPNQRASPGKGGSANQAVEPPQGNAPHEK
GTNSRRKKNVREELPGAKYDYTVKKNFELLHRKVEWFYHWFIESASNIEYDYRWSVILPYIVFKHDEEKKFTENNFIENL
NVQLLKNRSANVSVLPSVKLEAAAPPSVAVSNEEVSPPMGKDVETGNKKKHKRGATAAVREKKQVKKRKKGQGGAAGEQT
LECVGDRVGDRVGECFPEAANDLQSGREQPEGRVKKESSNKRENTQESHHDGHTEAVFDQNEYVLTSEIVIKAIENTLKD
VRSQDEEEYYAFHKNHDVIYLYSDLEKGGGEAATKGEAAARGAVQNTQAVTDVKGERKTTGRKGRDKQKSKAKRDAKGED
KKQSLYYFYLFGLATTYTFFTFQFDRNRISQFLIFPPMQSKGLGMKVLEKIYHLSIVNSNVKEITVEDPAVSFTQLRDII
TIKMCIDLRILSPTILYPSDYLKTKNIDKEYADLDKRKFMKVCKETHKQITRMIETLLLAGVLPHPAPSYADIGEDKASG
VRKKEKKNESPDSLNSMEHFESSDLCKDVRIKIKKRIKNDYIGNLINKNMNCMASDVFQDYVKEELYKLWKKQCKVYYR
```

226 - 245:	EEEEEEEEEEEEEEEEEEEE

A0A0J9SHY9 **A0A0J9SHY9_PLAVI** (941 aa)
RNase NYN domain-containing protein. *Plasmodium vivax India VII*

```
MIIELCNEMEYPNYTAIQLNRWRNFLFLLLGRRLGKGQPSDGRDNVAGKGQLAGGKNDRRDKSPQLKTGVKADCLSVGTS
KGENRNSKKRDDVGGNVLSAANVERSSRVGAEQKMGEGPEGEAKGEAHEETNEESHEETNEESHEEAKGLIFPSDIKLIY
GSITTTDREKNPNVKKKMTALLSKNLYDVVVLYYEMHFYNNIDSFQVDVNVYEIYNDLICLIDELYSMYIIDSEKKQSCY
PYEDVAERYLSKELSGGWGERTQEELLQEYYILRGDRNTLFINFKLMKMVYLSAVFDLEFFGDVCQESVFLPDGGSGVGW
GSGVGWGSGVDGGSGIDGLGCVDRVDYVDCVECVSRVRGCSCGADVCRVNCLSGVAPARTGDRRAGPPGRAVDRAVEAPR
NDNRGDKKKSNKRKGISKRADRRSDRREIPSPVLKSEVLRYRERKSAAAAAEEAAVGQEEEEEDEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEVFPVEDATPFEEPPPVKEVFPFEEAPPFEEAYIREDQKLCYRILCDEQPYKALLIKDE
LNLSSSDDGEGYRGRARTPVKEVPALRASSASRGAARNAAAALSVESSASLANLAVAPGLAVSPGVAVSPSLAVSPSTAA
LPNIATSAAESHQTSSENDRDSIAQGRHSRVYTKSKWNQGILSYASQHEKSVSIPKDILNITSLLSTPILSMSNIKSLNQ
VNFSYGYSKTKKDLYNYCYAYLLSIHNGYDVIPMEGYKFRPIIIDGANVSAKVIHKHISNVLDTDMSTIYDCFLLHEAYV
FFKRKKVDDIIIVLNPVTKKGEEYFLGNKKVCNYSYLENLIKQNAILICNEKYYHSYKGDVVKRRTYDDVLILELASHRN
GCVISNDNYTDIEADTACEEIKHVISHYVVKHHYDKQNGFGLDMTKKPLKFVLNSLFQKIN
```

465 - 484:	EEEEEEEEEEEEEEEEEEEE
466 - 485:	EEEEEEEEEEEEEEEEEEEE
467 - 486:	EEEEEEEEEEEEEEEEEEEE
468 - 487:	EEEEEEEEEEEEEEEEEEEE
469 - 488:	EEEEEEEEEEEEEEEEEEEE
470 - 489:	EEEEEEEEEEEEEEEEEEEE
471 - 490:	EEEEEEEEEEEEEEEEEEEE
472 - 491:	EEEEEEEEEEEEEEEEEEEE
473 - 492:	EEEEEEEEEEEEEEEEEEEE
474 - 493:	EEEEEEEEEEEEEEEEEEEE
475 - 494:	EEEEEEEEEEEEEEEEEEEE
476 - 495:	EEEEEEEEEEEEEEEEEEEE
477 - 496:	EEEEEEEEEEEEEEEEEEEE
478 - 497:	EEEEEEEEEEEEEEEEEEEE
479 - 498:	EEEEEEEEEEEEEEEEEEEE
480 - 499:	EEEEEEEEEEEEEEEEEEEE
481 - 500:	EEEEEEEEEEEEEEEEEEEE
482 - 501:	EEEEEEEEEEEEEEEEEEEE
483 - 502:	EEEEEEEEEEEEEEEEEEEE

A0A0J9SM15 **A0A0J9SM15_PLAVI** (1095 aa)
DNA repair protein rhp54. *Plasmodium vivax India VII*

```
MRKCPGRAKRSREDSPDRACITLVRATLLPILSIDKNEKTTLFHPFKSPLPGFVSDRRLYVQKTLGAKVRRTGWLNLMKN
```

SIPRRSDEAEASEQNKADEIKNEFVPLILYESENSKVEVDPILAQFLREHQREGVTFVFECLMNLRDDRISGCILADDMG
LGKTLQSISVLYTLLKQGIDKKPAVRRCLILCPASLINNWNDEINKWLPGRCNVTCVNDNAKEKIVSKLEGFKYDQKSTV
IICSYECFRINNDSLDKSSIDMIICDEAHRLKNDKTKTYMSIYKLAARKRLLLSGTPIQNDLSEFFALISLCNPDLFDDT
NSFRKKYANPILIGRDKDATEKEQEVASERLAELSTITNKFILRRTNNLLSKVLPVKYLINIFIKLNPIQEALYVLFLKD
KRILKNEQSTNKVNVLINIKKLEKICNHPLLLNPNDMKDVGHVSLAKLIEDAAKQHQGKRQAKQEKAERTEKPPLEGHPQ
GDRDRDRDRDRDRDRERDRDRRRAVEMDYDKPVKKLLEECRRDTHRCYYNMSCKFQLLHFLLKTIKQNTTDKVVIVSNYT
QTLDYMEILCKENFYKFVRLDGGISIKKRHKVISDFTHSSDIFIFLLSSKSGGCGINLISSNRLILLDPDWNPANDKQAL
ARVWREGQKKICYIYRLFCTGTIDEKVYQRQISKDGLSSMIVTNTNLSKDQLSDENVKKLFNYKMNTLCETHDNIECTRC
TIRNCTEKEVENFSEQLEDFEEEDVNTWAHHQNVESVPDEILAKAVKAATDYKRNDMNNFPVLKKLSDLFVTFAMSCKIE
FRDDLIKQKAQKAQKGERTCRPGAAADGPVEQDEEADYEGEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEGDEAEEEDDEDDEAEEEDAPPKRADKTSKLEYQHKLMEIMEYQRARRREKGAGEARKRS
DEGEGKRDGGAKREGAAKLEDGAKREDGTTREDGATREDAQQQAPRETPRETPRETQPGQKQDAKVSGKAKSQEGAGEEE
DPASKRVTRNMSQKNLMELLSQDEESKVTLSMSEDPDADADASVENVSTDSSYFI

843 - 862:	EEEEEEEEEEEEEEEEEEEE
844 - 863:	EEEEEEEEEEEEEEEEEEEE
845 - 864:	EEEEEEEEEEEEEEEEEEEE
846 - 865:	EEEEEEEEEEEEEEEEEEEE
847 - 866:	EEEEEEEEEEEEEEEEEEEE
848 - 867:	EEEEEEEEEEEEEEEEEEEE
849 - 868:	EEEEEEEEEEEEEEEEEEEE
850 - 869:	EEEEEEEEEEEEEEEEEEEE
851 - 870:	EEEEEEEEEEEEEEEEEEEE
852 - 871:	EEEEEEEEEEEEEEEEEEEE
853 - 872:	EEEEEEEEEEEEEEEEEEEE
854 - 873:	EEEEEEEEEEEEEEEEEEEE
855 - 874:	EEEEEEEEEEEEEEEEEEEE
856 - 875:	EEEEEEEEEEEEEEEEEEEE
857 - 876:	EEEEEEEEEEEEEEEEEEEE
858 - 877:	EEEEEEEEEEEEEEEEEEEE
859 - 878:	EEEEEEEEEEEEEEEEEEEE
860 - 879:	EEEEEEEEEEEEEEEEEEEE
861 - 880:	EEEEEEEEEEEEEEEEEEEE
862 - 881:	EEEEEEEEEEEEEEEEEEEE
863 - 882:	EEEEEEEEEEEEEEEEEEEE
864 - 883:	EEEEEEEEEEEEEEEEEEEE
865 - 884:	EEEEEEEEEEEEEEEEEEEE
866 - 885:	EEEEEEEEEEEEEEEEEEEE
867 - 886:	EEEEEEEEEEEEEEEEEEEE
868 - 887:	EEEEEEEEEEEEEEEEEEEE
869 - 888:	EEEEEEEEEEEEEEEEEEEE
870 - 889:	EEEEEEEEEEEEEEEEEEEE
871 - 890:	EEEEEEEEEEEEEEEEEEEE
872 - 891:	EEEEEEEEEEEEEEEEEEEE
873 - 892:	EEEEEEEEEEEEEEEEEEEE
874 - 893:	EEEEEEEEEEEEEEEEEEEE
875 - 894:	EEEEEEEEEEEEEEEEEEEE
876 - 895:	EEEEEEEEEEEEEEEEEEEE
877 - 896:	EEEEEEEEEEEEEEEEEEEE
878 - 897:	EEEEEEEEEEEEEEEEEEEE
879 - 898:	EEEEEEEEEEEEEEEEEEEE
880 - 899:	EEEEEEEEEEEEEEEEEEEE
881 - 900:	EEEEEEEEEEEEEEEEEEEE
882 - 901:	EEEEEEEEEEEEEEEEEEEE

A0A0J9SR47 **A0A0J9SR47_PLAVI** (384 aa)
Casein kinase II subunit beta (CK II beta). *Plasmodium vivax Brazil I*

MDEEGLSNNESSNDVVDEENLEEERGLSDASFGHREEEEGGLHGGSGEGGDGEEGGDCEDGLDGCDCDHGVDGGLDVEDL
EGQAADAPGEEKDAEGGGNEEEEEEEEEEEEEEEEEEEEEEEEEDDDEDDDDEDDDDDDYDDDEYDEDDFNEATVSWIE
WFCQLKQNIFLVEVDEDFIRDEFNLIGLQTKVPHFKKLLKIILDEDDDDDDDDDEEDDYDEEDDEINRGSDELYKNKDIY

```
EQNAACLYGLIHSRFILTSKGLALMREKYKSSIYGTCPSIYCDNAKLLPTAISEVPKFLSPLLYCPRCCESFYPHKNSLL
NQLDGSYFGTSFASFFALSFNIQSDKKRIYYTPQICGFTINRDIRETLYVGMNKDNSESSEEYS
```

100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE

A0A0J9SST3 **A0A0J9SST3_PLAVI** (588 aa)
TryThrA_C domain-containing protein. *Plasmodium vivax Brazil I*

```
MKGPKARRSPSRSSIAKKNKDYTLSNTSRKPVSSCIYVILFLLTYVVLPLSECSEFPRDHRANHDHRDRFKVEEPRDESR
SLAEVPKYRDNSTWLLFVKQFEQDWRDFNTDLTSKRDQWFEQKNVESEKWTKTMEDEKNKWFKAKDKELKILKKALEYKF
STVDPTLRKRRESAISGKPAMEPIVVKEADADDHIREIAQDPRAANFEKGKRIYRHPSEFAKQAQRTYSPQQKKIIKSKL
PEKDEIIQNEEMQRPEMGMPDMKKHPKGKPEMRRVPMEKHEMKKVPVKREELHPEDIYDEEEHPEGIMQQEEDYEEENPQ
EKDYEEEDHPKHAHQKGVHPEQAHQRAKDAEKSKMLDDRDKMFKQWDKVVEYKLATAAKDDPKLRANLEMLKRAQQMQDP
RNRRVQPNINEKFDEWRKELNEEEEEEEEEEEEEEEEEEEEEQQQQQQQQQQSEDEPLPHEERQPREERPPHEERQPR
EEQQPHEERQPQSHNHYNHKHYSHCYYNHCYYNTSHSYYNTSHSYCNTSHSYCNNKHGYCNNKPSYYNNKHSYYNNNHSY
YNNKHNSYNSNHIYYNNKQSYYNNKHSY
```

422 - 441:	EEEEEEEEEEEEEEEEEEEE
423 - 442:	EEEEEEEEEEEEEEEEEEEE
424 - 443:	EEEEEEEEEEEEEEEEEEEE

A0A0J9SXX7 **A0A0J9SXX7_PLAVI** (715 aa)
U3 small nucleolar ribonucleoprotein MPP10. *Plasmodium vivax Brazil I*

```
MELLKVKRYAELIEEFARQADELPPPERETAPQKKGTSQKEKKDVIEIIEYFANILARYFYSDYQHDDISIVDSGFDCEQ
LWLFIECLIKEKKLEGLLSFFERYERGLDSRVDSRLESGRGTQVGEEAEEEDDDDDDDDAALGTAQKRRAGNRVKVNVRA
PASKKRKVSPSWGGAQLSSDAAISVESDDAPEGDHFFDEDEMQQFLDEEEKKIVSGQSGESDSGGEVDLNEFEGDYEEGG
QLKYGDFYGGGEEEEEEEEEEEEEEEEEEEEEEEEEEEDDDEEEEEEEDDEEEEADDDDDDDEADEEDDDDLGSEDERARD
RCGPDRRSRKERDEEIERELREMNQFDSQHRGGGDQVGSEAEEEAGSGRGEETPQMERDKVERELIEKKHWSLTGEVSAH
DRPKNSLLSLNVEIPKLNSGGNDAYVSKAVGEEEDDDDKEEEAVGEGRRDGGKTPLSRNKRRNLLSDEIERVVKQRIQNM
LFDDVEKKRLEDLDVLLNDSKERGDGKDGRDGDVSFDHLNFSKSKLSLAEEYTKKYEEEIKSSRSEKKEINLQKLELMNL
YKKIIHCCDSLSNDFYIPKPALLNAPNRSDQFASLHIEETVPIILSEKDRRAPEQLFQPGHIKQLEEMHQKEKKAMRKSK
KVKRKKKLLHQFGVSELKKRNEHLSGKNREAKGEKESAARYGVGSRDQLRALPRTRYDFAGAISRAQARDAAGKR
```

252 - 271:	EEEEEEEEEEEEEEEEEEEE
253 - 272:	EEEEEEEEEEEEEEEEEEEE
254 - 273:	EEEEEEEEEEEEEEEEEEEE
255 - 274:	EEEEEEEEEEEEEEEEEEEE
256 - 275:	EEEEEEEEEEEEEEEEEEEE
257 - 276:	EEEEEEEEEEEEEEEEEEEE
258 - 277:	EEEEEEEEEEEEEEEEEEEE

A0A0J9SZA6 **A0A0J9SZA6_PLAVI** (772 aa)
Uncharacterized protein. *Plasmodium vivax Brazil I*

```
MLCDDEQGKPTWERPTWGEANLVTPPFPRSDTLKRHPFGGGRLHIPNEEATAGKRNTCPSVVTPVVPRQDGLLPRVASNR
ANQSPPQWADIPTDQKISSAPMGRDLPGGSRMGKVPYEQISHCTEEERAVLVDPFFYNCRGENPWECQWKKDTFADSRMG
MERNELTHAERLFASPYRHEGEGTREGPGGGSARTEATASNATTTNCTRRTEPGKEGGEEEEKEKEKENEEEEEEEEEEE
EEEEEEEEEEEENGEKLDEQKVDLLDEQKDDLLDEQKDDLLDEQKDDLLDEQKGGEELDDLLDEQKGGEELDDLLDDLPDD
GGEGMKGREPPPWRREKTILTIQWNIKKISLLCSSDSHFVVSPEYKTETLINEFFILLNINKDMHVHLLGENSFGLLFSY
TGFCDILFSVTCGVYQKKFCAYDCSTLPWFGFNNWGILKNCMQNDSISITVDIHEIRRKDSLKEVFLSNVILSMRSSNGS
FHFKEGASPVSPSAVVEAEEEKKKEAPSPTIATASATTAATTSPLDLGRHRRSAKCFFPQSAPATSDSCSRFAPPTVKRR
HPGSVHMVGSKHMAGNMHMAGSMHFAGTRANAPQWETKQTNASSWNGKVAKQQMIRANRETNPTQGNKLHKGIKKNLYAH
NLIDVCSPFEEHPGGNFIQLSQGLQEGTLAKCTSGSSAHRAAPCAVSGFANQPSVQQEGTPQMKKEGPFGRDPPRRGPTS
VKTFIGALPNDALPNEALPNEELPTEELPSREGKPRGGGATLEDRFSENGTP
```

230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE

A0A0J9T1D3 **A0A0J9T1D3_PLAVI** (2094 aa)
Uncharacterized protein. *Plasmodium vivax Brazil I*

```
MESYIRESKKLTFKGSKGKKLLRYVDISLNNKALHDSHIVELVNILKKYIKVVYNHFYCLNIDLSENYITCTGLKTLLKF
```

```
ILNYHDNIGVHILKLYKNNIKDDGVSLIKQLVYVQKIPMEELHLSHNFVQDDTCKELLLSFVQAKKENSYVYPRYEKYQS
HYKHLQIPVWIRLEYNCIQNPKEILKEVEEFAKKKRGYKSNLIICAALKSDKRCCPYKCLNATVRNTPIMHVYMFIHQKD
SPAYAISTNGKVGKEERKREFSSPSEVVDAGRMHASAHLQHKAQPEGVERQDGEAALPAKGEARSGAARSAAKSAAKGAA
KGAAKGAAKGAAKGAAKSGKDKKTAVRKGGANSGKRLSRGSLPHDVSADEEEEEEEEEEEEEEEEEEEEEEEEEEEEED
DDDDDDDDDDDDDDDYSEEEEEDDDDEEDDEDEDDDDDDDDDNDDDDDNDDDDNDYRHKRGKPLKGKEKNGQLPDAAPLY
ASKNGAAIGAQTNGRDEEDYDEEAEEGEESPNAADPAKKKKGKKKKKKKKKKKKKEQVEVSPLEGGCEEAKGSGERGEEG
SAVGGESGLGDGSGDESGDDNDNDNDNADRDDCDRRDHRYPREDLFRAVGGDPLRLDGGGEEDALPPELCPPRQDRLNLT
SDAASSLPLYIILDCTAVLDMKELWKDSSFLPFSFPGLLYLYNNKLLRSNAEGASGGRGVNGVSQNDAFICLMCSYVANE
LKLVCQKSEIIRQKMVNLKLNIWDKLSELGIIEFLSVPKDFKEKKKNFLNSSFLTEAQIKLANEYYDISQETLQMIQFSI
LWSTYIYKIGNKEIIIKNAAKEINKGGMKKSKKTIFTEVLYLTSSPNIYSFFEHLYGEDMNMILPLCVTVNQINKYIQDE
HSCVVELLSSGRPVGDKGGNFLLDKAFFKAFIKDKCARYLPDGEEGVASIGGATNGGTTNGLPSNGGIANGGTSNGLPSN
GGIANGGSSKKKKKKGAPPKRSADKLKDGFPSAHDNGTPSMSSLSAATPNCTSRSDKLSPGGKRSDDECVRGSLPIGGTH
INTNAYDYLDIKSVKSFSNENISKLCQLESSIQGGPFGMVGINGGGRMAAPMGGDRHSHYNDPSGGANKVKTNVGGRASG
EETHKGAEKGNAAVGMYASPIDANNGGNGFGMMMVTPPSGSAKENPQGGKENKGSSLYSMLVNAFNGKKKGAQKGAERGA
DRATDRATDRGVASGQDKSGNNMFMGAGPNQSVRDSVDPLSSHAGGENSQNEGGHGNNAAAAAAVATRPQLNMSNGKVKS
TGADLLDQLMHGGSESAPSQGKAASGLGANGGAATSPQMGIPSNDKATYLGSNNNSGSNHPPAHSLFAFNSSMLKGVAPS
GKGDLSFQSQMGTEGGGSGKSGSGIGAGLLGGVNFPMNGAGMGTLANRTTQGNSKQLQKNAVETIIGSDLLNVNEVELNN
FMGSIPKSFNDSLSMYLDSSNRNDSCYDGIARGENMMPFFNHSLLKGDAEQDLANLAARAEGHSRAEDHSRGADHSRVTD
HTRVADHNRVTDHNRVTDHTRLNEMKNVFELYKVDILNTSLLLEEMILNQNVCKYIPSELYNKILRCYERLDCLLAGLNR
VGSLSGLSGLSGLSGLRGVSGASGVSGMSGIGGIGGMSGIGGIGGIDAIGGMNQDILCEDFKSYWDYAFSKNESSPLALL
TSGGGSGIGGGGGAAHQDFTDGAGNISGNKSGNASNAMFYNTVSGNRGSKSALKSSMLNASSHSGNGGIGGGSGPLLASQ
LNSQNNGAVTPKKSRKKPPMNVSMGSGNNVELGINSMKNNSSQKKFMGGLSDGLDNTGFMNNSPGGNLSGSRNSQMGRNA
NYGLGQSIPPNRSGNGNQAGARNSGSGSNNAKSKDMKNHNAGPKDRNLNSVETDEYKNVNKLLLLGGNAQNVKMNGEKNP
YDHGGGGSGGNAHTEHQEHFPHKMNPYNDGGGSGACDSNLLALIHMKKNIKNGVSSSAGPKAGVNSGGANGGGANSGTAN
ELNGLRNRSYKKLLNNESIGLFNSPANKNTVNEMNLKYLEVLNSQFNFSARENRKNECDPNALNSSVMNFQNDLDKKYKN
PLVDLCDKGSVKKL
```

370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE
379 - 398:	EEEEEEEEEEEEEEEEEEEE
380 - 399:	EEEEEEEEEEEEEEEEEEEE

A0A0J9T2C8 **A0A0J9T2C8_PLAVI** (1088 aa)
DNA repair protein rhp54. *Plasmodium vivax Brazil I*

```
MRKCPGRAKRSREDSPDRACITLVRATLLPILSIDKNEKTTLFHPFKSPLPGFVSDRRLYVQKTLGAKVRRTGWLNLMKN
SIPRRSDEAEASEQNKADEIKNEFVPLILYESENSKVEVDPILAQFLREHQREGVTFVFECLMNLRDDRISGCILADDMG
LGKTLQSISVLYTLLKQGIDKKPAVRRCLILCPASLINNWNDEINKWLPGRCNVTCVNDNAKEKIVSKLEGFKYDQKSTV
IICSYECFRINNDSLDKSSIDMIICDEAHRLKNDKTKTYMSIYKLAARKRLLLSGTPIQNDLSEFFALISLCNPDLFDDT
NSFRKKYANPILIGRDKDATEKEQEVASERLAELSTITNKFILRRTNNLLSKVLPVKYLINIFIKLNPIQEALYVLFLKD
KRILKNEQSTNKVNVLINIKKLEKICNHPLLLNPNDMKDVGHVSLAKLIEDAAKQHQGKRQAKQEKAERTEKPPLEGHPQ
GDRDRDRDRERDRDRRRAVEMDYDKPVKKLLEECRRDTHRCYYNMSCKFQLLHFLLKTIKQNTTDKVVIVSNYTQTLDYM
EILCKENFYKFVRLDGGISIKKRHKVISDFTHSSDIFIFLLSSKSGGCGINLISSNRLILLDPDWNPANDKQALARVWRE
GQKKICYIYRLFCTGTIDEKVYQRQISKDGLSSMIVTNTNFSKDQLSDENVKKLFNYKMNTLCETHDNIECTRCTIRNCT
EKEVENFSEQLEDFEEEDVNTWAHHQNVESVPDEILAKAVKAATDYKRNDMNNFPVLKKLSDLFVTFAMSCKIEFRDDLI
KQKAQKAQKGERTCRPGAAADGPVEQDEEADYEGEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEGDEAEEEDDEDDEAEEEDAPPKRADKTSKLEYQHKLMEIMEYQRARRREKGAGEARKRSDEGEGKR
DGGAKREGAAKLEDGAKREDGTTREDGATREDAQQQAPRETPRETPRETQPGQKQDAKVSGKAKSQEGAGEEEDPASKRV
TRNMSQKNLMELLSQDEESKVTLSMSEDPDADADASVENVSTDSSYFI
```

837 - 856:	EEEEEEEEEEEEEEEEEEEE
838 - 857:	EEEEEEEEEEEEEEEEEEEE
839 - 858:	EEEEEEEEEEEEEEEEEEEE
840 - 859:	EEEEEEEEEEEEEEEEEEEE
841 - 860:	EEEEEEEEEEEEEEEEEEEE
842 - 861:	EEEEEEEEEEEEEEEEEEEE
843 - 862:	EEEEEEEEEEEEEEEEEEEE
844 - 863:	EEEEEEEEEEEEEEEEEEEE
845 - 864:	EEEEEEEEEEEEEEEEEEEE
846 - 865:	EEEEEEEEEEEEEEEEEEEE
847 - 866:	EEEEEEEEEEEEEEEEEEEE
848 - 867:	EEEEEEEEEEEEEEEEEEEE
849 - 868:	EEEEEEEEEEEEEEEEEEEE
850 - 869:	EEEEEEEEEEEEEEEEEEEE
851 - 870:	EEEEEEEEEEEEEEEEEEEE

852 - 871:	EEEEEEEEEEEEEEEEEEEE
853 - 872:	EEEEEEEEEEEEEEEEEEEE
854 - 873:	EEEEEEEEEEEEEEEEEEEE
855 - 874:	EEEEEEEEEEEEEEEEEEEE
856 - 875:	EEEEEEEEEEEEEEEEEEEE
857 - 876:	EEEEEEEEEEEEEEEEEEEE
858 - 877:	EEEEEEEEEEEEEEEEEEEE
859 - 878:	EEEEEEEEEEEEEEEEEEEE
860 - 879:	EEEEEEEEEEEEEEEEEEEE
861 - 880:	EEEEEEEEEEEEEEEEEEEE
862 - 881:	EEEEEEEEEEEEEEEEEEEE
863 - 882:	EEEEEEEEEEEEEEEEEEEE
864 - 883:	EEEEEEEEEEEEEEEEEEEE
865 - 884:	EEEEEEEEEEEEEEEEEEEE
866 - 885:	EEEEEEEEEEEEEEEEEEEE
867 - 886:	EEEEEEEEEEEEEEEEEEEE
868 - 887:	EEEEEEEEEEEEEEEEEEEE
869 - 888:	EEEEEEEEEEEEEEEEEEEE
870 - 889:	EEEEEEEEEEEEEEEEEEEE
871 - 890:	EEEEEEEEEEEEEEEEEEEE
872 - 891:	EEEEEEEEEEEEEEEEEEEE
873 - 892:	EEEEEEEEEEEEEEEEEEEE
874 - 893:	EEEEEEEEEEEEEEEEEEEE
875 - 894:	EEEEEEEEEEEEEEEEEEEE

A0A0J9T7B5 **A0A0J9T7B5_PLAVI** (345 aa)
Uncharacterized protein. *Plasmodium vivax Mauritania I*

```
MNLSSPLLALPEEGKKRRTKLIRLRNGHYRRIVDISNTDERKLIPSMCRCACVTPRKDEVENEGKWEDAKKAKSSQEYDE
TSDYVESEKKESYMLAVNEEDQTEDMYSKTISFTSITPTSIRSEEPEPRRKLSLLDVKEEEEEEEEEEEEEEEEEEEEE
EKEEEEEEDEIESTAEEKEEEKKQVPPEGKKLIEPSKTLMRGTKTNIYFLSNKEMVQTLMCYNYNCNAVVFEKDTFLRYL
YMKSISNIILNERMIDELCKQEDLKYVLTSNAIVLESTDFLKPLIIEFESSISKRVFVRHLKHNARKEIDMKKYHDYMGE
LNANEKIRLMKIERFHSFNKMIQCN
```

139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE

A0A0J9T8E4 **A0A0J9T8E4_PLAVI** (378 aa)
Casein kinase II subunit beta (CK II beta). *Plasmodium vivax Mauritania I*

```
MDEEGLSNNESSNDVVDEENLEEERGLSDASFGHREEEEGGLHGGSVEGGDCEDGLDGCDCDHGVDGGLDVEDLEGQAAD
APGEEKDAEGGGNEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDDEDDDDEDDDDDDYDDDEYDEDDFNEATVSWIEWFCQLK
QNIFLVEVDEDFIRDEFNLIGLQTKVPHFKKLLKIILDEDDDDDDDDDEEDDYDEEDDEINRGSDELYKNKDIYEQNAAC
LYGLIHSRFILTSKGLALMREKYKSSIYGTCPSIYCDNAKLLPTAISEVPKFLSPLLYCPRCCESFYPHKNSLLNQLDGS
YFGTSFASFFALSFNIQSDKKRIYYTPQICGFTINRDIRETLYVGMNKDNSESSEEYS
```

94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE

A0A0J9THC6 **A0A0J9THC6_PLAVI** (1089 aa)
Uncharacterized protein. *Plasmodium vivax Mauritania I*

```
MLCDDEQGKPTWERPTWGEANLVTPPFPRSDTLKRHPFGGGRLHIPNEEATAGKRNTCPSVVTPVVPRQDGLLPRVASNR
```

```
ANQSPPQWADIPTDQKISSAPMGRDLPGGSRMGKVPYEQISHCTEEERAVLVDPFFYNCRGENPWECQWKKDTFADSRMG
MERNERTHAERLFASPYRHEGEGTREGPGGGSARTEGGGRSVDGYRGDGYRGDGYRGDGYRGGTASFAAPTARPVPISTG
EKPWGDTPLALSLPISKAIKGCSPGGQIHTSCSDPHREKKIPREPYARGAANVGEARNALKDTNVNLLKCFKLSFERGRL
APLGGGGCTGVPTVGRTPESRTPPLSGFPLSGFPLREASPAVSHKGNLFESVDAFFYNFKKSGASLRGESRQVEEHVGAK
VVANDRANDRAKVVANDRAKVVANDRANTHPDCQSNSHVRASSSGVAQLANPSGSVTTTTTTTTTTTTMGAASAASAANV
VNAANVVNAANVVNAANVATASNATTTNCTRRTEPGKEGGEEEEKEKEKEKENEEEEEEEEEEEEEEEEEEEEEENGEKL
DEQKVDLLDEQKDDLLDEQKGGEELDDLLDEQKDDLLDEQKGGEELDDLLDEQKDDLLDEQKGGEELDDLLDDLPDDGGE
GMKGREPPPRRREKTILTIQWNIKKISLLCSSDSHFVVSPEYKTETLINEFFILLNINKDMHVHLLGENSFGLLFSYTGF
CDILFSVTCGVYQKKFCAYDCSTLPWFGFNNWGILKNCMQNDSISITVDIHEIRRKDSLKEVFLSNVILSMRSSNGSFHF
KEGASPVSPSAVVEAEEEKKKEAPSPTIATASATTAATTSPLDLGRHRRSAKCFFPQSAPATSDSCSRFAPPTVKRRHPG
SVHMVGSKHMAGNMHMAGSMHFAGTRANAPQWETKQTNASSWNGKVAKQQMIRANRETNPTQGNKLHKGIKKNLYAHNLI
DVCSPFEEHPGGNFIQLSQGLQEGTLAKCTSGSSAHRAAPCAVSGFANQPSVQQEGTPQMKKEGPFGRDPPRRGPTSVKT
FIGALPNDALPNEALPNEELPTEELPSREGKPRGGGATLEDRFSENGTP
```

534 - 553:	EEEEEEEEEEEEEEEEEEEE
535 - 554:	EEEEEEEEEEEEEEEEEEEE
536 - 555:	EEEEEEEEEEEEEEEEEEEE

A0A0J9TIK9 **A0A0J9TIK9_PLAVI** (1123 aa)
Histone acetyltransferase (EC 2.3.1.48). *Plasmodium vivax Mauritania I*

```
MKPKCSHKPSLASAEESKNEEIDREYYSCIKNCATDLQNLSLNFFPSINTYTCIPKINAINSITFHPCISSRDYFNNTYS
FKPLFTHHFFSDSEQVIGFDSLKIDFYYTCDNYEVFMKLSGSISDQYENSNYIMLMLLQNLYITTPYPGGFIETEEEFLR
ILRRNEGKTKASGAKQSAALTQEQIYKPPGFIIYEKRLSDDIYLQIRKCGFSSKYFKLESVSNADEEEEEEEEEEEEEEE
EEEEEEEEEEREKPGEKPGEKLEANLGGTDGSVYQNGFADMAQNENTPSKDQPCSPPKTDRSKHKRGSSVKETKSEHRKSS
KGGEINSSCINQNDNHNIKRGLPNEPCEDDSKGEGNEAATPKYVIHDDNCGSSTTSNEFNKEILRKKRDSKTSLVGSCTR
SNEESLSSKEKIKKEKKTKEPPTHPVVDGADCGNDNSPVELKKAKKNFTKHVTERDMSKLYRQYLRVVRAKRRNSLAARG
DSLKEKTPARRKLERQKCSGGSARGGAAVPVEENAAGNAAETAAETRGSSPKKGGSPNQRASPGKGGSANQAVEPPQGNA
PHEKGTNSRRKKNVREELPGAKYDYTVKKNFELLHRKVEWFYHWFIESASNIEYDYRWSVILPYIVFKHDEEKKFTENNF
IENLNVQLLKNRSANVSVLPSVKLEAAAPPSVAVSNEEVSPPMGKDVETGNKKKHKRGATAAVREKKQVKKRKKGQGGAA
GEQTLECVGDRVGDRVGECFPEAANDLQSGREQPEGRVKKESSNKRENTQESHHDAHTEAVFDQNEYVLTSEIVIKAIEN
TLKDVRSQDEEEYYAFHKNHDVIYLYSDLEKGGGEAATKGEAAARGAVQNTQAVTDVKGERKTTGRKGRDKQKSKAKRDA
KGEDKKQSLYYFYLFGLATTYTFFTFQFDRNRISQFLIFPPMQSKGLGMKVLEKIYHLSIVNSNVKEITVEDPAVSFTQL
RDIITIKMCIDLRILSPTILYPSDYLKTKNIDKEYADLDKRKFMKVCKETHKQITRMIETLLLAGVLPHPAPSYADIGED
KASGVRKKEKKNESPDSLNSMEHFESSDLCKDVRIKIKKRIKNDYIGNLINKNMNCMASDVFQDYVKEELYKLWKKQCKV
YYR
```

226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE

A0A0J9TJN2 **A0A0J9TJN2_PLAVI** (1010 aa)
RNase NYN domain-containing protein. *Plasmodium vivax Mauritania I*

```
MKKKKKTSKAEAKSPAEGELQISEGKLQISEGWRQGKRQINEGKQQISEGKRQINEGKRQISEGKRKIIEAKQSRGGLDS
AAGKGQPADGRDNVAGKGQPSDGRDNVAGKGQLAGGKNDRRDKSPQLKTGVKADCLSVGTSKGENRNSKKRDDVGGNVLS
AANVERSSRVGAEQKMGERPEGEAKGEAHEETNEESHEETNEESHEEAKGLIFPSDIKLIYGSITTTDREKTPNVKKKMT
ALLSKNLYDVVVLYYEMHFYNNIDSFQVDVNVYEIYNDLICLIDELYSMYIIDSEKKQSCYPYEDVAERYLSKELSGGWG
ERTQEELLQEYYILRGDRNTLFINFKLMKMVYLSAVFDLEFFGDVCQESVFLPDGGSGVGWGSGVGWGSGVGWGSGVDGG
SGIDGGSGVDGLGCVDRVDYVDCVECVSRVRGCSCGADVCRVNCLSGVAPARTGDRRAGPPGRAVDRAVEAPRNDNRGDK
KKSNKRKGISKRADRRSDRREIPSPVLKSEVLRYRERKSAAAAAEEAAVGQEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEVEVFPVEDATPFEEPPPVKEVFPFEEAPPFEEAYIREDQKLCYRILCDEQPYKALLIKDELNLSSSDDGEG
YRGRARTPVKEVPALRASSASRGAARNAAAALSVESSASLANLAVAPGLAVSPGVAVSPSLAVSPSTAALPNIATSAAES
HQTSSENDRDSIAQGRHSRVYTKSKWNQGILSYASQHEKSVSIPKDILNITSLLSTPILSMSNIKSLNQVNFSYGYSKTK
KDLYNYCYAYLLSIHNGYDVIPMEGYKFRPIIIDGANVSAKVIHKHISNVLDTDMSTIYDCFLLHEAYVFFKRKKVDDII
IVLNPVTKKGEEYFLGNKKVCNYSYLENLIKQNAILICNEKYYHSYKGDVVKRRTYDDVLILELASHRNGCVISNDNYTD
IEADTACEEIKHVISHYVVKHHYDKQNGFGLDMTKKPLKFVLNSLFQKIN
```

532 - 551:	EEEEEEEEEEEEEEEEEEEE
533 - 552:	EEEEEEEEEEEEEEEEEEEE
534 - 553:	EEEEEEEEEEEEEEEEEEEE
535 - 554:	EEEEEEEEEEEEEEEEEEEE
536 - 555:	EEEEEEEEEEEEEEEEEEEE
537 - 556:	EEEEEEEEEEEEEEEEEEEE
538 - 557:	EEEEEEEEEEEEEEEEEEEE
539 - 558:	EEEEEEEEEEEEEEEEEEEE
540 - 559:	EEEEEEEEEEEEEEEEEEEE
541 - 560:	EEEEEEEEEEEEEEEEEEEE
542 - 561:	EEEEEEEEEEEEEEEEEEEE
543 - 562:	EEEEEEEEEEEEEEEEEEEE
544 - 563:	EEEEEEEEEEEEEEEEEEEE

545 - 564:	EEEEEEEEEEEEEEEEEEEE
546 - 565:	EEEEEEEEEEEEEEEEEEEE
547 - 566:	EEEEEEEEEEEEEEEEEEEE
548 - 567:	EEEEEEEEEEEEEEEEEEEE
549 - 568:	EEEEEEEEEEEEEEEEEEEE
550 - 569:	EEEEEEEEEEEEEEEEEEEE

A0A0J9TLA9 **A0A0J9TLA9_PLAVI** (2094 aa)
Uncharacterized protein. *Plasmodium vivax Mauritania I*

```
MESYIRESKKLTFKGSKGKKLLRYVDISLNNKALHDSHIVELVNILKKYIKVVYNHFYCLNIDLSENYITCTGLKTLLKF
ILNYHDNIGVHILKLYKNNIKDDGVSLIKQLVYVQKIPMEELHLSHNFVQDDTCKELLLSFVQAKKENSYVYPRYEKYQS
HYKHLQIPVWIRLEYNCIQNPKEILKEVEEFAKKKRGYKSNLIICAALKSDKRCCPYKCLNATVRNTPIMHVYMFIHQKD
SPAYAISTNGKVGKEERKREFSSPSEVVDAGRMHASAHLQHKAQPEGVERQDGEAALPAKGEARSGAARSAAKSAAKGAA
KGVAKGAAKSGKDKKTAVRKGGANSGKRLSRGSLPHDVSADEEEEEEEEEEEEEEEEEEEEEEEEEEDDDDDDDDDDDDDD
DDDDDYSEEEEEDDDDEEDDEDEDDDDDDDDDNDDDDDNDDDDNDYRHKRGKPLKGKEKNGQLPDAAPLYASKNGAAIGA
QTNGRDEEDYDEEAEEGEESPNAADPAKKKKGKKKKKKKKKKKKKEQVEVSPLEGGCEEAKGSGERGEEGSAVGGESGLG
DGSGDESGDDNDNDNDNADRDDCDRRDHRYPREDLFRAVGGDPLRLDGGGEEDALPPELCPPRQDRLNLTSDAASSLPLY
IILDCTAVLDMKELWKDSSFLPFSFPGLLYLYNNKLLRSNAEGASGGRGVNGVSQNDAFICLMCSYVANELKLVCQKSEI
IRQKMVNLKLNIWDKLSELGIIEFLSVPKDFKEKKKNFLNSSFLTEAQIKLANEYYDISQETLQMIQFSILWSTYIYKIG
NKEIIIKNAAKEINKGGMKKSKKTIFTEVLYLTSSPNIYSFFEHLYGEDMNMILPLCVTVNQINKYIQDEHSCVVELLSS
GRPVGDKGGNFLLDKAFFKAFIKDKCARYLPDGEEGVASIGGATNGGTTNGLPSNGGIANGGTSNGGIANGGSSKKKKKK
GAPPKRSADKLKDGFPSAHDNGTPSMSSLSAATPNCTSRSDKLSPGGKRSDDECVRGSLPIGGTHINTNAYDYLDIKSVK
SFSNENISKLCQLESSIQGGPFGMVGINGGGRMAAPMGGDRHSHYNDPSGGANKVKTNVGGRASGEETHKGAEKGNAAVG
MYASPIDANNGGNGFGMMMVTPPSGSAKENPQGGKENKGSSLYSMLVNAFNGKKKGAQKGAERGADRATDRATDRGVASG
QDKSGNNMFMGAGPNQSVRDSVDPLSSHAGGENSQNEGGHGNNAAAAAAVAPRPQLNMSNGKVKSTGADLLDQLMHGGSE
SAPSQGKAASGLGANGGAATSPQMGIPSNDKATYLGSNNNSGSNHPPAHSLFAFNSSMLKGVAPSGKGDLSFQSQMGTEG
GGSGKSGSGIGAGLLGGVNFPMNGAGMGTLANRTTQGNSKQLQKNAVETIIGSDLLNVNEVELNNFMGSIPKSFNDSLSM
YLDSSNRNDSCYDGIARGENMMPFFNHSLLKGDAEQDLANLAARAEGHSRAEDHSRGADHSRVTDHTRVADHNRVTDHNR
VTDHNRVTDHNRVTDHNRVTDHTRLNEMKNVFELYKVDILNTSLLLEEMILNQNVCKYIPSELYNKILRCYERLDCLLAG
LNRVGSLSGLSGLSGLSGLRGVSGASGVSGMSGIGGMSGIGGIGGIDAIGGMNQDILCEDFKSYWDYAFSKNESSPLALL
TSGGGSGIGGGGGAAHQDFTDGAGNISGNKSGNASNAMFYSTVSGNRGSKSALKSSMLNASSHSANGGIGGGSGPLLASH
LNSQNNGAVTPKKSRKKPPMNVSMGSGNNVELGINSMKNNSSQKKFMGGLSDGLDNTGFMNNSPGGNLSGSRNSQMGRNA
NYGLGQSIPPNRSGNGNQAGARNSGSGSNNAKSKDMKNHNAGPKDRNLNSVETDEYKNVNKLLLLGGNAQNVKMNGEKNP
YDHGGGGSGGNAHTEHQEHFPHKMNPYNDGGGSGACDSNLLALIHMKKNIKNGVSSSAGPKAGVNSGGANGGGANSGTAN
ELNGLRNRSYKKLLNNESIGLFNSPANKNTVNEMNLKYLEVLNSQFNFSARENRKNECDPNALNSSVMNFQNDLDKKYKN
PLVDLCDKGSVKKL
```

362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE

A0A0J9TME3 **A0A0J9TME3_PLAVI** (1078 aa)
DNA repair protein rhp54. *Plasmodium vivax Mauritania I*

```
MRKCPRRAKRSREDSPDRACITLVRATLLPILSIDKNEKTTLFHPFKSPLPGFVSDRRLYVQKTLGAKVRRTGWLNLMKN
SIPRRSDEAEASEQNKADEIKNEFVPLILYESENSKVEVDPILAQFLREHQREGVTFVFECLMNLRDDRISGCILADDMG
LGKTLQSISVLYTLLKQGIDKKPAVRRCLILCPASLINNWNDEINKWLPGRCNVTCVNDNAKEKIVSKLEGFKYDQKSTV
IICSYECFRINNDSLDKSSIDMIICDEAHRLKNDKTKTYMSIYKLAARKRLLLSGTPIQNDLSEFFALISLCNPDLFDDT
NSFRKKYANPILIGRDKDATEKEQEVASERLAELSTITNKFILRRTNNLLSKVLPVKYLINIFIKLNPIQEALYVLFLKD
KRILKNEQSTNKVNVLINIKKLEKICNHPLLLNPNDMKDVGHVSLAKLIEDAAKQHQGKRQEKAERTEKPPLEGHPQGDR
DRDRDRDRDRERERDRRRAVEMDYDKPVKKLLEECRRDTHRCYYNMSCKFQLLHFLLKTIKQNTTDKVVIVSNYTQTLDY
MEILCKENFYKFVRLDGGISIKKRHKVISDFTHSSDIFIFLLSSKSGGCGINLISSNRLILLDPDWNPANDKQALARVWR
EGQKKICYIYRLFCTGTIDEKVYQRQISKDGLSSMIVTNTNLSKDQLSDENVKKLFNYKMNTLCETHDNIECTRCTIRNC
TEKEVENFSEQLEDFEEEDVNTWAHHQNVESVPDEILAKAVKAATDYKRNDMNNFPVLKKLSDLFVTFAMSCKIEFRDDL
IKQKAQKAQKGERTCRPGAAADGLVEQDEEADYEGEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEGDEAEEEDDEDDEAEEEDAPPKRADKTSKLEYQHKLMEIMEYQRARRREKGAGEARKRSDEGEGKRDGGAKREGAA
KLEDGAKREDGTTREDGATREDAQQQAPRETPRETPRETQPGQKQDAKVSGKAKSQEGAGEEEDPASKRVTRNMSQKNLM
ELLSQDEESKVTLSMSEDPDADADASVENVSTDSSYFI
```

838 - 857:	EEEEEEEEEEEEEEEEEEEE
839 - 858:	EEEEEEEEEEEEEEEEEEEE
840 - 859:	EEEEEEEEEEEEEEEEEEEE
841 - 860:	EEEEEEEEEEEEEEEEEEEE
842 - 861:	EEEEEEEEEEEEEEEEEEEE
843 - 862:	EEEEEEEEEEEEEEEEEEEE
844 - 863:	EEEEEEEEEEEEEEEEEEEE
845 - 864:	EEEEEEEEEEEEEEEEEEEE
846 - 865:	EEEEEEEEEEEEEEEEEEEE
847 - 866:	EEEEEEEEEEEEEEEEEEEE
848 - 867:	EEEEEEEEEEEEEEEEEEEE

849 - 868:	EEEEEEEEEEEEEEEEEEEE
850 - 869:	EEEEEEEEEEEEEEEEEEEE
851 - 870:	EEEEEEEEEEEEEEEEEEEE
852 - 871:	EEEEEEEEEEEEEEEEEEEE
853 - 872:	EEEEEEEEEEEEEEEEEEEE
854 - 873:	EEEEEEEEEEEEEEEEEEEE
855 - 874:	EEEEEEEEEEEEEEEEEEEE
856 - 875:	EEEEEEEEEEEEEEEEEEEE
857 - 876:	EEEEEEEEEEEEEEEEEEEE
858 - 877:	EEEEEEEEEEEEEEEEEEEE
859 - 878:	EEEEEEEEEEEEEEEEEEEE
860 - 879:	EEEEEEEEEEEEEEEEEEEE
861 - 880:	EEEEEEEEEEEEEEEEEEEE
862 - 881:	EEEEEEEEEEEEEEEEEEEE
863 - 882:	EEEEEEEEEEEEEEEEEEEE
864 - 883:	EEEEEEEEEEEEEEEEEEEE
865 - 884:	EEEEEEEEEEEEEEEEEEEE

A0A0J9TR37 **A0A0J9TR37_PLAVI** (378 aa)
Casein kinase II subunit beta (CK II beta). *Plasmodium vivax North Korean*

```
MDEEGLSNNESSNDVVDEENLEEERGLSDASFGHREEEEGGLHGGSGEGGDCEDGLDGCDCDHGVDGGLDVEDLEGQAAD
APGEEKDAEGGGNEEEEEEEEEEEEEEEEEEEEEEEEEEDDDEDDDDEDDDDDDYDDDEYDEDDFNEATVSWIEWFCQLK
QNIFLVEVDEDFIRDEFNLIGLQTKVPHFKKLLKIILDEDDDDDDDDDEEDDYDEEDDEINRGSDELYKNKDIYEQNAAC
LYGLIHSRFILTSKGLALMREKYKSSIYGTCPSIYCDNAKLLPTAISEVPKFLSPLLYCPRCCESFYPHKNSLLNQLDGS
YFGTSFASFFALSFNIQSDKKRIYYTPQICGFTINRDIRETLYVGMNKDNSESSEEYS
```

94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE

A0A0J9TZ11 **A0A0J9TZ11_PLAVI** (8584 aa)
HECT domain-containing protein. *Plasmodium vivax North Korean*

```
MKIQIPKDDNYILMLDKISEEEKFFIHVLSTCDEKNLIDHLFPFVDWVWLKSDLIAWAPVLNRFDDLLQRYIVHNKLSRE
ETSIARGAISGGVSEGVEAGESNTDKTSERKNERPNQKNRELLGDKTPELRGDKTPELRGENPPEPFVPPDLLVEQMLRF
TYHILDNCLSKSKYNSLDHLLVLLWSFNPKISILSAQILNIYYLFIKKTKKNENKINQIVNILSALINIPVPSFLHPYIN
SDIGRINDNNYISGLVLYYLHDSSDRRYMQNVYSKIDNRYLLDLIDYELNLDTVTINVEDHEIPFTSVLPKEVNYKNAKK
ALQQAYDTIVNKYQLDEKKTFDLRHKLRIYMGLICPKYRRKLFNLRYLIISGSLSINSILYPQIIPSNTIFLQEILYLLK
YHKFIAFNTLHIIFDLLTTAIEPHLHYQVVSDILGLRLHSGLFISVFKYYLNYFLSTYTVQKDICPLHIMNESPVEMYST
NDINALYVKKIQEEKAVGTSSPSLQGGSVHTAGRNGAIIARASIYSSLSELLPNEGMEQQPPRQQQQQQSRPPPHEEAAT
HYANDHQDVPQEEGRIRPTAAQTANQMSGTDQLSGSNQFSGSNQMSPANQLNPANQLSGTNDSSLFSADAFRGEDDPAGV
IGAMPPFLNNPPIGGGISSVQNLNIFDYMSNEGDTNNEGDSTHVRGLPNVGDLPNMGDLPNVEDLPNVGNPPNVRNLNLF
DFMNNMDEVDLLGGGPADSRLSSHPRDRNRFKEETQYENYISEEVIVSNIKKCKKNGESEFIKISKKQFKDFKKKKKEVS
MMLQLLTLYHTCIMEPCPILTIAQQNTLKFFPLYLQDSYTNNLPIVHLLLRIMETLLDFTPNFYFTAKNEEELYKILLSR
FQYEIFMMSDSFYHLNREHFLRFYFEPFDYRGYDRAFVEAVGEVEAAKEVEAADEANEAEAAGGADEANEGNAEVVTAGS
AGCAAPPPQASLFSRRNAKLVRLFQTYDINERASEETLLNRFAFWWKLHIYEERVKIIKMIIKALNLALKGYSPTDTLLD
IFTNNYISVKIIKYILKYPHKFGLCLYGYILGFIYEHIYEDPTILSTLLKEGLLNILLNSIVEDNLKDETVLIYVPSLLS
LMFIHSIGKSAMRKLNYSPIYNLFHYVIKIDYFFFDRFGDIAVSIGNIINELENYGFVMRDFLSFHVKLLKKLYLEGLNL
GYWRCLDYDYVQKYVEASAKQLHHVQLKDLNIDRYKHRRDNFFLDRLSILCRCILSYMKTSWVKSFLKLNGLKFLMAYTN
LISLPPNYIHIFEYHSIYTFVMKIYLYASFKNVYNQFLYPLYNYSNFVSYVQYVSLLFRGCCYFDLGDNIVVVKRSALLA
GELGRTTPMSEAPGSVGAAGKPPQRGSKYQRTDYFAGPFIDRNQLLLCNITQLFNILYFLISAYTDAKGLYSNEEKLYDL
SELSNRKILEIFSDVLVTIESVFDFYFTLYFYQTNDSNQNMFLHLKDKVCIHEHIKRTLRNSQNKSDYLLYNLFGSSRSL
FCYSINNNLYVLNQGQGKTHIICDHDSADDYKRTDHLSGLDNEDRVYKAIYRYTFSQVLIEFNTFVHKSMKLPSDIVTFK
SKEKSKFQKYFSSSEDSLVGGKTGRKRTASNLASSRNGINAAVAVHPLCNGAAAQCSAVKEARLLSGNPFEAASSGAEKS
QLNAQSVANMYAAYRGGSCEECHVAEKNKQQGGNNDPSVGRNENDAAKSEYNDYYIEDKDIHLHTRLAYDSKYVLCESLR
SLLVVIKKFFIMINLACHTRQLKLKPTPNYIFYNVIQQKHILCIIRCLTKCMMNVPVVSKPIQENPYLAGGAARNAAGGV
NNLYSVLSDHITAEKVSYLSEPSREHPQSPGLAATACKSGAKKWPKVGTKMDFPPCEGTAEANPTKEHLPHCGSANWGAE
RDAQQKDFNLYDYAYTPFTSHHVEKIENFYPEPFYMEEILFKRYNFNFSLIEVVPNKDLHQSGGATAGVEASVRVNVAAR
RSPPEEVEEEEAHHCRDPQGDLPSRDLSKYNKSYICTSVREADGTFRVVHHNGGFNFAKFAEEGANERGEGNQASRAASR
EGGGEGTGEMSHEGNHKTNVWNNPTSSNAAPGENRRASETPKERKLSPVGISIEHYSPMKTVKYIAELINILHKLLADNK
LEFISYFYFLDLLYKVGTFDFIFNMFNYVMSVYISLLALYYRKKKEMREVKKNKQNARPNYVTYIPIHISKNFTCTNTFF
VRYVIRVMEFYADADMSSLKIYLQIVVKGISAFLDFFVNLINIGKFNLMLFCTKMLHPLTRLHNDFESLSPQGKAREAAV
EAAAEGAAANTHSGDGAAPNGKAEEVNPLLASGSVQTPNNGAGGEANLLTPHMEGPNELSESSVEAAALENSHVGAFPNS
GEAKGKKKHDAAELSKGINSVSAAKESKKGGDALPDGRNAKEESSSSTPPQSAKRASEHTFTYNNNFIFSLDYFDIVNTI
RSVKCEITNNVFMWLTYINSTSVKIGNLGKNNIYINFNNNVVYTMLRIILKFIHHSVGVEPRIIDFWAKEKCRDKRSVGG
KDKERDKDKEKDKDKDKEREREKEKDKDKDKEREREREKDAFNYPHVNILEEWGLMGFDEKTIYDCLNYSGTTDLDCTLN
YLDKAKEKEFFLNIGRDKLPGERKNGVGRRPPYYDFDYNSSDENENSTAINRRVDNIRLGVNENASEEELNDAVQVAAER
NPVDGSSTTGGGHPTDANTSPPPLTPSDAPKNGNDKEDIFHKDDKYVLEKFPFMFEILKEAKAKSTHARVYYYQTVMDPN
```

SKRNMIFYLQYYLKLLKKNLFLTYEEKNEIKQFWDEENYLLLRQLIYKYIFNMLINIIITIPFNEGGYTNLYLSFLLVDI
DKKSVKLLLDHYRKTIQDKNTNKSRIFNHQDVKIIILYYFIENISKKIKMLKNDEAFPIEPFYHCHHLFMYVNKRKNKNV
KNGDDGGGKPEKKDNKNGSKGKFAQSRSGLPSDAGGVIPILAQTAEANVGSGGAIGAVGSGRQLGSDAGRAASSTAGMAP
NVSQNVPHNVPHSAPQSIPTSGGPSGGGALGSVRNMLVSSSNNPMSSANGRGRAGNPVSEFLAEYQLNSNYDVSNHSDDN
TTTAFYPGSDIVDDKNSVTNNHKKGKEHANHPDAELANDSNDPKNCIYGTKYIKGDLDVIYESQRDMEIYSYHFCLHMLF
FTLCNIIDKYTIARNLILHIDRNILDYCIFFLHKFNGAYVKSVEANVNHFLAESISQHCFATPGSSDEQMLSNTHGGCCE
ASANDNDAGKRNQEKNKRKRKFNKIGAASRIAPISNEQQNGLTNGDPCEQGALLTGQIPPLGSAHSNSVDGAPREDANEC
AQNGSHKKYAAHLCDERDNDYVHPTCGGSTHVGDSGTAGNNCQAETPQKEQKIINHMYNKGLVINKNIKTYGMLIPYWNL
ADTDAAEVNQKTAINYSPQENEENKYVSLYSKPPCIYTPLFMCLYKIVINYSLHNFNDKSRKVVKKQKEERTNDEKCGSG
LVRNVPSGKVEKATSQSEKKNLGQSAPTSASVATVQAVQAGQTGQAGQTVQTTQAVQTMSENVRFISAEKQHNIIKICID
TLYFFKGYNAQLCMSILQIIEYLTTTYSNVIFFISYTPPNVYRNFRKVFELEERKMERMRAGGKNPLDNRGSAHGRPNAA
GENPSEELFPSREEELSRGDLHKRETTISVGNVMEPPRDRSTEGMCSPPNVTMNEQQDNGGPFEQKCTPHVDVNELILNN
ISRSGLGILLTISKQAKFKDMLIILINILIQCFTDNYVIANRIEYSLKSYFLCHGIPVKCFMRKDDLKVLEDHKFSNALG
VSLSELNEALYPFIFKNPQMYEEILSCLCFFPNLKYVKKEEASDVQQQVGDAADFLSVNGFGETVGAHSAVGLASEQTRE
KRNGGNVHTGVCNGVEVAKGAKRGKHGGKDYGKDSGKDCGKDLDQEGRSAFQSATSSGAPSGAAQLGKKKGKSARESSAQ
QGAPPDGEGSGKGGAGSDNVGCGSGNGSGGGQFYLNLLPIPEHIKSIYMLSETANSTKYLRKYFLKNNFYNFYILAVLLD
FLNLFTIIQSKTRLVKLSEKEERLQFNKRLMEIYGTHADFDAELDYKVMYPFALTADNMLFIVNLIFKTFKHLIVYLVKV
PNSFNQKIMKTFFLNDYDELVQGCKGDAQQYSDAAAFAHPFQVNTTQGREAKMGSTVLAAAGINQGTSSRSKNCADVFSS
SCGVVYPPNGNHNSCGDDLNALIKGTPEQAANPPCGDNHVAVESSSAVLKLAKPELASNTPYTYREISEFYLQNYLQYYA
LFDLSKLTFRSCLFPFLMERGSGSGSGSGSGSRERGKDRGREKEKHIEREKEKPTEREKEKPTEREKEKPTEREKELLAG
HLLSANPPNNLVFTPLLIFLFKRILPQFICLSHPSIHTTYSPKKLEEKSKCTDYHYQSLLNSNEFKNVNYVKHIANFVQL
IFDIHSSSYDVHKKVVQEIMHLLKVYSIFQKRKEQPSGKASPEWHNNVFATLIDVFSYAVSALLYKLVNEEQNIKIENSH
LLEEKHLLGSGKYISKVLEFAQKGEEEQEAGNGGGGPNRDDDSDDCGDCGAGGSGSGGNHRGNASGGNAGGGNASGGNPS
GGNAGGGNHNRGNNNGGNHNGGSNNGGNHNGGNHNGGGGGGSGGDGGGGGEDHDEEEKAEKKDDGNKAFTYSREQLALFR
MALCSLLNKLDYTKEDFANTATSIIRCLSVLTSAPILGYPIKTKNNKLYMLKLNKLNERKNKKIKKIKRNKRRKNLSCVT
FLNPSYVRFRSDSSNNNSAGSDIPYSVDSDVSYEEHFVFDNDDSNEEDDLRYEYEEEMDDDYVDMVDGEDTEEDADDADD
AEDADDADDADDADDADDDDDEADDEVDDEVDDEVDDEVDDEADDEVDDEADDEADDDGEEDAGDEADAAAHGEGEDDEV
EEADDVDAVGEAEDRPRRRRRRGRRRRRRRRRRRNAELHNEREGHSEQRRNNNGSSNNPLSNAHLDTDENNENSPNEGAN
ETEGDYTNEEVEEEEEEEEEEEEEEEEEEEEEEEEEDIEEDEDVEEDVEEEDEDVEEEEDDDDDMEDDDDDMEDDDDMEDDE
EDDDEAMEEEEEYDEIDMEEEEDGGGRNGNEHDANRGLHVHAYLVQDRNVIDEDNLYDHSNNLLLPHEVDENEENMSHMG
DNNNNIVSNLELGSDSSNDMDEGQGVHRIREIDETEDYDEDDEDDDEDDEDDDDDDDDDDDDDDDDDDDDDDDDDDDDE
EEEEIDEDEDEEEINGNNGAFRISQADDNVRAANNNADLIDTEMNVNNSLLTCNENQHEILDILMEEDGVYNINDDIDEY
NDDYMDEGENNNRAASGTLNVGGAQLGGDDHVENAQLGGDNNGGSSSQNGSGGVDKNAHPDGAHRGDDKMGSGEAIQGDL
IGTTPDGISNRLNIPHADSPSEVKKGACGMNGSSAANMANVEDTADYPSGMTADAEVSTQNKGVCNELQNELATNGIHVG
MNNGEDQNGAYNCIQGGNFNPLVSSDNVNSLVSSDNVNPFVNARSDPGLPVPASDTPGETLFPPHMNQGTHKSVNAVANG
NVIKSEMNSVAAINQQDGAGGAEGGADNKLAARSTAAAITKQEENKKGGSPTGANASIAESGKKGESGGAFDKMQSPSAE
ATTSRTSVNENDINLIDLYYHFYNSNNRDVNTLLGENNSILYLNETGTIHPSAVKSSASGLPSGATADQGDGAGAIGVDA
PPSGFPTNGSLSNGVPTNGSLSNGVPTSGVSPNGAPPSVVPTNETSPMGLPPVEAAPMELIDREQGTLLSSRMENYGPVN
YTPTSTNIFALMDNLCSNLLTLNRRRNERLNSMLGTSVHIPDGVRNNSINIPMGINEDFNISGSISNENAAYDPTNMLHE
SGCTYYHLNLDRVNSFYSPPMFNTSPSMRSNNVSVRSINQTNHSLRNLFNIIRNYNISDNNINYTRNSSPTLNDLGRRGE
GSAEAVSGSNSGVVSGAISGAICGANNGSNVMSAENGEAPVGDAFSERGSNDAPAEMNTLANKIKSGNTIKEKNEGVKEE
KFCLADTVLDNDKKLKSSICNMMYNRLCKAIPKVHINLPIENLLEEKKKIIQSMRRKEEEKKELGSKKEAQRGKAGKQEQ
AKRGGPQKGEAPLKGEEVENGVENDAEGHAEGPVEGPVEGHTEGHTEGEEKPRDNGAAPPEADSTPSQNAPAEIAPSGAA
DPPFEAVLYDGNSSPDVPSSDIMGAEQSNAADPNQAAEQNDHPGESIPNEEDYKNINYEEIFDNVLRIESLLIICCALGI
NEGQFFQLLNVDRSFLIELPNNLIDEIIVQHLKNITLAGVNELAQENTQNGKKISIELYKKYLKFQEFSRTHPGGQQAGA
HNETADALTDQQNGSGSDPNASAIATAHVEGNAAGNNGSGALSDQMGEAVVETVQGGANNGDATVEGNGLPVENAANVVS
AASVENAANVESAANMESATNVESAPREEAPPQGETTAHPENPAKSEGEKNLLIYNSIKKSYLEALPSSVRAEIKKRIIG
NRSQRNETQDETNIAFIDSLTPELRRDVLSSASLRFIRTLTEEMIEEARNLRFVVLNSRSNLLTGSNRPRQNAVANAVSE
GDSADASANFRGSSSGNASGGGGISSGPNASGMNASEINASRIGASETNAVGVSEGANRSNNNVSGSGASSANGQTDSAH
VSSARLNTIRNDIQERITNTVLRNAVSNLNNMSSSENSNSNSNSNSNSSSNNNVPVISSGSSRHARNNRTLFNVLSRANA
NNRRRLNASLRNPLTTGSQRNNFIRITYNENNNPIIMINTGHENYDSLTVSRFLDHFLGGRSFNGAISNLPLSDSGTISA
SFSLIPTNPGGEGGHGGASSGNLNGGMSGHSGSRGHGGMGNHAVSRSHGGMSNHVVMSNHVGMSTHGGNNAGSSGNAGGS
GHLNASHRSGNNNTGGGSANNGMNETRLFINQENRLNYADPNFSLFTDDKFAEKEDDITLSRYLKNLFPTKNKADAESSK
GNALYVCLEEPVSSQALIDICRLLFLKKEINKKIMFTLFCNLTCSYQKTKICALQLFMSILWSASVDLHGKNNAPRVVAL
RQAVNFPPKMLYHNVNKKNYGLFSDNYFTTAYVSAERVLEQVQSLLITIPHITSFFSMLLVHPALFVPKDIIEHKVVGQK
RGGNGESRKGPSGGAFPEEGSPEGAHSLAGKKEEQVVSQQPVNPSQSNANKINDDEAAILQYELKRKRPKMDQKNSPHAL
ALSAKMDHAKQGDKSKNEYPINILFKLLNSFIYLTSKKLMSHLLSVIFNLLINCGKKWHTYSNFTKWVYTENLEELLDVE
NANNEEEVGAKKSEDVSNNDASNNNEGAALNNTSDSRSGRSNNGNKRNTTTGKGKKQRQHSSNLREFYHSSSKINRELLM
SIRNVKQNEPDSSSSGSRKDSTKRPFYLLEVISADALSNLSKLICNYKTNFLWINSNGSGGNSNANTPANSNNLEQVHKQ
DISSLTQIVVLFFSHYKLKKWHIQTLKYHTHVLIRRIIYDLKKIIQSIHNRTFNVYAVDHSDSLEQKLIAFYRVITILFN
APSLIDNLINRSEVSRNSSAEEISTPPSKSVLDFSAGSTTAPHNAGTISTGDAAPGGKEANLGDIPAGGGATRTDQAVHH
AMEKKSADEETKFDICADFFLSINIDELWEEFNKAMQVINNALIDKNYKFTYNNRSNMQFPAEEGKAEQHDGGAHLPSHI
KGESNVVEGGAVPGAPTPPCTNGKNDRGEAPLGGEISQSFYELDSSSSETSEQGSPNSVTAGSPQQEEEPPLPRSGANAA
ENANSNPVEEKKKDNEDDPPPTILNYLLPLMEAYLFIEEVILVSQYKLKKFKDLEKKVANLNIESIKINEKLAYDDSPFY
ISIYHKKEKRSASDSNTGGDLQSGKFNTGSRVSSNVSNKMKRKKELSALSDEELQKEGQHKQPKKEDVSMAHLAEADASA
AGFKQLGNDGGEKGQQGAGGGGGDGDGDGLISKREEMTGYLASDAEEGKKEGVVEPKKSAKPGESPIGERNRGSSSPNGD
HTEEAAQQRGGEVGPYADEYEGEDAEEEMLMRAFGDANEDGNNGDNGSRYDRHDRYERRDLDDDEYIQIKLEDSAGSIN
GRHKKLIKFVYINRRVINSLIKQTPILLHHNFKSLIKLTSSCINFENKRHYLRKKLKHLKSGVRSEPIRLNIRREKVFTD
SYYQLRNKSGNDLKGKLVVTFKNEEGVDAGGLTREWYSILAKEIFNPNYALFCREGKKSEFNHPNPLSYINPDHLHFFKF
VGKFIAKAIYDGQVIDAYFCRSFYKHMLGRKILPADAESVDPEFYNSLIKIAEYKLEDLNLEINFSTEIDEFGKTKVIDL
IPNGRNIPVTDENKHKYIELLCEMKVTNSIKEQLEAFMDGFKELIQPKLISIFDDKELELLISGIPTIDLNDLKENVEYH
NYSPNSIQIIWLWDVLQEFDENKKASFLQFVTGTSRVPLGGFKNLMGMRGAQKMIIYRAYGEDRLPTAHTCFNQLDLPEY
SSKELLRSKLIRAIMEGKEGFGFI

5052 - 5071:	EEEEEEEEEEEEEEEEEEEE
5053 - 5072:	EEEEEEEEEEEEEEEEEEEE
5054 - 5073:	EEEEEEEEEEEEEEEEEEEE

A0A0J9TZ34 **A0A0J9TZ34_PLAVI** (1646 aa)
Uncharacterized protein. *Plasmodium vivax North Korean*

MPSKSSPKKDVHLGELPSEGMPSKGVPSKGVPSEGVHPGVHRGMHREAYAAQGEMPLNQWGGDSEGGPTNRTRTNLVDAL
QMIKTNEVTLLESLNDASCEGVKDRQVGLAQGGERPNGRALLNTIEEESNPIEKPNPAGDLYKHILSLYRRKHPEGQLPC
EVTSLQMMGGEIHAEDTRVISRRDELEDATYGGAERDEAMSGIHSWGDYIVFGRGEEPQGHVETAFCLGRSDANCFARAA
GGEDSSDGERLPGGDTPPGEYCLRGAPPVGLPNKGEDATLNHLHKRECSFGPSERSPPPDGYDRRGCHCIGGGAPHVESP
LLKSPLLKGGGLYYGVKFDGEEEDEMGAAPKGGCFPPLANKCGGCSSSGALPGDCPEGGREKRFALNQLSSCEDKQVVYA
QTEATQMRLNLSGVPAGPKQPQQSQPRQPQPPADGTALANAASCLHRRAKDPLYEDPSVGGSCKGESFLLGSRASQRGSA
DGDPSKNRLNFPPFEGIHMSDANVMRRKQENGKMRLRGDLNEESVAGELMRLREKCFQNERLNHLYIGEQPFCRLRRDGG
SNEYPCGESKGGGPNAEGALDLQDPPKLIRCENLHWGESTLGRDPHNVQRDKTDRQHLIRVEKMFEEEAVGAVGRSERGG
APQLMLCDDEQGKPTWERPTWGEANLVTPPFPRSDTLKRHPFGGGRLHIPNEEATAGKRNTCPSVVTPVVPRQDGLLPRV
ASNRANQSPPQWADIPTDQKISSAPMGRDLPGGSRMGKVPYEQISHCTEEERAVLVDPFFYNCRGENPWECQWKKDTFAD
SRMGMERNELTHAERLFASPYHHEGEGTREGPGGGSARTEGDLCPSPRGRNHGAIKGCSPGGQIHTSCSDPHREKKIPRE
AYARGAANVGEARNALKDTNVNLLNCFKLSFERGRFAPLGGGGCTGVPTVGRTPESRTPPLSGFPLSGFPLSGFPLREAS
PAVSHKGNLFESVDAFFYNFKKSGASLRGESRQVEEHVGAKVVANVRAKVVANDRANDRENDRANTHPDCQSNSHVRASS

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SGVAQLANPSGSVTTTTTTTTTTTTTMGAASAASAANVVNVVNVVNAANVATASNATTTNCTTRSEPGKEGGEEEEKEKEK
EKEKENEEEEEEEEEEEEEEEEEEEEEEEEEEEEENGEKLDEQKVDLLDEQKDDLLDEQKGGEELDDLLDDLPDDGGEGMK
GREPPPWRREKTILTIQWNIKKISLLCSSDSHFVVSPEYKTETLINEFFILLNINKDMHVHLLGENSFGLLFSYTGFCDI
LFSVTCGVYQKKFCAYDCSTLPWFGFNNWGILKNCMQNDSISITVDIHEIRRKDSLKEVFLSNVILSMRSSNGSFHFKEG
ASPVSPSAVVEAEEEKKMEAPSPTIATASATTAATTSPLDLGRHRRSAKCFFPQSAPATSDSCSRFAPPTVKRRHPGSVH
MVGSKHMAGNMHMAGSMHFAGTRANAPQWETKQTNASSWNGKVAKQQMIRANRETNPTQGNKLHKGIKKNLYAHNLIDVS
SPFEEHPGGNFIQLSQGLQEGTLAKCTSGSSAHRAAPCAVSGFANQPSVQQEGTPQMKKEGPFGRDPPRRGPTSVKTFIG
ALPNDALPNEALPNEELPTEELPSREGKPRGGGATLEDRFSENGTP
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1127 - 1146:	EEEEEEEEEEEEEEEEEEEE
1128 - 1147:	EEEEEEEEEEEEEEEEEEEE
1129 - 1148:	EEEEEEEEEEEEEEEEEEEE
1130 - 1149:	EEEEEEEEEEEEEEEEEEEE
1131 - 1150:	EEEEEEEEEEEEEEEEEEEE
1132 - 1151:	EEEEEEEEEEEEEEEEEEEE
1133 - 1152:	EEEEEEEEEEEEEEEEEEEE
1134 - 1153:	EEEEEEEEEEEEEEEEEEEE
1135 - 1154:	EEEEEEEEEEEEEEEEEEEE

A0A0J9TZY6 **A0A0J9TZY6_PLAVI** (1342 aa)
Uncharacterized protein. *Plasmodium vivax North Korean*

```
MKPKCSHKPSLASAEESKNEEIDREYYSCIKNCATDLQNLSLNFFPSINTYTCIPKINAINSITFHPCISSRDYFNNTYS
FKPLFTHHFFSDSEQVGEPGEPSAHEREHPTASPLPPLYFPPPPPPPPPPPPLPPPPPPLQVIGFDSLKIDFYYTCDNYE
VFMKLSGSISDQYENSNYIMLMLLQNLYITTPYPGGFIETEEEFLRILRRNEGVEGVEVVGPLERAGPVERNAQGRAKEK
TKASGAKQSAALTQEQIYKPPGFIIYEKRLSDDIYLQIRKCGFSSKYFKLESVSNADEEEEEEEEEEEEEEEEEEEEEEG
EKPGEKPGEKLEANLGGTDGSVYQNGFADMVQNENTPSKDQPCSPPKTDRSKHKRGSSVKETKSEHRKSSKGGEINSSCI
NQNDNHNIKRGLPNEPCEDDSKGEGNEAATPKYVIHDDNCGSSTTSNEFNKEILRKKRDSKTSLVGSCTRSNEESLSSKE
KIKKEKKTKEPPTHPVVDGADCGNDNSPVELKKAKKNFTKHVTERDMSKLYRQYLRVVRAKRRNSLAARGDSLKEKTPAR
RKLERQKCSGGSARGGAAVPVEENAAGNAAETAAETVAIPAAIPAAVPPAVPASIPAAVPPEMGAASESAAPLDSSSPKR
GSPPKRGGSPKKACSPKRGSSPKKGGSPNQRASPGKGGSANQAVEPPQGNAPHEKGTNSRRKKNVREELPGAKYDYTVKK
NFELLHRKVEWFYHWFIESASNIEYDYRWSVILPYIVFKHDEEKKFTENNFIENLNVQLLKNRSANVSVLPSVKLEAAAP
PSVAVSNEEVSPPMGKDVETGNKKKHKRGATAAVREKKQVKKRKKGQGGAAGEQTLECVGDRVGDRVGECFPEAANDLQS
GREQPEGRVKKESSNKRENTQESHHDGHTEAVFDQNEYVLTSEIVIKAIENTLKDVRSQDEEEYYAFHKNHDVIYLYSDL
EKGGGEAATKGEAAARGAVQNTQAITDVKGERKTTGRKGSAAEGGKEIPLKEEEPVEDVNEQDGEKKRKKSKNKNEAKSE
GKSEGKNEAQNEGTSEAKSETHNEGKHKSKDKRRDKQKSKAKRDAKGEDKKQSLYYFYLFGLATTYTFFTFQFDRNRISQ
FLIFPPMQSKGLGMKVLEKIYHLSIVNSNVKEITVEDPAVSFTQLRDIITIKMCIDLRILSPTILYPSDYLKTKNIDKEY
ADLDKRKFMKVCKETHKQITRMIETLLLAGVLPHPAPSYADIGEDKASGVRKKEKKNESPDSLNSMEHFESSDLCKDVRI
KIKKRIKNDYIGNLINKNMNCMASDVFQDYVMGRESQAKHHSLAVKEELYKLWKKQCKVYYR
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298 - 317:	EEEEEEEEEEEEEEEEEEEE
299 - 318:	EEEEEEEEEEEEEEEEEEEE
300 - 319:	EEEEEEEEEEEEEEEEEEEE

A0A0J9U247 **A0A0J9U247_PLAVI** (2072 aa)
Uncharacterized protein. *Plasmodium vivax North Korean*

```
MESYIRESKKLTFKGSKGKKLLRYVDISLNNKALHDSHIVELVNILKKYIKVVYNHFYCLNIDLSENYITCTGLKTLLKF
ILNYHDNIGVHILKLYKNNIKDDGVSLIKQLVYVQKIPMEELHLSHNFVQDDTCKELLLSFVQAKKENSYVYPRYEKYQS
HYKHLQIPVWIRLEYNCIQNPKEILKEVEEFAKKKRGYKSNLIICAALKSDKRCCPYKCLNATVRNTPIMHVYMFIHQKD
SPAYAISTNGKVGKEERKREFSSPSEVVDAGRMHASAHLQHKAQPEGVERQDGEAALPAKGEARSGAARSAAKSAAKGAA
KGAAKGAAKSGKDKKTAVRKGGANSGKRLSRGSLPHDVSADEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDDDD
DDDDDDDDDDDDDYSEEEEEDDDDEEDDEDEDDDDDDDDDNDDDDNDYRHKRGKPLKGKEKNGQLPDAAPLYASKNGAAI
GAQTNGRDEEDYDEEAEEGEESPNAADPAKKKKGKKKKKKKKKKKKEQVEVSPLEGGCEEAKGSGERGEEGSAVGGESGL
GDGSGDESGDDNDNDNDNADRDDCDRRDHRYPREDLFRAVGGDPLRLDGGGEEDALPPELCPPRQDRLNLTSDAASSLPL
YIILDCTAVLDMKELWKDSSFLPFSFPGLLYLYNNKLLRSNAEGASGGRGVNGVSQNDAFICLMCSYVANELKLVCQKSE
IIRQKMVNLKLNIWDKLSELGIIEFLSVPKDFKEKKKNFLNSSFLTEAQIKLANEYYDISQETLQMIQFSILWSTYIYKI
GNKEIIIKNAAKEINKGGMKKSKKTIFTEVLYLTSSPNIYSFFEHLYGEDMNMILPLCVTVNQINKYIQDEHSCVVELLS
SGRPVGDKGGNFLLDKAFFKAFIKDKCARYLPDGEEGVASIGGATNGGTTNGGTTNGLPSNGGIANGGTSNGGIANGGSS
KKKKKKGAPPKRSADKLKDGFPSAHDNGTPSMSSLSAATPNCTSRSDKLSPGGKRSDDECVRGSLPIGGTHINTNAYDYL
DIKSVKSFSNENISKLCQLESSIQGGPFGMVGINGGGRMAAPMGGDRHSHYNDPSGGANKVKTNVGGRASGEETHKGAEK
GNAAVGMYASPIDANNGGNGFGMMMVTPPSGSAKENPQGGKENKGSSLYSMLVNAFNGKKKGAQKGAERGADRATDRGVA
SGQDKSGNNMFMGAGPNQSVRDSVDPLSSHAGGENSQNEGGHGNNAAAAAAVATRPQLNMSNGKVKSTGADLLDQLMHGG
SESAPSQGKAASGLGANGGAATSPQMGIPSNDKATYLGSNNNSGSNHSPAHSLFAFNSSMLKGVAPSGKGDLSFQSQMGT
EGGGSGKSGSGIGAGLLGGVNFPMNGAGMGTLANRTTQGNSKQLQKNAVETIIGSDLLNVNEVELNNFMGSIPKSFNDSL
SMYLDSSNRNDSCYDGIARGENMMPFFNHSLLKGDAEQDLANLAARAEGHSRAEDHSRGADHSRVTDHTRVADHNRVTDH
NRVTDHNRVTDHTRLNEMKNVFELYKVDILNTSLLLEEMILNQNVCKYIPSELYNKILRCYERLDCLLAGLNRVGSLSGL
SGLSGVSGMSGIGGMSGIGGIGGIDAIGGMNQDILCEDFKSYWDYAFSKNESSPLALLTSGGGSGIGGGGGAAHQDFTDG
AGNISGNKSGNASNAMFYNTVSGNRGSKSALKSSMLNASSHSANGGIGGGSGPLLASHLNSQNNGAVTPKKSRKKPPMNV
SMGSGNNVELGINSMKNNSSQKKFMGGLSDGLDNTGFMNNSPGGNLSGSRNSQMGRNANYGLGQSIPPNRSGNGNQAGAR
NSGSGSNNAKSKDMKNHNAGPKDRNLNSVETDEYKNVNKLLLLGGNAQNVKMNGEKNPYDHGGGGSGGNAHTEHQEHFPH
KMNPYNDGGGSGACDSNLLALIHMKKNIKNGVSSSAGPKAGVNSGGANGGGANSGTANELNGLRNRSYKKLLNNESIGLF
NSPANKNTVNEMNLKYLEVLNSQFNFSARENRKNECDPNALNSSVMNFQNDLDKKYKNPLVDLCDKGSVKKL
```

362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE

366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE

A0A0J9U363 **A0A0J9U363_PLAVI** (1066 aa)
DNA repair protein rhp54. *Plasmodium vivax North Korean*

```
MRKCPGRAKRSREDSPDRACITLVRATLLPILSIDKNEKTTLFHPFKSPLPGFVSDRRLYVQKTLGAKVRRTGWLNLMKN
SIPRRSDEAEASEQNKADEIKNEFVPLILYESENSKVEVDPILAQFLREHQREGVTFVFECLMNLRDDRISGCILADDMG
LGKTLQSISVLYTLLKQGIDKKPAVRRCLILCPASLINNWNDEINKWLPGRCNVTCVNDNAKEKIVSKLEGFKYDQKSTV
IICSYECFRINNDSLDKSSIDMIICDEAHRLKNDKTKTYMSIYKLAARKRLLLSGTPIQNDLSEFFALISLCNPDLFDDT
NSFRKKYANPILIGRDKDATEKEQEVASERLAELSTITNKFILRRTNNLLSKVLPVKYLINIFIKLNPIQEALYVLFLKD
KRILKNEQSTNKVNVLINIKKLEKICNHPLLLNPNDMKDVGHVSLAKLIEDAAKQHQGKRQAKQEKAERTEKPPLEGHPQ
GDRDRDRDRERDRDRRRAVEMDYDKPVKKLLEECRRDTHRCYYNMSCKFQLLHFLLKTIKQNTTDKVVIVSNYTQTLDYM
EILCKENFYKFVRLDGGISIKKRHKVISDFTHSSDIFIFLLSSKSGGCGINLISSNRLILLDPDWNPANDKQALARVWRE
GQKKICYIYRLFCTGTIDEKVYQRQISKDGLSSMIVTNTNLSKDQLSDENVKKLFNYKMNTLCETHDNIECTRCTIRNCT
EKEVENFSEQLEDFEEEDVNTWAHHQNVESVPDEILAKAVKAATDYKRNDMNNFPVLKKLSDLFVTFAMSCKIEFRDDLI
KQKAQKAQKGERTCRPGAAADGPVEQDEEADYEGEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEDDEDDEAEEEDAPPKRADKTSKLEYQHKLMEIMEYQRARRREKGAGEARKRSDEGEGKRDGGAKREGAAKLEDGA
KREDGATREDAQQQAPRETPRETPRETQPGQKQDAKVSGKAKSQEGAGEEEDPASKRVTRNMSQKNLMELLSQDEESKVT
LSMSEDPDADADASVENVSTDSSYFI
```

837 - 856:	EEEEEEEEEEEEEEEEEEEE
838 - 857:	EEEEEEEEEEEEEEEEEEEE
839 - 858:	EEEEEEEEEEEEEEEEEEEE
840 - 859:	EEEEEEEEEEEEEEEEEEEE
841 - 860:	EEEEEEEEEEEEEEEEEEEE
842 - 861:	EEEEEEEEEEEEEEEEEEEE
843 - 862:	EEEEEEEEEEEEEEEEEEEE
844 - 863:	EEEEEEEEEEEEEEEEEEEE
845 - 864:	EEEEEEEEEEEEEEEEEEEE
846 - 865:	EEEEEEEEEEEEEEEEEEEE
847 - 866:	EEEEEEEEEEEEEEEEEEEE
848 - 867:	EEEEEEEEEEEEEEEEEEEE
849 - 868:	EEEEEEEEEEEEEEEEEEEE
850 - 869:	EEEEEEEEEEEEEEEEEEEE
851 - 870:	EEEEEEEEEEEEEEEEEEEE
852 - 871:	EEEEEEEEEEEEEEEEEEEE
853 - 872:	EEEEEEEEEEEEEEEEEEEE
854 - 873:	EEEEEEEEEEEEEEEEEEEE
855 - 874:	EEEEEEEEEEEEEEEEEEEE
856 - 875:	EEEEEEEEEEEEEEEEEEEE
857 - 876:	EEEEEEEEEEEEEEEEEEEE
858 - 877:	EEEEEEEEEEEEEEEEEEEE
859 - 878:	EEEEEEEEEEEEEEEEEEEE
860 - 879:	EEEEEEEEEEEEEEEEEEEE
861 - 880:	EEEEEEEEEEEEEEEEEEEE
862 - 881:	EEEEEEEEEEEEEEEEEEEE
863 - 882:	EEEEEEEEEEEEEEEEEEEE
864 - 883:	EEEEEEEEEEEEEEEEEEEE
865 - 884:	EEEEEEEEEEEEEEEEEEEE
866 - 885:	EEEEEEEEEEEEEEEEEEEE

A0A0J9U434 **A0A0J9U434_PLAVI** (988 aa)
RNase NYN domain-containing protein. *Plasmodium vivax North Korean*

```
MKKKKKTSKAEAKSPAEGELQISEGKLQISEGKLQISEGWRQVSQGKRQINEGKQQISEGKRQINEGKRQISEGKRKIIE
AKQSRGGLDSAAGKGQPADGRDNVAGKGQPSDGRDNVAGKGQLAGGKNDRRDKSPQLKTGVKADCLSVGTSKGENRNSKK
RDDVGGNVLSAANVERSSRVGAEQKMGERPEGEAKGEAHEETNEESHEEAKGLIFPSDIKLIYGSITTTDREKTPNVKKK
MTALLSKNLYDVVVLYYEMHFYNNIDSFQVDVNVYEIYNDLICLIDELYSMYIIDSEKKQSCYPYEDVAERYLSKELSGG
WGERTQEELLQEYYILRGDRNTLFINFKLMKMVYLSAVFDLEFFGDVCQESVFLPDGGSGVGWGSGVDGGSGIDGGSGVD
GLGCVDRVDYVDCVECVSRVRGCSCGADVCRVNCLSGVAPARTGDRRAGPPGRAVDRAVEAPRNDNRGDKKKSNKRKGIS
KRADRRSDRREIPSPVLKSEVLRYRERKSAAAAAEEAAVGQEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEVFPVE
DATPFEEPPPVKEVFPFEEAPPFEEAYIREDQKLCYRILCDEQPYKALLIKDELNLSSSDDGEGYRGRARTPVKEVPALR
ASSASRGAARNAAAALSVESSASLANLAVAPGVAVSPSLAVSPSTAALPNIATSAAESHQTSSENDRDSIAQGRHSRVYT
KSKWNQGILSYASQHEKSVSIPKDILNITSLLSTPILSMSNIKSLNQVNFSYGYSKTKKDLYNYCYAYLLSIHNGYDVIP
MEGYKFRPIIIDGANVSAKVIHKHISNVLDTDMSTIYDCFLLHEAYVFFKRKKVDDIIIVLNPVTKKGEEYFLGNKKVCN
YSYLENLIKQNAILICNEKYYHSYKGDVVKRRTYDDVLILELASHRNGCVISNDNYTDIEADTACEEIKHVISHYVVKHH
YDKQNGFGLDMTKKPLKFVLNSLFQKIN
```

528 - 547:	EEEEEEEEEEEEEEEEEEEE
529 - 548:	EEEEEEEEEEEEEEEEEEEE
530 - 549:	EEEEEEEEEEEEEEEEEEEE
531 - 550:	EEEEEEEEEEEEEEEEEEEE
532 - 551:	EEEEEEEEEEEEEEEEEEEE
533 - 552:	EEEEEEEEEEEEEEEEEEEE
534 - 553:	EEEEEEEEEEEEEEEEEEEE
535 - 554:	EEEEEEEEEEEEEEEEEEEE
536 - 555:	EEEEEEEEEEEEEEEEEEEE

A0A0J9VBR3 **A0A0J9VBR3_PLAVI** (351 aa)
Uncharacterized protein. *Plasmodium vivax Brazil I*

```
MNLSSPLLALPEEGKKRRTKLIRLRNGHYRRIVDISNTDERKLIPSMCRCACVTPRKDEVENEGKWEDAKKAKSSQEYDE
TSDYVEPEKKESYMLAVNEEDQTEDMYSKTISFTSITPTSIRSEEPEPRRKLSLLDVKEEEEEEEEEEEKEKEEEEEEEE
EEEEEEEEEEEEEEDEIESTAEEKEEEKKQVPPEGKKLIEPSKTLMRGTKTNIYFLSNKEMVQTLMCYNYNCNAVVFEKD
TFLRYLYMKSISNIILNERMIDELCKQEDLKYVLTSNAIVLESTDFLKPLIIEFESSISKRVFVRHLKHNARKEIDMKKY
HDYMGELNANEKIRLMKIERFHSFNKMIQCN
```

153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE

A0A0J9VEQ7 **A0A0J9VEQ7_PLAVI** (584 aa)
Uncharacterized protein. *Plasmodium vivax Brazil I*

```
MEDTLLKHGIVDFGGNKNALELWKKYATEEAQRESAKRREAKRGDTWLNLCGQRVHHWRDPNCFPECQSDELPPNDGRQC
GQGEEGKNDTLMSEKNKCRKDSPEKLVPPPERGKKKKKEEEEEEEEEEEEEEEEEEEEEEEEEEKEKALLPRERKTYVEGF
EKLLEKLNEDTEQNFKKHQNDQKGETPAQCIVTYKNFECRNADVTYKEDADFFRFFYSSVCLIKENKTLIPRGNYLYELI
HPQTSSSFPVPNKLNDYLVKLYINNKWRLVFVHLTGLPQNGRNKFSSCHSLDETELWPHILLDALLTCFEAFHLPDYHFY
LLEMLTGLKCINKPCDFIPFGDHLRAQKCFFIPCAVLFGQGSDTSGERSSVNLCDPADVAGSPPCLHEEQSANLCVVPKS
SPPHEDHPPGRFFFLICSVEKGHIKIKCENVKPRHCTPYPDYQQSVLKAKKNVLLKGYAYINDRGNIRIKDTELVPVSNL
TPPNGSPQGGDEADQGEDKNGSTHNMTREPQTDSCNDAYGGRCDITVNEGNAQQVLQLIRRNLPDEKKSTKRHKPVSEES
DGRLHRMGTSKLAKKVTPTLFPFR
```

119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE

A0A0J9VP73 **A0A0J9VP73_PLAVI** (1005 aa)
RNase NYN domain-containing protein. *Plasmodium vivax Brazil I*

```
MKKKKKTSKAEAKSPAEGELQISEGKLQISEGWRQVSQGKRKINEGKQQISEGKRQINEGKRQISEGKRKIIEAKQSRGG
LDSAAGKGQPADGRDNVAGKGQPSDGRDNVAGKGQLAGGKNDRRDKSPQLKTGVKADCLSVGTSKGENRNSKKRDDVGGN
VLSAANVERSSRVGAEQKMGERPEGEAKGEAHEETNEESHEEAKGLIFPSDIKLIYGSITTTDREKNPNVKKKMTALLSK
NLYDVVVLYYEMHFYNNIDSFQVDVNVYEIYNDLICLIDELYSMYIIDSEKKQSCYPYEDVAERYLSKELSGGWGERTQE
ELLQEYYILRGDRNTLFINFKLMKMVYLSAVFDLEFFGDVCQESVFLPDGGSGVGWGSGVDGGSGVGWGSGVGWGSGIDG
GSGVDGLGCVDRVDYVDCVECVSRVRGCSCGADVCRVNCLSGVAPARTGDRRAGPPGRAVDRAVEAPRNDNRGDKKKSNK
RKGISKRADRRSDRREIPSPVLKSEVLRYRERKSAAAAAEEAAVGQEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEVFPVEDATPFEEPPPVKEVFPFEEAPPFEEAYIREDQKLCYRILCDEQPYKALLIKDELNLSSSDDGEGYRGRA
RTPVKEVPALRASSASRGAARNAAAALSVESSASLANLAVAPGLAVSPGVAVSPSLAVSPSTAALPNIATSAAESHQTSS
ENDRDSISQGRHSRVYTKSKWNQGILSYASQHEKSVSIPKDILNITSLLSTPILSMSNIKSLNQVNFSYGYSKTKKDLYN
YCYAYLLSIHNGYDVIPMEGYKFRPIIIDGANVSAKVIHKHISNVLDTDMSTIYDCFLLHEAYVFFKRKKVDDIIIVLNP
VTKKGEEYFLGNKKVCNYSYLENLIKQNAILICNEKYYHSYKGDVVKRRTYDDVLILELASHRNGCVISNDNYTDIEADT
```

ACEEIKHVISHYVVKHHYDKQNGFGLDMTKKPLKFVLNSLFQKIN

533 - 552:	EEEEEEEEEEEEEEEEEEEE
534 - 553:	EEEEEEEEEEEEEEEEEEEE
535 - 554:	EEEEEEEEEEEEEEEEEEEE
536 - 555:	EEEEEEEEEEEEEEEEEEEE
537 - 556:	EEEEEEEEEEEEEEEEEEEE
538 - 557:	EEEEEEEEEEEEEEEEEEEE
539 - 558:	EEEEEEEEEEEEEEEEEEEE
540 - 559:	EEEEEEEEEEEEEEEEEEEE
541 - 560:	EEEEEEEEEEEEEEEEEEEE
542 - 561:	EEEEEEEEEEEEEEEEEEEE
543 - 562:	EEEEEEEEEEEEEEEEEEEE
544 - 563:	EEEEEEEEEEEEEEEEEEEE
545 - 564:	EEEEEEEEEEEEEEEEEEEE
546 - 565:	EEEEEEEEEEEEEEEEEEEE
547 - 566:	EEEEEEEEEEEEEEEEEEEE

A0A0K0D5S5 **A0A0K0D5S5_ANGCA** (121 aa)
Uncharacterized protein. *Angiostrongylus cantonensis (Rat lungworm)*

MNNFRIEEYEAALKEWEESKPPGSATSADPFGHYKKKFEERESSRQSEIDNQSVKASGTMDEDQDVEDNEHVALANGKLE
EEDAEKDREDEEAEEEEEEEEEEEEEEEEEEEEKDEEEEEE

94 - 113:	EEEEEEEEEEEEEEEEEEEE

A0A0K0DBJ8 **A0A0K0DBJ8_ANGCA** (129 aa)
Uncharacterized protein. *Angiostrongylus cantonensis (Rat lungworm)*

MPVLAGRDSLYVRKEAELLKSQWKSSDETRFVMGSEEEEEEEEEEEEEEEEEEEEEEEEEEEKEEEEEKEEEEEKEEEEE
KEEEEEEEEEEEEEEEEKKRKKRKNRKRRKRRKNKKKKKKEDKKRLRSV

36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE

A0A0K0DJR5 **A0A0K0DJR5_ANGCA** (74 aa)
Uncharacterized protein. *Angiostrongylus cantonensis (Rat lungworm)*

MLKTKGENANEMRIPAINNGNNGTIAFAFVFMKRKKKNAVSNEKKEEKEEEEEEEEEEEEEEEEEEEEEEKK

49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE

A0A0K8LNW7 **A0A0K8LNW7_9EURO** (783 aa)
Uncharacterized NOC2 family protein C1142.04. *Aspergillus udagawae*

MAGSQKKSTKKFEKKHLKDVLERRKANAKIKQRMHLKEKRKADNARARPENGDVEEESPEERKKQNAFAEMNVDDFFAGG
FEIADADTDKGKKARKKDVTPKIGKRKRSEEQKEEDEEVSSAASSEGEEDGGVSDDDAESQASSAPDDFEAHKDQLQALK
DRDPEFYKYLKENDSELLDFGEHGDLTEVLELSEDEEEEGPAKKKKKKAAKDEDEEAADNTLTIAMVKKWQKLMEEQNSI
RAMRQAVLAFRCAAYINEAETQEQKYSISDPDVYHQVLVTALGTVPKVLAHHLPVKETASGKVKVSLDSKKFKTLTPLIK
SHTSSVHQLLVNLSDASTLKLTLSSIEPMLPYLLQFRKLLKVLIKTIVGIWADVSTTEATRITGFLLLRKLMVIGDSGLK
ETVLKASYEGVVKGSRNTTVHTLSGVNLMKNSAAELWGIDQNISYTTGFSFIRQLAMHLRSSITNTSKESYKTIYNWQYT
HSLDFWSRVLSQHCDGLVEAKVGKQSALRPLIYPVVQITLGAMRLIPTATYFPLRFQLTRALLRLSRATGTYVPLAPALL

```
EVLNAAEMRKPPKSSTLKQLDFSTAIRAPKSYLRTRIYQDGVGEQVAELLAEFFVLWTKHIAFPELSVPIVAALKRWLKQ
VGSRTAGNKNAKVNQAILLLVQKVEANARWIEEKRLNVTYTPRNRAEVETFLKDVDWESTPLGAFVKTQRKLREEKAAIL
EQGRREEEKRRAAEKKADEDEMMEDAPSDDDDGSEESSGEEEEEEEEEEEEEEEEEEEEFEEE
```

760 - 779:	EEEEEEEEEEEEEEEEEEE

A0A0K8R9M8 **A0A0K8R9M8_IXORI** (165 aa)
Putative nad+ binding protein. *Ixodes ricinus (Common tick) (Acarus ricinus)*

```
MLLLKLTLVVLISEIGERALCAGSGSTSSAKDNEYTNQNQLPPNSYINATDNNGCWYPLLIDYSGTDNFLATKTVNQKPD
PVRTENGNSTLNRKKSDIATLQFSAKDTVKVMVGSCSHGSCNPDTPTKNRVITLLEEGDEEEEEEEEEEEEEEEEEEEE
EEEEE
```

140 - 159:	EEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEE

A0A0K8RY61 **A0A0K8RY61_CROHD** (232 aa)
CDC42 effector protein (Rho GTPase binding) 4a. *Crotalus horridus (Timber rattlesnake)*

```
MPILKQSPVSHSKKRPRLDRAMISAPLGDFRHTMHIGRGGDAFGDTSFLSNHGGTKTNGLPHDVAVSPGSLGSPGDVSGC
FELLSPPGSGNGVVQSPATSTPDGSFVVLQSPEKADWKPPNGEGWDLQQNFSLESPTLDHAESLLSFQLDLGPSILEDVL
GVMDKDWDNIKGQDQDVLRDESSSPLGCSQQEDEKEEEEEEEEEEEEEEEEEEEEGQGYSFEDEQDEEIGL
```

196 - 215:	EEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEE

A0A0K9QFG5 **A0A0K9QFG5_SPIOL** (332 aa)
DUF2052 domain-containing protein. *Spinacia oleracea (Spinach)*

```
MEEEKERREVKEEAMERITERLSALENLYFPQALLSKAATPSLRKPLLLDLLRRDVPVFLERYGPQLTSQELQEFDVLKD
DYETNWHLKHLRSKLTPTSEQMRFQSLTKKNRRTAYMDKLISEGHYFSEDSMREREPYLHHEYVGKFQDPYGRSMPRPGE
RWSETLMRRAEEAILLAKIRGEQQRLGVDESEWVGNEGASRMEEEEDEEEEEEEEEEEEEEEEEEEEEEGEKANVHGNG
VTTSEVQPVHDQDGAAINGIASASENVERPMLSPAEIQDQLDQFTYIMQQKFLSGQDHEHVNYSKIDEDETLDDHWSKEA
NCDAEEKYFEED
```

208 - 227:	EEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEE

A0A0K9QV30 **A0A0K9QV30_SPIOL** (698 aa)
F-box domain-containing protein. *Spinacia oleracea (Spinach)*

```
MNRRKTSWSDMPPELLSDIAGRLETQSEFRKFRAVCKTWRRSAPITLLRRKNLLSSLLPHKISTPTPPLLGKNRSSIGYI
EITGNSLMIVPSSVYLLKSSQNPELPPWLITVEELNPGKFYLRKPLSRINIEKLPDNFPKHLQLSGLKVTEMGRFCTLRL
ADRPRDMFEKKHFTYCTNKVVLFVDPKCKNNPTINNCTAMVLYDNGNLSAIRLNNEVEKHLSPKCRKFDDILEFNGRVYA
VDRRGRLYCTDYHSPKMLEIISNTLGKGFSTDKKKLLVVLLGELYVVYRNQDCGVSIDFEVYRMQEEVGEWERVKNVDKV
FDGRLLFVTLDGCFFGDRNDFPGWRGNSIVFYKNSFPQYDGPSLDIKVFGKYYDDELDVGIFHFDDGCAGVSGYGLPAAS
SPSYSEVFWPPPAWLSRKPDTGFATSSSEEEEEEEEMDEEEDEEEEGEEEGEEGEEEVQSCYHGEINQEEEEEEEEEEEE
EEEEEEEEEEEVEEEEEVQSGYPGEINQQPIWYVENLPTLIQVDGIPYVQVGTTFPKVVQNGVSQAKFLGFNVSPHSVPI
LKKIWHKHGNIIQGHVLQNNGMISQALDSLANVILLLQSESGMSMNVAQAQYLDSTMCFLQGARFRLDWLFPFTQKAMAI
HYGQQQIHYIKGLEMSKSVLVSQLHDLDYRLAEQTKFLVEKTVAEAPLVPINLKNVLG
```

469 - 488:	EEEEEEEEEEEEEEEEEEE
470 - 489:	EEEEEEEEEEEEEEEEEEE
471 - 490:	EEEEEEEEEEEEEEEEEEE
472 - 491:	EEEEEEEEEEEEEEEEEEE

A0A0K9QV77 **A0A0K9QV77_SPIOL** (668 aa)
Rx_N domain-containing protein. *Spinacia oleracea (Spinach)*

```
MAELGICIAETLIAMVGSTVIKEICDMWGYQSELEQLNKTVFTIKNVLLDAESKRELSNEASGYIEDLKAAVYDADDLFD
EFLTLAELKQLDGNKDDKMFKKVRRFFSSKKKGVSQAYKMSHQVKDIKKQLDTIVGINKLTSLRKLPYFVVGKRKSYKER
```

```
CDGELKYLKALTELKGNLRIEIHDEEGMNDSGGKYLKSMKYLTEVIIDFSRCCGGHEVLMGKLEPNSNLKGLISWGYEGT
KIPGWGRATDNWAISFPHLVKIELSNCKNLEYIPLLSQLLYLKSLSLENLSMLEYMENTGSRCSSSGEGFTSFFPSLETL
HINCHENLKGWWRGEGLIVDDEHLLMRSLGFPRLSKLTIRGCPSLISFPPCPSLEVLDFCPGNKALQISTRDSENETTTA
TGISQDGVKLRIVKVDNIGYLRLLHPLCLTDLCIDNDPELESLSQVEDVLQICGSSLRCLTLLNLRNLRRLSGEWSKHLT
SLESLKLVRCSQLRNSDEDEEEEEDDDDDDDEEEEEEEEEEEEEEEEEEEEEDDEGGNTPWISLHKSLHSLVILMSEMR
SLPKGIQYLTSLQSLQLSWCSNMKTLPEWIGCLSSLQSLSIENCRELKSLPESMQNLTSLQRLHIVCCPDLQERCRKPNG
EDLPKIQHIPIVSFSYHPDHKFKNGMYY
```

512 - 531:	EEEEEEEEEEEEEEEEEEE
513 - 532:	EEEEEEEEEEEEEEEEEEE
514 - 533:	EEEEEEEEEEEEEEEEEEE

A0A0L0BL95 **A0A0L0BL95_LUCCU** (393 aa)
Troponin T, skeletal muscle. *Lucilia cuprina (Green bottle fly) (Australian sheep blowfly)*

```
MSDDEEYTSSEEEEEVVEEVEEVHQGEGDPEFIKRQDQKRSDLDDQLKEYINEWRKQRAKEEDELKKLKEKQAKRKVTRA
EEEQKMAQRKKEEEERRVREVEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDQGVLGLSSAAMERN
KTKEQLEEEKKISLSFRIKPLAIEGLGESALRDKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALK
KGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYDTLYKETREKIWQERQERFMQRSKSKLPKWFGERPGKK
AGEPETPEGEEDAKADDDVVEDEDEVEEEVVEEEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

359 - 378:	EEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEE

A0A0L0CSI7 **A0A0L0CSI7_PLAFA** (3138 aa)
Transmission-blocking target antigen s230. *Plasmodium falciparum RAJ116*

```
MKKIITLKNLFLIILVYIFSEKKDLRCNVIKGNNIKDDEDKRFHLFYYSHNLFKTPETKEKKNKKECFYKNGGIYNLSKE
IRMRKDTSVKIKQRTCPFHKEGSSFEMGSKNITCFYPIVGKKERKTLDTIIIKKNVTNDHVVSSDMHSNVQEKNMILIRN
IDKENKNDIQNVEEKIQRDTYENKDYESDDKLIEWFDDNTNEENFLLTFLKRCLMKIFSSPKRKKTVVQKKHKSNFFINS
SLKYIYMYLTPSDSFNLVRRNRNLDEEDMSPRDNFVIDDEEEEEEEEEEEEEEEEEEEEEEEEYDDYVYEESGDETEEQ
LQEEHQEEVGAESSEESFNDEDEDSVEARDGDMIRVDEYYEDQDGDTYDSTIKNEDVDEEVGEEVGEEVGEEVGEEVGEE
VGEEVGEEVGEEEGEEVGEGVGEEVGEEEGEEVGEEEGEYVDEKERQGEIYPFGDEEEKDEGGESFTYEKSEVDKTDLFK
FIEGGEGDDVYKVDGSKVLLDDDTISRVSKKHTARDGEYGEYGEYGEAVEDGENVIKIIRSVLQSGALPSVGVDELDKID
LSYETTESGDTAVSEDSYDKYASNNTNKEYVCDFTDQLKPTESSPKVKKCEVKVNEPLIKVKIICPLKGSVEKLYDNIEY
VPKKSPYVVLTKEETKLKEKLLSKLIYGLLISPTVNEKENNFKEGVIEFTLPPVVHKATVFYFICDNSKTEDDNKKGNRG
IVEVYVEPYGNKINGCAFLDEDEEEEKYGNQIEEDEHNEKIKMKTFFTQNIYKKNNIYPCYMKLYSGDIGGILFPKNIKS
TTCFEEMIPYNKEIKWNKENKSLGNLVNNSVVYNKEMNAKYFNVQYVHIPTSYKDTLNLFCSIILKEEESNLISTSYLVY
VSINEELNFSLFDFYESFVPIKKTIQVAQKNVNNKEHDYTCDFTDKLDKTVPSTANGKKLFICRKHLKEFDTFTLKCNVN
KTQYPNIEIFPKTLKDKKEVLKLDLDIQYQMFSKFFKFNTQNAKYLNLYPYYLIFPFNHIGKKELKNNPTYKNHKDVKYF
EQSSVLSPLSSADSLGKLLNFLDTQETVCLTEKIRYLNLSMNELGSDNNTFSVTFQVPPYIDIKEPFYFMFGCNNNKGEG
NIGIVELLISKQEEKIKGCNFHESKLDYFNENISSDTDECTLHAYENDIIGFNCLETTYPNEVEVEVEDAEISLQPENCF
NNVYKGLNSVDITTILKNAQTYNINNKKTPTFLKIPPYNLLEDVEISCKCTIEQVVKKIKVIITKNDTVLLKREVQSEST
LDDKIYKCEHENFINPRVNKTFDENVEYTCNIKIENFFNYIQIFCPAKDLGIYKNIQMYYDIVKPTRVPQFKKFNNEELH
KLIPNSEMLHKTKEMLILYNEEKVDLLHFYVFLPIYIKDIYEFNIVCDNSKTMWKNQLGGKVIYHITVSKREQKVKGCSF
DNEHAHMFSYNKTNVKNCIIDAKPKDLIGFVCPSGTLKLTNCFKDAIVHTNLTNINGILYLKNNLANFTYKHQFNYMEIP
ALMDNDISFKCICVDLKKKKYNVKSPLGPKVLRALYKKLNIKFDKYVTGTDQNKYLMTYMDLHLSHKRNYLKELFHDLGK
KKPADTDANPESIIESLSINESNESGPFPTGDVDAEHLILEGYDTWESLYDEQLEEVIYNDIKSLELKDIEQYVLQVNLK
APKLMMSAQIHNNRHVCDFSKNNLIVPESLKKKEELGGNPVNIHCYALLKPLDTLYVKCPTSKDNYEAAKVNISENDNEY
ELQVISLIEKRFHNFETLESKKPGNGDVVVHNGVVDTGPVLDNSTFEKYFKNIKIKPDKFFEKVINENDDTEEEKDLESI
LPGAIVSPMKVLKKKDPFTSYAAFVVPPIVPKDLHFKVECNNTEYKDENQYISGYNGIIHIDISNSNRKINGCDFSTNNS
SILTSSVKLVNGETKNCEININNNEVFGIICDNETNLDPEKCFHEIYSKDNKTVKKFREVIPNIDIFSLHNSNKKKVAYA
KVPLDYINKLLFSCSCKTSHTNTIGTMKVTLNKDEKEEEDFKTAQGIKHNNVHLCNFFDNPELTFDNNKIVLCKIDAELF
SEVIIQLPIFGTKNVEEGVQNEEYKKFSLKPSLVFDDNNNDIKVIGKEKNEVSISLALKGVYGNRIFTFDKNGKKGEGIS
FFIPPIKQDTDLKFIINETIDNSNIKQRGLIYIFVRKNVSENSFKLCDFTTGSTSLMELNSQVKEKKCTVKIKKGDIFGL
KCPKGFAIFPQACFSNVLLEYYKSDYEDSEHINYYIHKDKKYNLKPKDVIELMDENFRELQNIQQYTGISNITDVLHFKN
FNLGNLPLNFKNHYSTAYAKVPDTFNSIINFSCNCYNPEKHVYGTMQVESDNRNFDNIKKNENVIKNFLLPNIEKYALLL
DDEERQKKKKQQEEQEEQEEQQEQILKDQDDRLSRHDDYNKNHTYILYDSNEHICDYEKNESLISTLPNDTKKIQKSICK
INAKALDVVTIKCPHTKNFTPKDYFPNSSLITNDKKIVITFDKKNFVTYIDPTKKTFSLKDIYIQSFYGVSLDHLNQIKK
IHEEWDDVHLFYPPHNVLHNVVLNNHIVNLSSALEGVLFMKSKVTGDETATKKNTTLPTDGVSSILIPPYVKEDITFHLF
CGKSTTKKPNKKNTSLALIHIHISSNRNIIHGCDFLYLENQTNDAISNNNNNSYSIFTHNKNTENNLICDISLIPKTVIG
IKCPNKKLNPQTCFDEVYYVKQEDVPSKTITADKYNTFSKDKIGNILKNAISINNPDEKDNTYTYLILPEKFEEELIDTK
KVLACTCDNKYIIHMKIEKSTMDKIKIDEKKTIGKDICKYDVTTKVATCEIIDTIDSSVLKEHHTVHYSITLLRWDKLII
```

KYPTNEKTHFENFFVNPFNLKDKVLYNYNKPINIEHILPGAITTDIYDTRTKIKQYILRIPPYVHKDIHFSLEFNNSLSL
TKQNQNIIYGNVAKIFIHINQGYKEIHGCDFTGKYSHLFTYSKKPLPNDDDICNVTIGNNTFSGFACLSHFELKPNNCFS
SVYDYNEANKVKKLFDLSTKVELDHIKQNTSGYTLSYIIFNKESTKLKFSCTCSSNYSNYTIRITFDPNYITPEPQSRAI
IKYVDLQDKNFAKYLRKL

280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE

A0A0L0CUE3 **A0A0L0CUE3_PLAFA** (1977 aa)
Uncharacterized protein. *Plasmodium falciparum RAJ116*

MNVCKMKVQQKKNLKDCNLKSKNTILTSFEKKKNEKDENNLLKFSKLIDNKNKVVNSKLLKNDNYKFNERKESLTRCSTN
ESLKLKNIKTLTKDFDYNNNNNINNNNDYNNNNNNNNNNNNNNNNNNNNNNKNNNNNNNGHSKLVFKKNDKDIESKVREE
DGKKSEKKNNDLINNKNEFKVNNKLILKSKEFKSNNNNNNNICKLNNIDDKNKKQQMDTYSPKENEEDNSNNMKKSSSLK
NIKKNQINEMEIISNSVEENHDTHSKGDKENNGVSTKNVKRMNTMSKEINHKNNNLKKHVSKSNSLELKKGKKGEKSKDK
LSNNVSGKKGMNKEKEVVQSSSVRRNSSRYSIDYGRRDSSRRGSVKQEKGKERRGSKNVSKKVSNSKYTRKKSKRIKEES
DESDDDDEEEEEEDDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDNDNSDNNDESDEVYTNRSRR
STRCSIVKRKSSLCIGKKNSKIIKKSTSKTKNNKKKKGSVIKLVKKKEKLSKKGILKKTNKKTKGKLRKNSKLYHRKKNI
KNEKDGIDEEDIDEEDIEEEEEPSYFDEYNLSYEERKKDLEEKEKKKEIKEKYIKQIKLPKYADDESIIFINNPNYVMVL
LFLTVYKDVLKMNWNFKDIEEMFQNKETTEFGRNFILKLFFFLGRYFNSKSIFMYKYISRIFEDKEESLSRVVNFHELFP
VLETKKEIKNSGVGSKRKKDKRGKKMKIHQKEDELLYDEEVIGNEDVHIFEEEEDNEHSNDDEDEEEEDNEHSNDDEDEE
EEDNEHSNDDEEKEDVHYNDEEEKKSDLNNDSTKNTVIKEEKDGLHISEGSHNLVNIVNDSMKREESCKNGHIGDNERSG
DINTNDDKNNADNNDDVDGEKIVDSKNNIENKLDNTVEGKHDINSTEGIIKSENVDDEKGLLTNKLFLEWDDLSVISKLR
IIRMLLNLVLCESNNLKKMLGDEKLNYNNGYLGKINNEKYWFIFNDTINIEYKLYLEREEEGSFIFICDDDDMLYTIGYN
FLRNSDTKFMGEALIERYNKVCRERRNRSRMLKQQKKLLCADINLNDPLLGTKKRQHKQVEYFNFDNNEKMRRKKSDMNN
NNPYSVPPTKSYQKNDRSFRLAARNAQKGSVDDLEAWKLNEGSLGIENQGATSGNYNIANDGTNMTETNNINDNHNNDNN
NNNDGVVNADGNNIYGPNNNNVIGSDGNVNNANNTTTNNNNNLGTVKIPLKRGRKKKSEKKKRGRKKKILSVDGIGEIAN
NLSALNVDENRRKSMPNIGRGRRGTYTKRNTKPSVSIKYGTRSHSINKYENDVMSFNEYSLNPGLSMDDFYKNMVMDPKF
FHANMNMNNYMNGGFNMPNNNNSMMNMRNGSKMGNMNNIGGYNFPYMCTPPPMYNQYYMYNGNNMYLPNGGPNNNMNMSN
ANNGASVVMGGNVVSNQNTVKDVKAENMHMAKNSIMENRNSIIVNNMNNMNNINMNSMPHKNSFMGNDGINNMNSMNNNN
NNNNVNNNNNNVSNNNNNNVSNNNNNNVNFMDNMGNNNNNNNNNNNNPMNKYNNYMMNRNVLNNMGGTNPLYNNMYNMKFP
YMNNDMMNYNYNINSFQNMNYDKMNKSMFKRYPNFMGGYPYNNMNPYNNFNAFNMNYQQNDQMNQLPNMQGGYKSKLMND
NLSNYQSFNNNNVKQNHHDNNNNDNNNNKNNSEGGNKNMDDSNKNNDINKNDILDSTKLTEQPVGGVVPNNDCITRGEDN
HRIDLKGDIAEALVGNNNEKMNSSDHNLNSLKNLPNINNTYNMDHMSHMRNSVSASSIGMINPGHMNSSHSGSIMNKDKF
RDLQLNSNNNNNNNNNNYVKVNPFDHPMKNMNPNLMDDKYPKDNNNMMMMMMNSVYNMMGSDHFHMNNSHMMDPMGSPK
MNDNMYNHNNMNFENTNTNHNNHNNHNNHNNLNNLNNLNNLNNHNNHNNRIQDKLPE

416 - 435:	EEEEEEEEEEEEEEEEEEEE
417 - 436:	EEEEEEEEEEEEEEEEEEEE
418 - 437:	EEEEEEEEEEEEEEEEEEEE
419 - 438:	EEEEEEEEEEEEEEEEEEEE
420 - 439:	EEEEEEEEEEEEEEEEEEEE
421 - 440:	EEEEEEEEEEEEEEEEEEEE
422 - 441:	EEEEEEEEEEEEEEEEEEEE
423 - 442:	EEEEEEEEEEEEEEEEEEEE
424 - 443:	EEEEEEEEEEEEEEEEEEEE
425 - 444:	EEEEEEEEEEEEEEEEEEEE
426 - 445:	EEEEEEEEEEEEEEEEEEEE
427 - 446:	EEEEEEEEEEEEEEEEEEEE
428 - 447:	EEEEEEEEEEEEEEEEEEEE
429 - 448:	EEEEEEEEEEEEEEEEEEEE
430 - 449:	EEEEEEEEEEEEEEEEEEEE
431 - 450:	EEEEEEEEEEEEEEEEEEEE
432 - 451:	EEEEEEEEEEEEEEEEEEEE
433 - 452:	EEEEEEEEEEEEEEEEEEEE
434 - 453:	EEEEEEEEEEEEEEEEEEEE
435 - 454:	EEEEEEEEEEEEEEEEEEEE
436 - 455:	EEEEEEEEEEEEEEEEEEEE
437 - 456:	EEEEEEEEEEEEEEEEEEEE
438 - 457:	EEEEEEEEEEEEEEEEEEEE
439 - 458:	EEEEEEEEEEEEEEEEEEEE
440 - 459:	EEEEEEEEEEEEEEEEEEEE

A0A0L0CV02 **A0A0L0CV02_PLAFA** (4547 aa)
Cysteine repeat modular protein 4 PbCRM4. *Plasmodium falciparum RAJ116*

```
MEMGSIDEFNNKDKFIKDFTFSTDYLDQLKLNIVPVFVFLPGPVEYKEYVCFAGIPCNATIKIKRSAQTRLSTGNKQIIG
EKKDVANPYTGSYGNRNKANIKKGEEKKEQKRNDKKEGEIGYKKEGEIGYKKEGEIGHKKEDELGDKKEDELGDKKEDNN
EDQNQDNKQDKIENMNKDINKDKEIKTKETNIEEEEEVEEEEVEEEEEEEEEEEEEEEEEEEEKEEKEEKEEEEQEQEE
QFDHNEHEVKGADKNKDKNFNQNKGESQNVNPNTQQNQYDEQIISEEEQDNIENSLLGKHQYIYYTLNDTKECKNEYETV
YKSNASSIYVSQEINYLHHEFIDGVYNLKIDIVPTDITKRYEICASFYEDDKYFYNIGNIIFYGIFNESNTLDIISGVPF
SFEINQFYSKYDLFIRLIYEKHGDSKTCRLYNNNFENVFLEGTIERTIVQHDKKVLDNYITNYKWKDVTIILDTDNNNYM
TSYQNVDGSYNLYVCSCYELTEGHCQSGNYFSTQVMKFYVHTVELKEPKMNSLMHFLKPFTLKLETTKILNGSIKVIPID
IISDLSKLCLELNLKNIYLKYQAEINEYEQTYNITINFLSQGFIICWCGKDNCKDHEYLTKVAFFRLNSPNFIDVHTDLN
GNFSFHFLNQFVNINDRVRFVGQASSCLDDENVDLFNNHIVIKNVQNKKGKTSNGGNTKKEQQKNNNKINSNNNEEDEND
NENKNERKDEDDNYESYSIDWEQIIEIFGKPRNIFKGINQNWTWVSENYKMKTSNEKYIKICYCFHFYYKNCKDTKNFLY
IGLVHNHIWDSKTTIMQNELDTNYEISNMIYFNKDSIKFVAINSFNDLNRNVCDNINYEKNIIMPFFSGYNKFHNTTINQ
KNILNILKTYYHNEFIFILCYNTEYYKKKTNYLLTTKDMTELNDFTTYYNEEINTYNIIQSSFSYHSDIKDISTTNENIE
KYEHMQLLLQNRGNTPNIFENYFYQKDVYKKNNMSIYNMNLYNMSPYVVYNNNKKKITNIQVKNRLKIILTKMYHMTSVD
INEVIYYKGKGELLTDLNLQNIFILPKQKKVILCCYNDDYIEVIINDDNKIGMKKSNKIQELIDILKKYHPNFERNKKKQ
NDILEQFNNINDILFKYDYIRDVNKNQIYYDTGFFRNNIYIQLINQPFDLKIYGSNIQKKKNKDYILYIIEFHNICYNNM
NKNGFFLEHKRYNEMENYIHFLQISMNKINNYKLCLYDKERDIYSNVGILNITDYFVIKESSFFDNEDIGNIKKKNMETD
SYNYNNDNNYDGNYDNNYDNNYDNNYDQNNNKYYIKNYNQDVIKNVCLIMDNNTNQIIVIKGKGSFYFNLQIEKGIFIEK
KGQKLNELFPDIKNHEPISCKNKKKNTIILTKTHIFFYTNNNDISFSTKHNLPFPYDIDFDDQYIYVNDLYLNKIARIQI
LSNKDNKTPIPIINNKQRSKRSIINHGHESQQNIQKTHQTYDHFTPLHKVEKKEILQNNNIVQLKENEFPITNLKNIEYS
KNNIPNQKISSKDDIYKMSDFQAFINKYANLITTNSFRLYNYFEKKKYYGTPNYFIKRVWFNKVGPSREENYSTESKIEQ
NDKNNNNNNNNNNINNNYNYNYNDLHNNNHNIILNSNNYNNNNQSSRHQNFIYSYHVSLDGKKKQSENLLTHSLNNFIQFF
QNKKNSILKKEKEKRKNIPSYNIMYKNINHITNTLNKRKQQELTSSIIKKRTKRNVQEKRMSQSAYNELVLASIKKYTNK
VEPAHFVNNKLDYLNYITNLKSPLNISVQNNILYILDSIKNTFFSYNLINKEIKELEKYDFNDHPLILKNPLHFSIYNGI
ITEYTEHKNNLAFVTQIDSNEIKVIDLNSSKKYKIIKAIKLRKGYKHNHINYVIGIKQKLLIITSQSQNIDHYKNIIYHY
HFNSFDQYFSISFNYTFAKNYNANDNLYITPDIDKYSDNIIYFCFLNSNNKCTNIDELTKLSISHETGIITGKLNYFGTF
SLKIFAKTYFQYKINTYSNLYSYCGISQEYNKTKSTCESCPIGTFWNSEKLLCENCQKYIENTSTLKNGSKLKTDCLCSP
GYEYSDKSSKCEKCKPGYYKRSVGNFICIKGCPINEKSITYGAKSYGEMDCKCIEGYYRKKDKCVLCLSNYYCPGNELIK
PCDKNKISKEGVIHKNDCICKENYIKDNKNNNCVYCASIAKILGKPIYCSLCDPIYFHEDIYKNIFLLPNNIHNYGLINN
IYNYDEDLSLQGNIMKYAYFHKTTNIERNFTHYINIKNIYHTFNNNINNYDYLTNSKFAIEIDIPEPKKCIFCDSGYYIK
KKKCISCTTKYCEGFNHNPKACPKNSVVNKMKASSIFDCSCKRGYGILNERRNAYSNTITCQICPQNFFKHIISDDSCFP
CPLYTYTLNQGATSILQCLPKKGYFIYMFKSINIDYLRYKFDINTENRIYNYFENNNKIFDEDVYNFFLNKQYSKFFYNT
ENKTNTNNNHNNNNNNNHNHNNHNNNHNNHNNNNNNKYTKDNHFDNQVGNINKHTNNLQIKITENIYNIQYLEHLGFIKK
TSLFYIYMILLRNIEERYNFNMDKMLKITCHINLHLKKNPHFTITYKKNLQECIDSCKTNIYCTGIEFSRKRVEYTQIIL
KNNKKIILGYFKCKQFYFQNIYDYSSYNLDSYLNEHIENQINIKSTLTYTNFIMRNKPDIIYTCSIDRDPKYLLYKNYKL
VECVIGKFCPGNNTPYMISCPINSTTIIPASEDVNKCLCLKGYSYVGVTSYRCSLCDRGSYKNSVGNNKCDNCPLTFSTT
HRGSTNIKDCSCTSGNYLTFDTLGNFIRTENMQHKNISDQYFVIPIKQESQPENEIKDDNKNINIYNANNINNHDIVYKT
KMIKINLHKENDNHNDYMNNILKQTIGLCKPCTLENHYCEGGLESDITFNNKLIKGKFHTLPKKCPRGLGIPNIIKERNS
INNCLCIHGKVQRTTENKNVECFPCPPNTFKENEYDNSCSGACPPFSTTFVGSSYENQCFCKNNYYLVSTDDENDTNGNS
INNNKNIYNNNNIYNNNNNNNNNNNNNNFNNKSDVKKKSCKICPIGAICNRGFNIYIYLKLLNDRSYNNINVIDHETPFPK
YGYYAVYREKTNPTKSWDTLDDSAILNYVYPYHKLLLFIQKNIQKGNYFFLEKGNKFFLNDDFVEKMNEKSKYEEENANK
FVTKSEIIHNVNTNNLKGKHNTLNNNNNNNNNNINKSSSFLNQNNYNNDNIQLSSYENNPFKNLSSTSEVSSNNNVISFI
QNNDKTNNSTNDNNIENLVDIFNKYVQEAKELQIQNRKFERIPDIHPCTIPNRCLGTLINLCSDGSTGYQCNNCSKNYDM
SYFKSKCKKCQNLFYEILHFILLKLLYYIIVIFICSLNGNILNKLHVSGILMRIWLNCSFTFIAYGFFIPNMNSFISKYW
YLYKTAFSYHMKIFAYYLRVQCLLNSLNINLSYNQMWYIQKYMNICTPIFDSIFITILLFAVIHIYKFFFYKKNIDIFEQ
LLCTIPELNTLYKKNCIDNIHKVKNKKFANKVESFEENENQNKEEKNKKNIKRKNKAKNKHNNDNNDNNDDNDNNNDNNK
ININSKDEHINHFEKCSSITTILNNLELNNEEKNKESKKKKIFDIKKKTSIENIKENETNHLWNDTHNNVKNKESNINTT
NISNNINYELKYIKNKEWYNIFLNKTIQYIYKEKKIFGLWHFIFTKNDNWFKNMGTFLNDTLPCYVLIMILSIPYILLEL
VQLTYCTPIKYKTQKTYFYLTYLITQKCSLSSKLFITGLIVTITMFALYIFLWILLLYLYSKRKRLNLFDLLTTNLLSGF
RKGKVKEFTLSIHFIKTENIVNIQTIGYDPENIKNKNYKIYYKVMNKIKYFLNKNQKKNISNINENKDKHLNKNNNSKDH
VKFEPIENIIKRYNLKLNKGILKDANNNNNNNNIKNMSDQVEDNKKDILFIKKNVLPVNVHNVASIWYDEQNEDLLFQMP
YQNKFCLNMNNEANENNDQINDLTKDKTSEEENNNDHVNDPTKDQTNDEKKKNKNKKNKNNNNNNNENNCHSNDNSNNNN
NKEVHKNDDNINHNNINNHNKSSNISTTNKKNYFNKFSDYIIDKRNKKSIKYFITSLMEVIEKFLDSSTHGFIYENWFDF
TIRFAFVYISWIKKCNKKNNIMLPMNIQQLHIHMDLFIFTPIFPKNNSTCINEQNIQNYSKKKKIYNKINMYDEKIETGE
LLEKHNSFENTEIKISRSFGSHNYMPNIKNRKNNYDKKEDITSINDINVDIIKQDDQKEDSNINHLINEHNQKEPSQHIY
NINDKNIMDYNIDENISKNNEKEKHIKIPPKNISITQKEYYNNNDIFNYSLDIFSSEMFNEKMFHSIISLFELYMAIKTL
KLMNPHIFNKLYQMYNKKIITFDTSVMFYINKLRDDIKSEIEQIDKEINTGDTTEKERIQNYYYYKEELFKRKKLEEELL
SKIKSLEECIEVNKRSQSLRNMLLTKKKKNNNLNNENLEEHINYIFSHLHNEGTYKLNHSQNMDKKN
```

204 - 223:	EEEEEEEEEEEEEEEEEEEE

A0A0L0RWQ4 **A0A0L0RWQ4_ALLM3** (1159 aa)
Uncharacterized protein. *Allomyces macrogynus (strain ATCC 38327) (Allomyces javanicus var. macrogynus)*

```
MPLPDAPPSRHATAPATTRSPVRYADIVQLLLDLARTHSPNAAQDLSTNNGPHAPRTTSAFLAAPSPCAGSAVHRGPSRS
HLSLLSADPSDYADYLVAGDTPMTLSLASLLADSSVAALLSDKVRKADSVLLLREHNFAADQPASANPRIIVSFFHEDDG
HDSALPDAELEGNARRAHDPDPNPDPARNVFDLNANVVLDDPGLELSLIDLTSQPAVAAMTKPGITAFLLRNHPLLASQ
ANCASDQSANEQTDCDATQSPRLGMLIRLLGNDLHAPDAIPADYPRERVFSSDNGEDDDYDDDAHDGEDLDDQVDNGLSP
DYLVSPSNSSDANTSDSSTPAYPPSPRSTDLDTPPNPLDQSPDTAPDPSVRSSIASVQHNPDNSPIALSMASLPPAAARL
RPTMLVAPANTPMLSMLLHPHPQGGVYLHPHGPSHPTPTHGHAFGPSPSLVAFPVPVNSPTESVAASQFYLVAIPPPANA
PAGSVYHLVGDAGGPWSGAHAPPAAHTYVAVGPHGPVRYATTATPLNTPMPSMTRLDAGTGAWAVLGGGHHVPAAHSTVL
LAPHATPMPSAMNLASDEINAGAGPANTPMPSTANLAHTSSPFYAHGPSTAHLAAGTAPFNTPMPSTANLSACPFYAHVA
STAHLAATGGGVPFNTPMPSMVHLAATPAHVRNVPQNTPASSTADLRTRSPRGPATRLTPGGLRAPPPTTLPSRAVLAEA
QEEEEEEEEEEEEEEEEEEEEEEEEREACAPENTPAPSVAHLATADTFATAADAPHNTPMLSIAHLAATAVPANTPAPSMYQ
LATAPANTPAPSMFHLAGAPQNTPVPSLAHLAPGAARRVPTNTPAPSTPGLASHSRPAAAAAATAPAVATAAPTANEAMP
APPPVANPAAAPSGHVYWIPAPTTSGVPYAASNVVFPPHGAAWAGSPPTHIAPAASPQQQQPTVASVVHDLTTHLNTIPT
ASAASLAIQLETGRRMHELHVAALQAAADRDAYRSVLERTVETLRGMEIAPAALVGAAPAVPYGADRGQPWIWTLAVPQH
EMDGSRGNAPVPAPAAAGVTTPGSSPTTPTGPAAASAPAPVPAAATSAPAAAHDQDTVGDGIKVPRADPPRPRRPRRPRR
PLRPSSRGPAKPTTTGGPASIDPAAAGVASRAAGPALRP
```

722 - 741:	EEEEEEEEEEEEEEEEEEEE
723 - 742:	EEEEEEEEEEEEEEEEEEEE

A0A0L0TDI2 **A0A0L0TDI2_ALLM3** (419 aa)
Uncharacterized protein. *Allomyces macrogynus (strain ATCC 38327) (Allomyces javanicus var. macrogynus)*

```
MSPLAEFRQKLIASVSRFAEEVAQSASEDIQLSEEDRILEVEQKPLRSTCTGNKKAVCIGITYQNCPEPGLGKLRGPVND
ANRVKQLLHDNYGFTEQNTLLLTDDGQGDYEPTADNILQAMQWLVKDASAGDSLVFSFSGHGGGVADQDGDELDGRDEVL
```

```
WTCDGKFVRDDTIHSIMVKDLPAGVRLTALLDCCESGTAFDLPYVYDIDGAILDPAHEHLQDGIAKLIEAHSEFEKGRKG
ANATMADMIKGIEYLLGPAGADPETALKKGMSKGGAADVICISGCRDTQTSKDTSIDGLPTGALTDAFIKALTGAGAVPE
VAAAAEGGDEEEEEAEEEEEEEEEEEEEEEEEEEEEEGEEEEEENEYEPDGGEEEEEETGPLTYVGLLHRLRANLEHTYMQ
QPQLSASRPLDLVSSEFGL
```

336 - 355:	EEEEEEEEEEEEEEEEEEEE
337 - 356:	EEEEEEEEEEEEEEEEEEEE
338 - 357:	EEEEEEEEEEEEEEEEEEEE

A0A0L0UUT2 **A0A0L0UUT2_9BASI** (355 aa)
SUN domain-containing protein. *Puccinia striiformis f. sp. tritici PST-78*

```
MNNPCPTIQLRISYYKTQSPRPRLLFSFLVDTNYKREKKTLSNLSHCHRVVASTNTCLSNNRFLAKIFNYYNKKKDKYLL
TPYQNQNKENFVLFGLCDKIEIDHITITNFEFFSSMFKLIKLTVSSSSAEPGVEVGYLKTHDTRGFQVKNLFMFNTYSLW
AQLRSSILNISTLKEEEQLSSNLSAIYSVLYVPANLSFMEAGQKEVHGEEELGGHQKEEEEEKVSDELDMDLVTPLTKKE
ETINKQESVVVELDLEQAIDQRNPHPLEEQSNKNLIGNTTKEEEGEEEEEEEEEEEEEEEEEEEVKNLIKIKAQSSTPP
PPIQLVNNLPGNTYSLGTHESIFGQIMNSNLAQKL
```

286 - 305:	EEEEEEEEEEEEEEEEEEEE

A0A0L0VAH3 **A0A0L0VAH3_9BASI** (888 aa)
DBF4-type domain-containing protein. *Puccinia striiformis f. sp. tritici PST-78*

```
MINSNGKRRTTIEQQQQQQERIPLEQLSPAKRQRLNNTPTTTIKRSTQKDSLKREIAQWQDKYRVAIKSFVFYLDRLDPT
TTSDLKTRIKSYGARVDQFFSKDVTHIITDAHVPTNISIPSPSPRKKNNPYTLPSPTTATTTRNNKENAQFLAGLRRNPK
RISAPICSPEKSTATTDSVHPLIRKALELKIKIWKSEKLLNVLYRLGDQRSPVKQAQIAKPSLPSLLLKEAQQGHTNEFD
PISLRSDYYYFGPKAMFIMVEDTTQEHKPIIVKEYTRPKTRESTSWPIMWGGTEGKSAFSRHTAKQSYVHVRNRIRQLFE
IRARDSDRQIKLISNTVNRHQRSCSVDYMVDTHLPRDRTPPITTTTKTSNLRRAVSMNILQRRQSGKFTRTGGVIQHQHA
ENEEEDDDDEDEEECREIDHVNKVAPDHYRGGHERVFLGASGNSVTVTSNLASATSTRSSAIRSANIGRLLVDKRLAALG
KRPTFEINPTGIINSSSLKQEIHSSIDTHHNQQKNRLDILRNQLQPINLTNKLKRCQSLDSSLIARKKSLRDSGNKKGCR
VGLGVRAKLGNGFDLLDLNKIARNLVGSAVKSGYCENCRLKYSDFKKHILTRKHRKFALDEDNWLDLDETLKKITRKLKP
HVLVPPSVREMILLTGGSDEEEEEEEEEEEEEEEEEEEEEEEEEEAEMVPVEDEEHNEVVEDEMVPVEEEEADEDNDDDED
DEEDEEVEVVRGAEQSITKTLTHKDDHVQGEEELEEGEYDETEEENEDEQVQLVDRQEEEGREGEEDEEDEDRERED QKR
NQDRFNQSLQHIHPLLHPNPYPHHPRPNLPQQQQQQHNFNQHYTHQQLFQHPHKHHLHHHQIVNGQAPLELEEGEWDHEP
DHSDIVFL
```

660 - 679:	EEEEEEEEEEEEEEEEEEEE
661 - 680:	EEEEEEEEEEEEEEEEEEEE
662 - 681:	EEEEEEEEEEEEEEEEEEEE
663 - 682:	EEEEEEEEEEEEEEEEEEEE
664 - 683:	EEEEEEEEEEEEEEEEEEEE
665 - 684:	EEEEEEEEEEEEEEEEEEEE

A0A0L0VC57 **A0A0L0VC57_9BASI** (488 aa)
Uncharacterized protein. *Puccinia striiformis f. sp. tritici PST-78*

```
MASGDSTKSDAPLYHNNSHKTKEVRFQDFQESYLQMFKLIREEVASYPKPDPEDEYEEPSSIEKNDIPYRLEKKLLPELK
ETLEKLSSITDPANVKDESTSKHLAFFEFLSQLTERLVELRETTDKMSDGIVSEQLLPDSQDVKPLSAFKRQRILEKVHH
LFVVTLSKLLSESGVFLWSFDPSNKTADDQLILKRRQELEQLFIPANKEIDEIIKWLQKPLLSVTRQGWQRLVVRIEERL
DTLLHNRNHKEDNYKSPERLRCIQAGIIFLQFSRLFFNKLSRPENSQDMFFTDSLMDPEVDRLQELIEVTETVPAALERF
LDSILSPCSPRGISRPAAMLHHHLDKLVQILRQHFISLNVNKNPAIDPVQIDNASRWLEFWVSQLRYVKRRMERATDRVI
DWSYEPKDSDDSAISSDTAMEESEEESEEEEKEEEEEEEEEEEEEEEEEEEEEEEEESEDEIYRVNDCSCFNCVNRAFKNRW
ESGRWGDC
```

433 - 452:	EEEEEEEEEEEEEEEEEEEE
434 - 453:	EEEEEEEEEEEEEEEEEEEE
435 - 454:	EEEEEEEEEEEEEEEEEEEE
436 - 455:	EEEEEEEEEEEEEEEEEEEE

A0A0L0VIP7 **A0A0L0VIP7_9BASI** (1765 aa)
Vps54 domain-containing protein. *Puccinia striiformis f. sp. tritici PST-78*

```
MSGQSSSRGKQDPNNGNGKQNENEDEIEDEHENENEQTTRPFVLNPSSHYHPNYPISTVMNQVSSQNITLTAFNAIRSSI
PINLKPPPLSSFVKLPYGQSQSVLAPSNKRSAPSPIKLSRSPTIPLSDFDSYLEQVQVQYDRWQTNLTTNSKVIKSLQSN
STTELIANQSNHSDPPSNSTPTLPSLSSVPHVFFDQKFSLNDPSTFDLLTQQPSPSSPAISTSESDRHTSNQAPKPSASS
THNTTDLTTDHIIIDKLSHYLDLIELHLVQEISLRSSSFFSALGNLQSLHAQTSSSVAQIAALKNQLEQLKRTVSDKALT
IIRYGIRRRNITSIELALNKLNEVWQTVHGIEELIQSGEWQSALGLIQELEQLWQSSTVLSSTSPHHMTDSDHVSPPDRP
IKLRLSKLKALAALPKRLSVFRTTISKALVAELSSILSHDLKVNLIEFASIHSLDQTESKDLNSNSPTHSSSSTSNQNGG
PQIRDHIKSRAQERLRERVRPTFDGLIRAGGMEKALAAWRESVVKQIREIVKNGLTDVIEGDLDDRDDSSDISQFNSKDK
RNGLSEKTMTLARNLKALKHREFLKIAQTAYRDLLGCLELVDTQSKALLELAEQLKTQTNHPVPSQSDQLTDAPLDSNTA
RNEPPDVESVNESNQSNTITTIDLEGFQLKLTEVVQSTAELANSRFAKVIGVRTEIHSQLNFIEFFSIFDSSWKFVVQCE
TISRRMIIALRGVMVNQAKSFLLTFHQNKITESAKIVEMELWSPVDVPYQIQLIVNSIISSAMEDPKKLIIDYQKLQEDQ
EQVNDESSSSNPSPSKLLEIEGNFYHPVSASLQTLKTISEYLQIIINCSLLTTDLMGKIIEFLKAFNSRTCQVVLGAGAI
RSAGLKNITAKHLALASQALSTMISLIPYIRECLRRHLNMKQAVMLIDFDKLKRDYQEHQNEVHSKLISIMADRLGVHKQ
TLESIDWDSSSLDNSKDEKDELGANPYLESLLKEVGTLHRVLGRYLPSSTLQDILSQVFMSIHGALEEEFNQVEIKSIEG
```

```
KRRILRDAEYFSNKLIELKATEDCQSKGRALIELIHTRFFPELLKGGGTTKANSGGGGSSSTDIKSPDPTQVILPPSPIT
ERTGSFRDKFRFLSTRAKAVDSSGSLLAEVTNAALATPTTSSLIGGETSPTRGVSPVGSGAGVETGADGDKSTVKLDDDS
KPIGSKDESDEQPNSTQNIESTSTSSAPDSKSVETSVAPVPSSKEDPPLPNSSSSTASLSSKPLKLTLSQRLAALASSRR
GSHSSIITNTTSSPVQNGPPTIPEHLPTEGSELTPTLRVTTNSPPEDDQAKTVQDSRESGYLNFDTIPLSPIGSNAGVES
SKATGMSSASQEKAKEDSSREEVSSPSQMKAQQYSSTGICKTDQRPESTTTLSQDITSPLSPTPQPIKPTLSQRLAALAS
LRRGSQSSSLAPSPIQTGQTTIPDPLPKESAPINISTNQEQPDRGTQLSPDRHPLPLDSVHSDIPTSLADNEEEDETVES
IEIKQEEEEEEEEEEEEEEEEEEEEEEEEEEEGAHEGGGEELVTMENESENRDGNEAEKVEEKGEGESVEIEMELEDEIVGE
ENVEDDTEVVNVIETAVEEEELEKQSVGVNEEKKEDEKGGEEVAKEEAAEEEEDRKVAEVVEEEAAETAAEDQKVGDEKV
QGKVVEEAEEEERENGDGDGDGDGEEEKGEEGEVGEKEVEEKEVKKGKEQEDVVVDPPPTKAPLKERLAALAAARKGSHP
SSSST
```

1526 - 1545:	EEEEEEEEEEEEEEEEEEEE
1527 - 1546:	EEEEEEEEEEEEEEEEEEEE
1528 - 1547:	EEEEEEEEEEEEEEEEEEEE
1529 - 1548:	EEEEEEEEEEEEEEEEEEEE
1530 - 1549:	EEEEEEEEEEEEEEEEEEEE
1531 - 1550:	EEEEEEEEEEEEEEEEEEEE

A0A0L0W2H0 **A0A0L0W2H0_9BASI** (1094 aa)
Uncharacterized protein. *Puccinia striiformis f. sp. tritici PST-78*

```
MNLAAVQSQQAFPSTPLPDPEPQQQAIHYAACQSQQAFPLTPLPDPQPQPQAIHFAARQSQQPFSLTALSNPQPRPQATH
FADRQSQQAFLSTPLPNTQPISQPQQQAINFAACHSEQLFTSTHLPNPQPQQRALDQGSCQSLQAAVNQATRQSLQRLSS
TPLSNGHPPPHATNQTSRQSLQAFSFLSTPAADGHPLTDSTSRPASPQPRKSRANPNRPSQTSSTQASQTGTSKSNPSAR
SKKATQSQATDPTQPRFAALPSLQAELRRAIDANAKTTKAKAANAAKAAERATAKALALAEEAKAAEAAEEAVQANERGQ
PALTILQLTAESPTTTSRNSAFNATHAPELDLNLDFSGLRSVPASPKATLHAIEDFPINHSDRPGGHDADDARNEDDGHH
HEDDDHHHDDRRYEDDGQPRDDGRDADDGQLPDRQAMDTSVHDHDEDSVDDINCDIVRLVNGNTRLRLKPQTVQRLEGMA
LDELRERCYKHKHYSRLVAEDKADLDEATDEYDKHILRIACRNKLKLKTVEAYLGQGHRARGTNRYSEFCRYNLEARIAT
ADGSKPMHQRWVESGRLWRQLTKEEQEQYDDPDFLAQHANPFEELELEDGQILPACKRPTGPNGVNLAKPSKFDATRWCK
SIQTTMVNLAKSHGVEGVVFVVYPTKKGRALLTGGSRLGQAYYVNILPDEGNPAQDFLAFSDGQLSTQRLARCEVALPKK
VRQPKAAKNRMENCEFSLGTLKANRPPIREQLGWAIHKASKGKWCNGWPGADTVNQLKLLKLSLRVDENPLQVGPEEFCK
PISNMQIGEQERILTAIGKGWVHLERRDTSNPTRAIGDVEEEADEAAPDVQVVSVTVGPVPPGESVPKKPSVKLKAGKGK
GNGKGKGKGKGKGKGKGKGKAVRVQDETDDEEEEEEEQEEEEIEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEGEGE
GEEEEEEEEELPDAHNLKSSRMKKYVGAARAGSTSKNHVHVNHRLDGKRVSRRRDDPATADGEPRESIATREASVGQDRS
GASKKRKRIGSPPGASGDRDTIRNHRGGGTGPKKHRPTKVARTATIAPTDSNSE
```

924 - 943:	EEEEEEEEEEEEEEEEEEEE
925 - 944:	EEEEEEEEEEEEEEEEEEEE
926 - 945:	EEEEEEEEEEEEEEEEEEEE
927 - 946:	EEEEEEEEEEEEEEEEEEEE
928 - 947:	EEEEEEEEEEEEEEEEEEEE
929 - 948:	EEEEEEEEEEEEEEEEEEEE
930 - 949:	EEEEEEEEEEEEEEEEEEEE
931 - 950:	EEEEEEEEEEEEEEEEEEEE
932 - 951:	EEEEEEEEEEEEEEEEEEEE
933 - 952:	EEEEEEEEEEEEEEEEEEEE
934 - 953:	EEEEEEEEEEEEEEEEEEEE
935 - 954:	EEEEEEEEEEEEEEEEEEEE

A0A0L1I9I9 **A0A0L1I9I9_PLAFA** (381 aa)
Casein kinase II subunit beta (CK II beta). *Plasmodium falciparum IGH-CR14*

```
MEFVSNDESADDIIQDESNEGEVELTDADFYDLTVINDKIDEEIIEDDEEEADNDDQENDNVQEVYNIDDEDNDIHNDKL
LLDQQRDNDVNEEEEEEEEEEEEEEEEEEEEEEEEEEDEDDDDDDDDDDDDDDDDDDDDYDDDDEYDEDDFNEATVSWIEW
FCQLKQNLFLVEVDEDFIRDEFNLIGLQTKVPHFKKLLKIILDEDDDDDDDDDDDYDDEDDEINRDSEEMYKNKDMHEQN
AACLYGLIHSRFILTSKGLALMREKYKSGIYGTCPSIYCENAKLLPTAISEIPKFLSPLLYCPRCCETYYPSKNSLLNQL
DGCYFGTSFASFFALSFNIASDKKKVYYTPQICGFTINRNIRETLYMDVNKDNTESSEECQ
```

92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE

A0A0L1IBS0 **A0A0L1IBS0_PLAFA** (3131 aa)
Transmission-blocking target antigen s230. *Plasmodium falciparum IGH-CR14*

```
MKKIITLKNLFLIILVYIFSEKKDLRCNVIKGNNIKDDEDKRFHLFYYSHNLFKTPETKEKKNKKECFYKNGGIYNLSKE
```

```
IRMRKDTSVKIKQRTCPFHKEGSSFEMGSKNITCFYPIVGKKERKTLDTIIIKKNVTNDHVVSSDMHSNVQEKNMILIRN
IDKENKNDIQNVEEKIQRDTYENKDYESDDKLIEWFDDNTNEENFLLTFLKRCLMKIFSSPKRKKTVVQKKHKSNFFINS
SLKYIYMYLTPSDSFNLVRRNRNLDEEDMSPRDNFVIDDEEEEEEEEEEEEEEEEEEEEEEEEEYDDYVYEESGDETEEQ
LQEEHQEEVGAESSEESFNDEDEDSVEARDGDMIRVDEYYEDQDGDTYDSTIKNEDVDEEVGEEVGEEVGEEVGEEVGEE
VGEEVGEEVGEEEGEEVGEGVGEEVGEEEGEEVGEEEGEYVDEKERQGEIYPFGDEEEKDEGGESFTYEKSEVDKTDLFK
FIEGGEGDDVYKVDGSKVLLDDDTISRVSKKHTARDGEYGEYGEAVEDGENVIKTIRSVLQSGALPSVGVDELDKIDLSY
ETTESGDTAVSEDSYDKYASNNTNKEYVCDFTDQLKPTESSPKVKKCEVKVNEPLIKVKIICPLKGSVEKLYDNIEYVPK
KSPYVVLTKEETKLKEKLLSKLIYGLLISPTVNEKENNFKEGVIEFTLPPVVHKATVFYFICDNSKTEYDNKKGNRGIVE
VYVEPYGNKINGCAFLDEDEEEEKYGNQIEEDEHNEKIKMKTFFTQNIYKKNNIYPCYMKLYSGDIGGILFPKNIKSTTC
FEEMIPYNKEIKWNKENKSLGNLVNNSVVYNKEMNAKYFNVQYVHIPTSYKDTLNLFCSIILKEEESNLISTSYLVYVSI
NEELNFSLFDFYESFVPIKKTIQVAQKNVNNKEHDYTCDFTDKLDKTVPSTANGKKLFICRKHLKEFDTFTLKCNVNKTQ
YPNIEIFPKTLKDKKEVLKLDLDIQYQMFSKFFKFNTQNAKYLNLYPYYLIFPFNHIGKKELKNNPTYKNHKDVKYFEQS
SVLSPLSSADSLGKLLNFLDTQETVCLTEKIRYLNLSINELGYDNNTFSVTFQVPPYIDIKEPFYFMFGCNNNKGEGNIG
IVELLISKQEEKIKGCNFHESKLDYFNKNISSDTDECTLHAYENDIIGFNCLETTYPNEVEVEVEDAEISLEPENCFNNV
YKGLYSVDITTILKNAQTYNINNKKTPTFLKIPPYNLLEDVEISCQCTIKQVVKKIKVIITKNDTVLLKREVQSESTLDD
KIYKCEHENFINPRVNKTFDENVEYTCNIKIENFFNYIQIFCPAKDLGIYKNIQMYYDIVKPTRVPQFKKFNNEELHKLI
PNSEMLHKTKEMLILYNEEKVDLLHFYVFLPIYIKDIYEFNIVCDNSKTMWKNQLGGKVIYHITVSKREQKVKGCSFDNE
HAHMFSYNKTNVKNCIIDAKPKDLIGFVCPSGTLKLTNCFKDAIVHTNLTNINGILYLKNNLANFTYKHQFNYMEIPALM
DNDISFKCICVDLKKKKYNVKSPLGPKVLRALYKKLNIKFDNYVTGTDQNKYLMTYMDLHLSHKRNYLKELFHDLGKKKP
ADTDANPESIIESLSINESNESGPFPTGDVDAEHLILEGYDTWESLYDEQLEEVIYNDIESLELKDIEQYVLQVNLKAPK
LMMSAQIHNNRHVCDFSKNNLIVPESLKKKEELGGNPVNIHCYALLKPLDTLYVKCPTSKDNYEAAKVNISENDNEYELQ
VISLIEKRFHNFETLESKKPGNGDVVVHNGVVDTGPVLDNSTFEKYFKNIKIKPDKFFEKVINENDDTEEEKDLESILPG
AIVSPMKVLKKKDPFTSYAAFVVPPIVPKDLHFKVECNNTEYKDENQYISGYNGIIHIDISNSNRKINGCDFSTNNSSIL
TSSVELVNGETKNCEININNNEVFGIICDNETNLDPEKCFHEIYSKDNKTVKKFREVIPNIDIFSLHNSNKKKVAYAKVP
LDYINKLLFSCSCKTSHTNTIGTMKVTLNKDEKEEEDFKTAQGIKHNNVHLCNFFDNPELTFDNNKIVLCKIDAELFSEV
IIQLPIFGTKNVEEGVQNEEYKKFSLKPSLVFDDNNNDIKVIGKEKNEVSISLALKGVYGNRIFTFDKNGKKGEGISFFI
PPIKQDTDLKFIINETIDNSNIKQRGLIYIFVRKNVSENSFKLCDFTTGSTSLMELNSQVKEKKCTVKIKKGDIFGLKCP
KGFAIFPQACFSNVLLEYYKSDYEDSEHINYYIHKDKKYNLKPKDVIELMDENFRELQNIQQYTGISNITDVLHFKNFNL
GNLPLNFKNHYSTAYAKVPDTFNSIINFSCNCYNPEKHVYGTMQVESDNRNFDNIKKNENVIKNFLLPNIEKYALLLDDE
ERQKKKKQQQEEEQQEQILKDQDDRLSRHDDYNKNHTYILYDSNEHICDYEKNESLISTLPNDTKKIQKSICKINAKALD
VVTIKCPHTKNFTPKDYFPNSSLITNDKKIVITFDKKNFVTYIDPTKKTFSLKDIYIQSFYGVSLDHLNQIKKIHEEWDD
VHLFYPPHNVLHNVVLNNHIVNLSSALEGVLFMKSKVTGDETATKKNTTLPTDGVSSILIPPYVKEDITFHLFCGKSTTK
KPNKKNTSLALIHIHISSNRNIIHGCDFLYLENQTNDAISNNNNNSYSIFTHNKNTENNLICDISLIPKTVIGIKCPNKK
LNPQTCFDEVYYVKQEDVPSKTITADKYNTFSKDKIGNILKNAISINNPDEKDNTYTYLILPEKFEEELIDTKKVLACTC
DNKYIIHMKIEKSTMDKIKIDEKKTIGKDICKYDVTTKVATCEIIDTIDSSVLKEHHTVHYSITLSRWDKLIIKYPTNEK
THFENFFVNPFNLKDKVLYNYNKPINIEHILPGAITTDIYDTRTKIKQYILRIPPYVHKDIHFSLEFNNSLSLTKQNQNI
IYGNVAKIFIHINQGYKEIHGCDFTGKYSHLFTYSKKPLPNDDDICNVTIGNNTFSGFACLSHFELKPNNCFSSVYDYNE
ANKVKKLFDLSTKVELDHIKQNTSGYTLSYIIFNKESTKLKFSCTCSSNYSNYTIRITFDPNYIIPEPQSRAIIKYVDLQ
DKNFAKYLRKL
```

280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE

A0A0L1ICU4 **A0A0L1ICU4_PLAFA** (769 aa)
Uncharacterized protein. *Plasmodium falciparum IGH-CR14*

```
MIKIIIGVIGYYILYSSYHIYENIKSPIFNDGNVIKNNEGDKNEQLVIPKEGKKRNSINEEEEEYINKPFKNVLKKDDII
DYHLYFSCEEDIDINKHMQDKYLEKDERFISVYKILNGKYSWNNNVDLLDEKRKKNSFFFLFEKVHPSFDISIPKELIDQ
RKDIYLHILTYVNKELYRYGSRTVVITKRKEKTTTRGKKKFLWKSLIDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEKKYQHGNYEKGGSYKVHKNISNNKPNNKNPNDKRDIKHNNNNNNNKMKKDNFIKSNQNSLNIHKKKKKRKHKDFLF
YIPKKIRFGPVIEYNDFHISKLGFFSNMHVDKDTNTYLLPIYINNDLTPDDEYRMIKMKNSDDMMKKKLKKKRSSEKNDP
YYKENVRNDNNNNNNNNIKNNYLEIYDLSKRTYEMRNERNKKIYEKNSSINNNVHKLEHELMDYIINIEYVPINYNYYNL
LNMLKFNVSYVKKKYNFISFDMDSITTFLCCHITCSMIIYILCIIYIIMEITYLLFDIKMWKRWNNLYTFTYNNDIVMNI
TLLFFILLYLRNIDYGRVIMIYYIMKMMVLIFKIIYNYDICILNDYPYICMNKKSLKEMNKEMIMDEEFEKKIKKKVNIF
MIFSIILIFIYNYFYTKYDSYYSYVIHTLGFSSYLYKFILMLPQIITNIYTRTVQRMSFPFFLFLLVNVLINDLFIIFLR
MPKVHKYYLFADDFILFLFIIQYCIYKKENKIFGAREKLVLLKNAKKNK
```

209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE

224 - 243:	EEEEEEEEEEEEEEEEEEEE
225 - 244:	EEEEEEEEEEEEEEEEEEEE

A0A0L1IE45 **A0A0L1IE45_PLAFA** (1988 aa)
Uncharacterized protein. *Plasmodium falciparum IGH-CR14*

```
MKVQQKKNLKDCNLKSKNTILTSFEKKKNEKDENNLLKFSKLIDNKNKVVNSKLLKNDNYKFNERKESLTRCSTNESLKL
KNIKTLTKDFDYNNNNNNNNINNNNDYNNNNNNNNNNNNNNNNNNNNNNKNNNNNNNGHSKLFFKKNDKDIESKVREEDG
KKSEKKNNDLINNKNEFKVNNKLILKSKEFKSNNNNNNNICKLNNIDDKNKKQQMDTYSPKENEEDNSNNMKKSSSLKNI
KKNQINEMEIISNSVEENHDTHSKGDKENNGVSTKNVKRMNTMSKEINHKNNNLKKHVSKSNSLELKKGKKGEKSKDKLS
NNVSGKKGMNKEKEVVQSSSVRRNSSRYSIDYGRRDSSRRGSVKQEKGKERRGSKNVSKKVSNSKYTRKKSKRIKEESDE
SDDDDEEEEEEDDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDNDNSDNNDESDEVYTNRSRRST
RCSIVKRKSSLCIGKKNSKIIKKSTSKTKNNKKKKGSVIKLVKKKEKLSKKGILKKTNKKTKGKLRKNSKLYHRKKNIKN
EKDGIDEEDIDEEDIEEEEEPSYFDEYNLSYEERKKDLEEKEKKKEIKEKYIKQIKLPKYADDESIIFINNPNYVMVLLF
LTVYKDVLKMNWNFKDIEEMFQNKETTEFGRNFILKLFFFLGRYFNSKSIFMYKYISRIFEDKEESLSRVVNFHELFPVL
ETKKEIKNSGVGSKRKKDKRGKKMKIHQKEDELLYDEEVIGNEDVHIFEEEEDNEHSNDDEDEEEEDNEHSNDDEDEEEE
DNEHSNDDEEKEDVHYNDEEEKKSDLNNDSTKNTVIKEEKDGLHISEGSHNLVNIVNDSMKREESCKNGHIGDNERSGDI
NTNDDKNNADNNDDVDGEKIVDSKNNIENKLDNTVEGKHDINSTEGIIKSENVDDEKGLLTNKLFLEWDDLSVISKLRII
RMLLNLVLCESNNLKKMLGDEKLNYNNGYLGKINNEKYWFIFNDTINIEYKLYLEREEEGSFIFICDDDDMLYTIGYNFL
RNSDTKFMGEALIERYNKVCRERRNRSRMLKQQKKLLCADINLNDPLLGTKKRQHKQVEYFNFDNNEKMRRKKSDMNNNN
PYSVPPTKSYQKNDRSFRLAARNAQKGSVDDLEAWKLNEGSLGIENQGATSGNYNIANDGTNMTETNNINDNHNNDNNNN
NDGVVNADGNNIYGPNNNNVIGSDGNVNNANNTTTNNNNNNNNLGIVKIPLKRGRKKKSEKKKRGRKKKILSVDGIGEIA
NNLSALNVDENRRKSMPNIGRGRRGTYTKRNTKPSVSIKYGTRSHSINKYENDVMSFNEYSLNPGLSMDDFYKNMVMDPK
FFHANMNMNNYMNGGFNMPNNNNSMMNMRNGSKMGNMNNIGGYNFPYMCTPPPMYNQYYMYNGNNMYLPNGGPNNNMNMS
NANNGASVVMGGNVVSNQNTVKDVKAENMHMAKNSIMENRNSIIVNNMNNMNNMNNINMNSMPHKNSFMGNDGINNMNSM
NNNNNNNNNNNNNNNVNNNNNNVSNNNNNNVSNNNNNNVNFMDNMGNNNNNNNNNNNPMNKYNNYMMNRNVLNNMGGTNP
LYNNMYNMKFPYMNNDMMNYNYNINSFQNMNYDKMNKSMFKRYPNFMGGYPYNNMNPYNNFNAFNMNYQQNDQMNQLPNM
QGGYKSKLMNDNLSNYQSFNNNNVKQNHHDNNNNDNNNNKNNSEGGNKNMDDSNKNNDINKNDILDSTKLTEQPVGGVVP
NNDCITRGEDNHRIDLKGDIAEALVGNNNEKMNSSDHNLNSLKNLPNINNTYNMDHMSHMRNSVSASSIGMINPGHMNSS
HSGSIMNKDKFRDLQLNSNNNNNNNNNNNYVKVNPFDHPMKNMNPNLMDDKYPKDNNNMMMMMMNSVYNMMGSDHFHMNN
SHMMDPMGSPKMNDNMYNHNNMNFENTNTNHNNHNNHNNHNNHNNLNNLNNLNNHNNHNNRIQDKLPE
```

414 - 433:	EEEEEEEEEEEEEEEEEEEE
415 - 434:	EEEEEEEEEEEEEEEEEEEE
416 - 435:	EEEEEEEEEEEEEEEEEEEE
417 - 436:	EEEEEEEEEEEEEEEEEEEE
418 - 437:	EEEEEEEEEEEEEEEEEEEE
419 - 438:	EEEEEEEEEEEEEEEEEEEE
420 - 439:	EEEEEEEEEEEEEEEEEEEE
421 - 440:	EEEEEEEEEEEEEEEEEEEE
422 - 441:	EEEEEEEEEEEEEEEEEEEE
423 - 442:	EEEEEEEEEEEEEEEEEEEE
424 - 443:	EEEEEEEEEEEEEEEEEEEE
425 - 444:	EEEEEEEEEEEEEEEEEEEE
426 - 445:	EEEEEEEEEEEEEEEEEEEE
427 - 446:	EEEEEEEEEEEEEEEEEEEE
428 - 447:	EEEEEEEEEEEEEEEEEEEE
429 - 448:	EEEEEEEEEEEEEEEEEEEE
430 - 449:	EEEEEEEEEEEEEEEEEEEE
431 - 450:	EEEEEEEEEEEEEEEEEEEE
432 - 451:	EEEEEEEEEEEEEEEEEEEE
433 - 452:	EEEEEEEEEEEEEEEEEEEE
434 - 453:	EEEEEEEEEEEEEEEEEEEE
435 - 454:	EEEEEEEEEEEEEEEEEEEE
436 - 455:	EEEEEEEEEEEEEEEEEEEE
437 - 456:	EEEEEEEEEEEEEEEEEEEE
438 - 457:	EEEEEEEEEEEEEEEEEEEE

A0A0L1IGG9 **A0A0L1IGG9_PLAFA** (677 aa)
Glutamic acid-rich protein. *Plasmodium falciparum IGH-CR14*

```
MNVLFLSYNICILFFVVCTLNFSTKCFSNGLLKNQNILNKSFDSITGRLLNETELEKNKDDNSKSETLLKEEKDEKDDVP
TTSNDNLKNAHNNNEISSSTDPTNIINVNDKDNENSVDKKKDKKEKKHKKDKKEKKEKKDKKEKKDKKEKKDKKEKKDKK
EKKHKKDKKKKENSEVMSLYKTGQHKPKNATEHGEENLYEEMVSEINNNAQGGLLLSSPYQYREQGGCGIISSVHETSND
TKDNDKENISEDKKEDHQQEEMLKTLDKKERKQKEKEMKEQEKIEKKKKKQEEKEKKKQEKERKKQEKKERKQKEKEMKK
QKKIEKERKKKEEKEKKKHDKENEETMQQPDQTSEETNNEIMVPLPSPLTDVTTPEEHKEGEHEEGEHKEEEHKEGEHKS
KEHKEEEHKSKEHKSKGKKDKGKKDKGKHKKAKKEKVKKHVVKNVIEDEDKDGVEIINLEDKEACEEQHITVESRPLSQP
QCKLIDEPEQLTLMDKSKVEEKNLSIQEQLIGTIGRVNVVPRRDNHKKKMAKIEEAELQKQKHVDKEEDKKEESKEVEEE
SKEVQEDEEEVEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVEEDEDDAEEDEDDAEEDEDDAEEDEDDAEEDDDDAEEDD
DEEDDDEDEDEDEDEDEEEEEESEKKIKRNLRKNAKI
```

575 - 594:	EEEEEEEEEEEEEEEEEEEE
576 - 595:	EEEEEEEEEEEEEEEEEEEE
577 - 596:	EEEEEEEEEEEEEEEEEEEE
578 - 597:	EEEEEEEEEEEEEEEEEEEE
579 - 598:	EEEEEEEEEEEEEEEEEEEE
580 - 599:	EEEEEEEEEEEEEEEEEEEE
581 - 600:	EEEEEEEEEEEEEEEEEEEE

A0A0L1JEN9 **A0A0L1JEN9_ASPNO** (1410 aa)
Telo_bind domain-containing protein. *Aspergillus nomiae NRRL 13137*

```
MDANEQFPTSEPLHANRIPIAQLSPTLERFSKSSIHASVTLLWPYSSSTKSLSLLLAEPDFRLRHSNGQVKTVFHGHIAE
SVAKSQIGIGDIVYLSLDGARLSDNVTAPGAPGKSVAWDIHFDDRVFLEIWRSSNHLSTVKVDPPTPSPNNDTTNAPPAT
PISKGYDRSDQNFSIDGLSSWQSPAFLGRSRTSLGGLADSALDPFAEEDGFVPGKGRKRPRFSMRSNEWRVIDEPESPGE
RGEVPDWTHIFDEDWESESEHSPEDAAEKEERPSDATKMTNPETDSEGVSLTVPVLEADVAMEDVSPASSTTSPERHIAQ
AADGIRLPPPGVSGIAGFSRKRGVLNYSAHLPIETPRLHPIPSPGLPIPSPLVTMSNSPQGYFTPVTATPHSHTSQIPTT
LSQEVTDSENEIPGAQPDTSQRAKCKGTLITSETEDRAIDISEFGAESNATKITLKATSQPHTMANTGSEELSPDEDSKV
AAEPVKVDQFTPRISKKDTGRLDGHLGDTDQLRSPKREGKEVEVDENFIDAQVEAESEKDKEETHQGEEVVNEDKLEDDG
QQIKRINRSLVSGDTQVSGVSRMVEYGPTGSGEEDTETLETLRSYHGLATKSETNPPEMDRGDQTEAVHAGVNEWEREGS
EDESEEELGEEEESEGEQAQEIRKTDREEYADNKEIERDGLEGEWDDEEGWYEEELEEEEEEEEEEEEEEEEEEEEAEDV
YEDEYDDGAESEIISDQMSVDTPTQPPATKKIHPEVIVLDSDSEDEVATASRAYPMSSSRQEASTQEIESSEPEASASEE
GCLRSRSSDNSESSEDEEGEDWSDGNSESEQLMDKNEEMVVDECEQANGEQQGAGHAIYEVSDSGRTRDEKVDEEYQAEN
KAIEEPELKRGQVSVSQPTDIGGASPDAHEQPSPQHHQEEHTIKTPSQASDSGNLDHHSFIMSFVQEPHHDSRNASHELE
TVIDPELQNTGLGKEQVKKEAKEGPHSDSVHAEPRTGVFAKISEAAQNTAQSSFLDGTSFSQALHDSHEAVSERPPQLQH
LVPMDTQLVEPGPPSTDFTTIEILPTSEHTQGSMTAQVQGQMPPAIQTTTSAPAERHLNLAEDVENEARLVSTPQEGQDE
LEDFSGNGDVGTPASFSGDHGQEDDLYSDDEYVGDPDEVHLIGVDRHYPGLHSRLSYFAPLATLVDHYNALVDTISVVSE
VQPVFRAASGKKDFILTLQLTDQSMAGTTLYAQISRPSKAALPLVEEGNVVLLRNFRVKRFSRSIILASVDTSAWAVLKG
LDDKALAHDPPVEYGSEEQACATDLRQWYQEAGMAMVADNQLQASINRESREGTPTSSAALSDSGSIDSTPRDMRGESSF
SSRGSRRGKRSHRRITIHELRDGRRYTEVGSPSGKESIHELRDGTVYANL
```

697 - 716:	EEEEEEEEEEEEEEEEEEEE

A0A0L7K6V7 **A0A0L7K6V7_PLAFX** (3131 aa)
Transmission-blocking target antigen s230. *Plasmodium falciparum (isolate HB3)*

```
MKKIITLKNLFLIILVYIFSEKKDLRCNVIKGNNIKDDEDKRFHLFYYSHNLFKTPETKEKKNKKECFYKNGGIYNLSKE
IRMRKDTSVKIKQRTCPFHKEGSSFEMGSKNITCFYPIVGKKERKTLDTIIIKKNVTNDHVVSSDMHSNVQEKNMILIRN
IDKENKNDIQNVEEKIQRDTYENKDYESDDKLIEWFDDNTNEENFLLTFLKRCLMKIFSSPKRKKTVVQKKHKSNFFINS
SLKYIYMYLTPSDSFNLVRRNRNLDEEDMSPRDNFVIDDEEEEEEEEEEEEEEEEEEEEEEEYDDYVYEESGDETEEQ
LQEEHQEEVGAESSEESFNDEDEDSVEARDGDMIRVDEYYEDQDGDTYDSTIKNEDVDEEVGEEVGEEVGEEVGEEVGEE
EGEEVGEEVGEGVGEEVGEGVGEEVGEEEGEEVGEEEGEYVDEKERQGEIYPFGDEEEKDEGGESFTYEKSEVDKTDLFK
FIEGGEGDDVYKVDGSKVLLDDDTISRVSKKHTARDGEYGEYGEAVEDGENVIKIIRSVLQSGALPSVGVDELDKIDLSY
ETTESGDTAVSEDSYDKYASNNTNKEYVCDFTDQLKPTESSPKVKKCEVKVNEPLIKVKIICPLKGSVEKLYDNIEYVPK
KSPYVVLTKEETKLKEKLLSKLIYGLLISPTVNEKENNFKEGVIEFTLPPVVHKATVFYFICDNSKTEDDNKKGNRGIVE
VYVEPYGNKINGCAFLDEDEEEEKYGNQIEEDEHNEKIKMKTFFTQNIYKKNNIYPCYMKLYSGDIGGILFPKNIKSTTC
FEEMIPYNKEIKWNKENKSLGNLVNNSVVYNKEMNAKYFNVQYVHIPTSYKDTLNLFCSIILKEEESNLISTSYLVYVSI
NEELNFSLFDFYESFVPIKKTIQVAQKNVNNKEHDYTCDFTDKLDKTVPSTANGKKLFICRKHLKEFDTFTFLKCNVNKTQ
YPNIEIFPKTLKDKKEVLKLDLDIQYQMFSKFFKFNTQNAKYLNLYPYYLIFPFNHIGKKELKNNPTYKNHKDVKYFEQS
SVLSPLSSADSLGKLLNFLDTQETVCLTEKIRYLNLSINELGYDNNTFSVTFQVPPYIDIKEPFYFMFGCNNNKGEGNIG
IVELLISKQEEKIKGCNFHESKLDYFNENISSDTHECTLHAYENDIIGFNCLETTYPNEVEVEVEDAEISLQPENCFNNV
YKGLNSVDITTILKNAQTYNINNKKTPTFLKIPPYNLLEDVEISCKCTIEQVVKKIKVIITKNDTVLLKREVQSESTLDD
KIYKCEHENFINPRVNKTFDENVEYKCNIKIENFFNYIQIFCPAKDLGIYKNIQMYYDIVKPTRVPQFKKFNNEELHKLI
PNSEMLHKTKEMLILYNEEKVDLLHFYVFLPIYIKDIYEFNIVCDNSKTMWKNQLGGKVIYHITVSKREQKVKGCSFDNE
HAHMFSYNKTNVKNCIIDAKPKDLIGFVCPSGTLKLTNCFKDAIVHTNLTNINGILYLKNNLANFTYKHQFNYMEIPALM
DNDISFKCICVDLKKKKYNVKSPLGPKVLRALYKKLNIKFDNYVTGTDQNKYLMTYMDLHLSHKRNYLKELFHDLGKKKP
ADTDANPESIIESLSINESNESGPFPTGDVDAEHLILEGYDTWESLYDEQLEEVIYNDIESLELKDIEQYVLQVNLKAPK
LMMSAQIHNNRHVCDFSKNNLIVPESLKKKEELGGNPVNIHCYALLKPLDTLYVKCPTSKDNYEAAKVNISENDNEYELQ
VISLIEKRFHNFETLESKKPGNGDVVVHNGVVDTGPVLDNSTFEKYFKNIKIKPDKFFEKVINEYDDTEEEKDLESILPG
AIVSPMKVLKKKDPFTSYAAFVVPPIVPKDLHFKVECNNTEYKDENQYISGYNGIIHIDISNSNRKINGCDFSTNNSSIL
TSSVKLVNGETKNCEININNNEVFGIICDNETNLDPEKCFHEIYSKDNKTVKKFREVIPNIDIFSLHNSNKKKVAYAKVP
LDYINKLLFSCSCKTSHTNTIGTMKVTLNKDEKEEEDFKTAQGIKHNNVHLCNFFDNPELTFDNNKIVLCKIDAELFSEV
IIQLPIFGTKNVEEGVQNEEYKKFSLKPSLVFDDNNNDIKVIGKEKNEVSISLALKGVYGNRIFTFDKNGKKGEGISFFI
PPIKQDTDLKFIINETIDNSNIKQRGLIYIFVRKNVSENSFKLCDFTTGSTSLMELNSQVKEKKCTVKIKKGDIFGLKCP
KGFAIFPQACFSNVLLEYYKSDYEDSEHINYYIHKDKKYNLKPKDVIELMDENFRELQNIQQYTGISNITDVLHFKNFNL
GNLPLNFKNHYSTAYAKVPDTFNSIINFSCNCYNPEKHVYGTMQVESDNRNFDNIKKNENVIKNFLLPNIEKYALLLDDE
ERQKKKKQQQEEEQQEQILKDQDDRLSRHDDYNKNHTYILYDSNEHICDYEKNESLISTLPNDTKKIQKSICKINAKALD
VVTIKCPHTKNFTPKDYFPNSSLITNDKKIVITFDKKNFVTYIDPTKKTFSLKDIYIQSFYGVSLDHLNQIKKIHEEWDD
VHLFYPPHNVLHNVVLNNHIVNLSSALEGVLFMKSKVTGDETATKKNTTLPTDGVSSILIPPYVKEDITFHLFCGKSTTK
KPNKKNTSLALIHIHISSNRNIIHGCDFLYLENQTNDAISNNNNNSYSIFTHNKNTENNLICDISLIPKTVIGIKCPNKK
LNPQTCFDEVYYVKQEDVPSKTITADKYNTFSKDKIGNILKNAISINNPDEKDNTYTYLILPEKFEEELIDTKKVLACTC
DNKYIIHMKIEKSTMDKIKIDEKKTIGKDICKYDVTTKVATCEIIDTIDSSVLKEHHTVHYSITLSRWDKLIIKYPTNEK
THFENFFVNPFNLKDKVLYNYNKPINIEHILPGAITTDIYDTRTKIKQYILRIPPYVHKDIHFSLEFNNSLSLTKQNQNI
```

```
IYGNVAKIFIHINQGYKEIHGCDFTGKYSHLFTYSKKPLPNDDDICNVTIGNNTFSGFACLSHFELKPNNCFSSVYDYNE
ANKVKKLFDLSTKVELDHIKQNTSGYTLSYIIFNKESTKLKFSCTCSSNYSNYTIRITFDPNYIIPEPQSRAIIKYVDLQ
DKNFAKYLRKL
```

280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE

A0A0L7KBI1 **A0A0L7KBI1_PLAFX** (381 aa)
Casein kinase II subunit beta (CK II beta). *Plasmodium falciparum (isolate HB3)*

```
MNKKGIGIFNIYKKYNEGEVELTDADFYDLTVINDKIDEEIIEDDEEQADNDDQENDNVQEVYNIDDEDNDIHNDKLLLD
QQRDNDVNEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEDDDDDDDDDDDDDDDDDDDDYDDDDEYDEDDFNEATVSWIEW
FCQLKQNLFLVEVDEDFIRDEFNLIGLQTKVPHFKKLLKIILDEDDDDDDDDDDDYDDEDDEINRDSEEMYKNKDMHEQN
AACLYGLIHSRFILTSKGLALMREKYKSGIYGTCPSIYCENAKLLPTAISEIPKFLSPLLYCPRCCETYYPSKNSLLNQL
DGCYFGTSFASFFALSFNIASDKKKVYYTPQICGFTINRNIRETLYMDVNKDNTESSEECQ
```

89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE

A0A0L7KFW2 **A0A0L7KFW2_PLAFX** (1982 aa)
Uncharacterized protein. *Plasmodium falciparum (isolate HB3)*

```
MNVCKMKVQQKKNLKDCNLKSKNTILTSFEKKKNEKDENNLLKFSKLIDNKNKVVNSKLLKNDNYKFNERKESLTRCSTN
ESLKLKNIKTLTKDFDYNNNNNNNINNNNDYNNNNNNNNNNNNNNNNNNNNNKNNNNNNNGHSKLFFKKNDKDIESKVR
EEDGKKSEKKNNDLINNKNEFKVNNKLILKSKEFKSNNNNNNNICKLNNIDDKNKKQQMDTYSPKENEEDNSNNMKKSSS
LKNIKKNQINEMEIISNSVEENHDTHSKGDKENNGVSTKNVKRMNTMSKEINHKNNNLKKHVSKSNSLELKKGKKGEKSK
DKLSNNVSGKKGMNKEKEVVQSSSVRRNSSRYSIDYGRRDSSRRGSVKQEKGKERRGSKNVSKKVSNSKYTRKKSKRIKE
ESDESDDDDEEEEEEDDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDNDNSDNNDESDEVYTNR
SRRSTRCSIVKRKSSLCIGKKNSKIIKKSTSKTKNNKKKKGSVIKLVKKKEKLSKKGILKKTNKKTKGKLRKNSKLYHRK
KNIKNEKDGIDEEDIDEEDIEEEEEPSYFDEYNLSYEERKKDLEEKEKKKEIKEKYIKQIKLPKYADDESIIFINNPNYV
MVLLFLTVYKDVLKMNWNFKDIEEMFQNKETTEFGRNFILKLFFFLGRYFNSKSIFMYKYISRIFEDKEESLSRVVNFHE
LFPVLETKKEIKNSGVGSKRKKDKRGKKMKIHQKEDELLYDEEVIGNEDVHIFEEEEDNEHSNDDEDEEEEDNEHSNDDE
DEEEEDNEHSNDDEEKEDVHYNDEEEKKSDLNNDSTKNTVIKEEKDGLHISEGSHNLVNIVNDSMKREESCKNGHIGDNE
RSGDINTNDDKNNADNNDDVDGEKIVDSKNNIENKLDNTVEGKHDINSTEGIIKSENVDDEKGLLTNKLFLEWDDLSVIS
KLRIIRMLLNLVLCESNNLKKMLGDEKLNYNNGYLGKINNEKYWFIFNDTINIEYKLYLEREEEGSFIFICDDDDMLYTI
GYNFLRNSDTKFMGEALIERYNKVCRERRNRSRMLKQQKKLLCADINLNDPLLGTKKRQHKQVEYFNFDNNEKMRRKKSD
MNNNNPYSVPPTKSYQKNDRSFRLAARNAQKGSVDDLEAWKLNEGSLGIENQGATSGNYNIANDGTNMTETNNINDNHNN
DNNNNNDGVVNADGNNIYGPNNNNVIGSDGNVNNANNTTTNNNNNNNLGTVKIPLKRGRKKKSEKKKRGRKKKILSVDGI
GEIANNLSALNVDENRRKSMPNIGRGRRGTYTKRNTKPSVSIKYGTRSHSINKYENDVMSFNEYSLNPGLSMDDFYKNMV
MDPKFFHANMNMNNYMNGGFNMPNNNNSMMNMRNGSKMGNMNNIGGYNFPYMCTPPPMYNQYYMYNGNNMYLPNGGPNNN
MNMSNANNGASVVMGGNVVSNQNTVKDVKAENMHMAKNSIMENRNSIIVNNMNNMNNINMNSMPHKNSFMGNDGINNMNS
MNNNNNNNNVNNNNNNVSNNNNNNVSNNNNNNVNFMDNMGNNNNNNNNNNNPMNKYNNYMMNRNVLNNMGGTNPLYNNMY
NMKFPYMNNDMMNYNYNINSFQNMNYDKMNKSMFKRYPNFMGGYPYNNMNPYNNFNAFNMNYQQNDQMNQLPNMQGGYKS
KLMNDNLSNYQSFNNNNVKQNHHDNNNNDNNNNKNNSEGGNKNMDDSNKNNDINKNDILDSTKLTEQPVGGVVPNNDCIT
RGEDNHRIDLKGDIAEALVGNNNEKMNSSDHNLNSLKNLPNINNTYNMDHMSHMRNSVSASSIGMINPGHMNSSHSGSIM
NKDKFRDLQLNSNNNNNNNNNNNYVKVNPFDHPMKNMNPNLMDDKYPKDNNNMMMMMNSVYNMMGSDHFHMNNSHMMDP
MGSPKMNDNMYNHNNMNFENTNTNHNNHNNHNNHNNLNNLNNLNNLNNHNNHNNRIQDKLPE
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418 - 437:	EEEEEEEEEEEEEEEEEEEE
419 - 438:	EEEEEEEEEEEEEEEEEEEE
420 - 439:	EEEEEEEEEEEEEEEEEEEE
421 - 440:	EEEEEEEEEEEEEEEEEEEE
422 - 441:	EEEEEEEEEEEEEEEEEEEE
423 - 442:	EEEEEEEEEEEEEEEEEEEE
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439 - 458:	EEEEEEEEEEEEEEEEEEEE
440 - 459:	EEEEEEEEEEEEEEEEEEEE
441 - 460:	EEEEEEEEEEEEEEEEEEEE
442 - 461:	EEEEEEEEEEEEEEEEEEEE
443 - 462:	EEEEEEEEEEEEEEEEEEEE

A0A0L7KIY2 **A0A0L7KIY2_PLAFX** (773 aa)
Uncharacterized protein. *Plasmodium falciparum (isolate HB3)*

```
MIKIIIGVIGYYILYSSYHIYENIKSPIFNDGNVIKNNEGDKNEQLVIPKEGKKRNSINEEEEEYINKPFKNVLKKDDII
DYHLYFSCEEDIDINKHMQDKYLEKDERFISVYKILNGKYSWNNNVDLLDEKRKKNSFFFLFEKVHPSFDISIPKELIDQ
RKDIYLHILTYVNKELYRYGSRTVVITKRKEKTTTRGKKKFLWKSLIDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEKKYQHGNYEKGGSYKVHKNISNNKPNNKNPNDKRDVKHNNNNNNNKMKKDNFIKSNQNSLNIHKKKKKRKHKDFLF
YIPKKIRFGPVIEYNDFHISKLGFFSNMHVDKDTNTYLLPIYINNDLTPDDEYRMIKMKNSDDMMKKKLKKKRSSEKNDP
YYKENVRNDNNNNNNNNNNNNIKNNYLEIYDLSKRTYEMRNERNKKIYEKNSSINNNVHKLEHELMDYIINIEYVPINYN
YYNLLNMLKFNVSYVKKKYNFISFDMDSITTFLCCHITCSMIIYILCIIYIIMEITYLLFDIKMWKRWNNLYTFTYNNDI
VMNITLLFFILLYLRNIDYGRVIMIYYIMKMMVLIFKIIYNYDICILNDYPYICMNKKSLKEMNKEMIMDEEFEKKIKKK
VNIFMIFSIILIFIYNYFYTKYDSYYSYVIHTLGFSSYLYKFILMLPQIITNIYTRTVQRMSFPFFLFLLVNVLINDLFI
IFLRMPKVHKYYLFADDFILFLFIIQYCIYKKENKIFGAREKLVLLKNAKKNK
```

209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEEE
225 - 244:	EEEEEEEEEEEEEEEEEEEE

A0A0L7LWH3 **A0A0L7LWH3_PLAF4** (3140 aa)
Uncharacterized protein. *Plasmodium falciparum (isolate Dd2)*

```
MKKIITLKNLFLIILVYIFSEKKDLRCNVIKGNNIKDDEDKRFHLFYYSHNLFKTPETKEKKNKKECFYKNGGIYNLSKE
IRMRKDTSVKIKQRTCPFHKEGSSFEMGSKNITCFYPIVGKKERKTLDTIIIKKNVTNDHVVSSDMHSNVQEKNMILIRN
IDKENKNDIQNVEEKIQRDTYENKDYESDDKLIEWFDDNTNEENFLLTFLKRCLMKIFSSPKRKKTVVQKKHKSNFFINS
SLKYIYMYLTPSDSFNLVRRNRNLDEEDMSPRDNFVIDDEEEEEEEEEEEEEEEEEEEEEEEEEYDDYVYEESGDETEE
QLQEEHQEEVGAESSEESFNDEDEDSVEARDGDMIRVDEYYEDQDGDTYDSTIKNEDVDEDADEEVGEEVGEEVGEEVGE
EVGEEVGEEVGEEVGEEEGEEVGEGVGEEVGEEEGEEVGEEEGEYVDEKERQGEIYPFGDEEEKDEGGESFTYEKSEVDK
TDLFKFIEGGEGDDVYKVDGSKVLLDDDTISRVSKKHTARDGEYGEYGEAVEDGENVIKIIRSVLQSGALPSVGVDELDK
IDLSYETTESGDTAVSEDSYDKYASNNTNKEYVCDFTDQLKPTESSPKVKKCEVKVNEPLIKVKIICPLKGSVEKLYDNI
EYVPKKSPYVVLTKEETKLKEKLLSKLIYGLLISPTVNEKENNFKEGVIEFTLPPVVHKATVFYFICDNSKTEDDNKKGN
RGIVEVYVEPYGNKINGCAFLDEDEEEEKYGNQIEEDEHNEKIKMKTFFTQNIYKKNNIYPCYMKLYSGDIGGILFPKNI
KSTTCFEEMIPYNKEIKWNKENKSLGNLVNNSVVYNKEMNAKYFNVQYVHIPTSYKDTLNLFCSIILKEEESNLISTSYL
VYVSINEELNFSLFDFYESFVPIKKTIQVAQKNVNNKEHDYTCDFTDKLDKTVPSTANGKKLFICRKHLKEFDTFTLKCN
VNKIQYPNIEIFPKTLKDKKEVLKLDLDIQYQMFSKFFKFNTQNAKYLNLYPYYLIFPFNHIGKKELKNNPTYKNHKDVK
```

```
YFEKSSVLSPLSSADSLGKLLNFLDTQETVCLTEKIRYLNLSMNELGSDNNTFSVTFQVPPYIDIKEPFYFMFGCNNNKG
EGNIGIVELLISKQEEKIKGCNFHESKLDYFNKNISSDTDECTLHAYENDIIGFNCLETTYPNEVEVEVEDAEIYLQPEN
CFNNVYKGLNSVDITTILKNAQTYNINNKKTPTFLKIPPYNLLEDVEISCKCTIEQVVKKIKVIITKNDTVLLKREVQSE
STLDDKIYKCEHENFINPRVNKTFDENVEYTCNIKIENFFNYIQIFCPAKDLGIYKNIQMYYDIVKPTRVPQFKKFNNEE
LHKLIPNSEMLHKTKEMLILYNEEKVDLLHFYVFLPIYIKDIYEFNIVCDNSKTMWKNQLGGKVIYHITVSKREQKVKGC
SFDNEHAHMFSYNKTNVKNCIIDAKPKDLIGFVCPSGTLKLTNCFKDAIVHTNLTNINGILYLKNNLANFTYKHQFNYME
IPALMDNDISFKCICVDLKKKKYNVKSPLGPKVLRALYKKLNIKFDTYVTGTDQNKYLMTYMDLHLSHKRNYLKELFHDL
GKKKPADTDANPESIIESLSINESNESGPFPTGDVDAEHLILEGYDTWESLYDEQLEEVIYNDIESLELKDIEQYVLQVN
LKAPKLMMSAQIHNNRHVCDFSKNNLIVPESLKKKEELGGNPVNIHCYALLKPLDTLYVKCPTSKDNYEAAKVNISENDN
EYELQVISLIEKRFHNFETLESKKPGNGDVVVHNGVVDTGPVLDNSTFEKYFKNIKIKPDKFFEKVINENDDTEEEKDLE
SILPGAIVSPMKVLKKKDPFTSYAAFVVPPIVPKDLHFKVECNNTEYKDENQYISGYNGIIHIDISNSNRKINGCDFSTN
NSSILTSSVKLVNGETKNCEININNNEVFGIICDNETNLDPEKCFHEIYSKDNKTVKKFREVIPNIDIFSLHNSNKKKVA
YAKVPLDYINKLLFSCSCKTSHTNTIGTMKVTLNKDEKEEEDFKTAQGIKHNNVHLCNFFDNPELTFDNNKIVLCKIDAE
LFSEVIIQLPIFGTKNVEEGVQNEEYKKFSLKPSLVFDDNNNDIKVIGKEKNEVSISLALKGVYGNRIFTFDKNGKKGEG
ISFFIPPIKQDTDLKFIINETIDNSNIKQRGLIYIFVRKNVSENSFKLCDFTTGSTSLMELNSQVKEKKCTVKIKKGDIF
GLKCPKGFAIFPQACFSNVLLEYYKSDYEDSEHINYYIHKDKKYNLKPKDVIELMDENFRELQNIQQYTGISNITDVLHF
KNFNLGNLPLNFKNHYSTAYAKVPDTFNSIINFSCNCYNPEKHVYGTMQVESDNRNFDNIKKNENVIKNFLLPNIEKYAL
LLDDEERQKKKKQQEEQQEQEEQQEQILKDQDDRLSRHDDYNKNHTYILYDSNEHICDYEKNESLISTLPNDTKKIQKSI
CKINAKALDVVTIKCPHTKNFTPKDYFPNSSLITNDKKIVITFDKKNFVTYIDPTKKTFSLKDIYIQSFYGVSLDHLNQI
KKIHEEWDDVHLFYPPHNVLHNVVLNNHIVNLSSALEGVLFMKSKVTGDETATKKNTTLPTDGVSSILIPPYVKEDITFH
LFCGKSTTKKPNKKNTSLALIHIHISSNRNIIHGCDFLYLENQTNDAISNNNNNSYSIFTHNKNTENNLICDISLIPKTV
IGIKCPNKKLNPQTCFDEVYYVKQEDVPSKTITADKYNTFSKDKIGNILKNAISINNPDEKDNTYTYLILPEKFEEELID
TKKVLACTCDNKYIIHMKIEKSTMDKIKIDEKKTIGKDICKYDVTTKVATCEIIDTIDSSVLKEHHTVHYSITLLRWDKL
IIKYPTNEKTHFENFFVNPFNLKDKVLYNYNKPINIEHILPGAITTDIYDTRTKIKQYILRIPPYVHKDIHFSLEFNNSL
SLTKQNQNIIYGNVAKIFIHINQGYKEIHGCDFTGKYSHLFTYSKKPLPNDDDICNVTIGNNTFSGFACLSHFELKPNNC
FSSVYDYNEANKVKKLFDLSTKVELDHIKQNTSGYTLSYIIFNKESTKLKFSCTCSSNYSNYTIRITFDPNYIIPEPQSR
AIIKYVDLQDKNFAKYLRKL
```

280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE

A0A0L7LYD8 **A0A0L7LYD8_PLAF4** (2629 aa)
Uncharacterized protein. *Plasmodium falciparum (isolate Dd2)*

```
MGSQSSKSLEPIVDTNESEKSARNVLDVLAQNIRNKAENDAKNYASSLKGKLLQAKFYQPLLVAARIENKVPSNPCELDY
IFHTNVRNPKPKNRCPCLLRDKKRFSNEGEAECGSDKIRDNGERSAGGACAPYRRRHMCDYNLEFINEQNVLTTHDLLGN
VLVMAKSEGKSIVENHPNKGSSEVCIALARSFADIGDIVRGKDMFKRTDKDYVENGLREVFRKINDDLKKSKITDYDNDP
NYYKLREAWWTANRDQVWKALTCTAPDNVNYFRKYSDGSSNFSSEGKCGHKEGTVPTYLDYVPQFLRWFNEWAEEFCRIR
KIKLGRVKKACRDESSKLYCSHNGYDCTKTIRNKDICIRESKCTDCSTKCKLYEIWLGNQRKEFEKQTKKYENEKKKNVS
KNGIFNSNINNEYYEIFYKQLIEKKYENYNDFLKLLNEGKYCKEKISGERNIDFTKSGDEKGTFYRSDYCQICPECGVQC
SGTTCTPKTVIHPNCKDKETYEPGDAKTTDITVLYSADQEGDISNKLSEFCNEEIEKNSQKWQCYYVSSENNGCKMEKKN
GNNTSEEKITKFHNFFEMWVTYLLTETITWKDKLKTCMNNTKTADCIHECNKNCVCFDKWVKQKEDEWNSIKKLFTKEKK
MPKQYYLNINYLFEFFFFLVMYKLKKEAKWKELMDELRNKIELSKEKEGTKDLQDAIELLLEYLNEYAKICKDNNTNEAC
ENSKKSKTNPCANTTGAVSVTKSVMQLASEMQKKAKAQLGSGSDKGESVLKGHIKNAQFKNGASQSQLENICSITEKYTN
DSRYGRSDFKGPCTGKDRDNGGVRMKIGTEWQTGSNIQILDPYLFLPPRRQHICTSNLEKIDVKSVTGYSNVNDSFLVDV
LLAAKMDAAKIKDLYKSQNSKTGLTEENDKESICRALRYSFADIGDIIRGKDLWEHNDFKNLERYLVTIFEKIKAQLPEN
KDKYVNDNEGNKYINLRKDWWEANRDQVWNAMKCKTSPSVTTNCDKEPTPIDDHIPQRLRWMTEWAEWYCKMQKEEYEKL
VTGCGGCRSKGGKCMNGDNECKTCKEACAKYKAKIETWKKQWDKIQQKYEDLYKKATESGDTKSDKDQHVVEFLRKLHEQ
NGGGKSGATTAYSTAAGYVHQEVSHMNCKEQKIFCDNTTSGNNKNYAFEPYPYDYKDKCNCKDDTRPQEKKKDDVCDMVK
ARIGNNDGTKEIEHCKPKKGPFVWKCGDKSLVKDEGVCMPPRRQKLCVINLEHLTENTSDGLRKAFIKCAAAETFFLWHK
YKKDKNGGDADTKLNSGTIPEDFKRQMFYTFGDFRDLCLCTDISARNYTISAVKNNIDKCFNKKCDKGKNDNTERKQWWD
EHKEAIWEAMLCALSYDTTHYNVKPETRKNLSEKNDYSNVKFNGDKATLEEFAEIPQFLRWMIEWSEHFCKEQKEAYRKL
VTGCTGCDVSTDGNCTQKGNCKNCSSQCKEYQKFITQWKVQWEKQRNKYTELYEKTNNDSNHLTDAIERSVIDYFKTLSS
NGTTYSTAGKYINEKGYIHDCNGSKQNNFDENKNGGSNDNYAFREYPHNYKDQCTCTDKSTPEPPPPPPRPPPTPRAAGN
SGNDHRARSERGEDGAARPRPPPAPAGEGGVGRSATSPNGPPRAQQPQPKSKPTGEGLGRSLKPRDPEEPEEEESDEDGD
KGDGGEGDGQQEDEPQEGSPTTKEEVNPCKIVETLFSNTKNFEDACGLKYGPNASSSWKCIPSGDSTTTGKDGAICVPPR
RRRLYIHKVGNGGEDITDDKSLRDWFVKSAAVETFFLWHKYKQDKIKEDKEKKEANGGLVQRETSDDPEQKKLQESGNIP
DEFLRQMFYTLGDYRDILYSGNKDAKNGFNYIFSGDKEMKEKEEKIRTAINSYFSNSVSTSPPTPGPQNSGQPITRESWW
QAHGPDIWNGMICALTYKDSGGKEQPPEVDDAVYKKFFGENSESKDGNPLPQPGTTSTQNGTYQSTYNYHTVTLKDESGA
KPAGGDDTINNPKLSDFVKIPTFFRWLHEWGSDFCVKRTEMLEKIKEECMDGTKQKYSGFGEDCEDQLKDNPTNFKDLGY
SCPKSCRFYKKWIERKKIEFTKQSGAYSEQKQKYEEQNKGAESNSNDGNGFSKILKSLSEAADFLNRLKNGPCSKKDNEN
ENGKENEEDKLNFTNPNETFRPATNCKPCSQFKIDCQKANCTVDEKKEKCKQNGNDFISPEDIKKEGGSTEDINMLVNDD
DTKKFDGLEACKDKGIFEGIRKEEWKCRNVCGYVVCKPKNGNTETGSGENKDQIITITALVTHWVHNFLEDYNKIKQKIS
HCNKKGEEPKCIKECVEKWIKEKEKEWKEIKKRFNEQYNVNGSHDYNVRSVLETFLVQIGAAKDKNKVIKLSQFDKSKGC
CVSPNSEKSKDEDAIDCMLNKLQQKAEKCQQDHKPSDETHQTSCEKSPAPVEDEDDTLHEEIEVKAPNICPVLPKPQAEK
EDACITDAPQPDVKEEEEEKEEEDDDDEEDDVDDDAEEEEEEEEEEEEEEEEEEEEEEENVEEDTAENHTEEESPQPAAP
QPPTPQLLDDPLLKTALMSSTILWMVGIGFAAISYFLLKVLYIYMYMCVLCECVCVWIYVYVLYIFMYL
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2517 - 2536:	EEEEEEEEEEEEEEEEEEEE
2518 - 2537:	EEEEEEEEEEEEEEEEEEEE
2519 - 2538:	EEEEEEEEEEEEEEEEEEEE
2520 - 2539:	EEEEEEEEEEEEEEEEEEEE

A0A0L7M205 **A0A0L7M205_PLAF4** (382 aa)
Casein kinase II subunit beta (CK II beta). *Plasmodium falciparum (isolate Dd2)*

```
MEFVSNDESADDIIQDESNEGEVELTDADFYDLTVINDKIDEEIIEDDEEEADNDDQENDNVQEVYNIDDEDNDIHNDKL
LLDQQRDNDVNEEEEEEEEEEEEEEEEEEEEEEEEEEDEDDDDDDDDDDDDDDDDDDDDYDDDDEYDEDDFNEATVSWIE
WFCQLKQNLFLVEVDEDFIRDEFNLIGLQTKVPHFKKLLKIILDEDDDDDDDDDDDYDDEDDEINRDSEEMYKNKDMHEQ
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NAACLYGLIHSRFILTSKGLALMREKYKSGIYGTCPSIYCENAKLLPTAISEIPKFLSPLLYCPRCCETYYPSKNSLLNQ
LDGCYFGTSFASFFALSFNIASDKKKVYYTPQICGFTINRNIRETLYMDVNKDNTESSEECQ

92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE

A0A0L7M2Z2 **A0A0L7M2Z2_PLAF4** (1984 aa)
Uncharacterized protein. *Plasmodium falciparum (isolate Dd2)*

MNVCKMKVQQKKNLKDCNLKSKNTILTSFEKKKNEKDENNLLKFSKLIDNKNKVVNSKLLKNDNYKFNERKESLTRCSTN
ESLKLKNIKTLTKDFDYNNNNNNNINNNNDYNNNNNNNNNNNNNNNNNNNNNKNNNNNNNGHSKLFFKKNDKDIESKVR
EEDGKKSEKKNNDLINNKNEFKVNNKLILKSKEFKSNNNNNNNICKLNNIDDKNKKQQMDTYSPKENEEDNSNNMKKSSS
LKNIKKNQINEMEIISNSVEENHDTHSKGDKENNGVSTKNVKRMNTMSKEINHKNNNLKKHVSKSNSLELKKGKKGEKSK
DKLSNNVSGKKGMNKEKEVVQSSSVRRNSSRYSIDYGRRDSSRRGSVKQEKGKERRGSKNVSKKVSNSKYTRKKSKRIKE
ESDESDDDDEEEEEEDDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDNDNSDNNDESDEVYT
NRSRRSTRCSIVKRKSSLCIGKKNSKIIKKSTSKTKNNKKKKGSVIKLVKKKEKLSKKGILKKTNKKTKGKLRKNSKLYH
RKKNIKNEKDGIDEEDIDEEDIEEEEEPSYFDEYNLSYEERKKDLEEKEKKKEIKEKYIKQIKLPKYADDESIIFINNPN
YVMVLLFLTVYKDVLKMNWNFKDIEEMFQNKETTEFGRNFILKLFFFLGRYFNSKSIFMYKYISRIFEDKEESLSRVVNF
HELFPVLETKKEIKNSGVGSKRKKDKRGKKMKIHQKEDELLYDEEVIGNEDVHIFEEEEDNEHSNDDEDEEEEDNEHSND
DEDEEEEDNEHSNDDEEKEDVHYNDEEEKKSDLNNDSTKNTVIKEEKDGLHISEGSHNLVNIVNDSMKREESCKNGHIGD
NERSGDINTNDDKNNADNNDDVDGEKIVDSKNNIENKLDNTVEGKHDINSTEGIIKSENVDDEKGLLTNKLFLEWDDLSV
ISKLRIIRMLLNLVLCESNNLKKMLGDEKLNYNNGYLGKINNEKYWFIFNDTINIEYKLYLEREEEGSFIFICDDDDMLY
TIGYNFLRNSDTKFMGEALIERYNKVCRERRNRSRMLKQQKKLLCADINLNDPLLGTKKRQHKQVEYFNFDNNEKMRRKK
SDMNNNNPYSVPPTKSYQKNDRSFRLAARNAQKGSVDDLEAWKLNEGSLGIENQGATSGNYNIANDGTNMTETNNINDNH
NNDNNNNNDGVVNADGNNIYGPNNNNVIGSDGNVNNANNTTTNNNNNNNNLGTVKIPLKRGRKKKSEKKKRGRKKKILSV
DGIGEIANNLSALNVDENRRKSMPNIGRGRRGTYTKRNTKPSVSIKYGTRSHSINKYENDVMSFNEYSLNPGLSMDDFYK
NMVMDPKFFHANMNMNNYMNGGFNMPNNNNSMMNMRNGSKMGNMNNIGGYNFPYMCTPPPMYNQYYMYNGNNMYLPNGGP
NNNMNMSNANNGASVVMGGNVVSNQNTVKDVKAENMHMAKNSIMENRNSIIVNNMNNMNNINMNSMPHKNSFMGNDGINN
MNSMNNNNNNNVNNNNNNVSNNNNNNVSNNNNNNVNFMDNMGNNNNNNNNNNNPMNKYNNYMMNRNVLNNMGGTNPLYNN
MYNMKFPYMNNDMMNYNYNINSFQNMNYDKMNKSMFKRYPNFMGGYPYNNMNPYNNFNAFNMNYQQNDQMNQLPNMQGGY
KSKLMNDNLSNYQSFNNNNVKQNHHDNNNNDNNNNKNNSEGGNKNMDDSNKNNDINKNDILDSTKLTEQPVGGVVPNNDC
ITRGEDNHRIDLKGDIAEALVGNNNEKMNSSDHNLNSLKNLPNINNTYNMDHMSHMRNSVSASSIGMINPGHMNSSHSGS
IMNKDKFRDLQLNSNNNNNNNNNNNYVKVNPFDHPMKNMNPNLMDDKYPKDNNNMMMMMMNSVYNMMGSDHFHMNNSHMM
DPMGSPKMNDNMYNHNNMNFENTNTNHNNHNNHNNHNNLNNLNNLNNLNNHNNHNNRIQDKLPE

418 - 437:	EEEEEEEEEEEEEEEEEEEE
419 - 438:	EEEEEEEEEEEEEEEEEEEE
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425 - 444:	EEEEEEEEEEEEEEEEEEEE
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431 - 450:	EEEEEEEEEEEEEEEEEEEE
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438 - 457:	EEEEEEEEEEEEEEEEEEEE
439 - 458:	EEEEEEEEEEEEEEEEEEEE
440 - 459:	EEEEEEEEEEEEEEEEEEEE
441 - 460:	EEEEEEEEEEEEEEEEEEEE
442 - 461:	EEEEEEEEEEEEEEEEEEEE
443 - 462:	EEEEEEEEEEEEEEEEEEEE

444 - 463:	EEEEEEEEEEEEEEEEEEEE
445 - 464:	EEEEEEEEEEEEEEEEEEEE

A0A0L7M8W0 **A0A0L7M8W0_PLAF4** (174 aa)
Uncharacterized protein. *Plasmodium falciparum (isolate Dd2)*

```
MNKEKEVVPSSSVRRNSSRYSIDYGRRDSSRRGSVKQEKGKERRGSKNVSQKVSNSTYTRKKSKTIKEESDESDDDDEEE
EEEDDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDNDNSDNNDESDEVYTNRSRRSTRCSIV
KRKSSLCIGKRTVK
```

86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE

A0A0L7QQ84 **A0A0L7QQ84_9HYME** (232 aa)
Uncharacterized protein. *Habropoda laboriosa*

```
MSSSLSRIVCIAAYGDGCSGGLTDSMNLHFVAIPVSGQKNWNKALRLPQDEGIRRKDVGIGERDGFNRGVCYCFGGTSRA
GTNRVLLARTWMRVVKGGNHGWVKLKLKYQSAEGRAKKAREGRKARLWRRCNRERRTETEDKDSGRESEKESGETKENAT
VSKTKPGGGGGHVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDGEGGRERDEGGKTRIPR
```

174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE
180 - 199:	EEEEEEEEEEEEEEEEEEEE
181 - 200:	EEEEEEEEEEEEEEEEEEEE
182 - 201:	EEEEEEEEEEEEEEEEEEEE
183 - 202:	EEEEEEEEEEEEEEEEEEEE
184 - 203:	EEEEEEEEEEEEEEEEEEEE

185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE
190 - 209:	EEEEEEEEEEEEEEEEEEEE
191 - 210:	EEEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE
194 - 213:	EEEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEEE

A0A0L7QQ87 **A0A0L7QQ87_9HYME** (226 aa)
Uncharacterized protein. *Habropoda laboriosa*

```
MQFPGDGSVFVRNQDNFIVLMAIRGRDVYGRFAVDRKRTELREVSLMRTAIMRDGTNASGAEPSIEMMIPGKKEAAKLHR
LCVRMRISDPSARAPKKECRVRTKGKEEEEEEEEEEEEEEEEEEEEERRRAGKKGNSEKECTLQRRRSISGFHFVLGKRPG
MRSMREYARRAYAYVGRDQRAKRVEERRVGSEINVFVLRPPSYAPGKDSGLARRFDGEADGRDNGA
```

107 - 126:	EEEEEEEEEEEEEEEEEEEE

A0A0L7QQT1 **A0A0L7QQT1_9HYME** (751 aa)
Zinc finger protein 28 like protein. *Habropoda laboriosa*

```
MELSHEILDTIDINNDKDVMEILKQAISEENIILESEATEDSVETEIEEIIEIIEEIEEDKEESSQDNVTFTENKIIKLE
VNEESIERLQNEQFDKNSEIEDYAFDEDNSDFRTEADKESEKKDQFHNSSNKQVITYDVDEDWQDEDMEEEEEEEDEEEE
EEEEEEEEEEEEEEEEEEEEEEEYEQNSDILNDCTESLQGQRILSSDKKSVNNQTISFTSQTNRLESRDNVEPSDKIERS
KSSHDFKNNVNNDENVDNNINHEIVKNVENNLLYTVLGTKKQSSVKTLQADKSSDAHYIKMEQLDENTIPVGGTIYYEGE
NIETLYVAQTVDDNEQYPYDTATMENDDQTWEACNSDTNQNQEKENSQDQIFLHEDEDGQLYFKDDTGALQPVYLTEDGH
YAIADTTDDYEGKELQAKSQQNVRQMEEESFSVTDNELKSTHSNKQNSIVSTTDLDNEDNTVTISLIISEDEHGQKRTQV
IIPTTDNLKCDICNKSFKTSFQLLRHNRLKHAREEDITTRNFPCDLCPKRYPDQNSLARHRKTHTGDRPFQCLECHKNFP
TSTALRRHLTLHNSKSRPLPCIYCGRRFVEKASLVKHEQSHLAGDQRNHTCDVCHKSFLHATELSLHKKYHDPDKKFDCE
VCGREFNRLNNLQRHMMVHQQQGANEEILSCDVCGITYKFMSSLTRHMVTTHMNPEKLRQQAEEQRRKRENNYRRYLENR
KMYDTQNSGGYGTKRNYHNTRILSGNNDDAA
```

157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE

A0A0L7QSA5 **A0A0L7QSA5_9HYME** (560 aa)
Hydroxyisourate hydrolase (EC 3.5.2.17). *Habropoda laboriosa*

```
MITTNPTVLHANLLTPTGQRLTPTGKISHAKTRVYTQRYRKEWEQMPDFQGWLTSVPFQPTRAYCMYCKKNLHAHRLSLL
KHTCTMKHQRSALLHQAEEKKKVTAVKTCVGEDVEVEEVDEIEAVEHVQTEVEENEDEVEYVVERLETDDELDEKEIKED
VGCEVEEEEEEEEEEEEEEEEEEEEVEVDVAHMQIPSDEEDMKHSIKKVKIERLDSCQDSLTEAMDHMQSEYLEDTDNQE
AVQMEMVVESEEQSNQEMQVMSILPDSEYTDKESPKESRENGRASRRNDSKLDRKSVKLLQDECKEQGESGIVMACPLPI
LGTTYQINSSVAPTSNTIGVLQPVNTIPIAPAQNRTITLTTGGKTLTLTGGTFQPGAQYVLSKLKGKFPTLVVADQKPAI
AANQAQDATKGVQINKDQLAVASTSYQSPKKHVLLKTVKYPSIKKPRISTHVVDTSKGLPVGGLQVSLYKLMDGRWTFLN
ESNTSANGRCVDLVDNMKVNFTAGRYKIHFDVDKYFTLRRIETMYPFIEIVFDVKNPAGHYHIPVLLSPFGYTTYRGSER
```

166 - 185:	EEEEEEEEEEEEEEEEEEEE

A0A0L7QTK5 **A0A0L7QTK5_9HYME** (396 aa)
Molybdopterin synthase catalytic subunit (EC 2.8.1.12) (Molybdenum cofactor synthesis protein 2 large subunit) (Molybdenum cofactor synthesis protein 2B) (MOCS2B). *Habropoda laboriosa*

```
MVTPKDIVKLQHEELNFGEIIDLVTSPNCGAISNFIGITRDNFDNKKVLKLEYEAYEPMAYKEMNSICSKIRSQWNVHHI
AIYHRLGEVPVSKASVMIAVSSPHREESLEAVKYAINSLKASVPIWKKEVYDTQDAQWKENRECAWSNIEDTIDLQESEN
ITISNDTVETVVEYDGEEEEEEEEEEEEEEEEEEEEEDEFRVVIDPNLVQIRATPDELNHRISSFIERKRQQVNIVNVQE
FCCHRHQSDENEDSCARVDAILIRRKDSKSHVKVHRVLNAWGPQMVDQYTLRKATMLGASTANNYSYVLDDRISTTERIL
GMNRPVPKDVYERLKNIEDRILYLEGISPEYKDFWNTDDIINLKGVFKPVRKRTYSMAELDSKLHELEDKYVKKMK
```

177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE

A0A0L7QU22 **A0A0L7QU22_9HYME** (446 aa)
Troponin T (Fragment). *Habropoda laboriosa*

```
RDSGENIEFMKRQEQKRSDLDEQLKEYIAEWRKQRAKEEEELKRLKEKQAKRKITRADEEKRLAQKKKEEEERRQREIEE
KKQRDMEEKRRRLEESEKKRQAMMQAMKEQSKKGPNFTITRKDLAGNLTSAQLERNKTKEQLEEEKKISLSIRIKPLEIE
GFSIEKLRSKANELWDTIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQVASKYER
RVDTRSYDDKKKLFEGGYDTLLAEYNEKLWKQKTEQFMKRTKTPSSPWRDLYGNISQTKERVQASGHPRHLLRVTIYPSM
PFCPLVLQGLTEQQKEVIEKQWAQQKEQFLGRQKTKLPKWFGERPGKKPGDPESPEGEEDVKAAAEDEELEEPQFDEEEE
EEEEEEEEEEGDEKKEGEGEGEEEEEEEEEEEEEEEEEEEEEEEE
```

422 - 441:	EEEEEEEEEEEEEEEEEEEE
423 - 442:	EEEEEEEEEEEEEEEEEEEE
424 - 443:	EEEEEEEEEEEEEEEEEEEE
425 - 444:	EEEEEEEEEEEEEEEEEEEE
426 - 445:	EEEEEEEEEEEEEEEEEEEE
427 - 446:	EEEEEEEEEEEEEEEEEEEE

A0A0L7QYA2 **A0A0L7QYA2_9HYME** (342 aa)
Uncharacterized protein. *Habropoda laboriosa*

```
MDEDISLQDFNDIDVLEEIYGTSKEKNSDEKNVLDETDNQFDEILQIPSNEEIFEKFVNIPGVNEINDNVEPLEEVESIE
PEEYVNDIDVKPEIEEVEEESASVAMKFGVGVALVVAAHFVLVKRWNNEVIFVQNQSKLITSEKQKTEEKITSKKEEIFK
TAKYKAGQGKCEKIERKENKKEENEEVEEDEEEEQEEDEEEEVEIKKEINKNVEWNRNIRKYKESKTKETEMKQEDEIVI
AQETMSEEEEEEEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
ENFDDSELIAKLEAKYGKLQTT
```

257 - 276:	EEEEEEEEEEEEEEEEEEEE
258 - 277:	EEEEEEEEEEEEEEEEEEEE
259 - 278:	EEEEEEEEEEEEEEEEEEEE
260 - 279:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE
262 - 281:	EEEEEEEEEEEEEEEEEEEE
263 - 282:	EEEEEEEEEEEEEEEEEEEE
264 - 283:	EEEEEEEEEEEEEEEEEEEE
265 - 284:	EEEEEEEEEEEEEEEEEEEE
266 - 285:	EEEEEEEEEEEEEEEEEEEE
267 - 286:	EEEEEEEEEEEEEEEEEEEE
268 - 287:	EEEEEEEEEEEEEEEEEEEE
269 - 288:	EEEEEEEEEEEEEEEEEEEE
270 - 289:	EEEEEEEEEEEEEEEEEEEE
271 - 290:	EEEEEEEEEEEEEEEEEEEE
272 - 291:	EEEEEEEEEEEEEEEEEEEE
273 - 292:	EEEEEEEEEEEEEEEEEEEE
274 - 293:	EEEEEEEEEEEEEEEEEEEE
275 - 294:	EEEEEEEEEEEEEEEEEEEE
276 - 295:	EEEEEEEEEEEEEEEEEEEE
277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE

287 - 306:	EEEEEEEEEEEEEEEEEEEE
288 - 307:	EEEEEEEEEEEEEEEEEEEE
289 - 308:	EEEEEEEEEEEEEEEEEEEE
290 - 309:	EEEEEEEEEEEEEEEEEEEE
291 - 310:	EEEEEEEEEEEEEEEEEEEE
292 - 311:	EEEEEEEEEEEEEEEEEEEE
293 - 312:	EEEEEEEEEEEEEEEEEEEE
294 - 313:	EEEEEEEEEEEEEEEEEEEE

A0A0L7RAZ1 **A0A0L7RAZ1_9HYME** (940 aa)
Unconventional prefoldin RPB5 interactor. *Habropoda laboriosa*

```
MAYKKGHEKVAKALQTFEKDLYVNCMVPIGKRALIKGKLIHTNEVLACLGGGYFAKYTAAGAAALCERRIERSEEMLKHL
NTERDLYETRIMLSENDFFNDCAGRDIVEHWNENEITEWKKKHREMERKYHQKLAKLRQEERKKIETEEDLFERLDQLEI
EEELADELNRLKEEGYEYFGEEFEEEEYLYESEESSECVEEEELCKSEESLSVKEDDSKEQPEDVVQTCKIKKSVSFAEP
EDSLKKKEDNLAKKQKECSKTTENSDDILWIEFTHSENNPAAVSDGNSIETPADICRIFSKPKSILKRSPNDLNPEQAPP
PEYSTEEEEEEEEEEEEEEEEEEEEEEEEEEEEETIKPSAYEIVVKDIQERNVTAVASNSMENKEASKDTRPVSKFKRDRFN
FQLSLALMVSMGIVHCEPPLNAQYGVPGNYAGGNSNNNNNNNHVASGGNGFGNHHYDNGNDNDYVDQPMSYEFGYAVKD
QATGNDFGRRESSDGETVRGEYRVQLPDGRTQIVTYTADWRTGFHADVRYEGTATYPDQYNTQNNGYNNNNNNNNNSNNN
NQAGGQSFGFHGNNAAGGYSAGNSGNNGGYNYQAPSGNFNSVPQATPMDSPQIVPTVNHQGAVMSITWFPRAMRDGHSNT
YWLIRGYAALRINCNKGSAQYINSSVDHLLSSLRVFAHNSNMNYHQLTKALLVLSCLASDALAGLLPGGNAGGTGYQYNR
PGGGGGFGGPGGFSGNLGGGRGGDFGGSFSGRPSTSYGPPGGGGSGGGDTGAFSGGRPSNTYGPPGGGQFGGGYQDGGFQ
GGYGGRPQPYSFQYEVYDPPSGNDYSQRESSDGNVVQGEYRVLLPDSRTQIVKYMADDANGYTADVQYEGQAQYSRGGAG
AYGGGAGGSGGYQGGAGGYQQGGYQGGKYDFNTAQLCVQIKKIIHTTRYCIIFIFYLYTK
```

326 - 345:	EEEEEEEEEEEEEEEEEEEE
327 - 346:	EEEEEEEEEEEEEEEEEEEE
328 - 347:	EEEEEEEEEEEEEEEEEEEE
329 - 348:	EEEEEEEEEEEEEEEEEEEE
330 - 349:	EEEEEEEEEEEEEEEEEEEE
331 - 350:	EEEEEEEEEEEEEEEEEEEE
332 - 351:	EEEEEEEEEEEEEEEEEEEE
333 - 352:	EEEEEEEEEEEEEEEEEEEE

A0A0L7RB14 **A0A0L7RB14_9HYME** (1561 aa)
Uncharacterized protein. *Habropoda laboriosa*

```
MKEHGSELPAEQPAKILKSLLKKPGQSKAGSQKNRVVINEKLNEFFAADYIILIKEECCTDYEEDCDCCCQEHELIRLGN
CKECRAELNLRFGVSDNGRYHRENAAGQGCGGETFDCVELRVEDEDEEEEYEVETEGDEEEIEDVQDEKEVVVEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEKEGMNRTKYQPPVTPQPLLERPSSSDQQETLSPPEGYKDVYSNGDFSNVAECCLRSS
LDYLHCQRTTGTKVEEESRRYDQETKKNKDVETTGEQLQKAASNESRHRYLVETITMTTVTERRIVREISQEEDVDSSNS
RVAAERKAGGSHGRGTIEDDDSTEQKESSISNREEEEEDGKEMKELSLVFKLGNSSLTGNSLKPNSAVRQLFPNPRFVSP
PPAPIGKLISSVRSSSLDDDSPAFLVNAENLRFLDIAKRSNISENRTDQASFLNDQSANPIKRTIERNTLRRSLLDKYRA
NSRKKIPPSNNLSLEERIRRLTCVDQEEDDDDTEIEGGLLVRAPPSRQEETTTSTKTFVRNTTAVGQVLPVAIHLATKFS
GALSDAITTTITTTTTTTANTTMTATAVTSNSSLVITTATATTATTTTITGSNYCYKLNASTDSSTITDNVQNQSTYKKLT
DLFAYKRNVHANMPDLGLGNNGKSSSSNNSKNSLKTSNSDMRKQFLASLAPLSCVTVDNTDAREDYYQRSSSYNAFSPYQ
NIEMTLQENDRNYVGPPDVTKGTPIITSRLDIGDSATDELLAFVEQDKFRTERIKRRYNEVENQYRPILTNNTNGFTVDD
TRQQLTHRENAKRGNNGDKKNRGGEMANRSYNNGNDNNGGGDNEEDNEDDELNDYGFNRRPSVTGIKQRQSDNIGQEAFH
RRATLENDNANIPKTSFHSSLPSCYENNCVKVNSRIALYDETIDDSMRNSFVGAALVTDEPDTSTINRINTMQKQIDDIY
RIVEKNTTVTAQNSLERESYTDEAFARQHSRLPPPPNDAATFRFYQDPRNGQQYFQEQLNVANTRVARGIATGAEDIDGG
SIVAPTRDYTANGRSNYRCNVVPTTVYTGLPANGKCYRTVYFVPYNGLSDPTYQNIQRILPSHPSPSYANHIERYPYPRS
NKNDRRLQAQTQPPPPPPPPPPSTAQQLGYYHLGNRSMSPIPPNLPRNDHASSGHSAGSSSAPFDSRLASIPSSPNPPIA
ALHHPTRQTLHLHLHRHQQPDDFRISGLTLSSVPRAADNRALQFRRHAQRQHHHQPTFYRLPSTIPTVPSSSSSSSSSSS
YTVIAPSRCAAFAGTGTTEGSYRYYQVHLGRTVXXXXXTQTLLSSSASISIPSCSTTFSPSLPQHSPLYSPSFSSLPTVT
SVTPRQTSSSFLPPNHISETVHDVNFDGICRAAEVVQSVPNLTGITTPSTTTITTTTTTTTTTTTTTTTTTTTTTTTTT
TTTPILSSSFSVVSSSSSSSSSSSSSSSASSCSFSSSSSSCSSSSSLQIPCSPSKLLQQREIIGAYSAIERGVPEGAASAP
SHDASQPGILLTANSYITHNSTGVQVLPTHAQNSVYYAMNV
```

154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE

A0A0L7RB33 **A0A0L7RB33_9HYME** (255 aa)
Uncharacterized protein. *Habropoda laboriosa*

```
MFLKVDFRRKDARQKEIVVVFYFLYNRGKKGKAVSRGGEEEEEEEEEEEEEEEEEEKEETGRGMVKEEEAGWVCHLSLVK
SLTYIPKVTRSLVDFDKARYHGTEANAGFCFGTVVSHSVENNGAIIDGGGRSIDDGVCTKVEIATEFPVAKSVGEGNVVA
EPNGFEGASTDQSEEEEEEEEEEEEEEEEEEEEEEEEEGEVRYGVLTGLTFTSFPVQGTYSSRTEGTTVVQGSIRDLLGMFI
DVNPYSGKTIMSAFC
```

174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE

A0A0L7RCR5 **A0A0L7RCR5_9HYME** (1174 aa)
Testis-expressed sequence 2 protein. *Habropoda laboriosa*

```
MSSKHSPRKVTLAMIKGKPITTSVPVIHYHASDDELEEIYPSTDEEKRSTPEFERLSSKVTCIPSDVSENNSESRSVGTE
NVLPEGTPPSLHAWKVLSDIKGKITKTFEEKLSEIKSDKRKRCHSRAESSSISDLEDLGSVTLYDENIDEKQSSEPATMI
IRRRGNPARYVGFSGVKTGLKDKSLQDECVESGIEASEFSQDISEDVPGYSSNAKPPDENNFTTLRRQMYTRPSDAFPKQ
INFKTMFSRSIQRLICQGMYKFFTALIAISCIYYVIPLPEYLLGFTMGIFITVAIYDIVTKLKKILTTLPDERYVSSPTV
PVLEIPAVEEHAVVERFQGWLNELPYSYEPNNYHVARTKSVFFKLEGNILRIMETRMKVPKKAVWDEPKHKLKFVRRRVY
NLTGAKVELAPRGLARRRRWSKKYPICVTVEKGALISNVTLKSSTNGECSMDNYHQEEEAEEEEGGEGRLRRNARKVYTS
TDESRKKHRRREAANETKIGKRMSMLKKWNKKKEIWEEEGEEEEEQQRRGIEKREKEEEEEEDEMQNEEEDGNVEEEEVE
EEEEVEGEEEGEEEEGEEEEEEEEEEEEEEEEEEEEEEDEDEAAVVKVINSDDRRDGDVAEFKKLKNTKKYLAKKDERRKE
LKIFVFARTDREKEDWYRRLVSAAASRCVKKQDSLLFTIDPSTDTSNTTQSSTTVQKSTGESRSSFSANNSHENVPELNY
NAYMAKYLNTGECSASSESGFSASAENTLWINCLIARILFDVRKCPETISLIQDKIQRKLSNIKLPYFMECLLVSEVAIG
QGAPVIRSVTKPVSNERGLWLDLDVTYKGSLTMTVETKLNLMKLTRTGSVPGSANVVIPSGKHGELVTRSPIFDSDLEDT
PETSTEDDYDAPGTQSCNTAKEATSAQSSGKKFLSMVDRIAANKYFQHATELYYVRKAMEGVSNTEIRLMVTVSSIEGCL
SVNIPPAPSDRLWYGFKPVPKVSLTVKPAVGERTVNIVYVTKWIETKLLREFEKLVVLPNMDDLVVPLCLFYTVVAEQNK
DYIAYIYSADTRKLSTCVSRFSQRTTSMLSLQNFACVVFQACMVLDDVGITAIYSSLDYTYTYVHIVVSVLINSTIKRSI
ISETRTCNHNSRIVVNCVLKSHEFFFFFFFCTCYSFVKRKCRFVIFRTVAYIDS
```

577 - 596:	EEEEEEEEEEEEEEEEEEEE
578 - 597:	EEEEEEEEEEEEEEEEEEEE

A0A0L7RDK2 **A0A0L7RDK2_9HYME** (893 aa)
Glycogen [starch] synthase (EC 2.4.1.11). *Habropoda laboriosa*

```
MSRERGARRFYRMDSSNDLLEFMDRGYSAQHENRWNFEVAWEAANKVGGIYTVIRSKAFVSTEEMGDQYCLIGPYKETSA
RTEVEEADFPHNSPLHLAVQTLRDQGFKFSDKGKCVIRLRTSKTYITIKVRSLIEVVTGTWLVDGNPQIILFDIGSAAWK
LDEYKQELWNTCNLGIPHLDIEANDAVILGYLVCQFISEFRQVAEEYSDVPPRVVVHCHEWQAGVGLIALRTRHVDVATV
FTTHATLLGRYLCAGKTDFYNNLDKFNVDEEAGKRQIYHRYCMERAASHLAHTFTTVSDITGFEAEHLLKRKPDIITPNG
LNVKKFAALHEFQNLHAVSKEKIHEFVRGHFYGHYDFDLDKTLYFFIAGRYEFGNKGADIFIEALARLNHYLKSSRPDTT
VVAFLIFPARTNNFNVESLRGHAVTKSLRDTISDIQQKIGRRMYELCLSGRMPDAQDLLQKEDTIKIKRCLYALQRNGLP
PVTTHNVVDDWNDPVLNSIRRCNLFNTVNDRVKVVFHPEFLSSTNPLFGLDYEEFVRGCHLGVFPSYYEPWGYTPAECTV
MGIPSITTNLSGFGCFMQEHIADPMSYGIYIVDRRYIGLENSVQQLAHYMFDFARLSRRQRIIQRNRTERLSDLLDWRNL
GIYYRQARIKALMTVYPELASEYAEGGVGRFSYPRPISEPPSPSSSRHTTPAASVHGSDDEDEDVDDEKEREEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
LQPAAGKNWKVVATGWPRVTSACAFSKWLRCTTPNATINSGVETRQVDVATRGEPLTQRRYVEFARENDSGIGKTDLDIV
QQLHGLAGIPDAR
```

712 - 731:	EEEEEEEEEEEEEEEEEEEE
713 - 732:	EEEEEEEEEEEEEEEEEEEE
714 - 733:	EEEEEEEEEEEEEEEEEEEE
715 - 734:	EEEEEEEEEEEEEEEEEEEE
716 - 735:	EEEEEEEEEEEEEEEEEEEE
717 - 736:	EEEEEEEEEEEEEEEEEEEE
718 - 737:	EEEEEEEEEEEEEEEEEEEE
719 - 738:	EEEEEEEEEEEEEEEEEEEE
720 - 739:	EEEEEEEEEEEEEEEEEEEE
721 - 740:	EEEEEEEEEEEEEEEEEEEE
722 - 741:	EEEEEEEEEEEEEEEEEEEE
723 - 742:	EEEEEEEEEEEEEEEEEEEE
724 - 743:	EEEEEEEEEEEEEEEEEEEE
725 - 744:	EEEEEEEEEEEEEEEEEEEE
726 - 745:	EEEEEEEEEEEEEEEEEEEE
727 - 746:	EEEEEEEEEEEEEEEEEEEE
728 - 747:	EEEEEEEEEEEEEEEEEEEE
729 - 748:	EEEEEEEEEEEEEEEEEEEE

730 - 749:	EEEEEEEEEEEEEEEEEEEE
731 - 750:	EEEEEEEEEEEEEEEEEEEE
732 - 751:	EEEEEEEEEEEEEEEEEEEE
733 - 752:	EEEEEEEEEEEEEEEEEEEE
734 - 753:	EEEEEEEEEEEEEEEEEEEE
735 - 754:	EEEEEEEEEEEEEEEEEEEE
736 - 755:	EEEEEEEEEEEEEEEEEEEE
737 - 756:	EEEEEEEEEEEEEEEEEEEE
738 - 757:	EEEEEEEEEEEEEEEEEEEE
739 - 758:	EEEEEEEEEEEEEEEEEEEE
740 - 759:	EEEEEEEEEEEEEEEEEEEE
741 - 760:	EEEEEEEEEEEEEEEEEEEE
742 - 761:	EEEEEEEEEEEEEEEEEEEE
743 - 762:	EEEEEEEEEEEEEEEEEEEE
744 - 763:	EEEEEEEEEEEEEEEEEEEE
745 - 764:	EEEEEEEEEEEEEEEEEEEE
746 - 765:	EEEEEEEEEEEEEEEEEEEE
747 - 766:	EEEEEEEEEEEEEEEEEEEE
748 - 767:	EEEEEEEEEEEEEEEEEEEE

A0A0L7RJ18 **A0A0L7RJ18_9HYME** (2404 aa)
Death-inducer obliterator 1. *Habropoda laboriosa*

```
MSSSYVIEPPEGGSEKKDDTLIIIVNDDGTISVDQETLQSLILNQSNANVSVVRVGQAETDTENGDITLTVDPPSFTSAA
VNSTGTSTDASSLVDPFMEMDPEQLERLETALQSEEAKQILGENVTAMLDMLTVEEQQNSIRYSVKLDHCYTSRLSPSDP
KPRDPLPVIDSPTSDDGLQYARQLSPAPGTSKTSSPIGADTENTIVIKPKVVGKTGKPVGRPRKNPLPASVSVYNNSKSS
VGITSTPKSVTHTVPRNLTDQARSNDEDEDEITSSSTESSDSDPPSDNDSDFGPRGPKRGGMRARGGRKGLTTRGGSMTA
TRRRGSNKQMDMEQVRRLDMEMAAAVNAMKSPEKDEKLGGFGLVKGKRQFKTAVGRKKEESQRIESSSAMSEDVPVNFDK
PLQTTNQVKANLINANMIKGDMILTKPGQGRSNQKVTFVQKQVLMKPNDLKNIDIKKQVVLPKGKFLGQTGAKFFATKDG
KLLQIPVTTKTITSNVSVAQMKGAIPQVSPTQQSVAVIQNQTFNLLVGTKKHLKKENRKSPAYMVDSLGPALFSTPDIIR
RVGSNGESKIQENVVTSLISTTPSTVASGNALTQQATHSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS
ISTSLAAPNRSVESKPGIKTNATEEIQPTLDSGGIIEGEEHLLATLEMEASKHEEELLAEALLLQEELGVDLAEHAALVE
QGGSATPESLTSNNILIPPLITSEPEGTKPLGDAPTAIIVTATMSSTTTVVTASNASTNVSRESGRKVGKEDKEPIQIIR
GGRVITLPPIEAPATRSKRLQAKTEAVQKTFELVKRTEKLNYSVQQQRPSQSVKHEIRPNIVDEGGDQKEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDNSDSEDDPDRLWCICKRPHNNRFMICCDVCEDWFHGKCVHVSKAMG
QQMEEKGIEWVCPNCSKKKDEEAKAKMNIQNVSGKQQRIQSNAVSDNSKNLATLHQTSFGRETSSSIHSACDYDSVQYSS
GMQCVVCKKEARNSSIYCSDACILAHAQETLTKDKPVAATGPTISPKGTRASPFDPAAKPKIDARVIVFERKSGRVLTGS
DAPTRSNLRAWLKEHPTFEVVGTNNLGTVQIGKTISTIQTQIPGKMGKSTLLSPVKGQNLPKMTYTKVPGSKQMILTAGN
KKITTNKSPLLLKTATAKSVGQAQTKQLSGVVSPKQTAANMKKQELKQASLQSKQQQVKPSPQKKPETEPIRVNIRKTLT
ELLSSRIKETEDLKLTNEEIIDLAYNIELELYKYFKDTGAKYKAKYRSLVFNIKDTKNLTLFRKIADRSLTPDAVVRLSP
DEMASQELAEWREKETKHQLEMIKKNELDLMAQAKSIVVKTHKGEQIIENDGGIDHVDPKTPVQDIVTALNSADSITSTV
DDTEKELERMNEGEDRSRVKEDGKKSRSLDDKRRKDKDKDRGREKEKDKERDKEKERGREKKTSDSRRGRSMSRSRHNKH
GREDRERSKTREKSRERKSRDKEGKRERERKDRDKDKERDRGRERERERERERERKTTKQKERERERERERHRSNENSSRNRGS
DSFLHYDLSKDAEKRGEEEDDDEEEKKRETEKKEEFQSGLTMGTSGEKSIDDRLWRHVEDEMTSNNTIDGGNDSDVSDRE
PTSTVTIKTPDINEEIDKEREQEQGMTVERETPKGGGGWQTVWRGFVNMVDVAKFFITAQEVSGHAKDLMDDLPDTVDVV
GRISHETVWDYISKMKKTGSKEILVIRLTAANDEEKIPYITLYSYLNSRSRLGVVGNVSKNIKDFYIMPFSSQSTIPQVL
LPLNGPGFEEHRPHLLLGIIVRNKRKRLAAGITSSSVPMKLSKKDTDRSYTPPLMMVTGSKDKPMRGATGGMQRETTESA
KEKQHHPVTQTTLDSLNRAHIGMSRSTLLDTATICKIVPELSSKIDLTSSPGKVPIEDDGDEPYSPGQMDEEEQEVDLDL
RASSTSTATVISSMSNSMSIDGTTIDNGIISSSKNSNELQRKMEELNRQIEEQKQQIQSISSSFLGESTPTLPGLGLDPP
VNDECEEAYSPSDARSFTPPPPPGISKFTQPILEKVSNITIPPNLQEILANVKRQESSKVDPYLPSKPSATFLTTVNSSM
YQNSEKYSSSPPAVKLSVGGSGKTNSEKASSLDISSNHRESVSKEKENKSTLSSLSDLDLIRKAEEELAAVAAASAAAAA
AAAIASSGSIVAENSVPSSLSTTTSPQPQPQPQPQALPTIIGTCSSSPSLLSALASESPSSHESTSPYKSPFPEPFKRNI
APEQPKPPGLEDEDFPPFPSTPPNVENNLSKTMLSSRSKFVPKSGIVLSIKRKINDDGSIASCTPNKAPRVKSRWGQGPS
ESVD
```

870 - 889:	EEEEEEEEEEEEEEEEEEEE
871 - 890:	EEEEEEEEEEEEEEEEEEEE
872 - 891:	EEEEEEEEEEEEEEEEEEEE
873 - 892:	EEEEEEEEEEEEEEEEEEEE
874 - 893:	EEEEEEEEEEEEEEEEEEEE
875 - 894:	EEEEEEEEEEEEEEEEEEEE
876 - 895:	EEEEEEEEEEEEEEEEEEEE
877 - 896:	EEEEEEEEEEEEEEEEEEEE
878 - 897:	EEEEEEEEEEEEEEEEEEEE
879 - 898:	EEEEEEEEEEEEEEEEEEEE
880 - 899:	EEEEEEEEEEEEEEEEEEEE
881 - 900:	EEEEEEEEEEEEEEEEEEEE
882 - 901:	EEEEEEEEEEEEEEEEEEEE

883 - 902:	EEEEEEEEEEEEEEEEEEEE
884 - 903:	EEEEEEEEEEEEEEEEEEEE
885 - 904:	EEEEEEEEEEEEEEEEEEEE
886 - 905:	EEEEEEEEEEEEEEEEEEEE
887 - 906:	EEEEEEEEEEEEEEEEEEEE
888 - 907:	EEEEEEEEEEEEEEEEEEEE
889 - 908:	EEEEEEEEEEEEEEEEEEEE
890 - 909:	EEEEEEEEEEEEEEEEEEEE
891 - 910:	EEEEEEEEEEEEEEEEEEEE
892 - 911:	EEEEEEEEEEEEEEEEEEEE
893 - 912:	EEEEEEEEEEEEEEEEEEEE
894 - 913:	EEEEEEEEEEEEEEEEEEEE

yle="background: #FFFFDD;margin-bottom: 12px;margin-top: 24px;padding: 5px;"> A0A0L8FF58 **A0A0L8FF58_OCTBM** (1988 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MDLFNDCSDVLPDNSPTKKGEARNDRFYPNILDAEENQISETVEEQIESNNISLAKPAPICQPVNILPEGENTIISSSQT
NTLKRSRKDIVETCSNDFRNFCNNACVLDIEEVEDKITGQSSKNMNSDYKNLDVSRNLTGACYSNSDVGENRSNANYGNS
GKSDNKQEVSYKSNSGLIETEPTCQPIEVLSYCDDAANKKISLPYTCSSQKNIFNGCNDISNYSKNSKDVIRTDRFYPQI
QVDEENRKSDKKEKYVESNNNCSAKLGLRCQPIVIPPNDRDAVIYSSPTNVLNYNRNDIVEVCSNNVRNNVPLDNNAEEG
DNETSQSTNMMNTNYRNLNVNRNATDEDYSNPDGMQTNSSSGNSDESDDPMNANRSKTDVKGKWTNTNYGNSNVRGNLLN
SNYVNLHITNNSLNENCRNQTYTNHKKEKVEEERETEEDESMKLDNSKSGLAETDPRCQPTEVPFLCYPAASEKENVYHR
SCSKMKNFNGCCDAELDYEHTNKDVLRNDEFYLKIQVDENWRNEKKAGYVESNNCYLEKSKSISQSVVNSPKSRDVLEHS
RNDVVKTCSNNANNFYNDTPVFTNSEEDKERAESLMSINANDRNPDVTGSPMRVNDGGLDVGGERMATDYGNLDVSGNQQ
KANNGDSDLNGTGMKTNYNKPEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDRQHHQESLEVDDRNKSLVEMECHPNVVLL
TCSDATSERTSFSHTTSSQMVIFNDGTNAVSDYGLLHEDVTRNDRFHPTILAGEEDRRSKNAGECVEVDNGNTRLEQSDS
CKGVICRSQTKILDQNRNDIVEACSGDVHNFCNDVDILKNVEEIKEKDQSPKHTNLDYENPHASQNPTKENPNNPNVCGN
RTNANYGTSDINENLTNKNCGKSGITKIPTTEKKCGKSKESLTHCNASYNELNVSSNQMNTSYRISEVNGKLTNEKLSIT
EDDNDDEKEKSNKIHKSTKNLVETEPKCHHAEVSLMCNECNGNANFSHTSSSQTNIVNGCSYTDENVIRNDEENQRRQKV
EEHEKNNKSNRRKPESKCQSVVSPSRHRDVSIHGLQTNILDRSRNGIVQTFSNAVLNFCNNVHAVGNVEEKENETGHSSA
RINTKYRDPGVCRNPTNADYSDVCENWNNTNYENSYIRGNSENLKHKTSEANGSQTKANHKNSEKGDKKREGKLVTKILK
GNNGLAEIETKPHTIEGHYGNNAASDRANISYRSNSQMDRFNGDTNNDVTNDRFYPQTQEDKEDRISQKEGGHTETGNCS
SSLSKLGSICQSVGNPVICSDAISSLQTNILNPISNDIVERGLNNLYYFRNNVPALVSAQDDETNQTSNKMNATNGNLDV
SRTTTQISCDNSNDIGKWTNSICENLEAHENRVDASCGNWNVNRKRASENCENLYVSGDQPGNTDVSEHSRNLNYVYSDI
SGDRVNLYRGKLENGDIEGEEMSMNIHKNNNDLGETEPERHPREVPFPCNITVNAKANLSEVNSSKVDSFNGCSDVVSDT
GHVIKDATRDDRFYLKTMPGDEDQREKEVEVEYVETFNSNSSLAKPELRCQSVDNSTTDSHTTVHESQEAILSDNNNSSK
DVVGRSNGSRNSGSTVPFFNNAEDNSPKQFSNGTNPNYGNSDVIGNSTNGNYGNSEYEEDKDQEISKKIDNGNSYLGEAQ
LTHNSTKVPFLCNAAASKKTDFPYTSRSLIHDSHGCSDVVSNYNHIEEDVARDDRFSPKTQANEEARGGQKEEECVKSDN
SSNSSLPTISPVCRPVANPPVCSDAVNCSQSRNDTVKKCSNDVRNCCSKTLSALDNANDGGLTGEISNRTNTNCKTMDVD
GNRTNANNLAQGLSGNSTNASYGISDLNRNHANIPLFQIENPNCSDDQRVPAANDKIASSPMILSIDQQESFYSDLPSKR
HFNYKGNFTWKKPLEDCSVTLSTNSAETAAIVDTPTMNIRKILRIGLSKRQKIPALHPYIKRRRIDDE
```

662 - 681:	EEEEEEEEEEEEEEEEEEEE
663 - 682:	EEEEEEEEEEEEEEEEEEEE
664 - 683:	EEEEEEEEEEEEEEEEEEEE
665 - 684:	EEEEEEEEEEEEEEEEEEEE
666 - 685:	EEEEEEEEEEEEEEEEEEEE
667 - 686:	EEEEEEEEEEEEEEEEEEEE
668 - 687:	EEEEEEEEEEEEEEEEEEEE
669 - 688:	EEEEEEEEEEEEEEEEEEEE
670 - 689:	EEEEEEEEEEEEEEEEEEEE

A0A0L8FG31 **A0A0L8FG31_OCTBM** (86 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MVNKERRQKIIMKQKKPQEVVGDDGNKKEMENGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEQEEEQEEKEEEEEERQIM
EESKSR
```

34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE

A0A0L8FG54 **A0A0L8FG54_OCTBM** (88 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MDEEEEEEEEEEEEEEEEEEEEEGLEEEEEEEEEKEEREEEKEKEKGMKENTIKKRKVKKRIKRRRVRRKKRSTRMRRMVM
VMMTTMKT
```

3 - 22:	EEEEEEEEEEEEEEEEEEE

A0A0L8FG68 **A0A0L8FG68_OCTBM** (147 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
ELIRKEEEEEEEEKKEEEEEEEEEEEEEEEEEEEEEEEEGEVVEEEEEEEEEEEEEEEEEKKKKKKKKKINKSCKKLIKK
DEWNMKKRMRIRKQKGDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEANEEKKKKKKKRI
```

16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE

A0A0L8FG82 **A0A0L8FG82_OCTBM** (63 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MGEKEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEGENIEDDDESVQHSNNFAKLPLNS
```

8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE

A0A0L8FHJ5 **A0A0L8FHJ5_OCTBM** (58 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEETAAAAVINASIKISSFNCC

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE

A0A0L8FJ82 **A0A0L8FJ82_OCTBM** (49 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERPGILMGRVLTDSIDHIT

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE

A0A0L8FJW9 **A0A0L8FJW9_OCTBM** (84 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

MSIAVMKRRNNKEEEEEEEEEEEEEEEEEEEEEEEEEEEERQQQQQQQQQQQKQQEDILNIELIKLMKRKKDSKNDKKKF
NVRK

13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE

A0A0L8FKI6 **A0A0L8FKI6_OCTBM** (131 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MHLAFINNVEWFVKLKHLTFNCRQLTMTQKGEEGEEEEEEEKEEGEEEEEGEEEEEEEEREEEEEEEEEEEEEEEEEEE
SEVFYMKTDDLEERKDDKNARKTNEKESEKKIMLVLANVYRQMLGSHVYWQ
```

61 - 80:	EEEEEEEEEEEEEEEEEEEE

A0A0L8FKI8 **A0A0L8FKI8_OCTBM** (54 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEHHHHHHSDFFFC
```

2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE

A0A0L8FKV1 **A0A0L8FKV1_OCTBM** (59 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEWVYKKEVQTGGEEI
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE

17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE

A0A0L8FLA1 **A0A0L8FLA1_OCTBM** (447 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EEEEEEEEEEDEEEVEEEVEEEEEEEEEEEEVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVEEEGE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEE
EEEEEEEEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEEEEEEEEEEEEEKEEGEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDIHDDDNDVNTVTIIIISPSSAFVVIIIIITTT
TTIIIIVIIIIIIIIIVVAAIIIIIIIIATAATAPLPHYTQHHGHNR
```

33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE

92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE
180 - 199:	EEEEEEEEEEEEEEEEEEEE
181 - 200:	EEEEEEEEEEEEEEEEEEEE
182 - 201:	EEEEEEEEEEEEEEEEEEEE
183 - 202:	EEEEEEEEEEEEEEEEEEEE
184 - 203:	EEEEEEEEEEEEEEEEEEEE
185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE
190 - 209:	EEEEEEEEEEEEEEEEEEEE
191 - 210:	EEEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE
239 - 258:	EEEEEEEEEEEEEEEEEEEE
240 - 259:	EEEEEEEEEEEEEEEEEEEE

241 - 260:	EEEEEEEEEEEEEEEEEEEE
242 - 261:	EEEEEEEEEEEEEEEEEEEE
243 - 262:	EEEEEEEEEEEEEEEEEEEE
244 - 263:	EEEEEEEEEEEEEEEEEEEE
245 - 264:	EEEEEEEEEEEEEEEEEEEE
246 - 265:	EEEEEEEEEEEEEEEEEEEE
247 - 266:	EEEEEEEEEEEEEEEEEEEE
248 - 267:	EEEEEEEEEEEEEEEEEEEE
249 - 268:	EEEEEEEEEEEEEEEEEEEE
250 - 269:	EEEEEEEEEEEEEEEEEEEE
251 - 270:	EEEEEEEEEEEEEEEEEEEE
252 - 271:	EEEEEEEEEEEEEEEEEEEE
253 - 272:	EEEEEEEEEEEEEEEEEEEE
254 - 273:	EEEEEEEEEEEEEEEEEEEE
255 - 274:	EEEEEEEEEEEEEEEEEEEE
256 - 275:	EEEEEEEEEEEEEEEEEEEE
257 - 276:	EEEEEEEEEEEEEEEEEEEE
258 - 277:	EEEEEEEEEEEEEEEEEEEE
259 - 278:	EEEEEEEEEEEEEEEEEEEE
260 - 279:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE
262 - 281:	EEEEEEEEEEEEEEEEEEEE
263 - 282:	EEEEEEEEEEEEEEEEEEEE
264 - 283:	EEEEEEEEEEEEEEEEEEEE
265 - 284:	EEEEEEEEEEEEEEEEEEEE
266 - 285:	EEEEEEEEEEEEEEEEEEEE
267 - 286:	EEEEEEEEEEEEEEEEEEEE
268 - 287:	EEEEEEEEEEEEEEEEEEEE
269 - 288:	EEEEEEEEEEEEEEEEEEEE
270 - 289:	EEEEEEEEEEEEEEEEEEEE
271 - 290:	EEEEEEEEEEEEEEEEEEEE
272 - 291:	EEEEEEEEEEEEEEEEEEEE
273 - 292:	EEEEEEEEEEEEEEEEEEEE
274 - 293:	EEEEEEEEEEEEEEEEEEEE
275 - 294:	EEEEEEEEEEEEEEEEEEEE
276 - 295:	EEEEEEEEEEEEEEEEEEEE
277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE
287 - 306:	EEEEEEEEEEEEEEEEEEEE
288 - 307:	EEEEEEEEEEEEEEEEEEEE
289 - 308:	EEEEEEEEEEEEEEEEEEEE
290 - 309:	EEEEEEEEEEEEEEEEEEEE
291 - 310:	EEEEEEEEEEEEEEEEEEEE
292 - 311:	EEEEEEEEEEEEEEEEEEEE

293 - 312:	EEEEEEEEEEEEEEEEEEEE
294 - 313:	EEEEEEEEEEEEEEEEEEEE
295 - 314:	EEEEEEEEEEEEEEEEEEEE
296 - 315:	EEEEEEEEEEEEEEEEEEEE
297 - 316:	EEEEEEEEEEEEEEEEEEEE
298 - 317:	EEEEEEEEEEEEEEEEEEEE
299 - 318:	EEEEEEEEEEEEEEEEEEEE
300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE
306 - 325:	EEEEEEEEEEEEEEEEEEEE
307 - 326:	EEEEEEEEEEEEEEEEEEEE
328 - 347:	EEEEEEEEEEEEEEEEEEEE
329 - 348:	EEEEEEEEEEEEEEEEEEEE
330 - 349:	EEEEEEEEEEEEEEEEEEEE
331 - 350:	EEEEEEEEEEEEEEEEEEEE
332 - 351:	EEEEEEEEEEEEEEEEEEEE
333 - 352:	EEEEEEEEEEEEEEEEEEEE
334 - 353:	EEEEEEEEEEEEEEEEEEEE
335 - 354:	EEEEEEEEEEEEEEEEEEEE
336 - 355:	EEEEEEEEEEEEEEEEEEEE
337 - 356:	EEEEEEEEEEEEEEEEEEEE
338 - 357:	EEEEEEEEEEEEEEEEEEEE
339 - 358:	EEEEEEEEEEEEEEEEEEEE
340 - 359:	EEEEEEEEEEEEEEEEEEEE
341 - 360:	EEEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEEE
344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE

A0A0L8FLX3 **A0A0L8FLX3_OCTBM** (182 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EEEEEEEEEEEEEEEEEEEEGEEEEEEEEEEEEGEEEEEEEEEEEEEEEEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEVEEEEGGINIFEIVMRLIKKTIDEEQEIEKIVQVAWYQPKEKAPEFSVLITYDQTTIKGNK
AVTTTKTPTASFCANNGITSNY
```

52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE

63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE

A0A0L8FM38 **A0A0L8FM38_OCTBM** (63 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
MNETKKKKEEEEEEEEEEEEEEEEEEEEEEEKEEEEEEEEEADVEERKLTEKINGNGNYTEETK
```

9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE

A0A0L8FMV6 **A0A0L8FMV6_OCTBM** (96 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MEEGRNVTAYRRADIQADGDCRSLWSVMMQQKEDALDSSKVKRNAKDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDPH
ETANFKKSTKVKVGFI
```

48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE

A0A0L8FN93 **A0A0L8FN93_OCTBM** (74 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MNKTDKRKKKKEMGELIKVDEEEEEEEEEEEEEEEEEEEKEKKKKKKKKKKKKKKKKKKNIVIAIVRNYFLWR
```

21 - 40:	EEEEEEEEEEEEEEEEEEEE

A0A0L8FNN9 **A0A0L8FNN9_OCTBM** (115 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MHTFVFGNSKEKREKKEVGEEEKDEEEEVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEETHGNRFRKISILKHAYIHTYIHTYIQR
```

30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE

A0A0L8FNX4 **A0A0L8FNX4_OCTBM** (149 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MLMTTYYLKCGDYMIGFSIVSMKKKKTKKKKKKKKKKKKKKKKKKKKKKKKKKTVSIRKLMFGDHGTETGQVFSGITA
CRSGTLGMEVVGGICRKISRKVVNSIKEEEEDNDEEEDNEEEEEEEEEEEEEEEEEEEEEEEEEETEV
```

120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE

127 - 146:	EEEEEEEEEEEEEEEEEEEE

A0A0L8FPE2 **A0A0L8FPE2_OCTBM** (89 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEQEEEEEEGRYCCCDGG
KDDNDVFAS
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE

A0A0L8FQ79 **A0A0L8FQ79_OCTBM** (119 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
AVVVKKEEEEEEEEEEEEEEEEEEEEEEEEEDDDDDDDDDDDDDDDDDEKKKKKKKKKKKKKKKKKKKKKKTEKNEEQQME
GIRRKIEKSNSKHHVNNNNSSGSSNQGNQGRHIGNTDTS
```

7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE

A0A0L8FQW7 **A0A0L8FQW7_OCTBM** (1729 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MEVTKEHIRHILLYEFNKGNNATESARNINAVYGDRTISVSQCQRWFQKFQSRSYSLEDEPCPGRSVELNEGVLQILVEQ
NPIVTVEELAEKLGFVDKWCWCVYVQEDIVCLSCLASTARENDSGERYCLAAEGFGNRICSLINISNKDVPPDMSVCAFV
LEQALSVRALQEMVTSASHDSRATQSGHRTLLYGHAVLLRHLHSSMYLSCLSTSSSNDKLAFDVGLQEMAEGESCWWTIH
PASKQRSEGEKVRVGDDLILVSVSSERYLHIGYGVSVIASFQQTLWTVVPMCSGAIRLKSLGFVFGGDVVRLFHGHMDEC
LTIPRSGSENEDNAVMYETGAVCSHARSLWQLEHIRTKWSGGFLGWGSQCRIRHITSGRYLSIHSDNQVVTVHRNRATEE
LTTFLLLMTKDEKKQSEGREDEGMGKADIKYGDSMTFIQHCASGLWLSYMTYETKKRGVGRVEEKKAVLLLEGHMDDAFT
LSRAQEEESRSARVIRKCQSLFHRFNKALDSLKTEGRTSHAWSRITLEEVLKSLEDLIEYFAQPGEDEEHEERQSKLKAL
RNRQDLFQEEGMIALVLETIDKFIQYKSRRHFAHYAGEEAAEKWDDISSYLYLLLAAMIRGNRANCAQFAQSYRLDWLVS
RLESQQSSTGVLDVLHCVLIDSPEALNMIKEKHIVTIISLIDKHGRDPKVLDVLRSLCVGNGIAVRTNQNLICDNLLPGR
DLLLQTKLVDHVTSMKPNTYVGLHEGSAMYKKWYFEVVIAFIEQCTHQTPILRIGWGNTEGFVPYPGGGEHWGANGVGDD
LYSYAFDGVNLWTGGKPKQVRHESQVFEKGHTIGCALDLSIPQISFTVNGNKVHGVFKDFNTDGMFFPVVSMSARVSLRF
MLGGEHGRLKFGPPDGHSPVLESLLPREKLKIDPCFYFGEQHKNIVSGPTEVLEYNAFVPSPIDTTHVQLPAYIENVRDK
LAENIHELWSMNKIEQAWTYGEVRDDARKKHPCLCTFEQLPMSEKKYDITLAFETLRTLLALGYHISIQHKKESSRLKMV
KLGSYYLQGNGYKPCPLDLNTIHLNEKMEELVDLLAENTHNVWAKDRIKQGWTYGLCEDNVNKRSPYLVPYSKVDEHIKK
ANRDTASETVKTLMAYGYILEPPTNEGGDGGSQVTQTIAEKKCTSRTYRAELTYAISHGKWYYEFEVITPGYMRLGWAKA
SFDPGCELGTDGLSYGFDGFLARKWFQGSEPYGKCWQAGDVIGCMLDLNDKIITFSLNGELMMDALGQEIAFRNIDTNEG
YVPAFTFGAHQQARVSFGQDINKLKYFTCYGLQEGYEPFCVNMTRQMTLWYSKNQPIFEPLTSDHSRLEAVRIPGGTNIT
PALKISSKNFGTLEHVCLEYVRLSLPVTCMEEYVAKDRTIQSEIDHKMNLENIRRHEMDIEEERNAYADMPGQNYSDANI
SDASVEKGSKVIADTLKRIAGGTSDSSTTESHREGSLNISDTTEKSDGGTHDLEGGAQLEFSSGRVADPAQKEYKRHHDN
IARLVHWTLCNKYGLDRAKNWYDHKLEGIVENRNAKILWDFMIQCDHEIENRKPDIVLIEKENKLCWIIDIACPADNKVC
DKEERKVERYNRLAWEIKQLWSMRKVAVVPIIVRALGTASKNLEKYMEQIGGAIRVEHLQKTALLGTARILQKFAKAKEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEMRIMTKIQ
```

1679 - 1698:	EEEEEEEEEEEEEEEEEEEE
1680 - 1699:	EEEEEEEEEEEEEEEEEEEE
1681 - 1700:	EEEEEEEEEEEEEEEEEEEE
1682 - 1701:	EEEEEEEEEEEEEEEEEEEE
1683 - 1702:	EEEEEEEEEEEEEEEEEEEE
1684 - 1703:	EEEEEEEEEEEEEEEEEEEE
1685 - 1704:	EEEEEEEEEEEEEEEEEEEE
1686 - 1705:	EEEEEEEEEEEEEEEEEEEE
1687 - 1706:	EEEEEEEEEEEEEEEEEEEE
1688 - 1707:	EEEEEEEEEEEEEEEEEEEE
1689 - 1708:	EEEEEEEEEEEEEEEEEEEE
1690 - 1709:	EEEEEEEEEEEEEEEEEEEE
1691 - 1710:	EEEEEEEEEEEEEEEEEEEE
1692 - 1711:	EEEEEEEEEEEEEEEEEEEE
1693 - 1712:	EEEEEEEEEEEEEEEEEEEE
1694 - 1713:	EEEEEEEEEEEEEEEEEEEE
1695 - 1714:	EEEEEEEEEEEEEEEEEEEE
1696 - 1715:	EEEEEEEEEEEEEEEEEEEE
1697 - 1716:	EEEEEEEEEEEEEEEEEEEE
1698 - 1717:	EEEEEEEEEEEEEEEEEEEE
1699 - 1718:	EEEEEEEEEEEEEEEEEEEE
1700 - 1719:	EEEEEEEEEEEEEEEEEEEE
1701 - 1720:	EEEEEEEEEEEEEEEEEEEE
1702 - 1721:	EEEEEEEEEEEEEEEEEEEE

A0A0L8FRP1 **A0A0L8FRP1_OCTBM** (55 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

MTHEEGAGEEGVKEEMEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDDDDDDDDDCIC

17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE

A0A0L8FRT7 **A0A0L8FRT7_OCTBM** (52 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

GSRQQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEESRKEERR

6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE

A0A0L8FS63 **A0A0L8FS63_OCTBM** (107 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

DDHAGDNNSDDDDDDDDDGDDDDGGGDDDDDDDDDGGDDDDDEEEEEEEEEAEEEEEEEEEEEEEEEEEEEEEAEEEE
EEEEEEEEEVEEEEDDDDDNDEEEEEG

54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE

A0A0L8FS72 **A0A0L8FS72_OCTBM** (100 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

RREKRDEEGYQWGEGGGEEEEEEEGEGEEEEEEEEGEEEEEEEEEEEEEDEEEEEGEVVEEEEEGEEEEEEEEEEEEEE
EEEEEMKEVEEEENDHGKER

66 - 85:	EEEEEEEEEEEEEEEEEEEE

A0A0L8FS98 **A0A0L8FS98_OCTBM** (77 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

MEIGRKGHGVKRKIDKKGEKTENSEIIGVVEEEEEEEEEEEEEEEEEEEEEEEEEDGEGKEEEEEEEEEEEEEEEED

31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE

A0A0L8FUI3 **A0A0L8FUI3_OCTBM** (71 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

NVREGKEIDDDGYQEEEEEEEEEEEEEEEEEEEEEEEEEGKNEEEKRHEESNNETLENDKFKEIECKEEKG

15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE

A0A0L8FUJ4 **A0A0L8FUJ4_OCTBM** (63 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

MKNKRREQRKSEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERMVVVCKRTMREKEAMEEDK

12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE

A0A0L8FV96 **A0A0L8FV96_OCTBM** (114 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

EQTTNGNDDDTDNDDDDDDDDDDGGDDGDDDGDDDNDDDDDVNVDDDGGGHDDDDDDDDDDDDDDVDDVEAKNKEEEEEE
EEEEEEEEEEEEEEEEEEEMEEVVAAHPTLKLRE

75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE

A0A0L8FVM0 **A0A0L8FVM0_OCTBM** (96 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

NTIGYNNDNNDDSDDDDDDDDDDDDDDDDDDDDDEEEEEEEEEEEEEEEEEEEEEGFRGVLFHLEGECCGHSEYGMFGCILG
SITFLILIRPLTTSKQ

34 - 53:	EEEEEEEEEEEEEEEEEEE

A0A0L8FVQ5 **A0A0L8FVQ5_OCTBM** (62 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

RRLKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEIWLLLCFILSKFL

5 - 24:	EEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEE

A0A0L8FWG7 **A0A0L8FWG7_OCTBM** (68 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

ERGRKRKQKDEDEVRKQNCEKKRKEEEEEEEEEEEEEEEEEEEEEKSKKRWLKEIEKNDGKKRAKKQ

25 - 44:	EEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEE

A0A0L8FX43 **A0A0L8FX43_OCTBM** (50 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

EEEEEEEEEEEEEEEEEEEEEEEEEEVDDDDDGDDDDDDDDDDDEKGNA

1 - 20:	EEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEE

7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE

A0A0L8FX52 **A0A0L8FX52_OCTBM** (96 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
MEGNIEDGDEKREYVRKVVQHDAFPVLPTMIGNRQQKEEEEEEEEEEEEEEEEEEEEEEEEEEEKEKEEEEEEEEEEEEE
EEEEEEEEEEEEEDGR
```

38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE

A0A0L8FYF0 **A0A0L8FYF0_OCTBM** (145 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
ATVYAPTGAAAAAAAAVADDDDDDVVVEEEEEEEEEEGGTKRKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEELQQ
QKVTTSAAAVATTATTATAAAATTTTTSTTTTTTTTTTTTTTTTTTTTIIIIQLTLSITFLNMSIA
```

45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE

A0A0L8FYK4 **A0A0L8FYK4_OCTBM** (64 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
YLDDDNEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEINRIRKAGRMH
```

7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE

13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G0C7 **A0A0L8G0C7_OCTBM** (109 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
MEKKKKKHNEEEKGMKKNKCRRQKEDKKQEDGGENEKEVNEGRYGTEEEEEEKEEEEEEEEEEEEEEEEEEEEVEEEEEE
EEEEEEEEEDDDEDEEEYGSRWNRKQKRK
```

54 - 73:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G0R4 **A0A0L8G0R4_OCTBM** (85 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
RKKRRKRKRRRRRRRRRRRRDDEEVEEEEEEEEEEEEEEEEEEEEEEKEEEEEEEEEEEGASFIKISKSFVEAPNKQME
CSDKA
```

26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G114 **A0A0L8G114_OCTBM** (56 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MEEEEEEEEEEEEEEEEEEEEEEEEEEEEDTCHRSSFLIYGVFYAWDISDIMGHVI
```

2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G193 **A0A0L8G193_OCTBM** (71 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

KKKKKEKKKKKKKKKKKKKKKKKKKKKKKKKKKKNNNXXXXEEEEEEEEEEEEEEEEEEEEEQQQQQQQQQ

42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G1K1 **A0A0L8G1K1_OCTBM** (114 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

RKKEKKRIESEGQHEEEEEEEEEEEEEEEEEEEEEEEEVEVEEEEEEEEEEVEEEEEEEEEEEEEEEEEEKEEEEEEEEEE
EEEEEEEEEEEEEEEEEQQQQQQKQGKLKRRSRR

15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G1R8 **A0A0L8G1R8_OCTBM** (73 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

MRKKENDDDDGDDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGGGGGGDDDANDGSSEVEKN

14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G265 **A0A0L8G265_OCTBM** (100 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

HHFTKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKXXXXEEEEEVEEEEEEEEEEEEEEEEEEEEEEERDSDDDDDDDD

DDDDDDDDDVKMMAVMTRRN

46 - 65:	EEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEE

A0A0L8G297 **A0A0L8G297_OCTBM** (200 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

MKKKEVEKQQEQQEKKKKEAKKMKMKKKEKDEEEEEEEEEEEEEEEEEEEEEEEEEQKRIKTTTKRRKKRKRSRKRGKRR
RRRRRRRRKRKRRIRRRGKKKKKKKKKKKKKKKKNKKKKKKKKTKKKKKKEKKKKEKKKKKKWLKMMKKQKRRSRRRRRKR
RNEKKKRDEDDDDDDDDDDDEQQKQKKNNEGWKEDEKRGD

32 - 51:	EEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEE

A0A0L8G2B9 **A0A0L8G2B9_OCTBM** (87 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

DVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEREIKRGEDEML
KHTQLNY

3 - 22:	EEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEE

32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G2G2 **A0A0L8G2G2_OCTBM** (70 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

LHVIHCICVCVCIFDRVRICTYRSRNIGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEEEEEG

29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G2X6 **A0A0L8G2X6_OCTBM** (73 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

RGKERQREREREGNIERQREREREREREREVVEEEEEEEEEEEEEEEEEEEEEEEEEEEERAITKGRKNSI

35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE

43 - 62:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G340 **A0A0L8G340_OCTBM** (158 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MQGKNEIRGIKREMKKDAEEKRKISTRVKKNIGSYEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGWGDEEKLA
KGKQKSLTRGEYRKEYLRETSRAKERRKEDERDSERERERKEQCVRMVGMREYRRTFQNIIEYTLTDKEFEMKDRKRK
```

36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G394 **A0A0L8G394_OCTBM** (52 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EEKEEEGEEEEEEEEEEEEEEEEEEEEEEEEAVKVFFMIKEKKMNGKIANKY
```

8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G3B9 **A0A0L8G3B9_OCTBM** (117 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MKRRRGREKEVKERREVDKKIKKGQEEEENEEEEEEEEEEEEEEEEEEEEEGTRGEEKTKMKLRRKKMKKKEKERKNKD
VQEKLAEKIRKEINMRSHTKKEKKVNAMMAKVEEKYN
```

31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G3Q4 **A0A0L8G3Q4_OCTBM** (154 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MMMMATVGEGLMLKMTTVKKWKNLKTQEEEEEEEEEEEDDDEEEEEEEEEEEEEEEEEEEDDDDDDEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEMEEGEVEEEEEEEEEEEEEEEEEEEEEEEDDDDDVEKCRNYKLNK
```

66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE

72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G3Z1 **A0A0L8G3Z1_OCTBM** (49 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EDEEEEEEEEEEEEEEEEEEEEEEEEEEEEKQEEAEEEEKQEEAEEEAE
```

3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G411 **A0A0L8G411_OCTBM** (90 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MAEERLSCSPRRKCHKSKQKGSGARQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEEETKEMK
GVRGSSGRRS
```

27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE

37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G469 **A0A0L8G469_OCTBM** (91 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
LEQIAQNEERLEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGTTITTITTTTASSSKLINFLFWSVIRVTYCFVF
FFLLYFRLDQF
```

12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G4A0 **A0A0L8G4A0_OCTBM** (65 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MTSSERDRQKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDSQREKCGDKK
```

11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE

21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G4P4 **A0A0L8G4P4_OCTBM** (197 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
KFSKKVLHLVSDKYCDLYNNDNNNNNNNNNNIDNNNNDNNNNNNNNNNNNNNNNNNNNNNNNNNNNNKNIEKYLKNENPGY
RKIEEEEEDEEEEEEEEEDDDDDDEDDDDDDDDGEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEDDDDDDEDDDDDD
DDDDDIEDDDDDDDDDDDDDDGKDDDQDNHGYDHDLN
```

122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G4R6 **A0A0L8G4R6_OCTBM** (182 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MEEGEDGEEVEEKEEKEAEEEEEEEEEEGEEEEEEGEEEEEEEGEEEEEEEEEEEEEEEEEEEEEDENEKDQAAKGGEGE
VEKRGNGGEEEEEEEEEEEEEEEEERRRRKEKEETVEVDEQEEEEQDRKEQEKKKKKKIKKKKEEEEEGGEEEGEEEEEEE
EEEEEEEEEEEEEEEIEKKLDE
```

45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G4Z9 **A0A0L8G4Z9_OCTBM** (98 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MKSGRKKTEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKDDDGDDDDEVEEDDDDDDDDDNIDVDYVEDDDDDDGSDDDD
DNDDDDQDEDDEEEEEDH
```

9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE

17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G5C7 **A0A0L8G5C7_OCTBM** (56 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
KHCELREEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEELSSSGC
```

7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G5L3 **A0A0L8G5L3_OCTBM** (112 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EEEVVVVVVVVVVVVVVEEEEKEEECEDDVEDMKIDEGDDDDDDDDDDDDEKEEEEEKEEEEKEEEKEEEDEEREEEEE
EEEEEEEEEEEEEEEEGEIVMEENFKEKAEEV
```

76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G5M4 **A0A0L8G5M4_OCTBM** (112 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
MIYDVQRTQQLSHGTIFGCACNNNSSSVLVPALMVVPAAGLMIIEGGKEVVIVEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEKEEEEEEEGWRVYQLKRCTNNKQ
```

54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE

61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G610 **A0A0L8G610_OCTBM** (50 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
MLKVVGGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEKRKEEEEEEQE
```

8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G625 **A0A0L8G625_OCTBM** (84 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EEEEEEEEEEEEEEEEEEEEEEEEANKQQTKGKDEKRRRIWSEGKYKERKSRECNMQVVSSYTEIGKAEMAYEENFRNVSF
HLQV
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G634 **A0A0L8G634_OCTBM** (262 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
GGGGGGGDGRRRKKKEKVCVGGKGTRNWERKRKEKLKREEVEEKEKRETVKERKTDVEKEEVVVVVVVVVVVVVVAAAA
TATEEEEEEEEEEERRRRRRTEKKKKKKKKKKNGEEEKEEEEEEEEEEEEEEEEERRRRRRRRRRRRRRRRRRRRRR
RRRRRRRRRRRRRRRRTEKKKKKKKKKKKEKKKKKKKKKEKKKKKKKKNGEEEEEEEEEEEEEEEEEEEEEWKRRRRR
RKMEKKKKKKKKKKKKKKKKKK
```

212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G6A9 **A0A0L8G6A9_OCTBM** (212 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MSLPPVSRTGRQSVFSRTRRCFKRLFGSCTRRNSVGPDPNPTERVSGHRVPRSLFINAEPRTVTVKDAEEEKLEVEEEEE
EEEEEEEEEEEEEEEEEVEDSEYDEKTEQGKEQEEGKVEGREVETRHQSELKELGMMRMTERKSLEDLELAELKELEDEV
MQELEELDWLVKRKKQLREKAKSEKLAQMMENPELVKEIEYLERWKSWMFHH
```

76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G6W3 **A0A0L8G6W3_OCTBM** (179 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MKTKKKKRRRRRRRRRRRRDVQETKEEKYKNKREGRIATNKEEEEEEEEEEEEEEEEEAEEEEEEEEEEEEEEEEVEEEE
EEEEEEEEEEEEEEEEVEEEEEEEEEEEEEEEEEEEEEIAMEENLKEKLEVNEENGDDNDDLNEDQSNDDGLVEELGLMG
KEEEGDEEEEQQVKDMFNN
```

77 - 96:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G7C0 **A0A0L8G7C0_OCTBM** (94 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
MAQSAFKYHHVVFKMRNILDELGYKEEEEEEEEEEEEEEEEEEEEEEEEEEEEDLRPKNATKECGRTEEKAEDKQEEKNK
EIREKERDKGRGGI
```

26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G7E1 **A0A0L8G7E1_OCTBM** (101 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MKQGERKERKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEILKKTSSLPTTTKERRNILLLLLLFLFLLH
FLLLKARRVINTYITNFKSNK
```

11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G7F4 **A0A0L8G7F4_OCTBM** (60 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MHQQHIHTYICMCGEGKEEEEEEEEEEDDDDDDDDDKEEEEEEEEEEEEEEEEEEEEDAF
```

38 - 57:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G7F7 **A0A0L8G7F7_OCTBM** (342 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
DGGGDGGGGVNVGGEGNGGEGYGGEGGTGFDGGGGDGGGCEGGGGGEGGSSDGGSGDGGDVNGGGSSDVIGDCVLVVVVM
VVAVMAAXXXXSGDEGSSGDGGGDEGSSGDGGGCEGGGGGEGGSSDGGSGDGGDVNGGGSSDVIGDCVLVVVVMVVAVMA
AIEAVVVSMLVALTVAAEVGAILVVVVVVVALPLKVTLVIFIMAAVALMILEMVVVIILMAAALVVVMVMVLVLFRVITL
VSNFGIRPPILEWEDDEGRTRKRIWRVRRRRKGKGRGGEEEKKKKKKKKKKIPVMKEEKEEEEEEEGGGGEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEDT
```

311 - 330:	EEEEEEEEEEEEEEEEEEEE
312 - 331:	EEEEEEEEEEEEEEEEEEEE
313 - 332:	EEEEEEEEEEEEEEEEEEEE
314 - 333:	EEEEEEEEEEEEEEEEEEEE
315 - 334:	EEEEEEEEEEEEEEEEEEEE
316 - 335:	EEEEEEEEEEEEEEEEEEEE
317 - 336:	EEEEEEEEEEEEEEEEEEEE
318 - 337:	EEEEEEEEEEEEEEEEEEEE
319 - 338:	EEEEEEEEEEEEEEEEEEEE
320 - 339:	EEEEEEEEEEEEEEEEEEEE
321 - 340:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G7R0 **A0A0L8G7R0_OCTBM** (56 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
YQKRKIKRRNKKEEEWEEFEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEENGR
```

20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G8A8 **A0A0L8G8A8_OCTBM** (81 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MVEEKEEGEEEEEEEEEEEEEEEEEEEEEEEEEEQEQEQEQEQEQEQEQEVVLLLEVESGGEVEGGGGKEGGRGKRKRRK
Q
```

9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G8C0 **A0A0L8G8C0_OCTBM** (147 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MPKLTLPINHSRNVRISNAQKATEKKYLRGGGDDEEEEDDDDDVDDEEDEEDDEDEEDEQEEDEEDDEQEEDDEQEEDDG
DDDDDDDDYDEDGDDEDVDDKSDHEDDDDACDDDDEEEEEEEEEEEEEEEEEEEEEDGDEGVVVYVV
```

116 - 135:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G8Q0 **A0A0L8G8Q0_OCTBM** (156 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MRAKRRNKDSGTSRSLLDTYLDEFMWRQKYANGCLRDTLRGLHVGKFGSSQTKNPSQVLFHLSSPINGEGGYKDGESTFS
QNWDPKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEEEEEEEEEEEEEEEDIRITCCCGWR
```

87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G933 **A0A0L8G933_OCTBM** (163 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MTEEEEEEEEEEEEEEEEEEEEDGRRRRGRRRRKKKKKKKKKKRRRKKKKKKENKKKKKKKKKKKKKKKKKRKKKTEEEE
VEEKDGRRRRRRRRRKEKEEKEEEEKEEEEEEEEEEEEREEEEEEEGEEEEEEEKEEKEEKEEREEEEEKEERQEEKEEE
EKE
```

3 - 22:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G9I4 **A0A0L8G9I4_OCTBM** (108 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
CGQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEREREREREKERVGWMRLNNKRKRRAGETQS
KTGKEKKCQRKEYKISTEKSLREENRLN
```

4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE

10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G9M6 **A0A0L8G9M6_OCTBM** (86 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MNQLKTKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEVEEE
```

8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE

53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE

A0A0L8G9T6 **A0A0L8G9T6_OCTBM** (87 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MVDPQEMEEEEEEEEEEEEEEEEEEEEEEEEEEEEVEQEEEEDNDGDNDEGSSFVFVCEYVCVYLCSLYLCDWDGTYIFVY
VHAYLFL
```

8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GA93 **A0A0L8GA93_OCTBM** (236 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MERIQKRHTSAGGHSSMYNSSNVLEDRDKAGKKENEDEEVEEGEEGEEKEEKEKEEVEEEEEEEEEEEEEEEEEEEEEE
EEMEEEEEEGEKEEEEEGEEKKKKKNNNNKKKKKKRKKKKKKKKMKEKKKKKKKKNNNNNNKKKKWKKKKKKKKKKKK
KWKEKKKKKWKKKKKKERKMKKKQSKKKNKKKKEKKKKKKWKKKRKRWKKKGKKKKKKKGKRKKEKKKKKRKKKMQ
```

58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GBP9 **A0A0L8GBP9_OCTBM** (67 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MCMEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEASI
```

4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE

15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GBY4 **A0A0L8GBY4_OCTBM** (97 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MTIMKQKRYRRKRTIIRTTATRRRRRGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEEERRRPSK
RSEETDKGELHKEHEEK
```

28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE

44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GC30 **A0A0L8GC30_OCTBM** (101 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
TKETKGEKRQQRREDEGDEYEEGEEGEGERGDGEEEEEEEGREEEEEEEEEEEEEEREGGGGEEEEEEGEGGGGEEEEEE
EEEEEEEEEEEEEEDADEKLA
```

75 - 94:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GC59 **A0A0L8GC59_OCTBM** (120 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MTVDGDSYDNDEASVGWVGEEKADDDDDDDDDDDDDYDDDDDDDDDDDDDDDDDDDDDDEDDDDNKNNNDEVGKKSRQEE
EEEEEEEEEEEEEEEEEEEEEEEEEEKEEEEVMHKKKLYG
```

79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GC96 **A0A0L8GC96_OCTBM** (119 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EEEEEEEEEEEEEEEKEEEGGGGGGGEEEEEEEEEEEGGGGGGEEEEGEEEGEEEVEEEEAEEEEKEEEEEEEEEEEEEE
EEEEEEEESRQLLNRYSIYNILWTKTPPKYLVVGPRRHL
```

67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GCH5 **A0A0L8GCH5_OCTBM** (58 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
LEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEIRRRKRTHSRN
```

2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE

14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GDC2 **A0A0L8GDC2_OCTBM** (51 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MKGKNHLRESDEKEDEEEEEEENEEEEEEEEEEEEEEEEEEEEEESIPGI
```

24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GE39 **A0A0L8GE39_OCTBM** (60 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MWGGRGGGGGGGGEEEEEEEEEEEEEEEEEEEEEEPNANNNKSICNQRRQKSNNVVKESN
```

14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GEQ6 **A0A0L8GEQ6_OCTBM** (163 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
IYQTSKVNSYEDQSLLISTIPTKKTKLVLLGDFNGQVETYRRTWWNVLVTNGINNYNIDGKLLLHHFCTVNHSLLTSTTF
KLPLRNRGGAAGEEEDEETEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAEQQQQQQQQQQRKQLRILFHC
SCQ
```

100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE

115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GEX2 **A0A0L8GEX2_OCTBM** (79 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDVFVEKRKLNKRNEVCRYENEKNRKKKKEKVYKKRKRKNEE

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GF01 **A0A0L8GF01_OCTBM** (78 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

KRFTFSKRKVNKEEEEEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEEEEEEEEEEEEEKATKAIKQNTELN

21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GF46 **A0A0L8GF46_OCTBM** (57 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

EEEEEEEEEEEEEEEEEEEEKEEEEEEEEEEEEEEEEEEEEEEGPSWFGGTKDYEN

1 - 20:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE

23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GF88 **A0A0L8GF88_OCTBM** (56 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

KKQNYRKIQHQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEINF

12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GF93 **A0A0L8GF93_OCTBM** (130 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

MKERQIPIKKKKKKKIKEKEKKKKKKKKTKKKKEKKEKKTKEKKKRKRGKKKTKKKRKQWKKKTKKMEKKKKEDEDEEGE
VGGAEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEHQQQQ

93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GFU7 **A0A0L8GFU7_OCTBM** (57 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKKEEEEDTSPKTLRSCFELETTWL

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GFX6 **A0A0L8GFX6_OCTBM** (82 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MYERPTIRSTSQQQEQRRANKYGSTKLLNLIDSKAKRERRRGGEEEEEEEEEEEEEEEEEEEEQQQQQQQQQQQQQQQH
QE
```

44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GG17 **A0A0L8GG17_OCTBM** (51 aa)
TFIIS central domain-containing protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
KEEEEKEEEEKEEEEEEEEEEEEEEEEEEEEEKEEEKEDEEEEEEGDVCIT
```

12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GGF5 **A0A0L8GGF5_OCTBM** (55 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
KTFIQLEENASNGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGGHRLKILWLFM
```

14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GGG5 **A0A0L8GGG5_OCTBM** (739 aa)
PWWP domain-containing protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
MNGISSTLVTQLPPIPAVGVNPKLTPNPISLSTGLNSEQASYPVLHFQSPLKTSPPEGGGERDGRTSEPVCEKQQIEVPA
LMSMDQSTRRRIRHVPKHEPLSESTAITTTSTTTSATIATTTTATAIVNSTSDDKMKVPVKDPTSKVETTSKENQSVQKK
TDPLLEKHEKPAKWFVGDLIWSKVSGHPWWPCLIACDPVEGIYTKLCVKGKGCVRNYHVQYFYDEPERAWVSENATLGFE
GKDKFFKYVEDMLERAPAKQRSQISQKYGVSKHKRPVWDRAVRSAEVALPLSHSERKLCYINNFDKHPEKKKQESPEKLA
VEVSKPDKAGPKAKKQKTESSSGAGVTSGGDGGGKVKIESSSASKLPSIVNGTLAKKRHASPGSFANDSDSIASPQRKRP
KAAGGTESGGGAAGGSGCVTTPKSGKDDGSFDMFCQKHREGVLSEHSDFDEQMVVEYLRQQWSMMSQKQRARYKSKFGGG
GGGGGGGVITSRGTSSEEPEVKLEPINVDIINFKKGSTVKKPTSHPSRPALKKSESDEQTPSKNEVKLKRSPRISKPSIK
KLEAEEDNKLFTEYQKQMINSKPNSTRKRRSVQSKGFGSKMFQDSSSLAEHHQMNNSSSKSIDGHGKSAEFRHASSHQRG
QLIPKVELDRDGVKLLVKQEENNEEEGHEEEDEEEEEEEEEEEEEEEEEEEEEEDDEYELEIFKLSSSWPVKRENVCQIC
EKPGDLTDCEGPCLGSYHL
```

673 - 692:	EEEEEEEEEEEEEEEEEEEE
674 - 693:	EEEEEEEEEEEEEEEEEEEE
675 - 694:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GGL6 **A0A0L8GGL6_OCTBM** (795 aa)
PWWP domain-containing protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
MNGISSTLVTQLPPIPAVGVNPKLTPNPISLSTGLNSEQASYPVLHFQSPLKTSPPEGGGERDGRTSEPVCEKQQIEVPA
LMSMDQSTRRRIRHVPKHEPLSESTAITTTSTTTSATIATTTTATAIVNSTSDDKMKVPVKDPTSKVETTSKENQSVQKK
TDPLLEKHEKPAKWFVGDLIWSKVSGHPWWPCLIACDPVEGIYTKLCVKGKGCVRNYHVQYFYDEPERAWVSENATLGFE
GKDKFFKYVEDMLERAPAKQRSQISQKYGVSKHKRPVWDRAVRSAEVALPLSHSERKLCYINNFDKHPEKKKQESPEKLA
VEVSKPDKAGPKAKKQKTESSSGAGVTSGGDGGGKVKIESSSASKLPSIVNGTLAKKRHASPGSFANDSDSIASPQRKRP
KAAGGTESGGGAAGGSGCVTTPKSGKDDGSFDMFCQKHREGVLSEHSDFDEQMVVEYLRQQWSMMSQKQRARYKSKFGGG
GGGGGGGVITSRGTSSEEPEVKLEPINVDIINFKKGSTVKKPTSHPSRPALKKSESDEQTPSKNEVKLKRSPRISKPSIK
KLEAEEDNKLFTEYQKQMMSGSIMDNDQTQDQIALHKGASTARCPSAAVGRRSCTVAIDNRTNNILNVTPPSSAINSKPN
STRKRRSVQSKGFGSKMFQDSSSLAEHHQMNNSSSKSIDGHGKSAEFRHASSHQRGQLIPKVELDRDGVKLLVKQEENNE
EEGHEEEDEEEEEEEEEEEEEEEEEEEEEEEDDEYELEIFKLSSSWPVKRENVCQICEKPGDLTDCEGPCLGSYHL
```

729 - 748:	EEEEEEEEEEEEEEEEEEEE
730 - 749:	EEEEEEEEEEEEEEEEEEEE
731 - 750:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GGR4 **A0A0L8GGR4_OCTBM** (183 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
NCFGHGREVEVEGGRREVEEEEEEEEEEEEEEEEEEEEEEEEEEEQQQQQQQQQQQQQQQQQQQQQQRQQEQQQQQRKEQGK
ECREGRKQSEIGYEYVTKRIKRHKLRPGKKGGKKIQDPRTPATATMRERANGIATTINGKENERYNNNNSSNINNNSSNI
NNNNNNNNNNKRNEAGINLKTRK
```

19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GGV0 **A0A0L8GGV0_OCTBM** (144 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MKIRKRCERSRMIRQRKRNERKGQSGAKGKINEGEEEQKQELQQQMHQEVKKEEKEEGERTAEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEDGKEKKKKKKKKKKKKKKKKKKKKKKKKKKKKRSCRRRWKIKRRTGLIRSLN
```

63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GGY7 **A0A0L8GGY7_OCTBM** (149 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MRIHDEDEEEEEKEDNDESGGTESEIDGNIGDVEGKSIIAGIDIQKQKLNGDDDDDDDDDDDDDDENDDDNDDDETGDTE
SEIDGNIEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEERI
```

90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GGZ1 **A0A0L8GGZ1_OCTBM** (95 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
LLSLLLLLIQNDNGGQKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEEEEEEEEEEEEEEEEKEEEEEEEEEEEEEE
EEEEEEEEGCIKMAG
```

18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GGZ7 **A0A0L8GGZ7_OCTBM** (51 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EEEEEEEEEEEEEEEEEEEEEEELEEEEEEEEEEEEEEEEEEEERGGERKLL
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GH83 **A0A0L8GH83_OCTBM** (70 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MFDALIGCDIVLPEKRKRYCNFIWSGGGGGGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGLFY
```

32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GHP5 **A0A0L8GHP5_OCTBM** (85 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MERERERERERERERKEKEKEGKITAADRDKTRWKVNEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEIP
```

37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GIA2 **A0A0L8GIA2_OCTBM** (53 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDFCFFFYTCF

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GIL7 **A0A0L8GIL7_OCTBM** (151 aa)
ANF_receptor domain-containing protein. *Octopus bimaculoides (California two-spotted octopus)*

MGIFALFILNNPISHHVVQAYSNALHLPVFVLNVATRHQLPSYPFEIHMSPSYMPAITELINFYRWRRIFYIFDSDDVVS
SQGISSSVDQSKRFKEEEEEEEEEEEEEEEEEEEEEEEEEEEQQQQQQQHQQQQQQQQQKQQQQKLSVL

96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GIR5 **A0A0L8GIR5_OCTBM** (60 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

IERRRTKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEYRKYLSNENPGAKFSQDTC

8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE

13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GJ59 **A0A0L8GJ59_OCTBM** (84 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EEEEEEEDGEEEEEEEEEEDEEEEEEEEEEEEEEEDEEEEEEEEREEVEEEDEEEEEEEEEEEEEEEEEEEEEEGVGKE
EDGD
```

53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GJA9 **A0A0L8GJA9_OCTBM** (98 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MQSSGMMEFSEDQESYFVASILFVCVLILITVWILGSKSTGPEEAAFHVDKEEEEEEEEEEEEEEEEEEEEEEEEEEE
ISRGQTRRRNRSTWSKML
```

52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GKN3 **A0A0L8GKN3_OCTBM** (205 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EGEEEEDEEEEEEDKGEGEEEEEEGEEGEEEEEEEEEEEDGDDEQQEEESSCVHACICVCVCVCVHTREARGGGKKMRGN
DDDDDDDDDDADDDDDEEEEEEEEEEEEEEEEEEEEEEAEEEEEEEEEEEAEEEAEEEGGGGGEEEEEGGGGGGGGEEEEEE
EEEEEEEVEGGGGEGEEEKEEEEEEEEEEEDEEEEDEEEEDEEEE
```

97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GKY3 **A0A0L8GKY3_OCTBM** (183 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
RRGKVEEEGGGGGEGEEEEEEEEEEEEEEEEEEEEEEGEEEREEAKKKKEKKTERDKEEEEEEEEEEEEEEEEEEEREEA
EKKKEKKMERDKEEEEEKRRRRRRRRRRRRRRRRRRRRKWKGIRTKKKKKKKKKKKKKKKKKKKKKKKKKKKKNMKKMRT
EKKKQQQEEQMQPIFTWYLFQIY
```

16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GLE5 **A0A0L8GLE5_OCTBM** (62 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

SEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEEEEEEEEEQQQQQQLQQQQQQQ

4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GMF1 **A0A0L8GMF1_OCTBM** (103 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

RRRRRRRRRRKRRRRREGGEEEEEDEEEEEEEEEEEEEEEEEEDQLENNNENGYDDEGHDDDNDVDDDGNDDEDEDDD
DDFDEFDSRCRWWRKKIKGSSKQ

26 - 45:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GMP6 **A0A0L8GMP6_OCTBM** (87 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

FFTAKAAGFLCVLGIGLGIGSLLIYRLFKKYQCSNDLPDKSDDECYVRLRGGEEEEEEEEEEEEEEEEEEEEKEEEEG
EGVVREQ

53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GN40 **A0A0L8GN40_OCTBM** (58 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDDDDKRLRKSSKYYVKNCQGCKNVF

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GNA3 **A0A0L8GNA3_OCTBM** (66 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

QVVVVEEEEEEEEEEEEEEEEEEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEESAAEAAIAAGEWY

6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GNK5 **A0A0L8GNK5_OCTBM** (56 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

MQNRKDDDDDEEEEEEEEEEEEEEEEEEEEEEEEEEKAEKKKKKQKKKRNNKKRYVD

11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GNN5 **A0A0L8GNN5_OCTBM** (118 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

MWKWGGELIEEEEEEEEEEEEEEEEEEEEEEEGEEEEEEEQQQQQQRGGEAGEEREEKQQEGGGEREEGEQEQQGGGGEEE
VEEEEEEEEEEDEEEEGILHTIQTSQNLEVKDGKKKKH

10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GNZ8 **A0A0L8GNZ8_OCTBM** (187 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

MGRRDDDEEEEEDDDDDGDDDDDDDDDDDDDDDDDDDNDDDDDDDDDGDGDDDGDDEIQLHGTTDEKMESFKKRLVIELA
AAAAEEEEKEEEEEEEEEEEEEQQQQQQQQQQQEQEEEQQQQKQQQQQHGEEEEEEEEEEEEEQQQQQQQQQQQHGEE
EEEEEEEEEEEEEEEEEEEEEEEEEE

159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GP21 **A0A0L8GP21_OCTBM** (115 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

MFGEHEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAKKVKKKKKKKKKKKKKKKKKLRRRKEEEEEEEEEEEEEEE
EEEKEEKKKKKKKKKKKKKKTKKKKKKKKKLRRRS

6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GP28 **A0A0L8GP28_OCTBM** (119 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
GGGQEEQEGDKEVDDDDDDDDDDDDDDDDDDDDDDDNDYDDDDDDDDDDDDGDDDDDVDDDDDDDDDDDDDDDDEKQEEEEEE
EEEEEKEEAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEG
```

90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GP31 **A0A0L8GP31_OCTBM** (53 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MKKRMKKGKLVIPVVVTKGEDREEEEEEEEEEEEEEEEEEEEEEEEEEEEVD
```

23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GRB4 **A0A0L8GRB4_OCTBM** (112 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MLMVGTVLMEGKENDEGRERLRRGEKRKEAVNGGWTRWKVIWEGGKRSVNGGGKGSGRREGGKGEEEEEEEEEEEEEEE
EEEEEEEEEEEEGKKSEKLQEEKNVEVKRKIE
```

65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE

67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GRC0 **A0A0L8GRC0_OCTBM** (63 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MSFMAIIEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDWMKNRQM
```

8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GS89 **A0A0L8GS89_OCTBM** (115 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDDDDDDEADDDDDDDDDDDDDDDDDDDELIKKGRKRTSEEITVTEINNR
RVIQTEKKKKNNHVWVGQGRSRGSKECSGRKIKLY
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE

7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GS93 **A0A0L8GS93_OCTBM** (83 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
REKEEEEEEEEEEEEEEEEEEEEEEEDEEEEEEEEEEEEEEEEEEEEVCLCVQTYALRNLDVIFVYEEDVYMTYMFEGGRC
VDV
```

4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GSE4 **A0A0L8GSE4_OCTBM** (118 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
ISPLPDHYVLTRLELPSRFRRSTEHITKRLSNDNRHRKGGKMTDYVTQCVAGLKFSKYGFSPVDKLLACFRQLEKEEEEE
EEEEEEEEEEEEEEEEEEEEDDDDDDDEEEEEDYIYI
```

76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GSF4 **A0A0L8GSF4_OCTBM** (54 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EEEEEEEKEEEGEEGGEEEEGEEEEEEEEEEEEEEEEEEEEEEEEGCGGGRG
```

22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GSQ1 **A0A0L8GSQ1_OCTBM** (108 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
REKERKKEGRKEGKNEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERYATRVCSEAEIFAKGKKMLIINNNNKNDDDDAGD
DDDDDDDDDDDDDDDRGDGGDGGGGGGG
```

16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE

24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GSX2 **A0A0L8GSX2_OCTBM** (78 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
VICCDVCEEKEEEEEKEEEEEEEEEEEEEEEEEEEEEEVYQMGSARKKATHVGARNTSEPVAPKYVKEQNSEEKQIHQ
```

17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GTB1 **A0A0L8GTB1_OCTBM** (102 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
CVTLSINDDNDDDDDGDDDDDDDEEAKHYGCVHLEEEEEEEEEEEEEEEEEEEEEXXXXKKKKKKKKKKKKKKKKKKKK
KRHDVSWKTVCVEELSHTHKYM
```

35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GTP8 **A0A0L8GTP8_OCTBM** (215 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MKQKEKRKEEKKENSKQRNAKESEGKKLNQKEDIGNNTERKESAERNEERTNNEIYRREVIYKHRDGERERERERERERG
ERERKRGRERERSWVKQILGMCEKHRWTDRREKKKRERLREMKDKKWKEGEKEKETGSERYRFGMQHKLTDAKIHDEKER
ERERERERREEQTVIEGEKRGKRREREEEEEEEEEEEEEEEEEEEEEEEESILVQD
```

185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE
190 - 209:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GTZ8 **A0A0L8GTZ8_OCTBM** (134 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MTIAVIGVFDVSASVSVVVGIVIIHFIIIVFVAIVVLIIIVISLGRNEEREKDDDDDDDDDDDDDDDDDDGDDGDDEE
EDVEDDDEVALEEEEERIEEEEEEEEEEEEEEEEEEEEEEEEEEETVWLSIYQ
```

99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GUL3 **A0A0L8GUL3_OCTBM** (61 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MQTKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEQQQQISAVKDNGKVLFWCLIPC
```

5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE

7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GV45 **A0A0L8GV45_OCTBM** (60 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MYVCMYACTYPVHTCMCVCVYVNRSSRTQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEQE
```

30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GV87 **A0A0L8GV87_OCTBM** (99 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
NKEEEEEEEEEEEEEEEEEEEEEEEEEEEQQQQQQQQQQQQQGGGGGDWRTTNTETVGNLIEGRQDIDDDDDDDEDVHHH
HHHHHHHHHDDHDETVEEK
```

3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GVG4 **A0A0L8GVG4_OCTBM** (53 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MIIIIIEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEECIKMYTR
```

7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE

18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GVH2 **A0A0L8GVH2_OCTBM** (70 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

MMMLTLTMNRQSKKLREKKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEECSKLLKLKKERTKMMQSS

21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GVK8 **A0A0L8GVK8_OCTBM** (67 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

EEEEEEEGGGGGEEEEEEEEEEEEEGEEGEDEEEEEQEQEEGGEEEEEEEEEEEEEEEEEEEEEEEEE

43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GVN6 **A0A0L8GVN6_OCTBM** (71 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

MEVSAYYRYNDDDDDVDDDGDGDGGAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVEGQRKGGGLYS

27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE

36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GVX4 **A0A0L8GVX4_OCTBM** (128 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MQMKQRKTNVKKRKKRKKLMMMMMMMMERKKDENEKEEELETKERKGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEDDKAKKERKNTLLSFECSEIPLNNKYTDITRSIDFNLNNNNNNKCG
```

48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GWD7 **A0A0L8GWD7_OCTBM** (87 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MHYAVIRVVGEKEEEEEEEEEEEEEEEEEEEEEKEEEEEEEEEGGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EELKEDI
```

44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GWJ1 **A0A0L8GWJ1_OCTBM** (64 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

KNNSRNDIREEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEIEGEEVEGENKK

10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GX79 **A0A0L8GX79_OCTBM** (154 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

MTLQCKQEEEEEEEGGGGGGGGGEEEEEEEEDEEDGEGGGEEEEEEEEEEEVVVVGRGGGGGGEEEEEAVVVVVGEEEEE
EEEEEEEEEEEEEEEEEEEEFPVFCTRLTVLRGWAHRLHQRQCSTGPVFKRSSNSIVPFLHRSGIAKLKVPTKP

76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GXM3 **A0A0L8GXM3_OCTBM** (111 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

MLHGQQPIFHTAQTWIVLKSYVGEIELDNTLERTLRSRLWSRHNPGKYIKFKQHRDSSQVSEKKRKQEVEKLEEEEEEEE
EEEEEEEEEEEEEEEQQQQQQQQQQQQQQQQ

73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GXV5 **A0A0L8GXV5_OCTBM** (75 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

MADGGKIATEVKSKGNRGSRGMKAMKTKKEKRRRKKKKKEENGEEEEEEEEEEEEEEEEEEEEEEKEDGSGGEEI

44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GYZ1 **A0A0L8GYZ1_OCTBM** (85 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
AVVVVVVVVVVVVVVVIEEEEEEEEEEEEEEEEEEEEEMEEDEMLEEIKEKMEERKKSKINKELEEEEEGGGGGREEERW
TQRKN
```

18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GZN3 **A0A0L8GZN3_OCTBM** (418 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MHVYNPLLVLKISESVHKHSILKPHIKYIGNIHGNEVVGRELLLHLIDYLVTNYRRNSTVTRILQTSVVHILPTINPDGY
ARATLGDCTSVVGRYNRRMSDLNRNFNENPASSKKIEPETRAIMNWIRSNTFVLSASFHGGAVVVNYPFDYTRGNMDKIA
YSKSPDDDVFVYLALNYSRSHHDMHHSINCSTNEYFKDGITNGAAWYPLKGGMQDYNYYHGVMEITVELSCCKYPPAETL
QVYWEKNKRALINYLQLVHMGVKGLIMDESGNPVFRAKLSIDDRYITFRSSKFGEYWRLLLPGNYILKVKARGFRDYLSQ
PFRVIPGRVHRLDVVLTRRNSLTTNRRKSQKTVVVAKEGGGNEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEIE
```

366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE
379 - 398:	EEEEEEEEEEEEEEEEEEEE
380 - 399:	EEEEEEEEEEEEEEEEEEEE
381 - 400:	EEEEEEEEEEEEEEEEEEEE
382 - 401:	EEEEEEEEEEEEEEEEEEEE
383 - 402:	EEEEEEEEEEEEEEEEEEEE
384 - 403:	EEEEEEEEEEEEEEEEEEEE
385 - 404:	EEEEEEEEEEEEEEEEEEEE
386 - 405:	EEEEEEEEEEEEEEEEEEEE
387 - 406:	EEEEEEEEEEEEEEEEEEEE
388 - 407:	EEEEEEEEEEEEEEEEEEEE
389 - 408:	EEEEEEEEEEEEEEEEEEEE
390 - 409:	EEEEEEEEEEEEEEEEEEEE
391 - 410:	EEEEEEEEEEEEEEEEEEEE
392 - 411:	EEEEEEEEEEEEEEEEEEEE
393 - 412:	EEEEEEEEEEEEEEEEEEEE
394 - 413:	EEEEEEEEEEEEEEEEEEEE
395 - 414:	EEEEEEEEEEEEEEEEEEEE
396 - 415:	EEEEEEEEEEEEEEEEEEEE
397 - 416:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GZS8 **A0A0L8GZS8_OCTBM** (90 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EEEEEEEEEEEEEEEEEEEEEEEEEAIGGGKERRGGEENVNFIRWNDDDDDDNADDDDDDDDDDDEDDYEEEEGSGKEGN
TSILTSVMRT
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE

A0A0L8GZY5 **A0A0L8GZY5_OCTBM** (131 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
WTEEEEEEEEEEEEEEEEEEEEEEEDDDDDDVDDDDDGSFTYLHIHIFVLLPIIHLLRERTQHFHQHQSPPPPPPRLKILL
PSSSSPSMPYHQRHIVLRLHSHFRTLLHTIRQSSCCNTHKCTSQNAKLTLQ
```

3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE

A0A0L8H0H1 **A0A0L8H0H1_OCTBM** (52 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EYREKEKERGREEEEEEEEEEEEEEEEEEEEEEEEEGTNRLEIRCKNNKRCVR
```

12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE

A0A0L8H0P2 **A0A0L8H0P2_OCTBM** (59 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
NSYIYTRTVHTHKRQKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEECDMKRTRTRSAMR
```

17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE

A0A0L8H0U2 **A0A0L8H0U2_OCTBM** (99 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MEKGRKIERSGRRQRQEEEEEEEEEEEEEEEEEEEEEEEDVGEVDDVGYKNYKERKKKKKKKKKKKKKKKKKKKKKKKK
KKKKKKKKKKKISNRRRNE
```

17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE

A0A0L8H0U7 **A0A0L8H0U7_OCTBM** (66 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVEDGHKRRRNQQKKILLKKVKTKKINQ
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE

A0A0L8H1F8 **A0A0L8H1F8_OCTBM** (69 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MGLVCPYQTGSHVGYIGLHMFVLQYHFDGMCCSFTQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE

A0A0L8H1H9 **A0A0L8H1H9_OCTBM** (240 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
KKKKKKKKKKKKKKKKKKKKNSNKNNNNNNNNNNNNNNNNNNNNGNGNNNNNNNNNNDDDDDDDDDFFIGRKGSKHGGQYR
RTSLQHTRTKQKQNNRKTEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEIH
NLPRYGLEPHNQLLFKKYVCQSNSRSLKSEGRGASSREQDIIDRDSGGGRGAVCLSLVHGGGGGGGGRGGGGGDNDGDDG
```

99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE

103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE

A0A0L8H1U2 **A0A0L8H1U2_OCTBM** (49 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
SNNIEEEEEEEEEEEEEEEEEEEEEEGEEEEEEEEEEEEEEEEEEESGGK
```

5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE

A0A0L8H1Y1 **A0A0L8H1Y1_OCTBM** (75 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MSDIEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEASKATCSPEGEEKEDMKNNNNNNNLYVGNIRKNTAKHK
```

5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE

A0A0L8H259 **A0A0L8H259_OCTBM** (163 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
AHDNIATASLDAVVAFVDIINMEIIIIVFILVIVVIVVGTDTIVDIVIPINIAIVIFFIIIIIIVIICLTSSLRERGGGG
EGGGGGGEEEIEEEEEEEEEEEEEEEEEEEEDDDDDSKKMKLAVSSASLSSSSSSSSSAAATTTATTVTAAAAAAAAAAR
TPS
```

92 - 111:	EEEEEEEEEEEEEEEEEEEE

A0A0L8H2E1 **A0A0L8H2E1_OCTBM** (73 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEECVLFYFDRKFDLEIFNVRDGKKKKLDCNGIQCDKI

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE

A0A0L8H3I3 **A0A0L8H3I3_OCTBM** (172 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

MGGNVGSGGGSCGAGSSGDVSVVGGVGGSGCNGSSVGGEGGGDGGGVGDGGSDGASSNGVRDEKSDVVRAGVGGKCSETA
VEGSGSDDGDDDNDEVDADNDGERKTKGKREVESGSKDDEGKPNEEEEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEE
KEEEEEEEWGCS

132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE

A0A0L8H407 **A0A0L8H407_OCTBM** (141 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

MEEKFGFLHSYIYIYGGGDDDDDDDDDDDDDDDVDDDNDNDDDNDDDDGNDYDDDDYGNNVDDQVDDADDDNNDENDSEDE
NDDDDDDEEEEEGGRGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVKKDSDKIS

97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE

108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE

A0A0L8H4R8 **A0A0L8H4R8_OCTBM** (91 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
REGESDGKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGGGRGEGGGEGGEGGEEEEEEEEEEEEEEEEEEEEEEEEEEEESE
TGRVIERLLLN
```

9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE

A0A0L8H564 **A0A0L8H564_OCTBM** (68 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EEEDEEEDEEEEEEEEEEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDLLNPSRLNY
```

22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE

A0A0L8H571 **A0A0L8H571_OCTBM** (50 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

EEEEEEEEEEEEEEEEEEEEEEEEEEEEQQQQQQQQQQQQQQQKEEEGQY

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE

A0A0L8H5B9 **A0A0L8H5B9_OCTBM** (55 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

RERGGEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVYGTE

8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE

A0A0L8H5K2 **A0A0L8H5K2_OCTBM** (79 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

MKNEREWRRKIGSIWQNDREEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEERREKA

20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE

26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE

A0A0L8H5Q0 **A0A0L8H5Q0_OCTBM** (52 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
KRGGGGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVIAILSKIAAPLK
```

7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE

A0A0L8H5W1 **A0A0L8H5W1_OCTBM** (90 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
KQKKKQKKKQKKKKKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEVKDRRRGGSETSSVHVYSWFRPFNLTRLSNFKLHTY
NNGHSEKCKM
```

17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE

A0A0L8H5Z5 **A0A0L8H5Z5_OCTBM** (138 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MRIRKRKTKQEKEEEGNEEEEEEEEEEEEEEEEEEEEEEEEEERKKKKGRRRMRRTMRWRRKPQKRRNYEFKIMMIKSIVV
SLEAQNGIESPLLKQTGKGLNPIFIAENNPYSTIDQPVFLWRIIPVKNQRKYRKILET
```

18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE

22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE

A0A0L8H605 **A0A0L8H605_OCTBM** (123 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EELEGEEEYEEVEKYEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKVGGSSRRRKSRRWEGKRSRRNEENNKKKKKE
RDETTTTSKKKEKRRKKNKKKKKKKKKKKKKKKKKRERREEGRNN
```

18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE

A0A0L8H684 **A0A0L8H684_OCTBM** (237 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EEEEEEEEEEEEEEEEEELEEEELEEEEEEEEEEEEEEEEEEEEEEEEEMEEEEEEEEEEQQQQQQQQQEKQEQEEQVEQE
QEEQEQEEENNKKKYKKKNKKKNNNNKNNNKKNNNKKNKKKNKKKKNNNNKIEESMMLTTGVFSIADYDDYDDDDDDDDD
EDKGAQFVEEEVEEKEEEEEEEEEEEEEEEEEEAEEVVVVVVMDDDDDDDDDDDDDDDDDDDDDDYDGDDDDEQRKDI
```

24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE

A0A0L8H6D5 **A0A0L8H6D5_OCTBM** (93 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MTSCCEGIDNTLLLLGLHDLSELRDFITNWKQSLIRERESEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEMKI
```

43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE

59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE

A0A0L8H6E6 **A0A0L8H6E6_OCTBM** (109 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEQEQEEEEEEEEEEEEQEQEQEEEEEEEQEQQQQQQQQEEEEEEEEEEEEEEE
EEEEVLSILSDEEPVNLNRIYCKKWFYCT
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE

A0A0L8H6G4 **A0A0L8H6G4_OCTBM** (70 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
NASKQTNKEEEGEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVGGI
```

15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE

35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE

A0A0L8H749 **A0A0L8H749_OCTBM** (132 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MFEKGLVPGKFQGGVEWEEGEEDDEEAEEEEGEEREEGRKDFPEEAGIWVEEMIRLHQPQYSAEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEGEEEEEEEEEEDEEEEEEEEEEEEEADDDYEEFSKQRILK
```

64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE

A0A0L8H7H4 **A0A0L8H7H4_OCTBM** (52 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEYMTRESKILRIVVSLVSL
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE

A0A0L8H8B2 **A0A0L8H8B2_OCTBM** (52 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MTGAEVAKVGNWPLTSEREEEEEEAEEEEEEEEEEEEEEEEEEEEEEERDWK
```

26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE

A0A0L8H8H7 **A0A0L8H8H7_OCTBM** (191 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MPICTLIVCVLYSMFVCLYMRLYPSSGDIAVPFSQSHNLSVALNYLNIFKLLNIFMFAFIIIVVVVVIILIIIIMLIIHI
ITVSSIISFTITVTPPLSLLTLLLRRRDGISSVLTFKLRREEEEEEEEEEEEEEEEEEEEEEEEEEEEEDPSIGIDSYIL
FELMIFNVGGHDNLVGLQYFVIIACLFELLQ
```

121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE

A0A0L8H923 **A0A0L8H923_OCTBM** (137 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MRERRGRRRWMEWSEREGCKGRERERSKAERGRERERERERERERERKRLEKGRRRMNERKERIKNKENLIERRKEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERRMKREKQNG
```

74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE

101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE

A0A0L8H9K3 **A0A0L8H9K3_OCTBM** (75 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MREVLLYEGVVHLETILTEIRVLPEEEEEEEEEEEEEEEEEEEEEEEEENEEDEMNGDLEYREEEEGRMARTRKR
```

25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE

A0A0L8H9L7 **A0A0L8H9L7_OCTBM** (105 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MTIPIDINVSVKTYQKLSKYKDLEIEIGKMWNLKTKTIPVVIGALGMVAKGADCYLAQIPGNSKIAEIQKLVLMEPAHIL
QEEEEEEEEEEEEEEEEEEEEVQ
```

82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE

A0A0L8H9S8 **A0A0L8H9S8_OCTBM** (159 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
KSINNNESKTNNNDNEEDDDDDDDDDDDDDDDGGGYDDDGLTTTAATTTTTTTTTTTTTTVPVLLPLLTLLLLMVMLFGDVD
DDGADAQGNDDDDDDDDDDDDDDDDDDDDDDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEERPLIAVECQQI
```

111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HAC7 **A0A0L8HAC7_OCTBM** (51 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
LFWERDRVELVGEKEEEGEDEEEEEEEEEEEEEEEEEEEEEEEEEEKEKERG
```

21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HAK3 **A0A0L8HAK3_OCTBM** (70 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
FTGERRRRRRRRRRRRRRRRRRRRRRKGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEESEEKQETKKKKA
```

29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HB26 **A0A0L8HB26_OCTBM** (76 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EQEQEQEQEQEQEQEQEEEGGGGEEEEEEEEEEEEEEEEEEEEEEKEEEEEEEEEEEEEEEEEEEEEESRYLVSEV
```

24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HCP7 **A0A0L8HCP7_OCTBM** (99 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EEEEEEEEEEEEEEEGGGEDEEEEEEEEEEEEEEEEEGGEDEEEEEEEEEEEEEEEEEEEEEEEDEEEDEEGGGGGGGDYR
KLAKSKERMASGIPFCVQK
```

42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HCV6 **A0A0L8HCV6_OCTBM** (117 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MKEEEEEEEEEEEEEEEEEEEEEEEEEEEKDEETNDDGDDNDVYDDNDYVRDDNYGDDDEGVGSDDDDDEEESKRKRRKKS
NQIRIRAIDDRFSLIIVDTHSDHHAWNVVSFLNFSND
```

3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE

9 - 28:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HCY3 **A0A0L8HCY3_OCTBM** (74 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

IDGYFLYYISYCLWYFIYLGEESDNERGKREGGEEEEEEEEEEEEEEEEEEEEEEEEGGGGGEGKEEEEEEEEK

34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HDP0 **A0A0L8HDP0_OCTBM** (57 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

IDIIISPEKNKSRLESVKQERESGEQQQQREEEEEEEEEEEEEEEEEEEEEEEEEN

31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HE58 **A0A0L8HE58_OCTBM** (75 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

EEEEEEEEEEEEEEEEEEEEEEEEKEEEEEDKSLEGKIPQVQYHRKCCSVFTMKKSLGTIIAKSNSVEAVEVGAK

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HED0 **A0A0L8HED0_OCTBM** (53 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

MITELKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGGGGLIVAREAYDHYSNQ

7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HEK2 **A0A0L8HEK2_OCTBM** (72 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

MSTRVWYSTLPFQPFPLFSEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEETYVAMGNIFTFIISYKPIINK

24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HF17 **A0A0L8HF17_OCTBM** (77 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEIKINWLCCNVLQ

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE

40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HF77 **A0A0L8HF77_OCTBM** (53 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

EEEQEEVEAEEEEEGEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEILIF

18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HFH8 **A0A0L8HFH8_OCTBM** (67 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

EEEEEEEEEEEEEEEEEEEEEEEEEEEEEDMMRKKERKKWFKLSISLSREIVERKIKSMKKSRSMNN

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HFK7 **A0A0L8HFK7_OCTBM** (53 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

KRIKEVENEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDS

11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE

21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HFV5 **A0A0L8HFV5_OCTBM** (54 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EEEEEEEEEEEEEEEEEEEEEEQQQQQQQQHTSTYHLICAYMQQQVEAEIINLT
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HG43 **A0A0L8HG43_OCTBM** (161 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MEKSRRKGEREEEERKKKDKNKLEEEDKNKMKKDEKVEKVEEVVVVMVVVVVVVKKNEREEKGEEEEEEEEEEEEEEEE
EEEEEEEEEEEEQEEEEQQQQQQQQRRRRRREGKENDDSSDAGDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDYDDDDE
V
```

64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HG57 **A0A0L8HG57_OCTBM** (198 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MCWRTRHDNASFVCSASDPGRNVSHLRKPKAYSVGEVFKEADKYKQEIILRNKYEVEEDEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
LELEQQRTMIKRWQEKPRHAKYWAKLNGKETDRENSQQ
```

60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE

71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HGH1 **A0A0L8HGH1_OCTBM** (93 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
PGLYNSGITKEAIRAKIIDSYETYGGFRKVKVVSSYSHNTTIGECKQYRCIRVFVNVRGGGGGGGGEEEEEEEEEEEEEE
EEEEEEDNTDQLQ
```

67 - 86:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HGJ3 **A0A0L8HGJ3_OCTBM** (52 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EEGEGNEEKIVVVREEEEEEEEEEEEEEEEEEEEEEEEEEDNDDAEWHKQREQ
```

15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE

20 - 39:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HGR1 **A0A0L8HGR1_OCTBM** (1451 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MPLLGKKIFVYAKPLVNRKSEEVIYSIAHTKEQFRSKQDYEKRVALYKNRIWTCQSTGHTNLTHEEAWNSEKNVKKSVQS
QFQTCYEKPVLEIVHHSILSLDTLVDQAWLKLQQVLSINECVSLKVKTSGKVVKAKVVRIDTCGIEANPTSNCSSPSSDK
ENTDENSSNKDTGQKKWVPPKLLPYKYSIKLNEEEKIINCVPAADLTRVDRPPPKELLRLFIRTHALRAGVTSSSPWVVD
DIMIKKHSIQNKLADVFLSPMKIQDHSLDECAKKRKLSSSKSQNSSNAKKSKLDKSKPAKTSKKKKDESESSSKKKAKQG
KLNTSSSSSNSSCTTKRKPSISKNSNSGSPSKKSKLVNDVDSSDEDSDTSEDCTLGKLKKKLPLSKDDDDVPLSTLKMQR
TPTKSKKTDSRQSTPKKPKTVQKDQGKGSAKKSSSKSSEKKKSSKESDKKKKVSGEKDKKKSSSSSSSNKSKDKETPKKN
KSMKQMTLLEMSTKKGPKTPEKKKPSTTSSPQKPPPLVRKLMAAMKTKDSNRNEYKKILEKVVIHLSAQQREKLPPDVKD
IVLKAFQSHEERKKLKAMTAEQREEYLQKKREESKKKQAEDRRARQEAIRKKKRELSRRYEDQDLDQKSLPVPKLISHPK
VLPIEAFGDVAMVTEFINCFAGLLMPQGEKVYYTDTLMKALVDKEKGSSYIAEILVILLQTLLQDEISEDYAELKTSLSD
IPVNHYTATELVRLALRKIDTDVADEAQSDDSSTSGVEEELELNEELIDMLENHELNDLEPAQKLQILKGLCLRIMGTYS
VQDFMEQKQAEASDLWRRRLFSLKEKKQQRFLANANKITLKEDQSDSKENDPKNGNVKTEPRNIKASGESGLTIRDFYGN
KVAEEEEANFSDDGLASVVKRRQRRAAVVAKEKEKRDKEERERREKEYAVLRKIKEEEAFEKEFNDGISFAKLVLRLSPI
GTDRNHSRYWVFSRCTPGLYVEKGWIPDEIAFSFKNESDDSSCSSDDEVLSNSQNSHYNNKPVETSVPEPGQNTWSVYET
EEEFDNFIASLHPQGIRESALKSELLKRRDDIVKNMNATKKSSSKDVTVKKTEEEESDNPLDMKEAFKRELRETETRLRN
GGLGGVFDQEEWEKKIETSVAISDMANCMLDTQSYVLERFLQGIMGKSKSKSSDSEKKEENTDSSVKEEEDKELINMGLL
KWKEAVEHSKTYSRLHVLLGILDACIKWEKSAENAKCKICRKKGIGEQLILCDDCNQAFHLYCLRPALPWIPEGDWYCPA
CLPQSERRSRRTASRKKYGEDTDDEKGDSDDGDTEGDDLRQSEKEHYENCVVCDGQDDLIQCSQCPDVYHIECHDPPLRH
PPRGQWICTQCKSGGRRSRSRQAVAKQRQERAQRRKKYMKESEEEEEEEEEEEEEEEEEEEEEEEEEESEEDIPKSSKSKK
KVQLRTYCKFI
```

1403 - 1422:	EEEEEEEEEEEEEEEEEEEE
1404 - 1423:	EEEEEEEEEEEEEEEEEEEE
1405 - 1424:	EEEEEEEEEEEEEEEEEEEE
1406 - 1425:	EEEEEEEEEEEEEEEEEEEE
1407 - 1426:	EEEEEEEEEEEEEEEEEEEE
1408 - 1427:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HGV2 **A0A0L8HGV2_OCTBM** (87 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEETLLCNEIRGNGSKNGIWLGEIVGKTRIANPAKKELRNERREDKTNE
NVRQNDV
```

7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HH98 **A0A0L8HH98_OCTBM** (152 aa)
Thyroglobulin type-1 domain-containing protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
ILKFTRMFPALALLILYHTLETVHTNECLRLRAAGLNSHLINIFIPKCEEDGTYTAVQCHANGCYCADEFGAPITDVDIS
LEEVKRTNMNCMSMLSMKFIMMKMMMMIMEGKGGGGGGGEEGGEEEEEEEEEEEEEEEEEEEEEEEMDGFE
```

125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HHE0 **A0A0L8HHE0_OCTBM** (50 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MHSQNMTKNILDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVEEDKKLKI
```

13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE

16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HHZ5 **A0A0L8HHZ5_OCTBM** (133 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MEENEEEIRKRKERRERRSGEKEEEKGGMRGRERRARRKETRRKESKDEEEQRGRRARMKESKEEGKQGGRKKRKTTRRE
RGEEVEEKRGEKRRKRWEEEEEEEAGEEEEEEEEEEEEEEEEEEEEEEEEEG
```

107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HIU0 **A0A0L8HIU0_OCTBM** (58 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
HILKTHRAALGSAVKAPYKNKTSEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEA
```

24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HJ96 **A0A0L8HJ96_OCTBM** (66 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MTKPKKEEEEGEEEKKKKKEEEEEEEEEEEEEEEEEEEEEEEEEDQRISVNDAEKDKKKRTKRKGNK
```

20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HJQ3 **A0A0L8HJQ3_OCTBM** (132 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
MLVFIRINVCVPLYRSINIMTCICFLVCITYMQMCIGATSLHQSIYLNIYGTVMLHTIISNMFMRTIYIYIYNGYCHTHT
```

QAYTHTDENVPEILCFGKQEEEEEEEEEEEEEEEEEEEEEEEEEEEENKGDVE

100 - 119:	EEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEE

A0A0L8HJT0 **A0A0L8HJT0_OCTBM** (52 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

KGMEEGRCGKVEEEEEEEEEEEEEEEEEEEEEEEEEEGGGGEGGVEINEKKTE

12 - 31:	EEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEE

A0A0L8HK86 **A0A0L8HK86_OCTBM** (97 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

MVRNQTKVKAENIVAAQVMSSLNDDDDDDDDDDDDGDDYDDEDDDGDNDDGGGCEEEEEEEEEEEEEEEEEEEEEEEE
EEEEDEEEEEEEKKEEE

55 - 74:	EEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEE

A0A0L8HKD6 **A0A0L8HKD6_OCTBM** (90 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

MTAMRRKDTLEKREEKDWTKQKKKVYEKENDEGDYDEQNEEEEEVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEGGGGGGRG

46 - 65:	EEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEE

56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HL59 **A0A0L8HL59_OCTBM** (75 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEECVCLPYSIDSSMPPGHILNVVFLTEEKPFH

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HLJ5 **A0A0L8HLJ5_OCTBM** (81 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

DDVREIRRKLRTRESKREQRCEIGKELTAIEEEEEEEEEEEEEEEEEEEEEEEQQQQQQQQQQQQQQRLRRRRRRRRRRRR
L

31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HLK2 **A0A0L8HLK2_OCTBM** (58 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

MVMVKNKRKKERKKEKRKKEEEEEEEEEEEEEEEEEEEEEEEEEEEGFIDCDNHEQQI

20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HLN6 **A0A0L8HLN6_OCTBM** (72 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MVVVVVGNEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEECLNLYVCSYVYVQFVSM
```

9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HMI7 **A0A0L8HMI7_OCTBM** (77 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
ITTLHKTIALGTTIIDEESSKRSSVNKIISEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEFFYGSKP
```

31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE

38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HMK1 **A0A0L8HMK1_OCTBM** (58 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MSFSALSEEEEEEEEEEEEEEEEEEEEEEEEEEEEERLRLAIHFVVVIFFASSLKIVNR
```

8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HMZ9 **A0A0L8HMZ9_OCTBM** (56 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MIATTTVLIVTVIIMRRRRRRRRRGGEEEEEEEEEEEEEEEEEEEEEEEEEVYLH
```

27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HN69 **A0A0L8HN69_OCTBM** (109 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
RQCAEEEEGEGEEEEEEEEEEEEEEEEEEEEEEEEEEEQQEYENEEQEDQEEYEVQEEQEEQEEEVEEKQEDSNKSNELE
EKEGKKQDKIRQKKRKKKKRGVKMKTKKK
```

12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HNK5 **A0A0L8HNK5_OCTBM** (155 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
TGKESHDRESHDKETHDKETHDRETHDRETHDMETHDRETHDRETHYRETHERERESHDRGCQESAKKKTDRQTDRDRQT
DRDRQTDRDRQTDRDRERSKCKDFSWETRLLEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDCADGRN
```

112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HNK9 **A0A0L8HNK9_OCTBM** (55 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MSGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKERNKREESRMENMKGKN
```

4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HNQ6 **A0A0L8HNQ6_OCTBM** (63 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EEAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEELLQVFHKKLSHKSCSDYSLCYMNDYSEK
```

4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE

10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HNW9 **A0A0L8HNW9_OCTBM** (50 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
MRIDEEEQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGNYQLP
```

9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HPA8 **A0A0L8HPA8_OCTBM** (51 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDDDDDDDDNDDDDDDNIRKKN
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HPE4 **A0A0L8HPE4_OCTBM** (77 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
MIVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEETGGGGGKEEKQEEEKKKTKKGKKKRKTKERKEKKKEKERKMK
```

4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE

8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HPS2 **A0A0L8HPS2_OCTBM** (54 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MMREEEEEEEEEEEEEEEEEEEEEEEEEEEQEEEEQEEEEEEEEEEEEEEKKTIV
```

4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HPZ6 **A0A0L8HPZ6_OCTBM** (49 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MIEKEDEGGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGKHF
```

10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HQC8 **A0A0L8HQC8_OCTBM** (175 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
KKKKKKKKKKKKKKKKKKKKKKKKKQEEEEAKRRRMTTTTAAVKLVKEVKRRERKQKRYMRRQRCKRKQERKKERKKERK
KERKKERERERERKERKRERKEKEEEEEEEEEEEEEEEEEEEEEEYEVVEDADDDDYNVDDDENTNKMDEVEKEEQYSNFKI
QKSIQINGISFASFP
```

102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HQF7 **A0A0L8HQF7_OCTBM** (64 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

EQRKKRKKLTKCETDSVRERGGESGDGGREEEEEEEEEEEEEEEEEEEEEEEEEEEEIFSYHEW

30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HQI5 **A0A0L8HQI5_OCTBM** (62 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

MRRHLLRLRSGRIGKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERREKGQEEQDIFQR

16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HQQ5 **A0A0L8HQQ5_OCTBM** (100 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

RKSRRNVVVVVVEEEEEEEEEEEEEEEEEEEEKEEEEEEEEKEEEEEEEEEEEKEEEEKEEEEEEEEEEEEEEEEEEEEE
ELKEDAKRNNINMNNKRLIT

59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HR66 **A0A0L8HR66_OCTBM** (59 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

MSVSGKDEKMRRRRRRRGGGGEEEEEEEEEEEEEEEEEEEEEEEEKEEEERRNDGGCGK

22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HRA5 **A0A0L8HRA5_OCTBM** (49 aa)

Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EKKNTKKMKKVKAEEEEEEEEEEEEEEEEEEEEEEEEEDEEEEELEGDVD
```

14 - 33:	EEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEE

A0A0L8HRB8 **A0A0L8HRB8_OCTBM** (91 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EEEEEEEEEEEEEEEEEEEEQQQQQQQQQQQRKMVLLTYDSGKYKNTYQVADNNEHISANREKGREIRDNHKIRCVRKRK
HTNLCKRRKKF
```

1 - 20:	EEEEEEEEEEEEEEEEEEE

A0A0L8HRG9 **A0A0L8HRG9_OCTBM** (126 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
MEHRKKQGERIKNQHQTVEEEEEEEEEEEEEEEEEEEEQEEEEQEEEEEEEEEEEEQEEEQELERTSSSSSSRSSSSSSSS
SSSSSSSSSSGGGGGGGSGSSSSSSSSSSSSSSSSSRLEVGGIGNQ
```

19 - 38:	EEEEEEEEEEEEEEEEEEE

A0A0L8HRH3 **A0A0L8HRH3_OCTBM** (52 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EEEEEEEEEEEEEEEEEEEEEEEEQQQQQQQQQQQQQQSEKEGTKQRKERRI
```

1 - 20:	EEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEE

A0A0L8HRS9 **A0A0L8HRS9_OCTBM** (81 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MYLLEYIQPLLMMTLIYCKYLRMLTIKYYAHIHSQKKERERERERKEEEEEEEEEEEEEEEEEEEEEEEEEEDRQTDRLL
D
```

46 - 65:	EEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEE

A0A0L8HSR0 **A0A0L8HSR0_OCTBM** (55 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MCVYFIEGGEEEEEEEEEEEEEEEEEEEEEEEEEEEGDDDDDDDDDDDDDDNVQ
```

10 - 29:	EEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEE

14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HSW0 **A0A0L8HSW0_OCTBM** (305 aa)
WSC domain-containing protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEIKRKETERQINRKRKQREGERERAMKREKR
KGGKDIKRESRRQTDTEKAEKTAKADKAEKTAKAKKTEKAVKAEKAEKAAKTKKAAKTKKAEKTAKAEKAEKAAEAKMVE
KNAKAAKAEKSAKTAKAGKAAKTEKQKAKDEPNDESLKNNDGRIIGCFKITNSRRLKKDMNLQLVVLNKSQKSCMFRCRL
YGLKYAVVYNGKVCFCGSNKPPTKKAIKSIDCSKICSGKKSKCHQKNTVRIYETMTPVSKVGKTK
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HSW8 **A0A0L8HSW8_OCTBM** (148 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
RKKKKKKKKRRRRKRRRKRRRRRRRRRRKLRGKEDEADEEEEEEEEEEEEEEEEEEEEEEKEEEGKEDERKDEADEEEEEEE
EEEEEEEEEEEEEEEEEEDRRXXXXEKKKTKGERRRSRRRRRRRRRRRRRRRRRRRRRRRRRRRRRPTES
```

38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE

77 - 96:	EEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEE

A0A0L8HTH9 **A0A0L8HTH9_OCTBM** (105 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
TEEEEEEEEEEEEEEEEEEEEEDSGGDGDDEDDVHDRDNNYDDGDNGADADDDDEKEEDMEADLEENEGIDLIRDPGRKR
LEMSNEVKKSVKEMEEWGEDRVRDR
```

2 - 21:	EEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEE

A0A0L8HV35 **A0A0L8HV35_OCTBM** (141 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MNYPITHKVRMYRYSANVCSLEIVIVNLIDEKQPVNTMMTKCSKAAPDAIGSNVDDGSDAFAPDDDNGGGGDDYDDDNDD
DEDDDEGEEEREEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVYVGLKFLHNASSFV
```

92 - 111:	EEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEE

A0A0L8HVG6 **A0A0L8HVG6_OCTBM** (63 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EEEEEEEEEEEEEEEEEEEEERERERSKEREKERKREREKEREKITEKWRSEKKSYNNNESRR
```

1 - 20:	EEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEE

A0A0L8HVW8 **A0A0L8HVW8_OCTBM** (63 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
KSEEEEEEEEEEEEEEEEEEEEEEEEEEEEELVRLNIGGKRKDGCFETICLVNNGPRVSESGQ
```

3 - 22:	EEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEE

12 - 31:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HW62 **A0A0L8HW62_OCTBM** (172 aa)
ATP-dependent DNA helicase (EC 3.6.4.12) (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
YCILDTIYEKNYHLYSQDFLNNLNLSALPLHKTKLKTNCPIMLLKNLDPANGQCNGSTYTVAELNSNIIEAVIATGPHNG
KRLFIPRITLVPADNQLPSQLRRRNGETFKIQRLGNRGNSNVGSSGTVLEEEEEEEEEEEEEEEEEEEEEEEEEEEEEID
KSNLEKRNFSYE
```

130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HWR7 **A0A0L8HWR7_OCTBM** (50 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MPKTEEEEEEEEEEEEEEEEEEEEEEEEEQQQQQQQQQQQQQQHRSTPSK
```

5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HWT4 **A0A0L8HWT4_OCTBM** (297 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
KKKRKKKRKKTKKKKKKKKKKKKRKKKKRKKTKKKKKKKKKRKKKRKKKKKKKKEKKKKRKKKKKKEEKKKKRKRSRRSR
KKKKKKKKKWKKKKKKKKKKKWKKEKKKKKKKKKKEEEQEEEEEEEEQQQQQQQQQEEQEEQEGGGGEEEKEEEEEEEEE
GEEEEEEEEEEEEEERKGEIYGEDGLTKEEKKKTGRQVINGERGREREREREREKEKINIDEGEEGVKEKEINENGKQ
KGRKKEKRKEEEEEEEEEEEEEEEEEEEEDDDDDDDDDDDDDDDCGGDGGGGGSGSG
```

250 - 269:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HX42 **A0A0L8HX42_OCTBM** (80 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
TTNEEEEEEEEEEEEEEEEEEEEEEEDEEKEEIEEEEEEEEEEEEEEEQQQQQQQVDGVTKIATALGEKEKERKKKRKKS
```

4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HXZ9 **A0A0L8HXZ9_OCTBM** (113 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
KAKEKNRKEKERKEEEEEEEEKEEEEEEEEEEEEEEEDGEEEVEDGEEEEEEEEEEEEEEEEEEEEEEEDEEEEEERQQE
ERRRSWVVSTSTGSPLSSRFVGWHTMYLTTQRY
```

47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE

50 - 69:	EEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEE

A0A0L8HZ31 **A0A0L8HZ31_OCTBM** (56 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

KRKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDGVDDDGKEEDMYILNIDISTC

4 - 23:	EEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEE

A0A0L8HZK0 **A0A0L8HZK0_OCTBM** (108 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

MLLGAFLMSAMICIFYYIDIKYYFVLEQGLSKLKSYKVYQVVSEMVTQFSIEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEQRQQQQQQQLHLKQH

52 - 71:	EEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEE

A0A0L8HZR9 **A0A0L8HZR9_OCTBM** (63 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

GRDGGERGENNETNDVVVEEEEEDQEEEVKYVEEEEEEEEEEEEEEEEEEEEANEKTEENEEE

33 - 52:	EEEEEEEEEEEEEEEEEEE

A0A0L8HZW6 **A0A0L8HZW6_OCTBM** (115 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
VVVVVVVVVVVEEEEEEEEEEEEEEEEEGGEEEEEEEEEEEEEEEEEEEEEEEEEEEMKQRSKIKEKDKNGIKNKESLRKW
NGKKRGRVGGKIIAKEKQRRKERMKERKEKEEQKV
```

30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE

A0A0L8HZY8 **A0A0L8HZY8_OCTBM** (159 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MTTRLVRVHQACASQPYVRDTHDLAESLIIAPINDDDGDGDKEEEEEEEEEEEEEEEEEEEEEEEEEEKEEEEKEEEEEEE
NDVDSEKEMDDDNSEDEEDNTTDDDDDDDDGDGDDVDNDDDNDGPLRTGRRDRDDAKIIRHKRTRRKSRRERRRLMMTE
```

43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I049 **A0A0L8I049_OCTBM** (68 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
HIPKAHRAALGSALEARYKIKTTDEGGGRGGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEESFLLEAQ
```

32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I079 **A0A0L8I079_OCTBM** (55 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
KEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAEEEEVGGGGGGGGGERSL
```

4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE

12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I0C6 **A0A0L8I0C6_OCTBM** (87 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
VEIRCREDEEREEERWGEKEEEEEEEEEEEEEEEEEEEEEEDDDDDYDDDDDDDDDDDDENEDDDDDDDADDDDDDDDDD
VDDVDDD
```

20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I0R0 **A0A0L8I0R0_OCTBM** (73 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
LLKRVQEKNLRHVALVNRLVYYIISEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEV
```

26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I1Q8 **A0A0L8I1Q8_OCTBM** (81 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MMKKKKLKKKEGEEGEEEEEEEEEEEEEEEEEEEEGEEGGDEEKEEGGRGGGGGGEEEEEEEEEVEEEEKKNKEEGEGEEE
C
```

16 - 35:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I1Q9 **A0A0L8I1Q9_OCTBM** (908 aa)
Fibrinogen C-terminal domain-containing protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MKAAFFGVFALFLIVCLSTTSTAPVDPSEDAVGTSNDSQPIIPLPKPVAAGKAEPEPQPEPETTVDPETLPISIKSGSAS
LTWLPEADRRIVDLNWYVDHLVKKNRALKLKFEKFEEILKNLHDEEKKMSEELNRWNMGLFFPGMAHVHETIGITGHILN
KVGAKVEGGLQPCRLNNLLRRLDTVCPKIRDDEIKVLEETIEGVAGNMKAIDDIIKQEEESQNLKEDISQIWKDFRGPSV
SVLPDDTYLNVINITVPGELSETEESEEEEEEEEEEEEEEEEEEEEEEEEVAEAVAEEKEEEITEIKETVEVDIEGDKKTE
VDEEEIEEKAVEVEKEDKKAEEIEEKKEEKAAEVEKEEDKKAEEIEQKEEKAAEVEKEEDKKAEEKEEKAVEVEKEDKKA
EEIEEEKEEKAVEVEKEDKKAEEKEEKAVEEDKKEEKAVEVEKEKDKKAAEAEEKEESELGKVDPKVDPVSIPEPESDEP
VEKKTDAPVALPENDAGVATAQPSAAAVTTDAPKRGTKSPKKPKKKPRRKPKKPRRRGTKAPKKVTTAAPKVVITTTPKV
VTTTTPKVVTTTTPKVVTTTTPKIVTTTTPKVVITTTPKIITTTTLEPCVDVFSVEEKRYQCKGYWKRGLTILGLQINKL
KKDNHELFLKVIDANGKIKLAQESIAEHKINVKALKKKFAWPDKDNLGNTHKDCSDALKKDHKKPGVYLIHPVGSPYKVH
LLCVDGWTVIQRRFDGSENFHRSFDEYLSGFGNFSGEFFVGLENLHRMTLSQAYTLRVDVKSAAGKWYFAVFNNFAVSDE
TDQFRLKLGNMTASNSDDVMDQSRDRPFSTYDRDNDDWSGGNCAQHFRGGWWSGNCITNLNQMWCSNGCLRWGDTRVVSS
IMRIRPTSTADPDDMTETPNPVGFSIKE
```

267 - 286:	EEEEEEEEEEEEEEEEEEEE
268 - 287:	EEEEEEEEEEEEEEEEEEEE
269 - 288:	EEEEEEEEEEEEEEEEEEEE
270 - 289:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I1T3 **A0A0L8I1T3_OCTBM** (56 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MCEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGGGGGQRLS
```

3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I2C0 **A0A0L8I2C0_OCTBM** (54 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
GGGENNKEEEEEEEEEEEEEEEEEEEEEEKEKEKEEEEEEEEEEEEEEVEEEEEY
```

8 - 27:	EEEEEEEEEEEEEEEEEEEE

9 - 28:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I2G9 **A0A0L8I2G9_OCTBM** (223 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MRQYDDDDDDDDDDDDDDDDDDEDDEDEDDEDEDDDEDDDEDDDEDDDDDDDEEDEEEEEEEEEDDDDDDDDDDDDDEEDD
DDDNVDKRRKGVEKKKEDEGEKEEVKEEERGRRTKRRGEGRKRRGEGRRGEGGGEMENEKEEEEEKEEVEDVEEEEEEEM
WWWRRRRMWWWRSRKRGEEEEQEEEEEEEEEEEEEEEEEEEEVGKEEKEYQEYGSDMTAVGC
```

183 - 202:	EEEEEEEEEEEEEEEEEEEE
184 - 203:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I2H9 **A0A0L8I2H9_OCTBM** (79 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MRIVFEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEWCFTEARGCGYTYLYVCVYLIDCRGIITSPLTMFRFAAVL
```

6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I2J7 **A0A0L8I2J7_OCTBM** (99 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MREEEEEEEEEEEEEEEEEEEEEEXXXXNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNDDDDDDDDHDMRKRRTRAKGGGE
DDRDNEYQGRCKEKKINEK
```

3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I2P5 **A0A0L8I2P5_OCTBM** (169 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
RRRRRRREEEEEEEEEEEEEEEEEEEEEEEEEEEEEENNNNNNNNNNNNNNKKKKKKKKKKKKKKKKKKNEKEEKRRKFRREG
NKNMEGAEKMKLKKRAVEEKKRKKNSSSSSSSSSSSSSSSSSSSSKRKILGIKKMKKIDGDGDDDGGDDDDDDDDDDE
NKNKNKNKK
```

8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I2V4 **A0A0L8I2V4_OCTBM** (67 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MVISYQDKQRMTSQQEEEEEEEEEEEEEEEEEEEEEEEEEEQQQQQKGIRCEKLYYLFFNTYSTTGLD
```

16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I3D5 **A0A0L8I3D5_OCTBM** (196 aa)
C2H2-type domain-containing protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MCVMRLCAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAKPRIRKLLGIKWQDRIPNTEVLIRANLLSIHTILMQSQLRWA
GHVARMSDDRLPKGLIFAELQKGKRSQGGQKKRFKDILKASLESWRSAVHKGANTCETNRIAAAEDRRQTRKNRANNPVA
GSTIPCPHCQRLFRAQIGLTSHLRTHKASPPPPQDD
```

9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I3G8 **A0A0L8I3G8_OCTBM** (100 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
RKESGRERKKKEKVEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEXXXXXXXXXXRKKKKKKKKRKKKRRRRRRRKKKK
KKKKKKKKKKKRKRKKKRMQE
```

19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I3L6 **A0A0L8I3L6_OCTBM** (270 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
VCEKQDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDSEEGEDVTVPPLTTATSTTTTTETSVITRPSSQSEESSLSATAVA
GRTAATAATAYVLASSSLLSLSSSSSPTATTTTTTTTTTTPASLSGHCRRPLLLSRPFTPPSSPLPLYSARDLSTSTPGF
PDESPPLSPARAERKPLKVGFVDMEDEEDDGLDGEQDADEDGRHRNTSKFGLRKGMNCKRYHQPRMSLLGKPLHFHGHRR
DAKYRKLQARIYNFLERPKSWPSALYHIFV
```

7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE

12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I3R7 **A0A0L8I3R7_OCTBM** (49 aa)
TFIIS central domain-containing protein. *Octopus bimaculoides (California two-spotted octopus)*

MSREEEEEEEEKEEEEEEEEEEEEEEEEEEEEEEEVEKKEEEEEEEGYH

13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I3Z4 **A0A0L8I3Z4_OCTBM** (89 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

TKHEQNEKLFSVFKEADKYKQEINLPNKYEEEEEEEEEEEEEEEEEEEEEEEEEEEEEETKAIKHMKSKLRLEQQRTMI
KRWQEKPLH

30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I440 **A0A0L8I440_OCTBM** (69 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

MTKQVKMRSRLKNRNNSSNKEKRRKTFSGQNKEEEEEEEEEEEEEEEEEEEEEEDGGGAEEDKHNFWYK

33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I4I0 **A0A0L8I4I0_OCTBM** (70 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

PSVSDNDKVCVLSDESACDSVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDSHNDFDEH

22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE

32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I4Z5 **A0A0L8I4Z5_OCTBM** (84 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEESGEEQRERRGRISTIKRYGLQVIRRHIAKQTNQNDMIGDISQD
SFFG
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I584 **A0A0L8I584_OCTBM** (56 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
TGATNTKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAHSKQAAVDQKQKT
```

9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE

22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I5L7 **A0A0L8I5L7_OCTBM** (57 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
GGGGGGGEERGKGEGAEEEEEEEEEEEEEEEEEEEEEEEEEEEDDHKQQQEEQSEVHR
```

17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I5Z2 **A0A0L8I5Z2_OCTBM** (91 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
MMMMMTTTTNRGKNHYKRREGGEGEEEEEEEEEEEEEEEEGVGGEEEGRGRGREEEEEEEEEEEEEEEEEEEENEKEEG
GRKEEGGRRRE
```

55 - 74:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I673 **A0A0L8I673_OCTBM** (529 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MTVTIVIMVMMRRRRRKKKRKKKTRKKERKKKTRKKERKKERKKERKKKRKKKRRKKKRKKKRRKKKRKKRRRKKKRKK
KRKEEEEDEKEGEEEGEEEGEEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEEEEEAEEEEEEEEEE
EEEEEEEEEEEEEEEEEDEEEEDEEEEEEEEEEEEEEEEEEEEEEEEERRKKRRKEEVEEEEEEEEEGEEEEGEEEEGEEEE
EEEEEEEEGEEEEEEEEEEEEEEEEEEEKEEEEEEEEEGGRRRGRRRKKRRKKEEEEKEEEEDDNDDDDDCCTYDGGDEDD
GGGDNGGGSGAGGAGGAGSGGGDSNCNGSEDNTHVSECNDDDDDDDDDNDDDDDDDRGGGAVFSGLHEDVCRSEVLDSFF
SRRAGSNIRFNQACSPYPGVQKQSLWLNTHFSWGTPLRFFCQTEESKNIRTSFIRFLSKNGAQPSFHKIHTSLVTADFPP
RSVRYFLQKIGLEHKQLKKGTKELRPRQLKSILDGCGWQETTEASWQKR
```

110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
184 - 203:	EEEEEEEEEEEEEEEEEEEE
185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I676 **A0A0L8I676_OCTBM** (137 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EKTKENYTTSTKGVCQQHRHQQKHLKGGEEEEEEEEEEEEEEEEEEEEEEEEEEGEGEGEGEGEGEGEEGEGEEEEEEEE
VEEEEEEEEEEEEEEEEEEEEGEEEEEKKKKTENNSNNYNNDDNRSFIGHKSRTQNK
```

29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I6Q0 **A0A0L8I6Q0_OCTBM** (166 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MNVLLFKQDQQGDREEEEEEEEEEEEEEEEEEEEEEEEEEVEEEEEEEEAETRRRRRRRRRRRRRRRRRRRNKKKKKKKKK
KKKEKKKKKKKQEEEEEEEKQEQEEQQRKKKKKNKNKKKKKKKKKKKKKKKKKKKKKKKNNNNNNNNNKKTTRIIIIMLTI
WHARLQ
```

15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I6V9 **A0A0L8I6V9_OCTBM** (49 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
KSKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEQQQQQQQQQQQQQQEEL
```

5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I6X8 **A0A0L8I6X8_OCTBM** (93 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
TTKKEGDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEEEEEVVVVVVLVVLVEKEVEEKEKKYHKNSNKSNKKRPRSMDI
NLAVITAVAPSKI
```

8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I748 **A0A0L8I748_OCTBM** (71 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
NNADGDADDIEKEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKRRGEGWRSGRAHSDFSTTVQ
```

15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I7A1 **A0A0L8I7A1_OCTBM** (65 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
KKKKEEEGGGGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEYNWFDVHDDVDDD
```

12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I7G4 **A0A0L8I7G4_OCTBM** (119 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
PTAEEIEEEEEEEEEEEEEEEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
DGSVKLSFATSINKSQGLSIKGVGLNLTPPSFLPSWAII
```

7 - 26:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I7M6 **A0A0L8I7M6_OCTBM** (126 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
PVVGGSSHEGVEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEHIAYEGKEGEKGDGEGRRGEEEEEEEEEEESADGDEEKEE
DTDVDGNEVHKANRHCLDPVLFHENGELPHGPKVSSFHVFWGSSPS
```

15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I7M7 **A0A0L8I7M7_OCTBM** (60 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEATSAQTSSFIIV
```

3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I7V8 **A0A0L8I7V8_OCTBM** (68 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MKSISCRKYTERNLGCKEEEEEEGEGEGEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVSEKIL
```

31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I7Z3 **A0A0L8I7Z3_OCTBM** (176 aa)
CPSF100_C domain-containing protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
SVYKQNFGICSYLSWRIVYYYVVAQVICALLYIQYFTEQHISIHRSTEEDGGGGGGEEEEEEEEEEEEEEEEEEEEE
EKEEEEEEEEEEEEEEEEEEELTIVLNMYCIYEPEMMKCKGTSAGFEMKRNKHPLRIPLNHWLNERTNPCDFSSLSVVVC
HVINSSEISLKAHPAG
```

58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE

60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I8E9 **A0A0L8I8E9_OCTBM** (97 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
NIGLQLRQLRSTEVQSDDEVVNDDSDCDDDDDDDDDDDDDDDDDLDGDESSNDVDDDDGEEEEEEEEEEEEEEEEEEEE
EEEEEERGGGKGRCEES
```

60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I8J8 **A0A0L8I8J8_OCTBM** (199 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MKTEGKGESDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDHDDDEDEEDDKVENDDHDDEEEEEEEEEEEEEEEE
EEEEEEEEVEEEEEEEEEDNIINDRPRRTRPRTKRRRCRRWGRELRKVDDDEDKNDNDDDGGSGGGSGVYDDVDDDDDDD
SYDSDNDDDDDMKAELSGVCHSSNISMELKALLTDIEDL
```

65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I8N1 **A0A0L8I8N1_OCTBM** (97 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
MKMRNSNSDSNTNNNIVKRKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKTTNKNRKEVEEERRRGKKKRKEEEKEEEEEEE
EEEEEEEEEEEEEEITG
```

74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I8Z4 **A0A0L8I8Z4_OCTBM** (70 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
MSYTHHRHTLIVSNYAFKENYDDDDDDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDRTGSRRRGEKEVY
```

28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I8Z7 **A0A0L8I8Z7_OCTBM** (79 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

IDTQTETEIPMLEFYSSRSYLKHSVLCNDDDEEEEEDDDGSGGNGRSGDGCRAEEEEEEEEEEEEEEEEEEEEEEEES

54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I908 **A0A0L8I908_OCTBM** (53 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEEDSYTVPGSGFRRLTS

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I9C8 **A0A0L8I9C8_OCTBM** (73 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

KRNYGEANDDGDKEAKVEGERQNVRWKKQEEEGEEEEVEEEEEEEEEEEEEEEEEEEEESIMILVVVVTTTSR

39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I9F1 **A0A0L8I9F1_OCTBM** (171 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

GKDNNENNNYSDTNNKEKEEEEEEEEEEEEEEEEEEEEEEEEEEEKNSNSASNSAGTTATITTALITTITIVAAAAVAVTT
TTPTATTTTKTTKTTTTTTTNNNNNNSNNNIKWNCGSSSSSSPSSSSSSTSSSSSSSSPSTSSPTNIIISATVVTAAASP
PSSHSSFSTTS

19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE

A0A0L8I9W1 **A0A0L8I9W1_OCTBM** (51 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

GKEIKEEEEEEEEEEEEEEEEEEEEEEEEEEGKYKLAEDEEHRGGSFQNVI

6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE

A0A0L8IAP8 **A0A0L8IAP8_OCTBM** (56 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

MIMMLPVIMMTLLQFEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDFK

16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE

A0A0L8IAR3 **A0A0L8IAR3_OCTBM** (86 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

MEKEEKMEKEEKMEKEEKMEKEEKMEKEEKMEKEEKEEGRRKKKKKKKKKKKKKEEEEEEEEEEEEEEEEEEEEEEEAD
EEEQEQ

55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE

A0A0L8IAV1 **A0A0L8IAV1_OCTBM** (78 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

MGNEKEKKRRKREGGEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEEEEEEEVKKHERTVGYCCEEPPRKEVAPYGLTCY

16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE

19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE

A0A0L8IAY0 **A0A0L8IAY0_OCTBM** (88 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
KEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEELVESYRRNKTAFYTISSKYFPQHTV
VNFKVLPQ
```

2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE

A0A0L8IAZ1 **A0A0L8IAZ1_OCTBM** (59 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
DADEEEEEEEEEEEEEEEEEEEEEEEEEEQQQQQQQQQQRRRQQQRQYTHEEEHKKNPWR
```

4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE

6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE

A0A0L8IB32 **A0A0L8IB32_OCTBM** (67 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
TERKEATKGRQVMEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEEEEKEEKEERAFERKESETQQ
```

14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE

A0A0L8IB41 **A0A0L8IB41_OCTBM** (118 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
TYTYMYTYMRAHTYDDNDVGDDDDDNDDDDDDDDDDDDDDDVDDDDDDSGGGGGGGGDDDDDDDDDDNDGDSDDDERDDM
EEDKDKNTVGIEEEEEEEEEEEEEEEEEEEEEEEESESA
```

92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE

A0A0L8IB74 **A0A0L8IB74_OCTBM** (128 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MFNNGISFYGDFKSLLTNVSPLNHVHKNKIIFNSCKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGGGGGGGGEGEG
AEGEEEEEKTTTTTTSTTTTTTTTTTTTTTTTTTTAVTKTTKIGVGGGR
```

38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE

A0A0L8IBG1 **A0A0L8IBG1_OCTBM** (61 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MKKKKKKNEEEEEEEEEEEEEEEEEEEEEEEEEEGAVVENERNGFRGQSKNKGTVQYERTNQ
```

9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE

A0A0L8IBL9 **A0A0L8IBL9_OCTBM** (57 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
GEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEETKTDEESYANGDGLVKE
```

2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE

A0A0L8IBQ4 **A0A0L8IBQ4_OCTBM** (116 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MPRIVLLPLLYILVRLYPKVGDKGDYQKSLAMIKVAVGSPNNAKKNNKYEQEQQQQQQQQQKQEKETRAKRRKVNGDREE
EEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERGG
```

86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE

A0A0L8IBU2 **A0A0L8IBU2_OCTBM** (53 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MSEPTAKKAKLRDYKEDCIMLEEEEEEEEEEEEEEEEEEEEEEEEEEERREEDR
```

22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE

25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE

A0A0L8IC23 **A0A0L8IC23_OCTBM** (156 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
NLHRYRIRLLNKRKEEEEEEEEEEEEEEEEEEEEEEEDDDDDDDDDDDDDDDGDDDGDDDDDDDDDDDDDDSDDNDDDEWR
LMTIIIIVRIRMRMRRRKRRRRKNRRRRRKNRRRRRKNRRRRRKRKKKKKRRRRRRRKKKKKKKKRRRRRKNRRRRK
```

15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE

A0A0L8ICG2 **A0A0L8ICG2_OCTBM** (145 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
RKGGGGGGGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGGAAAVAEGGGDLVRNLDQPRLFNGTMVHVWLLVNGSLTL
SKQKSSLHVNTANTNRCPVPFHFKRVQFPVRAIYRITIDRSQGQTLQVAGLHLEEGCFSYGQLYV
```

10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE

A0A0L8ICJ3 **A0A0L8ICJ3_OCTBM** (55 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MKQTLYMYEEEEEEEEEEEEEEEEEEEEEEREDEEEEEEEEEEVETFFSFEITRQNV
```

9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE

A0A0L8ICN1 **A0A0L8ICN1_OCTBM** (65 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
SGGFEKDDGKEEEEEEEEEEEEEEEEEEEEEEEEEEEEGNEGGRKRRKRCRLNNEDVLYGYVVIHL
```

11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE

A0A0L8ICZ5 **A0A0L8ICZ5_OCTBM** (75 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

RKDSKDDEEERKEEEEEEEEEEEEEEEEEEEEEEEEEEEVEEGEGEEGGEEGEEERRKKKKKRTTTTGKKKKEKKG

13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE

A0A0L8ID25 **A0A0L8ID25_OCTBM** (63 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

MILVTYLVSYPGIQRRREEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVGFWPLRPKVLRTIK

18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE

A0A0L8ID87 **A0A0L8ID87_OCTBM** (50 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEQQQQQQQNTHSNSMK

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE

A0A0L8IDA9 **A0A0L8IDA9_OCTBM** (160 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

MDCLSLVSLVLNWRLGGRGWSELSRWWTGNLSVSDEGEGEVEEEEKEEEEEEEEEEEEEEEEEEEEEEEDEEEEEEEEE
EEEEEGDDDDDGNEDGEDDDEEDVGAVEREEEVGGKRIDDDGDADEDLKDGDGEEDVDDGESNIGDISSDDDEGEDDVCV

47 - 66:	EEEEEEEEEEEEEEEEEEEE

48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE

A0A0L8IDB4 **A0A0L8IDB4_OCTBM** (60 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
DAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEQEQQQQQQRQQQQQEEEMCMEGVEK
```

3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE

A0A0L8IE63 **A0A0L8IE63_OCTBM** (120 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MDGSGSKEHRQPNTDNHNEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEEEEEEEEEEEEEEEEEEEEEEGDGDDDDDEKE
EEEEEEEDDGDDDDDDDDDDDDNDDDDDDDDNDEAISKY
```

19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE

A0A0L8IE98 **A0A0L8IE98_OCTBM** (54 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MAASIRILQTKNIHITIINSEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGDD
```

21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE

29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE

A0A0L8IEI2 **A0A0L8IEI2_OCTBM** (64 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

RINNNKGGGGRGGGRGRGRGGGGRGGRGGGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEYIQAS

31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE

A0A0L8IF47 **A0A0L8IF47_OCTBM** (67 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

FKTTPTTHSTQTCIYKEQTKEGEEEKKKEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEENTVN

32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE

A0A0L8IF52 **A0A0L8IF52_OCTBM** (84 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

ENEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEESIQVGDVYKNRFRKISSK
KHYK

5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE

16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE

A0A0L8IFA8 **A0A0L8IFA8_OCTBM** (4085 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MSCNSSSLGEVSGEKPSTATLQAISVPHSTADGSIGTEGISWSLDAILPAVHGTEEKNPFLEHLQQFDQVLSCDDVKEAL
QQTRVPSLGLDGSGAMSAVVYAIDDGRSNVDTNLILFSQHQSNIGIADGDLGYGEEAGNKPNIDSPAAAVGSVSNNSNSN
NNNDDSHSATNKVELFADDQSMNLQHLDALSGHTSPEINQIYDPCISSSRDDFRGLASVAVTDHAYAIPANREPRDPSYP
LMSSKSVQTPFEQSDYEQLCLTSQEEEDTSTNLSDVAAVHSSPVKENDIDDDDTNNKPKRLQPQQQQKKSSPVVTPTNIR
RSTRISEAEQREMAEKIRQENRQKEKEAQEAMKKQSEEVSQVEQQQSEVAEVLGDAEASSVVVTKPDAVMSLVQPLITST
PVKSDQLNTTLDTTTTTTTSTSNTTSQPTAATDITTSTTSIITTTTTIATITDPTAATRGRSRTPRNKAKILNKDTPVGV
GRVTVAKGGSAKGKTTAVAGRGHARGKAVGSSTSRKKKGDSTRVDSESNGEVIDDSVTDLASDSEKDMSVVSKAESTSNS
EQANKSVCETASRPVRKRMKKIIRDIPLQKEVSKKSGKASVTGKNNTGKIGVKGKTNTGKNSVKGKKNIGKKTVSTPTNQ
SVNIAESSESSDDTSLNLSSIVSASADLLPVSGQISENSMLLSQTNSSADGSLQSPASSALCNLLQPPDKDGAQTVSDLA
DSSPLAKLQKGMSPISKTGSSVDKLEPTASEKSTVPKTPRGSRRPAISLTKSQKKKEVQKANDSEISLKDLSVSQQEETG
KEDDKKDGETAKENIDDSKDANVSGKEPTEESNKGIPLMKSGRPKRQARIRKEEREKAAKASELEEREKKKLKRKRKLPV
KDVNSSVEVDKTTENEEEEEEEEEEEEEEEEEEEEEEEEDEEEVPLFRLKKMQNSAEVKAASSEVPVTPVKKLTKKEKKAA
ALQAKAEQEELARLEEEKARLAAEEKARAEQKARAEKEAKKRRKQRKSEESLDKTMIDLFKPDGVIVHESSTQAKKENET
DIQADAISQTLPEKSSVTTATPSSLQSSNSATKTVSFSSSELQSKVSTTGNKTAIAPSKPVQSSPSHHKPSVVSYSVNSS
QTDSEKMSSDNGKDIPSSIDDKTATSSSIDSVTSMTVDVADKFVSVNFDHTEEPVRAETSLDEPAPEKQIRSKADSVQSA
SNETQSATSVKMEAETTMSNDAFTEDIDNKSLAVSIGCQADEDSEYEYVSCTEEMEDDRHLQPRLQGKTCTICNMVQDNQ
YLVDCDICRKSFHGHCAELTLEDMQRILQDGEKFVCDNCPLEGTTLPVTTEPAKEESTTSEAAVPVQVDASTSDKSTAVV
KSREDSSESTKKTKNKKSVSGESNVSKAASKESVNNSDVTTTPKKMLTSSAKKEKLTAASNEATHKKEALTHIATPVTTS
KPTSVSSTKSAPVSTAKTTPTSTTKSTPVPTAKTTPVPTAKTTPVPTTKTPAVPTAKITLVSTTKPTTKTTPVSTTKTPV
SSTVTTPVATTKATSISTTDTTPISTTNTTSVSTTNTTPVSTTNTTPVSISKKAPSESKTPRKSSRDGDPEKEKQKTPVS
KDNKRKLSTEHYESKEAKDRQNSKERAEVGSKERRYKDRKDYSRDKLKPSSKERDRRDSKDYANNSPSTKSFGNLTPRKP
EVSSAQVSSSTSTENEKKTSPTSDSSKKKKLLHFKDMDLKKRTFQQCIGAGCKRDARTGSVYCSDECIVRHAQESLALLK
NERHFQQTGQKPSEKSINPQPTPQLLPSLKKESNSKVVVLERKSGRILTGPTAPTESVLREWLTEHPTFEVLQPSQGLHK
TPTFYGKDKDKRQPQPEKKNSTEPKKKEPELKQGNQVPKGPDDVRLNVKKSLHEALSNRAREANDINHHNSSIRNLVINI
EEELHRLYNDSGQKYKARYRSLIFNIKDSNNKGLFRKILNKQIKPYRLVRMTADELASPELSQWRQKEVKHTLEMIEQRE
VEAIQDAAKCHVVKKTHKGEVDVAGEDLSTLETSIIHYQAKPVPVEKVKVDQKVDIVGDLVTDTTDCHRKHLFDLNCKIC
TGKIPPPSDEPLAKKAKKEILAPSTSSSPGILDKNQPKPAIPKTEKTTPKTITKVQEDTFKDDEVKTIMETIRSVTQSET
TSESKASNSPRPSAMKSSSNSRNVTVRSPDSVLQSGLEKKVKFSPSSPLVWKGFIHMQDLVKFMTTAYRLSGPTEHLELQ
DTVHVCGRIAPELIWDYLNRIKQTGSRDICVLRFLPGTFDEKNAYVMLYSYLNSRGRCGVVGNNSRHIKDMYIVPLASHS
KIPAVLLPFDEPGLEDNRPHMLLGVIVRQKVCKRPGEQLAASAGQAVMLSEAELQTKRLKYDPTLPSTTVNIPKIESSAA
SQPVRYDPFQPATLPKYTPSSTLQDTPADLQSSGSSSLTSGKETKYYNPVPVKEQFYTPSLVLSSSKNDRLKQPSPSPVD
SSTSDSPENVSSCINDPIVKAYGKLNSDSELNSSTPTEDLSTAPYSPTQYEPTQTSFLDSHEDKISGGVGSVDQDSDELD
NEKPYDPEECDFDAEDDSPPPPPPPPPPLSTTVGLNALKNQISSTVSTTTATTTAASTVEDLFNKIKKSTLPSSLAAAST
SGQQNKPEMKDLLGEFTQRIADKKPESTAPKPAAGSLPTALQNLFSQVSRSTLSANQPQSSGPAPKATNAAANVLLPIKL
AAGGNSVLSNLVTSSMSQPSGTYSNSSNSSMGLASEPVNTNTGALNLLSLTTTSSIQPTPSPLASVASSLPKDQALSSLV
QSSPISVAGWSKIAETLASLAKVHSVNLPAQNQAAGLHSNSTTGCITAITPTTTTTTINSNTSLPSTPTIDTAITTSTAI
HSTTTTTATTTNNSGLTQSSFSAFSLGGNRSNLSGSQKTVSQYEKFDSTASHLTNIEKKPENAASKTSETNKGSSVRIAF
STGPKHPLIPHAVFKEDEKPKVTALMSEPKIPGLGLDEEEEIVTVSNQALKDNAFLSRAKFETLTTLGKTDTFLPSGVKT
DSFPSRGLNPDSFINNWKGVENSNESVNVSGKSENDEKVQLEPSKAAEILLDSTKIQSSESLVDNQKNETPQYEVSNVVK
SKFENNKESIKNRSFEGHQEPPARSRESHHDSKSRPSSDSSKDSRRQSDSDRKRSHYSDSGSSKSSSSRYSERSERHGYS
RHSRSRDYSDKRDRDYRKDYSNTESRNRDRDYDRDRDRDRDRDYEHSSSRSRDRSRDRKDYRRSSSSKGDERSSSKKSSE
```

```
KGDKFVSTASEESNRYGDVDERKKMYSTTPAYPEAGSRFSADKKDMASFHSGAKQFKDADGKSEGKDYKAISFMSQDQDL
RKGLSGVPNTSIPAVAQPIPTLTSNIHEEFPRDVDHRKHSLSWQGAYEPNNKDTTEESNASFWSSHGDVDYRTQTSSVIA
ASRTAAHPPVLPSGNLAGWGSHPVPGQPTASAPSNFQPISTVLHQRSVNAKPGNLMETGNQADQDMRKQSRPGIPPKIDV
ILPRPTAKDFFGSVESESSDSVTQPPSLFEVDSSIHSRTSAPFKSHGNSNESLGSLHPVMSKWSTTQEKLVPPGLASPLD
VDDRPNAYRTANTAVSPAGQGLPGDSLSSSQLLKVPPVDSSHTQEAVFYTTAATSHSELTPNSSGGTTMSAAPQETRPLM
SVANSSSVIDPDSLSSVGKGQIPLPYCTPNPTSSHQGYAPPPPPPPPPPQHMQPAVEISSDRLQQSAQWEGCTSTSSIA
LSEHSAPPPPPQQQQPPSQPQAKLQQHITGRTEHEVSNSSLLKSHHQLQQTWSQVDSSKQPQLPPPPPPPPPPHQQPLVV
SVGQYYEHASYSDVSPVTVASNISFSSTPPPPPPPLSSSSSSTPSSTTTVASGGTPGSLPPPPPPPPSQTPTIPPVGQSS
VRPGLGGQYTQLRERGGGYGGESAVSGGSPSQPPPPPSSLHRGSRFLNPPPPPPPMQSAPSQPQPLQPPIPGSGGSSSSS
SSSPYNMPPRTDFPTGQLPGQRGFAGGPRQGFQPPRTNFNAGPHGSVGGNGGSNNNNNNNSSVPRDEQGSGSGQYSHHRG
VSRFN
```

896 - 915:	EEEEEEEEEEEEEEEEEEEE
897 - 916:	EEEEEEEEEEEEEEEEEEEE
898 - 917:	EEEEEEEEEEEEEEEEEEEE
899 - 918:	EEEEEEEEEEEEEEEEEEEE

A0A0L8IGF2 **A0A0L8IGF2_OCTBM** (67 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MKRANNVRKKLVQKEKKVKKRGEKEEEEEEEEEEEEEEEEEEEEEEEEEEEGNNEVEADKYEEKEKK
```

25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE

A0A0L8IGF9 **A0A0L8IGF9_OCTBM** (139 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MEVEEEEEEEEEEEEEEEEEEEEEEEGGEEGEGEVGGGGGGGGGGEEEEEQEEEQQEQQQQQQQQQQQQQQIQSDEQKRN
DSIILENNENVTMKSNEINKENSLEHIQSTNLSSNSNNSSKNYDEKNGSNQEYTNIAEI
```

4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE

A0A0L8IGG5 **A0A0L8IGG5_OCTBM** (62 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
NHVVWWGRQEKEEKQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEANNINKLGGAIYNKSLYLN
```

16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE

A0A0L8IGQ4 **A0A0L8IGQ4_OCTBM** (323 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
GEEEEEEEEEEEEEEEEEEEEEEEGEREKEEEEEEEEEEESEEGEESEEEEEEEEEEEEGSEEEKSEEEGSEEEKSEEEKS
EEEKSEEEKMKKKKKKKKKEKKKKKKKKVKEKKVKKVKKVKKKKKKKKKKKVIEKKKKKKKKKKKKKKKKVKEKKVKKKKK
KKEVKKKKVKKKKKKKKKKKKVKKKKVKKKKKVKKKKKVKKKKKVKKKKKKKKKKKKKKKKKKKKKDNNNNNKMEEKRIENRRE
REREKIGEREREREREDKDRERYEGRERYKDRERDTKRERDTKREKEIQRERDVQRQRERYKDRERCTKLKRERGRDWERL
GDI
```

2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE

A0A0L8IH17 **A0A0L8IH17_OCTBM** (55 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEINQMMAKELEWAKY
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE

A0A0L8IH88 **A0A0L8IH88_OCTBM** (58 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EEEEEEEEEEEEEEEEEEEEEEEEGGGGGEEEEEEEEEEEEEEIFLVEMRWVIDLVNER
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE

A0A0L8IHE3 **A0A0L8IHE3_OCTBM** (118 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
MEEGEEEKEEVEEEQEEKEQKDEEELGEAEKEEEAKVEEVTGEEKVEEVEEEKKEGRKMWRKKRGKEKERIIETDLEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAQLR
```

77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE

85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE

A0A0L8IHF7 **A0A0L8IHF7_OCTBM** (64 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
LSFHFLVSLEINTSISTEVFGLSLSLFCLLQQEEEEEEEEEEEEEEEEEEEEEEEEQEQEQEE
```

33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE

A0A0L8IHQ2 **A0A0L8IHQ2_OCTBM** (129 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MLFWRKEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDDDDDDDDGGGGGSSKFCQKGSNFGEVMSRLHRPQCSTDDDDDDDDG
DDDDDSDDDDDDDDDDDDDNHDGDDDDDDDDDDDNHDGDGDDDDDLRFI
```

7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE

A0A0L8IHY2 **A0A0L8IHY2_OCTBM** (111 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
ILQIRQRRQQQLQEEEEEEEEEEEEEEEEEEEEEEEEEEEKEEEEEEMIYTKQEITSTQLSYPWHQKKRSAIKAEEVTMTAT
AATATIQTCSATTVIISSTDILSTARMKNLI
```

14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE

A0A0L8II03 **A0A0L8II03_OCTBM** (97 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EEEEEEEEEEEEEEEEEEEEEEEEEDEEEENKKRRRKWWRRMKNKKKEEKEERRKKEKGEGRKRKRKNERRKKEEERRQ
KKKEDNEVPKSAKNKKK
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE

3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE

A0A0L8II38 **A0A0L8II38_OCTBM** (92 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDDNVDDDDDDDDIDDIDANLYSNRLSLCLCVCFCVYACIQCPCM
SLRLYVLMCFCA
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE

A0A0L8II50 **A0A0L8II50_OCTBM** (213 aa)
Uncharacterized protein. *Octopus bimaculoides (California two-spotted octopus)*

```
MHARTDETTISRHTPTYTLKTLDVVCFLMAYEEGGGGGEEEEEEEEEEEEEEEEEEEEEERKKERKKEGKKENKKERKKI
RRKERKKERKKERKKTKTKKKKKKKKERKKEGKKENKKERKKERKKERRKKRKRKRRRKRKKERKKERKKERKKERRWKER
KNEIKKQGKKERKKERRRRRRRRRRRRRRRRRRRRRRRRRRKRSDGGSGSWDDVE
```

39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE

A0A0L8IIX3 **A0A0L8IIX3_OCTBM** (51 aa)
Uncharacterized protein (Fragment). *Octopus bimaculoides (California two-spotted octopus)*

```
EEAEEEESEEGEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEESETYAD
```

15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE

A0A0L8RLK7 **A0A0L8RLK7_SACEU** (1379 aa)
SPT7-like protein. *Saccharomyces eubayanus (Yeast)*

```
MTEKIPITNYQRTNAKPLLKLTEKLFRRNIFDLYLTAQQLVVLGYLLAIPSEEDKLKAWDYFMKGNITLNVEKSFPSTQE
KEQGSIISSTGDAQPDNVSSETVEITTENHNNNNNDTNNNNDNSNSNSESQCEDKGPEPNTNDEDNVNNDVEEDLFKLDL
EDLKQQISGPKFIGNLSLKIRYVLWQCAIDYMYSDHNEFDDGDEMEYALLDVEKEEEEEEKEKEKDDETEAPQNQENIPK
FTEDENYDDEDDNYEEDTTFEKKDDFIENGNGIPSSNIEIDDERRLLLNISISKETLSKLKTSNVEGIMGNWNKIYHSLE
YDKETMIKRLRLEESDKMIEKGKRKRSRSDLEIASDEENNKNIDSKPETNDILSAIEGETFSDTGNKRPKQNKLDLTVNL
GIENLSLKHLLSSVQENKSRLGISDYELKHLIMDVRKNRSKWTSDERIGQEELYEACEKVVLELRNFTEHSTPFLNKVSK
REAPNYHQIIKKSMDLNTVLKKLKSFQYDSKQAFVDDVMLIWKNCLTYNSDPSHFLRGHAIAMQKKSLQLIPMIPNITIR
NRADLEKEIEDMEKDKDYEVDEEEEVAGSGRKGLNMGAHMLAKENDKGSKRGTSKTTEKETSTDIDKATSTILEGGEDEL
DSPKEEKEDDQTASPNVTFSETGGKKELRENEKYDEHQSVEESKKAEGCEKENENGRDGEVSKNDTENKRQSKVDEGNEV
REENDGEGEKVNENEEEEEEEEEEEEEEEEEEEEEEEEDEEDMADSQSYLLEKDDDKDDLEISVWKTVTAKVRAEICLKRAS
YFKNGKLNIDSEAYLKNPQRMKMFDQLFSEYKEQKALESYRQKMEQDSIMKNGFGTVLKQEDDDQLQFHNDHPLNGNEGF
EKQPNDIELDDTRFLQEYDISNAIPDILYEGVNTKTLDKMEDISVERMLQNGMTRQSLFLANKDLGLTPQMNQNITLVQQ
IRHICHKISLIRMLQSPLSAQSSRNNPNAFLNSHIYNYTVIDDSLDIDPVSQLPTHDYKNNRELIWKFMHKNISKVAMAN
GFETAHSSAINMLTEVAGDYLSNLIKTLKLHHETNSLNRGTNVEMLQTTLLENGINRPDDLYSYVESEFGKKTKKLQDIK
HKLENFLRALLRPTLQELSERNFEDESQSFFTGDFASELTGEDFFGFKELGLEKEFGVLSSSVPLQLLTTQFQTVDGETK
VQDKKIQPEESDSITYSKITKGLLDAGSFWNTLLPLLRKDYERSKAYIAKQSKSSATNDRILPTSTEDNSFALLEEDQFI
SKKSASKARLPPTGKISTAYKKKPISNAFILPEEDPEKSEKGDPNTTIHSTVHTENEMGSSLFLETPQPLDSLNMDDPFN
DSNVGTNSSFSLSLPRLNQ
```

735 - 754:	EEEEEEEEEEEEEEEEEEEE
736 - 755:	EEEEEEEEEEEEEEEEEEEE
737 - 756:	EEEEEEEEEEEEEEEEEEEE

A0A0L8VFY3 **A0A0L8VFY3_9SACH** (1036 aa)
TAF1p TFIID subunit, involved in RNA pol II transcription initiation. *Saccharomyces boulardii (nom. inval.)*

```
MKQRISALDLLLLARELKQDLEGYRLSNIYNIADSSKQFLLKFNKPDSKLNVVVECGLRIYLTEFSRPIPPTPSGFVVKL
RKHLKAKRLTALKQVDQDRILVLQFADGHFYLVLEFFSAGNVILLDENRRIMALQRVVLEHENKVGQIYEMFDESLFTTN
NESADESIEKNRKAEYTSELVNEWIKAVQAKYESDITVIKQLNIQGKEGAKKKKVKVPSIHKLLLSKVPHLSSDLLSKNL
KVLNIDPSESCLNLLEETDSLAELLNSTQLEYNQLLTTTDRKGYILAKRNENYNSEKDTADLEFIYDTFHPFKPYINGGD
TDSSCIIEVEGPYNRTLDKFFSTIESSKYALRIQNQESQAQKKIDDARAENDRKIQALLDVQELNERKGHLIIENAPLIE
EVKLAVQGLIDQQMDWNTIEKLIKSEQKKGNRIAQLLNLPLNLKQNKISVKLDLSSKELNTSSDEDNESEGNTTDSSSDS
DSEDMESSKERSTKSMKRKSNEKINVTIDLGLSAYANATEYFNIKKTSAQKQKKVEKNVGKAMKNIEVKIDQQLKKKLKD
SHSVLKKIRTPYFFEKYSWFISSEGFLVMMGKSPAETDQIYSKYIEDDDIYMSNSFNSHVWIKNPEKTEVPPNTLMQAGI
LCMSSSEAWSKKISSSPWWCFAKNVSKFDGSDNSILPEGAFRLKNENDQNHLPPAQLVMGFGFLWKVKTSGNEDNGDDDE
EEEEEEEEEEEEEEEEEEEEKEEEEKEEEQQQDEDDSNEVNGLEKGGDSNDSTKNNSFEHDNLEKDIEKHCTISSDTDS
DSGNAKAKNDNSSTQRILDEPGVPISLIENINSNVRGKRGKLKKIQKKYADQDETERLLRLEALGTLKGIEKQQQRKKEE
IMKREVREDRKNKREKQRRLQALKFTKKEKARVNYDKHKSELKPSLDKGDVVDDIIPVFAPWPALLKYKYKVKIQPGSAK
KTKTLTEILHYFKSRPLDGSSTDKEMDWPQEHEMIKGLKEQDLVLLLCVDKLKVTIAGQKSTKNGGNSSKKGKKKR
```

720 - 739:	EEEEEEEEEEEEEEEEEEEE
721 - 740:	EEEEEEEEEEEEEEEEEEEE
722 - 741:	EEEEEEEEEEEEEEEEEEEE

A0A0L8VKF5 **A0A0L8VKF5_9SACH** (754 aa)
DRS1p Nucleolar DEAD-box protein required for ribosome assembly and function. *Saccharomyces boulardii (nom. inval.)*

```
MVVGTKKYSNLDFVPTISDSEDDVPILDSSDDEKVEAKKTTKKRKGKNNKKKVSEGDNLDEDVHEDLDAGFKFDLDADDT
TSNFQGWNFLAEGESNKDDAEAFVKKDVDLDKIIRRKGGLVKMAHIDSKQEEETEKEKVEKENDSDDEELAMDGFGMGAP
MNNGDENQSEEEEEEEEEEEEEEEEEEEEEQEEMTLEKGGKDDEIDEEDDSEEAKADFYAPETEGDEAKKQMYENFNSLSL
SRPVLKGLASLGYVKPSPIQSATIPIALLGKDIIAGAVTGSGKTAAFMIPIIERLLYKPAKIASTRVIVLLPTRELAIQV
ADVGKQIARFVSGITFGLAVGGLNLRQQEQMLKSRPDIVIATPGRFIDHIRNSASFNVDSVEILVMDEADRMLEEGFQDE
LNEIMGLLPSNRQNLLFSATMNSKIKSLVSLSLKKPVRIMIDPPKKAATKLTQEFVRIRKRDHLKPALLFNLIRKLDPTG
QKRIVVFVARKETAHRLRIIMGLLGMSVGELHGSLTQEQRLDSVNKFKNLEVPVLICTDLASRGLDIPKIEVVINYDMPK
SYEIYLHRVGRTARAGREGRSVTFVGESSQDRSIVRAAIKSVEENKSLTQGKALGRNVDWVQIEETNKLVESMNDTIEDI
LVEEKEEKEILRAEMQLRKGENMLKHKKEIQARPRRTWFQSESDKKNSKVLGALSRNKKVTNSKKRKREEAKADGNGARS
YRKTKTDRIADQERTFKKQKSTNSNKKKGFKSRR
```

170 - 189:	EEEEEEEEEEEEEEEEEEEE

A0A0L9T533 **A0A0L9T533_PHAAN** (521 aa)
Uncharacterized protein. *Phaseolus angularis (Azuki bean) (Vigna angularis)*

```
MTRGDLLLVHLPFSPSTHLLLLDAPLDREGSVARVVGKCWMPPLELKGNQYVIGINSPDLDFPGAGRLDIADVRPPPERT
FKRLKQSTLQLSPQPFELEEVEEVEEVDEVEEVDEVDEVDEVTEVDEEEKEVDVVEEVEEVEEDVEVEEVEEHEEDEATE
EDEANKVEEEDEVDDVDEMDEVDKVEEEVEEEEEVEEEEEEEEVEEVEEVDEMDEVDEEDEEEGEEIEEVDKVEEVEEVE
EEEEVEEEEEEVVDQVDEEEDEEVEEVDEDDVDEVEEMDEVDEVEEVDEDVEVDEVEEVEEEQEDEATEEDEAEEADEVD
KVEEEEDEVDEVEEVDEVDEVDVVDDVDNVEEVEEVEEMDEVDEVDEVDEVEEVDEVDEVDEVDEVEEVDEVDKVDKVDE
VDEVDELDEVDEVEEVDEVNEVEEIEEEDEANKEDEVDEADEVDKVEEEREEEDGVDEVVEVEEVDIMDELDELDEVEEV
DEEDEEDEEEEEEEEEEEEEEEEEEEEEEVDKVVEVDEGRS
```

488 - 507:	EEEEEEEEEEEEEEEEEEEE
489 - 508:	EEEEEEEEEEEEEEEEEEEE
490 - 509:	EEEEEEEEEEEEEEEEEEEE

A0A0L9T641 **A0A0L9T641_PHAAN** (344 aa)
Uncharacterized protein. *Phaseolus angularis (Azuki bean) (Vigna angularis)*

```
MDEVDEVEDMEEVDEVDKVNKVDEVDEVEEVDQVNKVDEVDEVDEAEEEHEEEEEEEEEEEEIVDEVDELDEVEEVEEQEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVDEVEEVDEVDEVDKVDIVDEVD
EVDEVEEEHEEEEEQQQQQEEEEKEEEEEEEEDEEEVDGVEEANEVNEVDEVKEVDEANEVDEVEEEDEEEEEQQQEEEEE
EKEEVDDMEEVDELDEVKEVVEQEKEKKKKSEEGERWNQKRHQKVQKEKPQLPLNGSLPLSGTQEFTGDPLRGKMAAEGK
KPTHALTAERHFYGLGPNFSVIYK
```

79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE

A0A0L9T648 **A0A0L9T648_PHAAN** (795 aa)
Uncharacterized protein. *Phaseolus angularis (Azuki bean) (Vigna angularis)*

```
MDEVEEVEEVDEVDKVDEVDELDETYEADEADEVEEQEEEKKKTKKKKKKKKKKKKKNWTTWKKWTTWKKWTNWTKWKN
KNKKRRTRIRKEEEEEEEEAEEEEEEEEDEEEEEVDKVDEVHNVDKVDELDEVEEQEQEKKKKKNKKKKKKWTKWTRRRKWT
KLTKWRGGRSERSVQSGRSRRSGRKDEAEKEEVDEVEEVDEVDEVEEEDEEEEEEEEEQQQQQKQQEVEEEEEEEEEEEVEE
VEEVDEADKVNEVDDVNEVDEVQEDEEDGGVDEVDEVIQVDKVDEVEEVVEVDEVEEEDEEEKEEAEEEQEEDEEEEEEEE
EEVDEVEEEDEVEEDDEVVEVDEVDEADKVYQLDEVDELDEVEEVEEQEQEKKKKKKKKKNKWTKWTRWTNWTKLMNWTR
WTKCTKWTKWTKLKKWKNEKKRRRRRSGPSGRSGGSGQRERSGQCGRTDEVDELNEADEVEEVEKQEEEEEEEEEEEEEE
EEEEEEEEEVDDTEEVDEVDKLDEVEEEFDEANEVDEVDEVDEVDEVDEVHEVDEVDEVEEEYEEEEEQQQQEEDEEEE
```

```
EQQQQQEEEEQEVDEVHDVDEVDKLDEVVEMEEDVEEEEEKRRRRRRRTTRKEEEEEEEEEEKVDEVDEVEEVDEVEEVDE
VDEVDKVHEVHKVDEVDEVEEEHEEEEQQQQEDEGEEEEEVDEVDEAEEENEQEEEQEKEEEVDEVEEMDEVEEVDEVGE
MYEVDEVHEVDEVNEVDEVEEEDEEEEEQEEEEEEDDEEKEEEVDDMEEVDELHKVEEVEEQEREKKKKKKKKWT
```

468 - 487:	EEEEEEEEEEEEEEEEEEEE
469 - 488:	EEEEEEEEEEEEEEEEEEEE
470 - 489:	EEEEEEEEEEEEEEEEEEEE

A0A0L9TB55 **A0A0L9TB55_PHAAN** (649 aa)
Uncharacterized protein. *Phaseolus angularis (Azuki bean) (Vigna angularis)*

```
MDEVDEMDEVNELDEMDEVDEVDEVDEVDEVDKVDEVDEVDKVDEVEEEEEEEEEEEEEEEEMEEEEEEDAEEVEEVEEV
EEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEE
VEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVE
EVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEV
EEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEE
VEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVEEVGEGDEINEVDEVDEVNEVDEMDEVDEVD
EVDEVDEVDEVDKVDEKDKVDEVDEVEEEEEEEEEEEEEEEEKEEEEEEEEDEEEMEEEEEEEEEEEVEEGEEVGEVDEV
EVEEVDELNEVDEVDEVEEVDEVDEVDEVDEVGKVDEVGEVDEVDEINEVDEVNEVEEVDEVHEVDEVDEVDELDEVDEV
DEMDEEEEE
```

507 - 526:	EEEEEEEEEEEEEEEEEEEE

A0A0L9TB73 **A0A0L9TB73_PHAAN** (1365 aa)
Uncharacterized protein. *Phaseolus angularis (Azuki bean) (Vigna angularis)*

```
MDEVVEVGEIEVVGEVDELDEVDEVDEVHNVDEVNDVDEVDEVDEVDKVEEVDEVDEVEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
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A0A0L9TBJ9 **A0A0L9TBJ9_PHAAN** (473 aa)
Uncharacterized protein. *Phaseolus angularis (Azuki bean) (Vigna angularis)*

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MDEVDEVNEVGELDEVDEVDEVDEEDEVNEVDEVEEEEEEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEMEEEEEEEEEM
EEEEEEEEEKMEEEEEKEEEEEEVEEVEEVDEMDDMEVEEEELDEVEEVGEVDKEDEAEEVEEVDELDEVDEIDEVDEVD
KVDDVDEMDEVGEVEKVGEADEVDDINEVDEVDEVDRVKEVEEVEEVDELDEVDEMDEVEEVEEVEEVDELDEVDEMDEV
NEVDEVDKLDEVDEVDKVDEMDEVDEVGVVEEVGEVDEVEKVDEVEEEEEEEEEEEKEEEEEEEKEEEEEEEMEEEEEME
EVEEVGEMEEVDEVDERDEVDEVEEVDEVEDVDEHDEVDEMDEVDEVDEVDEADEADEVDKVGEVEEVGEVDEVDKINEL
DEVDEVDEVDGVKEVDEVDEVEEVEEVDELDELDEMDEVDEVDEVEEVEEVDEVDKEDEVDEVEEEEEEEEEQ
```

44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE

A0A0L9U4R2 **A0A0L9U4R2_PHAAN** (831 aa)
Uncharacterized protein. *Phaseolus angularis (Azuki bean) (Vigna angularis)*

```
MEEEDEEVEEVDEVEEVEEVNEMEEVEDVEEEAKVDEVDEVDEVDEVEEVEEEAEVDEVDEWSKWTKWEKLTKSPKLMKL
DEVEEEEEVEEEGEMEEEDEEVEEVDEVEEVEEVNEMEEVEDVEEEAEVDEVDEVDEVEEVEEVNEVEEVEDVEEEAKVD
EVDEVDEVSEVNEVEELDEVDEVDEVDEVEEKEEEEEEEEEEEEEEEEEEEEEEEKEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEEEEEEEEEEEMEEEDEEVEEVGEVEDVDVVDEVEEKL
REFIKYVYVERRYTGESSSNLSRIRLSEKEPNASKRSSSFRLEFRTPNSSPGPYPKSDDKNLRYLYDESRSPRYAQKYSR
NGGHIRSPIQIEVVDDRYKDDERRNRRLANIEAKLKETSSDDLKKVETVAAPLAEVSKEKAQPLKWKPWSRRHNIVVTPP
QHRRHTATALSPHRHSTTTEPPNRHKRSTTTTHKAASPNLAPNPQTAVNEPTKQRRREHHKIVETTTTPLIHGTSTMGKE
REGELETRKGEGNWGNFEYMGTNTEIENLNYCGHYRRPKTLVEVEEVEEEAEVDEVDEVGEVDEGDEVDEVDEVEEEEEG
EHEKEEEEEDEDEEQEKKKKWKKNKKKWKRLEKWKKWMDKVDSVHEVDEVEEEEEEEEGEEEGEMEEENEEVEEVDEVEE
VEEVNEMEEVEDVEEEGEVDEVEEVEELNEVEEVEDVEEEVEVDEVDEVDEVGEVDEVDKLEEVDEVNEVDEVEEKEEEQ
EEEEEEEEEEEKEEEEEEEEEEMEEEDEEVG
```

193 - 212:	EEEEEEEEEEEEEEEEEEEE
194 - 213:	EEEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEEE
196 - 215:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE

218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEEE
225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE
239 - 258:	EEEEEEEEEEEEEEEEEEEE
240 - 259:	EEEEEEEEEEEEEEEEEEEE
241 - 260:	EEEEEEEEEEEEEEEEEEEE
242 - 261:	EEEEEEEEEEEEEEEEEEEE
243 - 262:	EEEEEEEEEEEEEEEEEEEE
244 - 263:	EEEEEEEEEEEEEEEEEEEE
245 - 264:	EEEEEEEEEEEEEEEEEEEE
246 - 265:	EEEEEEEEEEEEEEEEEEEE
247 - 266:	EEEEEEEEEEEEEEEEEEEE
248 - 267:	EEEEEEEEEEEEEEEEEEEE
249 - 268:	EEEEEEEEEEEEEEEEEEEE
250 - 269:	EEEEEEEEEEEEEEEEEEEE
251 - 270:	EEEEEEEEEEEEEEEEEEEE
252 - 271:	EEEEEEEEEEEEEEEEEEEE
253 - 272:	EEEEEEEEEEEEEEEEEEEE
254 - 273:	EEEEEEEEEEEEEEEEEEEE
255 - 274:	EEEEEEEEEEEEEEEEEEEE
256 - 275:	EEEEEEEEEEEEEEEEEEEE
257 - 276:	EEEEEEEEEEEEEEEEEEEE
258 - 277:	EEEEEEEEEEEEEEEEEEEE
259 - 278:	EEEEEEEEEEEEEEEEEEEE
260 - 279:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE
262 - 281:	EEEEEEEEEEEEEEEEEEEE
263 - 282:	EEEEEEEEEEEEEEEEEEEE

A0A0L9UUI4 **A0A0L9UUI4_PHAAN** (1100 aa)
Uncharacterized protein. *Phaseolus angularis (Azuki bean) (Vigna angularis)*

```
MKMTKFTKWTKLTKRMKWTKWTKWSNWTKWMSGRSGLSGRSRRNGRSKRADVVNEVHELEEVDDVDKVDEIHELNEVEKE
AHEVGEVDELDEVDELDELDELNEVVEADEVNEVEEVDKGDEGEEEEEEEEEEEEEEEEEEEGEEEVDEMEELDEVDEV
VEVNEGDEGDEVDEGDEVDEVDEGGEGDEGDEVDEGDEGDEVDKVEEVEEVDEDDQVFKVEEEVEEVDEVDKLDEVDQVV
ELDEVEEVDEREEGDVGDEGDEVDEVEEVEEGDEVHEDDEVEEVDEVEEVDEEDEVDEVDKVIELDEVDEVDEVDEVDEV
DEVEEGDEGDELDEVDEVEEVHVVDEVDEVEEVHVVDEVDEVEEVHVVDEVDEVEEVHVVDEVDEVEEVHVVDEVDEVEE
VHVVDEVDEVEEVHVVDEVDEVEEVHVVDEVDEVEEVHVVDEVDEVEEVHVVDEVDEVEEVHVVDEVDEVEEVHVVDEVD
EVEEVHVVDEVDEVEEVHVVDEVDEVEEVHVVDEVDEVEEVHVVDEVDEVEEVHVVDEVDEVEEVHVVDEVDEVEEVHVV
```

```
DEVDEVEEVHVVDEVDEVEEVHEVEEVDEFDELDEVDEVVELDKVDEVDEGDEGDELDEVDEVDEEDEVDEVEEVYEVNE
MDGVIEVDEVDEGDEVDDVDDWTKLKKLTKWTKWMKWIKWMKGQGGEGDEVDVVEEVEEGDEVHEDDKVEEVEEVDEEDE
VDEVVELDEVGEVEEGDEVDEVVEVDEVVEVDEVDEEDEGDEGDEGDEEGDEVEEVVEVKEVDEDDKVDEVDEEDELDEV
DKVDEVVELHEVDEWAKDEVEEGDEVGEVDEVEELDELDEVELVDEVVELDEVDEVGQKVNEGDEGDEGDEVDEVEEVEE
VDEVEEVEEVDEVEKVDEDNEVYKVDEELHEVDELDEVDELEEVDEVGELDERDEGQEEEEEGEEEEVHEMEELDEVGEV
VEVDEGDEVVEVDEVDEGDEGDEGDKVDEEDKEDEVDEVEEVDEVDEGDEVEEVEEVDELDELDEGDEGDEGEEVDEVDE
VEEVEEADEDDEAYKVDEVDEDNELDEEDKVDEVVELDEVDEWAKLKRLTKWTKGTKWTK
```

124 - 143:	EEEEEEEEEEEEEEEEEEEE

A0A0L9UY37 **A0A0L9UY37_PHAAN** (220 aa)
Uncharacterized protein. *Phaseolus angularis (Azuki bean) (Vigna angularis)*

```
MRAFFLQSKKIPPLAAGHLQIYQRECCCWTLDTVSPCCCVLPCAPPILSKHTPVGSAVRASQSSQQRVFSGPCVALLPSL
LDVRPSPSWMILLGASATGQLAWTLDEVDDVDEGEKREEGEAEEEEEEEEEEEEDVDKVDEVDEVEEVEEVEEVEEVEEM
EEMEEVEEVEEMKEVDEVDKGEEGEEGKEEEEEEEEEEEEEEEEEEEEEEVEEVDEVDEVD
```

189 - 208:	EEEEEEEEEEEEEEEEEEEE
190 - 209:	EEEEEEEEEEEEEEEEEEEE

A0A0L9VCJ5 **A0A0L9VCJ5_PHAAN** (125 aa)
Uncharacterized protein. *Phaseolus angularis (Azuki bean) (Vigna angularis)*

```
MKEKEEEEEKEEERKEEEEEEEEEEVEEEEEEQEEEDEEEDKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEERRGRRGRRRRRRGRKKRKKRKKRKKKRRRRRRRKKKKKKF
```

43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE

A0A0L9VKQ2 **A0A0L9VKQ2_PHAAN** (615 aa)
Uncharacterized protein. *Phaseolus angularis (Azuki bean) (Vigna angularis)*

```
MKDVKKDRYGIKKELKKCKRREAASTAQCHFIAERHYLTLVGTVEGLQVFGTIFGVQKFVINPLPPIPPLPTHSPLPPLP
PLPSLSLLPPPREEEEEEEEEDEEEVNEREEADEADDVDEVEEMDEVDEVEEVDEVEEVKEVDEVEEAEEVDEVDEVDEV
EEVDEDDEKVDEVDKVDEVDEVDEMDEVDEVDEVEEVEEVDEVEEVDEEEEVEEVEEVHEVDEVDDVDEVEEVEEVE
EVDEVNEVDEVDEVDEVNEKFVINPLPPIPPLPTHSPLPPLPPLPSLSLLPPPREEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEDEEEVNEREEADEADDVDEVEEMDEVDEVEEVDEVEEVKEVDEVEEAEEVDEVDEVDEVEEVDEDDE
KVDEVDKVDEVDEVDEVDEMDEVDEVDEVEEVEEVDEVEEVDEVDEVEEVEEVDEVEEVDEEEEVEEVEEVHEVDEVDDV
DEVEEVEEVEEVDEVNEVDEVDEVDEVNEVDEVDEVDEGAPAPSLCTSQAHTCFYVTTRPGRYYCRSCCPCETLRVQAGP
```

NHFCSCSCSFFGQNRAAPNPWTCLLDRFLQACWTLLQVASVGRSFCAQRKAKMTL

295 - 314:	EEEEEEEEEEEEEEEEEEEE
296 - 315:	EEEEEEEEEEEEEEEEEEEE
297 - 316:	EEEEEEEEEEEEEEEEEEEE
298 - 317:	EEEEEEEEEEEEEEEEEEEE
299 - 318:	EEEEEEEEEEEEEEEEEEEE
300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE
306 - 325:	EEEEEEEEEEEEEEEEEEEE
307 - 326:	EEEEEEEEEEEEEEEEEEEE
308 - 327:	EEEEEEEEEEEEEEEEEEEE
309 - 328:	EEEEEEEEEEEEEEEEEEEE
310 - 329:	EEEEEEEEEEEEEEEEEEEE
311 - 330:	EEEEEEEEEEEEEEEEEEEE
312 - 331:	EEEEEEEEEEEEEEEEEEEE
313 - 332:	EEEEEEEEEEEEEEEEEEEE
314 - 333:	EEEEEEEEEEEEEEEEEEEE

A0A0L9VLE0 **A0A0L9VLE0_PHAAN** (1060 aa)
Uncharacterized protein. *Phaseolus angularis (Azuki bean) (Vigna angularis)*

MWTKWKKWTKSKKWRSGRSGRSGRRRRRRRRRRRRRRRRSRRRGRSLRSGRSGRSGRSRQRGRSGIRRRSKRSGRSGRSE
RSGRNGRSGRNGGSGRSVRREEEEEVEEVEEVEDVEEVAEVDELEKVDEVDKVHEVDKVDEVDKVDEADKVDEVAEEDEV
DEMEEIDEVDQVEEGEEGEEVEEVEEVEVVEEVDEVVEVDEVVEVDEVVEVDEVDDVDECTKWKKWTKLKKWTKWIKWTK
WKKWTKWKKEKKEKKEKKEEKSKKWKKSKKWTKWSKWTKGTKWTKWNKEKKQKKWKKWTKWTKKGEEREAVEEVEEVEKV
DEVDEVEKGEEVKEVEQVEEMEEVNELEKVDEVGDVDEVDKVDEVEEVDEVEEGEEGEEGGEVEEVEEWKIGPSGPSGRS
RRSPQSGRSGINRRRRRSGRSGRTGRSGQMVEVDEVDDVDEVDEVELGEEEEEVEEVEEVEDVEEVAEVDKLDKVDEVDK
VHEVDKVDKVDEVEEEDEVDEVEEIDEVDKVEEGEEGEEVEEVEEVEKVDEVDEVDEGEEGEEVEEVDEVDEVDEVEEVE
EVEVVEEVDEVVEVDKVVEVDEVDDVDEVDEEVNKVDEVDKVVEVDKVDEVDEVEEVDEVEEVDEVDEVEEVDEVEEVDE
VDEVEEGEEGEEGEEVEEVEEVEKVDEVDEVEIGEEGEEVEEMEEIEEVNKADKVEEGEEGEEGEEGGEVEEVDKVVEVN
KGDKMDEVEGGSRRSGQSGRNGKGQEREEREEVEEVEKVDEVDEVEKREEVKEVEEVEEMEEVNELEKVDEVGDVDEVDK
VDEVEEVDEVEEGEEGEEGEEGEEGGEVEEVEEDEGDEVDEVDELDELEEVDEVEYGEDGEEGEEVDEVEEVEDVEEVAE
VDELDKVDEVDKVHEVDKVDEVDEVEKVDEVDEVEEEDEVDKVEEVDEVDEVEKGEEGEEGEEVEEVEEVEKVDEVDEVD
EVEIGEEGEEVEESGESGRNEEVEQVDEVNEVDEVDKVDEVEEVKEMDEVEEVEEVDEVDEAEEGEEEEEEEEEEEEEE
EEEEEDVEEVDEVDEVDEVE

1026 - 1045:	EEEEEEEEEEEEEEEEEEEE

A0A0M4FAR5 **A0A0M4FAR5_DROBS** (374 aa)
Up. *Drosophila busckii (Fruit fly)*

MSDDEEYTGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRAKEEDELKKLKEKQAKRKVTRAEEEQKMAQRKKEEEERR
VREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKETGVLGLSSAAMERNKTKEQLEEEKKISLSFR
IKPLAIEGFGEQKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQ
VASKYERRVDTRSYDDKKKLFEGGYNTVYAETLEKAWQERQERFTTRTKSKLPKWFGERPGKKAGEPETPEGEEDAKADE
DIVEDEDEVEEEVAEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE

345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE

A0A0M5L630 **A0A0M5L630_9GAMA** (518 aa)
ORF73. *Felis catus gammaherpesvirus 1*

```
MDPSAPRKRREESPPPQQEGRLPRSKCCGPGQPCPLMSAPYTTPPLGHRPRPRKTPKPVPEPEPEPEPEPEPEPVPVPVP
VPVPEPEPEPEPEPEPEPEPEPEPEPVPEPEPEPEPEPEPEPEPEPEPVPDGLTALMLAYQGDSDGDGDESDGDESVITV
SSGTGSDNGNHEEPILISSEDSEGQEGQEGQEGQEGQEGQEGQEGQEGQEGQEGQEGQEGQEGQEGQEGQEGQEGHGEDE
EDEEDEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEPMNPDLHGDHTYANVQSSGPRRRKRIRSPSTSSSGSSTLCQPKKR
RKRPRRLSSSSESDETAGPSTAGPSTAGPSTAGPSTAGPSTAGPSTAGPSTAGPSQQSRATGHWHTPRRPPYDPGHIPKK
YQPTHEYFKHKLGELREFIDHKPWKWGVLAVSLNFTVLYRLHRSLQFPGVVSSPVSVLPATCHTTPGSLTKYSLQLYTQT
KEQAFALKAAILAYGERRHDSPYINCILSKFQSPVPLD
```

253 - 272:	EEEEEEEEEEEEEEEEEEEE
254 - 273:	EEEEEEEEEEEEEEEEEEEE
255 - 274:	EEEEEEEEEEEEEEEEEEEE
256 - 275:	EEEEEEEEEEEEEEEEEEEE

A0A0M8MYX5 **A0A0M8MYX5_9HYPO** (1444 aa)
Protein MGA2. *Escovopsis weberi*

```
MGDPFSASEYHGFSDDDFADTSLFDASNSPDGIQDTASIAENKNHIDPRELAAIRAPDSPTESLFDTASDSTSSDQRCSS
AASKEGIETLGDVSMDGESPHTDNIQWGQPSQTHFENGFHVFGLASPSEGFIDYGNHNDAIQEASFEIETAASSSPPLPG
KDTHGSMVFFQIPQSKSLGKTTSTHPEKTQHSIPSPRAGRKREATGEPSPMSMGTSNGLSPVSHVPGFPSPQILGTDVSM
LNSLSSFTANQAMQSAFGFCSFPPHLAFQPTFQLDQQIPQQAQPFNAHPIGAFSGPCGLWIDTLPVKSRVETQIPIRMIM
SPMPPGITKLHLPTHTISKPKLMARPPATPSPDTLELFVSLVCTSAMDNPALKQKALERAKATPQGHLPDPDDEENSPQN
GGEVRICGGCITRERKRAARKKIKKPEEDMLWSQDEARRVVVFNTHEIKEWQPYTGLQNPNGRPEPPRNGATMQLDAPMR
IACYCRHHNEKLGFNVIFTIKNWQGLVIAQDMSQRIMITDDHKTNPITQFSTTTHSALNEVFTDMAAPRHHSMALETGNA
PMPPPAVNGGFGGFSPSPSSSMQMSINMQQPSYGTATPAKTTPTVTSAVPCRPMSRDPSPSRMGPLAKKRKSSAPNVPKT
LTMTRMDSSPNQAPKPPASAQPASAPSPYPPHSTSSPNANLNQTPNPASFAQTEALFGQLLSQGQFALGPSGLGGPHDMP
FFGDRRSGSTDNRAMAQLFSSAPASNHASRAPSPNGLRTGQLLQPLNGSMGAMPMSLDRPRPPPIIHKVIPNEGPTMGGI
EVTVLGASFYQGIEVWFGDIKATTTTFWGESSLVCLLPPSPAAGAVPVTIGTQVVATPHMQLKSPPFFRYLEESEDQLIR
SALSVLGSKMSGQLLNVNDLARRILSAGSSGWTSGASGNSPTNGPLMNQGSQGHLEAQVLNVLELARLEESAHPVHLDIP
SPTGHTMLHFASALGQHRLVAALLDMGANVNARDRGGFTPLHIAAIRNQAPIVERLRGAGADATIKSLSGLRPSDVAGSR
AVERAIRHPHRHVRTQSGGLPQSRPARISSRVHSWVPRSSSHMHPERRSVDSDEESLEYTSGDFDDEDPDDNWYLAMRRL
SHASFASGETAELEEQDSPHQEGDEDAKEQEEAEAEEEEEEEEEEEEEEEEEEEEDEDEDEDEAEQDDAGEINGGKASNP
AAMAAALKDQIQAQLNQLQQTMALCLQNVATLRQAGMPQMPTFSSDYQAYLPQAPFMRKVQQLVPGIAGNRTDAAGGDHH
HREPDSRKLDDSVNPPAYHDLFPRRNMDTKTESAVRAAADAEADMKCASLYDEASTSAAAPASSSTQGIPVVLEIGRKNA
ITREQQENLLRARERNLKRLSKDRNLFFLWIPLLLAMICALLYSYVPSLFHFLWTSLRAVVQSSNLCVGRATRSAAAPNR
MVEV
```

1156 - 1175:	EEEEEEEEEEEEEEEEEEEE

A0A0M8ZPU6 **A0A0M8ZPU6_9HYME** (763 aa)
Scavenger receptor class B member 1. *Melipona quadrifasciata*

```
MSANLVASVAKLFSVDRVTQISVELDSRAWETKPEDSDGSVEERERKKEEKELSVGGERGWKPDVSTVSGNLENNTTGPL
LELTAGGSQRRRARCWAYGFVTLLSVATFVLFWCTSAFRDAILWNLELRNGTRSFLLWQRPPVGLQINVYVFNYTNVHEF
ESGTARKLKVQEVGPFVYRESLSRANVHLHENRTVTYQEKRSFQWISGLSERQKVIVPNVLLMSALAYSRDLNYLLQIGF
TVLMTGLNLRAKPFLELPVGEYFWGYEDELFEMAKRFSPLKQSLPYDKFGILAFVRYELTNLRTYNSSGLNADRITMHTG
TDDLGLIQRINGHESYWIWGDEKCDRIYGTDGSMFPPNWIQQQPNATIYIYAKEFCRQLPFRECVVARNTLHQSNRYKLP
SNVFTSTRNKDSCFCPKESYDSVTRICPPAGTFNISACQFGTPLIVSFPHFYSGDESLFQKIEGLTPQQDRHESYVDLHT
VGIGTDRPYLPCSSMHLGVTVATRMRFQLNLEVRKAVGMPFSGNLEDGSILPLIWVDTLIEDLPESIRQMLYLSHYLVNA
VEAGLQWCSLIGVVISEFEPITSKWEEEEEEEEEEEEEEEEEEEEEEKEEEEEEEEEEEEKEEEEKEEEEEEEEEEEEEE
EEEEEEEEEGRMTRNWMLRAKVDHYISQFWLRRRFPVIQRLIELLCPYVRPQVFRCKHFGGLFSLSYVLPIGFVWKPSMR
ISSLTAIFPVLTLQIRAKDSTNSQIQRTCTYIRSRMRQIYEYR
```

586 - 605:	EEEEEEEEEEEEEEEEEEEE
587 - 606:	EEEEEEEEEEEEEEEEEEEE
588 - 607:	EEEEEEEEEEEEEEEEEEEE
627 - 646:	EEEEEEEEEEEEEEEEEEEE
628 - 647:	EEEEEEEEEEEEEEEEEEEE
629 - 648:	EEEEEEEEEEEEEEEEEEEE
630 - 649:	EEEEEEEEEEEEEEEEEEEE

A0A0M8ZSV1 **A0A0M8ZSV1_9HYME** (272 aa)
Uncharacterized protein. *Melipona quadrifasciata*

```
MADSRLESCLKGTLISSRIGGAEKLQTADRRHFVHAMLQYQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEELYSRARSR
ATLEKLALFRSRPGTIKCAAIQKQPASTPSAHAGKQQRRNSVATCVGETSPTARETFASSKPIEEVGSHGRSKESVEEGT
EEGADLDRQRGPFSIAVTLIGKGEQHPYANGSRTDCETALNHEIEDEAQLGPQARDRKTTVAINRCGGFERNEPVSLFGA
FKQVYRVDFTTEQTTDSVVNVSQFTGQTVSAR
```

42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE

45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE

A0A0M8ZTD0 **A0A0M8ZTD0_9HYME** (1755 aa)
PH-interacting protein. *Melipona quadrifasciata*

```
MEGNVTRNETAIAPELYFLIAKFLAAGPCREAADVLKRELERAKVLPQRLDWEGYVHNQTFEELEKKYSHIGSNHLLQIC
ARIGPVLEKEVPPCIPGAISLLGVGRQSLLRTHEDVQHQVHGIISYSGRVGGKPFLDSPYSLLVPNIVHVLQGRENSGPL
SRREAIPTKFYNKMQLYRHTLGHLSAVYCVLFDRTGKYIITGADDLLVKVWSSIDGRLLATFRGASAEIMDIAVNFDNTL
LAAGSLDRILRVWCFQTMSPVAVLSGHSGMITSVNFCPISCNGVYYLVSTSTDGSVAFWSHMKKGNERAVFQPKPIQYHE
KMRPGQAQMICASFSPGGAFMAAGSADHHVRVYAMLGDDGPCRVLEVEAHSDTVDSIQWAHNGLKFISGSKDGTANVWHF
EQQQWMYKRLLMTTKLPGESETEDDSNKKAKVTMVSWDVSDEWVITAVNDSCLKVWNAKSGELVKILRGHKDEVFVLESH
PIDPRVILSAGHDGQLIIWDVLNTEPIACFQNFIEGQGNGAVFDAKWSPDGTMLVATDSHGHLLIYGFGSGVEKLKIVPK
ELFFHTDYRPLIRDANNYVLDEQTQTAPHLMPPPFLVDVDGNPYPPALQRLVPGRENCRGEQLVPNIAVGAGGMQEVIEG
LPAQEPRSNIDQLIEALAQRQNINADAENPDEREENAAEQPVRQMASPRGSRSGLRRVGDVEGVRQSSGNWQRDSTTPWN
KPILARPMNPGVRETQFKALHATAEMELENFKREMRKRPQPVSNTANTEGNISSRIANRKRNRTTRHGYRTRATRGEEQE
DDEFENPDNAATTGSSASSNSNDSTAHEEDLCSDSSTSESSTEYSDWIADHGLNLEPPKRSKRKPVKKRSLTPPSDMDKR
RNRRPKKKDIPLSTGIDDIPEVFRPSEWLTEIIPRKAPYYPQMGDEIVYFRQGHQFYLDAVRNKKVYELGPRCEPWNKVH
IRAQEFVKVVGIKYEIRPPRLCCLKLALTDVDGRLTGENFTIKYHDMADVLDFLVLRQTFETALARTWSEGDRFRCMIDD
GWWMGQIQSMEPLDEDFPESFFMCFRVRWDNGEYERMSPWDLEPIDENRLPAELGGAVPVLPEEIRTILYQPHAEEWPMG
DREATCRRIIRGLDQVMSLAIAEPFMAPVDLNAYPSYAFVVEYPIDLTTIKARFENHFYRRITSAQFDVRYLATNAEQFN
EPHSQIVKHARIVTDLCLRIIKETTELDVPAIYHQLVDTYHSSESEVDVEDAKDRPSTSTQRVTSSRNLRSQEVSTDWKI
ACRQLLETLWQCEDSIPFMEPVDRLEHPDYHQIIDTPMDLRTVKEDLLGGNYETPLEFAKDMRLIFTNSRNYNTNKRSRI
YSMTIRLSAMFEEHMRKIISNWKSARRRNNNAKNMKGKAKKTKVRLTNGTASSKSKPACSDDDDDDEMNSEDDDLDEIEK
DSSNVFGPGPSRMTNGHTKRSTNVTRPTIKLRISRSAVPKKPKESESEASDSEASTESESSGSVPIRRTRARKTVPSVSA
DSDSGEIYTPSGRGKQTRKNRAKNSKNSKQVKSKSKLSLYENSKNNYEAFSTNELSDDESEEEVINKSRTRSRKLVSTPE
QENSIKNTTKSGRNNTESQSEEEEEEEEEEEEEEEEEEEEQSQNEINNQDSDSEESDKGFVSSRSQRRIRATREIQSRET
VQNSRRTGKRPRYNEESDESNTVPVRNRRKIKRRYYAEESDESLEPENVPRISISSRGRVRKMTERARAFLLDSP
```

1621 - 1640:	EEEEEEEEEEEEEEEEEEEE

A0A0M8ZUH6 **A0A0M8ZUH6_9HYME** (335 aa)
Uncharacterized protein. *Melipona quadrifasciata*

```
MKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGGERRERKRTRAGGQKAKRETSCGGEGKRKSAEKRHSDRLR
KTQRALNEGTKYPGAFLFEIDKCRNYDVLVAVKRDPWPVKEDLIKFQATVVDNLGKVEFAAAGKLGRQDGGGEPDRHPAK
ILRIYPNSEGIETRYIRYGTVRYGTVRYGTVRYGTLRHDTTRHDTIRYDTIRYDTIRYGTIRYDTVRYGTIRYDTVRYGT
IYGGTIRYDTVRYGTIRHDTHGTARHGTAPHGTAGTAGTARHGTARYGTVRHGTVRYGTVQYGTVRYGTVQYGTVRYGTD
TIHDITRYDTTQCMI
```

3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE

A0A0M8ZUI8 **A0A0M8ZUI8_9HYME** (761 aa)

CCHC-type domain-containing protein. *Melipona quadrifasciata*

```
MALNHPAFTYEQKSVFGNIYIKLQEEEARLNLSKSNSSYKQGCAPCINTNERLMDTEMQGNCMMGPPPMQTYHGEMSMRN
NMVTGVPPGLSMPPPGLCLPTPEQMPMGSGGATQYLHLGFPSVNHIPPWTGQVMMGNQLMYHTGDMLAYPPSPLVSRQSS
PSQSRSPSRSNSPMGRRNNTMPRTSSQVTQSTSNTLTSTSASNSQTSICSSNVNSLPPLPTMGTNRSHPSQPPLLPSRSV
PLSISSSTTFSRHNSIENTPSTLIPAAPQSKQPPPPRLRSSISGDSLRETLGKEMPNFKGNLQNFSLDEIRRMSDEDLRE
IGLTPNAVGQLRSIVKSQTSNGLNQISTDKKLDNTNSTTHTVDSVENEGIPGMEMLNDNGNQSSKSMPLQEQHPAMHHHH
NHAATPNLRRYPTMPPLDPAQIQMYPAPPPMYAAQNAPCYACLTLPVAGVQNRYSRCNAQHVYCLTQLQALRLDPESSKH
CSQSSSSDSTGSRSPPETPPAAPWVSGSETNAPPVTDHLSSAPVHSTSVSHPASQQPIQSGPERQRNRRNQTHVIKYNHK
NQMVNGGGPPNLSQCVSFPAPPSQSQVTYLPHGHFPALRPSSGIYSNFSHGPYARPAYPATYQPNGEMMYQYPGHPSSGG
TPPPPPNAATPVQAPYMPPTPVVTYSPAAVPPTKISCYNCGSSSHLAIDCKDQTMEDLTKKAQYRLDYSIMKQPGECPSS
DKKERKKEGGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEG
```

731 - 750:	EEEEEEEEEEEEEEEEEEEE
732 - 751:	EEEEEEEEEEEEEEEEEEEE
733 - 752:	EEEEEEEEEEEEEEEEEEEE
734 - 753:	EEEEEEEEEEEEEEEEEEEE
735 - 754:	EEEEEEEEEEEEEEEEEEEE
736 - 755:	EEEEEEEEEEEEEEEEEEEE
737 - 756:	EEEEEEEEEEEEEEEEEEEE
738 - 757:	EEEEEEEEEEEEEEEEEEEE
739 - 758:	EEEEEEEEEEEEEEEEEEEE
740 - 759:	EEEEEEEEEEEEEEEEEEEE
741 - 760:	EEEEEEEEEEEEEEEEEEEE

A0A0M8ZVW9 **A0A0M8ZVW9_9HYME** (72 aa)
Uncharacterized protein. *Melipona quadrifasciata*

```
MAHIPQVITWEEILALAGLGRIHSSQDVTGFSSTLADVWPGEEEEKEEEEEEEEEEEEEEEEEEEEKYKKEE
```

47 - 66:	EEEEEEEEEEEEEEEEEEEE

A0A0M8ZWM6 **A0A0M8ZWM6_9HYME** (975 aa)
Uncharacterized protein. *Melipona quadrifasciata*

```
MDCCVQPAFQPGPTPKRDLLTHFEKDGAIFLGMDRQNSISEIFADSKRTLVSTLDENGINALATHTHAATMTHTDAATMF
HNNYLFEQDEKYFHFGTYRCKNIVILAYACCNAKLLYFLFVVWFLVKTLTGGGNIPFADEDGAVSSGVEHRRAERRSNVT
RRELTKETTASSPCPRTNVQSFTTFRSIVQPKIGEEGERRIVSMLQKGAATFAQRESQAQHRQSKQSPAPRRNKNETVLE
TGFEHPLQRYENAVLKHQTRQRDRGKRQASGDRQQQQQQQQQQSYSQHGYSSSDESVVRNKSKSISSIDTQSVNNILDEY
EDLDYRRSSDLSDVGSISVSNFEAVMMDQQKKQQQEKSRVLAAAARMQPKCSPPGREKSQPVLKVNQQTQVRQRSRERQK
ESGVRHVLPPSPTEPDNSSSSCVSPAAAVTVDNSRIRVPEVLLRKGEVQKRVDEWLNQTQSQNFSAPTREKPLTRSNSSA
EQKSQRRYRQDSRSRSIDEGRGDKLNGTSSSYDDLSRADKKQAERKLVDKVNVGVNTSRGTYKEYLASKNRGKQQDYGFS
ASNTGIGRSRDISPSTGSRIPQRGPLSSSFRSRRLESSNAASQADIVGGESSSQLHQAERNCRARNATDGRLTNLAKTRN
ESDHGRISGVIGVATGGSTVTTSSGTLSVIPCRKASFKRSQAHDQSTAGATARALVKEETGQRARGACGGNSDSKGPSNL
GDQGEPISPNKDGESRRPALTSDSPRADDKPADAACKSATEFSRSVDRPTRDVLRITTGESAESSRVYAALQLLNEQNSA
KSRSAAGNNGVQPLERSPCRSHYSSPNHVEKIYERSLQPQVIHVDDLQSILRPPLQISAYGEGGTGGRSDLKSPPKEAVI
LDERNEKQPEEEEQEEEEEEEEEEEEEEEEEEEEEEDDDEEENEEEEEEEKGEEKETEVYERVGELRYEHLETXXXXXPGD
RIESVPENSAMPAEW
```

895 - 914:	EEEEEEEEEEEEEEEEEEEE
896 - 915:	EEEEEEEEEEEEEEEEEEEE

A0A0M8ZX22 **A0A0M8ZX22_9HYME** (592 aa)
Uncharacterized protein. *Melipona quadrifasciata*

```
MEKKLESTFYSPANTNLSIRFNLIKMNQPTVATRQLVEEEEEEEEEEEEEEEEEEEEEEEEEEAKKKKKKTKTKKKKKKRGM
RKRRRRRGRGGEDETGNLTGLLQRNLHRSIDGTCSSITSENANCLTETVGKTDNSGDRKVMSFLRMSIFVCHLSAHCVLQ
SCAKDILRSEALWGINVFLHRGTYVVIIRGHSFVNSSVDDDDDDDDVKDEDEKCSGTTRRCGDCTGCCVISRKIGPRVIL
HTKIQLRFRTRYISIKFLFMHIPLTTNIGGLSQDTLILKRSTVRSTELDIPDELQFTSSSWKVNVRKNSAKVLAITNSMH
KSNSILPKSRCHRIHGGESWSMLRDNVTTSRCATRSRAVPMGDSPLSRQGPRGGAAAGRKRKDIERNTSNFSDPTIVCNP
MIIPKDPRSVIIVNANNPEYSHRRSKMENVLILYYASEADYILIICCISKVDYNRYILIDIGPFKSINDYLCSHFVYEKG
EKESLSVAILDEFYMQRTCDKIHLDLEFQGVSCQTYDDNNCAIRIQNNNYDENTSLSVMHVRHLKDIEWRKSNLSMVFGF
GDNWVGFVVCINVIVNFLDFIYQLCPLTVVLI
```

38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE

A0A0M8ZXJ6 **A0A0M8ZXJ6_9HYME** (302 aa)
Uncharacterized protein. *Melipona quadrifasciata*

```
MKWCLGLRRYTSNYKEEKISAQSHLPLPPGLVATTTATTSITTTTTTTTTTTIATVIITSASLELEVLDFKILEIMVACLE
TVENCDKIYDTARSCISVIRVRKRDLLLLRKIFRIGSSRFEKMCFDEIIGDCLDRSIMNRSDYLFSFVINNKIHAFHFER
NAKSVQQNILALVPFTQLGQRQPLTGGEAAECVPGEERETKWQGRRGKIPAIRGPRNFKQQRQQRVSSLTRRSTTRAEIR
DEGEEEEEEEEEEEEEEEEEEEEEVGETGAQGEEKQPLWAIKQLREGGKYLQLYGNSTMFRR
```

244 - 263:	EEEEEEEEEEEEEEEEEEEE
245 - 264:	EEEEEEEEEEEEEEEEEEEE

A0A0M8ZXM6 **A0A0M8ZXM6_9HYME** (361 aa)
Uncharacterized protein. *Melipona quadrifasciata*

```
MGDVALNIGSILYLICASSGNEALCTSRKPAIYRAIYVLIDILELLYSYAHNEPDIGASHGGKICTRPLDFISILPAISG
IVMMVIGLTTLLSVPCNSKLNGSSITTPSKNCLLKRVTHIATFATVSMERSRRDHLKSIETDEIKVDERLRGLEQRKVIK
SKAVSKERTRNEEEEEEEEEEEEEEEEEEEEEEEEEEGEEKIKRETKRRKEMRRSVFVSASPEHWCRIPELENLTDLMTLE
ERKALSLPYVEKSDGKVKKYSKCKMYDVNYTAIVESWLENAVLENATEEEVEAQRTRSRNGLPPPPVGNPDWPVTKCRHG
WIYDNRDYDSTLVTEFEYLSLIIYTFQTKNQTTIRACNYNN
```

172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE

A0A0M8ZZZ5 **A0A0M8ZZZ5_9HYME** (308 aa)
Uncharacterized protein. *Melipona quadrifasciata*

```
MAGMAEAAPVLGNPSRHVRLLTPPRFGNARRLKPPSLHPTPSRTFERDSPTQSQCPRNKGELNPRACPNRQQTPVPGWLP
TAPQAASGCAPSVDVLPIFDVKQQSVRNPARMGANQPSRFSYNNKRLGCKDVSRSHDVFLISRESERSRRERRKLATRGC
EDREKKKEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEGVENDAGKFHQSFPSPTLLQTELGKRHKGIFYSEDSYENCLYM
VVLLFNTLRDPTFLGALRSQLLHTTSSPASLKPRLQLPAGVHRPVRRYLAVDASSPPAIRPGLVVSIS
```

171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE

A0A0M9A0H3 **A0A0M9A0H3_9HYME** (1659 aa)
Uncharacterized protein. *Melipona quadrifasciata*

```
MLYLDAPRSHKIFGSYVNNDTETTQLNSEFTIYFSKGASHVLKLGIGNFDGMKLLEEGRGEVTDISASPGRQAPANQLRP
KEPPPMVIQGDFRKKDESVEQFHEVLFILNASVHDMAWLKWKDLSLQVSGISTEIFKQIETVENDHDASTAAALEAVERR
GEMVVRVIEPRQMGRQASEAAKKFIAMQDPKHPIHFVEIIKRPGQTLGLYIREGNGVDRNDGVFISRIALETAVYNSGCL
KVGDEILAVNLVDVTHMSLDDVVIIMSIPRRLVLATRHGQHQPVSHSRQTEHKAPPVVVIKRELNEDESDHATSNHVRDG
NRRRGDGREMLPSRSRLGLSGLGSSQDLGSSNGDLYYNSRPEGHWSYQPPPPPVITHQPKPSATQHFQPYERGYPKTLES
LAEKVSPCDALLVPRDFDAGRGFHKGKETTNSFLISRLMLCSNPLHRAPPGQWTTRTSKNLSQKAQKSVTFMVSQFNLDV
FVENSKKMLNISPGVQVHSFYTGPVMPSNGGRRMSTGAGMQSVGSRLSSQTQSSHYGYGQHAGSGRIMPRSGSDQHLPRV
DYTSITTPARHTLLRSSLKSVYKTLDSYFTTGTSALRYNTRYGSQGDSTTATQRQGQFGTLTRRHRPSLDYASDTEATCS
SSPKSAYYYYRHNMNNPPQSSAVSHLATLSRSQIGQSSSGLRSNSLPRSGRTLPQQPGLRSGLSTVASGLIDQEDSDGAL
SAPELPSIRRDRGRIPSSPSVFTSDEYRAWLSRTPSTSALYEQIRASTTRPPRYTYSAENIHAAANQGEYGSYGAYRPLS
STLDRLSTRSASAQQVNLANLRASTAISSTCHRGTANPRPASVASSARTSLTSQKPSLSSSATQRATSVRRIRNLLDLES
TRSIPTPTPTRTQDQRLLDINPAGDIQVLEFLKYKIEKPPTVGTPSSTNSLLSSLGETSSGDLAGGVSGLLWVHLLAGRG
LRSTTSSSAATTPSTPSGQPNLASCGLRDLYCVLECDRVHKARTVMRTGDLMFDWDETFELDLVGNRQLDLLVYSWDPQY
RHKLCYKGSVHLATLLKESPVHQLAVKVEPRGTIYLRLRYTDAQQTFRRRGLPTGGVPGGVSTALAMGVPNVPIIVWRCV
EEVERRGLDIIGLYRLCGSATKKRILREAFERNARSVNLSPDNVPDINVITGVLKDYLRELPEPLFTKCLYQMMVDALAV
CLPDDPQGNAKLMFSILDCLPKVNRCTLIYLLDHLAMVVSQCNKMSPASLAVCFGPVLMLHSEENGPPLDFQQPIAVLKY
LLEIWPVKSVRKISSVASTLPRVTPAVEHNNSHQPLQQQQQPQPQQQQVQQQVQQQVQQQLQGTLGRTGLPWQPPHSLHQ
QPPTTAPAALAASIRPPPPVKPRQEMTLFGTAFLFVQVIVSSPGSPSSEESEASPEPINKSLLGGLGLEKSNEGATANST
GPGTEQITPTSSVDTEEGNTTHPEEGEKGVEGDAEASDDDRHQHMIWKDVFNKVLNKNKSQVSQRENKETKKKEEYSISK
IDLQESTNIFGKLQKIRRTGLISSGGLSDWPSDLNYRKIQKDQACIYWTLKTPTSRGIRGTEVRFSSQSKEKEEEEEEEE
EEEEEEEEEEEEDITLHKSKKTYAYQGRSWLSWGQVIYSDSWCTVLKAVERHESPRTEL
```

1593 - 1612:	EEEEEEEEEEEEEEEEEEEE

A0A0M9A0T4 **A0A0M9A0T4_9HYME** (278 aa)
Zinc finger matrin-type protein 5. *Melipona quadrifasciata*

```
MGKRYYCEYCDRSFKDDPDARKKHLSSLQHVKIRANHYNMFKDPEVILKEESSKIPCKWYLSCGSCAFGIGCRYSHYTLP
MIWELQRLVAMKHQSKLNVTLENSWPNPDDTIKEYFENTASTSNTDDFIYPTWHRPLELQNYSMLPPSLWPITPESLANT
TTFKEWIAFHVPAPKGDGRSKKRAASWPSERRPRQPTEEEEEEEEEEEEEEEEEEEETQQADAVCAVYALRSLVKTFARN
KCYDDEITTTLGLDYNWNSCFRYRRPAFQNFSNGYRLV
```

198 - 217:	EEEEEEEEEEEEEEEEEEE

A0A0M9A2G3 **A0A0M9A2G3_9HYME** (411 aa)
Uncharacterized protein. *Melipona quadrifasciata*

```
MAPIKLNYQFVYVIICEDNQVSAQEDKASSGDQDYASQHQLFDIFWEKFNVGSKARNTRLKKKKENLLQKCKSTNLEPNQ
ALPWKKNKNQLTGLDELLELVEEGTTGRTMASLETEMSLVAVGRILRNEVRVAARLETISIVRFDISTKLRLLRNLCQFQ
IVQQTIHADIELRVHRQSELGVQHLHLVILIRNEANHGIPREEPDPSIQQPTPFQYYRTLFFVKLQVQVGLVRETGLPDT
WRIIFQLSRHFLAAGFPNANQSQEEITASFRELKALRSVNPNGGFRSNESNGVIVIVAGTNDERKSCNEPTNTSPVNQQT
KKTSKTTRQTGKRVEEKEEEEEEEEEEEEEEEEEEEEEEEEEEDEEVGRRRCVVNRAKSVFNLTTGCFISGRVAVNLQPRL
QQEWGLGGGWL
```

338 - 357:	EEEEEEEEEEEEEEEEEEE
339 - 358:	EEEEEEEEEEEEEEEEEEE
340 - 359:	EEEEEEEEEEEEEEEEEEE
341 - 360:	EEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEE

A0A0M9A379 **A0A0M9A379_9HYME** (998 aa)
Uncharacterized protein. *Melipona quadrifasciata*

```
MVLPPSFVACGGNSGSNAGNGESPSLALKSFDGNSLETHAEIKLNANSELMQPRFMSPAVATAGYKGLAFVAEEAKTRQR
FGVDRVAGRFEQELELVFPLARLISVGEISSGFLRPAKAQWLSNAITLIASGNPCARLMLIAVRATRCQDSASQDVGMAE
CQDSSQLRVTDTGDIDGDVGPFITVANRSPNFGLLPDNFQLLSSLSGRQYPLGGYGCKFGQLIVRFKLYQLLNRIKFCTM
SKNDVAYEHKFKRTKVILKKIKSRKFRGNEMSSNFERNIPDTTISFRIRVWILSRFFTILQNRRKLESAACCSVFNPSTT
NVQTSKIPPLVARIWETARRTDGLARVAASREKSVERCGRGCEEEEEEEEEEEEEEEEEEEEEEEEEEEETNRGEKGERT
KEGETGWKQREKSEEDGENSGFDNQLVLVQHLSASLVNTLGSVGLDQLRPENIGSVTTLGKWPASTANSSLICQEININA
KRLVGKAKGALAIKNEIDRQVTRIQSIEKIEATAEIPVLAIGRGVDKRMPVEKLWTEEQHRPAPRNGRGSAATKGLSGDY
LCIIDGTTLETICAECKVLDKETNATNDNEHGSEPEILFSLQVSTGWQKVISSEVRVETSPMILKIKIHARDKGDASLAA
THQENYDEIIHEPQITIFEYFYWINLPSEEINPEYLIYRENGDIRRADGGGRFDEMNLCVELLADSNFKLYFIIQQVRKR
EEEAESTKEKLVEAKLWKTTGMAFRVERLGEVAGVAEAGNATSRSVRAEVGLRDDPTGADEFTCTAVMLGWHWYSLTAKS
RFAGGCLRKKTCDNVTCTSGARMPVTLTSAFTSLPTTPIHRHPLSPPPPPPPPPPPSPPPPPPPPTRERVNNQIALKAL
FLPEWELGFQDSTGLLTLRERLVKVEWNPTCKISETDLLFQTLVETNSRSRRLQRRPQSSEVSSLKKASFVQSDSTSYHL
QIQIYWVYPAIAAEEENKSEGQDVIFRRAFVNTGIIDL
```

363 - 382:	EEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEE

A0A0M9A3Q1 **A0A0M9A3Q1_9HYME** (740 aa)
Tubulin polyglutamylase TTLL4. *Melipona quadrifasciata*

```
MDFLHFNLLSRLERIEMKQPVNFNLFKHREEEEEEEEEEEEEEEEEEEEEKEEEEEEEEEKDGTKKYVYTMLACNRKDYQN
ISKYITHCEMNCIVKICVGNSKPRWDIILQRNEADLGHPNPRRFEDTPGGCATTGTSNGVINLDADSDEEWLVYEKLTAI
AFARSRTKSPAPSVANVTLRDNQSKSADIERRRSVKLTKNKSVASKVEARPVIFDERADGDKAARDASPLPIRKSLFPYV
SPYVLLQSHDHAPETLPKDFAQLLKWKFTTSTPRILMKILINSGYQVVNKGTDWSGVWNLSCKDTARYRSMKNFQKLPDS
LFNEIAELITKYRQQRPIVDAPECEMSRKFVEEYSFMPKTYALPREMQKFEGMWNRHGMGVAWIIKPPSAGRGQGIKIVN
QWWEIPKWQSVIIQPYISRPKLINGLKFDLRIYVLLTSINPMRIYVYKEGLVRFASVRYVRGANSGDKYMHLTNSSVNKQ
NPAYITNDGVNSFKGHKWSFASLWSYLRQENVWQDVADLWCQIKDIVVKTFISVESSMNAAVSENLASSYTCYELYGFDV
LLDANLRPWLLEVNVLPSLQTDSPLDTAVKGAPMNDVLNTAGYQIPRKTSKFQATVRARKKYDSIAHNYRLYSTALNLRE
KMKQNEINAMGTRDEYLDGILRNLTRDDLGQLVRYEDELSQADNFEILFPTSSSYLYFKFFEVERYYDRLLDAWEHRYSG
DKAKGIRRLQRHCETMEHLE
```

30 - 49:	EEEEEEEEEEEEEEEEEEE

A0A0M9A5U1 **A0A0M9A5U1_9HYME** (265 aa)

Uncharacterized protein. *Melipona quadrifasciata*

```
MQSVHFHHVVRLIAVLCHLKQLSQNTLSCLIDCNVSTMESLEIQKIIKCNINYCYNTIMKAGTGPFPSMKRGRRRKSNEG
FIEEEWRKREEEEEEEEEEEEEEEEEEEEEGKSGGMDESGVEVNTIQGPYAARRGVGEQLRVQQHNATDEVESEEHRQRQG
DVVRHPFRAEVTALVRQLGRPQEDKQYYSVLVKMESDGGSFCRSIVSFAINQRERCNRKGCSQSEIKARSLQSIVQDIII
TLLNRIYRVLGATKEENLIKIGKME
```

90 - 109:	EEEEEEEEEEEEEEEEEEEE

A0A0M9A674 **A0A0M9A674_9HYME** (435 aa)
Troponin T. *Melipona quadrifasciata*

```
MKHQRLFTLCRFPDCAQRQEQKRSDLDEQLKEYIAEWRKQRAKEEEELKRLKEKQAKRKITRADEEKRLAQKKKEEEERR
QREIEEKKQRDMEEKRKRLEESEKKRQAMMQAMKDQANKKGPNFTITRKDLAGNLTSAQLERNKTKEQLEEEKKISLSIR
IKPLEIDGFSIEKLRSKANELWDTIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQ
VASKYERRVDTRSYDDKKKLFEGGYDTLLAEYNEKLWKQKTEQFMKRTKRSRRVPLSPRVTIYPSMPFCPLMLQGLTEQQ
KEFIEKQWTLQKEQFLGRQKTKLPKWFGERPGKKPGDPESPEGEEDVKAAAEDEELEEPQFEEEEEEEEEEEEEEEEGEK
KEGGGDAEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

408 - 427:	EEEEEEEEEEEEEEEEEEEE
409 - 428:	EEEEEEEEEEEEEEEEEEEE
410 - 429:	EEEEEEEEEEEEEEEEEEEE
411 - 430:	EEEEEEEEEEEEEEEEEEEE
412 - 431:	EEEEEEEEEEEEEEEEEEEE
413 - 432:	EEEEEEEEEEEEEEEEEEEE
414 - 433:	EEEEEEEEEEEEEEEEEEEE
415 - 434:	EEEEEEEEEEEEEEEEEEEE
416 - 435:	EEEEEEEEEEEEEEEEEEEE

A0A0M9A6I2 **A0A0M9A6I2_9HYME** (196 aa)
Uncharacterized protein. *Melipona quadrifasciata*

```
MRENAPTSAVSEENARKGIKPPKLTADSSLFNNKSDNRERTEFSKPPRYYCGQNGQLEQAGGKEKQDGRTHRGQGTRGRE
GRKLVVGAVEEEEEEEEEEEEEEEEEEEEEEEREAHFEHYCKSTGSEDQFVAMNRLFSGNPIHASIFHSGILTSPLVIARRT
KVKGHTHPLRLYSHGSAPSGLSATVAFGHGVNFSFE
```

90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE

A0A0M9A7C5 **A0A0M9A7C5_9HYME** (587 aa)
Putative cytochrome P450 6a14. *Melipona quadrifasciata*

```
MSLSITETLGLVVAVFLLIYYYSVSKFEFWQKRGVKGPKPIPLFGNFKDVFLGKGSLHDCFEKVYYDYKDEPVIGLYAGY
SPLLVLRDPDLIKNVLIKDFSKFADRTLPPHREVEPLSEHLFRLEVERWRPLRARLSSVFTSGKLKEMFHLLLECSEHFG
QFLEGMVAKGELIECREISAKFTTDVIGSCAFGIEVNALASEDSEFRKMGRKVFETSWKTMIRDRLRDYPFLFKLIGRFF
VDMDVADFFTRITKETIDYRIEHNVRRHDFVDSLVDLKQNPEKAHLPEMDDLFLTAQAFVFFVAGFETSSLTISHFLYEL
AVNPSIQEKVREEIKNVLQKTNGVVTYDSIREMKYLDACFQETLRKYPVLVWLSRTVLVDYTFPGTKISIPKGQHVFIPI
YAIQMDPEIYPNPQVFDPERFTDDNAKSRHPMSFLPFGDGPRICIGKGRARRVRTIYEIHRDSNIYPESDLPRIPGVQFK
NEDSVSANPMSHLAALAKVQGTASVDYPSIIEIMTNHEKSSIRCIITLRHLKIPSTPHRVAKEEEEEEEEEEEEEEEEE
EEEEEEEEEEENVQRAAVAPRGMTVRL
```

543 - 562:	EEEEEEEEEEEEEEEEEEEE
544 - 563:	EEEEEEEEEEEEEEEEEEEE
545 - 564:	EEEEEEEEEEEEEEEEEEEE
546 - 565:	EEEEEEEEEEEEEEEEEEEE
547 - 566:	EEEEEEEEEEEEEEEEEEEE
548 - 567:	EEEEEEEEEEEEEEEEEEEE
549 - 568:	EEEEEEEEEEEEEEEEEEEE
550 - 569:	EEEEEEEEEEEEEEEEEEEE
551 - 570:	EEEEEEEEEEEEEEEEEEEE
552 - 571:	EEEEEEEEEEEEEEEEEEEE

A0A0M9A7D0 **A0A0M9A7D0_9HYME** (218 aa)
Uncharacterized protein. *Melipona quadrifasciata*

```
MSPLRQITNAKWWGEEEARRIEQRMQQSSAHSVRDKVLRCVTKGCMTKTQHSRGFVYELTESNVDKYSWALTVLRSCHAV
LRLPPAYLYPRIVRSKLKLSGTTAQKPANITTYQYHFSPTSISVEQFQQTTPINRKIVSNEQAWEIAEDQEQEKEEEEEE
EEEEEEEEEEEEEEEEEEEEGGEEEEEKEDKGRGRKPRHCKKKKEEEKLEKEERERL
```

155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE

A0A0M9A8N4 **A0A0M9A8N4_9HYME** (492 aa)
Uncharacterized protein. *Melipona quadrifasciata*

```
MQEISRSVDSRNDAKRNLWNLRRGAENAREKDLDKKGATSESPTYRRWRYNDSETYWLLIVSPCYQLMTVIKSLGYTSRV
RPYPWLQAPDDERLPRDHGTLARFVSILDIRIWIGETIGGAMWHDVIVKGGDGSNEILNETSYTRIVPSPRATIVIVNLS
YPEKLWLSTLGGYAVLFFPPPALSYLLLFHPIRPESPEWCVSPGPCSASVPRTDLVCVPGGDRFRIEIGLEIGDSNPRAA
KLAARPWRTGPRVVVTAGGGGGGGDGGGGGGGGGGGNGSGGGGVRNARNTLEEARKWGRVDDGGGGGGGGDTCGPEGVEE
GKEEEEEEEEEEEEEEEEEEEEEEVEEEGRRRVPQPRNSRPNGRRYAPCRTKDTLEEEIVDATNRSVFGRTTKELRFVRS
IRNLHIFTLNVRAFPDPKKHVLKVRAKRRAGLAPEGEQPPLPPPPPPPPPLEGRQKEDGPRGRGDESREDSATLKYPLFM
IETRIYCPNSRG
```

323 - 342:	EEEEEEEEEEEEEEEEEEEE
324 - 343:	EEEEEEEEEEEEEEEEEEEE
325 - 344:	EEEEEEEEEEEEEEEEEEEE

A0A0M9AC50 **A0A0M9AC50_9HYME** (733 aa)
Regulator of G-protein signaling 20. *Melipona quadrifasciata*

```
MLARSHHKDKIAGSNITLGSKPTTLCLSCLLSKLNLYFRDNNFSLVTTTVSTYTQGRLNNYTVIGNQVHRMFLVPLRKTE
NFISKSEISKILEEEVSKDEPGSHRISFMFLACVAMCSKLIEFEVNETRKLRIKTTTGLFRTKVEIIMDREQRGRGEEEE
EEEEAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
RLAVIEAEGVGEVFVVEGIVREQTTKESDESQESDLDDRTVAEFLIHCEFEMCAIVMILCGWKIGGGLKFGRFELVLDVC
KFSRRLQTRNVEPGNTYRSINPKPTVTLTIAQWESLDVLAAVGGNSTGAGGAADQEKKKGNAGVEHSELCETGNGLDGLD
GLDGNAECSLEEIRSWGSSFDKLMRSPIGRKFFREFLLSEYSDENIAFWLACERMKRESNSEKIEEDARLWVFVHQEILG
NFGKFIEMYDIRKMSKGSSVFYRGRIVSLDSRVREIVNRNMVQPTPHTFDEAQLQIYTLMHRDSYPRFVNSELYRRVARL
GATGTTGANNQEQDGGTGKSKGKKGATRRNSAIEPHVCLPKTPSARSTSQLRTSTEKVSINKKADSNVCKFSTSVSNGRM
RTIVSRVNFGVIFGWFSDRWRHRGHLDGTCSARLRVLKDWVFAYCGIQIRKEIFEYCKKYKLWYSQTVIPPKYDTSKIRY
SQSVVLPNYNTPN
```

166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE

A0A0M9F0F5 **A0A0M9F0F5_FUSLA** (1164 aa)
Developmental regulatory protein wetA. *Fusarium langsethiae*

```
MDSTKASSALMHTPPSASASGRRGNFQCEDSSSSQDIPPGAGVRAPSPPSPTSLVGCPSHPTSSIKSVPFSSGGLFASPQ
TPDTGAGCRHGWNPPSPARTDSWPQKEPCADDYISRLLRRVRHHPERGHRANTSPVMADFLASLGFGGAQTTTVSNNSQC
DSVEQLQHQLRGIIDAKVTPTRAEHVAITTELKATVRFQLNVSELENGTCENSNNLDPSVEGAQSIGVNDDQDAGQSSRV
VFANDMIMNQPQDDPTLQRSVAKHIISTISSADGGTWTVREVSRGAQGWTFTYFCKDSVQYWSRQNAKNPSKTIVCEFSQ
REPDPTLYTRPAFDCRGSIVIAFNRSTRSIAVKYDHTPLHKTVAELAAHFKPLPRQLGPGAQKLQEQQQKAKEKTPKKPR
GEKKDKKERKKRESVKAQDENGNPRKRKKKTNGASQSEATDGPMIPPDYPGAPAINGQADPSYMNGGQAPDNTGQQGFND
YPQELMGDASGATNGAGSQQAGGQPGSVTFPVNVSAAEVARRREAATTMLSNAGVDPTTLSPEQFGIFSNQAPELQRESL
NMLVKYGAERLRIVHPSNREGSAQANASAAQSSQSSTGPRTTKELVPHAQSNPNIDSEAQAMSQTADDISSPKRKARKVG
KSRTACFPCKARKTQKPRNRGNKTKKSEEIVIDDDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGQQEDAGDAA
DAEDAEAEGDEEEEDDDQQTASQDYSYPQMNIGNMVTDTTAQDTHATPNSYYHQSTSNLAMPQANTYPINLQPLATAASR
RDSYSRALPEVTQPVHHPLPHIPAPAGTIAPSETRRWTAFGSGELNGASDSGKTRRSLPSEPPHPTVQSASTTNSQPSDW
GQGPNTTMSSIPASNTATVSPQMSYDTRSSQRSRQNNQSLSNDSAQQAAAMAGTVMQQAQARQSPVAAAAMMAQARKSPY
QQVAVPRTTSRTGQRNQSRTPVTDQARGYQPPPPVDTNQQQTARPSAHYDTSSHMPSGSGYNDYGRYGGTSTAANHQSAI
SAASATPSSMGTSYQSKTSTANQWSGSLSRNDRSYQTPNVHAQTSASGQNFKMRPGTQQQQQWQQQQQQANYPAYSGSTH
QNQQGQTSNQQQQPPSWYFQNSHNPSMHPGGQSSGYNYEPWSGV
```

676 - 695:	EEEEEEEEEEEEEEEEEEEE
677 - 696:	EEEEEEEEEEEEEEEEEEEE
678 - 697:	EEEEEEEEEEEEEEEEEEEE

679 - 698:	EEEEEEEEEEEEEEEEEEEE
680 - 699:	EEEEEEEEEEEEEEEEEEEE
681 - 700:	EEEEEEEEEEEEEEEEEEEE
682 - 701:	EEEEEEEEEEEEEEEEEEEE
683 - 702:	EEEEEEEEEEEEEEEEEEEE
684 - 703:	EEEEEEEEEEEEEEEEEEEE
685 - 704:	EEEEEEEEEEEEEEEEEEEE
686 - 705:	EEEEEEEEEEEEEEEEEEEE
687 - 706:	EEEEEEEEEEEEEEEEEEEE
688 - 707:	EEEEEEEEEEEEEEEEEEEE
689 - 708:	EEEEEEEEEEEEEEEEEEEE
690 - 709:	EEEEEEEEEEEEEEEEEEEE
691 - 710:	EEEEEEEEEEEEEEEEEEEE

A0A0M9VP69 **A0A0M9VP69_9BASI** (773 aa)
Uncharacterized protein. *Malassezia pachydermatis*

```
MSHAGSWAESRRSRAMHTHRRSAFDSFDESQWLYGLREHVRSVLLERRRPLSRDQAPPSTPPLIRAQHQAPRMVASDHEE
EAPESIPEDPEAKSHLRLAADAMKELLALGGVVDEESEQPVEMDGFAEKVWRVDEPQEEGPSSLFSLFQTQSNGPVDVDA
LLRFRAGMTEAQAEEEAMPPPRPKIEVVESDASASSATSDSDDDEGSGDPAEDDAMEADEDEDHEGKNDSQDDDDDGDND
DTTGDSPRQDNASPFLRDLAHAASTHSYEDTEQATPAELLIPGQGGQHAPIVVLSDSEEEEEEEEEEEEEEEEEEEEEE
TTSPPSLPKLWSYAVDDALAEGNSNEEDEEEGDGENMLAEDNMLEEEEEDSMLAEQEEEEEEEEENMLEDENEGDNDEDI
GLSQRNTEPTAHMDMPASLIADASPFTEEEPALHPSLPIDEASETRTNLTEVMDEDAITASLLPTSETAENTSTVDTSAE
ATTAPRSEVVIELPTYERDETSGPSSMTDPVPVSETPATDAQPAHVSPMDSLASQDEPTMIDPSLLSVQADASRVSSADA
ATNQVTTASDDTSEAHDTYPTSQGKDEPAELATQPSPDRDVSDASTEALSEDEEADTSNLLEQPDEHDIMFSSPSQHATR
SHCAFQRLTLTKEDGAPTFIVRSCTLNPTVLEEEGAEQTDVITDSLEMQPLDADSLPESVYHALCRIVGPALLDDVYVLP
QSLGAQWMKTDPEHADIEASPSKRPRTNTPSPPRRMRLRTAQERRRRQPFSPS
```

298 - 317:	EEEEEEEEEEEEEEEEEEEE
299 - 318:	EEEEEEEEEEEEEEEEEEEE
300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE

A0A0N0BDY0 **A0A0N0BDY0_9HYME** (766 aa)
Homeobox protein aristaless. *Melipona quadrifasciata*

```
MRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGAGQ
SHLSRIMDHLGCLARILRFLMTISWKPISIVIYVLIPRIRRKVFLHYHNLKRYLDERFCVPTRKKKKIKDPVVQSNLSVT
PGYNTCIFIHFNSNQILTPNQLQRRMEIYVIRGSMFQPEEKSGEKEVASLIYNRAKNVSQDRAGEGQDHSTRGGGGGGGG
GGVGGGGSGSVSEQAVPQTSPASSTSSSGQVNQSLQQASQQVHQQPPPTTTAPQSAQMGISTEEVRAEEESNHPRAAPTS
PESETEVDDFAPKRKQRRYRTTFTSFQLEELEKAFSRTHYPDVFTREELAMKIGLTEARIQTFIENTYMCIDGPVVNTVV
YCNKTYNDKLARQEREDIYFLRLILYPLISHNWDQNAWMDVWFQNRRAKWRKQEKVGPQAHPYNPYGLGSGAPPPSAVVA
PTLPNPFAHLGTFALRKPFDAFRYPPLGHGPVLPGSYTAHPYHRAPPPLLPPGMPLPYTSAASFQSLLANISAAQRPKLI
RNSPPPPPPPPPTAGISLPHPPPVPPPPPPQTVSSPQGSPTGTVGLPDIDRRTNSIASLRLKARDNDVGRCFELYAYTYN
REGNKYFGSYDVKCELKDFYRSPPLVMDNRRRINFVGKDIPENEKMHVHGWCTLSEYLCVIKKTYGTLFAILSRVSDVVL
FVTMTATANAVTASAANLHGFAVARFARTICGDTANFKGYCGIPRK
```

36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE

52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE

A0A0N0BE46 **A0A0N0BE46_9HYME** (499 aa)
MAGUK p55 subfamily member 7. *Melipona quadrifasciata*

```
MKHSQDIDIEPDDEPLTESGTRGNRQKNFLISQISSDIICKELSDHLCPVEIPTVNGDEEKRKVFRGDAGRTSPEEGTGN
GGGTSSIISELNLFSQCLASVTEKKKKKKKKKKKLPCLGNGKKEEEEEEEEEEEEEEEEEEEEEEADRLGSKLVGCCA
RARNKNPKREEDDEHNSERTWTGREERVGNEEEEEEDEEEEEEEEERGDEQDREDEDNDDDEDDEEEEEEEKQESKELNA
LVNVHNKILNNVKDDKFFPVLSNSMDVEVLDLLSTKTHVSKDCKELFHLLQKPRMHTGLAVRSRRSRPEGLPSPIAGDPS
GEVDEDEETVKIVQLVKSNEPLGATTKTCEVTGKIAIARIMHGGAADRSGLIHVGDEVCEVNGISVEGQRLRTLSQNSEG
TIFKTFKIVSADSKGESKVRVRRHRNVRAGLIPSRAFHGSYSRDWKDDNTKNDDFNREEIPIYSSKTLSETGSLPTGGSN
QAIGCRQKAQEAAHGHRFR
```

124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE

A0A0N0BES5 **A0A0N0BES5_9HYME** (1623 aa)
Disintegrin and metalloproteinase domain-containing protein 10. *Melipona quadrifasciata*

```
MILSYIEVVLKGGNLEGTKGSPCAVWLSGGRENEQDIVVCEASVASLGYSGGGLVGESGPGNSRDFFDTSTSNRIIEKNR
LVVILISNNVWKSSLDSFNTCQRSMTHWEIERERPIFAFKEIRSTEKLQNLGIAPLVIAGPENVEPMRATTLAVDEGGEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEAKEEKGEEDEGGKDRGGQNGAQRAAIFFRKMENVTQRSHLLESTNRMTKADDL
PFIGQKHFKRDYFVTTTPYTEDQYQDQLEEFIYILFTLYIQKIQIRKVETNLKTHVDKRYKPHVQHEYAFKYMERGGNYA
NYHVIVLVELTGLFWIKQWTLRLIRDEGLFSKDATFESTNGPIDFDSSHSYVGTVLDIPKTKNSLGGNVRAVVDKQKFKA
ICDNSLPRLISGAAADGSDSLPQTPVIVTKPAIRLVRQPILPSGVPQHSACLTSKIGRRSTLGAQPLAACASRVFETHLQ
NKRNGILGLSYPDYSDWRYLLAFAVHRIPTQQQKYTCRHCGLLSLCKFAVLYSQAVTSNFIFRHIGAATLLRSRAIEDEN
AMVQGIVTEDGLFDGTVVTGFEEYYIEPTNRYLNKEEDTSPPYHSIAYRASDVLTPRRSLPCASHHLHQSASHDSTEREG
DEGQIKFKKKRKDEKRGERGKHGYANDSRTLYEPLLGERRALYSKENGARVLTTERDKSAARMETVSDADRIARHLHKRA
TVDPRKTTCMLYLQADHQFFARYGTEEACIEVMTRHVQRVNSIYKHTDFNQDGRPDNISFMIKRVKVHSEDALRDPNYRF
PGNYGVEKYLELFSEEDYDAFCLAYMFTYRDFEMGTLGLAWTGDLKNAGGVCEKNGHYRGSMKSLNTGIVTLLNYGKHVP
PAVSHVTLAHEIGHNFGSPHDPEQCTPGGEDGNFIMFARATSGDKRNNNRFSPCSLSAINPVLNSKARSPKGCFTEPQVS
LCGNGVIEEGEECDCGWEEDCRDSCCFPQRRYPPPGETPCTLTPGSICSPSQGPCCTAECNLRFGDKCRDDNGCRDASFC
DGRSPYCPPSINKPNKTICNREFVCFMGECTGSICLAYGLESCQCIPGPNDPSTKACELCCRLPGENQPCLSSFDWNSPP
YDIPDMFSKPGTPCNDYNGYCDVFQKCREVDPSGPLATLRKLLLSDESLATFRRWIIDHWYAAALIILAAVSLLVASMRL
LGKRPDLKLKSVTIIHSSTTETVRLPPEGTEGVTVHPPAVRAKLPLSRKVREKRRHRKHKDSHGNGDKSGKDPSKKKKQS
QTKRTSATNEDLPRKRSADAMVQESKRKKSFPSRDKQNTNGNSSNADNEKRKRKKQHKKEVIDYSAIQAEKETEPNADPK
SKVRSWLLASSQCRPETGRGNATGLPKSKSTPVGLTGAGARLPATRQQQVALRRPTESKEAKITANSGARKERAKLQVVY
KPPFRFSVKLRKSDKVAQVPAVAANATHATGRPKLPRTGVLLRTAKKKDRVRIGRARQIAPTGIGNSAGDLPEPANSDLH
TLKLVCPYEVSLKINNCRQLDYFLSALAIVNPTYYSDGSYSPAIPNRGVKPAGLFAFPVDNCIASQVITTSNVRCLFVLN
GFQFGALCDSVTKTTAVTASTLV
```

159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE

A0A0N0BEU5 **A0A0N0BEU5_9HYME** (451 aa)
Uncharacterized protein. *Melipona quadrifasciata*

```
MYKYVIPDPGKHFKQSSWQKSHSPGKRSGVTATLVGSGATKTGSLSFWSSTTILAVTVEANCSPGGARSDALRISVYSAL
SSLSSGLANVRAPVNESTAKLPLDGNSATRPYRRSPFKPLSRSTAVKLYMVEPITALSDTRTVIGSCGHRGELSLASSIT
IFTETAMLWGLPIDVVSNARISKWPAKVTKSTGAAREKGGREDDEEKEEQEQEEEEEEGGGGGRGGGSTVKLLLAWTTAY
LSRAFLPRSGSEALTEPTSVPEGRFSSSSNPARISVRLCARVRGGGAITTAFSTRQVREERACFAAHNSARNAGIETGKQ
TNRASYTRKTSRSADAAKWSGMADECTRGEEEEEEEEEEEEEEEEEEEEEEEKEEEEKRRGGLETEGGKNDKTMDGDNKIF
FPQVRISCSGLGFLKYGFRTLDWHKPQVAARLASMSYRSSTLSSGVCGTPL
```

350 - 369:	EEEEEEEEEEEEEEEEEEEE

351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE

A0A0N0BFU3 **A0A0N0BFU3_9HYME** (189 aa)
Uncharacterized protein. *Melipona quadrifasciata*

```
MNGFGVIINIEYRVGACWILGEDGTKGRRMSRKEGKEEDEEEEEEEEEEEEEEEEEEEEEVGEAGGWFLYNRSQGEEEEE
EEEEEEEEEEEEEEEEEGEEEKEEETSTRAKKKRGRCSEEEHGDTNWHCEKREKKGEGATRDSERKTMKQYAEENIYGWL
GIITVELCNFQQYVTLQMKSNMCTVVQKS
```

40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE

A0A0N0BG81 **A0A0N0BG81_9HYME** (3044 aa)
Cadherin-related tumor suppressor. *Melipona quadrifasciata*

```
MKIYRLPPKMPPFPLHGGGGGGGGGAPGPWSVSIVLRTGNSRSCRCTGDPLFGERSGCLAGDDDDDDDNDDDTRRGEYDR
ELRIVGSSPNVHRFVLCIKKRKDTCKEAGYEYRGFVGPKERKETKKQRETKRKGEEEEEEEEEEEEEEEEEEEEEGRSG
GVGQSGVRVTVLDKNDVAPTWGSGTWKFKISEEAPPNTVVTVLKAFDPDTIGTLTYTLVPNHRAGTSPGLADPTEVEETQ
CQFRLHPTTGQLTLAEALDREAREKYILKVRADDGLQHTDIALTIQVTDTNDNAPTFQSTAYSFDVPENMPRGSRIGQVV
ATDADADGPNSQLSYTLISDWANDVFSLNPSTGVFTLTASLDYEQVQHYILVVQATDGGIPALSSTVTVYCNVVDLNDNA
PIFEAGPHAADIVENTTIGTSILSVAAQDLDSGDNGRVIYAVAGGDENGDFGMAPNGTLFTRKLLDREQKPLYNLILSAT
DSPLPPALPLSSTVQQELNLAGFLGATCDGGVAGRERHVAGVHIANEDFDNRERAEQHDGLLRVSGSLDRELRSNYTLEV
TAKDRGEPPRSSSTTVTVTVLDENDNSPVFDPRQYSATVAENASIGASVLQVSAMDRDEGANGRVRYSIAMGDDNRDFTI
SEDGGVIRVAKNLNFERKSRYYLTIRGEDCASEVGETPRGDTAQVTVTVLDINDNAPVFLDSPYLAHVMENMVPPGGGFV
IQVKAYDADTPPYNDQVRYFLKEGDTDLFRINASTGDIFLLRPLDRELVPEYTLTLVAMDTGSPPLTGSGIVRIVVLDVN
DHIPEFTRQEYRATVTENSASGTWVTKPHATDKDEGLNAKIRYSLLGENSERFTVEPETGDVFTVVPLDREQTSVYHLTL
VAQDSSPTEPQASAVNLTIFVKDVNDNAPRFSSPRYTAYVPGATKPGDFVFGAKAVDDDDAENSRIVYRLQGIDAERFAI
DSNSGVIRTTQELANDETTYQLQIQASDCGVKPQSVTADLVIHLWERQLFPSFRSTINTRFTLAEDVPEGRVITKLSATT
PKVGTASNLVYGMAGGNVGDALKIDPHTGEVLVASGFDYETAPHYEAWVEVRDSDTPALRSVVELFVNVTDANDNAPIME
APIYNATVPEDEYPPLFVSKVSAKDRDSGENGQVSYHLVNDFAETFIIDSDTGEISTNAKLDREEIASYELIVEARDQGQ
PSLTGTTTVLLTVLDKNDNPPQFTRLFSVNVTENAEIGTFVIRITSSDPDIGQNANVTYRFTENPGQKFAMDALSGNVTV
DGHLDREEQDEYLLKLVAADGAWQAATALTITIQDQNDNPPEFDEESYHFHFPELQPPVAHVGQVTAIDRDKQGPNSVIS
YSLLQPSDLFTVDPANGDVFSKKTLKYKHTHRPSSPENLYSLTVVATDNGKPPLSSKTVVYVNVVDANNNAPRFEQRSYL
YPVPENYAVGKKVVQLTAKDDADFGVNAEISYSLEDVNGTEYFAIDERSGWMYVRNSLANVPVGTTFLLKVQAIDRGVPP
QKDQVSLTLVISGENKHAPTFAAVSHQVRVPENEPVNTTILTVSATDGDDGPNGMIRYKISAGNEKNEFFVHSITGAVTI
LEPLDYDLVQEYKLNITATDLGFEPKQAVAILTVNVSDINDNPPTFNQSVYEAYLPENSPPDSFVYKDTLNCDNLKKKNC
VTIYSSGNSEFIFLHRAASENFIFTNCARSLSVRQRYSYSRSTARPLTNHVTQINQSLIFVALALHLKKPDFLGVGYSLS
VSGNDGRHPNVVSKVTVEFLVFTNSTIENSVTLQVAKLNARDFLSQYYRALLDILQEEIDVGDTFKIFSLGETDSDLNIH
LAVESPQGYRSKYEVTELLNRNRDKIRSLLEGMTFTVGYSPCKQIPCENGGSCSDRLVIYDDARITDSQALILTSPRMMH
EMTCKCRDGFTGDKCDRRQDPCSPNPCLLGGQCRRMAYDFQCTCPIDREGKLCELERGDACASNPCRNGGSCRKSPDSFS
FFCLCRAGYRGNHCEAITDSCRPNPCLYGGLCVGEKPGYRCSCPEGRYGRHCERSTFGFEELSYMAFPALDSNTNDITIV
FATTKPDALLLYNYAPQTGGRSDFVVLELVDGRVVFSYGGARSAITSITIKTESSVSDGEWRKVTATRNGRVVSLSVSTC
REHGDICDDCKPGDGTCYADDVGPTGTLNFNNNPLLVGGLENADPVLERPGQVHSDDFVGCVHSVSINGRALNLSNPLAS
RGVKSTCIRSKNNPCLRSGKDSISTCGANSKCYDKWHQVSCRCGSVIAPNCEGALEPITLSEGGYVEFKISEKHRRMQLL
EYLYRGSTMWQKNRAKRTVSEDTSFITNPSPFKTLIYAATNKHFTSVELRNGQLFYASLLGSPVNMTASIEGGLADGRWH
NLTLHSYLRGLRLLVDGVQTGEELDPVSVHDFLDPYLSVLSIGGVSQDLYYAHSAGARSFEGCLANFTINNEIQPFNGSG
SIFKEVLYHAKVSTGCRGPIGISAAATADPLSIGITLVIVFFVILLIAILVSFIVFRLRRQNKEKSAPSVVNKNTNAIMT
GNPLVGSGNDNLMSRHENTYISDTSDLRGVGHMGPELISKKYKEREINATAEHRPQRPDIIEREVTKSPPIRDEHPPLPP
PAQTSLHSHEHNPEPDMPEHYDLENASSIAPSDIDIVYHYKGYRDGMRKYKATPPPINNYANHHKHTGQQHRHTGPFPPR
ALPPPNVNQPPGPTQKLLQSTPLARLSPSSELSAQQPRILTLHDISGKPLQSALLATTSSSGGVGKDALNSNSERSLNSP
IMSQLSGSTASRKAPQSNNENSVNNVSSGPMGLTAEEIERLNSRPRTSSLVSTLDAVSSSSEARGPPAHGPLHLHRRHTP
PVERLERRNSSTTDESGNDSFTCSEYDNTSLVGDKRSDNPFAKQDDEEVNQRSNESSQTTKPPLPPNVNYDGFDSSFRGS
LSTLVASDDDLSTHMGGLYRPNNSGSPSTTTTALSWDYLLNWGLNFDSLVGVFIDIAELPDSASRVPSTLRLPTSIPKPS
EEYV
```

135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE

A0A0N0BI47 **A0A0N0BI47_9HYME** (1598 aa)
LIM/homeobox protein Awh. *Melipona quadrifasciata*

```
MKANKDIRKIVELSDTGCDARLPAFKASRNTDRSHFPKLPERMKQNENWKSHCDEKIKKKSCGERSRASNGLDAVDTEEY
LFTLKEDGANQYYWQSYSPREDLTESIEFKRKPECRDLRNKLRTSPDRSRPNSYKQDNSFCEVSNTVRNNPNVVRQNLLN
DVKKENLSQSNPTRPKSAGAKLRFVHSNYPSKSLDPNLNDQIVINREKVVSTKQDYPEDFVSKDTPRNSSKNQKSHWRRT
SDVENHIDEILQRDRRFSRFDNSRNESAANSNEVSRDWIEPTPSRIRSRTCSPPVDRQKKTRSFLKNPYETETRQDNEND
ECSKFSRMRDANSDRSVDRRFVDRAVDKDSLSDLQNVCASAEQISKLTDQVEKSNARANFWEFIPLDESDERYKGIPENK
EITYQPQNKSSAKNSDVRRWKDRFLQRHSKNSGFCNDPSLIKPQVTSEIDNNKYTLRNEQPSNNEAKEKSNPDFDKDRVA
GPNVYKNFKVVDSTKSQRQCKYESKSQSKVVSKITFGWTNKTNTYLKRSGSASDENDDKKKRITNAGISSSVTDDQKVRT
NIVERTAACLKRKLNRSENREVSNQHSPIAVKKKIRSEEFGHSKLPIRVGNRLRSSNPMTKNQFNFKYVAREENKEKETN
EEPCRFGSISVRSRTKPRIKPSVIVGEAIDFADTSKNFQSGGFNPENKGKVKDPLVNDPKAESNLIEGRIGNRGGKENFK
NEKLETNIENKDDTEKMLNVEENERKCINRGREMDYKKGFTNKVVDGRSGLKEKCCFHLNAEQNVIYNDYCNKEHRNLAC
SSQIGAEIPIQTFLQPEQRSHLLKLLGDRSQRTEKAQATTPEKRNIQPLERKDREPHLEEEAFNERARLQFIVATLPVFL
KTRTAQNTEVEDMTSDGVCEGTGPNLAAGENTGGLMGPEMSPSVMECGGCGERVRERTVLCVGGRTWHSRVYCRHDYALR
VACKTRACDTTHARTARMNGWKGGCYGCTGTFGAKCAKCGRSVGAGDWVRRARERVYHLACFACDACSRQLSTGEQFALL
DARLLCKAHYLDVVEGNNTSSDEGGDSESGHKSGNKAKRVRTTFTEEQLSVLQANFQLDSNPDGQDLERIAHVTGLSKRV
TQVWFQNSRARQKKHLHTGKMKGQHVHQSPPNSTASGDFSRHINLHLTYSFQHQQQHHHGQQPPQLSPATCKSPTPSLYH
NHGENFRNLACMYVCVPNVFYDFETKSAHEIVVNPLRLPARKEKIGKKRQKYRRGGNFLRLDGSTALSHWITVYNIAVMC
VQHRAEGQYQILMHDFLQIYVQKLQDLSIGTIKKQSFKPRRKQEFKEKEDEGAILVRAAGCENSKADMCVACRVTSKRLP
```

```
VFQTIVEGIRLPTIRVRSKEEEEEEEEEEEEEEEEEEEEEEEEENFCQKYDMEIVTVLSPVTTDEWLGWTLNEREEDTKNSF
NIVMISKAHVCVTLFCSVVFDTIRQFGTLQNTLHVNLRKDQRTLLSNSKSHKNGKCPIYSLLDGGALGVFQYRFVRPMNL
GILKTDKYPPQPMDSQNPQHPLVLELATARHNESPSGKSVRRHAFVTRGTFGTLQVDCGFLCVCWKFGDAKVHAFMKK
```

1380 - 1399:	EEEEEEEEEEEEEEEEEEEE
1381 - 1400:	EEEEEEEEEEEEEEEEEEEE
1382 - 1401:	EEEEEEEEEEEEEEEEEEEE
1383 - 1402:	EEEEEEEEEEEEEEEEEEEE

A0A0N0BIP7 **A0A0N0BIP7_9HYME** (215 aa)
EPL1 domain-containing protein. *Melipona quadrifasciata*

```
MEAFLARLTTISSAAKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEEEKRKRELIMIISFRRQANQTPDKKKHRRY
SSSMSTDAPAGATAKGAALGNVGLVGTTVPLFPSCPAVGTRWDWKARSLCNCPQFLSSDCWLEGLKMTWITEKTAWQAGL
AASHNPRPRGTKNEQVSVDKPSHSDYSNPPTTIYSTLLAVAGNNAGFQVFPRPQK
```

17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE

A0A0N0U304 **A0A0N0U304_9HYME** (452 aa)
Forkhead box protein O. *Melipona quadrifasciata*

```
MLAKDFANGRTAPREVLAITLEYTEETNMMDSVPVSSGSKTGLQPQQGVPYDLESGFEPQTRARSHTWPLPRPEEYIEGN
VVPSVSASKEGVEGVESGTPPQHGTLGQGTGLLPVKKNSSRRNAWGNHSYADLITQAITSAPDERLTLSQIYEWMMQNIP
YFREKGESNSSAGWKRPYWKSKIAGSSYEEEEEQEEQEDEEDEEEEEEEEEEEEEEEEEEEEEEEEEETATAATASRARE
TGKVLSEPITGYLNTFAIFKIQAAWVKQYQEFVIYGAGLAPAAQENHSTGDYPVEFHVSCTRDTMYRDRGDNLADSVSAR
TGIGLGRKDSTCVVLVNGSQDSPKFCEWNVRIALNVVCHEIFEQSDIDGSSGKALPDQTHRDAFLLRTMRYLKRNNKAKN
IGRSDGGVELSERLSWLRVRTTLGKLFSSIRYQSRCPFQQIFLCEIHYVLED
```

203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE
208 - 227:	EEEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEEE

A0A0N0U3H9 **A0A0N0U3H9_9HYME** (2835 aa)
Uncharacterized protein. *Melipona quadrifasciata*

```
MARGLLLFVAVKVSLCPRSCNGVKVTQPDSLIHRLKQRNQVVVLLSSIDVNAEKDSKDDVDLNERKENNETTIVASIKIN
DDSFRNRTNKVRENQLGKIRAPLNNGSRQNVSRELVLPKSVDIARVISDDSTGDEEGLEELPEASAKKFIMPSLRKRPSY
RPPPRRPSSLNRRNVYADLSRTPLIRPPRRPTEAKRDPTEKECTFFTKTVCLEAADYPHDAIARSLRSNKEMVTALLTDY
KSQDFDDSGESPPIALPLENKYENRYESNEIRRRSDMSSSFENVEEGFTCPSVIKYARPQLARAASGIWKYIINTGEHTQ
TLRLEKCSLLAWDNKLGLHMDIFKVPSCCSCHVHGYAEIFPPHQKDPPSRVKESFPGSDFATSEQKDDYEDSSKLNYLHK
YTFDSSLGSSNKKPVIESTPSRPPFVLPVRTRPKKPSSTSSRPFDKLPQQHAPNTRAPGYTGPLLKGSRPSRPNRPPYRR
ESISHIEEQTEAANSTILNRYSQPYDLEMDATSRLQNGGFDDEYQEPQRRVNYNYHPIIDFFRPEAMMLQSSEASPTSDQ
NNSNSWKPGCLTPTEVLQPQSWAGAIANTLRSKEEEEEEEEEEEEEEEEEEEEEEEEEGEPEGPPDHAIPYSEHEEPRNVPT
KPKYTGPGEWARPPKGKEDRSEFVPTKVYAQVRRTHTLRKLPRKKAIQNAESEEERKNAARLRAVVRNTKVNTVYTEEGY
EDSAYDHAGHARDADFHEGYARKLHDHLDLKKKAGDGDRDDQAEENETKNEKYEMIEPEEFEEFDEDNDDYGSSTASKIS
DNVLVNPKLVVEKGVEELQDDLEREAEEMEKGIEISKLGKAQTVKERSDGEILAESRKRDGKVGRRRKTKRRKSSSSDEN
VENTTAVSMDENVISTDRGVETTTVNENLENLPKGSLYKYEVDDSQDPTTVSYGQVFWDYFKTRQDPLTATESPLTLEST
TLSQAHVQSYFVHEETTTSLPTIGPEILRTQEVTPDGISMDSEYSKNSGQNSESLLDSTDLDELWRSINSNEQLKTETYS
DQGIPSSNFQNNLGNDEAFEQNFGTSLFSPALDSANNRKLRYKITVRHKPKEPEKPSNPEIQSSSREPSTSNVISRPSKL
IETASKEPLLLNENYMKVLMHVRNEKNSKNSHHPNSLHRYNLQRNNHFSSGGSKNDLEDLTRMRPPLPQTAPDYYYYNNF
VARNKPEIDLTAHFNRISFPVSQNYRRAYANPRTYQIYLDMPQTRQLPTSWQKNAKLSFDFARSAPPLPRNDPTRQKEPI
DYVNGGGNRWKQGRNFSQTTNRGIRAKRRERRFVDDDESGVARGCSVPANNGTSNRGETEVAAKNLSSAGRNCRQKVTRL
LQVGLGLDTSQAKRKKSRYRGNDHVGEGSRAVERESTTANEKFQLGEREEKDSTVNNKLKEHEKLFDTTEKKEKEYIINT
IRRREKKDVGKEDSKKHAELLDEAPKIAEDVINEEINARFNKDGQTNRQKENEEKEDDNEEQVEVEIPGFDYVEELAEEG
QAEDHTATTEATIDPEKYPFYNNEKMPIPSALKYAIDPQRLPAKTYGAMEFYNSRDAYKQCDEIEPNLKVLPEKEEPVAD
```

```
KGPETNVPRLTGLGDKLDCYKAKYFDENPFDNPLFLEKQVEEPVAPAEIDSKQFASRIMMFPKEDDDHVTQKSSRRPENY
RQPRKQASTPVVLQKRRRIRYKTYPRTSQQVRIRKRPQSYVVQNSRIKYAKNPRRNPLKVEKRPVASASEVSLIKLSDSV
PYQSQVYEDVMGTIKNLANSYQVYEITTIPASEGIATVNGTVNEVKTNSSTNSTSSKKKERNNASKDIVDRPNNVKVGIN
IKGFVPSNNYQNRYRMYKRPRAPQNGRLRVQPMQKPVAGVRTVKRRRKIRIYKRDLSLNSTHDGKLPVASIELDSRSDRM
EKKDEMRGKLSNSEEEKPRKAVYTIQDRIRYSRPKGDVWKVGKFSNKTEAEVDKRRKEPKYSYIRRKSSSNPVLITAQSF
SPSLTNRTNWTESATTTEKVIELDSETVGKENREVEYKIGETEDGRLNAPENFNDTKQDLIGRSNEEIVNKTEAGYAVYE
NVNEGEATTTQKPQLSTSSAFFDLKTFLDGDPPEHAELSNENFEKSSSLNDNSNVTLSSVNSSESQEEKESKTGEGNDED
VSTTFPQSYYFDEDSSSKTKEKARSSTESSEESSVASKEIESGEQRPFFSYSSRPSSPAENYEDERYSELGPRVNKPAFY
HPPFFNYKRSRESSEEMQGSNEGKEEHVFPWYRDEEDERKRRRRRYRGRANGRYEYPWEKRERLEREERRRTEEKRKGFD
EEEEAEEASAAKYRRNIYPRGRLRFWGRLDSDTLEDSTSDNVESSSEYRPTTRYSSRYSSGNVKLAVDEKSRSAEEIGRS
VKKTLEDGSEEKGTLEGKETTSEKKEPAASYKSRGISRGTIVSEDERKREKSVDNSSTSISPRNRNSSDSAASTLDDDTE
SRVTVIEGPRGIENSTKQEKTIKKKRRPLKNAVSKKSVSWTNRARQRQKPSSTTPAAVQSTFSVATTTPAPRFVRRRIQK
AKDSRRKNYVLNNSGSGTNGTSETGAVGQSSRGRKGSRTNEILADVKSPAKSHRDQELSVKSLTKQENLTANSDRGKGPE
SETVEERFVDDDVKRSKEAEEVKRTFPPVSNDERFEFKDDRIETSSEFDKIDNDYEMDGDFTPQNRALQLREQSSREITS
SIILLSVGLLNLSTAAPDSAGIVEMVNGLAYGGIPYGSVTGMVAKYPGFTGQQFNSNQARQLNQFRNEVPLIVNPNFRAT
RLVGTQSQSVQIYKDSGVLGSVNYIGYYAPLVAKS
```

594 - 613:	EEEEEEEEEEEEEEEEEEEE
595 - 614:	EEEEEEEEEEEEEEEEEEEE
596 - 615:	EEEEEEEEEEEEEEEEEEEE
597 - 616:	EEEEEEEEEEEEEEEEEEEE

A0A0N0U471 **A0A0N0U471_9HYME** (742 aa)
Homeobox protein ARX. *Melipona quadrifasciata*

```
MAQLYPYMRRNNAAKRFVLEKCGSNPFTLGCRSFVLQTDMVERRLAIARGGGGGGGVSSGDRCLGLTAGVFSHALDRRPG
CIALTSRDALSYVPTVSLLIKTISKNGRSSSQRFFELTDLSIEDRLRKLSRDSATGKGGKRRRCRPAISMAQTYNQKRNV
YSIDQILGHGKEDDHATSSDAIGDAGDGELGHLSDHQINDALHDPLNLGESDRLNLGESDRPRKVRRSRTTFTTYQLHEL
EKAFGNTQYPDVFTREELAMRLDLSEARVQVWFQNRRAKWRKKEKVLGRDTSFMHEQSGVNELSLHARLLQTAGGVPGAD
PSGGPTGAFPWFIPPVFPPPWPASAPKLPPLHAILSQYIGLPLPQNLASLSTVLPVGLNPASTLNHNNVNGHTLGSHIPG
HPLNLGVQSLPQNLSSKHDKEEDSASSDDEIRRQSAEVLRVKAEEVLRKMLKIEWCVLEKEQEHVRRSSDRWNTIVQTNK
ARTGQAANNGGKKVEERRKKGGGKEEEEEEEEEEEEEEEEEEEEEEEEEEEKMEPITGKFLVRVFPKLQWNRPTSDRSAI
HSILFLLSNTRERARNQVNVEKQGYSNCTKKLCIEILPNLIRWTDHPESERRLPDNHALRRFLFLVIVAGHWLFAKSTET
FGLRCLSEVYDYQTIMLITGRKFLPERGIVQLGDPVDVEGKRGLNRTQDAGTGRYKAEIIQSTYENPAAFLVKEIPTDSD
NDKKYGSKLDSELSFSYFCKRN
```

505 - 524:	EEEEEEEEEEEEEEEEEEEE
506 - 525:	EEEEEEEEEEEEEEEEEEEE
507 - 526:	EEEEEEEEEEEEEEEEEEEE
508 - 527:	EEEEEEEEEEEEEEEEEEEE
509 - 528:	EEEEEEEEEEEEEEEEEEEE
510 - 529:	EEEEEEEEEEEEEEEEEEEE
511 - 530:	EEEEEEEEEEEEEEEEEEEE
512 - 531:	EEEEEEEEEEEEEEEEEEEE

A0A0N0U479 **A0A0N0U479_9HYME** (1731 aa)
Uncharacterized protein. *Melipona quadrifasciata*

```
MARKSDNIKTINVAIVGLSGTEKDKGQVGVGKSCLCNRFMRSLNDDYNVDHISVLSQSDFSGRVVNNDHFLYWGEVTKTA
EDGTEYQFQVIEHTEFIDDASFQPFKGGKMEPYAKRCAATKITSAEKLMYICKNQLGIEKEYEQKVLPDGKLNIDGFLCV
FDVSVVPNRSIEKQIEIVANILNSLMKTKKPIVLVTTKNDDANEQYVKEAEKLIMRKEYKGSILIVETSAHENINIDLAF
MILAQLIDKTKMRSKVTPFAEAARARKELLDASTESLQRLIRVHVTDYRALWSQASKKLAQHKEFSTFVELFGIDATQRL
FRRHIKKLKDEQVAKKIQGYLDMLPDILHEICPDVTNLINEEWSAVQQYIKEHPDFHQYFYECPEDIPWIDCDFGENNET
KIPYDVLETPDVETVFKNHINILQQEQRRLELPKRWKKQFKQLLEEAGYVTPGKHLSEVRVLFMGRECFEALSHHDCQEI
YDQHQKEIIENAKHSFQELLLEHADLFYHFKSIAPTGTITQDDIKEITDALVDDFRYKTLDRLDQDRKLMLFQHLGFVHC
PIREHCPAYPNCMDALIERILGTKAHRPSSWNHSSQWQLTSDNNQLNLVILGSSGLGEEFAREIRAQTEDDEVEIDCQLY
TLGYRIIDGDVGLPHNSFTTSDFMPHGSFCIYADDYSFEYIRSSLEKTLLSNLEQEDRLPFQGLPIVIMFVPESTIDEME
AIRLRKEGQNLADSLQCPFIDVCIEDLEQDKRFPAPLVKDALQQLIQSINHRAGFLNIYQSVIECLEPDIRIIMCMFCGD
PYSVENVLGPLLNHQCCFLSGDRSIVLETFLGESKRRVEVIISSFHGANAFRDELVHGFILVYSTKRKASLATLNAFSMN
IPNLPIQIMAVTDTGGANAFFSNDLSHLLITEGNAIADKLQAHFMTSASSCQQKKPGNLNDSGEGTLEYSALHPMPPPRH
ESYHLQTPDDGSGSESYEQLTPDGDLGDTGLNEQFADNRATPSDDSDIYSQVEFYREERERDLLKPGDIANKLSGWVKDT
FMHQDGVTNSYSHRAFTTGRRHISQTKPRPQGNSQTLKQPGKINLKDFSNVTDAIARMTVGEKDEHGPKITMGHAPLATP
ELVDLGSEYAQVKDVVPSLYPSYDGDYMYASVQDSIGNSKPKLRHRREKGQPSYSDSDSEWSSLERQRVADVLGKVNKKP
PSHKRIRKKRTAIPVAAPKVPSLASMGSGDGIVGLNYNVKEDKNWRINLTERVSSESPDSSESSDPEHSRSRAKQYKHAA
ASLRKRFGNSLPQQHLPTSLQHPYNVKHMTQEMFSASLKQRSDIMFGNIPDDESSLDVSSPREINSPSVKDGDKLNRKKD
KQKAKEDEKLEKRRQKEEKLKKHAEKEKEREKKKQEKIKQTKGVTPALSMSQQPLIEDFAQSEKNRIPLFLEKCVQFIED
EGLDSEGIYRVPGNRAHVELLFQKFEEDENVDIHSLDIPVNAVATALKDFVSKRLPPLIDTERMSELEDISGAHGISKPM
SATCMNMEDRSCRLLALRLMLNKLKQVNFNVLKFIFHHFVKVAENCKLNSMDSKNLAICWWPTLLPIEFNDLTIFEAMRP
YLEDLVQTMIDQYPFLFCGEEAIVMVTSGFVEREFDEVHVPSANEYVARKRIEEEEEEEEEEKEEEEEEEEEEEEEEEE
EEEEKEEKEEEEEEEEEKEEEEKEEEEGGEEEERKKERRRRKKERKKERKK
```

1664 - 1683:	EEEEEEEEEEEEEEEEEEEE
1665 - 1684:	EEEEEEEEEEEEEEEEEEEE

A0A0N0U4Y8 **A0A0N0U4Y8_9HYME** (618 aa)
Uncharacterized protein. *Melipona quadrifasciata*

```
MCLICSSIDIQGRLRPVYQSSPGYALARRYRTSGNSNTSIDKTAMHRGEEKARVFQAGKPVISQRSCLMKSAKASKNFTT
```

```
KWQRMFHCTPEARDILVVLLATEIRSLPPSRLAHRAGNTNRDQVFASRQVDRNVCFKYEFVISTLVSLRIHPSNQLFLLF
QSHGVNWLGNADDNSTAYDTDTYIVQSYRRTTFRNGREFFTLCREMGYATSIIGCFEEILNGTSGVSSALNRGKYTTITW
QQHRRIYRRCVTSLERRVPLLFLEFTRTLITVRLEGRRNNEHWVQLNSGSQNILAVKCDDHEVKKGPCHQLDTDVNNRNG
TEEEEEEEEEEEEEEEEEEEEEEEEEEEVEKEGKRLTATLELAFSEKPKLQVMGEKRNGNNSAIRGEEIGSEECAVKLG
MSEETAPFAWHIVDGQAHERFLPITSWPWRHCILGPHHENVYDAAWVVFPIQEVSEIGNKAIFGGIVSCNRGLFRRNADA
TKISDWLIWVTSSVGVAATPRDRLPGFMVQATPRVTSPSHLRCTTKDFREAAETLLFKEPYTIPGRQKDATAIRISSYFS
LACLLFSSLLFFFLHPLLHHHLCPLMVRVFERRVLSRELHFTSRRSESEESFDSSFDH
```

322 - 341:	EEEEEEEEEEEEEEEEEEEE
323 - 342:	EEEEEEEEEEEEEEEEEEEE
324 - 343:	EEEEEEEEEEEEEEEEEEEE
325 - 344:	EEEEEEEEEEEEEEEEEEEE
326 - 345:	EEEEEEEEEEEEEEEEEEEE
327 - 346:	EEEEEEEEEEEEEEEEEEEE
328 - 347:	EEEEEEEEEEEEEEEEEEEE
329 - 348:	EEEEEEEEEEEEEEEEEEEE
330 - 349:	EEEEEEEEEEEEEEEEEEEE

A0A0N0U547 **A0A0N0U547_9HYME** (1221 aa)
Toll-like receptor 4. *Melipona quadrifasciata*

```
MHRIPAGAAGIDIVNSNISKIRTGAFSKYSDSLTELNITGCGVEEIEPDAFTGLNKLRVLGLVNNKIRKIDASWIRGLSS
LKALILWRNRIVDIDPAIYDLLPELRVWDIAHNELRACLSPDMLRKLRNLRRILIADNPWSYKCRSSMTWYLGSNHIRFI
KDWSISDLLIEECLAHEPGAEEDDVVLEKCVDRRIGSADTLPYSVGELNEQVRELARKISGLQADVAALKKSKMYTFLFK
KNRGRVEICGKYLHRVDKAFDSFIRKLKCTADSYLGHAIFVVEIIDNDQRRCEAQRHKTQSSCQRDQKKELPFCNEVRLE
KATRKFCRFVIIRINLTAMIRTLALSLSRIIKRAGSQNEMEHLKGRRLLLLRRIVKLRSTDITDTADDVYERPNRALPKS
SDPKWIRTLLDGQISILGQPNEDEEEEEEEEEEEEEEEEEEEEEEEEKEEEEEEKEKENVEGDERRGGSEDGRRGYAFPP
CLPVTCIIYKDVETTFTVKQLIMLIEMNLLYLAMETKCGRQSLFSENCRDSDLMETTDRGLQKRKESSESGLSTRLMPYI
AERVSEAGEGGGRDGLGRDESGARVVEGILKCVKITSMSLVLPKLQIGRIEQKKQSILDINIEIIESAVLNAHQSPRDQP
QNLLYFVSSLEFDILSQTSESRWISDQVLFVIDCNRDSVYVHVNYSTKCRIFVKVKELNFQHHPYKFSFREQTAKKSFFT
LPSNHRRVSVSFVQFNAKLEKVFKLQMADVFLNFQQLHYILHQESQLLTPVKNSITVSGKCYNYHYLLLNNNEFVARLTI
IHTVALINIDIDTSVGENLENLENLEQKIKQNPHYYYLHDIIFITIHIQLKKLHDSYPKMREYTKTVCDAILTSLKKYYM
QEHANPSRGRANHLIGTEVIRTSNLQIGEYLNLPDLGTSNQRNSTFEPRSAATPTICTVVIRNTEETEETLRVGKPSENH
GQRYNIGNFHLLKFSVLSKEKKKKKKKFKILNFLEYLDNPDDLDIPGEPKINRPDIFGFSRISVRKRNDKRQQMENNADD
EKEVTLLRNSTWGLYGNWKPSVYTRWDFRMQFYSVSLFFLLERTGIEVTLENSTTGSESSTMNNGLAMQSQFKDKHERLL
KFKEQKDTAQHAYRLSKKRPSPIRTAGVQLLEFNRDNWPRGFRTVTGETSSISDIDHAIQGADLVLTIFHQVAAQNSTDF
SNVTATVVEKTRRRDVSNIIL
```

424 - 443:	EEEEEEEEEEEEEEEEEEEE
425 - 444:	EEEEEEEEEEEEEEEEEEEE
426 - 445:	EEEEEEEEEEEEEEEEEEEE
427 - 446:	EEEEEEEEEEEEEEEEEEEE
428 - 447:	EEEEEEEEEEEEEEEEEEEE

A0A0N0U5V5 **A0A0N0U5V5_9HYME** (131 aa)
Uncharacterized protein. *Melipona quadrifasciata*

```
MIDDRLISPRQSGKPWRLSNKLNLWNLEQNGTSDMSETFIPRERNEPVHQEEEEQEDEEEEEEEEEEEEEEEEEEEEETG
WLEERGQGNGGERVGKGARNKESGEQRPATTRNGRSTKGIRGGGEGIKRTS
```

58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE

A0A0N0U6P6 **A0A0N0U6P6_9HYME** (680 aa)
Uncharacterized protein. *Melipona quadrifasciata*

```
MGSCEANRVERCGWTYVRICICKAGISPVLIKISQFLVCLNFTDEQLLRQFLHIEQFLLTFYGHLLCSVGTFEELKSEKD
FDTTNTVDCTQRVLQISYKSVNTYSPSVNGGNLFFGKELKNSIVAISIQGKEGDGSCEGGEQDDEEEEEEEEEEEEEEEE
EEEEEEKVSEWKFYASIIGSFSIKSSITHTLEFELIITDFIQKEKLEIVRNETFLKRICHNIRSTLPYALCIYTYRDAHT
GYRAYRSFEWIGFPCPTEREGGTNRRFPPDVPRCSISQALIVEETRRLQEEARWMPWNSSGYYLIKAMVIVTAHSDECFE
IAKCRDFCAFKGTKFTEWMYKIVQSIQSGISVVTFNRSESSSTFSVLCARVYQRYGKQSSTSRKCEVTSGSCESRTQLEA
KVETRIQPCLAVEGTIEERGIAIQRARSMILILIQPLQKVSQECMIRREIFDTIQLKVRAKGCHILEGNCVINGTERNSN
AMCETSRIEAIACYALLRHRDYGSCIPTLTFVFIIDTIIQLYNKIVSTPIILFRSLGRKHRLLSEECVGSQLTERTPGSF
AWHFHRFAASRENMYLSTNTLGTDGSCLYKTAKVMLTRLLTLTARHCDTLSRGTTLYTSDIGVLERSTWWGNFDNGQAWA
ENWFRNLDEFSCARSTLIFAFEQFVPSLDGHFEVRKINLI
```

145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE

A0A0N0U6X1 **A0A0N0U6X1_9HYME** (1412 aa)

SNF-related serine/threonine-protein kinase. *Melipona quadrifasciata*

```
MNFCSSKFEETSEGRGELRSVCTVGEDSIETIEDLNFGCHAPPVNVTRCFGEFYDLQLEIGMMKFESTPWCSRSLDSQVR
KRSKEVARETAKEKEEEEEEEEEEEEEEEEEEEEEAEEEDDNDGTDQIFKQLLLWIYDRCLDRFVQLYLFRHEMHRRVGYS
NYDGKIAGLYDLEETLGRGHFAVVKLARHVFTGEKVAVKVIDKNKLDEVSRAHLFQEVRCMKLVQHPNVVRLYEVIDTQT
KLYLILELGDGGDLYDYIMRHDSGLSEEVARTYFRQIVRAISYCHRLHVVHRDLKPENVVFFEKLGTVKLTDFGFSNRFC
PGQKLETSCGSLAYSAPEILLGDSYDAPAVDVWSLGVILYMLVCGQAPFQEANDSETLTMIMDCKYSIPPHVSEGCKRLI
ARMLVREPEGRATLEEIAADPWLAIGPDSDPVEALPLVSRQQVSDDHHNHIITKMVNGNIATKEEILEALDKNEYNHITA
TYFLLAERKLRAHRQELMQNIRPEILEVSASRQDDAAANIRADQNSLSTINQSLLSVPRTPGDVSQNVRTRKCSIVQEEE
DEDDVSSCSGRDERGSNSTLNSFNRRGSRSEGKLSHILQERLSQLPEKTSHKPMSSQRNSQKDINVVSTVAEGEERLKSS
SPKSGNSDSSSPVQTMVRLQAGIQLADKVPAATMFDPISQENLKSRFDDGSSPVWSRRGGSSESRPKSVSDCLKSVGPVP
ANKWRMGSQHRSSVSSLDSSSAIGPSKSSESSATTTTTTTILTESSTVSIPLRPLTGLSDSLSLTPKYKTMPSPGSTGST
STPLNEILEDGDALPVSGSESSGSKCRVVRRTGYEQRKSKFHKTRTTSCSSSDASDDDSESRKKRAHKLSASASKSMSSR
RDSHDDSSDSQDPGSGGGGGGEGGGGGGGVGHGEHTTETPSSETSRKDHGSNTSTTTTTTTTTGGRHRCSENQAIFGRR
HRAGRRRTGETRLRESQSLNRITEVQEAEGPSSCHNHCHVSRNSTVLGVQSISSSSSSVSQSSTGSHGLPQTLSQAAATV
QKAKGFGARLLQSWSLSAGKSSSLSQPSNKQTNCNSNGGRCSGARQETQRNACQRIEMCDERELNGGSVNQIPSNDKENR
NGSMNRNDCKNRKIRLLSRLFAVKITMTTIWNRLSARIRDFNCLVLSSSARYYTVLVLVVRDRGTLLENSQEQTIRRSFV
RHLPELNETCGACQKSIADEKIEKAKRCNIVNINPSSTTVNIMENTACVLIRTAAWILGSLKGSISVFASIAKLTQDGDA
TNTAKLIKEKALPNLIQHFNGHRRVPDFSRINDDTVLLTFSPGYRNKISRSVSRLKLPCPKLCSRSFNGLELNKQASRRV
RQSRHEGAVPSTQQQEPKVRTQGSSRLEVSSDGDTEGDSAPVDEREESARSP
```

95 - 114:	EEEEEEEEEEEEEEEEEEEE

A0A0N4TVL5 **A0A0N4TVL5_BRUPA** (135 aa)
Uncharacterized protein. *Brugia pahangi (Filarial nematode worm)*

```
MKEKKLLKRREEEEEEEEEKEEEEEEEEEEEEEEEEEEEEEEEEKEEEEEEKEEEEEEEEEEEEEEEEEKEEEEEEKEEE
EEEEEEEEEEKEEEEEEEEEEKEEEEEEEEEEEEEEKEEEEEEKEEEEREEGEKEE
```

21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE

A0A0N4V7Z4 **A0A0N4V7Z4_ENTVE** (1895 aa)
Protein kinase domain-containing protein. *Enterobius vermicularis (Human pinworm)*

```
MQFQAILSPLFRRGDMTIGVAGGSRAASRNSRSAKFSTSKLLNNQYGSSSATSGSQLGGQPLNGPAPGSSSGRGDIKHRF
EIIKKLGSGTYGKVSLAYDHKTEREVAVKLIRKSAIENKQDLVRIRREIRIMSALKHPNIIQIYEVFENKDKIILVMEYA
SGGELYDYVSTYGSLPEAEARRIFRQITSAVLYCHKHKVAHRDLKLENILLDADNNAKIADFGLSNYFSDKSLLSTFCGS
PLYASPEIINGTPYRGPEVDCWSLGILLYTLVYGSMPFDGRDFNRMVRQIKRGAYFEPDTPSTASMLIRNMLRVNPERRA
DIDDIASHWWLNLEENMPVIQELPENQIIDHTPLTERAETMVVQDLADETDVFMDFGHLSANTRKKIEEFRRRRIEAEEY
NESSPIKPPKTRKTDGRDSKKELTSIEKSLRHDVPPKQEEPKPTFEELKNRFADPLERLKQLENRLQTGALGDKGITSLP
TTVLEQVESGPVSMNLIARIKNHPYYESRQMVKELLESIIAAQPPAVQEQATKVIQQHSQDLLQKQQLNASTKKEVEAEE
KKTKKNESAESGTTVTANVRAQKPEAGAKELTKPQQRTMFEGRTWHSVEVGFDPDEDMETGQDSRRQSVNTDATEETVQD
TSFEDESEEELQFTKTERKSQEEKTATPDATNDERAGRQTTETGNEVINKVKKPDHDDEGDEEEEEEGEEEDEAEDEEEE
EEEEEEEAVGEYHAQIDALGKEVEQVEEDEDNTSFASAVSHVNSEPNPPPDPPSQSNGSQFLEPFDRGLIKRQSKGKYQH
SKVEHYGRGVSTECESPTFMHRRIGGPQPTIERSPFLFDKLIQIGKNNVDCVKKLFKYTFATVKLYIMTYPKYLDDSDDE
FPEKFSKKNKEKKMNWLKTQDPDVPESSVENQPESSNPSASLDKFSSARSQAVGGTKSEDEEVSGSEGEEEEEEEEEEEE
EEEEEEEEEEEEEEEEVVEAEAGKKDKENKRDSDQKKAGSSSSSRKEDIDRKDEKFHVQPALSAPNSRDITNTSLTFPPN
ATTIGQATVSIVLKTPPPKRNSVISAMQSAPASIHNTPSPEPNNTVQVATSSTEDSKPYVHVGDLKVSDSKPDRLQTSVV
PLNFGGNIAVTKSALERKATEREARRYIPHHAENERFYPRSPSPATVTQDKHDVAGETGIQAWESAASYIRRRNRERRLR
NRTIGTPEDVLRNVMEYRDYASNAGAGLNANKERSSVSEAAPSNEDPNLPARATSPLSGITLRNLGTTDPFYHHTRPVSI
ASTKDSVISGNPAGSLFNFVRPRYHDESYRRRDIENEPPSPSRFNLENNQTTLSHTDKNKSKSIHDLTPDRPESTVTTTA
HTSPWYGTGTTHHYGARYENEPVSSYIGSSFQPESKRFHVYQTRAEREAERNAALSNLHPPSTFRTGSAWYTGNDRPLTS
YTPGSYRSRFDDNFIYRRSAYDVERPTTPTPIGESTNSGTTAASSSTQPPHDRGGGGVGGLFSRFRPVARRVASAVGNSE
RRNSRSQSMDRKTSATEDNEYRANLRNRLVTPEVTTDRAEYSYINYYDTSSNAGSVPREPDQTRMPSRGILKNKQSADLE
PRAATTPISENGRGLVGGKDRSPATSGVKNMLDRLKRRLSTEKSLSPAPQEPLGHIHTQQGSSVGLRHRFGLGTGLGNSR
EGFHGPNELAYSNFNEGRKTPAKVEEAKVKKRSFLNLGRRKTAEISIGADGKIVTSGVDDDLKRPSSPIEKIKSFFRKSK
ENTSANDHGNNQSNVNTNNNINNKTINNNISVSNNPSTITSNSAYPHLRDYVRYSPVESQPSTTNRYGLTDKVFGVYPSS
NLSPIAARDSYASQYRKYTGSINGNVSKNLNRYSYTPGYGSDRPMRHWYEESHLY
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949 - 968:	EEEEEEEEEEEEEEEEEEEE
950 - 969:	EEEEEEEEEEEEEEEEEEEE
951 - 970:	EEEEEEEEEEEEEEEEEEEE
952 - 971:	EEEEEEEEEEEEEEEEEEEE
953 - 972:	EEEEEEEEEEEEEEEEEEEE
954 - 973:	EEEEEEEEEEEEEEEEEEEE
955 - 974:	EEEEEEEEEEEEEEEEEEEE
956 - 975:	EEEEEEEEEEEEEEEEEEEE
957 - 976:	EEEEEEEEEEEEEEEEEEEE

A0A0N5A803 **A0A0N5A803_9BILA** (2000 aa)
Protein kinase domain-containing protein. *Syphacia muris*

```
MTIGVAGSSRAASRNSRSTKFNASKLINNQYGSSSITSGSQLGGQPLSGPAPGSSSGRGEIKHRFEIIKKLGSGTYGKVS
```

```
LAYDHKTEREVAVKLIRKSAIENKQDLVRIRREIRIMSALKHPNIIQIYEVFENKDKIILVMEYASGGELYDYVSTYGSL
PEAEARRIFRQITSAVLYCHKHKVAHRDLKLENILMDANNNAKIADFGLSNYFSDKSLLSTFCGSPLYASPEIINGTPYR
GPEVDCWSLGILLYTLVYGSMPFDGRDFNRMVRQIKRGAYFEPDTPSTASMLIRNMLRVNPERRADIDDIASHWWLNLEE
NMPVIQELPENQIIDHTPLTEREETMVVQDLADETDVFMDFGHFSANTRKKIEEFRRRRIKAEEYNETSPIKPPKTRKTD
ENESKELTSHEKSLRSDSQSKKDEAKDSVKDMKSKFTDPLERLKQLENRLQTAGKDSAHGDRGISTLPTTAPANKEIHRF
KPPNIDDSKSTTTKSTRRPSYYAIPKRERYSPDQPDDPTTSSSRISQKANAVEESRKPAFVAVDTPAGSFSNTDLRNRRT
SVSAQKNWHIEADSLNMLMNQVLEQMESGHVSMNLIGRVKSHPFYDSRPMVKELLESIIAAQPASVQEHATKLIQQQSQE
LIEKQKSVSNSRKLEADFSETKPPKVNQDNKTRAISSSEFQRREGASKESAKSQPRTLFEGRTWHSVEVGFDPDEDMETG
QSSRRQSVHTEATEETVQDTSFEDETEEELEFIKADEKSREEKTTTPEVATTEKTIPLTATANLRVVATSNGADAEEEEE
EESEEEQEEEQEEEDDEKAGNEEAEEVEEFNVEIDELGKEVEQVEEEEEEEEEEEEEEEGEDNASFASAVSQLNNNQNPPP
DPLTPSTTSQFLEPFDRGLIKRQSKGKYQHSKVEHYGRGVSTECESPTFLHRRIGGPQPTIERSPFLFDKAKKYIMTYPK
YVDDSDDDLLEELKKKNSNKKMNWLKTQDPDVPESSAEKQTGYSNMSLSLEKFSSARSQPSGTKSEDEEVSDDGEDEESE
EEEGEEEEEEEQEKGGVGNGEVVEEEEEVGEEEEEEEEEEEEEEEEEEEEEGEEEEEEKEKEEEEEEEDEDEEGEEEEEE
GKKEETEEDDGVEEEGKASNGANKENNPAGAAPDAHSNRESQSRYDAAAKHSLLSTSKYYSQSPLSVSNSHDFTNANLTL
PPSSAQLNSSRRVTSVDRDDSKIYLNVGDVKVAEPKTDSHLQTPVVPLNFGGNVAVTKSALERKVTERDQGRYIPYSTES
DNVPRSPTPTTYGQEKLDLPTGTGIQAWESAASYIRRRNRERRLRNRTIGAPEDVLRSVMEYREYGSNAADLYNSANEPV
TSSDNQSLSASGRSSSPLLGLTTRPYGQTDTFYQHSRPSAATNETATSNSNGTGSLFNFVRPRYHDESYRKRDVENETSL
SLTHFSLENPQTTLTYNDKNKSKSVHDLAPDRLESTAVGLGYSSPWYGTGTAHHYGNHYENDPPSSYALSSVQPDNKRFH
VYQTRAEREAERMAALSNFHPTPTYRTGSTWYSSDRPFTSYTPGSYRSRYDDNFMYRRSAYDVERPTTPTPIGESTNTNL
TANGTNQQSHDRGGNGVSGLLSRFRPVARRVASVTGDSERRSARSQSMDRKISAPDDLEYHYRNRIASPEPDRSEYSYIN
YHDTSLAPSSTLREPDQTRLPSRGILKNKQSAEFEPRGATTSVSENGRGLVGGKDRSPTTSGVKYMLDRLKRRLSTEKSL
SPAPQEPLHHIHTQHGSSAGHRHRFGMGTALENSRDGFQGSNEFSYVNFDDGRKVLSKPEETKAKKRSFLNLGRRKTAEI
SMGADGKIVTTGIDDDIKRPSSPIERIKSFFRKSRDPATTNVNGASNVNNHMNGNAVAANSPTVTSASAYPVGRDYARYS
PVESQASSTNKYGLTDKVLGAYPLSNLSPIAARESYGAQYRKYPGGINSNVSKELHRFSYTPGYATDRPIRHWYEESHLY
```

1071 - 1090:	EEEEEEEEEEEEEEEEEEEE
1072 - 1091:	EEEEEEEEEEEEEEEEEEEE

A0A0N5A8V1 **A0A0N5A8V1_9BILA** (419 aa)
Uncharacterized protein. *Syphacia muris*

```
MSPLESRNDRALKDYGNSQDEKPVKKKWTLEQLRGGHTFLSLQAGTNKFDSQKGMTAPGMPRWNITKDKHLGFIEPDRKS
EEVLRVQCGTNQYASQKGLTPIGANRFQVPKVVYKKDWETVLDKEGEKIMPKQAGDFGLATQSGERSMGSHRNQVANIRG
RLPHDRRTHGVLCYQYGTNLFASQTGMSAPPGVGAVRQATMEIEGLGFSEDSMRKGTAITPWYSGQNKFANQAGTGGFMK
VRDVLPHSKGGKDIDEDLRRKSEGIVPLQSGTNRLASQRGMTGFGTPRNTMLKQGWKKEWIEEYEQALKEWEETRPPGSA
SSVDPFGHYKQKFEERQQAKSENGESNEKSDEKADENNDEEKENEEAKEEEEEEEKEEETKEEEEEEGKEEEAEEEEEEE
EEEEEEEEEEEEEEEEEEE
```

394 - 413:	EEEEEEEEEEEEEEEEEEEE
395 - 414:	EEEEEEEEEEEEEEEEEEEE
396 - 415:	EEEEEEEEEEEEEEEEEEEE
397 - 416:	EEEEEEEEEEEEEEEEEEEE
398 - 417:	EEEEEEEEEEEEEEEEEEEE
399 - 418:	EEEEEEEEEEEEEEEEEEEE
400 - 419:	EEEEEEEEEEEEEEEEEEEE

A0A0N8NZW2 **A0A0N8NZW2_DROAN** (397 aa)
Uncharacterized protein, isoform I. *Drosophila ananassae (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAK
RKISRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKEAGVLGLSS
AAMERNKTKEQLEEEKKISLSFRIKPLAIEGFGESKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQL
RHKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYNTVYAENLEKTWQERQERFTQRTKSKLPKWFG
ERPGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE

A0A0P0VL97 **A0A0P0VL97_ORYSJ** (177 aa)
Os02g0602300 protein. *Oryza sativa subsp. japonica (Rice)*

```
MQAKESKKSRDRGRDRVKWNEENLNDIESTKPVREKITEPKTPYHSMIDEDDGTVSPKRTIEESVDKSTHADAIKTALME
AVSSGKLSAREHLESCSNEEEEEEEEEEEEEEEEEEEEEEQEEEEEEEEEEEEEEEEEEVAIKQGTDFEEQRKAHYDEFR
KMKELRRRGTPSQEGDE
```

99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE

A0A0P8XKX7 **A0A0P8XKX7_DROAN** (394 aa)
Uncharacterized protein, isoform C. *Drosophila ananassae (Fruit fly)*

```
MKSTPPRRRRLSRRPVRRRKKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAKRKI
SRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKEAGVLGLSSAAM
ERNKTKEQLEEEKKISLSFRIKPLAIEGFGESKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHK
ALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDEISKDVNEKIWNEKKEQYTGRQKSKLPKWFGERP
GKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE

A0A0P8XKX8 **A0A0P8XKX8_DROAN** (395 aa)
Uncharacterized protein, isoform F. *Drosophila ananassae (Fruit fly)*

```
MKSTPAPRRRRLSRRPVRRRKKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAKRK
ISRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKEAGVLGLSSAA
MERNKTKEQLEEEKKISLSFRIKPLAIEGFGESKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRH
KALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDEISKDVNEKIWNEKKEQYTGRQKSKLPKWFGER
PGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE

A0A0P8XKY8 **A0A0P8XKY8_DROAN** (374 aa)
Uncharacterized protein, isoform L. *Drosophila ananassae (Fruit fly)*

```
MSDDEEYTGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAKRKISRAEEEQKMAQRKKEEEERR
VREAEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKEAGVLGLSSAAMERNKTKEQLEEEKKISLSFR
IKPLAIEGFGESKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQ
VASKYERRVDTRSYDDKKKLFEGGYNTVYAENLEKTWQERQERFTQRTKSKLPKWFGERPGKKAGEPETPEGEEDAKADE
DIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE

347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE

A0A0P8XKZ3 **A0A0P8XKZ3_DROAN** (388 aa)
Uncharacterized protein, isoform E. *Drosophila ananassae (Fruit fly)*

```
MSDDEEYTSEEEEVVEETREETGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAKRKISRAEEE
QKMAQRKKEEEERRVREAEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKEAGVLGLSSAAMERNKTK
EQLEEEKKISLSFRIKPLAIEGFGESKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGL
DPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDEISKDVNEKIWNEKKEQYTGRQKSKLPKWFGERPGKKAGE
PETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE

A0A0P8XL01 **A0A0P8XL01_DROAN** (374 aa)
Uncharacterized protein, isoform N. *Drosophila ananassae (Fruit fly)*

```
MSDDEEYTGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAKRKISRAEEEQKMAQRKKEEEERR
VREAEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKEAGVLGLSSAAMERNKTKEQLEEEKKISLSFR
IKPLAIEGFGESKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQ
VASKYERRVDTRSYDDKKKLFEGGWDEISKDVNEKIWNEKKEQYTGRQKSKLPKWFGERPGKKAGEPETPEGEEDAKADE
DIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE

A0A0P8Y0W7 **A0A0P8Y0W7_DROAN** (373 aa)
Uncharacterized protein, isoform B. *Drosophila ananassae (Fruit fly)*

```
MSDDEEYTGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAKRKISRAEEEQKMAQRKKEEEERR
VREAEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKEAGLGLSSAAMERNKTKEQLEEEKKISLSFRI
KPLAIEGFGESKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQV
ASKYERRVDTRSYDDKKKLFEGGWDEISKDVNEKIWNEKKEQYTGRQKSKLPKWFGERPGKKAGEPETPEGEEDAKADED
IVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

344 - 363:	EEEEEEEEEEEEEEEEEEEE

345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE

A0A0P8Y0X5 **A0A0P8Y0X5_DROAN** (394 aa)
Uncharacterized protein, isoform K. *Drosophila ananassae (Fruit fly)*

```
MKSTPAPRRRRLSRRPVRRRKKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAKRK
ISRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKEAGLGLSSAAM
ERNKTKEQLEEEKKISLSFRIKPLAIEGFGESKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHK
ALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDEISKDVNEKIWNEKKEQYTGRQKSKLPKWFGERP
GKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE

A0A0P8Y899 **A0A0P8Y899_DROAN** (373 aa)
Uncharacterized protein, isoform G. *Drosophila ananassae (Fruit fly)*

```
MSDDEEYTGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAKRKISRAEEEQKMAQRKKEEEERR
VREAEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKEAGLGLSSAAMERNKTKEQLEEEKKISLSFRI
KPLAIEGFGESKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQV
ASKYERRVDTRSYDDKKKLFEGGYNTVYAENLEKTWQERQERFTQRTKSKLPKWFGERPGKKAGEPETPEGEEDAKADED
IVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE

A0A0P8ZKV1 **A0A0P8ZKV1_DROAN** (388 aa)
Uncharacterized protein, isoform J. *Drosophila ananassae (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAKRKISRAEE
EQKMAQRKKEEEERRVREAEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKEAGLGLSSAAMERNKTK
EQLEEEKKISLSFRIKPLAIEGFGESKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGL
DPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYNTVYAENLEKTWQERQERFTQRTKSKLPKWFGERPGKKAGE
PETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE

A0A0P9AAY7 **A0A0P9AAY7_DROAN** (397 aa)
Uncharacterized protein, isoform D. *Drosophila ananassae (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAK
RKISRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKEAGVLGLSS
AAMERNKTKEQLEEEKKISLSFRIKPLAIEGFGESKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQL
RHKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDEISKDVNEKIWNEKKEQYTGRQKSKLPKWFG
ERPGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE

A0A0P9AAZ6 **A0A0P9AAZ6_DROAN** (389 aa)
Uncharacterized protein, isoform M. *Drosophila ananassae (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAKRKISRAEE
EQKMAQRKKEEEERRVREAEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKEAGVLGLSSAAMERNKT
KEQLEEEKKISLSFRIKPLAIEGFGESKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKG
LDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDEISKDVNEKIWNEKKEQYTGRQKSKLPKWFGERPGKKAG
EPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE

A0A0P9BVD4 **A0A0P9BVD4_DROAN** (396 aa)
Uncharacterized protein, isoform H. *Drosophila ananassae (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAK
RKISRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKEAGLGLSSA
AMERNKTKEQLEEEKKISLSFRIKPLAIEGFGESKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLR
HKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYNTVYAENLEKTWQERQERFTQRTKSKLPKWFGE
RPGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE

A0A0Q2LBC0 **A0A0Q2LBC0_XYLFS** (149 aa)
Uncharacterized protein. *Xylella fastidiosa*

```
MLSMTITVNAETPATLKALLADLIPAIADSGAPLQTVATTQRIRRKLTKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEIKITRNRALAALSETASTFGKKEAKRVLARFNADNVEGVHKKDLNALIEQCKQCFIANGCEHAWVDV
```

50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE

A0A0Q3JPT5 **A0A0Q3JPT5_BRADI** (1415 aa)
Uncharacterized protein. *Brachypodium distachyon (Purple false brome) (Trachynia distachya)*

```
MPPAADFPASKRKSRIEIPDSDDDADRRRESRSSVGTGGQRERSAEAGRSGGLERRLAAAIARRRTRAAAASRPEVVNLT
GDDDDDIRDEEAAGRREVLGRVKEEPLDDRGLDPEASVARRGRGRGRARAAAASAPVASRKRRREDDSGSRGRGGRRATR
SAKQCTRGRRGGLRSLPSRPSSSDEPLGDSGRAKRVRRGHAEGGGSGRHGAAPSKQAGSLVASSSRSRKGKQRAALPPKH
QFPLVSQSESSSESDDDDDDEEGDDGLDDVCSETSDESWQPRYNSEFQVAMKGEKKVEGRRNSVEEEATEKELGENGNGI
PVLEEAAEKELRENGNSIPVQEEAAEKELGENGNSIPVLEEAAEKELRENGKSIPVEEEAAEKELGENGNSIQDDRYDGE
DEEATDDAHAAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEQDDESDEAGEELHPVPNSNADAGGNARSGGEG
TPIGKRVFEGLCLVDNADNAVTTKSIRQRTRSNFKDRACLDKKLLGQGTCSKPYCIDTESEEDVPPPPQPQPSSAECEDD
GSGGDDRMPAKRRRGKEQITDSDDTQNDSEDSDENRTLARNARKGSSSRRPKNGASYQQNVKEGSRNYDSPSNPRHVKNY
AANAGNPTDRFNMQSGDICFNTNTLLPQRMKHGRVWTKQDTDNLLNSLLDEIENGSAPAQAQNEDRLPLVFSFGDEDQVE
EQSDHNKLQDELWAEMDFCMESTNVCPQSCEEGEKSNNGQEKPGDKATLCSQGKHDLVTDEQIGVWCRRCNFIQLEIRHV
VADMGKVSTERELRADRQLDLSINNLLTSMGYEGTCKIVDHKAGSVWDLIPGVKEGLFTYQAAAVEFMWKNLAGGTKIQD
VKNNINSDDLRGCWISHAPGTGKTRSTIAFLQSYRVLFPRSCVLIIAPKAMLATWQDEIGKWNAKVPIHVYSSCDINWGG
DETIKRIVDNDEDFAQRLSVNKFGPKVRKVLKVRSWCEGSSVLGMSYEMFSKLAKQNSNDETMRKLLLEKTDLLILDEGH
KPRNKKSIIWKVLAEVRTKKRIILSGTPFQNNFEELYNVLCLLQGTCDADSKLLGKDEDKGFWTSMSVDNITDERVNEIR
DKLKPFLHIYNGEFLQKSLPGLRESVVILNPFPHQKKIIKMLEDSRTKSGTNGHLDFEYKISLASVHPSLITSTQKLPYQ
LTSVMDKPLLESLRLNPCEGVKTKFVFEIVRLCQPLKERVLVFSQYLQPLDLIMQQLRSEFLWTKDKEILSMSGDDDAET
RQKLMNDFNNMESEAKVMLASTKACGEGITLIGASRVVLLDVVWNPSVGRQAIGRAFRIGQKKIVHTYNLIAEGTQEKSK
YDRQAQKDHMSKLLFSNETQPAECSKSPEFIVSSDKILEKMTEDTNLKTMFANIL
```

412 - 431:	EEEEEEEEEEEEEEEEEEEE
413 - 432:	EEEEEEEEEEEEEEEEEEEE

414 - 433:	EEEEEEEEEEEEEEEEEEEE
415 - 434:	EEEEEEEEEEEEEEEEEEEE
416 - 435:	EEEEEEEEEEEEEEEEEEEE
417 - 436:	EEEEEEEEEEEEEEEEEEEE
418 - 437:	EEEEEEEEEEEEEEEEEEEE
419 - 438:	EEEEEEEEEEEEEEEEEEEE
420 - 439:	EEEEEEEEEEEEEEEEEEEE
421 - 440:	EEEEEEEEEEEEEEEEEEEE
422 - 441:	EEEEEEEEEEEEEEEEEEEE
423 - 442:	EEEEEEEEEEEEEEEEEEEE
424 - 443:	EEEEEEEEEEEEEEEEEEEE
425 - 444:	EEEEEEEEEEEEEEEEEEEE
426 - 445:	EEEEEEEEEEEEEEEEEEEE
427 - 446:	EEEEEEEEEEEEEEEEEEEE
428 - 447:	EEEEEEEEEEEEEEEEEEEE
429 - 448:	EEEEEEEEEEEEEEEEEEEE

A0A0Q3TIV5 **A0A0Q3TIV5_AMAAE** (159 aa)
Uncharacterized protein. *Amazona aestiva (Blue-fronted Amazon parrot)*

```
MKKQHTHCLGQHLTRSHHHMKKRRRRRRRKKKKKKEEEEEEEEEEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEERRRRT
RRRRRRGRRKGEEAEEEEKEEITWNDIAPPVVDEMIHKLHVFEDNLTPSIISTVEKLSQDLKQLRDNLSDLSSSSCLSY
```

51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE

A0A0Q9WCU6 **A0A0Q9WCU6_DROVI** (389 aa)
Up, isoform D. *Drosophila virilis (Fruit fly)*

```
MRNTLPKRRRLSRRPERRRKKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRAKEEDELKKLKEKQAKRKI
SRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKETGLGLSSAAME
RNKTKEQLEEEKKISLSFRIKPLAIEGLGEQKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKA
LKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDEITKDVNEKIWNEKKEQYTGRQKSKLPKWFGERPG
KKAGEPETPEGEEDAKADEDIVEDEDEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEE
```

364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE

A0A0Q9WCW4 **A0A0Q9WCW4_DROVI** (370 aa)
Up, isoform B. *Drosophila virilis (Fruit fly)*

```
MSDDEEYTGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRAKEEDELKKLKEKQAKRKISRAEEEQKMAQRKKEEEERR
VREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKETGVLGLSSAAMERNKTKEQLEEEKKISLSFR
IKPLAIEGLGEQKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQ
VASKYERRVDTRSYDDKKKLFEGGYNTVYAENLEKTWQEKQERFTQRTKSKLPKWFGERPGKKAGEPETPEGEEDAKADE
DIVEDEDEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEE
```

345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE

349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE

A0A0Q9WD96 **A0A0Q9WD96_DROVI** (390 aa)
Up, isoform E. *Drosophila virilis (Fruit fly)*

```
MRNTLPKRRRLSRRPERRRKKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRAKEEDELKKLKEKQAKRKI
SRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKETGVLGLSSAAM
ERNKTKEQLEEEKKISLSFRIKPLAIEGLGEQKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHK
ALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYNTVYAENLEKTWQEKQERFTQRTKSKLPKWFGERP
GKKAGEPETPEGEEDAKADEDIVEDEDEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEE
```

365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE

A0A0Q9WMQ1 **A0A0Q9WMQ1_DROMO** (370 aa)
Uncharacterized protein, isoform I. *Drosophila mojavensis (Fruit fly)*

```
MSDDEEYTGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRAKEEDELKKLKEKQAKRKISRAEEEQKMAQRKKEEEERR
VREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKETGVLGLSSAAMERNKTKEQLEEEKKISLSFR
IKPLAIEGFGEQKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQ
VASKYERRVDTRSYDDKKKLFEGGWDEISKDVNEKIWNEKKEQYTGRQKSKLPKWFGERPGKKAGEPETPEGEEDAKADE
DIVEDEDEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEE
```

345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE

A0A0Q9WMW9 **A0A0Q9WMW9_DROMO** (392 aa)
Uncharacterized protein, isoform F. *Drosophila mojavensis (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRAKEEDELKKLKEKQAK
RKISRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKETGLGLSSA
AMERNKTKEQLEEEKKISLSFRIKPLAIEGFGEQKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLR
HKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDEISKDVNEKIWNEKKEQYTGRQKSKLPKWFGE
RPGKKAGEPETPEGEEDAKADEDIVEDEDEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEE
```

367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE

A0A0Q9WMZ7 **A0A0Q9WMZ7_DROMO** (393 aa)
Uncharacterized protein, isoform E. *Drosophila mojavensis (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRAKEEDELKKLKEKQAK
RKISRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKETGVLGLSS
AAMERNKTKEQLEEEKKISLSFRIKPLAIEGFGEQKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQL
RHKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDEISKDVNEKIWNEKKEQYTGRQKSKLPKWFG
ERPGKKAGEPETPEGEEDAKADEDIVEDEDEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEE
```

368 - 387:	EEEEEEEEEEEEEEEEEEEE

369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE

A0A0Q9WN06 **A0A0Q9WN06_DROMO** (390 aa)
Uncharacterized protein, isoform G. *Drosophila mojavensis (Fruit fly)*

```
MRNTPVPKRRRLSRRPERRRKKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRAKEEDELKKLKEKQAKRK
ISRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKETGLGLSSAAM
ERNKTKEQLEEEKKISLSFRIKPLAIEGFGEQKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHK
ALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDEISKDVNEKIWNEKKEQYTGRQKSKLPKWFGERP
GKKAGEPETPEGEEDAKADEDIVEDEDEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEE
```

365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE

A0A0Q9WP92 **A0A0Q9WP92_DROMO** (391 aa)
Uncharacterized protein, isoform C. *Drosophila mojavensis (Fruit fly)*

```
MSDDEEYTSEEEEVVEETREETKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRAKEEDELKKLKEKQAKR
KISRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKETGLGLSSAA
MERNKTKEQLEEEKKISLSFRIKPLAIEGFGEQKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRH
KALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDEISKDVNEKIWNEKKEQYTGRQKSKLPKWFGER
PGKKAGEPETPEGEEDAKADEDIVEDEDEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE

A0A0Q9WRP3 **A0A0Q9WRP3_DROWI** (395 aa)
Uncharacterized protein, isoform H. *Drosophila willistoni (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAK
RKVTRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKEAGLGLSSA
AMERNKTKEQLEEEKKISLSFRIKPLAIEGFGESKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLR
HKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDEISKDSSEKIWNEKKEQYTGRQKSKLPKWFGE
RPGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE

A0A0Q9WRS4 **A0A0Q9WRS4_DROWI** (372 aa)

Uncharacterized protein, isoform C. *Drosophila willistoni (Fruit fly)*

```
MSDDEEYTGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAKRKVTRAEEEQKMAQRKKEEEERR
VREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKEAGLGLSSAAMERNKTKEQLEEEKKISLSFRI
KPLAIEGFGESKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQV
ASKYERRVDTRSYDDKKKLFEGGWDEISKDSSEKIWNEKKEQYTGRQKSKLPKWFGERPGKKAGEPETPEGEEDAKADED
IVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE

A0A0Q9WS07 **A0A0Q9WS07_DROWI** (372 aa)
Uncharacterized protein, isoform I. *Drosophila willistoni (Fruit fly)*

```
MSDDEEYTGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAKRKVTRAEEEQKMAQRKKEEEERR
VREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKEAGLGLSSAAMERNKTKEQLEEEKKISLSFRI
KPLAIEGFGESKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQV
ASKYERRVDTRSYDDKKKLFEGGYNTVYAETLEKTWQERQERFTQRSKSKLPKWFGERPGKKAGEPETPEGEEDAKADED
IVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE

A0A0Q9WS17 **A0A0Q9WS17_DROWI** (373 aa)
Uncharacterized protein, isoform J. *Drosophila willistoni (Fruit fly)*

```
MSDDEEYTGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAKRKVTRAEEEQKMAQRKKEEEERR
VREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKEAGVLGLSSAAMERNKTKEQLEEEKKISLSFR
IKPLAIEGFGESKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQ
VASKYERRVDTRSYDDKKKLFEGGYNTVYAETLEKTWQERQERFTQRSKSKLPKWFGERPGKKAGEPETPEGEEDAKADE
DIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE

A0A0Q9WSG9 **A0A0Q9WSG9_DROWI** (394 aa)
Uncharacterized protein, isoform B. *Drosophila willistoni (Fruit fly)*

```
MMKSTPAPRRRRLSRRPERRRKKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAKR
KVTRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKEAGLGLSSAA
```

```
MERNKTKEQLEEEKKISLSFRIKPLAIEGFGESKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRH
KALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDEISKDSSEKIWNEKKEQYTGRQKSKLPKWFGER
PGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE

A0A0Q9WTM9 **A0A0Q9WTM9_DROWI** (396 aa)
Uncharacterized protein, isoform F. *Drosophila willistoni (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAK
RKVTRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKEAGVLGLSS
AAMERNKTKEQLEEEKKISLSFRIKPLAIEGFGESKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQL
RHKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYNTVYAETLEKTWQERQERFTQRSKSKLPKWFG
ERPGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE

A0A0Q9WV15 **A0A0Q9WV15_DROMO** (369 aa)
Uncharacterized protein, isoform D. *Drosophila mojavensis (Fruit fly)*

```
MSDDEEYTGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRAKEEDELKKLKEKQAKRKISRAEEEQKMAQRKKEEEERR
VREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKETGLGLSSAAMERNKTKEQLEEEKKISLSFRI
KPLAIEGFGEQKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQV
ASKYERRVDTRSYDDKKKLFEGGYNTVYAENLEKSWQEKQERFTQRTKSKLPKWFGERPGKKAGEPETPEGEEDAKADED
IVEDEDEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE

A0A0Q9WYI4 **A0A0Q9WYI4_DROMO** (392 aa)
Uncharacterized protein, isoform H. *Drosophila mojavensis (Fruit fly)*

```
MSDDEEYTSEEEEVVEETREETKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRAKEEDELKKLKEKQAKR
KISRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKETGVLGLSSA
AMERNKTKEQLEEEKKISLSFRIKPLAIEGFGEQKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLR
HKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYNTVYAENLEKSWQEKQERFTQRTKSKLPKWFGE
RPGKKAGEPETPEGEEDAKADEDIVEDEDEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE

369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE

A0A0Q9WZ97 **A0A0Q9WZ97_DROWI** (373 aa)
Uncharacterized protein, isoform G. *Drosophila willistoni (Fruit fly)*

```
MSDDEEYTGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAKRKVTRAEEEQKMAQRKKEEEERR
VREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKEAGVLGLSSAAMERNKTKEQLEEEKKISLSFR
IKPLAIEGFGESKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQ
VASKYERRVDTRSYDDKKKLFEGGWDEISKDSSEKIWNEKKEQYTGRQKSKLPKWFGERPGKKAGEPETPEGEEDAKADE
DIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE

A0A0Q9WZZ2 **A0A0Q9WZZ2_DROMO** (369 aa)
Uncharacterized protein, isoform B. *Drosophila mojavensis (Fruit fly)*

```
MSDDEEYTGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRAKEEDELKKLKEKQAKRKISRAEEEQKMAQRKKEEEERR
VREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKETGLGLSSAAMERNKTKEQLEEEKKISLSFRI
KPLAIEGFGEQKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQV
ASKYERRVDTRSYDDKKKLFEGGWDEISKDVNEKIWNEKKEQYTGRQKSKLPKWFGERPGKKAGEPETPEGEEDAKADED
IVEDEDEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE

A0A0Q9X2B8 **A0A0Q9X2B8_DROWI** (394 aa)
Uncharacterized protein, isoform D. *Drosophila willistoni (Fruit fly)*

```
MSDDEEYTSEEEEVVEETREETKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAKR
KVTRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKEAGLGLSSAA
MERNKTKEQLEEEKKISLSFRIKPLAIEGFGESKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRH
KALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDEISKDSSEKIWNEKKEQYTGRQKSKLPKWFGER
PGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE

A0A0Q9X3R0 **A0A0Q9X3R0_DROWI** (396 aa)
Uncharacterized protein, isoform E. *Drosophila willistoni (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAK
RKVTRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKEAGVLGLSS
AAMERNKTKEQLEEEKKISLSFRIKPLAIEGFGESKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQL
RHKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDEISKDSSEKIWNEKKEQYTGRQKSKLPKWFG
ERPGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE

A0A0R0HYP5 **A0A0R0HYP5_SOYBN** (75 aa)
Uncharacterized protein. *Glycine max (Soybean) (Glycine hispida)*

```
MSFISSFFSAIRLCTKAQKTLGDKIKTRKKSQTHAKGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVLT
```

38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE

A0A0R1E9X7 **A0A0R1E9X7_DROYA** (394 aa)
Uncharacterized protein, isoform O. *Drosophila yakuba (Fruit fly)*

```
MKSTPPRRRRLSRRPARRRKKPPQTPAEGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAKRKV
TRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSSAAM
ERNKTKEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHK
ALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDEISKDSNEKIWNEKKEQYTGRQKSKLPKWFGERP
GKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE

374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE

A0A0R1E9Y4 **A0A0R1E9Y4_DROYA** (397 aa)
Uncharacterized protein, isoform G. *Drosophila yakuba (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETKPPQTPAEGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAK
RKVTRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSS
AAMERNKTKEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQL
RHKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDEISKDSNEKIWNEKKEQYTGRQKSKLPKWFG
ERPGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE

A0A0R1E9Y8 **A0A0R1E9Y8_DROYA** (388 aa)
Uncharacterized protein, isoform C. *Drosophila yakuba (Fruit fly)*

```
MSDDEEYTSEEEEVVEETREETGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAKRKVTRAEEE
QKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSSAAMERNKTK
EQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGL
DPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDEISKDSNEKIWNEKKEQYTGRQKSKLPKWFGERPGKKAGE
PETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE

A0A0R1E9Z2 **A0A0R1E9Z2_DROYA** (394 aa)
Uncharacterized protein, isoform M. *Drosophila yakuba (Fruit fly)*

```
MKSTPPRRRRLSRRPARRRKKPPQTPAEGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAKRKV
TRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSSAAM
ERNKTKEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHK
ALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYNTVYAETLEKTWQERQERFTQRTKSKLPKWFGERP
GKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE

373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE

A0A0R1EA04 **A0A0R1EA04_DROYA** (389 aa)
Uncharacterized protein, isoform S. *Drosophila yakuba (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAKRKVTRAEE
EQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSSAAMERNKT
KEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKG
LDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDEISKDSNEKIWNEKKEQYTGRQKSKLPKWFGERPGKKAG
EPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE

A0A0R1EA67 **A0A0R1EA67_DROYA** (386 aa)
Uncharacterized protein, isoform B. *Drosophila yakuba (Fruit fly)*

```
MKSTPPRRRRLSRRPARRRKGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAKRKVTRAEEEQK
MAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSSAAMERNKTKEQ
LEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDP
EALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYNTVYAETLEKTWQERQERFTQRTKSKLPKWFGERPGKKAGEPE
TPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE

A0A0R1EA82 **A0A0R1EA82_DROYA** (373 aa)
Uncharacterized protein, isoform R. *Drosophila yakuba (Fruit fly)*

```
MSDDEEYTGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAKRKVTRAEEEQKMAQRKKEEEERR
VREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGLGLSSAAMERNKTKEQLEEEKKISLSFRI
KPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQV
ASKYERRVDTRSYDDKKKLFEGGWDEISKDSNEKIWNEKKEQYTGRQKSKLPKWFGERPGKKAGEPETPEGEEDAKADED
IVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE

351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE

A0A0R1EA94 **A0A0R1EA94_DROYA** (373 aa)
Uncharacterized protein, isoform D. *Drosophila yakuba (Fruit fly)*

```
MSDDEEYTGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAKRKVTRAEEEQKMAQRKKEEEERR
VREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGLGLSSAAMERNKTKEQLEEEKKISLSFRI
KPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQV
ASKYERRVDTRSYDDKKKLFEGGYNTVYAETLEKTWQERQERFTQRTKSKLPKWFGERPGKKAGEPETPEGEEDAKADED
IVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE

A0A0R1EAA8 **A0A0R1EAA8_DROYA** (396 aa)
Uncharacterized protein, isoform T. *Drosophila yakuba (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETKPPQTPAEGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAK
RKVTRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGLGLSSA
AMERNKTKEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLR
HKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDEISKDSNEKIWNEKKEQYTGRQKSKLPKWFGE
RPGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE

A0A0R1EAF9 **A0A0R1EAF9_DROYA** (396 aa)
Uncharacterized protein, isoform P. *Drosophila yakuba (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETKPPQTPAEGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAK
RKVTRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGLGLSSA
AMERNKTKEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLR
HKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYNTVYAETLEKTWQERQERFTQRTKSKLPKWFGE
RPGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE

373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE

A0A0R1EAK8 **A0A0R1EAK8_DROYA** (389 aa)
Uncharacterized protein, isoform F. *Drosophila yakuba (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAKRKVTRAEE
EQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSSAAMERNKT
KEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKG
LDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYNTVYAETLEKTWQERQERFTQRTKSKLPKWFGERPGKKAG
EPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE

A0A0R1EAM7 **A0A0R1EAM7_DROYA** (388 aa)
Uncharacterized protein, isoform L. *Drosophila yakuba (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAKRKVTRAEE
EQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGLGLSSAAMERNKTK
EQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGL
DPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYNTVYAETLEKTWQERQERFTQRTKSKLPKWFGERPGKKAGE
PETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE

A0A0R1EBP2 **A0A0R1EBP2_DROYA** (388 aa)
Uncharacterized protein, isoform E. *Drosophila yakuba (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAKRKVTRAEE
EQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGLGLSSAAMERNKTK
EQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGL
DPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDEISKDSNEKIWNEKKEQYTGRQKSKLPKWFGERPGKKAGE
PETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE

364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE

A0A0R1EDP1 **A0A0R1EDP1_DROYA** (394 aa)
Uncharacterized protein, isoform J. *Drosophila yakuba (Fruit fly)*

```
MKSTPAPRRRRLSRRPARRRKKPPQTPAEGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAKRK
VTRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGLGLSSAAM
ERNKTKEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHK
ALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDEISKDSNEKIWNEKKEQYTGRQKSKLPKWFGERP
GKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE

A0A0R1EFL0 **A0A0R1EFL0_DROYA** (393 aa)
Uncharacterized protein, isoform H. *Drosophila yakuba (Fruit fly)*

```
MKSTPPRRRRLSRRPARRRKKPPQTPAEGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAKRKV
TRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGLGLSSAAME
RNKTKEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKA
LKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDEISKDSNEKIWNEKKEQYTGRQKSKLPKWFGERPG
KKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE

A0A0R1EG79 **A0A0R1EG79_DROYA** (374 aa)
Uncharacterized protein, isoform I. *Drosophila yakuba (Fruit fly)*

```
MSDDEEYTGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAKRKVTRAEEEQKMAQRKKEEEERR
VREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSSAAMERNKTKEQLEEEKKISLSFR
IKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQ
VASKYERRVDTRSYDDKKKLFEGGYNTVYAETLEKTWQERQERFTQRTKSKLPKWFGERPGKKAGEPETPEGEEDAKADE
DIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE

349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE

A0A0R1EG89 **A0A0R1EG89_DROYA** (397 aa)
Uncharacterized protein, isoform K. *Drosophila yakuba (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETKPPQTPAEGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAK
RKVTRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSS
AAMERNKTKEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQL
RHKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYNTVYAETLEKTWQERQERFTQRTKSKLPKWFG
ERPGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE

A0A0R1EGK5 **A0A0R1EGK5_DROYA** (385 aa)
Uncharacterized protein, isoform Q. *Drosophila yakuba (Fruit fly)*

```
MKSTPPRRRRLSRRPARRRKGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAKRKVTRAEEEQK
MAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGLGLSSAAMERNKTKEQL
EEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPE
ALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDEISKDSNEKIWNEKKEQYTGRQKSKLPKWFGERPGKKAGEPET
PEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE

A0A0R1EHP1 **A0A0R1EHP1_DROYA** (374 aa)
Uncharacterized protein, isoform N. *Drosophila yakuba (Fruit fly)*

```
MSDDEEYTGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAKRKVTRAEEEQKMAQRKKEEEERR
VREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSSAAMERNKTKEQLEEEKKISLSFR
IKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQ
VASKYERRVDTRSYDDKKKLFEGGWDEISKDSNEKIWNEKKEQYTGRQKSKLPKWFGERPGKKAGEPETPEGEEDAKADE
DIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE

348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE

A0A0R3NZP9 **A0A0R3NZP9_DROPS** (395 aa)
TpnT, isoform K (troponin T, skeletal muscle isoform X18). *Drosophila pseudoobscura pseudoobscura (Fruit fly)*

```
MSDDEEYTSEEEEVVEETREETKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAKR
KISRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGLGLSSAA
MERNKTKEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRH
KALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDAITKDSNEKIWNEKKEQYTGRQKSKLPKWFGER
PGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE

A0A0R3NZS0 **A0A0R3NZS0_DROPS** (388 aa)
TpnT, isoform B (troponin T, skeletal muscle isoform X12). *Drosophila pseudoobscura pseudoobscura (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAKRKISRAEE
EQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGLGLSSAAMERNKTK
EQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGL
DPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDAITKDSNEKIWNEKKEQYTGRQKSKLPKWFGERPGKKAGE
PETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE

A0A0R3NZS3 **A0A0R3NZS3_DROPS** (388 aa)
TpnT, isoform O (troponin T, skeletal muscle isoform X13). *Drosophila pseudoobscura pseudoobscura (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAKRKISRAEE
EQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGLGLSSAAMERNKTK
EQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGL
DPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYNTVYAETLEKTWQERQERFTQRTKSKLPKWFGERPGKKAGE
PETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE

361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE

A0A0R3NZT2 **A0A0R3NZT2_DROPS** (388 aa)
TpnT, isoform F (troponin T, skeletal muscle isoform X11). *Drosophila pseudoobscura pseudoobscura (Fruit fly)*

```
MSDDEEYTSEEEEVVEETREETGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAKRKISRAEEE
QKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSSAAMERNKTK
EQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGL
DPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDAITKDSNEKIWNEKKEQYTGRQKSKLPKWFGERPGKKAGE
PETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE

A0A0R3NZT6 **A0A0R3NZT6_DROPS** (373 aa)
TpnT, isoform E (troponin T, skeletal muscle isoform X17). *Drosophila pseudoobscura pseudoobscura (Fruit fly)*

```
MSDDEEYTGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAKRKISRAEEEQKMAQRKKEEEERR
VREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGLGLSSAAMERNKTKEQLEEEKKISLSFRI
KPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQV
ASKYERRVDTRSYDDKKKLFEGGYNTVYAETLEKTWQERQERFTQRTKSKLPKWFGERPGKKAGEPETPEGEEDAKADED
IVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE

A0A0R3NZU4 **A0A0R3NZU4_DROPS** (397 aa)
TpnT, isoform L (troponin T, skeletal muscle isoform X2). *Drosophila pseudoobscura pseudoobscura (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAK
RKISRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSS
AAMERNKTKEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQL
RHKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYNTVYAETLEKTWQERQERFTQRTKSKLPKWFG
ERPGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

368 - 387:	EEEEEEEEEEEEEEEEEEEE

369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE

A0A0R3NZX5 **A0A0R3NZX5_DROPS** (374 aa)
TpnT, isoform H (troponin T, skeletal muscle isoform X15). *Drosophila pseudoobscura pseudoobscura (Fruit fly)*

```
MSDDEEYTGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAKRKISRAEEEQKMAQRKKEEEERR
VREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSSAAMERNKTKEQLEEEKKISLSFR
IKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQ
VASKYERRVDTRSYDDKKKLFEGGYNTVYAETLEKTWQERQERFTQRTKSKLPKWFGERPGKKAGEPETPEGEEDAKADE
DIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE

A0A0R3NZZ3 **A0A0R3NZZ3_DROPS** (394 aa)
TpnT, isoform N (troponin T, skeletal muscle isoform X8). *Drosophila pseudoobscura pseudoobscura (Fruit fly)*

```
MKSTPAPRRRRLSRRPERRRKKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAKRK
ISRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGLGLSSAAM
ERNKTKEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHK
ALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDAITKDSNEKIWNEKKEQYTGRQKSKLPKWFGERP
GKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE

A0A0R3P036 **A0A0R3P036_DROPS** (396 aa)
TpnT, isoform M (troponin T, skeletal muscle isoform X5). *Drosophila pseudoobscura pseudoobscura (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAK
RKISRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGLGLSSA
AMERNKTKEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLR
HKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYNTVYAETLEKTWQERQERFTQRTKSKLPKWFGE
RPGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE

A0A0R3P049 **A0A0R3P049_DROPS** (396 aa)
TpnT, isoform P (troponin T, skeletal muscle isoform X19). *Drosophila pseudoobscura pseudoobscura (Fruit fly)*

```
MSDDEEYTSEEEEVVEETREETKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAKR
KISRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSSA
AMERNKTKEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLR
HKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYNTVYAETLEKTWQERQERFTQRTKSKLPKWFGE
RPGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE

A0A0R3P473 **A0A0R3P473_DROPS** (374 aa)
TpnT, isoform C (troponin T, skeletal muscle isoform X14). *Drosophila pseudoobscura pseudoobscura (Fruit fly)*

```
MSDDEEYTGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAKRKISRAEEEQKMAQRKKEEEERR
VREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSSAAMERNKTKEQLEEEKKISLSFR
IKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQ
VASKYERRVDTRSYDDKKKLFEGGWDAITKDSNEKIWNEKKEQYTGRQKSKLPKWFGERPGKKAGEPETPEGEEDAKADE
DIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE

A0A0R3P4R4 **A0A0R3P4R4_DROPS** (396 aa)
TpnT, isoform Q (troponin T, skeletal muscle isoform X4). *Drosophila pseudoobscura pseudoobscura (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAK
RKISRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGLGLSSA
AMERNKTKEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLR
HKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDAITKDSNEKIWNEKKEQYTGRQKSKLPKWFGE
RPGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE

A0A0R3P4R7 **A0A0R3P4R7_DROPS** (389 aa)
TpnT, isoform I (troponin T, skeletal muscle isoform X9). *Drosophila pseudoobscura pseudoobscura (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAKRKISRAEE
EQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSSAAMERNKT
KEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKG
LDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDAITKDSNEKIWNEKKEQYTGRQKSKLPKWFGERPGKKAG
EPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE

A0A0R3P549 **A0A0R3P549_DROPS** (397 aa)
TpnT, isoform D (troponin T, skeletal muscle isoform X1). *Drosophila pseudoobscura pseudoobscura (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAK
RKISRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSS
AAMERNKTKEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQL
RHKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDAITKDSNEKIWNEKKEQYTGRQKSKLPKWFG
ERPGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE

A0A0R3P565 **A0A0R3P565_DROPS** (389 aa)
TpnT, isoform G (troponin T, skeletal muscle isoform X10). *Drosophila pseudoobscura pseudoobscura (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAKRKISRAEE
EQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSSAAMERNKT
KEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKG
LDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYNTVYAETLEKTWQERQERFTQRTKSKLPKWFGERPGKKAG
EPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE

A0A0R3P5V0 **A0A0R3P5V0_DROPS** (373 aa)
TpnT, isoform J (troponin T, skeletal muscle isoform X16). *Drosophila pseudoobscura pseudoobscura (Fruit fly)*

```
MSDDEEYTGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAKRKISRAEEEQKMAQRKKEEEERR
VREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGLGLSSAAMERNKTKEQLEEEKKISLSFRI
KPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQV
ASKYERRVDTRSYDDKKKLFEGGWDAITKDSNEKIWNEKKEQYTGRQKSKLPKWFGERPGKKAGEPETPEGEEDAKADED
IVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE

A0A0R3P9D0 **A0A0R3P9D0_MOUSE** (716 aa)
Phospholipid phosphatase-related protein type 3. *Mus musculus (Mouse)*

```
MLAMKEKNKTPKDSMTLLPCFYFVELPIVASSIVSLYFLELTDLFKPAKVGFQCYDRALSMPYVETNEELIPLLMLLSLA
FAAPAASIMVGEGMVYCLQSRLWGRGPGGVEGSINAGGCNFNSFLRRTVRFVGVHVFGLCATALVTDVIQLATGYHTPFF
LTVCKPNYTLLGTSCESNPYITQDICSGHDTHAILSARKTFPSQHATLSAFAAVYVSMYFNAVISDTTKLLKPILVFAFA
IAAGVCGLTQITQYRSHPVDVYAGFLIGAGIAAYLACHAVGNFQAPPAEKVPTPAPAKDALRALTQRGHESMYQQNKSVS
TDELGPPGRLEGVPRPVAREKTSLGSLKRASVDVDLLAPRSPMGKEGMVTFSNTLPRVSTPSLDDPARRHMTIHVPLDAS
RSRQLIGEWKQKSLEGRGLGLPDEASPVHLRAPAEQVAEEEEEEEEEEEEEEEEEEEEGPVPPSLYPTVQARPGLGPRVI
LPPRPGPQPLVHIPEEGVQAGAGLSPKSSSSSVRAKWLSMAEKGGGPVAVAPSQPRVANPPRLLQVIAMSKAAGGPKAET
ASSSSASSDSSQYRSPSDRDSASIVTIDAHAPHHPVVHLSAGSTPWEWKAKVVEGEGSYELGDLARGFRSSCKQPGMGPG
SPVSDVDQEEPRFGAVATVNLATGEGLPPPGASEGALGAGSRESTLRRQVGGLAEREVEAEAESYYRRMQARRYQD
```

439 - 458:	EEEEEEEEEEEEEEEEEEEE

A0A0R3U639 **A0A0R3U639_9CEST** (215 aa)
Uncharacterized protein. *Mesocestoides corti*

```
MNRYGGVMTFKRHQHRALFKCTALWAQGHCSIKPSRRESLHVHVKVCEGLHSAKLRQQLARNNSTCGDGGTAVYEYEDEE
EVEKEEEEEEEEEEEEEEEEEEEEEEEEEEKEVEEEEVEEEEEEEEEEEEEEEEEEKEAEEGEDNVRVETIKKNAETMFPEV
MGGEEAASWGQLPGVRASGGDSGTATSGVFFNEIRVVAYAGLGVSATHHTLFEVV
```

85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE

87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE

A0A0R3XAG6 **A0A0R3XAG6_HYDTA** (56 aa)
Uncharacterized protein. *Hydatigena taeniaeformis (Feline tapeworm) (Taenia taeniaeformis)*

```
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEEGEGRGRTSALLLSCIKVIN
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE

A0A0R4J114 **A0A0R4J114_MOUSE** (768 aa)
UTP25 small subunit processome component. *Mus musculus (Mouse)*

```
MGKRRNRGRSQMLSTMTKKQKKHLRDFGEEHPFYDRVSKKEAKPQICQLPESSDSSHSESESESEQEHVSGYHRLLATLK
NVSEEEEEEEEEEEEEEEEEEEEEDDSAVGDAEMNEEAGSEDGSVGEAAVSEAAEEAAETQEHMSLADNSKEKDGEEPPG
VSQKSSEEFTDVKHESLFSLETNFLEEDSGGSCSQRPSQDPFQQHVNKELKEKEIQAAASSPPATQQLKWPVLGHLVFSS
KFQKTETFKPPKDIDLKLLHLQKPLESTWAKTNSQFLSGPQKSNSSFTPLQKELFLIMNSYRDLFYPERTALKNGEEVRH
VYCLHAINHVLKANAQVLANNSRRRSQKLGVGEDDDFRDQGLTRPKVLIVVPFREAALRVVQLFISLLEGDSKKKIIVSN
KKRFQGEYGSDPEERPPNLKRPEDYEAVFVGNIDDHFRIGVAILQRSIRLYAPFYSSDILIASPLGLRTIIGGEGEKKRD
FDFLSSVELLIIDQADIYLMQNWEHVLHLMNHMNLLPLDSHGVDFSRVRMWSLNNWSKYYRQTLLFGALQDAQINSVFNK
HCINAQGQVAVRNVPMTGSISHVLVQLPHVFQRMEAQDLSSVIDARFHFFINKILPQYRDAVMSHTLIYVPSYFDFVRLR
NYFKKEELNFTHICEYTQKSGISRARHFFLQGEKQFLLLTERFHFYKRYTIKGIRNLIFYELPTYPHFYSEVCNMLRATS
RGEEATWTCTVLYSKYDAQRLAAVVGVERAAQMLQSPKNVHLFVTGEK
```

84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE

A0A0S3SQJ6 **A0A0S3SQJ6_PHAAN** (885 aa)
Uncharacterized protein. *Vigna angularis var. angularis*

```
MVRGGRFSGKRNFRKRVRSKEGGSDDSDEDYVVSDDGREVSDYYCSSFDGCASEESFGSFLSEEDEEFQTVRNFNRSKAK
RGTARRPKNASKNSHKRERIKYAEEEVEEVEEEEEEEEEEEEEEEEEEEEEEEEEEYKVEEEEEEEEEIQEARNFSRPK
AKSGVCSKKRSAGKISSKRGRKLHTEELEEEEEEVKLEEEEEEKEKVDIGGDDKEEEGDREGEDEDFDYEDEDDEFFPEE
DDYSDEEEEMRGKKKNNDGMTMVKKVFRKKRSSVVSTRGRKRQSSRASKKPLRKKRKNGRLRKKVRCEDEDEDDFIDNSP
TMRTSRKKRGQKRKRVLLSDSEYPSSGSSDFEFTISEEEREQVREAKRLCGNLRNNLRSSSQLINNEEVGVHEEQIQLRK
PPARKGKEKIEEPQGRKGKEKVEVKSEMGKQVCGICLSEEDKRRVRGVLNCCTHFFCFACIMEWAKVESRCPLCKQRFKT
ISKPARSTTGIDLREVVIQVPERDQVYQPSEEELRSYIDPYEYVICSECHQGGDDGLMLLCDICDSPAHTYCVGLGREVP
EGNWYCDGCRPVALGSSSSQVQEGVADPRLTIQNLPVRAPPTLHVRESIDLNLISSPRAAFNQGFGHLPSSRFSGRSVEG
SSPVSGGAPTLSERRWIHRQIQQLLSIDRMTATPGRTTNGISATSSTSNLYSSQIDQSRGTATLHVRTQDVGTSYHTFLD
DRLCNNTSPLMQNGPLWPGLMATPPVPDCEQVHQFSRSSIVPDDGLSTAIREETNFHTAKEQLQSMVKSHLKSLSQNIDL
GHSTFKDIARSSMHTILAACDLEHKNSEVCNVPPPSACPHMELMAGGPTSLIKGCCSSCFDSFVGDVVKRILDARVSSQW
LRLGL
```

111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE

117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE

A0A0S4MI72 **A0A0S4MI72_ECHMU** (356 aa)
RNA directed DNA polymerase. *Echinococcus multilocularis (Fox tapeworm)*

```
MDESILECPVCLDEFKHPVMPPCQHAFCFSCILKYIRESGAKCPICRTVFAEEDLRRSLHIEQLLSANSGGLEADEEEEE
EEEEEEEEEEEEEEEEEEEEEEEIGDESGTLVAALADLPPFKDDMDFEVWLKLAKFNLPLYPRRQRILRILRALPQDLFL
AAIDAGITPDTNLEQCCDTLSQLVIDKEEQTLARDFFIATKKWVKMTRIVQFKHGVRPPIMVEKLCGMKANSLSQLVKFA
TRKRQELLKIPHYNILSRRSNPAPSYRASSRYPPRSADLRRNLQAVKLLSAKNSEPVPPCESDGYPKSFDFSSKPRSQQQ
VDRSKWVTTLAAGAAGVLIGVIGAAIGFSAASKRRR
```

76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE

A0A0S4MI78 **A0A0S4MI78_ECHMU** (158 aa)
Calmodulin. *Echinococcus multilocularis (Fox tapeworm)*

```
MTSCIVKKKKKKKKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEGRGGSNALTHGIELRLATVAASASKAVSHHEPLAQSTRQSASQPASQSFCLAAYR
```

16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE

45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE

A0A0S4MLW7 **A0A0S4MLW7_ECHMU** (121 aa)
Phosphotidylinositol phosphatase PTPRQ. *Echinococcus multilocularis (Fox tapeworm)*

```
MLTKLTKKKKKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEALLQLLTWPPASPLQHKSTPRNVSLEATNSHTVHMT
REPPAEFYDGTTCYIIFWLINEEPQGSIKVSPSGFYNFTGL
```

13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE

20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE

A0A0S4MM78 **A0A0S4MM78_ECHMU** (171 aa)
Aromatic l-amino acid decarboxylase. *Echinococcus multilocularis (Fox tapeworm)*

```
MPSLASSQHSLLNFITPISSSSSSSPSSFNMHLRCSLCTFSPTSPPIRCCTPRPPPPFSRKPQPTEDASYSTLPHHTLRL
GWLCCCPYCCAPIALLAEGINTYCAFLKNCIADTRQVTLTTSHCDNRAKEEEEEEEEEEEEEEEEEEEEEANRYSERRCK
LLIVVSVEMLG
```

130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE

A0A0S4MQH7 **A0A0S4MQH7_ECHMU** (181 aa)
Aromatic l-amino acid decarboxylase. *Echinococcus multilocularis (Fox tapeworm)*

```
MGDLTDLRCPPWHPSQHSLLNFITPISSSSSSSPSSFNMHLRCSLCTFSPTSPPIRCCTPRPPPPFSRKPQPTEDASYST
LPHHTLRLGWLCCCPYCCAPIALLAEGINTYCAFLKNCIADTRQVTLTTSHCDNRAKEEEEEEEEEEEEEEEEEEEEEEE
ANRYSERRCKLLIVVSVEMLG
```

138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE

A0A0S4MR35 **A0A0S4MR35_ECHMU** (159 aa)
Hypothetical transcript. *Echinococcus multilocularis (Fox tapeworm)*

```
MMGKFLIPLVMENAVSLARQHTPNSITLTHQPEMESVTYHRLRLFESIQVAIEPVSEISPWSLMKEQKHLTFLQEVESVD
SLELSSIYTLPEFALETSATWEPSPYERKIAIMFQNPRIDHLRGQWEEEEEEEEEEEEEEEEEEEEEMLQCRTDHHMLP
```

127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE

A0A0S4TFD2 **A0A0S4TFD2_CRYHO** (371 aa)
Thioredoxin domain-containing protein. *Cryptosporidium hominis*

```
MKLKLAVLNLILLLVIGIRGDEINASINGHNRAQRHAKPTASASSYTPQKHHPTVSVNSEKKIQSFVKELNDSNFEHLTQ
SATGSTTGDWFVLFYLPNCQQSQMSLAELDKLSVIARESLNVAKIDVSKNQQLINRFGIVAVPSFRFFRNGKMYTYTGMR
NAEVIKAFIWNKDYKKLTPQPVPDPLSTLDIIISEIKHTINDINKLIKLAPLVTIIILLIGFFTGIGVTNIFSRSSNRSK
TTTSNNRVKRDKYSDDECVDHEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEAPKQLKTPQRGRRAAENIAKEDDRLNNTYNTSVRRSNRLKKL
```

262 - 281:	EEEEEEEEEEEEEEEEEEEE
263 - 282:	EEEEEEEEEEEEEEEEEEEE
264 - 283:	EEEEEEEEEEEEEEEEEEEE
265 - 284:	EEEEEEEEEEEEEEEEEEEE
266 - 285:	EEEEEEEEEEEEEEEEEEEE
267 - 286:	EEEEEEEEEEEEEEEEEEEE
268 - 287:	EEEEEEEEEEEEEEEEEEEE
269 - 288:	EEEEEEEEEEEEEEEEEEEE
270 - 289:	EEEEEEEEEEEEEEEEEEEE
271 - 290:	EEEEEEEEEEEEEEEEEEEE
272 - 291:	EEEEEEEEEEEEEEEEEEEE
273 - 292:	EEEEEEEEEEEEEEEEEEEE
274 - 293:	EEEEEEEEEEEEEEEEEEEE
275 - 294:	EEEEEEEEEEEEEEEEEEEE
276 - 295:	EEEEEEEEEEEEEEEEEEEE

277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE
287 - 306:	EEEEEEEEEEEEEEEEEEEE
288 - 307:	EEEEEEEEEEEEEEEEEEEE
289 - 308:	EEEEEEEEEEEEEEEEEEEE
290 - 309:	EEEEEEEEEEEEEEEEEEEE
291 - 310:	EEEEEEEEEEEEEEEEEEEE
292 - 311:	EEEEEEEEEEEEEEEEEEEE
293 - 312:	EEEEEEEEEEEEEEEEEEEE
294 - 313:	EEEEEEEEEEEEEEEEEEEE
295 - 314:	EEEEEEEEEEEEEEEEEEEE
296 - 315:	EEEEEEEEEEEEEEEEEEEE
297 - 316:	EEEEEEEEEEEEEEEEEEEE
298 - 317:	EEEEEEEEEEEEEEEEEEEE
299 - 318:	EEEEEEEEEEEEEEEEEEEE
300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE
306 - 325:	EEEEEEEEEEEEEEEEEEEE
307 - 326:	EEEEEEEEEEEEEEEEEEEE
308 - 327:	EEEEEEEEEEEEEEEEEEEE
309 - 328:	EEEEEEEEEEEEEEEEEEEE
310 - 329:	EEEEEEEEEEEEEEEEEEEE

A0A0S4TFR4 **A0A0S4TFR4_CRYHO** (1259 aa)
Uncharacterized protein. *Cryptosporidium hominis*

```
MIPEKILEEDLLEHDLQGSNALVLPTSKIERKRIHQENNHSESDQNSRRSCKEKKMSNRKKRKLKQLEEKKRLNKIHEDL
TNDLKKYTLSDQELQLMMGITNTRINNKQKQILRSRYLAAKLELPDFLKLKDCSSKSKNYISESESESESKHEFKPESEP
ENSKVDDLVHLADYDKELKSENENFDSESKLELKKNEQLKEENQKKESKGRYIRKYTSLVIKNDNDRPIINRTPEIEFQR
SELPVRVYEFEILDAIENNDVVIVTGATGSGKSTQVPQLLYESGYCQLKKGQNNNHVNESEKRYMIGLTQPRRIAATSLS
NRIGEELNDSKVVGYQIRYDKKNCTNETVIKVMTDGVLLQEIQKDLLCSKYSVILIDEAHERTVNTDILIGLLSRIVIFR
REEYIRKTKQGLEDILPPLKLIIMSATLRVTDFSENPKLFSKPPPVINIETPNFPVTLHFSKNTPKDYISAAYKKIQQIH
NRLPPGSILVFVTGKKEVNLLVNLINNKGKNKAKRNCLLNNTTNSKMNMLLDFTENNLEEEELEELEEEEEEEEEEEEEE
EEEEEEEEEEEEDDDDELEEEQLDELEQEELEEEEKEQQKEQENEVSEGSKNVWESFGKKDIRKRKIRLHKDVDSSVWKG
GGVIEEDDSEEEKDSVKKEERNKNKKPENIKIQLIAIPLYASMSFDEQKKAFKLPESNNIRHVIISTNVSETSITIPNVR
YVIDTGKEKRREYTKGSDSSHFTVEWISKASASQRSGRAGRVGPGHCYRLYSSPIYENIFPKFAPIDILSIPLDSVLLYM
HSLGIPDIVDFPFPTPPEKSQIDQAYQLLTILGSVESRKSKYILTNQGISISSFPLPPRYAKILLLTTAYIRKNLINDDL
KSSIELLQQVCILVSYLSIGNLRDESFSSDTQKEHNQGIKNVDHQNLNDDFESFPSNLGNDIEINLWFCIKYLEYYGSGR
KHERSLSDKFCKKFELNSRGLSEIRLMSIQLFNITKKKYLDKLINSEANLNIKWPPSLPNYTQKNLLRTFFISSFIDHIA
VRNDGNLVSKVSYQIPNESPNSYSAFIHPRSVLKSSKPKLLIYSQIISSTDKNRHNLCDCLLITTDDISKATSLKHSLVD
CSKILSFPTPYYNIESDSIIGYCTPKYRNNSVVIDLPSSEIQLETNNNIVFEVFARAILNGQVFKEFKNQRILKGLKSKN
NNSNQFKLLVNTLEQNLIFNKSRLISKFQTKRDFLLKNILQLYEISVHNDIRSFWPPIK
```

547 - 566:	EEEEEEEEEEEEEEEEEEEE
548 - 567:	EEEEEEEEEEEEEEEEEEEE
549 - 568:	EEEEEEEEEEEEEEEEEEEE
550 - 569:	EEEEEEEEEEEEEEEEEEEE
551 - 570:	EEEEEEEEEEEEEEEEEEEE
552 - 571:	EEEEEEEEEEEEEEEEEEEE

553 - 572:	EEEEEEEEEEEEEEEEEEEE

A0A0S4TJX9 **A0A0S4TJX9_CRYHO** (324 aa)
18S rRNA aminocarboxypropyltransferase (EC 2.5.1.-). *Cryptosporidium hominis*

```
MKSRNSTKTQIETDFVSEFISETDSSEIESKFESEKNEELDKKEEEKVSKKADKDEVIEVNKEEKADEKDDEEKGEEEEE
EEEEEEEEEEEEEEEEEEEEEEKEEEEEKEEEEPTIKIGLWDFCQCDVARCSGRKLLRFNYAKKLQFSSNYARKWPGII
LSPRAKKKVSMEDLPLILKGGVGVIDCSWNKIDQVPFHKIHNGNERLLPFLVAANSTHYGRPYELSCAEAISACLFFFGF
PKQAEKLLGIFKGGHHFLELNKEAFDFYKSKGINSQSIINAEQDFINKYMNKQQQRESRDYDSLFSSSYEDDDYDDNDDN
DGKA
```

76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE

A0A0S4TKA6 **A0A0S4TKA6_CRYHO** (1307 aa)
Uncharacterized protein. *Cryptosporidium hominis*

```
MSIFVEEINVNNPGLLQGQIESSKKNKCLEENVSNKDFIENKIQNVGFSAKTAVDHLDSNLILKDDKKGMTILEQSELEM
KLKKLLEATNQYSYLLSGESKNSKHLESKSKSGSNCRQHFITEKEEDDILIKEVEDDSFQNEDEEINYSIEKVAEQPDCI
TGKMKFYQLEGLNWMFQLYKHNINGILADEMGLGKTLQTISILGFLKSTFKVEGPHIILTPRSTLDNWFCELKRWCPSLR
VVKLHGDRQLRDEIFSSLLFPGSKVSAGTLYCNESNELAEDEEKDVELRQNSEERPTFANFDYNDGNLHYNVCLTTFEMA
IKEKWRLQKISWKYCILDEAHRIKNEKSLLSEVVRLLKSKNRLLITGTPLQNNLRELWSLLNFLMPNLFSSSEDFESLFD
FSKLESDDQQKCVIKTLHQILRPFMLRRLKADVERDLPPKRELYVYIGLSKLQKKIYSELLTRNLDVLNSASSNKTQMLN
LLMQLRKTCNHPYLFDGVEPGPPYVEGFHMVEASGKMVLLHKLLPKLFSQGSRVLLFSQMTRLLDIIDDYLRWSGYPYCR
IDGSTPGIERQERIDIFNKEGSEKLIFLLSTRAGGIGINLATADVVILFDSDFNPQMDLQAMDRAHRIGQKKPVTVYRFV
TEKTVEERIVERAAKKLKLDSLIIQQGLISNASHSAPDNRELHEMIQFGAQEVYHTRDSSSVTDEDIDTILAAAQERTNE
MNAKMKKLSSELDLQNLRLDGGIKASMHPESKDDELKSGDDSKTKDLPTIQSDITWFDLGERKTKWKLETSSNNTISIKK
QPKPKLIGWRAQVGGGYDHQFFNIKRLDELEEIEKKWNEYLKENEIQQKNNLNDSVCAKLSNFNEDSLKDVFSVPPELKE
LNENQLIRLLDVAEEHMDVSIDKSSWPKKKLFSRAKELFSSGFVLPRCNFKEALADLRLMFNDGRAWDMNIPCARQRSKK
KNNKEKNLENSQNPTVFTELMKQEMMELISQGFATWTKGDFQRFCRAAELYGSDLHSITDSMENKSFEEVSRYYNVFLKR
YKELPGGERIMGRIKMTEEIQNWFSDANNAIKYIVCEQIKKNKLKKLSLENISLPFKVKSTSNKFESFSHLQDNALLIAM
YKLGVQSYNDVSISFKYLLNSITSVNSLYYSHYSVEFITERCNEISKAAINYYKKCSQHKKPNKLKISKHNFQDKLGDTN
KVSSLNKKKKTKIQDKKSDSTDGQHNSGKNYEMDFEDQEEEEREEEEEEEEEEEEEEEEEEEEEEEEDDDDDDDEDEQ
GHHNSRKKRSINIRKNNRKCSKRKRFN
```

1244 - 1263:	EEEEEEEEEEEEEEEEEEEE
1245 - 1264:	EEEEEEEEEEEEEEEEEEEE
1246 - 1265:	EEEEEEEEEEEEEEEEEEEE
1247 - 1266:	EEEEEEEEEEEEEEEEEEEE
1248 - 1267:	EEEEEEEEEEEEEEEEEEEE
1249 - 1268:	EEEEEEEEEEEEEEEEEEEE

A0A0S4TLN5 **A0A0S4TLN5_CRYHO** (2719 aa)
DNA-directed DNA polymerase (EC 2.7.7.7). *Cryptosporidium hominis*

```
MKRSKSYRDNGRKKFERKTTERKKGRFELGGSSNIDKKFGINFQKIGVNHREIGYLYNVQVSSELISESGTAFDGMEIGT
LESSSELIESYKERSCLNLYFINKQGMTFKSPFFFRPYFYLEAQKAVDIHWILTNLEHKYRDTTIEFTNIMKEDLTLDNH
LIGEKREVIKASFDNVKELVSIRNEILDHIKRNKLEKKKNESLGAYYDQDQQNNYENKTLDVLDSISEIYEYDVQYEARV
MIDNSISIGMWYDSVRWTHELLELKCLDHDTSAPDLRSLAWDIETTKDPLKFPNVEKDQIMMISCMFEGQGYLITNREIV
SADIYDFEYSPKKEYESFFKCINYPDEKELIWGFIKLIQTLRPHIIASYNGDNFDFPFLYERAKKYDIDVSKEWGIRMEI
DHSSGGGGLQSSNKTIFSGTNIIHLDCFRWVERDSYLPCGSRGLKSVTKAKLRYNPVELDPELMVPYAKTNPQGLAEYSV
SDAVATYFLYKTYVHRFIFALATIIPLSGEDLLRKGSGTLCEHLLMKEAFTKNILFPNKKVQETMEFYQNRPILNSTYVG
GTVESLCSGVFRADIPEKFCLNTDTLKNLIKILDTTLNFGIKDSGTTIDNIENYEQVRNEILEKLQSLLESPRIKIEPLI
YHLDVAAMYPNIILTNRLQPTAVIEETTCMKCPFNSESKLCQRRMNWRWKGDVFPISKGEMERMMNHIQIETFENVKNEL
GAVNKKKKFEDHESDSENDEKMEFTGENVNINNKEKIKWSSLTPRQQSEILIQRMKAYCNKIYRKQTENIEETRSSIVCQ
RENPFYIDTVRRFRDRRYVYKGKKKEAEEKLKRAELLGDLLAVQEAQNEELLYESLQLAHKCILNSFYGYVMRKGSRWFS
MEMAAIVTWVGGNVIREARSLMEGIGRPLELDTDGIWAILPKGFPEEITFRLKDGGKKKIHYICTLLNQQVHKSWTNDQY
LEYDADLGKYNIKVENSIYFEVDGPYKCFFIPASDKQNKLLKKRYAVFDFENRLKELKGFELKRRGELQLIKILQEELFP
AFLKGNSKKEAYDHVASISKKWLSLIDTKGRGILDDEQLFFLISESKNMSKSVQQMGNAKSMSITTAKRLFEFLQNPSYI
QDKNIVCKFIVSEFPKGEDKSQRAVPLSIFSTPLETRISWLSKWLRISKSGGRREKDELVEHRRKADVDITSGSGSGNGI
LNKENETNKWNVRNILDWEYYKNRLTNTILKIVIIPAINQGVPNPLPELEVPSWVRYHSEIVGTNQQKISEYFNVVKKEE
KKKSSFSELPNYNSIIQGRSQDQGQVQDQGQIQNQGQIQNQGQIQDHGQIQDQNQTQDHGQTQDHGQTQACKIVETRNNS
SISKFNGKLTKKERIELFKKKGFKSWLEYHKKFWLESFHAFNEKQLELEKKLKNIDIEKLEYFGKGSTAKGIEFLSEYIF
LTKGRFHILDIYPLSIQQRSIKRNYDEDLLGFYNVVMYSEETGDCFTVTFEFLRRFYIATNVQIQIMDNDDDGEFITKSI
ATGKELPRGVPYNHLTEVIISERRFQKSKSTLICDNNTVGIYETNLPLEFSILEKFGNVIESNTPNVEKLLLKNGAITDK
FWNSTGGLKEKNLNYGDIIHWLFLSICTFEERKCFSLTDLSKKRIYFFLGLGPNISNNILKSELDRQIKQDQRLEKITEI
HVNYFKTTKDCLEELDRLLKDLIQEFPKEPIVLLIQSMVRLEELKTHNSELNLYKTILREYISEMEHNKKVIETKVVTLW
EEIIDFDSSNSIFSRFDWHKDSIRYSLKALKEAINKLQLSLELSKALRLPVLYLLQFKNNLTNFLYDIIYSRELHSMGLL
SWGSLRSTPDLGNPKLIQLSKSDWDLRRLGYLMPTKDLNNSKGGRGCGGHSNCNINSLDEFDVLEVVRPGIYRNYGVQLD
FKQWLIIESVRNCRILSDKYNLDDFEQGEKRILGADCKKKNSEKDDKKKDVLIYNLGSRKHLSNPNNKQGLLISQPLYNH
SSLSTSSAFLCLEKTINKMRSVIENHEKVESIFRIYNGQKTCENEQFDQKNENILGKEEEKGEREERKRRREERKRRREE
EKGEEDEGEGEGEGEGEGEGEGEGEGEGEEEEEEEEEEEASSLLFEFMVTLQERFYSWLSSPNSLLYDPALIEMTKDYAHWY
```

```
FKSLESDMREMGIQVVYGNIRKMILTFNLDELKNNSIRNNSDLQNQFSKLMQILNNRELYSGISLDPTVEYKAMIQIDRT
NYIRRTLGGGGSGGLEDPYEMNLSLLNYFPVNSRKYIVGEISNFLMEPLRELRNYFKKNSNLSLKESLQILGDIVLEQFG
PFSENFQNFLQAISNPNTYIVRKYGIQQFDDPLNDIGWNDDIMREGEEVKENRKIIEEEEKEEKEEEEEEEEEEEEEEEE
EEEEEEERRRKKKNANSILEEDNDTLLLKKNLENLDINNRRDDIPFAIYPNSIKKKGNSHSLMIETSKKRMEEKGIRKRR
NFKDLFEFPPCIGKAYNGNKPSLSLELIKLFIYIWGLDKSFSMDESKQKQYEQIIFMVCQTVDISEFNPIVTEKWTSPLI
PYIIKDFSCPNCFEIEDFDFTGNAIQDEDDLGLSSNNYNNIIRPRFTWYCSHCNFSIDNEILEEKLLLEFFERLEVIQSQ
DILCSRCNSVQISYMQKHCDECMGELTTRLGNHKTFHNFFTLFNSVAQYYSDLNSEEDENPQFQGLIEFKNMYDNIFYI
```

2385 - 2404:	EEEEEEEEEEEEEEEEEEEE
2386 - 2405:	EEEEEEEEEEEEEEEEEEEE
2387 - 2406:	EEEEEEEEEEEEEEEEEEEE
2388 - 2407:	EEEEEEEEEEEEEEEEEEEE

A0A0S6XQD1 **A0A0S6XQD1_9FUNG** (463 aa)
Uncharacterized protein. *fungal sp. No.11243*

```
MSVSEQERVYRSSSGIQQQHFPARRTAVKSSWRPGRLSGRQQSTLTQLDFCSPQSSSVVHETDSEDDKHGKQPRRKRRKV
RDGRRQATLTQLLPDLEDVQLERDLSDLDRPEMRIIQETQWDAESLHIDEDETASESSPVLARRSLSPSTEIVKDSPLAQ
KSTTPPVQSPIVLSTPTKHHRDEVPSSQTPLSILYTNGSRCSRDTPSNSPLKDRSVNVVDVPASPSHVSCPERQPASNSQ
QRPKVDSPIKFLIPALPSPKKVTRIRETQYPPPRMVVQDSQFDDLEMALVEGQSGGLSRVPATCFPEHYKTQLQSSLDGF
TQYMDNIDPACTHTYDALSSPQEIQDSDADSDDDADELQLESPQNGMVGDRRRRRLRLATEVLPDSLLEFTVLPAPAWSS
SPAFAEREQTEEQQEEEEEEEEEEEEEEEEEEEEEEEEEKSVDYSLPPPSSEWRSSGRQTRA
```

415 - 434:	EEEEEEEEEEEEEEEEEEEE
416 - 435:	EEEEEEEEEEEEEEEEEEEE
417 - 436:	EEEEEEEEEEEEEEEEEEEE
418 - 437:	EEEEEEEEEEEEEEEEEEEE
419 - 438:	EEEEEEEEEEEEEEEEEEEE
420 - 439:	EEEEEEEEEEEEEEEEEEEE
421 - 440:	EEEEEEEEEEEEEEEEEEEE

A0A0S7DZU6 **A0A0S7DZU6_9EURO** (844 aa)
RNA helicase (EC 3.6.4.13). *Aspergillus lentulus*

```
MAPNSAIKKRAAAKDDDFVLTLSDDENDVLENGVEEDGDNAEEDTLSSSRKRKREAAEAPKGKNKKQKQSKKSKKGESAA
GAVSDDQSGEEGEAEAMDAGEDDGALDSEFEFDVGGNANTGVIEGFDGWEARNGDGSADAAKNGNKKAVDIDDIISRRKA
KKDAELKKKQQKEKKRREEEEEEEEEEEEEEEEEEEEEEEGEDSENEDADSDGGMSVDFQDDELLAADGFGMGADGADESGD
DMEKDSSDGDDSDEQGSEDEEDDDDDDAASDNDSVATPVHHPDDEAASDDESEAESEVDAEEAEKRKAFFAPEEKSTAAS
TSNRSFQDFNLSRPILRGLASVNFTTPTPIQQKTIPVALLGKDIVGSAVTGSGKTAAFVVPILERLLFRPRKVPTSRVAI
LMPTRELAVQCYNVATKLATHTDITFCQLVGGFSLREQENILKKRPDVIIATPGRFIDHMRNSPSFTVDTLEILVLDEAD
RMLEDGFADELNEILTTIPKSRQTMLFSATMTDSVDKLIRVGLNRPVRLMVDSKKNTSMNLTQEFVRLRPGREDKRLGYL
LYLCNEIYTGRVIVFFRQKREAHRVRIVFGLLGLKAAELHGSMSQEQRIKSVENFREGKVAFLLATDLASRGLDIKGVET
VINYEAPQNHEIYLHRVGRTARAGRSGRACTIAAEPDRKIVKSAVKAGKAQGAKIVSRVVDPAVADEWAAKAKGLEDEIE
EVLQEEKLEKQMAQAEMHLTKGENMIKHEAEIMSRPKRTWFETERDKRAARKLGATELNGPSQKDKVKLSNKDKKRLDDA
RQRHEGNIGWKKGKADREAPKQGKNKESKNKSDKKNKIKMKGKK
```

178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE

A0A0S7E532 **A0A0S7E532_9EURO** (780 aa)
Uncharacterized NOC2 family protein C1142.04. *Aspergillus lentulus*

```
MAGSQKKSTKKFEKKHLKDVLERRKSTAKIKQRIHLKEKRKADNARSRPENGDSEESPEERKKQNAFAEMNVDDFFAGGF
EIADADTDKGKKSRRKDVTPKIGKRKRSEEQKEEGEEDSSAASSEGEEDGGVSDDDAESQASSAPDDFEAHKDQLQALKD
KDPEFYKYLKEHDSELLDFGEHGDLTEVLELSEDEEEEGPAKKKKKAAKDEDEEAADNTLTIAMVKKWQKLMEEQNSIRA
MRQAVLAFRCAAYINEAETQEQKYSISDPDVYHQVLVTALGTVPKVLAHHLPVKETASGKVRVSLDSKKFKTLTPLVKSH
TSSVHQLLINLSDASTLKLTLSSIEPMLPYLLQFRKLLKVLIKTIVGIWADVSTTEATRITGFLLLRKLMVIGDSGLKET
VLKASYEGVVKGSRNTTVHTLSGVNLMKNSAAELWGIDQNISYTTGFSFIRQLAMHLRSSITNTSKESYKTIYNWQYTHS
LDFWSRVLSQHCDGLVEAKAGKQSALRPLIYPVVQITLGAMRLIPTATYFPLRFQLTRALLRLSRATGTYVPLAPALLEV
LNAAEMRKPPKSSTLKQLDFSTAIRAPKSYLRTRIYQDGVGEQVAELLSEFFVLWTKHIAFPELSVPIVVALKRWLKQVG
SRTAGNKNAKVNQAILLLVQKVEANARWIEEKRLNVTYTPRNRAEVESFLKDVDWESTPLGAFVKTQRKLREEKAAILEQ
GRRDEERRRAAEKKADEDEMMEDAPSDDDGSEESSGEEEEEEEEEEEEEEEEEEEEEFEEE
```

757 - 776:	EEEEEEEEEEEEEEEEEEEE

A0A0U1LRC5 **A0A0U1LRC5_TALIS** (103 aa)
Uncharacterized protein. *Talaromyces islandicus (Penicillium islandicum)*

```
MSTTLDRPPEEKEPPKVESDRDAELNNNKKKLTGVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEGKKHSITNRVS
```

36 - 55:	EEEEEEEEEEEEEEEEEEEE

37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE

A0A0U1LUN5 **A0A0U1LUN5_TALIS** (2407 aa)
Alpha-1,3-glucan synthase (EC 2.4.1.183). *Talaromyces islandicus (Penicillium islandicum)*

```
MKWFSRLFTWVSIQSWFQSITALPYTPDQIDFNLNQNQSATDPLDYWGQWQDHEFHPSPRNWRMPFYTIFLDRFANGDPS
NDNANGTQWEHDILSNQFRHGGDVLGLVDSFDYLQGMGIKGLYLAGVPHINQPWAADGYSPLDLTLLDAHFGTIDDWRTM
ISEAHRRGMYIIVENTMATMGDLIGFSEYLNESAPLNNREYDYLWKTSRRYHDFQPGNEWLEECKWHYPRFWDDYGHGLT
KTSLGPGCKDSEFDQYGEVASFGNYTEWERQITKFAFVQDRLRDWRPDVRQKLELFSCITIAMLDVDGFRIDKAIQVTLD
TQGEWSDSIRQCAQRFNKTNFYIPGEIVSGNSFGAIYVGRGQQTNQTYDNITDAVTMTNSSVPDLHIRSAKNSALDAAAF
HYTLYRALTRFLGMDGTFEAEGDPATNFVDMWDGLIQTNDMINTNTGEFDPRHLYGTSNQDVFRWPSIRNGTEKQVLGLY
VVSLLIPGSPIVYWGEEQAFYVLDNTNANYVFGRSPMTSSVAWQLHGCYKVGSVRYNDFPIDRALDGCMDDNVSLDHRNP
SHPVRGVVKLMFEMRENYPVLNDGYYLQQLSNMTYNIYLPGSNGTRTETGLWSVLRSRFELTQDLTGLGQGNQSVCQRAL
VSPFDEGTVVKNLFPPFEEHTLQSSIHSLGLEGSKKPNGCLNNLTISPWGFKAFVPKEAFTAPSPFITKFEPGHDARILS
TVTTGETIPISFLFSEDMDCDSITNGIYVSSTALSGQQAQFDKGSVSCNSIPEHQSVSWQGAYTSAYNYSIDMTNVFHGI
HEVLVKNVTNQGKNRTTGSVDHFIIRIGSTDNPMVWPSQANYSRNLLYADSSDNGTLWVSHKAAGADKWRYTLDFGASYS
PWVVYMGLNTSIPPNNWSGTKLQAWDGEHIMVQYWNKITGSSNHYQHGDLEWNDKPPRRFPNLWVQGELNQFGYDSGYHS
QMHLSNLSGQWEYNLMTEWPCQVALNAWGVNSDGTPDITQVYGDIDGDMVLDRIPPISLLSNFINVTDPPPWPYLSWKIS
LDDGNLRYWTTPQGSQKVQLCLYVCLAILPILSGAAAVWIYLKAFYQVKFNDVGVSRERNHRESIYARRSITANRSLENT
DVGPTYIDKIMQLFHRSSTIAASAHRQALNADAGDSRRTVLIATMEYDIEDWDIKIKIGGLGVMARLMSRNLGHQNLIWV
VPCVGGIEYPVDQVVEPMNITVMEKTFQVQVQYHCVRNITYVLLDAPVFRAQSKSEPYPPRMDDLDSAIYYSAWNSCIAE
TLKRFPVDLYHINDYHGAAAQLHLLPKTIPCCLSLHNAEFQGLWPMRTERECKEVSQIFNLKLSVIKQYVQFGDVFNLLH
AGASYLHIHQSGFGAVGVSRKYGKRSWARYPIFWGLKEVGSLPNPDPSDTAEWKRDEQIEQALVDPVFEAARADLKHRAQ
AWAGLEQMPDAELLVFVGRWSMQKGVDLIADVFPSILEMYPKTQLICIGPVIDLYGRFAAIKLNRLMEMYPKRVFSKPEF
TILPPYIFSGTDFALIPSRDEPFGLVAVEFGRKGALGIGSRVGGLGQMPGWWYTIESMTSKHLIHQFKQAIQEALNSKPS
VRAIMRARSGKQRFPVAQWVEELEVLQSSAIAKHKAHTKPGHRRNLLRQMSVSVSRRLGKQQVSEKSPCNSKSGESSSEI
STRISPGNDRPGLYRRSISQVLSWLGSALQETSLDEREGSRSTEQNSQSSSRTASNSPQHTQTETRDNGELVEAVPASRR
MILLSTQDESTSGSEANSHSPSGVNTPIPTASEDTISQATTTYGQHDNSSRQTLLSVDNVIREKTGFNLQSVNPFFTDST
RVYAKKFERRLSHLDGRNSQDQLCIEEYLSKSEKDWFNRYRDVKLGRNSSFHGTSASSIFKVRVNSSFTESDGTSPTAPG
```

```
ASEEEKNLDDFELPRDYVPPSGLRKLLLYRLGDWPLYSVFLAFGQIIAANSYQVTLLNGEVGEPAEKLYIIASIYLVSSI
VWWMLFRWFKSIFVVSIPFLLYGSAFVFIGFSPLANNPLGRWWMQNVATGLYAAASSSGSIFFALNFGDEGNAPVQSWVY
RACVIQGTQQIYVTFLWYWGSKLAAGSQAGSTQISLTDSHPRLLIGIGIGIAAVLWMIGAAVYLGLPDYYRQAPGKVPSF
YKSLSRRKIILWFFYAVFIQNYWLSAPYGRNWLYLWSSKHAHRWEIILLVVVFFIGVWAGTLWIFSILSKRHVWFVPIFA
IGLGAPRWCQMLWSTSNIGSYVPWAGSPLASALLGRGLWLWLGVLDSLQGVEEEEEEEEEEEEEEEEEEEEEANRRDTGF
GMILLNTLTRFHIAFTLIAAQVIGSIGTILARATAPDKLGPGDVFPDFSAGIHAGLSKADFWVCLLFILSVNILCFSFFR
KEQLQKP
```

2292 - 2311:	EEEEEEEEEEEEEEEEEEEE
2293 - 2312:	EEEEEEEEEEEEEEEEEEEE

A0A0U1M1L9 **A0A0U1M1L9_TALIS** (843 aa)
Putative transcriptional regulatory protein C3C7,04. *Talaromyces islandicus (Penicillium islandicum)*

```
MNGMSFQGWTMQPGGYALPYQEVELFSPPSATVRAILLKLQYHELCGGGGGGGGEEEEEEEEEEEEEEEEEEEEEEEE
EEEEAKNPNCREAGIICCYTDGKREKSKRQLATLSAKVQTYEEVIRKMSLRFGVSDEQLMSNAMTCDSNQIVLAEQSETA
SAFSRGRSLFANDNSERKSRSPSAASHAGTDRVQEDFNRDDSTRATGYIGKSSEVSWLQKLRKRVNEDVPDIKQSSPTPE
ANDDNLVTANNFYEDNKNVDIIEDVQSHGMPRQKIAELLLRAYFKSVHPSFPIIGMSTFISQYQLFFSQPTVKPGNKWLA
ILNLIFAIATVYAHMISADWRSDLEDHSVYFSRARTLSLQDTLLDHPDLQQLQIEGLTSFYLLATGQINRSWKLCGFAVR
GAIALGLHLRNVDPSTSDTSKEIRYRVWWALYWMDHLLSVITGRPCCISDGACTTPVPIPYDESDFQKQEAAQMLSNHSR
RGLWVHDWTPAPSTLASPSQLEDSKSTTETAGAKSDASETDWLKSLPSSMSLYFFHLATLTSIAKRANMKLYSAEAVQAP
WPSLEFTIQSLTLEANTWLAHLPESYDFKLLHTTQTMITQKTSLAFSYYSTKISITRPCLCRLEKHCQTDGTYEFCCKTA
ADCVEAATGLISLLPDSLETSLLHKISPWWCLLHYLMQATTVLLLELSFRAEHVPERAVEVSHAAKKSVKWLHELSHSSA
PAHRAWKRCNDLLHSLSQPLNLDISDLPSDEIMVDPPDSFVSVLESSLLEQQIPTPLPYLEPDALDFLDKQQTQSESQSS
SRSNIFDEYLPYDPNTGQITGSFFPAASSLDLDFGYMLDRSVY
```

55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE

A0A0U1M7K0 **A0A0U1M7K0_TALIS** (170 aa)
Molybdopterin synthase sulfur carrier subunit (Common component for nitrate reductase and xanthine dehydrogenase protein G) (Molybdenum cofactor synthesis protein 2 small subunit) (Molybdenum cofactor synthesis protein 2A) (Sulfur carrier protein MOCS2A) (MOCS2A). *Talaromyces islandicus (Penicillium islandicum)*

```
MTTPKEAREQNLFQIHYFASAASYTGKQSESLPAPLPLSRLFPLLEGRYPGITQRVLSSCSVSVGLDYVDVPGETENGDS
GKEHGEEEVIIQAGEEVGIIPPVSSGHRLFSLLLNDKLYLTPLASPRNALDIGTVEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEKP
```

136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE

A0A0U1M8E2 **A0A0U1M8E2_TALIS** (436 aa)
Uncharacterized protein. *Talaromyces islandicus (Penicillium islandicum)*

```
MAPKIFSLDGKSLKLDTSEDIEAHIKPLLEDTTHTEVHLGGNTFGIAASERLATVLATQKNLEVADLADIFTARLLSEIP
```

PALSALLNALLEIPTLHTVNLSDNAFGLNTQAPLVDFLSRAVPLRNLILNNNGLGPNAGTHIADALTKLAERKEEARKEG
KDVPLLESIVCGRNRLENGSMAAWANAYKAHAKGMRSVKMTQNGIRQEGISHLLKEGLSHATALEVVDLQDNTFTNLGSI
ALAGVIQGWTSLRELGVGDCLLSARGGIKVAQALAAGKNQKVETLRLQYNDINAEGVKQFLFASKTALPALRRIELNGNK
FTEDDDNVEELRDLLEKRKEEHGSDEDPKDTWGIDELDELEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKPHS
ADKTLKETVRAEDELVTQKKDAAVDKLADTLSKTGL

361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE

A0A0U1M9P7 **A0A0U1M9P7_TALIS** (158 aa)
Uncharacterized protein. *Talaromyces islandicus (Penicillium islandicum)*

MRYIAVLASILAVAAADDFGSWSLYCGSSCSGGTLIGTGDLDTNIINSCTNLGATYDYCHLEVQEYPNMYRAVLSSDGSC
SDSSNPVIVSGYKLNKGSKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEESKQQSEDERMSEFTSEKLDK

100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE

A0A0U1MA58 **A0A0U1MA58_TALIS** (1133 aa)
Uncharacterized protein. *Talaromyces islandicus (Penicillium islandicum)*

MSTSPPRSATSSPDVLGPEGDALYLISSPVPDFRGRQSWLPPYTVRTPRRKERLPSRSPGKSAQTLRFDDIVLPPKSPSR
PRSISPTKMQPDGSLSPWRIRVTVEAEQDEDGENTQGSPRKKLKPSAITTKVPLKDEEGNTPSEKRRRGRPRKSDLRTTS
PFPIKGSPGHTPKLKPPTPGKRPRGRPRKSLQSQTVAQSIETDHHPATTPTVETLHGIANRNSPVPLLEVDEGSVADSQS
DSDPFLDMVESGSLNSEQLATNIPRRFSPSGSENSPPQRTKGVRVIEGTSELTPIKSVAAARRNQAVSPENTLHAGHTPR
LRRSYPTPASSSLVDEHRGDQKRQQLREDEDAPIVMDPTDEHHEFDTIMESEGFSMVSLESLPSAKQAGFSSILNSAKGA
LKPFFEREKPVPFNEKSQVTATLGNNNTGLPESSPIELDPTQNSIGNATARRPEQPMPKETRSLPSLARIVRIGLALHGT
MRQRHGEYPVDDEELRNSRKRLEKTFSTFNEDMQYQLQAGLRFGEQLARSRIEAEHHRALVIEDEDEEEEDDEEEELVEE

```
VEEREEETQEEDEGDENENEEEKEEEEAEETEETEQAEEGEETEPRESDTSFQEESGLRHNLPQKVSLSLSQREAEWQHE
REVVSQQINMAASSDVIVLGSDEDSQPQPENEEPESPLDGDDEQDDDGDFDDIWQEEARDRSFDKRTGRAFQAEEKSLIL
PASPKRLEQHDSNTDRKAYYEWNPDKGEIPPLGRSRMAQLQDEEVDLSLLLRPRDTPKSRKYYANSSPHTVVSQKPQPNP
NAAIEVVHNERRSPRDIRLSRGLNRTDPSMTSDGVRDYENTHDDENYHEEYEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EDGGYEEEPQEERRDDEVHAIQISDQSATPEHDSDVQNSVITPDAGISVSKPSWFRRLTNNVTPGWWAKSEKEQFVETEW
PLDESVSPPFNGNIDELYPPVMESTPNLKRAREPEPEPLSSVNVRHQPHKKARSMALATSGYFTDAHYVALRRLYSTAKR
FPEQFPYHSNAYRDEMIGDSFWTSDGEHGLPIAEIQFGILDRFVSDLSEADLQNGGSGEIGWTEDDLHKRLFSIIVGEQI
RREEKELQTRSRR
```

852 - 871:	EEEEEEEEEEEEEEEEEEEE
853 - 872:	EEEEEEEEEEEEEEEEEEEE
854 - 873:	EEEEEEEEEEEEEEEEEEEE
855 - 874:	EEEEEEEEEEEEEEEEEEEE
856 - 875:	EEEEEEEEEEEEEEEEEEEE
857 - 876:	EEEEEEEEEEEEEEEEEEEE
858 - 877:	EEEEEEEEEEEEEEEEEEEE
859 - 878:	EEEEEEEEEEEEEEEEEEEE
860 - 879:	EEEEEEEEEEEEEEEEEEEE
861 - 880:	EEEEEEEEEEEEEEEEEEEE
862 - 881:	EEEEEEEEEEEEEEEEEEEE

A0A0U5FSQ9 **A0A0U5FSQ9_9EURO** (866 aa)
Uncharacterized protein. *Aspergillus calidoustus*

```
MAPTTSSARQKHARQQTSLRRLVKQHKIHFYSIGDHLPASLEREEAAVQAIGNATYQANLERSSQVTQERGEEMWEAVRW
CLKNENNEENWRHEVETNILNRLTKYHACVKCGKRLWRADFEFPIGDEQGARWENLRRRRDRRDKCACKSRIMGDRRPKD
RVFQSLRGDEVRYGPDLRDRIPGGIRPDLVVGLFNGPKSTTLLDAPSRADPAKRVGDLVKSDIFAKEDPDVQDDSAMIFP
FLILEAKRARAPDSLEDIERQMAFPAYEMLRAQNRLLENAAGSEGSDRLPRVWLVSFKAQIWRLYVATMEQDEKEEYNYN
IYNVWGGDVSGRSDALKLVLLLDCVFDWALDIYRLDIFESLQSMVAPNPRITARNVAPTVSDLSESLEGLVIMDPVDLRV
ENLNTIQEDTSEDVLKYKHGWIRDGRQVLTPGEGLLITQANIADIFDNFEHPDHAKRFARMIWALLSKEAWLFSSELILD
KVREVWTGQKEHRQQVPDVPIYVQLEVYVYFDTSWQLTRKLIFVAVTKDSIPELFKRTQYPKRRSGEIDIARHQIHEEKF
TAELRDRRKPRVPDRPSEAHFNIEEAVRRWHCSLSPSRGSWDRDPLGWSRVSVPSCDKAFQEIFRMYQVGQREPSESFLK
IWHSVQSTRFEVALDQDWLVVGDTDEGDWRHIHPHNRAPRLCVFVFEDLHDLDTTEFGEFFAYYEKEGFKAIDYHYTVLR
GKYLSGSTHFDDNRLESESCWLMGPISPSGGRGPIYPSLALLLGEWVRELRNGEPEHSDAGSDGEEYCTDDSDHREDLGN
LKSGKASVDSIDGEEGVDSDEYEGSETESSDYVEEEEEEEEEEEEEEEEEEEEEEGKGGGRGRWK
```

834 - 853:	EEEEEEEEEEEEEEEEEEEE
835 - 854:	EEEEEEEEEEEEEEEEEEEE
836 - 855:	EEEEEEEEEEEEEEEEEEEE
837 - 856:	EEEEEEEEEEEEEEEEEEEE

A0A0V0HBB9 **A0A0V0HBB9_SOLCH** (206 aa)
Putative ovule protein (Fragment). *Solanum chacoense (Chaco potato)*

```
MEKGFVKIFSPEKSGKRLKIPTCFTYYKNEKLPKKIYLRDRFGNMWPIGVNKIGGKFYFQYGWEKFIEDNTVEVGDFLIF
DYDGNRIFDFKLLGRTKCEKKGVGGLKLTVKEEEVEEMSVEHQKSADPKGKNWASNNFNSSSSDDNDVEYMGEEEEEYKE
TKKVPCHAEEEEEEQEDDEDEEEEYEEEEEEEEEEEEEEEEEEEE
```

186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE

A0A0V0RVW9 **A0A0V0RVW9_9BILA** (124 aa)
Uncharacterized protein. *Trichinella nelsoni*

```
MCSQLRIELFPNGEWAVSDPSPRYSKKMEMRCAEVMQEKSTKSKIKGDVEEEEEEEEDNDADADDHNSQKEETEEEEEDK
EEEGGGEEEEEEEEEEEEEEEEEEEEEEEEEEKEEKEEEEEEEEE
```

87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE

A0A0V0THI3 **A0A0V0THI3_9BILA** (102 aa)
Uncharacterized protein. *Trichinella murrelli*

```
MRGILTKEEEEEEEEEEEEEEEEEEEEEEEEEEEAINHLRMKSNSIRVESCSSTSRHYHQRRINDPNRSVIDLCKCPLVE
GRTDGKANLFTFVSFSVKEWKI
```

8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE

A0A0V1BRG0 **A0A0V1BRG0_TRISP** (164 aa)
Uncharacterized protein. *Trichinella spiralis (Trichina worm)*

```
MPNYWANDWYLFESLETSNSLYGETYSMLLRNYDEVVQITIRLVDVVETLVLFQECEVLNYVITTMCSGDAQLLLDNQVI
RIYPLCEVLTNSVLIRCSCINETVMFVIVEXEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERIFLSDFYLYRNSSY
RMDQ
```

112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE

A0A0V1F3V4 **A0A0V1F3V4_TRIPS** (74 aa)
Uncharacterized protein (Fragment). *Trichinella pseudospiralis (Parasitic roundworm)*

```
LEVSGEEEEEEEEEEEEEEEEEEEEEEEEEEVEEVEEVEEVEEVEEVEEVEEVEEVEEDSSVGSRLILAAVMQT
```

6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE

A0A0V1FA45 **A0A0V1FA45_TRIPS** (102 aa)
Uncharacterized protein. *Trichinella pseudospiralis (Parasitic roundworm)*

```
MLAARSFSNKNHTQKKQEGSSSGSGSSSSSHSGSSGSSSSSSNSNSSNSSSSSSSSSSNSSSSNSSNNNRKKKEEEEEEK
EEEEEEEEEEEEEEEEEEEEEE
```

81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE

A0A0V1FFC0 **A0A0V1FFC0_TRIPS** (690 aa)
Mucosa-associated lymphoid tissue lymphoma translocation protein 1. *Trichinella pseudospiralis (Parasitic roundworm)*

```
MNSSSSGNKDFSCDSCMDASSNSKFSSKTTLADIPWLTAKHLSSSLATNSKWRQLVKHIPLENMTSSDVIQSLQQSCSPA
EALLQFLGKRQTTVADMLNYCHEAHLLEPQLILHRKFQHVKIVEQLHLIVENSSMSNGILACAATGFPYPEYHWYCDGHR
IDTDESNCTLFIDNKNLSQGAWYYCIVSNEVKRSDIWDEFYFKDDKQYKSALQTISIHVDSTGFKFEEKDDDEQGEEEGE
DEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEANSQNSSVYSKDEGVSDISDLKSKDIVSSGNIDLESRLYAVDK
VALIICNSKYENIPTLLTPFQDGSTLAECLIQLGFKTVTLSDLTLSEMHFMIKEYCQLLGSGVYAVLYFVGHGFEVGGQC
YLLPTDVKSHMVSFTECLCTEEILTMMQEMDPAVSVIFLDICRRQENFEIPEKDFKRYTPRVKRNCIIGYATSFGEGAYE
IVGESNGVFMKYLKKYVKLEKPIAEVLTLVMQDLEMDDRARKFQFPEIRTNLSKSRSLADPLIYTGHTETFDLRTCRWQQ
IHQLPEPLQVVFETFDVYIMIWFDFCAFFSNLVLVYASVFSLCSSNPDYSKKYSTNLIFPEILKPISSVVELGRRKRLTL
KTQLNQLQKLKQPLVIDVELIYNSTGEMMGRRTVTVGDILISSLHHHTVH
```

242 - 261:	EEEEEEEEEEEEEEEEEEEE
243 - 262:	EEEEEEEEEEEEEEEEEEEE
244 - 263:	EEEEEEEEEEEEEEEEEEEE
245 - 264:	EEEEEEEEEEEEEEEEEEEE
246 - 265:	EEEEEEEEEEEEEEEEEEEE
247 - 266:	EEEEEEEEEEEEEEEEEEEE
248 - 267:	EEEEEEEEEEEEEEEEEEEE
249 - 268:	EEEEEEEEEEEEEEEEEEEE
250 - 269:	EEEEEEEEEEEEEEEEEEEE
251 - 270:	EEEEEEEEEEEEEEEEEEEE
252 - 271:	EEEEEEEEEEEEEEEEEEEE
253 - 272:	EEEEEEEEEEEEEEEEEEEE
254 - 273:	EEEEEEEEEEEEEEEEEEEE
255 - 274:	EEEEEEEEEEEEEEEEEEEE
256 - 275:	EEEEEEEEEEEEEEEEEEEE
257 - 276:	EEEEEEEEEEEEEEEEEEEE
258 - 277:	EEEEEEEEEEEEEEEEEEEE

A0A0V1IK40 **A0A0V1IK40_TRIPS** (60 aa)
Uncharacterized protein. *Trichinella pseudospiralis (Parasitic roundworm)*

```
MHRDLSSAFSFKLLMLLNQISVFKWRTTIKTEQEEEEEEEEEEEEEEEEEEEEEARQETRP
```

34 - 53:	EEEEEEEEEEEEEEEEEEEE

A0A0V1LKN0 **A0A0V1LKN0_9BILA** (123 aa)
Uncharacterized protein. *Trichinella nativa*

```
MSTLEVMTLSCRTEKIVKAKQLEQTKQKERKRLDEEEEEEEEEEEEEEEEEEEEEDDDDDEVALMLYGGFKLRTAEPLIL
HARMENESHKFPNLPILYCLCVNNFSRKMKVPVICFDTMKSLP
```

35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE

A0A0V1NWL6 **A0A0V1NWL6_9BILA** (1570 aa)
Tyrosine-protein kinase receptor (EC 2.7.10.1) (Fragment). *Trichinella sp. T8*

```
MTVVNGNRTEINRSENCSHVTAMTTTTSRLFGRNVRAGGGLLLLMLWSSVAVVMLLLPLVVPPCRGMDEVVCSGFAMRNS
PRQFYADLDDRLRLLHSKCTVVEGDVRLTLMTSQNLTDDDFRLVTMPNVREITGSILVFQVLGLQSLGSLFPNLRLIRGN
SLVHNYALVLFQNPNLREIGLTNLMEISKGGVRIVNNPELCYAKTVAWEELCREPYAHVVIEGGKNANLCSEKCVGDDRL
CLERRNGRACWNHDHCQLACPVDCARQGLACNGTTADGQRPFCCHRSCAGSCTGPADHQCMACRRVTHNGRCMDQCPDGL
FELEQRRCVTRRQCRERRPVVDQRTGHSLLYKAVDAGRLCSLHCPAGYDEHPADRRLCTPCAGACSKKCPGGDVRSLAEA
AQFRGCDVVLGALDITMQGGLTKNVAGKLEEYLGNISEITDYLKVSFSPPLVSLNMLRNLRLIRGRKLWNNKYALSVFEN
HHLSMLWDFDDSAGARQLRIENGRLQFHNNPHLCYKTIVDLAVQVGLGDNLQDLDVSPMSNGDKAVCEELELEIECRFVG
SDLVVIQWDSWNTSMMDHRMFLGYQLYYRPVEAGNVSIAENRDACHDSWKMMFFQTSERGAFVTDLQPYTRYAFYLATLM
VNSPGARGGVSKVIYVRTAFGHPSPVLVTRAESLTPDSITVEWLPPVKPNGDVTHYMLSVLPKKRPLWSERNFCDEPPDY
SSQTDRGKNSSSGQGGSSNGVCAQFKCCECQPSLWNQQHQLNTTNNGTVNSPASALLDPELLVNEQKERALFENIIHNIV
FVRNSRHRRHHGLQEPVDLTLTNSNNSSNNNNNSNNNNNNRWLKPMVVNVSDRRYTVTGLRHFTTYEIRIWACQNRSVVE
NFCSRREALVIQSTLMVESKDAIDENSVSVSNGSAHSPYHLFVRWAAPAEPNGGAVVSYEVEYAREADPADSGAAKPKRE
CTTGADFAAVGGMHFRHLSAGNYSFRVRAVSLAQRGPWTRKFHFVIVDAPRQLDTSVLVVSVGCSLVLIGVGVVLAVALS
RRHLKRMLPGYVQHVFSANPEYISQLEVYEPDEWELRRQDVELLNELGRGSFGTVYAGHGRNVVSSCGVRFGDCAVKTVS
QNGSVYDRWHFLVEASVMKKFNTAFVVKLYGVVSEGQPALVVMELMSNGNLRDYLRSRRPGAATPAPGRLELYAMAAEIA
DGMAYLEAIRFCHRDLAARNCMVSASGCCKIGDFGMARDVYVKDYYRPRGRRLMPVRWMAPEALQDAKFTSKSDVWSYGV
VLWEIATLASQPYAGLSNEQVFERVVERRQLLPRPADCPPGFYELMRLCWSANPRDRPSFGEIAFALCGHIPDNLLAGSF
SESKLFLAARNSSELADHHRHNDDIVTVQPAPQQLCKTVTPRLIPDRIFEMLVSGNALPEEEEEEEVEDLDDDDHHHLEG
RHLRLNAAGICRQSRTPAAIPPLFRPHRSWPQLNSQIQCADGACRCHSGDIIMTAWLCVLCGRIEKERKRKKSFYFIARD
VDGQMDEKLWTIHQALHASIIPHFSPIESEEEEEEEEEEEEEEEEEEEEE
```

1550 - 1569:	EEEEEEEEEEEEEEEEEEEE
1551 - 1570:	EEEEEEEEEEEEEEEEEEEE

A0A0V1PYJ3 **A0A0V1PYJ3_9ASCO** (1075 aa)
CBF domain-containing protein. *Debaryomyces fabryi*

```
MDGSKLSLASLKDKISSKMNLLNKSNEKPKKKENKKSEQKEAKQESAKPKENKRSEHKEYKATDRKSVSKEQTKSKQINN
DKEKTEEDILREEAFALGATEEDLALLKGIEDGEDSEQEFDGDSKSIDKTFSTDLSQFMKGIGLGKGEAVVVEDDEAVPE
LVDVEENDEEEEEEEEEEEEEEEEEEEEEEDEEEEEESSDSSSESESEVQEKEMNKKELASKSKEGVKDKSRRDPDKITDLS
SVSSNNLIVPSRTDWYNTPLERIDEPEKLDRFGVERLYERAKTVVEKDNKTYLEEFTSNNSQKKFLSQILADGTLNDKIS
ALTLLIQEAPLHNMKAFDTLLGYCSKKSRTAALQSINALKDLLLNGVLPDRKLVAFNKQPLTKNLSDVQVAIYYFEDYLK
KSYFKLISTLEVLSHDPIIHVRMNVVSHLFDLIKAKPEQEVNLLRLGVNKLGDIDNKVSSKTSYQILQLEQTHPAMKKVV
TDSVVDIIFKSNSDYHAQYYSIVTLNQTILTRREDELANTLVRTYFALFEKILVETDHHNAETNKEDKALGKSEKGRKNN
RKNFKKGKKGGKSVKNQEKSENEIIEDKNTRLFSALLTGLNRAFPFSSLPNETYQKHLDTLFKITHSSNFNTSIQALVLV
NHIITSQKLDSDRYYRTLYESLLDPRLVTTSKQGIYLNLLYKSLKNDTENVPRVLAFVKRILQICSHWLHVGAITGMLFL
LMQLSKTYPQIQDLSIDFASRPDEDDFENEEANNADRTYDSRKRDPKFANADKSSLWEIGQFLTHYHPTVAIYAASLLDG
NDQPKPDLGLFTLSHFLDRFVYRNSKLKPMTKGSSIMQPLGGAHTGSLLVKATNVANNEIPANTENWLNKKVENIQPDEK
FFHQYFTTKVSKLKNKESKKEGEEEIENEEEAAEMEDDEIWKALVKSRPEVEEASDEDDFSDFDADDFSDMSDDEETAEA
EGEDAALEGEEQEIEDEPQTVAADESDGEENDEESAMFAINDEDEYDSDEAPKMLGEDDLSSAESEPESDQGSKKRKASD
EKSAKSKRSKLKSLPIFASVDDYSQYLDSEDEDYS
```

169 - 188:	EEEEEEEEEEEEEEEEEEEE

A0A0Y9UZ33 **A0A0Y9UZ33_PLABE** (294 aa)
CCAT-binding transcription factor-like protein, putative. *Plasmodium berghei*

```
MKTNLVFALFFLFISVCESNASLRGQSESNISPEGKNADHSHQKDSGAQNEGSTSITGNSDTVLGGVGSTPGGVGVGGVP
GGVGVGTNVPGTGGAGAVPGVSPETEEPQTVLKEIPIESSENNKITEEELAVCEEIEESYDEIEEEEEETEQEQIPEDFE
INNEEEEEEEEEEEEEEEEEEEEEQTSSTENVEAGEQGNTQTQESNSTSGGESSTQVNTDENGQNKRKNTTGSTVPLINS
KFHDPINEDSRNVIESKQEAKEIMKTLVTMFDNIDVIDEPVIDFSDDISQFLII
```

164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE

A0A0Y9X279 **A0A0Y9X279_PLABE** (2962 aa)
NAD(P)H-dependent glutamate synthase, putative (EC 1.4.1.14). *Plasmodium berghei*

```
MKKKKSAKHGLYDSRYEKDACGVGVVADINGKSSRMVIQKAMQILLRLSHRGGVQSNNGDGAGILVGMPHEYFQMLSDTC
QLPFLLPEKGDYAVAQIFLPHNEERRLFLYHEIEREVYNHGLVVLGWRSPIPVRSDVISATVKKSEPFIAQMFVCKRSVF
KNYDDFNIYPFSDINFTDDTNLNLNELPGDIELLSFFIRKKLVRHNDMYFCSFSSRTIVYKGLLTPSQIYLYFEDLLSEQ
FTTYLAMVHVRFSTNTSPTWYAAHPFRRICHNGEINTISVNSLLFKERMQLAKAPNFFKSVSIKDLKPINEEKYIIYDND
DEIIHKRDTFEDIMLTKNRLKKKSRRNLLLKLKRDYTYNSSALNYQIKREYMNSDINSNSEFLNNMNEQSKSSSDELLDI
NEKNNHMKNAKNFIAGNTGISNPNDFGKSMKSQIKYGESKKTKGELSFPSDSSLFDNAIDFLTMTGREIEHAVMMLMPRA
YQKDPNITPLEKAFYEYHTCLMEPWDGPALVIFTDGNKVGASLDRNGLRPARYSITNYGLFVLSSETGVVDLPYDKITHK
GCVYPGKVVLVDFKEKTFLRHEDVLSKFLKLNNYKKWLDHYSIHLDNIIKPVSNMENIRMTAYKYGAILNKDNYYHHTNH
INNNSTSKIGQINNPDHHDDSLIKKLKAFGYTYDAFNIIISPMVKHAADGLGAMGNDTAFPFLSYLRRNLVYYFQQTFAQ
VTNPAIDPIREENIMSLMSILGKEGDILHCTYTNCQRIFINGPILNEPLYNMLLQLPDFPHIIIDMTISLDLLEHLMSKE
NSNSPTANGENDDDNFIKFDVVKSFSSPKKSFIQDYTPKAEDSAKKNGKDDPTTNNTGGNKKPRIFSKYLIKFIDRINTK
VESAIRRGSQLIILSHGNVSESRVPIFSIIIVGALHKYLLSKNLRTKCSIIVKAGDCFEIHHLAVLLSFGADCIYPFILY
ESLQFIKYGSNEARLSNHQLISNYRHATNYGILKIMSKNGISTLPSYKGCGLMQPLGISDEILKKCFINACDSIIGGVTF
EFVEKEILRIFNHAYPKRILALNVKNANDELDDFGEYHFRNIGNAQIHMNHPETINLLQRATKTGNFDTYKKYSELQNEL
INHCEIRGQLEINYKKCPSYNKKKKKNEPININLVEPINKILLRFCTGAMSFGSLSEEAHTTVATAMNSIGLKSNTGEGG
EAEDRIIQPNNNNNNEPNTSSAVKQIASARFGVTAYSLVNAHELQIKVAQGSKPGEGGELPGYKVNAKIASVRRSTPGIG
LISPPPHHDMYSIEDVGQLVYDLKNINKEAKISVKLVSKLGIGVITSGVVKGNCEQILISGMSGGTGASKWTSIKHAGLP
WEIGLAEAHQTLCKSKLRKRVILQIDGQLKTGRDVILGALLGAESFSFSTQPLITLGCIMMRKCHLNICPVGICTQDPEL
RKKFAGKPEYVINFFFMVANEVREYLASMGFRKFSHIIGRSDLLKKKSHLKYDEKRKLLDFSKLLFPGWKYYTEEQNKED
GDKGYTNSEKRKKKKKEIEKEREKEKKKKTLSVYSMHSSIINKYKEQQSGSLTLSEKNIRKQVLINENLNTDIKYDISKE
EKNGVNAIKERVGKLSYEQIEVEDGDDEEEEEREEKDNSSSEEDEEEEEEEEEEEEEEEEEEEEEEEEEYDETDGDDV
IEKNLSLTYREDMLKNVDKLNFQNKGLRKKSKSISEKKSHLKKKKSKPIPIFCCETQNHKLCDIIDRELIRRSKIALLNC
TPVNINMPIKNTDRAVGAMLSYHIIQKYGEQGLPMDTINVKFRGTGGLSFGVFLTSGCNFELEGDANDFVGKGLSGGIIS
VHFPKSSLFINECQKNMIVGNSVLYGATKGRAFFAGRAGERFAVRNSGAIAVVEGVGCHGCEYMTKGIVVILGEIGCNFA
AGMSGGIAYVLDINEKNVNHQMVDLKICKTMDEKMTLEKLLHEHYDRTNSYTAKMLLNDFDKNLERFTKVIPRDIKRVLT
EACIEFVKTGNEEAASILDDWASLLKSVDHPENMYKKAMQFFTTISDDISGLSKTLALRNVDGLIIYDILQGSNHRKLLR
MKNLGSNLVSGSHFNTEGNISFEADQNKIFDFEKFTYNLELCRANNRKWRRYAQIPFKCNAFSDFKSIFPNSLDDKSKEI
IKKYMLNEQYLLDVHLKSLNSNQFIEGLLNREDERDAYINQKQINPNIYSFKNMFYPADYNDLLCITDEKKSEQSICINH
DTNKLNTEYIENINKTDKGTGENTTINTQIAIHEKIAKKINIINSNENETVEKIPRKSIDNINQTKDVNSIKPFLVANPN
KVTGFMEYERLSHPLKDISSRVLDYSEIIVPINVKSKLHNQLLKTQSSRCVDCGTPTCHYPNSRGGGCPLGNRIYDWNNL
IYENEWKKALERLLDTNNFPEITGRVCPAPCEDACILSINEKPVSIKFIELSIIECGFIKKWIQPIIPHTRTGKTVAIIG
SGPSGLTAAQQLNKAGHHVVIYEKGEYFGGLLMNGIPSVRLDKKIIERRISLMRKEGITMKNNINIGVDIKLTELMQNYD
AILLATGYEIPRKLNIPGSNLNNIFYAMDFLSSFQKSLIKSDLMDDQYIDVSEKHVIILGGGKTAADCISLAIRMGAASV
LQFTRKESPSINKNKNSWPGLKNIFKVEYSHDEAIVIQGKDPREFCIRSLEFIPSNKDPKRVSGIKAIKVKPKRCNITRN
GVNNSIKRDLSKRTPSPQYNKSTTNINTSINGVTTGNESTNTNGSLSTILANTPSMNTNSQKNSTKKQCINKSNKLKQNK
HTDKRNSDESPISNNSNYNHKITNMNNEVVKNYQIVKPEKEYVDIPFTERVYKADIIILALGFLKTDDSIWENDTIKIEL
DNYNCIKTYNNIYQTAHKKIFACGDCRIGPSTVVQAIAEGRDVASKIDEFLTNSTSILPPCNTYYYYPKNYKYTPFSSAH
WG
```

1646 - 1665:	EEEEEEEEEEEEEEEEEEEE
1647 - 1666:	EEEEEEEEEEEEEEEEEEEE
1648 - 1667:	EEEEEEEEEEEEEEEEEEEE
1649 - 1668:	EEEEEEEEEEEEEEEEEEEE
1650 - 1669:	EEEEEEEEEEEEEEEEEEEE

1651 - 1670:	EEEEEEEEEEEEEEEEEEEE
1652 - 1671:	EEEEEEEEEEEEEEEEEEEE

A0A100ITT5 **A0A100ITT5_ASPNG** (500 aa)
Unnamed protein product. *Aspergillus niger*

```
MPNKKSTSSKKGTAANDDAPGTCQSTSGRKETREPRIRSRSSSPVRRTKTESTTTLTGVDPVSEIADKPQNLEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
CGEKSFNWHNVHKPLAIDYQHAYPKEWPTEIQRPFGLALDWALHLLLVKECISRFFTNPFWYLVPNPRPVNDGDDKGNLA
ANASDFGAQILELFEKMRESEPAAAQLWRLWTTRFSHPDHKLGYDMIAHRDSVADKICEEVLGQELVKSLLRSTVKCDLD
RAFLDMQKVFRSAAELSVKISCNLERLEFKTLNTLGHAFHHPSAEIELAEDYGGAEKEHCFDDRQILFLEFPAMYCCGDL
KDPFYKGILHKAVVYVEDVD
```

73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE

115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE

167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE
180 - 199:	EEEEEEEEEEEEEEEEEEEE
181 - 200:	EEEEEEEEEEEEEEEEEEEE
182 - 201:	EEEEEEEEEEEEEEEEEEEE
183 - 202:	EEEEEEEEEEEEEEEEEEEE
184 - 203:	EEEEEEEEEEEEEEEEEEEE
185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE
190 - 209:	EEEEEEEEEEEEEEEEEEEE
191 - 210:	EEEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE
194 - 213:	EEEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEEE
196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE

A0A103XT77 **A0A103XT77_CYNCS** (508 aa)
Homeodomain-like protein. *Cynara cardunculus var. scolymus (Globe artichoke) (Cynara scolymus)*

```
MEKQMLFDLQGKYGNKWAKIATYLRGRSIYHVKNVWCNHQTKMARFNKDEDEEEEEDEEEEEQKKKKKKKKKTKKKTKKK
TKKKKKKKKKKKKTKKKKKTKKKKTKKKKTKTKKKTKTKTKKKTKKKTKKRKKKRKKKRKTKRKTKRKTKKRKTKKKKTK
KTKTTKTTRRGRRRRRRRRRRRRRRRRRRRRRGISRGRRRGRRRGRRRGRRRGRRRGRRRRRRKRKKTKRKTKRKTTKKKK
KTKKKTKRKTKRKTKKTKTKTKTKTKTKTKTKTKTKKKKKTKKKKTKKKKTKKKKTKKKKKKKKKKKKKKXEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEKEEEEEEKEEEEEEEEEEEEEEEDFKQLDSGMTRAPCKNFGSIICNGDFQMETTDNFIITMATTKI
AFKPKILCNIMSTRSERVDDLCRHDEFNNAEYETPSLTASTEIDDKESEQNCAPRSIASSSSSCAGQRDYKNKQEQVQVG
KQVQTRQQRVSDGNRKSARRLERFSALK
```

304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE
306 - 325:	EEEEEEEEEEEEEEEEEEEE
307 - 326:	EEEEEEEEEEEEEEEEEEEE
308 - 327:	EEEEEEEEEEEEEEEEEEEE
309 - 328:	EEEEEEEEEEEEEEEEEEEE
310 - 329:	EEEEEEEEEEEEEEEEEEEE
311 - 330:	EEEEEEEEEEEEEEEEEEEE
312 - 331:	EEEEEEEEEEEEEEEEEEEE
313 - 332:	EEEEEEEEEEEEEEEEEEEE

314 - 333:	EEEEEEEEEEEEEEEEEEE
315 - 334:	EEEEEEEEEEEEEEEEEEE
316 - 335:	EEEEEEEEEEEEEEEEEEE

A0A103YFC9 **A0A103YFC9_CYNCS** (73 aa)
Uncharacterized protein. *Cynara cardunculus var. scolymus (Globe artichoke) (Cynara scolymus)*

```
MSHDPQESVLEDEGEEEEEEEEGEEEEEEEEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEETNSEDESNEVE
```

36 - 55:	EEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEE

A0A109UVW8 **A0A109UVW8_9SACH** (612 aa)
HBL351Wp. *Eremothecium sinecaudum*

```
MGPIVKIKKPKNTGDDQGDGQPKLKKIKLKSSTVRDDTKKTTHQSPQPSNAANTKIKLMIKKKDIEPSPSSDSKQSMKLK
LNIKRDSITPVPSASSGAKTKAPKIRVKPPRIPGEGYDSEASDIEEDPLIEEGIILRVLPDIQAEFVKNSIESGDYSGIS
IKWKGERHAIVRINDYQYGAVLVNIPTLLEVNKSVDGKNLLKTFDVSQMLLCIAMINREEEVFDLHPPDTEDLVKKHFER
YQAEITESRKKILTGFQGGSLTDAESKHLDAIAEKAYDYKHGITPPLYNVRNRRFRRRMGSTEMDYVEKTVELLLKQDAE
AEEFSYDLVDEDSLAQKTSSNIDLVNYAKQNSTNAMSPSQTAAANLSVDSTLFGDKFDNVDHEDHEDFELELEQALQDSS
DREKGRTLSGDEQPPADEAGDEVEQDNGEEEDEDEEDEEDEDEEDEFGQKNPKPETNEDLQHNELLKDELGELESILQQN
KDKLAKATNPLLKSRFIDSINKLEKEVEIKRKQLLASEETLQNSNTIAPEVPVAPTSRPPRAEDEEEEEEEEEEEEEEE
EEEEMEEEEEEEDEEEEENNEQQPTDQRSQQDEELDQDDMDMMILFGAEGDD
```

545 - 564:	EEEEEEEEEEEEEEEEEEE

A0A117NL39 **A0A117NL39_9EURO** (191 aa)
Uncharacterized protein. *Penicillium freii*

```
MYQNRISNAQRDPFEEEEDEYNNDDIEVDYYKYSGIDYKEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEGANHNGYYKDEIEYSDEYDNDDHREEERYIGYTDTENKDGYDKREGEYSEDRIDQESLDHNSINEGPEFAYHT
ERELECIDIGLIRRRAQNHYRLLLTSGFILG
```

47 - 66:	EEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEE

68 - 87:	EEEEEEEEEEEEEEEEEEEE

A0A117NLA1 **A0A117NLA1_9EURO** (46 aa)
Uncharacterized protein (Fragment). *Penicillium freii*

```
EEEEEEEEEEEEEEEEEEEEETRVFLLMVVVIAGSDAYGYGYAYAG
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE

A0A118JVB9 **A0A118JVB9_CYNCS** (119 aa)
Uncharacterized protein. *Cynara cardunculus var. scolymus (Globe artichoke) (Cynara scolymus)*

```
MKMRHRRQQLLGGEGVGEDEREAGRGTCGSLESGASLFSREEEEEEEEEEEEEEEEEEEEEEEEEEEEEEQGEGIHRFFG
QFFLGGENFSRRWREETRLYLGMERRDAMVAMEAMEAVD
```

41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE

A0A118K2K7 **A0A118K2K7_CYNCS** (248 aa)
Uncharacterized protein (Fragment). *Cynara cardunculus var. scolymus (Globe artichoke) (Cynara scolymus)*

```
RRRRKRRRKRRRRRRRSKRRRRSRRRRRRRRRRRRRRSRRRKRRRKRRRRRRKRRRRRRRRRRSRRRRRSRRRRRRRRR
RGEGEEEGGEGEEEGEEGGEGEEEGEEEGEEGGEGEEEGEEEGGEGGEGEEEGEEEGEEEEEEGEEEEEEEEEEEEEE
EGEAEAEGEGEEEGETEGEEEGEAEEEGEAEAEGEGEEEEEEEEEEEEEEEEEEGEGEGEEEEEEEEEEEEEEEEEEE
EEEEEEGE
```

221 - 240:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEEE
225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE

A0A122IQI6 **A0A122IQI6_PLABE** (2623 aa)
Uncharacterized protein. *Plasmodium berghei*

```
MNKNFNISNYNLDLIKCLQNESGIYFILDPTKAIHDKKHSDVYDIFIPENSDGVTLHVQKVNNEYKCIGVSITKRGIDIN
TGTRIFNTKIADWLEQLFNFNKTLGSNNNESNNANSNSNENEDGNNNTENRTNNLNGKNNWSNMERNGANNHGFGAIVNN
KNTSINANPINNIGATNNNEQGDAIGDDKDANGGDGNDNLENSDDNNNSIINNGNNNKYNNNYNNVRHNLSNNQAGAPIA
NLIKNSKGGYDNFENNDNYNNAINMPNKTKNSKNAINQGNCNLNVNSNLSAHIIPSSNLSSPQSKKQNQHTKQIRLNQMN
NSHKSHLMQYHNSNYDDKNSKLYNNVNSSNTVINKHISSENSGVLHASASNNNDAVKVNKIGCNTRQKNGPHILHNGNNN
RDGNNNSYKVQQQVYNENLGYRPTLFNLLEVLSNHNITTPDQRVCIRGIVTDFLNNELPHGKIYAYIGAVVGHDILHDII
KKLEKDPNRNAVPDASGLARIEASFGLSKSSYDFMNHNSTNSSMNNIPNVLFNNRNLNSALLNNHIYSNILSNVANNNNG
NIGDNMGHSGMLNADTEKIANNKTANDINNMMMKYGDNDKSGGSYNNNMLNINKKKALNMLNMRYMDNNNMTDMGNLGIT
NMNNTDNSYMNQMNIDLANLENLNNAKNSGLSVHDYLYASKNFHNGNPLNRNNNIGEDEEELMKVIKKNIETYKMNNIKN
ILISSVFGRIKWLKIMNESPHAYLYGHSIVKYGNKLYMFGGTNNKHKKVPFNHTLTFSLIYYNYKLLPLSGNYPEERDGH
TTHLVSLKSGLSVFLFGGANNNVYYNDIYILDMETRKWSKRIVNGKLPLPRHQHCSLVYPAKSEHLRGEKLNLTEGVIVY
GGKCLYNNNIVNLNDMWIFLFQANMWIRINYLGDQIPNGRYGMNLIWSDTNTLCLFGGEYLYSDKNCKTRKLLDDMWTFR
LNTPVLINNAEDIGTDIKHLPCENAINTQSELHKHQKGTKSDPHLNNQNGNNGISIHDNNNNNDNCYGQTNNLNDKNGIN
EIDNKMGNNNNESQFVDNKGSIENNNINNNNNINNNNINNNNINNNNINNNINNSNNNNNSNNNNNSNNNNNSNNNNNS
NNNNNSNNNNNNSNNNNNSNNNNNSNNNNSNNLINKIKITGEWKREIYEGNIGPRSNYSNIFITQRHQDFKGAEPKTIEKL
MLLCSGITYDNKLKIVSSDEIYVYFFSQKRWYLLKGKLYNEEYMYSARQRHVGCFFESKNVLGRSNRNPVPCIFIHGGFK
KNSVFGDAWLLSLTGENPLRLYEYDTCREKISTTQMPLYYFRDTHSISLLYTFCTLQKWLFGAFANLVDNSVYAINPAEN
VFIKYELTPEHDGMVSIQDDGEGLDFNAMNRILRMYGNYKNYDNNSFYNNNNNNNIKKHSLPNNDDSDSYEMDNYNENEE
EQEYNEETNNTNELNNNENNNADQNNNQYVNNNTKVDQMQQNAENYMKSEKGDGEKIYNNNLSGSNCEGMIKKENDTRNK
NVIVGKKKCTWSDSFYYKKKNQHYFYNDISNSIFDIKYGVGFKTAFARIASSCAIMSRTINTIGIGLLSLELMNHCDAKE
LATPLCMWKLPNKELINRNIANKSEHRHHQKLLMSYTPFNSPSLLAEQINILGTYSGTRLLYWNFRDDMDFIIFNPTNNN
IYLSSSPLSIDELKNKKQKNAQGEGSNFNSKYQGVKDIKFANRVIKRKGVFGDDENLKKLKTDIDNPDEEIEKDEDIVAD
DKNNNKYNNIDDKYNKDEDNIKKELDNMSTSSKNNIILDGDNNNNDENKNVNSTHYKEKLKYEDQLKYNNDNYFKKRMNL
```

```
FEYNSHLTSSISKEKYNMNQIFPLWDHPKDSIDYCLSTYLYWLYLRRSTNIFLQNTLLIPTSMRREKDMNPNKNNNDNNG
KKKGTKSTKLRNKKTTKQNDVNNIQNDEKIADIEENNGEIGNVSEIVPENNNSFVKFEQIQEKNDDNNHSNVQNEADTNN
ERGENISEQNQNTEINNNGIKNENVCTNKVEEEKEENNNPEDGKENNHCENDTNGGLTKLEKQKLEEALEYGISQDLQPQ
NSANKNEADGEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEETSKNNEDNGINETNNDVENEGNNNVENEGAKVEGEVNEV
GAGVVKTETPNEMETENNADDTEKNKKSKKENKNNVGKTIDNANEDSIANRRKRRKKKDGLSTGTVANGKKNGEIEKMKK
ENYVNVYMENFKIKDEYYINDPSKYTLYHFLRRKLYKMVESHYLFTPSDHTYGSFIMMGFLNDNNNTSIEVNRVCETGIL
LYYKNRLIKRLDAPFIDTPYNLFLSKYPPNPSLYEGNLYKYALTVIVNVPNWLKPSVSKQEFVHENNHAFLVFKKKLVTL
IKHYLSICEDIVKLNKWRESRDMKLKKYLEKMQNQSVKSRNDSDYENDIDNNKSKNFNIIYNNDEEGDNYMNDQNDGNKK
KNEEINYSGKNKTPYTNDNEPILHKNKKTKTNNNDDLNKRDHNPTSENESANIDNENNQENDVLEGEKEQEDDEYDEADQ
EAEDRPNFEDEKDEHEENEEEAEEEDPDDEEYNGEMDDQKNRSVEQETEEEMIEDEEYEPDDE
```

2091 - 2110:	EEEEEEEEEEEEEEEEEEEE
2092 - 2111:	EEEEEEEEEEEEEEEEEEEE
2093 - 2112:	EEEEEEEEEEEEEEEEEEEE
2094 - 2113:	EEEEEEEEEEEEEEEEEEEE
2095 - 2114:	EEEEEEEEEEEEEEEEEEEE
2096 - 2115:	EEEEEEEEEEEEEEEEEEEE
2097 - 2116:	EEEEEEEEEEEEEEEEEEEE

A0A125YRB8 **A0A125YRB8_TOXGM** (149 aa)
Uncharacterized protein. *Toxoplasma gondii (strain ATCC 50611 / Me49)*

```
MQPVKEKEGGVNERDTEAQSTERDKATISRARKGRDAEREEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGGEEGDKDGGEKVEGDGDDEEDDEEDGGGGYLI
```

40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE

74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE

A0A127Z7I4 **A0A127Z7I4_9BASI** (1013 aa)
Related to ITC1-subunit of Isw2 chromatin remodelling complex. *Sporisorium scitamineum*

```
MPLVKRKPVEPFPPPAASGSDDPDVFYLAATGEVFADFETYSNRLSFYNQKIFQCELTGRINLSYFEALKSERKEAIALH
KVFPEQLKGPVLKAVQFQITGRIDELVDRVYDRFKDRFFPAETVFFDLDGDKYYARLSKADPPAKPASAANGDHVDTDLK
PEPNGHAESWRSSPRASPSSTQIHTVGTNLTLELEQANQLDDPTKYVYTVDLIDDQDEPAGGTYVTSSQKLSRDRLAFSK
TILRKYLRDCIIRAANIGAEWRVKQWLAVKYGIPLEPTDEISQMNEALKDAKLSKRKKYLLTDGEDSSASTSKKLKSDGK
KLSASAQRKADEAEKAAIEKAREEERLRKKNLKYPIEDLELDPITKRELMFKMPGELERRKERPQPARGDHALPVPSELF
ETFLGTYFFLISKGKPLSLSPFTMDDYEQALQHKLSDPSCTLINEIHRTLINLIVRDGGSSLVANTSALAASLDVTASAP
ASVNGDADEGAASKAASDVDELETTPNGVYANGNGTNNNNNAEVEAIASLLEAARELSQGWEKLTIRPDNRRERWENSLI
GLIAARATPHVLPRMIGILSHLTAVEHAQGYIDGKFEADLYDTPSQRYPLLSLTDKLQIIDFLCMLAVETKPIKAFYDDC
EVQLTELRKEKIEVSRAKKELATAWEEFEGNKKDEEKDGDAAKGEAEGEEGEGDEGDENEKAEEEEEEEEEEEEEEEEEE
EEEDELASDSDTRSTREDSSFSDSGRGGRGGGSRQEILRQKALEKQAQEAARRIKEAKAREAHKAKLAENKILTAQRKKL
EEEENKLVRRDETIDREFRRLILASRMVPLGRDRFGDKYWWFDGVGSCSLVTGSEKYTYQTGRLFVQGATEDEVSLLIPD
PSTTVVNASPYAHLFHQPITASLITTRKSAELGGDQGTLQPGEWAVYSDPERIEQLFAWLRPKGHREHHLKQQLSKLKWY
IESGMKKRNADLTAHLRDNFADAVRRSARSSKVDNSTNGLAYMAWKNTLDKVK
```

703 - 722:	EEEEEEEEEEEEEEEEEEEE
704 - 723:	EEEEEEEEEEEEEEEEEEEE

A0A127ZGG7 **A0A127ZGG7_9BASI** (690 aa)
Related to NSP1-nuclear pore protein. *Sporisorium scitamineum*

```
MKRQADKQIRREDGDDASDDESPSQTGSMPATPAAGRVIRGLPKRRGAPSTPGTPGAAPAPAAPPASPLTFGAAASSSPF
GASTGGSNPFASLGGSTGFGSASSTAAPAAPTSTPTFSFGAASTTTPSSSSAAASQPPAKANPFGGFTGFGTAKPAAAPA
ASTASTTSTPSFSFGAPADSSAPSTSNAATVPSKTSTIVSGILGGMSSAPTAAAASSSTSTNGSTSSEEKEKLRKLRGLN
ISLQTTLSQKIKERLDADPFGDLTKLIESFREQYRKHRDGIESVNGSSSAANTATTSSLSSNATPLKPATNGASSSAASA
TSAPQSTSLPSFSFGKPVSTVSSSTPAATTTSSFSFGSSSSTATKPASSGFSFSPLPSTASASTTAPAPAAAKSSFSYGS
STKWSNPDVQEVEDDEQDEAADQGDDGEEDDEEQDDDDDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDAEDAEDSDDEV
EVIGTKTASSTSAPVKPPSFSLPTGGFSFDGKPVSTGSSEEDAKKAQATQNMTGAPKLDLPQTGFTFGGKPVNFGSSTAK
PAATTPAGDGASSSTSAAKPATPAFSFGTTSTTPAFGGFASSTPTTGTGFTFGSSKPASTPAFGSSTPVAGTNAAPTFSF
GTSSTNSPSGAGSNFANFSASTASKPGAFSFGSQTIKLSDSQGEKKDDAK
```

440 - 459:	EEEEEEEEEEEEEEEEEEEE
441 - 460:	EEEEEEEEEEEEEEEEEEEE
442 - 461:	EEEEEEEEEEEEEEEEEEEE
443 - 462:	EEEEEEEEEEEEEEEEEEEE
444 - 463:	EEEEEEEEEEEEEEEEEEEE
445 - 464:	EEEEEEEEEEEEEEEEEEEE

446 - 465:	EEEEEEEEEEEEEEEEEEEE
447 - 466:	EEEEEEEEEEEEEEEEEEEE
448 - 467:	EEEEEEEEEEEEEEEEEEEE
449 - 468:	EEEEEEEEEEEEEEEEEEEE

A0A132AK47 **A0A132AK47_SARSC** (412 aa)
Troponin T-like protein. *Sarcoptes scabiei (Itch mite) (Acarus scabiei)*

```
MSDEEEYSEEEEVEEVEEPVKKPQPPKQTEKPPEAVSEAEMAMDEKIRKKKQEEEEQWTDYIEQRKKQKQKEEEDLKKLK
ERQALRKQKRAEQERKLEEWKQQQEAQRIKELEERRAKEAEAKRKRLEDAERKRAAMQAALNKQNTTGKVERNFVITKRT
DGGPGAALARSEMGKTKEQLAEDKRIAMSFRVKPLDIDGLSVDDLKKKATQLWDMIVQLESDKYDLEERKKRQDYDLKEL
AERQRQINRNKALKKGLDPDALSGKFPPKILTASKYERQVDRRTFNDKKSLFEGGYDAMVEAQLEKMWQDRVKDFKEKEK
STLPKWDPEHPKNKETYEPGARTYDANDEDDLDLLDAFIKPPGFESSASEEVSKPASKPAAAAQEEEEEEEEEEEEEEEE
EEEEEEEEEEEE
```

385 - 404:	EEEEEEEEEEEEEEEEEEEE
386 - 405:	EEEEEEEEEEEEEEEEEEEE
387 - 406:	EEEEEEEEEEEEEEEEEEEE
388 - 407:	EEEEEEEEEEEEEEEEEEEE
389 - 408:	EEEEEEEEEEEEEEEEEEEE
390 - 409:	EEEEEEEEEEEEEEEEEEEE
391 - 410:	EEEEEEEEEEEEEEEEEEEE
392 - 411:	EEEEEEEEEEEEEEEEEEEE
393 - 412:	EEEEEEEEEEEEEEEEEEEE

A0A135SV53 **A0A135SV53_9PEZI** (770 aa)
Chromo domain-containing protein. *Colletotrichum nymphaeae SA-01*

```
MVDFSERSKKTMSRPSKKLVWFGGQPPTPADTSNGAATTNNTTTSSTSSIPSRQPQPPRKNPETEPRKLAVVLEDLPTYR
RYKRGSGPPLRPITLAPPRDSTAYIRDEFFVPPALSDDGKKRLQYVVGWTDLPAARVVVDAEQICDYVSPMAYEEWCAAR
AEERDEEERRLEEAENVRAVEEAVARERGVAISGEKGGKGAKRGRKRKHVAAELRTPPPAVDGEKKKRGRPRKNAPSLST
PSKSALVDEFRELDTEAEADVDVEMEDAADDEADDEAIFRQLNGTGTTTPLLLTEDSYDSGEQSSLPAGLEPPTKKQRTG
SPRPAFSRFMPGIETDTSSRSTPFDSSRGATSSPALPPLPQPPAPGLQGSSGRPRETPIFPPIPPASANHTSTPTAPRVA
KTQQPPKRSLLSIRDPPSTPQQSSSPKVQTPTPKASSMLPPPATAPPALNSTQNGTGADTSWTHTPIPKPGTTPLIQNTT
PWTISLAASKSSFYSQLTPSQPVQSIEQPISTTPIPIPKIPGPKPHIAPASRAPHQAPLPQTASAPPATTTGSKTVGANS
KPITTKLHTARKTGTPAAPTATQGDDEEEEEEEEEEEEEEEEEEEEEEDEQVYEVLRIEGFEDRVSRRSGKKLGRFFQVR
WKGNWPSSMNPTWEPESNIPQHVIQRFYFEKGTTPKRNVQAGAMDKYLVPKKYASVSRAVEGEDELVRGHGDHRNGNGNR
APAAAKAALATEGSDENAMDQIKVEGDDDEGNDMMLVTDFRNLLDPERRF
```

587 - 606:	EEEEEEEEEEEEEEEEEEEE
588 - 607:	EEEEEEEEEEEEEEEEEEEE
589 - 608:	EEEEEEEEEEEEEEEEEEEE

A0A135V8G3 **A0A135V8G3_9PEZI** (864 aa)
DNA-binding protein RAP1. *Colletotrichum salicis*

```
MSVGGITYDGVPGASGILFKDLKFFVSLRVPDRENGGTIAKLETQADHYITFANGPTPAGSLDWKFIRHSVDNGAIQETD
KYEMHQTPRASRPVGGSHPAGGSRPAAKANSAPVKGTRTPFSAADDASLAKWVLSHAANKKSGNEIYQVFETINNRHTWH
SWRDRWVKKLSKLPPAELEKLAAAAPEMVFSLPPAAATSSKRPEATRPAVKKAPSPAAQTISQLPPAKAAAKPRAESSSA
THQPDVKAPLTPAKRTEFTGAEDDLLIREAGRFGVTPDTKFFKKFSEKHSSHSEGAWRRHWTQILEPWLRESSKESLEES
GSLPEGPPTVDRKTRPNTASSGKSSRQGESSHNERPNESSGQSMEILAPEVAPSSASPMRKKGEAKQVLEPRVKEPTAVT
REKFYGDLGGYRIHNNLDTQINPEINDQPIDLWRLWQAVGDQYQKGAVEPDWAAVADGLGFHVEDAQLIQQCYTDYVAHF
ATCGILDEPDVESSEHDEVSQPDDEDAVPDVPLEPLQTQRAATPGASRKRRAITVETSGFPSTPNGRKKRQRLGPDDEIP
STPDDKLGLASFKNLGPSPSLSVKRWTASEEQVEVAEEMAIEEEEPRQDPAGKPRRLEPETQDFGFDDAFNAPDKSQDSI
EFDISPSQQLLGEEESVTPLPLSFKRDKGKGVDRNQSPTPAQVQESPAEEGEEEEEEGLEEGEGEEEEEEEEEEEEEEEE
EEEEEEEPDEAPKEATDQAMVDSQESTDQTVELEDLMNRFVSFGYPREDIILALMATSLCTPLATSLVKYLKEHRDLPNN
WQGVWTANDDKRLRRIDAAGSEGGPDGAKIQKYWDYLESKHTRIRIAQRRKFLAYLDETGQSSQ
```

705 - 724:	EEEEEEEEEEEEEEEEEEEE
706 - 725:	EEEEEEEEEEEEEEEEEEEE
707 - 726:	EEEEEEEEEEEEEEEEEEEE
708 - 727:	EEEEEEEEEEEEEEEEEEEE

A0A139A7F2 **A0A139A7F2_GONPJ** (215 aa)
LysM domain-containing protein. *Gonapodya prolifera (strain JEL478) (Monoblepharis prolifera)*

```
MSHKQDEYEEDVEQEEEEQEEAKAEEEADEEEEEEEEEAAEEEEEEEEEEEEEEEEEEEEEEEEGEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEASAVQVKSQPKKTTSKTSVTKQVTARNVTSTSSSGPGCKPASKTASSGSKQKVQARSVARAAESNH
GHGQAQNKGQWHTICSGDTYYKLSQKYCTTVQNLEKLNPGVNYNNLQIGHSIRIK
```

40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE

A0A139I258 **A0A139I258_9PEZI** (381 aa)
Uncharacterized protein. *Pseudocercospora musae*

```
MFESRRGKAKNVSGSSTTTTTTTTTTTLPVGLFACLLACRLAPAQAPAPEGLVSSCIASHRIMAGPVLRYDELEAEILGE
LGTMQDDQSRINFVIKELGASVKQTEDSEIKCHIYSKWLFTQHPTTSAKWRQQYSRIEELETITDRVTKKQNEANRRIDG
INKIWVGWDWTFPADSTPPSWPNGLLKSLRTLAGVNKDWRFATKEVAKASRVRRRTKGGRKTAHISTADVVEVIRKLKEP
EPEPEPEPTSEPSPSIEIGRGEPSCKRRKTGEEEEEEEEEEEEEEEEEEEEEEEEEEEEQEGRELPSYNGDSVFGGVGR
NSIIMKVLVQTAPCETKLAEQAERAVSAELRETASSQLAEHRAFQQRLMAFLERKAPQFWF
```

272 - 291:	EEEEEEEEEEEEEEEEEEEE
273 - 292:	EEEEEEEEEEEEEEEEEEEE
274 - 293:	EEEEEEEEEEEEEEEEEEEE
275 - 294:	EEEEEEEEEEEEEEEEEEEE
276 - 295:	EEEEEEEEEEEEEEEEEEEE
277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE

A0A139XP19 **A0A139XP19_TOXGO** (121 aa)
Uncharacterized protein. *Toxoplasma gondii ARI*

```
MQPVKEKEGGVNERDTEAQSTERDKATISRARKGRDAEREEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEGGEEGDKDGGEKVEGDGDDEEDDEEDGGGGYLI
```

40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE

54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE

A0A139XVG8 **A0A139XVG8_TOXGO** (133 aa)
Uncharacterized protein (Fragment). *Toxoplasma gondii ARI*

```
EEEEEEEEEEEEEEEEEEEEEEEEEVRGLAYVSRRRIVILLLRTAFVSRRGKTKTKGCKVPRQASDEETEGRRSSFSTQAR
PSGIRRASRGNWSRNEASRPQKNATQTKSKSRRAWTARKKEIEVCLLFARWND
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE

A0A139XWG2 **A0A139XWG2_TOXGO** (899 aa)
Daxx family protein (Fragment). *Toxoplasma gondii ARI*

```
EGEETQEGAHEELGRVEAEEDEEDEEEEDDEEDEEDDEEENEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEGDEED
EEEGEDLKLKTEQYSTCASASAGKYLPPHLRNRAQRELSNEAEFDGDNPGRNSTRQHGAAPASEASDKANFVASKLPLSC
LEKARQTATDAGRGLTQRLRGSLNRVSEGNVEVILQQISQEVKAALTQVLSGALPVPATSPALTPRDVRGLRREQEISFF
QEVNCIIVRLLMQSMVESKFSTASLVATQTALCCGLSCLLDASLCSQLLAALGEAFRKFFPLALAQADRRTETGEPVGLY
VRHTLMALCFLFDFNVVQPAVFLGLLQRLSGKVATTKEKGEAKNGERNEPLVEFQVECLLMVLRLGGGKLRNDNPVLFKE
AWNFLMTRVKGGEGEREVQVHSGREERPFEEQTREEQRARLARVSTSFSGALRQRQEGEQPATTGRLHYLARELEELKNN
KGNTIHLASKASQEAMRRWLQTSPLLAQSPLRQCAGEGKSVLVGVSSWQEVEDGVVSVSPSSHRPPVSPHKSVRVEKEKQ
SCLGDTGSEKALLDLAAKLRLHSEEQKKIFLAIMSAESPNDAVKRLLQLVPRTNKKKNFVTTAVAVLLHISLQQSAFNPF
YALVIARLCARCSCASWGRLEAEAEQPPLLGPLGSGRASVNQRRARGPCACLLPPDKEGKVFRRVTQRGLAAQNSAAHGF
PLRRLLHLARLEAFLIRIGVVELRVTRFVSFEGEKGQTDAHMGLSGKLGVFLKELCTELLCSPAFASVPLPGPSTASPLL
PFLSLSALPDVREAFLLVLEDVLLPEARKNACSENGKGAKESVNAACMPGRQGKCVRAKGAMCTPACGIRKDVISRVIWF
MKKQERYEEEDPNTFAFDA
```

42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE

A0A139XWI9 **A0A139XWI9_TOXGO** (439 aa)
Uncharacterized protein (Fragment). *Toxoplasma gondii ARI*

```
MRGRRPSQQRKKAASLGASSLLSSLPSSLPSSLFSRGDSVGRRLGKRRGIEEEGGKRKRARGGRSARHNFPEVDQQGGSD
LDELPSSEADPREAQQDGEGSFGHEQELAETLKKSKRAVLERKRRRHEERRQKKQIHRKQQQLWKLERQKALLERQLDMQ
KAAISGVRVNQGTGSGVRTPCGPEADSEDEEEDVSPRREKKTPSSLSSSLSSSLSSLDVRGSVLSALSAKDKKHTVSGEV
LLLSGVSSRSTEEHRKAEERRLALDAAGRQLDAELAFLESKLGIGKDSSKAGEKKKKKLAQELLDDGFDEDLQTLLDDIL
GGKAENRKRKTKTDYDHDEGEMEGEETQEGAHEELGRVEAEEDEEDEEEEDDEEDEEDDEEENEEEEEEEEEEEEEEEEE
EEEEEEEEEEEGEEEGEEEGEEEEEEEEEEEEEEEEDR
```

384 - 403:	EEEEEEEEEEEEEEEEEEEE
385 - 404:	EEEEEEEEEEEEEEEEEEEE
386 - 405:	EEEEEEEEEEEEEEEEEEEE
387 - 406:	EEEEEEEEEEEEEEEEEEEE
388 - 407:	EEEEEEEEEEEEEEEEEEEE
389 - 408:	EEEEEEEEEEEEEEEEEEEE
390 - 409:	EEEEEEEEEEEEEEEEEEEE
391 - 410:	EEEEEEEEEEEEEEEEEEEE
392 - 411:	EEEEEEEEEEEEEEEEEEEE

A0A139Y3V3 **A0A139Y3V3_TOXGO** (978 aa)
Ribonuclease type III dicer (Fragment). *Toxoplasma gondii ARI*

```
MRPAWSRLRRDQCWTLSSAGFCLSVCRSPAPPPGVTRLFLHRVWCTPLTAREAALERLWEPNEKQRRRRRRVLKKLAESR
GFLPSPLYESGGFCGLWRIFADAEAPLQAADLALDGASRWRQEKAKEKEQIEPDAGDGDGDEDGLWWTGNRRQREACFEK
REREGGDGKHDQCKEDEKCGAEKEEEEEEEEEEEEEEEEEEEEKKWSWQEEEKNRQRREILELIRSRIDAVVEGRRGPDS
VLQPLCLLLAHPIPATVAFHALHPEASEKAALHRGRRPRTGRTSFSLRASKAEKGSNAWTELEADEEGEEGDEEGEEEEG
EEEGEEEEGEEEGEEDGEEEGDEEDVPGLMRVEVEKPAKTMFIDLPTEYVEKVLLRFTHIHLFRLLQLSNFSPNGTCNSL
LLTVLQFLSALPFRRFPFRTVPSSSSLSSSASASASASCLGGDGEPRSRFVSLPLPACASASRLLPSHALSLFALPPSLF
SLLSLLSLAAEEAEESTESTLHSQSPPSSPRSSSPRSSSPRSSSPSTSAEQLKRQMVEACSSLAKAGVVDLQRVMFPFFL
LAPLSPLDAKSVDLDFIHRLASLRLFLRSGQRRSSGFLEAGACPPSLMLQHDRRLLRGAVESLHCLPSLSAVARLFCLGN
SARKLDYGGGRSLQKAERRSARKEQNEGDAAEENGAFNWPRSLLGTLPSSDRESESAKDTKEKRTPGSEKGERGEADGER
REEDGEKGATKEDGLFSKEEQFFRRLQSYKGSIFSRGDDAANAWTTEEQKLLTFFQQRNENALSVKEALREEGMEIFYHL
RSRGFEPVALRMTHQFGRSFRFYRLQTIHRNLTPRNVVINSDAGFTLGTLCRVYLSRFKQRLAEPHPDSQRGPQGNCFLV
QGVKRRQGARQLFSRERVVDGDEFAGLHAPQFAHLLPISEPMFQEISWMPAILYQLEVQGKHCDLVRRLRQEMRPFLFTA
EENISPPLGIVMHDIRIR
```

184 - 203:	EEEEEEEEEEEEEEEEEEEE

A0A139Y8H7 **A0A139Y8H7_TOXGO** (121 aa)
Uncharacterized protein (Fragment). *Toxoplasma gondii ARI*

```
EEEEEEEEEEEEEEEEEEEEEECWSAVDEEGEAGESGCREEERKVKGERDPSAEDVRRIGSSRTSETNWFSEVAGDPKKR
AVRGTDQQRERDIVEPGVARTASDDSGDAWVIAKSASVEYE
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE

A0A140KLX5 **A0A140KLX5_9BASI** (770 aa)
Uncharacterized protein. *Sporisorium scitamineum*

```
MSLKPLTPPLRFSTVAFAVTDQPQPYRQSDADEDHSDPRSHPHHRESVYRGAYPKARNLSFLSRLHLRTVLSLTPRPLDN
DAALLAWSSSAAEPSSSTSSTTETVAYNVSKHGIQLLHVRCEKPKDESGGLTREGAARALSILLDRRNHPIYIHCLDGVE
VTSTLVACMRKVQAWSNPAILAELGRALRDSNSSEWTEVPSHLSSFLTKFGQPDGIRLPPRNHIPSWLWPAPNPLSILAD
PYAWAGSAHPPSHLVTGHGQNGANSSSAPSSETNMSRNPSHTNNGTSDSHSSATPSTSAHRPTPSHLRRDRQLPIHHPTL
KLHFEHDPDLPPEPLASSTSASAASTTASSVQRPTTPSRPLHHPSLAASFHANANLRTPPHSRPASRAGRAPTSSSHHTA
SRSASLAPDETSARSPASTPRNPAPSLIVPRPASPTLQLPASAIPTVAAFLEDQVRNRNTGDSHVAPQRENESPSRRSRS
VVGSEVHLDLPQSNKSLYHPAQAPVSAQLAPTNTTSPIDADTDEIDVSTPRARPTTSSNFHIGIAGTIFHHDDDITDNEA
EHALSSRATGTTSTARVVVPLEQRRRRPVLDEVDGEQTPTKANSLAQRQALHASGQSTIENQAPTPARVQTASREGEPSQ
GSTSSPCSSFDKQRDDEQSKDIVQSPSTYGPDDDDYKSDSAKNTKIYQDQDENQASDKEQAQADAEVDEEQEKEEEEEGE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDEDEDDLALEALDLEGY
```

720 - 739:	EEEEEEEEEEEEEEEEEEEE
721 - 740:	EEEEEEEEEEEEEEEEEEEE
722 - 741:	EEEEEEEEEEEEEEEEEEEE
723 - 742:	EEEEEEEEEEEEEEEEEEEE
724 - 743:	EEEEEEEEEEEEEEEEEEEE
725 - 744:	EEEEEEEEEEEEEEEEEEEE
726 - 745:	EEEEEEEEEEEEEEEEEEEE
727 - 746:	EEEEEEEEEEEEEEEEEEEE
728 - 747:	EEEEEEEEEEEEEEEEEEEE

729 - 748:	EEEEEEEEEEEEEEEEEEEE
730 - 749:	EEEEEEEEEEEEEEEEEEEE
731 - 750:	EEEEEEEEEEEEEEEEEEEE
732 - 751:	EEEEEEEEEEEEEEEEEEEE
733 - 752:	EEEEEEEEEEEEEEEEEEEE

A0A140LHH9 **A0A140LHH9_MOUSE** (1664 aa)
Predicted gene, 35339. *Mus musculus (Mouse)*

```
MEDRLIETGNLYSSEGDHLPLDVDIYDHDIYDIPDPGVLIEKNELGLLGGPQVPHLFTNSQRWQNMSLRRRARLLWLHLR
AYLHDIVEKEKRAELRVARMTHGLEPLRHLEVEAGLCSVAQDPVGERFMVLDGEGYLHQHTKDGWEQAKLKPPVILNGLV
TVPGPLGEIGRFVGWGPAGLSILGPDFHLLWLSKPRVNKSLDQEPFCCLPVPSLSLLIVAQMGGSLELWKFRSGGRCLVP
CGSPLRPPPGLSGSFKCLALGLEPDHCSWHCFAAYGSAVLTFDLDDWALINVSQDLHKTIISDLDYCEEMDAMVTASRDS
TVKVWEADWQIRMVFVGHTGPVTAMTVLPNSTLAVSASQDGTIRTWDLRAAAQVGEVTLGCWTEDIISEKVSHLLAPASP
GWPVLSLCSKSIELWRVRTLYSPLAQLSAPVLHIQVAPVLPAPTDPSLPARLVCACADGSVHLVSATTGRTVSSLLLEPE
DCAAGVAYCLSREALWVLTRSGHLVRANAARCPMVVVHRLRPPPPPAPQPCCLHLYSHLTDSRSAFACWEIVRQNQGDML
RSAIAWAWKNKNRFLPVMGHSDGTLSVLDWRTSVTVFHTEAHSPGPVTAIGSTWSSIVTSGGDLTVKMWRVFPYAEECLS
LLQTFSCCHPVVMLCVLGKRITAGFEDPERATYGLVQFGLGDKMRCDHRPQDDPMDHITGLCCCPTLKIFACSSLDCTIR
IWTRENHLLRLLQLDGPPQALAFASNYGDLVFSLGSRLHLVSYSTYLPTSYLVKKLCLKASDVISDPPLPLTSKKPLTSS
QLQRLANLRGAASLSVALPFGYYKRSEPQQPVLKKDLETIIARDQDLQELIQGLVAPATRPPLTLKQRHKAFDNYLRLVY
GSDLMDINPERESQQWGTSALSTEKESSDQESQPGPVMIVGQAAFSNDVQPVFPLSFPQPPGGAPGKRFARPPRVSLPIP
PTYRRVHSRASQLLARSSLSCELGLGLDLQVQWDQFAVKAIDLDASIDYMKNRVPLLLQRKPAEPLSKLMGFFPATIKPY
RLRSRPIKFPGCVPNSVVLRQMWLQAEVSGLGSLAELSSQSRTKAESEDEQWSRRRKHSSLRWRNKLFGLLRLTRRKGGE
EEEEERRKEEEVFERDLIPSSQTSATEPEHWKPDTDSATDLISKLCNEASKTKGYSQPLQFGRSFLEERYGHLPKFLHYF
VVQNWFKKLFPIFTLEAYPEMGTIEGLASMFLDFLLKASWADRVNILNSLLRLLPDITGNLRIRLQAKLLYLLNQDDPPK
LQDPTQKEFVMIALQLLLACNLDVLEVVLEIISYYLYSPISCRQELKKLLEGLGLHDPEGVLFKEIMTWVEDLKVESKAT
IRIQCQQKLEDIYLQADTLEQSTVSIFVEPSRQVSQTSLISGGSLPAMSTSWTFSRASEMSLVPSPVEPIESMEQVTSIV
SIPELQMASSQAHMRIQKTKRVLADMLQTFGLEDSEYPFKFDVPRRESPLAQTLWARSQIVDLFHMDMLNLFCEKRRVQQ
QRSSMGEEKEEEGKEEEEEEEEEEEEEEEEEEEEHLPVSLLRRHQLRPNAVLRPRRERWLYPILRLQEAKAPDFGVFLRS
HKMQSRELTTDGSLRVLKLPLPRVDLQPFPPGWPTPPRALPPLLLQPSLQRYFLLQDTYPGAFS
```

1535 - 1554:	EEEEEEEEEEEEEEEEEEEE

A0A140LHU3 **A0A140LHU3_MOUSE** (172 aa)
Olfactory receptor 93 (Fragment). *Mus musculus (Mouse)*

```
IVQIPPTLTLPFCSHRQIDDFLCEVPSLIRLSCGDTTFNEIQLSVAGVIFLLVPLSLIIVSYGVIARAVLKTNSSKGRRK
AFGTCSSHLIVVTLFYSSVIAVYLQPKNPYAQERSKFFGLFYAVGTPTLNPLVYTLRNKEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEE
```

140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE

A0A143ZY09 **A0A143ZY09_PLAF7** (3135 aa)
6-cysteine protein P230. *Plasmodium falciparum (isolate 3D7)*

```
MKKIITLKNLFLIILVYIFSEKKDLRCNVIKGNNIKDDEDKRFHLFYYSHNLFKTPETKEKKNKKECFYKNGGIYNLSKE
IRMRKDTSVKIKQRTCPFHKEGSSFEMGSKNITCFYPIVGKKERKTLDTIIIKKNVTNDHVVSSDMHSNVQEKNMILIRN
IDKENKNDIQNVEEKIQRDTYENKDYESDDTLIEWFDDNTNEENFLLTFLKRCLMKIFSSPKRKKTVVQKKHKSNFFINS
SLKYIYMYLTPSDSFNLVRRNRNLDEEDMSPRDNFVIDDEEEEEEEEEEEEEEEEEEEEEEEEEYDDYVYEESGDETEEQ
LQEEHQEEVGAESSEESFNDEDEDSVEARDGDMIRVDEYYEDQDGDTYDSTIKNEDVDEEVGEEVGEEVGEEVGEEVGEE
VGEEVGEEVGEEVGEEEGEEVGEGVGEEVGEEEGEEVGEEEGEYVDEKERQGEIYPFGDEEEKDEGGESFTYEKSEVDKT
DLFKFIEGGEGDDVYKVDGSKVLLDDDTISRVSKKHTARDGEYGEYGEAVEDGENVIKIIRSVLQSGALPSVGVDELDKI
DLSYETTESGDTAVSEDSYDKYASNNTNKEYVCDFTDQLKPTESGPKVKKCEVKVNEPLIKVKIICPLKGSVEKLYDNIE
YVPKKSPYVVLTKEETKLKEKLLSKLIYGLLISPTVNEKENNFKEGVIEFTLPPVVHKATVFYFICDNSKTEDDNKKGNR
GIVEVYVEPYGNKINGCAFLDEDEEEEKYGNQIEEDEHNEKIKMKTFFTQNIYKKNNIYPCYMKLYSGDIGGILFPKNIK
STTCFEEMIPYNKEIKWNKENKSLGNLVNNSVVYNKEMNAKYFNVQYVHIPTSYKDTLNLFCSIILKEEESNLISTSYLV
YVSINEELNFSLFDFYESFVPIKKTIQVAQKNVNNKEHDYTCDFTDKLDKTVPSTANGKKLFICRKHLKEFDTFTLKCNV
NKTQYPNIEIFPKTLKDKKEVLKLDLDIQYQMFSKFFKFNTQNAKYLNLYPYYLIFPFNHIGKKELKNNPTYKNHKDVKY
FEQSSVLSPLSSADSLGKLLNFLDTQETVCLTEKIRYLNLSINELGSDNNTFSVTFQVPPYIDIKEPFYFMFGCNNNKGE
GNIGIVELLISKQEEKIKGCNFHESKLDYFNENISSDTHECTLHAYENDIIGFNCLETTHPNEVEVEVEDAEIYLQPENC
FNNVYKGLNSVDITTILKNAQTYNINNKKTPTFLKIPPYNLLEDVEISCQCTIKQVVKKIKVIITKNDTVLLKREVQSES
```

```
TLDDKIYKCEHENFINPRVNKTFDENVEYTCNIKIENFFNYIQIFCPAKDLGIYKNIQMYYDIVKPTRVPQFKKFNNEEL
HKLIPNSEMLHKTKEMLILYNEEKVDLLHFYVFLPIYIKDIYEFNIVCDNSKTMWKNQLGGKVIYHITVSKREQKVKGCS
FDNEHAHMFSYNKTNVKNCIIDAKPKDLIGFVCPSGTLKLTNCFKDAIVHTNLTNINGILYLKNNLANFTYKHQFNYMEI
PALMDNDISFKCICVDLKKKKYNVKSPLGPKVLRALYKKLNIKFDNYVTGTDQNKYLMTYMDLHLSHKRNYLKELFHDLG
KKKPADTDANPESIIESLSINESNESGPFPTGDVDAEHLILEGYDTWESLYDEQLEEVIYNDIESLELKDIEQYVLQVNL
KAPKLMMSAQIHNNRHVCDFSKNNLIVPESLKKKEELGGNPVNIHCYALLKPLDTLYVKCPTSKDNYEAAKVNISENDNE
YELQVISLIEKRFHNFETLESKKPGNGDVVVHNGVVDTGPVLDNSTFEKYFKNIKIKPDKFFEKVINEYDDTEEEKDLES
ILPGAIVSPMKVLKKKDPFTSYAAFVVPPIVPKDLHFKVECNNTEYKDENQYISGYNGIIHIDISNSNRKINGCDFSTNN
SSILTSSVKLVNGETKNCEININNNEVFGIICDNETNLDPEKCFHEIYSKDNKTVKKFREVIPNIDIFSLHNSNKKKVAY
AKVPLDYINKLLFSCSCKTSHTNTIGTMKVTLNKDEKEEEDFKTAQGIKHNNVHLCNFFDNPELTFDNNKIVLCKIDAEL
FSEVIIQLPIFGTKNVEEGVQNEEYKKFSLKPSLVFDDNNNDIKVIGKEKNEVSISLALKGVYGNRIFTFDKNGKKGEGI
SFFIPPIKQDTDLKFIINETIDNSNIKQRGLIYIFVRKNVSENSFKLCDFTTGSTSLMELNSQVKEKKCTVKIKKGDIFG
LKCPKGFAIFPQACFSNVLLEYYKSDYEDSEHINYYIHKDKKYNLKPKDVIELMDENFRELQNIQQYTGISNITDVLHFK
NFNLGNLPLNFKNHYSTAYAKVPDTFNSIINFSCNCYNPEKHVYGTMQVESDNRNFDNIKKNENVIKNFLLPNIEKYALL
LDDEERQKKIKQQQEEEQQEQILKDQDDRLSRHDDYNKNHTYILYDSNEHICDYEKNESLISTLPNDTKKIQKSICKINA
KALDVVTIKCPHTKNFTPKDYFPNSSLITNDKKIVITFDKKNFVTYIDPTKKTFSLKDIYIQSFYGVSLDHLNQIKKIHE
EWDDVHLFYPPHNVLHNVVLNNHIVNLSSALEGVLFMKSKVTGDETATKKNTTLPTDGVSSILIPPYVKEDITFHLFCGK
STTKKPNKKNTSLALIHIHISSNRNIIHGCDFLYLENQTNDAISNNNNNSYSIFTHNKNTENNLICDISLIPKTVIGIKC
PNKKLNPQTCFDEVYYVKQEDVPSKTITADKYNTFSKDKIGNILKNAISINNPDEKDNTYTYLILPEKFEEELIDTKKVL
ACTCDNKYIIHMKIEKSTMDKIKIDEKKTIGKDICKYDVTTKVATCEIIDTIDSSVLKEHHTVHYSITLSRWDKLIIKYP
TNEKTHFENFFVNPFNLKDKVLYNYNKPINIEHILPGAITTDIYDTRTKIKQYILRIPPYVHKDIHFSLEFNNSLSLTKQ
NQNIIYGNVAKIFIHINQGYKEIHGCDFTGKYSHLFTYSKKPLPNDDDICNVTIGNNTFSGFACLSHFELKPNNCFSSVY
DYNEANKVKKLFDLSTKVELDHIKQNTSGYTLSYIIFNKESTKLKFSCTCSSNYSNYTIRITFDPNYIIPEPQSRAIIKY
VDLQDKNFAKYLRKL
```

280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE

A0A146F1C5 **A0A146F1C5_ASPKA** (444 aa)
Similar to An07g03710. *Aspergillus kawachii (White koji mold) (Aspergillus awamori var. kawachi)*

```
MWLPINAGDTTPLVLDESTRTLYSRAISNPSSLTDQERRLITYRPPPDEEDTLCRNACGLSMGELIAKAINSSNNTGNDI
PLSSLGLSHEEASLLTTGVVEGQSGRILSEVARLSPEDRDLKARAIVAARTDDIRAAMEVAHRVLQRWRKVELAAANALN
DDDIRNILFALKVPWQEHVLQSSSASARDSVPGCESGLGEAGGRFGLVVFYPKEEEEEEEEEEEEEEEEEEEEEEEEEE
GRLPEYKSLIGTAVSHGLHYSARLIKNETRDRFALHWVAVPGSTRNNSMDPSALRRRFSTMLPNGEIPAGFRRDAFLYVN
DEAFRSRETTRPYIWLAEPEPQSEAKREPEPEPEPEPEIKMGSGTGSGTGAATGAQSEALQPLKVDIKHIAPTLFARLVQ
RDLQGEARRKPYRHTSELTRLHAAVNAKFREDRDGIWPPPARFQ
```

214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE

A0A146FP86 **A0A146FP86_ASPKA** (175 aa)
Ribosome assembly protein Noc2. *Aspergillus kawachii (White koji mold) (Aspergillus awamori var. kawachi)*

```
MAATDILMTSVEAIPKVLPTQKLDDGSMLNQETTMCFYQILVYSCGCTTPGPFKQCPPQLGTNVRCTRLGPRQQQPVGNY
CPRHLVTRGARIVYARPGGQWQPVADNWGQEEQGGNGDDAEAEEDKAEEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEK
EDDESDNNRDPDWHP
```

134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE

A0A147A261 **A0A147A261_FUNHE** (835 aa)
B-cell lymphoma/leukemia 11B (B-cell lymphoma/leukemia 11B-like). *Fundulus heteroclitus (Killifish) (Mummichog)*

```
MSRRKQVNPQHLSLTHRETVQAEVNHDSGAQSPSPEQSTPSPRRMGQGEHDLLTCGQCQTNFPLGDILVFIEHKRRLCRG
PGGGPAAFSKPGEAGGIMGVPISPRTRSLELGRGSVPVEVGIQVTPGGEDDEQRRLTPAKGICPKQEKGDKDEPSSYICT
TCKQTFTSAWFLLQHAQHTHGIRIYLDNHLANCSLTPRMALPPPPGADALPRSPLPTFLGDTNNPFHLLRMAAPLLREHP
```

```
HPPGYMETRLPATPPFVSPPPPPRPPLERLGPEEMGLLSQHPSAFERVMRMTPMEPPSMDFSRRLRELAGNTTNNGGPTP
PLSPNRVPPMHRLLSPTLFQPGAKPPTFLTYAPQPPASQGGHGSSSPPDAQGQNQAPGKSKSCEFCGKIFKFQSNLIVHR
RSHTGERPYKCHLCDHACSQASKLKRHMKTHMHNKSGNMTGSPEQGSRGEEGEGEGKNREGDARVMEMENEEEEEEEEEE
EEEEEEEEEELRNGSRPDSNLSEDSQEFSQNRENGPRQSPEEKSMSGDRVNDNGGVGIMHPYNHLDNHLRLNPNKRNLER
QPNGDSGERNDTERENDREPDREREEQEDIRPLMNGRISVSEAESFPGLFQRRPTPITSPSPSNNKRIKIEKEHLDMPPT
IPLISPENVYSQLLAGYAASRHFIREPFLGFTDSRQSPFATSSDHSSSETGSLRYSTPPGELIEGGSASGRSGSSTPHLL
RGPGPGRPPSSKEKRNDTCEYCGKVFKNCSNLTVHRRSHTGERPYKCDLCSYACAQSSKLTRHMKTHGQFGKEVYRCDIC
HMPFSVYSTLEKHMKKWHGEHLMASEVKLEQADRG
```

471 - 490:	EEEEEEEEEEEEEEEEEEEE

A0A150FYX0 **A0A150FYX0_GONPE** (263 aa)
ANK_REP_REGION domain-containing protein. *Gonium pectorale (Green alga)*

```
MLVQLEMRAVESSPGPVENTNTAVVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDCEDVRLALVAAAIIGDADAV
RHFLRQDADPNSMDPAGVTPLHLAAASGSCNMVELLLRFGATLEAEDRMGLHPLHHAAEEGCAEAISVLLNAGADIHACD
SEGRTPLHTAAGQGHYKAVSVLLDAGADIEAVEVKLQNQTPLHFAVEAANLAMVKVLLEKGADVNAQDLDMCTPLHGAAS
WGYLHIAKVLLSMGAFMEARDKV
```

26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE

A0A150G289 **A0A150G289_GONPE** (1585 aa)
Uncharacterized protein. *Gonium pectorale (Green alga)*

```
MNKNNELVARRRQATASAITNGVKPVGGGSAEGNDLDWRALFGTSLTLPSASAGAVAAGTPKTARQAGSFFTAYGNAHGN
ELETDSSGGLGHGPSPLHDPVFGDFGYDDDWLDMDLDAEMEEFLSEPGLQPRSALLPYAGGISAAALTQEASFDLTDAAD
VGPVLEADSALERLRSADALLRAVVAAAEAVRPGLYMDSAEQLRDQLEQSRLDVMLRAVDAARGELLLRSGGGTAGGGSG
GGSGGDSDAGGSCDRGGLAAAALEARVGAARGRLARAGAEGRRLAAAGLRENGWRSARQAAARLGRVDLNELRWQSLGLL
DEATVVAPARVHLRPDSVAAREAWERLGKLAREQEEGGLAGDQAQAPAGMSRTRALDRDCGCEELMRSAVLGLVLLGGGG
PCLPDVGPLGAPDPLACALIVPLLRRLKAEADLDGSLGPVAAASPVVLYDLLVYGMLHERRAPAAASVGGGGRVVGPSAA
APPLPVRLSLGHLEQLTSSLGGSQEEVETALLWAALGRAVHADGDASSPAASERAKDVAALQELQRLWAAEGQGGAGELR
RLRTCGSKSGGSGGDGSTGGRVTRLAMTSAALAKAASSRKGRDDDVEEEEEEEEEEEEEEEEEEEDLWGYLGGSDGLLP
PAGKGRGRDRTRDRTRAHAGQGSGFGSELEASIGTATDTEGEGAFDSDEGEGEDDEPGSGPFGSLYSDTWVCTPPPELER
PPAAAAAAAAKLNRLVNMLRDWALIQVTHDSRAVRRLHELLHRAYDAQQLLVLQAVGPVSEPECSRSGSGSESRPGRPGS
PRAGGAAARSRRCGGGGSDGGGSDGSSDLICRESAGGDLDTERSAVHALAAGAVARSRARWAAWAAEHAAWVAANATLWG
AVEVGLLQRRGPRALRSETARMLADGLQPGLAGAHPDTWGALLLVFDRAEKRADAPPGDTAVPGDLEGMREVIHAALVGL
VVLAGRAPPLPRLTLTSCAAVGAFALSHGAVGATTARAVGTGSGGGGTALGAAVELFQFLSHVPCPMLVWPERCWLGGRF
WLSSPEEHAEWVRGALTPLRTSPDGQEAMETLLHHSLDRYEQVPYLAGALAAWMSTRGAHDAAAAAATAAAAAAAEFKAM
EAEAEATAQAEATLRQLRSLEEDVAALALLAQTTGHSLDSGSVSADELSSASHISVAELVRLGRAQEREEREEEEHQEEE
EEEEEEEEAEEQAEVVVRNVPDCLGTTTPAQEAAAAMLRTISRARLFGAATDARAAAAAAASASLPPMPPPPSLTLVGPE
PICLALLLLHLVWLESEQKQPFAFEPLADEATAREARRLPVGHKVALFPPPAGEPAVLRLAGVRPADLPGEGAEAYRSAY
EWKRIRSVSDGLLVGGTARWSELYKAAEAALVKKRLGALYLAAEGVEGVQRAMMLGAKLRAALREKHGTTLYATVEAVDG
PELRPRAARRGGGGGGYHELLLGRRMPEQVEKSLQNLARLLDYMQRKRATVRKEAWVWDGVIEAVGTVWPHLVGAAPPGP
ADPRVGEGRRPPPPRPAPAGLREGLLVVVRLVECEEGRPDRPVLPSERAARGQKQPKGVKEALMR
```

607 - 626:	EEEEEEEEEEEEEEEEEEEE

A0A150G4H0 **A0A150G4H0_GONPE** (129 aa)
Uncharacterized protein. *Gonium pectorale (Green alga)*

```
MDTARFANSAGVRRDEQAHTDGGLKRSDPEPASGHVAMPLSDPTAHGMHKRVPKDLHQVYLDAHQAQPEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEVVVQHIQMKEYDRQGMFMRWGTGLQATTDM
```

69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE

72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE

A0A150G644 **A0A150G644_GONPE** (522 aa)
Uncharacterized protein. *Gonium pectorale (Green alga)*

```
MASPDHDATTAARIWIPSIIDRIARFLPRNEVACNLRVVDKATAAMLQTPEFSTVRLSEPVPHHAFAWRWGRPGAMRDLT
RARRSELLCLTAASGATDNLALAAQSVGCPLANKVGYAAGKAGQLGSCALLAGLGCDVGRALLGAAAGGHLALCEELMSW
AGFDHDSQEEKLQGCAFQAARAGHDCILDWALSCDKLMCYRLGIVPTWLLMRAVAQGCDLAALQRYHAKLIWRNGVVEEE
EEEEEEEEEEEEEEEEEEEDEEEDDHDDEKFQMWVVAAAAGSPTPDWRAKLEWLESRSFPKTWKAFVAAAKRPDALERFA
WLVQRVYPSRPEDGYGKENEALVAPADAGNAAAVLYLAEGLPVDMDLAGAWRAAAAKGHLPVLQALHAVGRHVGACGAAY
DAARNGHLHVVAWLVEVPHLGVVLDEKLFEAAAGSGSVELMAWLREHGCLWDAQTFKATASSGCVAALEWLAEQGCPMPD
DNSPIVDAVKAEDFVVLECLRRLGCAWGPTGHLFDVCFEDNW
```

238 - 257:	EEEEEEEEEEEEEEEEEEEE
239 - 258:	EEEEEEEEEEEEEEEEEEEE
240 - 259:	EEEEEEEEEEEEEEEEEEEE

A0A150G669 **A0A150G669_GONPE** (555 aa)
Uncharacterized protein. *Gonium pectorale (Green alga)*

```
MLGAPVGSWVHSLRVVDKATAAMLRTPEFMTVRLSEPVPHHAFAWRWGRPGSMRDLTRAQRLDLLCLTAASGAIANLALA
AQSAGCPLTVEVGYAAGKAGQPGLCALLAELGCDMGRAVEGAAAGGHLALCEELLTGGAGGLSSFLSCAFAAAKAGHIHV
VEWMVGRYEELKLLGPRSWGAWELVKAVAEGCDLAALQRYHAKLIAPDGAEEEEEEEEEEEEEEEEEEEEEKEEVDEDWL
EDVKSGVVAIAAGSPTPDWRAKVEWLEAQRFLQTWESFEAAAERPDALERFAWLTQRGYPRRPGDGYDEEAPLVAASAAG
NTAAVLFLAERWLLGKGLVDVWCAAAAKGHLPVLQALHAAGRRVGARDAAHIAACNGHLHVLAWLVEAPGLGVVLDDELF
RAAAASGNVEMMTWLRERGCSWDVHTFTAAAKSGCVAALEWLDDGCTFVNAVKVEDFAMLECLRRLGCNWGPTGHVSKAC
LKVYIKDQVAMMSWLLAAGCPIDWPMAVAKTTAAVVQATGRVAWEPASKYYADLLEKRQGVHAWVCAEARRHQQQ
```

211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE

A0A150G6Z1 **A0A150G6Z1_GONPE** (3341 aa)
Protein kinase domain-containing protein. *Gonium pectorale (Green alga)*

```
MGAAPSRCVQCFGGAHKPPPEEDASAGVPAGASSAPEEAPQSEQQPAQRLGAEGAQSQQLDLQHPQNPEASSGRPTAISL
SVQSFCSPFAAQAGNGADASTSSTPTGSTPSGGDADPDAPPVRAGLTAAQKYLQSARARARAAEATHVANAATDTAAPHA
SAAASRNFSGPSASGLPPRPARANSGKPQGLQSAPPALSTAAPPPAPRPPRGLHALPSPSQSSLQITEYAYQPMMMSLGS
VGASVASSAATGSAVLVTIGNVVSSSAATSGCAASAAAGPPLPPPGSLVAAAAPQALALRRVRHEARRHSAEGQLGGGGG
ATTAAGASDAGFPGKPSSSTALPEVLRGPRGILKLPAASPGAPAAPAAAAASAGPLAAPPPQGTSQDVLRSPPRHQPASA
VDSGVTSGYLGSGSDAGAVHSAGSGSLNAGRLSTTTERLLGSRHGRTPEQVALALASYLGTADSEAAAERLSPNGQNQNR
NCQLLREAQGQLELRREPEQLQLQQQQHRHHHQHFRSRHTLPQEALTFSQPSSNEDSPTGSTRSISDPSGHGIGAVPGPA
TPAKAAPAHAAPQMSPEAQRGGGGGGDTARASAAERGAAWQQWGLPRVGMAAAEERAVGGGSLGDSGGGSSGGGSGGYPA
VPKRGAFSATLGSIFRNKESSGLGGSSGTVGGSAAGPSHVASCIPAAQFPPSAPGGAAEQRHAVQQQQSASVQLPAVRQP
PQQQQRPVGHKFRERFGTMAAAMGLKTAPDRRSRPAVHTAPGNLRAQMLAAAAAAAAAAAAPADGSEAAAAAAGNSGPLAA
ASGFEGGLAPRGTQSARLASPFVSPVNSGASGGDGTGIGIFVGTGHEMPATRMFGAASGAYGSGGGAGLRARMASTIVED
EQEGEDASLASSAAHIHPPKPLPPPQPLPSRVQPAALQQPQPQPQQVLTAGGDDSGASGAAAEPALGSAPGSMWSGAMVS
TLSAASGAGTVPSLPSCLGSAASRHHPGGPSQQGHQLAPASPSELTSSLASVASVAEYRGGGTASGGGAAGGGTGHGRPP
THGSRVSGLYNGGGGSGHLLPLQRGMTRGSAFAAASRTASRADAPAGGSDLGPSFIHQGAVLGSGRGAATAAVTGGRRGE
PSAAAMRKSPVGDGSSGLSHLAAADGAAGAAVGPVEGGGGGSMAWALRTTPVMWSELERTTSPPDDAAGATDRPGSADRL
QQLLLGASSVASAAHALLGQPGAGAQAETTEPQFTFGEPGRWQGQRPRRASVAVVVAVRTASDVAARMTAHMRVDDVGRH
GGGGAAAAAGGTPRAGLTSAASLPAGHIRLHARGAAAVAAGDVGSSESGGGAPGEVDSPFESPFGSSLALTSSPTLASIT
KTAAPARPELAGGGGGPRKVGAPRRVRTSGALRVGRAAAAEPAPSAGAADLAGGAGDEEEEEEEEEEEEEEEEEEEEAAA
AAAASGAPVPVTPRAAAAGAAAAADAPAPFIFTLEPCPPGSEVDNLLSLVANVFQMPVVMVAAHLPGTIYVRINKAAVAS
AAAAAAAAKPAAAVGSSHGTSAGGPRLQAPAQAAAAAAAAAAAGAAAASDIEEDMEWQLRLGAWAITSSVADGPWGQDAV
EAGNGVVVVEDAAQDDRLSREAFVRMAPPIRFLMAAALEEDRPAAAKGAAVFAPPAGAVSTAGSSSVHEMVRERSGALSR
ASGEGGDGDAEPAADGSGSGGGGEGRGGGAAAVVDACRTRLLGTLCVADFHPRPAASVATPLLANIRQLLLTQLSRDVTL
YDERQRSRAVLSELLLSLQRMLDRHERCLLLVDLAAGPTGRWPVLYANHAWTAITGMARGDVVGRDIKEIVSTAAVVRSA
TSTTVTSGAAPSGAATVFGGGTTSSAATDGPSSQSNGGGTAGGGSADPRVAGGAPRPVPIQWELFAAAFPRHSDIVIDNA
RLPAAGRRAEEGEEGSAATLATLRFRFVAREAAQDSGLLPLGWRPLIGAILERGPARALLLVTPNPPPATPSGADAAGRQ
EPYAHALRPGGGGRIHIPGLELKHLLGRGGFGAVYYGTLNGLPVAVKTLDMGNNNLSVHGASLEAVMGQALDHPNIVKTL
MYVESERRQPPRTGGGTGGRASASEGGGGGAAARVSAMGGSAPVADMGEGMAAAAPPAAAAEAHQHQQRQPPAEAEAQAA
ETAPPPLPSGRWSAADRFAGFRTLMRQGSSVHGPGEGSTGPNFFMLGGAPGSPTAGGGRGSGGRTAMGVGAAGPGEGTEG
TSGLAGFVRSGPAVGGGFSGGLGGGDGGGGSSGATGHVLMLGSGTRGYSTTLRTRSSALTTEPTFGGAASPAAAGRTLTP
VAELAAELAAGSSSLISDGVGADSTAAAAVAALAGVAGAAGLFGTTARQPAAAAPVGQRTLRSAQHHQQHQPLEAAPEDA
PMPIFTTAAATAMRALFSGAGGEGSAPSTAGALGFASGPGGGAFGFTSGPCGGTTNTGDGSVNLSQSGSGLWASMNSAQI
AAAARLTSASALRRHQPSGAFDGSSGDAIAAIATLAAADASAGAQFHAHHPAATAAAAAAAAAMPRLNPRGGGGGHTSGP
GGGDGSSGTVAGGSRPRGGWMGMAPRAAAGAVEDSPGRRLPPLPHAPSRRSFWSGPAGMLLQGDYGSLGSTGPQPGRPLA
ALAAALQAAADAGPVGTDTGGGGGGGGGGGGGDGGVVTAVAADWLVHGPPALASHMAAVRDGPTAAAVGAASAAVSAPA
ALPPPPLPPAYRAASMVPNLPPVPQSSETSSGHSRPLPGGGGGGTLAPNQSPVPYAYLAAAGGLPTGGGRQLSAPAAAAA
QRFFNASGAPVGPAATAAAASPTTPPRPEPPPSPPPPPSLPPSNPPSTPSVPSMPSGLSPPSARSFPSGPSAPPSAPSAP
SAAPSAPLSGLSAPSGTVDGPRGDDGDDGSFSVIDSDSDLMAPTLDSPRTAARKERQAKKAAAAASAAAAVAAAAAAGDL
```

```
SMGLQRGAHASGDIASAAAAAAAARRRRCSGNGGDDRRRVATRGGLDRHGDALERGLFALPPDPAGPIHPSGGPKAAAAAA
TATAVSGASRRASAVIFNPSALAALGGAPIAVISGGGAAERAAGPSRRRGPGGSGGGGGSGGAPAAREVDMRALLATALE
VASALRYLHCLGVVHGDLTGHNVMLVSLERAALPYERTASNSSSAPGGGDGGGGGGGGASASSAATDAGVGAAAPLVCRM
CGRSFVAKVADFGLSRMMQAQSKIRTRSFGTITFMPPETLVAGTVSKAADVYSFGVLLWQMYTGARPWAGMNTGQIVYNV
GMKNMQLPFPPGAPPALVELSRSCTAADPDKRPTFERVQEKLAGIAADMGLELDRRAAVGL
```

1418 - 1437:	EEEEEEEEEEEEEEEEEEE

A0A150P194 **A0A150P194_SORCE** (1051 aa)
Uncharacterized protein. *Sorangium cellulosum (Polyangium cellulosum)*

```
MFGPGCTAGADRAEADDVAANTAEAAEFLGDATSFVSADDLPRVFYGEEEEEEEEEEEEEEEEEEEEEEERELEEGDIYRVLG
DGHLLNLNNYRGLQVIDIHDPQSPTVVGQMPVAGTPVEMYVDGDRAIVLMNNWVGFRAMPGRLAVERQESAAVLLIDISN
RNAPRLLSQLGVPGYIQTSRYANGATQDALYVASSHWEWVDLGNGESEYRNRAVVKSFDVTDRGLIGRSQLDLGGYVTGI
HAERDVLLVARGPEGWSHEDSQVSLVDISRLDGSMTLHDTVTVDGYVRSQFHMDFRDGVLRVFSGPNWGGGTSYLQTWDA
SNPDDLTPIDKEGFGEGESLFGAVFLDDRAFAVTYFRTDPFHAFSIDPGGYVEEKSEFIVSGWNDFFRPVLGATRLIGIG
VNDEGGGRRLAASLYDITDLTNPSPMIARSEVAGDDDGWNWSEASWDHRAFTVLDGAVSVAAPTGETETGLVLLPFSGYS
WENDRWNSAVQIFTFSSTTLTRRGVMQHATPVRRTFRTGPDTAANVSETQLSLYDQRDLDNPEKLGELDLAPNYAAILGY
GDHRVRIRNPERSSWERAPDEMAVAEVIDASDLADAAVPLATFPVTPDAIYYKIGDDLLATVTSRYAGWPGYETTISVFD
LSDPRRPRAAGRLVTTDLPPHNGYYHDDEAYAPTRVHVTNRSLTFVSKVGTWTDIGPAEHCRSYVAFEHGDYACSGVDDC
PYIAGQRTCHALEGGPEYCEGWFATCRTRLVDGNDVCTPVADEAALDGLLQSRCYDGTARRVMTRITLNVVDLSDPDHPA
LVPPLALPADESGVSSLAHQGDVYVSVKLPAALPDDPRPHARYFVRRVDMSRPEAPALGPAINVPGEVIAIRGTKVFTRD
RVWGSHFIEPAIARATLHNGRAHLNHHQELSGKAISGAILIDEHQRALMTYGDRIWPSYWRWSYGYEADKLAILRPGGTL
SPTGFDVLSETPIDRWTTFMRFVAERRAFINVDYGTLMVDYEDPRRPVAQAFFMGAWSPHVLVDRARDEVLVSAQRYGIY
QLDLDATNLLP
```

48 - 67:	EEEEEEEEEEEEEEEEEEE

A0A150RRP5 **A0A150RRP5_SORCE** (1062 aa)
Uncharacterized protein. *Sorangium cellulosum (Polyangium cellulosum)*

```
MTCWLGVALLAVGPGCTAGADREGQGALAEETAEFADPLGRTTSFVSADDLPTVFYGEEEEEEEEEEEEEEEEEEEEEEREL
EEGDIYRVLGDGHLLNLNAYRGLQVIDIHDPESPAMIGQMPVSGTPVEMYVDGDRAIVLLNDWVGFRATPGSLTMERRAG
GAVLLIDIGNRNAPVLLSQLDVPGYIQTSRYANGATRDALYVASTSWGWVDLGNGDYEYHNEAVVKSFDVTQGALVERSQ
LDLGGYVTGIHGEGDVLLVARGPEGWDNENSQVSIVDVSSIDGFMTLRDTVTVDGYVRSQFHMDFRDETLRVFSGPQWGG
GVSHLQTWDASDPDDLTPIDEEDFGDGQSLYGAVFLDDRAFAVTYRRTDPFHAFSIDPDGNVEEKSEFIVSGWNDFLRPV
LGATRLIGIGVNDEGGGRRLAASLYDITDLTNPSPMIARAEVAGSEGGWNWSEASWDHRAFTVLDGAVNVAAPTGEAETG
LVLLPFSGYSVTGDRWTYESAVQIFTFSGTTLTRRGVMKHGSPVRRSFRAGPDTAANVSETQLSLYDQRDLDHPEKLGEL
DLAPRYSTILGYGEYRVRIRNPEQESWEREEGQMAVAEVVAAADVAAVATPLASFPVTPDASYYKVGDDLLAVVTSRFVS
WPSHETTIGVFDLSDPLRPRAAGQLVTTDLPPTYDDYYDYYYYAPTRFHVTNRSLTFASKTDSWTVVGWVEQCESYVTYS
RGDDSCWGLDGCTYTTGQRSCQSLDGGPEYCSGGFAECTTRLGSEDACAPVVDEAALDGLLESYCFEGEASRQHRQMTVH
VVDLSDPDHPALAPPLALPAEEDAVSTLAHEGDLYVSVKLPATVPDDPRPHARYFLRRVDLSRPGAPALGPAINVPGEAL
AIRGAKVFTRDRVWGSYFIEPAIARSTLHGGLAHLNNYQVLAGKAIDDTLVIDQHQRALMTYGERSWPTYWRWSYGYKSG
SLAILRPGDTISTTGFDVVSEAPIDRWMSLVPFAAERRAFFNVYSGTLMVDYEDPRQPVAQAFFTGAWRPEILVDRARDE
VLVAAERVGIHQLDLDVSNLLP
```

58 - 77:	EEEEEEEEEEEEEEEEEEE

A0A150UVV2 **A0A150UVV2_9PEZI** (354 aa)
Uncharacterized protein. *Acidomyces richmondensis BFW*

```
MPTIKNITLTLHSQYDDTRPIPIAPLPVSAAEDDPNTLTSMLLTSHPGAQFWLTYSCSPPEEGEGWRYMYFTLHSHHLGS
AVVGWGVGAAEQWRGRTVFGLRAVADEEVERWGFFFPSSLRLGKGGAWWEVKTYRCRGRRREKVCVGVGVTSEVDRQEGG
LSLARMGRLKKGEPCRLYNYALLDPIDAPYAVFRFHMSSGSDDDPTVIARSNQEEGEDEEREEEEQQQQQQQQEEDEEEE
EEEEEEEEEEEEEEEEEEEETFPLSLKTTIHRRLSVPPPTLLQPSTTHSEPGSPVKKPFSDNLIPDTSSSSLPDTLSSDS
LRERGRALRKEGSMGGGLRDVIRGALWRRRKREG
```

237 - 256:	EEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEE
239 - 258:	EEEEEEEEEEEEEEEEEEE
240 - 259:	EEEEEEEEEEEEEEEEEEE
241 - 260:	EEEEEEEEEEEEEEEEEEE

A0A150VFY1 **A0A150VFY1_9PEZI** (715 aa)
Uncharacterized protein. *Acidomyces richmondensis BFW*

```
MMKYSSDWDLNLPADWDVSLDRDDNNTFRPLVAPFNGGDGIGSNLIVPPEFHDGYLQHYASSQFGDRRIDSPVFFQQQQR
EVEDEEEEEEEEEEEEEEEEEEEEEEEEEEEHKYHQQLGLQQDYPSIAQHEQIYHTQHFPHQDHQHTLLVPPTHYYLQPPIL
LSHGDEGQYAGVPAHARAPPPFITPNLLLLTPHQQRIFHRHSHPGVRNLLTQQAEVGYPCAQPLAGSHQMGDSNHLQGLG
FNGTTGIDHTMALSARMDGNDVTNFEVNTGIENNMTATMDDTMASAMHDTMDATTPANPPPSIDSTAGFNTLLDVNTPSA
SDILPTVETFPSVDPFTTVNSPEVVNSSPPINITTPAVATSPSNPTTTEMLHVPAMDAPPGVAAASAMPSSKINPSNWIP
PSEGQKPFLAFHFAFARHFAGFSPAISSYNSICAANDAKKLTPVELYKAIYRILYFTSAFPLLQRWQSLRPPQWDVSVIG
PQFGGSVQAFHRAIEDEAEQYWPITAEKLRGFGKWRATSTYVNPEEEMLDLLVRTLDGEFGPRQVNEDGRTPRRAAERAK
KGLKMTAVWEKEHEEQGRLVVKLPVPRENLESLILHDDVQRTVPSAHKPAQKKRKNAVGESLQGAWPPGFSKPGPKKKRR
AEAWETVAPTGRISKEKGIEKEGADEAMGAGLVEIVPQERVARKVRRMVVAGGDEDNEEAKEEKARVLMAQRTGR
```

85 - 104:	EEEEEEEEEEEEEEEEEEE

86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE

A0A151GQM5 **A0A151GQM5_9HYPO** (78 aa)
Uncharacterized protein. *Drechmeria coniospora*

```
MHQSASASKNGSPSVAESGARGSWGWIVARREEEEEEEEEEEEEEEEEEEEEEEKQQEVVEEERRGWSSWKREAHLISK
```

32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE

A0A151GRQ6 **A0A151GRQ6_9HYPO** (66 aa)
Uncharacterized protein. *Drechmeria coniospora*

```
MGEAGEPPALADDVQCRLVEEMEEEVEEEEEEEEEEEEEEEEEEEEETGMGREQSMMGGGWMTGRP
```

27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE

A0A151H0Y3 **A0A151H0Y3_TOXGO** (130 aa)
Uncharacterized protein (Fragment). *Toxoplasma gondii TgCatPRC2*

```
EEEEEEEEEEEEEEEEEEEEEEEVRGLAYVSRRRIVILLLRTAFVSRRGKTKGCKVPRQASDEETEGRRSSVSTQARPSG
IRRASRGNWSRNEASRPQKNATQTKSKSRRAWTARKKEIEVCLLFARWND
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE

A0A151H4K6 **A0A151H4K6_TOXGO** (1245 aa)
MI domain-containing protein. *Toxoplasma gondii TgCatPRC2*

```
MRGRRPSQQRKKAASLGASSLLSSLPSSLPSSLFSRGDSVGRRLGKRRGIEEEGGKRKRARGGRSARHNFPEVDQQGGSD
LDELPSSEADPREAQQDGEGSFGHEQELAETLKKSKRAVLERKRRRHEERRQKKQIHRKQQQLWKLERQKALLERQLDMQ
KAAISGVRVNQGTGSGVRTPCGPEADSEDEEEDVSPRREKKTPSSLSSSLSSSLSSLDVRGSVLSALSAKDKKHTVSGEV
LLLSGVSSRSTEEHRKAEERRLALDAAGRQLDAELAFLESKLGIGKDSSKAGEKKKKKLAQELLDDGFDEDLQTLLDDIL
GGKAENRKRKTKTDYDHDEGEMEGEETQEGAHEELGRVEAEEDEEDEEEEDDEEDEEDDEEENEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEDEGDEEDEEEGEDLKLKTEQYSTCASASAGKYLPPHLRNRAQRELSNEAEFDGDNPGRNST
RQHGAAPASEASDKANFVASKLPLSCLEKARQTATDAGRGLTQRLRGSLNRVSEGNVEVILQQISQEVKAALTQVLSGAL
PVPATSPALTPRDVRGLRREQEISFFQEVNCIIVRLLMQSMVESKFSTASLVATQTALCCGLSCLLDASLCSQLLAALGE
AFRKFFPLALAQADRRTETGEPVGLYVRHTLVALCFLFDFNVVQPAVFLGLLQRLSGKVATTKEKGEAKNGERNEPLVEF
QVECLLMVLRLGGGKLRNDNPVLFKEAWNFLMTRVKGGEGEREVQVHSGREERPFEEQTREEQRARLARVSTSFSGALRQ
RQEGEQPATTGRLHYLARELEELKNNKGNTIHLASKASQEAMRRWLQTSPLLAQSPLRQCAGEGKSVLVGVSSWQEVEDG
VVSVSPSSHRPPVSPHKSVRVEKEKQSCLGDTGSEKALLDLAAKLRLHSEEQKKIFLAIMSAESPNDAVKRLLQLVPRTN
KKKNFVTTAVAVLLHISLQQSAFNPFYALVIARLCARCSCASWGRLEAEAEQPPLLGPLGSGRASVNQRRARGPCACLLP
PDKEGKVFRRVTQRGLAAQNSAAHGFPLRRLLHLARLEAFLIRIGVVELRVTRFVSFEGEKGQADAHMGLSGKLGVFLKE
LCTELLCSPAFASVPLPGPSTASPLLPFLSLSALPDVREAFLLVLEDVLLPEARKNACSENGKGAKESVNAACMPGRQGK
CVRAKGAMCTPACGIRKDVISRVIWFMKKQERYEEEDPNTFAFDA
```

384 - 403:	EEEEEEEEEEEEEEEEEEEE
385 - 404:	EEEEEEEEEEEEEEEEEEEE
386 - 405:	EEEEEEEEEEEEEEEEEEEE
387 - 406:	EEEEEEEEEEEEEEEEEEEE
388 - 407:	EEEEEEEEEEEEEEEEEEEE
389 - 408:	EEEEEEEEEEEEEEEEEEEE
390 - 409:	EEEEEEEEEEEEEEEEEEEE
391 - 410:	EEEEEEEEEEEEEEEEEEEE
392 - 411:	EEEEEEEEEEEEEEEEEEEE
393 - 412:	EEEEEEEEEEEEEEEEEEEE
394 - 413:	EEEEEEEEEEEEEEEEEEEE

395 - 414:	EEEEEEEEEEEEEEEEEEEE
396 - 415:	EEEEEEEEEEEEEEEEEEEE
397 - 416:	EEEEEEEEEEEEEEEEEEEE
398 - 417:	EEEEEEEEEEEEEEEEEEEE
399 - 418:	EEEEEEEEEEEEEEEEEEEE
400 - 419:	EEEEEEEEEEEEEEEEEEEE

A0A151HI59 **A0A151HI59_TOXGO** (631 aa)
DNA gyrase/topoisomerase IV, A subunit domain-containing protein (Fragment). *Toxoplasma gondii TgCatPRC2*

```
EHWSTVFLRVCRNVVLLSAPALVRRLPLSVYPTLRRGALGVRSLSRSLASAESPDLDRDEADEAQTRGVKGKSAAVGASS
LQGVWSCWTKDRLLFLSANGYVSMLPAYRVPLGSRISRGTSLPQLLFEGWKKPAALRRLGESAAAAGALAEDAANREKKR
EEKERTLLREAAQVAAVLAVPPPTQREKARGVRQASESSRKSRKAKFLVVVTDQGRIAKIKLKRILGRRCETKVKKLVSL
VQGDSIRAAALLEEEVEPLARGRVSGAGKEIKHLRGNGSECNATDEERGARKKGREEEDEETTEKEEEEEEEEEEEEEEE
EEEEEAGSRLVEDEDDVGGEGAEGERTDLKSEEKRDTNSPSIVIVTRQGMGLRFPASSLRASGSSKTRGVRAIRLRAGDS
VASVAVVPPEVKEDEARTESRKEGDSDETQSKNESSNEKAEPSLLIVTAAGFGKRIRVSALRMQRRRGVGVRVIRLVKRK
KVAREGDDRGLSDEAVGQESQGFPDEEPDSEERADPRSVSQEKDPQSPETEGDNYVVAVLALPASDLPNRPKKSKGSDNA
ELLSVTQNGFLLRQSCRSIPMPRGRLARGVSLQRLPATGKSRSSTDLIVAADIVHGASEQQRRRKRRTPED
```

306 - 325:	EEEEEEEEEEEEEEEEEEEE

A0A151HIZ9 **A0A151HIZ9_TOXGO** (1886 aa)
IgA-specific metalloendopeptidase (Fragment). *Toxoplasma gondii TgCatPRC2*

```
MTSARTREGLVGAEAPLGEGEEDLQDSIACSVPRAPTNSFEEGYEVECVDECPYIKFQHASKLPLSPLLFDASSSPAPLP
ERLLAARCTDSLCLLHCCGVLLLPGLDSILAVDATEAACGSPISRGRLPLHASKEGETKDAFPSLLLLSPDARFLAVAVD
CQVKLVQLGGCGGPSCSKSAGEASREGNAEARLGGQQGGDSCISEKTQVLSLAGFASPVKDISWIWPSGDRTETWCEGDT
QGDAERLIGLAVLTESGEAFILSPRGAQAFPLPAHGLAIHALPRRSPAAAKSEGAGPGGLAPLTAVVSCCAPASLWLVGL
QETALLPEGSGQGESLYDFGHRRPDVSRETANEEKRKGRRKIRVEGLADIPGYEDEAQALHKGRGRFVGVHCLGASLDSA
AGESPLPLALAWFVPDADLSTGEDDWEKPELESDSAEPRLDPLRQAPASAEDCGDSWSCFILFGFLARRPYTPSDARALP
GDIGEAESADEKEELVFRVYAASRNEMFLRSVAASTVCRFRWIPQWHCLWVFSNACTQVICFALPHSFSRNGDPLPSPRS
SSFLGSGEVPWRCFTMPEGRALETADEDAFPQGLALFFNFKESMFREHSTTDTPPLEHPPVFFLLQSDGQVCVHLADCCE
CYVDDAGIGKEKRLLPRLEWTPVSPPSSFLLTSWTETRRRACGEQPATPVPKVSPPALSPSSSSLASPLFASLQQGKPTP
SLFGTPSTNAASAPLFSSSSGTSLFPSFASSTSSLFTPAKSEEEARKTGWVVPTTHLKVTSASSAANDPSASNGASASNN
LSALDGSSPRPLSSSRKDCVDQARPAAKETREEAPTRRLPAKSSSRDPQRRGHCLHCGAVDVGDRRGGREAERRRREKKL
RRRVEAKNASLRQAAAAANEVIEATLQAARGTKAEPAREKNAKKRILLTEEQSEVKALLDEFDEKKHAFCSFSRFLPSSL
FRPLLLSARCFENALRHEERRDVLLESSPVSSSASSSASSSASSSSSSSSSSSPGSLFVSRCGEKDAPVDCGAEQEKSTAA
LLPAAAAGLARTGRLADKLKDEQRNVRTKQETETEVVETLQEAQQHLVAWRSCLEAVRDELLLRMQFAEKSENPTERNGE
QTDAAGREEGRRDREADGREEKRERQAERGNSVTEEDVIACMQKIQSESGARRNLFEALQTLLPADSEHAQLNTDTHIKC
VLTHLESGLLRAERRLLLLLQRFRFYTSFQTRFPSSLDPESGSSVRRLAASGWPGSWKINSGLSSLSSYGDKGVSSLPLA
HGKDSDRDARTKRGSVHTPDTACGRGRPGGCYGLRFEWLEEDEFPDKREESVVDSHRRVSSTTHPVSEGTPGARPSLAFS
LSASPPSAFHLSLFGSPRGAGDSRIACSQGPGGSVKDGGLAGSRSGAASGDFLLDMHAEHRAAGLVAELEAAVSEFLSSV
RQLEIDLAKLEWKATDLQSPARQSPSSSSSTSSFAASLSLLSSSVFGEPLPPSGPSGLPDVAGAEKPAKDGEQRFPVSSL
REQRERFDERRKLRRQLLEVWRATTSTDPQQEGEEETETDADEEEEEEEEEEEEEEEEEEEEEEEEEEDEEEEDEEEEEEDE
SDAFEVLENSSSVSHDEESDEWEPVGSASPENPQTPPRQSVVSRRLGASLRSGRRTSRSKQRAKFAPLSGDEDSSENACS
SSPSSPDDVSPRRPGAELSDSEGAPEDGASCSNSHDESASLPVCGVPGETHSISHSSLFSIKPEDVTQPPQSASFQFASS
LAPRRASGLGHTLFSFASNSSSLPPDPTKPSSASSALLPPDPTKPSSASSALLPPDPTKPSSSTSALLPHDPTKPSSASS
ALLPPDPTKPSSSTSALLPHDPTKPSLFTSAPLPPDPTKPSLFTSA
```

1563 - 1582:	EEEEEEEEEEEEEEEEEEEE
1564 - 1583:	EEEEEEEEEEEEEEEEEEEE
1565 - 1584:	EEEEEEEEEEEEEEEEEEEE
1566 - 1585:	EEEEEEEEEEEEEEEEEEEE
1567 - 1586:	EEEEEEEEEEEEEEEEEEEE

A0A151HL05 **A0A151HL05_TOXGO** (121 aa)
Uncharacterized protein (Fragment). *Toxoplasma gondii TgCatPRC2*

```
EEEEEEEEEEEEEEEEEEEEEQCWSAVDEEGEAGESGCREEERKVKGERDPSAEDVRRIGSSRTSETNWFSEAAGDPKKR
AVRGTDQQRERDIVEPGVARTTADDSGDAWVTAKSASVEYE
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE

A0A151I0T7 **A0A151I0T7_9HYME** (1142 aa)
MOG interacting and ectopic P-granules protein 1. *Atta colombica*

```
MEGTLEELASKDASQSQDSSDKHLKDMIIPNGVNGNYSADNEEYMDTSDNTSKIALKDVITEEEEEEEEEEEEEEEEEEE
EGDEDEEEEDVDEQYDEDDHERAVDIQEGKDEDSDRNEEIGNTSKEGETFDLKNDFKISNSPDGVSETNNSSEVSKTEIS
ECVKNTSCEAMDVDEQSNNSDIECLDESITEIQLDNDDVFLSKKTIEKHDNDVSSNCSCDSSEIADSSMEKSDVKLCEEN
GSCGSPDIEEITDNAKSNDHDSSLDRAIKDPTKQRKPRKQVDLSNITPRRSSRNIKRTSYIEKELEEEVEDDGSDIEEIK
PEDPLAGIDSKDKENSKLKSPVRNSKTTIVVNDTKRLVEIAAGSKSIKGGKKEPTLVIIDTNSILSGRGGVPVSNNKPHH
TVSNSNPFSVVPMSGMTTQTMYPNMRTTITPVPMTSKAAQLSPKTSSMTTVTPTIPPILPTLTDDMFVVEAPSFIVPYVY
EKPPLKPLKEFVTKLERNIEEIEKEERKRLADENKDNEDYKEDSLDVKRGNDKSEDSDMEGKGKREGDDRGDNSIDLIEH
GFSSLSDKHDLRQDDRNKIPTYFDLPLGKFFMQIGMNLVQEYVQTDLLRTQKRKQGKGSTSAETQLAINSLIKNLEFSKE
NNEPFHLEMKKCEFCSFKTESTLVMQHHLETPHMRNYVYKCNFCPMEVRSPHDILYHMEAEHNTRGRLERGPAFHQCPNC
```

PFEDNQKGKLTRHILACTKKFRPERNLEPAVDWEPPAKIPRVNRARPVGPTNPNALAAMAMSAKGPQPLLPKLLPAPITG
RGRGRPPMQPRYSDLKTLRPGATPMRQDNVAGMMYRPTSSGLLVPTSYQFSSNQIFQVVGGSGTVMSAVSGVSSSSGGSS
GQPTPIALVPNVIDSLSRLSSSQNTTASSKNPTAKLLSQPSISITPLPRTTSQTSIPGSGTSSKSGGKNTFVICEICDGY
IKDLEQLRNHMQWIHKVKIHPKMIYNRPPLNCQKCQFRFFTDQGLERHLLGSHGLVTSSMQEAANKGKDAGRCPACGRVY
QWKLLNHVARDHGMTLKPAHLSYKCTVCTATFGMYKQFENHVYSAHSVVAKRVMDKKNTPASPSSRSNDSLLKPLKINDE
ITIIPQPAKPTTRSGAIQGRGK

62 - 81:	EEEEEEEEEEEEEEEEEEE

A0A151I2R2 **A0A151I2R2_9HYME** (631 aa)
Radial spoke head protein 4 like protein A. *Atta colombica*

MEHMFYAVKERWASKETASDLEKCPSYLGHPIDDKYDHLIELLAKILAEQPPNVVDIFEEYSRKLKEERFKIKKDYLRDL
YIPPVQYDDAKKLIKLFQDVKQINKDEQERMEDKEQNDKKKKVPNLLDLLFYFEQTGIGLPRHEIVSLNLSIWKFASTMP
LENIRFWGKILGKPKNYYILEAELQADELARRLEQEKHEVQSKKEKGEIKIQQNATKLTEEEMVTKTQQTEDIERIVKPT
KNLRKDKKSKRKPLKLIFPSLPVNLWTPLPEIPIERIGSGLNRKVYFVCNTPGVDEWIELPMVTPQQIVIARQIVRYCTG
NLETPIHSFPPFPGTEKNYLRAQIARISATTHVSPIGFFTFSRKEDEETEEERKKKDELLENMNYDPLPIKDLVDPSMSN
WCHHSPYILKQGRTVWWNPQEENIVNVKEEKENVETDEVKIMMKEIGPPLLIPLSEDAIIDSVIPWTVRQSSYIQPDVTI
ALIRSNIWPGAFAFADGGKHFATMYIGWGHKYNAYNYNPSHMPPVQDQYKIGPEILEISDPTVKEEQAFQLMRLPLTEEE
EEEEEEEEEEEEEEEEEEEEKEEEEKEEEEEKEKKKEEEEEEKEKKEEEEEEEEEEEEKEEEEVNKEDDE

558 - 577:	EEEEEEEEEEEEEEEEEEE
559 - 578:	EEEEEEEEEEEEEEEEEEE
560 - 579:	EEEEEEEEEEEEEEEEEEE
561 - 580:	EEEEEEEEEEEEEEEEEEE
562 - 581:	EEEEEEEEEEEEEEEEEEE

A0A151I5Q5 **A0A151I5Q5_9HYME** (155 aa)
Uncharacterized protein. *Atta colombica*

MTRYVSNAIERDKVQIPRVSRVIRVASENRSRVQELIALISCFTSDLKTLGSTAGKRSNVGEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEKEEEERRPRNAVALRGLSIQLTARERDGDEKGRDGMGRKGTRRDEMGRDGTGRDGTGRDGTEAGK

62 - 81:	EEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEE

A0A151I7T4 **A0A151I7T4_9HYME** (1683 aa)
WASH complex subunit FAM21. *Cyphomyrmex costatus*

MAMIFPLLSTSDAMISNISNPLAALDGSAIGRRPGATSSNTSKARYKLLDMDVSDDIDKAWDHPWTTEEMRNKRREWSLA
GDVGLLKHLQQFSENLVSKATKTQAALDTLTTQLKETEILVDNVTNTSLALANTQFIESRVQEDDIEIKENVDEKQENAK
TQESTPENLLASISESVKQGLSIMDEKYKVMDVACSDSEEEDEGGVVFSVIVGPNDPYQDRPLPYIIGSDKWIASNKIGL
ESSSSESEQADEEREESESEKEDAGVHKVFNSRHNPEINIARLSSSSDSDNYNDHSNNISYENNKTDIASQNNINSASES
VTPNNVSKSNEAAPNFAEELAKRLGTVRQAQKPVAVDETNESSINRFKDDLFASEKDEDVFNGSDNLFSSKKDLFDDQVS
ANLWKEKPIKSYKNSNIIPASIDVPPPISIVSTKPKSAIDDLFADADSEEDSDDIFSSKNAIKKRTKESVASDNAYPANM
EDVPKKFMDVIATNKIATSTPESNINSTSLFSDDENDDADLFGNSKKQSHKPTNTPLSTNTQESSKKKPVGGEWILGNVL
ASDIESKLSSRIMQRRQESESSDSDAPGNSDCATRSNVESASMTTNHSSQNPTENVSAIVGSTISSGISVQPPSIDITVG
SGLSNIFSPCMTSTRVKSEEIYRERITSDSLFEARTHYPANANSDNQQQQQQQQLEQQQQDISSALLQDDVFENDDLFGP
PPLPNKSDSKRTNKSKVSSLFDDSDSGDEFFSVASSGSRSQKSTDFHNTVSSSDRTKSVSKSGDLFDDNVNIFGGKDAPD
VDIFGVAPGSKNAASNGPSSVIPKNNNDNSRNTRMEPKKISLFDDNDDDGDLFGAKPMKLKNERKIDLFEDEDDLFLTKT
SSIEKDVAKIDVKPKIDVSKNVSSLETEKKNRNDPSDHLDELFSKRTRPHNLLFEDDDYDDLFSKKDTASCDKDQLKSKD
EIKKDIAEQAQELPEENKSPVESSNLNRDVKTIIESNVVARNNVDEEKSETEIKETSSNEEDGIVKKNSPPKTLSIRTIS
PPSEEHGNQQVPRRLVSGKIKNLMGKMSDLKILSPMDAPPLWRKSEDKTDEEEDVVDRDIADLGISGHVSPPSISEGSTL
KESSYSTISTTSNAEAAINFDDLAQVETLSTTASKSRVRIQAKRRPQSRHARKSALRHSGIDFDTVDNADNDNSQEESHT
STCSSSKDPSAALTISVSDRLTANDNIHRSAVDPASTDDKSELGSISKESSMSVNKNTLLSPSTDEEDLFDVPPDLPEDP
QKEDTLFGRAPILSPIDGQSDKTLVVVKPLDTVIRKIDDMDTGVDAMNNESNKRNSSEFAQLNVNTKSDTLESPKKKDDK
HKEVDDEQDKVIRASSEELSDPLRDSTHDPLKDPSQLFAFVTKTPSPEKSKGLLFSESDDSLFSSGSAKKPNEPKKKVLD
LFADDNVGGDLFSTAPLKRTVKKPLRDTKIGLFGDDDAQNDDDDSLFGNSSSKAKLNNQSSSSISTGRKKDNIFDDDDDD
DEEEEEEEEEEEEEEEEEEEEEDDDSSVFVESSGLSQKSDSASFSELKQDSQVDFQTKSSNLKDIFGNVSHDGDDDDSDL
FATKKIVPKKVVAPKLSKSLFLSDDDDDDGYIFGKQPSASTQSKASTTIAPSSRSVVKKPVTKDLKKTAEKIIEDPLSLL
QDD

1522 - 1541:	EEEEEEEEEEEEEEEEEEE
1523 - 1542:	EEEEEEEEEEEEEEEEEEE

A0A151IK59 **A0A151IK59_9HYME** (617 aa)
Pescadillo homolog. *Cyphomyrmex costatus*

```
MVVIGKKKYQSGEGAQFMSRRAALRKLQLTLNDFRKLCILKGIYPREPRNRKRAQKGEPGIKTLYHKKDIQFLMHEPIIW
KLREYKIFNKKIGRAKAMKDFAKVKRYLSNHPTLKIDHIVKERYPTFIDALRDLDDCLTLCFLFSTFPSLPHIPRDQSLL
CRRLTIEFLHAVIAAKALRKVFVSIKGYYYQAEIKGQTVTWIVPHHFCFEPQAKNEVDFKVMSTFVEFYIVMLGFVNYRL
YHTLNLHYPPKLINSENIEKTLVDEETYVSERISALNVLLINLNSSISTTEDDDIEIDQFSNETDATKIEAAKAEAEKIR
KLKNLFKGIKIFINREVPREPLVFILRCFGGEVSWDKLLFVGATFDENDETITHQIVDRPSMNKQYISRYYIQPQWVFDS
VNARELLPIEKYLMGAVLPPHLSPFTENRQDQTYIPPEERALMDPDYKLNNLEEEEEEEEEEEEEEEEEEEEEEGKEDKN
GNEENKIETENDLSSGSDEEMEEIQENDDNDVQIAEEKEKEKMKKQAQLQKKKMKVQTGEIMKENPWEEARLEKQEYRLR
EKMIKKKHRKLYQSMMKGREGRAKEIWLLRKKRRIHEAKEKEKRKEQKKANRNKSNK
```

453 - 472:	EEEEEEEEEEEEEEEEEEEE
454 - 473:	EEEEEEEEEEEEEEEEEEEE
455 - 474:	EEEEEEEEEEEEEEEEEEEE

A0A151J0R0 **A0A151J0R0_9HYME** (1126 aa)
MOG interacting and ectopic P-granules protein 1. *Trachymyrmex cornetzi*

```
MIIPNGVNGNYSADNEEYMDTSDNTSKTALKDVITEEEEEEEEEEEEEEEEEEEEEGEEREEGEEGEEGEDEEEEEDVDE
QYDEDDHERVVDIQEGKYEDSDRNEEEVGNTSKEGETFDLKNDFKVSNSPDGVSETNNSSEVSKTEISECVKNTSCEAMD
VDEQSNNSDIECLDESITEIQLDNDDVFLSKKTIEKHDNDVSSNCSCDSSEIADSSMEKSDVKLCEENGSCDSPDIEEIT
DSAKSNDHDSSLDRIKDPTKQRKPRKQIDLSSITPRRSSRNIKRTSYIEKELEEEVEDDGSDIEEIKPEDPLAGIDSKDK
ENSKLKSPVRNSKTTIVVNDTKRLVEIAAGSKSIKGGKKEPTLVIIDTNSILSGRGGVPVSNSKPHHTVSNSNPFSVVPM
SGMTTQTMYPNMRTTITPVPMTSKAAQLSPKTSSITTVTPTVPPILPTLTDDMFVVEAPSFIVPYVYEKPPLKPLKEFVT
KLERNIEEIEKEERMKRLADENKDNEDYKEDSLDIKRGNDKSEDSDMEGKGKREGDDRGDNSIDLIEHGFSSLSDKHDLR
QDDRNKIPTYFDLPLGKFFMQIGMNLVQEYVQTDLLRTQKRKQGKGSTSAETQLAINSLIKNLEFSKENNEPFHLEMKKC
EFCSFKTESTLVMQHHLETPHMRNYVYKCNFCPMEVRSPHDILYHMEAEHNTRGRLERGPAFHQCPNCPFEDNQKGKLTR
HILACTKKFRPERNLEPAVDWEPPAKIPRVNRARPVGPTNPSALAAMAMSAKGPQPLLPKLLPAPITGRGRGRPPMQPRY
SDLKTLRPGATPMRQGMMYRPTSSGLLVPTSYQFSSNQIFQVVGGSGTVMSAVSGVSSSSGGSSGGSPTPIALVPNVIDSL
SRLSSSQNTTASPKNPTAKLLSQPSISITPLPRTTSQTSIPGSGTSSKSGGKNTFVICEICDGYIKDLEQLRNHMQWIHK
VKIHPKMIYNRPPLNCQKCQFRFFTDQGLERHLLGSHGLVTSSMQEAANKGKDAGRCPACGRVYQWKLLNHVARDHGMTL
KPAHLSYKCTVCTATFGMYKQFENHVYSAHSVVAKRVMDKKNTPASPSSRSNDSLLKPLKINDEITIIPQPAKPTTRSGA
IQGRGK
```

36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE

A0A151J9N2 **A0A151J9N2_9HYME** (1391 aa)
Uncharacterized protein. *Trachymyrmex cornetzi*

```
MSNHEINKRDHNYSESKPQHANNSTSNTISKISQTGSVVGQIRDIDELKKIAPRVRLQDTESLNELTRISSLSNSKSQQN
DISILERTRQELRKYCRTCAGLKLPLVDIFSEKGIKLRLSQQIKHLEVNPYDSSLSTQMCMDCICDLRMSYKFFMQIKKA
EIKLKSIHVNLTTDNATKKVTSIDDSLIVKEDKQPSYSEIKPEYQLSSAIQQNPSLSSTEHVNQAIPENQIDDSVPKICA
IFSLNESKMGQDFEIEKEMEKEKEEEEEEEEEEEEEEEEEEEEDKDTEEKEVTQVGGGIFEEVAEGEDEESIEEFDPEDP
ALLVDEEEEEKSLKTVYNYDMAADSYVRVEGNEGISVKSEVSQTSEGENQREGMWQPNILKRKLIPMISNNGGEDEIQSI
VEKHKVQKLDTNSLLNMNNPSEEEGIMYVTVKGSKPNEILLVKVKKMDKLTEPKRAVVPVSADLKPVERFLKRYETLTKD
FSSRRPDAREQIIEEQIEEYKKKREKVLGNQAAVTHTANETQKEVQEEDISIKSNFERTEEEMIVIKEEDEERETRKEEK
MKDKEEEEMKEEEENEKQKEKEKMENDVKIEKGQERISDNTEEHLKLSRMKKLEETKRKKESLQKELDESCNEENLEKLA
KVLEKTENLQEFLEYLKQRKIILARLKDEDIISLYEAQFSTTIKSSSKSLPDLVDTQHPSGLLFDLLSDEDNYLECDYCS
ETFPNCDLLEGHLKSHDYRILHCCDDCGEEFQTNKAKRNHNMLCVKKFICKYCEIVLDSKGKKRQHEQKHVDTLYGQLCE
ICGERFKHQGTLDQHQKTQHTSLEKIYQCPKCPKKFAFKQKLSFHLKSVHTTLRAYLCEDCGADFKNPASLRHHRIRKHQ
PVGNKRECPVCRKLVPFYSLSKHMHTHKAYSIQCPHCDKMFKNSSTLKQHVRIHEDQRQFRCDTCGVGFNRRDGLRLHLR
VHEKTGSRGLKECSCQVCGEKFPNHSTLVIHRNREHKDGKQYTCHICNRSMISTRSLEWHMSHIHNQLVPGITRNESGLL
EKKRVSCYHCNKTFKTELILRTHIKNTHMEKDPLKCTDCEDIFNSEVRLRHHLMVVHNRLEGTLACPHCPKRFVNQLRLK
THMISHSEERPYTCEICGFNLKTKIQLIKHHQNRHSDERPLQCKYCPWRCKQVSALVCHERTHTNERPYSCSVCRQRFKY
LGDKNKHERRHESLGGSGFKRIVPGRNLKQKNSNPACVNSDVESDQDDIVKRSVSQLDMHVTEEQFEEGQMVKFEEVKFE
NGEQYEHVYEQEYEETSREASEATELIMNIEDSNMYTEEVTADSIESGAEIITDEIITNDILQSGTAVVLQSEDDSGKIQ
VIPIPVVLSLPDLSDANTEVNLPTASIMYNN
```

264 - 283:	EEEEEEEEEEEEEEEEEEEE

A0A151L7J6 **A0A151L7J6_PLARE** (384 aa)
Casein kinase II subunit beta (CK II beta). *Plasmodium reichenowi*

```
MEFVSNDESADDIIQDESNEGEVELADADFYDLTVINDKIDEEIIEDDEEEADMDDQENDNVQEVYNIDDDDNDIHNDKL
LLDQQRDNDVNEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEDDDDDDDDDDDDDDDDDYDDEYDEDDFNEATVSW
IEWFCQLKQNLFLVEVDEDFIRDEFNLIGLQTKVPHFKKLLKIILDEDDDDDDDDDDDYDDDDDEINRDSEEMYKNKDMH
EQNAACLYGLIHSRFILTSKGLALMREKYKSGIYGTCPSIYCENAKLLPTAISEIPKFLSPLLYCPRCCETYYPSKNSLL
NQLDGSYFGTSFASFFALSFNIASDKKKVYYTPQICGFTINRNIRETLYMDVNKDHTESSEEYQ
```

92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE

98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE

A0A151L9P7 **A0A151L9P7_PLARE** (1987 aa)
Uncharacterized protein. *Plasmodium reichenowi*

```
MNVCKMKVQQKKNLKDCNLKSKNTILTSFEKKKNEKDENNLLKFAKLIDNKNKVVNSKFLKNDNYKCNERKESLTRCSTN
ESLKLKNMKTLTKDFDYNNNNDDYNNNNDDYNNNNDDYNNNNINNNNNNNNNNNGHSKLVFKKKSKDIESTVIEEDEKKS
EKKTNDLINNKNEFKVNNKLILKSKEFKSNNNNNNNNNNNNICKLKNVDDKNKKQQMDTYSPKENEEDNSNNMKKNSCL
KNIKKNQINEKEIIPNTVEENHDTHSKGDKEHNGVSTKNVKRMNTMSKEINHKNNNILKKNLSKSNSLELKKGKKGDKLK
DKLINNLSGKKGMNKEKEVVQSSSAKRSSSRYSIDYGRRDSSRRGSAKQEKGKERRASKNVSKKVSKSKYTRKKSKRIKE
ESDESDDDDDEEEEDDDDDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDNENNNSDNNDESDEVYTNRS
RRSTRCSIVKRKSSLCIGKKNSKIIKKSTSKTKNNKKKKGSVIKLEKKKEKLSKKGILKKKNKKTKGKLRKNSKVYHRKK
NIKNEKVGIDEEDIEEEIEEEEEPSYFDEYNLSIEERKKDLEEKEKKKEIKEKYIKQIKLPKYADDESIIFINNPNYVMV
LLFLTVYKDVLKMNWNFKDIEDMFQNKETTEFGRNFILKLFFFLGRYFNSKSIFMYKYISRIFEDKEESLSRVVNFHELF
PVLETKKEIKNSGVGSKRKKDKRGKKMKIHQKEDELLYDEEVIGNEDVNIFEEEEEEEEEEDDDEEDNEHSNDDEDEEEE
DNEHYNDDEEKENVNYKDEEEKKSDMNNDSTKNTVIKEEKDGLHISESNHNLVNIVNDSMKREESCKNGHIVDNERSADF
KINDDKNNEDNNDDGDKIVDSKNNIENKLDKSVDGMKDINSTEGIIKNENVDDEKGLTNKLFLEWDDLSVISKLRIIRML
LNLVLCESNNLKKMLGDEKLNYNNGYLGKINNEKYWFIFNDTINIEYKLYLEREEEGSFIFICDDDDMLYTIGYNFLRNS
DTKFMGEALIERYNKVCRERRNRSRMLKQQKKLLCSDINLNDPLLGTKKRQPKQVEYFNFNNNEKIRRKKSDINNNNNNN
NPYSVPLTKSYQKNDRSFRLAARNAQKGSVDDLEAWKLNEGLLGIENEGGISGNYNIENDGNNMVETNNINDNNNDNNKK
NNNNNNNNVVVKADGNNVYGPNNNNVIGSDGNMNNGNNTTTTNNNNNNNNNNLGTVKIPLKRGRKKKSEKKKRGRKKKIL
SVDGIGDVGNNLSSLNVDENRRKSMPNIGRGRRGTYTKRNTKPSVSIKYGTRSNSINKYENDVMSFNEYSLNPGLSMDDF
YKNMVMDAKFFHGNMSMNNYMNGGFNMPNNNNSMMNMRNGSKMGNINNLGGYNFPYMCTPPPPMYNQYYMYNGNNMYLPN
GGAINNMNMSNTNNSASVGIGGNVVSNQNTVKDVKAENMNMAKNSIMENRNSISVNSMNNINMNNMPHKNSFLGNDGINN
MNSMMNNNNNNNNVSNNNNNNNNNNNVNFMDNMGNNNNSNNNSNNSNNPMNKYNNYMMNRNALNNMGGTNPMYNNMYNMKF
PYMNNDMMNYNYNINTFQNMNYDKMNKSMFKRYPNFMGGYPYNNMNPYNNFNAFNMNYQQNDQMNQLPNMQGAYKSKLMN
DNLSNYQSFNNNNIKQNHHDNNNNNNNDNNNNINKNNSECGNKNVDDSNKNNDINKNDILDSTKFTEQAVGGVALNNDCT
TRGEDNHRIDLKGDVVEALVGNNNEKMNSSDHNLNSLKNLQNINSTYNMDHMSHMRNSVSGSSIGMINPGHMNSSHSGSI
MNKDKFRDLQLNNNNNNNNNNNNNNNNNNYVKVNPFDHPMKNMNQNLMDDKYPKDNNMMMMMMNSVYNIMGSDHFHMNNS
HMMDPMGSPKMNDNMYNHNNMNFENTNTNHNNHNNHNNHNNHNNHNNHNNHNNHNNRIQDKLPE
```

420 - 439:	EEEEEEEEEEEEEEEEEEEE
421 - 440:	EEEEEEEEEEEEEEEEEEEE
422 - 441:	EEEEEEEEEEEEEEEEEEEE
423 - 442:	EEEEEEEEEEEEEEEEEEEE
424 - 443:	EEEEEEEEEEEEEEEEEEEE
425 - 444:	EEEEEEEEEEEEEEEEEEEE
426 - 445:	EEEEEEEEEEEEEEEEEEEE
427 - 446:	EEEEEEEEEEEEEEEEEEEE
428 - 447:	EEEEEEEEEEEEEEEEEEEE
429 - 448:	EEEEEEEEEEEEEEEEEEEE
430 - 449:	EEEEEEEEEEEEEEEEEEEE
431 - 450:	EEEEEEEEEEEEEEEEEEEE
432 - 451:	EEEEEEEEEEEEEEEEEEEE
433 - 452:	EEEEEEEEEEEEEEEEEEEE
434 - 453:	EEEEEEEEEEEEEEEEEEEE
435 - 454:	EEEEEEEEEEEEEEEEEEEE
436 - 455:	EEEEEEEEEEEEEEEEEEEE
437 - 456:	EEEEEEEEEEEEEEEEEEEE
438 - 457:	EEEEEEEEEEEEEEEEEEEE
439 - 458:	EEEEEEEEEEEEEEEEEEEE
440 - 459:	EEEEEEEEEEEEEEEEEEEE

A0A151LDY5 **A0A151LDY5_9APIC** (388 aa)
Casein kinase II subunit beta (CK II beta). *Plasmodium gaboni*

```
MEYVSNDESANDIIQDESNEGEIELTEAEFYDLTNINDKIDEEIIDDDEEEVNKDDQENDNVQEVYNIDDDDNGVNNDVN
NDVNNDVLLLEQQRDNDVNEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDDDDDDDDDDDDDDDDDDDYDDEYDEDDFNEA
TVSWIEWFCQLKQNLFLVEVDEDFIRDEFNLIGLQTKVPHFKKLLKIILDEDDDDDDDDDDDDYDDDDDEINRDSEEMYKN
KDMHEQNAACLYGLIHSRFILTSKGLALMREKYKSGIYGTCPSIYCENAKLLPTAISEIPKFLSPLLYCPRCCETYYPSK
NSLLNQLDGCYFGTSFASFFALSFNIASDKKKVYYTPQICGFTINRNIRETLYMDVNKDNTESSEECQ
```

100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE

A0A151LV11 **A0A151LV11_PLARE** (3073 aa)
Transmission-blocking target antigen s230. *Plasmodium reichenowi*

```
MKKIITLKNLFLIILVYIFIEKKDLRCNVIKGNNIKDDEDKRLHLFYYSHNLFKTPERKEKKNKKEYVSKNGDIYNLSKE
ITMRKDTSVKIKQRTCPFHKEGSSFEMGSKNITCFYPIVGKKERKTLDTIIIKKNVTNDHFVSSNMHSNVQERNMILIRN
IDKENKNDIQNVEEKIQRDTYENEDYESDDKLIEWFDDNTNEENFLLTFLKRCLMKIFPSPKKKKTVVQKKHKSNFFINS
SLKYIYMYLTPSDSFNLVRRNRNLDEEDMSPRDNFVIDDEEEEEEEEEEEEEEEEEEEEEEEEEEEYDDYVYEESRDE
TEEPLQEEQHEEVAAESSEESFNDEEEDYVETQDGDMIRVDEYYEDQDSDTYDSTIKNEDADEEVGEEEGEYVDTYEDEK
ESQGEIYRVGDEEEKDEGGESVTYEKSEIDKTDLFKFIEGGEGDDVYKVDSSKLLLDDDTISRVSKKHAVRDGEEGEDVE
EGEDEESVIKIIRSVLQSGALPSVGVDELDKIDLSYETTESGDTAVSEDSYDKYASNNTNKEYVCDFTDQLKPTESSPKV
KKCELKVNEPLIKVKIICPLKGSVEKLYDNIEYAPKKSPYVVLTKEETKLKENLLSKLIYGLLISPTVNEKENNFKEGVI
EFTLPPVVQKTTVFYFICDNSKTEDDSKKGNRGIVEVHVEPYGNKINGCAFLDEDEEEEEKYGDQVVEDEHNEKIKMKTF
FTQNIYKKNIIYPCYMKLYSGDVGGIMFPKNIKSTTCFEEMIPYNKEIKWNKEKKSLTNLVNNSVIYNKEMNAKYFNVQY
VHIPTSYKDTLNLFCTIILKDEESNLNSNSYLVYVSINEELNFSLLDFYESFVPIKKTIQVAQKNGNNKEHDYTCDFTDK
LDKTIPSTVDGKKLFICRKHLKEFDTFTLKCNVNKIQYPNMEIFPKTLKDKKEVLKLDLDIQYNMFSKFYKFNTENSKYL
NLYPYYLIFPFNHIGKKELKNNPTYKNHKDVKYFEQSSILSPLSSSDSLGKLLNFLDTQETICLTEKIRYLNLTINELES
DNNTFSVTFQVPPYIDIKEPFYFMFGCNNNKGEGNIGIVELLISKQEEKIKGCNFHESKLDYFNKNISSDTDECTLHAYE
NDIIGFNCLETTHSNEAESDDGTEISLQPENCFNNVYKGLNSVDITTILKNAQTYNINNKKTPTFLKIPQYNLLEDVEIS
CKCTIEQVVKKIKVIIMKSDTVLLKREVQSESTLDDKIYKCEHENFINPRVNKTFDQNVEYTCNIKIENFFNYIQIFCPA
KDLGIYKNIQMYYDTIKPTRVPQFKKFNNEELHKLIPNSEMLHKTKEMLILYNEEKVDLLHFYVFLPIYIKDIYEFNIVC
DNSKSTWKNQLGGKVIYHITVSRREQKVKGCSFNDEHAHMFSDNKTNVKNCIIDAKPKDIIGFVCPSGTLKLTNCFKDAI
IHSNLTNINHILYLKNNLANFTYKHQFNYMEIPTLMDNDISFKCICVDLKKKKYNIKSPLGPKVLRALYKKLNIKFDKYV
TGTDQNKYLMTYMDLYLSHKRNYLNELFNDLDKKKPAETDSNPESIIESLSINESNESGPFPTGDVDAEHLILEGYDTWE
SLYDEQLEEIIYNDIESLELKDIEQYVLQVNLKAPKLMMSAKINKNKHVCDFSRNNLIVPESLKKKEELGSNPVSIHCYA
LLKPLDILYVKCPTSKDNYEAAKANISESDNEYELQVISLIEKKFHNFEVLDSKNPGNGDVAHNGVVDTGPVLDNSTFEK
YFKNIKIKPDKFFEKIIIKTDDTEEEKDFESILPGVIVSPMKILKKKDPFTSYAALVVPPIVPKDLHLKVECNNTEYKDE
NQYISGYNGIIHIDISNSDKKINGCDFSTNNSSILTSSVELVNGETKNCEININNNEIFGIICDNETNLDPEKCFHEIYD
KDNINVKKFREVIPNIDIFSLHNSNKKKVAYAKIPLDYINKLSFSCSCKTSHTNTIGTMKVTLNKDEKEEEDFKTAQGIK
HNNVHLCNFFDNPELTFDNNKIVLCKIDAELFSEVIIQLPIFGTKKVEGVQDEQYKKFSLKPSLVFDDNDNDIRVIGKEK
NEVSISSALKGVYGNRIFTFDKNGKKGEGISFFIPPTKVDTDLKIIINETIDNSNIKQRGLIYIFVRKNVSENSFKLCDF
TTGSTSLMELNSQVKEKKCSVKIKKGDIFGLKCPKGFAIFPQACFSNVLLEYYKSDYADSQHINYYIHKDKKYNLKPKDV
IELMDENFRELQNIQQYTGISNITDMLHFKNFNLGNLPLNFKNHYSTTYAKVPDTFNSIITFSCHCYNPEKHVYGTMQVE
SDNRNIDNINKNENIIKNFLLPNIEKYALLLDDEEREKKQKNLKDQDETLTTHDDDFNKNHIYMLYDSNEHICDYEKNES
LISTLPNDTKKIQKSICKINAKSLDVVTIKCPHTKNFTPKDYFSNSSLTTNDKKIVISFDKKNFVTYIDPTKKTFSLKDI
YIQSFYGVTLDHLNQIKKIQEEWDDVHLFYPPHNVLHNVVLNNHIVKLSSALEGVLYMKSKVTTDETSTKKNTTLPSDGV
SSILIPPYVKEDMTFHIFCGKSTTKKPNKNNTSLALIHIHISANRNIIHGCDFLYLEKHTNDSINNNSYSIFTHNKNTEN
NLICDISLIPKTVIGIKCPNKKLSPQTCFDEVYYVKEDDVPSKTITADKYNTFSKDKIENILKNAISINNPDQNDNTYTY
LILPEIFEEELIDIKKVLACTCDNKYIIHMRIEKSTMDKIKIDEKKTIGKDICKYDVVTKVATCEIIDSIDSSTLKEHHT
VHYSITLSRWDKLIIKYPTNEKTHFEKFFVNPFNLKDKVLYNYNKPINIEHILPGAITTDIYDTRTKIKQYILRIPPYVH
KDIHFSLEFNNSLSLTKQNQNIIYGNVAKIFIHINQGYKEIHGCDFTGKYSHLFTYSKKPLPNDQDICNVTIGNNTFSGF
ACLSHFELKPNNCFSSIYDHNEANKVKKLFDLSTNVELDHIKQNTSGYTLSYIIFNKESTKLKFSCTCSSNYSNYTIQIT
FDPNYITPEPQSRAIIKYVDLKDKNFAKYLRKP
```

280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE
287 - 306:	EEEEEEEEEEEEEEEEEEEE
288 - 307:	EEEEEEEEEEEEEEEEEEEE
289 - 308:	EEEEEEEEEEEEEEEEEEEE

A0A151LWI7 **A0A151LWI7_9APIC** (3061 aa)
6-cysteine protein. *Plasmodium gaboni*

```
MKKLLTLKNLFLIILLFILTKKKDVRCNIIKENNIKDDEDKRFHLFYYSHNFFKTPETKQKKKKKKKQLYKNVGISNLSK
EISIRKDTYVKTKQRTCPFDKEESSFEIGSRIITCYDPIIWKKERKYMNKTVIKKNVTNHQFVYSDINKEYKNDIKNVEE
KIQRDTYEKKDYENNDNLVVGYDDNFLLSFLKKCLMKIFSSPKKKKTVVQKKHKSNFFINSSLKYIYMYLTPSDSFNLVR
RNRNLDEEDMPPKDNFVIDDDDEEEEEEEEEEEEEEEEEEEEEEEEEEEEYDDYVYEQSVDETEEPLQQLQEEQQDEVAVEG
SEESSNDVGEDYVEGEDEDMIRVDGYYEDQFADTYDSKIKDEREDDAVDEYLDEYLDEYSDEYSDEYSDEYEKERESQGE
TYSVDDEGEESFTYEKSDISKTDLFKFIEDSEGDDIYKVDSSKVLLEDDTTISKVSKKSADVEGEEDEESVIKMIRNVLQ
SSVLPSEGADEFDKIDLSFETTESGDTSVSEDSFDKYASNNTNKEYVCDFTDQLKPTESTPKVKKCEVKVDEPLIKVKII
CPLKGSVEKIYDNIEYIPKKSPYVVLTKEETKLKEHVLSKLIYGLIISPTVNEKENNFKEGVIEFTLPPMVKKPTVFYFI
CDNSKTEDENKKGNRGIVEVSIEPYGNKINGCAFLDDDEEEEKYGDQGEVDENNDKIKLQRFFTQNIYKKNNIYPCYMKL
YSGDIGGIMFPKNIKSTTCFEEMIPYNKEIKWNKEKKSLTNLINNSVVYNKDMNAKYYNVQYVHIPTSYKDTLNLFCSII
LKEDESNLNLNSYLVYVSINEELNFSLLDFYESFVPIKKTIQAAQKNVNNKEHDYICDFTDKLDKSLAPLIEEKKLFICR
```

```
KYLKEFDTFTLKCNVNKTQYPNIEIFPKNLKDKKEVLKLDLDIQYQMFSKFFKFNTENSKYLNLYPSYLMFPFNHIGKKE
LKNNPIYKSHKDIKYFEQSSLLSPLSSSDSLGKLLNFIDTQETVSLTEKIRYLNISINELESDNNTFSLTLQVPPYIDIK
EPFYFMFGCNNNKGDGNIGVVELLISKHEEMIKGCNFHETKLDYFNNNVSNSKDECTLYAYENDIIGFNCSETNNASDEE
EDGVEISLQPENCFNKVYKGLEIIDINTILNNAQVYNINNKKTPVFIKIPPYNLLEDTKLSCKCTIDHVVKNINVILTKN
DKVLLKREIQNEFKLDDKIYTCEHENFINPRVNKIFDEKVEHTCNVKIEKFFNYIQILCPAKDLGIYKDIQIYYDIIKPT
RVPEFKKFNNEELHKLIPNSEMLHKTKEMLILYNEEKVDLLHFYVFLPIYIKDNYEFNIVCDNSKTTWNNQIGGKVIYHI
TVSKREQKVKGCSFNEEYTYMFIDNKSNVKNCVIDANPKDIIGFVCPSGTLKITSCFKDAIVNTNLTNINHILHLKNNLA
NFTYKHYFNYMEVPALIDYDISFKCICVDLKKKKYNIKSPLGPKVLNAIYKKLNIKYDKYVTGTLQNKYLMTYMDLHLSH
KRNYIKELFNDLNKKKPADTDANPEAIIESLTINESNESTPFPTGDVDAEHLLLEGYDVWENLYDETLEDVIYKDIESLE
LKDIEQYVLQVNLKAPKLMMSSQINNNRHVCDFSMKNLIVPDSLKKKKEEGGNNPIDIHCYALLKPLDTLYVKCPTSKDN
YEAAKVNISESDNEYELKVISLIEKRLQNFEVLDSKRNGNGHAILTNGVVDPTSVILDSSIFEKYFKNIKIEPDKFFEKV
IKEVDDTEEEKELESILPGVIVSPMKVLKKKDPFTSYAGLVVPPVVSKDLHLKVKCNNTEYKDEDENILGYNGIVHIEIS
SSDQKIKGCDFSTDDSSILTTSIKLVNGETKNCEININNNEFFGIICDNDTNLDPEECFNEIYDKDKSNVKKFHELIPNI
DIYTLPNSNKKKVAYAKIPLDYINKLSFSCSCKSSHNNTIGNMKVILNKDEKEEDEFKTSLSIKHNNINLCNFFDNTELT
FDNNKIILCKIDAELFSEVIIQLPLFGNNKTLEGDQNEEYKKFSLKPLLPINEDDNDIKVIGKEKNEISINLALKGVYGN
RTFKFEKDGKKGEGISFFIPPTKIDTDLKFIINETIDNSNIKQRGLIYIFVRKNVKENTLKLCDFTTGSTSLMELNSQMK
EKKCNIKIKKGDIFGIKCPKGFAIFPQACFSNVLLEYYKSNHTDNEDINYYIHKDIKYNLKPKYVIELMDENFRELKNIQ
QYTGISNITDMLHFTNYNLGNLPLNYKNNYSTAYAKVSDNFNSIINFSCNCYNPEKHVYGTMQVESDNTNFDNIKKNENI
KKNVLLPTIDKFPLLLDDEQRQKFKLKLRDTNDIFNTNDIFNTNDINHIYMLYNSNEHICDYQKNETLISNIPSDNKKIQ
KSTCKINAKSLDVVTIKCPHTKNFTPKDLLDNSTLQSNDKKIVITFDKKNFVTYIDPTKKTFSLKDIYIQSFYGVTLDHL
NKIKKIQQDWDDEHLFYPPHNVLHNVVVNNHIVKLSSALEGVLFIKSKVTGDETNTKKNTTLPTDGVSSILIPPYVKEDI
TFHIFCGKSTTKKPNKNNTSLALIHIHIASNTNIIHGCDFIYLEKNTSVTSTVNNTSTIFTHNKNKENNLICDISLVPQT
VIGINCPNKKINPPTCFDEIYYIKEEDVPPKTITADKYNTFTKDKITNILKNAISITNPDEKDNTYSYLILPDKFEEQLI
DTKKVLACTCDNKYMIHMKIEKNTIEKIKNDEKKTIGKDICKYDVTTKVATCDIIDVIDSSSIKEHHTVNYSVTLSRWDK
LIIKYPTNEKTHFEKLFVNPSNLKDKVLYNYTNPINIEHILPGAITTDLYDTRTKLKQYILRIPPYVHKDIHFSLQFNNT
LSSTKQNQNVIYGNVANIFIHINQGYKEIHGCDFTGKYSHLFTYSKKPLPNDNDTCNVTITNNTFSGFACLSHFELKPDN
CFSSVYDNNEANKVKKLFDLSTNVELDHIKQNTSGYTLSYIIFKKESNKLKFSCTCSSHYSNYTIQITFDPNYITPEPQS
RAIIKYVDLQDKNFGKYLRKH
```

263 - 282:	EEEEEEEEEEEEEEEEEEEE
264 - 283:	EEEEEEEEEEEEEEEEEEEE
265 - 284:	EEEEEEEEEEEEEEEEEEEE
266 - 285:	EEEEEEEEEEEEEEEEEEEE
267 - 286:	EEEEEEEEEEEEEEEEEEEE
268 - 287:	EEEEEEEEEEEEEEEEEEEE
269 - 288:	EEEEEEEEEEEEEEEEEEEE

A0A151NA22 **A0A151NA22_ALLMI** (923 aa)
General transcription factor 3C polypeptide 3 isoform A. *Alligator mississippiensis (American alligator)*

```
MSDFSPELIDYLEGKISFEEFERRREERKKRQRKDEENSPTEDNTENLDAPSSSRKGSSKSQCLNDTEGETSDGVSKSVH
RVFASMLGENEDEEEEEEEEEEEEEEEEEEEEEEEDDEETSEQPSAGDVFALEMVLNRENKKMMKEKRPRSKLPRALRGLM
GEANIRFARGEREEAILMCMEIIRQAPLAYEPFSTLAMIYEDQGDMEKSLQFELIAAHLNPSDTEEWVRLAEMSLEQDNI
KQAIFCYTKALKYDATNVRYLWERSSLYEQMGEHKMAMDGYRRILNLLSPFDGERFMQLARDMAKSYYEANDVTSAIEII
EEAFTKHQSLVSMEDVNIAAELYISCKQYDKALAVITDFSGIVLEKKATEKGSSEENKETNTVAVVKIQESQVEVMDYQD
VPPESSAASPEKVSCLIPDGVPIDITVKLMICLVHLSILEPLNPLLTTLAEQNPEEMGDLYLDVAEAFLDVGEYNSALPL
LSALVCSERYNLAVVWLRHAECLKALGYVERAAESYAKVVDLAPLHLDARISLSTLQQQLGRPEKALEALEPMYDPDTLA
QDANAAQQELKLLLHRSTLLYSQGKMYGYVDTLLTMLAMLLKVAMNRAQVCLISSSKSGERHLYLIKVSRDKISDNDDQE
TANCDAKAIFAVLTSVLTKDDWWNLLLKAIYSLCDLSRYKEAELLVDSSLEYYSFYDDRQKRKELEYFGLSAAILDKNFR
KAYNYIRIMVMENVNKPQLWNIFNQVTMQSQDVRHHRFCLRLMLKNPENHALCVLNGHNAFVSGSFKHALGQYVQAFRTN
PDEPLYSLCIGLTFIHMASQKYVLKRHALLVQGFSFLHRYLGIRGPCQESYYNLGRGLHQLGLVHLAIHYYQKALELPPV
VLEGIETDQTDLKRDIAFNLSLIYLSSGNTTVARKMLYTYGVM
```

93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE

A0A151NA59 **A0A151NA59_ALLMI** (926 aa)
General transcription factor 3C polypeptide 3 isoform B. *Alligator mississippiensis (American alligator)*

```
MSDFSPELIDYLEGKISFEEFERRREERKKRQRKDEENSPTEDNTENLDAPSSSRKGSSKSQCLNDTEGETSDGVSKSVH
RVFASMLGENEDEEEEEEEEEEEEEEEEEEEEEEEDDEETSEQPSAGDVFALEMVLNRENKKMMKEKRPRSKLPRALRGLM
GEANIRFARGEREEAILMCMEIIRQAPLAYEPFSTLAMIYEDQGDMEKSLQFELIAAHLNPSDTEEWVRLAEMSLEQDNI
KQAIFCYTKALKYDATNVRYLWERSSLYEQMGEHKMAMDGYRRILNLLSPFDGERFMQLARDMAKSYYEANDVTSAIEII
EEAFTKHQSLVSMEDVNIAAELYISCKQYDKALAVITDFSGIVLEKKATEKGSSEENKETNTVAVVKIQESQVEVMDYQD
VPPESSAACEQSPEKVSCLIPDGVPIDITVKLMICLVHLSILEPLNPLLTTLAEQNPEEMGDLYLDVAEAFLDVGEYNSA
LPLLSALVCSERYNLAVVWLRHAECLKALGYVERAAESYAKVVDLAPLHLDARISLSTLQQQLGRPEKALEALEPMYDPD
TLAQDANAAQQELKLLLHRSTLLYSQGKMYGYVDTLLTMLAMLLKVAMNRAQVCLISSSKSGERHLYLIKVSRDKISDND
DQETANCDAKAIFAVLTSVLTKDDWWNLLLKAIYSLCDLSRYKEAELLVDSSLEYYSFYDDRQKRKELEYFGLSAAILDK
NFRKAYNYIRIMVMENVNKPQLWNIFNQVTMQSQDVRHHRFCLRLMLKNPENHALCVLNGHNAFVSGSFKHALGQYVQAF
RTNPDEPLYSLCIGLTFIHMASQKYVLKRHALLVQGFSFLHRYLGIRGPCQESYYNLGRGLHQLGLVHLAIHYYQKALEL
PPVVLEGIETDQTDLKRDIAFNLSLIYLSSGNTTVARKMLYTYGVM
```

93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE

A0A151RB78 **A0A151RB78_CAJCA** (1055 aa)
Uncharacterized protein. *Cajanus cajan (Pigeon pea) (Cajanus indicus)*

```
MHSVPCSSQQWGHEDVNRHRNMVFDAAGLNHEQQNEEEPPNMEASKFYEMLNSAQQPLWPGCKSTSELSVALTMLSLKSK
HNMSQACFNDVMKFMKESSHPENVIPSNFRETKKLVAGLGLSSIKIDCCIDGCMLYYKGDSTLIECKFCQKPRYKEPRAY
KKNSKYVPYKRLHYLPLIPRLQRLYASVRSAKHMRWHYENRREEGVLCHPSDGKAWKHFDQLYPEFASEPRNVRLGLCAD
GFTPFNQSGKTYSCWPIIVTPYNLPPELCMMTPYMFLTLIIPGPHNPKGKIDVFLQPLIDELQQLWNDGVITYDASRKQN
FKLRAALMWTINDFPAYGMLSGWSTAGKFACPICMKKTKAFRLDNGNKISWFDCHRQFLPHNHAFRRNKDAFYKNRIEKD
DPPSRLSGEQVWQMVYGIPKTTEVRICNVPGHGRSHNWTKRSIFWDLPYWKHNLLRHNLDVMHIEKNVFENVFHTVMDTK
EKTKDNENARLDLPEHCHRKELFLKINSNGNYIKPKAKFCLSKEQKNDVCEWVKRLKMPDGYASNIARCVDTNSTKFFGM
KSHDCHIFMECLLPIALRALPEPIWKPLTEVSQFFRDLCSTILHEDHLLQMEQNIPVILCKLERIFPPAFFDSMEHLPIH
LPCEAMLGGPVQYRWMYPFERFLNKIKKTVKNKKNVEGSICEAYLVQETSYFSSHYFLSPIGVIEGIQQDHIQPMLSIFK
PFGQTAGKHKERWLNDQELLAAQLHVLLNCNEVKPFIDIYVQRLKGMYGNLSDDIIDKQIEADFPRWFQEYVRISFKNKL
SIIILFMGPLRLAKSWPIYFVNGYKFHTKARGEGKTTYNSGICVSGIGHDEASNDYYGVLIDILELEWPSQATKTLVLFY
CDWFDPSNRGMRTHKQYKIVEVKKGRKYGKFDPFIFPKAATQVYYLPYPGRQKDKVDWLVVIKTKPRKVVDNRHTLEVVY
QVHESQVSAIIEDDPIDHLQDDEIGGEEVHLKESNFIGNGEENAFIDDEDVEEEYEEEEEEEEEEEEEEEEEEEEEEEE
EEEDDDDDDDDENDN
```

1016 - 1035:	EEEEEEEEEEEEEEEEEEEE
1017 - 1036:	EEEEEEEEEEEEEEEEEEEE
1018 - 1037:	EEEEEEEEEEEEEEEEEEEE
1019 - 1038:	EEEEEEEEEEEEEEEEEEEE
1020 - 1039:	EEEEEEEEEEEEEEEEEEEE
1021 - 1040:	EEEEEEEEEEEEEEEEEEEE
1022 - 1041:	EEEEEEEEEEEEEEEEEEEE
1023 - 1042:	EEEEEEEEEEEEEEEEEEEE
1024 - 1043:	EEEEEEEEEEEEEEEEEEEE

A0A151TVP5 **A0A151TVP5_CAJCA** (480 aa)
Uncharacterized protein. *Cajanus cajan (Pigeon pea) (Cajanus indicus)*

```
MPGSRQRDVKAKNPESPEGNGEREKPTDSDEQVDLDGNNDQQQTMEEEVEYEEVEEEVEVEEEEEEEEEEEEEEEEEEEE
DEMRVADTKDGVEKKKHADLLALPPHGSEVYIGGIPQNVSEEDLRLFCQSVGEVSEVRIMKGKESSEAKGYAFVTFKTKE
WASKAIEELNNSEFKEKRIKCSTSQAKHKLFIGNVPRNWTEQDMKKAVEEIGPGVIAVELLKDPQSSGRNRGFAFIGYYN
HACAEYSRQKMSNSNFKLDSNTPTVSWADPRNSESSANSQVKALYIKNLPENITQDRLKELFEHHGNITKVVLPPAKAGQ
EKRRFGFVHFAEKSGAMKALKNMDKYEIDGQTLDCSLAKPQANQKSSGAANTQNSVALPAYPPHIGYGIVGGAYGAIGPG
YGGAGFAHPLMYGPGATPAGMGMTPMLLPDGRIGYVLQQPGLQHPAPMPVSRHGRSGRSSGGKRSNGNNRNRGQSRYYPY
```

61 - 80:	EEEEEEEEEEEEEEEEEEEE

A0A151X0G9 **A0A151X0G9_9HYME** (3945 aa)
WD_REPEATS_REGION domain-containing protein. *Trachymyrmex zeteki*

```
MSYSNFGRGRGYPQGTRAARRFGRPRFPRPPFRHAVPPPRPGHPAQFGAPWQPNNMFFQPHTSQPLRGSPPFRADGRRRR
FCNYDVRFPAPNRLPVPPRFEKSAVLPEELIMQEETNIIETVPQLLLLGSEEERQQKIIETADRLKQKLSSFNSDDIPDI
WNEDIPSNIIADNPEDNAQIRIPVVGYKSSEINLTYNDLRDIGKINSDNMQHTTNELDIINNTDSDVMILDENKDETRLM
IPNDQMTILENVPDDNQYMEVDKEWIENGQGVDWELQEPVDDSQNLEQSDLHGDNTIENELLESNFQYQYDTPLVSISQE
QDDQQRDISQGIEIYPTDVTKEPDESETLNLEADVSFPIDSTDQDILQKDVSQEKEELFENLDVQESALNSHVHAENSNS
SNCTLIQTPLIDTPVSNVTLDNQLPRMKENSFQSGPPKLSPHTEQELPVDFDPTTPPPMLLKQDQPCILPPYSIPDLPLF
DPTEPPPNIKCLLGTKMSHEDANPPWSNAQNPIPAVYNNMEVHTGLNTHGGFMPQQLPLEIVNQSNVFMPSHIDSVNFSP
MFPMLPSNPVINTHVPSLPQVHATSLNTCVSSSFLPELSSSSNLHCSVNKDDGLNDMQEAMRFAKEMTSITGKTDEESKS
SSKSLSKSSTPIDPASDVESIALPPGKPKTKTNKQKKIKESDTSSKKKILEEQSTADYPSSEETIQDANVKSKNTLLMND
LVNELERPKVVFNLNNKVKVVNTKSWKENNEKKNGMTHPIELEKTLAEPSITKKNLENTSKHNKEEEKNLKRKENNFENA
ISSEIANQNIILHHKKPQKDVHTEKSQHSNVSLPKVNVQNLRSRIEKNENTKMDASWKNRIISRFLKMSKNDIYNMVNNT
SLRKFDIIMKRLVKEKKPTLSLEMRHAQDEKMKLYDQQEFMKQLNAMLDTDAIVSITDLPTEFIHHLNEVLQLDVQPDIH
AESAAASSSQYGHLEDTNRTFNPVITQIPECTNKTTMLNDISQECVKSKGHAVKTGSNKNVPAHNTRNNDVNLKGDTCNP
IVTNVSNVNNSLLTLQHDLDDIFSEVTKKIQTPAAVKERKRCSMGQQSAKKFDVGAISRSMEKEAFMEDDRTHRLENSPH
WDEKCDRWKRKEREDPHAYRNLTKEEWEAKYGMQTNLTVCIPSDNPKRIGVTKRGRGLLNRGRGRKVYPRRRYSSESSKQ
QLNTRYRSLEKEKHKKSRRHSDDRKHTTEYLEYDINQDSDSSSSSTSSSSSSNSSDNTNVTKLLRAIKENEKVAKQMSLN
EAIRDEVNAEIERERKSKKSRKTYKNSKSRKQRKVRYKKKKRQNKEMTSSSDSSSEKDNDNEMTDRLLTEKEIKKEVIEN
QVVQEVIVKEEVDINQEENTRDAEFRDVNASNHLMTMENKAAHFFSQNRVESPLAQEIPLTSINATQLHAEERLPIGSPT
QLKTKAQLKQMPETSDMNDNKVPLNIFTCIPENWNAFNSPSFSEYIEDSNKTCETSDTGCNQDKTVLSTNNSVMNQSNIT
YESACSSEVNENAILQQSDATACILTESSVKIQDSKSVAEISATDNDMSKASTAAKSTSLVSSVPTSTASPKQGGSKKID
IKTYYERTIHRRMNDKLESKKPAENPTTSTQNLITPKSIEPEIAVNKFTLISTSSSSIQDPRLASKRSEENSNRTVNNDS
VVQKSNQIKSKDEVSLATSSVNALPNIVTTSKIAASKAKKCSEVKNSATDKTLQSKAASDPKRFKNIRSEGSKELKLKKE
MAKEQKAKKKFATASKSDNLISTKIYFPLEETSTEEKEKKINNINDRNKVKIIGIQSLSSHENKVNTSNVKTSTISSGNA
DNDGNELPHNTIKTKERSLNLEICERGNAEKTANNIESTDTREHSSKTTPDETHNIKRAKDTASVKIADKKGHKKIRNII
PESLDASTVSKIALKVPESKNSSIEKINKDVSTEIQQSNTIKNMELSLNNTDGSQIKKSDRDLTESTINRDSDISELDAV
SRVDSIDKQSKENLLVNIETSSTKENDMKLNVLDATNKSASANKDDSASKKTAESSSTSNENSQERQSIENNAISSDSVG
SPFKGFLQETMMDFEQSNLFDVNYVTTSTADCKDMKIEGRQDYETLEPGTDYADDTNINANANFNIAFGNDLLASNKECM
NEKSDKSDLTADENGEGHVRKSSSEIVTTMLHDDDNDISIGRGNETDRQLTVSKEGYASCAGLVIKESMLLDNEEEIIQS
EARSKDLTSKLKTTTDPSLSDALEATISDDALRLPDCQSAEHLDNHIYLETNISAEKAPCDKLPGFDSDEHLDNDIFYLD
DRLQSTTTFDTKDDECVHFSVDQQSPEFDIMPAVIPETTIIAPCADLSRSEKSEGCKFDMKHISSTENNLLVGTSPMECS
PIDSPRTLNIPTKAALKEAANLFLKSLSNVSTATKALEILDKTQQSETDINYQTPTWRVEEQNNRKTSMPEIDNNATAAQ
KAHNTMTVQVNLNVNKISAHNSIRGESVHKDVSANANHGKFTVSPTTLTNIEKRLHSNMQREPVVELLKMKELDKLLEKK
NQENFEKIKEKVHEEKRSQEIFRMREKVYEGQKKHNDSILYRLKDKRQMKYRPKETPRKNSLVKRLKKMRRSGKIVGNTK
EAILARMLKIDLEIHKLMTEKLKLHELLRSNVPSSENSITNGSVVLRTAKDNTVPDQPEIPSTSQNSEINHAKQGRHVSP
SKSSRLIKDRKRALSSQDNKNTNYTPRSKTPVIRWKKKPRLEQTVKQEKDNEEDGGGEEEEEEEEEEEEEEEEEEEEED
FNEVTKEQASTSVSKKMENDLIDTSENLRKSNAMKNNKVRKDKIAGKKIDKEADINSKRSIYSDKSGTDKSADERSECRD
FTEGETERAKHFDTDKSNDISPSSEVAKINSQPSNKHVHSTPESLSIYTDDSTWDSLVQNTASEIHKKASGLALLNESFK
KELARSKMKSIVRKKKKKQLDNFLRTVNNLTGEEEELPLSKLYIKKLRQKRDLLDSLSQREGNANLVEPDVLKNVDETIN
EVTENKEENLFEPQSEARASDDTPPMSNASPILHSDKHQILVDAEANANSDWPYREKENIEEVALQQDSNDVPDGSNHVF
KAVSQDKVPFYNERNVEPDSSITPEETQAESHSSDCERDGVKNSNDVASRNFDIKVSVPKTLIKNDFSLGILLQKNKQTE
DSVVDTDLVDSTTNAFPAHTDRLEEKNKNSTTNAFSAHTERLEEKDENSQSTSQADNSTAEKDKKDKKDEAKDKRTANAN
EKEEAIDRASNTPSAPQLVTANSDVTENERSNNNVESNDKITIIDTGCDSNVLEKTDTKQKKPDAESEQLSNDTISVKQD
CQNIKNAIKAAKEEEKNNPENISGTFEKILNNDQGTGNSVPVDLTCERSEDEVSVEQMSGLEHTSTSTFSSNKAKSKEMS
KKLRRKHDTSIPIRRSTRNSNESKSSKINEIDANSSSSGPSSRETSVFHENDLTMRSKSKSPTWTKRDEKVVNNVIRKNR
VSQKVQNTNSRKVGTESETKIENQTKYLDTITESAVSKNKIVVTARKRKHRTDWQMKHCKVRLIDCKSILYKYINPKVLD
```

```
RLGIIAINSSASSDLSCMQHTTCDHYAAIISTAASNKSFFDPAEFCDKEKSEIEMLEEKLITESSEKDLDQEFVSHTVES
NEDDSTRMQYTVHKGPILDLMIFENSFLAASEDGKIYRYSQKSNGILNIYKGHKSAVTCLYIYKSDDAGVDKNLMYSGSL
DGTLRCYNIMTGALVGHPAQTKSPIQCMDQAWGIIFIGTKSGHVSRFNIEAGAIKEDSIPFSEKSVLALKATNEGPRRIL
IIASRNQPINIRDALTGLLLRMISGQNNSTVYSLLRHNNLIYCGTSSTSINVFDFTANNHELVHSIRGPGNMLLSIEVVN
NKIIAGSKDKRLHMWQMPTQVRALL
```

2778 - 2797:	EEEEEEEEEEEEEEEEEEEE
2779 - 2798:	EEEEEEEEEEEEEEEEEEEE
2780 - 2799:	EEEEEEEEEEEEEEEEEEEE

A0A151X4F4 **A0A151X4F4_9HYME** (447 aa)
Troponin T. *Trachymyrmex zeteki*

```
MEFWGISRDLPESGLNRRDLKRVTFVFTPASFRESGENPEFMKRQEQKRSDLDEQLKEYIAEWRKQRAKEEEELKKLKEK
QAKRKVTRADEEKRLAQKKKEEEERRQREIEEKKQRDIEEKRRRLEESEKKRQAMMQAMKDQSKAKGPNFTITKKDLSGN
LTSAQLERNKTKEQLEEEKKISLSIRIKPLEIEGLSIDKLRVKATELWEAIVKLETEKYDLEERQKRQDYDLKELKERQK
QQLRHKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYDTLLAETNEKTWKQRTEQFMKRTKTLTSP
REDSYNPEKATVRRERVFPGDPDGLTDQQKEIIEKMWTQQKEQFMGRQKTKLPKWFGERPGKKTGDPESPEGEEDVKAIV
DDDLEPQFDEEEEEEVKEEEEEEEEVEEEEEEEEEEEEEEEEEEEE
```

427 - 446:	EEEEEEEEEEEEEEEEEEEE
428 - 447:	EEEEEEEEEEEEEEEEEEEE

A0A151X8G2 **A0A151X8G2_9HYME** (2616 aa)
Uncharacterized protein. *Trachymyrmex zeteki*

```
MELKKEAAFDMNKEKAKSFKAKIKQLAEYNEIVSAETISAIGDVTKDVTKDMIKDDAPSSDEFDEDLEEEYRNLNNMLDL
PNDTYSLTKITAELPLCVKYGVRSGLIHSNMSYFSPLSRGYQGGAIAIAAFATTAIHKSRCWNEAVIDQIVEDGDTFYCE
SYKDVNTDDRRTMTILDLKRNLLLQKKFNVEVKIEDPAYAGKFRSRNPTELHLAKALELFFERHNAGILTSPVLNIAIWK
DSKYYYVFDGQARQESGEPAVDRVSGSAKLFLVKDLIGLLFIILEKSNVRNEPFVIYPIFISNVEMILPEDAEEAAKILE
KPRRRPSGYKICEKYRVIVQGSYHLTHPAIPEALRGKGHLIIAVAALIYSRLINANKWTTALINLIFNQANIYLVDLVRV
LEKKLDYKFELCLDDLMSDVILGVYSAKVKVDANVISSQTQKGKSSIENGLKEFFETQELGIVEIKKIFYAIWKDGDSYY
FFDPFACDDEGFRIDYSDRERTTHDTTRDVACVTMNSTVNDVMEIVLENTGNEESDPFLIHGVKVLYVKTGVTPSGPFEK
VIYRESGTNRRPRAPPPPVPMDTTKVDLIDATPRLRPESRKFAEVSIQYPELMQDIDQYMMGVDEPVTYTIENGKIEKIK
KIEEEGKEKEKEEEEEEEEEEKEEEEEEDDEEEVKEEDEKEEDVIGSIRGYNLINDHCLIVRGSLTCMSGTYDLRSQGRQ
GLIIALTALAYRKLKDPTRWRCLDVDQILNIGNKAYKQVIRWIQQGRPEIKEVKVVEKKLKEEEEEEEEEEEEEEEEEAE
EEEEEEEEEEEEEEEEEEEKAVIRKVARAPSHLDISLLPPRLKLAENDVFFKTKMNVANGDANPLANLAEALERYFERYP
EVILENNRLMYAIWKEDEKFFLFNPYGSDEEGWRHWQYSAGFNVTDRFNELIKLLYGILEYHDSRFSLHFVALDAIEPGK
YRSSVEIVIPDEKTEKFQTKFLPITDDDLLELEEKKLDVDIEVTKEFVDKKDVVEEEKEEEEEEEEEEEEEEEEEEEEE
KEEEEEEEEEEKEKHIIEQKEFDEFREKDPTKLIEESVQPDAPYRLNLALLTSTVKIQDPTEEELKSLPEEIIMEKMKYDH
PPPYVMPPRGTLRVLLEAKSANKSIPSLVSRFSIDSRLEIKKGDVPMDSILTTIVPLLRDTKPSKMIKLSLRKYLYSRLP
PIRMVPLRAIDESYIQDKEIDKAIDERYLGREKLEKKEDKTLGKLPRVSYVRPELIPRGPIIKTPVLVIKHLTYPDERKK
VLKTEEVAPTIKETITDAEQLLFKLKFLKFQFDVPLQPLVKKNDDKIKEKKKMLIKAEYINKKVGLLLSEVIGLKPLNKK
NDKAKEMKKMIIKAEYFDKKVDSSSPEIIGFKVVDEDAEIIRGNHSLSDRTRIEPSHFKPCFISAILCILAKNMLNVDRF
CDSILDYLIFSASNIDQQIGKLRYNGYRTFDKIIILDTSFNIILKEIIYANPESTPSDELDAVVGKFLENNQTGTLVLAN
CAYAFWTADDKYYLFDPYSCDERGKANEEGYCCLMRFRNLKSMLDRIKENAGETVRKPFRIYTVSVTYAEMKRRKRRKDI
KRRPKLEEVTKELILSEEKRDVSTPTVKSEVSLIELTEWVTAGPELDPRCDVAVTGFTPMRHYEASMLEEIVLENDITTP
TLAPFELFLDNQGLIKMANVRKIPSERIFHNNSSIQIPIDLCIMAWSLIHDPASWSERTIDGLIEAATDYAYDSVLANED
TSVSDMTDAVLPEFEIANYVFRVVFAPLHYGFLYATEGWNLAMTLEKIFETMIYTGAIIVCHSAHIGVSKCGKNYFAWWT
VTGTKNLRMIATSSFDEFLKMIVKVINMPQTIAFTVRAITISHALKMAPDFSDVKGLHEPRVTTASLPEIYRKELQDSYD
VKAIFKPIDPAQKPIFILGTVALRNRDSLLEPLIKRCYFIALLAVVIKRDIVQSPLPGMIDRILEVAESLYRGFPAEPKF
HTEHILRNVPLMNRFFDLRDCALPLVVLTTNSQTGRNDFYVQVKHHLKRYFKMHTSGILHFTNCCYGFWYSRATNCYYYL
DPYQCDTDGRKTCANGNACLCIFSSIRQMVKHMCLNQYEGTTGFFLHRIHVNSIDAPSFDKFQEDPMWLYLDYHWNFTHS
IMRSRKKAKYGDRSKTNRRFWNNYAIEVIGLIYSIWGTIGAYDCRFGERAGKNCIAICVAVLAMRNLCHPSRWSPAILDS
AVICGDSYYTESLKSLMQNYSKSDNRFGLQTSFKIFPHSWTIDFDTSICGILYSGDQNNLTLTDALNLAFEEARNVIIEC
NRIALAALATKDAYYVADPCWIGPPLFPRNRGAIYVLRCKNMNVLIYAITKMFNTNQRLNVYVTPLSLAFDREDFEADLC
TTRRKILPTSVQKVPGRIEDPAIPIPGAVVVPDEDSYLHIYRQRLAEDIARDSQLESLQLRCAECVLNPENANNALVSTK
WRMNLGQARSRKRPKLPLDSVESKDDLLEFDSLTDPYKTRISITNLITASNRYPRPIDFTSDEPPPRIELLKNVSERGFI
REQSRIDFNKSVAEMSQENYASYQHRLPKNETARIKTKIPNIYSDSSNVTTDIERE
```

800 - 819:	EEEEEEEEEEEEEEEEEEEE
1019 - 1038:	EEEEEEEEEEEEEEEEEEEE
1020 - 1039:	EEEEEEEEEEEEEEEEEEEE
1021 - 1040:	EEEEEEEEEEEEEEEEEEEE

A0A151Z609 **A0A151Z609_9MYCE** (789 aa)
Uncharacterized protein. *Tieghemostelium lacteum*

```
MHENVSDALYLNHNTIHCHDRMDKEIYSNISNGNYQSCKMEQQMYSSNGSNNSNHGNNNTTPITKGKMLSPNLASLKVQV
FENDNTADIQEIHLKDSSEEDTQEDFNDYEDEEDEYIDDDELYDQDDLEEEEEEEEIGELELEDLEEEEEEEEEEEEEEE
EEEEEEEINDSTLSCSTITKPEKEENQVSTETKEEELLYLEYEWTFFYDEGVPKGQSSDSYKLFIKNLGNFNTAQGFWRY
WDNFIDIGRLPEGANLRLFKQGIEPMWEDPENSKGGKWVLHSSSGRDTSQVVLKIILFIIGEQLQHSYDICGFVVSVRAN
RHIISVWNKSGENQEIIDQTIQDFTEKLNICNFKYSLHNKPVTPTSPHPSLHSSLNGFLPDSPQVQQPQHSNSNNYRHKK
SQSTSSLPIGINFKNSSNGFSSPSNQYYNQRNTNNGNNRFTLTNSQNGSSDNLAKTPNTNGTPQHHNRRTIDKHISSPSI
TIPFSLNTSKKDKVDRKKSSSTPLSKSSSSTSLSNEEQQSSTPSPPPPPPEDIIVSKSVELKQSPTSSTTCNNIETSPLS
QPVPIAISIVNAIECEEPVLEKVLEQQVSVPNVEQQQQQQQQLQQVVKEDEMLISTPPQAVESSEENSKVATKNDEVERE
EEEEEFVEDELVSQQSELDDCSDIPTDASSTAAKISTGSINYKPSNKILDTPSKSKKNTQNKKKNGNSKSSNSSKQQPVS
QLHNVNKNNNSTSKKHSHSVTSNNKSKVIVNRKPSKIQDVILLFLQEHIIIINMLVLIVIFTLIYQNYS
```

146 - 165:	EEEEEEEEEEEEEEEEEEEE

147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE

A0A151ZFW0 **A0A151ZFW0_9MYCE** (1345 aa)
PHD zinc finger-containing protein. *Tieghemostelium lacteum*

```
MVMNTSNTMSSKPKRNSSTSSPNKTPTKTRLQKNNNDDSSTSSLGDSEIEDDSITTTPTKSPKSINNKKSQKNKEINETV
TDVMEIDNTNTNNNNNNSSSGNSTPTKLLKPKFTKELYKQKLQILNPENTDPSEITKIFEQSQESEVYYESDNKPNNSYK
KTITTNNNSLNEEKLYTERHGYLKSNEELLNRASYKEIDFNNRPSNNDSDSDSDSDAESELAPWVKPTSYIIYQEKSNED
LDNEVEYDMDSEDEQWLQAWNSKGGPQYTEDDFEFIIDRLEKETFQYKQDSGSDMFPHFNSEEAGDVCAVCFDGTSDDTN
QIVYCDGCDIAVHQECYSIVLIPEGHWFCQKCESSEKDVVKCQLCGKKNGAFKQSVDKEWVHLVCINHIPELNGILQKKV
HSPRDPIGPSGLLSHINKQRYKLNCTICKEKVGCCIQCRQRNCSVAFHPYCIKVNQKARYEENLTPHIIFCNKHFKNHKE
DSSDPIAKLKDLDLPSDTHESEKDSDNDTDDNDNDEEEEEEEEEEENSDSDYIDENDNTEEPKELTSDDEILNILPNSKS
NNNVNKKNLKVCASKPAAIIKLSPSTPTTTTISSSPNKKKLNQPIKPITPVKLPIKKATISTPTITRSHNDSNNINGNGK
TKTETGITAKKAGLISFKRACKVIKYPTKFLNGVYDFWVKKRISRSGLAIIKRFQPSILYSLRPTLQSQDPGINTMDNYN
QLIDIRKDLERARTILELVRKREKSKRNYVHNLRSFIDSHMMQSHYLHTQIINILSEVETFEPFAQPVTEDQAVNYFKII
KEPMSFSLIAQKLKVYSYESDDQFWSDLLLISQNAKFYNGSKTNIYKSAVVLEKLSGHLENDLPEQLTINQLSLFINKFV
TTGFIPKKYSTSPVKSQTKSPTKLTTTITSTTTTTTTTSTSTKTTTTNNNNNNNNNNNNNRNLPLILTRDKKHQIGRKVS
FSDNITTHNIESIKNILAKQNITPHSKSTAAKLLKSKVPTSTTPTTIKKSTEKPLRLMPTRNTPVVELSKPTGRSRRQSK
KLKNNNNNNININNNNKKEEEVEEEEEEVEIVEEKVNEEEEEEEEEEEEEEEEEEEEEEEEEEEEENDDGEEKTVDNEHIQS
SVVPTKPVPLSLRLRKNKPLGEETLPPPKLKMKKKKRRSEFSQLLDQQTIPSLKKHLSKSFKPTRVNLDKFHNDLKENNL
TSTTPTTDIQMTDISKESNIQETISNGIAVDSNKSNHEPNDIEMVNNNEEEEEIVPPKERFLYAISEMSNADESGFFKKR
GRVCKSSDPLKHLDNIFFRVEKEFYRTWDQFWHDVSIMTKNTPRKYAKFSRKVQARADELMETLK
```

1078 - 1097:	EEEEEEEEEEEEEEEEEEEE
1079 - 1098:	EEEEEEEEEEEEEEEEEEEE
1080 - 1099:	EEEEEEEEEEEEEEEEEEEE
1081 - 1100:	EEEEEEEEEEEEEEEEEEEE
1082 - 1101:	EEEEEEEEEEEEEEEEEEEE
1083 - 1102:	EEEEEEEEEEEEEEEEEEEE
1084 - 1103:	EEEEEEEEEEEEEEEEEEEE
1085 - 1104:	EEEEEEEEEEEEEEEEEEEE

A0A152A0Q6 **A0A152A0Q6_9MYCE** (224 aa)
Uncharacterized protein. *Tieghemostelium lacteum*

```
MDELKKFQRSPVNKEHTMKSTPLSYSRLSFLYDYIDFGSDIAFGFIGDHPLIVNFIDRIGSVKFDFGQTKQFIDQEQLKY
NGLRSGLVYVNYDITDKNGMIWIYSKTGIQPGDSGSLVVDNNNVIIGVLGQQVKNPTASNLVYGLVYPLREAYLDAFIDN
LGKLPSDLTDLEEEENESNDEEEEEEEEEEEEEEEEEEEEEEEEEESSEDGNPNIHCKLFPTCSMF
```

181 - 200:	EEEEEEEEEEEEEEEEEEEE
182 - 201:	EEEEEEEEEEEEEEEEEEEE
183 - 202:	EEEEEEEEEEEEEEEEEEEE
184 - 203:	EEEEEEEEEEEEEEEEEEEE
185 - 204:	EEEEEEEEEEEEEEEEEEEE

A0A154P016 **A0A154P016_DUFNO** (63 aa)
Uncharacterized protein. *Dufourea novaeangliae (Sweat bee)*

```
MDQRERVQRNGNKRDRDDRVRIEIEEEEEEEEEEEEEEEEEEEEEDCSSLPSGANRSGETKKRF
```

25 - 44:	EEEEEEEEEEEEEEEEEEEE

A0A154P1E8 **A0A154P1E8_DUFNO** (306 aa)
Uncharacterized protein. *Dufourea novaeangliae (Sweat bee)*

```
MARGPSHHHHHHHQHYRTSSSSSHRPRPRHHHHHHHYHHRHVSLHQQSQPEDDEEEEDAEEEDEEEEEEEEEEEEEEEEE
EEEDEDEDDLDRQQRRRLPQHRPLTTHHRHHHNQYQHRYHSHQPRSASFSALHTVFEGPVRISSLRPARYSFKSSTRSSQ
SSSPSPSPIADRRGTATSLPITHRGGTTTSFPITYRPGTATSLPITYRPGTATSLPITYRGGTATSSPTIIPPQQEDEEE
QDFQQFERRTTPFQRAKRRFCGLLPRGWFTCRAEGSARIDIIARIAFPLTFILFNMGYWFTYVIWR
```

64 - 83:	EEEEEEEEEEEEEEEEEEEE

A0A154PB68 **A0A154PB68_DUFNO** (886 aa)
NAD-dependent histone deacetylase Sir2. *Dufourea novaeangliae (Sweat bee)*

```
MASGSELPEYSSPAKRRKVDGNDYVGTSIAKPEFQDYETSRVTPNEDPEETYGGDSGFNELSDESKSTSVSPDTTHLTTG
LSRIDSTSDDTGCPIDTADEKDEVSSTVSNLSDLSGLSDFSGEGEINHQWRNASSWVQKQMLIGADPRDLLHHILMDSTQ
IPEQVDDLTLWKIIVNVMSEPPRRQKLRHVNTLCRDGIYSRLAQDFPDLPDPQAMFDINYFGQDPRPFYKFAREIYPGQF
KPSPCHRFIQMLDKQKKLLRNYSQNIDTLEQVAGIENVIECHGSFATASCTRCKYQVKADDIREDIFAQRIPLCPKCRVN
```

```
ALPPISEINLNENYRARLVRSRTEFADSLVSSHFAEISSTNTTCVAIERKKNAQSDLVTHGIMKPDIVFFGEGLPDAFHD
AMAKDKDDCDLLIVIGSSLKVRPVALIPSSIPSHVPQILINRESLPHLKFDVELLGDGDVIINQLCHLMGDTYKEICWNN
MILREATQLAPMRYLPEDSWEQSQDTTTNTVLSRDSVEKDTCSIGSQDIEQSTENMNVCVSSFRKDHANNTEERFDLHQG
SPKRRLGESSEESSPKRMNFGGSSVLEFRSSSSTAENSNCWNDYKIHVVSMESTSKENGKVYNLEECQVCPRTVEFSSES
AELEPTLQSNRCTEDTIISTTEIDKINFKPRQASIDSALDSGIGDSCNSVDSGEGKCDDRKTELKNGRLSGRHCWQSKVR
ESLASRLPENSYYQLTPGKYIFPGAEVYSDPEDYDQCNFSINSESSESDSVSSSAEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEDEEEDDEDVEEVVEKERAKRGEVEEDKSAMMDLQQEETNKERELEKRSQNDESLEMKIVTTGIDAVCEKRKWTT
NCSHNG
```

776 - 795:	EEEEEEEEEEEEEEEEEEEE
777 - 796:	EEEEEEEEEEEEEEEEEEEE
778 - 797:	EEEEEEEEEEEEEEEEEEEE
779 - 798:	EEEEEEEEEEEEEEEEEEEE
780 - 799:	EEEEEEEEEEEEEEEEEEEE
781 - 800:	EEEEEEEEEEEEEEEEEEEE
782 - 801:	EEEEEEEEEEEEEEEEEEEE
783 - 802:	EEEEEEEEEEEEEEEEEEEE
784 - 803:	EEEEEEEEEEEEEEEEEEEE
785 - 804:	EEEEEEEEEEEEEEEEEEEE
786 - 805:	EEEEEEEEEEEEEEEEEEEE
787 - 806:	EEEEEEEEEEEEEEEEEEEE

A0A154PE90 **A0A154PE90_DUFNO** (426 aa)
Troponin T. *Dufourea novaeangliae (Sweat bee)*

```
MKRQEQKRSDLDEQLKEYIAEWRKQRAKEEEELKRLKEKQAKRKITRADEEKRLAQKKKEEEEPRQREIEEKKQRDIEEK
RKRLEESEKKRQAMMQAMKDQSKKGPNFTITRKDLAGNLTSAQLERNKTKEQLEEEKKISLSIRIKPLEIDNLSIEKLRY
KANELWETIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDD
KKKLFEGGYDTLLAEYNEKQWKQKSEQFMKRTKKIRTMTRKPSKGSQTSVLRVTMYPSMRFCPLVLQGLTEQQKETVEKQ
WTQQKEQFLGRQKAKLPKWFGERPGKKAGDPESPEGEEDVKAAAEDEELEEPQFEEEEEEEEEEEEEEEEGGDEKDGEGE
EEEEEEEEEEEEEEEEEEEEEEEEE
```

400 - 419:	EEEEEEEEEEEEEEEEEEEE
401 - 420:	EEEEEEEEEEEEEEEEEEEE
402 - 421:	EEEEEEEEEEEEEEEEEEEE
403 - 422:	EEEEEEEEEEEEEEEEEEEE
404 - 423:	EEEEEEEEEEEEEEEEEEEE
405 - 424:	EEEEEEEEEEEEEEEEEEEE
406 - 425:	EEEEEEEEEEEEEEEEEEEE
407 - 426:	EEEEEEEEEEEEEEEEEEEE

A0A154PHA7 **A0A154PHA7_DUFNO** (1916 aa)
Zinc finger protein 91. *Dufourea novaeangliae (Sweat bee)*

```
MYNLENFYDFRTACVNAVALLERCLPPSEKADGVTTTLMCFNDAELLKQKESIPMLIPEAPIVNPNAALGTPPRLNSDGE
AEHEAEEIVDNSGTDEATIVDESEDRRSEEYEMDMETNPSDFLEMTSIVTEEPEEPESRHREHSGNVPEITSQQYEVYVC
SLCNKAFSSKGHLSLHARIHVGAGDVIGEKVLTDDHTSYKRPYQCDLCHKSYSTAKHRWGHVSTTHRGHPAVTCGYCSRI
YSTRTNLEEHIKSRHAGLPAPIKIPANNTCRQETRYQCNPCGKMCIDATELNLHGRICIDEKRSDHLARNENRDTKTMDS
SEGSSIIGSDEDSKDYRSAEAKLAKNPQLTILKQALTKGDSLKRDFEDKFMTNCKPKKLPKTVENLKEHEVVHDGDKPYI
CILCKKDFVLKSSLSRHIQTLHGVDPLPIIESDKCLKKIVSRNWNESMDLEYEGKTSEFPLSPETNAENEEEDHESGQEN
LIEIETVFVCEICTRDFNDRASLWLHIRATHKEFAAFACGVCLKICADNTQLLNHVNMYHGGSKLLLSEQRRYSCTICGR
QHDSRKKLIAHVSIHSVDSNYDPATFVQLNSNYYGENINGTETTETMLDYEEEGDKVDCYICYKSFPNEDHLIRHQRNAH
RSEQLMPAGDSLNSSNLNGGGNRAQYHLFFVCELCGSSHPSKWERWLHVSSSHANEAAIKCDREDCGKIFATKSLRNDHV
QHHAIQGSSPNTCEICGKLWGSRVDYWKHVMGVHSDTVPLICGVCLKVFPNVMQLSGHVKSKHWPLTNGDFSCDICGRPY
SNKSKMSRHRKIHGFEESCDNNGAENSERKADGRIRETELSCEHCMDLKFPSLEKLSNHRRIVHGLFPCDLCNKCYGRTS
HLWKHVNRVHKGHEDITCPYCLKTSASKVHLAGHISKIHRYAPDSREDGIDGKDTRQLLKTEEVSLHYCEKCNKGFHKRY
LLRRHMKGCQNYRKDPGALLTRCRACERIFKDRASLQKHIENHHSTYACHLCNETITSKLGIMTHNRVKHMDHPDLTCNF
GACRKLFRTREDLEAHKNDHRYHTNPNVCDFCGDTVENKLKLKMHVLSLHRNEIGVSCGVCLIPMKDPKELKSHVEQVHS
SVLSRPNTCQVCGKQYASKWKAFDHTKKCHGKVFRTCKQCLAVFTEDTAIRDHYEMVHNISKDQLAAFEYRLDIRSKNED
FEMESPDIIVKEEPDDLEYDIDLCDEDSSDSKRRRSLTDTFDCEMCPEMFLNSDALSKHYRNMHNTDPERMFKRLKQEEQ
RRMRAKMSFLCKNCKRQFSTKTLYWNHVATCRRSASRKKEDHLPLRNDMSDNQESVLDNREEILKNNNQIKQEETTSNLN
IPDFNLFEDINLQLSGQRPLPNLMPLSQRVKPSMKCSRKDSRKVYDESTNTECACEVCGKQWPAKKHLWQHLIRFHRAEA
AVTCGVCLKLCKDYNDLADHLKATHEAILSCEGNNFTCKTCGRYHNARSKLLLHTSIHIGHASNGVTCPKCHKNVTDETD
HFNTCTGKIEEEEEEEEEEEEEEEEEEEEEEEDLKDEEKPEEGSLIADDAMVEEVEEGDFESEAEEADTEESDSGSSTEAE
EENDSEGESRATGEITYNSDSEDSEELDNIEIQEKSMQHFALKRLQASNETEPEKNDGLSDDDGPPVLSPMMPLLPENIS
DEQSMGHKLGSIVTLTEKDIDMCDLTEIQNQSSPKSMNFYEKGLSTNESLNFETEAYINRSDDDYDDTKNEYDENSMEGN
DEENEDNEETEGNEENDDNDEIGQNEENDGNNEIEVNEESDEGNELNEETEDIEENRLNEEIEDDEDNEEDEENYENEDN
EEIEENEGSEEIEGNEEKEDGMQLGDLEGAVLMVTEGNEILIQQNILENGTENVNQAYVYSTLAYSSEEDSDDEGK
```

1530 - 1549:	EEEEEEEEEEEEEEEEEEEE
1531 - 1550:	EEEEEEEEEEEEEEEEEEEE
1532 - 1551:	EEEEEEEEEEEEEEEEEEEE

A0A154PKH3 **A0A154PKH3_DUFNO** (401 aa)
Uncharacterized protein. *Dufourea novaeangliae (Sweat bee)*

```
MADGLFAEDAATDLGDSDFRLTRDRHKRQDGPFPMTSPSTGLDTARRIHEDALVAESHLHHRQHQLHQHRPPRRNCHTHP
HLLRRHPNNNSNTNNNNNNHHHHHHHHHNFHRCDRENINDNNNEVVVDGHERVSKIESVNSAGADTKRVLPPFASLICGD
YEEDEDEDEEEEEEEEEEEEEEEEEEEEEEEDEDRSVDGNGVSKKCRSSVRNDVAKTVINEESCNSNSSSNNSGSSGAEG
ATMTSGGSASRGDKTTSSADGRRSRSVFHESNGPNYRVDDADDDEDFEDADALQKVNRLGCDNGGIERGVDDEDAARKTD
DIASDDSSVGSGSSGSSGGAAAAAAVSASGAAGVTGNGMAAVRHQGSPFKGQVRTAEDTLVGPYGKKRCADRYDSSESSD
R
```

169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE

A0A158NAG0 **A0A158NAG0_ATTCE** (1142 aa)
Uncharacterized protein. *Atta cephalotes (Leafcutter ant)*

```
MEGTLEELASKDASQSQDSSDKHLKDMIIPNGVNGNYSADNEEYMDTSDNTSKIALKDVITEEEEEEEEEEEEEEEEEEE
EGDEDEEEEDVDEQYDEDDHERAVDIQEGKDEDSDRNEEIGNTSKEGEMFDLKNDFKISNSPDGVSETNNSSEVSKTEIS
ECVKNTSCEAMDVDEQSNNSDIECLDESITEIQLDNDDVFLSKKTIEKHDNDVSSNCSCDSSEIADSSMEKSDVKLCEEN
GSCGSPDIEEITDNAKSNDHDSSLDRAIKDPTKQRKPRKQVDLSNITPRRSSRNIKRTSYIEKELEEEVEDDGSDIEEIK
PEDPLAGIDSKDKENSKLKSPVRNSKTTIVVNDTKRLVEIAAGSKSIKGGKKEPTLVIIDTNSILSGRGGVPVSNNKPHH
TVSNSNPFSVVPMSGMTTQTMYPNMRTTITPVPMTSKAAQLSPKTSSMTTVTPTIPPILPTLTDDMFVVEAPSFIVPYVY
EKPPLKPLKEFVTKLERNIEEIEKEERKRLADENKDNEDYKEDSLDVKRGNDKSEDSDMEGKGKREGDDRGDNSIDLIEH
GFSSLNDKHDLRQDDRNKIPTYFDLPLGKFFMQIGMNLVQEYVQTDLLRTQKRKQGKGSTSAETQLAINSLIKNLEFSKE
NNEPFHLEMKKCEFCSFKTESTLVMQHHLETPHMRNYVYKCNFCPMEVRSPHDILYHMEAEHNTRGRLERGPAFHQCPNC
PFEDNQKGKLTRHILACTKKFRPERNLEPAVDWEPPAKIPRVNRARPVGPTNPNALAAMAMSAKGPQPLLPKLLPAPITG
RGRGRPPMQPRYSDLKTLRPGATPMRQDNVAGMMYRPTSSGLLVPTSYQFSSNQIFQVVGGSGTVMSAVSGVSSSSGGSS
GQPTPIALVPNVIDSLSRLSSSQNTTASSKNPTAKLLSQPSISITPLPRTTSQTSIPGSGTSSKSGGKNTFVICEICDGY
IKDLEQLRNHMQWIHKVKIHPKMIYNRPPLNCQKCQFRFFTDQGLERHLLGSHGLVTSSMQEAANKGKDAGRCPACGRVY
QWKLLNHVARDHGMTLKPAHLSYKCTVCTATFGMYKQFENHVYSAHSVVAKRVMDKKNTPASPSSRSNDSLLKPLKINDE
ITIIPQPAKPTTRSGAIQGRGK
```

62 - 81:	EEEEEEEEEEEEEEEEEEEE

A0A158NDY9 **A0A158NDY9_ATTCE** (406 aa)
Uncharacterized protein. *Atta cephalotes (Leafcutter ant)*

```
MPELATRRFKQPPICLTTRNNTPARRKSRKCKQPEKKTEGRASQKESGENPEFMKRQEQKRSDLDEQLKEYIAEWRKQRA
KEEEELKKLKEKQAKRKVTRADEEKRLAQKKKEEEERRQREIEEKKQRDIEEKRRRLEESEKKRQAMMQAMKDQSKAKGP
NFTITKKDLSGNLTSAQLERNKTKEQLEEEKKISLSIRIKPLEIEGLSIDKLRGKATELWEAIVKLETEKYDLEERQKRQ
DYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGLTEQQKEIIEKMWAQQKE
QFMGRQKTKLPKWFGERPGKKVGDPESPEGEEDVKAAVDDLEEPQFDEEEEEEVKEEEEEVEEEEEEEEEEEEEEEEEEE
EEEEEE
```

382 - 401:	EEEEEEEEEEEEEEEEEEEE
383 - 402:	EEEEEEEEEEEEEEEEEEEE
384 - 403:	EEEEEEEEEEEEEEEEEEEE
385 - 404:	EEEEEEEEEEEEEEEEEEEE
386 - 405:	EEEEEEEEEEEEEEEEEEEE
387 - 406:	EEEEEEEEEEEEEEEEEEEE

A0A158NDZ0 **A0A158NDZ0_ATTCE** (386 aa)
Uncharacterized protein. *Atta cephalotes (Leafcutter ant)*

```
MSDDEEQYSSEEEVEEVGRASQKESGENPEFMKRQEQKRSDLDEQLKEYIAEWRKQRAKEEEELKKLKEKQAKRKVTRAD
EEKRLAQKKKEEEERRQREIEEKKQRDIEEKRRRLEESEKKRQAMMQAMKDQSKAKGPNFTITKKDLSVSGNLTSAQLER
NKTKEQLEEEKKISLSIRIKPLEIEGLSIDKLRGKATELWEAIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKAL
KKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYDTLLAETNEKTWKQKTEQFMKRNKTKLPKWFGERPGK
KVGDPESPEGEEDVKAAVDDLEEPQFDEEEEEEVKEEEEEVEEEEEEEEEEEEEEEEEEEEEEEEE
```

362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE

A0A158NDZ1 **A0A158NDZ1_ATTCE** (378 aa)
Uncharacterized protein. *Atta cephalotes (Leafcutter ant)*

```
MSDDEEQYSSEEEVEEVESGENPEFMKRQEQKRSDLDEQLKEYIAEWRKQRAKEEEELKKLKEKQAKRKVTRADEEKRLA
QKKKEEEERRQREIEEKKQRDIEEKRRRLEESEKKRQAMMQAMKDQSKAKGPNFTITKKDLSGNLTSAQLERNKTKEQLE
EEKKISLSIRIKPLEIEGLSIDKLRGKATELWEAIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEA
LTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGLTEQQKEIIEKMWAQQKEQFMGRQKTKLPKWFGERPGKKVGDPESP
EGEEDVKAAVDDLEEPQFDEEEEEEVKEEEEEVEEEEEEEEEEEEEEEEEEEEEEEE
```

354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE

A0A158NDZ2 **A0A158NDZ2_ATTCE** (372 aa)
Uncharacterized protein. *Atta cephalotes (Leafcutter ant)*

```
MSDDEEQYSESGENPEFMKRQEQKRSDLDEQLKEYIAEWRKQRAKEEEELKKLKEKQAKRKVTRADEEKRLAQKKKEEEE
RRQREIEEKKQRDIEEKRRRLEESEKKRQAMMQAMKDQSKAKGPNFTITKKDLSVSGNLTSAQLERNKTKEQLEEEKKIS
LSIRIKPLEIEGLSIDKLRGKATELWEAIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYP
PKIQVASKYERRVDTRSYDDKKKLFEGGLTEQQKEIIEKMWAQQKEQFMGRQKTKLPKWFGERPGKKVGDPESPEGEEDV
KAAVDDLEEPQFDEEEEEEVKEEEEEVEEEEEEEEEEEEEEEEEEEEEEEEE
```

348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE

A0A158NDZ3 **A0A158NDZ3_ATTCE** (372 aa)
Uncharacterized protein. *Atta cephalotes (Leafcutter ant)*

```
MSDDEEQYSESGENPEFMKRQEQKRSDLDEQLKEYIAEWRKQRAKEEEELKKLKEKQAKRKVTRADEEKRLAQKKKEEEE
RRQREIEEKKQRDIEEKRRRLEESEKKRQAMMQAMKDQSKAKGPNFTITKKDLSVSGNLTSAQLERNKTKEQLEEEKKIS
LSIRIKPLEIEGLSIDKLRGKATELWEAIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYP
PKIQVASKYERRVDTRSYDDKKKLFEGGYDTLLAETNEKTWKQKTEQFMKRNKTKLPKWFGERPGKKVGDPESPEGEEDV
KAAVDDLEEPQFDEEEEEEVKEEEEEVEEEEEEEEEEEEEEEEEEEEEEEEEE
```

348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE

A0A158NGG1 **A0A158NGG1_ATTCE** (1125 aa)
Uncharacterized protein. *Atta cephalotes (Leafcutter ant)*

```
MSGAPAWGTVPRRQRRHHHHHHHHHHQKHQKRVRDDESRNETLDEPEEKRPKVNPIFLWASQREQKIIEVRCEDYDKRNRI
KLTKTAQGWRSIPRTTSMYTIALAATCKKTSSIADTSPASSVSSNDEKENGKRCLQEPASATASSLRCHPLIYSPNGTTN
GLLTGEGVGKKKQGYDEETNRRGYSSPLRARDKVNDSEDREVNNEEDKNCEQNKPKDCLPNLNSEDSQGWINLQRLQMNK
LFQPRVVLELLQLSQLPESANQNVVHHAKNKDATTNETKRIEQSNEQNEENVEEEDKKKREQKMDNEEVEEEEEEEEEE
EEEEEEEEEEEEEEEEESSEKSNRMNKTGIQDILNMIDATASPVLATDTPSADLPVDSTKTYEVLDEKPSVERQQVKDAKL
DEKDQTKSASSYETEIVDQDGEIDDKLEVHEEKILKDCCLQEMEDRKIQMENNLGLLSLENNAETTPNSCKIAEADGGFI
IGRSKCRSKSVITWQSSKPIEEEEAPDEPGDPLKLDYDSSRILDALRNTPGISVSIMRNDTPEVGKNPIVSPARPPSKAS
SSSRSPDSQAECVEKLLKNANFDGSSRNLPGLSIVIPNYRYKNVSDQLTTSPSIKQRVESPESTVSFNKVDAYPEEMKMD
EFPHEEDRDEEEDEDCDSQVMEDLRQQKADSLAYDGTDADYYNGHRTKNNQEDRKSLMEKKSDSAWISSGKNSEAQAKGK
GSGYRDLEHFDEQVLEELRSRGTVVVSPQPSGIPCSPASRRPSSAYLERLLPSPPCSVSCSEDAKSEITLKSILASSNCV
DPRDYERTKEGVIRSDQNIDQPISRPVHSNIDRNMKRTNQHSFQERLNVHNQEVRNSGRPMSSGDIHSTFYAMIERATPK
RPMSAEWQIGQRHRNQAVCYQKTVDRTRGHFIDQEQDQITCTTSSSTDKLLDPARQLRELIETVGHLIPDPLLVPRGYLP
GLAAAPATEIPKLLASRPELRLPEALTRPDLLRDPDLLVISLAHLQHVLDHGEGPVSRSQQSQPQQPSATVNGTIIKGLS
GSTNSNGTKDGGFTVITGRPKLSCKPICTLMPTQPMDLSNGGRSRINHYSPLLRVRSGLLKQEPEVSSTASSPDESQLWH
PLFGR
```

310 - 329:	EEEEEEEEEEEEEEEEEEEE
311 - 330:	EEEEEEEEEEEEEEEEEEEE
312 - 331:	EEEEEEEEEEEEEEEEEEEE
313 - 332:	EEEEEEEEEEEEEEEEEEEE
314 - 333:	EEEEEEEEEEEEEEEEEEEE

315 - 334:	EEEEEEEEEEEEEEEEEEEE
316 - 335:	EEEEEEEEEEEEEEEEEEEE
317 - 336:	EEEEEEEEEEEEEEEEEEEE

A0A162XQA3 **A0A162XQA3_DIDRA** (221 aa)
Transferase. *Didymella rabiei (Chickpea ascochyta blight fungus) (Mycosphaerella rabiei)*

```
MGGGVPVVWSQKCHTGACTDPVVLRSFALPPNIQHDCPVSPSDTPPTSAAESSPVPIGLPWLLSLRHVGCRHALHRSSCA
TTARGEVSILPFGQGSVADSSGVALHAGQPSLAAQNFNMPALSPTMTEGNIASWKIKEGTIDPAHRDRTEEEEEEEDDDD
DEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDGGTHANALQQGHERAFLGSDGLHPATALT
```

162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE

A0A162XSU9 **A0A162XSU9_DIDRA** (1579 aa)
Alpha-galactosidase (EC 3.2.1.22). *Didymella rabiei (Chickpea ascochyta blight fungus) (Mycosphaerella rabiei)*

```
MYAALTCHPPLGQTTTVPAHKQSVRFTVLIESSAGSGKIWEVALWHNFDGREEWASLSLKPAPEPSLTVIKSSHANIRRQ
FFSIDLPGCPKHGGSLSYTVTFRSGKDEPWKWANEQFSTSDGRLIYQSEDALSEDLTNYIDGLPPYLQIGREQSESPETL
LWSITSPVNGASGATSGYSNNNLGRPLDLTRWFALVRLWSPWLAPRQGKDRFQPDKEAVLATFEREDGSHLVVLAVSGVD
DVLTTLGHDGEGRIVIHSRNDSEEDGISRLVAAVGKDLNHAIAAVMYHARKLVMKYGMGSEEAEAEFKALTDDFKPEWLE
NWYDGLSYCTWNGVGQHLTEQKLFDALESLAKNEINISNLIIDDNWQSLNHEGGDQFKNAWIEFEASKNGFPRGLKATVG
DIRSKYKNIKHIAVWHAIFGYWGGIAPEGKLAKEYKTTVVQKKDGVSGGKFTVIAEEDVNRFYKDFYQFLSSAGIDSVKT
DAQFFLDELDDAPDRRSLIKSYQDAWNIAQLRYFSARAISCMSQTPQMIFHSQLPSNKPRILLRNSDDFFPEVPASHPWH
IFCNAHNAILNQYLNILPDWDMFQTSHDYASFHAAGRCVSGGPIYITDVPGQHDINLIGQMSGNTPRNDTVILRPHTVGK
STSAYNSYDAPVLLKVATYVGMAHSGVSILGVFNCTQRPLSELIGLDSFPGAEKGAYVIRSHTSGQVTKPTTSETNDAFV
HLELPTRGWEILSAFPLQSFKLKRSHDAEGPEEVQVANLGVLGKMTGAAAIVNTDSYVDRSSGRLRVWTSLKVLGTYGLY
ISDLRERNLDDDVMALIFGRPIARHCVKISDKCENVLEIDTTRAWKESDSKASWSNEVAVEVVVRQDFNLSNHYNSRAQN
SSTTMADPTANYAAHLAAIWAHPHTRALLMMTGGAIMTGLYYEQFRLSEYTIDEPDPKPPVAIEVFEDEQKMFDNVVVVE
DMSEPLSPAPNVPVPSIWGHPNSISYTPGKPWNQATKSYINDGYVQVNPTATLLSFLVPLVMLVCLPVWFVRKCSKTSRN
CAAPTSDTDGGIPKDLVCNRTLPPSKTPTTPRNTPPSTPTCSSDALPSSVLHAMVGGRNHAGAQIPLQGRFPSLQTSPPK
EWTELGRQVEKPKHKHQASQAQAHKNLDDREKIEQTLSDRITGLEARVVLLQGELEAASDCTSDSDRAATTNPGPPQDHM
IEIGVDKASIAPEEMASELVEAYYLLGNRDGEGSRSHTEHSDLARWSVEFMDTDVETDDLSPASTAAAETRIDKGNFAVL
PEQSTAIVGPQDHPTGTTTSIAIVDDQTASFKGIFEQNANEKAERESEHETTEGAKNSTRPEDNGDKLERTLEKTTEVDT
SRSDRIPVNLSKPEALMGNPASTGSTLGPADQHANSPVLAPKNIVLPPMPSPRLADSYKGTKWMKASRHASKLPDSLNFT
APQLKSAPSNNTPLHMLGGSRHATPAAAAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEARKTDDQSQKTKRSQPRAQKE
SEQNGRKSNGPAILQIGDQEQSMLQAAGETPTHPDPELNLSLASAGPAASAVPAASITS
```

1470 - 1489:	EEEEEEEEEEEEEEEEEEEE
1471 - 1490:	EEEEEEEEEEEEEEEEEEEE
1472 - 1491:	EEEEEEEEEEEEEEEEEEEE
1473 - 1492:	EEEEEEEEEEEEEEEEEEEE
1474 - 1493:	EEEEEEEEEEEEEEEEEEEE
1475 - 1494:	EEEEEEEEEEEEEEEEEEEE
1476 - 1495:	EEEEEEEEEEEEEEEEEEEE
1477 - 1496:	EEEEEEEEEEEEEEEEEEEE
1478 - 1497:	EEEEEEEEEEEEEEEEEEEE
1479 - 1498:	EEEEEEEEEEEEEEEEEEEE
1480 - 1499:	EEEEEEEEEEEEEEEEEEEE

A0A163KPQ2 **A0A163KPQ2_DIDRA** (103 aa)
Uncharacterized protein. *Didymella rabiei (Chickpea ascochyta blight fungus) (Mycosphaerella rabiei)*

```
MGIAEEMEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEETVALRPK
HNQHTNAPGAVVGPRTCLGRGPW
```

13 - 32:	EEEEEEEEEEEEEEEEEEEE

14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE

A0A163KZK3 **A0A163KZK3_DIDRA** (92 aa)
Uncharacterized protein. *Didymella rabiei (Chickpea ascochyta blight fungus) (Mycosphaerella rabiei)*

```
MGPPLRVLHRAGRSLEIAYYRLLGTLHEPVCAPALLCLRLLDQLRSSHVKVPARGVQVALESVGWGEAEEEEEEEEEEE
EEEEEEEEENRA
```

69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE

A0A163M5A4 **A0A163M5A4_DIDRA** (365 aa)
Holocytochrome c-type synthase (EC 4.4.1.17). *Didymella rabiei (Chickpea ascochyta blight fungus) (Mycosphaerella rabiei)*

```
MGWFWADTTPSAPAAPVAPHPMPTGNAEPPCPMHKKATPPAKAEVPKGACPYVPPANPASTPEPKTGLLAKLNPLNNMFS
ELDNKKAEIQSRDLPLSREASTIPKGDGSLWEYPSPQQMYNAMLRKGYTDTDVTAVESMVSVHNFLNEGAWAGIMGWERR
```

FSRGLKEGYEICKNGEQLANLKLGIHEDAFDTTTWDVRDVQPPKLLRFTGRPTERTPKATIAQWLGWLNPEKYGTAPPFD
RHDWFIERCNEQGCKEVRYVIDYYEGEAVSDDEPVFHLDIRPAVDGPTSAAERLIRSGTELWWQASGGSVRMLRKLEEAK
KKREEELAATRRQEGEEEEEEEEEEEEEEEEEEEEEEEEIDDVIRT

336 - 355:	EEEEEEEEEEEEEEEEEEEE
337 - 356:	EEEEEEEEEEEEEEEEEEEE
338 - 357:	EEEEEEEEEEEEEEEEEEEE
339 - 358:	EEEEEEEEEEEEEEEEEEEE

A0A164PZM0 **A0A164PZM0_9AGAM** (1394 aa)
Uncharacterized protein. *Sistotremastrum niveocremeum HHB9708*

MWMTTRFRKKQEDAQAAQAGHPPAQEPEDRLDEPDDATSQLPNTLWRGGTSQAVQKTPKSQTRVKDLPHGKSGVKVYHAP
ESPQDMPPVEPQRPKRPRPKQTTVEKVQSRRAAAEDGFMGPTTKNKLKIVHEVQEPEDDAPADKIIPVPSVRAPSPNPFD
VAGAELSDDEDEKRGRQLLQQHQWAEDDEQTQPRAHGDHECRDAPDASAQDHPEDNEHGQKQHKADAEDSTEEDAVEEEQ
VEDEEDAEEEEEEEEEEEEEEEEEEEEEEEEEREADEQDDSPSTSRQRSKAKSRRTVNPRGLQYRPPIDTEDAVESSSSSE
DDTGSSSSLEDAHPPDGPANGDDQEYRDTQQHTPLTPEPTHAADDHPPPHSPRLLSESSGDDDSDNDFEKTAAKETKAFE
HKRKKTQFKHLVTQEEADAIDQQEFEAEVAAEEQSRAKGKGKAVERPQSPSPSDLDNLIRFPPSDDDGDDNTGVKYKIRP
GPLSVEALKQLQLIWQTAETSLEEFAVLHGKSLNFVARKAGFKPKWIKTKTRTDNAWKAMVAAVCEQIPLLKELYPDENW
NEECMATFYAVRDAYEELGEREEWEKSLIEEFEQELRDNMKANQTAASDNKSVNEISSQLSDFAKHFLINYGVVVVGEVY
GSLDLPGRGSISSFGAGSTWQRLIRDRADLLHDHALVRQAALRLASAEIRKEILARANGEDVSPVQTVTKEELIKAATKR
PRYTLPTETRGDRDFKRRFPSHLIKEEFAFWTGNTDPRKVLWKNILDKLFAHQLRVVGWSCLLSTDIRHYDAAKMNQTTI
DIFYDQIVRFSQASSEEQATWEGLHIEEWSKAEKAVDPAEQGNICLVRDEKDNDMLFVRHAKVWLKAYGKNTPNPSTKKR
KVSADTDADQPSDSPQEGTSKRAKGAGNAKRSRSQKSQVFVPSDADDESDETEQLKAKEKSRTAELRKEKEREKTKTKTK
AKAKDTRTEKEKSKKTHEIDQTEEMDTSTKGKGKGSVGTTALAKRGRDDVDNADEDEVGRPAKKTKRMRNMQPIHPPPPP
PSPPRRDPSTDPDISSSPVPHVIPKPRPSAPRSDATELPKSTIVTQPSKPDTATKQTVEDDSSDEDTSDSDSRLNLKANL
HAPIEDTQKKKSSHTTAGRAKGLARPHPAPSSHIVPVSDQTLRASAPEVSTHVSDIHNQASGKGKGKATNTDLEVMNNNP
VDKVKDAALRRAVPPPPPPRPTHQHFVQTLESRMPLPPIDYVDKGKTQVTRDHPEASMSQPRPKQVTKTSSQPNRFTNHA
RPGPSTIPEATIEDVTKAKDTSAGGSKNKREDEDDDEEDDEDDDEDDDEDTIIWQNILALPKEKRKKQVTRMMAMAKFPP
KWFDKKVSGRITQFLRDGLRGEQTRSWSDGIIEG

248 - 267:	EEEEEEEEEEEEEEEEEEEE
249 - 268:	EEEEEEEEEEEEEEEEEEEE
250 - 269:	EEEEEEEEEEEEEEEEEEEE
251 - 270:	EEEEEEEEEEEEEEEEEEEE
252 - 271:	EEEEEEEEEEEEEEEEEEEE

A0A164ZB60 **A0A164ZB60_XYLHT** (879 aa)
Protein SQS1. *Xylona heveae (strain CBS 132557 / TC161)*

MAKGKKGARRNQAKNPLSGGRIEFRNSGFSPKVESPRTQSSSQEQSHFSLQQEARNTERRHSYWTSASKLRHNGVAFVSA
GNFDANRLVGEEDAAIACEQEEANKRQAGARIDFDANNPAKIQPDQDVASSFMAGTVAQPTEDESQRESSLFAVDVVGSS
LNFETGLPHPRVRSSSPAASDSSEEVILFSGRNRPLAHISETLDETPLTISSSVGGGHQARFEGQPTDDSAGDASRRRCD
PAFKEPSRDATEERSNGNRSFQPKHENIQSRDHFSKQALFQNRKSHSVVTKSGQEDDPIVADYIANMKENDDRGFTEGHT
TYTLRDLGDVDQAYQVDICRKTPTNQSSSSRAPQPLRGSCKSVDRKPRLSHLVGGSVNDAFHTTEQSEAVEARSVHTPQR
ATSDELEVQLRTNKDVSTRLEGLEPSADSVNEPQSTYKIKQPTRHLDEAAYRKKVQMNGNEGESKIGQRVAEDDEDEFEG
GEEEAEENEGMEEGEEAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGSDIGLDYLEDMQDEEDLIERRIQRMTDEKIA
RLLEKQEELGLGSGELILFDGDDGDEEVGEELENFPMWNTSPGRRPQSRPKHQFPSANLMADVLDNDPYDGFDVMDFDRP
SLKRKPKGRRGTLPFGLSDSEMEISLHSTWEKDRKKKQLKKKEREELRAQGLLGKSKKGKPQLKAKYKEGVGLEDIKVEI
KQFLRAEHTSLALPPMDKRNRKLVHEIANAFYLKSKSVGSGKSRFPVLYKTSRSREIDVYSSGHIDRILGRKRFLPRMDV
SQKNGALRNAGGKSVSAGVAYRDGDVVGATAPELGAENKGRAMLEKMGWSSGTALGAVHNKGILQPVAHVVKTSKAGLG

498 - 517:	EEEEEEEEEEEEEEEEEEEE
499 - 518:	EEEEEEEEEEEEEEEEEEEE
500 - 519:	EEEEEEEEEEEEEEEEEEEE
501 - 520:	EEEEEEEEEEEEEEEEEEEE
502 - 521:	EEEEEEEEEEEEEEEEEEEE
503 - 522:	EEEEEEEEEEEEEEEEEEEE
504 - 523:	EEEEEEEEEEEEEEEEEEEE
505 - 524:	EEEEEEEEEEEEEEEEEEEE
506 - 525:	EEEEEEEEEEEEEEEEEEEE
507 - 526:	EEEEEEEEEEEEEEEEEEEE
508 - 527:	EEEEEEEEEEEEEEEEEEEE
509 - 528:	EEEEEEEEEEEEEEEEEEEE

A0A165GZL8 **A0A165GZL8_XYLHT** (84 aa)
Uncharacterized protein. *Xylona heveae (strain CBS 132557 / TC161)*

MCIQYMHLTLCNCSNRSNRFKCSEEEEEEEEEEEEEEEEEEEEERAKEAVNATTTINNDNKSDQTKLLPLPLPPITTKQAT
ISDE

24 - 43:	EEEEEEEEEEEEEEEEEEEE

A0A165IQ05 **A0A165IQ05_XYLHT** (2390 aa)
Ras-GAP domain-containing protein. *Xylona heveae (strain CBS 132557 / TC161)*

```
MSTMQLVSQFRVDEDKLAIIFQQTSFSFPVLPSPVQYYVARLLTPAILRWLEQRQCRSTDGERPPIEIAQAAKALCNTCC
EHSDPYHIDAQFWQLICCLMAVQWKYLPEAVTETDGKNQMINDLCAFIEMIRKNLRSPKQCNAAAKCLIFLCKLTHIFPS
DSGVWTCIMEVKAQLEKELFTPQQPQLEVDGIPFGFNTTVEALIVLSQLDPDSILANILSQLSESEYHEKLAFIILNACC
ELAIQPDPRRFFSIFRKMAPFAWMNLLAAQHWVQGDAFSDGPLPPEYIKDGYAATQNTAIIRVALTFFILLPEMLCLKDI
NKVVQLKDEEERQYQCLLQYIIAPNPEISRLGGQVIVESMAVTVLDREELRTGGGRSPTAFWNFSSKIMLMLARGLLNTI
DEPSSKTLLDYSATFLESRLCIISADKMISGETQHHDLRLAASSDLETALLLYLCSSDLAMCAKAMSSLTYICDEGRLYE
KELEEVKSLISVAANLEVYCEISSRSFRLTGMVAFQKRLRRCLLKISKPTAGLIRAWRTVFLRWSRLNQHFLDDKSWKET
LPERNFDMSEASYFTEWRNYSGFLAALGSVCKPDGDVDLDPRSTSLEVSNDKESLAFLSQKYLLESLKILVCGKIYAQEA
IKDVLGSELHAVLHPQLLLALDSELETMIGPQTSMTSERQLLFIEQAASILRLIVSSRLDHPKESSSPVDFGQISLRLCR
FLHALRDTNNVLRVKIKICHLFEGVAWKAEILILRHDLRIRNQMAEVLFDWLSRSSPAGLEKIKADLDRSCLRALMRLTY
HMPLQFMDDTSENDSADLRIDRFRNYFTSFISVLKEADTNRPPQKDIFSSSSAREEQHTASDLAITGLSNLLSANVDVGL
KQVLDLGYHNDPRLRIVFMRVLCDVVVQGSELTRLSDPALIQNYAALLQLLIRNPRIGIALAECSPNNGLDEVTVSLIDV
FEARGLGYEFLKELIVHEIELTENESEILRRNCIATKVLSHYARWKGSCYLQKTLGRTLSQLLSSPGELDIELDPTRVGR
AEDVESNILKLQKVAIALIDSICRSGRHAPASFRRICSTIASAVSGRFPEAKFIAVGSFVFLRFFCPAIVAPDVEQLIDI
PITKSARRGLLLVAKVLQNLANNVLFGAKEYYMLPLNDFLCTHIYRVSTFLRELSQQNSTKLEEDDAEEGEGKEEEEEEE
EEEEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEEVGNETFEFGSSVALHKFIYDHWEMIKHRLNALERTMR
KDMASNTSRATSFSRSKTAPERFTDLLSKLGAPPVEMTWVPPQIFSSSPQSYCRFQEFMIRNAAGTGALRPAASAIYAGG
ESKDGLPVICVVLRELELEGLDEDLILYCFFKIASRMWQRKFGVVIDATCYSSMNEPQDDLFRKLSLFAPQEMANNFSRI
YTYNMNSGYRKCFRRVVRNAIYDVNHILNPRNVEYRTIGSLQELQAHFNLGALHLPKSTISVVTDSKFVFQPVTRLSKTR
GKVDVVIKIGGYFVQVTTTRKQEIIPGSRQQAAINDIFRLADLEEASHSTQGRDNDSFGFKTGDGKIIMLFTSPRKVDIL
QAMRAAKSKILKGSDKVVGSERIIKSDDVPGSLINICLTNLTSEYPSLRTSSYRLLCSLGKKHRFSLTDLATNAGAISTL
PLLPQTISPEAHSLRSILVPAHPAALVLDISKHLAFSQVHLTYDLLMEFFIGWDCISESQRANYLSYITPWVSNLRSDVL
SSDEDSTRGREKLASVVRKMIALIVKHPELDFLIQNTICSAIAKDDWLIDSVVEEMLRYLQVAVDDETTTDVFSSILKRL
GTGLVLGKVVARIRKALNRSSLRPTKSLCENDVWPELISLLKILQALSFECPHLVQSFLPEMFHVIVITYNCGSRNAAAI
TRALLITTIRSVSLVAPGRQGDLNPLEVLLSSILRKGSHLFHWMLQSDSQMESSGSSNIAAIESLTMTLVDVIRLGATSV
DLANTWRARWMSIVSSSAFQSNPAVQPRAFASLGCLAQGGADDDLLYQILVALRGSIKAFAADDEDEMLIVILGSLSKLM
ENLTTSSRYTVQIFWLALSLFRVLPLNCINNAASLLETSLRAISKFSNLKGRDLLLLIFRGRAPMIKGLSKLDDWCGVQF
SLEFFHAAVVTTLIQAIGGPLPRQIGKTTANTFLEIFSSDIPETKCFPEDPSLIPYLTYLLPRATEAEEKNEILWLTGGP
RTIVTEVPGRIYDMFDLERLSLTELALDAALCLDDCSAQDDSIRGQILSFLVPVFRTKPEVTAMMAPSLMGILHNLLKNS
RDVQTLEIAHILTRLVSSTQPQNSHTPDLLRKLATSAGFSGLKVAKEDEGEQEDQIKIETVIGLIEDIVN
```

1209 - 1228:	EEEEEEEEEEEEEEEEEEEE
1210 - 1229:	EEEEEEEEEEEEEEEEEEEE
1211 - 1230:	EEEEEEEEEEEEEEEEEEEE
1212 - 1231:	EEEEEEEEEEEEEEEEEEEE
1213 - 1232:	EEEEEEEEEEEEEEEEEEEE
1214 - 1233:	EEEEEEEEEEEEEEEEEEEE
1215 - 1234:	EEEEEEEEEEEEEEEEEEEE
1216 - 1235:	EEEEEEEEEEEEEEEEEEEE
1217 - 1236:	EEEEEEEEEEEEEEEEEEEE
1218 - 1237:	EEEEEEEEEEEEEEEEEEEE
1219 - 1238:	EEEEEEEEEEEEEEEEEEEE
1220 - 1239:	EEEEEEEEEEEEEEEEEEEE
1221 - 1240:	EEEEEEEEEEEEEEEEEEEE

A0A165UKX3 **A0A165UKX3_9AGAM** (502 aa)
Homeobox domain-containing protein. *Neolentinus lepideus HHB14362 ss-1*

```
MPKVKKEPQEMTALPPAAKKPVVIVRANKEQTRILKAAYAAIPSSTPTIQDLDELSRQTGLTRDWIHNWFGRQRKQARQE
AMKIKVEEPPNSLLSQKHTRTTRNAGRTTADTPARAEKTTAYMDVQKIPSVNRKRKYACVDSLPSSSVPPSSPPSATFSD
VTFDSDPVRTSDFDSTPAPIQSRPKSCRTLPQESASTAYNNSKTHGPGIETFDVSDPCWLCRPPDWTPMRHQASENDIFF
PGVSVPSSSDRFGPPNPLVSSCAPNLPLSVHQDHTRSLPYQYNRPLGAPQSTSSQYSPSNSTGHRPVAGAYPMQVPLSRA
ARPAGQLNYALPLTSAVHSMSAVHSTSAVLSASSIPPNFTSSLTSALLPNHASTHTSALLARPQQHSAPPPQAQLDSAST
NPTRLQKYPLRQEEEEEEEEEEEEEEEEEEEEEEEGPLSFCPGPAYQPFLPLPVDPAPKNPVLDNDPALVKEALELLHPDR
CADNPFLATMVLVDLARRGFRW
```

413 - 432:	EEEEEEEEEEEEEEEEEEEE
414 - 433:	EEEEEEEEEEEEEEEEEEEE
415 - 434:	EEEEEEEEEEEEEEEEEEEE

A0A166MD50 **A0A166MD50_EXIGL** (418 aa)
Uncharacterized protein. *Exidia glandulosa HHB12029*

```
MAAVQLFKTPDLDRELFYLDPSLPRGLRRDLIALVEASKHGGNVLEYPPRQGYVLTDMTSASGLALFREKDSPDGGRYVL
HYQWAQLCVRSATKLPPTLRRPPLFLKHLRPLRIYVHAGSLGHAAAEKLSARIHRHGGQCLDNHHRADVAIIGLGREADR
ASELLKDSVPTITTSDWVARCIGKGEIIVQDRDEVAADATLAAQTRLLREAVQQIVGGPRRPRNCRNGFSAEELRHFLMF
LVDNVGSEYGLCGNRLYQPNSNFTWFGQLHWGRRHTWMSWRERYVKHQQEWTPLIADELEKRLALMAAEKRPVFVESMAL
RMNMLRAQNGNGQEPELFEAVDDVLSNHGSLHQHRSPSLAASSRNVGHRGRHADPEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEELAPPDGDAEFL
```

376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE
379 - 398:	EEEEEEEEEEEEEEEEEEEE
380 - 399:	EEEEEEEEEEEEEEEEEEEE
381 - 400:	EEEEEEEEEEEEEEEEEEEE
382 - 401:	EEEEEEEEEEEEEEEEEEEE
383 - 402:	EEEEEEEEEEEEEEEEEEEE
384 - 403:	EEEEEEEEEEEEEEEEEEEE
385 - 404:	EEEEEEEEEEEEEEEEEEEE
386 - 405:	EEEEEEEEEEEEEEEEEEEE
387 - 406:	EEEEEEEEEEEEEEEEEEEE
388 - 407:	EEEEEEEEEEEEEEEEEEEE

A0A166V0J7 **A0A166V0J7_9HYPO** (657 aa)
NOL1/NOP2/sun domain protein. *Moelleriella libera RCEF 2490*

```
MSDPPPPQIMLGLHLMSLYHEAAEILSASHEGGSLKSRVFRRKNAKAPLNQLYALVFETCKWSAVLKEVIDGIRRKASSF
EQLKRLVDEEAAAAGGEEGEVYRHPRWIRINALKSSLEEQLESTFRAFTRVFSIEELMTSSSTADSNRILLDAHVPNLVA
IPPGHDMSKTEAYAAGKIIFQDKASCFPAYLLDVRSEDGDVVDACAAPGNKTTHLAAIVHAHTPDEFESMPQTIFAFEKD
AQRAKTLEKMVRVAGAKNMVRIGLGQDFLQTDPMADTFKNVGALLLDPSCSGSGIVGRDAMPKLHLPQDHHPAPRSRAQS
QTGTQGAAATSVAATAAKEDHAPSRSSKKRKLEQTTDQNHHSVLLDDDGNEAVLLKTQEELQQRLEALSSFQLALLLHAF
RFPGARKITYSTCSVHAQENEHVVTAALRSDTARERGWRILRRDEQVSGMKAWPVRGLAEACAGDRNAAIVADGCIRAHK
DDGRGVMGFFVAGFVRDVSLAGTEEQEGDEGPYVRDENGGIVRDVLGMPTLKATGHPVTLVPREDRAADAAGVSESTEEE
DEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEDEKDGDSEWGGFDD
```

562 - 581:	EEEEEEEEEEEEEEEEEEEE
563 - 582:	EEEEEEEEEEEEEEEEEEEE
564 - 583:	EEEEEEEEEEEEEEEEEEEE
565 - 584:	EEEEEEEEEEEEEEEEEEEE
566 - 585:	EEEEEEEEEEEEEEEEEEEE
567 - 586:	EEEEEEEEEEEEEEEEEEEE
568 - 587:	EEEEEEEEEEEEEEEEEEEE
569 - 588:	EEEEEEEEEEEEEEEEEEEE
570 - 589:	EEEEEEEEEEEEEEEEEEEE
571 - 590:	EEEEEEEEEEEEEEEEEEEE
572 - 591:	EEEEEEEEEEEEEEEEEEEE
573 - 592:	EEEEEEEEEEEEEEEEEEEE
574 - 593:	EEEEEEEEEEEEEEEEEEEE
575 - 594:	EEEEEEEEEEEEEEEEEEEE
576 - 595:	EEEEEEEEEEEEEEEEEEEE
577 - 596:	EEEEEEEEEEEEEEEEEEEE
578 - 597:	EEEEEEEEEEEEEEEEEEEE
579 - 598:	EEEEEEEEEEEEEEEEEEEE
580 - 599:	EEEEEEEEEEEEEEEEEEEE
581 - 600:	EEEEEEEEEEEEEEEEEEEE
582 - 601:	EEEEEEEEEEEEEEEEEEEE
583 - 602:	EEEEEEEEEEEEEEEEEEEE
584 - 603:	EEEEEEEEEEEEEEEEEEEE
585 - 604:	EEEEEEEEEEEEEEEEEEEE
586 - 605:	EEEEEEEEEEEEEEEEEEEE
587 - 606:	EEEEEEEEEEEEEEEEEEEE
588 - 607:	EEEEEEEEEEEEEEEEEEEE
589 - 608:	EEEEEEEEEEEEEEEEEEEE
590 - 609:	EEEEEEEEEEEEEEEEEEEE
591 - 610:	EEEEEEEEEEEEEEEEEEEE

592 - 611:	EEEEEEEEEEEEEEEEEEEE
593 - 612:	EEEEEEEEEEEEEEEEEEEE
594 - 613:	EEEEEEEEEEEEEEEEEEEE
595 - 614:	EEEEEEEEEEEEEEEEEEEE
596 - 615:	EEEEEEEEEEEEEEEEEEEE
597 - 616:	EEEEEEEEEEEEEEEEEEEE
598 - 617:	EEEEEEEEEEEEEEEEEEEE
599 - 618:	EEEEEEEEEEEEEEEEEEEE
600 - 619:	EEEEEEEEEEEEEEEEEEEE
601 - 620:	EEEEEEEEEEEEEEEEEEEE
602 - 621:	EEEEEEEEEEEEEEEEEEEE
603 - 622:	EEEEEEEEEEEEEEEEEEEE
604 - 623:	EEEEEEEEEEEEEEEEEEEE
605 - 624:	EEEEEEEEEEEEEEEEEEEE
606 - 625:	EEEEEEEEEEEEEEEEEEEE
607 - 626:	EEEEEEEEEEEEEEEEEEEE
608 - 627:	EEEEEEEEEEEEEEEEEEEE
609 - 628:	EEEEEEEEEEEEEEEEEEEE
610 - 629:	EEEEEEEEEEEEEEEEEEEE
611 - 630:	EEEEEEEEEEEEEEEEEEEE
612 - 631:	EEEEEEEEEEEEEEEEEEEE
613 - 632:	EEEEEEEEEEEEEEEEEEEE
614 - 633:	EEEEEEEEEEEEEEEEEEEE
615 - 634:	EEEEEEEEEEEEEEEEEEEE
616 - 635:	EEEEEEEEEEEEEEEEEEEE
617 - 636:	EEEEEEEEEEEEEEEEEEEE
618 - 637:	EEEEEEEEEEEEEEEEEEEE
619 - 638:	EEEEEEEEEEEEEEEEEEEE
620 - 639:	EEEEEEEEEEEEEEEEEEEE
621 - 640:	EEEEEEEEEEEEEEEEEEEE
622 - 641:	EEEEEEEEEEEEEEEEEEEE
623 - 642:	EEEEEEEEEEEEEEEEEEEE
624 - 643:	EEEEEEEEEEEEEEEEEEEE

A0A166VW90 **A0A166VW90_9HYPO** (467 aa)
Pyridoxal phosphate-dependent enzyme, beta subunit. *Beauveria brongniartii RCEF 3172*

```
MADLSTTAPLNRASVQAAHALIAPHIHCTPVVTSQTLTALASTPRADLASTRFAGRTPAKPTLRLWFKCENLQRMGAFKA
RGAFHALSRLLQEPGWVEGGGKQRGVATHSSEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEETTNTDTVKHAGNHAQALALAAKEHGIPAHIIMPSISAPAKIAAARGYGAHIV
FSGSTSSERQVVADQVVASTGARFVPPYDHPDIILGQGTLGLELQAQASEMMTSPNRPYAGSKTRLDAIMTPCGGGGMLS
GVALSCEATGIRVFGAEPSFQGADDAKRGFESGARIEAASSLTVADGLRTPLGAHPWDVVYTRGLVDGMYSVGEDEIVAA
MRLVFERMKMVVEPSACVPLAVALFDEDFRAMVEREAGEEGWDLGIVLSGGNVGADTLGKLFGVRED
```

112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE

124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE

A0A167A8P0 **A0A167A8P0_9HYPO** (200 aa)
Uncharacterized protein. *Beauveria brongniartii RCEF 3172*

```
MLEKKDEEEEEEEKEEKEEEEEEEEEEEEEEEEEEEEEEERDEEEEEEEEEEEEEEEEEEEEEERDVEAETLDVPDALACG
NSSSVYAGGWEVCDAECLVETVLSVAEDEDVLVVLDEEEVEQTLSASLELLADFGGVVEASEVVVEEIVEVAKDVAKVVE
QDVLEVANEDIADEPDWDADETIADKMDVVSQLELELVSD
```

18 - 37:	EEEEEEEEEEEEEEEEEEEE

19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE

A0A167IC07 **A0A167IC07_9HYPO** (211 aa)
Uncharacterized protein. *Beauveria brongniartii RCEF 3172*

```
MKSIPSHENHRRQKREEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERKKERKSENMSKSIRFVSS
```

16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE

58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE

110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE

162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE

A0A167ISE7 **A0A167ISE7_CALVF** (484 aa)
Uncharacterized protein. *Calocera viscosa (strain TUFC12733)*

```
MTEEIITERLHVDGLTPFSSFGSVLAVDGLDLLDGVGQPRKFAYVTLSATPTKLTRCMNLLSGMLYKGAELRIGEAKPDW
EEQWSKDHEPEETLLRKKRRMAGCQAPPDIKAQAQGPRTSNARRVVLDPPKWGAVHLTGELLEAGVVALPEMEEVGAVAV
EEPAEKVKTKKRKGRERGELEADIGHAEPAPGPTASSSKRAKLPLAIEPATTEDPLLASFVAETHAGLGLLKQMFGEGLE
KADEWAEADSEVEELEGRVGGLKVVVQEEEEEEEEEEEEEEEEEEEEEETEEEGVVPEQQMQPQGQDQEEVAGETEEEAQ
SDDEDEVPTAAEARKPVAGEEQEDTASSLDGDVEDKPEQESLKDMFAPTYAVSMPTQRSTATYEPADSPKTDFSSYPLFF
PTWDEEGNPVENHTTLGGRRKSNTFWDVAREKGWMDGWKRETEDEARQRWEEVRGQLTQEWKKRSREARRRKKATGLAGA
GEGM
```

268 - 287:	EEEEEEEEEEEEEEEEEEEE
269 - 288:	EEEEEEEEEEEEEEEEEEEE
270 - 289:	EEEEEEEEEEEEEEEEEEEE

A0A167J1A3 **A0A167J1A3_CORFA** (851 aa)
SET domain containing protein. *Cordyceps fumosorosea (strain ARSEF 2679) (Isaria fumosorosea)*

```
MAQPTTPPPRSSRPTVPQRNWNQPDLTKALQDLLRAVRQDHSRLVAHAIESTTPTEWRVHHGANLFEGMGPGPVPQKQEE
TMRVKFKQHLKARKDAREEHHDIISIRTLKDRVPRYRFHHVGIRKNVLTPNTMLTFVPHLRDLESSEESKYNVWLKELEE
IDTKSGFKPMNREEKVILTIQTERAATVSLYLDTWLEKLGMASCTKSALVACMTSQESDDNVTPQRGIAVMRSSRELIDG
NPTVGDSSKAAALFTAAFSRAFDNKDMPLASRIQLRRVLLLEQSTDGLLDSKSVARDAGDPDDVAEAYVEIAVPSMPSLS
HWLSHRYKQQAQGHRDSKRCPGKTCQAKQKEKPCICVQLNRECDPDLCGTCGVLERTDPLNADFEMLHETGCQNCELQRG
CGKQLVLGQSQLDGVGYGLFTAENIAQDDFVIEYVGELITHDEGVRREARRGDVFDQGSNISYIFTLLDNEGIWVDAAIY
GNLSRYINHASEHDQAGSNITPRILYVNGDYRIKFTALRDIRAGEELFFNYGENFPNLTKKLLKNRTSEKPAVPRKPGRP
AQSAARKDVARKAPRPEQKKIGRKKPAVRGRVQRIVVKDDDYDDADDGGGGLRAPHASLLTRPVKRKRALAGMDSDDDGY
RAPQSMVQNKWMDCAAEDEEGVEEEVTPNGGATTRRSLRNRAPETPTKAKAKVTGRRGGARPGSGRPRKHPLRVPKAVLE
TTEASRSLQESPKKSTWNEESLRKSPLPAYQSRTEQARAEEIQDSEEWSTGGEDNALRSYGLKAEGAAVRESDGQAEVEE
EEEEEEEEEEEEEEEEEEEEDQDVVVRRRLVRATRNRRPPAKFRGDDFFY
```

799 - 818:	EEEEEEEEEEEEEEEEEEEE
800 - 819:	EEEEEEEEEEEEEEEEEEEE
801 - 820:	EEEEEEEEEEEEEEEEEEEE
802 - 821:	EEEEEEEEEEEEEEEEEEEE

A0A167YBB1 **A0A167YBB1_PENCH** (67 aa)
Uncharacterized protein. *Penicillium chrysogenum (Penicillium notatum)*

```
MCREGEICTDQGTQGEEEGGRWKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEENHSKLRLRIEYIV
```

24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE

35 - 54:	EEEEEEEEEEEEEEEEEEEE

A0A168CGS9 **A0A168CGS9_9HYPO** (1234 aa)
DEAH-box RNA helicase. *Moelleriella libera RCEF 2490*

```
MAKFVPRQRKHKVLAREKAKTARHHDEDTNHEILPAVHTERQEKRDRLRRELQQDGVAVNAKKAKRLEKYIDNKLRKDEG
RELLAKLAARRIDTSLFASSKSLGQGRETKKQAMSRALREQRAGLEGDAEVFLEKRSEKTVKQAEEEEEEEEEKKKEEEE
EEEEEEEEEEEEEEEEEKGEEDEEALKSQKSQIAPVAQPSQSCESVIAEKCSRSFGSGLKRPLGQDDDGRPMIKKKQKRG
GLKTKLSFDSDRNAQDGGPEETIYEEWNGFMGDHDANGDSQMKTDDDKTDDDNEETDVDSSDSASDEDDHNEDEDEDEED
NEQPIQRSSAFKAWAFQQRNEALGYRPANGDAGPLQIPKPENFIPRAVEQDALPAELQPTENDSRKAFSTPVIRTADIQE
ARLKLPVVAEEQRIMEAIHNHDTVVICGATGSGKTTQVPQFLFEAGYGCPQSPTPGMIAVTQPRRVAAVSMSNRVATELG
DRSDAVAYQIRFEGTASEKTAIKFLTDGVLLREVAQDITLRRYSAIVIDEAHERSVNTDILIGMLSRVVKLRGDLAKEDS
TVRPLKMIIMSATLRIEDLTMNPKLFPKPPPVLEVEGRQHPVTIHFARKTHHDYVEEAFRKIVRGHRKLPPGGFLVFLTG
RNEILQLSKRLRAAFGGPSSADGPKVRIPGTEAPMEVEDVELGDLDGDDGDTAGLDSDSEEDEEEFRIEEDQEAAPLKMQ
ISQLYSLLPTREQIKVFEPAPEGTRQVVLATNIAETSLTIPGTRFVFDCGRSKERQYDRLSGVQSFEIGWISKASANQRS
GRAGRTGPGHCYRLYSSAVYERDFSPFSDPELLRMPIEGVVLQLKSMGLDNVVNFPFPTPPERQSLAKAEKLLTYLSALS
ATGHVTEIGRAMSVFPLAPRLARILLIGHLHQCLPYAVALVSGLSAAEVFLSEIQAIPEAAANGDEEIRTNAQVIAETQQ
ANARRRFNQVHKDFCDLDGKSDAIKLLKVVGEFPYEPTEQWCESHFVRFKVLKEIQQLRKQITDLLRNNISAHANLRFQD
KLDPPTPLQVNALKQMVAAGFIDQVAIRGDIAPAPPELYRKPKRAIDVPYIPLIPLSDRPGSEGDDSLVYIHPSSPLAHL
STQECPEYVIYSHLHRASLAGTDSGAKKPKIRMHSLTDVTAEQLIGLAKDTTLLTYGKPIKEVRPTVAGPGSGLTRECWV
VPYLREENTGGQGWPLPVKKVKQKRIAGKGWVVV
```

157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE

A0A168EDJ9 **A0A168EDJ9_9HYPO** (2233 aa)
Uncharacterized protein. *Moelleriella libera RCEF 2490*

```
MSSPDPLNDSTVAALSSPMRRVTRSQSLQPAASPSRRRSGRPSQEAASPQRLLATHRQHQNGGDKAVGSNARRKLFPAPM
ASSTPPAPRRPAAAATRTTTTTVPLRESIEGEGEGEGEGDATRPGPRTRQRKSNGTPMPGAGTKRTAAATPLPRAARRRR
TLSVQESAVPGIQATPFVRGNQSSRKTTPGTVASASDLAANDRTPRPSTSRRGKRRRQALAPSELLELVDEAADVDVDVT
ILPPVTSDDEVDLVRAPSDSSDADGQETARRLRPPPSRAAAPSSPSPANGGPAEPESDIWIATLSHETTPRLIVPAPTKD
YAPGLSPQPPSDSLPPLHGDADFETSPAGDYSRYGYNDPAPAASERSSLDELLDRQERPVSAAPVADSDHSSFDELLEPE
PLAGPAAPAVYDTIAQGEEFSMIFMDSIQSMQPNFNSSVHPVTHDELGDETSLIIQNTLESLRQEGNHVEMEQISAFDHV
PPNTEPARVAEPETHPDSQAVQELVSEQPPPSPRLRLSPRRSLSPRKAAGAPSPLRYRVLKYYAKQAEESVAAQFRAGEA
QSPPRTGPQMRQGSDAGAEQANLYDDSFSEIPESVLTAATPKRPRARYTPADARDDVDQVQQQQQSVNGSDEPEIDQADE
DLAGAALVAAPQEEEEEEEEPEVRYPDLSRGMEETEQDDLRQGDGGDDQDYEEASGPQVESEELEEQLDESGNGESEHLP
HGGQLPHGGQESHDESQQSAREASEDEEQSIAGKMEQSIAGEMEDDKQASEVEDELQRVSAAPAISHVEDEYDYGEVADS
EENVETAEEEAKAEYATTVPGATPTAADVDGEQQLGDFEGVTQDATGFTGLDHDQQYESVESNDHDQLTSVLPDEAAEGF
DEEQLSVPGRETDQQVRGREASDVEMDDGSMHEDEEQDDLVDAGYGAGISAPNTAPRHSPTPDRASRLAKSPVVDEDREQ
APDRSSRPSPRTASRSNSPRPQAQPAQPVLPAPTPSSAAVPSPRYPGRYGDVSRAASTRTSPAKSPRMPGSRVDAEQPPA
FSARAASSSPGYTRRSVERLQASLIARWPAKRPSPDKGEQNEIPDSTIAAPREPASRSPERQQFTPVSRSPIKPQGISAN
PGLRAEQPALARRSLSKAASSSPQRPTGQTGRPKSSQPSILPTVSNTTIYDTTEQLGSESRTPTRKPSFRDNGFGLARPE
LTFKPRFMSLSPRHRPVADKSESAFRSRPARSSTSESRARLKAPVRAPGLDMAMDDELLHHHQQQQQQQQQEQTQDETLD
TEPRHRSPKPGAARTHRRASLRDAPRRPLSSPAPAAADSAINDDDPRRASAAEETPTHQISSPPAPAPTTTTQRLQSPQQ
PQPQPEPALPKKVLPQLSAIVRAGQALQSVTADPLSPERREKQLRSPFQRSTSKDSGSVSRESHASRRLSRSPSAPTTLQ
GQGEALASAAGNESQSVYSSPARRDGQEASGLSARRESRPRYSTSPTRYDGEEAPVESARNESRPAYSSPSRHDEQEASL
ASTRNESRPTYSSPSRHDEQEASLVSRRNESRPMYSSLTRHDKQPSLEEEHHSLLRPSPASSLRLSPTSDGAMSWVAREG
PISPSLRGDMSLRQAAGLPESLIARSSPVNHGLQASVQPAETRSAEGAAVEQEPTAEGQEIRDDETDIWELEAQRETPRP
ARQQSFGKRMPTSNHRRSTIPSPWTKRGVYRPAASRMISQAVPDLSHLTEEPSVAPDRPTSEVSEEDEFSRLAQRLKDEE
EAVAAAAARAPESAAKGKRFDLSSFFSSPAVVPGMSTQQQQQQQQQGMSTADQQRAFTRQPGPNRLTGQAAPVVPTSSMF
PQVSHRAIQPVTTNTTNTTTGSTRSDALSTPVGSAPAEPPSPATPEPVLPAIAQKRNFTPRPRQASQTFSQPPTAAAATT
TTTTTPPRTQPSRADIHRWNEQTSAASNEPSSTPPPPSSSPFARQRRPLLRPLPPKNASPTKSALRSPLKPHTPGRVVEF
TSSVLSPAEQALARRLTATTTNTDEDVYMADQEEAATPDEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
SSSSARLVAQRFLGRTVASHGQAMVLQQWHLDCVQVFRAYVARWDEGALVKRLFALMLGEARRREARSSPMFH
```

2044 - 2063:	EEEEEEEEEEEEEEEEEEEE
2045 - 2064:	EEEEEEEEEEEEEEEEEEEE
2046 - 2065:	EEEEEEEEEEEEEEEEEEEE
2047 - 2066:	EEEEEEEEEEEEEEEEEEEE
2048 - 2067:	EEEEEEEEEEEEEEEEEEEE
2049 - 2068:	EEEEEEEEEEEEEEEEEEEE
2050 - 2069:	EEEEEEEEEEEEEEEEEEEE
2051 - 2070:	EEEEEEEEEEEEEEEEEEEE
2052 - 2071:	EEEEEEEEEEEEEEEEEEEE
2053 - 2072:	EEEEEEEEEEEEEEEEEEEE
2054 - 2073:	EEEEEEEEEEEEEEEEEEEE
2055 - 2074:	EEEEEEEEEEEEEEEEEEEE
2056 - 2075:	EEEEEEEEEEEEEEEEEEEE
2057 - 2076:	EEEEEEEEEEEEEEEEEEEE
2058 - 2077:	EEEEEEEEEEEEEEEEEEEE
2059 - 2078:	EEEEEEEEEEEEEEEEEEEE
2060 - 2079:	EEEEEEEEEEEEEEEEEEEE
2061 - 2080:	EEEEEEEEEEEEEEEEEEEE

2062 - 2081:	EEEEEEEEEEEEEEEEEEEE
2063 - 2082:	EEEEEEEEEEEEEEEEEEEE
2064 - 2083:	EEEEEEEEEEEEEEEEEEEE
2065 - 2084:	EEEEEEEEEEEEEEEEEEEE
2066 - 2085:	EEEEEEEEEEEEEEEEEEEE
2067 - 2086:	EEEEEEEEEEEEEEEEEEEE
2068 - 2087:	EEEEEEEEEEEEEEEEEEEE
2069 - 2088:	EEEEEEEEEEEEEEEEEEEE
2070 - 2089:	EEEEEEEEEEEEEEEEEEEE
2071 - 2090:	EEEEEEEEEEEEEEEEEEEE
2072 - 2091:	EEEEEEEEEEEEEEEEEEEE
2073 - 2092:	EEEEEEEEEEEEEEEEEEEE
2074 - 2093:	EEEEEEEEEEEEEEEEEEEE
2075 - 2094:	EEEEEEEEEEEEEEEEEEEE
2076 - 2095:	EEEEEEEEEEEEEEEEEEEE
2077 - 2096:	EEEEEEEEEEEEEEEEEEEE
2078 - 2097:	EEEEEEEEEEEEEEEEEEEE
2079 - 2098:	EEEEEEEEEEEEEEEEEEEE
2080 - 2099:	EEEEEEEEEEEEEEEEEEEE
2081 - 2100:	EEEEEEEEEEEEEEEEEEEE
2082 - 2101:	EEEEEEEEEEEEEEEEEEEE
2083 - 2102:	EEEEEEEEEEEEEEEEEEEE
2084 - 2103:	EEEEEEEEEEEEEEEEEEEE
2085 - 2104:	EEEEEEEEEEEEEEEEEEEE
2086 - 2105:	EEEEEEEEEEEEEEEEEEEE
2087 - 2106:	EEEEEEEEEEEEEEEEEEEE
2088 - 2107:	EEEEEEEEEEEEEEEEEEEE
2089 - 2108:	EEEEEEEEEEEEEEEEEEEE
2090 - 2109:	EEEEEEEEEEEEEEEEEEEE
2091 - 2110:	EEEEEEEEEEEEEEEEEEEE
2092 - 2111:	EEEEEEEEEEEEEEEEEEEE

A0A168R9N5 **A0A168R9N5_ABSGL** (909 aa)
Uncharacterized protein. *Absidia glauca (Pin mould)*

```
MLKPPILGSVSVILVWLFLGLIHASKEDRIAVAHESLSKLISNADSPTLMKRFTTYNDDNDENENDENDDDEFIHDDTEG
QDEYDYLYGKGNDEQNEDAKNDENLDVRQPSVQLQQHRQPLIATQYTTVTGSCIPADTGPRYYTHYNNLQRYFQMGIYGP
TNAQCNGPLAVCDPNVEWAQARNHWTGVFFGNFHVGDGGRRSLGPLAVQGDFIGGDYQIHHDSVVCPPYKDLSSTALVVG
GKVSGSQITLPLGGASYIQHGIVEDGHVSITGDDSCRTHQGTTGPVDFDAYYTYWTRLSQTFSEKMPTHILDDAKHVRTI
NFNPEDSAIHVFTFNTCNCFKCDLWPGLLSTPDHIFSGYDAWNGPSSDYPSTGTIVFNIPVDDGTTFAIDSLQPSINMDC
CRTIYNIYPVDPEGNYLSNGHITVLRNCEDTIRGLVLAPQADILDGESGRFAGLVIGDNYSWQNMEEGPDLGDWAAGDCA
CTEFQGCVPLPTPTRPPSFIMTTPGLPPPPRITGPPPLTPPGPRTLPPPSPPATKPDCKTAVTITDCHTTISNCISVATP
PPSGTVTATVTKISCPTPNSRQLWATVTNNQVKTVTQISCPTPNSNRLFATVTSHHVQTITSCTDTVISLFPVTDHAVTR
LVTVPGPPGSTHDNIKVQTPPPPVTSYLTVTSTVHHTKTIRPPECENHEEEEEEEEEEEEEEEEEEEEEEEEEEEDNNE
EEEEEEEEEEEEDNNGEEEEEEEEEEEEEEEDNNEEEEEEEEKEEDNNEEEEEEEEEDHWKKKKHQCDYDHHGKKHKKWW
HKKKKHHKDEKDEDDDEDEEEEDNDDDNEEGNNDDDNDDEEDDDEEDDDDDSGGDDDGGNEYWHKKKWHHHHKKHKDEDF
WKAKKKQHGQENKDSRKWLDKEEVDWLPW
```

689 - 708:	EEEEEEEEEEEEEEEEEEEE
690 - 709:	EEEEEEEEEEEEEEEEEEEE
691 - 710:	EEEEEEEEEEEEEEEEEEEE
692 - 711:	EEEEEEEEEEEEEEEEEEEE
693 - 712:	EEEEEEEEEEEEEEEEEEEE
694 - 713:	EEEEEEEEEEEEEEEEEEEE
695 - 714:	EEEEEEEEEEEEEEEEEEEE
696 - 715:	EEEEEEEEEEEEEEEEEEEE
697 - 716:	EEEEEEEEEEEEEEEEEEEE

A0A169XD14 **A0A169XD14_PENCH** (109 aa)

Uncharacterized protein. *Penicillium chrysogenum (Penicillium notatum)*

```
MRFGGWGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAEEEEEEEEKDEDEEKERRAADGRNPVTKHSRT
RGRPLIPIVGRSNDCPPGNIGRVNSSTIF
```

8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE

A0A174IFI0 **A0A174IFI0_CLOSY** (447 aa)
FliB family protein. *Clostridium symbiosum (Bacteroides symbiosus)*

```
MSGKKKIQIRKPDYFERFQCSASDCTDNCCIGWEIDIDERTAERYKKVQGELGQKLKDRILREWEDELPHFILQGERCPF
LGDNNLCELINELGESSLCDICREHPRFYEWFDGLTEMGLGLCCEEAARLILESPEKADFVVSFKEEEEEEEEEEEEEEE
EEEEEEEGGRPRLFASLLEARDTAFGLLQNREYRIGERLALYLMLAEDIQDYLDLYGEYREASAQTARSCTDAKIQPDEI
RAIEIQTAERILEVVERYGRPEFLSGLLCGCRKEEGGASDRDKVQEWYADTLQFLCTLEPVSPKWPSLLNRLMEELPLLF
EKEEAFTNYFESREYEYEHLAVYFTYRYFLKSYFDCDLLSRAVFAAAGILIMRLFAISRFAQEGKVSAEDQVEIAKFYSR
ELEYSLENLAAFSEETWFSDTLCSERLIEIMLLPGMGAAPLLSDERK
```

146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE

A0A175VQ78 **A0A175VQ78_9PEZI** (1382 aa)
Vacuolar protein sorting-associated protein 41. *Madurella mycetomatis*

```
MTESSPQPGDNGTHDGTTGPDREADAIQPNLGTPARPSLGGGGVGIGNGSEGAAEHSSIEEDDGGDDDESEGEDEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEDEDEDEDEDEEPKLKDSRLTQDLGP
VYRNGDATSSFLVAGDKMIIGTHNGNIHVIQLPVFQSLRTYHAHSASVTSVSISPFPPPLPNIGAEAAARSAPNSPFRPA
TGTTEGHASPAAASRRAREASAVPNAPSNNIYIATSSMDGNICVQSLIDVKDVQLRNFARPMQAVALSPEYKHDRMYLSG
GLSGQLILTVGASTGRSTAMTTGATAQAAGWLGSMVGSGSGKDTVLHSGEGTISTIKWSLSGRYIVWLNEHGIKIMRTKL
HLESTDADDAWKRIGHIDRPQTEEWDTMASVWKGRAEWIDEQAVEPDEDDGVRRDAALSPAAESLRQQQLRSSKMIERLL
IGWGGTIWIIHVHPGGIGVGKDAGERTAGRAEIVKILRMDCIISGISLYTQNLLLVLAYCLPDAEDEEEETSPGHGRSLS
GDSTRSRPSGGIQRKQNNLPPELRLIDLASQAEADKHGLSISRFERLSSNDYHLGVLPAQNVAAATQSSRGALEALAGFG
ADMLNVALNPRSLFSSGASIKSKDSDGASGYQVAAGGAVHRRNSAHLSLAKPGIKIFIHSPYDCILATKRDLSDHLTWLL
EHQQYQQSWELVDQHPEIMSTTSDATPTSPQHTQSTDDFYEETASVTDGMRNLYSSAEKEKRRIGELWIRDLIDAGDWTR
AGQVCGKVLGTPDRWEKWVWTFAGAKKFDEIVNYIPTQRTRPPIPGTLYEIVLGHYLQASKPRFRELLERWSPDLFDVAT
ITTALEDQLRFRDVREDSVEDGEVGRDWRIVMESLAKLHEANGRNREALKCHIRLQDADSAMRLIREDHLADAVADDIPS
FIGLRVPQDRAKKMTHSELEDATSEAITLLVDEAQHGLVKPDIVINQLQGKNLDLYTFFYLRGLWRGEGMHEHSGESRAR
LVTDSQTLVDQFADLAVHLFAAYDQSLLMDFLKTSTAYAFEKACLSRVKQAAQECEALNYIPELVYLYSKTGQTKRALYL
IIDRLGDVSRAIAFAKEQDDPDLWEDLLTYSMDKPRFIRALLEEVGTAINPITLVRRIPEGLEVEGLREGLKHIMKEHEI
QHSISEGVARVLRSEVARAQGLLRAGQRKGVKFEVVVKGIGHVDVASAFDMDPLPPAADKEENVGDGGRVGVNGDAVARR
APARKWVPGHCAQCCEPFVEWEIETLVGFACGHVFHLTHLLERLHPGEEVDEALLNGLAEQRSAAAHLIGAKVTHARLLR
DRIAGGCPVCVDREDVGKALVR
```

75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE

79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE

A0A175W9W8 **A0A175W9W8_9PEZI** (181 aa)
DNA-directed RNA polymerases I and III subunit RPAC2. *Madurella mycetomatis*

```
MSTRSKSRKEEPSDAGSDVVMEEVPTSHQPESKDDDMSVDQDGNDQVEEAEEDEFEEEEEEEEEEEEEEEEEEEEEEEV
QRVKLLPGSTPTAASFEFLDEGHTLGNALRYVINRNPDVEFCAYAIPHPSEAKMNVRIQTFESTTAIEALEKGLRDLQDL
CDVVTDKFIDARECFAANSSS
```

56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE

A0A175WE07 **A0A175WE07_9PEZI** (832 aa)
AP-3 complex subunit beta-2. *Madurella mycetomatis*

```
MESIARISSLLENARELTLDAASAARSVRSSSKPLDRAQVKKLLDSRNEREVLDGLRRVISMMYRSQKTLPLFSSVVKNV
ASPNLEIKKLVYIYLIHHAEQEPDLALLSINTIQKSLSDPNPQVRALALRTMSGIRVPVISQIVSLAIRKGAGDMSPYVR
RAAALAIPKCYRLDPSQLPQLLEYLSTLLGDKLYYVAGAAVTAFMEVCPERIDMIHKHYRNLVRMIVDMDEWSQLSTLRL
MTIYARKCFPRRMKTVKSGERGADLQEFYDEAADGSSEGEQVLVLDPDLESLLNGIRPLLQSRNSGVVVAVARCYSAVGT
PAYVKLAIGPLIALLRGAQDIQQVALFNIVSICLGCPADFVKYTTHFLVRATDTKPVWELKLELLTLVFPHAPGHVKSLI
```

```
LNELEHFSRGSDKVLVREAVRAIGRCAQADTAAAPRCLRLLLGQITSLDGILAAESLTVIRHLIQQDPTAHVATVVRLAK
NLDSATDPQARATIIWLVGEFSGLNGEDNIAADVLRILLKDFASESEIAKRQIILLGAKVYLHHLNRQIEQAQQSQEPSP
PSERFQTQQPAQSPLLLEDDPHPIAKLWSYVLLLARYDTSYDLRDRTRLYKALLSVPQLATLMLLAPKPAPQAPSPSEAR
KGYTLGSAALVLAGGGGVHGLRGYEDLPPWVEEGKEPDAKLRDREGDRGGAVEGKGTRLPPAAEVLDAAAGAGRSSSPSV
SGAVGGKVVGANGVGEKTLDDWLAEDEVKVEAKVDDEEESEEEEEEEEEEEEEAEDSEDEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEESDEYEEESDEEEENTRLMRPS
```

780 - 799:	EEEEEEEEEEEEEEEEEEEE
781 - 800:	EEEEEEEEEEEEEEEEEEEE
782 - 801:	EEEEEEEEEEEEEEEEEEEE
783 - 802:	EEEEEEEEEEEEEEEEEEEE
784 - 803:	EEEEEEEEEEEEEEEEEEEE
785 - 804:	EEEEEEEEEEEEEEEEEEEE
786 - 805:	EEEEEEEEEEEEEEEEEEEE
787 - 806:	EEEEEEEEEEEEEEEEEEEE
788 - 807:	EEEEEEEEEEEEEEEEEEEE
789 - 808:	EEEEEEEEEEEEEEEEEEEE
790 - 809:	EEEEEEEEEEEEEEEEEEEE
791 - 810:	EEEEEEEEEEEEEEEEEEEE
792 - 811:	EEEEEEEEEEEEEEEEEEEE

A0A176WG42 **A0A176WG42_MARPO** (849 aa)
ARID domain-containing protein. *Marchantia polymorpha subsp. ruderalis*

```
MTEPETEIGNGASATIDSQPTVTDAPQEPVEAEVVKTSSGEHTESLRPRDVKQAPNVSTEGLFAKKAESEEVVNKEDDKK
VAEMKIDEKDVEEKEVQAKVGERKDGAKKERVLKEEDKHEEELEEEEEEEEEEEEEEEEEEEEPLQARMVSSKDEKMEEE
EEEEEEEEEEEEEEEEVEEEEVEEEEVEEDEVDDKDGSIEEQIAFTRVLENFFRDRNLEYKAPKFYGEELNVLKLWKAVT
SLGGYEQVTSGKLWRQVGEQFKPPKTCTTISWSFRGFYEKALLDYERFQTGGCLPSSFGGKDLNQGDALLSGFENQAAMS
PTTPSSQPNAAAASGSGRARRDAAARAMQGWHSQRAGNGEVGDPIIKVELLDQHVGVTNGGEVLSEKSGVLKKEKQLKSL
GGTKRKETASLVERAVKVARAKGVRSRSLDDVPSENALSAGANISKAGPLLKKSAKQDRSKHGTKSTSMEPMKGLKLVIT
DDGPPADWVKINAYRNTDGYEIYALVPGLAREEVRIQCEEGGRVVICGSPEQPSNPWGVTAFRKVINLPSKIDAHHTSAV
VTLYGQLFEEPNKWTPSENSGWANVIRVGSVDQEGERSKVVPGSGSEVKKRKKKRKRKHGGREGGNEEAQEGDKRAEREG
GREKNSSLGLSGVIAKSVDLLQLVRFVREFEGWNQKLELRIVVVGCGPGIIEEHRVKLEVVMLGLDAAGKTTILYKLHIG
EILSTVPTIGFNVEKVQYKNVEFTVWDVGGQEKLRPLWRHYFNNTDGLIYVVDSLDRERIDKAAAEFQTIVQDPLMRNSA
ILVFANKQDMTQRDPVIKPMHQRPTFYFKSAPRPDHNHQQRPKPTHAHP
```

124 - 143:	EEEEEEEEEEEEEEEEEEEE

A0A176WQ23 **A0A176WQ23_MARPO** (576 aa)
RING-type domain-containing protein. *Marchantia polymorpha subsp. ruderalis*

```
MPLSAKKVAASYGSGGVRVPRAPLILCLTCPLCGDLFREATTVSECLHTFCRDCIQGRLSDGETNSCPICNVSLGTLPLE
KLRADHQLDDVKAKLFPDASRKRKNGPGSSPAVSAAPIRRKERSLYSLGIGAQPQSANPGFATRATRGSPGKSLAVRDTS
SSEEEEEEEEEEEEEEEEEEEEEEEEEDADEVDEQDEEEDEPTDAEDYVGKEGTNGMVESAPFSTTGAKRMEVEHEINDL
DFIPFRPSRPKEEPRRAPIREPPAPSSDVGIYHARRSVLTANGVARTRSGSGMEPMVSADETGAGSAKGPANSQDGRGLG
SDNLLATLAEVAEASGIGKASRGEQPQTGASGLANNGPDISRGRDIVSHDAKSIETRPSSAITQALDSSTLHASPPRARR
SSPQLQRNPSLKLFVNGGVERPAILMHPTPPANGSLLASTSFAPNSCGIWFALQAARNQSADNPLPQLSSPYLRIKDGKL
PVSHVKKYLVKKLGLSNETEVEITCRGQPVVSSLPLESVRNIWFATAAAPNTKDQENQGLAANETTTGLMHLDASSAKEL
IMVLTYQRHRRNTRIC
```

163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE

A0A177BX39 **A0A177BX39_9PLEO** (86 aa)
Uncharacterized protein. *Paraphaeosphaeria sporulosa*

```
MRHPAAPTVIAFLLGLLAFFLLWGKLRGDGHHEGNPHPDDVPPKAKEEIVEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEAGEG
```

51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE

55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE

A0A177DDI4 **A0A177DDI4_ALTAL** (662 aa)
Photolyase. *Alternaria alternata (Alternaria rot fungus) (Torula alternata)*

```
MPPKRKASIPPNAASARNYTDVSGDAPNKRSRIAKPLSKAFADSAPPIDSIARNTENGAPGEAVKKEEEEEEEEEEEEEE
EEEEEEEEEEGEEGEEGEGEFDHSRPEERAGIVDRRYYPAEMSNERCALYNANEIPRPIEILAKTLESTKDRRMAIREANK
AQFGDAVVHWFKRDLRIRDNTGLSQAAQLAKAKGVGVIGVWFMSPQDWEAHLVSPPKCDFELRSVESLKQELEEFDIPLY
VETIAERKNVTKRLVELAESWNAKNVFCNLEYEPDELRREERLVRKMLEKGINFDPQHDDCVVPPGSLKTGGGKQYAVYS
PWYRAWVAYLHAHPHLLNERPIPERNSPNFRQKFTQLFDSKVPDLPDCKSLTQEEKERFHRLWPAGEAAAIDRLERFLIE
KIGKYKDTRNFPAKNSTGRVSVHHAAGTLAARTSVRMARDVNSAKKLDGGKDGVKGWIGEVAWRDFYRHVLVHWPYVCMN
KPFKFEYTNIEWEYNDAHFQAWTQGRTGYPIVDAAMRCMNHTGYMHNRLRMIAASFLAKHLLLDWRLGEQYFLTHLVDGD
FSSNNGGWGFSASTGVDPQPYFRIFNPWTQSERFDEEGEFIKLWVPELEEIEGPAIHNPYGAGGKAAQAAKSKGYPEPVV
EHKFARERCLARYKAGIGRETA
```

67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE

A0A177EZQ9 **A0A177EZQ9_9EURO** (143 aa)
Uncharacterized protein. *Fonsecaea monophora*

```
MSLRDCSIRKSDILGSLEIGDSVLEGVIVATSLVHWSVLCEFPWRSETVFLRNRRFNIRDGFVTQDKEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDCPPEAREKIEDNVEDDGDGGEQLNW
```

68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE

93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE

A0A177FII9 **A0A177FII9_9EURO** (669 aa)
AA_permease domain-containing protein. *Fonsecaea monophora*

```
MAEPSKKEIVSHDESSASRYDASGTNRDIDPEKLNDPKMQKLAGEITYDDETDPVNRQHNPLAQKLRSRHMQMIAIGGSI
GAGLFVGSGSALHKGGPGSVLLGFIIIGFMLLCTMQALGELAILYPVNGAFYTYIVRFVDPSLGFAVGWDYAIGWLTVLP
FELTAASITIEYWRDDIHVSVWITVFLVFLCLVQIFGVLGYGEVEFVLAMIKITACIGFIIFGIVVDCGGVSSDDRGYIG
ARYWHNPGAFQNGFKGFCTVFVTAAFAFGGTELVGLAAAEAADPHRSLPKATRQVFWRIATFYVLSLFIVGLIVPSDSTD
LLGASGANTKASPFVLAIKYAGVKGLPSVMNAVITISVISVANSCTYGSSRTMQALAARGMGPKFLMYVDRQGRPLWCVV
IQLLFGCLAYIGEANASDTIFTWLLSLSGLSFFFLWMSINLSHIRFRHGWYAHGFTKHQLPYQAAFGIWGSYIGFSLNAL
AIIATFYTSLFPLGSDPDAEVFFENFLAAPIVIALFIGWKLYSRDWKLFIRADEMDVTMGIRRGSLEIAAEKGRSGRLKE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEDDDDGEDEDDDDDDDEEEFDPLKASKPNADNEVEVRIDNYKEL
GPWLDGYSVTPELAASSAKEKSGRKHYYR
```

560 - 579:	EEEEEEEEEEEEEEEEEEEE
561 - 580:	EEEEEEEEEEEEEEEEEEEE
562 - 581:	EEEEEEEEEEEEEEEEEEEE
563 - 582:	EEEEEEEEEEEEEEEEEEEE
564 - 583:	EEEEEEEEEEEEEEEEEEEE
565 - 584:	EEEEEEEEEEEEEEEEEEEE
566 - 585:	EEEEEEEEEEEEEEEEEEEE
567 - 586:	EEEEEEEEEEEEEEEEEEEE
568 - 587:	EEEEEEEEEEEEEEEEEEEE
569 - 588:	EEEEEEEEEEEEEEEEEEEE
570 - 589:	EEEEEEEEEEEEEEEEEEEE
571 - 590:	EEEEEEEEEEEEEEEEEEEE
572 - 591:	EEEEEEEEEEEEEEEEEEEE
573 - 592:	EEEEEEEEEEEEEEEEEEEE
574 - 593:	EEEEEEEEEEEEEEEEEEEE
575 - 594:	EEEEEEEEEEEEEEEEEEEE
576 - 595:	EEEEEEEEEEEEEEEEEEEE

A0A177FN82 **A0A177FN82_9EURO** (205 aa)
Uncharacterized protein. *Fonsecaea monophora*

```
MAYGAIGGTPGRALGPIKPKQGEFFDREELPARFRRKAWSEEEIEAAQAQSTRQLGMTASATTTTDTANAASAVKLTVEL
SYIPTEDRAAWGGGGEKRRKEGSRFQAAVNQAGENRTEQVPGDVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEI
```

125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE

140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE
180 - 199:	EEEEEEEEEEEEEEEEEEEE
181 - 200:	EEEEEEEEEEEEEEEEEEEE
182 - 201:	EEEEEEEEEEEEEEEEEEEE
183 - 202:	EEEEEEEEEEEEEEEEEEEE
184 - 203:	EEEEEEEEEEEEEEEEEEEE
185 - 204:	EEEEEEEEEEEEEEEEEEEE

A0A177TIH5 **A0A177TIH5_9BASI** (841 aa)
Uncharacterized protein. *Tilletia indica*

```
MIFDANSRLEREKHAQDQLQRMQQQRERERQHQESLAAQRRQEGGQQQRSRQLDQAGQQQQRNTHQTQPQQQQGAGEIRQ
QRQQRRNTAEIPNQAFEGSRSDAVVQGPVQQYLPPPAAPCYPSPLLRPTMAPQPQVATTTASLPHQISGTSNMTAIPSGS
NLQQAAGLQMAATGQTKWIEARDSPSSEAIDACQQLRDYNRAAQHWISQTFGLSHVQISEIRDLIIEGNGCFSVKTMSDF
NQFQKWYAQTKQEPCRQAGESVNDHNATLGLYWESLEDHERAEVMIKVKTWFGKNIRTNKVQTKAAVRKLRTKLLRLSAE
AEDLWGISLVSFIASCSPKVKAQYVGRSHGIGVFSTALERSKGDLTPETVASAFWCCSVADLPPSVRDPNSASKAPSTSP
AQKTRIVANFDIHERTDHCFSQVVELLSRSIVQVLHAALQSRSEEFVTPAKIAAWEEWNSRSDGGNQRMYKRLFTLVESM
GFAVAGWPKHCRKMIDEEWRHQTGLQQDTITLTHGGLANFNEWSRPKAKLLLAQLINDSTTLHLKRISADGQEVDLKSIP
```

```
SGGGQDSGSVNGTPGTGTLSNGSEDVGTGAIAARSDSNSGSLPSTQTTVTPGRNQQAGTGDAEGQRGREQPLTKRKRRAP
KAGEQAVQGTPETNEFSEDDDPNVPRQRRTTKTPRQTKRKTQKRRRRPSSTDSDCDDSDAVNYAEPELATEEISEEARRR
LQSNAQRRNANSSNAQLRPAESSSMGTHAATLGDDIRQRTEDSVRNDEEDDEGGEKEGGEGEDDEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEDGDDDEDDDDEDDYDGIEDLMAALTS
```

785 - 804:	EEEEEEEEEEEEEEEEEEEE
786 - 805:	EEEEEEEEEEEEEEEEEEEE
787 - 806:	EEEEEEEEEEEEEEEEEEEE
788 - 807:	EEEEEEEEEEEEEEEEEEEE
789 - 808:	EEEEEEEEEEEEEEEEEEEE
790 - 809:	EEEEEEEEEEEEEEEEEEEE
791 - 810:	EEEEEEEEEEEEEEEEEEEE
792 - 811:	EEEEEEEEEEEEEEEEEEEE
793 - 812:	EEEEEEEEEEEEEEEEEEEE
794 - 813:	EEEEEEEEEEEEEEEEEEEE
795 - 814:	EEEEEEEEEEEEEEEEEEEE
796 - 815:	EEEEEEEEEEEEEEEEEEEE

A0A178AEN6 **A0A178AEN6_9PLEO** (553 aa)
Uncharacterized protein. *Stagonospora sp. SRC1lsM3a*

```
MATTPRPPMPLAPAELSPQAQPSTEPLSSNYSSSPPRPIKPMPRKRSRPTKSPFPPPDPTRSVYGDMHAHTSSSLMSTHA
AYMLAQGMISAHMARQLSQPWHKSGVLEVRYDEAYLAGFEGRVEGMDEVVPKKQKKKGGNKNGKGKDGEDDDVDGEWERW
LEEGELKEEEEEEEEEEEEEEEEEEEEEEEEEEEDINGEEEEGDLGDGECDEDWVDDTDVDSDITSSNAATKSDSEQLD
FDDPAAEKSPELSEISSDAQSALGESEADETDVNTGVVRKRRLRESALGERAVKRMKSNNGSGFIKTTSSRNVEGTTISP
AKPQTRRRSTNTGGVEESVRKKAPLKKEKKETATSSEVSTKLGVEGNSTKTKVPSKKVKKTASTDGPRDDKSPTIAAPFK
KKPAPLITTPPPSAPTPYDSTNYFALLALCRTRNLPGGGKERDLRTRLFGDDENVRLGRERVLNAARKGGRRKGWKHDGE
GKLIGEKVVRKGKVEDQGREVEDGSVGKGGGKKGKVGEAGKRKRDDDDVDEEGDEAKEPTHEEKKLKTMEAQN
```

168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE

A0A178AP40 **A0A178AP40_9PLEO** (529 aa)
Uncharacterized protein. *Stagonospora sp. SRC1lsM3a*

```
MGQQKKKVAASRSAFSAQQKHHVRSRAATGISVPRTTTTSTKTSAKRPIPAMPTIQLSNFSKITMNPFRPLMLGAAVQIP
PVPAPTMQIKPLAPAIQIKPPSQMPSEVPSGGRLNPSKLAAPPRKDVVPQNRLKHDLNNMQGGSLKKEVITKKDLFKPGL
FSRKQSKKIIAAEDPLKKKVPENALAKEDLLNKDLPLKKMSEGILPDQNRTKNGQPKKGLLPLKKTPPDPLKKKGIPNKD
RKKDMPAKDAKEGLLSEDVKKGRLGEDVKQDMLDKDARKGILDRDAKKCILDKDPKSDNKGKQMQLTKPLPKKDSWVKTL
FEKGPPKNRLPTLPRPARTRPLNQEREPATNEQSEEESDIDDEPGSEESDDPPATVAPQLRANVPPRWPPPILMPRPHAI
RAPVQRPQAAPEIQRVPRPPQHMPIRKPVPSHAQSLVRLPPPVPAHEEEDDDDDDDYDELEVDEEEDEEDEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEDLNSIAATPPQYQPPSRPLLPPTQRCAP
```

471 - 490:	EEEEEEEEEEEEEEEEEEEE
472 - 491:	EEEEEEEEEEEEEEEEEEEE
473 - 492:	EEEEEEEEEEEEEEEEEEEE
474 - 493:	EEEEEEEEEEEEEEEEEEEE
475 - 494:	EEEEEEEEEEEEEEEEEEEE
476 - 495:	EEEEEEEEEEEEEEEEEEEE
477 - 496:	EEEEEEEEEEEEEEEEEEEE
478 - 497:	EEEEEEEEEEEEEEEEEEEE
479 - 498:	EEEEEEEEEEEEEEEEEEEE
480 - 499:	EEEEEEEEEEEEEEEEEEEE
481 - 500:	EEEEEEEEEEEEEEEEEEEE
482 - 501:	EEEEEEEEEEEEEEEEEEEE

A0A178AYC7 **A0A178AYC7_9PLEO** (521 aa)
Uncharacterized protein. *Stagonospora sp. SRC1lsM3a*

```
MGKVTVRRCESPGRKGIPLLEHLSPRSIVLPVFNNTHSRSTRREQRRRFQVRKMTVGQGKPRTKKELPSLQEKRGRMPKP
TEQQNSQVSRRHQSSTQGSRAASRTAFRQSMIGPGTRLGATKYAPIIIREEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
VEVVDREEDSPRYVGLFSNSFVASTPASPRTSIYAPSPSTPSDSSSPIRRSIPSLIGGAWTPPSSTASDEGRYRETSIYV
STRRHTTTGAQPAPHSPSAYSGGNEYRSCPPRTSGIFASATAAITPKSRSAKTSRGETTLANIPNAITRKKVADLMAVAP
ALPVEDLHDLLIEFEHDVPAARSRAMRASRGPSAKPAIKSEWEESHEPSRNARLMGYGYDGDEVMIKIDPNESFLEYDTD
SPPPEDIPSSAKVRTSKHSGKTKSVAENIKQSSRKRAKIGSLYKFGRKGKGNSLECTVIDADNVVHLETDCSSSDTDSSA
LVDSSDTEMEDAAEDVAEDLRIDMRSRYTFNYNILKKAKKR
```

130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE

A0A178CG34 **A0A178CG34_9EURO** (1820 aa)
AAA domain-containing protein. *Fonsecaea nubica*

```
MPAGRGSKRTLEEVVNYEDSDDEDYDDRAAGPSKSRSAKPRRRGAPARKKRKRGYAGSDVDSDSDEVVSDEDSFSDEDED
DDIETNAIGRPVRRAAKKAANKYEESSEDEEDELANSSGEDRPRRQATTSPRKKLIITLKTTPARSARSLRTRSGSYGIN
QPATSSAPHPTVTRRSSRLSHDPEESLVKLTDSGNHVEIVREGSRDPEGIPPRAMKGGKGLKYPSKSTIDEESQSQPKEE
EVEEVLEIQASQHELLESDPQTMEEHAAEELPNITSDIINIAEFEGVESDGDFNPEPAATQEEAAVEVEKEDIEEEQEEE
EDEEEDEVRPARGRLTRGSSKRKVDSPEFEPHKSPKRLRGRTLAGEANSGASGSRRRKAPDESSDFHPEDETANQDDMSS
SSESNASPRKKNGDDDDYESENQGRRSRRLRSQAASRQRSEESDDDLAAEVAELKRDGRKSRRPREEEIIYEPRGRRGGK
KPNYDLLRNLAPLEEEEEVAAPSPSARARKTGGGGWSRTLFNTYGPFGGGGGLPPVLGGGPQRAQGGVDSDSSDDETMKQ
PRQLGGTVGMTPTTAGGFNLFPQTLNADAAQATAGTPANLGKIKDKQTLADADPLGVDQNVTFDNVGGLQGHIDQLKEMV
ALPLLYPEIFMRFKITPPRGVLFHGPPGTGKTLLARALATSVSSQGKKVTFYMRKGADALSKWVGEAERQLRLLFEEARK
NQPSIIFFDEIDGLAPVRSSKQEQIHASIVSTLLALMDGMDGRGQVIVIGATNRPDSIDPALRRPGRFDREFYFPLPGTA
ARKSIIGIHTKGWDPPLPEAIKDELAELTKGYGGADLRALCTEAALNAVQRHYPQIYNSNEKLAIDPRKIEVTPKDFMIS
LKKMTPSSERSASSGAAPLPPSVAPLLQSQLDQISQLLGEILPQRKRLTALEEAQFEDTADGHSFGREKMQQTFETTRVF
RPRLLIHGKLGMGQQYVASALLNHFEGLHVQAFDIPTLFSDTASSPEATVIRLFSEIKMHKPSVIYIPNVQEWYNTVGQA
VISTFVGLLRSIKPTDPVLLLGFAEGDYDDMDDNMRREFFGYSKKNQFQLREPNLEERSQFFRSIKDYISTAPDDFPDPK
HRKKRELEKLAVAPPEPEKPKPPPTKEELKAQKRRDRQTLNMLKIRLQPIMDQIRTKYKKFRTGVIDESHIRYLYDEADP
GTVTSDLHTEILARASYRPFEIGKDAHGVPGLIDQSNGNFYYNLDSVTIEKRLSNGYYKRPKDFLADIKRLAKDAKAIGD
EDRLLKANELLANVEVDIGSMEVNEPALAAECERVYQRELEREREALEKAEQGKMPPPPNVTNIAQGSGTTTTNDTGPIL
LGEPMHRRNDFAQRLAATSTQAKSTESIVTNGIHPSQNHSGHLTNGSHANGHEIDVEGDTFMGGGDSHPSSHNKSNDTQQ
TNTTSSYGARASAQTRPWSAYTAPSQQLMKESGLSAPPSQTGPFTPMPQGSQPGEFQNDASTTQSPNEKKPSSNNTQQEI
HQDSGPDLYPFDERRSAGGSQIPSTQGQNSQSQAAVGVRPSSPQGANQESNSQPSMIMPPPIEAPSQRHSNASRIDDLLN
PSSSPRPTSPPSPTSRPNLIQVEEHALENLHTEIADQTSGLSVEQLEQVNSVLMDTIWKTRSEWDRNKVKESVAEAFNEV
MEDMVGAGQQFGDGSWGRKAQRVSTSTITIIITVTIRVLGPEDPVLGVEVEVEVEVEVEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEGAHWGRPQQGSGKAPESLGWRNLWLFTRSIYAFWFVPAL
```

1739 - 1758:	EEEEEEEEEEEEEEEEEEEE
1740 - 1759:	EEEEEEEEEEEEEEEEEEEE
1741 - 1760:	EEEEEEEEEEEEEEEEEEEE
1742 - 1761:	EEEEEEEEEEEEEEEEEEEE
1743 - 1762:	EEEEEEEEEEEEEEEEEEEE
1744 - 1763:	EEEEEEEEEEEEEEEEEEEE
1745 - 1764:	EEEEEEEEEEEEEEEEEEEE
1746 - 1765:	EEEEEEEEEEEEEEEEEEEE
1747 - 1766:	EEEEEEEEEEEEEEEEEEEE
1748 - 1767:	EEEEEEEEEEEEEEEEEEEE
1749 - 1768:	EEEEEEEEEEEEEEEEEEEE
1750 - 1769:	EEEEEEEEEEEEEEEEEEEE
1751 - 1770:	EEEEEEEEEEEEEEEEEEEE
1752 - 1771:	EEEEEEEEEEEEEEEEEEEE
1753 - 1772:	EEEEEEEEEEEEEEEEEEEE
1754 - 1773:	EEEEEEEEEEEEEEEEEEEE
1755 - 1774:	EEEEEEEEEEEEEEEEEEEE

1756 - 1775:	EEEEEEEEEEEEEEEEEEEE
1757 - 1776:	EEEEEEEEEEEEEEEEEEEE
1758 - 1777:	EEEEEEEEEEEEEEEEEEEE
1759 - 1778:	EEEEEEEEEEEEEEEEEEEE
1760 - 1779:	EEEEEEEEEEEEEEEEEEEE
1761 - 1780:	EEEEEEEEEEEEEEEEEEEE
1762 - 1781:	EEEEEEEEEEEEEEEEEEEE

A0A178D380 **A0A178D380_9EURO** (423 aa)
Uncharacterized protein. *Fonsecaea nubica*

```
MAEEASSTFSLAGKGLKIDTKEDLEKHINALTSSPSVTHIDLSGNTLGVSACAALAPILASKSTLQSADLHDIFTSRLLD
EIPLALSSLLTALLECPNLHTIDLSDNAFGLKTKDPLVDFLSKHTPLKHLVLNNNGMGPEAGIAIAEALIKLAERKEAAR
KEGKNVPYLESIVCGRNRLENGSMPAWARAYQAHKAGIKSVKMTQNGIRPEGISHLISSGLSKCENLEVLDMQDNTFTLK
GAQALAEALGGWSNLKELGVGDDLLGARGAIKVFEAFSGGNSENVEILRLQYNDITPAGVKSLLRAAKHDLPKLRRVELN
GNKFEEEDPSIEELAALLSDRKDELGKNEDPEDHWGLDDLDELEGEEEEEEEEEEEEEEEEEEEEELAERIVKEAEEAEE
EKVAEEKDKEVDELAKALEKTHV
```

366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE

A0A178D7H8 **A0A178D7H8_9EURO** (982 aa)
C2H2-type domain-containing protein. *Fonsecaea nubica*

```
MADDFKCKVAPPAQGNEASTDGWIAHPAADDKADRIMCGTADTGEKPFRCLHCQKHYGRRDVLRRHIRDHHGEAGEFLND
AGGVEVYERNEGNLFAGHAQSLRSPRRGLGEGHEPLITSTLKGSNNVVDEANSIDDLPPLAGLAFEEIFDSITDPVISAA
RIDNMMDAAVYPHHTSQALPEQADDGTTESFSVTDVISICGVNEDNNLDPYIHSSDSNVGQLTTTEFFDGTGDQHLDDCL
SPTTSFALTFTETSLHGPELGEQFEWTLEETAKGQPESIEANHTKHYSGDERYQVEIPEPVSTSGINGRPWFSLASSRLP
KHLLLPSESVWPSKVMGRGHQQASRNWWEFVICCCEANIFCRQSVHTATESTESPTLDSHAFGFNEECRSQLMQAFCLSQ
SNRRPDMADVLPSQQIWSRGGRPSSLEAQFPSREALSASLGLYFRHFHPLMPFIHRATFHAPTANLSVLFAMCLIGLMLL
DDARAKRCIAVMLPTAIQTCRRDLDLHAHQTHFSAEVLASLASAMLLLCICHMANFYDDTSRLMYIEAMSLSQRRHLFPT
DDGNETLRGLLNGASQREKWKAWARVESTKRLCVCLLMGDAMFSHKYEVKPMLRFELLEYIVPGDLATFEAPNQAVWWRR
LLQSPSGRMVTLHTLSLPRSIGNYEMHGLLAICWAQVLEGQLDRPGGAVDSDCARAGRHDRQVGDHSRIQRTAAVLSGLY
DAYKDAFTSLNPNCLVSWHNTCMSLAADPLLFQDAAGRNGVARARIARNAVAQWCRTPTARRACLHAAQTFRIMSQRKIS
EGMMFQSETALFESALVLGLYLYLRPAVPGVSAWASWVVSGGGCDEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDA
QGEEYELLDDVDWTRIGVLGLSDSVECLGDDVPRSSNSNSPSRRFIRDGGLTSLSFDGVTCAPGFASAQRIFLAFSTLLS
QVAPWNAGRYCPILRSLSDCNL
```

848 - 867:	EEEEEEEEEEEEEEEEEEEE
849 - 868:	EEEEEEEEEEEEEEEEEEEE
850 - 869:	EEEEEEEEEEEEEEEEEEEE
851 - 870:	EEEEEEEEEEEEEEEEEEEE
852 - 871:	EEEEEEEEEEEEEEEEEEEE
853 - 872:	EEEEEEEEEEEEEEEEEEEE
854 - 873:	EEEEEEEEEEEEEEEEEEEE
855 - 874:	EEEEEEEEEEEEEEEEEEEE
856 - 875:	EEEEEEEEEEEEEEEEEEEE
857 - 876:	EEEEEEEEEEEEEEEEEEEE
858 - 877:	EEEEEEEEEEEEEEEEEEEE

A0A178FIX5 **A0A178FIX5_TRIVO** (807 aa)
Uncharacterized protein. *Trichophyton violaceum*

```
MSFVSSQQSYAAFCEEFDEDANVAIPETRRVANISAKRSKPDLHPVIISADGASDSGYSSRTAATIGSSGESLASGTSGA
SSSYAVSMNNAMAGRDIPRVRSRGDGVDREKQHSRKAKEREQKDLDGMKNEGMKPPSSRGSNRPTALTHAPKTRRRESMS
AGRHPPGVCAECDRFGYHTQGMIPNMMDASSYFNQIPGYDVPPSPQTPRYQPMDIGMSITPAITHSRRSNSSSYHQQSRP
VSFHPGIVPDMNMMYMAGGPSAPYGNSHAGPPLSASAYTNAYMGSPFDSSYTQPSPIMGSSYENSSQVMMHYERPRTASM
SRPSSERPRRGSVYGPPVVENTPPTPSHMPNLDRKLERRPSREQRARRQSRSYHDEDYYRMPPPRLPAAKPAQPQPPVQV
IPITKRPTPKKAVTTPAATTVVHRPPSFDMSSMREALPAPRANQYHHQPPQSQRRTSRSTAREPSPERGTTQVIASTRPR
RTATYYDAARPARVTVEAPRRPRRVSTYGIEQENLLEQKQREVEAYQAARAPKAPQLTTEMVRKASRRVSKARTIHQRQP
EPEPEPEPEPEIESPSETDTDTESEEEEEEEEEEEEEEEEEEEEEEPPMQVYPMSRVHRQQPRQQLRQQHPPAPPAPPAPP
APQAPPAPVPLTTEMLRKAASRRPPPIPHSETESDDDDDDAIEDDSSSESSDSEDDTSDVNTKNGSATGSRVDDDSITMI
IRGVKIGLSSDAIDGKTINFRSGEEGGVELNIGGRKRDRYFLPRSDTASTSSRREADDIRRLREEHRAERDSRRSSRSGY
SGRGLLE
```

585 - 604:	EEEEEEEEEEEEEEEEEEEE
586 - 605:	EEEEEEEEEEEEEEEEEEEE

A0A178Z416 **A0A178Z416_9EURO** (743 aa)

WD_REPEATS_REGION domain-containing protein. *Fonsecaea erecta*

```
MAGSTQDISRVSVNDHSRAAVGTFHGPVYLGNNESEYLNNVLNSLPIAADAPFNAYKRQHDPTCLPDTRSNLLRKIYDWA
DGKNSPSIFWLSGMAGTGKSTIARTVASRYSEKEALGASFFFSRGGGDIGYARWFVTSIAVQLAYKVPGLKRPICDSVVN
HGDIAGQSLRDQWRHLVIGPLSVLPGDSCLFRYILVIDALDECEDEDNVRTILQLLAEAQALERVQLRVFLTSRPEVPIR
NCFIQMPDAEHQEFILHGILPSVVNHDIRIFLEHNLKLIAQERSLPAGWPGEEIIKRLVQKASGLFIWAATAYRFIREGK
RVAAKRLHQILEHGSSTVNGPEGHLSEMYIAILRHCISEYPDGERKEPQSILKSLLGNIVTLLSPLSTQSLTKLLQDGVD
QTLYDLHAILDIPEDISAPLRLHHPSFRDFLYAETRSAEFWVDEKEAHLTLATKCIQLMSRCFGQEDRIVRPKALIAICD
TSRPGTLVTEVNREQVEQHLPPEMQYACRYWIQHLQKSGDQLRDDQLHDDGPVHRFLRDHLLHWLEALAWVGKVAEGIHN
ISTLNLMATSQKCPQLSKFVYDAKRFTLYSRSAIEQAPLQIYCSALVFAPMESIVKKQFSDCAHQWMRRLPKIQEKWDAS
LQTLEGHSDSVNAVAFSPDGNLLASGADDGTVRVWDTSSGEVKQTLEGHSDSVNAVAFSPDEEEEEEEEEEEEEEEEEE
EEEEEEEEEEKEEEKEEGITICL
```

702 - 721:	EEEEEEEEEEEEEEEEEEEE
703 - 722:	EEEEEEEEEEEEEEEEEEEE
704 - 723:	EEEEEEEEEEEEEEEEEEEE
705 - 724:	EEEEEEEEEEEEEEEEEEEE
706 - 725:	EEEEEEEEEEEEEEEEEEEE
707 - 726:	EEEEEEEEEEEEEEEEEEEE
708 - 727:	EEEEEEEEEEEEEEEEEEEE
709 - 728:	EEEEEEEEEEEEEEEEEEEE
710 - 729:	EEEEEEEEEEEEEEEEEEEE
711 - 730:	EEEEEEEEEEEEEEEEEEEE

A0A178Z7H1 **A0A178Z7H1_9EURO** (333 aa)
Rhomboid domain-containing protein. *Fonsecaea erecta*

```
MVTTSGFSNTPVARLLILTSVGLSILTSTLSIQYLLPIRPHPHLWPYLQVSRLLTYQVAHTSSTELLFAAVLLYQFRVLE
RLWGSRKFASFVAVVFWCNLAVVPLLVVLLKLITLGWYNYLPSGSTGLVFALLSAWAEEVPRIYRYKIATGGTPATAATT
TGNSGPQSQSQQQQVPGVILSDKSTTYLLAAQLALSQFPYSLLPAAVGWTVGSAWMGELLPGGLGRWRIPAWMVGESSRR
KERDRYEGLRRRLEEEGSSADGMRTAQMRKPPAAAAAAAAAAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEE
```

284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE
287 - 306:	EEEEEEEEEEEEEEEEEEEE
288 - 307:	EEEEEEEEEEEEEEEEEEEE
289 - 308:	EEEEEEEEEEEEEEEEEEEE
290 - 309:	EEEEEEEEEEEEEEEEEEEE
291 - 310:	EEEEEEEEEEEEEEEEEEEE
292 - 311:	EEEEEEEEEEEEEEEEEEEE
293 - 312:	EEEEEEEEEEEEEEEEEEEE
294 - 313:	EEEEEEEEEEEEEEEEEEEE
295 - 314:	EEEEEEEEEEEEEEEEEEEE
296 - 315:	EEEEEEEEEEEEEEEEEEEE
297 - 316:	EEEEEEEEEEEEEEEEEEEE
298 - 317:	EEEEEEEEEEEEEEEEEEEE
299 - 318:	EEEEEEEEEEEEEEEEEEEE
300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE
306 - 325:	EEEEEEEEEEEEEEEEEEEE
307 - 326:	EEEEEEEEEEEEEEEEEEEE
308 - 327:	EEEEEEEEEEEEEEEEEEEE
309 - 328:	EEEEEEEEEEEEEEEEEEEE
310 - 329:	EEEEEEEEEEEEEEEEEEEE
311 - 330:	EEEEEEEEEEEEEEEEEEEE

312 - 331:	EEEEEEEEEEEEEEEEEEE
313 - 332:	EEEEEEEEEEEEEEEEEEE
314 - 333:	EEEEEEEEEEEEEEEEEEE

A0A179UAE8 **A0A179UAE8_BLAGS** (117 aa)
Uncharacterized protein. *Blastomyces gilchristii (strain SLH14081) (Blastomyces dermatitidis)*

```
MFISLLFFGMAVKLPSRPGTAREILPSTDHSHGVETEGERGRGAGEVGNEIENIEEEGEEEEEEEEEEEEEEEEEEEE
EEEEEDEEEEEMSSTSDYHSEFEDGLFCLTPSVTDYL
```

59 - 78:	EEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEE

A0A180FYU8 **A0A180FYU8_PUCT1** (163 aa)
Uncharacterized protein. *Puccinia triticina (isolate 1-1 / race 1 (BBBD)) (Brown leaf rust fungus)*

```
MARRKRADPRAPPSQLRPIPWKSLLLQAHAGKSNRRLPLPFPMDHEARHRSSDLGEKHNQSGSKTQQRKDNSNVPVGGKP
RTAEQQEEEEEEEEEEEEEEEEEEEEEEEEVDQEEQENVGGMVEEPVEPDENLVIDDSAQEQLSTGRVAPREDLNYGTER
YRL
```

87 - 106:	EEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEE

A0A180G093 **A0A180G093_PUCT1** (168 aa)
Casein kinase II subunit beta (CK II beta). *Puccinia triticina (isolate 1-1 / race 1 (BBBD)) (Brown leaf rust fungus)*

```
MDHDARHRSSDLGEKHNQSGSKTQQRKDNSNVPVGGKPRTAEQQEEEEEEEEEEEEEEEEEEEEEEEVDQEEQENVGGM
VEEPVEPDENLVIDDSAQEQLSTGRVAPREDLNYDTDTSASVTDSLTWISWFCSLAGHEYFAEVAEDFIEDDFNLTGLTT
YVPFYKEA
```

45 - 64:	EEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEE

A0A180GR73 **A0A180GR73_PUCT1** (814 aa)
Uncharacterized protein. *Puccinia triticina (isolate 1-1 / race 1 (BBBD)) (Brown leaf rust fungus)*

```
MNRPLPFTHPDLQQYTYAFQQGQEQGEYDEEDGSQEDDEGEEEGDGEEDEGEEEVAEVEDGINEGEEEEEDEEEEEEEE
EEEEEEEEEEEEEVEERGPSTLPDPAAHQMTFALVQKPMTVRQRKELEKIARQQERQRKKELKEREKAERLAKREQEKLA
RIAKKEQLLLQSKAAKKAKATLDGDQRAWSIGRPMKTTGSSSQLLTTRKIKVDSRIETVRRLITHAENGELHIHPSGAAL
DPSGNTRWCETKVHQGVTYLVEDDELTLPSDPKGDTKVTPEGVLLGGRQYKIPTFTSKDRANHNKHFVLSIDAARAAGYR
DSLYFFRRNPLIQKLPCTQLEKDELICAGFLSGNLKSRAVTMCSARNAFKVMGARFLKDGRHVVDDYYEDAALASGANSG
EIALADGSEPQDRAASNSAPGQPGDPSALPDMPESTTRLPCQSAFRLALNRVNPSAAGSASLGLKTIFGGDGKAPSIAIP
NDSKERRRRMASHLTAKNWMIHYCRAISEMNRHLRGIRNERMVPFPKYPSIARLAADPSTNGAIGTLANNAVEEEMEWRE
VEVEMRLNTDGKIMEPGEEMDTKEEPDDDDDNNSNAGGPSASAPEPAQVFSRITNPLPPSSIITIYGVKNSSTSQEQTNT
GEGTPGQGGGGADSSRVGGSGLHPARARSPHKRPFKLRGKKSQNDWWTTTTRVLEQRPKQPVMGLLDVHTGQPHVRQDTQ
STMAIWETADDLDDWTRCNKRQKLNGSQIDPQAGYDPSLLESRTIMNGPGIGRPGLSSVNDTILIETIFDDELTRPKYEL
LPGMWDFRSIDPQA
```

72 - 91:	EEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEE

A0A182FK60 **A0A182FK60_ANOAL** (3294 aa)
Uncharacterized protein. *Anopheles albimanus (New world malaria mosquito)*

```
MLLPSYAMAELTRPPLGDIKRPEEVVKMSMTDNLKFAVLIGLIEVGQVANREVVNTVLHLLVGGEFDIELNFVVQDAQNV
KHMLELLDHCPANLQAEVWSVFIAILKKSVRNLQACTEIGLIEHVLARLYQAEPIVADLLIEMLGVLASYSITVKELKLL
FGAMKAVNGKWPRHSAKLLNVLKQMPHRNGPDVFFSFPGRKGSAVVLPPLAKWPYENGFTFSTWFRLDPINSVNIEREKP
YLYCFKTSKGVGYTAHFVGNCLVLTSMKVKGKGFQHCVKYEFQPRKWYMIAIVYIYNRWTKSEIKCLVNGQLASSTEMAW
LVSTNDPFDKCYVGATPELDEERVFCGQMAAIYLFSEALTTQQICAMHRLGPGYKSQFRFDNECYLNLPDNHKRVSDEAA
KSNASVAMLSLSPTSHVPLESNIHRNLVSGGSAAAGFAAAATLSAATTTAGSGASLAPSATDPSGESFDFVSVLYDGKLS
SAIVFMYNPVATDGQLCLQSAPKGNLSYFVHTPHSLMLQDVKAVVTHSIHCTLNSIGGIQVLFPLFSQLDMPYEGTDVRK
DPTLCAKLLGFICELVESSQTVQQHMIQNRGFLVISFMLQRSSRDHLSLDVLGSFLSLTKYLVTCLSANSDLLLKQLLDH
VLFNPSLWIYTPATVQARLYAYLATEFLSDTQIYSNVRRVSTVLQTVHTLKFYYWVVNPRSKSGITPKGLDGPRPVQKDI
LAIRAYILLFLKQLIMIGNGVKDDELQSILNYLMTMHEDENLHDVLQMLISLMSEHPSSMVPAFDVKHGVRTIFKLLAAE
SQLIRLQALKLLGFFLSRSTHKRKYDVMSPHNLYTLLAERLLLYEESMSLPTYNVLYEIMTEHISQQILYAKHPEPESHY
RLENPMILKVVATLIRQSKQSEQLIEVKKLFLSDMTLLCNNNRENRRTVLQMSVWQEWLIAMAYIHPKSSEEQKLSDMVY
SLFRMLLHHAIKYEYGGWRVWVDTLAIVHSKVSYEEFKLQFAQMYEHYEKHRTDNITDPALRQQRPISTISGWEHQGSGS
TGKPNTESELLLDGHRGCGGPPHHQSVASIGTSSTIATSAGCICGPETGDTVIKSPVMKNTTDDGFKGNSLPQNGAGGKH
DNVVNDQIEDGEEPVTKLNTYKAESAAGDEELEDDEEEAEEVEEEGKADEGDEEENDPGQRRKLVADVKDVVAGQMAASG
SSDAMVVQRIVDEIVDKSTANLLLVGWNERAEGAHCEKNSKQQIQTKETPTEPTSSPVIKDEEIELAVNEVVKMSQLKPL
EDEGRSGHQQASDGLPLVDTETKSNSENVNDDARRITATEPLYKDENDEAKIAAYVHRYVEEVIDRVFSEPEAAVEHSVD
ATESVACEIQQMVQSIITDAVERAEKTNGATTSGTAAECQCAPDSGGTMFLPSANHHDGATKSYAKISVVSEAMEGMAGN
DKIVLVREEEDERAMEEDENDEEEEDEEMEQGSEEENEDEKDEKKRETKVAMQKVEEEEDDDEEEEEEEEEEEEEEEEEE
EEEEEDDEHEEEEEEDNASKSGVLVAAIESNQLSTKHETVAKSIAQPSGAAEIMITGTAPSTVIVAPEQMDTHKHSSANG
AQPQTHASKGSSNGVNSGKPLSSTTSTNSQPSLAQTMAGGANDGVYDGQPKRSSKQSSSSSGNRPMFSPGPTRPPFRIPE
FKWSYIHQRLLSDVLFSLETDIQVWRSHSTKSVLDFVNSTENAIFVVNTVHLISQLADNLIIACGGLLPLLASATSPNSE
LDVLEPTQGMPLDVAVSFLQRLVNMADVLIFASSLNFSELEAEKNMSSGGILRQCLRLVCTCAVRNCLECKERTRGLYNG
MALKDIPGGVHLQALIRGAQSTSSKTIIESLSGPLSPVKDPEKLLQDMDINRLRAVIYRDVVGGFWREGTGCGICKANGN
LKKRLFQEETKQAQFLSLAIVYFISVLMVSKYRDILEPPVELQIHRNTSPVVHQRATPTQGTQSMQDGEYEVIVVDESNS
SVIADDSHSSGPLSIKSVDSDGGSLNLNSTENDPQEVETSSEIMPDDHKPTNSNDESWTDVNLNDDGVGDLKTRVADVPV
AVLSSDGTCVGASAIGVGGNESGMLSIQTVGGGGLRLDGSGEPPVGSGEAVKHESSDISVVRMPEGYGPSSVSSAVMVGS
GEVGGTNRGRSTDEINLKTPFVGQIPLTIPSREASLTQKLEIALGPVCPLLREIMVDFAPFLSKTLVGSHGQELLMEGKG
LTTFKNSHSVVELVMLLCSQEWQNSLQKHAGLAFIELINEGRLLSHAMKDHIVRVANEAEFILNRMRADDVLKHADFESQ
CAQTLVERREEERMCDHLITAARRRDNVIASRLLEKVRNIMGNRHGAWGDMNANYSRQIYWKLDAWEDDARRRKRLVQNP
RGSSHPQATLKASLVNGLGTAALAAVAASAATTASEEAGGDDSAGLASGNSRVALGRSSRDELYSQIAVPRSQQPDLLDD
SELLIEDRELDLDLTGPVNISTKAKLIAPGLVAPGTMSITSTEMYFEVDEENGEFQSIDAEVLKYCDHLHGKWYFSEIRA
IFSRRYLLQNVALEIFLASRTSILFAFPDQHTVKKVIKALPRVGVGIKYGIPQTRRASMMSPRQLMRNSNMTQKWQRREI
SNFEYLMFLNTIAGRTYNDLNQYPVFPWVLTNYESRELDLSQPSNYRDLSKPIGALNPSRREYFEERYETWDTPGIPPFH
YGTHYSTAAFALNWLIRIEPFTSMFLALQGGKFDHPDRLFSSVALSWKNCQRDTSDVKELIPEWYFLPEMFYNASEYRLG
QRDDGTLVGDVELPPWAKTPEEFVRLNRMALESEFVSCQLHQWIDLIFGYKQRGPEAMRATNVFYYLTYEGSVDLETIGD
LVTREAIENQIRNFGQTPSLLLMEPHPPRSSAMHLSPMMFNTMPDDVCMSLKFHLNSPIIHISANTYPQLPMPSVVTVTA
GHQFAVNRWNCQYTASIQSPSYAESAQNMNANLPLTMDPLLSQINGHNSSSNQQNRRHLGDNFSQKLQIKSNCYVTTVDS
RFLIACGFWDNSFRVFSTETAKIVQIIFGHFGVVTCLSRSECNITSDCYIASGSADCTILLWHWNARTQSIVGEGEIPTP
RATLTGHETAVTSVVISAELGLVVSGSISGPVLVHTTFGDLLRSLEAPKGFMSPENITLSREGFIVVNYDEGSVAAYTIN
GKLLRYESHNDNFQCMLLSRDGEYLMTAGNKGIVEVWRTFNLAPLYAFPACNSGIRSLALTHDQKYLLAGLATGSIIVFH
IDFNRWHHEYQQRY
```

1503 - 1522:	EEEEEEEEEEEEEEEEEEEE
1504 - 1523:	EEEEEEEEEEEEEEEEEEEE
1505 - 1524:	EEEEEEEEEEEEEEEEEEEE
1506 - 1525:	EEEEEEEEEEEEEEEEEEEE

A0A182FR73 **A0A182FR73_ANOAL** (365 aa)
Uncharacterized protein. *Anopheles albimanus (New world malaria mosquito)*

```
SEEEVVEETKEEQGDDPEFIKRQDQKRSDLDEQLKEYINEWRKQRAKEEDELKKLKDKQAKRKVSRAEEEQRMAQRKKEE
EERRVREIEEKKQREIDEKRKRLEEAEKKRQAMLQAMKDKDKKGPNFTITKKDSSFGMSNAQMERNKTKEQLEEEKKISL
SFRIKPLEVDGLSADALRARATELWETIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPP
KIQVASKYERRVDTRSYDDKKKLFEGGFDTLNKEVLEKNWAERKEQFGGRQKSKLPKWFGERPGKKSGDPETPEGEDEVK
PEDEEVEEVEEEVVEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

339 - 358:	EEEEEEEEEEEEEEEEEEEE
340 - 359:	EEEEEEEEEEEEEEEEEEEE
341 - 360:	EEEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEEE
344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE

A0A182GIW8 **A0A182GIW8_AEDAL** (375 aa)
Uncharacterized protein. *Aedes albopictus (Asian tiger mosquito) (Stegomyia albopicta)*

```
MSDDEEYSSEEEEVVEEQHEQGDDPEFIKRQDQKRSDLDEQLKEYINEWRKQRSKEEDELKRLKEKQAKRKVSRAEEEQR
MAQRKKEEEERRVREIEEKKQREIDEKRRRLEEAEKKRQAMLQAMKDKDKKGPNFTITKKDSSFGMSNAQMERNKTKEQL
EEEKKISLSFRIKPLEMDGLSADALRTKATELWETIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPE
ALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGFDTLNKESLEKQWSERKEQYVGRQKSKLPKWFGERPGKKAGDPET
PEGEDEVKPEDEEVEEVEEVVEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

346 - 365:	EEEEEEEEEEEEEEEEEEEE

347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE

A0A182GJG7 **A0A182GJG7_AEDAL** (842 aa)
Uncharacterized protein. *Aedes albopictus (Asian tiger mosquito) (Stegomyia albopicta)*

```
MPVNGSNRPPWLKDRLETVNKNVPPAWARKNPTTTGPGTDSKDSKSTSKAETSDSSKTAPIVKKPTTAATASAAAKENGE
PPKTSVKLQSREIKVPVVVKQKKPVQPPLTKPEPLIKNTTPQMTVLREPAKPKPKPKEPTPSDSEEEEEEEEEEEEEEEE
EEEEEGSTEYETETESEEESPPPPPVKKPQPKREPSPPKPKIPVQLKKVSKSPEKTDTESKSSKSEKSSSPEPKTFIKPP
LKKVIRPQQDEPQKERSKSPEPKGFRVQLRKVPSNLKAPRLKEKLPEVQLKRVEKPLLEEKPKKEEAYPHKPSMLKSESS
KRIPPPPPMPKSNIPPPPPPPPKLAPPSDFKKEEVSEKHKEMIEKLKKRPRRRPDWSDMMKEVEQGKKLRHVECNDRSKP
IVHCKSITKVKDQFIFETEKATAHNVLLKEIQSGVRLKPTKCNDRSKPILEGLRKFRRQMTLEEQLAKSESRANLEAPPP
EEDEVDEMDDIDRVRDDLQSTKQLLAMELRNNEALERENKRLLQRVQNLEAELSRERWNPLSGEEKSSIAGPDAELIHSL
KKEAVEAQQQSKQLEEKYQTVAKELDTATKQNEEQKRKIADLEKKLQSLTDDDFYLKEPQGITDIAPRRTAEAPNQKESS
PELEPEEEEEEEEEDEEKKAEKAAKRLNREVNMLSARLIRLKEKEEERHAERQALKYAMKTNQYALKNELKKYKKLQKEV
EKMAAMMKMEDEDEDGEEAKEPPPEEPEEEEEEEESEEESESESESESDNESANEAEDAPDEKKKANLEPRVKRHENRLA
SLKKGNYFLQANVDRIKDEINKTREMCCTLQSDLDSVIADLG
```

145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE

A0A182IAC4 **A0A182IAC4_ANOAR** (1199 aa)
NRF domain-containing protein. *Anopheles arabiensis (Mosquito)*

```
MVANRRLLLAGGLLCLLALLLVVGEADGFRLREHGQEEGLAVVKRKVAARGKGDAPWSAVTRKPWPVKDDDDEDDEDEEE
DDEEDEEEETEEQAAIRRATQQRLLRARHGLKSRDKRPAAASERRETVRGRGDAAAAAADNDDDDDEDEVAEAEPRSIFN
LFGLLGSRQRTDSDDERRTADGDVDDDDDDDDDGEKETRQHTKEKQRETVRPARKGQEPTDEASWLEGLKRALETVLKPAA
DDHAAKEEASDGGLLRWVQSFRADADRKEKDNPIINLLASWLASADGGADSQEEIRFRPAGSYADDGESDADDGNAPARQ
RGRPKTAPDSKLVQLLNHSPIASLFHPAELPAEPPVEAGPKRTKRSAADGPARVVKQRIAISPEDFEQLLLRVPSFVPDY
TRVRGAECRRQGEIFERQLRGKRLWALQMIDASARLASGLLRGNANQLGDFDLCTGIATRVRVREDELVRLRGKYCLAHV
DVVAEDAELRVPVHLLQGGGFVKSTLNDDAGSIVQHFVRPYNSTGIKLFLELEEANCHVRQVRTWSRLLKDHWQLVAVFG
FYTFVAVVTLVATLNDYEIFIKIEPPSAQDSPLDPPERRTTNAFHQTLMAFSLKQTLPQLFGAAGGASDDHLPCLDGLKA
LAGGALFLALRLVPLGYQPFTNRNEFTDSFNAPWSVAVRLLMLYADVFLVVSGFLAAYRMVREYRERARVSWFKRIAGRY
LRLVFPLVPVLMFYAWVWEHLGSGPQWGDVVTKNANLCKHGYLSNLLFMHNWYPIEETCAPHTFQLAIEMQLSVLAPFLL
VILVRSPFYGTAAYVLLSALSTAIRFASTTEDRLAPYVFHGVRLTQLYRTLNLSFAETLHRLTPYLAGFGLGYLLQEVGR
SRPERGVRYAGWLGAAVALLWCVCFPLDIVRKDFRYEPADAAQFAALAPLSWSVGLCWTIYYCLTEPASLLNRLLSSRPL
VCLGRLTYSLTLVQFLVFFYFAGTTRGTSVFSFAGYVNRTEVCIALGAALALTLLFDLPIQNVKRLLDQYGVFEGLEVRP
SVQPQQQPAEAAAEAEPVAEPELEKSEPPEAAASEGAAPEQADFVSPFDDQEEEDEGLWLRKRTAAPVEEPTAPEEDFWA
QSSEPEVQEEAAPKEIATEHESPSATNPPEQEEEPEQEEEEEEEEEEEEEEEEEEEEEIDEEKEVKRRPATNGASWSRL
```

1158 - 1177:	EEEEEEEEEEEEEEEEEEEE
1159 - 1178:	EEEEEEEEEEEEEEEEEEEE

A0A182J3N1 **A0A182J3N1_9DIPT** (374 aa)
Uncharacterized protein. *Anopheles atroparvus*

```
MSDDEEYSSEEEVVEETREEHRGDDPEFIKRQDQKRSDLDEQLKEYINEWRKQRAKEEDELKKLKDKQAKRKVSRAEEEQ
RMAQRKKEEEERRVREVEEKKQREIDEKRKRLEEAEKKRQAMLQAMKDKDKKGPNFTITKKDSNFGMSNAQMERNKTKEQ
LEEEKKISLSFRIKPLEVDGLSADSLRARATELWETIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDP
EALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGFDTLNKEVLEKNWSERKEQFGGRQKSKLPKWFGERPGKKSGDPE
TPDGEDEVKPEDEEIEEVEEVVEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE

A0A182JCP0 **A0A182JCP0_9DIPT** (190 aa)
Uncharacterized protein. *Anopheles atroparvus*

```
MLYFFDGPGGTGISFLLEVILAYTRRKTKIAFTEASTTKDPFSSCGGSSSLFIAMCFFLLLDRPAVFIEVTNVEEEEEEE
EEEEEEEEEEEEEEEEEEEDGEEEDGEEDGEEEDEEEDEEEDEVDDDVDRTSPEEEEEDGEEEDGEEEDGEEDGEEEDEE
EDEEEDEVDDDVDRTSPVAQEEAIASSLRL
```

74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE

A0A182M209 **A0A182M209_9DIPT** (336 aa)
Uncharacterized protein. *Anopheles culicifacies*

```
LDEQLKEYINEWRKQRAKEEDELKKLKDKQAKRKVSRAEEEQRMAQRKKEEEERRVREIEEKKQREIDEKRKRLEEAEKK
RQAMLQAMKDKDKKGPNFTITKKDSSFGMSNAQMERNKTKEQLEEEKKISLSFRIKPLEIDGLSADSLRARATELWETIV
KLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGFD
TLNKEVLEKQWAERKEQFGGRQKSKLPKWFGERPGKKSGEPETPEGEDEVKPEDEEVEEVEEEVVEEVVEEEEEEEEEEE
EEEEEEEEEEEEEEE
```

310 - 329:	EEEEEEEEEEEEEEEEEEEE
311 - 330:	EEEEEEEEEEEEEEEEEEEE
312 - 331:	EEEEEEEEEEEEEEEEEEEE
313 - 332:	EEEEEEEEEEEEEEEEEEEE
314 - 333:	EEEEEEEEEEEEEEEEEEEE
315 - 334:	EEEEEEEEEEEEEEEEEEEE
316 - 335:	EEEEEEEEEEEEEEEEEEEE
317 - 336:	EEEEEEEEEEEEEEEEEEEE

A0A182M919 **A0A182M919_9DIPT** (1241 aa)
NRF domain-containing protein. *Anopheles culicifacies*

```
MLRVRLVAAGLLCLLVVALVVGDADGFRLREHGQDEGLVLLRRRDVSRTRGNAPWSSVTRKPWSVRDDTDDEDEEEADEE
EDDEEDAEAEEQAAIRRATQERLLRARHGVKSRDKRHQPADSRRKVMDHDAADVDDDEQEDEAEPRSIFNLFGLLGTKQR
KGDDEVGAKSTTGDDDAGNDDDDDDDDDEDDDDDNLKNVRKPSANVNERRKQTKVTQARKSVKKEEPDQKQKTNDEDDAS
WLDELKRVFESVVQPTAGKEGEQSDPPEEGGFVRWLQSLTSRDGEVAPRDDEPKEKENPIINLLTGWLQSAEGGDSNEEI
RFRPIGSYADDDDDDDSNERSKRKKAPTKGPTDSKLVQLLNHSPIASLFSAEDLPAESPIDNGPKRPRQPAPGVRGPARV
VKQRIAISPEDFEQLLLRVPSFVPDYSQVQGAECRRQGEIFERQLRGKRLWALQMIDASARLASGLLRGNANQLGDFDLC
TGIATRVRVREDELVRLRGKYCLAHVDVVAEDAELRVPVHLLQGGGFVKSTLNDPDHFLPRFTTINWGICLPAACSFEDA
GSIVQHFVRPYNSTGIKLFLELEEANCHVRQVRTWSRLLKDHWQLVAVFGFYTFVAVVTLVATLNDYEIFIKIEPPSTQD
SPLDPPERRTTNIFHQTLMAFSLKKTLPQLVGSGTDEVHHLPCLHGLKALASGALFLALRLVPLGFQPFTNRNEFTESFN
APWSVAVRLLMLYADVFLVVSGFLAAYHMVREYRERARVPWFKRIAGRYLRLAFPLVPVLVFYAWVWEHLGSGPQWGDVV
TKNANLCKHGYLSNLLFMHNWYPIEETCAPHTFQLAIEMQLSVLAPFLMIVLVRSPFYGTAAYVLLSALSTAIRFASTTE
DRLTPYVFHGVRLTQLYRTLNLSFAETLHRLTPYLAGFGLGYLLQETGRPRQERGVQYAGWCGAAIALLWCVCFPLDIVR
KDFRYEPGDAAQFAALAPLSWSLGLCWIIYYCVTVPESLLNRVLSSRPLVGLGRLTYSLTLVQFLVFFYFAGSTRGSEVF
SFTGYVNRTEVCLALGASLILTLLFDLPIQNVKRLLDQTGVFDRLEVPPETPTASATEPTDTPTAPLDEKPVPESEPEPA
EEPTAEQTDFVSPFDDQDDEDGGLWLRKRTTDIANESSSTPDEDFWAEESKDTTVKDERPEKDADECAAPTVPAPEEEIE
EEEEEEEEEEEEEEEEEEEIDEEKEVKRRPTTNGPASWSRF
```

1200 - 1219:	EEEEEEEEEEEEEEEEEEEE

A0A182N4M7 **A0A182N4M7_9DIPT** (374 aa)
Uncharacterized protein. *Anopheles dirus*

```
RGDDPEFIKRQDQKRSDLDEQLKEYINEWRKQRAKEEDELKKLKEKQAKRKVSRAEEEQRMAQRKKEEEERRVREIEEKK
QREIDEKRKRLEEAEKKRQAMLQAMKDKDKKGPNFTITKKDSSFGMSNAQMERNKTKEQLEEEKKISLSFRIKPLEIDGL
SADTLRARATELWETIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQVASKYERRV
DTRSYDDKKKLFEGGYSAFYQEKLNKKWAQRQELFMARTKKVLEKQWSERKEQFGGRQKSKLPKWFGERPGKKSGEPETP
EGEDEVKPEDEEVEEVEEEVVEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE

351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE

A0A182PA23 **A0A182PA23_9DIPT** (375 aa)
Uncharacterized protein. *Anopheles epiroticus*

```
MSDDEEYSSEEEVVEETREEQGDDPEFIKRQDQKRSDLDEQLKEYINEWRKQRAKEEDELKKLKDKQAKRKVSRAEEEQR
MAQRKKEEEERRVREIEEKKQREIDEKRKRLEEAEKKRQAMLQAMKDKDKKGPNFTITKKDSSFGMSNAQMERNKTKEQL
EEEKKISLSFRIKPLEIDGLSADTLRARATELWETIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPE
ALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYSAYYQEKINKKWSQRQELFMARTKTKLPKWFGERPGKKSGEPET
PEGEDEVKPDDEEVEEVEEEVVEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE

A0A182QQN0 **A0A182QQN0_9DIPT** (3599 aa)
ANK_REP_REGION domain-containing protein. *Anopheles farauti*

```
MQNVEQSGVKNREKIVKSVNQQTSSKSQLQQQQHTIPSSSSLSSSCSSTSAEGEKATAFASASLGETAPGAPAKSSSSTS
LKPSKNNSSNSSTIGGGSSSVGSGVVGNSGNSEAISSGAAATAATTVDDVATGVVDVSAPVPSPASLSAALPAVKDVDGC
VGSGVGTSHQHPRRAEGEGSDSRHRVSSSRLTPSSGESAEDSADVSGVAGAEHIRPQVPGSDGSSRNNFQANNDKTMSST
KSSTTAAKPALPQPTGAAASTSGASGGGDGDGSKTAATGGTGSSCVGAPKQPTGGVSAVVRPNNNKLSSNNSSPAKSDTE
TFSEIQPRVSDSSESEEESVSEILLACLCLRPDLLVDSFPLDQQSIEIPETECSDSCENDVDMDESDSCDNDADDNDDSE
EDDEEEDDDDEDMGHSAAPRKFLLENDDDTDHERDEAAHALTRMKSSDGSPRDKNLLSRSLIAACTDNDVNTVRRLLGEG
NSLSEATEEGDSLLSLACSAGYYELAQVLLAMSAQVDDRGQKNDCTPLMEAASAGHVDIIELLFKHGADVNAQSSTGNTP
LMYACAGGHEKAVKLLLEHGAKVEDHNENGHTPLMEAASAGHVGVAKILLDHGAGINTHSNEFKESALTLACYKGHLDMV
RYLLEAGADQEHKTDEMHTALMEASMDGHVEVARLLLDSGAQVNMPTDSFESPLTLAACGGHVDLAMLLIDRGANIEEVN
DEGYTPLMEAAREGHEEMVALLLQQNAQINAQTEETQETALTLACCGGFIEVAEFLIKNGADIELGASTPLMEAAQEGHL
DLVRFLLQNGANVHAQTQTGDTALTYACENGHTEVADILLNYGAELEHESEGGRTPLMKACRAGHWCIVKFLIEHGADVN
RHTTNNDHTPLSLACTGGHQSVVELLLKNNADPFHRLKDSSTMLIEAAKGGHIGKAKIQFISDVKGPPSTLLPPMETYIN
IASPNMQAGKPIIDGNSNNGALFFASTLSGNLPQPQHLQLATIAANAASAAPASVIPSSEASVQMLQQSMANLNLQSQSP
VMASSTTTVQSVGTLLSGGKSSEVKTFGTVATAANEAKKSDVNDATDTKPSVSATGSVKSIPKPSANNSTVITSATAAKR
AVAATPAAATVAKDAAVDVVEAVSSNVKEKRQSSSSNSSSVVSGGVTDEEVAPAAAPAVPSGDSVTADGSDGASSSSSTS
DLEYPELSRILCSFSRSDILPAPEFVQVHQHMQNIIQHKGSSNPIKLGDASDGHQYAEEGEEHLSMFNIEESEGDGMAEC
VGGMYPSLDETLEPFHGEDGSVAQAHGSRESMYNYEWVDSIDDVIHVLNGCPDIPMALHDMAANFSCQDIDMYANLIGLN
SFCKTRWAGNQNQLTSGTSSPAEEDGSNAVALSDEQCAYRQGQAAASQLLTFDPQQFSMDQIQLLNQFHQASASGSAVLH
HPASGAGSDGQQPKLVFNVDADKASQTVGVGGKMGGGGGAGVTGGGGGKKGEKNRKEKNRLTVPPAVRQAPAGQQSGGQQ
LANYQYDTNGGRGAGSGGGSAVMDVPPPGSAAAGTVQPFHGAGGVIAQQAGSVVTERTIDVDSETDSNHDTALTLACAGG
HEDMVELLINRGANIEHKDKKGFTPLILAATAGHEKVVDTLLRSGAEIEAQSERTKDTPLSLACSGGRYEVVELLLSMNA
NREHRNVSDYTPLSLAASGGYVNIIKLLLQHGAEINSRTGSKLGISPLMLAAMNGHVAAVKLLLDMGSDINAQIETNRNT
ALTLACFQGRHEVVSLLLDRKANVEHRAKTGLTPLMEAASGGYIDVGRVLLDKGADVNAAPVPSSRDTALTIAADKGHLK
FVELLLSRGALVEVKNKKGNSPLWLAANGGHLGVVEMLCTAGGDIDSQDNRKVSCLMAAFRKGHTKVVKWMVGQVTQFPS
DQEMTRYINTISEQELLEKCHDCVKVIRAAKDQQATKANINASILLKELDLERSREESRKAAAAKRRERKKRRRAEKREQ
QRKLEMGEEGGEAGDGQDDEDEDEEADEDKEEEEEEEEEEEEEEEEEEEEEADSEHDEDELLLSAAMIQQSSAAGNKHKN
RNVNNAQLHSNSKSQQQNHREKERESRRLQEKEHLQQQCAGRDNGKREKTLEKENVAPRDHDGRTGASAGGATKNESKKS
SSASGNNDHHHHQNGPQQTGATHQHQQQQQHQSNAAGNRKSIIVFGSGNRHAADQNDDQQNFYHAGGALGSGTGGKKTHS
QKTFYNTTTNNDDHHHGGGHHGKMASSASPMKQHQQAGLQQHNGSQPNAMGGGAKREEGWKEVVRKSSVQQGGGGGGGGG
SSSSPMECRKVQVPVHAISRVIGRAGSNINAIRAATGAHIEVEKQGKSQGDRSITIKGSQEATKQAHSLIVTLIKDPDVD
ILLMLPKHNTTAGSSSQKTYGSSSANSGGGSGSSSTAGQSSGGGSSSGTGTVPAQPPAIISSNASAARPPAAKNLFLSSS
NSSTQQHQQTSSRVMTAGSSNNGVVPNSVPYAVAASSSASQVKDSKRQPAASGGIQQQQQQTIGTKGGSQHHHPGLATSG
PSGAGGNSTATPPFGSVGMKPKNTSNVNKPTPQNTANASVPLNSGINGGGVGNTSSGTTGAPAATPAAPMAGSFAKLVAS
DNHQKKSSPSVGPIGVASGQQQQQQQSGTGVTTGRGGPTPMQVQQSPAKSGGAGPPGGLPVPFAGGSSNSAAQSTAAPGP
IGSHIISSNSHPQTSATATASVGGGGSGNTGQQQKISSFIPPIATTGPGPTIVEASAIPPLPPISVPNTANPLAAPGSGR
SITPIGQPPSSASSAASTSAVSSITTISTASSSSGSVTGPIGSRAVTTPSPLLHQQQTSGSSITSATVGGQLHAKMQAIG
QQQHHQQLAPSPPPSNVYSLFNDPGVGGAGTSGVLGPFMENPPTLQVDASKAPGYRGNTISSPVSSKASSNATTPPSSSM
SSHQHQQPPPLHQALQHQANGGQHGGPMHHPPHTLQQQHPSLGLAHMLSAGSSSSTSPLSGLGGQQPPPTVVSRDSGVIN
IVSGGGGHSVSSASASVPTSTVAGGPHQQQQPTSYQSSNDSSNVGMKPNAPPPSMLGGGGAAGSNNQGGGLGMLRSMMNL
TSHMRPPVGGNGPPDFLGGSSGGGGGRDHASGMVPQPQPPVGSSRPPPPLMFDNVGSLGSGGPPDALQSSYQQHLGGLGG
SGNAGLPPISRLNPKASAFAGGIGPSIMPPSQQHQPGKMNLSNNHPPYGGGNSVGAGAGMFHTPPPIGLGSGGGGSGGGG
GGTSGKYTSMSSYSLAPGRPNNQQQHGGSGAGGPPPPVGTIHHRGGVGSGGGSSGGNNWYSSDLSHLQRDNLMGMENGLA
MALNAASPTISPNNNNAQQQHAINGGLMTPHQQQSQQQSMMDDARKQLPRAIGTERAWKFGGNGNVGPIGSGGGGVGASG
ANNTSSGGNMYNAAMVSAYVGLDGADLMNGSGASPAALAAAAAAASGNQPWMNIDKNQFMAGSGGGGVGGGSQQQHQQQP
PLPWLTMGRQYMDDIHLPDHFQQLQMDYHGNIGGSGPNQPNMNFMQYPFTPSNDMVGTGDLRPPWEHEKQGWSQKWSGH
```

2031 - 2050:	EEEEEEEEEEEEEEEEEEEE
2032 - 2051:	EEEEEEEEEEEEEEEEEEEE

A0A182QYZ0 **A0A182QYZ0_9DIPT** (375 aa)
Uncharacterized protein. *Anopheles farauti*

```
MSDDEEYSSEEEVVEETREEQGDDPEFIKRQDQKRSDLDEQLKEYINEWRKQRAKEEDELKKLKEKQAKRKVSRAEEEQR
MAQRKKEEEERRVREVEEKKQREIDEKRKRLEEAEKKRQAMLQAMKDKDKKGPNFTITKKDSSFGMSNAQMERNKTKEQL
EEEKKISLSFRIKPLEIDGLSADTLRARATELWETIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPE
ALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGFDTLNKEVLEKQWSERKEQFGGRQKSKLPKWFGERPGKKSGEPET
PEGEDEVKPDDEEVEEVEEEVVEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE

A0A182RCW0 **A0A182RCW0_ANOFN** (367 aa)
Uncharacterized protein. *Anopheles funestus (African malaria mosquito)*

```
MSDDEEYSPAAKSEGDDPEFIKRQDQKRSDLDEQLKEYINEWRKQRAKEEDELKKLKDKQAKRKVSRAEEEQRMAQRKKE
EEERRVREIEEKKQREIDEKRKRLEEAEKKRQAMLQAMKDKDKKGPNFTITKKDSSFGMSNAQMERNKTKEQLEEEKKIS
LSFRIKPLEIDGLSADTLRARATELWETIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYP
PKIQVASKYERRVDTRSYDDKKKLFEGGFDTLNKEVLEKNWAERKEQFGGRQKSKLPKWFGERPGKKSGEPETPEGEDEV
KPEDEEVEEVEEEVVEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

340 - 359:	EEEEEEEEEEEEEEEEEEEE
341 - 360:	EEEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEEE
344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE

A0A182U8M5 **A0A182U8M5_9DIPT** (366 aa)
Uncharacterized protein. *Anopheles melas*

```
SEEEVVEETREEQGDDPEFIKRQDQKRSDLDEQLKEYINEWRKQRAKEEDELKKLKDKQAKRKVSRAEEEQRMAQRKKEE
EERRVREVEEKKQREIDEKRKRLEEAEKKRQAMLQAMKDKDKKGPNFTITKKDSSFGMSNAQMERNKTKEQLEEEKKISL
SFRIKPLEVDGLSADSLRARATELWETIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPP
KIQVASKYERRVDTRSYDDKKKLFEGGFDTLNKEVLEKQWAERKEQFGGRQKSKLPKWFGERPGKKSGDPETPEGEDEVK
PDDEEIEEVEEVVEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

338 - 357:	EEEEEEEEEEEEEEEEEEEE
339 - 358:	EEEEEEEEEEEEEEEEEEEE
340 - 359:	EEEEEEEEEEEEEEEEEEEE
341 - 360:	EEEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEEE
344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE

A0A182VD87 **A0A182VD87_ANOME** (971 aa)
Nucleolar complex protein 2 homolog. *Anopheles merus (Mosquito)*

```
MKIKQSKKKEDFQNMSLDNFLDNMDADVGDDEPEAKPKSKLKSNGIEKAKYKQDAKDDKKKVKSVGKVKKVAASTAEPEE
EVNGAEEKKSRKTKKVKSADAEQNEAMNGKVKKRKNLNSEAQRPELTGKEKKKKRKLAEPEEADGSDHDTAGSNANSVLK
```

KKTKKVKKVAEQAEMNGNKKKAKTESQPVQLNGKESKKTKGKQAAAEKSDKELTKSSMKQVEKEHKEALARLETTDPELF
AFLKKNDEKLLKFGQLGGSDSEFSDSENEAEDEEGAVHELPDKLDVASDESDFDPNEDEDEQGPGEGDDEDEDGEEEEKA
ADDDDGTPGKRVTFKMLKAWTNDLTTLPVKHVHGIRNICKAFNSALYTVTGDKSVIPPYRVEGSAMFNGIVQTCVLYLGP
ALRSYLALTEKRQFKDLKNDFRFKKVRASIKTYLIDLTNLLENVSSSHIMSVLLKHLHEFSSILICYQNLTKPILKRLIG
IWSTAEEETIRVLAFMCILKITHAQQSFFLSNVLKVMYLAYVKNSKFVSPNTLPNINFMRRSLAEMFLLNFNVSYQHMFL
YIRQLAIHLRNAVILQKKESLQYVYNWQYINSLKLWGDVLGSAHAHGGALEPLIYPFVSITIGVMKLIPSAQYFPLRFHC
CRTLIQLNAKTNIYIPVLPFLVEVLRSHSFNEDHKKLSMRPVNLTCLLRFSPANIQENAFKDAVIDQIYELVLEFAANES
ASIGFPEIVLPIILQLRQYAKTTKQYKYSRKMKQLSDKLMENYEFMEKRRRKMDIPLKETDRIRAWEELVRAEGTPLAKF
YATIAKETEAVKRRHATDSEKISDYKLPTLKKVVKKTPTKKDGPVTLFPSDDEDEDDDDDDEDGLEDMEDDTDGDESMSD
MEEGSDDEEMMGSDDDEDDDEEEEEEEEEEEEEEEEEEEEEVVPKKSNKKKLVKEQKKPNKKIVENYPLEDGTDADQVDI
LKDLKLDDWDD

901 - 920:	EEEEEEEEEEEEEEEEEEEE
902 - 921:	EEEEEEEEEEEEEEEEEEEE

A0A182VGS4 **A0A182VGS4_ANOME** (1215 aa)
NRF domain-containing protein. *Anopheles merus (Mosquito)*

MVANRRLLLAGGLLCLFALLLVVGEADGFRLREHGQEEGLAVVKRKVAGRGKGDAPWSAVTRKPWPVKDDDDEDEEDEED
EEDEEETEEQAAIRRATQQRLLRARHGLKSRDKRPAASERRETVRGRGDAAAAAAADNDDDDDEDEVAEAEPRSIFNLFG
LLGSRQRTGSEDERRTADGDDDDDDDEKETRQHPKEKQRETVRTARKGQEPTDEASWLEGLKRALETVLKPAADGHAAQE
EASDGGLLRWVQSFRADAARKEQDNPIINLLASWLASADGGADSQEEIRFRPIGSYADDGEADADDGHTRPKQRGRPRTA
PDSKLVQLLNHSPIAALFHPAELPAEPPVEAGPKRTKRSAADGPARVVKQRIAISPEDFEQLLLRVPSFVPDYTRVRGAE
CRRQGEIFERQLRGKRLWALQMIDASARLASGLLRGNANQLGDFDLCTGIATRVRVREDELVRLRGKYCLAHVDVVAEDA
ELRVPVHLLQGGGFVKSTLNDPDHFLPRFTTINWGICLPAACSFEDAGSIVQHFVRPYNSTGIKLFLELEEANCHVRQVR
TWSRLLKDHWQLVAVFGFYTFVAVVTLVATLNDYEIFIKIEPPSAQDSPLDPPERRTTNAFHQTLMAFSLKQTLPQLFGA
AGGASDDHLPCLDGLKALAGAALFLALRLVPLGYQPFTNRNEFTDSFNAPWSVAVRLLMLYADVFLVVSGFLAAYRMVRE
YRERARVSWFKRIAGRYLRLVFPLVPVLMFYAWVWEHLGSGPQWGDVVTKNANLCKHGYLSNLLFMHNWYPIEETCAPHT
FQLAIEMQLSVLAPFLLVILVRSPFYGTAAYVLLSALSTAIRFAATTEDRLAPYVFHGVRLTQLYRTLNLSCAETLHRLT
PYLAGFGLGYLLQEVGRSRPERGVRYAGWLGAAVALLWCVCFPLDIVRKDFRYEPADAAQFAALAPLSWSVGLCWTIYYC
LAEPASLLNRLLSSRPLVCLGRLTYSLTLVQFLVFFYFAGTTRGTSVFSFAGYVNRAEVCIALGAALALTLLFDLPIQNV
KRLLDQYGVFEGLEVRPPVQPQQQPEPAVEDEPVAEAEPEKSEPTEGAASEGAAPEQADFVSPFDDQEEEDEGLWLRKRA
AAPVEQPTAPEEDFWAQSSEPEVQQEAAPKESVAEPESPLATNPPDQEEEPEQEEEEEEEEEEEEEEEEEEEEIDEEKE
VKRRPATNGASWSRL

1174 - 1193:	EEEEEEEEEEEEEEEEEEEE
1175 - 1194:	EEEEEEEEEEEEEEEEEEEE

A0A182VN10 **A0A182VN10_ANOME** (367 aa)
Uncharacterized protein. *Anopheles merus (Mosquito)*

MSDDEEYSSEEEVVEETREEQGDDPEFIKRQDQKRSDLDEQLKEYINEWRKQRAKEEDELKKLKDKQAKRKVSRAEEEQR
MAQRKKEEEERRVREVEEKKQREIDEKRKRLEEAEKKRQAMLQAMKDKDKKGPNFTITKKDSSFGMSNAQMERNKTKEQL
EEEKKISLSFRIKPLEVDGLSADSLRARATELWETIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPE
ALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYSAYYQEKINKKWAQRQELFMARTKTKLPKWFGERPGKKSGEPET
PEGEDEVKPDDEEIEEVEEVVEEVEEEEEEEEEEEEEEEEEEEEEE

345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE

A0A182VQ91 **A0A182VQ91_9DIPT** (404 aa)
Uncharacterized protein. *Anopheles minimus*

MSDDEEYSSEEEVVEETREEQKGDDPEFIKRQDQKRSDLDEQLKEYINEWRKQRAKEEDELKKLKEKQAKRKVSRAEEEQ
RMAQRKKEEEERRVREIEEKKQREIDEKRKRLEEAEKKRQAMLQAMKDKDKKGPNFTITKKDSAFGMSNAQMERNKTKEQ
LEEEKKISLSFRIKPLEIDGLSADTLRARATELWETIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDP
EALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYSAYYQEKINKKWAQRQELFMARTKSKLTGFDTLNKEVLEKQWA
ERKEQFGGRQKSKLPKWFGERPGKKSGEPETPEGEDEVKPEDEEVEEVEEEVVEEVVEEEEEEEEEEEEEEEEEEEEEE
EEEE

378 - 397:	EEEEEEEEEEEEEEEEEEEE
379 - 398:	EEEEEEEEEEEEEEEEEEEE
380 - 399:	EEEEEEEEEEEEEEEEEEEE
381 - 400:	EEEEEEEEEEEEEEEEEEEE
382 - 401:	EEEEEEEEEEEEEEEEEEEE
383 - 402:	EEEEEEEEEEEEEEEEEEEE
384 - 403:	EEEEEEEEEEEEEEEEEEEE
385 - 404:	EEEEEEEEEEEEEEEEEEEE

A0A182VW13 **A0A182VW13_9DIPT** (856 aa)
Uncharacterized protein. *Anopheles minimus*

```
MPVNSRPPWLKDRLETVNKAVPPAWTRKASVTPATDTKESSPSTKANATEGSPTGSTKTTTPAATTVKKAVNSPAKENGD
TTAKATTTAKLQSKEIKVPVVVAQKKPANPPLSKPEPSVGLKNTTPVMTVHREVAKPKPKPTAKEPTPESDEEEEEEEEE
EEEEEEEEEEEGSTEYETETESEEEPPSKPAIKKPEPSQQKRQDADASQPPKLPVQLRKVTPTKSPEKSDTESKSSSKSE
KSSSPEPKVFVRPPLKKVVRPQQDPPPKERSVSPEPAKNFRVQLRKVPSNLKAPRVKEKLPEVQLKKVEKPLLEDIPKKE
EAYPHKPSMLKSESSKRIPPPPPMPKSNIPPPPPPPPSLKPPPDFEKKEISSKQKEVIDKLKRRPRRRPDWSDMMKEVEQ
GRKLKHVECNDRSHPIINSKSITKVKDQFIFETEKATAHNQLLKQIQGGVQLKPTKCNDRSKPILGGLRKFRRQMTLEEQ
LAKSESRANMEAPPADEEEDELDDIDKVRDDLQSTKQMLAHELRNNEAMERENKRLQARVQNLEAELSRERWNPLSGEER
TTVTGPQSDLIQSLKDEALTAQKQSKQLEEKYQTVAKELDTAYKQVDEQKRKIADLERKLQCLTDDDFYLNEQQGITDDR
RATESAQKESSPELQPEEEEEEEEEEDEEKKAEKIAKRLNREVNMLQARLTRLKEKQEEKHAERQALKYAMKTNQYALKA
EKKKYKKLQKEVEKMAAMMKLEDDDDESAEAKEPPPEEPEDEQEPEEEEEEESESEESESESENESENEAEDAPDDKKKA
NLEPRVKRHEGRLASLKKGNYLLQANVDRIKDEISKVREECCTLQTDLDNVIADLG
```

152 - 171:	EEEEEEEEEEEEEEEEEEEE

A0A182W4K5 **A0A182W4K5_9DIPT** (1245 aa)
NRF domain-containing protein. *Anopheles minimus*

```
MLFRVRLVAAGLLCLLVVALYVGEADGFRLREHGQEEGLAMVKRRVITRTKGDVPWTSVTRKPWSVRDDTDDDDEEEADD
EDEEQDDDDDEEDAETEEQAAIRRATQERLLRARRGVRSRDKRHQPAESRRKATDHDAADVDDDEQDDEAEPRSIFNLFG
LLGTKQQKGDDEGSAKSTAGVDDAGNDDDDNDEDDDEDEDDDNEKNVRKPSAKVHERRKQIKVVQTRKSVKKEEPEQKQV
AEEDDASWLDGLKRVFESVVQPTADKEAEQSDAPVEGGFVRWLQSLTSRDDDVPPRADEPKEKENLIINMLTGWLQSAEG
GDSNEEIRFRPIGSYADDDDDDDSNERGKRKKPPTKGGTDSKLVQLLNHSPIASLFSAEELPAESPIDNGPKRPRQPAPG
VRGPARVVKQRIAISPEDFEQLLLRVPSFVPDYSQVQGAECRRQGEIFERQLRGKRLWALQMIDASARFASGLLRGNANQ
LGDFDLCTGIATRVRVREDELVRLRGKYCLAHVDVVAEDAELRLPVHLLQGGGFVKSTLNDPDHFLPRFTTINWGICLPA
ACSFEDAGSIVQHFVRPYNSTGIKLFLELEEANCHVRQVRSWSRLLKDHWQLVAVFGFYTFVAVVTLVATLNDYEIFIKI
EPPSTQDSPLDPPERRTTNVFHQTLMAFSLKKTLPQLVGAGTDELHHLPCLHGLKALASGALFLALRLVPLGFQPFTNRN
EFTESFNAPWSVAVRLLMLYADVFLVVSGFLAAYHMVREYRERARVPWFKRIAGRYLRLAFPLVPVLVFYAWVWEHLGSG
PQWGDVVTKNANLCKHGYLSNLLFMHNWYPIEETCAPHTFQLAIEMQLSVLAPFLMIVLVRSPFYGTSAYVLLSALSTAI
RFASTTEDRLTPYVFHGVRLTQLYRTLNLSFAETLHRLTPYLAGFGLGYLLQETGRPRQERGVQYAGWCGAAIALLWCVC
FPLDIVRKDFRYEPGDAAQFAALAPLSWSLGLCWIIYYCVTEQESLLNRVLSSRPLVGLGRLTYSLTLVQFLVFFYFAGS
TRGSEVFSFTGYVNRTEVCLALGASLLLTLLFDLPIQNVKRLFDQTGVFDRLEVPPETPASVTEPTDTPTVLDEKPAPVS
EPEPEPEEPAVEQSDFVSPFDDQDEEDSGIWLRKRTTDVANESSSTVEDFWAEESKDTNVKDERPENSDESAAPAEPVPE
DEIEEEEEEEEEEEEEEEEEEEEIDEEKEVKRRPTTNGPANWSRF
```

1204 - 1223:	EEEEEEEEEEEEEEEEEEEE

A0A182XID3 **A0A182XID3_ANOQN** (353 aa)
Uncharacterized protein. *Anopheles quadriannulatus (Mosquito)*

```
GDDPEFIKRQDQKRSDLDEQLKEYINEWRKQRAKEEDELKKLKDKQAKRKVSRAEEEQRMAQRKKEEEERRVREVEEKKQ
REIDEKRKRLEEAEKKRQAMLQAMKDKDKKGPNFTITKKDSSFGMSNAQMERNKTKEQLEEEKKISLSFRIKPLEVDGLS
ADSLRARATELWETIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQVASKYERRVD
TRSYDDKKKLFEGGYSAYYQEKINKKWAQRQELFMARTKTKLPKWFGERPGKKSGEPETPEGEDEVKPDDEEIEEVEEVV
EEVVEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

325 - 344:	EEEEEEEEEEEEEEEEEEEE
326 - 345:	EEEEEEEEEEEEEEEEEEEE
327 - 346:	EEEEEEEEEEEEEEEEEEEE
328 - 347:	EEEEEEEEEEEEEEEEEEEE
329 - 348:	EEEEEEEEEEEEEEEEEEEE
330 - 349:	EEEEEEEEEEEEEEEEEEEE
331 - 350:	EEEEEEEEEEEEEEEEEEEE
332 - 351:	EEEEEEEEEEEEEEEEEEEE
333 - 352:	EEEEEEEEEEEEEEEEEEEE
334 - 353:	EEEEEEEEEEEEEEEEEEEE

A0A182Y7A2 **A0A182Y7A2_ANOST** (453 aa)
Uncharacterized protein. *Anopheles stephensi (Indo-Pakistan malaria mosquito)*

```
MTALLLLLLWITVRAITSAGRDPPYTYAPRKLHHKPSVSGVLFFLFSFFCGLTGSVLLSLAYALVPCDNRGDDPEFIKRQ
DQKRSDLDEQLKEYINEWRKQRAKEEDELKKLKEKQAKRKVSRAEEEQRMAQRKKEEEERRVREIEEKKQREIDEKRKRL
EEAEKKRQAMLQAMKDKDKKGPNFTITKKDSSFGMSNAQMERNKTKEQLEEEKKISLSFRIKPLEIDGLSADSLRARATE
LWETIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKL
FEGGYSAYYQEKINKKWAQRQELFMARTKSKLSGFDTLNKEVLEKQWAERKEQFGGRQKSKLPKWFGERPGKKSGEPETP
EGEDEVKPEDEEVEEVEEEVVEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

426 - 445:	EEEEEEEEEEEEEEEEEEEE
427 - 446:	EEEEEEEEEEEEEEEEEEEE
428 - 447:	EEEEEEEEEEEEEEEEEEEE
429 - 448:	EEEEEEEEEEEEEEEEEEEE
430 - 449:	EEEEEEEEEEEEEEEEEEEE
431 - 450:	EEEEEEEEEEEEEEEEEEEE

432 - 451:	EEEEEEEEEEEEEEEEEEEE
433 - 452:	EEEEEEEEEEEEEEEEEEEE
434 - 453:	EEEEEEEEEEEEEEEEEEEE

A0A182YHW6 **A0A182YHW6_ANOST** (835 aa)
Uncharacterized protein. *Anopheles stephensi (Indo-Pakistan malaria mosquito)*

```
MPVNSRPPWLKDRLETVNKSVPPAWTRKASVTPATDTKESSPSNKSNATEAAPTASTKPTAPASTTGVKKTAVSTPAKEN
GETGAKATTTAKLQSKEIKVPVVVAQKKPANPPLTKPEPTVGLKNTTPVMTVHREPPTPEPSDDEEEEEEEEEEEEEEEE
EEEEGSTEYETETESEEEPPAKPVLKKPEPVKRQEADTSSKLPAVQLRKVTPTKSPEKSDTESKSSSKSLSEKSSSPEPK
PFIRPPLKKVVRPPQDTPPKERSVSPEPAKNFRVQLRKVPSNLKAPRVKEKLPEVQLKKVEKPLLEDIPKKEEAYPHKPS
MLKSESSKRIPPPPPMPKSNIPPPPPPPPSLKPPPDFEKKEISDKQKEVLDKLKRRPRRRPDWSDMMKEVEKGRKLKHVE
CNDRSHPIINSKSITKVKDQFIFETEKATAHNQLLKQIQGGVQLKPTKCNDRSKPILEGLRKFRRQMTLEEQLAKSESRA
NLEAPPAEEEELDELDDIDKVRDDLQSTKQMLAHELRNNEALERENKRLQARVQNLEAELSRERWNPLSGEERTTVTGPQ
SDLIQSLKDEALEAQKQSKQLEDKYQTVAKELDTAYKQVDEQKRKIAELERKLQGITDDRKATESAQKESSPELQPEEEE
EEEEEEDEEKKAEKMAKRLNREVNMLQARLTRLKEKQEEKHAERQALKYAMKTNQYALKAERKKYKKLQKEVEKMAAMMK
LEDDDDDTAEAKEPPPEEPEDEQEEEEEEEESESEESESESENESENEAEDAPDDKKKVNLEPRVKRHEARLASLKKGNY
LLQANVDRIKDEISKVREECCTLQTDLDNVIADLG
```

145 - 164:	EEEEEEEEEEEEEEEEEEEE

A0A183B6M4 **A0A183B6M4_9TREM** (484 aa)
CW-type domain-containing protein. *Echinostoma caproni*

```
LRQIRRLRTTAAELRNLVTVRQNAVARKQKSIRDPKTLTFYFGVNVMNRACDGMFVYNCSRLIKMYQRIGPQQDSSMMCR
GVVGIVDVPYMVLEPTHNKQDFADAKEYRQLMRAMADHLMQYWDDLGIDKEAEDLVRFWKSFGYLSARWRDPPSGEDKYA
RRRCCSVSICVQCDKCLKWRVLPFSQSLVGRDVPDTWQCRDNPDHKHKRCEDPEEDLSPPMGVLKRKIKTKEQRQAELEK
QIRKKQLELIQDPDDENDARSGGNTRSSRSLTGSFAKPAVQVSSPRKRPPAVSPGSTLPTKRPTHPVTPPSRAMTVAEKK
RQITNSNGCASTQKRTGLPLPTTNQRQPPSGGLVPKVQREAPAKNRRVVVMDEEEEEEEEEEEEEEEEEEEEEKVEKMAR
KNASRAKPSDKTKPTKAPPSTAVETTSEPKTLVSHLGIFPSNYDMHATRHEITIVQTNFGYLRGFAIGTEYKYYMSGLIY
LHPS
```

373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE

A0A183BPW9 **A0A183BPW9_GLOPA** (1915 aa)
Uncharacterized protein. *Globodera pallida (Potato cyst nematode)*

```
MDNVAIQIESIATGQVPSSTGKECGDVDVELGIGREQKDSDGIPLQKIGTHSLSTERLIPPGDADGTSARREEDEALSSK
ASLSRPPWHRGVLSSFAQIGSFVSTTKVFWVVVVYTIFGAYLFMWLEVQKDLEEKRKAYEYHLVVRDALLFKIEQINKES
FLEKSQHWKRAILEFEEHSGFQPPQRDTSWTLIATEQVPSLTGKECGDVDVELGIGREQKYRDGIPLQKIGTHSVSTERL
IPPGDADGTSARREEDEALSSKASLSRPPWHRSVLSSFAQIGSFVSTTKVFWVVVVYTIFGAYLFMWLEVQKDLEEKRKA
YEYHLVVRDALLFKIEQINKESFLEKSQHWKRAILEFEEHSGFQPPQRDTSWTLWMSILYCATIYTTVGYGNIACATTGG
RVATIVYAICGIPLMIVVLDQLGTFLLRKMKELSNFVDDLLFFLGVKYRLIRLEDQEAFVRYIAICRILARLRLIPSTIT
LSITEEDIDHFNTAKSPSSASGASTSSRSSSPDSRASSVIKICKPSSNSAAIHFRERVSLRLAISRGSVLQNIGPFYVES
IDAESADNLLVELDKQLLLPPTTVKETSKCQKQSLRRASKTSVTTVHIKLEEADKILNITPKSGEISRKSSAVVSVHSET
VPNETPQLGKAGRSPPLLIALAVTTAWIAFAAAVFCLWEEWSYFTSIYFFFISMSTIGFGDVTPQHPQYMIMTFFVVVVG
LSLVSVCINVVQEKLNISRKNQGIRIMNKFKEEAKAMGVELPEVMTELNEETGKPAFCRIFDEKSDQKVNQFLEQAQHQG
KMRRNAHTQTKMPLPKTHKFFISRAEADKEEFEVQTEMEMDPKTEKGTQTATSECSDSGIQCSPIMSDEWTECIEEIGPE
LFDRWTSTQTQAVTTRNTGVQPEVSCIMRIIDEDESDFPLSSDYGDEEECAAALSSSGLSRLGSPADALSSQQSQLLSGS
SREGELERRLSVGSKRSAQMKRVPEIELDDEGFVVGGPYRAISRPAGPETFSCHGFAPPLSPPPLVTIRMASKALTEEEI
GETMKPEAGRAKKKRKMRAGLRYMKNAAVQVESVKNMEQLRDFACQFGHESGKALLAEEITDERMERKSTQNDQKIMLQD
KWAQCNILTLLQNVGQNVGTQTDLDRGETLSTAEENGISTSPIGQLRPVADIFETADNWRSSFGVQTEFPCCRCKRTQTD
RPLLVSRPVQTQLSSTFRRSYRDGEGPRGEGKAGEESEAQIETHFESEREEEMKRVFGLESEDIDQLRERVREVKRKRR
EERQRRKRQQAQGGRRGDGEARGDTEGMSGGNGGSLRAITSSEEDEQMEEEEKAMLIEEIRRIKKRRRLAKEQRLEAEEG
EEEEEEEEEEKEEEEEEEEEEEEEEEEEEEEEEEEKEEIRAFPGQKRKRMLQSRKGRGENERVEEFTLQINQPAERGHIIR
ANYEETILDIQLIRSPFFETRYLPQSKEQLIFDEVELKARESIKPKEKDEKAEIEKLLGKLNRLEALSAKEEELEQLESI
RREIGQMSREEEEKIFQFTAESSAQTVEDGQMSEMVTFCKNNPDVAVNDLSDMLKNIDEFKQFKERRAKTWPIAATSAAP
IDLSQIVLVQTQAETVEFRKIQKRSASAGAGEETETEPDTCPLEPNELAKLRELFPGLMEGFSGKEMGKPMEKQQSQRQF
ISSYAPSSSTQFGSPKESNKRRKEWKQQQKHVTMMSRTEGGRVESARGSGADGREDKIRLVSLVSILKGDDEETIVPSTG
IQPWPIPPGPPRFGQTQLHYIRQWIEHLLELDRDQKQPQSLYDVPLRSISEFLRERRRELDELEKQKQQLERLAELASRE
ESAERMAGVHSRVVPILGARDGREGILPSEEFNYLTNPMYPIVRIPLELTGRGREDIDGEKEQDEQGEGQKDNGQ
```

1372 - 1391:	EEEEEEEEEEEEEEEEEEEE
1373 - 1392:	EEEEEEEEEEEEEEEEEEEE
1374 - 1393:	EEEEEEEEEEEEEEEEEEEE
1375 - 1394:	EEEEEEEEEEEEEEEEEEEE

A0A183CKA2 **A0A183CKA2_GLOPA** (90 aa)
Uncharacterized protein. *Globodera pallida (Potato cyst nematode)*

```
MFMHLLDVKETADDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEEEEGGIFLAEESTVVTNKLSERQTLDEEWEEVEKRG
GRDGTDQRFR
```

15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE

17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE

A0A183G1Z2 **A0A183G1Z2_HELPZ** (67 aa)
Uncharacterized protein. *Heligmosomoides polygyrus (Parasitic roundworm)*

```
LRTPPRSGTNADEEEGEEEEEEEEEEEEEEEEEEEEEEEEEDMITHVFYRFVLSRYNSTPLFFALYNA
```

17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE

A0A183GT19 **A0A183GT19_HELPZ** (133 aa)
Uncharacterized protein. *Heligmosomoides polygyrus (Parasitic roundworm)*

```
MREARLRRYGHVLRAKDDTVRKTGLNLDVLGKRVPQLGGTNAEEEEEIEGEGEEEEKEEEEGEEEEEEEEEEEEEEEEGE
DEEEEEEEEEEEEEEEEEEEEEVEEEEDDDEEEEDEEEEEEEEEEEDVEQEE
```

82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE

A0A183GTQ6 **A0A183GTQ6_HELPZ** (37 aa)
Uncharacterized protein. *Heligmosomoides polygyrus (Parasitic roundworm)*

```
LRLRGTKRTGEEEEEEEEEEEEEEEEEEEEEEEYVSCH
```

11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE

A0A183IJG2 **A0A183IJG2_9BILA** (156 aa)
Uncharacterized protein. *Soboliphyme baturini*

```
MTLLALGCNPSSGADQELNPNLFRLKLTTSFRLLRRAAAHGAYDARLQTDADDSDEIDRKEEEEDDDDEKEEEEEEEEEE
EEEEEEEEEEAEEXXXXXEEEEEEEGHWVSLKYRFKLTESNFCGWGRAGHISSSKMHQNSVYDFRCNGWPKSCGSP
```

71 - 90:	EEEEEEEEEEEEEEEEEEEE

A0A183IMR4 **A0A183IMR4_9BILA** (231 aa)
SCP domain-containing protein. *Soboliphyme baturini*

```
MYALWWMLMIPVVAAKLEDLIVLHNFNQEIVDAIVRKHNDLRAMVANGTIEPKQPTAKRMNEVRKQEEEEEEEEEEEEEE
EEEEEEEXXXXXXXXRSPTFRTASKSGLQQGCRTRCKGAGAEVCVYRHEGPSDKLGYWWIGQNIWAGTYGIKDPLPNDRV
KAMMESAIGRWFNEIKNFKYPKCDEGKVCGHYTQVVAEDTDYIGCALAQCRDLEPIKWKNAFFVVCNYAPG
```

67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE

A0A183JS53 **A0A183JS53_9TREM** (79 aa)
Uncharacterized protein. *Schistosoma curassoni*

```
MAVTSTSDSRDSAGILSDPAAIPPLIIQHGEDVDMKLNGLEVGEDEDEDEDEEEEEEEEEEEEEEEEEEEEDKHTKTQ
```

52 - 71:	EEEEEEEEEEEEEEEEEEEE

53 - 72:	EEEEEEEEEEEEEEEEEEEE

A0A183JZ33 **A0A183JZ33_9TREM** (125 aa)
Uncharacterized protein. *Schistosoma curassoni*

```
MKREEEEEEEEEEEEEEEEEEEEEEEEEEGGGGGGEEEEEEEEGEEEEKEGGEGGGGEKEEEEEEEEEEEEEEEEEEEEED
EEGGGEEEDEEEEEGEEEEEEEEKEEEDEEGGEEEEEEGGEEEEE
```

4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE

A0A183K0U7 **A0A183K0U7_9TREM** (91 aa)
Uncharacterized protein. *Schistosoma curassoni*

```
MRKMNKNLMELEKKAEWDRVGWRMLVGGLCSIRSNRQEEEEEEEEEEEEEEEEEEEEEEEEGNEKKTVDITNHLHNYLCI
ICLDQSTYQSI
```

38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE

A0A183K6F6 **A0A183K6F6_9TREM** (92 aa)
Uncharacterized protein. *Schistosoma curassoni*

```
MVSGDQRLVHTPFVPSGYWNPCEPLVDSPSPPNRFKSHMFDFRPLNFVNNTRDARRQSLEEEEEEEEEEEEEEEEEEEE
TTKNVHTSLVNI
```

60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE

A0A183K7B6 **A0A183K7B6_9TREM** (89 aa)
Uncharacterized protein. *Schistosoma curassoni*

```
MVAGDQQLVYTKFVASGYWSPCATLVWNPVKAPDIRFSSFHFPKQHPRHEKANMYIHEEEEEEEEEEEEEEEEEEEEGEA
VTQSTVVTQ
```

58 - 77:	EEEEEEEEEEEEEEEEEEEE

A0A183KAW2 **A0A183KAW2_9TREM** (95 aa)
Uncharacterized protein. *Schistosoma curassoni*

```
EEEEDEEEEEEEEEEEEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
AEEEEGEEEVATHEH
```

22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE

31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE

A0A183KG90 **A0A183KG90_9TREM** (46 aa)
Uncharacterized protein. *Schistosoma curassoni*

MKIKRSTRQIKDKKEEEEEEEEEEEEEEEEEEEEESTLVMLIYYPEW

15 - 34:	EEEEEEEEEEEEEEEEEEEE

A0A183KV50 **A0A183KV50_9TREM** (38 aa)
Uncharacterized protein. *Schistosoma curassoni*

LSQISEEEEEEEEEEEEEEEEEEEEEEEEEKNTPFPNQ

6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE

A0A183NQA9 **A0A183NQA9_9TREM** (38 aa)
Uncharacterized protein. *Schistosoma mattheei*

MNDDDDEEEEEEEEEEEEEEEEEEEEEEEEEEEDDDDD

7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE

A0A183NU03 **A0A183NU03_9TREM** (76 aa)
Uncharacterized protein. *Schistosoma mattheei*

```
MLFKLPKKIQSKEEEEEEEEEEEEEEEEEEEEEEQEEQETLRKCHQDEMNEERSYNFKCGVSVSKKRCDGRLPGYLIL
```

13 - 32:	EEEEEEEEEEEEEEEEEEEE

A0A183PDM5 **A0A183PDM5_9TREM** (50 aa)
Uncharacterized protein. *Schistosoma mattheei*

```
IQNEIEEEEEEEEEEEEEEEEEEEEEEEEGELTVINPIYIINVYCVICNLL
```

6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE

A0A183Q8F6 **A0A183Q8F6_9TREM** (31 aa)
Uncharacterized protein. *Schistosoma mattheei*

```
EEEEEEEEEEEEEEEEEEEEEEEEXXXXFSE
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE

A0A183QHU9 **A0A183QHU9_9TREM** (105 aa)
Uncharacterized protein. *Schistosoma rodhaini*

```
MPGRSIGERYWSPCALLVWNQGFPTPLSGFFVLTDLVKAPGIRYFSSQFHKQHPCCEKAMSRTSLAEAIYAWPCGSHVEE
EEEEEEEEEEEEEEEEEEEEEGND
```

79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE

A0A183SF27 **A0A183SF27_SCHSO** (83 aa)
Uncharacterized protein. *Schistocephalus solidus (Tapeworm)*

```
MIKECEEDEDEDEEEEEEEEEEEEEEEEEEEEEKEEEGGGGGGGGCGGGCGGGEGGGGEGGGGGGIRGYFRKWRVLACVSN
LIA
```

13 - 32:	EEEEEEEEEEEEEEEEEEEE

A0A183SKL4 **A0A183SKL4_SCHSO** (1423 aa)
PDZ domain-containing protein. *Schistocephalus solidus (Tapeworm)*

```
MRHFFTLRSSRNAKSSERSSIFNAFPNIETELSLADLDKSNGTGGRCLRIFCEKVKEGTYFKTISIKDTTTVSECIAALI
```

```
HLIFEPPEQHRLVNPESLLMFEAVGRIKPSMETAGEMSARRPSVCTEFMEVSSRPLVPSQRVMEVFSLMIPASGLSRRLE
LRPKQPPARRSSASKSNRLSSETTYFGQDGTSSSPHSNGMDMPLDVNILHNKKPPPTLAHQPHLLLLKGSRPERDSLVHD
LSPLFSGSRGKLSIGFSSKDDIRLYLAPGSNKSKSDTATASPLNLCIRDVGTRKSLYLVSPSQWKLPQTGDVIQVFHNWI
EVSREIPLESYLQPGDILRFEAKGLAYIFLFKDASSVPEHELKLGFLSTPPATPPSASPISTPSSNRSALRTARISASRD
AKTVDRHPAHHTPFSSSSTLNSKNSAGSCPPEGVFPSTDSVNPVLRMLFPNSGPGLATDDFVTFITPKPWTGLPNVTVAS
ACYAHLTRSTATACAAARSSEKQLYLTLEHLLDTVGRTLTNEIDDLESVTMKHLVPAIWKVAFCFYISQYFSPGWLKPTL
TPTEEPRDSWTLETPETETNGELMISPAEIESMSEVGKLRELSIEEADRTLDSAVQHTLGSKVCGDVLQALYLEVKVVMC
VFSIVDRRSFVGKKIYQDKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDGDDGVKRDDDGKKVILEDVTSLCQMVGNNHR
AAENVKLAEQRLFDKLGQIRDNLLLGLSGTASDYPVALVQAEDYVDNQDNGSINDTSNRSATTASSDVDSASTSEDVADI
ATAKLNIDSSTGRQLLNFIRSLDTWMTNAGINRYKEPLRMIYQFAKLLSTDRNTLFQMRVQDMHRKFPEIPVPVLYFLVE
NYENGLGIRQAEVWQYDDIGTISYDDSPGESLAECTRIWKRDDRLKQREGRRGRVDQRYAGNKPLDLASLFHLAETKDII
SKFDEELGKQECKFRWTRFLRHYPPPGLRSTTTTSNTIDSPNIYTARIRSREASTSRGNQELGFVGGSLPSNMVSKIARP
TTLEFGSALLPVPIHSDGRPTRSIMGLRLPTYCASELGGTMDLRSAKNNLSSRYTQNPRSRAARLAGMYDLGSSSPYLAG
DFTDSRPFMTRYQGAGRGGGGSLLGISRLPNRFASAVNLARSTEFDMVDGEEVRRVREEWSQFKRENSRPPSLSADDGVV
KLRRPSQLPVETDFAFVQPFTPPVSQQMEKHRNSSVGHYPLMTESLHDFPYSRLQPPSNHLSRTQSGLSINIASSTTRPA
TLEVARSLRGSTSHLGMSYEFGRLGSQSSLLGVDASRTSESTIFNVMLQRQGNESFGINLVEGHRTSLDQPGIYITHVTP
NSPADRSGKLTLGDRILAINGTDLNGLTYKESVALLKSSKERITLTIQKGSLDNPDALLELNS
```

660 - 679:	EEEEEEEEEEEEEEEEEEEE
661 - 680:	EEEEEEEEEEEEEEEEEEEE
662 - 681:	EEEEEEEEEEEEEEEEEEEE
663 - 682:	EEEEEEEEEEEEEEEEEEEE
664 - 683:	EEEEEEEEEEEEEEEEEEEE
665 - 684:	EEEEEEEEEEEEEEEEEEEE
666 - 685:	EEEEEEEEEEEEEEEEEEEE
667 - 686:	EEEEEEEEEEEEEEEEEEEE
668 - 687:	EEEEEEEEEEEEEEEEEEEE
669 - 688:	EEEEEEEEEEEEEEEEEEEE

A0A183SQA5 **A0A183SQA5_SCHSO** (175 aa)
Uncharacterized protein. *Schistocephalus solidus (Tapeworm)*

```
MQHRPWSNDDVGTSSTFDNRPTTPLLSSSAEFYSSPTYAVPCDSPSEEEEEEEEEEEEEEEEEEEEEVTNVIQRLCKKKIS
GEYGIQAEVCKSSVDTLASLLHEVIGQECKKEVGPEDRDPGVLVPVRKKIYKPRSENYRGISLIDVAVKMFGLCLTRGRD
ATKSESILDMDVRDF
```

47 - 66:	EEEEEEEEEEEEEEEEEEEE

A0A183SSI9 **A0A183SSI9_SCHSO** (336 aa)
Uncharacterized protein. *Schistocephalus solidus (Tapeworm)*

```
MLQRRDAEYRESITIGKSIDVFSVAIDKDCVEVVLRAFQTTEPVNFKEILLVYTASISLDIWQHITVVYSDDFSEAEEQP
NGDLAGLTLLRGTTLDTAQLQCFVDCHARFSLDSGAFRGISPDTRVSWEIPFDRILIDSFDSQQVVLLLRRLRVLNLESR
LASRDSRTTLRLTGYITANLHLLILLCASRLADLVSCLLFTVINGRHPSCEDSGEILHTKPTIIAVTGTDSAGFAEEPGQ
RFPFGSVHSEDTSLEVGSSTKGVERENGEEEEDAEADLTDNQPCTYRLRLHSALIDSQAGRTLRVTGLGAGDGQLLEEEE
EEEEEEEEEEEEEEE
```

317 - 336:	EEEEEEEEEEEEEEEEEEEE

A0A183STZ0 **A0A183STZ0_SCHSO** (69 aa)
Uncharacterized protein. *Schistocephalus solidus (Tapeworm)*

```
MFVQGERRGGVLAPGRDYRCCCCCAMYAGESQSAFTANVSFAPRDRLEEEEEEEEEEEEEEEEEEEEEFV
```

48 - 67:	EEEEEEEEEEEEEEEEEEEE

A0A183SX50 **A0A183SX50_SCHSO** (258 aa)
Uncharacterized protein. *Schistocephalus solidus (Tapeworm)*

```
MVLVVQTATGGIGMMCMQAHKPPSESLSLPAIWQGITEKAPSYCGFLSNWLLARASGAAIPGVGYDWLMTVNKSEMAIPV
SFVFVSNVILSTSLDALRLLAGLYRELQETTGRVSLITDRQIDGVAMGSPLGPLLADVFMGKLEKFQLSGQINKLRYYGR
YVDDIFAIVTEETNVDELLYTICDLNRQYGHMREIEIGGSRKHATLNSGLGSRRRTTTLKRRKKKEEEEEEEEEEEEEE
EEEEEEEEEEEEEAITGT
```

226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE

231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE

A0A183T2T4 **A0A183T2T4_SCHSO** (173 aa)
Uncharacterized protein. *Schistocephalus solidus (Tapeworm)*

```
LAGGTNHDSTSTVNAFKFFLIIFYQNHVSLTTCRKSPGGWRRQFTSTAISSPSPPPKEGIAVIEASRRGPGRVSEEEEEE
EEEEEEEEEEEEEEEKEDTAAVAAADDDDDSGGGGGGGAAAAAAAADDDDDDDDDDDDDDDDDYDGDDDDEEEEDEDDDD
DEDVIVGTRSLLA
```

75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE

A0A183T4Q4 **A0A183T4Q4_SCHSO** (94 aa)
Uncharacterized protein. *Schistocephalus solidus (Tapeworm)*

```
MSITMPMPDAFILKREEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGVVLLVPHSRSAHKLTELERATGTGWEGVKRETDF
ARSLCIKKNLKPIS
```

16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE

A0A183T545 **A0A183T545_SCHSO** (126 aa)
Uncharacterized protein. *Schistocephalus solidus (Tapeworm)*

```
MEVYVRSSGVCISEEEEEEEEEEEEEEEEEEEEEEEEEKEEGCSFTGIMAYTSSDTVRRDYVKSLCSKLVVVNADYQKLAQE
FEAFKLDNVSDMSSKPKLARLRAVLKGIEAMLPPPDSLGQRYVLFR
```

14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE

A0A183T556 **A0A183T556_SCHSO** (753 aa)
Uncharacterized protein. *Schistocephalus solidus (Tapeworm)*

```
MNRSTESLKSRLPDDKRAHKASEDLNSQRKHDQDYQVTPLCLSSSNSKLLASLSRSAETVQTSASNDDSEATLVRRGTHH
HHQRRSYDDAYVSRLLTPGKRASQMDEGRSSTSSLLGERPDILQEVTLYTSGSEAPAFSCSYCILPALSTIMELLLPQSP
KSFPIPKTDAEPSSYLPITVGLRSLAMHLFFHAHYLLTGIRAETGASGTTLTGAISDCVLAAIRQEQVPGNLPPQREDEP
SAGSSLKVLLNSATEKLCTLIFGRNREPLPEMGSGSERGDGQELERAERAHLVQQAMKQVELVLPAYLVTCFMIHYLSLS
SSSTSTEQTDRNFVDSWLQQHRPIYQTLDLVSPLNIEPIVDAIGSMSKEFWDQLEEEEASFAFSYELGKEGSNNERPKMT
GASNAEFTPLFMRLLASMQIASLQNPANLSGIGKGETLSNLDFEVWDVLDSTSGIAFSDGEAAPTLVVEKRPDNGLVANS
LTRSLDHLESLSVSLMQQRKFLLQRSRSKESDLLPVKSSDQDAVDYARAVAALRRQHEEEIKEIWDNVQANWVPKEEFET
FAAETDCLLIEAKKEVTESSTEIEGEEEEEEEEEEEEEEEEEEEEEEEEEEXKAWEYQKTLFILLRQLEKANEAFTSF
LRSETFREDFEHKGANRQAGEMAEGVRKALADLTSAAVFLRARLYGKDFEGIEEDEKELPSNYDCDDEVNGDKSDNVHNK
WTPRCPSPLPFPVILHSPRMHYHALNEDEESEI
```

586 - 605:	EEEEEEEEEEEEEEEEEEEE
587 - 606:	EEEEEEEEEEEEEEEEEEEE
588 - 607:	EEEEEEEEEEEEEEEEEEEE
589 - 608:	EEEEEEEEEEEEEEEEEEEE
590 - 609:	EEEEEEEEEEEEEEEEEEEE

591 - 610:	EEEEEEEEEEEEEEEEEEEE
592 - 611:	EEEEEEEEEEEEEEEEEEEE
593 - 612:	EEEEEEEEEEEEEEEEEEEE
594 - 613:	EEEEEEEEEEEEEEEEEEEE

A0A183T7M0 **A0A183T7M0_SCHSO** (61 aa)
Uncharacterized protein. *Schistocephalus solidus (Tapeworm)*

```
MVREEEEEEEEEEEEEEEEEEEEEKGGGGASERPQVSRQAGRRRRRRGPTLQLYRQLGSSVW
```

4 - 23:	EEEEEEEEEEEEEEEEEEEE

A0A183TB60 **A0A183TB60_SCHSO** (350 aa)
Uncharacterized protein. *Schistocephalus solidus (Tapeworm)*

```
MPLGSIKPVSSPRIPPRVQWTSSSGSRAGATTPCSSGSSSLAVATTTNSDTAHRSKTPPQTVMAIKLASPRSAITVTPPS
PVSCSPVASERSPRAQPSPERCPVEASPGERMVTPPALVSVEAYFPPAAPNRRVRFLPRHSLQQRHEESQKPSLSKSVPD
EASNPPGGTDEFTDAMHAGDHKAVNPPTDRRATINDAEGGHQETNRQGDSNETPSDSRMEPANAPAVKANNGRAVPGGG
GNASLDETKLNEEGEEEAEEEEAEEEEEEEEEEEEEEEEEEEEEEVDGEGREQVEQDGGPSHDGGGGHGIVRDGGSSSNSS
SGSGDGGGVDGGDGGGVDVGGGIGGREGGR
```

264 - 283:	EEEEEEEEEEEEEEEEEEEE
265 - 284:	EEEEEEEEEEEEEEEEEEEE

A0A183THT8 **A0A183THT8_SCHSO** (194 aa)
Uncharacterized protein. *Schistocephalus solidus (Tapeworm)*

```
MNTRLEAFRGNVNQSGRFAVLPPPHYIYEFALRSSHDTASAAEESEGDVQFFLSSKAGRFADLSTGPIARDSERDSCPGG
GSISRAPPTGRTAELLQEKRSTLLTNVKKQNEEEEEEGEEKEEEEREEEEEEEEEEYEGEEEEEEEEEEEEEEEEEEEEE
GGRRGRKKEEEEEEEDEEEEKEEEDGEEEEEEDD
```

140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE

A0A183TNY7 **A0A183TNY7_SCHSO** (890 aa)
Uncharacterized protein. *Schistocephalus solidus (Tapeworm)*

```
MGVVTQERAPDPTAGAGIQDTSTWFLDEAGVREQLRLDLAAVAACAASPAGTSVSTTVAAAASVNSPMDFYTLSNFGPGA
FRAASASTTANTSDQHVGASSRPNHSSDEGPSAAPSTTGRAATFTTGTRSGTMSTASTARPLRPFARAWLENYRQLQKSM
PIWSFCSSSTSSLSWPMAASRWATAVGQSPATMQASANLSMTTTASVTTATNLGGPASTPVGGNGGTALSVYSPGSQIAM
IFAKACELLSTRDANGPRLLAIITEELINCARLSLPKLRRSFRGVVTTPERSVWESFSDATTPDLDDLDTNDITDLDAVV
APPRYLAHQQQSEGTTLTANSSQPPPAWTIPLWEEATRLWTCFLLSPGTSESSRQKWRSRLLAWSQSPRSPRDETYLVPQ
LTTPPAVEQLTSSVVPTQSPLLRPPSCFTNNQRPARNSSVFKLAIEAGSLPLQKGLWLLSGTNPCAGVRAQLSPNALSDL
SLSMPSNVQQCTCPFCGVSLLLSKTWCLNETFVALCHRVSSLASTGYREEATNLAVSLSVLLLDCVDEVSRRTLPGAARV
WHPEEGAEAAASAQWSRLYSAPCSPPAYAPPGKGASPCSLSVNTSCANAGPNGPGWYHSTSPLPGPSGGASALPLPPPRT
PPTFKSPPPPISPGCYGASSRYGRSFSIGDGAGAQWQSVPGAPFIHPPPPLYPLPPHPPHQSYYAYSNASFECAQIASCE
AGLRSLITGPLRRGPVGVSGLPFAVPRPPSRSPLPPPPPASRYINRSPSVTDPLSEAFLSSLLLSEASSSCPSHECGWLV
LPGRPIISLVECLFKAAAVRLQQEEEEEEEEEEEEEEEEEEEEEEEEEEEXLRLSACNRKRKKRKKKKKRKKKKKRVQR
RHFWQKRTNQ
```

824 - 843:	EEEEEEEEEEEEEEEEEEEE
825 - 844:	EEEEEEEEEEEEEEEEEEEE
826 - 845:	EEEEEEEEEEEEEEEEEEEE
827 - 846:	EEEEEEEEEEEEEEEEEEEE
828 - 847:	EEEEEEEEEEEEEEEEEEEE
829 - 848:	EEEEEEEEEEEEEEEEEEEE
830 - 849:	EEEEEEEEEEEEEEEEEEEE
831 - 850:	EEEEEEEEEEEEEEEEEEEE
832 - 851:	EEEEEEEEEEEEEEEEEEEE

A0A183TPN1 **A0A183TPN1_SCHSO** (110 aa)
Uncharacterized protein. *Schistocephalus solidus (Tapeworm)*

```
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEAEEVEEEISTRKSTPPVNLDSVYSPILPSPSATGPLMVSGVAGNLSENFVA
DETGVCAKTAQGNVATAFLTVEKYRKLPSI
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE

2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE

A0A194PVU8 **A0A194PVU8_PAPXU** (110 aa)
Uncharacterized protein. *Papilio xuthus (Asian swallowtail butterfly)*

```
MRQYVLYLNLPTSPPNQRRASTNNQRRIIIIRRRIRRRIRRRIRRRIREEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEVEEEEEEEEEEEEEEEEIKIEY
```

49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE

A0A194QAB5 **A0A194QAB5_PAPXU** (178 aa)
Uncharacterized protein. *Papilio xuthus (Asian swallowtail butterfly)*

```
MLTWYSSAPCTEARPRRLQLRLSGVLPQVGRQRVVVRGHSHQGLSCAPKINHYKSGLRVLFFPQLSTAVKTSHIGDPDVI
ETWKINKAKINHYKSGLRVLFFPQLSTAVKTSHKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGLKLFFSDIVIALCF
WMSDFYNSFFICKLVLVN
```

115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE

126 - 145:	EEEEEEEEEEEEEEEEEEEE

A0A194VRN2 **A0A194VRN2_9PEZI** (1175 aa)
Ribosome biogenesis protein MAK21. *Valsa mali*

```
MAKKSKAQKEAVPAFDEAALTKLTAKIDTELSKPKPEPKPKAQKSKAQKPKEQKPKEQKPKEQKPKEKQNDERPAKRKRS
DNDTKDATPQKRQAQEATNGHVKPQKAQKPQKSAAERKSELLEEIKALGGDEADLDLVAGIDSDAEEGQTKPSKASEDLD
KSLKNELAKFAAGLGFEQVRDEVLAADDEEEEEAEEVDREDSEDEQEGEEEEEEEEEEEEEEEEEEEEEEEEEEEMAP
FVEEPKKRAGAGKLIFDPRPDWHALSQEWLPLPSADDIRNFSTTINSMKDYAKALLESDAAAYNSTVAASSTRKFMSTXE
EEEEEEEEEEMAPFVEEPKKRAGAGKLIFDPRPDWHALSQEWLPLPSADDIRNFSTTINSMKDYAKALLESDAAAYNSTVA
ASSTRKFMSTIMSSGTMSDKVSALTLAVQESPVHNMKALENLINLAGKKSRDQAVAALGALVDLLGNGVVLPSDRRLRLF
RAQPCLLGTLQKYSVTAWKSDKPLPGKITKAHLMMWAYEDWLKETYFKVIQLLELWCGDEIEYTRHRSLDFVFALLKEKP
EQEANLLRLLVNKLGDRERKIASRASYLILQLLITHPAMKAIVVDTIEQEALLRPGQTIRTKYYSIITLNQTILSQKEPQ
IADTLVRIYFDLFVSLLKMGALGVATSSDAKKKPWERNKKQWEKGSNATPLGGKKDPAAGKAAAVPDTETAEKLVSAILT
GVNRAVPFSTADEVTLEKHLDTLFRITHSANFNTSIQALKLVQQLSLSKHIAVDRFYRTLYESLPDPRLIHSSKQADYLN
LLYRSLKSDVDVRRVKAFVKRMLQICYLHQPSFVCGILFLVAQLEAAFPDLRTLLNEPEEDGDEEEVYRDAPAEGAAEEP
ATAQDSRQKKAVYDGRKRDPQYSNADQSCLWEVMPYFKHFHPSVSVFAENLLKPQKTLPKPELANHTLMQFLDKFIYKNP
KAADTKRGGSIMQPVLAASSSANVVMAGKANAKHQPSVNSAAFWNKKQEDVAAEDVFFHAYFSQIGKPGQEAKTKKDKKA
SAEGDDEEADEDEIWDALVNSRPDIEGPDDSDADMDMGEDDESDLGSLLEDMSDDDEDEDMDSAGEDVDMGEEDGPGEED
GWVDGADLASESEEEPVEKKGKDGKKGRMTKRDFKKLPMFATADDYAALLAEEEE
```

209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEEE

A0A194X5F3 **A0A194X5F3_9HELO** (260 aa)
Uncharacterized protein. *Phialocephala scopiformis*

```
MNRLEMTLVTSLKVGAPKKTDERITRPFTFAQKFANYFSEADNIRHVTLNHITDFREPSDVVHFTTELPFWLKGFKSLRT
LTVDIPVVRQIFDADLQDKLLNALISRINKKVGVTADIQTWTWKAPAGRTMDWSQDLGWEWTFTRLLGIDDDEGEHDGIL
VERELDAEKRYRGFDIPYSSDDEVRLGESYIVKSEEEEEEEEEEEEEEEEEEEEEKEGKEESEVEEGTRENSSAAGEEDK
DAGVQQAIEVAAEGGNGTQE
```

195 - 214:	EEEEEEEEEEEEEEEEEEEE
196 - 215:	EEEEEEEEEEEEEEEEEEEE

A0A194X8T0 **A0A194X8T0_9HELO** (192 aa)
Uncharacterized protein. *Phialocephala scopiformis*

```
MCFPVALDGLFTHAASWACKVAVAQVQMVLLLHTMSKCKYDHGQGTLPSESPVSLSRKHNNNNNNKNNNNGDDDDDKMPR
RSRRLEIAAARRLVAAAPTARARRAATRFVRRLQLQPEQQHRLRVVRPREEEEEEEEEEEEEEEEEEEEEEEGEEDDDWS
WHGEEEEEEEVDSGAGEPSYIPPDAEYLYEED
```

130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE

A0A195AVH1 **A0A195AVH1_9HYME** (139 aa)
Uncharacterized protein. *Atta colombica*

```
MADRQPESSEVRKRDVIIYSAPERPTEADEREERMRANGCIRMPKCRVTCNARKADTCTRPYPPDVPRSEREHEEGEEED
EEEEEEEEEEEEEEEEEEEEEIMKDEKVLPRKRRERSVAPVHQLPRPMASLRVDEFHGE
```

81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE

A0A195AZK9 **A0A195AZK9_9HYME** (2569 aa)
Uncharacterized protein. *Atta colombica*

```
MELKKETSFDMNKEKAKLFKTKIKQLAEYNEIVSAETINAIGDVTKDITKDMTKDTPSSDEFDEDLEEEYRNLNNMLDLP
NDTYSLTKITAELPLCVKYGVRSGLIHSNMPYFSPLSRGYQGGAIAIAAFATTGIHKSRCWNEAMIDQIVEDGDTFYCES
```

YKDVNTDDRRTMTILDLKRILLLQKKFNVEVKIEDPAYAGKFRSRNPIELHLAKALELFFERHNAGILTSPVLNIAIWKN
SKYYYIFDGQARRESGDPAADRVSGSAKLFLVKNLIGLLFIILEKSNVRNEPFVIYPIFISNVEMILPEDVEEAKILEKP
RRRPSGYKICEKYRAIVQGSCHLMHPVIPEALRGKGHLIIAMAALIYSRLINANKWTTALIDLIFNQANIYLIDLIRVLE
KKLDNEFELRLDDLMSDIILGVYSAKVKVDANVISSQTQKSSIEIGIKEFFKMQELGILEIKKIFYAIWKDGDSYYFFNP
FACDDEGFRIDYSDRERMTHDTTRDVACVTMNSTVNDMVEIVLENISNEENDPFLIHGVKVLYVKTGVTPSGQFEKVIYR
ESGTNRRPRAPLPLVSMDMTKVDLIDATPRLRPESHKFADVSIQYPELMQDIDQYMMTVDEPVTFIIAQEKVKKIKKIKE
KKEEEEEEEEEEEKEEKEEEEEEEEEEVKVGFIRGYDLINNHCLIVRGTKTCMDLTYNTRSQGRQGLIIALTVLAYRKLKDP
TRWRCIDVDQILNIGNKAYEQVITWIQQGRPEIKEMKEKKLKEEEEEEEEEEEEEEAEEEEEEEKEEEEEEEEEEKEEEE
EEEEEEAVVRKVARAPSHLDISLLPPTLKLAENNVFFKTRMNVANGDANPLANLAEALERYFERYSETILENNRLMYAIW
KEDGKFFLFNPYGSNQEGWRFWQYSAGFNVTDRFNELIKLLYGILEYNNSRFSLHFVALDAIEPGKYKSSVEIVIPEEKT
EKFQTKFLPITDDDLLELEEKKLDVEVVKELDKKDIEEEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEEEEEEE
EEKVEVEEKELSEFLKEDPTLFVEESVQPDAPYSLNLALLTSTVKIQDPIEEELKSLPEEIIMEKMKYDHPPPYVMPPRG
TLRVLLEAKLANKSIPSLVSRFSIDSRLEIKKGDVPVDSTLATIVPLLRDTKPSKMIKLSLRKYLYSRLPPIRMVPLRAI
DESYIQDKEIDKAIDEKYLEREKLKKREKDKMLEKLSRVSYVRPELIPRGPIIKTPVLVIKHLTYPDEQKRALKTAFTIK
KIITDTEKLLFKFKFLKFQLDVPLQLLNKISGNKMKKRKKMIIKAEYFDKKIELPPSEIIGFKVVDEDTEIIQGNYSLLD
RTKIEPSHFKSCFISAVLCILAKNMLNADRFCDNILDYLIFPANSIDQQIGKLRYNGYRTFYLKIIVLDTSFNIILKKII
YANPESSPSDELDAVINKFLENNQTGILVLANCAYAFWTADDKYYLFDPYPCDEKGKVNEEGYCCLMRFRNLKSMLDRIK
ENADKTVRKPFRIYSVSVIYAEMKKRKRRKGIKRRPKLEEMTKELISSEEKLAVSTPTVKSEVSLIELVKWVTEGPELDP
HCDVAMAGFIPMRYYKASVLDKVVLEKNITTPTLAPFELLEAQDNEKMEKVRIIPFERIFYNNSSIQIPIDLCIMAWSLI
HDLASWSERTIDGLIEAAIDYAYDSVLANEDTSVSDMTDAVLPEFEIANYVFRAVFAPLHYGFLYTKKGWNLAMTVEKIF
ETAIYTGGIIVCHSAHIGVTKCGKNYFAWWTVTGTKNLRIIVTSCFDEFLKLIVKVINVPQTIGFTVRAITISHALKTAP
DFSDVKGLHEPRVTMASLPEIYLPEKELQDSYDAKAIFKPIALAPKPIFILGTVALRNRDNLLEPRMKRCYFIALLAVVV
KRDIVQSPLPGMIDRILEVAENLYRGFPAESKFHAEHILRNVPLMNRFFDLCDCALPLVVLTTNSQTGRNDFYVQVKHHL
KRYFKMYTSGILHFTNCCYGFWYSRATNCYYYLDPYQCDTNGRKTCANGNACLCIFSSVCQMVKHMCLNQYEGTTGFFLH
RIHVNSINAPPFEKFQEDPMWLYLDYHWNFTHSIMRSCKKAKYGDRSKANRQFWNNYAIEVIGLIYSIWGTIGAYDCRFG
ERAGKNCVAICVAVLAMRNLCHPSRWSSAILDSAVICGDSYYTESLKSLMQSCSKYDNRFGLQTSFKIFPHSWTIDFGTS
VCGILYGEQNSLTLTDALNFAFEEARNVIIVCNRIALAALATKDAYYVADPCWIGPPLFSRNRGAIYVLRCKNMNVLIYA
ITKMLNTNQRLSVYVTSLNLMFDREDFEMDLYTTRRKILPTSIQKVPGKIKDPAIPIPGAVIVPDEDSYLHIYRQCLAER
IARDSQLESLQLPCAEYVLNPENVNNALVSTKWRMNLGQARSRKRPKLSLDSVEIKDDLLEFNESNFLTNLYKMRISITD
LITASNRYPRPIDFTNNESPPKIELLDNISERGFINEQSYVNFDKSVAEMSQKNYANYQHRLPKNNKNPIETKSIYSKSS
DVTTDTERE

1003 - 1022:	EEEEEEEEEEEEEEEEEEEE
1004 - 1023:	EEEEEEEEEEEEEEEEEEEE
1005 - 1024:	EEEEEEEEEEEEEEEEEEEE
1006 - 1025:	EEEEEEEEEEEEEEEEEEEE
1007 - 1026:	EEEEEEEEEEEEEEEEEEEE
1008 - 1027:	EEEEEEEEEEEEEEEEEEEE
1009 - 1028:	EEEEEEEEEEEEEEEEEEEE
1010 - 1029:	EEEEEEEEEEEEEEEEEEEE

A0A195BBC3 **A0A195BBC3_9HYME** (816 aa)
Uncharacterized protein. *Atta colombica*

MYTHIYIKVRTGGKEGGEEEEEEEEEEEEEEEEEEEEEEEEEEEVAIVVEEGKEEEERDLQGTGKRGKKSGSAITEHLRGAQ
PNMEQSQISIRPNREYTPAPPFALLGSRRVGRCRGCRLRRRRCRRCRRFIPRPPLSRWRCRRCSRLLLVHFTLARNSAKR
GTMQTEEVVPRTQSIGIDSSLIDGAGLQHHLHHSVHLRCPLSPLIHMAVKQEPQEEEERSRDASTLSSQVDVGNVVGSMD
SKHGQQGGNQIQALEENLALTSPDSSSRGRTSRGRRKSRWKLKFHHQALPPEYLDHYEASLAQENLNLSPPRIIEPTASS
PAPTNSTSTPSPIADVHGWLQRIAAMQQELCPQIAPPQCPTTLGHNQVTASTRRSVITSVSSQTCNTTYPSHHIQQTQTS
SRPPMKYSDLPYMGEITLDNSKPRRGRKPKKADICHLIYKNYGTILPGTPEPVNYSESVGHRSNNSFVNHNNNVIDPMIG
HNSGFVYWPNAGVFIHPMALQSQLLYYQKVAQNDKGPPSTTDQPPREQKIVPKSIYSMMETKNAAQSSLPIAQTIPVSVA
TSTSPRPKRNAPLNQQQSQPTKRKRSAIFIPPMPTENNNNPATEVSICKFKFTGGAKPSLQEKKSLSVDSGGNFRYYSGT
GDKSMRGYEFFPREALQQPAGQSGTTSAAGAFLNAAGERIQPPTVCQRSPTGQDDGRRKRKTRKSLQREKLEQTFKEKGF
LIQTQQLESAEGATYCKFRQLRKFTRYLFRSWKDYLPGNVRELSGCGTGAAVAIENDVADVEVDGDTTLVPSPLPRGNLL
DVPNSFVEDHRTLPLT

18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE

A0A195BK30 **A0A195BK30_9HYME** (651 aa)
Suppressor of cytokine signaling 2. *Atta colombica*

MMLRMVCPKCHHHFPVLGCCLKWNDETNQKEMKEEEKEEKKKKEKEKEKNEEEKKEKEEKKKEEVRKEEEGEEEEEDEEE
EEEEEEEEEEEEEEEEEKKKEKMTANTICSKAATYYVSSLPVSHGCTSDSSCFINPSTKIQEPTIFQSRAVNCGSNVEIT
DSDTLELFYDIQTSIKHNHHPLLTSPIYQLNDQDPFITMTENLNYEMASSEQYIASTCELTGGSVTIATPDIQSGGCLIQ
HTEPEILVQASQIKIEPKLTGGGCLVQKKLTEENQRLVTSKCTKNFAAVNNRTFVTPPNGYSELPANIRVISSGTIRDNE
NNVITSAESRPRKIPNTIKINNCCDCKSTFQQNHCQYHHRRIFDASLADNRDSLLLEPIGSSVQFRVNATVQLPANLGQC
TVNITATTTTPPNQVVAMKLPGRGRNNFHGGGLVQPNELDCAMVNQIVAENNKSCNNTEQVDETLTTPVSWPLTAWSPDV
HVNRLREVKRLLQICGWYHEGISRQQSENLLKDASIGRWLMRDSSDYRFTFAVSVKTTKGPASIRVHYFLEHFRLETTDP
KLALAMPFFDCPIKMLEYYVAYSKRMDEHRREVWVDYSGQLYSQIYLTSPLVKEVRSLSHLARLAVNRNKLPIDCLPLLI
KNYIKEYPYTL

78 - 97:	EEEEEEEEEEEEEEEEEEEE

A0A195BM48 **A0A195BM48_9HYME** (207 aa)
Uncharacterized protein. *Atta colombica*

```
MATVIAVRVSASFTSSTLSSPRETRYAESVCEYLELTIFPPKWQFKYLGSGDLFVSSPYPKHYFKRSVHTPRRAEEQEAE
EEEEEEEEEEEEEEEEEEEEENDGGEGCFAGGKIFLTAFASPPTSDFSYSSLRSLPPFQGTFSTDACAFPDFISLGKIIVA
LARALFGSALCARLSTRVSMICTCAYMLRVCMCERRKNNGTELASNR
```

80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE

A0A195BPR4 **A0A195BPR4_9HYME** (447 aa)
Troponin T. *Atta colombica*

```
MEFWGISRDLPESELNRDLKRVTFVFTPASFRESGENPEFMKRQEQKRSDLDEQLKEYIAEWRKQRAKEEEELKKLKEKQ
AKRKVTRADEEKRLAQKKKEEEERRQREIEEKKQRDIEEKRRRLEESEKKRQAMMQAMKDQSKAKGPNFTITKKDLSGNL
TSAQLERNKTKEQLEEEKKISLSIRIKPLEIEGLSIDKLRGKATELWEAIVKLETEKYDLEERQKRQDYDLKELKERQKQ
QLRHKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYDTLLAETNEKTWKQKTEQFMKRNKTLTSPR
EDLYNPEKATIKRERVFPGDPDGLTEQQKEIIEKMWAQQKEQFMGRQKTKLPKWFGERPGKKAGDPESPEGEEDVKAAVD
DLEEPQFDEEEEEEVKEEEEEVEEEEEEEEEEEEEEEEEEEEEEEE
```

423 - 442:	EEEEEEEEEEEEEEEEEEEE
424 - 443:	EEEEEEEEEEEEEEEEEEEE
425 - 444:	EEEEEEEEEEEEEEEEEEEE
426 - 445:	EEEEEEEEEEEEEEEEEEEE
427 - 446:	EEEEEEEEEEEEEEEEEEEE
428 - 447:	EEEEEEEEEEEEEEEEEEEE

A0A195C4W5 **A0A195C4W5_9HYME** (450 aa)
Troponin T. *Cyphomyrmex costatus*

```
MEFWGISRDLPESGLNRRDLKRVTFVFTPASFRESGENPEFMKRQEQKRSDLDEQLKEYIAEWRKQRAKEEEELKKLKEK
QAKRKVTRADEEKRLAQKKKEEEERRQREIEEKKQRDIEEKRRRLEESEKKRQAMMQAMKDQSKAKGPNFTITKKDLSGN
LTSAQLERNKTKEQLEEEKKISLSIRIKPLEIEGLSIDKLRVKATELWEAIVKLETEKYDLEERQKRQDYDLKELKERQK
QQLRHKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYDTLLAETNEKTWKQRTEQFMKRTKTLTSP
WEDLYNPEKATIRRERVFPGGPDGLTDQQKEIMEKMWAEQKQQFMGRQKTKLPKWFGERPGKKSGDPESPEGEEDVKATV
DDDLEEPQFDEEEEEEVKEGEEEEEEEVEEEEEEEEEEEEEEEEEEEEE
```

429 - 448:	EEEEEEEEEEEEEEEEEEEE
430 - 449:	EEEEEEEEEEEEEEEEEEEE
431 - 450:	EEEEEEEEEEEEEEEEEEEE

A0A195CL58 **A0A195CL58_9HYME** (677 aa)
RIC3 domain-containing protein. *Cyphomyrmex costatus*

```
MAEVTDFGPRKTFFILAVVIGCFTVLWPRILHPMFIGFVTPHHSTTDVCCEVIFESDVTAVDIMQEMCQNILRHHPIDPR
VRDALKLSKLTPQTASLCREEVLARCGIDLSSFLAERESLGKTYKQVLEEIRSFNSSLCLKMNFGVPLSQLGTPHLIRYH
ILMPHNTMPQERRTPPHAGGMHPALRERGRAIPSSHIIPKIGSDHPMPKMRPPLGGPGHVVSAPKGSSTMGIIMPLYTIG
IILFFVYTIIKVLKKNTESEIISEYPGAAAEKEFRRKVFSPETFATAMTGGTPYYLKEKSPHKITPTIEELNDPIIRTYI
LNTFGDVLHAGTQEAAGDIEIDQLRQRLVETEAAMERIVVQMGNISRSVKHNASSQPEIKVYQINFDAIHIDGSPKSNGL
AGVDRGSKEDTADQESHSKEDEELDVAEQPPTVKVMGMEMTASCESGQKCSRPTTPIIPAPSIIEREKTPPTPIYLEGAL
PSQCELLVTDSETQAEKSEDDDDAIVLSGKMTLSLISLDQIPADSDAENPDNKRKRVLDTQMEIRDVKDTKNIILQKEEN
RGKEDENEEEVLEIEEAIEMEESEEEVEEEENDQEKELHEEKNKEVIEEEKLEQEKGKMEEKDEEEEEEDEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEDEDEDKEYEDEEDDDKLD
```

631 - 650:	EEEEEEEEEEEEEEEEEEEE
632 - 651:	EEEEEEEEEEEEEEEEEEEE
633 - 652:	EEEEEEEEEEEEEEEEEEEE
634 - 653:	EEEEEEEEEEEEEEEEEEEE
635 - 654:	EEEEEEEEEEEEEEEEEEEE
636 - 655:	EEEEEEEEEEEEEEEEEEEE
637 - 656:	EEEEEEEEEEEEEEEEEEEE
638 - 657:	EEEEEEEEEEEEEEEEEEEE
639 - 658:	EEEEEEEEEEEEEEEEEEEE
640 - 659:	EEEEEEEEEEEEEEEEEEEE

A0A195D4J2 **A0A195D4J2_9HYME** (2561 aa)
Uncharacterized protein. *Cyphomyrmex costatus*

```
MELKKETAFNMNKEKAKSFKTKIKQLAEYDEIVSAETINVIRDVMKDVMKDMVKDAPSSDEFDEDLEEEYRNLNNMLDLP
NDTYSLTKITAELPLCVKYGVRSGLIHSDMPHFSPLSRGYQGGAIAIAAFATTAIHKSRCWNEAVIDQIVEDGDTFYCES
YKDVNTDDRRTMTILDLKRTILLQKKFNVEVKIEDPVYAGKFRSRNPTELHLVKALELFFERHNAGILTSPVLNIAIWKD
SKYYYIFDGQARRESGEPATDRVRGSAKLFLVKDLIGLLFIILEKSNVRNEPFVIYPIFISNVEMILSEDAEETAKILEK
PRRRPSGYKICEKYRAIVQGSYHLTHPAIPEALRGKGHLIIAVAALIYSRLINANKWTTALINLIFNQANIYLVDLVRVL
EKKLDNEFELCLDDLMSDVILGVYSAKVKVNANVISNQTQKDKSSIKSSIKEFFETQELGILEIKKIFYAIWKDGDSYYF
FDPFACDDEGFRIDYGDRERTTHDITKDVACVTMNSTVNDVVEIVLENTGNEESDPFLIHGIKVLYVKTGVTPSGPFEKV
IYRESGTNRRPRTSPLLAPMDTTKVDLIDATPRLRPESRKFADVSIQYPELMQNIDQYMMTLDEPVTFIIAQERAKKIKE
VEEEEEEEEEEEEEEEEKEEKEVKKGEKKKKEEEKTQVTPPVYFIRGYALINGHCLTVRGSKSCASFTYDLLSQGKQGLI
IALSALAYRKLKDPTRWRNIDVNQILDVGNEAYEQVITWIQQGRPEIKKVKEAEKELKEEEEEEEEEEEEEEAEEEEEEE
EEEEEEEEAVVRKVARAPSHLDISLLPPKLKLAENDVFFKTRMNVVDGDANPLANLAEALERYFERYPEVILENNRLMYA
IWKEDGKYFLFNPYGSDEEGWRYFQYPAALNVTDRFNELVKLLYGILEYNDSRFLLHFVALDAIEPGKYKSSVEIVIPDK
TTEKFQTKFLPITDDDLLELEEKKLDVDVEVTKELVDKKDVVEEEEVEEEEEEEEEEEAEEEEEEEEEEEEEEEEEEEE
KELDQFLEDPLILIEESVQPDAPYRLNLALLTSTVKIQDPTEEELKSLPEEVIMKKMKYDHPPPYVMPPRRTLRVLLEAK
LANKSVPSLVSRFSIDSRLEIKKGDVYVDSTLTAIVPLLRDTKPSKMIKLSLRKYLYSRLPPIRMVPLRAINESYIQDKE
IDKAIDEKYLGQDKLEKKEEDKTLGKLPRVFYVVRPELIPRGPIIKTPVLMIKRLTYPDEQKRVLKTEKVAPIIKKTLTD
AEKLLFKLKFLKFQFDVPLQTLNKKNGDKVKDMKKMIIKTENFDKKIDLLSPEIIGFKVVDGDAEIIRGNNSLSDRTRIE
PSHFKPCFISAILCILARNMLSVDRFYGSILDYLIFSANNIDQQIGKLRYNGYRTFDKVIVLDTSFNVILKEIIYANPES
SPSDELDAVINKFLENNQTGILVLANCAYAFWTADDKYYLFDPYPCDERGKANEEGYCCLMRFRDLKSMLDRIKENAGET
TKKPFRIYTVSITYVEMKRRKRRKGIKRRPKLEEVKKELIPSEEKRDVSMPIVKSEVSLIELTEWVTAGPELDLRRDVAV
AGFTPMRYYEASMLEEIVLENNITTLTLAPFKLFQNDEGRIVMAKVRETPSERIFHNNSSIEIPIDLCIMAWSLIHDPSS
WSERTIHGLIEAATDYAYDSMLANEDTSVSDMIDAVLPEFEIANYVFRAVFAPLHYGFLYATEGWNLAMTLEKIFETTIY
TGAIIVCHSAHIGVTKCGKNYFAWWTVTGTKSLKIIATSSFDEFLKLIVKVINVPQMIGFTVRAITISHALKMAPDFSDV
KGLHEPKITTASLPEIYRKELLESYDAKAIFKPINLASKPIFILGTVALHNRDSLLEPQMKRCYFVALLAVVIKRDIVQS
PLPGMIDRILEVAESLYRGFPIEPKFHTEHILRNVPLMNRFFDLRDCALPLVVLMTNSQTGRNDFYVQVKHHLKRYFKMH
TSGILHFTNCCYGFWYSRATNCYYYLDPYQCDTDGKKTCVNGNACLCIFSSIRQMVKHMCLNQYEGTTGFFLHRIHVNSI
DAPPFEKFQEDPMWLYLDYHWNFTHSIMRSCKKVKYGDRSKTNRQFWNNYAIEVIGLIYSIWGTIGAYDCRFGERAGKNS
VAICVAVLAMWNLCHPSRWSPAILDSAVICGDSYYTESLKSLMQNYSKSDNRFGLQTSFKIFPHSWTVDFGTSVCGILYG
DRNSLTLTDALNLAFEEARNIIIECNKITLAALTAKDAYYVADPCWIGPPLFPKNRGAIYVLRCKNINVLIYAITKMFNT
NQRLSVYVTPLSLAFDREDFDADLCTTRRKILPTSVQKVPGKIEDPGIPIPGAVVVPDEDSYLPIYRQRFVEGTARDSQL
ENLQLRRTECVLNPENANNALVSTKWRMNLGQARSWKRPKLPLDFIETKDDLLKFDSLTDPYKTRVSFTDLITASNRYPR
PIDFTSDEPPPRIELFENVSERGFIREQSRVDFDKSVAEMSQENYASYQHRLPKNEKTLIKTEIPNIHSESSDVTTDTEQ
E
```

1020 - 1039:	EEEEEEEEEEEEEEEEEEEE
1021 - 1040:	EEEEEEEEEEEEEEEEEEEE

A0A195D7Z8 **A0A195D7Z8_9HYME** (448 aa)
Troponin T. *Trachymyrmex cornetzi*

```
MEFWGISRDLPESGLNRRDLKRVTFLFTPASFRESGENPEFMKRQEQKRSDLDEQLKEYIAEWRKQRAKEEEELKKLKEK
QAKRKVTRADEEKRLAQKKKEEEERRQREIEEKKQRDIEEKRRRLEESEKKRQAMMQAMKDQSKAKGPNFTITKKDLSGN
LTSAQLERNKTKEQLEEEKKISLSIRIKPLEIEGLSIDKLRGKATELWEAIVKLETEKYDLEERQKRQDYDLKELKERQK
QQLRHKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYDTLLAETNEKTWKQRTEQFMKRNKTLTSP
REDLYNPEKATVRRERVFPGDPDGLTDQQKEIIEKMWAQQKEQFMGRQKTKLPKWFGERPGKKSGDPESPEGEEDVKATV
DDDLEPQFDEEEEEEVKEEEEEVEEEEEEEEEEEEEEEEEEEEEEEE
```

424 - 443:	EEEEEEEEEEEEEEEEEEEE
425 - 444:	EEEEEEEEEEEEEEEEEEEE
426 - 445:	EEEEEEEEEEEEEEEEEEEE
427 - 446:	EEEEEEEEEEEEEEEEEEEE
428 - 447:	EEEEEEEEEEEEEEEEEEEE
429 - 448:	EEEEEEEEEEEEEEEEEEEE

A0A195EF44 **A0A195EF44_9HYME** (2560 aa)
Uncharacterized protein. *Trachymyrmex cornetzi*

```
MEFKKEAAFDMNKEKAKLFKTKIKQLAEYNEIVSAETINVIGDVTKDVTKDMTKDDAPSSDEFDEDLEEEYRNLNNILDL
PNDTYSLTKITTELPLCVKYGVRSSLIHSNMPYFSPLSRGYQGGAIAIAAFATTAIHKSRCWNEAVIDQIVEDGDTFYCE
SYKDVNTDDRRTMTILDLKRILLLQKKFNVEVKIEDPAYAGKFRSRNPTELHLAKALELFFERHNAGILTSPVLNIAIWK
NSKYYYIFDGQARRESGDPAADRVSGSAKLFLVKDLIGLLFIILEKSNVRNESFVIYPIFINNVEMILPEDAEEAAKILE
KPRRRPSGYKICKKYRAIVQGSCHLTHPAFPEVLRGKGHLIIAVAALIYSRLINANKWTTALINLIFNQANIYLIDLVRV
LEKKLDNEFELRLDDLMSDIILGVYSAKVKIDANIISSQTQKGKSSIDIGIKEFFETQKLGILEIEKIFYAIWKDGDSYY
FFNPFACDDEGFRIDTDSDREHTTHDTTRDVACVTMNSTVNDVVEIVMENIGNEESDPFLIHGVKVLYVKTGVTPSGPFE
EVIYRESGTNRRPRAPPPPVPMDTTKVDLIDATPRLRPESRKFADVSIQYPELMQDIDQYMMTVDEPVTFIIAQEKAKKI
KKIEEEEKEEEEEEEEEEEMKVGFIRGYNLINDHCLIVHGSKTCMDLTYNLRSQGRQGLIIALTALAYRKLKDPTRWRSI
DVDQILNIGNKAYEQVITWIQQGRPEIKEVKEKKLKEEEEEEEEEEEEAEEEEEEEEEEVEEEEEEEEEEEEEEEEEEKE
AVVRKVARAPSHLDISLLPPRLKLAENNVFFKTRMNVANGDANPLANLAEALERYFERYPEMILENNRLMYAIWKEDGKF
FLFNPYGSDQEGWRFWQYRAGFNVTDRFNELIKLLYGILEYNNSHFSLHFVALDAIEPGKYKSSVEIVIPDEKTEKFQTK
FLPITDDDLLKLEEKKLDVDVEVIKELVDKKDVVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEK
ELKEFLKEDPTLLIEESVQPDAPYRLNLALLTSTVKIQDPTEEELKSLPEEVIMEKMKYDHPPPYVMPPRGTLRVLLKAK
LANKSIPSLVSRFSIDSRLEIKKGDVPVDSTLATIVPLLRDMKPSKMIKLSFRKYLYSRLPPIHMVPLRAIDESYIQDKE
IDKAIDEKYLGQEKLEKKEEDKMLGKLPRVSYVRPELIPCGAIIKTPVLVIKHLTYLDERKRVLKTEEIAPTIKKTITDA
EKLLFKLKLLKFQLDVPLQPLNKINNNKAKKMKKMIIKAEFFDKKIDLSSSEIIGFKVMDEDTEIIQGNHSLSDRTRIGP
SHFKPCFISAILCILAKNMLNADRFCDSILDYLIFSANSIDQQIGKLRYNGYRTFDKVIVRDTSFNVILKEMVYANPESS
PSDELDAVVSKFLENNQTGILVLANCAYAFWTADDKYYLFDPYPCDERGKANEEGYCCLMRFRNLKSMLDRIKENAGETA
RKPFCVYSVSITYAEMKRRKRRKGIKRRPKLEEVRKELIYSEEKQNVSTPIVKSKVSLIELAEWVTAGPELDPRCDVTVA
GFTPMRHYEASMLEEVVLENDITTPTLAPFELFLDDEDRAKMAKVRIIPSERIFHNNSSIQIPIHLCIMAWSLIHDPASW
SERTIDGLIEAATDYAYDSVLANEDTSVSDMTDAVLPEFEIANYVFRAVFAPLHYGFLYATEGWNLAMTLEKIFETAIYT
GAIIVCHSAHIGVTKCGKNYFAWWTVTGTKSLRIIATSSFDEFLKLIVKVINMPQTIRFTVRAITISHALKMAPDFSDVK
GLHESKVTTASLPEIYRKELQDSYDVKAIFKPIDPAPKPIFILGTVALCNRDSLLEPRMKRCYFIALLAVVIKRDIVQSP
LPGMIDRILEVAENLYRGFPAEPKFHAEHILRNVPLMNRFFDLRDCALPLVVLTTNSQTGRNDFYVQVKHHLKRYFKMHT
SGILHFTNCCYGFWYSRATNCYYYLDPYQCDTDGRKTYANGNACLCIFSCVRQMVKHMCLNQYEGTTGFFLHRIHVNSIN
APPFEKFQEDPMWLYLDYHWNFTHSIMRSRKKAKYRDRSKVNRQFWNNYAIEVTGLIYSIWGTIGAYDCRFGERAGKNCV
AICVAVLAMRNLCHPSRWSPAILDSAVICGDSYYTESLKSLMQSCSKFDNRFGLQTSFKIFPHSWTVDFGTSVCGILYGE
QNSLTLTNALNFAFEEARNVIIECNRIALAVLATKDAYYVADSCWIGPPLFPRNRGAIYVLRCKNMNVLIYVITKMFNTN
```

QRLSVYITPLNLAFDREDFETDLCITRRKILPTSVQKVPGKIEDPAIPIPGAVVVPDEDSYLHIYRQRLAEGIARDSQLE
SLQLCHAECVLNPENANNALVSTKWRMNVGQARSRKRPKLPLDSVETKDDLLESDSLMDPYKTRIFITDLITASNRYPRP
IDFTSNEPPPRIELLENISERGFIREQSRVDFDKSVAEMSQENYASYQHHLPKNEKTPIKTEILDIYSESSDVTTDTERE

995 - 1014:	EEEEEEEEEEEEEEEEEEEE
996 - 1015:	EEEEEEEEEEEEEEEEEEEE
997 - 1016:	EEEEEEEEEEEEEEEEEEEE
998 - 1017:	EEEEEEEEEEEEEEEEEEEE
999 - 1018:	EEEEEEEEEEEEEEEEEEEE
1000 - 1019:	EEEEEEEEEEEEEEEEEEEE
1001 - 1020:	EEEEEEEEEEEEEEEEEEEE
1002 - 1021:	EEEEEEEEEEEEEEEEEEEE
1003 - 1022:	EEEEEEEEEEEEEEEEEEEE
1004 - 1023:	EEEEEEEEEEEEEEEEEEEE
1005 - 1024:	EEEEEEEEEEEEEEEEEEEE
1006 - 1025:	EEEEEEEEEEEEEEEEEEEE
1007 - 1026:	EEEEEEEEEEEEEEEEEEEE
1008 - 1027:	EEEEEEEEEEEEEEEEEEEE
1009 - 1028:	EEEEEEEEEEEEEEEEEEEE
1010 - 1029:	EEEEEEEEEEEEEEEEEEEE
1011 - 1030:	EEEEEEEEEEEEEEEEEEEE
1012 - 1031:	EEEEEEEEEEEEEEEEEEEE
1013 - 1032:	EEEEEEEEEEEEEEEEEEEE
1014 - 1033:	EEEEEEEEEEEEEEEEEEEE

A0A195ERG3 **A0A195ERG3_9HYME** (423 aa)
Troponin T. *Trachymyrmex septentrionalis*

MEFWGISRDLPESKLNRDLKRVTFVFTPASFRESGENPEFMKRQEQKRSDLDEQLKEYIAEWRKQRAKEEEELKKLKEKQ
AKRKVTRADEEKRLAQKKKEEEERRQREIEEKKQRDIEEKRRRLEESEKKRQAMMQAMKDQSKAKGPNFTITKKDLSGNL
SSAQLERNKTKEQLEEEKKISLSIRIKPLEIEGLSIDKLRGKATELWEAIVKLETEKYDLEERQKRQDYDLKELKERQKQ
QLRHKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYDTLLAETNEKTWKQRTELFMKRNKTLTGLT
DQQKEIIEKMWAQQKEQFMGRQKTKLPKWFGERPGKKAGDPESPEGEEDVKAAVDDDLEEPQFDEEEEEEVKEEEEEVEE
EEEEEEEEEEEEEEEEEEEEE

399 - 418:	EEEEEEEEEEEEEEEEEEEE
400 - 419:	EEEEEEEEEEEEEEEEEEEE
401 - 420:	EEEEEEEEEEEEEEEEEEEE
402 - 421:	EEEEEEEEEEEEEEEEEEEE
403 - 422:	EEEEEEEEEEEEEEEEEEEE
404 - 423:	EEEEEEEEEEEEEEEEEEEE

A0A195EWC3 **A0A195EWC3_9HYME** (1124 aa)
MOG interacting and ectopic P-granules protein 1. *Trachymyrmex septentrionalis*

MIIPNGVNGNYSADNEEYMDTSDNTSKTALKDVIAEEEEEEEEEEEEEEEEEEEEEGDEDEEEEEEEDMDEQYDEDDHERA
VNIQEGKDEDSDRNEEIGNTSKEGEMFDLKNDFKVSNSPDGVSETNNSSEVSKTEISECVKNTSCEAMDVDEQSNNSDIE
CLDESITEIQLDNDDMDNDDFLSKKTIEKHDNDVSSNCSCDSSEIADSSMEKSDVKLCEENGSCGSPDIEEITDSAKSND
HDSSLDRAIKDPSKQRKPRKQVDLSSITPRRSSRNIKRTSYIEKELEEEVEDDGSDIEEIKPEDPLAGIDSKDKENSKLK
SPVRNSKTTIVVNDTKRLVEIAAGSKSIKGGKKEPTLVIIDTNSILSGRGGVPVSNSKPHHTVSNSNPFSVVPMSGMTTQ
TMYPNMRTTITPVPMTSKAAQLSPKTSSMTTVTPTVPPILPTLTDDMFVVEAPSFIVPYVYEKPPLKPLKEFVTKLERNI
EEIEKEERMKRLADENKDNEDYKEDSLDVKRGNDKSEDSDVEGKGKREGDDRGDNSIDLIEHGFSSLSDKHDLRQDDRNK
IPTYFDLPLGKFFMQIGMNLVQEYVQTDLLRTQKRKQGKGSTSAETQLAINSLIKNLEFSKENNEPFHLEMKKCEFCSFK
TESTLVMQHHLETPHMRNYVYKCNFCPMEVRSPHDILYHMEAEHNTRGRLERGPAFHQCPNCPFEDNQKGKLTRHILACT
KKFRPERNLEPAVDWEPPAKIPRVNRARPVGPTNPNALAAMAMSAKGPQPLLPKLLPAPITGRGRGRPPMQPRYSDLKTL
RPGATPMRQDNVAGMMYRPTSSGLLVPTSYQFSSNQIFQVMGGSGTVMSAVSGVSSSSGGSSGQPTPIALVPNVIDSLSR
LSSSQNTTASSKNPTAKLLSQPSISITPLPRTTSQTSIPGSGTSSKSGGKNTFVICEICDGYIKDLEQLRNHMQWIHKVK
IHPKMIYNRPPLNCQKCQFRFFTDQGLERHLLGSHGLVTSSMQEAANKGKDAGRCPACGRVYQWKLLNHVARDHGMTLKP
AHLSYKCTVCTATFGMYKQFENHVYSAHSVVAKRVMDKKNTPASPSSRSNDSLLKPLKINDEITIIPQPAKPTTRSGAIQ
GRGK

36 - 55:	EEEEEEEEEEEEEEEEEEEE

A0A195EYV9 **A0A195EYV9_9HYME** (313 aa)
Uncharacterized protein. *Trachymyrmex septentrionalis*

```
MAVPPDSSRVRDNVRGQTLMIFSAGVVTPPRNITFQRHSQNGRTFRSLGNEMVRGKIAATYAGNLFGGNLRASFRVRTNT
WALLTWNLKRSATRALALTSRSRECNAGEITARPDRTNISPEGEGAGAAGRISSESITARYAKYATTVHSTPVIVDTMAR
NDCFTPPLARELGNKLAVGLISLSRPMATRKARPDEEFRRNHQKIAKGEATRRRSWKKVEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEARPQRRDEEGARALADGGESLRRVARRSYRRYHGGSALSSKSVSSPLVFSLSLVSPTNPSDTPT
```

220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEEE
225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE

A0A195F640 **A0A195F640_9HYME** (303 aa)
Uncharacterized protein (Fragment). *Trachymyrmex septentrionalis*

```
SFLSRFFPCLTHRIIQSSTIGNVENYYVMDGHVEFTLLSIEIRNGKQWLSFKRRSTNSFELTVRHHHESLRKYYTGWPKI
SGCTDVGSKRERKGEGERCVFLSEFPVVIYQTGKIVSDGWTAARNFSSKSREEEEEEEEEEEEEEEEEEEEAKREKREEE
ECFGIASRGHAPRVHVCPHPLIRGLIGRAGAIECQTGRTVRKSPVGAVSLSHATTRGQRAPSRGAFDVSHTGTLGTLPTR
QADVTARGNAQGVSSKPEEPCRCSPYALYLGPRAGQIRLLRTNGVHPSGAFLGGRTPPSRIFL
```

132 - 151:	EEEEEEEEEEEEEEEEEEEE

A0A195FFC5 **A0A195FFC5_9HYME** (167 aa)
Uncharacterized protein. *Trachymyrmex septentrionalis*

```
MFRVYFSTFVLPYQLIAAEEMVGVRHVTNLYLKRLADVVDIEITQRDIRGTSIVGSSKKSLHNDQPIYGGIIVTYRSYSI
RRRGERTEEEKEEEEEEEEEEEEGEEEEEEEEEEEEEEEEEEEEEEDGLYLFGRREGRPSDSIRYKKGRRTPSARMRKVM
SRKITGR
```

105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE

A0A195FGU2 **A0A195FGU2_9HYME** (242 aa)
Uncharacterized protein. *Trachymyrmex septentrionalis*

```
MLGSKEREKGTTTTNDDDEKRGRGWKEFENFLRGGKIVALLAPRSQLTGDNPKVTSGAGYWRHEKQSSIAIAGRNRERET
TVSPGPIPISQLDIRFIDIFSQSFERQTRSNRSHSEISRILEEEEEEEEEEEEEEEEEEEEEEEADKRKEKETSWLVVPS
RVAAVYFIGNSRREKSSVHCTVDESCPGLPEEPNEPSRFMFVRAVMALTPREVSSKAKPSAIFPNQRARLDVEGTISKGI
RD
```

122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE

A0A195FUA1 **A0A195FUA1_9HYME** (138 aa)
Uncharacterized protein. *Trachymyrmex septentrionalis*

```
MYREEEEEEEEEEEEEEEEEEEEEADEDEEEREEEDDNNDDEEETTTIEGVCPLGRRRCFSILFLVDAPLVRFCCPCSTLL
IFLPTFCPLVSDQSSRWPFCVRCAGGEGENNRRECHGRKGEPSPIHGLFTGIVDRKIN
```

4 - 23:	EEEEEEEEEEEEEEEEEEEE

A0A195FVX9 **A0A195FVX9_9HYME** (2571 aa)
Uncharacterized protein. *Trachymyrmex septentrionalis*

```
MELEKEAAFDMNKEKAKLFKTKIKQLAEYNEIVSAETINAIGDVTKDVTKAMTKDDAPSSDEFDEDLEEEYRNLNNMLDL
PNDTYSLTKITAELPLCVKYGVRSGLIHSNMPYFSPLSRGYQGGAIAIAAFATTGIHKSRYWNEAIIDQIVEDGDTFYCE
SYKDVNTDDRRTMTILDLKRILLLQKKFNVEVKIEDPVYAGKFRSRNPIELHLAKALELFFERHNAGILTSPVLNIAIWK
NSKYYYIFDGQARRESGNPAVDRVSGSAKLFLVKDLIGLLFIILEKSNVQNESFVIYPIFINNVEMILPEDAEEAAKIVE
```

```
KPRRRPSGYKIYEKYRAIVQGSYHLTHPAIPEALRGKGHLIIAMAALIYSRLINANKWTTALINLIFNQANIYLIDLVRV
LEKKFDNEFELCLDDLMSDIILGVYSAKVKVDANVISSQTQKNLIEIGIKEFFETQELGILEIKKIFYAIWKDDDSYYFF
NPFACDDEGFRIDYSDTERTHDTTRDVACVTMNNTVNDVVEIVLENIGNEESDPFLIHGVKVLYVKTGVTPSGPFEKVIY
RESGTNRRPRMPSPIPMDTTKIDLIDVTPRLRPEFKADVSIQYPELMQDIDQYMMTVDEPVTFIIAQEKAKKIKKIEEEE
EEEEEEEEEEEEEEEKEEKEKKEEKEKEEEKEKEEEKEKEEKEKKEKEKEEEEEEEEEIEVDVIKGYDLINNHCLNVRGTK
TCMDITYNLRSQGRQGLIIALTALAYRKLKNPMRWRCIDVNQILNVGNKAYEEVITWIQQGRPKIKEVEEKKEEEEEEEE
EEEEEEVEEEEEEEEEEEEEKEEEEEEEEEEAVVRKVARAPSHLDISLLPPILKLAENNVFFKTRMDVATGDANPLANLAEA
LERYFERYTEMILENNRLMYAIWKEDGKFFLFNPYGSDQEGWRFWQYSAGFNVTDRFNELIKLLYGILEYNNSRFSLHFV
AVDAIEPGKYKSSVEIVIPDEKTEKFQTKFLPITDDDLLELEEKKLDVDVEVITEFVDKKDTVEEEEEEEEEEEEEEEEE
KEEEEEEEEEEEEEEEEEEEKEKDKVEEKELDEFLKEDPTLLVEESVQPDAPYRLNLALLTSTVKIQDPTEEELKSLPE
EVIMEKMKYDHPPPYVMPPRGTLRVLLEAKLANKSIPSLVSRFSIDSRLEIKKGDVPVDSTLATIVPLLRDTKPSKMIKL
SLRKYLYSRLPPIRIMPLRAIDESYIQDKEIDKAIDDLEREKLKKREEDKTLGKLPKVSYVRLEMIPRGPIIKTPVLVIK
HLTYPDERKRALKTEEIAPTITDVEKLLFKLKFLKFQLDMPLQPLNKINNNKAKKMKKMIIKAEYFDKKIDLPSSEIIGF
KVVDEDTEIIQGNYSLSNRTRIKPYHFKACFISAILCILAKDILNVDRFCDSILDYLIFSANSIDQQICKLRCNGYKTFD
KVIVLDTNFNIILKEIICANPESSPSDELDAVVSKFLENNQSGILVLANCAYAFWTADDKYYLFDPYPCDVRGKANEEGY
CCLMRFRNLKTMLDRIKENAGKTARKPFRIYSVLFTYTKMKRRKGIERRLKLEEVTKELIFSKEKQEVLTPTVQSEVSLI
ELAEWVTAGPELDPHYDIAVAGFIPMRHYEASMLEEVVLENDITTPTLAPFELFLDDEDHVKMAKERIIPPERIFHDNSS
IQIPIDLCIMAWSLIHDPASWSERTIDGLIEAATDYAYDSVLANEDTSVIDMTDAVLPEFEIANYVFRAVFAPLHNGFLY
TTEGWNLVMTLEKIFETAIYTGAIIVCNSVHIGVTKCGKNYFAWWTVTGTKNLRIIATSNFDEFLKLIVKVINMPQTIGF
IARAITISHALKMAPDFSDVKGLHKPKVTTASLPEIYRKELQDSYDVKTIFKPTDPISKPIFILGTVALRNRDSLLEPQM
KRCYFIALLAVVIKRDIVQSPLPGMIDRILEVAENLYRGFPAESKFHAEHILRNVPLMNRFFDLRDCALPLVVLTMNSQT
GRNDFYVQVKHHLKRYFKMHTSGILHFTNCCYGFWYSRTTNCYYYLDPYQCDTDGRKTCVNGNACLCIFSRVRHMVKHMC
LNQYEGTTGFFLHRIHVNSINAPPFEKFQEDPMWLYLDYHWNFTHSIMRSRNKAKCSDRSKANHQFWNNYAIEVIGLIYS
IWGTIGAYDCRFGERAGKNCVAICVAVLAMRNLCHPSRWSPAILDSAVICGDSYYTESLKSLMRCSKPDNRFGLQTSFKI
FPHSWTIDFGTSVCGILYGEQNSLTLTDALNFAFEEACTVIIECNRIALAALAAKDAYYIADPCWIGQPLFLRNRGAIYV
LRCKNINVLIYVITKMFNTNQRLTVYITPINLAFDREDFETDLCTTRRKILPTVVQKVPGKIKDPPIPIPGAVIVPDEDS
YLHIYRQHLAEGIVRDSQLESLPLYCAEYVLNPENVNNALVSTKWRMNLGQARSRKRPKLPLNSVEIKDDLLESDSLTNL
YKTQISITDLITASNRYPRPIDFASNEPPRIETLENISKRSIREQSHVDFDKNVAEISQENYASSQQLPKSLIKTEISDI
SANVTTDIEQE
```

1042 - 1061:	EEEEEEEEEEEEEEEEEEEE

A0A199UQM3 **A0A199UQM3_ANACO** (330 aa)
Zinc-finger homeodomain protein 1 (zinc-finger homeodomain protein 2-like). *Ananas comosus (Pineapple) (Ananas ananas)*

```
MEFEEHDEAEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEMEVAAAGSSYEGPSGAGNSRREDQGGGAASGRGGGGAEGGPG
GSSIIINRKMTGAGGGGGRYRECLKNHAVGIGGHAVDGCGEFMAAGEEGTLDALRCAACSCHRNFHRKESPDSAAAITDA
ALPTAAAAALQYQYHHHQQFSPYYRTPAGYLHQPPPHLQISASAAGQQHRAPPPPPALALPSTSGGGREEGEDVSNPAMM
MMMMMGGGGAGAGAGAASGSGGGASGKKRFRTKFTQEQKDKMLAFAERVGWRLQKHDEAAVQQFCTDACIKRHVLKVWMH
NNKHTLGKKP
```

10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE

A0A199US15 **A0A199US15_ANACO** (586 aa)
Tetratricopeptide repeat protein 1. *Ananas comosus (Pineapple) (Ananas ananas)*

```
MPRSDDSSHVLVASFVWNLAMSDPDDPELPSAGALRCMALLIARALDDDAGPSWLRRHQNVYIPYYAAHVIGSYTIRVPS
LAALAVEEGAVAPLLGLMRGSMTWVEQRVAVRALGHLASYDATYPAVARHADELVPLAMHIASACLGRVYAEFLAVSPPQ
RERYHRDLLTRGLGGAETENRKAEEWASQLQCWSLYLLSCFAFRDRRTHGLVCRDAEFLNDLCRMWGGVVNADSPAGAGL
MRLLCRSRVGRCSIVACPRVVDSLCSLSRSSDDWQYMGIDCLLLLLDDPVTRLRAANIAAPCLVDLAELRCLGPRKNVGD
AIARSLLQQQQQQLDNYDDTSPQNLSQEAELAIKNLWVLKIERKEREEAMSLDELGKRKALAALKKQEGNEKFYTGDLEG
AMASYTEALELCPLKRRKDRVVLYSNRAQCRLLLREPDAAVSDATRALSLPRQANGHGKSLWRRSQAYDMKGMAKESLMD
CLMFANRWWFEEKKGSGAKLPYYVVRMINKQMGAAWLFADAALRSKVVNKDGDVDGDGGGGGGDEWEEEEEEEEEEEE
EEEEEEEEEDNVLETSVSGKLLTISP
```

548 - 567:	EEEEEEEEEEEEEEEEEEEE
549 - 568:	EEEEEEEEEEEEEEEEEEEE
550 - 569:	EEEEEEEEEEEEEEEEEEEE

A0A199UXQ1 **A0A199UXQ1_ANACO** (306 aa)
Coiled-coil domain-containing protein 97. *Ananas comosus (Pineapple) (Ananas ananas)*

```
MERSAMEGIAARLSAIQGLYFPGAIHRGGAPDPSSLRHSALLRLLSRDPPLFLERYGSELTAEELDAFDALGNDYEVAWH
LARLRRVRETPTVQETRARLATVKNRRRAYMERLVRGGEYFSEEAMREREPYLHHEYLGQFQDPAGRAMSRPGERWSETL
LRRCEEAAIVEKIRGEQQRRGVDRREWVGGCAREEEEEEEEEEEEEEEEEEEEEEEEEAAKMPPDEGRESNTGGAEGEATE
NFQPTLSGEEMQDQLEQFTLIMQQKFLAGEDTEHFDYSQIDNDERLDDHWVREANYDAEEKYFEED
```

194 - 213:	EEEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEEE

196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEEE

A0A199V1Y4 **A0A199V1Y4_ANACO** (438 aa)
Putative chromo domain-containing protein LHP1. *Ananas comosus (Pineapple) (Ananas ananas)*

```
MRGARKKKKIAAEVGAEHHQKQKPQGGRRRRGGDDERGEEEEKRRGEEEEEEEEEEEEEEEEEEEEEEEKGEEEGKEEEE
DRGAPKLEDGFYEIEDIRKKRVRKGQTQYLIKWRGWPESANTWEPYDNIESCKDMIEAFEERSRFPRSSGSAGASAGPHF
IAKKKRSSSAPAADKSPAEHPASVAVVDGDGRDMTTEACIAAGREEGLVGVETNKDTNNKKKRKKKKKKKKSNNNGKKNS
ADDEAVANGPPREVREDEQMRKSAVPAASEQEGPKSMPQGVISISLPGRQEEEGPTDGFSKIESAQPALSQQGNQVTGAK
RRKSGCVRRFKVDSLQNGAERGGRGEKAGNEDVDSTEDDTGDKNKLDECSNQVSITKIIKPVRYFASITNDVQEVSITFK
ALRSDGKEVLVDDKELKANYPLVLINFYEQHIRYNPNS
```

47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE

A0A1A5ZTV6 **A0A1A5ZTV6_9TREE** (1849 aa)
Uncharacterized protein. *Kwoniella dejecticola CBS 10117*

```
MLRSHVLPNGGAKGIKQPGPYDLFPPPAVASWLDDLQAKIARGLNPPDSPGPSRSPSPVVPTIEREEESQYVENDVELYG
KETDESDTGLIGEDEEEDDSEGVFGHEERDGVSGNGEDQDVYENGQKEVLDAQDDHGVFDDESLANQDELDNHDVGGDPD
QTQEDEENPFETPQQPLFEMYDGQEAEDNDDDEEDVLAEEGTPSPLAQSVNEEERDVEQDEEDELFDTRSEAGYDPEYGV
VPEEDGAAYVGSDGDVYGDEDQTEEEDEEGEESEEEEEEEQEEVEEEDDGIEYLGTSESPAPKQPSSLPMNTLYPTLPAP
PSGFVEHDTTFESQDQINQLPAAFSEDAIDPSLLAEIVQQVHEAMPEDAGSSLHLPHVQQPENIPTGSSSFDPALPIEQI
IEGTEHGYGHGDSQGENAYEQGLPDENDDQDELADGDEVEIGSRASSDDNQEEEVQSKVPIFTEVIEIGSSSDEDENEDE
EEGAQYYGYPSEEEEEVESDGQIQEDTDEEPNAISGDAQPHSSEDEEEAMEDHEDELLMEAGGSFDVTHEVEMRAEEASL
GESREQPPQEAIMYDGEVIEDRHSYIPSVEEPATPAVTDGTAFFFEPDQPIQVDDIQMMETTGSIDLEQPFAVETPLTEA
GLFSFTTMPSTYIDTVVEELMEDGEPITEGSSSTSEHTIVHLQTNEVGIELSTVTTPNFTDEVMTSVDTMKELEDANFSP
MRTPGGEDAIGPFNAEEFMSFDVPEFTASTSGGSDMALHSLSSSTGDLADPITDPLVEAQTLVQDQVLHAEDVNTAESSF
HNLADGTATYQDPPSEFVITQDLAADSRFGDAQPGPREELPDPKLSPPDANTLMPLVPHDTRPSVERSPSLAVEPPEHDP
LPEDVPTSAVSRSSTPTALPDPTVPPPNTSAHQPLDIHTMIPHENDTPSLVVEIPQDPIPAEIASAIPSRAATPTALPDP
SLPAADTFTIGPLDPHDLVPHPPSSPSLIVEPPGKDPIPSDIYSAPATREATPTELPDPKLPPPDSYLDAPITPHQLTPS
EAVQTPSLQVEAATDSPAPNMSRIPSALAASSHLSNVDVMSESADEDIQVHIRWNEPDAPAGADFEPTVDETDIQGEPPA
MQGHDGNSPAEVGDKADKESKDAEIRVDDLDRQTPSREDKASSPPVQVQDGTDGRSDDGDIQIEVRRISPAADQGSPAAH
GDDADVAEEPNNTPLAGESSTSRLDSAVEINDTKDSGSAAMFDALEEYVKAADEASSTVAEKIADITAHDGEPLKTESPL
KPPFLPHVSESTLERLFHRHGSPDKASASGPSLTTATHRRTRSRGRPSASLEPPATRSHCYYEKLRVSDDDLTAVILVPH
CAIPDVKQLEQETSQSEGKSTTEEEAEGRLQPIDHEHPMLQPQLTTKIRRLVGAQLFDEGHCYILYAHDDARLPDREASD
TPRGTPVQRGRKRKSFGSNSRLSAEIDEDQDISVKVEDFATPAKRPAVSPPATRSGRKRISASASGSLEPDAELDITPAR
RGRGGSARPSSAKKGKARESSIISETGSRTSTTASPGPPLRRSARMSVARGENIPEVDEGTPQAEIEYDTPPAPSAVDRL
DSLPPPEVQPRRSTRKSLRGKQASPTHTPEPQAKNADQDEATPVPEDVEMSTSSSSKSRSPRKPLSLATKADEAPYRPYE
DEEEAEEEEEEEEEEEEEEEEEEEEEVEPLSSTKSTFSVEIPSTKKRKSRASEQVEDEQENPGSSSTPKKRKARKHSEGG
VAIADEGPRRETRGMKRRAIESESSPDKPQAVTAKDEDEDGDGDGLENEGGNIVAKTGTEVVSASSREESKEERKGSGGF
WNKFGWGKR
```

1686 - 1705:	EEEEEEEEEEEEEEEEEEEE
1687 - 1706:	EEEEEEEEEEEEEEEEEEEE

A0A1A6FWA3 **A0A1A6FWA3_NEOLE** (401 aa)
DUF3496 domain-containing protein (Fragment). *Neotoma lepida (Desert woodrat)*

```
MFNVFYVKPCCIKAIQKKERRRRRRRRRRRRRRKKKKKKKKKKKKKNNNKKKKKKEEEEEEEEEEEEEEEEEEEEEEEKKK
RRRKEEKKKKKKKRRRTRRTRRTRTRRTRRRKRKKEKKRKEKKREKKRKEKKRKEKKRKEKKSNPWVIPHNVAINDDL
TAKLETASSKCQHLHQENQLLQQELLSMKIIQKKCEKLKKNKKKLEQEIVNLKSHMEKNMIECGQIEQYKWEIEEKTKQD
LVEKLKQVNLFLQTQAAYEDKLEKLRHKQNASVRTQMELRIRDLESEFSKMKSQVDCNQIEMENYKHLYLEEVKIRKLLS
NKLSKTDERLAKVKTKLLLERKQNRASQYSTINTRSVLESTCPRDLSNRLFIPRSFSGENVMVPTSNLWHSIETMENCKT
K
```

55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE

A0A1A6FXD6 **A0A1A6FXD6_NEOLE** (676 aa)
Uncharacterized protein. *Neotoma lepida (Desert woodrat)*

```
MLQYDTTMLYYDITMLYYDNIMFYYDITMLHYDITMPHYDITMPHYEITMLYYDITMLYYDKRMVYYNITMLYYDITMLH
YDITKLYYDVTMLYYDITKLYYDITMLYYDITKLYYDITMLYYDITMLYYDNRMVYYDITMFHYDTTMLHYDITMFYYDV
TMLYYNFTMPHYDIKMLYYDITMLYYDNRMLYYDITMFCYDITMLHYDITISPMVLNWALWRLQTGDDDDEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEXKRKRKRKRKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKTASTLH
SCFEIPLDFYCSTQSTGLGFMARMPLSLQGASCTYLGDVKSKIPSCEETGGAAFYLGVFLMQLPVWLRLHHPHLKRLGLL
ARVQASTGPQAAEPAFRARQNMAPSQRGQDHSLSLFKQHPETRRSLPSGLSPRSPVCGARESPWKGKQQEQQQQQLWLHA
VGRAYGPSGGSGLAGSYGMSRIIAVVIEYTYIIMDPSLHLAFHISRKLNKHVSQKDQSPVTVLPDTIIFAVDKIIAKPPT
YKNEESMSQNGFKKKTAGFANKTFKTLSITVSSLLSGCLYEDPGQIQVVHQNLAGIFKSLPKELCCCYYNIRAPERNGLT
GKMVTCGVTKYNIVFEENTADKQFAVILWNLISAGM
```

231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE
239 - 258:	EEEEEEEEEEEEEEEEEEEE
240 - 259:	EEEEEEEEEEEEEEEEEEEE
241 - 260:	EEEEEEEEEEEEEEEEEEEE
242 - 261:	EEEEEEEEEEEEEEEEEEEE
243 - 262:	EEEEEEEEEEEEEEEEEEEE
244 - 263:	EEEEEEEEEEEEEEEEEEEE
245 - 264:	EEEEEEEEEEEEEEEEEEEE
246 - 265:	EEEEEEEEEEEEEEEEEEEE
247 - 266:	EEEEEEEEEEEEEEEEEEEE
248 - 267:	EEEEEEEEEEEEEEEEEEEE
249 - 268:	EEEEEEEEEEEEEEEEEEEE
250 - 269:	EEEEEEEEEEEEEEEEEEEE
251 - 270:	EEEEEEEEEEEEEEEEEEEE
252 - 271:	EEEEEEEEEEEEEEEEEEEE
253 - 272:	EEEEEEEEEEEEEEEEEEEE
254 - 273:	EEEEEEEEEEEEEEEEEEEE
255 - 274:	EEEEEEEEEEEEEEEEEEEE
256 - 275:	EEEEEEEEEEEEEEEEEEEE

A0A1A6G2T1 **A0A1A6G2T1_NEOLE** (1032 aa)
Uncharacterized protein (Fragment). *Neotoma lepida (Desert woodrat)*

```
HFRMSDDMQSLGKVTSDVAKRRKLNSGSLSEDFGAARGSGDVTLEKGEPRPLEEWETVVGDDFSLYYDSYSVDERVDSDS
KSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPR
AKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKC
MATESVDGELSGCNAAILKRETMRPSSRVALMVLCEAHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQ
LNGMVFCPHCGEDASEAQEVTIPRGDGGTPPAGTAAPAPLPLAQDAPGRADTSQPRYWPLPPLPPAPCPILSPLPSDLRT
FSHSARMRGHGEPRRPPCDPLTDTIDSSGPSLTLPNGGCLSAVGLPPGPGREALEKALVIQESERRKKLRFHPRQLYLSV
KQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMV
QLGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIDVIRMLLTRGADVTLTDNEE
NICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVW
FALQLNRKLRLGVGNRAVRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVD
DCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRSCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTI
PQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAF
FSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELSSLPPINT
```

93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE

A0A1A6GG34 **A0A1A6GG34_NEOLE** (918 aa)
Uncharacterized protein (Fragment). *Neotoma lepida (Desert woodrat)*

```
MSAVKSQDRKRSEVQCSLTLTPDKFDAPLSGSAKKEREEEEEEEEEEEEEEEEEEEEEEEEEEEEEXKKKKKKKKKKKK
KKKKKKKKKKKKKKKKKVVTALQQRHCSENHMNHQASARGFLSEQESSQSIDLWVDHKSSPYTCYDKSFSSDPQSVPFFTK
WLFSPIGVLEPSGNIVTTFHVTVQDDNNIVVSLEASDLVSPASVYVVRVAGESKNYFFEFEEFNSTLPPPVVFKATYHEP
LPVTSVSIYDYKPSPETGVLFEIHYPEKYNVFSRVNISYLEGRDFRTMLYKGKSQEEPGEMMLYKGKSQEESGEMMLYKG
MSQEEPGEMMPYKDFFKGKTVFNHWLPGICYSNITFQLVSEATFNKSTLVEYSGVSHEPKQHRTAPYPPRNISVHFVNLN
KNNWEEPSGSFPEDSFIKPQNAIGRDRLFHFPEXTPETPPSNVSSGWPDPNSTDYESTSQPYWWDSASAAPENEEDFVSV
LPMDYDSDTTLSRTEKPTSDPFSAFPVQMTLSWLPPKPPTAFDGFNILIEREGPTGEWIEELTEKPQHVSVHVLSSTTAL
MSWTSSQENYNSTIVSVVSLTCQKQKESQRLEKQYCTQVNSSKPVIENLVPGAQYQVVMYLRKGPLIGPPSDPVTFAIVP
TGIKDLMLYPLGPTAVVLSWTRPYLGVFRKYVVEMFYFNPTTMTSEWTTYYEIAATVSLTASVRIANLLPAWYYNFRVTM
VTWGDPELSCCDSSTISFITGDIYNLSVTACTERGSNTSMLRLVKLEPAPPKSLFAVNKTQTSVTLLWVEEGVADFFEVL
CQQLGSSHDAKLQEPIAVASHVVTISSLLPATAYNCSVTSFSHNSPSVPAFIAVSTMEMNPNVVVISVLAILSTLLIGLL
LVTLVILRKKHLQMARECGAGTFVNFASLEREGKLPYS
```

38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE

A0A1A6GGA1 **A0A1A6GGA1_NEOLE** (131 aa)
Receptor protein serine/threonine kinase (EC 2.7.11.30). *Neotoma lepida (Desert woodrat)*

```
MAISLAYLHIEIVGTQGKSAIAHRDLKSKNSLVKKNGTCCIANLELAKKKKKKKKKKKKKKKKKKKKKKKKKKKXEEEE
EEEEEEEEEEEEEEEEEEEEEEEVVVVMNGLIFGSQSKKLQRTNKSTNATG
```

77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE

A0A1A6GGH7 **A0A1A6GGH7_NEOLE** (393 aa)
Alpha-type protein kinase domain-containing protein. *Neotoma lepida (Desert woodrat)*

```
MNTKTLQLPFSFPVSESGLLQLPEAEMDSKEKRAELEVQRAKCTQAALRASILVQDCAAAAAIVFLMDRFLYGLDVSGKL
LQVAKGLHKLQPSTPIAPQVVIRQARISVNSGGLHPLAPAGPHPACSQLLDLYRRSRASAGKLLKAEYILSSLISNNGAT
GMWYEAAELIWASVALLKEFDHRLLSAAEACKLAAAFSAYTPLFVLTATESEFQNCSLLEFSSILDSEISRYVGKEYKEW
KGLRHHFTDVERQMTAQHYILEDMTIKGCISVEPYILGEFVKLSNNTKVVKTEYKATEYGLAYGHFSYEFSKHRDVVVDL
QEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEILKPLKLLLFAFPAATTDETVPPGQSHEVDTKKAKHSYILEK
```

322 - 341:	EEEEEEEEEEEEEEEEEEEE
323 - 342:	EEEEEEEEEEEEEEEEEEEE
324 - 343:	EEEEEEEEEEEEEEEEEEEE
325 - 344:	EEEEEEEEEEEEEEEEEEEE
326 - 345:	EEEEEEEEEEEEEEEEEEEE
327 - 346:	EEEEEEEEEEEEEEEEEEEE
328 - 347:	EEEEEEEEEEEEEEEEEEEE
329 - 348:	EEEEEEEEEEEEEEEEEEEE
330 - 349:	EEEEEEEEEEEEEEEEEEEE
331 - 350:	EEEEEEEEEEEEEEEEEEEE
332 - 351:	EEEEEEEEEEEEEEEEEEEE

A0A1A6GKU5 **A0A1A6GKU5_NEOLE** (385 aa)
Protein kinase domain-containing protein (Fragment). *Neotoma lepida (Desert woodrat)*

```
MVMEYVSGGELFDYICKHGRVEEVEARRLFQQILSAVDYCHRHMVVHRDLKPENVLLDAQMNAKIADFGLSNMMSDGEFL
RTSCGSPNYAAPEVISGRLYAGPEVDIWSCGVILYALLCGTLPFDDEHVPTLFKKIRGGVFYIPEYLNRSVATLLMHMLQ
VDPLKRATIKDIRWNKCFDMYLLWNIQRVVNAYHLRVRRKNPVTGTYVKMSLQLYLVDNRSYLLDFKSIDDEVVEQRSGS
STPQRSCSAAGLHRPRSSFDSTTAENHSLSGSLTGSLTGSTLSSASPRLGSHTMDFFEMHAPEGEELLDVQHIPQAVPLE
GPPLEFVSRKEGEGEEKKEEEEGKQKEEEEEEEEKEEEEEEEEEEEEEEEEEEEEEAHQRLHLSD
```

356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE

A0A1A6GMR4 **A0A1A6GMR4_NEOLE** (260 aa)
CSD domain-containing protein. *Neotoma lepida (Desert woodrat)*

```
MSTDNKRILLRRAAGHIVLQEAQSTDFSAKNDTKEDVFVHQTAIKKNNPRKYLRSVGDGETVEFDVVEGEKGAEAANVTG
PDGVPVEGSRYAADRRRYRRGYYGRRRGPPRNVALVLKSRDTNQGGCPSFRSARKEEEESKKRRSRRKRKRKRRRRRKKE
KEEEEEEEEEEEEEEEEEEEEEEEEEEKKKKXXXXXXXXXXXXXXXXXXXXXXXXTGPPAMQGIGQPSLKYRLTLPTGLX
SDWGKYTGTYPPSTTITPVP
```

162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE

A0A1A6GUH1 **A0A1A6GUH1_NEOLE** (259 aa)
GST N-terminal domain-containing protein (Fragment). *Neotoma lepida (Desert woodrat)*

```
RQEEXEEEEKKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEASEDGESVGHCPSCQRLFMVLLLKGVPFTLTTVDTRRAL
DVLKDFAPGSQLPILLYDGDAKTDTLQIEEFLEATLRPPEYRESNTAGNDIFHKFSAFIKNPVPTQDNALYQQLLRALTR
LDSYLRTPLDHELAREPQLRESRRRFLDGDQFTLADCSLLPKLHIVDTVCAHFRQMPIPEELCGVRHYLDSALQEKEFKY
TCPHSAEILAAYQPAVHPR
```

13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE

A0A1A6GZN7 **A0A1A6GZN7_NEOLE** (182 aa)
GST C-terminal domain-containing protein. *Neotoma lepida (Desert woodrat)*

```
MSVITVYYKAELEKRPENLEDLPEKMKSYSKFLEKQPPWLARDETTFVDFLNYDSLDQQHVVELKCLDMFLSLKNLMACF
EGLQKISTFMNCFLLGVLYTKTTLWGLSPGSPHPGVVRHQSGATAPDESDLKKKKKKKKKKKKKKKKKKKKKKKKKKKE
EEEEEEEEEEEEEEEEEEGSL
```

160 - 179:	EEEEEEEEEEEEEEEEEEEE

A0A1A6H071 **A0A1A6H071_NEOLE** (130 aa)
Ribosome biogenesis protein NOP53. *Neotoma lepida (Desert woodrat)*

```
MEWECHFEMREGVSHHSGSMPSSAKLPESTGSPSPVFNAYQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERKKKKKKKK
KKKKKKKKKKKKKKKKKKKKERKTIRDSELGNLYRLPVKEKLIAFIQSSSL
```

42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE

44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE

A0A1A6H5D1 **A0A1A6H5D1_NEOLE** (190 aa)
KCNQ_channel domain-containing protein (Fragment). *Neotoma lepida (Desert woodrat)*

```
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEQEKEKKRMCMQYFVAKKKFQQARKPYDVRDVIKQYSQGHLSLMVCIKEL
QRRLDQSIGKPSLFIPIPEKSKDRGSNTIGARLNQVEDKVTQLDQRLVIITDMLHQLLSLHQGGPSCNSRPQVVASDEGD
SINPQLFLPSNSLPTYEQLTVPQMGPDEGS
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE

A0A1A6H7Z5 **A0A1A6H7Z5_NEOLE** (339 aa)
Uncharacterized protein (Fragment). *Neotoma lepida (Desert woodrat)*

```
KAIYLRNSSSIQVSSPPKPFLLYSSGPHHQGKQQALKDFFTSAVLPWKLIDPSHLRSIMQCKLLSSTSIAPSPAVVTSEL
FNKVFSGQVQLERLPQTGTKGFRPQKVTKQANGSRLSAGASGAPDILEIEEEKEEEEEEEEEEEEKEKEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEGEGWGRGGGEGEGMLRRLPQEQLVNPVSGLRDFNRNSFHLRCFDEKFEQQASPSQLNALA
DNTDRRLLPAQTPQQLASLGTVPPTSGYSLNLAAEHCHGCSRVQTDLKHPHCMATLLSPKLPYPLLAKGPLLLETPRNAK
RTSQHTLFSLNYFEEAGSG
```

149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE

A0A1A6H928 **A0A1A6H928_NEOLE** (776 aa)
acidPPc domain-containing protein (Fragment). *Neotoma lepida (Desert woodrat)*

```
MIAMKEKNKTPKDSMTLLPCFYFVELPIVASSIVSLYFLELTDLFKPAKVGFQCYDRSLSMPYVETNEELIPLLMLLSLA
FAAPAASIMVGEGMVYCLQSRLWGRSSGGAEGSINAGGCNFNSFLRRTVRFVGVHVFGLCATALVTDVIQLATGYHTPFF
LTVCKPNYTLLGTSCEANPYITQDICSGHDTHAILSARKTFPSQHATLSAFAAVYVSVSESPQCCTLCPPVGSSYNLDPA
YLLAQMYFNSVISDTTKLLKPILVFAFAIAAGVCGLTQITQYRSHPVDVYAGFLIGAGIAAYLACHAVGNFQAPTAEKVS
VPAPAKDALRALTQRGHESMYQQNKAVSTDELGPPGRLEGVPRPVAREKTSLGSLKRASVDVDLLAPRSPMGKEGMVTFS
```

```
NTLPRVSTPSLDDPARRHMTIHVPLDASRSKQLISEWKQKSLEGRGLGLPDEGSPVHLRAPAEPMAEEEEEEEEEEEEEE
EEEEEEGPVPPSLYPTVQARPGLGPRVILPPRPGPQPLVHIPEEGVQAGAGLSPKSSSSVRAKWLSMAEKGGAPVAVAPS
QPRVANPPRLLQVIAMSKAAGGPKAETASSSSASSDSSQYRSPSDRDSASIVTIDAHAPHHPVVHLSAGSTPWEWKAKVV
EGDGSYELGDLARGFRSSCKQPSMGPGSPVSDVDQEEPRFGAVATVNLATGEGLPPPGASDGAMGAGSRESTLRRQVGGL
GDREVEAEAESYYRRMQARSNNRKQKNRAVSWQRNSGSGKKKNWEGRGGKKKVAKH
```

467 - 486:	EEEEEEEEEEEEEEEEEEEE

A0A1A6HE68 **A0A1A6HE68_NEOLE** (173 aa)
Uncharacterized protein. *Neotoma lepida (Desert woodrat)*

```
MLCRPFRRSLAVQVKFFPSNYSASLQELTPALVQPAKGHNHRFLHLAAARSVLIHSRLSSIYARRASMEXQKEAQRIMTL
SVWKMYHSRMQRGGLRLHRSLQLSLVMRSARELYLSAKGEKKKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEKGK
```

125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE

A0A1A6HG76 **A0A1A6HG76_NEOLE** (45 aa)
Uncharacterized protein (Fragment). *Neotoma lepida (Desert woodrat)*

```
MQNMILEKKNRRRIGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE

26 - 45:	EEEEEEEEEEEEEEEEEEEE

A0A1A6HL26 **A0A1A6HL26_NEOLE** (531 aa)
Uncharacterized protein. *Neotoma lepida (Desert woodrat)*

```
MMMMINYNNNNNNNNNNNNNNNNKKKKKKKKKKKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEXEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEECPAFPPNCPPVNVSCNIFINSFGSIAETTMDYRVNIFLRQQWNDPRLAYNEYPDXSLDLDPSML
DSIWKPDLFFANEKGAHFHEITTDNKLLRISRNGNVLYSIRXVXEPTTRITLTLACPMDLKNFPMDVQTCIMQLESFGYT
MNDLIFEWQEQGAVQVADGLTLPQFILKEEKDLRYCTKHYNTGKFTCIEARFHLERQMGYYLIQMYIPSLLIVILSWISF
WINMDAAPARVGLGITTVLTMTTQSSGSRASLPKLVQYAVSIFLCSFHPNIXAEEQWAVGKVTEDWVSYVKAIDIWMAVC
LLFVFSALLEYAAVNFVSRQHKELLRFRRKRRHHKDDEGGEGRFNFSAYGMGPACLQAKDGISVKGANNNNTTNPAPAPS
KSPEEMRKLFIQRAKKIDKISRIGFPMAFLIFNMFYWIIYKIVRREDVHNK
```

34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE

A0A1A6HPC0 **A0A1A6HPC0_NEOLE** (134 aa)
Uncharacterized protein (Fragment). *Neotoma lepida (Desert woodrat)*

```
LTTRPCREQQRQALLCDFWVAVWHQQHSGPSQGTRGKKVLVTKEEKEKEKQKQEKEEEEEEEEEEEEEEEEEEEEEEEER
KLLKEILMASACFVSGFVFTTHLISSTQILEFLLGLGIIRVPNIDKVPSNLYDS
```

56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE

A0A1A6HR72 **A0A1A6HR72_NEOLE** (91 aa)
Uncharacterized protein. *Neotoma lepida (Desert woodrat)*

```
MRTQTLSLTGKLVFQVVLEHTQRPPLTERLREAIAGGVASKILAKSLKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVV
VISGATRVSEQ
```

49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE

53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE

A0A1A8A812 **A0A1A8A812_NOTFU** (708 aa)
Retinitis pigmentosa GTPase regulator b. *Nothobranchius furzeri (Turquoise killifish)*

```
MAEEAEDEIPDSGAVFTFGKSKFAENIPSKFWLKNDVPQTIACGDEHTALITENGKLFMFGSNNWGQLGLGSKLTLFMFG
SNNWGQLGLGSKLTVNKPTCVKALKSEKVCLVACGRNHSIICTAQGRVFSCGGNSEGQLGLGDCEERTTFQRVGFFDSHG
PIRMLAAGSNTSAALTASGKLFMWGDNTEGQIGLGKESQASSPQEVSVGRPISWVSCGYYHSALVTVDGALYTFGERDSG
KLGLGTEQLSAHRLPQRVKNIKAPVRKVACGGGHTVALTEDDVYTFGLGQFGQLGHGTFIFESRLPRSVEHFRKNRARHV
SCGENHTAVIAGGGLLYTFGDGRHGKLGLGEENFTNQFKPTLCPRFLKYDVQAVACGGCHMVVLARPRDPLAAEVTLEED
DVTEDFLEKPYVELLGETNDSSTLQRSLSARVRRRERERSPDQFGTTLQTLPSMMPSLRQLPLPVSRQTAPPGLPLPELS
HRKVPNQQESSDSTQQEQPNGEADGVVASLTDTDSVGGLGETTDFLNMTHVMKMDPSDKSLTLSPLQKDVETLRNKGERE
EEEEEEEEEEEEEEEEEEEDSVIDADDGEEEEGNASRCLTESAEEEPNREAAPDGEQKVEVIRQNDTAAEEKTGKESKAA
NGKRDGNGNSLSGSNMKISFFRRLSSTRFKQTEDMEVDQSVLEEEPPSPAAVKSSGPRRPRSGACSLL
```

560 - 579:	EEEEEEEEEEEEEEEEEEEE

A0A1A8PVY6 **A0A1A8PVY6_9TELE** (443 aa)
Translocation protein SEC62. *Nothobranchius rachovii (bluefin notho)*

```
MAERRRHKKRIQEVSEPTKEEKVVAKYLRFNCPTKSTNMMGHRVDYFIASKAVDCLLDSKWAKAKKGEEALFTTRESVVD
YCNRLLKKQFFHRALKVMKKKPEKDPKKEKEKEKCKTDSSKEDEKKGKKEKEKDKEKKKETEVVETKKEKSDDSPKKKKE
VKKKFKLEPHEDQLFLDGNEVYVWIYDPVHFKTFAMGLILVIAVIAATLFPLWPAEMRVGVYYLSVAAGCFVASILLLAV
ARCILFLIIWLVTGGRHHFWFLPNLTADVGFIDSFRPLYTHEYKGPKASDKKGSDKTNEKDSSSSNKAQKSDSEEKSDSE
KKDADDEEEDEEEGGREERKEADGEGKEDSQDTDSDRQDEGSQHSNGNDFEMITREELEQHTEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEETQVRKEGGSSETKPQTAET
```

383 - 402:	EEEEEEEEEEEEEEEEEEEE
384 - 403:	EEEEEEEEEEEEEEEEEEEE
385 - 404:	EEEEEEEEEEEEEEEEEEEE
386 - 405:	EEEEEEEEEEEEEEEEEEEE
387 - 406:	EEEEEEEEEEEEEEEEEEEE
388 - 407:	EEEEEEEEEEEEEEEEEEEE
389 - 408:	EEEEEEEEEEEEEEEEEEEE
390 - 409:	EEEEEEEEEEEEEEEEEEEE
391 - 410:	EEEEEEEEEEEEEEEEEEEE
392 - 411:	EEEEEEEEEEEEEEEEEEEE
393 - 412:	EEEEEEEEEEEEEEEEEEEE
394 - 413:	EEEEEEEEEEEEEEEEEEEE
395 - 414:	EEEEEEEEEEEEEEEEEEEE
396 - 415:	EEEEEEEEEEEEEEEEEEEE
397 - 416:	EEEEEEEEEEEEEEEEEEEE
398 - 417:	EEEEEEEEEEEEEEEEEEEE
399 - 418:	EEEEEEEEEEEEEEEEEEEE
400 - 419:	EEEEEEEEEEEEEEEEEEEE
401 - 420:	EEEEEEEEEEEEEEEEEEEE
402 - 421:	EEEEEEEEEEEEEEEEEEEE
403 - 422:	EEEEEEEEEEEEEEEEEEEE
404 - 423:	EEEEEEEEEEEEEEEEEEEE
405 - 424:	EEEEEEEEEEEEEEEEEEEE

A0A1A8UMA8 **A0A1A8UMA8_NOTFU** (689 aa)
Retinitis pigmentosa GTPase regulator b. *Nothobranchius furzeri (Turquoise killifish)*

```
MAEEAEDEIPDSGAVFTFGKSKFAENIPSKFWLKNDVPQTIACGDEHTALITENGKLFMFGSNNWGQLGLGSKLTVNKPT
CVKALKSEKVCLVACGRNHSIICTAQGRVFSCGGNSEGQLGLGDCEERTTFQRVGFFDSHGPIRMLAAGSNTSAALTASG
KLFMWGDNTEGQIGLGKESQASSPQEVSVGRPISWVSCGYYHSALVTVDGALYTFGERDSGKLGLGTEQLSAHRLPQRVK
NIKAPVRKVACGGGHTVALTEDDVYTFGLGQFGQLGHGTFIFESRLPRSVEHFRKNRARHVSCGENHTAVIAGGGLLYTF
```

```
GDGRHGKLGLGEENFTNQFKPTLCPRFLKYDVQAVACGGCHMVVLARPRDPLAAEVTLEEDDVTEDFLEKPYVELLGETN
DSSTLQRSLSARVRRRERERSPDQFGTTLQTLPSMMPSLRQLPLPVSRQTAPPGLPLPELSHRKVPNQQESSDSTQQEQP
NGEADGVVASLTDTDSVGGLGETTDFLNMTHVMKMDPSDKSLTLSPLQKDVETLRNKGEREEEEEEEEEEEEEEEEEEEE
DSVIDADDGEEEEGNASRCLTESAEEEPNREAAPDGEQKVEVIRQNDTAAEEKTGKESKAANGKRDGNGNSLSGSNMKIS
FFRRLSSTRFKQTEDMEVDQSVLEEEPPSPAAVKSSGPRRPRSGACSLL
```

541 - 560:	EEEEEEEEEEEEEEEEEEEE

A0A1A8VLT0 **A0A1A8VLT0_9APIC** (732 aa)
U3 small nucleolar ribonucleoprotein protein MPP10, putative. *Plasmodium ovale curtisi*

```
MEQVNVKMYTDFISSFCKRSEEILSFGKVSEEDKNKLMEMIEYFCNILISYFYNDMNMDRISISESGFDCEQLWFFIECI
IKQKKLDSLLLFFNNFERKINETKNCKQEDRCRIIEEGDTKVRRKRKLEKASLRRNPGTKRTNRRGDQDDNAATEDGSAA
TEDGSATTEDESATTEDGDDAAMHEDDDAAMHEDDDAAMHEDDDAATDKDDDAATDEDDDAATDEGNGEEGDRFFNRVEM
ETFIEEEEKKFLRAADESSSRGNSSGEESDGEYNLNDFECDYEGAHKLKYRDFYKGEGEQLEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEEEEDDRSSRRAHGRTRKGKKEDEKIERELDEMNERELNEEEDEAVSAKTG
EADRERIERELVATKHWSLTGEVFANQRPKNSMLELNVDIPKINTYNNDAFVSKTVGSIEGSEEDTEEAAGRTRSSRQNL
LNEEIELVVKQRIKNMLFDDVEKKTIEDLDAMYGVSEGDGGEVNFDSLNFTRSKLSLADEYAKKIEDDIKNSHSMNKEIS
LQKIELMNMFKKIMHCCDALSNDYYIPNPVYINGKRSDINAKLHIEENIPIILSEKNKNAPEENYKPGFMKEIHEMSKKE
KKALRKQKKNKRRKILLSQFKDNGGGISEWKNRNSHLLEKNKKKKEEKLNRMKYGVISKEKLTQGPGQHSKYNFSRDITK
AIAYDKRRKGDS
```

302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE
306 - 325:	EEEEEEEEEEEEEEEEEEEE
307 - 326:	EEEEEEEEEEEEEEEEEEEE
308 - 327:	EEEEEEEEEEEEEEEEEEEE
309 - 328:	EEEEEEEEEEEEEEEEEEEE
310 - 329:	EEEEEEEEEEEEEEEEEEEE
311 - 330:	EEEEEEEEEEEEEEEEEEEE
312 - 331:	EEEEEEEEEEEEEEEEEEEE
313 - 332:	EEEEEEEEEEEEEEEEEEEE
314 - 333:	EEEEEEEEEEEEEEEEEEEE
315 - 334:	EEEEEEEEEEEEEEEEEEEE
316 - 335:	EEEEEEEEEEEEEEEEEEEE
317 - 336:	EEEEEEEEEEEEEEEEEEEE
318 - 337:	EEEEEEEEEEEEEEEEEEEE
319 - 338:	EEEEEEEEEEEEEEEEEEEE
320 - 339:	EEEEEEEEEEEEEEEEEEEE
321 - 340:	EEEEEEEEEEEEEEEEEEEE
322 - 341:	EEEEEEEEEEEEEEEEEEEE
323 - 342:	EEEEEEEEEEEEEEEEEEEE
324 - 343:	EEEEEEEEEEEEEEEEEEEE
325 - 344:	EEEEEEEEEEEEEEEEEEEE
326 - 345:	EEEEEEEEEEEEEEEEEEEE
327 - 346:	EEEEEEEEEEEEEEEEEEEE
328 - 347:	EEEEEEEEEEEEEEEEEEEE

A0A1A8VQV5 **A0A1A8VQV5_9APIC** (2213 aa)
B30.2/SPRY domain-containing protein. *Plasmodium ovale curtisi*

```
MNTKLVSHNCVEQYINCKDVVEGQKKELRIKENKQIGSAILYTRKGNTRMEELISILGGRRKDAKQIFFYNNCANKRYGK
INSLYKKKKEMKKNIYSVEEILERPAFNKTVEKKKNIFCFHRIPYIGYISEIIKSLIMRKKIYCSVSFNIIFSENGETFL
LRCLTFLLKYNKKNLSKSETFSLILKNECSSNKDRSFITRGVQYFLPHFNSKEGKYYEVKVVMEENIFLSLSHDNVLKIR
TYFFSKDVNFVENTPFANTYFELNYRGSTLFYDNIEIHNLKNHPIVRSVKDNFLEITVNCSEMKCNQCKKRKNEMGDSRY
SRAIRDAVSPLALLKNPFFSIIYKKENSKIGVNILEVHAFCCTKICTIQVFINVFTFPEIKTIFNYPSMKYGMSILYYVS
IFSYMINTHGVIFYHIVITEMVKVVLLMLFCTYICIMNLIFLRTRIYNNTHFSKHFTKKWEQREICVISLLCHTVVHIPF
SKKSYKEYITNRKNEHWSIGNPVLCLEKVPITFHFARRKMEKRRHFPIYSLPRYNTCHNGYFITTSFIDQFYHVLLEFYN
IVIYAVGMILHFFYIYMSTMISEFFCSLCCFLCLIIQGIVFFLNVMLNFVKYKMDLFLKMKNKKIEKYPTLFWIPREIRK
WNFPDLNQVTQEDTDENEDIKHQKWEEKIKTGNDYVARFDNKSELSHGCPRVGREVSGERLQCAACSSGFGNINNGRRRR
RRNVDSCGYLLPGIRNSVLCDAKKGVSKEYHESGNKKKRTFSSGRVVIKKKKNGTIHTKNGNMHCAIFSPVLYFKYSLYF
KETHEYNFAQFHGTPFQPLLLPSDSCSSHMSTGKKKSQRHANRRKNKKKKTNKEGKQQRGGKDKRNSNGSGSGSDSGSDS
GSDSDLESGSDEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEEEEEEEEKEPEDKFGDGEEEDDNDDDDNHNDDDDDNDNDD
DNDDDNDNDNDDDDDDGDDSYSERERKKRKQKNKKIKGRGMYGDDPSIESEGEKQKGDSYYDKKKNLYLKKKKKKFKHNF
IYLKNLFKENVCINTTNVSNFISISKDKLTATYTAWGKHTDIACVQVNKCALRDCSIYYFEVEVLNCTNFSKIVIGMTSK
NYTINKNPGTEYNSFGYKNDDGKKIIDGKVDNYCNGYTKNDIIGCGINYYDNSAFFTKNGKYLGKACTINAKYDYYATVG
LSTLGDRIKFHLNSFHFDIYNLIYEESEKERKIIKSIYIQKDIFSDIIKSHLIKCGYFNTYQSFVNYLEKNKNSDDNNSI
```

```
SNSSNCKNGINKIFEKNTDSIKAKDNNDHKLYDGKKLKDSEGMKKENLTISGINGKGENNEKNDNPNKGNNTDISGRMKC
IITITPEENNSVKFNEGNSKFKTEEGTCTEHGDVVGNIGEKHKNEHIEEDCFTSQIKSDTVKSAAEGEVVAAAEVVATAE
VVAAAEVVAAAEVVAAAEAVATAETATGKKCESKEEKSNIDRNKDDKICDKSNDKSILNAFLVNYLDVYEKLNKEGNTEK
EVKDQGTIKTTEKKNDKGMNASDKSPHRPNKNGEGEGKYGEGEHGEKQETQIKTKSDEGKRSNKKTDCEDRKGRKEENVH
LVKCPIEETAEEGRKSQVGGTDPQLDILKSYEFSPYNNYGGVSSQNIQLASRRNSLSNLINARKESSSLLLSRLRNKRSL
STKDDLNILATNFLNTKKEAKKNDSDINKKIHLLRDKSNIVKNEKKKLNKKEGGKNYSNDKEYITKYFVNLYLSEEKLRK
MKESLEMRHIIRKNIINGNIINALNILEEQYTELFTNERASFHIAMLFTQQLIEILKPHKKFIKNISSRKIKYKNEGKYE
KQDDLSSESSYKSYNTLSDDHFYDDIKTEYDSSDSLFCDSSNGEESNFTISQLEKLGKIHISKRGNQAEVKIGNKFESGH
NDKAANSSAKGFLNNGNVMLPLDNDPSKEETVGKDQKPSPVLSESKNLDNNASTIDNPKTNAEDGGVSVSPMNITQLNDI
DFVKEKKIEHMIFKSMQCNYDEEFYKKNNLQEEYESHYNKLSKEYEFFKDDNPYNYKHKKKCYDKMHREDELGKDVKDIC
TSSTDDSTSDYDSNDSNFKRKYYEFNDINFDQIYQYIYKNNFSPNNQLKFKKDHLYLALLWIREKLSLFNKSPHVNVRQC
IQDSTSLIAYHKPYKQKLVRMFFSKNRNLLTFNSVNEGILGNILFIYVPSVSR
```

892 - 911:	EEEEEEEEEEEEEEEEEEEE
893 - 912:	EEEEEEEEEEEEEEEEEEEE
894 - 913:	EEEEEEEEEEEEEEEEEEEE
895 - 914:	EEEEEEEEEEEEEEEEEEEE
896 - 915:	EEEEEEEEEEEEEEEEEEEE
897 - 916:	EEEEEEEEEEEEEEEEEEEE
898 - 917:	EEEEEEEEEEEEEEEEEEEE

A0A1A8VRU9 **A0A1A8VRU9_PLAMA** (750 aa)
Peptidyl-prolyl cis-trans isomerase, putative (CYP81). *Plasmodium malariae*

```
MKRKKKYVYLEFSINSITLGKVYFELFSDEEIKKSVENFVSLCKGNLNYSIYTDDEMLSFKNCKIEKIKKNKCIKSGYLK
NKVYLHNNEWKNKYPIYQNKKYENVECIYGKYYNKEYTKRRHLNAGLLTVVQVENKKYSSIFKITLNKVPTYNNKNIIIG
RVIKNMHILRAIEIIPVTSNWEPKINVYISDCNEVSESFFKERKASSRQSYIDGLFENLNHNEQGNEESDGVETGEREES
DEGGEPYDGDDNSALYANHPFKKHSPFLSNFDIKKERNKKIKITEKQKGIELLNKILSELDSASKEENFSKRSTKKSASE
HPQSKHHPYPQLQPEPQSSSSLQERTVRGDYPSKGTDDTSKNFETMEEEEEEEEEEEEEEEEEEEEEEEEEEEKEEEEEEE
EEEEEEEEEEKEEEEKKEEEEKKKKKKKKKKKKXXXXKKKKKKKKKKKKSNEGDSQQDQPLPCSNALPYDNNINKQMTE
RERRMFEIQLKINQSKCLNEMEIRRERMMMMSQGPNRGMGKFGEYTHYNFAQNANVKSVIQRRISTEGSGGREEKEKEKQ
KEPTGAHHSGSNRGCDIGGDKVSENDHANGCDNADNHGIDLRKDDEDGKKSQLYNTSAVRVQSALNRKKKKREDTYELDN
DINLYKKIKFNFSINRKLYEDKKKEFKNNFYGYNLLINDNSTCTDKDKNKVVEFCKKQEELRSKISRKRKNDEGVFKNYI
NRRNKIYNKKLDRYFNKHTVEIRQNLERTF
```

367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE

A0A1A8VS39 **A0A1A8VS39_PLAMA** (764 aa)
Uncharacterized protein. *Plasmodium malariae*

```
MMHCTIKYRREFLTLFNVWMNRKNNYICTNIVKLFTTHSAESTRVDDNEDVLGNVYKSGVEEKEENKKSKSKQKDLKEGK
QQKEYERYNEYRQHNEHTQIPPQNLPPHDYKETSFVKPRSFVYGPRASNTLTSELYNKIVNEHKLCEEIPYDSGKKKKRH
AQTLSQSVIKTKYRTVGETKENPLYDMNKKYFNKGDNTGTPLNEEHMSTNSEHLMIENKRFTEGTMKCNDNPSVDDKKDE
VLHGKLNSDRNNDLIISSNIKMDAKSIIKNKGKNNMENKIIKRKGYDVVHNTVDKHINNMLMKSKDNQLSISEKKKNDHF
YKIFFSSKKVKIIKSQNHPVFIHLYKLATDRKYREKQEKILLTSKKIILERQKNYLCRIYTNSIDNLKDFHSFDNFILLS
NKLLKKLSFLYSFKNGVLAEVLHKFHFDNVGLPHLAFCFYNVNWGEEHQVGAEVKMNHVDEAKEEKEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEDGEDEWKERQKIPFEVKQSEQNLKIYDIHFEEKENANDRAVKRDDCSLNSESAQQYDIKNNVEY
LCNGDIGTIIRSCFLLKWQCIFNIENLKKKNKNKIASYKTLDINSIYNIDFFHPFTIRASSGYLLDIPYKNTDLNELHKY
AKENKILLLKYSSHSDLYINYKKNYSEHDHTFLNLVNKAKGVFLIMDNCNNIEKKYKSVHKNFINMSNNLHNKDEIFDNI
YYVNLKQNKDRPLGLVATYSIFMYILKTNFFKHLPQSSYVCIED
```

467 - 486:	EEEEEEEEEEEEEEEEEEEE
468 - 487:	EEEEEEEEEEEEEEEEEEEE
469 - 488:	EEEEEEEEEEEEEEEEEEEE
470 - 489:	EEEEEEEEEEEEEEEEEEEE
471 - 490:	EEEEEEEEEEEEEEEEEEEE
472 - 491:	EEEEEEEEEEEEEEEEEEEE
473 - 492:	EEEEEEEEEEEEEEEEEEEE
474 - 493:	EEEEEEEEEEEEEEEEEEEE
475 - 494:	EEEEEEEEEEEEEEEEEEEE
476 - 495:	EEEEEEEEEEEEEEEEEEEE
477 - 496:	EEEEEEEEEEEEEEEEEEEE

A0A1A8VSD4 **A0A1A8VSD4_9APIC** (84 aa)
Uncharacterized protein. *Plasmodium ovale curtisi*

```
MGNNGKGGATRKKKKKEVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEYTLNEYLLCSPFSPFCLELIIQMCISLI
VHAE
```

19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE

A0A1A8VSX7 **A0A1A8VSX7_9APIC** (1123 aa)
Vacuolar protein sorting-associated protein 33, putative (VPS33). *Plasmodium ovale curtisi*

```
MSKKTKTQGKKAVRHKNDYFEFSGRMNTLNELKEQGRLLLLNILQSFSGVKCLFFEKSLHILLNVVLNDEDVNKEKIEHI
FVVSNEMDVQTSKLDNISNILFFIRPYFYEIENIFKIIEKIEKVKSSEKKYVFIFIPYMTYMCEQEILKNNIFEVSIKII
IYPLYFIPLYNDVFSLEIKNIFKDYYVDNDFSNLIFCAFSLMFLQHLFNGVFKNIKSLGYLSHFISEQLIQLRKEIVASN
FHIQAPNNFDEDFLDILSNIQHLQDNQHFKNSTELAVVPVNSFEQNEELPKRYVDAHRINSVTKKIEGRGKTPNGELPVE
EACGEEEVEEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEGEEEEGEEEEEEEEEEEEEGEEEEEDDDVEENV
KSESAEKRTGGREKREKRKHELGDEQYEEKEALKCAASMEQNVMGKESKAGIATPEEVQTKDIVSTLGTNVDVTPNPNDK
NSLCSDSPSGRSCSNISPFCEDVCKTEQEQFVEEEQEKENESQERNRQKGGEMDKQESEVYMYVNPGVRKYTRKTTTKNK
ASSSKGGKELSITKGNKFRDCLSPDIQKRKMEPAHITVDAAADAGAEVGSEKKDPSEEPSRREKQKKEQQKRREGKGKTK
WGSAHGRRHWDEAEVIYKKNRKQGVTRKEGKVSPGFMATMDNTKFLMKKKDREKAEREEKKEKNYLLEKIGISSFQFLLN
VCDKIDSCVIIDRRIDMVTPFCTPFTYEGLIDHLFCIENLQIEIPRYIIFNDQRGRNGTIASTPSVAGENNFSAGGSTGG
GGDLRVRVKLRSSVDVLYNHIKDLSQNEIGSFLHKRASDIQKTYQEKDSLKDIGQINEYMRKFKEKHYEHNSLSTHVNLA
SFILSVIKKEHNFSKLKLEDEIIQLNTNSSKSKIHNVVKKIQLLIYTKENIYEVYRILCLFSVITNGFSDNYMNELKKDI
IEQYGINEIVRLNKLHLCNILKYQPKQKFIWNCLKNNFNLLSNEENDISYVCNGYAPLSVRLIEYMGILKNNVQVFPEFF
NLLNGPTYDIIQNAVGYEHVQDKENHLDINNKKKFVILFYVGGISYAEIAAIRRLNRNNQDYHYLIFTTEVTSSRKILQA
MGA
```

334 - 353:	EEEEEEEEEEEEEEEEEEEE
335 - 354:	EEEEEEEEEEEEEEEEEEEE
336 - 355:	EEEEEEEEEEEEEEEEEEEE
337 - 356:	EEEEEEEEEEEEEEEEEEEE
338 - 357:	EEEEEEEEEEEEEEEEEEEE
339 - 358:	EEEEEEEEEEEEEEEEEEEE
340 - 359:	EEEEEEEEEEEEEEEEEEEE
341 - 360:	EEEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEEE

A0A1A8VVI6 **A0A1A8VVI6_PLAMA** (1427 aa)
Uncharacterized protein. *Plasmodium malariae*

```
MYSKDENDENNKINLNNYKNILHNKKKILGLLNKDPLEKKGNYILAEKKDNKGVVSTSECKKGQSGGIDQVKSNLEEVEE
VLDESEEEEEEEEEEEEEEEEEEEEEDEDDDEDYEVDEEEEEDDDDEFDEEEYDDEQREINFNSYNNSYYETYNDEEGEK
YRNNIEQLLKNKNRNEKCKNKEEKNEIMFEKYNKLLSNYRVRKEKLSKDYIKDCIKDCVEEDSANSCCFSCKSEERNKNM
PLNVQADVKENLKSHQGINWNNRDSNTNNIEYEEGDFIRDVLDRIDEIYYKESRYKNLKSVNNNNNNLCINDLNLNLISE
YLNVDISVFHKKTTILLLGNTQSGKSSFINWFSETYVQNTSSLAKKNQITYVDIKSNFKFQFNKLQNQNYQFGVVNRLTD
EGYDHYTGKAQYYGKAHANYDSTYGGKYGGTYENTCGNTRGNTRGDRYIDHDMNGPTHHNVDDHCYNENDSCGGGGKKIM
FSGEHCYYLFKPFQQLRKKGHDIKKYIYGKLYYQNNLTKYMNRVNSVSFIDTSGIDDGSGIDDMSNVEYDEIIMNLSKYV
DLIFIFVDSNKFSINNRLLRIINYLLDNQINKVTICLTRIDIIKKINLYRVVFYLTQYFLRNLNIFKYQSLNDTSNKRKE
DEEFNDYEDETIQRHGKSFFNKNKMEKINILFNRSIRSFQNVLLFPNMLAKMITSQKNTTEKGSIKRKGINAPSSGSYYL
NNITGEDGVEEKSPFSRYTSRRSAGRWMGGYDQAEVEEKDETEENCGVMSGPIRAESTVRINAGKEEEKKEEKSILKKIL
TTSYNSFKEKIMGSEETDQNSNKAAKHWRRQEDTTHHGGHFNYNDGQNYEGNFVRSDVKNERNDVFAKVYKRNNHQLEYV
ERTSNSYQERDGIINELNRSKHVKENNRLENIFEKKINYSDGLKNMSIFLFVLMYEVVTTVYSLVHTTINRYITANGSRR
VVNVEKMQKLDNAHKMRYINPDDAITTGTRKRSSNINNNNNINNNINSNNNINSNGNRGESASGSSNGNAYKILEFLTIY
LPEMPYDLLKREKWKYEESNIHCNHDRRKRFSCNIQYEHTEYTGMMQNDTTNYNTHDVINNNRFNKKKNYPQRRSIPEDF
ILLSKGNKNNNDDCYNDSIEHVSYINNNKFRGINEISRNSYITDSVYNTNNERASNYLVENDPRESSPYSSKGKYYHVGE
```

EARLHQRVHHRDHPQVHPQYEPSNYPYTHSNNRNFNYMRMRNEDVKELNMIHELLFKIDESIDLKTNQSIYMLKRDLQNI
QNSCLKKISDNNEIIKKNRSLRIQNIKFYFFKYMAIFFGFIISLLRYDLLVYFNFIKPELFFSIFSKYFLFLASYNKNSL
FIAVNMLLVVAYFALYIRYNRRNYFKSLDKSDLNKLKIILLFTQIIFDEINQLHLKLLGRTDKDVRR

86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE

A0A1A8VVU2 **A0A1A8VVU2_9APIC** (1619 aa)
SET domain protein, putative. *Plasmodium ovale curtisi*

MFRVALLKNLERGGTGDEEEEEEEEEEEEEEEEEEEEEEEEEEEEKISEESNKVSRKEKEELLEVAKELPILYENNDKEVI
EALISSFVERYPKSVDAYECFSNFYIKMKDYKSALSMLYAALYVEKKNKTIVRMLHECEGRLVSQVYKIPTRYKNWVSFP
ESRPYKEDVYSWESNCGNYGRSGGENVRGRGDRTDNNQDDEFIERKSLGKKVHLVRQGQQYIALARTNLEPGEIIFQEKP
LVLTQHIFSNYFTYSTCYHCFRERNISQKSYACPVNPHTCSYIFCNWKCLVDNIKIHKIECNILPIIYAASKKCKLGYYN
VLHIFRVLIKTRIDRDYKDKDHNMLNDIFTFPSYYYAVKENQKDIFNSFNTLANIIILKFPCSFYLYLKQQELVEFMLII
WQYSTFVKYYSPSSIIQQINPETTFGFVFSPQLAKLHHSCIPTCTFYYDDNGKITVRSLCTIPEGGKLCINILPDQYLPL
KIRKSFKAIPRIFTCGCARCSDPTENNLHLRSIKCPKCILGYICPMKTDSLVETLKLHWYGQKGMNEEEERAYSREEVIA
KRSGSPSKCSDSSTKRGGSPSNCSYSPAKRGDPSSNYYASPSRSKPLLTDKEKKILDRLEKEMERWVCSNCGKLSIQGNK
RCIMLENKIYMLYNKGENEYMRGNLISSRNILLQLYKEFCHVLHPNHYIIFNTNVLLAGLLRYNPNKEIYESLVCLRKAI
IAAENVLSVCSLEKVHLYINLAHYTFNCLNVYKLHHKGIGISSEFVIDPIYTAIWNSSVVTGFNSTLTIVLMQQLRMYAI
YMNKFTPYMDIHFSIERKENFCTFYHKVTQKKSEPFRYIKKKTEDDPFYPIYMACQCFDLKFEKNKYFRNIFKSFKNIPY
FGNGLDALSLACSFGNINLVKLLLKLKYSIFLKNELHMNALLYMASSFLPEEKTSYHYNYYYTLLKEIELQNINFGHVEG
NYLSQEMFTHEENKKSFLLPQNGLNYMNSCHIKNEIEKPFPFDIVLDEEFIYGEKCKEIDTNQKIILILFLKHLHKIEVK
KKKLYKKRLGLSERFHRFGNTNARFLKRAERRGKGGKRGKKKGMKKREKKGVEKREDKTELTPYNNLAGNNEEEDGNWGS
TRKKPDNTKRHGSHLKELSSSGSSLFSDNPSHGSSQTGESDFLNGSNLSEESDIPSRGSNLSEESNTSSGSNLSEESDTS
HGSNPSEESNLSSDNSEDVLNNKVKNYYSQKLLVQSVSHKLLGFNNVLHYACARGKRELAKQLIISGVPVMLLNGEGSTP
LHMASFGGHNEIVKTLITYKSDINFVSSHGETPLMLAIYGLHIDVVKSLIENGANIMTKRNNNMTVLHCLVHGLLRTETI
HYKNVITMDDIPYLSLHGFTELSSSKCNIQRLTNLNINVLNSHITIIEQMSHDFFLLPFKLLHRLKKAITILKYIMSYCP
IFIYEIKNVNGYNPFELLKTTWKKLCERRLEVLSMSDLKISSFSERQKNIISQAWTLITSLVNAILSILRPDRSILTSIY
KNLLHMRGTTTWGNQGNAQVADVKKPVEDTKKPVEDTKKPDEDMKKPDEDMKKPDEDMKKSGEDAKVPSESSNTVVAKAS
ALKKVVLKKMKPPMLKNKG

18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE

A0A1A8VY47 **A0A1A8VY47_9APIC** (739 aa)
Uncharacterized protein. *Plasmodium ovale curtisi*

MIKFVVGIICYYILYCSYNVYENIKTPIYDYSLEGSNLKKEKDNHVDGKYINKPFKNMLRKNDKINYHFYLSCIEEINLN
KYAKEKYIDNDKNFINVYNLTNVSYNWDYGHKLGDISKWLFFSGSKYPSVNLIIPQKLINKNKHIYLHIITYVNDELYRH
GFVTSLLTKSKNGRRDNVIKKKKKYLWKWLFDDEEEEEEEVEGIQIGEKTMEEDDRKGEEEEGEEEGEEEGEEEEEEEEE
EEEEEEEEEEEERSTSSKTTSGVTIGKTTSGATFGKTTSDATTGKATYGSTTGETKQKNEQQRSSVKNVRHNSLYIPRRVR
FGPIIEYNDINVNRIGFFSNVLLDKSTSTYLLPTYFNNYLTPEDEYQLLQGDYEEETDEDEFEAEKRKKKKERLKSASHG
SSNMIEGIRWNEVTVEYAPISYTHFNLFNIIIFNINHLKEKYSFSSYDLDSLAVHLCGNIYFSLFIYTICLVHIIIDLIA
LLFDIKSWTQLNSLYSFLPNTIYLKFFFTSFILLYLKNKSDCKIVMVFCLVKMAVCICRLVSNYDIHFLPIYPYIYIGNN
KIGLDAKDSIVQQLEKTIKMKIQNVMICAMVILLTYNFLYNKYDSIYSLLIHTVGIYSYVFNFLFMCPQILRNYCDKRVQ
HIPALYFFFLFLTALMDDLFALLLRMPIAHKFNALGDDIIFVIFLAQHLFYEGRNQEGRGYMGREYAGRERTNRGAIKQK
PLKGLEKTPKKFTSSSPYP

232 - 251:	EEEEEEEEEEEEEEEEEEEE

A0A1A8VY93 **A0A1A8VY93_9APIC** (1838 aa)
Leucine-rich repeat protein (LRR6). *Plasmodium ovale curtisi*

MLALKRQVRTRKGKTGRVLSLQHISKVHVLSNRSDILVYCRAKGGESVADECTFAETRELVTQAIFDEAGYFSFLPSLPL
HLSEFLLSLISTMLLDLSKCNLQSLEDTDIILEKLIDLNCDYTSITYLDVSYNQLRCLKGLRHFENLKVLNISNNKLESL
DGDYIPSSTEKILAGYNNLTDICFKGAHTSKTLCREIISDIVDGEDTSPVCSPIYHPFNSSTLNEKREYTNRNLPLNRLT
YLDVSYNNIKRLITFEKYLHIMNKKRKNKKYESYLEDGYINNYIQSKTEKDVMILFFNSLQTLHLKGNKLTNLKGLSVFK
NLKTLDLRSNMINHPVQLFYLLDNKNWLKRYQQRGGTSNRDTKKEMKNGTNNCSKGGRENRNGSYYSYFIYILKKYRNFK
HLQNLLLLGNQKCLRPKHLFMSVFNVLRNVNERGELLTDVTDGEALINTNGAVETDVQSTATTGQFKWEKESQGKCSHND
IKSSIRQVHRGISNAYPGCGENSTQDAPESSLHLGGVAERESVEADEDWEGEGEEWEEWEDKEEEIEEEEIEEEEIEEDD
IEEDDIEEDDIEEDDIEEDDIEEDDIEDDDIEDDKIENDKIENDEIEVQEVDDTEKAMRRKSDTGVHPKGGDEMVLNEGI
KTKDQETGRDSDEAKYWAPRSSERETLNECHVGGSNENQEEGETEEAKEETAEEDSEMDAKIWVQKAMQNVRENAAEMSP
SLLSFYNKLRKNICGRSSNDDLYDPNGQRVLENMKKEFTKLTKGQFRDAEYETDCYDNEDEWVQMKNGNHDTLKVQEGEG
MKSKKGEDLSSTGGAKALRKDEAHEKVNEEMHGEVHDEAHRETQKQAHKARDVANPEPVLTVQSSLDSQENKNDKLKFLP
TKSLKRVSSHHSGGNTTITASANLNNDEYHFHRCGQIKEKEVNTEENETSCSFTSILKRKRTNSLLREMLIGNKYPERYS
LVNFSSMDSDVFDSNSDDMSKTSLDEDSQAGGLQLLSGKKDGEGAVGGEDKEKEEKMEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEKEEVREEEDEIVGEQMPHMPRAKGSLTQERPHQHNSNRRNEYNDDETRPSGRFGSISKKHNITQNSSNC
GKGKNILHRDQTGNDVVKEEGEGKKWREEVYRQSKNRRNNFENNDHLTGEENIMSLGRKNRTTRDSDKNGGMQNGGMNEN
KILEVRGGDRNHYTGKDKGKEWKQKEKKEQKGQIDHTEKTKQTEQKNQSEHTEKTKQTEREKLMKLLRLNLCKEERPCPP
NSKTNNLEEYNLKLKKSQNYSSSLKSESTDVTERNVHGHNIRSDKYAPKDFVYNHNKTGNMLNFDVQEMVKEVNICAYPV
RITHNGAVNLGGGKEDNLAFPGKGDSKEAYLVTEKGSNGSNRSSGGSEKGGCDEEGEGGNIDEDRSDTKQPITSADFFSK
MCTPQLSNTKDLALSNTLALYLRDVCLKLGKEKQHSNMLLKEKKRLEIKIKLLNENKQLYKKKIKSLEKNCNEKMKMTRK
YQIMKEKFKSMENIKMEMPKDDINLQNEYIENAMEQLYNIFSDVFGENHIITKRIENLADVYIKKEKKIEIQMVTQRKEL
DLLKNVEEIVKKKNEYHKELEKKNDIINSLNNNLTKITRSVANMKCSIIENEKKSKSLLEELAKKDSLLKELDERSSQMA

KEKEMAFQKERTQLLELLNDRDEDRKRAKQYKEEIKGLEEKLKSYLDTNVHKIHDKNYEIMVDRLHDEQIKMHSLLTEKE
KLINEKNLQIENLESQLQSWADEATNWIVVADKHTKLITNHNILKQNYEELKFKYIMDMKYIQTNKNEKVKELMRKFS

1018 - 1037:	EEEEEEEEEEEEEEEEEEEE
1019 - 1038:	EEEEEEEEEEEEEEEEEEEE
1020 - 1039:	EEEEEEEEEEEEEEEEEEEE
1021 - 1040:	EEEEEEEEEEEEEEEEEEEE
1022 - 1041:	EEEEEEEEEEEEEEEEEEEE
1023 - 1042:	EEEEEEEEEEEEEEEEEEEE
1024 - 1043:	EEEEEEEEEEEEEEEEEEEE
1025 - 1044:	EEEEEEEEEEEEEEEEEEEE
1026 - 1045:	EEEEEEEEEEEEEEEEEEEE
1027 - 1046:	EEEEEEEEEEEEEEEEEEEE
1028 - 1047:	EEEEEEEEEEEEEEEEEEEE
1029 - 1048:	EEEEEEEEEEEEEEEEEEEE
1030 - 1049:	EEEEEEEEEEEEEEEEEEEE
1031 - 1050:	EEEEEEEEEEEEEEEEEEEE
1032 - 1051:	EEEEEEEEEEEEEEEEEEEE

A0A1A8VYN3 **A0A1A8VYN3_PLAMA** (1890 aa)
B30.2/SPRY domain-containing protein (Fragment). *Plasmodium malariae*

LLLINILDFDKRASIKFGCLRCSIAPHLDYTVIIYSFFVLLKNYKQFSALKIWKNDNLFYRLNIGVGNKCIATTHGREEV
QTLKDISPFTDVRFNFHFLRIFIDDSNFYLNNIDRIIIDCSSKVVRHYFPSTFSSVFRSGCNKDLFHLFVLIKKEEDNLL
VFFKPEKIREFYMHNFNQAVQKGKDIRDRINLSINKKKFLRNANMSSSCDESKMEKYNRRMSTNDPWIYGVHVNEDAKNY
KNHKKRTCNYVDSEKSDEEPYNWTNQLSPANIFSKKNDTLFRYTKWRVLKDYCKYKSNKNKKKIIYKRRVKIKKNGKIHV
KHLLPLLFLNEVAYFRHAHEYKPCQSLIMPFKLLVFSSDNSNNISSRRKKTESHSNRRKNKKNKINEQKENKEKERKKKN
SSNDSDSDMDSDSDSDSDDDEVEEEEEEEEEEDEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEDE
EEGEGEEEKEDEEEGEGEEEKEDDEEGDEFDNDDEDEEEEEEQDKDEEDKEDEDKEDEEDEGNEENEEDEEPRETEDTDD
NEEEYKEDEVETDDEKDEDEGEDSFNDNERKNRKKKKKKIKNKNNNNKNRKRNRNKNKKCKYEHNGVENNASDEEIQKEE
DSYYNKKKKLYLKRTNKRFKHNYIYLKNLFKEHVCINTTNVSNFISVSKDKLTATYTAWGKHTDIACVQVNKCALRDCSI
YYFEVEVLNCTNFSKIVIGMTSKNYTINKNPGSEYNSFGYKNDDGKKIIDGKIENYCNSYTKYDIIGCGINYFDNSAFFT
KNGKFLGKACNINSKYDYYATVGLSTLGDRIKFHLNNFYFDVYNLIYEENEKERKIIKSVYIQKDIFSDIIKSHLIKCGY
LNTYKSFVNFLEKNKNSDDNNSVGSSSNSKNEIDKFFMNKTDLPNVLEKKVVDESSQNISNNHEDKENKKNVTDETKKKM
DIIIKSNNAKDNANIFVENTTAKCTPLNVDNTKNSSNNDNISSVELKKEGLIHRENDNNTENTEEKCRTDHIKKEEDTFT
PINSNSSIKNTVDVDVPKYVSLLSENIPEKEGKVSKDEGSTKGDKNVLSTFLVKYLDAYEKCDEQGKSDKEKNDMEHIDN
DSSKMEMTNKETTNKESTTKGTYNQEKNEECTSATVEVKEDKKMSKLPDSPSSLNKKDESKLEEKSDTSEKLEKSENSSA
TLIVASDQAKGNNKLIVSETGKSGKDENVNSIKIPNEQKHSTEENVEKMEKNQIIDTTSSILKCYDFSQYSFAGGSIQNS
LWVSRKNSLSNLINVRKDSSSTLLNRLRNKRSLSTKDNLNILPTNFLSTKKESKKNDSDINKKIHLLLKDKSGIIKNEKK
KLSKKEGSKNYSTDKEYITKYFMNLYLSEDKLNKMVDSLETRYLIRNNVINGNIIDVLNILEEQYSDLFTNAHASFNIAM
LYTQQLIEILKPHKIFIKKISSKKRRKCKKSVAYDEEEDLLSESSYKTYNTLSDDRFYDDIKTDYNSSDSLFCDSSNNEE
NNYAAFNIEKLNKRRNQKKCSKINDEEDRYSRDKNILASYRKNGKDKSSDSSRSNGSRSGSISSSSNKSANKLGRDSFDN
GNVLPVCATKLKEKMSNIDNSYSNSNNNNNFYNKHNNNKHLLNIGDKKGLEHGKYTRNDCQKTKVNCEEGATISPIKHTQ
LNHNDFLKEKKIEQMSLRSIRSNYNEEFYKKNNMLEEYEDHYKKLSKEYEFFKEDNPYNNKCKKECYKTLYKEVEEEEKK
RFYYMSSNDDITSDYDSNDSNFNEKFYQFNDINFDKIYQYIYKNNFSPNKQLKFKKDHLYLALLWIKEKLSVFNKSPFVN
VRQCILDSTSLIAYHKPYKQKLVRMFFSKNRNLLTFNAVNEGILGNISFF

441 - 460:	EEEEEEEEEEEEEEEEEEEE
442 - 461:	EEEEEEEEEEEEEEEEEEEE
443 - 462:	EEEEEEEEEEEEEEEEEEEE
444 - 463:	EEEEEEEEEEEEEEEEEEEE
445 - 464:	EEEEEEEEEEEEEEEEEEEE
446 - 465:	EEEEEEEEEEEEEEEEEEEE
447 - 466:	EEEEEEEEEEEEEEEEEEEE
448 - 467:	EEEEEEEEEEEEEEEEEEEE
449 - 468:	EEEEEEEEEEEEEEEEEEEE
450 - 469:	EEEEEEEEEEEEEEEEEEEE
451 - 470:	EEEEEEEEEEEEEEEEEEEE
452 - 471:	EEEEEEEEEEEEEEEEEEEE
453 - 472:	EEEEEEEEEEEEEEEEEEEE
454 - 473:	EEEEEEEEEEEEEEEEEEEE
455 - 474:	EEEEEEEEEEEEEEEEEEEE
456 - 475:	EEEEEEEEEEEEEEEEEEEE
457 - 476:	EEEEEEEEEEEEEEEEEEEE

A0A1A8VZX3 **A0A1A8VZX3_PLAMA** (1677 aa)
AAA_23 domain-containing protein (Fragment). *Plasmodium malariae*

```
EEEEEEEEEEEEEEEEEEEEEEEEEEREREKRRKNSHVDYVEGENTKKKRKRNEANGMVRKNRNEANGVVRKNRNEANGVV
RKNRDKENSIVRKNRDKENSIVRKNRDKENSIVRKNRDKENGVVTRRHHEIEGKNEVDLFMNSSTSNYEKTSVSSPSRDD
HFEKKRCAKNDEIKVSSTNFKQLKGKNRKKNFNKTIKRSNNTEDGVMGKKHDEVNISNEEESSRSSFGNDKKERSAKGGA
TDEAVGTDEVDEMAEADGADEVDEMAEADGADGTDEVDEMAEAGGANEPGNGKDFTKGCANRKGAQNADQNYFDFSNLKD
ADVKSFYGSTGKIIKLRIRNFLNHENLELSFNSSKNIIIGKNGKGKSAIAQAVAVGLGSQGKQAGRDISLANYIKDYDKN
KKNLVCNIEIFLSNSGKNSYKRDIYGDIVVIKRVFTSHSSKFFLYGLRQGRNSVSHSETVTTNMTSNFCTNTNTENMDKR
ISSNVSTHSRGVEDSSNGRNAVANNSSSEEYPMRQARKKAYIDNYLNVIKLNIRSPCVYLDQEKGKQFFSTINEKALHKF
FMSSVGLNIVEDEIEKENEMLQNCLKEIKQKEILLCPLEEELKNMKEKNDMLRDEFDKLKYYDKGYKIAIFYDLLKNTIL
MFNEYLKAENFKNEKVINSIQNKMNTLVEQSEYLKEVVKLVIEKDTFAYNFIKKNQDKMIKYNEMVKELISIKDRYTKRK
DEIVNYVSSFEKAKDNKKLLRDHLNKYKDEIKDIKQKIKIQTDKEIELQSEINKRENSIYEMEYQVSKCQNSVELINKQI
NVITAHLNKIQKIKNNQIKKKMYIYGYDIYTVRKDIIKNYNVYNESDRSSFLPSLDAQPNLANLAMDGIHGSSSYDCHFK
YEPIGPVGEYIKLRGNIENEKILSIIEKHLGDLFYAWLVSCYEDKNILTNIEIENKNKFSIIVTNAFQHVRRDSLLQNIQ
SLLSKINGNSIYSFLNIDLLPTSLLFYLYDNFKIVQTLICNNSTELQELLRTNDKKIVKSIYVIDDFVLVKVLANGGLHY
QPAKEEYYRNPIFLNRPFNENNLYDESNDSHLPTQNDAFVNVPAGDSVSIAQFTSINTAADTRAADSSPINNNEKNGTHK
TNEEELKELEKEKEEMDEEILRTSKKILSYKNIIESLNESLKKCKFAQDELKYQLQNIDELMENHDSIFSEQLDLEIKEK
NKDIYNINESVNSIDEYIRVLEGKKRNALDTCSLHKYLISHHSEYLKKKKEQLTQLIEEYYNLKEVLIKLEKDKKKNEEV
ATRSKKSFLLSLNKLHNVYFECLTSNFLLDDIFLESPFLILKGRNSTTTITNIAIRRTHFGEDASNVDKVGECNCSDNNS
PLEGRSGNELTESGCSVKVTFTTESLNKSLCGNEIIQAEVPLSSLSSFNKLFLLSGNDENIMKSKENASLNKSPNLYSNN
KNMGMEIKDIKKLEMYIENIMNNNGRVDNKSSCDNIISSNKILFDEDKIEISSYEKYSDILWKKRCEKKKEIIEILKVNG
FKEIDNTDNSLKNYFDSLIEQYTNDEKGYIAQMKQINELKNNYDMHLSNIKLRRSKFSTILKKTKEQITVHFKNILKSMN
NYKGKIEFDDLNRHVKVLVSINQDISNNIFMEINSLSGGERSTIQMALLASLSLTETSSFHIFDELDVYMDELTRVK
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE

A0A1A8W140 **A0A1A8W140_9APIC** (637 aa)
snRNA-activating protein complex subunit 3, putative. *Plasmodium ovale curtisi*

```
MAERKYQSFTLPIPHFSPNLIFNPDEYDFYKIKHKEGHKASPNGNTLKKGANAKVEGSPKNRDGSDNERGSGSGSGSGEE
SENEKLFMRYLKHIGKKDVSRRGDNQASKSSPCSRDSGKDNASVAKDQPGGNSNKLDVVRKKVHLFEKYPHITIKEELKM
EWLYHMVPKSFVTRRVNISAFEEECRRVRDRLKVRPCHVRKEVDEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEAGMEEEEKEENEGEQERDNKRDETDDVGEEIVERAKSKIYSRLIRVLLSGVRTPSVEEIINHIVYHNCN
NWQYKIDMDVLKKVANTEKTRKVLNRTKCYLDWLPNMESNPFSKYEIIAKLKEKTISKTFKLVCDFNNTILKSLYINQNV
INIFYTLTEYPTYAKDSLKNLSSETIFIISVSFYHPIRGIKIAEYDILSNQTLAHLTDVFFCFDTSNYGFPKFAGSLYYI
DGILYPDLRKKEALDYSTCILNFYKKMKNNDFVRPPYKIPQHKAILRDIEIPLYERCCFLHQGNCEHRVVFTNVRQHNSY
RDKEFSQYPLRTFKPNITRKFCTCCHKNEAKKIVLDCYLLKENPSYVCNGCFDLFLLNESGDFVDPSMKQFDYINDV
```

209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEEE
225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE

A0A1A8W2P8 **A0A1A8W2P8_9APIC** (425 aa)
Uncharacterized protein. *Plasmodium ovale curtisi*

```
MNDSNASLSRKFSCPTNEKPEDGNKKRTKLIRLRNGHFRRIVDISNIDEKKILPNSCTFPCSTPRTEANGMLLALRGVQQ
TGARNMVATWSQHGHHISATCFASFLQFSYHPFSNYIHFSPVLILSSLDNKEKKWEEVSEVPSPNVYRKRRNSSMPPPSY
IVTVEEEKSSEQPSVRTISEFSLTCTSAKDEENESVKTQPEEEEVGEEQDEDVEEEEEEEEEEEEEEEEEEEEGEEEGEE
EGEEEDFMAEKEEEKVEEKEEEKEEVPPEDKQLIAPSKTLMRGIKTNIYFLSNKEKVQALMCYNYKCNAVVFEKDTFLRY
LYMKSINNIILNERMIEELCKQEELKYVLASNSIVVESTDFLKPLIIEFESSISKKIFVKHIKLNAKKEMDMKKFDEYLY
ELDPNEKLRLRKVERFHSFNKLVAE
```

214 - 233:	EEEEEEEEEEEEEEEEEEEE

A0A1A8W3U3 **A0A1A8W3U3_PLAMA** (3145 aa)
Uncharacterized protein. *Plasmodium malariae*

```
MNKNYEFEYYQNLMQKELKEYETHSDISCKIGYSDSESEGVASIKEVPYYSYNNSLKNYKKEKLEKPVWKSLYDIEETAK
DSYSDYEYSKNDKSESEIESPRFGNSSEDEKGKEVDGLNGEDEQNEEDKLYEKDELNGGDEPYEMNERYEEGEHKEETAR
IKNFVNGVNNSENFFAFDKINDELKNSKSNDPFGNFSNKENISISSSINYNFREELENNMYNNLSMFKSIKNRYDDTTKH
FMKPKTCKDINGIYYDVSDEKVDIDLLKREHEKLKKGHILEKLSTSEYDYLTRGNSSNSHYRNVQYTSAKNSSKLKKGVL
DDNTLKKISKNFGISSDNSTSDTFDQILVDQNIAYKGKKLHERKITDYSNSVKKKNTRLRKIANRGVEQVEKEVEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEGEEKNEEEEDAQKNTDIKEDEDKEEEEQHNKV
GGNTEEEDEGNEEEDNAVLENSKCKRNTNKAASKIRTDNINSKNIPNFQKKNNETKKRNSNKKKIAKDKVFTCKKITEII
DEKNSSERVTTSSTTSESNDEIISYIHNKNIIINKTETEKQNDLVNEQIAKEMNFEWWKPNEKTVHTQMENLQNMKEDID
NKLNNEKRVIKSEKEILNKERILNRYEIPKDISYYVEKYQKRKEEHDKNSSNVHINVNNDANRKEVVNESENILAHNNTN
DILSEKKDLFNTRNSENKNQDIEAEKGLEHLYHDRFNRYDDSLKVPNNRTTIQDCNKEMIPISTNDQVDSLKSCNIIDEF
FSDKPKIKNDVNYENGANINNSNTFLKEEKVPYINSINMNQISNSNNTCEVYNNSFFNNDHKNKGKDLLGIPRNMLQNEI
CNGQISGDTYTIYDKIYDSIYDQINNYSEKNNEECFNKSTENNNNNEKNLPFFQNIDESKENCMYIKEKGDTRIYSDEEKN
EKIKMFLKYLKCIDDNSLTKVFEHIVQRENDDKLKKQLEMYLIGKKNINKIENNECEQETRHILRSNQNTQTTDKHFKNE
EIQTSIKDTNKSDSCMQTEINDINNKLYVQNDMISKKTSIDSIFFRNLSKDSYPLDVDNCAVKNSHVESKERKYFASDRN
DDLNNDEYNELKKINDLKAKILEKIKSCYENTNENNDEAAAILMLQDKKEFKNNSNSCRIYDNNTCNSRSVEKRRSNNSS
KNSSSHIDNNRNNGNISGKSNKSVSTLETLESMKSFEKEMNLLISHNERLKRRIEKLYEEKEKIKNDYKKIEKIKESQDN
LFLATEKHIEKLHGELDNLSKQNESMKGDIKKKKMKIIALESQIDESNTNNDVNDSDDLTLKRHTHMIKDELTYIDINNR
LDEFKGQIIDKKKIKTQIDQLQKQLHILKDEIKKTEFLKLENEELKKLLTMKNSNINDYEKSTMKLEKHIEKLNEHNLRI
YKENFNLCENIVMLKKENTTVPYSSEEIHDKPTNIEKELHADGASIQTIGSKVNEKGARDLQKHGNIIKKLEKTVDLLNE
QNFHLNEKICDLKEQNMKLRKTALLSNKENGNILDSNKHIEMIQTETEKIYIDKINLLKCNLEASKNKINMLNILLKTSN
NQTTQLNKKVKYIIKENKTLQKKYEKCLTYLEKLKIKYDDEILKVNYEKSGISLYDSKDINNNKDEEAIHKMNKIHDMQL
LKEGEHINILEHKLYEKDEKSTEVFNDTKEEGNMGSIVQKRNINGKCSTGIGTLVGIKEENEDNKKKNKEVSKLLKFNDL
ISNNEDENIYQNWLDSENKYVHVNNIFEIDSITKDLQNMFCSDTENTSKKLLKDSMSDNDNSIINTRVNTQEGVKNIEST
NSISNERSLRNIEKRFVSDKIKKMNENINKYIDEKKNNIKNICYNDNFPYSKSHMKEDYQGHYSDIDPKNRIIKEQKGNE
QDINRMYNNKTDGNIIPMNSVDQTYNKKQLGNMNNADYKNNTNNTYSMNNSSYNNSLARSTNSYHMYKENVGDSLINNDS
DNFKSVLRTYQIYDDKEDMQIKNNGLNNEYPLQKCNATNLEKTNENDVKSNDYMNKLHLCNENNTSAHNNNNLVNNSFNN
YKLNSSENMYIAYNKQNDITIYGNPEYSNRNAPATSQNMNNGVEANDKYQNAKNEKKGEAWIIDIKNNEIMPYRKLQSTI
LTEEVERGTENRGKYGVKDGINRTKNKAKNREKNGMKNWLHQNRYMNNHTKLKPLLHHKKFSKGSAYNNGKNKDKLHLLV
NNISKLVKGKIEEELKSKNISKDILNFEITKIKKKKAVPNSSLKNKSQETTIILSDSMSLSSGTLNSTFETIDDHKNNQI
TPNFLRNMQESNLTFNTDCASNLSKNGKGRHVYIGKNNNSFVDHKDRDDKNNFQLTNMNKSIINGGTYVNEANYLYGGSY
LNNDTLLNNFIVNKNYMQDIGSLNENLFLNDQSVLPEVPLNNIGDIYYKQNLSCDYVGNVQLQHNIDYLNFSGLSNKNQL
NQSSLSNNRNNYKSNNIVVNEYINIKNNSTSSNNNNNGSSSSNTNVNNGSNNNDALNSSIKNKAVNAEENANIMNSRNI
RKDEEAFIVDEDVNNSIENTNNNLNMNMVINNYQDINNNFINDPVSNVYDTNQCLLYNGVLSNKNGKEASTIFDVDKMNN
SYLFDINTIKQGMIPPFYDDASLNYNLIDRNDTNDMNDTNDVNDMDEGSKGGSLGNNLNSSSNKNDNSSSSNKIIGKSEH
NFKNADGSIAFFPEYCVDKNISNKTQKEVKVCEKINVNKKGNNQLLKENIVDEKHKTLERNTRRSKSVDIRRFETKNDLA
SKGDSTRNKMKTQIFNYSDYKNNGLRDMSTYADKVLQDMKSLIPSNVSNLINKANLKGKTGRSITKMVSNNSNISSSNNS
ISSSRSSSCNSCGSRGSCNSNTFNSANYKLCTKHEPGKLNKNKDKIHSNHGGTLLKSTSTKNLYQNYRYDETNNVSENIM
NNINILGLEKGDYINKCPSINKNETRIIYNDSNDSNNNNYLVGEGVNNIMIGKTNENALLSSRNSSSNNNENNIKKNLMS
MNAKNGEHTRLNAGINSNINNNMHYDLNNFNYNLNKFENILKEDQFKNYSNNAHNIIYKQVNSNQHLVKNSIILNRKEEG
NAFQSETRRSLSCFREALKKQGILG
```

395 - 414:	EEEEEEEEEEEEEEEEEEEE
396 - 415:	EEEEEEEEEEEEEEEEEEEE
397 - 416:	EEEEEEEEEEEEEEEEEEEE
398 - 417:	EEEEEEEEEEEEEEEEEEEE
399 - 418:	EEEEEEEEEEEEEEEEEEEE
400 - 419:	EEEEEEEEEEEEEEEEEEEE
401 - 420:	EEEEEEEEEEEEEEEEEEEE
402 - 421:	EEEEEEEEEEEEEEEEEEEE
403 - 422:	EEEEEEEEEEEEEEEEEEEE
404 - 423:	EEEEEEEEEEEEEEEEEEEE
405 - 424:	EEEEEEEEEEEEEEEEEEEE
406 - 425:	EEEEEEEEEEEEEEEEEEEE
407 - 426:	EEEEEEEEEEEEEEEEEEEE
408 - 427:	EEEEEEEEEEEEEEEEEEEE
409 - 428:	EEEEEEEEEEEEEEEEEEEE
410 - 429:	EEEEEEEEEEEEEEEEEEEE
411 - 430:	EEEEEEEEEEEEEEEEEEEE
412 - 431:	EEEEEEEEEEEEEEEEEEEE
413 - 432:	EEEEEEEEEEEEEEEEEEEE
414 - 433:	EEEEEEEEEEEEEEEEEEEE

415 - 434:	EEEEEEEEEEEEEEEEEEEE
416 - 435:	EEEEEEEEEEEEEEEEEEEE
417 - 436:	EEEEEEEEEEEEEEEEEEEE
418 - 437:	EEEEEEEEEEEEEEEEEEEE
419 - 438:	EEEEEEEEEEEEEEEEEEEE
420 - 439:	EEEEEEEEEEEEEEEEEEEE
421 - 440:	EEEEEEEEEEEEEEEEEEEE
422 - 441:	EEEEEEEEEEEEEEEEEEEE
423 - 442:	EEEEEEEEEEEEEEEEEEEE
424 - 443:	EEEEEEEEEEEEEEEEEEEE
425 - 444:	EEEEEEEEEEEEEEEEEEEE
426 - 445:	EEEEEEEEEEEEEEEEEEEE
427 - 446:	EEEEEEEEEEEEEEEEEEEE

A0A1A8W417 **A0A1A8W417_9APIC** (391 aa)
Casein kinase II subunit beta (CK II beta). *Plasmodium ovale curtisi*

```
MTPRTYDAVHKNSMEFISNNESSNGVVEEENQEEDVELSAASLDEHARNDFKAEESEEAERDEVERDEIEKKEVGEEEVE
RDEVEKEAERNEVEGAEVEGAEAEGAEEEEEEEEEEEEEEEEEEEEEDDDEEDEDDDDDEDEEDDDDDYDDDEYDEDDFNE
ATVSWIEWFCQLKQNIFLVEVDEDFIRDEFNLIGLQNKVPHFKKLLKIILDEDDDDDDDDDEEDDYDEEDDEINRDSEEM
YKNKDLYEQNAGCLYGLIHSRFILTSKGLALMREKYKSGIYGTCPSIYCDNSKLLPTAISEVPKFLSPLLYCPRCCETFY
PHKTSLLNQLDGAYFGTSFASFFALSFNIQSDKKKTFYTPQICGFTINRDIRETLYMDMNKDNSESSEEYS
```

107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE

A0A1A8W4X1 **A0A1A8W4X1_PLAMA** (372 aa)
Casein kinase II subunit beta (CK II beta). *Plasmodium malariae*

```
MSYNESSNEIVQDENQEEGMNVSDESLCGKGAEHWEDVKYEIADDVFDGDANDYSNDYCNYGGGDNNVQRSDPILEEAEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDDEEDDDDDDDDDDDDDDYDDDEYDEDDFNEATVSWIEWFCQLKQNIFLI
EVDEDFIRDEFNLIGLQNKVPHFKKLLKIILDEDDDDDDDDDDEEDDYDEDDDEINRGSEEIYKNKDIYEQNAACLYGLIH
SRFILTSKGLALMREKYKSGIYGTCPSIYCDNAKLLPTAISEVPKFLSPLLYCPRCCETYYPHKNSLINQLDGSYFGTSF
ASFFALSFNIQSDKKKIYYTPQICGFTINRDIRETLYMDMNKDNSESSEEYS
```

79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE

A0A1A8W548 **A0A1A8W548_9APIC** (1141 aa)
Vacuolar protein sorting-associated protein 33, putative (VPS33). *Plasmodium ovale curtisi*

```
MNTLNELKEQGRLLLLNILQSFSGVKCLFFEKSLHILLNVVLNDEDVNKEKIEHIFVVSNEMDVQTSKLDNISNILFFIR
PYFYEIENIFKIIEKIEKVKSSEKKYVFIFIPYMTYMCEQEILKNNIFEVSIKIIIYPLYFIPLYNDVFSLEIKNIFKDY
YVDNDFSNLIFCAFSLMFLQHLFNGVFKNIKSLGYLSHFISEQLIQLRKEIVASNFHIQAPNNFDEDFLDILSNIQHLQD
NQHFKNSTELAVVPVKYALHKIFLSEKKKNKSEQEKKKKKKSHKKGNVNKKEKNFKIASSFEQNEELPKRYVDAHRINSV
TKKIEGRGKTPNGELPVEEACGEEEVEEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEGEEEEGEEEEEEEEE
EEEEGEEEEEDDDVEENVKSESAEKRTGGREKREKRKHELGDEQYEEKEALKCAASMEQNVMGKESKAGIATPEEVQTKD
IVSTLGTNVDVTPNPNDKNSLCSDSPSGRSCSNISPFCEDVCKTEQEQFVEEEQEKENESQERNRQKGGEMDKQESEVYM
YVNPGVRKYTRKTTTKNKASSSKGGKELSITKGNKFRDCLSPDIQKRKMEPAHITVDAAADAGAEVGSEKKDPSEEPSRR
EKQKKEQQKRREGKGKTKWGSAHGRRHWDEAEVIYKKNRKQGVTRKEGKVSPGFMATMDNTKFLMKKKDREKAEREEKKE
KNYLLEKIGISSFQFLLNVCDKIDSCVIIDRRIDMVTPFCTPFTYEGLIDHLFCIENLQIEIPRYIIFNDQRGRNGTIAS
TPSVAGENNFSAGGSTGGGGDLRVRVKLRSSVDVLYNHIKDLSQNEIGSFLHKRASDIQKTYQEKDSLKDIGQINEYMRK
FKEKHYEHNSLSTHVNLASFILSVIKKEHNFSKLKLEDEIIQLNTNSSKSKIHNVVKKIQLLIYTKENIYEVYRILCLFS
VITNGFSDNYMNELKKDIIEQYGINEIVRLNKLHLCNILKYQPKQKFIWNCLKNNFNLLSNEENDISYVCNGYAPLSVRL
IEYMGILKNNVQVFPEFFNLLNGPTYDIIQNAVGYEHVQDKENHLDINNKKKFVILFYVGGISYAEIAAIRRLNRNNQDY
HYLIFTTEVTSSRKILQAMGA
```

352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE

A0A1A8W936 **A0A1A8W936_9APIC** (2214 aa)
B30.2/SPRY domain-containing protein. *Plasmodium ovale curtisi*

```
MNTKLVSHNCVEQYINCKDVVEGQKKELRIKENKQIGSAILYTRKGNTRMEELISILGGRRKDAKQIFFYNNCANKRYGK
INSLYKKKKEMKKNIYSVEEILERPAFNKTVEKKKNIFCFHRIPYIGYISEIIKSLIMRKKIYCSVSFNIIFSENGETFL
LRCLTFLLKYNKKNLSKSETFSLILKNECSSNKDRSFITRGVQYFLPHFNSKEGKYYEVKVVMEENIFLSLSHDNVLKIR
TYFFSKDVNFVENTPFANTYFELNYRGSTLFYDNIEIHNLKNHPIVRSVKDNFLEITVNCSEMKCNQCKKRKNEMGDSRY
SRAIRDAVSPLALLKNPFFSIIYKKENSKIGVNILEVHAFCCTKICTIQVFINVFTFPEIKTIFNYPSMKYGMSILYYVS
IFSYMINTHGVIFYHIVITEMVKVVLLMLFCTYICIMNLIFLRTRIYNNTHFSKHFTKKWEQREICVISLLCHTVVHIPF
SKKSYKEYITNRKNEHWSIGNPVLCLEKVPITFHFARRKMEKRRHFPIYSLPRYNTCHNGYFITTSFIDQFYHVLLEFYN
IVIYAVGMILHFFYIYMSTMISEFFCSLCCFLCLIIQGIVFFLNVMLNFVKYKMDLFLKMKNKKIEKYPTLFWIPREIRK
WNFPDLNQVTQEDTDENEDIKHQKWEEKIKTGNDYVARFDNKSELSHGCPRVGREVSGERLQRAACSSGFGNINNGRRRR
RRNVDSCGYLLPGIRNSVLCDAKKGVSKEYHESGNKKKRTFSSVRVVIKKKKNGTIHTKNGNMHCAIFSPVLYFKYSLYF
KETHEYNFAQFHGTPFQPLLLPSDSCSSHMSTGKKKSQRHANRRKNKKKKTNKEGKQQRGGKDKRNSNGSGSGSDSGSDS
GSDSDLESGSDEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEEEEEEEEKEPEDKFGDGEEEDDNDDDDNHNDDDDDNDND
DDNDDDNDNDNDDDDDDGDDSYSERERKKRKQKNKKIKGRGMYGDDPSIESEGEKQKGDSYYDKKKNLYLKKKKKKFKHN
FIYLKNLFKENVCINTTNVSNFISISKDKLTATYTAWGKHTDIACVQVNKCALRDCSIYYFEVEVLNCTNFSKIVIGMTS
KNYTINKNPGTEYNSFGYKNDDGKKIIDGKVDNYCNGYTKNDIIGCGINYYDNSAFFTKNGKYLGKACTINAKYDYYATV
GLSTLGDRIKFHLNSFHFDIYNLIYEESEKERKIIKSIYIQKDIFSDIIKSHLIKCGYFNTYQSFVNYLEKNKNSDDNNS
ISNSSNCKNGINKIFEKNTDSIKAKDNNDHKLYDGKKLKDSEGMKKENLTISGINGKGENNEKNDNPNKGNNTDISGRMK
CIITITPEENNSVKFNEGNSKFKTEEGTCTEHGDVVGNIGEKHKNEHIEEDCFTSQIKSDTVKSAAEGEVVAAAEVVATA
EVVAAAEVVAAAEVVAAAEAVATAETATGKKCESKEEKSNIDRNKDDKICDKSNDKSILNAFLVNYLDVYEKLNKEGNTE
KEVKDQGTIKTTEKKNDKGMNASDKSPHRPNKNGEGEGKYGEGEHGEKQETQIKTKSDEGKRSNKKTDCEDRKGRKEENV
HLVKCPIEETAEEGRKSQVGGTDPQLDILKSYEFSPYNNYGGVSSQNIQLASRRNSLSNLINARKESSSLLLSRLRNKRS
LSTKDDLNILATNFLNTKKEAKKNDSDINKKIHLLRDKSNIVKNEKKKLNKKEGGKNYSNDKEYITKYFVNLYLSEEKLR
KMKESLEMRHIIRKNIINGNIINALNILEEQYTELFTNERASFHIAMLFTQQLIEILKPHKKFIKNISSRKIKYKNEGKY
EKQDDLSSESSYKSYNTLSDDHFYDDIKTEYDSSDSLFCDSSNGEESNFTISQLEKLGKIHISKRGNQAEVKIGNKFESG
HNDKAANSSAKGFLNNGNVMLPLDNDPSKEETVGKDQKPSPVLSESKNLDNNASTIDNPKTNAEDGGVSVSPMNITQLND
IDFVKEKKIEHMIFKSMQCNYDEEFYKKNNLQEEYESHYNKLSKEYEFFKDDNPYNYKHKKKCYDKMHREDELGKDVKDI
CTSSTDDSTSDYDSNDSNFKRKYYEFNDINFDQIYQYIYKNNFSPNNQLKFKKDHLYLALLWIREKLSLFNKSPHVNVRQ
CIQDSTSLIAYHKPYKQKLVRMFFSKNRNLLTFNSVNEGILGNILFIYVPSVSR
```

892 - 911:	EEEEEEEEEEEEEEEEEEEE
893 - 912:	EEEEEEEEEEEEEEEEEEEE
894 - 913:	EEEEEEEEEEEEEEEEEEEE
895 - 914:	EEEEEEEEEEEEEEEEEEEE
896 - 915:	EEEEEEEEEEEEEEEEEEEE
897 - 916:	EEEEEEEEEEEEEEEEEEEE
898 - 917:	EEEEEEEEEEEEEEEEEEEE
899 - 918:	EEEEEEEEEEEEEEEEEEEE

A0A1A8WC34 **A0A1A8WC34_9APIC** (315 aa)
Uncharacterized protein. *Plasmodium ovale curtisi*

```
MKVNSKKFKHFSDKPEKLISKSPFDKSSTSSVNYNSVYGGRTKKLTKSNHNGVQVNLLFNLFALLLNKCNRNGISKFRVV
IVLYEVLVLHVTGKSGVEANSDKLQEGTNGTSFASFFDLSTMQAYLQKFVCYLKYQIICVTTQDDDEYCKNSHIVFLGIA
FFIIAVIGIIIIIFQKCGLCPCVPSISRKKKEVDFYRKQFEEMQLQMQMQEDYLLRALMSGESNGQEGEEGEEEEEEEEE
EEEEEEEEEEEEEEEEEEKRDKRKKKDEDKEKDEDKEKNKKEDDTKKKKVSMSTHNAENANSRNDNINIGYNATT
```

232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE
239 - 258:	EEEEEEEEEEEEEEEEEEEE

A0A1A8WC86 **A0A1A8WC86_9APIC** (2501 aa)
Transcription factor with AP2 domain(S), putative. *Plasmodium ovale curtisi*

```
MNDDMCAKEKLSKVEKLRKKKEGYNVSDNCKLSKNEHFDHEENLRYSKFCEHNNNAYDSYDLVNIPSTNRISDDEVKPSS
ISGRTISSAYAYVDDMRNISDSINSTNSNCNSTLYGNSSQGQNVEGSYKGASKDDQTNFNAGLNIPLMKLLSMRCSTNVD
LGNNTNCDSVSSKSIFKQGFERDSISKVNSAYTVHGENIDEDCDEKKDTMRSTNVMNQIMQNSEENEGNCEQSNNTMDSP
RFADTFSGEYQKSSVVYQQKEANIMSTIMDSKNMYDCSKTFDKVLTRKKKKQSKDNEDELNVSYGKIDYTNRIVQNMNMF
SMNGKKCINMVTSENDDISSENENILSNDIAKKFFDNMDLLHSLNKIADNDNAKSEQLSKFNSMNYVKNVLSDMSNMHSG
IGNSHNNAGRILGNVINSSEETNYINEQDSYINLVNMDRKNLKDSQNYLYSSDYLGIHNAKLGSKRSNKKGATLSTKNNE
NVITPHDAFTHNTYIGMNKDSCDMSLYNNGSSRNGVIQNGVAPNEVIQDGMSNKIVYRKQPSSDMHGETLKSAECMKINS
PLSTYDYDYDYDYCNFALNNFPNSGIELIKSQKKFMNTKCENTMAANSSSSNVCNINNKKSSNSKLETKDNAEFYGNVDN
DSYKKKTINDKFINVNKTNEDMDNSRNYAIPLVLKTSKDLGNSVKKNISSSVDVITNACGMSQSNNLSERKNINSGDMKM
SGKLINMNHHNRGNNTYENAGDSSSNYGNAFDKENFLLTCNQEDIDNFRIMNNSDGLMTGDTLLYNAQEMKHKEKLKNVC
YNDVFSSRMKKIPEEQFRYLSQKEESFSSHSFCPDVNVVAVSNGANVVGEAFLGNPKRRNQSIDFQTHRSFSCDEERAEN
DDFVDKVRRYQSFETHEEFGEKKNELDMYNVLRGGAPFISTTSSDIRTSYKSDNYCNKNETDIEEEYEDAPLLCERMQSN
NNERVNEQREIASEHAGEEEIEEASNNERKIFTEWNESFRGEIAGEKRKMRNSAKLKILKNDNTRSKKDMNNVEPSIISK
DKNNYISQYYDDLNKALFNIKNNSNIDELTKKKLLSRIENSFFPGKNPNMHFSNEEHDEQAQSSAVHANYMKQGRTNATQ
EVHRGSNNASHSGMRSTEHGEDCDPFEKCNDYDNSKRSRKCDLKPPRSSVRSEKAPRDIKMEKHREYFYKNSFASMGTST
SVVPNVTANANSCSSVNAQLLMGKQCEQGFLNKYNYAHDGSRICDVGINEDAKVFTVKERKNKKQKKIMNVLGEKNRADD
MLQQGVGVNEKYDTHDNCMNEEFYNDISNENNTNEVICVGDFKNRSMNNAGMEKFQMNILNAPFKKKGKVTLSCGDDMND
ELRKIIISKNELTKALEQNDRNIIENVEGRMFMYSSNSNNSNNNNSIGKSTSDVWKKGNNNDPMLRKGKMIMDEGSSRNF
SIMKDELNASMDTKKLLYKKNKEDMEEEEEEEEEEEEEEEEEEEEEEEEEDEEGEEEEEEEEDEEEDKLVNVRNGYEENAD
MGINGKKYDSDDLKSRKFGEIQNNEKKQKLCMSDVMKSNELQNNDNYFKFHSNLPSNLLSTSTSSSYSNDNLKVSSANYS
MNELSSNACTNKYYTEESMPSNLNVNTQINKNNNISYGKKKKKNDKKYVTSSFNSATNYVSNVNYANGKITDNDANVDGF
CQSQKGKGQHLLNVLHRMDAESKVIPNGILIDECVKKELINSSKNQFMMKNHHVGEKQKQNQKQRERKEEEETEETEET
DEADGADEGGEADEVDEKEHVDHAHHENVCSTGMSNNSHFGHHLGDSNLHDNSKKVVWGNANEINGVDVRRCYEDKFVEN
SQSNYAKSDVQFRKNNLQKSKSHSENDKLLNLYLKRKMSVFSDYAESDETNLKKHKLYNNYGKEDNEFLLSRTNSLNINM
SRMKKEQLDCENEANSNLNNDNSGNKQVGGGRLYDPLVRVKGEQEMLSNITDSSKLLEEKFDLQKGSRNQFDDNKIGAQV
KGENMVGEKGEKPNEPGNDASNRLEKDTSNGQENETLNGLENDTSNGLENDTSNETSNEASNAGGGTVKNEIDVSVCTLA
NCPTHNPQSYTRNVSRRGDSQGEGGMVKEENDELKRIPGVYYDKNSQRWFGEHKINGVKCAQSFAVKKHGCEEAKRLAIE
WKKARIRGEVWDRFINKKKKSNNNSSCINKTNKTSRPSVEELRIKYLSMSKNMPKVRGVWFNSTPQRMGWVGQAYKKCKR
IERIFSVNKYGFEGARKLAIAFRNSQKPSNEDSDEDSWSKDDKGNIKNGDENLNSYEFKTGYSSCVTRTKSSHDDMNDAN
DMNDINDGNDVNDINDTNDSNDNNDSHYGNDDNDGNDDRYNNDNSYSRPMSNNMNKIENKDTRINLCRDAILFILHDLET
ILELNIPMLNKNVNIYKICIKHHLNYLTLIKSEEQIIPYLNVFGDYIQRCILPTDLPYAELYVLIDSLIHNDILPSFDHK
ENFAECSVAEDPGIITPSMLL
```

1466 - 1485:	EEEEEEEEEEEEEEEEEEEE
1467 - 1486:	EEEEEEEEEEEEEEEEEEEE
1468 - 1487:	EEEEEEEEEEEEEEEEEEEE
1469 - 1488:	EEEEEEEEEEEEEEEEEEEE
1470 - 1489:	EEEEEEEEEEEEEEEEEEEE

A0A1A8WCM9 **A0A1A8WCM9_PLAMA** (2466 aa)
Separase (EC 3.4.22.49) (Fragment). *Plasmodium malariae*

```
NNNNNNNNNVSKTKECKNDNIVCIKKTAISGEEFKETISLESSISLNNNKEENNQRCSSEINDFENESLRCFNSCNKKKE
KTFFNFFLEKLFLINNVDTDMFNISLDDEQDITSIIKSYVMSDIKSLNVINFQNEYYNFNNFIRFGESANNDDDDDKCVQ
NISRMKSNSKIEDQTNELKNRRSILNLHACAFKVNDISVLNYLYLNYDFEKNIIYTENYINNRLFKYNCKRMNSYFIRVV
LYYINLVFLKIKNIFCDDCIYTIKKQQFLNSSANDCSRNIFFILFLKLFYFFNFSKQIVSEICINYFPGNKDYRTYLYML
SKNKQKENNNKTIVPSNHDGNTNRSLNTYYQKNNNAKNYNNGTTTNLDKIIFLHFAEIFLYPTKNCSYFEVLTVCYEFLT
NMKDAKNKVNRKKHKEKLYGFLISIMVGKQSRNIENNDISSSGNSVNSSSISSNSNNNIGDGTVYYFQTVLIYLSLLLYN
TCKKSFTHEMRKVAQFFLDFIFFFIENIKNNLIILQIIESYLNDVHSENENNVNTDNRCDNGKEIKYFYLLKFYFRKLLS
LLYLYTDELIFYTIKNNIDQEISQKKYYRKNVNRNLNIGIICNYEYISHMNLSEFCFYWDYAIVSMSHDKSDLYISRCYK
NFLLVLIQIIKNIQENNGSGNGKHLLDEASSSKSKEESFFSNGEEKISSLNNDEQKYNYFYEQIGNFFDILNNQQEDQQI
VDPNDNTYFIEDNNLMVSSNNNLYHSIKDIQEYLKANPYDEFHTRSDNNKYNKYGSMFHNNSTLKEKEGYEYEHDNGCIV
DGTSNYEKCGEKKKENKTIHDNIENEKSKKTKKKLYNISGENIFFTFDVNNVFSVYNIHNTPNSVNISNVSNVLNDKIEK
NEEYTRSNLKVLYFFSCLYKNACKCINKKRFEYFHVDKIHLNIEKFSFKEKWNYIKKLEKILKQYQHMIKIMCEILHKSK
NVDRSKSNLKIFIDLWWNNRYTLEQHLKILNLDISNLLGFSIHKLISVPLISLNVSRKFLLHPTTNCVEEEKTRKHLLNE
ENSPIDSNCIYNTISLVNNQKDYLKTNFDIFVVLYYYSNMLNIISWINKWRNFFLHLKYWDEINFINVLITLTVFSIVMK
NCNVQITHVKKKYLASNPILKKDNSSKKSNSEEMDKLNDHNSEKRKTQRNSIHINKTVVTSYLPFINKDIETILTLDKKL
QKRKSTNDAYFENANANININEGATWKENITLDVSKNLRSNISQDRQKKNRNSNCNYSYNYNEIEEFKNAGGESSIDKSY
RIIVPKAKEKQRYSYYTTNNRGNDKNSNGNSSENKYNVKRSRRKTINIINDNPDNFVDEDYNKSSVYEETRRKDEKKINS
TVYEYLSSMKDECFENSEKKYENKLRKNRKKATVEGTLILNDLKKERVKKMDEDKDGEKIYKENNYLKYLDLRKKCDRGS
LKCSFLKLRMYLYNILIDIFENNEVLPEDIFNIFNNITHSFATDILKCNLLEDDLDKERYIYVRNVEQHRTRKNPIIIYL
HSNLNRLPFENLEPLKDSYIVRGVHKIVTAYLYERLLRKIKNEEAQKDREIFSKMGEQVKEEETEEEEEEEEEEEEEEE
EEEEEEEVEKEEVKEEHVSDDYDNESDNMLQNEYIKNEYSEKWKIDMCKNKEQNIYTSNKNSVYNPLELKDKKNKNTDVV
IDSIEYRSHVPPKENLKDNNICFSKKNKNMFYEIFSNSTNNISKNDSTKNCHLYNNSEKSKTSDVNYEKCKLIYSIDNCN
TKERETRKTLYFDEREKSGESRYVRVKDLECKKEALVKGRYSLINTIEEKKQMKEDHVEIAKTVKSEIQIKDVRQTHEKE
KRRKYRRKSVRIEHSFLNPFNRSNYNNNNHKNERYSNNDKKNCNVLLFNEYDLGVQDKIYKKNEKKGVYNTLTVRDKHKW
GTHTTIRRSCVKDKDVPSYSSSSPSPSSASSNSSVELVQKEEELRRIFMNARKSMNIHNIMSICGKDEFSFFNSKKKRKK
SVSESEAHIDEEKMFLSSIVEPCKKERKRRSYSADPEHLSKLSKIKYIKYIPYYIKSSRLIDPRKSKIFFVINPNGDLKR
TEDATYPFIYFKNKEKYKYKNWNGYFGKVPCEMALLKHLCNDDLYLYCGHQGGEQYIKKEIIQNAFLRCNYEFVEEKRDG
KKHNSNKKGNIRSVSKHKKGKEKNRSLLLLENKNKKRRRRRYSCVIDSNKCIMDKRMKRKTVGDLIGVYDRSNVSTSNDT
SIYTHNETDEDSPLSDNNNYGINCCVFLIGCSSGLVSSHGFDLDVWGTPYDYIVGGCIFIFGNLWNVTDGEVDGFTQNFF
WKWTQPNSSSLFYSCSNYYNNVQMKNVLKISFSFFTKLLKECCSVQDNEDVQNEVSDNKNILIDVGDNFVTLDLHTYTYL
KQNNFFYKYFQQFYNCKIILNKNLFNINQNRKYIWLSMTEALAEAKQFCRLPNTTGSAVVIYGLPV
```

1585 - 1604:	EEEEEEEEEEEEEEEEEEEE
1586 - 1605:	EEEEEEEEEEEEEEEEEEEE
1587 - 1606:	EEEEEEEEEEEEEEEEEEEE
1588 - 1607:	EEEEEEEEEEEEEEEEEEEE

A0A1A8WCQ5 **A0A1A8WCQ5_9APIC** (703 aa)
GTP-binding protein, putative (Fragment). *Plasmodium ovale curtisi*

MRLSPLLLRKSSKFEKRHFSSSLTKGNESGRKKEIIVLHPILKKINNDKSFEEIIYDAQEALGLARSAGFRIASGISMPS
GGWAFTAESNSGREKSEGRDVHSSVAEGGNCINDTGSFDEIEKKIAESIMIKVNRVDNKFFFSKGKLNELSRYFLKNPTP
YIFINTILSPEQFRNIDFLFNNLLRSYHDELKLMSEKRSEGNFLSKRTLDSVLDVGNTKELDNRNCGYFDLYNSYTHAED
DNNVEEDDQTMEDNYDEEENHGDVDNTESDRRRGVVPMYVELLDRYSIILYILKSRAKSNLSKLQLELARANFIFTTYSE
NNKSRMKYIKYVENNILGKCHFDYEEKSNQVNIYHVEKQKSKKNFDYLGYTSNYIKSTETYKEYEKRIINNLYIKLRKEL
KICKNNNNLQNNARKHKALIAVVGYTNVGKTQLINYLTKSNLKSRNILFQTLDNTYKNLNISNSFSTIFIDSIGFIQNVP
YSLYESFKISLDAIKNSDIVIHIIDISHPYKDKHKKCVIDTLKKIGISDEFIKNNIIEVWNKIDKLKEKQLYQLYKDKPK
NVLPISAKYGINCDALIHIIKNLTNHIKNVQVLTLIFPTKEAKERISYLTKNFKVIPDSISYSTDGNTTFIRVVDNPSNL
KRINSWMYTTVCEMGNNGKGGATRKKKKKEVEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEKEE

672 - 691:	EEEEEEEEEEEEEEEEEEEE
673 - 692:	EEEEEEEEEEEEEEEEEEEE
674 - 693:	EEEEEEEEEEEEEEEEEEEE
675 - 694:	EEEEEEEEEEEEEEEEEEEE
676 - 695:	EEEEEEEEEEEEEEEEEEEE
677 - 696:	EEEEEEEEEEEEEEEEEEEE
678 - 697:	EEEEEEEEEEEEEEEEEEEE
679 - 698:	EEEEEEEEEEEEEEEEEEEE

A0A1A8WF66 **A0A1A8WF66_9APIC** (79 aa)
Uncharacterized protein (Fragment). *Plasmodium ovale curtisi*

EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEYTLNEYLLCSPFSPFCLELIIQMCISLIVHAE

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE

A0A1A8WJM9 **A0A1A8WJM9_9APIC** (737 aa)
Uncharacterized protein. *Plasmodium ovale curtisi*

MIKFVVGIICYYILYCSYNVYENIKTPIYDYSLEGSNLKKEKDNHVDGKYINKPFKNMLRKNDKINYHFYLSCIEEINLN
KYAKEKYIDNDKNFINVYNLTNVSYNWDYGHNLGDISKWLFFSGSKYPSVNLIIPQKLINKNKHIYLHIITYVNDELYRH
GFVTSLLTKSKNGRRDNVIKKKKKYLWKWLFDDEEEEEEEVEGIQIGEKTMEEDDRKGEEEEGEEEGEEEEEEEEEEEE
EEEEEEEEERSTSSKTTSGVTIGKTTSGATFGKTTSDATTGKATYGSTTGETKQKNEQQRSSVKNVRHNSLYIPRRVRFG
PIIEYNDINVNRIGFFSNVLLDKSTSTYLLPTYFNNYLTPEDEYQLLQGDYEEETDEDEFEAEKRKKKKERLKSASHGSS

```
NMIEGIRWNEVTVEYAPISYTHFNLFNIIIFNINHLKEKYSFSSYDLDSLAVHLCGNIYFSLFIYTICLVHIIIDLIALL
FDIKSWTQLNSLYSFLPNTIYLKFFFTSFILLYLKNKSDCKIVMVFCLVKMAVCICRLVSNYDIHFLPIYPYIYIGNNKI
GLDAKDSIVQQLEKTIKMKIQNVMICAMVILLTYNFLYNKYDSIYSLLIHTVGIYSYVFNFLFMCPQILRNYCDKRVQHI
PALYFFFLFLTALMDDLFALLLRMPIAHKFNALGDDIIFVIFLAQHLFYEGRNQEGRGYMGREYAGRERTNRGAIKQKPL
KGLEKTPKKFTSSSPYP
```

228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE

A0A1A8WLQ9 **A0A1A8WLQ9_9APIC** (1646 aa)
SET domain protein, putative. *Plasmodium ovale curtisi*

```
MFRVALLKNLERGGTGDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKISEESNKVSRKEKEELLEVAKELPILYEN
NDKEVIEALISSFVERYPKSVDAYECFSNFYIKMKDYKSALSMLYAALYVEKKNKTIVRMLHECEGRLVSQVYKIPTRYK
NWVSFPESRPYKEDVYSWESNCGNYGRSGGENVRGRGDRTDNNQDDEFIERKSLGKKVHLVRQGQQYIALARTNLEPGEI
IFQEKPLVLTQHIFSNYFTYSTCYHCFRERNISQKSYACPVNPHTCSYIFCNWKCLVDNIKIHKIECNILPIIYAASKKC
KLGYYNVLHIFRVLIKTRIDRDYKDKDHNMLNDIFTFPSYYYAVKENQKDIFNSFNTLANIIILKFPCSFYLYLKQQELV
EFMLIIWQYSTFVKYYSPSSIIQQINPETTFGFVFSPQLAKLHHSCIPTCTFYYDDNGKITVRSLCTIPEGGKLCINILP
DQYLPLKIRKSFKAIPRIFTCGCARCSDPTENNLHLRSIKCPKCILGYICPMKTDSLVETLKLHWYGQKGMNEEEERAYS
REEVIAKRSGSPSKCSDSSTKRGGSPSNCSYSPAKRGGSPSNCSYSPAKRGDPSSNYYASPSRSKPLLTDKEKKILDRLE
KEMERWVCSNCGKLSIQGNKRCIMLENKIYMLYNKGENEYMRGNLISSRNILLQLYKEFCHVLHPNHYIIFNTNVLLAGL
LRYNPNKEIYESLVCLRKAIIAAENVLSVCSLEKVHLYINLAHYTFNCLNVYKLHHKGIGISSEFVIDPIYTAIWNSSVV
TGFNSTLTIVLMQQLRMYAIYMNKFTPYMDIHFSIERKENFCTFYHKVTQKKSEPFRYIKKKTEDDPFYPIYMACQCFDL
KFEKNKYFRNIFKSFKNIPYFGNGLDALSLACSFGNINLVKLLLKLKYSIFLKNELHMNALLYMASSFLPEEKTSYHYNY
YYTLLKEIELQNINFGHVEGNYLSQEMFTHEENKKSFLLPQNGLNYMNSCHIKNEIEKPFPFDIVLDEEFIYGEKCKEID
TNQKIILILFLKHLHKIEVKKKKLYKKRLGLSERFHRFGNTNARFLKRAERRGKGGKRGKKKGMKKREKKGVEKREDKTE
LTPYNNLAGNNEEEDGNWGSTRKKPDNTKRHGSHLKELSSSGSSLFSDNPSHGSSQTGESDFLNGSNLSEESDIPSRGSN
LSEESNTSSGSNLSEESDTSHGSNPSEESNLSSDNSEDVLNNKVKNYYSQKLLVQSVSHKLLGFNNVLHYACARGKRELA
KQLIISGVPVMLLNGEGSTPLHMASFGGHNEIVKTLITYKSDINFVSSHGETPLMLAIYGLHIDVVKSLIENGANIMTKR
NNNMTVLHCLVHGLLRTETIHYKNVITMDDIPYLSLHGFTELSSSKCNIQRLTNLNINVLNSHITIIEQMSHDFFLLPFK
LLHRLKKAITILKYIMSYCPIFIYEIKNVNGYNPFELLKTTWKKLCERRLEVLSMSDLKISSFSERQKNIISQAWTLITS
LVNAILSILRPDRSILTSIYKNLLHMRGTTTWGNQGNAQVADVKKPVEDTKKPVEDTKKPDEDMKKPDEDMKKPDEDMKK
TDEDTKKSGEDAKVPSESSNTVVAKASALKKVVLKKMKPPMLKNKG
```

18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE

A0A1A8WQW9 **A0A1A8WQW9_9APIC** (799 aa)
Tryptophan-rich antigen, putative. *Plasmodium ovale curtisi*

```
MEPEIEIENPIPETPPISTLKINNSDILFCVSGSFFKSCVEFLCFATSIYIIGKYLYPSLLNKRKNVFDDLDYENNASHG
RHVNKKVPNKSKTLETVVEEGDEDEEFIDALENIEDNATNEGKEEMTEEEEEEEEEEEEEEEEEEEEEDEEEDEEEEEE
NGKSKNGIDAQNGNANNSMKEEEMNIETKDTSYNMEEESLETIHKKGIIDDYKMKEGESVSANEKSHSNYVLEVVHGEKD
EPNDKLTIESENNMEDRTSVDSGKKNESQYAEYESSNLYVVKESGENFDSKETKNNGVKEGETDVGTKETNTNEIKEGES
SLSKTEAHINDVKEGETDMNIKEANNEVKVGEKKPFHNETDEYEITVDGENIEKKDIISDEIRERLKGLIKKGKNNNVVK
EGEIESDKKETNANMEKEEEIKSVNKETNDKKVKEEEDHMEKKGANHQVEENAKEEHTKGLNDNKLKVDENNVQKNLSND
DKIKEDEKNAYRKGKIDDKTKVGEKDEHKNVGSFDKIETAKTKMKKELAQEKKVYNDEKSVANDIRRSVSVDAIYKNDYD
SKDEELLDEKSEEWKKKEWNNWMINTEEEWKLFNSTIEKKKEKWLEGKEKELEIWVRNMKNKWRNYKIDSDNEHIADVLK
KSIGWNEQQWEQWMKIEGKKCMEADLKKWINDCETNLDEWVSKEWVQWKNERIVLWLSVDWKHKEDENWENWKSGKISKI
LHIKKKKKFTKWKERTNKEKEEWNNWVGEKENLYVNAKWDKWIKWRKDKRVLFNLKVGTFINKCISAKLWTSWIKHRRL
```

128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE

A0A1A8WSJ4 **A0A1A8WSJ4_9APIC** (442 aa)
PIR Superfamily Protein. *Plasmodium ovale curtisi*

```
MLKDVFTDVLTLLYVIKPVILNFFFMSSEKGPRVEKEDKVEEKARNVRTRQGKSGKEEEDDEEEDGEDEEEEEEEEEEEE
EEEEEEEEEDEEEEEAVEDKENHVDNTLNNILSEISSNDCHMHKLNLCQKKDIKLLDHYLEKYSDYTKKRSVEREISNSS
```

```
YCESFNKIIELYNDETNCKVHNFNNEFCQEVKKCKKQYSYNSIPILTCAVKESSSIPEKQDTDKALLQVGVSGIATPDVP
YDNLPSGESHDPKKPTASEIFDAGVSYNTVIRNEKQTMEKTESFAHSDQVLSQMTPASEQNGSDTIISTSSTSCPHSSRK
ESCDQLLTTSKGTQREDTNKLSQSNQGYTVDHVETHMDSQEESRSTSTIIISASSVLGIPFFLFILYKFTPIGSKINNRK
RKEHIWKMNEEQYDQHLMYNPEIGNTNSNNNKYNIRYYSLIN
```

69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE

A0A1A8WSN7 **A0A1A8WSN7_PLAMA** (104 aa)
Uncharacterized protein. *Plasmodium malariae*

```
MSFVYPRVDVPESSKLVNNFIEQGENGIKEEKDKKNDEVVESIKHIKNINRTKQRTGKKIVPIETETAYEHENNEYKEEE
EEEEEEEEEEEEEEEEEEEINICL
```

78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE

A0A1A8WT47 **A0A1A8WT47_9APIC** (1840 aa)
Leucine-rich repeat protein (LRR6). *Plasmodium ovale curtisi*

```
MLALKRQVRTRKGKTGRVLSLQHISKVHVLSNRSDILVYCRAKGGESVADECTFAETRELVTQAIFDEAGYFSFLPSLPL
HLSEFLLSLISTMLLDLSKCNLQSLEDTDIILEKLIDLNCDYTSITYLDVSYNQLRCLKGLRHFENLKVLNISNNKLESL
DGDYIPSSTEKILAGYNNLTDICFKGAHTSKTLCREIISDIVDGEDTSPVCSPIYHPFNSSTLNEKREYTNRNLPLNRLT
YLDVSYNNIKRLITFEKYLHIMNKKRKNKKYESYLEDGYINNYIQSKTEKDVMILFFNSLQTLHLKGNKLTNLKGLSVFK
NLKTLDLRSNMINHPVQLFYLLDNKNWLKRYQQRGGTSNRDTKKEMKNGTNNCSKGGRENRNGSYYSYFIYILKKYRNFK
HLQNLLLLGNQKCLRPKHLFMSVFNVLRNVNERGELLTDVTDGEALINTNGAVETDVQSTATTGQFKWEKESQGKCSHND
IKSSIRQVHRGISNAYPGCGENSTQDAPESSLHLGGVAERESVEADEDWEGEGEEWEEWEDKEEEIEEEEIEEEEIEEDD
IEEDDIEEDDIEEDDIEEDDIEEDDIEEDDIEDDDIEDDKIENDKIENDEIEVQEVDDTEKAMRRKSDTGVHPKGGDEMV
LNEGIKTKDQETGRDSDEAKYWAPRSSERETLNECHVGGSNENQEEGETEEAEEETAEEDSEMDAKIWVQKAMQNVRENA
AEMSPSLLSFYNKLRKNICGRSSNYDLYDPNGQRVLENMKKEFTKLTKGQFRDAEYETDCYDNEDEWVQMKNGNHDTLKV
QEGEGMKSKKGEDLSSTGGAKALRKDEAHEKVNEEMHGEVHDEAHRETQKQAHKARDVANPEPVLTVQSSLDSQENKNDK
LKFLPTKSLKRVSSHHSGGNTTITASANLNNDEYHFHRCGQIKEKEVNTEENETSCSFTSILKRKRTNSLLREMLIGNKY
PERYSLVNFSSMDSDVFDSNSDDMSKTSLDEDSQAGGLQLLSGKKDGEGAVGGEDKEKEEKMEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEKEEVREEEDEIVGEQMPHMPRAKGSLTQERPHQHNSNRRNEYNDDETRPSGRFGSISKKHNITQNSS
NCGKGKNILHRDQTGNDVVKEEGEGKKWREEVYRQSKNRRNNFENNDHLTGEENIMSLGRKNRTTRDSDKNGGMQNGGMN
ENKILEVRGGDRNHYTGKDKGKEWKQKEKKEQKGQIDHTEKTKQTEQKNQSEHTEKTKQTEREKLMKLLRLNLCKEERPC
PPNSKTNNLEEYNLKLKKSQNYSSSLKSESTDVTERNVHGHNIRSDKYAPKDFVYNHNKTGNMLNFDVQEMVKEVNICAY
PVRITHNGAVNLGGGKEDNLAFPGKGDSKEAYLVTEKGSNGSNRSSGGSEKGGCDEEGEGGNIDEDRSDTKQPITSADFF
SKMCTPQLSNTKDLALSNTLALYLRDVCLKLGKEKQHSNMLLKEKKRLEIKIKLLNENKQLYKKKIKSLEKNCNEKMKMT
RKYQIMKEKFKSMENIKMEMPKDDINLQNEYIENAMEQLYNIFSDVFGENHIITKRIENLADVYIKKEKKIEIQMVTQRK
ELDLLKNVEEIVKKKNEYHKELEKKNDIINSLNNNLTKITRSVANMKCSIIENEKKSKSLLEELAKKDSLLKELDERSSQ
MAKEKEMAFQKERTQLLELLNDRDEDRKRAKQYKEEIKGLEEKLKSYLDTNVHKIHDKNYEIMVDRLHDEQIKMHSLLTE
KEKLINEKNLQIENLESQLQSWADEATNWIVVADKHTKLITNHNILKQNYEELKFKYIMDMKYIQTNKNEKVKELMRKFS
```

1023 - 1042:	EEEEEEEEEEEEEEEEEEEE
1024 - 1043:	EEEEEEEEEEEEEEEEEEEE
1025 - 1044:	EEEEEEEEEEEEEEEEEEEE
1026 - 1045:	EEEEEEEEEEEEEEEEEEEE
1027 - 1046:	EEEEEEEEEEEEEEEEEEEE
1028 - 1047:	EEEEEEEEEEEEEEEEEEEE
1029 - 1048:	EEEEEEEEEEEEEEEEEEEE
1030 - 1049:	EEEEEEEEEEEEEEEEEEEE
1031 - 1050:	EEEEEEEEEEEEEEEEEEEE
1032 - 1051:	EEEEEEEEEEEEEEEEEEEE
1033 - 1052:	EEEEEEEEEEEEEEEEEEEE
1034 - 1053:	EEEEEEEEEEEEEEEEEEEE

A0A1A8WVD4 **A0A1A8WVD4_9APIC** (629 aa)
snRNA-activating protein complex subunit 3, putative. *Plasmodium ovale curtisi*

```
MAERKYQSFTLPIPHFSPNLIFNPDEYDFYKIKHKEGHKASPNGNTLKKGANAKVEGSPKNRDGSDNERGSGSGSGSGEA
SENEKLFMRYLKHIGKKDVSRRGDNQASKSSPCSRDSGKDNASVAKDQPGGNSNKLDVVRKKVHLFEKYPHITIKEELKM
EWLYHMVPKSFVTRRVNISAFEEECRRVRDRLKVRPCHVRKEVDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEAGMEEEEKEENEGEQERDNKRDETDDVGEEIVERAKSKIYSRLIRVLLSGVRTPSVEEIINHIVYHNCNNWQYKIDM
DVLKKVANTEKTRKVLNRTKCYLDWLPNMESNPFSKYEIIAKLKEKTISKTFKLVCDFNNTILKSLYINQNVINIFYTLT
EYPTYAKDSLKNLSSETIFIISVSFYHPIRGIKIAEYDILSNQTLAHLTDVFFCFDTSNYGFPKFAGSLYYIDGILYPDL
RKKEALDYSTCILNFYKKMKNNDFVRPPYKIPQHKAILRDIEIPLYERCCFLHQGNCEHRVVFTNVRQHNSYRDKEFSQY
PLRTFKPNITRKFCTCCHKNEAKKIVLDCYLLKENPSYVCNGCFDLFLLNESGDFVDPSMKQFDYINDV
```

205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE

207 - 226:	EEEEEEEEEEEEEEEEEEEE
208 - 227:	EEEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEEE

A0A1A8WXF7 **A0A1A8WXF7_PLAMA** (1315 aa)
Calcium-dependent protein kinase 3 (Fragment). *Plasmodium malariae*

```
MLVSAKRKKKKNSILEDESEKDIRFIESGNHEDSYNICELYGDIENNGNRTNTNYSFQNLNKKEHITKNSFKEFYINSKE
NMQYGTNENEIFTEDILENDNFDDINFVEDENIEYKTYSSYTNRDFKLFSKYPSESIKKKIVQPDRKYNQLDGKYKKYWY
NNERFKNNLNEEDSDKMEFLNKNKKSVEYNKQNGIHFKKGIARSSTRNNNYIQENYKKYKGNCIGSNNYEYFNRGDSSYY
EYEDDDEDAYEGDDDENNQEIKRKKNLENTGVVRQSRGNAENEDYEYEEYYNDTKEEVEYNEEEEEEEENEEENEEEEDE
EEEEEEEEEEEKEEDKEEEEEEEEEEEEEEEEEEEEKAFRDSVRESEQKCTSALRNRRNNFNLKNEYKENENSNKRENE
NFEKEIISYEKEENKMIVPMHNIINYNGKNNNKNYDVNVSIYEKDRYINNLRTMEKKQSEELATMYNANQNNLKKNDLRK
NIQSRVKSSNIENKSKSNIISAKYTNVCIDKNKYNTFNNMDDKTIMFNIIGSTASTPTSATTTITTAATSGNVKLKYKDE
MINNVEYMNNSLYKSTAYKDSNYIIKKMEAGYKELKYTGKYAREPIQDSNVEDKKKNKIKNFLEKIKHRKNNEENLIKKE
HRNYEQEQKKDKLKMKFIDILHTGTLGNFFHRSKSNYAKSLSPQRKRDNSFNSVSSSNDVYKISLDYSKKSKIMNTLHHH
ESNNTPFQFSIKDEAKYYNRQELKREIYYNSNEESKVKNNLVYDSLSNERSQHIKDDIKYIELINKKDKIKYLQFSNNLN
DKEKSVKNGKCLRSEYSKYLEVNKKDYQDDFTKSRPTYTNNISLDVNNEQPNTSENIFPIHQHLSKKTIFWSDNEMKELK
QIQKENEINTKKLSTKEEDLEVKINQTLSKKMIENNELKKQNENNEDLIVTPFYIKSKIDKVLKNSEIFEKSARATFQQF
DVKNKNFLHFSEIESLIQQMCYNLELPPVDKNILSIVYKDYDSSKNNSMNYTDFRQMYWDLLKQIKKKYYPTKNFKIKRN
CIISRKKLGGYDYSSIYNYLSFKKILGCGAFGEVHLVEDNICKLYKVVKILKKKNMKNIKINEEINVLIYLDHPNIIKIF
DVYENVDCTYIVMELCEGGELMSKIRKSENFNEAYIKNIMFQILCAIAYMHSNNIAHKDLKPENILFKTKEDDTLKIIDF
GLAELINKSEGVSKTAAGTVLYMAPEVFKKNITIKCDIWSAGVIMFFLFTKNLPFSGTTYEQVKHSVFKDEPNYKSLKQK
LSQPALHILKLMLEKDHKKRPMASVVKINIHQNVH
```

337 - 356:	EEEEEEEEEEEEEEEEEEEE
338 - 357:	EEEEEEEEEEEEEEEEEEEE

A0A1A8WYA4 **A0A1A8WYA4_9APIC** (430 aa)
Uncharacterized protein. *Plasmodium ovale curtisi*

```
MNDSNASLSRKFSCPTNEKPEDGNKKRTKLIRLRNGHFRRIVDISNIDEKKILPNSCTFPCSTPRTEANGMLLALRGVQQ
TGARNMVATWSQHGHHISATCFASFLQFSYHPFSNYIHFSPVLILSSLDNKEKKWEEVSEVPSPNVYRKRRNSSMPPPSY
IVTVEEEKSSEQPSVRTISEFSLTCTSAKDEENESVKTQPEEEEVGEEQDEDVEEEEEEEEEEEEEEEEEEEAGKEEGE
EEGEEEGEEEDFMAEKEEEKVEEKEEEKEEVPPEDKQLIAPSKTLMRGIKTNIYFLSNKEKVQALMCYNYKCNAVVFEKD
TFLRYLYMKSINNIILNERMIEELCKQEELKYVLASNSIVVESTDFLKPLIIEFESSISKKIFVKHIKLNAKKEMDMKKF
DEYLYELDPNEKLRLRKVERFHSFNKLVAE
```

214 - 233:	EEEEEEEEEEEEEEEEEEEE

A0A1A8X313 **A0A1A8X313_9APIC** (2493 aa)
Transcription factor with AP2 domain(S), putative. *Plasmodium ovale curtisi*

```
MNDDMCAKEKLSKVEKLRKKKEGYNVSDNCKLSKNEHFDHEENLRYSKFCEHNNNAYDSYDLVNIPSTNRISDDEVKPSS
ISGRTISSAYAYVDDMRNISDSINSTNSNCNSTLYGNSSQGQNVEGSYKGASKDDQTNFNAGLNIPLMKLLSMRCSTNVD
LGNNTNCDSVSSKSIFKQGFERDSISKVNSAYTVHGENIDEDCDEKKDTMRSTNVMNQIMQNSEENEGNCEQSNNTMDSP
RFADTFSGEYQKSSVVYQQKEANIMSTIMDSKNMYDCSKTFDKVLTRKKKKQSKDNEDELNVSYGKIDYTNRIVQNMNMF
SMNGKKCINMVTSENDDISSENENILSNDIAKKFFDNMDLLHSLNKNADNDNAKSEQLSKFNSMNYVKNVLSDMSNMHSG
IGNSHNNAGRILGNVINSSEETNYINEQDSYINLVNMDRKNLKDSQNYLYSSDYLGIHNAKLGSKRSNKKGATLSTKNNE
NVITPHDAFTHNTYIGMNKDSCDMSLYNNGSSRNGVIQNGVAPNEVIQDGMSNKIVYRKQPSSDMHGETLKSAECMKINS
PLSTYDYDYDYDYCNFALNNFPNSGIELIKSQKKFMNTKCENTMAANSSSSNVCNINNKKSSNSKLETKDNAEFYGNVDN
DSYKKKTINDKFINVNKTNEDMDNSRNYAIPLVLKTSKDLGNSVKKNISSSVDVITNACGMSQSNNLSERKNINSGDMKM
SGKLINMNHHNRGNNTYENAGDSSSNYGNAFDKENFLLTCNQEDIDNFRIMNNSDGLMTGDTLLYNAQEMKHKEKLKNVC
YNDVFSSRMKKIPEEQFRYLSQKEESFSSHSFCPDVNVVAVSNGANVVGEAFLGNPKRRNQSIDFQTHRSFSCDEERAEN
DDFVDKVRRYQSFETHEEFGEKKNELDMYNVLRGGAPFISTTSSDIRTSYKSDNYCNKNETDIEEEYEDAPLLCERMQSN
NNERVNEQREIASEHAGEEEIEEASNNERKIFTEWNESFRGEIAGEKRKMRNSAKLKILKNDNTRSKKDMNNVEPSIISK
DKNNYISQYYDDLNKALFNIKNNSNIDELTKKKLLSRIENSFFPGKNPNMHFSNEEHDEQAQSSAVHANYMKQGRTNATQ
EVHRGSNNASHSGMRSTEHGEDCDPFEKCNDYDNSKRSRKCDLKHPRSSVRSEKAPRDIKMEKHREYFYKNSFASMGTST
```

```
SVVPNVTANANSCSSVNAQLLMGKQCEQGFLNKYNYAHDGSRICDVGINEDAKVFTVKERKNKKQKKIMNVLGEKNRADD
MLQQGVGVNEKYDTHDNCMNEEFYNDISNENNTNEVICVGDFKNRSMNNAGMEKFQMNILNAPFKKKGKVTLSCGDDMND
ELRKIIISKNELTKALEQNDRNIIENVEGRMFMYSSNSNNSNNNNSIGKSTSDVWKKGNNNDPMLRKGKMIMDEGSSRNF
SIMKDELNASMDTKKLLYKKNKEDMEEEEEEEEEEEEEEEEEEEEEEEEDEEGEEEEEEEEDEEEDKLVNVRNGYEENAD
MGINGKKYDSDDLKSRKFGEIQNNEKKQKLCMSDVMKSNELQNNDNYFKFHSNLPSNLLSTSTSSSYSNDNLKVSSANYS
MNELSSNACTNKYYTEESMPSNLNVNTQINKNNNISYGKKKKKNDKKYVTSSFNSATNYVSNVNYANGKITDNDANVDGF
CQSQKGKGQHLLNVLHRMDAESKVIPNGILIDECVKKELINSSKNQFMMKNHHVGEKQKQNQKQREREKEEEETEETEET
DEADGADEGGEADEVDEKEHVDHAHHENVCSTGMSNNSHFGHHLGDSNLHDNSKKVVWGNANEINGVDVRRCYEDKFVEN
SQSNYAKSDVQFRKNNLQKSKSHSENDKLLNLYLKRKMSVFSDYAESDETNLKKHKLYNNYGKEDNEFLLSRTNSLNINM
SRMKKEQLDCENEANSNLNNDNSGNKQVGGGRLYDPLVRVKGEQEMLSNITDSSKLLEEKFDLQKGSRNQFDDNKIGAQV
KGENMVGEKGEKPNEPGNDASNRLEKDTSNGQENETLNGLENDTSNETSNEASNAGGGTVKNEIDVSVCTLANCPTHNPQ
SYTRNVSRRGDSQGEGGMVKEENDELKRIPGVYYDKNSQRWFGEHKINGVKCAQSFAVKKHGCEEAKRLAIEWKKARIRG
EVWDRFINKKKKSNNNSSCINKTNKTSRPSVEELRIKYLSMSKNMPKVRGVWFNSTPQRMGWVGQAYKKCKRIERIFSVN
KYGFEGARKLAIAFRNSQKPSNEDSDEDSWSKDDKGNIKNGDENLNSYEFKTGYSSCVTRTKSSHDDMNDANDMNDINDG
NDVNDINDTNDSNDNNDSHYGNDDNDGNDDRYNNDNSYSRPMSNNMNKIENKDTRINLCRDAILFILHDLETILELNIPM
LNKNVNIYKICIKHHLNYLTLIKSEEQIIPYLNVFGDYIQRCILPTDLPYAELYVLIDSLIHNDILPSFDHKENFAECSV
AEDPGIITPSMLL
```

1466 - 1485:	EEEEEEEEEEEEEEEEEEEE
1467 - 1486:	EEEEEEEEEEEEEEEEEEEE
1468 - 1487:	EEEEEEEEEEEEEEEEEEEE
1469 - 1488:	EEEEEEEEEEEEEEEEEEEE
1470 - 1489:	EEEEEEEEEEEEEEEEEEEE

A0A1A8X5I5 **A0A1A8X5I5_9APIC** (442 aa)
PIR Superfamily Protein. *Plasmodium ovale curtisi*

```
MLKDVFTDVLTLLYVIKPVILNFFFMSSEKGPRVEKEDKVEEKARNVRTRQGKSGKEEEDDEEEDGEDEEEEEEEEEEEE
EEEEEEEEEDEEEEEAVEDKENHVDNTLNNILSEISSNDCHMHKLNLCQKKDIKLLDHYLEKYSDYTKKRSVEREISNSS
YCESFNKIIELYNDETNCKVHNFNNEFCQEVKKCKKQYSYNSIPILTCAVKESSSIPEKQDTDKALLQVGVSGIATPDVP
YDNLPSGESHDPKKPTASEIFDAGVSYNTVIRNEKQTMEKTESFAHSDQVLSQMTPASEQNGSDTIISTSSTSCPHSSRK
ESCDQLLTTSKETQREDTNKLSQSNQGYTVDHVETHMDSQEESRSTSTIIISASSVLGIPFFLFILYKFTPIGSKINNRK
RKKYIWKMNEEQYDQYLMYNPEIGNTSSNNNKYSIRYYSLIN
```

69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE

A0A1A8X6X5 **A0A1A8X6X5_9APIC** (283 aa)
Uncharacterized protein. *Plasmodium ovale curtisi*

```
MKVNSKEFKHFSNKREKVISKSPFDKSSTSGVNYNVVYTGKTKKLTKYNHNGVQVNLLSNLFALLLNKCYRNGISKFLVV
IILYEVLILHSTGESGVAANTDDSQEETNGTNSASFFDLSTMQNYLQNVVCYLKEQIMCVITQEDDESCKNSHTVFCGLC
PCVPSISRKKKEVDFYRKQFEEMQLQMQMQEDYLLRALMSGESNGQEGEEDEEEEEEEEEEEEEEEEEEEEEEERDKRKKK
DEYKEKNKKEDDTKKKKVSMSTHNAENANSSNDNINIGYNATT
```

212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE

A0A1A8X8Q9 **A0A1A8X8Q9_9APIC** (734 aa)
U3 small nucleolar ribonucleoprotein protein MPP10, putative. *Plasmodium ovale curtisi*

```
MEQVNVKMYTDFISSFCKRSEEILSFGKVSEEDKNKLMEMIEYFCNILISYFYNDMNMDRISISESGFDCEQLWFFIECI
IKQKKLDSLLLFFNNFERKINETKNCKQEDRCRIIEEGDTKVRRKRKLEKASLRRNPGTKRTNRRGDQDDNAATEDGSAA
TEDGSATTEDGSATTEDESATTEDGDDAAMHEDDDAAMHEDDDAAMHEDDDAATDKDDDAATDEGNGEEGDRFFNRVEME
TFIEEEEKKFLRAADESSSRGNSSGEESDGEYNLNDFECDYEGAHKLKYRDFYKGEGEQLEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEEEEDDRSSRRAHGRTRKGKKEDEKIERELDEMNERELNEEEDEAVSAK
TGEADRERIERELVATKHWSLTGEVFANQRPKNSMLELNVDIPKINTYNNDAFVSKTVGSIEGSEEDTEEAAGRTRSSRQ
NLLNEEIELVVKQRIKNMLFDDVEKKTIEDLDAMYGVSEGDGGEVNFDSLNFTRSKLSLADEYAKKIEDDIKNSHSMNKE
ISLQKIELMNMFKKIMHCCDALSNDYYIPNPVYINGKRSDINAKLHIEENIPIILSEKNKNAPEENYKPGFMKEIHEMSK
KEKKALRKQKKNKRRKILLSQFKDNGGGISEWKNRNSHLLEKNKKKKEEKLNRMKYGVISKEKLTQGPGQHSKYNFSRDI
TKAIAYDKRRKGDS
```

301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE
306 - 325:	EEEEEEEEEEEEEEEEEEEE
307 - 326:	EEEEEEEEEEEEEEEEEEEE
308 - 327:	EEEEEEEEEEEEEEEEEEEE
309 - 328:	EEEEEEEEEEEEEEEEEEEE

310 - 329:	EEEEEEEEEEEEEEEEEEEE
311 - 330:	EEEEEEEEEEEEEEEEEEEE
312 - 331:	EEEEEEEEEEEEEEEEEEEE
313 - 332:	EEEEEEEEEEEEEEEEEEEE
314 - 333:	EEEEEEEEEEEEEEEEEEEE
315 - 334:	EEEEEEEEEEEEEEEEEEEE
316 - 335:	EEEEEEEEEEEEEEEEEEEE
317 - 336:	EEEEEEEEEEEEEEEEEEEE
318 - 337:	EEEEEEEEEEEEEEEEEEEE
319 - 338:	EEEEEEEEEEEEEEEEEEEE
320 - 339:	EEEEEEEEEEEEEEEEEEEE
321 - 340:	EEEEEEEEEEEEEEEEEEEE
322 - 341:	EEEEEEEEEEEEEEEEEEEE
323 - 342:	EEEEEEEEEEEEEEEEEEEE
324 - 343:	EEEEEEEEEEEEEEEEEEEE
325 - 344:	EEEEEEEEEEEEEEEEEEEE
326 - 345:	EEEEEEEEEEEEEEEEEEEE
327 - 346:	EEEEEEEEEEEEEEEEEEEE
328 - 347:	EEEEEEEEEEEEEEEEEEEE
329 - 348:	EEEEEEEEEEEEEEEEEEEE
330 - 349:	EEEEEEEEEEEEEEEEEEEE

A0A1A8YQY2 **A0A1A8YQY2_9APIC** (1241 aa)
Vacuolar protein sorting-associated protein 33, putative (VPS33). *Plasmodium ovale wallikeri*

```
MNTLNELKEQGRLLLLNILQSFSGVKCLFFEKSLHILLNVMLNDEDVNKEKIEHIFVVSNEMDVQTSKLDNISNILFFIR
PYFYEIENIFKIIEKIEKVKSSEKKYVFIFIPYMTYMCEQEIIKYNIFEVSIKIIIYPLYFIPLYNDVFSLEIKNIFKEY
YVDNDFSNLIFCAFSLMFLQHLFNGVFKNIKSLGYLSHFISEQLIQLRKEIVASNFHIQAPNNFDEDFLDILSNIQNLQD
NHHFKNSTELAVVPVKYALHKIFLSEKKKKKSEQEKKKKKKPHKKGNVNKKEKNFKIASSFEQNGELPKREVDGHRTTGV
TKKIEGRDKTPNGELPVGEAGGEGEEEEEEEEEEEEGEEEEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EDDDVEEEEEEEEGEEEDDDVEEEEEDDDVEKNAEGGASAEKRTGGREKSEKRKHELGNEQYEEKEALNCAASLEQNVMG
KESKGGIATPEKVQTKDDIVSTLGTNVEVTPNPSDKNSLCSDSHSGRSWCSNISPFCEDVGKTEQEQFVEEEPEKENESQ
ERNRQKGGEMDKQGSEADMYVNPGVRKCTRKATTKNKANSGKGGKELSATKGDNFRNCLSPDIKKGKMEPAYRTVDAGAV
EGGAVEGGAEVGSEKKAHKEAPPRREKQKREQQKRREIKGKTKWGSAHGRKHWNEAEVIYKENRKEGAKRKEVAKRKKGA
KRKEGKVSPGFMATMDNTKFLMKKKDREKAEREEKKEKNYLLERIGISSFQFLLNVCDKIDSCVIIDRRIDMVTPFCTPF
TYEGLIDHLFCIENLQIEIPRYIIFNDQRGRNGTIASTPSSVVGENNFSAGGNIGGGSDLRVRVKLRSSVDVLYNHIKDL
SQNEIGSFLHKRASDIQKTYQEKDSLKDIGQINEYMRKFKEKHYEHNSLSTHVNIASFILSVIKKENNFTKLKLEDEIIQ
LNTNSNKNNIQNIVKKIQLLIYTKENIYEVYRILCLFSVITNGFTDNYMNELKKDIIEQYGINEIVRLNKLHLCNIIKYQ
PKKKFIWNYLKNNFNLLSNEENDISYVCNGYAPLSVRLIEYMGILKNNVQVFPEIFNLLNGPTYDIIQNAVGYEHVHDKE
NHLADADDDTNSNSSSSNSSSNSSSNSSSNNSSSNNNSNNNNNNNNNNNNSSSSNNNSSSNNNSSSSNKKKFVILFYVG
GISYAEIAAIRRLNRNNQNYHYLIFTTEVTSSRKILQAMGA
```

367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE
379 - 398:	EEEEEEEEEEEEEEEEEEEE
380 - 399:	EEEEEEEEEEEEEEEEEEEE
381 - 400:	EEEEEEEEEEEEEEEEEEEE
382 - 401:	EEEEEEEEEEEEEEEEEEEE

A0A1A8YRB0 **A0A1A8YRB0_9APIC** (1628 aa)
B30.2/SPRY domain-containing protein. *Plasmodium ovale wallikeri*

```
MDLFLKMKNKKIEKNLTLFWIPREIRKLSFPDVNQVTQEDTDENEYIKHQKWEEKIKAGSDYAIRFDNKSELGDSRPRVG
REVSGERLQRAACSGGFGNNNNGRRRRRRNVDSCGYLLPGIRNSVLCDAKKGVSKEYHESGNKKKRTFSSGRVVIKKKKN
GTIHTKNGNMHCTVFSPVLYFKCSLYFKETHECDFAQFHGTPFQPMLLPSDSCSSHMSTGKKKSRSHANRRKNKKKKTYK
EGKQQRRGKDKRNSNGSGSGSDSGSGSGSGSDSDLESDSDEEEEDEEEEEEEEEEEDEEEEEEEEEDEEEEEEEEEEEE
EEEEEEEEEEEEEKEPDDKFGDGEEEDDNDDNDDDDNDDDDDDDDDNDDDDGDDSYSERGRKKRKEKNKKIKGKGMYGDDPS
IESEGEKQKGDSYYDKKKNLYLKKKKKKFKHNFIYLKNLFKENVCINTTNVSNFISISKDKLTATYTAWGKHTDIACVQV
NKCALRDCSIYYFEVEVLNCTNFSKIVIGMTSKNYTINKNPGSEYNSFGYKNDDGKKIIDGKVDNYCNGYTKNDIIGCGI
NYYDNSAFFTKNGKYLGKACTINAKYDYYATVGLSTLGDRIKFHLNSFHFDIYNLIYEESEKERKIIKSIYIQKDIFSDI
IKSHLIKCGYFNTYQSFVNYLEKNKNSDDNNSISNSSHCKNGINKVFEKNTDSLKTKDNDQKLQDGKKMKDTEGMKKENL
TISGVNGKGENNEKNGNPNKGTNTDMSGSAKCIITISPEENSSVKDNDGNSKFKTEDGACKEHDDVEGNIGEKRKNEHIE
EDCFSSQIKSDTVKSTEAEVVAEAEVVAAAEPVAVAEVVAVAEAVATADAITGKKCESKEEKIDIDRNKGDKSNKSSDKS
NDKSSDKSNDKSNDKSCDKSSDKSILNAFLVNYLDVYEKLNKEGSTEKEVKGQGTLNTAEKKHDKGMNAPDKSPQRPNKN
GEGEGKCSEGEHGEKQVTQIKTKSDEGKRSNKKTDCEDGKGREEENVHLVKCPTEETAEEGRKSQVGGADPQLDILKSYE
FSPYNNYGGVSSQNIQLASRRNNLSNLINARKESSSLLLSRLRNKRSLSTKDDLNILATNFLNTKKEAKKNDSDINKKIH
LLLRDKSNTVKNEKKKLNKKEGGKNYSNDKEYITKYFVNLYLSEEKLRKMKESLEMRHIIRKNILNGNIINVLNILEEQY
TELFTNERASFHIAMLFTQQLIEILKPHKKFIKNISSRKIKYKNEGKYEKQDDLSSESSYKSYNTLSDDHFYDDIKTEYD
SSDSLFCDSSNGEESNFTISQLEKLGKIHISKRGNLEEAKIGNKCESGDVGKSGDNDKAANSSAKGFLDNGNVMLPLDSD
PSKEETVGKEQKPSPVLSESKNLDHNSSTIENPKTNGEDKGVSVSPMNVTQLNDIDFVKEKKIEHLIFKSMQCNYDEEFY
KKNNLQEEYESHYNKLSKEYEFFKDDNPYSYKHKKKCYDKMHREDELGKDVKDICTSSTDDSTSDYDSNDSNFKRKYYEF
NDINFDQIYQYIYKNNFSPNNQLKFKKDHLYLALLWIREKLSLFNTSPHVNVRQCIQDSTSLIAYHKPYKQKLVRMFFSK
NRNLLTFNSVNEGILGNILFIYVPSVSL
```

308 - 327:	EEEEEEEEEEEEEEEEEEEE
309 - 328:	EEEEEEEEEEEEEEEEEEEE
310 - 329:	EEEEEEEEEEEEEEEEEEEE
311 - 330:	EEEEEEEEEEEEEEEEEEEE
312 - 331:	EEEEEEEEEEEEEEEEEEEE
313 - 332:	EEEEEEEEEEEEEEEEEEEE

A0A1A8YSC8 **A0A1A8YSC8_9APIC** (1251 aa)
Vacuolar protein sorting-associated protein 33, putative (VPS33). *Plasmodium ovale wallikeri*

```
MNTLNELKEQGRLLLLNILQSFSGVKCLFFEKSLHILLNVMLNDEDVNKEKIEHIFVVSNEMDVQTSKLDNISNILFFIR
PYFYEIENIFKIIEKIEKVKSSEKKYVFIFIPYMTYMCEQEIIKYNIFEVSIKIIIYPLYFIPLYNDVFSLEIKNIFKEY
YVDNDFSNLIFCAFSLMFLQHLFNGVFKNIKSLGYLSHFISEQLIQLRKEIVASNFHIQAPNNFDEDFLDILSNIQNLQD
NHHFKNSTELAVVPVKYALHKIFLSEKKKKKSEQEKKKKKKPHKKGNVNKKEKNFKIASSFEQNGELPKREVDGHRTTGV
TKKIEGRDKTPNGELPVGEAGGEGEEEEEEEEEEEGEEEEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EDDDVEEEEEEEEGEEEDDDVEEEEEDDDVEKNAEGGASAEKRTGGREKSEKRKHELGNEQYEEKEALNCAASLEQNVMG
KESKGGIATPEKVQTKDDIVSTLGTNVEVTPNPSDKNSLCSDSHSGRSWCSNISPFCEDVGKTEQEQFVEEEPEKENESQ
ERNRQKGGEMDKQGSEADMYVNPGVRKCTRKATTKNKANSGKGGKELSATKGDNFRNCLSPDIKKGKMEPAYRTVDAGAV
EGGAVEGGAVEGGAVEGGAEVGSEKKAHKEAPPRREKQKREQQKRREIKGKTKWGSAHGRKHWNEAEVIYKENRKEGAKR
KEVAKRKKGAKRKEGKVSPGFMATMDNTKFLMKKKDREKAEREEKKEKNYLLERIGISSFQFLLNVCDKIDSCVIIDRRI
DMVTPFCTPFTYEGLIDHLFCIENLQIEIPRYIIFNDQRGRNGTIASTPSSVVGENNFSAGGNIGGGSDLRVRVKLRSSV
DVLYNHIKDLSQNEIGSFLHKRASDIQKTYQEKDSLKDIGQINEYMRKFKEKHYEHNSLSTHVNIASFILSVIKKENNFT
KLKLEDEIIQLNTNSNKNNIQNIVKKIQLLIYTKENIYEVYRILCLFSVITNGFTDNYMNELKKDIIEQYGINEIVRLNK
LHLCNIIKYQPKKKFIWNYLKNNFNLLSNEENDISYVCNGYAPLSVRLIEYMGILKNNVQVFPEIFNLLNGPTYDIIQNA
VGYEHVHDKENHLADADDDTNSNSSSSNSSSNSSSNSSSNNSSSNNNSNNNNNNNNNNNNSSSSNNNSSSNNNSSSSNK
KKFVILFYVGGISYAEIAAIRRLNRNNQNYHYLIFTTEVTSSRKILQAMGA
```

367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE
379 - 398:	EEEEEEEEEEEEEEEEEEEE
380 - 399:	EEEEEEEEEEEEEEEEEEEE
381 - 400:	EEEEEEEEEEEEEEEEEEEE
382 - 401:	EEEEEEEEEEEEEEEEEEEE

A0A1A8YSS1 **A0A1A8YSS1_9APIC** (1223 aa)
Uncharacterized protein. *Plasmodium ovale wallikeri*

```
MYAKDENDENNKINLHNYKNILHNKKKNLGLLNQDLLGKKDVKHALGGGECIKLRADAKGEVKEVEEEEEEEEEEEEEEE
EEEEEEDEDEDFAAEVEDDDEDEDDEDYVAEGEEEEEDDEDEYDEEDYDDEEREITFNSYNNYYYETYNEEEEKKRNEIE
DLIREKQKQDEKNRNGDKKNEALFEKYSKLLTGYKLRKERNVKDYPVQGEDDSRSCCYSCKSEERENGHTKLGDSTHRER
THLRGDHHPTLEKSSAEEEGNFVADLLNRIDEIYYKESRYESLKSVNNNNNNVCINDLNLNIISDYLNVDISVFNKKTTV
LLLGNTQSGKSSFINWFTEGYVQNTSSISKKNQITYVDVKQNFKFNFGRLQNGNYQLGMINKLSDASATAADGQGTNEYE
```

```
SMGLPQENQKVILSGENCYCLFKPFQKLKKSAQNLKKYIYGKIYYQNNLTKYMNRVNSVSFIDTSGINDVTDFEYDEVVM
NLAKYVDLIFIFIDSNTFSINNRLLRIMNYMIDNQINKVTICITRIDLIRKINLYRVVFYLTQYFFRNLNVFKYNLSRTH
SNSNCVNDIGELSNEEEHPDACVNIKSKQKGGKGNNFFNMSIKSFQNILLIPKMVGNLVARNTANERRKKAYPGHPFNRK
NNQNGTDAEWEEDVEGDKTQWDGGPSFSHSPHHGKKEPPGTPDEEESIFKKILTKSYNSFKEKIMSVDAENPQRGTSRIH
QKGNSQHTDEHRGSSQELPFEERNIRENNTSNRLDSIFERKINYGDCLKNCSVFFFVLIYEVITTVYSLLHTSISNYLST
SNMKRVINVEKLYKLDDANKLKYRDKNSNSNNCYKILEFLTIYLPEMPSNVLKRERWKYDESNINYNHQRRNRFSCDVQY
DHTSYNYNIDRVEKNPNMNNNPEKNNNYYYSKRYPQRRSIPEDVLLLGKGSNQYDGYNRGEKKVRYPDANNDRYRHIDEN
EHSSYFPKSDYRGDKRDSSFLPQEQTRRRASYLVDHTWENSSANGYPGRVLRQESSEVACGEPWGNSFERPYGHPPRNEE
ARELNMIHELLFKIDEAIDLKTNQSIYMLKKDLEKIQNSCLQKIFENDEVVKRNKSLRMQNIKFYFFRYMAIFFGFFVSL
LRYDLLVYFNFIKPEIFLSVFSKYFLFLSSYNKNSLFIAVNAILLGAYFFVYFRYNRRNYFKSLDKSDLNKLKIILLFTQ
IIFDEINQLHLRLLGRRGKEDRR
```

66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE

A0A1A8YSZ0 **A0A1A8YSZ0_9APIC** (1633 aa)
B30.2/SPRY domain-containing protein. *Plasmodium ovale wallikeri*

```
MDLFLKMKNKKIEKNLTLFWIPREIRKLSFPDVNQVTQEDTDENEYIKHQKWEEKIKAGSDYAIRFDNKSELGDSRPRVG
REVSGERLQRAACSGGFGNNNNGRRRRRRNVDSCGYLLPGIRNSVLCDAKKGVSKEYHESGNKKKRTFSSGRVVIKKKKN
GTIHTKNGNMHCTVFSPVLYFKCSLYFKETHECDFAQFHGTPFQPMLLPSDSCSSHMSTGKKKSRSHANRRKNKKKKTYK
EGKQQRRGKDKRNSNGSGSGSGSDSGSGSGSGSDSDLESDSDEEEEDEEEEEEEEEEEDEEEEEEEEEDEEEEEEEEEEE
EEEEEEEEEEEEEEEEEKEPDDKFGDGEEEDDNDDNDDDDNDDDDDDDDNDDDDGDDSYSERGRKKRKEKNKKIKGKGMY
GDDPSIESEGEKQKGDSYYDKKKNLYLKKKKKKFKHNFIYLKNLFKENVCINTTNVSNFISISKDKLTATYTAWGKHTDI
ACVQVNKCALRDCSIYYFEVEVLNCTNFSKIVIGMTSKNYTINKNPGSEYNSFGYKNDDGKKIIDGKVDNYCNGYTKNDI
IGCGINYYDNSAFFTKNGKYLGKACTINAKYDYYATVGLSTLGDRIKFHLNSFHFDIYNLIYEESEKERKIIKSIYIQKD
IFSDIIKSHLIKCGYFNTYQSFVNYLEKNKNSDDNNSISNSSHCKNGINKVFEKNTDSLKTKDNDQKLQDGKKMKDTEGM
KKENLTISGVNGKGENNEKNGNPNKGTNTDMSGSAKCIITISPEENSSVKDNDGNSKFKTEDGACKEHDDVEGNIGEKRK
NEHIEEDCFSSQIKSDTVKSTEAEVVAEAEVVAAAEPVAVAEVVAVAEAVATADAITGKKCESKEEKIDIDRNKGDKSNK
SSDKSNDKSSDKSNDKSNDKSCDKSSDKSILNAFLVNYLDVYEKLNKEGSTEKEVKGQGTLNTAEKKHDKGMNAPDKSPQ
RPNKNGEGEGKCSEGEHGEKQVTQIKTKSDEGKRSNKKTDCEDGKGREEENVHLVKCPTEETAEEGRKSQVGGADPQLDI
LKSYEFSPYNNYGGVSSQNIQLASRRNNLSNLINARKESSSLLLSRLRNKRSLSTKDDLNILATNFLNTKKEAKKNDSDI
NKKIHLLLREKSNTVKNEKKKLNKKEGGKNYSNDKEYITKYFVNLYLSEEKLRKMKESLEMRHIIRKNILNGNIINVLNI
LEEQYTELFTNERASFHIAMLFTQQLIEILKPHKKFIKNISSRKIKYKNEGKYEKQDDLSSESSYKSYNTLSDDHFYDDI
KTEYDSSDSLFCDSSNGEESNFTISQLEKLGKIHISKRGNLEEAKIGNKCESGDVGKSGDNDKAANSSAKGFLDNGNVML
PLDSDPSKEETVGKEQKPSPVLSESKNLDHNSSTIENPKTNGEDKGVSVSPMNVTQLNDIDFVKEKKIEHLIFKSMQCNY
DEEFYKKNNLQEEYESHYNKLSKEYEFFKDDNPYSYKHKKKCYDKMHREDELGKDVKDICTSSTDDSTSDYDSNDSNFKR
KYYEFNDINFDQIYQYIYKNNFSPNNQLKFKKDHLYLALLWIREKLSLFNTSPHVNVRQCIQDSTSLIAYHKPYKQKLVR
MFFSKNRNLLTFNSVNEGILGNILFIYVPSVSL
```

310 - 329:	EEEEEEEEEEEEEEEEEEEE
311 - 330:	EEEEEEEEEEEEEEEEEEEE
312 - 331:	EEEEEEEEEEEEEEEEEEEE
313 - 332:	EEEEEEEEEEEEEEEEEEEE
314 - 333:	EEEEEEEEEEEEEEEEEEEE
315 - 334:	EEEEEEEEEEEEEEEEEEEE
316 - 335:	EEEEEEEEEEEEEEEEEEEE
317 - 336:	EEEEEEEEEEEEEEEEEEEE
318 - 337:	EEEEEEEEEEEEEEEEEEEE

A0A1A8YY79 **A0A1A8YY79_9APIC** (1708 aa)
SET domain protein, putative. *Plasmodium ovale wallikeri*

```
MTMFRVALLKDLERGGTGDEEEEEEEEEEEEEEEEEEEEEEKHISEEKHISEEKHTSEEKHISEESNKVSRREKEELLEVA
KELPILHENNDKDVIEALISSFVERYPKSVDAYECFSKFYIKTKDYKSALSMLYAALYVEKKNKTIVRTLHECEERLVSQ
VYKIPTRYKNWISFPESRPYKEDVYSWESNCGNYVRSGGENVRVNGDRSSNNQEGEFAEGKSLGKKVHLVRQGKQYIALA
RKNLEPGEIIFQEKPLVLTQYIFSNNFTYSTCYHCFRERNISEKSYACPVNPHTCSYIFCNWKCLVENIKIHKIECNILP
IIYAASKKCKLGYYNVLHIFRVLIKTRIDRDYKDKDHNMLNDIFTFPSYYYAVKKNQKDIFNSFNTLANIMILQLPCSFY
LYLKQEELVEFMLIIWQYSTFVKYYSPSSIIQQINPETTFGFVFSPQLAKLHHSCIPTCTFYYDDNGKITVRSLCTIPEG
GKLCINILPDQYLPLKIRKSFKAIPRIFTCGCARCSDPTENNLHLRSIKCPKCILGYICPMKTDSLVETLKLHWYGQKGV
NEEEERAYSSNEVMEKQSGSPSNCSDSSEKQGDPFNNSHASPSRTKPLLTDKEKKILDKLEKEMERWVCSNCGKLSIQGN
KRCIMLENKIYILYNKGENEYMRGNLISARNILLQLYKEFCHVLHPNHYIIFNTNVLLAGLLRYNPDKEIYESLVCLRKA
IIAAENVLSVCSLEKVHLYIHIAHYTFNCLNVYKLHHKGIGIPSEFVIDPIYTAIWNSSVVTGFNSTLTIVLMQQLRMYA
IYMNKFTPYMDIHFSIERKENFCTFYHKVTQKKSEPFRYIKKKTEDDPFYPIYMACQCFDLKFEKNKYFRDIFKSFKNIP
YFGNGLDALSLACSFGNINLVKLLLKLKYSIFLKNELHMNALLYMASSFLPEEKNSYHYNYYYTLLKEIELQNVNFGHGE
GNYLSQDMFTHEENKNGFPLPHNGLNYMNSCHLKNEIEKPFPFDIVLDEEFIYGEKCKEIDTNQKIILILFLKHLHKIEV
KKKKLYKKRLGLSERFHRFGNTNARFLKRAKRRGKGDKKRDKKRDKKRDKKRDKKRDKKRDKKRDKKRDKKRDTKRDTKR
DTKRDTKRDKKRDKKQDKKRDKKQDKKREDNTELTRYNNLAGNNEEEDGNWGGTHKKPDNTKLHGSHLKELSSSGSSLFS
DNPSDGSNISEESDIPYGSSSLSGDSSNPSRGSNLSEESNPSRSSNLSGDSSNPSRGSNLSEESSNPSRSSNLSEESNIS
SDNSEDVLNSKVKNYYSQKLLVQSVSHKLLGLNNVLHYACARGKRELAKQLIISGVPVMLLNGEGSTPLHMASFSGHNEI
VKTLITYKSDINFMSSHGETPLMLAIYGLHIDVVKNLIENGANIMTKGNNNMTVLHCLVHGLLRRKTIHYVNINTMDDNP
YFSLHRFTELNSSKCNLERLTNLNINVLNSHISIIEEMSHDFFLLPFKLLHRLKKAIIILKYIMSYCPIFMYETKNVNGY
NPFELLKTTWKKLCERRLQVLSMSDLKISSFSERQKNIISQAWTLITSLVNAILSILRPDRSILTSIYKNLLHMRGTTAW
GNQRNAQVADGKKPSEDGKKPSEDGKKPSEDGKKPGEHGKKPSEDVKKPGDEAKKPGDEVKKPGDEVKKPGDEAKKPGEE
ANTVVAKASALKKVVLKKMKPPMLKNKG
```

20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE

[A0A1A8YZ92](A0A1A8YZ92) **A0A1A8YZ92_9APIC** (1704 aa)
SET domain protein, putative. *Plasmodium ovale wallikeri*

```
MTMFRVALLKDLERGGTGDEEEEEEEEEEEEEEEEEEEEEEKHISEEKHISEEKHTSEEKHISEESNKVSRREKEELLEVA
KELPILHENNDKDVIEALISSFVERYPKSVDAYECFSKFYIKTKDYKSALSMLYAALYVEKKNKTIVRTLHECEERLVSQ
VYKIPTRYKNWISFPESRPYKEDVYSWESNCGNYVRSGGENVRVNGDRSSNNQEGEFAEGKSLGKKVHLVRQGKQYIALA
RKNLEPGEIIFQEKPLVLTQYIFSNNFTYSTCYHCFRERNISEKSYACPVNPHTCSYIFCNWKCLVENIKIHKIECNILP
IIYAASKKCKLGYYNVLHIFRVLIKTRIDRDYKDKDHNMLNDIFTFPSYYYAVKKNQKDIFNSFNTLANIMILQLPCSFY
LYLKQEELVEFMLIIWQYSTFVKYYSPSSIIQQINPETTFGFVFSPQLAKLHHSCIPTCTFYYDDNGKITVRSLCTIPEG
GKLCINILPDQYLPLKIRKSFKAIPRIFTCGCARCSDPTENNLHLRSIKCPKCILGYICPMKTDSLVETLKLHWYGQKGV
NEEEERAYSSNEVMEKQSGSPSNCSDSSEKQGDPFNNSHASPSRTKPLLTDKEKKILDKLEKEMERWVCSNCGKLSIQGN
KRCIMLENKIYILYNKGENEYMRGNLISARNILLQLYKEFCHVLHPNHYIIFNTNVLLAGLLRYNPDKEIYESLVCLRKA
IIAAENVLSVCSLEKVHLYIHIAHYTFNCLNVYKLHHKGIGIPSEFVIDPIYTAIWNSSVVTGFNSTLTIVLMQQLRMYA
IYMNKFTPYMDIHFSIERKENFCTFYHKVTQKKSEPFRYIKKKTEDDPFYPIYMACQCFDLKFEKNKYFRDIFKSFKNIP
YFGNGLDALSLACSFGNINLVKLLLKLKYSIFLKNELHMNALLYMASSFLPEEKNSYHYNYYYTLLKEIELQNVNFGHGE
GNYLSQDMFTHEENKNGFPLPHNGLNYMNSCHLKNEIEKPFPFDIVLDEEFIYGEKCKEIDTNQKIILILFLKHLHKIEV
KKKKLYKKRLGLSERFHRFGNTNARFLKRAKRRGKGDKKRDKKRDKKRDKKRDKKRDKKRDKKRDKKRDTKRDTKRDTKR
DTKRDKKRDKKQDKKRDKKQDKKREDNTELTRYNNLAGNNEEEDGNWGGTHKKPDNTKLHGSHLKELSSSGSSLFSDNPS
DGSNISEESDIPYGSSSLSGDSSNPSRGSNLSEESNPSRSSNLSGDSSNPSRGSNLSEESSNPSRSSNLSEESNISSDNS
EDVLNSKVKNYYSQKLLVQSVSHKLLGLNNVLHYACARGKRELAKQLIISGVPVMLLNGEGSTPLHMASFSGHNEIVKTL
ITYKSDINFMSSHGETPLMLAIYGLHIDVVKNLIENGANIMTKGNNNMTVLHCLVHGLLRRKTIHYVNINTMDDNPYFSL
HRFTELNSSKCNLERLTNLNINVLNSHISIIEEMSHDFFLLPFKLLHRLKKAIIILKYIMSYCPIFMYETKNVNGYNPFE
LLKTTWKKLCERRLQVLSMSDLKISSFSERQKNIISQAWTLITSLVNAILSILRPDRSILTSIYKNLLHMRGTTAWGNQR
NAQVADGKKPSEDGKKPSEDGKKPSEDGKKPGEHGKKPSEDVKKPGDEAKKPGDEVKKPGDEVKKPGDEAKKPGEEANTV
VAKASALKKVVLKKMKPPMLKNKG
```

20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE

[A0A1A8ZEG0](A0A1A8ZEG0) **A0A1A8ZEG0_9APIC** (3785 aa)
Uncharacterized protein. *Plasmodium ovale wallikeri*

```
MSDIKLSHVSSITFINSNGVIITTEIKEGNKRMKGTYTNDYEGNYVFFEKDLEHVKNIVLTLKPFHKEYEDNIIFRIKKR
DDKYRCEWVLLLKTKEEGGKKGRNGNTFADIRNSNKKNECEQKEEKEEIEEKTFDCSNIKDIMLKYVYCVTYFDNYILNL
RNEIGGSNSENEYLLNELIKINNNDIAKKSHKEGFVKATHIAARDDMMRSSVQLEAVHGTAQREAVHGTVQRETVHGTVQ
HDGMLRTVLYDDTGNNNGDDNGDHFMYDRATCKGNQLTLNGNSYNDRLGEKMEVFSSSGPYHFGEGDQENGNGNAIGIRR
NSSIRTSCNSSSNDVTGIRGRRLGARKIHCEKPKGEIKQRTHSSKMDRSEPDSGKPDSGKPDSGKPESGKYNSLKTVSNN
TTCNYGINHTACSSAKSRDLNKIPLEEKHLKDYNSDDIDFLKKLFYTNCNFENNNSAINERSTNIHGNKVISGEKKYSVQ
KGKEESMIRNGERNSIINKEEGFVVDPADCDRSFTVNKISNDDMVENIGNFNNVGVGGVSSFTENDNIGSDTFINKKGKL
LTKGEELKKELSCLLNVSEIKERMNEEKVNKNNKMERYYYLRSGQNSHLNLNENINNNNKLSSQKLSIYNKLNFDNLKYI
NEPFINTENILMNISPNNFLNLQKEFINNKNYNKNFDKNKIFNNSEFYDNSEFYDNSEFYDNSEINNNSEINNNSEISNN
LKHVNIELLKLILNQQDINNSSQAFMYDKNRIFEHLQSACKRDNNDALCSEESTKNDYMFTNKCAQNISNVHEKICNPYE
NSEMNNSFIKVQSAEENGKIGSNSKGGSNGNVVSGNSCGIGGGVDESVPHAHKPKYDFRAQKKRDRNGEYGKCVLHSKEK
QVSDRAESRGQKNNAEDSLHDGVISEIFNFMMKFNENCNAENGTCSTSHKCSGNIFGGHEQCSNERNDAIRLNNAIREFL
DNLTPSEMRHLVSNKEHIISKLISDRCTNANVSRKYNMHMKNGKCACTSGRKKERTDDCTQDCTQDCTQDCTEECTEECT
RECTDECTGGSSSTCSNCNVLSNIYSKSSTNRNDASRFFINSSTTHINMNVKKRSEQNMKEMILLNTNNNDNDVTNSKSS
NVLNVINLIKSGTGYVTNRCDDMGNVQSTSFRSDKNNKLNLSEDCSKNCVPEEDAVSSTIPTTLTTQGLNNFDPGDHFLI
EEKIKDTNSAHNTPMENKAKRDDDPPNGNDSDDGRGIHTKLHDDVDSKKDDSANVENCSDNANILGRSNGERFQLSSEKM
DFLYNYYLEACKNNAMHADFNNKLISLTDAHICNDLHNTLVNKRGMNRSPDCCINGLYNSTSSSVKGSSARNMKNVRKKT
VEGKDGINSDSGSMHSGPASINTIPCAHGGLNINFGDTYRNGENVADEVNNFFRNCLYSLKHMKGATTLDKFLEHEHNPG
EDIIKSRNQDEEENKTEQEKKNERRIENEGGKENDCEVDCGGGSPRRVHICSANGADEPGAQILYANGKGNDEQAYSDKS
TFEGSNLGKAKNGEKSKDIACDRDGKVEHDECAQTSGGTVRCLTELNEKMGENQIDNEFSSHINNKYENDEAVDKYPKNL
IHFVEDLSNQSIGGGEFYSSEVEANGNINEKYNDEHIIKAVLINMIKEMSNSKHGNNSGSSRDVPLSKGDYEGSNGAHTN
NVSGSCGCSYPQSNYNSLPSKCDGNRRNSINHKRDESKDTNGNTGFSNSPDDMNGNINFQANVDAFNHIYNSLVIKNNIN
NSNNYYNNYCQNNIININNCGGNNYFYNSSCGSGGGSNNSRASTKCDSNALRGGGVGRGNPEDGGTLHVQSNNVKLGMSN
NIHYLTSSGMGKKVKSGSFSSFNISNCKQFPVGGHSLVFESNACDHTSSNDANDPKSPNGPNDETVNTENTHDDVVNTDN
ANDVNANDDDVNERVDSGHLLGSDLLSGNSFRDNSSLKGERDANCMSNLKVGMDESEFGKVVFNKMDNNMDGINKRQSSY
EEEEDIFRMVRRNSHSNGNANDAEGSTVNDTVLNINDSNLNSLMITGDITDADVVGAVGAVGAPDEADNAEEAGDCEDDG
NGNKWNTKGWEIFEQFQARNREKYSFIFDTNVEEGSPFCKMRENSHDMRSVSDVNGNTSLDSVYGDVKSDLMHNLREDCD
LGLYKKDHYSVIDRNNVPFKEINDIMPMDIRNVKQNNVKELLLQKGWLCTGVKKCEEEEEEEEEEEEEEEEEEEEEEMYKE
EYNNMYFEKDKGKEDIYQDVFNKTFCDDKSTEVNIKTNVCNSYSSYSSLNINFFCLFDDMYENFFKNNFEDREKMIKILN
MNKDLCYNQLLTFYKKKLFFEGIKEGERSSTHTHLDLHNTYNQRIKESIAMQQKCTSTEGSTEGTTESSTYDVVHGEDAH
VGSITLIDKRESDFSGKIDYLLPPNNGDNINSSNNVLGCFTEYTVKGEYSGTTTLPLPLLLVKEETEHMCKDDDGVMNHL
KTDDHRVNNTLQLMNRSSSEEEATAMEPGEIPNNERTLHVGMKSGTEWKHVIGNTVNGTGGIGTRGGNIIKFKGEQEDVC
KGESSRGDCKDITNVRIDEIVKKDVKEVVEKKLADISCEHLSDYSFESDDAREMVEHILDSPKRMTKKDSSNGGSSSGYC
GGSECSTADDRGTLEFEINVRDMCEEEGSTMFKYIYHKIKCIRNNIWTQSIDEMQNREMHELFVMGRQKSEEVAKREEQV
QLTMQRMSPQQTQLEVHNEGISTVPPTDIYYFNVYTNLWENVDLNVSHKLLEAQGAKKKIINKFYRSDHVGEKYITFSEW
SIYNLLVSKICKHFDVKKFEDNQLKMYNMDKFQYELKKRNTYNFGIKIIGDSNGTSKGKQREKRGRRNCKRNRNRRLSRI
SEEFSDMNHDEEEEDEDDLDGGEDYIDGGEAEVDEDEVEEEEEEEEEEDEDEEEEEEEEDVEIDDVEIDDVEPFYEEEEQQ
TNSNNSSNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNSSNNNNSSNNNNAIPRSS
SRIFCRNKNRSGLKIYGSSSEMNGRNSIDRKRPVKELKDGKITIVSCEKNGKMDDTVSTTSRNGGEVGEGGEEGNAEEGLG
QASRSLSMSLRRKKRNSLLSGNSAESGLSRVNKRKSKRLKIGEKEGKYVDDLQQEEGVVSQRGHRSGHYGVIHRGHPVSS
SSCGRNRKVHIFKKRISRRSNFNTLTDKKMNVYHMIQLPDYVSHKELIRSKNECLPTYEQSLKHNEYLNNTLNNVKARLH
IKRLCLKKNITIRDRIFDVSSTYFNDLYTYDSKNNTYVFYKSKESRMNKMERAIDNQDYYYSMYVNDYIENELLNKGKRK
KKKNYHHHNSSHSGKSSGDNFDFASERAVVRKISSSYEHSGNHVDNMGDYGNDFPEKRETHHGSANHSIGGDNTRNDAYA
ISDVAKNEHQMCDQLNYINYFVDHVQYDEDNSNGETCKNVMSFSERTVEEEFLGEDMLGGGLLGDEILGAIEKSSIEQIE
SSSMGKMEKSRMEEVHTFSPEQSATFPPELLSTYSNNFEEESDKKEIIKTKNDFFNYYNQNDNESFFPNFQKQENGNEQD
FNNNNKEFYFNGSINHDDIIQARTDYTYRYIRPIVRVLGAPLIYCTTPFRCKVCPLDRASGCKSIQTRHGNFTCVFVPSL
AITLEETNLIERESKCSPFDRLLRVFIYHKYKTFSEPSLVPLAWVIRVIINAEFASYYFLFYLFFFFYFLKKIINFWHFL
RLLFSLLKSGKREEFQNWSIIINAN
```

2216 - 2235:	EEEEEEEEEEEEEEEEEEEE
2217 - 2236:	EEEEEEEEEEEEEEEEEEEE

[A0A1A8ZEU8](A0A1A8ZEU8) **A0A1A8ZEU8_9APIC** (1209 aa)
NTF2 domain-containing protein. *Plasmodium ovale wallikeri*

```
MDIHTLIGEMVGSGAVGGGAVGSGAVGSGAVGSGAVGSGAVGSGAVGSGAVGSGAIGSGAIGVGGKPNQKNAYHFHQRKD
AKNNYEDYIGSMQDASNGGNNVSLSHAQRAYKSYAAENNHDNYLNMGMSKNSNRYYEANDNAAAGINNLSGQKNINYYST
```

GQSNAHNGMMSGSEGARPQGYSGVSDRVLHMGDEGSLQKSLLAAGDNKKTLLSMISSNEGNKVKNKNKSKVSNDHYNFGE
GEDAEGGNKIGKMEKREEEHGKIGKIGRIGKIGKIGKIYKSNSNSRAPSICSSSNRSRSRSRSGSRSRSRSGSRSRSGSR
SRSNVPPKEMHENRDTSGGKNETACNESLVGNLNNAGPSGSAYSIAYMFIYQYYYVLHTKKEMMHNFYSEHATLLISFNY
QSGDKTGISDKGIETGGGAVSVGLGIGVEMNTDAMCGVGMSSGLVSGLTTGGVSINAGKFFNLNEIKVEGCQRSENMMKF
KSRKMIASYYENLDVNECTVHISSIEVVNLYNEIYMYIYGKIKKCKDTNVFYFFVQNIHLHKYNIYQYYVDVDFVHYYNT
FEEIFDANRKLEQRKSRQYETSKLLCNTFNVKVKEEDKKKKNKISTLNVGGTHVGITNSGDRPSRTNTGKNEKKNYHTSS
TCKSVLKRSGKVEVEEEEEDEEDEEEEEEDEEEEEEDEDEEEEDDEDGEEDDEVEDYDEDDEEEVEEVEEYDEEDYDEE
DEEEEEYDEEGEDDEDEEAEKCNEDKIVDMGKKKNISTVHSKGGELGHTKKVEESSSGGSKNVKKGIISTGEGGDVVVA
KSTSQPSSDKKPLEEDAVSGKTTGEQVKTLDEKEKPGESFTPSVADSKKGKEKEVPGSGKASTSSGKASIGSGKASISSG
KAVVGVDTALASSEKTSINNVKTVGDSGNYAIDGKGKKGKSENAWNVPNDVVIPKMENNLKEEKIASEVAKKKKKEKNKI
DPNSWVFRVMKNNQGANMGEKKSLAANIKVNNNQVKNSGDKRKTVLDGTENMKANDEEEEEEEEEEEEEEEEEEEEEKKE
EEINVNDKKIIIHNIHKNMDKKKINDCIIDRLKKYNDGHAVQIDIYQRSIKKLYANSYNYHNSYEKIKPTEYSYAIAELD
CRQSQQLLLDLGLYCNGIKLNIENFKNKRKTEIKKNTKKFSNTYNTSLEGSKMRDDKFKGSFYRGASATMTPVAASSSFR
SKRNNIFVK

1017 - 1036:	EEEEEEEEEEEEEEEEEEEE
1018 - 1037:	EEEEEEEEEEEEEEEEEEEE

A0A1A8ZFP4 **A0A1A8ZFP4_9APIC** (3715 aa)
Uncharacterized protein. *Plasmodium ovale wallikeri*

MSDIKLSHVSSITFINSNGVIITTEIKEGNKRMKGTYTNDYEGNYVFFEKDLEHVKNIVLTLKPFHKEYEDNIIFRIKKR
DDKYRCEWVLLLKTKEEGGKKGRNGNTFADIRNSNKKNECEQKEEKEEIEEKTFDCSNIKDIMLKYVYCVTYFDNYILNL
RNEIGGSNSENEYLLNELIKINNNDIAKKSHKEGFVKATHIAARDDMMRSSVQLEAVHGTAQRETVHGTVQHDGMLRTVL
YDDTGNNNGDDNGDHFMYDRATCKGNQLTLNGNSYNDRLGEKMEVFSSSGPYHFGEGDQENGNGNAIGIRRNSSIRTSCN
SSSNDVTGIRGRRLGARKIHCEKPKGEIKQRTHSSKMDRSEPDSGKPDSGKPDSGKPESGKYNSLKTVSNNTTCNYGINH
TACSSAKSRDLNKIPLEEKHLKDYNSDDIDFLKKLFYTNCNFENNNSAINERSTNIHGNKVISGEKKYSVQKGKEESMIR
NGERNSIINKEEGFVVDPADCDRSFTVNKISNDDMVENIGNFNNVGVGGVSSFTENDNIGSDTFINKKGKLLTKGEELKK
ELSCLLNVSEIKERMNEEKVNKNNKMERYYYLRSGQNSHLNLNENINNNNKLSSQKLSIYNKLNFDNLKYINEPFINTEN
ILMNISPNNFLNLQKEFINNKNYNKNFDKNKIFNNSEFYDNSEFYDNSEINNNSEINNNSEISNNLKHVNIELLKLILNQ
QDINNSSQAFMYDKNRIFEHLQSACKRDNNDALCSEESTKNDYMFTNKCAQNISNVHEKICNPYENSEMNNSFIKVQSAE
ENGKIGSNSKGGSNGNVVSGNSCGIGGGVDESVPHAHKPKYDFRAQKKRDRNGEYGKCVLHSKEKQVSDRAESRGQKNNA
EDSLHDGVISEIFNFMMKFNENCNAENGTCSTSHKCSGNIFGGHEQCSNERNDAIRLNNAIREFLDNLTPSEMRHLVSNK
EHIISKLISDRCTNANVSRKYNMHMKNGKCACTSGRKKERTDDCTQDCTQDCTQDCTEECTEECTRECTDECTGGSSSTC
SNCNVLSNIYSKSSTNRNDASRFFINSSTTHINMNVKKRSEQNMKEMILLNTNNNDNDVTNSKSSNVLNVINLIKSGTGY
VTNRCDDMGNVQSTSFRSDKNNKLNLSEDCSKNCVPEEDAVSSTIPTTLTTQGLNNFDPGDHFLIEEKIKDTNSAHNTPM
ENKAKRDDDPPNGNDSDDGRGIHTKLHDDVDSKKDDSANVENCSDNANILGRSNGERFQLSSEKMDFLYNYYLEACKNNA
MHADFNNKLISLTDAHICNDLHNTLVNKRGMNRSPDCCINGLYNSTSSSVKGSSARNMKNVRKKTVEGKDGINSDSGSMH
SGPASINTIPCAHGGLNINFGDTYRNGENVADEVNNFFRNCLYSLKHMKGATTLDKFLEHEHNPGEDIIKSRNQDEEENK
TEQEKKNERRIENEGGKENDCEVDCGGGSPRRVHICSANGADEPGAQILYANGKGNDEQAYSDKSTFEGSNLVKAKNGEK
SKDIACDRDGKVEHDECAQTSGGTVRCLTELNEKMGENQIDNEFSSHINNKYENDEAVDKYPKNLIHFVEDLSNQSIGGG
EFYSSEVEANGNINEKYNDEHIIKAVLINMIKEMSNSKHGNNSGSSRDVPLSKGDYEGSNGAHTNNVSGSCGCSYPQSNY
NSLPSKCDGNRRNSINHKRDESKDTNGNTGFSNSPDDMNGNINFQANVDAFNHIYNSLVIKNNINNSNNYYNNYCQNNII
NINNCGGNNYFYNSSCGSGGGSNNSRASTKCDSNALRGGGVGRGNPEDGGTLHVQSNNVKLGMSNNIHYLTSSGMGKKVK
SGSFSSFNISNCKQFPVGGHSLVFESNACDHTSSNDANDPKSPNGPNDETVNTENTHDDVVNTDNANDVNANDDDVNERV
DSGHLLGSDLLSGNSFRDNSSLKGERDANCMSNLKVGMDESEFGKVVFNKMDNNMDGINKRQSSYEEEEDIFRMVRRNSH
SNGNANDAEGSTVNDTVLNINDSNLNSLMITGDITDADVVGAVGAVGAPDEADNAEEAGDCEDDGNGNKWNTKGWEIFEQ
FQARNREKYSFIFDTNVEEGSPFCKMRENSHDMRSVSDVNGNTSLDSVYGDVKSDLMHNLREDCDLGLYKKDHYSVIDRN
NVPFKEINDIMPMDIRNVKQNNVKELLLQKGWLCTGVKKCEEEEEEEEEEEEEEEEEEEEMYKEEYNNMYFEKDKGKEDI
YQDVFNKTFCDDKSTEVNIKTNVCNSYSSYSSLNINFFCLFDDMYENFFKNNFEDREKMIKILNMNKDLCYNQLLTFYKK
KLFFEGIKEGERSSTHTHLDLHNTYNQRIKESIAMQQKCTSTEGSTEGTTESSTYDVVHGEDAHVGSITLIDKRESDFSG
KIDYLLPPNNGDNINSSNNVLGCFTEYTVKGEYSGTTTLPLPLLLVKEETEHMCKDDDGVMNHLKTDDHRVNNTLQLMNR
SSSEEEATAMEPGEIPNNERTLHVGMKSGTEWKHVIGNTVNGTGGIGTRGGNIIKFKGEQEDVCKGESSRGDCKDITNVR
IDEIVKKDVKEVVEKKLADISCEHLSDYSFESDDAREMVEHILDSPKRMTKKDSSNGGSSSGYCGGSECSTADDRGTLEF
EINVRDMCEEEGSTMFKYIYHKIKCIRNNIWTQSIDEMQNREMHELFVMGRQKSEEVAKREEQVQLTMQRMSPQQTQLEV
HNEGISTVPPTDIYYFNVYTNLWENVDLNVSHKLLEAQGAKKKIINKFYRSDHVGEKYITFSEWSIYNLLVSKICKHFDV
KKFEDNQLKMYNMDKFQYELKKRNTYNFGIKIIGDSNGTSKGKQREKRGRRNCKRNRNRRLSRISEEFSDMNHDEEEEDE
DDLDGGEDYIDGGEAEVDEDEVEEDEEEEEEEDEDEEEEEEEDVEIDDVEIDDVEPFYEEEEQQTKFGEEGGQSSGHKGV
AVITANSGLAKGGNNNNNNNNSSNNNSSNNNSSNNNSNNNSSNNNSNNNNSSNNSSNNSSNNSSNNSSNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNSSNNNNSSNNNNAIPRSSSRIFCRNKNRSGLKIYGSSSEMNGRN
SIDRKPVKELKDGKITIVSCEKNGKMDDTVSTTSRNGGEVGEGGEEGNAEEGLGQASRSLSMSLRRKKRNSLLSGNSAES
GLSRVNKRKSKRLKIGEKEGKYVDDLQQEEGVVSQRGHRSGHYGVIHRGHPVSSSSCGRNRKVHIFKKRISRRSNFNTLT
DKKMNVYHMIQLPDYVSHKELIRSKNECLPTYILQYEQLRKNECIFFNIQSHYNNFINNVYHFAISYEQSLKHNEYLNNT
LNNVKARLHIKRLCLKKNITIRDRIFDVSSTYFNDLYTYDSKNNTYVFYKSKESRMNKMERAIDNQDYYYSMYVNDYIEN
ELLNKGKRKKKKNYHHHNSSHSGKSSGDNFDFASERAVVRKISSSYEHSGNHVDNMGDYGNDFPEKRETHHGSANHSIGG
DNTRNDAYAISDVAKNEHQMCDQLNYINYFVDHVQYDEDNSNGETCKNVMSFSERTVEEEFLGEDMLGGGLLGDEILGAI
EKSSIEQIESSSMGKMEKSRMEEVHTFSPEQSATFPPELLSTYSNNFEEESDKKEIIKTKNDFFNYYNQNDNESFFPNFQ
KQENGNEQDFNNNNKEFYFNGSINHDDIIQYIDIQ

2201 - 2220:	EEEEEEEEEEEEEEEEEEEE

A0A1A8ZLM2 **A0A1A8ZLM2_9APIC** (186 aa)
Uncharacterized protein. *Plasmodium ovale wallikeri*

MHVQHSALMTPRTYDAVHKNSMEFISNNESSNGVVEEENQEEDVELSAASLDEHVRNDFKVEESEEAERDEVERDEVEKK
EVEEEEVERDEVEKEAERNGVEGAAVEGAELEGAELEGAEVEGAEEEEEEEEEEEEEEEEEEEEEEDDDEEDEDDDDED
EEDDDDDYDDDEYDEDDFNEATVINI

125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE

A0A1A8ZNL6 **A0A1A8ZNL6_9APIC** (1114 aa)

Uncharacterized protein. *Plasmodium ovale wallikeri*

```
MYARKKHQYYRSFTRAKSAKNREAAQNSGIRQGWAEQRPLHMIYLRHFCTYARTYTYYIPARTAARTASLTAALTATRIA
VGVRLLPFPPAETHVQYENEKSEKYNDFLTTFMNSNVHYCPLKANKKKLRSELIKYMRKNLNEDDVFNVGFTAVRHLGRI
KNAVLTALPGEGFKSDILSDHKKTARGTPDNGPGSIRSVWCSEEERLLFRDNLRILNLGLWNNREEGAYEEEGEKKKKKQ
SALKKNINRRCGKMDMDDAAEGGCAKEEVITETSAPRNSTVGKEVEVGVGAEVEAAAEGVEAAEEAAAEEVETAQGASLG
RTPPSCGSEAVHEHNNQTKRNKKNFILKKGNYKNEIKKGVILIAHPLTSSPLWNKSVILITQKDKNNLVCGLILNKHPLY
NHTMGLPNDKEIAKILNKLYSKKKKFLNDVADGIFTDQRKCIHTKGEKTTQTETGTPNVKMIGTGEEEQEQEQEEYDKII
TKEGKECVNMTNNERENRETALEKKHEMDLRKESNCVKNKSSNSDNSTTMQGESSEDFPTLKDLQEMFLRIQFRSSSKHY
MNKRIKRKNNLFIMMDEHLLDIITHYIIKLNKVPLYLRFLPSYNIGSMTDIKNEMKKLQFLNEFYKIYFEKYNKWKVVII
NNRIHIFDKNKNKKKVENMTTNVHVKNEEGIENKELTEEEKARIHRKIKNFKETNRLVEDYEDGDEAHYHQGSAETSHRH
RRRGKSGAALRGTVKQQGYNDGQEKSHGEDPEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEQDDLDEEQGDLDEEED
GLDEEEDDLDDAAVEQAERNLDKMTSERVTATLPPGRQDAVIGIGSDAIGKEKLVRRKKRGKRVKGDPSTKAVTSAKKVG
INTVHKNYFVGNPVHLFWLGGPLPGLTILHNIRKISKNIVINDFIYEGYNENVDTTSSCNQDVKDSMGYMVEEDPLTCAD
MGKVLVGSSENTNPSKNELMCQSSNIVEVGGKSTCGNVESEGCINRMEGKKLIKRFIGKTTWDMNQLMDELKNDYWIAIN
CENRDLLSHIIFNSGNDFLNGTYGECTTGVSAYKGEHLWEKILSSLSTDYEAISKIPQHVVDTVLKDFRGTDAE
```

752 - 771:	EEEEEEEEEEEEEEEEEEEE
753 - 772:	EEEEEEEEEEEEEEEEEEEE
754 - 773:	EEEEEEEEEEEEEEEEEEEE
755 - 774:	EEEEEEEEEEEEEEEEEEEE
756 - 775:	EEEEEEEEEEEEEEEEEEEE
757 - 776:	EEEEEEEEEEEEEEEEEEEE
758 - 777:	EEEEEEEEEEEEEEEEEEEE
759 - 778:	EEEEEEEEEEEEEEEEEEEE
760 - 779:	EEEEEEEEEEEEEEEEEEEE
761 - 780:	EEEEEEEEEEEEEEEEEEEE
762 - 781:	EEEEEEEEEEEEEEEEEEEE
763 - 782:	EEEEEEEEEEEEEEEEEEEE
764 - 783:	EEEEEEEEEEEEEEEEEEEE
765 - 784:	EEEEEEEEEEEEEEEEEEEE

A0A1A8ZQ39 **A0A1A8ZQ39_9APIC** (1305 aa)
NTF2 domain-containing protein. *Plasmodium ovale wallikeri*

```
MNRGSDTKQYNKSKNKFPVFFYKNKYPCFKQTNSNSCSNHHTNDNYNSAFNSSVNNTQGNSSSSNTGFFYKKKNSLTVHG
HNRNSSTNMLGYNDDMYSFEKQKALSGGGGTSSGVGPYHIDNGHSHVNRGNGSVSAVGSGAVGSGAVGSGAVGSGAVGSG
AIGSGAIGVGGKPNQKNAYHFHQRKDAKNNYEDYIGSMQDASNGGNNVSLSHAQRAYKSYAAENNHDNYLNMGMSKNSNR
YYEANDNAAAGINNLSGQKNINYYSTGQSNAHNGMMSGSEGARPQGYSGVSDRVLHMGDEGSLQKSHLAAGDNKKTLLSM
ISSNEGNKVKNKNKSKVSNDHYNFGEGEDAEGGNKIGKMEKREEEHGKIGKIGKIGKIGKIYKSNSNSRAPSICSSSSRS
RSRSRSGSRSRSGSRSRSNVPPKEMHENRDTSGGKNETACNESVVGNLNNAGPSGSAYSIAYMFIYQYYYVLHTKKEMMH
NFYSEHATLLISFNYQSGDKTGISDKGIETGGGAVSVGLGIGVEMNTDAMCGVGMSSGLVSGLTTGGVSINAGKFFNLNE
IKVEGCQRSENMMKFKSRKMIASYYENLDVNECTVHISSIEVVNLYNEIYMYIYGKIKKCKDTNVFYFFVQNIHLHKYNI
YQYYVDVDFVHYYNTFEEIFDANRKLEQRKSRQYETSKLLCNTFNVKVKEEDKKKKNKISTLNVGGTHVGITNSGDRPSR
TNTGKNEKKNYHTSSTCKSVLKRSGKVEVEEEEEDEEDDEEEEEDEEEEEEEDEEDEEEEEDDEDGEEDDEVEDYDEDDE
EEVEEVEEYDEEDYDEEDEEEEEYDEEGEDDEDEEAEKCNEDKIVDMGKKKNISTVHSKGGELGHTKKVEESSSGGSKNV
KKGIISTGEGGGDVVVAKSTSQPSSDKKPLEEDAVSGKTTGEQVKTLDEKEKPGESFTPSVADSKKGKEKEVPGSGKAST
SSGKASIGSGKASISSGKAVVGVDTALASSEKTSINNVKTVGDSGNYAIDGKGKKGKSENAWNVPNDVVIPKMENNLKEE
KIASEVAKKKKKEKNKIDPNSWVFRVMKNNQGANMGEKKSLAANIKVNNNQVKNSGDKRKTVLDGTENMKANDEEEEEEE
EEEEEEEEEEEEEEKKEEEINVNDKKIIHNIHKNMDKKKINDCIIDRLKKYNDGHAVQIDIYQRSIKKLYANSYNYHNSY
EKIKPTEYSYAIAELDCRQSQQLLLDLGLYCNGIKLNIENFKNKRKTEIKKNTKKFSNTYNTSLEGSKMRDDKFKGSFYR
GASATMTPVAASSSFRSKRNNIFVK
```

1114 - 1133:	EEEEEEEEEEEEEEEEEEEE

A0A1A8ZQF0 **A0A1A8ZQF0_9APIC** (1107 aa)
Uncharacterized protein. *Plasmodium ovale wallikeri*

```
MYARKKHQYYRSFTRAKSAKNREAAQNSGIRQGWAEQRPLHMIYLRHFCTYARTYTYYIPARTAARTASLTAALTATRIA
VGVRLLPFPPAETHVQYENEKSEKYNDFLTTFMNSNVHYCPLKANKKKLRSELIKYMRKNLNEDDVFNVGFTAVRHLGRI
KNAVLTALPGEGFKSDILSDHKKTARGTPDNGPGSIRSVWCSEEERLLFRDNLRILNLGLWNNREEGAYEEEGEKKKKKQ
SALKKNINRRCGKMDMDDAAEGGCAKEEVITETSAPRNSTVGKEVEVGVGAEVEAAEEAAAEEVETAQGASLGRTPPSCG
SEAVHEHNNQTKRNKKNFILKKGNYKNEIKKGVILIAHPLTSSPLWNKSVILITQKDKNNLVCGLILNKHPLYNHTMGLP
NDKEIAKILNKLYSKKKKFLNDVADGIFTDQRKCIHTKGEKTTQTETGTPNVKMIGTGEEEQEQEQEEYDKIITKEGKEC
VNMTNNERENRETALEKKHEMDLRKESNCVKNKSSNSDNSTTMQGESSEDFPTLKDLQEMFLRIQFRSSSKHYMNKRIKR
KNNLFIMMDEHLLDIITHYIIKLNKVPLYLRFLPSYNIGSMTDIKNEMKKLQFLNEFYKIYFEKYNKWKVVIINNRIHIF
DKNKNKKKVENMTTNVHVKNEEGIENKELTEEEKARIHRKIKNFKETNRLVEDYEDGDEAHYHQGSAETSHRHRRRGKSG
AALRGTVKQQGYNDGQEKSHGEDPEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEQDDLDEEQGDLDEEEDGLDEEED
DLDDAAVEQAERNLDKMTSERVTATLPPGRQDAVIGIGSDAIGKEKLVRRKKRGKRVKGDPSTKAVTSAKKVGINTVHKN
YFVGNPVHLFWLGGPLPGLTILHNIRKISKNIVINDFIYEGYNENVDTTSSCNQDVKDSMGYMVEEDPLTCADMGKVLVG
SSENTNPSKNELMCQSSNIVEVGGKSTCGNVESEGCINRMEGKKLIKRFIGKTTWDMNQLMDELKNDYWIAINCENRDLL
SHIIFNSGNDFLNGTYGECTTGVSAYKGEHLWEKILSSLSTDYEAISKIPQHVVDTVLKDFRGTDAE
```

745 - 764:	EEEEEEEEEEEEEEEEEEEE
746 - 765:	EEEEEEEEEEEEEEEEEEEE
747 - 766:	EEEEEEEEEEEEEEEEEEEE

748 - 767:	EEEEEEEEEEEEEEEEEEEE
749 - 768:	EEEEEEEEEEEEEEEEEEEE
750 - 769:	EEEEEEEEEEEEEEEEEEEE
751 - 770:	EEEEEEEEEEEEEEEEEEEE
752 - 771:	EEEEEEEEEEEEEEEEEEEE
753 - 772:	EEEEEEEEEEEEEEEEEEEE
754 - 773:	EEEEEEEEEEEEEEEEEEEE
755 - 774:	EEEEEEEEEEEEEEEEEEEE
756 - 775:	EEEEEEEEEEEEEEEEEEEE
757 - 776:	EEEEEEEEEEEEEEEEEEEE
758 - 777:	EEEEEEEEEEEEEEEEEEEE

A0A1A9A359 **A0A1A9A359_9APIC** (2327 aa)
Uncharacterized protein. *Plasmodium ovale wallikeri*

```
MDRMKNQPKNSKDLSAKTKNSKNSLLSSEKKKSVSSHDSSDMFNNKAVKSGGGSVESLGKKKNEKVNDKSENSNNSKSKS
SHSTTSTSSKGKNENSKSIEKKESLRSNTNESIKLKSINLRDSAKQSKSKGEKGGEEDIKGKSEKSEKIEKGEKSGKSGK
NEKSVKVDKNEKIEKSEKKGKNEKKEKNEKSDKNEKSDKNEKSDKNEKSDKNEKSDKNEASDKNEKSDKNDKNDKSEKSE
KSEKSEKSEKSEKNEKKEKSEKSEKNEKNDKRHPSEDKKKDQSNSKNDSKANSKIPPKSSKPKGGSTNPINNSSRSSNSN
SGCHTKGKNNETSSRSIASASSKEALKEQTSSSATRSKKNSSVSTSVRKDSSEEIANNDNNKKEKKGSLSSSSKNVKRSC
ERKGDEKGSIKGIEKGVEKLGERAIELASNSISSKEENTKVSRSSADLKRNSKSERAEKGENAKSDKSEKDAKSGKSEKD
AKSGKSEKDAKSGKSEKDAKSGKSEKDAKSAKSEKDAKSAKSEKDAKSGKSEKDAKSGKSEKDAKNAKSEKDAKNAKSGK
DLKSSTKSGKDSKSAKSASESDDNNSRQHHDKKKKMNTNNEGESGKNTVKSSKVSQDSSSKKEITKKGSSDQKKGKEKAN
LKATGSRESQRSETNSSRSKSKSKSKSKSRSTDKSRNKKKYREEEEDTEEGESELDLQEDDTISEEEEEVEGGVEEEEEEVE
EGANDEDAEIDETVDQQEEGEQEGEPEEEEEEEEEEEDDDDDDDDYRQQSDSKRRSKYDATKKKSSNAKSKNASVSSGVK
SISTKSSGIKHSVTRSSSTKSNSSKSKKKNTKASKEKIVIGKSNVKKEQKSVKRENELKDKEKDKEEEENSYFADNDYSL
EARRKMLEERERKRQLKENFIKRMKLPKYADDESILFINNPNYVMVLLFLTVYKDVLKMSWNFKDIDDMFQNKETTEFGR
NFILKLFFFLGRYFNSKSIFMYKYISRIFEDKQASLVKVVNFNELFPVLESRKKKKKGLRSSGGGNGGGSSSSKKKKEKK
GKKSKNDPKSEGLFEEETIENDDLNDFDEGEEVLEGLEVELEGEEGDDDEEEEEEEEEEEEEEEEEEEEEEEEGEDDGEG
DGEGDDEGDDEGDDEGEGETEEEEKRRGEEKSEKFLSGENKEYDRKVIERDDQYGDDLNEENRRDVDTSEGIIKMEMGII
GKGEGEEKDYEDEEKIGEKIKSENIEQGKKEMEGGCDGCGDEEGARGEKGLSKKLFLEWDDLTVTSKLRIIRMLLNLVLC
ESNNLKKLLLTEKINFNNGYLGKINNDKYWFILNDTVNIEFKLYIEKEEKGIFEFLCDDEDVLYSIGYNLLKDTDTKVMG
ETIIERYNKICRERRNRNRILKQQKKLFADFNMNSDQFLTSKKRQHKQVDYFNFDNDRMRKRKNENTTSNNNPYSVQKNN
YQKNDRSFRLAARNAQKGNVDDIEGWKFHNTSVDASDNTHYVQSGSTPNDLLLIGEAEKDTHANTVGVSAGGSSSTGIAG
VGGAVGGTVGGAAGGATGGATGAVVTPGEGAVVVKVPLKRGRKKKSEKKKRGRKKKIFTEGTGGGGVDGSSANPLVEETK
EELKKGSTKVRKTPYTKRSNKPTVSIKYGTRSHSINKYENEQMQFSEYGPPNHGIQSDEFYKNGNIDTKFFNPNMHLGNF
INHNANGPYNLQNNLINMRNGKMSSAGSGGASAAAAAAAAAGSGGAGAGAGAGGYNFPYMYNPQLYNQYYMYNGNMYMLN
NTGNHIFAQNNRNKEVKNENLYMAQNMGNGGMRNGGGVPPPIGAVNSVRGKGMLRMSNSPDGVVHNESSSMNGSGVSGVS
GVSGVSGVSGVSGMSGVIGVGNSGMGNSGMGNSGMGNSGMGNSGMGNSGMGMINGMDSSNSSMGNGMNYVDSMGGSTMNK
YNGYILNRNPMGGNLTNPLYNNMYNLKYPYINNDIMNYNYNLNNFQNINYDKINKNIFKRYPNFMNSSYSPYNNMNNPYT
NFNTYNIPYQRNEQQYNNISSQNNTFKNKLIGENNMTNYSVFNIKGKNINNDISNTMDNDNKHSTAYNNFPSNSGNAGNA
GNPGNPGNAGNAGNPGNPGNPGNPGNNLKKCEDTQRNNTTGGISLTDNIGDINEGNKSNISYNVTNNVNSLSTITNLSNV
TNMTCSENSSNAASANQTVNTDIKNGTNTSGIVKTIANTGNDGGKDHANGLTSEKTDNYNGMNVNMNMSSQTFGHPNSVG
NSGVVVSYRRDNNANAENAFDGNAPNNLHDSSNNSNERMHYTKDGNISMHADKVLLSLEKNSVLDNNVDATSFMNKADDA
HQSGADG
```

1090 - 1109:	EEEEEEEEEEEEEEEEEEEE
1091 - 1110:	EEEEEEEEEEEEEEEEEEEE
1092 - 1111:	EEEEEEEEEEEEEEEEEEEE
1093 - 1112:	EEEEEEEEEEEEEEEEEEEE
1094 - 1113:	EEEEEEEEEEEEEEEEEEEE

A0A1A9A3X7 **A0A1A9A3X7_9APIC** (2318 aa)
Uncharacterized protein. *Plasmodium ovale wallikeri*

```
MDRMKNQPKNSKDLSAKTKNSKNSLLSSEKKKSVSSHDSSDMFNNKAVKSGGGSVESLGKKKNEKVNDKSENSNNSKSKS
SHSTTSTSSKGKNENSKSIEKKESLRSNTNESIKLKSINLRDSAKQSKSKGEKGGEEDIKGKSEKSEKIEKGEKSGKSGK
NEKSVKVDKNEKIEKSEKKGKNEKKEKNEKSDKNEKSDKNEKSDKNEKSDKNEKSDKNEASDKNEKSDKNDKNDKSEKSE
KSEKSEKSEKSEKNEKKEKSEKSEKNEKNDKRHPSEDKKKDQSNSKNDSKANSKIPPKSSKPKGGSTNPINNSSRSSNSN
SGCHTKGKNNETSSRSIASASSKEALKEQTSSSATRSKKNSSVSTSVRKDSSEEIANNDNNKKEKKGSLSSSSKNVKRSC
ERKGDEKGSIKGIEKGVEKLGERAIELASNSISSKEENTKVSRSSADLKRNSKSERAEKGENAKSDKSEKDAKSGKSEKD
AKSGKSEKDAKSGKSEKDAKSGKSEKDAKSAKSEKDAKSAKSEKDAKSGKSEKDAKSGKSEKDAKNAKSEKDAKNAKSGK
DLKSSTKSGKDSKSAKSASESDDNNSRQHHDKKKKMNTNNEGESGKNTVKSSKVSQDSSSKKEITKKGSSDQKKGKEKAN
LKATGSRESQRSETNSSRSKSKSKSKSKSRSTDKSRNKKKYREEEEDTEEGESELDLQEDDTISEEEEEVEGGVEEEEEEVE
EGANDEDAEIDETVDQQEEGEQEGEPEEEEEEEEEEEDDDDDDDDYRQQSDSKRRSKYDATKKKSSNAKSKNASVSSGVK
SISTKSSGIKHSVTRSSSTKSNSSKSKKKNTKASKEKIVIGKSNVKKEQKSVKRENELKDKEKDKEEEENSYFADNDYSL
EARRKMLEERERKRQLKENFIKRMKLPKYADDESILFINNPNYVMVLLFLTVYKDVLKMSWNFKDIDDMFQNKETTEFGR
NFILKLFFFLGRYFNSKSIFMYKYISRIFEDKQASLVKVVNFNELFPVLESRKKKKKGLRSSGGGNGGGSSSSKKKKEKK
GKKSKNDPKSEGLFEEETIENDDLNDFDEGEEVLEGLEVELEGEEGDDDEEEEEEEEEEEEEEEEEEEEEEEEGEDDGEG
DGEGDDEGDDEGDDEGEGETEEEEKRRGEEKSEKFLSGENKEYDRKVIERDDQYGDDLNEENRRDVDTSEGIIKMEMGII
GKGEGEEKDYEDEEKIGEKIKSENIEQGKKEMEGGCDGCGDEEGARGEKGLSKKLFLEWDDLTVTSKLRIIRMLLNLVLC
ESNNLKKLLLTEKINFNNGYLGKINNDKYWFILNDTVNIEFKLYIEKEEKGIFEFLCDDEDVLYSIGYNLLKDTDTKVMG
ETIIERYNKICRERRNRNRILKQQKKLFADFNMNSDQFLTSKKRQHKQVDYFNFDNDRMRKRKNENTTSNNNPYSVQKNN
YQKNDRSFRLAARNAQKGNVDDIEGWKFHNTSVDASDNTHYVQSGSTPNDLLLIGEAEKDTHANTVGVSAGGSSSTGIAG
VGGAVGGTVGGAAGGATGGATGAVVTPGEGAVVVKVPLKRGRKKKSEKKKRGRKKKIFTEGTGGGGVDGSSANPLVEETK
EELKKGSTKVRKTPYTKRSNKPTVSIKYGTRSHSINKYENEQMQFSEYGPPNHGIQSDEFYKNGNIDTKFFNPNMHLGNF
INHNANGPYNLQNNLINMRNGKMSSAGSGGASAAAAAAAAAGSGGAGAGAGAGGYNFPYMYNPQLYNQYYMYNGNMYMLN
NTGNHIFAQNNRNKEVKNENLYMAQNMGNGGMRNGGGVPPPIGAVNSVRGKGMLRMSNSPDGVVHNESSSMNGSGVSGVS
GVSGVSGMSGVIGVGNSGMGNSGMGNSGMGNSGMGNSGMGMINGMDSSNSSMGNGMNYVDSMGGSTMNKYNGYIL
NRNPMGGNLTNPLYNNMYNLKYPYINNDIMNYNYNLNNFQNINYDKINKNIFKRYPNFMNSSYSPYNNMNNPYTNFNTYN
```

```
IPYQRNEQQYNNISSQNNTFKNKLIGENNMTNYSVFNIKGKNINNDISNTMDNDNKHSTAYNNFPSNSGNAGNAGNPGNP
GNAGNAGNPGNPGNPGNNLKKCEDTQRNNTTGGISLTDNIGDINEGNKSNISYNVTNNVNSLSTITNLSNVTNMTCSENS
SNAASANQTVNTDIKNGTNTSGIVKTIANTGNDGGKDHANGLTSEKTDNYNGMNVNMNMSSQTFGHPNSVGNSGVVVSYR
RDNNANAENAFDGNAPNNLHDSSNNSNERMHYTKDGNISMHADKVLLSLEKNSVLDNNVDATSFMNKADDAHQSGADG
```

1090 - 1109:	EEEEEEEEEEEEEEEEEEEE
1091 - 1110:	EEEEEEEEEEEEEEEEEEEE
1092 - 1111:	EEEEEEEEEEEEEEEEEEEE
1093 - 1112:	EEEEEEEEEEEEEEEEEEEE
1094 - 1113:	EEEEEEEEEEEEEEEEEEEE

A0A1A9APG9 **A0A1A9APG9_9APIC** (492 aa)
PIR Superfamily Protein. *Plasmodium ovale wallikeri*

```
MPEEDEDANLAVFMKLTNLFTGSDVERQIRGGFLPNECDKDPDTGNSNFFFMNSQNGDLVVVEGKGNQEGDRQKASVKVT
RIEVTGEGQNRKKGVRGEEGARDNEEEEEEEEEEEEEEEEEEEEEDEDEEDDDEEEEDEEGKREDKFDNNILFELNSNDC
SVQMLKLNRTKCMRLLCEYLENYNDQTKRANIENKISGSIFCNSFNEIINLYNNKSECISPNSHNEYCKEVQQYREKYQN
INISNLSCTGTKSQSHSQEHETRREQSQVEESEQTILGHGTRSDAATGNPTDELLDAKTKSAEGSPNPGLDARVLPNGGV
VIEKQPLGMDDQTSESVQVHSQTLTSSSINGKHTLISVSSTSCPNGSNKQPCDDSLQESAATERDNTNELGLPKQKQADG
HTEINVNSQEESGNTSATITSATSVLGIPFVIFMLYKFTPIGSLLNKRREKKPTLNINEAQYDQNLLYNSELRNANSNNI
KYNIGYYSLNNS
```

105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE

A0A1A9ARH8 **A0A1A9ARH8_9APIC** (101 aa)
Uncharacterized protein. *Plasmodium ovale wallikeri*

```
MPNVFIRQILNVSFCVCVCVCEHLKKKKKKKKKEEEEEEEEEEEEEEEEEEEEEEIFAKEAENYEHFFFFFATLELYATRR
PYHTAKEVYQKTGHGKKRKKK
```

34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE

A0A1A9UUG5 **A0A1A9UUG5_GLOAU** (148 aa)
Uncharacterized protein. *Glossina austeni (Savannah tsetse fly)*

```
MNLFMKLFYISFHKDINVAQEKQQAASSKQQAASSIVLCTIEKKKNETEIQNSFYHPESIDWCQMWQNIKQSNITKRQTC
AICLKTVLVKVYSSVTEAFLRFMSAKANRLHDSEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGLI
```

117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE

A0A1A9UZH9 **A0A1A9UZH9_GLOAU** (345 aa)
Uncharacterized protein. *Glossina austeni (Savannah tsetse fly)*

```
MSDDEEYTDDPEFIKRQDQKRSDLDEQLKEYINEWRKQRAKEEDELKKLKEKQAKRKVSRAEEEQRMAQRKKEEEERRQR
EVEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDSGVLGLSSAAMERNKTKEQLEEEKKISLSFRIK
PLAIEGFNEGKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQVA
SKYERRVDTRSYDDKKKLFEAKLPKWFGERPGKKAGDPETPEGEEDAKADEDVLEDEDEVEEEVVEEEEAEEGEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEE
```

314 - 333:	EEEEEEEEEEEEEEEEEEEE
315 - 334:	EEEEEEEEEEEEEEEEEEEE
316 - 335:	EEEEEEEEEEEEEEEEEEEE
317 - 336:	EEEEEEEEEEEEEEEEEEEE
318 - 337:	EEEEEEEEEEEEEEEEEEEE

319 - 338:	EEEEEEEEEEEEEEEEEEEE
320 - 339:	EEEEEEEEEEEEEEEEEEEE
321 - 340:	EEEEEEEEEEEEEEEEEEEE
322 - 341:	EEEEEEEEEEEEEEEEEEEE
323 - 342:	EEEEEEEEEEEEEEEEEEEE
324 - 343:	EEEEEEEEEEEEEEEEEEEE
325 - 344:	EEEEEEEEEEEEEEEEEEEE
326 - 345:	EEEEEEEEEEEEEEEEEEEE

A0A1A9VBF0 **A0A1A9VBF0_GLOAU** (586 aa)
Uncharacterized protein. *Glossina austeni (Savannah tsetse fly)*

```
MDLKSPRTKCLEFMLKGKLFPKYSHCLATIAATPPTALLAASKFVNSYSKANEITDSDAEDIRNTSAITFTERTHFVSGE
CSSEPSNLTQTFVLATCTEVKTASETPLMGAIITNNFILTATVLPEDGVTCAITYNIKGKRGEQTTKSFNIQSYIVESNI
SPHQTPQIQLLELQTPINFELPGPIPDIIVAKTVDLAKRRPKIRESAILHTIDNNGGVVQIEVKLTSRSDCEADYPHLHP
HVFCVTIAKKGCDGCNNVMPGSALVQYDHLIGLVSERVKCDPSKNILCANVYKVRNWIKSNTRISGAWGPLWNNTKMFVI
FIIYFILFVNRTHFVSGECSSEPSNLTQTFVLATCTEVKTASETPLMGAIITNNFILTATVLPEDGVTCAITYNIKGKRG
EQTTKSFNIQSYIVESNISPHQTPQIQLLELQTPINFELPGPIPDIIVAKTVDLAKRRPKIRESAILHTIDNNGGVVQIE
VKLTSRSDCEADYPHLHPHVFCVTIAKGECDGCKDLKPGSAVVQKDGDIDGLIGIVSERVPCDSSKKILCGNVYEVQEEE
EEEEEEEEEEEEEEEEEGEEEEIAQ
```

558 - 577:	EEEEEEEEEEEEEEEEEEEE
559 - 578:	EEEEEEEEEEEEEEEEEEEE

A0A1A9VYI5 **A0A1A9VYI5_GLOAU** (194 aa)
Uncharacterized protein. *Glossina austeni (Savannah tsetse fly)*

```
MIPNDTEHDVIENFLMEAPKKKKKKKKKKKKKKKKKKRKKEEEEEEEEEEEEEEEEEEEEEENSAFSFFVSPCSRECAPNKWF
ANSGKCNANLATWPPSHLDLIGQTVKKAMKSLPKSANTDITKKCNIDNETVSNHFRNIGYVKWFTVWVPHKSVFVKNLIN
RSRESLLIRGKIKAGFDSPPKNSSSSTINKINFQ
```

40 - 59:	EEEEEEEEEEEEEEEEEEEE

A0A1A9W691 **A0A1A9W691_9MUSC** (380 aa)
Uncharacterized protein. *Glossina brevipalpis*

```
MMRSTLLKRRRRLSRKPKSEKPPQTPADDDPEFIKRQDQKRSDLDEQLKEYINEWRKQRAKEEDELKKLKEKQAKRKVSR
AEEEQRMAQRKKEEEERRQREVEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDSGVLGLSSAAMER
NKTKEQLEEEKKISLSFRIKPLAIEGFNEGKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKAL
KKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYDTLYKEVVEKPKLPKWFGERPGKKAGDPETPEGEEDA
KADEDVLEDEDEVEEEVVEEEEAEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE

A0A1A9WVG0 **A0A1A9WVG0_9MUSC** (444 aa)
Uncharacterized protein. *Glossina brevipalpis*

```
MAIEDTFLKSKKRKKQKRKEEKQQKRNLHKREKFVSQKMKENTINYRQFVDKSVNAGEYKEEKKFGKLTKHVSSERITKN
SSDLNIYEVHCNGDDLKIIQLYKNDYFKVKEPNMVVRQLAGNSRRCSTVAGSSTIGYKEGRGDEYSEDVDNRENVERDDD
DDDDDDDDDDDDDDGNDDNDNDDGDEEEENSIGTRLVPAALQRESVTELISEKNKHQRIPIDSQTLIHKHIKSKLKHQGI
KEVEEDYAEVQDITAIRNRKVFHCKKQIMKFMKSKYRILAISVFKERFKKIDNLEKQVVSIRQNMNRMRKEFVPHVDLLQ
```

```
FNEFYERVKKLNSMLMNLKNFYPFDSSDYFNVEESSNLKTFTITQDLIEKKKTEILLNGINGAKIEEEEEEEEEEEEEEE
EEEEEVKEISSSSFSVIDAVVLVTAAAVLTFVTAFFSKRPILDF
```

386 - 405:	EEEEEEEEEEEEEEEEEEEE

A0A1A9X1Q6 **A0A1A9X1Q6_9MUSC** (111 aa)
Uncharacterized protein. *Glossina brevipalpis*

```
MTEQWFKTYFHENFRKRLQLTEFSLRYTTDAFINVCIVLPAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEEEEEEE
EEEATEKERERHREKERWKSINLLPNILNLK
```

42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE

A0A1A9YMB3 **A0A1A9YMB3_GLOFF** (357 aa)
Uncharacterized protein. *Glossina fuscipes fuscipes (Riverine tsetse fly)*

```
MSDDEEYTSEEEEEVVEETKDDDPEFIKRQDQKRSDLDEQLKEYINEWRKQRAKEEDELKKLKEKQAKRKVSRAEEEQRM
AQRKKEEEERRQREVEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDSGVLGLSSAAMERNKTKEQL
EEEKKISLSFRIKPLAIEGFNEGKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPE
ALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEAKLPKWFGERPGKKAGDPETPEGEEDAKADEDVLEDEDEVEEEVVEE
EEAEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

327 - 346:	EEEEEEEEEEEEEEEEEEEE
328 - 347:	EEEEEEEEEEEEEEEEEEEE
329 - 348:	EEEEEEEEEEEEEEEEEEEE
330 - 349:	EEEEEEEEEEEEEEEEEEEE
331 - 350:	EEEEEEEEEEEEEEEEEEEE
332 - 351:	EEEEEEEEEEEEEEEEEEEE
333 - 352:	EEEEEEEEEEEEEEEEEEEE
334 - 353:	EEEEEEEEEEEEEEEEEEEE
335 - 354:	EEEEEEEEEEEEEEEEEEEE
336 - 355:	EEEEEEEEEEEEEEEEEEEE
337 - 356:	EEEEEEEEEEEEEEEEEEEE
338 - 357:	EEEEEEEEEEEEEEEEEEEE

A0A1A9ZB08 **A0A1A9ZB08_GLOPL** (365 aa)
Uncharacterized protein. *Glossina pallidipes (Tsetse fly)*

```
MMRSTLLKRRRRLSRKPKSKKPPQTPADDDPEFIKRQDQKRSDLDEQLKEYINEWRKQRAKEEDELKKLKEKQAKRKVSR
AEEEQRMAQRKKEEEERRQREVEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDSGVLGLSSAAMER
NKTKEQLEEEKKISLSFRIKPLAIEGFNEGKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKAL
KKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEAKLPKWFGERPGKKAGDPETPEGEEDAKADEDVLEDEDEV
EEEVVEEEEAEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

334 - 353:	EEEEEEEEEEEEEEEEEEEE
335 - 354:	EEEEEEEEEEEEEEEEEEEE
336 - 355:	EEEEEEEEEEEEEEEEEEEE
337 - 356:	EEEEEEEEEEEEEEEEEEEE
338 - 357:	EEEEEEEEEEEEEEEEEEEE
339 - 358:	EEEEEEEEEEEEEEEEEEEE

340 - 359:	EEEEEEEEEEEEEEEEEEE
341 - 360:	EEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEE
344 - 363:	EEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEE

A0A1B0B6K6 **A0A1B0B6K6_9MUSC** (319 aa)
Uncharacterized protein. *Glossina palpalis gambiensis*

```
MPMCRKPPQTPADDDPEFIKRQDQKRSDLDEQLKEYINEWRKQRAKEEDELKKLKEKQAKRKVSRAEEEQRMAQRKKEEE
ERRQREVEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDSGVLGLSSAAMERNKTKEQLEEEKKISL
SFRIKPLAIEGFNEGKLREKAQELWELIVKLETEKYDLEERQKRQDYDGWEELGKEVNEKIWNEKKEQYDGRQKSKLPKW
FGERPGKKAGDPETPEGEEDAKADEDVLEDEDEVEEEVVEEEEAEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

288 - 307:	EEEEEEEEEEEEEEEEEEE
289 - 308:	EEEEEEEEEEEEEEEEEEE
290 - 309:	EEEEEEEEEEEEEEEEEEE
291 - 310:	EEEEEEEEEEEEEEEEEEE
292 - 311:	EEEEEEEEEEEEEEEEEEE
293 - 312:	EEEEEEEEEEEEEEEEEEE
294 - 313:	EEEEEEEEEEEEEEEEEEE
295 - 314:	EEEEEEEEEEEEEEEEEEE
296 - 315:	EEEEEEEEEEEEEEEEEEE
297 - 316:	EEEEEEEEEEEEEEEEEEE
298 - 317:	EEEEEEEEEEEEEEEEEEE
299 - 318:	EEEEEEEEEEEEEEEEEEE
300 - 319:	EEEEEEEEEEEEEEEEEEE

A0A1B0D1D5 **A0A1B0D1D5_PHLPP** (382 aa)
Uncharacterized protein. *Phlebotomus papatasi (Sandfly)*

```
MSDDEEYSSEEEEVVEETHEQPAAKPEGEAGDPEFVKRQDQKRSELDEQLKEYINEWRKQRAKEEDELKKLKEKQAKRKV
TRAEEEQRMAQRKKEEEERRVREIEEKKQREIEEKRQRLEEAEKKRQAMVQAMKDKDKKGPNFTITKRDTSSINLSAQMD
RNKTKEQLEEEKKISLSFRIKPLDLTGLGESKLRAKAQELWETIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKA
LKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYITMMDEMRNELWQKRNDRFTKRRRPKLPKWFGERPG
KKPGDAETPEGEEEGKADEIEEDEIEEVAVEEVEEEVVEEEEEEEEEEEEEEEEEEEEEEEEE
```

359 - 378:	EEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEE

A0A1B0DBP5 **A0A1B0DBP5_PHLPP** (122 aa)
Uncharacterized protein. *Phlebotomus papatasi (Sandfly)*

```
MIKLKTSVLICLAIILQGKFSDESTRFSATTAQNSEENEQDGQSPPDTPSEPAPEEGEEPNSQEEEPASEAEESASEEGT
GPTSGETPDEPDEEDITDGEEEEEEEEEEEEEEEEEEEEEEE
```

100 - 119:	EEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEE

A0A1B0GAG3 **A0A1B0GAG3_GLOMM** (457 aa)
Uncharacterized protein. *Glossina morsitans morsitans (Savannah tsetse fly)*

```
MSDDEEYTSEEEEEVVEETKEKPPQTPADDDPEFIKRQDQKRSDLDEQLKEYINEWRKQRAKEEDELKKLKEKQAKRKVS
RAEEEQRMAQRKKEEEERRQREVEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDSGVLGLSSAAME
RNKTKEQLEEEKKISLSFRIKPLAIEGFNEGKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKA
LKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYDTLYKEVLEKHWQEKQERFMQRTKCKLHFHIQIYLE
```

```
DTVSVTVRQLSLQVLCVVIAIKNQDNGWEELGKEVNEKIWNEKKEQYDGRQKSKLPKWFGERPGKKAGDPETPEGEEDAK
ADEDVLEDEDEVEEEVVEEEEAEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

426 - 445:	EEEEEEEEEEEEEEEEEEEE
427 - 446:	EEEEEEEEEEEEEEEEEEEE
428 - 447:	EEEEEEEEEEEEEEEEEEEE
429 - 448:	EEEEEEEEEEEEEEEEEEEE
430 - 449:	EEEEEEEEEEEEEEEEEEEE
431 - 450:	EEEEEEEEEEEEEEEEEEEE
432 - 451:	EEEEEEEEEEEEEEEEEEEE
433 - 452:	EEEEEEEEEEEEEEEEEEEE
434 - 453:	EEEEEEEEEEEEEEEEEEEE
435 - 454:	EEEEEEEEEEEEEEEEEEEE
436 - 455:	EEEEEEEEEEEEEEEEEEEE
437 - 456:	EEEEEEEEEEEEEEEEEEEE
438 - 457:	EEEEEEEEEEEEEEEEEEEE

A0A1B0GDI3 **A0A1B0GDI3_GLOMM** (319 aa)
ANK_REP_REGION domain-containing protein. *Glossina morsitans morsitans (Savannah tsetse fly)*

```
MYDNFENRPLAWQRAFLRLSVKVRNVDPVIKSRRVSEKTKYVNQEVFNEAEELESPHRDIETQSRDINAELRKAALEGNI
EKVKSLISEGAKVNAQDKDNRTPLHFAAQNNNKEIVDALIKAGADVNIKDEDGKTPLDLTTNEEIKTLLQPAEKSDDGSA
GGSSTDGEGGQEEEEEEEEEEEEEEEEEEEEEEDSNQSQREQDINGEKGADVQDKGVNPVAPTEPAQTEEQPGSFFGSLFS
ILMKPFSLVASFFGGFFSWLFGSDTDQSTSQTDADVSLLKPSNVKKTDESDIPLPTSNPLDKENNNNYDAMKSHDGVIE
```

172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE

A0A1B1E2N1 **A0A1B1E2N1_9APIC** (296 aa)
SICA antigen. *Plasmodium coatneyi*

```
MRKVQDEEITDDEHLEENVHAKIEEEKLKEEEEEEEEEEEEEEEEEEEEEEEEEKEEEKEEEKEEEKEEEKEEDGEASEEE
PRSDDTAQAEDPDQNPQDSQKSKQDVQPVVPEAPQSPGSEAAPAAQLGHRINQPNITSYLPLAPAVLGISIMSYLLWKYF
RMLRKTRKRYRRAHQGRGPSLEQQTVDHVDDQDDGPHAYTLVKERRHPRSTPIKRRKTRGVDRLAGRRGVRHRMIIDIHL
EVLDECQKGDTKLAQEYFFEILVKEFMGSEFIKEDFVPKEQVPSSDFGFREGRLCS
```

30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE

A0A1B1JH81 **A0A1B1JH81_TRYCR** (516 aa)
Deacetylase 2. *Trypanosoma cruzi*

```
MVFTDAVAGKTSLPPPVAIIVGHNIDASAMPLTYERNRFVIDMLQHYACPVFSHKKSGDAMNTVSSDVFEWVLEPLPVVG
VEDMTAFHDRAYLNYLSIREALSEVDERASTVKRSRAEGIQPPVSRRSSAQTQPPLRVLPDLVPIPADEEYGLVNENMPF
VGMWRTIQATVSGTLLAARLLAQPGRFAAIHWFGGRHHAKKSTAGGFCFANDVVLGVLELKKLLSSDKNGILVVDVDAHH
GDGTQSAFLHDNSVLTLSMHAHGVGIFPGTGGIEEIGAGLGRGFTMNVPLPEGATDILAVTLMYRSIHFAFKKLGEGLAA
IVIVCGSDALSGDPLGALNLTVGGMQSIIRLLLKEAARRSLKVLLLGAGGYVDTSCARLAGVVTKDVLSCAAAMRLGKTE
YFGDSANLGDNLGVAVPEGCEYFTRYGPSFLMHGLPPARVSKLYRLPYGSPLFMRMQRAATKEALRRRLNQEQDEEEDAE
DDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEP
```

483 - 502:	EEEEEEEEEEEEEEEEEEEE
484 - 503:	EEEEEEEEEEEEEEEEEEEE
485 - 504:	EEEEEEEEEEEEEEEEEEEE
486 - 505:	EEEEEEEEEEEEEEEEEEEE
487 - 506:	EEEEEEEEEEEEEEEEEEEE
488 - 507:	EEEEEEEEEEEEEEEEEEEE
489 - 508:	EEEEEEEEEEEEEEEEEEEE
490 - 509:	EEEEEEEEEEEEEEEEEEEE
491 - 510:	EEEEEEEEEEEEEEEEEEEE

492 - 511:	EEEEEEEEEEEEEEEEEEEE
493 - 512:	EEEEEEEEEEEEEEEEEEEE
494 - 513:	EEEEEEEEEEEEEEEEEEEE
495 - 514:	EEEEEEEEEEEEEEEEEEEE
496 - 515:	EEEEEEEEEEEEEEEEEEEE

A0A1B6CID0 **A0A1B6CID0_9HEMI** (378 aa)
Uncharacterized protein. *Clastoptera arizonana (Arizona spittle bug)*

```
MSDEEYSESEEEAPQAEPEKKTGGESAPQGDPEFIKRQEAKSSALDDQLKEYIAEWRKQRSKEEEELKRLKEKQAKRKVE
RADEEKRLAEKKKQEELQRQREVEEKKQRDMEEKRRRLEEAEKKRQSMMSALKDQTAKNKSPNFTISKKATDLSNLSNAQ
IERNKTKEQLEEEKKISLSFRIKPLNIEGLDANKLKAKAKELWECIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRH
KALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDTLILENSEKSWSSKYEQFSKRSKTKLPKWFGER
PGKKQGDPETPEGEEETKPSEPAPIEIEEEEVEEEEVEEEEEEEEEEEEEEEEEEEEE
```

358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE

A0A1B6ECS2 **A0A1B6ECS2_9HEMI** (386 aa)
Uncharacterized protein. *Clastoptera arizonana (Arizona spittle bug)*

```
MSDEEYSESEEEAPQAEPEKKTGGGGPSLKGGESAPQGDPEFIKRQEAKSSALDDQLKEYIAEWRKQRSKEEEELKRLKE
KQAKRKVERADEEKRLAEKKKQEELQRQREVEEKKQRDMEEKRRRLEEAEKKRQSMMSALKDQTAKNKSPNFTISKKATD
LSNLSNAQIERNKTKEQLEEEKKISLSFRIKPLNIEGLDANKLKAKAKELWECIVKLETEKYDLEERQKRQDYDLKELKE
RQKQQLRHKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWDTLILENSEKSWSSKYEQFSKRSKTK
LPKWFGERPGKKQGDPETPEGEEETKPSEPAPIEIEEEEVEEEEVEEEEEEEEEEEEEEEEEEEEE
```

366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE

A0A1B7SCM9 **A0A1B7SCM9_9ASCO** (359 aa)
PWWP domain-containing protein. *Ogataea polymorpha*

```
MFPPGSLVLTKIKGFPEWPSRVIDYEQLPEKIRNMKPGSAPGRKRRGAASDPQLVCVKFYGDDEYFWCTEKDLKPLTDDM
VTEYLVKKGELPDSDGNFRAKRASKVSSLTNAYLCANNKDVSPQDFALYGSYGRVGEEDEDYVEEADEEEEEEEEEEEE
EEEEEEEDSDSDEEAYGRSSKRKHNGTHGARKKAKVEVVEDLDSDWGLESDVEDAGLEIPLLNSAELVDEVKRSTKFFGD
IRVQIQKLAFPTDTPVDYAKTGKELEPLVNKLSGYRPVSRAVLKSTNIAKVLVVLLKKPEFARLRVAKKIGTVLKNWLDL
HVEPDPHWGDDYEPSSEPEASADEVKQEPTDQSVPANGE
```

148 - 167:	EEEEEEEEEEEEEEEEEEEE

A0A1B7TI34 **A0A1B7TI34_9ASCO** (776 aa)
Uncharacterized protein. *Hanseniaspora valbyensis NRRL Y-1626*

```
MFNSPFPPLNPNVKYKTAFQRAGFNTNLNEQDNNNNSNDDSKLYNVNDSSVIDSPNSTFINDESSSNKIQLINKALQKKQ
KLLLRKQQKAEEEKTKPQKKSFKKKSPLSKNKVKGESKTAQDTSSNDLNDQNLSNNDKNINTKNKILPLGLLFNKNSNNK
DKTIDSDLNEKHISPSANNRGLNIKTLNNDLSPTRKGDISHVSDLDSSDDEKEKIDPFQPQFLSQNFIELNLNPQPDKKE
EEKKEIKEIQANDYEEKDVINVDSTHIFEEEIEPPMNTIMNLQDLQFEQESFYSEIQSQDPRAVNGEPSEEKQHFIANQQ
QECEINELTPITFSNEQHIPPSGPITKSASNNDDDDDVEEEEKEQNDDDDDDRISTVESNEGEDTDDFNFKDNSNVYRSV
SNFAGTREDIFFTPTRTTFNNSGSMIHNNETTSSKEQLVENIFKNKRDSVVNTINEPTEELNFDNNSKINEAEEEEKEEE
AEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDKDDLEFSDNGINDTKELNFETDLPQNDNDNNNVINDEEMSLFRKPYE
ERHIPPAHLAADNTQTVNTDFYTKEEEEEETKEEELREEEHDKEKVVVREEKQFVEDSEITQSLPIQQSHSLIVDENVCR
GCHNQILPEEKKIYDKNGDLSGKWHKSCFTCTICLTKFSRNTPCYIHNDSPYCEPHFFEVTGLICFCCSEKILDDTCLDV
PGLGKAHIGCFTCNGCEMPINDEYFSNDTINLCGDCVKDMGKEKMQRRRTVLWDAN
```

485 - 504:	EEEEEEEEEEEEEEEEEEEE
486 - 505:	EEEEEEEEEEEEEEEEEEEE
487 - 506:	EEEEEEEEEEEEEEEEEEEE
488 - 507:	EEEEEEEEEEEEEEEEEEEE
489 - 508:	EEEEEEEEEEEEEEEEEEEE
490 - 509:	EEEEEEEEEEEEEEEEEEEE
491 - 510:	EEEEEEEEEEEEEEEEEEEE
492 - 511:	EEEEEEEEEEEEEEEEEEEE
493 - 512:	EEEEEEEEEEEEEEEEEEEE

A0A1B7W5S1 **A0A1B7W5S1_9NOST** (90 aa)
Uncharacterized protein (Fragment). *Anabaena sp. CRKS33*

```
EEEEEEEEEEEEEEEEEEEEEEEEEEELDYEDEDEDEDEDELDYEDEDELDYEDEDEDELDYEDEDEDELDYEDEDEDEDE
```

DEDEDMEFLK

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE

A0A1B7XQL3 **A0A1B7XQL3_COLHI** (108 aa)
Uncharacterized protein. *Colletotrichum higginsianum (strain IMI 349063) (Crucifer anthracnose fungus)*

MVRMVAEEVYLNAKRDEARAAEAARDAAAGHAALASLQEAGRAARTAAAKAAPAASEGPAEEEEEEEEEEEEEEEEEEEE
EEEEESDDSLGILDEEMLAILEHWESST

61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE

A0A1B7XU65 **A0A1B7XU65_COLHI** (115 aa)
Uncharacterized protein. *Colletotrichum higginsianum (strain IMI 349063) (Crucifer anthracnose fungus)*

MVLLPPPPSPGELVAPNVASESLTDPSEQTGTGSYTTDTQVRLQVARALSEKWRGRSDGSTLGNVWGVEEEEEEEEEEEE
EEEEEEEEEEEACLVNCGPVCLCWTEQFAASLGRV

69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE

A0A1B7YSD7 **A0A1B7YSD7_COLHI** (157 aa)
Uncharacterized protein. *Colletotrichum higginsianum (strain IMI 349063) (Crucifer anthracnose fungus)*

MMRLSSANIPHIRQVRAARAEIEVEVKSRSGTLLRKGAAGRGYTRAKWDIVQKYLGASRSPSGRSSRLGTGSCVAALQDL
MLLQIILGNWKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEENDDDNDVEDEEEEVVERQKSASHVPPRNFETGSV

92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE

A0A1B8A4X3 **A0A1B8A4X3_FUSPO** (203 aa)
Uncharacterized protein. *Fusarium poae*

```
MTELLNEKTDGFMIDTQLPQEVRESIRNANFAGKPLNAVDWSALPGSDDSVIFQLTHPLASEESDKEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
PGFSTPCPFQRHTQLHDSLRDLIREEIIVAESSYRATEDADIL
```

67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE

A0A1B8B3Y9 **A0A1B8B3Y9_FUSPO** (4208 aa)
TMF_TATA_bd domain-containing protein. *Fusarium poae*

```
MATAYILASTDSWTRSAIGLPTTRCQSNAPVEYSLRCRLSLVARAWVVQTLQQNAYSSLPHRKVAERPLIIPDHSPRWYR
RLPKSCDAPIPTDTTMPTNGTGRNANRRLPSWLTSSPLPPSDAQKERRQPNDKILSDPASDILIDFNSSEGFHEAAKKSK
KAKAPTAPPPPPPPPAAPPADDGQKDDMNGNGGGASGGSAAGGAGDGNDSNGGSAPPKPPTTFDNISLGASKLDLGLSPP
ENKSISSWGAKLGFGGGGWGWGGGSKNEPQPAPAPPPPEPKDEDNPWDKPKGSTGNLGMKDDDDAWGFGTKKDKKPSALW
GAEPEEEPKDAGDPWGWGNQKKKGKPGGILEELALDTEPEGPPGGKKDIWDTWGISKKDRAKKKGIMEEVALAAAPDPPS
```

```
MDDQWGSGWSGKNDKSPQNSLWGAQDPIPAAPDPPSFEDKDGDDFWSTFGSGKAKPVEDNPGGWGSWGISKTEPPKIEDD
GRDLWGTGKKKKKAGDLIQLEDEIPPPAPDPVEAVGTNDFLDSWGFGKKPKKPAADPFDFKTSDANDPNHAFWGSIDTKP
GAHDFLIDTTDPEQAAREAEDAEAAREDEEIASLAEKKAKRGGRLLKSDRERLTLLEDNAARRAEARAAREAEAAAAAEA
AQAEAQAVADAQAAADAEAAALQAAEDAEAAKENEEIALLLAKKQKRGGKLLKKDQERLTLLEGNVRRRAEAQAAREAAA
AAAADAAAVEVINDIPLDEAPPPECFEPDAAAQAATEAEAALASETAQEEAEIESLKSKKAKKGKLIKKDQERLNILIDN
AAKRAEQAAAKEAEEQAAKDAEDAAAAAAIEAAEAESAAQAAAEAEEAAKEEEEMAALKAKKAKKVKLTKVETARLMALV
GSSVKRAQAKSAKEAEEAAAAQAVREAEESAIREAEEKAAREAEEAATREADAAIAAEEEKELAALDALKTKRGGNLIKK
KDVDRYNVLTQRVTERAAKNAEAAATEVHAEATPEISDEPTGPAPEPAPEDPPVDADAAPAEPEPIPGPDATVIAAEDAE
LASLEAKKAKKGKLGKKDTDRYNLLSENALQRQAAKEAEETAAREAAEAEAAAAAADKAAAAQVTEAEALTASEAEAVLI
ADEEAELATLIAKKAKKGKLIKKDLERFNILTENATQRQASRDAEEAAVAAAAEAEAEAEAAKDAEAAAAAEAAEAEALA
AREAEAIAIAEEEAELAALTTKKAKKGKLIKRDAERFAILTENAERRAQEAAIVTEQPEDPTTIPEVEAEEPPPEPPVDE
LPVEGDDPDANATAIAEEESELAALVAKKERKGKLGKKDTDRFNLLTANATTRAEKAAEEEAAAQAAEAAAAEAEEAAAA
EAAAIEEAAAREAAEAEAAVIAEEEAELAALTAKKNKKGKLGKKDSDRFAVLTENATQRAEKAAEAVEVEPEPELEPEPE
PEPEPEPEPEPEPEPEEEAPPEVEDPLVDEFDDAAASEADDEEAAIAAEAAAIAATIAAEEEEEMEALIAKKNKKGKLGK
KDSDRLAILADNAAQRAEKAAQEEAAALGELEIVEDPPADIEEPAPECAPEAYPEEEAPPEEHDVAAAAEEQELADLDAK
KARKGKLGRKDTDRYNVLTENATKRAEEQAAAEANEIAATEAAAAAEAEEIATREAAEAGAAMAAEEAEKEAAKAEAEAA
IAQEEEELAALKAKKERKGKLGRKDTDRLNALMDSKAARDAQAFEEQAAKEAEEQAAQEAEEAAAREAAEAAEAEEIASR
EAAEAESAAIAAEEEAELAALTAKKARKGKLGRKDTERFDQLISNTAQRAEEQAARQAEAVAEEVTTEEIPLEEPEEPTP
DVEEPVEEAPEDLAPDIDDEAAAMAAEEEAELASLEAKKARKGRLGNKDTQRFNFLTENLAKRAEEQAAKEAEAQAAAEA
EAAAEEAAAEEAAAEDALEDAAEDDDEDAAAREAAEAEAAAVAEEEAELAALVAKKARKGKLGRKDTERFDVLTENAARR
EEEQAAKEAEAEVEEPALEQTEDTAEPEPEENLGDEDAAAEEAAEAEAQAIAAEEEAELAALNKKKAKKGRLGRSDTERF
NILIDNAARRVEMQAAKEAAEAAEVAEEEDDEFVDAEDGEDELAEEHEPEAEEAAELDEEDVAVAAAEAEAQAAAIAEEE
AELASLSKKKIKKGKLGRKDTERFQLLTDNAARRAEEAAAREAEEAAAAEVEPDPEAEAEAEAGPEVESEAEPEVEPEPE
LEADQEPEDDSNEIDETEQAAIAEEEAELAALIKKKAKKGKLGRKDTERFEILTENAARREDERAAKEAAAAAAAIAEAE
LEVAEGDPEADAIAEAEEPANEEGGEDFAEAEDGEAAAREAEEAAIADAEEEELESLKAKRVRKGRLGRKDTERFAVLEE
NAARRAEERAAKEAAAVEDEDDEPAEDDEPDEDEDGVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDNAAVEEEEAAREA
EEAAAREAEEAAAREAEEAAIAEAEEDEFESLKAKRARKGRLGRKDTERFVILEENAARRAEERATREAAAAAAAEAEAE
VNVDEEEEEEEEEEEEEKEDGEEGEDEDGAVDDDDDDEEEEEEEAVREAEEAAAREAEEAAARDAEAAAIAEAEEAELDSL
RFKKSRKGRLSRKDTDRLKFLEDSAAKRAEELAAKEAAATAEAEADKAPEEEEDDEDEDEGEDEDEDEEEDAAEKPTEVA
NDDVAEESGQEEVEAAPEEVEAEAPMDDEIVEVIDLSPKKDRRSRKSKSRRDAPPPPPVPDPPLTPPPEPKQSRRPKLAR
EGAPWGKWEATPREEPDDYYQEKYSRHRRREEKTSSKGSSSDKVEKNSRPTAPFGKPNFSRSASTREKRDGVSSKRRHSE
TARGIVSPPPEEMLVHEEPGSRRKSRKPRSREDDGAMMSGAAPVPERYERRHSHKTRSREDDDVIMVDPDLANDRRERRR
SHKTRSREDEDMVMADDIITPGLRDRRRRDRRSRDEEPVMVEPDVPTDHALPRGSKKGFAGLFSGLRTPKNERPDPLRRR
STYATTDDEALRTARMDGDAVIVDADREARRAARKAKRADPEEEARRAKDEARRERRRQREKGADTQRQDQDERRAERRA
ARQRGEEERRAQEEQQADEELQRAQEAKEAQRSERRRLRREQEAAAAAEQEEQEARRAARRERRRPRPVGPSEDEHERRR
RREAKRAARATDEAEGHQRRPRRHEEMQQPAWPHLGTSSWVQEHVDAPPPPDLPQADDASGGQDEDDEMARREARRAQHR
SKYSDETPDEAEERRKRRARREERDRGGRHRDRRSEGSDERHHTRRPSNVPNDLAILVMTAPGKGSRWGAFLSSAFEGVE
NRLDNLLDEEQQATQSSQQYEQQQGMKAAPPVPSPSPKPTTHAAVPKTNRANDRLQARLAKAIASRTSQSSPRSSVDTAR
GSVDKERPASTELVVSGQSTDTPEPKSTERENPVAEPTPVVVVEPSSTSAESQPTNSKDTPNTNQDAQDAKQEITPSPTI
IEPQSDTEPQTFSAQQGIDKTETQPQPLDHEPNVPKATETTQTTAASEEPPQKEPEPNQTDKARSGEIQEYIEQIDSLQA
KLQYLSKNAADAAKQAANSAAAGSTERKLAEKDEKIALLMDEGQKLSTSEQKFRTTVRKLRLQIAENEKQANELKKDREK
AVIEADNLRGQITSKEDQEKRNEEVRKASAVLQKEIDTLKRDKKAGEEAYRRLEQESKTKAEQAQAAHTETLNKALDVEK
KRQKELESSIATLRSEKEALVERLRLTEVEWQEKLDRAVERGRNVEEELKLELRAAESKLEAMRVAAEEASAGSGGDIKL
IRHIETLQSQYASASENWQGIETSLLTKTANLEKERDEAQRRESEMRKKARDSASRCKRLEDELQDVSPALATARQELEA
CHEELTTLRTQYKSAETALEQARSDLEKLQRAASREVSAEAERRQWADDVAISTPKSQSRPDSPLLSVARTFSSDLIGLP
VPGRQPRRVPTPGSQTDSAGEGFFFGRRMSSQPPRPSALSTTGPMMPPPPPFSPFEPPSESPRAASPPPDRDDLEDGDPS
SPRNMAQDMISVSTVGAGPSVQLVERMSAAIRRLEAEKVAAKEEMARVCSQRDEARSDIVNLMTELETQKGATARVTQLE
TEVENINSRYQTTLEMLGEKSELVEELKADVQDVKDMYRELVERTVMK
```

2438 - 2457:	EEEEEEEEEEEEEEEEEEEE
2439 - 2458:	EEEEEEEEEEEEEEEEEEEE
2440 - 2459:	EEEEEEEEEEEEEEEEEEEE
2441 - 2460:	EEEEEEEEEEEEEEEEEEEE
2442 - 2461:	EEEEEEEEEEEEEEEEEEEE
2443 - 2462:	EEEEEEEEEEEEEEEEEEEE
2444 - 2463:	EEEEEEEEEEEEEEEEEEEE
2445 - 2464:	EEEEEEEEEEEEEEEEEEEE
2446 - 2465:	EEEEEEEEEEEEEEEEEEEE
2447 - 2466:	EEEEEEEEEEEEEEEEEEEE

A0A1B8CTS1 **A0A1B8CTS1_9PEZI** (313 aa)
NADAR domain-containing protein. *Pseudogymnoascus sp. 24MN13*

```
MAMLFAAPDIAARIAHEPDVEDVRALARGVDNFDEKTWEEDRYGIVEEATYHKFAHSLVRERDLKAALLATGEDELVLAS
PLDGIWGIGYEAGEAVGLRETWGTNLLGKALMMVRAWIRMEETGSASWEKGGAFDVTAEQRRVDMPLEVQTYEASKGYIS
PSDHMYWDTERGEGLAAEYYDKTREFGPPGGYPDHGVPEEQTEGSRAIEGAPDASGSDNALAVLGALGAGGLVLHEARGG
SYGVEEEEEENSDDELRKEEEEEEEEEEEEEEEEEEEEEEPESESDSEEEEEEAEEKEEEEDAGSDSDGDSD
```

259 - 278:	EEEEEEEEEEEEEEEEEEEE
260 - 279:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE
262 - 281:	EEEEEEEEEEEEEEEEEEEE

A0A1B8D4R2 **A0A1B8D4R2_9PEZI** (432 aa)
Uncharacterized protein. *Pseudogymnoascus sp. 24MN13*

```
MEGYLLVPPERSAIIGRAVWKPRYVVLGTNGPRHPTAPKPSLPRSTSASKLHAARQGLKATSVFQSSDDLARVGQDQLWL
TVTKQKGDSEIISQNLLSSIRSCEIQSIQFRKPGPAVPTLILTFELDAAAERMRKRRSSRSGQLTSPSSTFPNSLLFRPM
PDERFNIYDWQVTIAPRIRPTTAERGDASSNDSASLFAFVNPFGNSQKPSERPTISNPIPQPEPFLHHRTSTKDHRRPPK
SIRPVLVEGDLEPASLSLAGMGTRIIPPAPRTVDTAEEEEEEEEEEEEEEEEEEEEEEEEEEEEADEEDEEDDDEEVDLDSTAFPQP
PSSPLPRSRTAPPTRPPLYHRHSSASSFLPVQTNVSSAAASSRNSHNSDASSGFGLPEAETVLGRGLSQARLSGLVRGTR
```

PGVLQRGVSEDTRCGGGWRGSGMLGGMEGGFM

277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE

A0A1B8EUG7 **A0A1B8EUG7_9PEZI** (422 aa)
NADAR domain-containing protein. *Pseudogymnoascus sp. 05NY08*

MPPIFFWRDTNPSFDFLSQDFHAPFHDNETETVWPTTEHYMLSKMAMLFGAPDIAARIAHEPRVKDIRALARGVDNFDEK
IWEEDRYGIVEEATYHKFAHSLVRERDLKAALLATGEDELVLASPLDGIWGIGYEAGEAVGQRETWGRNLLGKALMMVRA
WIRMEETGSASWEKGGAFDVTAEQRRVDMPLEVQTYEASKGYISPSDHKYWDTERGDGLAAEYYDKTREFGPPGGYPDHG
VPEAQEQTEGARALEGAPEASGSDNALAVLGALGAGGLVLHEARGGSYGVEEEEEENSDDELRKEVIENLFRKKPAEDED
SLADDSEDEKTPEPESEEEEEPEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEESESESEPESESEEE
EEEEEAEEEEEDAGSDSDGDSD

343 - 362:	EEEEEEEEEEEEEEEEEEEE
344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE

A0A1B8EWG0 **A0A1B8EWG0_9PEZI** (177 aa)
Uncharacterized protein. *Pseudogymnoascus sp. 05NY08*

MTTPKQHQATFSAKLPFRGKEANPPPPARINTRFTYLSLVNSVDSPPPHHYFEAVFAQSRRRYGFIYVDDILVCSATVDE
HAADVYDVLGLVKALGVKIDSPRSVFSQSRGYFGIGGETVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKKEEEEEG
VLDAAGIVRGVGSWLDN

121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE

131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE

A0A1B8FFL2 **A0A1B8FFL2_9PEZI** (581 aa)
Uncharacterized protein. *Pseudogymnoascus sp. 03VT05*

```
MSLSDAIAKRSQRQLERKSLDDQLPALKPRSKERERIIVEKKISDLDKEIQKDNSEIKKLEIEDAEKQQKLAEKAAAEEV
AKEAAANAAEEEARKAAEEKAAKEAADKKNQQMAAEEEAVKKTAEEEAAKKAAEDKGAKKTADNENPQMTEEEKAAKKAA
EDEAAKKAAEDKAAREPPSDNENDDIISRLRKGQPISKLKKPISISVEALLSPEQHVVGYKNGFGKPVIILDNTFPYARI
CRIRRDIAHDKSSPNIMLQRRGGELKPNSVEKWGVDDLSAVKMITIDVPLDYASSPVNLVKLIPKMTGTEKDAFKANNET
IPRQPDVQLYCEWNEPLILDTGKEVFSSWESRATCRLIWKKNADDYLLYVAKCIEEWYQKVSGGQYADEPMPTIEIFRAG
RSMSPGTEATPTPKNTPRQTPEPKVTPVPFRTKPPQGTGNKSPSILSSDDDEETEEEDEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEETEQELWEKRIREIEGQYRAKHNILPNAKLTSKQEKAIKKQELREKHIREIESQYRAKHNISSKD
TLTLKQEKAIKKKLTSTYGII
```

459 - 478:	EEEEEEEEEEEEEEEEEEEE
460 - 479:	EEEEEEEEEEEEEEEEEEEE
461 - 480:	EEEEEEEEEEEEEEEEEEEE
462 - 481:	EEEEEEEEEEEEEEEEEEEE
463 - 482:	EEEEEEEEEEEEEEEEEEEE
464 - 483:	EEEEEEEEEEEEEEEEEEEE
465 - 484:	EEEEEEEEEEEEEEEEEEEE
466 - 485:	EEEEEEEEEEEEEEEEEEEE
467 - 486:	EEEEEEEEEEEEEEEEEEEE
468 - 487:	EEEEEEEEEEEEEEEEEEEE
469 - 488:	EEEEEEEEEEEEEEEEEEEE
470 - 489:	EEEEEEEEEEEEEEEEEEEE
471 - 490:	EEEEEEEEEEEEEEEEEEEE
472 - 491:	EEEEEEEEEEEEEEEEEEEE
473 - 492:	EEEEEEEEEEEEEEEEEEEE
474 - 493:	EEEEEEEEEEEEEEEEEEEE
475 - 494:	EEEEEEEEEEEEEEEEEEEE
476 - 495:	EEEEEEEEEEEEEEEEEEEE
477 - 496:	EEEEEEEEEEEEEEEEEEEE

A0A1B8FW66 **A0A1B8FW66_9PEZI** (156 aa)
Uncharacterized protein. *Pseudogymnoascus sp. 03VT05*

```
MNTGAGEAGSTTEVCARRRRLGNGGNDGVNDTGDGDDGMQNAEGRDEAAIAKDKEQVEDEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEVCCREEKGFDRARRAGLIDAVAWKVVERNCGGSVSVGTVVGVGVGVGCKLPLGSSLLTLMCRVKL
```

60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE

A0A1C1C928 **A0A1C1C928_9EURO** (674 aa)
Putative sterigmatocystin biosynthesis monooxygenase stcW. *Cladophialophora carrionii*

```
MGSIGDIGTGGPAMDVPVPVSASVNGHNKADPSITIPMHNVPAFTPSKKLRVVTIGAGYSGMIFAHKLQYTYGPEFASLV
```

```
EHTIYEAKPCAGGTWVANTYPGVQCDVPSHIYVFPFAPNPEWSHFYSTGPEIREYFQRTVREWNLDRDVQYNTTVERAEW
DEERAQWRLEVRRRQQQSDGDAADTSSGTSTDTRVEWADVLVSARGILSHWRWPDIRGLHTYRGHKVHSAAWDHTFDYSH
KRIGLIGNGSSAIQILPEMASLADTRVTCFQRTPTWVVCRHTPAKLVGSDDPSPNPAYRDEDKARFRGDPAALKEYRKRI
VGNVNRGFRIFEKASPQQAEIRAFATRQMAEKLGHDPRLCAMLIPDFEVGCRRVTPGNGYLEAFTRDNVALTQSHIDYVD
ERGIRTMDGQYYELDVIICATGFDVSNVPPFPIVGRNGTDLRDKWKHEPESYLVSTAYLFFCMHATSYGRYATGDMLLAI
CHGRAHALAKQKAKLISAQSVACPEMPNFFMFMGPNATIGHGSLIYSLDWTAEWIVQWLRKLAREDIASVAPKQDVVDEL
VRYGDEVMKTLTWTGNCRSWYKNNRIDGRVTATFAGSAMLFREMVETIRPEDFDLRYRSRNRFRFMGNGFTKFELTDGVD
LAWYEEEEEEEEEEEEEEEEEEEEGCVNEHEQE
```

645 - 664:	EEEEEEEEEEEEEEEEEEEE
646 - 665:	EEEEEEEEEEEEEEEEEEEE

A0A1C1C9G9 **A0A1C1C9G9_9EURO** (1368 aa)
Uncharacterized protein. *Cladophialophora carrionii*

```
MDLPHPDPKHTDVWPATPANPSWNEASNVTASTSATSQRILNEHADLAEAIRLSLEHRQNSLLQKRLPVEGDSSGLPLEL
VLGLNNEFDPLDQPEDDVAIYFGAPPQEVGQTDQDYQYIKHHFDRVHALNWRTLRLMGDESRFTDNDLLNPTKSFRAERR
LRKEHRIVLERAERKHGGKFRCYIDLRPPKEDEEAVILITELSCTRGVLTWHQARDRYNLAPLSVLGHDDFGGQPPAQAA
GQQANPSGTVEETPADSTTSPPNLLELARKLVKAPTSLAPNSQPAVAAEYSALRHHSALERLLQAISGKDPKLDSAPKVW
TFFALARYFGCAAHERIARWITTWLYADNNANFIQNNPEVAYRIAMGIKSPNLIKVSFSILVGERALIEAYGEQRSDILT
PLRQNVHGRKLELLDDDERNRIDHAASSLVKRIRDITSHMCEHLTFLRESSMYDVLDKTIAETPEETSLLLSAKKTIHEY
VRSRIYYVLCQDQKPFEELEQDVKSTLRFRSATANSFSEVYNTLNPSTRPFTKTFWLALQHTQFDIGHTNIAAKGTTSFF
YDTDHTLEFKALYQKQPVYGITQILRSTFDDKIIEVNRMLRERELAKSRRLNGMEHPVSDMSPGVMHYPTDLALDKLAIK
TPPGSPLSRRAEEGSSPTKRRKTTKTEKFVDGFWDTGSSAPSSSNPGPTKKVAFPASPSNLGSASAAELGGGSDLFLSSP
DRATAPAVSEECRGMSSARKSTYGNPASPTPSLPSIDGRLASQVEKAPTVPSKSQPTLALRQKAMRMDASGPVQRGMEDQ
RLEEQQPTVEHIQPGPTQATAWTEKVAAFLAKHKSHKHNSTLPSHPEAKPMAMNTNEELIPPELPPLASFSESEAGGGIG
NGPNSSSSPPVATKELPSSEAGELPVNPTPQTAGSFPYSQASFNGSHKFMPVPQQPLQLTSGSSSRAVQQAFSNSNTHRQ
TKYLSGHCNATPSAELRKQALYPINPQEMLHEIGAAVGEICSGVLYPPHLFHHTGLLPTNLVDTVLNLGEDEFRYLPLWV
PGGNDDGSGGVFDETPVPNIDPARVTFESFGPGRIRRPYDQADSPISDSDIEEISSSQGISTVGKASKLATDGTHTVTSL
SSDTSSANGRPDADVVVVDPARDPWGAVDVGEGIPSRNAANGSEMTDPDTGLGFCETGDDANEADINNDNNDIDIDTING
DDPLEREMTASLRAFVAGGDDDADSASNEPYEGNDTSDPDALDIKPAAHPALFHSAAAAEEEEEEEEEEEEEEEEEEEE
EEEEKQAEVKAEGTGEGKETGKAKAQNHPFLLPNRHDDDDDDEIQHHAQIQTTHSAQSAQLTSNVRHGAMPHSQDEDEDE
DEDEYEFL
```

1260 - 1279:	EEEEEEEEEEEEEEEEEEEE
1261 - 1280:	EEEEEEEEEEEEEEEEEEEE
1262 - 1281:	EEEEEEEEEEEEEEEEEEEE
1263 - 1282:	EEEEEEEEEEEEEEEEEEEE
1264 - 1283:	EEEEEEEEEEEEEEEEEEEE
1265 - 1284:	EEEEEEEEEEEEEEEEEEEE

A0A1C1CJR5 **A0A1C1CJR5_9EURO** (84 aa)
Uncharacterized protein. *Cladophialophora carrionii*

```
MLAEEGKEDGGEEEEEEEEEEEEEEEEEEEEEEEEEEVLAVSCHPSIWSCCSRYNPTQWGGRRGVPPQPGVSLFPGLFSNYV
SEIA
```

12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE

A0A1C1CQG0 **A0A1C1CQG0_9EURO** (100 aa)
Uncharacterized protein. *Cladophialophora carrionii*

```
MTTLAILILGASSNEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGKQEKQQEEEDHHHGGKQRCDAEEAVDLISRQD
HLGSLSEGGVLRGETGLHHC
```

15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE

25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE

A0A1C1CSN2 **A0A1C1CSN2_9EURO** (569 aa)
RNA 3'-terminal-phosphate cyclase (ATP) (EC 6.5.1.4). *Cladophialophora carrionii*

```
MITLDGSTLEGGGQLVRVALSLSAICNIPVRITNIRAGRGPGSFYKKAPRKNGGGRHGNASQSGPRDESKSSKKSAAAGG
GLKESHLAALTWLARECGAAIEGAEVNSLEVVFRPQRTRRERVPVPVPVPVPVPAPGPAGRGATSEPEVIELRNPGSIWL
IWQAIFPYIVFAVLARSSEDASRKPPKEPAFRIRLRGGTNVPKSPSGEYMQQVFLPLCERIGLPKVHVDVTRRGWTTGAP
EIGEVEISVFAPRPTTRRAEVSSSSTGAKDACQNNGGTSHGRTNAAVSSEEEEEAKEEEEEEEEEEEEEEEEEEEEEEE
APRRGFRLPPFDISLGQDFDFTVESISITTISSSPQTHSLLHARLRDSLRSTPAFSDPRISITDHPSCSAHSGDERRLYI
LLTAHLAGGYVLGRDYLGPGKKITTDADRRRTVDEAVNQVVRDFQREVGRRRCVDEFAEDQLVIFQALAEGASLVDTTRA
GRSENARARATFETGSLHTRTVRWVCHEMLGTVFDGVGGCQGGGGGGGGGGGLRRGIPSDGVDEISQQISDDLVLGVDRR
DVKKGGDKS
```

297 - 316:	EEEEEEEEEEEEEEEEEEEE
298 - 317:	EEEEEEEEEEEEEEEEEEEE
299 - 318:	EEEEEEEEEEEEEEEEEEEE
300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE

A0A1C1CV77 **A0A1C1CV77_9EURO** (101 aa)
Uncharacterized protein. *Cladophialophora carrionii*

```
MSTAAKLKRPSQVSKKLMLCSAPLLYPKKFNNSPIPRKSGLGAMARSGHMKGTCREEDASALEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEDKEDIWKGN
```

63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE

A0A1C1CVT4 **A0A1C1CVT4_9EURO** (127 aa)
Uncharacterized protein. *Cladophialophora carrionii*

```
MRADLLKGADLGQLQCLKQVADELGFELYLANMEKEITKTDDGYDDRRYGYYDEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEISRSITLTYIADVAGSRMNHPVNSADRGLEVDQENIVDSHG
```

54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE

67 - 86:	EEEEEEEEEEEEEEEEEEEE

A0A1C3KEA8 **A0A1C3KEA8_PLAMA** (506 aa)
Uncharacterized protein. *Plasmodium malariae*

```
MKKIWGVVFYFIFLNKYIYTKNGNLRSNNDGKNTPEKKKKKNSKNGWIPYYYPQWNQNKVPDNLYDVPENKGNKNTTEYK
EKISGVTEEKKKLDELRDVNEDEAPYKLLSVGENSSASVNERVNESLTPGYNNDTSENTSQEFIVIDPNVETFDDVAVNE
IATHESDKAPSEYKSEEPNVVSHNNETIERDKNEASHDKAVIESSTFENAEETSENISKESNVICSDSQTVERNEKNSDG
GNVTYNTIRKQEIASEFGKNEIDQAEQSSDVVVTYDNKSEDSSVALDAQVESVFDKETHVNKEETEEQESKTDIQKINRV
EERNEPPYPGENTHKENVVEQRKEGSESRREKQVQVVHEPRLDNDKTQEQPKERTHNAVERMVQRNEENGVEEEEEEEEE
EEDEEEEEEEEEEEEEEEEEEEEDEEEEDEEEEDDEENHDSVIYNKKDSNTYFPPNDKHDNMNIMQTITKILLRNLLN
SLSHDYALNDPLMGLEMGLVNPFYLF
```

404 - 423:	EEEEEEEEEEEEEEEEEEEE

A0A1C3KGA5 **A0A1C3KGA5_9APIC** (571 aa)
Uncharacterized protein. *Plasmodium ovale (malaria parasite P. ovale)*

```
MKNKRKKLKQVPQKYKNFITKSLPKNNVLSLNNSNIYTGGNNKLAKCNYNSARDNLLSNLFTSSLNTNYNDAIIKFITLV
GICNVLMLRSVVAIAEDLANRSAYKGSKPEVESKTFDSASTVGEKISSAAQTVIQLIQEKFNCIFLDKTDSDCRKLRLTI
LFCILFFLLVFGMFYGFSTVCISSKNIRVKRQFVEEIEHSNRRAQMKHRQMHQNQRYQNCKIYNMEEVDEYEDKDEEEDE
DEDEEEEDEDEDEEEDEDEDEQDEQDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
ENKEENKEENKEESKKENKEENKGENKEESKKENKEENKEENKGENKEENKAENKEESKKENKKENEEESKKENKAENKE
ENKEENKAENKEESKKENKEENKVENKEGNKEENKNEDEKAGQKAKQKEKEKGKEKEKQKEEEDKEVTKMQEQKVKSEKT
QVQNAQPETEKQNTKEQNSIEKNREKKNTKEKKNTKGKNKEKKNTKGKNQKTKSKKEQKIEKKNFPAKIPKTKQGNSMND
ALLLGYHPSPK
```

267 - 286:	EEEEEEEEEEEEEEEEEEEE
268 - 287:	EEEEEEEEEEEEEEEEEEEE
269 - 288:	EEEEEEEEEEEEEEEEEEEE
270 - 289:	EEEEEEEEEEEEEEEEEEEE
271 - 290:	EEEEEEEEEEEEEEEEEEEE
272 - 291:	EEEEEEEEEEEEEEEEEEEE
273 - 292:	EEEEEEEEEEEEEEEEEEEE
274 - 293:	EEEEEEEEEEEEEEEEEEEE

A0A1C3KJE2 **A0A1C3KJE2_9APIC** (1664 aa)
SET domain protein, putative. *Plasmodium ovale (malaria parasite P. ovale)*

```
MFRVALLKDLERGGTGDEEEEEEEEEEEEEEEEEEEEEEKHTSEEKHISEESNKVSRREKEELLEVAKELPILHENNDKDV
IEALISSFVERYPKSVDAYECFSKFYIKTKDYKSALSMLYAALYVEKKNKTIVRTLHECEERLVSQVYKIPTRYKNWISF
PESRPYKEDVYSWESNCGNYVRSGGENVRVNGDRSSNNQEGEFAEGKSLGKKVHLVRQGKQYIALARKNLEPGEIIFQEK
PLVLTQYIFSNNFTYSTCYHCFRERNISEKSYACPVNPHTCSYIFCNWKCLVENIKIHKIECNILPIIYAASKKCKLGYY
NVLHIFRVLIKTRIDRDYKDKDHNMLNDIFTFPSYYYAVKKNQKDIFNSFNTLANIMILQLPCSFYLYLKQEELVEFMLI
IWQYSTFVKYYSPSSIIQQINPETTFGFVFSPQLAKLHHSCIPTCTFYYDDNGKITVRSLCTIPEGGKLCINILPDQYLP
LKIRKSFKAIPRIFTCGCARCSDPTENNLHLRSIKCPKCILGYICPMKTDSLVETLKLHWYGQKGVNEEEERAYSSNEVM
EKQSGSPSNCSDSSEKQGDPFNNSHASPSRTKPLLTDKEKKILDKLEKEMERWVCSNCGKLSIQGNKRCIMLENKIYILY
NKGENEYMRGNLISARNILLQLYKEFCHVLHPNHYIIFNTNVLLAGLLRYNPDKEIYESLVCLRKAIIAAENVLSVCSLE
KVHLYIHIAHYTFNCLNVYKLHHKGIGIPSEFVIDPIYTAIWNSSVVTGFNSTLTIVLMQQLRMYAIYMNKFTPYMDIHF
SIERKENFCTFYHKVTQKKSEPFRYIKKKTEDDPFYPIYMACQCFDLKFEKNKYFRDIFKSFKNIPYFGNGLDALSLACS
FGNINLVKLLLKLKYSIFLKNELHMNALLYMASSFLPEEKNSYHYNYYYTLLKEIELQNVNFGHGEGNYLSQDMFTHEEN
KNGFPLPHNGLNYMNSCHLKNEIEKPFPFDIVLDEEFIYGEKCKEIDTNQKIILILFLKHLHKIEVKKKKLYKKRLGLSE
RFHRFGNTNARFLKRAKRRGKGDKKRDKKRDKKRDKKRDKKRDKKRDKKRDTKRDTKRDTKRDTKRDKKRDKKQDKKRED
NTELTRYNNLAGNNEEEDGNWGGTHKKPDNTKLHGSHLKELSSSGSSLFSDNPSDGSNISEESDIPYGSSSLSGDSSNPS
RGSNLSEESNPSRSSNLSGDSSNPSRGSNLSEESSNPSRSSNLSEESNISSDNSEDVLNSKVKNYYSQKLLVQSVSHKLL
GLNNVLHYACARGKRELAKQLIISGVPVMLLNGEGSTPLHMASFSGHNEIVKTLITYKSDINFMSSHGETPLMLAIYGLH
IDVVKNLIENGANIMTKGNNNMTVLHCLVHGLLRRKTIHYVNINTMDDNPYFSLHRFTELNSSKCNLERLTNLNINVLNS
HISIIEEMSHDFFLLPFKLLHRLKKAIIILKYIMSYCPIFMYETKNVNGYNPFELLKTTWKKLCERRLQVLSMSDLKISS
FSERQKNIISQAWTLITSLVNAILSILRPDRSILTSIYKNLLHMRGTTAWGNQRNAQVADGKKPSEDGKKPGEDGKKPSE
DVKKPGDEAKKPGDEVKKPGDEVKKPGDEAKKPGEEANTVVAKASALKKVVLKKMKPPMLKNKG
```

18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE

A0A1C3KLC6 **A0A1C3KLC6_PLAMA** (741 aa)
Peptidyl-prolyl cis-trans isomerase, putative (EC 5.2.1.8). *Plasmodium malariae*

```
MKRKKKYVYLEFSINSITLGKVYFELFSDEEIKKSVENFVSLCKGNLNYSIYTDDEMLSFKNCKIEKIKKNKCIKSGYLK
NKVYLHNNEWKNKYPIYQNKKYENVECIYGKYYNKEYTKRRHLNAGLLTVVQVENKKYSSIFKITLNKVPTYNNKNIIIG
RVIKNMHILRAIEIIPVTSNWEPKINVYISDCNEVSESFFKERKASSRQSYIDGLFENLNHNEQGNEESDGVEAGEREES
DEGGEPYDGDDNSVLYANHPFKKHSPFLSNFDIKKERNKKIKITEKQKGIELLNKILSELDSGSKKENFSKRSTKISASE
HPQSKHHPYPQLQPEPQSSSSLQERTVRVDYPSKGTDDTSKNFEKMEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEKKKKKKKKKKSNEGDSQQDQPLPCSNALPYDNNINKQMTERERRMFEIQLKINQSKC
LNEMEIRRERMMMMSQGPNRGMGKFGEYTHYNFAQNANVKNAFQRRISTEESGGREEKEKEKEKEKEKEKEKEPTGTIHS
GSNSGCDMGGDKVSENDHANDNDNADNHGSDLRKDDEDGKKSQLYNTSAVRVQSALNRKKNKREDTYELDNDINLYKKIK
FNFSINRKLYEDKKKEFKNNFYGYNLLINDNSTCTDKDKNKVVEFCKKQEELRSKISRKRKNDDGVFKNYINRRNKIYNK
KLDRYFNKHTVEIRQNLERTF
```

367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE
379 - 398:	EEEEEEEEEEEEEEEEEEEE
380 - 399:	EEEEEEEEEEEEEEEEEEEE
381 - 400:	EEEEEEEEEEEEEEEEEEEE
382 - 401:	EEEEEEEEEEEEEEEEEEEE
383 - 402:	EEEEEEEEEEEEEEEEEEEE
384 - 403:	EEEEEEEEEEEEEEEEEEEE
385 - 404:	EEEEEEEEEEEEEEEEEEEE
386 - 405:	EEEEEEEEEEEEEEEEEEEE
387 - 406:	EEEEEEEEEEEEEEEEEEEE
388 - 407:	EEEEEEEEEEEEEEEEEEEE
389 - 408:	EEEEEEEEEEEEEEEEEEEE
390 - 409:	EEEEEEEEEEEEEEEEEEEE
391 - 410:	EEEEEEEEEEEEEEEEEEEE
392 - 411:	EEEEEEEEEEEEEEEEEEEE
393 - 412:	EEEEEEEEEEEEEEEEEEEE
394 - 413:	EEEEEEEEEEEEEEEEEEEE
395 - 414:	EEEEEEEEEEEEEEEEEEEE
396 - 415:	EEEEEEEEEEEEEEEEEEEE
397 - 416:	EEEEEEEEEEEEEEEEEEEE
398 - 417:	EEEEEEEEEEEEEEEEEEEE
399 - 418:	EEEEEEEEEEEEEEEEEEEE
400 - 419:	EEEEEEEEEEEEEEEEEEEE
401 - 420:	EEEEEEEEEEEEEEEEEEEE
402 - 421:	EEEEEEEEEEEEEEEEEEEE
403 - 422:	EEEEEEEEEEEEEEEEEEEE
404 - 423:	EEEEEEEEEEEEEEEEEEEE

A0A1C3KR10 **A0A1C3KR10_9APIC** (1196 aa)
Vacuolar protein sorting-associated protein 33, putative. *Plasmodium ovale (malaria parasite P. ovale)*

```
MNTLNELKEQGRLLLLNILQSFSGVKCLFFEKSLHILLNVMLNDEDVNKEKIEHIFVVSNEMDVQTSKLDNISNILFFIR
PYFYEIENIFKIIEKIEKVKSSEKKYVFIFIPYMTYMCEQEIIKYNIFEVSIKIIIYPLYFIPLYNDVFSLEIKNIFKEY
YVDNDFSNLIFCAFSLMFLQHLFNGVFKNIKSLGYLSHFISEQLIQLRKEIVASNFHIQAPNNFDEDFLDILSNIQNLQD
NHHFKNSTELAVVPNGELPKREVDGHRTTGVTKKIEGRDKTPNGELPVGEAGGEGEEEEEEEEEEEEGEEEEEEEGEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDDVEEEEEEEEGEEEDDDVEEEEEDDDVEKNAEGGASAEKRTG
GREKSEKRKHELGNEQYEEKEALNCAASLEQNVMGKESKGGIATPEKVQTKDDIVSTLGTNVEVTPNPSDKNSLCSDSHS
GRSWCSNISPFCEDVGKTEQEQFVEEEPEKENESQERNRQKGGEMDKQGSEADMYVNPGVRKCTRKATTKNKANSGKGGK
ELSATKGDNFRNCLSPDIKKGKMEPAYRTVDAGAVEGGAVEGGAEVGSEKKAHKEAPPRREKQKREQQKRREIKGKTKWG
SAHGRKHWNEAEVIYKENRKEGAKRKEVAKRKKGAKRKEGKVSPGFMATMDNTKFLMKKKDREKAEREEKKEKNYLLERI
GISSFQFLLNVCDKIDSCVIIDRRIDMVTPFCTPFTYEGLIDHLFCIENLQIEIPRYIIFNDQRGRNGTIASTPSSVVGE
NNFSAGGNIGGGSDLRVRVKLRSSVDVLYNHIKDLSQNEIGSFLHKRASDIQKTYQEKDSLKDIGQINEYMRKFKEKHYE
HNSLSTHVNIASFILSVIKKENNFTKLKLEDEIIQLNTNSNKNNIQNIVKKIQLLIYTKENIYEVYRILCLFSVITNGFT
DNYMNELKKDIIEQYGINEIVRLNKLHLCNIIKYQPKKKFIWNYLKNNFNLLSNEENDISYVCNGYAPLSVRLIEYMGIL
KNNVQVFPEIFNLLNGPTYDIIQNAVGYEHVHDKENHLADADDDTNSNSSSSNSSSNSSSNSSSNNSSSNNNSNNNNNN
NNNNNNSSSSNNNSSSNNNSSSSNKKKFVILFYVGGISYAEIAAIRRLNRNNQNYHYLIFTTEVTSSRKILQAMGA
```

318 - 337:	EEEEEEEEEEEEEEEEEEEE
319 - 338:	EEEEEEEEEEEEEEEEEEEE

320 - 339:	EEEEEEEEEEEEEEEEEEEE
321 - 340:	EEEEEEEEEEEEEEEEEEEE
322 - 341:	EEEEEEEEEEEEEEEEEEEE
323 - 342:	EEEEEEEEEEEEEEEEEEEE
324 - 343:	EEEEEEEEEEEEEEEEEEEE
325 - 344:	EEEEEEEEEEEEEEEEEEEE
326 - 345:	EEEEEEEEEEEEEEEEEEEE
327 - 346:	EEEEEEEEEEEEEEEEEEEE
328 - 347:	EEEEEEEEEEEEEEEEEEEE
329 - 348:	EEEEEEEEEEEEEEEEEEEE
330 - 349:	EEEEEEEEEEEEEEEEEEEE
331 - 350:	EEEEEEEEEEEEEEEEEEEE
332 - 351:	EEEEEEEEEEEEEEEEEEEE
333 - 352:	EEEEEEEEEEEEEEEEEEEE
334 - 353:	EEEEEEEEEEEEEEEEEEEE
335 - 354:	EEEEEEEEEEEEEEEEEEEE
336 - 355:	EEEEEEEEEEEEEEEEEEEE
337 - 356:	EEEEEEEEEEEEEEEEEEEE

A0A1C3KRF5 **A0A1C3KRF5_9APIC** (2321 aa)
B30.2/SPRY domain-containing protein. *Plasmodium ovale (malaria parasite P. ovale)*

```
MHTKLVSHNCVEQYINCKDVVEGQKKELRKKENKQIGSAILYTRKGNTRMEELVSILGGRRKDAKQIFFYNNCANERYGK
IKSLYKKKKEMKKNIYFLEEVLEKPSFNKTVEKKKNIFCLHRIPYSGYINEIIKSLIMRKKIYCSVSFNIIFSENGETFL
LRCLTFLLKYNKKNLSKWETFSLFLKNECSYSKGRSFITRGVQHFLPHFNLKEGKYYEVEVVEEENIFLSLSRDNVLKIR
AYFFSGDVNFVENTPFANSSFELNYRGNTLFYDNIEIRNLKNYPIVHSLKDTFFEITVNCSEMRCNQCKKRKSEMGDSRY
IRDIRDVVAPLALLKNPFFSIIHKKENSKMGVNILEVHAFCCTKICTIQVFINVFTYPEVKTILNYPSMIYGMRILYYLS
IFSYIINTHGVLFDHIIITEMVKIVLLILFCTYICIMNLFFLRTRIYNTTHFSKPFTKKWEQRENRVISLLCHTVVNIPF
AKKSYKECITNRKNEHWSIGNPVLCLEKVSIAFHFARRKMEKRRHFPIFSLSRRNRCHDSFLITTSFIDQFYHVLLGFYN
IVIYAVGMILYFFYIYMNTMINYFFCSLCCFLYFIIQSIVFFLNVMLIFVKYKMDLFLKMKNKKIEKNLTLFWIPREIRK
LSFPDVNQVTQEDTDENEYIKHQKWEEKIKAGSDYAIRFDNKSELGDSRPRVGREVSGERLQRAACSGGFGNNNNGRRRR
RRNVDSCGYLLPGIRNSVLCDAKKGVSKEYHESGNKKKRTFSSGRVVIKKKKNGTIHTKNGNMHCTVFSPVLYFKCSLYF
KETHECDFAQFHGTPFQPMLLPSDSCSSHMSTGKKKSRSHANRRKNKKKKTYKEGKQQRRGKDKRNSNGSGSGSDSGSGS
GSGSDSDLESDSDEEEEDEEEEEEEEEEEDEEEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEPDDKFGDGEE
EDDNDDNDDDDNDDDDDDDDNDDDDGDDSYSERGRKKRKEKNKKIKGKGMYGDDPSIESEGEKQKGDSYYDKKKNLYLKK
KKKKFKHNFIYLKNLFKENVCINTTNVSNFISISKDKLTATYTAWGKHTDIACVQVNKCALRDCSIYYFEVEVLNCTNFS
KIVIGMTSKNYTINKNPGSEYNSFGYKNDDGKKIIDGKVDNYCNGYTKNDIIGCGINYYDNSAFFTKNGKYLGKACTINA
KYDYYATVGLSTLGDRIKFHLNSFHFDIYNLIYEESEKERKIIKSIYIQKDIFSDIIKSHLIKCGYFNTYQSFVNYLEKN
KNSDDNNSISNSSHCKNGINKVFEKNTDSLKTKDNDQKLQDGKKMKDTEGMKKENLTISGVNGKGENNEKNGNPNKGTNT
DMSGSAKCIITISPEENSSVKDNDGNSKFKTEDGACKEHDDVEGNIGEKRKNEHIEEDCFSSQIKSDTVKSTEAEVVAEA
EVVAAAEAVAVAEVVAVAEAVATADAITGKKCESKEEKIDIDRNKGDKSNKSSDKSNDKSSDKSNDKSNDKSCDKSSDKS
ILNAFLVNYLDVYEKLNKEGSTEKEVKGQGTLNTAEKKHDKGMNAPDKSPQRPNKNGEGEGKCSEGEHGEKQVTQIKTKS
DEGKRSNKKTDCEDGKGREEENVHLVKCPTEETAEEGRKSQVGGADPQLDILKSYEFSPYNNYGGVSSQNIQLASRRNNL
SNLINARKESSSLLLSRLRNKRSLSTKDDLNILATNFLNTKKEAKKNDSDINKKIHLLLRDKSNTVKNEKKKLNKKEGGK
NYSNDKEYITKYFVNLYLSEEKLRKMKESLEMRHIIRKNILNGNIINVLNILEEQYTELFTNERASFHIAMLFTQQLIEI
LKPHKKFIKNISSRKIKYKNEGKYEKQDDLSSESSYKSYNTLSDDHFYDDIKTEYDSSDSLFCDSSNGEESNFTISQLEK
LGKIHISKRGNLEEAKIGNKCESGDVGKSGDNDKAANSSAKGFLDNGNVMLPLDSGPSKEETVGKEQKPSPVLSESKNLD
HNSSTIENPKTNGEDKGVSVSPMNVTQLNDIDFVKEKKIEHLIFKSMQCNYDEEFYKKNNLQEEYESHYNKLSKEYEFFK
DDNPYSYKHKKKCYDKMHREDELGKDVKDICTSSTDDSTSDYDSNDSNFKRKYYEFNDINFDQIYQYIYKNNFSPNNQLK
FKKDHLYLALLWIREKLSLFNTSPHVNVRQCIQDSTSLIAYHKPYKQKLVRMFFSKNRNLLTFNSVNEGILDICLKAPIY
SPLEIMVKHLILCRNLLREKKGNIGIKYDCRYVCQPYKRYMIKIKNNKIKRRYFKETTKQKNEKGSLNGKLIADKRLSIF
Q
```

921 - 940:	EEEEEEEEEEEEEEEEEEEE
922 - 941:	EEEEEEEEEEEEEEEEEEEE
923 - 942:	EEEEEEEEEEEEEEEEEEEE
924 - 943:	EEEEEEEEEEEEEEEEEEEE
925 - 944:	EEEEEEEEEEEEEEEEEEEE
926 - 945:	EEEEEEEEEEEEEEEEEEEE
927 - 946:	EEEEEEEEEEEEEEEEEEEE
928 - 947:	EEEEEEEEEEEEEEEEEEEE
929 - 948:	EEEEEEEEEEEEEEEEEEEE

A0A1C3KRJ1 **A0A1C3KRJ1_9APIC** (1223 aa)
Uncharacterized protein. *Plasmodium ovale (malaria parasite P. ovale)*

```
MYAKDENDENNKINLHNYKNILHNKKKNLGLLNQDLLGKKDVKHALGGGECIKLRADAKGEVKEVEEEEEEEEEEEEEEE
EEEEEEDEDEDFAAEVEDDDEDEDDEDYVAEGEEEEEDDEDEYDEEDYDDEEREITFNSYNNYYYETYNEEEEKKRNEIE
DLIREKQKQDEKNRNGDKKNEALFEKYSKLLTGYKLRKERNVKDYPVQGEDDSRSCCYSCKSEERENGHTKLGDSTHRER
THLRGDHHPTLEKSSAEEEGNFVADLLNRIDEIYYKESRYESLKSVNNNNNNVCINDLNLNIISDYLNVDISVFNKKTTV
LLLGNTQSGKSSFINWFTEGYVQNTSSISKKNQITYVDVKQNFKFNFGRLQNGNYQLGMINKLSDASATAADGQGTNEYE
```

```
SMGLPQENQKVILSGENCYCLFKPFQKLKKSAQNLKKYIYGKIYYQNNLTKYMNRVNSVSFIDTSGINDVTDFEYDEVVM
NLAKYVDLIFIFIDSNTFSINNRLLRIMNYMIDNQINKVTICITRIDLIRKINLYRVVFYLTQYFFRNLNVFKYNLSRTH
SNSNCVNDIGELSNEEEHPDACVNIKSKQKGGKGNNFFNMSIKSFQNILLIPKMVGNLVARNTANERRKKAYPGHPFNRK
NNQNGTDAEWEEDVEGDKTQWDGGPSFSHSPHHGKKEPPGTPDEEESIFKKILTKSYNSFKEKIMSVDAENPQRGTSRIH
QKGNSQHTDEHRGSSQELPFEERNIRENNTSNRLDSIFERKINYGDCLKNCSVFFFVLIYEVITTVYSLLHTSISNYLST
SNMKRVINVEKLYKLDDANKLKYRDKNSNSNNCYKILEFLTIYLPEMPSNVLKRERWKYDESNINYNHQRRNRFSCDVQY
DHTSYNYNIDRVEKNPNMNNNPEKNNNYYYSKRYPQRRSIPEDVLLLGKGSNQYDGYNRGEKKVRYPDANNDRYRHIDEN
EHSSYFPKSDYRGDKRDSSFLPQEQTRRRASYLVDHTWENSSANGYPGRVLRQESSEVACGEPWGNSFERPYGHPPRNEE
ARELNMIHELLFKIDEAIDLKTNQSIYMLKKDLEKIQNSCLQKIFENDEVVKRNKSLRMQNIKFYFFRYMAIFFGFFVSL
LRYDLLVYFNFIKPEIFLSVFSKYFLFLSSYNKNSLFIAVNAILLGAYFFVYFRYNRRNYFKSLDKSDLNKLKIILLFTQ
IIFDEINQLHLRLLGRRGKEDRR
```

66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE

A0A1C3KV45 **A0A1C3KV45_9APIC** (390 aa)
Casein kinase II subunit beta (CK II beta). *Plasmodium ovale (malaria parasite P. ovale)*

```
MEFISNNESSNGVVEEENQEEDVELSAASLDEHVRNDFKVEESEEAERDEVERDEVEKKEVEEEEVERDEVEKEAERNGV
EGAAVEGAELEGAELEGAEVEGAEEEEEEEEEEEEEEEEEEEEEEEEEDDDEEDEDDDDEDEEDDDDDYDDDEYDEDDFNEA
TVSWIEWFCQLKQNIFLVEVDEDFIRDEFNLIGLQNKVPHFKKLLKIILDEDDDDDDDDDEEDDYDEEDDEINRDSEEMY
KNKDLYEQNAGCLYGLIHSRFILTSKGLALMREKYKSGIYGTCPSIYCDNSKLLPTAISEVPKFLSPLLYCPRCCETFYP
HKTSLLNQLDGAYFGTSFASFFALSFNIQSDKKKTFYTPQICGFTINRDIRETLYMDMNKDNSESSEEYS
```

104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE

A0A1C3KVU2 **A0A1C3KVU2_9APIC** (3703 aa)
Uncharacterized protein. *Plasmodium ovale (malaria parasite P. ovale)*

```
MSDIKLSHVSSITFINSNGVIITTEIKEGNKRMKGTYTNDYEGNYVFFEKDLEHVKNIVLTLKPFHKEYEDNIIFRIKKR
DDKYRCEWVLLLKTKEEGGKKGRNGNTFADIRNSNKKNECEQKEEKEEIEEKTFDCSNIKDIMLKYVYCVTYFDNYILNL
RNEIGGSNSENEYLLNELIKINNNDIAKKSHKEGFVKATHIAARDDMMRSSVQLEAVHGTAQREAVHGTVQRETVHGTVQ
HDGMLRTVLYDDTGNNNGDDNGDHFMYDRATCKGNQLTLNGNSYNDRLGEKMEVFSSSGPYHFGEGDQENGNGNAIGIRR
NSSIRTSCNSSSNDVTGIRGRRLGARKIHCEKPKGEIKQRTHSSKMDRSEPDSGKPDSGKPDSGKPESGKYNSLKTVSNN
TTCNYGINHTACSSAKSRDLNKIPLEEKHLKDYNSDDIDFLKKLFYTNCNFENNNSAINERSTNIHGNKVISGEKKYSVQ
KGKEESMIRNGERNSIINKEEGFVVDPADCDRSFTVNKISNDDMVENIGNFNNVGVGGVSSFTENDNIGSDTFINKKGKL
LTKGEELKKELSCLLNVSEIKERMNEEKVNKNNKMERYYYLRSGQNSHLNLNENINNNNKLSSQKLSIYNKLNFDNLKYI
NEPFINTENILMNISPNNFLNLQKEFINNKNYNKNFDKNKIFNNSEFYDNSEFYDNSEFYDNSEINNNSEINNNSEISNN
LKHVNIELLKLILNQQDINNSSQAFMYDKNRIFEHLQSACKRDNNDALCSEESTKNDYMFTNKCAQNISNVHEKICNPYE
NSEMNNSFIKVQSAEENGKIGSNSKGGSNGNVVSGNSCGIGGGVDESVPHAHKPKYDFRAQKKRDRNGEYGKCVLHSKEK
QVSDRAESRGQKNNAEDSLHDGVISEIFNFMMKFNENCNAENGTCSTSHKCSGNIFGGHEQCSNERNDAIRLNNAIREFL
DNLTPSEMRHLVSNKEHIISKLISDRCTNANVSRKYNMHMKNGKCACTSGRKKERTDDCTQDCTQDCTQDCTEECTEECT
RECTDECTGGSSSTCSNCNVLSNIYSKSSTNRNDASRFFINSSTTHINMNVKKRSEQNMKEMILLNTNNNDNDVTNSKSS
NVLNVINLIKSGTGYVTNRCDDMGNVQSTSFRSDKNNKLNLSEDCSKNCVPEEDAVSSTIPTTLTTQGLNNFDPGDHFLI
EEKIKDTNSAHNTPMENKAKRDDDPPNGNDSDDGRGIHTKLHDDVDSKKDDSANVENCSDNANILGRSNGERFQLSSEKM
DFLYNYYLEACKNNAMHADFNNKLISLTDAHICNDLHNTLVNKRGMNRSPDCCINGLYNSTSSSVKGSSARNMKNVRKKT
VEGKDGINSDSGSMHSGPASINTIPCAHGGLNINFGDTFRNGENVADEVNNFFRNCLYSLKHMKGATTLDKFLEHEHNPG
EDIIKSRNQDEEENKTEQEKKNERRIENEGGKENDCEVDCGGGSPRRVHICSANGADEPGAQILYANGKGNDEQAYSDKS
TFEGSNLGKAKNGEKSKDIACDRDGKVEHDECAQTSGGTVRCLTELNEKMGENQIDNEFSSHINNKYENDEAVDKYPKNL
IHFVEDLSNQSIGGGEFYSSEVEANGNINEKYNDEHIIKAVLINMIKEMSNSKHGNNSGSSRDVPLSKGDYEGSNGAHTN
NVSGSCGCSYPQSNYNSLPSKCDGNRRNSINHKRDESKDTNGNTGFSNSPDDMNGNINFQANVDAFNHIYNSLVIKNNIN
NSNNYYNNYCQNNIININNCGGNNYFYNSSCGSGGGSNNSRASTKCDSNALRGGGVGRGNPEDGGTLHVQSNNVKLGMSN
NIHYLTSSGMGKKVKSGSFSSFNISNCKQFPVGGHSLVFESNACDHTSSNDANDPKSPNGPNDETVNTENTHDDVVNTDN
ANDVNANDDDVNERVDSGHLLGSDLLSGNSFRDNSSLKGERDANCMSNLKVGMDESEFGKVVFNKMDNNMDGINKRQSSY
EEEEDIFRMVRRNSHSNGNANDAEGSTVNDTVLNINDSNLNSLMITGDITDADVVGAVGAVGAPDEADNADEAGDCEDDG
NGNKWNTKGWEIFEQFQARNREKYSFIFDTNVEEGSPFCKMRENSHDMRSVSDVNGNTSLDSVYGDVKSDLMHNLREDCD
LGLYKKDHYSVIDRNNVPFKEINDIMPMDIRNVKQNNVKELLLQKGWLCTGVKKCEEEEEEEEEEEEEEEEEEEMYKEE
YNNMYFEKDKGKEDIYQDVFNKTFCDDKSTEVNIKTNVCNSYSSYSSLNINFFCLFDDMYENFFKNNFEDREKMIKILNM
NKDLCYNQLLTFYKKKLFFEGIKEGERSSTHTHLDLHNTYNQRIKESIAMQQKCTSTEGSTEGTTESSTYDVVHGEDAHV
GSITLIDKRESDFSGKIDYLLPPNNGDNINSSNNVLGCFTEYTVKGEYSGTTTLPLPLLLVKEETEHMCKDDDGVMNHLK
TDDHRVNNTLQLMNRSSSEEEATAMEPGEIPNNERTLHVGMKSGTEWKHVIGNTVNGTGGIGTRGGNIIKFKGEQEDVCK
GESSRGDCKDITNVRIDEIVKKDVKEVVEKKLADISCEHLSDYSFESDDAREMVEHILDSPKRMTKKDSSNGGSSSGYCG
GSECSTADDRGTLEFEINVRDMCEEEGSTMFKYIYHKIKCIRNNIWTQSIDEMQNREMHELFVMGRQKSEEVAKREEQVQ
LTMQRMSPQQTQLEVHNEGISTVPPTDIYYFNVYTNLWENVDLNVSHKLLEAQGAKKKIINKFYRSDHVGEKYITFSEWS
IYNLLVSKICKHFDVKKFEDNQLKMYNMDKFQYELKKRNTYNFGIKIIGDSNGTSKGKQREKRGRRNCKRNRNRRLSRIS
EEFSDMNHDEEEEDEDDLDGGEDYIDGGEAEVDEDEVEEEEEEEEEEDEDEEEEEEEDVEIDDVEIDDVEPFYEEEEQQT
KFGEEGGQSSGHKGVAVITANSGLAKGGNNNNNNNNSSNNNSSNNNSSNNNSSNNNSNNNSSNNNSNNNNSSNNSSNNSS
NNSSNNSSNNNNNNNNNNNNNNNNNNNNNNSSNNNNAIPRSSSRIFCRNKNRSGLKIYGSSSEMNGRNSIDRKPVKELKD
GKITIVSCEKNGKMDDTVSTTSRNGGEVGEGGEEGNAEEGLGQASRSLSMSLRRKKRNSLLSGNSAESGLSRVNKRKSKR
LKIGEKEGKYVDDLQQEEGVVSQRGHRSGHYGVIHRGHPVSSSSCGRNRKVHIFKKRISRRSNFNTLTDKKMNVYHMIQL
PDYVSHKELIRSKNECLPTYILQYEQLRKNECIFFNIQSHYNNFINNVYHFAISYEQSLKHNEYLNNTLNNVKARLHIKR
LCLKKNITIRDRIFDVSSTYFNDLYTYDSKNNTYVFYKSKESRMNKMERAIDNQDYYYSMYVNDYIENELLNKGKRKKKK
NYHHHNSSHSGKSSGDNFDFASERAVVRKISSSYEHSGNHVDNMGDYGNDFPEKRETHHGSANHSIGGDNTRNDAYAISD
VAKNEHQMCDQLNYINYFVDHVQYDEDNSNGETCKNVMSYSERTVEEEFLGEDMLGGGLLGDEILGAIEKSSIEQIESSS
MGKMEKSRMEEVHTFSPEQSATFPPELLSTYSNNFEEESDKKEIIKTKNDFFNYYNQNDNESFFPNFQKQENGNEQDFNN
NNKEFYFNGSINHDDIIQYIDIQ
```

2216 - 2235:	EEEEEEEEEEEEEEEEEEEE

A0A1C3KX89 **A0A1C3KX89_9APIC** (1282 aa)
NTF2 domain-containing protein. *Plasmodium ovale (malaria parasite P. ovale)*

```
MNRGSDTKQYNKSKNKFPVFFYKNKYPCFKQTNSNSCSNHHTNDNYNSAFNSSVNNTQGNSSSSNTGFFYKKKNSLTVHG
HNRNSSTNMLGYNDDMYSFEKQKALSGGGGTSSGVGPYHIDNGHSHVNRGNGSVSAVGSGAVGSGAVGSGAVGSGAIGSG
AIGVGGKPNQKNAYHFHQRKDAKNNYEDYIGSMQDASNGGNNVSLSHAQRAYKSYAAENNHDNYLNMGMSKNSNRYYEAN
DNAAAGINNLSGQKNINYYSTGQSNAHNGMMSGSEGARPQGYSGVSDRVLHMGDEGSLQKSLLAAGDNKKTLLSMISSNE
GNKVKNKNKSKVSNDHYNFGEGEDAEGGNKIGKMEKREEEHGKIGKIGRIGKIGKIGKIGKIYKSNSNSRAPSICSSSNR
SRSRSRSGSRSRSRSGSRSRSGSRSRSNVPPKEMHENRDTSGGKNETACNESLVGNLNNAGPSGSAYSIAYMFIYQYYYV
LHTKKEMMHNFYSEHATLLISFNYQSGDKTGISDKGIETGGGAVSVGLGIGVEMNTDAMCGVGMSSGLVSGLTTGGVSIN
AGKFFNLNEIKVEGCQRSENMMKFKSRKMIASYYENLDVNECTVHISSIEVVNLYNEIYMYIYGKIKKCKDTNVFYFFVQ
NIHLHKYNIYQYYVDVDFVHYYNTFEEIFDANRKLEQRKSRQYETRITNSGDRPSRTNTGKNEKKNYHTSSTCKSVLKRS
GKVEVEEEEEDEEDEEEEDEEEEEEEDEEDEEDEEEEEDDEDGEEDDEVEDYDEDDEEEVEEVEEYDEEDYDEEDEEEEE
YDEEGEDDEDEEAEKCNEDKIVDMGKKKNISTVHSKGGELGHTKKVEESSSGGSKNVKKGIISTGEGGGDVVVAKSTSQP
SSDKKPLEEDAVSGKTTGEQVKTLDEKEKPGESFTPSVADSKKGKEKEVPGSGKASTSSGKASIGSGKASISSGKAVVGV
DTALASSEKTSINNVKTVGDSGNYAIDGKGKKGKSENAWNVPNDVVIPKMENNLKEEKIASEVAKKKKKEKNKIDPNSWV
FRVMKNNQGANMGEKKSLAANIKVNNNQVKNSGDKRKTVLDGTENMKANDEEEEEEEEEEEEEEEEEEEEEEKKEEEINVND
KKIIIHNIHKNMDKKKINDCIIDRLKKYNDGHAVQIDIYQRSIKKLYANSYNYHNSYEKIKPTEYSYAIAELDCRQSQQL
LLDLGLYCNGIKLNIENFKNKRKTEIKKNTKKFSNTYNTSLEGSKMRDDKFKGSFYRGASATMTPVAASSSFRSKRNNIF
VK
```

1091 - 1110:	EEEEEEEEEEEEEEEEEEEE

A0A1C3KX98 **A0A1C3KX98_9APIC** (1057 aa)
Uncharacterized protein. *Plasmodium ovale (malaria parasite P. ovale)*

```
MIPKEKKKVLRSLARTVGKLSNFFDEHQIWKCFISNIYRYENEKSEKYNDFLTTFMNSNVHYCPLKANKKKLRSELIKYM
RKNLNEDDIFNVGFTAVRHLGRIKNAVLTALPGEGFKSDILSDHKKTARGTPDNGPGSIRSVWCSEEERLLFRDNLRILN
LGLWNNREEGAYEEEGEKKKKKQSALKKNINRRCGKMDMDDAAEGGCAKEEVITETSAPRNSTVGKEVEVGVGAEVEAAA
EGVEAAEEAAAEEVETAQGASLGRTPPSCGSEAVHEHNNQTKRNKKNFILKKGNYKNEIKKGVILIAHPLTSSPLWNKSV
ILITQKDKNNLVCGLILNKHPLYNHTMGLPNDKEIAKILNKLYSKKKKFLNDVADGIFTDQRKCIHTKGEKTTQTETGTP
NVKMIGTGEEEQEQEQEEYDKIITKEGKECVNMTNNERENRETALEKKHEMDLRKESNCVKNKSSNSDNSTTMQGESSED
FPTLKDLQEMFLRIQFRSSSKHYMNKRIKRKNNLFIMMDEHLLDIITHYIIKLNKVPLYLRFLPSYNIGSMTDIKNEMKK
LQFLNEFYKIYFEKYNKWKVVIINNRIHIFDKNKNKKKVENMTTNVHVKNEEGIENKELTEEEKARIHRKIKNFKETNRL
VEDYEDGDEAHYHQGSAETSHRHRRRGKSGAALRGTVKQQGYNDGQEKSHGEDPEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEQDDLDEEQGDLDEEEDGLDEEEDDLDDAAVEQAERNLDKMTSERVTATLPPGRQDAVIGIGSDAIGKEKLVRR
KKRGKRVKGDPSTKAVTSAKKVGINTVHKNYFVGNPVHLFWLGGPLPGLTILHNIRKISKNIVINDFIYEGYNENVDTTS
SCNQDVKDSMGYMVEEDPLTCADMGKVLVGSSENTNPSKNELMCQSSNIVEVGGKSTCGNVESEGCINRMEGKKLIKRFI
GKTTWDMNQLMDELKNDYWIAINCENRDLLSHIIFNSGNDFLNGTYGECTTGVSAYKGEHLWEKILSSLSTDYEAISKIP
QHVVDTVLKDFRGTDAE
```

695 - 714:	EEEEEEEEEEEEEEEEEEEE
696 - 715:	EEEEEEEEEEEEEEEEEEEE
697 - 716:	EEEEEEEEEEEEEEEEEEEE
698 - 717:	EEEEEEEEEEEEEEEEEEEE
699 - 718:	EEEEEEEEEEEEEEEEEEEE
700 - 719:	EEEEEEEEEEEEEEEEEEEE
701 - 720:	EEEEEEEEEEEEEEEEEEEE
702 - 721:	EEEEEEEEEEEEEEEEEEEE
703 - 722:	EEEEEEEEEEEEEEEEEEEE
704 - 723:	EEEEEEEEEEEEEEEEEEEE
705 - 724:	EEEEEEEEEEEEEEEEEEEE
706 - 725:	EEEEEEEEEEEEEEEEEEEE
707 - 726:	EEEEEEEEEEEEEEEEEEEE
708 - 727:	EEEEEEEEEEEEEEEEEEEE

A0A1C3L0E5 **A0A1C3L0E5_PLAMA** (156 aa)
Uncharacterized protein (Fragment). *Plasmodium malariae*

```
MEFMSYNESSNEIVQDENQEEGMNVSDESLCGKGAEQWEDVKYEIADDVFDGDANDYSNDYCNYGGGDNNVQRSDPILEE
AEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE

92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE

A0A1C3L339 **A0A1C3L339_PLAMA** (1176 aa)
Uncharacterized protein. *Plasmodium malariae*

```
MLNSKKYENLSKYDLNLSKNDIIKKKKKNDLKNILLFPSLFWFNGVFSPPIPLFKYDYGNTYNVRIKDYVTCSVHKHSVI
IRRIRKNEILSISMFNDKKVLSCLFYIEIGQLLELAYFSKRPFSFPPSTAFTNEKGDKEGEKKGKEEGMQVEVVEMENKS
MHVSPGRKTNYHLFCYNEKNEIHLYDVENNISVLSFCEKEQITSMHFNFLYINRKNSLYNKLQNDVYEGNIKVVNMDNVE
KKIEQKNRYCFELLQEIWTHVGSGSDSGSDSGGDSGSDSGSDSGSDSGSDRGSDRGSDRGSDRGSDILKSVFYALIYGDS
EGCVYLFIPQKKIKIKKILNKNEKIVFIETNVKEYFKIKSINDLLQKIKNNCYIFVAYKDKIHIINFYIFEIYFVVNLGE
DKIFSLTSTFNYDLEENYLSFSTKSYVKIFNINKREELLHIQLSAQHALERGNSSSVKSEAVNSNLMELYGDVVVRNNKL
ASSNCYYNDGGGVGVYCKADGVARIHAVEAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEQQGQKQKR
```

```
QQKRQQQQQKPQGRQGGGPSWEKIEKEQKNYICVYFSARESNIYISKGKGMIYVYNIRENKMINCFNLRCKCIFYLFHFT
LSKKEYLYVYDSEKYYCLYLINENNIIYKTFTLSAWVYHILCARTNILFSLGNENVYNIDLKRYKTAFFLKPIYYKNMNI
CVYLVKHPHLPIIAFINKNQLFGFFFQPLNVNGVDAGMEEVRCKRNETVIIPAIRENQNVISVCWFLKRKELLVADKRCI
NFEGYHNDEMLNVQGVCENGHHESTVTSIVYSEDSVQTREEWEQQKRKRRCERRCETEAIITSKKKYEHVHNKYYDTYLT
VLNENALYLYNIANAELIQLRHTHHDLLNSTIFPLKGRKKFTASTKLNDMYYMFIFSENSLLIFDENLKFASCKIKIDER
INKMYIQENIIFIHSNSYVYFSFLWPIVMCAYSKDILTSNTSTTEPIPDNHCHTKKYYYPEFTFTRIPLKQSLKIVLFDF
YYTGNDLYIAIYSKKKKIFVYRVVNVSGTSESVGASASASASANARNNDVTNKRADAWREDDKEKDKMNINLQIDSQLIA
QFHNFYIFDNINKVGSILSMKFFYSVPKKKIYLIFGGLEQFLFSWDFLKYPLVRRK
```

511 - 530:	EEEEEEEEEEEEEEEEEEEE
512 - 531:	EEEEEEEEEEEEEEEEEEEE
513 - 532:	EEEEEEEEEEEEEEEEEEEE
514 - 533:	EEEEEEEEEEEEEEEEEEEE
515 - 534:	EEEEEEEEEEEEEEEEEEEE
516 - 535:	EEEEEEEEEEEEEEEEEEEE
517 - 536:	EEEEEEEEEEEEEEEEEEEE
518 - 537:	EEEEEEEEEEEEEEEEEEEE
519 - 538:	EEEEEEEEEEEEEEEEEEEE
520 - 539:	EEEEEEEEEEEEEEEEEEEE
521 - 540:	EEEEEEEEEEEEEEEEEEEE
522 - 541:	EEEEEEEEEEEEEEEEEEEE
523 - 542:	EEEEEEEEEEEEEEEEEEEE
524 - 543:	EEEEEEEEEEEEEEEEEEEE
525 - 544:	EEEEEEEEEEEEEEEEEEEE
526 - 545:	EEEEEEEEEEEEEEEEEEEE
527 - 546:	EEEEEEEEEEEEEEEEEEEE
528 - 547:	EEEEEEEEEEEEEEEEEEEE
529 - 548:	EEEEEEEEEEEEEEEEEEEE
530 - 549:	EEEEEEEEEEEEEEEEEEEE
531 - 550:	EEEEEEEEEEEEEEEEEEEE
532 - 551:	EEEEEEEEEEEEEEEEEEEE
533 - 552:	EEEEEEEEEEEEEEEEEEEE

A0A1C3YJW2 **A0A1C3YJW2_GIBZE** (1214 aa)
Zn(2)-C6 fungal-type domain-containing protein. *Gibberella zeae (strain ATCC MYA-4620 / CBS 123657 / FGSC 9075 / NRRL 31084 / PH-1) (Wheat head blight fungus) (Fusarium graminearum)*

```
MDVTKDPAAFMHTPPSASASGRRDSFQWAARQDSGNNQDILPGTGVRAQSPTSLHIRSVPFSSSASAQLFARPQTPDAGV
GCRNRQNLPSPASTDLSPQKEPWADDYISRLLRRVRHHPNGGQRANTSPVMADFLASLGFGGAQTTAVSNNSQCDSVEQL
QNQLRGILDAKVTPTRAEHVAITTELRATVRFQLTASELENGNHDNPNNLDPALGGAQSTEVNGDQDAGQPSRVVFANDT
IMNQPQDDPALQRSVAKHIISTISSADGSTWTVREVSRGAQGWTFTYLCKDSFQHWSRQTAKNPLKTIVGEFTRPAFDCR
GSIVIAFNRSSRSISVKYDHTPLHKTVAELAAHFKPPPRQLGPGAQKLQEQQQKAKEKTLKKPRGEKKDKKERKKRDSVK
AQDENGNPRKRKKKTNGASQPETTDGSMTPLDYPGASAVGGQTDPSYMNGGQAPDNTGHQGFNDYPQGLMGDASGATNGT
GSQQAGGQPGSVTFPVNVSAAEAARRREAATAMLNNAGVDPTTLSPEQFGIFSNQAPELQRESLNMLVNYGAERLRIVHP
SNREGSAQASASTAQSSQSSTGPRTTKELVPQSGAHDSPNTDFEAQAASQTADDTSSPKRKVRKMGKSRTACFPCKARET
KCPRERPTCTECSNHGTACEYAPQKPRNRGKKTKKSEEIDIDDDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEQQEDAEDAEDVEAEGDEEEDDDDEQAASQDYSHPQMNIGNMVTNTDATTQDSHATQSNYYQSTSSLAMPQA
NPYPNNPQPLTTAASQRNNYSHALPEVIQPVHHVPPPIPAPAGTIAPSETRRWTAFGSGGLNGASDSSKARRGLPSEPPR
PTTQSPSTTNVQLSSWGQSSNTTMPAVPATTMATVSPQMSYDSRSSHRSRQKNQSLSNDSAQQAAAMASTAMPQAQVQVH
AQAQARQSPVAAAAMMAQARKSPYQQVAVPRTTSRTSQRNQSRTPVTEQARGYQPPPPVDMGQQQSARPGAHYDTSSSHM
PSGSGYNDYGRYCGANTAANHQAAMSAASATPSTMGTSCQSKPATANQWSGSSSRNDRSYGSNSSYQTPNIYTKTPAAKS
VSASGQNFKMRPGTQQQHQQQPQHAHGSSNSYSQQQQATYPAYSGSTHQNQQGQTSNQQQQQQPPSWYFQNSHNPSMHHG
SQSSGYNYESWSGV
```

685 - 704:	EEEEEEEEEEEEEEEEEEEE
686 - 705:	EEEEEEEEEEEEEEEEEEEE
687 - 706:	EEEEEEEEEEEEEEEEEEEE
688 - 707:	EEEEEEEEEEEEEEEEEEEE
689 - 708:	EEEEEEEEEEEEEEEEEEEE
690 - 709:	EEEEEEEEEEEEEEEEEEEE
691 - 710:	EEEEEEEEEEEEEEEEEEEE
692 - 711:	EEEEEEEEEEEEEEEEEEEE
693 - 712:	EEEEEEEEEEEEEEEEEEEE
694 - 713:	EEEEEEEEEEEEEEEEEEEE
695 - 714:	EEEEEEEEEEEEEEEEEEEE

696 - 715:	EEEEEEEEEEEEEEEEEEEE
697 - 716:	EEEEEEEEEEEEEEEEEEEE
698 - 717:	EEEEEEEEEEEEEEEEEEEE
699 - 718:	EEEEEEEEEEEEEEEEEEEE
700 - 719:	EEEEEEEEEEEEEEEEEEEE
701 - 720:	EEEEEEEEEEEEEEEEEEEE
702 - 721:	EEEEEEEEEEEEEEEEEEEE
703 - 722:	EEEEEEEEEEEEEEEEEEEE
704 - 723:	EEEEEEEEEEEEEEEEEEEE
705 - 724:	EEEEEEEEEEEEEEEEEEEE
706 - 725:	EEEEEEEEEEEEEEEEEEEE
707 - 726:	EEEEEEEEEEEEEEEEEEEE
708 - 727:	EEEEEEEEEEEEEEEEEEEE
709 - 728:	EEEEEEEEEEEEEEEEEEEE
710 - 729:	EEEEEEEEEEEEEEEEEEEE

A0A1C6AU91 **A0A1C6AU91_9CLOT** (420 aa)
Signal recognition particle receptor FtsY (SRP receptor). *uncultured Clostridium sp.*

```
MFKKLFKFNKKKEEENIVEENKKSEEIVELEDDNKESISEVVENEVESEEEKVSEASEFNVEPIEIKEEIIEVEKNVEDK
EDTENNSLEEEEEEEEEEEEEEEEEEEEEEEEEEEESVGLFARLKQGLTKAKQGITDKIDAVLNSYTTIDEDLLEELEEI
LITADVGVNTTMEMIDRLRDAIKSKGITDPLAVRDELKAIISDMLGEEDSKLDMEKGPNIILMVGVNGVGKTTTIGKLAN
RYTKQGKKVVLAAGDTFRAAAIEQLEVWANRSNVDIIKHQEGADPGAVIFDAVKAAKARKADILICDTAGRLHNKTNLMN
ELGKVFKIVDREYPEAKKEVLLVVDATTGQNAVSQAKTFKEVADITGIVLTKLDGTAKGGVVLAVKSEVDVPVKLIGVGE
QVQDLQDFDSKAFIDALFGN
```

89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE

A0A1C6DQ56 **A0A1C6DQ56_9CLOT** (421 aa)
Signal recognition particle receptor FtsY (SRP receptor). *uncultured Clostridium sp.*

```
MFKKLFKFNKKKEEENIVEENKKSEEIVELEDDNKESISEVVENEVESEEEKVSEASEFNVEPIEIKEEIIEVEKNVEDK
EDTENNSLEEEEEEEEEEEEEEEEEEEEEEEEEEEESVGLFARLKQGLTKAKQGITDKIDAVLNSYTTIDEDLLEELEE
ILITADVGVNTTMEMIDRLRDAIKSKGITDPLAVRDELKAIISDMLGEEDSKLDMEKGPNIILMVGVNGVGKTTTIGKLA
NRYTKQGKKVVLAAGDTFRAAAIEQLEVWANRSNVDIIKHQEGADPGAVIFDAVKAAKARKADILICDTAGRLHNKTNLM
NELGKVFKIVDREYPEAKKEVLLVVDATTGQNAVSQAKTFKEVADITGIVLTKLDGTAKGGVVLAVKSEVDVPVKLIGVG
EQVQDLQDFDSKAFIDALFGN
```

89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE

A0A1C6X2R4 **A0A1C6X2R4_PLABE** (2623 aa)
Uncharacterized protein. *Plasmodium berghei*

```
MNKNFNISNYNLDLIKCLQNESGIYFILDPTKAIHDKKHSDVYDIFIPENSDGVTLHVQKVNNEYKCIGVSITKRGIDIN
```

```
TGTRIFNTKIADWLEQLFNFNKTLGSNNNESNNANSNSNENEDGNNNTENRTNNLNGKNNWSNMERNGANNHGFGAIVNN
KNTSINANPINNIGATNNNEQGDAIGDDKDANGGDGNDNLENSDDNNNSIINNGNNNKYNNNYNNVRHNLSNNQAGAPIA
NLIKNSKGGYDNFENNDNYNNAINMPNKTKNSKNAINQGNCNLNVNSNLSAHIIPSSNLSSPQSKKQNQHTKQIRLNQMN
NSHKSHLMQYHNSNYDDKNSKLYNNVNSSNTVINKHISSENSGVLHASASNNNDAVKVNKIGCNTRQKNGPHILHNGNNN
RDGNNNSYKVQQQVYNENLGYRPTLFNLLEVLSNHNITTPDQRVCIRGIVTDFLNNELPHGKIYAYIGAVVGHDILHDII
KKLEKDPNRNAVPDASGLARIEASFGLSKSSYDFMNHNSTNSSMNNIPNVLFNNRNLNSALLNNHIYSNILSNVANNNNG
NIGDNMGHSGMLNADTEKIANNKTANDINNMMMKYGDNDKSGGSYNNNMLNINKKKALNMLNMRYMDNNNMTDMGNLGIT
NMNNTDNSYMNQMNIDLANLENLNNAKNSGLSVHDYLYASKNFHNGNPLNRNNNIGEDEEELMKVIKKNIETYKMNNIKN
ILISSVFGRIKWLKIMNESPHAYLYGHSIVKYGNKLYMFGGTNNKHKKVPFNHTLTFSLIYYNYKLLPLSGNYPEERDGH
TTHLVSLKSGLSVFLFGGANNNVYYNDIYILDMETRKWSKRIVNGKLPLPRHQHCSLVYPAKSEHLRGEKLNLTEGVIVY
GGKCLYNNNIVNLNDMWIFLFQANMWIRINYLGDQIPNGRYGMNLIWSDTNTLCLFGGEYLYSDKNCKTRKLLDDMWTFR
LNTPVLINNAEDIGTDIKHLPCENAINTQSELHKHQKGTKSDPHLNNQNGNNGISIHDNNNNNDNCYGQTNNLNDKNGIN
EIDNKMGNNNNESQFVDNKGSIENNNINNNNNINNNNINNNNINNNNINNNNNNSNNNNNSNNNNNSNNNNNSNNNNNS
NNNNNSNNNNNNSNNNNSNNNNNNSNNNSNNLINKIKITGEWKREIYEGNIGPRSNYSNIFITQRHQDFKGAEPKTIEKL
MLLCSGITYDNKLKIVSSDEIYVYFFSQKRWYLLKGKLYNEEYMYSARQRHVGCFFESKNVLGRSNRNPVPCIFIHGGFK
KNSVFGDAWLLSLTGENPLRLYEYDTCREKISTTQMPLYYFRDTHSISLLYTFCTLQKWLFGAFANLVDNSVYAINPAEN
VFIKYELTPEHDGMVSIQDDGEGLDFNAMNRILRMYGNYKNYDNNSFYNNNNNNNIKKHSLPNNDDSDSYEMDNYNENEE
EQEYNEETNNTNELNNNENNNADQNNNQYVNNNTKVDQMQQNAENYMKSEKGDGEKIYNNNLSGSNCEGMIKKENDTRNK
NVIVGKKKCTWSDSFYYKKKNQHYFYNDISNSIFDIKYGVGFKTAFARIASSCAIMSRTINTIGIGLLSLELMNHCDAKE
LATPLCMWKLPNKELINRNIANKSEHRHHQKLLMSYTPFNSPSLLAEQINILGTYSGTRLLYWNFRDDMDFIIFNPTNNN
IYLSSSPLSIDELKNKKQKNAQGEGSNFNSKYQGVKDIKFANRVIKRKGVFGDDENLKKLKTDIDNPDEEIEKDEDIVAD
DKNNNKYNNIDDKYNKDEDNIKKELDNMSTSSKNNIILDGDNNNNDENKNVNSTHYKEKLKYEDQLKYNNDNYFKKRMNL
FEYNSHLTSSISKEKYNMNQIFPLWDHPKDSIDYCLSTYLYWLYLRRSTNIFLQNTLLIPTSMRREKDMNPNKNNNDNNG
KKKGTKSTKLRNKKTTKQNDVNNIQNDEKIADIEENNGEIGNVSEIVPENNNSFVKFEQIQEKNDDNNHSNVQNEADTNN
ERGENISEQNQNTEINNNGIKNENVCTNKVEEEKEENNNPEDGKENNHCENDTNGGLTKLEKQKLEEALEYGISQDLQPQ
NSANKNEADGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEETSKNNEDNGNINETNNDVENEGNNNVENEGAKVEGEVNEV
GAGVVKTETPNEMETENNADDTEKNKKSKKENKNNVGKTIDNANEDSIANRRKRRKKKDGLSTGTVANGKKNGEIEKMKK
ENYVNVYMENFKIKDEYYINDPSKYTLYHFLRRKLYKMVESHYLFTPSDHTYGSFIMMGFLNDNNNTSIEVNRVCETGIL
LYYKNRLIKRLDAPFIDTPYNLFLSKYPPNPSLYEGNLYKYALTVIVNVPNWLKPSVSKQEFVHENNHAFLVFKKKLVTL
IKHYLSICEDIVKLNKWRESRDMKLKKYLEKMQNQSVKSRNDSDYENDIDNNKSKNFNIIYNNDEEGDNYMNDQNDGNKK
KNEEINYSGKNKTPYTNDNEPILHKNKKTKTNNNDDLNKRDHNPTSENESANIDNENNQENDVLEGEKEQEDDEYDEADQ
EAEDRPNFEDEKDEHEENEEEAEEEDPDDEEYNGEMDDQKNRSVEQETEEEMIEDEEYEPDDE
```

2091 - 2110:	EEEEEEEEEEEEEEEEEEEE
2092 - 2111:	EEEEEEEEEEEEEEEEEEEE
2093 - 2112:	EEEEEEEEEEEEEEEEEEEE
2094 - 2113:	EEEEEEEEEEEEEEEEEEEE
2095 - 2114:	EEEEEEEEEEEEEEEEEEEE
2096 - 2115:	EEEEEEEEEEEEEEEEEEEE
2097 - 2116:	EEEEEEEEEEEEEEEEEEEE

A0A1C6YQY0 **A0A1C6YQY0_PLACH** (1491 aa)
Uncharacterized protein. *Plasmodium chabaudi adami*

```
MKVQQKRNIKNKDEKNIIHSEKKTHTNSCDNNDTRHNKSSRLGGSNEISNKKNTEKDAKTDENMKSKTVSGSNNKSKMPE
KKTSSRNTTDTNTRDNAKMNKNEKGDTNDSKKKSVSNSKIKSSRHNYSNSSSNITKSSEDSNKKNKNGSSITSEDDTKEY
SEPITRNSLKRNSSLLKNVKKKNTSKNDSDDMLSDDNYEQSKSLKNSKNKNNKNSKNKNANDSDSDSNNSNEGNFYNLKK
RTRLSNCDSETLKKQANKKDGAKKGLLNNKKNAKGKNENDYSSSEDGTNKKGKNKRSGSSRYRGKSIVDSEEEEDDDEEE
EEEEEEEEEEEEEEEEEEEEDESDEGYKRSRSSRLSRSKNIKNKKNGKNMINRNSRNSKLLKKNKNIKSGKDKGVSNNKS
GKNQIKNVKNEEEYSYFDDYIYSNEERKAILEEREKKRQIKEGYIKKMKLNKYADDEAIEFINNPNYIMVLLFLTIYKNI
IKIDWNFKDIDEMFQNKENTEFGRNLILKLFFLLGRYFNSKSVFMYKYISRIFQDKQNALVKVVNFNELFPLLNEKQNDK
NGSGGTSKKRKDKRGKKNKNLVKTDEMDEELAEHDDANDDANDDGNEFDEDVLTHEEEGEEYDESEEEEHNNEVKENSEN
EQTLSEAEKDTNIVKEENNIDKKEDEVNCKDSLELEQNIKNEIENHGESKTEIVTDQVVKSEQNGEQVQDETGLSKKLFL
EWSDLSIISKLRIIRMLLNLVLCESSNLKKMLLTEEINYNNGYLGKINNDKYWFIFNDTINIEFKLYVEREEKGIFEFVC
DNDEVLYTIGYNMLRHADTKFMGDIIIEKYNKICRERRNRNRILKQQKKLFDDLNNEQLLYASKKRQHKQVEHFSFDNDK
MRKKKNENIITNPYSLQKNSYQKNDRSYRLATRNAQKENGGDDFESWKNGGNINGNGLGVDNNLNDNQIVGLNPMIDNVN
YQNVNDVNNLNGGVVVKVPLKRGRKKKSEKKKRGRKKKIIIEEGMDPNNPLPNEIKKPVKVKRAPYTKRASKPIVSIKYG
TRSNSLTKYEADQMQFGGYDMNNHALQNDEFYKNNNLDNSKFFNPNMHLNNFFNPNMPGAYNMHNNMINMRNQKANPPNN
YNFPYIYNPPIYNQYYMYNGSMYMYNAGMNGNPSTVKDGKGESGYMNDTMGVNLRNGIGPNTNNNAIRSDNESGKVAISE
NGNANDVSGITTPGMNANGGELGSMANMGSVNRPNNENNTIDPNNNKNNENDVNYNDSMNKYNSFMANRNNNPVNNMNAP
PMYNNMYNLKFPYVNNDMMNYNYNLNNYQNFNIDKMNKNMYKRYSNFIPNNFPPYNNMNMYPGFNSYNMNYQPGQVMKNF
GNEPGGFGEMNENNLTAPNNGGSDMMSGVENVSKMNEVSNLNRMGNMVSSPNVGTIPDMNQQENNPMNVNNEIMKNDGIL
YGNETANKGGYILNNDNGQMGDPNGINVDVTNNEANLSVENSTRDIDGNGI
```

318 - 337:	EEEEEEEEEEEEEEEEEEEE
319 - 338:	EEEEEEEEEEEEEEEEEEEE
320 - 339:	EEEEEEEEEEEEEEEEEEEE
321 - 340:	EEEEEEEEEEEEEEEEEEEE

A0A1C6YU60 **A0A1C6YU60_PLACH** (1492 aa)
Uncharacterized protein. *Plasmodium chabaudi chabaudi*

```
MKVQQKRNIKNKDEKYIIHSEKKTHTNSCDNNDTRHNKSSRLGGSNEISNKKNTEKDAKTDENMKSKTVSGSNNKSKMPE
KKTSSRNTTDTNTRDNAKMNKNEKGDTNDSKKKSVSNSKIKNSRHNYSNSSSNITKSSEDSNKKNKNGSSITSEDDTKEY
SEPITRNSLKRNSSLLKNVKKKNTSKNDSDDMLSDDNYEQSKSLKNSKNKNNKNSKNKNANDSDSDSNNSNEGNFYNLKK
RTRLSNCDSETLKKQASKKDGTKKGLLNNKKNSKGKNENDYSSSEDGINKKGKNKRSGSSRYRGKSIVDSEEEEDDDEEE
EEEEEEEEEEEEEEEEEEEEDESDEGYKRSRSSRLSRSKNIKNKKNGKNMINRNSRNSKLLKKNKNIKSGKDKGVSNNKSG
KNQIKNVKNEEEYSYFDDYIYSNEERKAILEEREKKRQIKEGYIKKMKLNKYADDETIEFINNPNYIMVLLFLTIYKNII
KIDWNFKDIDEMFQNKENTEFGRNLILKLFFLLGRYFNSKSVFMYKYISRIFQDKQNALVKVVNFNELFPLLNEKQNDKN
GSGGTSKKRKDKRGKKNKNLVKTDEMDEELAEHDDANDDANDDGNEFDEDVLTHEEEGEEYDESEEEEHNNEIKENSENE
QTLSEAEKDTNIVKEENNIDKKEDEVNCKDSLELEQNIKNEIENHGESKTEIVTDQVVKSEQNGEQVQDETGLSKKLFLE
WSDLSIISKLRIIRMLLNLVLCESSNLKKMLLTEEVNYNNGYLGKINNDKYWFIFNDTINIEFKLYVEKEEKGIFEFVCD
NDEVLYTIGYNMLRHADTKFMGDIIIEKYNKICRERRNRNRILKQQKKLFDDLNNEQLLYASKKRQHKQVEHFSFDNDKM
RKKKNENIITNPYSLQKNSYQKNDRSYRLATRNAQKENGGDDFESWKNGGNINGNGLGVDNNLNDNQIVGLNPMIDNVNY
```

```
QNVNDVNNLNGGVVVKVPLKRGRKKKSEKKKRGRKKKIIIEEGMDPNNPLPNEIKKPVKVKRAPYTKRASKPIVSIKYGT
RSNSLTKYEADQMQFGGYDMNNHALQNDEFYKNNNLDNSKFFNPNMHLNNFFNPNMPGAYNMHNNMINMRNQKTNPPNNY
NFPYIYNPPIYNQYYMYNGSMYMYNAGMNGNPSTVKDGKGESGYMNDTMGVNLRNGIGQNTNNNAIRSDNESGKVAISEN
GNANDVSGITTPGMNANGGELGGMANMGNVNRSNNENNTIDPNNNKNNENENNVNYNDSMNKYNSFMANRNNNPVNNMNA
PPMYNNMYNLKFPYVNNDMMNYNYNLNNYQNFNIDKMNKNMYKRYSNFIPNNFPPYNNMNMYPGFNSYNMNYQPGQVMKN
FGNEPGGFGEMHENNLTAPNNGGSDMMSGVENVSKMNEVSNLNRMGNMVSSPNVGTIPDMNQQENNPMNVNNEIMKNDGI
LFGDETANKSSYILNNENGQMGDPNGINVDVTNNETNLSVENGTRDIDGNGI
```

318 - 337:	EEEEEEEEEEEEEEEEEEEE
319 - 338:	EEEEEEEEEEEEEEEEEEEE
320 - 339:	EEEEEEEEEEEEEEEEEEEE

A0A1C7M999 **A0A1C7M999_GRIFR** (661 aa)
Uncharacterized protein. *Grifola frondosa (Maitake) (Polyporus frondosus)*

```
MSRQQYDSTTSEDQTPKTTPSRRSSEIESEQIAEHHHDPTTAYEGQSSTPQSPQAVSSSSEGYPSWLPKRPPHPAPRSTL
QSSVAGMFSEPGPSSEPLAVGRKPTPRSVRIVSLQSTAQAEKRREPTDQSRALSGPAHARFDGQLPKPRFRSPALHLELL
RNPSWQMHFLYFLYPVFVFAHIPLQTFFDFNAVFILLLVAKFPNPEAPGVPGSGRDWALAAAAYIACWFTWIVVVFIVYE
LTYSFYRRWRVKRPLMLPIYFSSAAFNYVSMTSYTNFCFMYHIRISAFTGEHGSLRDGLAETFYYYSQNLATVALLTPRA
ALSLALLLAFSSPQPGAVALADAGISSRDGTFFRADGTLTDYARGVLIANAAWTAWRMLLLIISWIGLWILSGQGCAGLC
GPRFRWEEEDAEKMAAVHNDTISEMDSLHWSWKECTLLRIKDAYDFCLTNKHPHVAKDGEQAVPLEGMERIFAAVGLPSG
HLPARRGVLSDQLFESPAHTPVLELDEKDARVESAPELPRVIPPAAAVQGREKQGPEPSGPLMKLPYPFTGYGSQVSSEE
VVPFPPSPAIEEREVPIENGDEEDGERAEEEEEEEEGGGEEEEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEILGNQ
LHLDTHSNSGDHGEAPRLRRT
```

608 - 627:	EEEEEEEEEEEEEEEEEEEE
609 - 628:	EEEEEEEEEEEEEEEEEEEE
610 - 629:	EEEEEEEEEEEEEEEEEEEE
611 - 630:	EEEEEEEEEEEEEEEEEEEE
612 - 631:	EEEEEEEEEEEEEEEEEEEE
613 - 632:	EEEEEEEEEEEEEEEEEEEE
614 - 633:	EEEEEEEEEEEEEEEEEEEE
615 - 634:	EEEEEEEEEEEEEEEEEEEE
616 - 635:	EEEEEEEEEEEEEEEEEEEE

A0A1C7N855 **A0A1C7N855_9FUNG** (419 aa)
Translation initiation factor eIF-2B subunit beta. *Choanephora cucurbitarum*

```
MTIPKALEAQVSQFILKLKTRQIIGSYEVAKETALILRQAISTTRWYDVDLXIEFITQLGSRLVAAQPKELAVGNIVRRV
LKIIREVARGELNDATNNDFDDEEEEEEEEEEEEEEEEEEEEEQNQTKSVFAHQKASIMNDKHRLLKQSSMFNLLSDGPGK
RHETTPQNTYNLKPLIIQEINEEIIADLESVYKGIADQATDFIHAKNKIVTETNSVDLSEVIMTIGKSRTVQEFLIRAAQ
KRKFQVIVAETSPTYQGHDMACTLSAAGIDTTVIADSAIFAAMPRVNKVVLGSHAVLANGGLVAVTGSHLLAAAAKHHST
PVLVCTALYKLSPLFSYDSDTFNVAVTPHDVLHYQEGSIVDKVTISNPYYDYVQPELVSLFIHNLGSAPPTYVYRLINDN
YDQQDATLTNIFTQEKMSP
```

103 - 122:	EEEEEEEEEEEEEEEEEEEE

A0A1D2J589 **A0A1D2J589_PARBR** (486 aa)
Uncharacterized protein. *Paracoccidioides brasiliensis*

```
MHGEGEFDLAILASQRNDNATMGVLSPIATATATMTEPARAKTTKTTTTTTTTTTTTDSSMHLPFSDSAIDMDTESSGNA
DQTPETTTIPTTRDTMNATGKSHLQSLTTITTTMIKERLIHLTHLITDSDSHPKPDNRHNKDQNSRNEYSNSSPYHPLTS
HATSPSTSLSWSPQKSIAINRYLDGIEALLLALHITGFSSGASSEEEEEEEEEEEEEEEEEEEEEEKEVKVDRGENERKTN
HCCTLSNNHHDPRLACISLEAGCQNANTKPHNQNQIQTKLDSQLDDVIRDLKVVTGSLEQRRAECLHLNAVFTMKCEKLA
QRILDLEEQMEELRAKKIENTIELEGLKGTVRGLEGWIKRWKMRQCEDEEGEEGRNSKHAWSETSDHGRGQWGKPGRLLW
GGDGDYDSNDGDVDEDTLMDGVSAWLRDWRDVEEGFRIRARLRERMKAVRRGPGKILLAANNLLQTFDKAVRAPLWENGG
GGEVGI
```

205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE

A0A1D2J690 **A0A1D2J690_PARBR** (619 aa)
Uncharacterized protein. *Paracoccidioides brasiliensis*

```
MAEEPEQIVPNMDSKSRRSFGDGLRRVVKKFTTRKGLIGEYNYAFLFTPNLPLMTSRQRSAPFFGLDDRMPVVLALILGL
QHALAMLAGSMSNLFPLCFLPPHSTLRGEGGEEEEEEEEEEEEEEEEEEEEEEEEEEEELITKHQNPVITPPILISSSSAAT
LPPSASQYLVSTSLIVSGFLSSIQMARFHLYKTPYYVGTGLLSVVGTSFATIPVAVGAFAQMYASGYCPIDKETGIHLPC
PHGYGAVLGTSCLCALLEVGLSFTSTRGLKRLFPPLVTGPTVLLIGVKLIESGLRNWAGGSGPCASRPTEAVYMLCPTSD
APHALPWGSAEFIGLGFLVFLTIILCERFGSPIMKSCAVVLGMLVGCVVAAACGYFDRSGVDSAPAVSFVWVHTFPLRLY
PPIILPLLAVYIVLMMEAIGDITATCDVSRLDVEGPLFDSRIRGGVLADGINGLLAGLCTITPMSVFAQNNGVISLTRCA
NRQAGYCCCIFLVVMGIFSKFAAALVSIPSAVLGGMTTFLFSSVVVSGMRIIATIRFTRRNRFILTATLSLGMGATLVPE
WFAFVFTYQGGNKAKQGLLDAVELVMTTGFAVAAFIALVLNLVLKEEEEEEEEEEEEEE
```

112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE

A0A1D2JNS5 **A0A1D2JNS5_PARBR** (247 aa)
Uncharacterized protein. *Paracoccidioides brasiliensis*

```
MSTRKRARGDEEEELVALPSDESEEEEEYEESDAGDEDEEHESVSEDESEGGFENGEAEGMEPIKPTNELSRIFPKFPST
PASIHSTQSPTFGGFWIIADISISPPTAVHKKRKVVPGPNAEVTGEADGVAEEEEEEEEEEEEEEEEEEEEEEEEEEEL
DETENGLEAEYEDGEGDAEADAETEAEKQKENGAASTVPTAKGAVASDVPEVPASAPAPAAKATANGAPAVASVTEVEGV
GGAGDGE
```

132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE

A0A1D2MKQ9 **A0A1D2MKQ9_ORCCI** (452 aa)
Troponin T. *Orchesella cincta (Springtail)*

```
MEGGLHSILITIRVKKHFSGKKEAKRSSLLLIPWLGSVSEFRTLRGSLRISHGVATSESHQLPKSISFLAFKNTSNQSCR
TKKNTLRRRSNRKSQASKKEDIQPDFVKRAQRKQGALDEELAVYIEEWRKQRRKEDDELQRLKDKQAKRKVVREQQEKDM
ELRKQKEEKDRQAAVEDKKRKEQEEKMRRLQDIERKRQEKRDKGGNTGGMGGSGASSAEFHKTKEQLEEEKKISLSFRIK
PLTLDGVSASGLKNKANDLWENIIKLETEKYDLEERQKRQDYDLKELQERKKQQLRQKALKLGLEPEALTGKYPPKIRLA
SKFERRVDTRTYEEKRALFDGGYTKLTKEHTDKVWSDRIEEFKARPKSRLPKWFGERPGKKKNDPPTPEEEEDQAAGAGP
LALDLDEPEIFLLPEDEPPAEEEAPAAEPEAEEEEEEEEEEEEEEEEEEEEE
```

432 - 451:	EEEEEEEEEEEEEEEEEEEE
433 - 452:	EEEEEEEEEEEEEEEEEEEE

A0A1D3JC48 **A0A1D3JC48_9APIC** (315 aa)
Uncharacterized protein. *Plasmodium ovale (malaria parasite P. ovale)*

```
MKVNSKKFKHFSDKPEKLISKSPFDKSSTSSVNYNSVYGGRTKKLTKSNHNGVQVNLLFNLFALLLNKCNRNGISKFRVV
IVLYEVLVLHVTGKSGVEANSDKLQEGTNGTSFASFFDLSTMQAYLQKFVCYLKYQIICVTTQDDDEYCKNSHIVFLGIA
FFIIAVIGIIIIIFQKCGLCPCVPSISRKKKEVDFYRKQFEEMQLQMQMQEDYLLRALMSGESNGQEGEEGEEEEEEEEE
EEEEEEEEEEEEEEEEEEKRDKRKKKDEDKEKDEDKEKNKKEDDTKKKKVSMSTHNAENANSRNDNINIGYNATT
```

232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE
239 - 258:	EEEEEEEEEEEEEEEEEEEE

A0A1D3JKD6 **A0A1D3JKD6_PLAMA** (724 aa)
Peptidyl-prolyl cis-trans isomerase, putative (EC 5.2.1.8). *Plasmodium malariae*

```
MKRKKKYVYLEFSINSITLGKVYFELFSDEEIKKSVENFVSLCKGNLNYSIYTDDEMLSFKNCKIEKIKKNKCIKSGYLK
NKVYLHNNEWKNKYPIYQNKKYENVECIYGKYYNKEYTKRRHLNAGLLTVVQVENKKYSSIFKITLNKVPTYNNKNIIG
RVIKNMHILRAIEIIPVTSNWEPKINVYISDCNEVSESFFKERKASSRQSYIDGLFENLNHNEQGNEESDGVETGEREES
DEGGEPYDGDDNSALYANHPFKKHSPFLSNFDIKKERNKKIKITEKQKGIELLNKILSELDSASKEENFSKRSTKKSASE
HPQSKHHPYPQLQPEPQSSSSLQERTVRGDYPSKGTDDTSKNFETMEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEKKKRKKEEEEKKKKKKKKKKKKSNEGDSQQDQPLPCSNALPYDNNINKQMTERERRMFEIQLKINQSKCLNEMEIRRE
```

```
RMMMMSQGPNRGMGKFGEYTHYNFAQNANVKSVIQRRISTEGSGGREEKEKEKQKEPTGAHHSGSNRGCDIGGDKVSEND
HANGSDNADNHGIDLRKDDEDGKKSQLYNTSAVRVQSALNRKKKKREDTYELDNDINLYKKIKFNFSINRKLYEDKKKEF
KNNFYGYNLLINDNSTCTDKDKNKVVEFCKKQEELRSKISRKRKNDEGVFKNYINRRNKIYNKKLDRYFNKHTVEIRQNL
ERTF
```

367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE
379 - 398:	EEEEEEEEEEEEEEEEEEEE
380 - 399:	EEEEEEEEEEEEEEEEEEEE
381 - 400:	EEEEEEEEEEEEEEEEEEEE
382 - 401:	EEEEEEEEEEEEEEEEEEEE
383 - 402:	EEEEEEEEEEEEEEEEEEEE

A0A1D3LG43 **A0A1D3LG43_PLACH** (188 aa)
Uncharacterized protein. *Plasmodium chabaudi adami*

```
MFNDKVDKGDKFDKKEPCNISDENAENEKTSSHSPNKDKQNEKNQEIDQDKAEEKQKNQQDIDAYEDDEEEEEEEEEEEE
EEEEEEEEENYARYKKTTGTMKRINENTGTAYRNIEMNKINSVWMIKDKNNKTINVKWENKIFEKLFFETFENYVKKYIN
DYHPNWRDYPYNGSKIITTKHSYLNNIK
```

69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE

A0A1D3LG93 **A0A1D3LG93_PLACH** (906 aa)
Phosphatidylinositol 3-and 4-kinase, putative. *Plasmodium chabaudi adami*

```
MGSNSIAISQQMYFSTHNALRINEENDVISTLFYEINGHRHISLLIFPFYDVQMLKRLLIKKLDLPDIKVNDILIFYKGI
KLPNYRIISTYLDNTNRVDNVKKKKKKKVNKLYWAIKDPNPNASIRVIDNKSYPPFFENILNDIKLAFKKNIAPKLTMDG
TGGTYLLFNSKKKVCSVFKPADEEAFSPFNPRGYEGKIYQEGFRAGVLSGEGASREIAAYILDNTYNNFSNVPCTIMVEA
CNPHFNNKSNLKYIYNENTLKWKCGSLQEFIDSRESVGNYDHKQFSIRDIHKIAILDIRVMNLDRNDGNILVSPLKSLKD
CCNQFLYRNNKRFSTNDEDILKRIITIDQKPSRYSLIPIDHGLIMPHIMDVAEIDLVWFDWPQTKIPFDNEVLEVIFAFD
PDKDADKIRNKLLIREDCIRTMRVCTRLLQIGARMHLNLHEIAKISTRKNIDEESILEHLVRDSIIQAYQMMDYTSLMST
NRLGHILDLAEIKINKKKKNNKNKTMELIDSNKTKDENSNDAKKNNSFQKEEENYETHNNTTYAKSKSLDIKKIENSFTT
VSFKDIKEHKSPSSFTLVNNATNENLKKSYEEKFGKYNINMNEQKEGEGNSTYKMLLQHQSDTKDSDDKYNKYINTKFNN
ISSKENIGGYYSWSKDNSIEIRNDNINDHVKEKNISETNSFSTKSEYTFVTATSNSKKEDNVHKSSNDVEQNSDGSENCV
ENFVDKGDKFDKKEPCNISDENAENEKTSSHSPNKDKQNEKNQEIDQDKAEEKQKNQQDIDAYEDDEEEEEEEEEEEEE
EEEEEEENYARYKKTTGTMKRINENTGTAYRNIEMNKINSVWMIKDKNNKTINVKWENKIFEKLFFETFENYVKKYINDY
HPNWRDYPYNGSKIITTKHSYLNNIK
```

787 - 806:	EEEEEEEEEEEEEEEEEEEE
788 - 807:	EEEEEEEEEEEEEEEEEEEE

A0A1D3LS99 **A0A1D3LS99_PLABE** (2604 aa)
Uncharacterized protein. *Plasmodium berghei*

```
MNKNFNISNYNLDLIKCLQNESGIYFILDPTKAIHDKKHSDVYDIFIPENSDGVTLHVQKVNNEYKCIGVSITKRGIDIN
TGTRIFNTKIADWLEQLFNFNKTLGSNNNESNNANSNSNENEDGNNNTENRTNNLNGKNNWSNMERNGANNHGFGAIVNN
KNTSINANPINNIGATNNNEQGDAIGDDKDANGGDGNDNLENSDDNNNSIINNGNNNKYNNNYNNVRHNLSNNQAGAPIA
NLIKNSKGGYDNFENNDNYNNAINMPNKTKNSKNAINQGNCNLNVNSNLSAHIIPSSNLSSPQSKKQNQHTKQIRLNQMN
NSHKSHLMQYHNSNYDDKNSKLYNNVNSSNTVINKHISSENSGVLHASASNNNDAVKVNKIGCNTRQKNGPHILHNGNNN
RDGNNNSYKVQQQVYNENLGYRPTLFNLLEVLSNHNITTPDQRVCIRGIVTDFLNNELPHGKIYAYIGAVVGHDILHDII
KKLEKDPNRNAVPDASGLARIEASFGLSKSSYDFMNHNSTNSSMNNIPNVLFNNRNLNSALLNNHIYSNILSNVANNNNG
NIGDNMGHSGMLNADTEKIANNKTANDINNMMMKYGDNDKSGGSYNNNMLNINKKKALNMLNMRYMDNNNMTDMGNLGIT
NMNNTDNSYMNQMNIDLANLENLNNAKNSGLSVHDYLYASKNFHNGNPLNRNNNIGEDEEELMKVIKKNIETYKMNNIKN
ILISSVFGRIKWLKIMNESPHAYLYGHSIVKYGNKLYMFGGTNNKHKKVPFNHTLTFSLIYYNYKLLPLSGNYPEERDGH
TTHLVSLKSGLSVFLFGGANNNVYYNDIYILDMETRKWSKRIVNGKLPLPRHQHCSLVYPAKSEHLRGEKLNLTEGVIVY
GGKCLYNNNIVNLNDMWIFLFQANMWIRINYLGDQIPNGRYGMNLIWSDTNTLCLFGGEYLYSDKNCKTRKLLDDMWTFR
LNTPVLINNAEDIGTDIKHLPCENAINTQSELHKHQKGTKSDPHLNNQNGNNGISIHDNNNNNDNCYGQTNNLNDKNGIN
EIDNKMGNNNNESQFVDNKGSIENNNINNNNNINNNNNINNNNINNNNNNSNNNNNSNNNNNSNNNNNSNNNNNSN
NNNNNSNNNSNNLINKIKITGEWKREIYEGNIGPRSNYSNIFITQRHQDFKGAEPKTIEKLMLLCSGITYDNKLKIVSSD
EIYVYFFSQKRWYLLKGKLYNEEYMYSARQRHVGCFFESKNVLGRSNRNPVPCIFIHGGFKKNSVFGDAWLLSLTGENPL
RLYEYDTCREKISTTQMPLYYFRDTHSISLLYTFCTLQKWLFGAFANLVDNSVYAINPAENVFIKYELTPEHDGMVSIQD
```

```
DGEGLDFNAMNRILRMYGNYKNYDNNSFYNNNNNNNIKKHSLPNNDDSDSYEMDNYNENEEEQEYNEETNNTNELNNNEN
NNADQNNNQYVNNNTKVDQMQQNAENYMKSEKGDGEKIYNNNLSGSNCEGMIKKENDTRNKNVIVGKKKCTWSDSFYYKK
KNQHYFYNDISNSIFDIKYGVGFKTAFARIASSCAIMSRTINTIGIGLLSLELMNHCDAKELATPLCMWKLPNKELINRN
IANKSEHRHHQKLLMSYTPFNSPSLLAEQINILGTYSGTRLLYWNFRDDMDFIIFNPTNNNIYLSSSPLSIDELKNKKQK
NAQGEGSNFNSKYQGVKDIKFANRVIKRKGVFGDDENLKKLKTDIDNPDEEIEKDEDIVADDKNNNKYNNIDDKYNKDED
NIKKELDNMSTSSKNNIILDGDNNNNDENKNVNSTHYKEKLKYEDQLKYNNDNYFKKRMNLFEYNSHLTSSISKEKYNMN
QIFPLWDHPKDSIDYCLSTYLYWLYLRRSTNIFLQNTLLIPTSMRREKDMNPNKNNNDNNGKKKGTKSTKLRNKKTTKQN
DVNNIQNDEKIADIEENNGEIGNVSEIVPENNNSFVKFEQIQEKNDDNNHSNVQNEADTNNERGENISEQNQNTEINNNG
IKNENVCTNKVEEEKEENNNPEDGKENNHCENDTNGGLTKLEKQKLEEALEYGISQDLQPQNSANKNEADGEEEEEEEEE
EEEEEEEEEEEEEEEEEDEEETSKNNEDNGNINETNNDVENEGNNNVENEGAKVEGEVNEVGAGVVKTETPNEMETENNA
DDTEKNKSKKENKNNVGKTIDNANEDSIANRRKRRKKKDGLSTGTVANGKKNGEIEKMKKENYVNVYMENFKIKDEYYI
NDPSKYTLYHFLRRKLYKMVESHYLFTPSDHTYGSFIMMGFLNDNNNTSIEVNRVCETGILLYYKNRLIKRLDAPFIDTP
YNLFLSKYPPNPSLYEGNLYKYALTVIVNVPNWLKPSVSKQEFVHENNHAFLVFKKKLVTLIKHYLSICEDIVKLNKWRE
SRDMKLKKYLEKMQNQSVKSRNDSDYENDIDNNKSKNFNIIYNNDEEGDNYMNDQNDGNKKKNEEINYSGKNKTPYTNDN
EPILHKNKKTKTNNNDDLNKRDHNPTSENESANIDNENNQENDVLEGEKEQEDDEYDEADQEAEDRPNFEDEKDEHEENE
EEAEEEDPDDEEYNGEMDDQKNRSVEQETEEEMIEDEEYEPDDE
```

2072 - 2091:	EEEEEEEEEEEEEEEEEEEE
2073 - 2092:	EEEEEEEEEEEEEEEEEEEE
2074 - 2093:	EEEEEEEEEEEEEEEEEEEE
2075 - 2094:	EEEEEEEEEEEEEEEEEEEE
2076 - 2095:	EEEEEEEEEEEEEEEEEEEE
2077 - 2096:	EEEEEEEEEEEEEEEEEEEE
2078 - 2097:	EEEEEEEEEEEEEEEEEEEE

A0A1D3LXA9 **A0A1D3LXA9_PLABE** (2603 aa)
Uncharacterized protein. *Plasmodium berghei*

```
MNKNFNISNYNLDLIKCLQNESGIYFILDPTKAIHDKKHSDVYDIFIPENSDGVTLHVQKVNNEYKCIGVSITKRGIDIN
TGTRIFNTKIADWLEQLFNFNKTLGSNNNESNNANSNSNENEDGNNNTENRTNNLNGKNNWSNMERNGANNHGFGAIVNN
KNTSINANPINNIGATNNNEQGDAIGDDKDANGGDGNDNLENSDDNNNSIINNGNNNKYNNNYNNVRHNLSNNQAGAPIA
NLIKNSKGGYDNFENNDNYNNAINMPNKTKNSKNAINQGNCNLNVNSNLSAHIIPSSNLSSPQSKKQNQHTKQIRLNQMN
NSHKSHLMQYHNSNYDDKNSKLYNNVNSSNTVINKHISSENSGVLHASASNNNDAVKVNKIGCNTRQKNGPHILHNGNNN
RDGNNNSYKVQQQVYNENLGYRPTLFNLLEVLSNHNITTPDQRVCIRGIVTDFLNNELPHGKIYAYIGAVVGHDILHDII
KKLEKDPNRNAVPDASGLARIEASFGLSKSSYDFMNHNSTNSSMNNIPNVLFNNRNLNSALLNNHIYSNILSNVANNNNG
NIGDNMGHSGMLNADTEKIANNKTANDINNMMMKYGDNDKSGGSYNNNMLNINKKKALNMLNMRYMDNNNMTDMGNLGIT
NMNNTDNSYMNQMNIDLANLENLNNAKNSGLSVHDYLYASKNFHNGNPLNRNNNIGEDEEELMKVIKKNIETYKMNNIKN
ILISSVFGRIKWLKIMNESPHAYLYGHSIVKYGNKLYMFGGTNNKHKKVPFNHTLTFSLIYYNYKLLPLSGNYPEERDGH
TTHLVSLKSGLSVFLFGGANNNVYYNDIYILDMETRKWSKRIVNGKLPLPRHQHCSLVYPAKSEHLRGEKLNLTEGVIVY
GGKCLYNNNIVNLNDMWIFLFQANMWIRINYLGDQIPNGRYGMNLIWSDTNTLCLFGGEYLYSDKNCKTRKLLDDMWTFR
LNTPVLINNAEDIGTDIKHLPCENAINTQSELHKHQKGTKSDPHLNNQNGNNGISIHDNNNNNDNCYGQTNNLNDKNGIN
EIDNKMGNNNNESQFVDNKGSIENNNINNNNNINNNNINNNNINNNNNNSNNNNNSNNNNNSNNNNNNSNNNNNNSNN
NNNNSNNNSNNLINKIKITGEWKREIYEGNIGPRSNYSNIFITQRHQDFKGAEPKTIEKLMLLCSGITYDNKLKIVSSDE
IYVYFFSQKRWYLLKGKLYNEEYMYSARQRHVGCFFESKNVLGRSNRNPVPCIFIHGGFKKNSVFGDAWLLSLTGENPLR
LYEYDTCREKISTTQMPLYYFRDTHSISLLYTFCTLQKWLFGAFANLVDNSVYAINPAENVFIKYELTPEHDGMVSIQDD
GEGLDFNAMNRILRMYGNYKNYDNNSFYNNNNNNNIKKHSLPNNDDSDSYEMDNYNENEEEQEYNEETNNTNELNNNENN
NADQNNNQYVNNNTKVDQMQQNAENYMKSEKGDGEKIYNNNLSGSNCEGMIKKENDTRNKNVIVGKKKCTWSDSFYYKKK
NQHYFYNDISNSIFDIKYGVGFKTAFARIASSCAIMSRTINTIGIGLLSLELMNHCDAKELATPLCMWKLPNKELINRNI
ANKSEHRHHQKLLMSYTPFNSPSLLAEQINILGTYSGTRLLYWNFRDDMDFIIFNPTNNNIYLSSSPLSIDELKNKKQKN
AQGEGSNFNSKYQGVKDIKFANRVIKRKGVFGDDENLKKLKTDIDNPDEEIEKDEDIVADDKNNNKYNNIDDKYNKDEDN
IKKELDNMSTSSKNNIILDGDNNNNDENKNVNSTHYKEKLKYEDQLKYNNDNYFKKRMNLFEYNSHLTSSISKEKYNMNQ
IFPLWDHPKDSIDYCLSTYLYWLYLRRSTNIFLQNTLLIPTSMRREKDMNPNKNNNDNNGKKKGTKSTKLRNKKTTKQND
VNNIQNDEKIADIEENNGEIGNVSEIVPENNNSFVKFEQIQEKNDDNNHSNVQNEADTNNERGENISEQNQNTEINNNGI
KNENVCTNKVEEEKEENNNPEDGKENNHCENDTNGGLTKLEKQKLEEALEYGISQDLQPQNSANKNEADGEEEEEEEEE
EEEEEEEEEEEEEEEEEDEEETSKNNEDNGNINETNNDVENEGNNNVENEGAKVEGEVNEVGAGVVKTETPNEMETENNAD
DTEKNKKSKKENKNNVGKTIDNANEDSIANRRKRRKKKDGLSTGTVANGKKNGEIEKMKKENYVNVYMENFKIKDEYYIN
DPSKYTLYHFLRRKLYKMVESHYLFTPSDHTYGSFIMMGFLNDNNNTSIEVNRVCETGILLYYKNRLIKRLDAPFIDTPY
NLFLSKYPPNPSLYEGNLYKYALTVIVNVPNWLKPSVSKQEFVHENNHAFLVFKKKLVTLIKHYLSICEDIVKLNKWRES
RDMKLKKYLEKMQNQSVKSRNDSDYENDIDNNKSKNFNIIYNNDEEGDNYMNDQNDGNKKKNEEINYSGKNKTPYTNDNE
PILHKNKKTKTNNNDDLNKRDHNPTSENESANIDNENNQENDVLEGEKEQEDDEYDEADQEAEDRPNFEDEKDEHEENEE
EAEEEDPDDEEYNGEMDDQKNRSVEQETEEEMIEDEEYEPDDE
```

2071 - 2090:	EEEEEEEEEEEEEEEEEEEE
2072 - 2091:	EEEEEEEEEEEEEEEEEEEE
2073 - 2092:	EEEEEEEEEEEEEEEEEEEE
2074 - 2093:	EEEEEEEEEEEEEEEEEEEE
2075 - 2094:	EEEEEEEEEEEEEEEEEEEE
2076 - 2095:	EEEEEEEEEEEEEEEEEEEE
2077 - 2096:	EEEEEEEEEEEEEEEEEEEE

A0A1D3PAT4 **A0A1D3PAT4_PLAMA** (1430 aa)
Uncharacterized protein. *Plasmodium malariae*

```
MYSKDENDENNKINLNNYKNILHNKKKILGLLNKDPLEKKGNYILAEKKDNKGVVSTSECKKGQSGGIDQVKSNLEEVEE
VLDESEEEEEEEEEEEEEEEEEEEEEEEEDEDDDEDYEVDEEEEEDDDDEFDEEEYDDEQREINFNSYNNSYYETYNDEE
GEKYRNNIEQLLKNKNRNEKCKNKEEKNEIMFEKYNKLLSNYRVRKEKLSKDYIKDCIKDCVEEDSANSCCFSCKSEERN
KNMPLNVQADVKENLKSHQGINWNNRDSNTNNIEYEEGDFIRDVLDRIDEIYYKESRYKNLKSVNNNNNNLCINDLNLNL
ISEYLNVDISVFHKKTTILLLGNTQSGKSSFINWFSETYVQNTSSLAKKNQITYVDIKSNFKFQFNKLQNQNYQFGVVNR
LTDEGYGHYTGKAQYYGKAHANYDSTYGGKYGGTYENTCGNTRGNTRGDRYIDHDMNGPTHHNVDDHCYNENDSCGGGGK
KIMFSGEHCYYLFKPFQQLRKKGHDIKKYIYGKLYYQNNLTKYMNRVNSVSFIDTSGIDDGSGIDDMSNVEYDEIIMNLS
KYVDLIFIFVDSNKFSINNRLLRIINYLLDNQINKVTICLTRIDIIKKINLYRVVFYLTQYFLRNLNIFKYQSLNDTSNK
```

```
RKEDEEFNDYEDETIQRHGKSFFNKNKMEKINILFNRSIRSFQNVLLFPNMLAKMITSQKNTTEKGSIKRKGINAPSSGS
YYLNNITGEDGVEEKSPFSRYTSRRSAGRWMGGYDQAEVEEKDETEENCGVMSGPIRAESTVRINAGKEEEKKEEKSILK
KILTTSYNSFKEKIMGSEETDQNSNKAAKHWRRQEDTTHHGGHFNYNDGQNYEGNFVRSDVKNERNDVFAKVYKRNNHQL
EYVERTSNSYQERDGIINELNRSKHVKENNRLENIFEKKINYSDGLKNMSIFLFVLMYEVVTTVYSLVHTTINRYITANG
SRRVVNVEKMQKLDNAHKMRYINPDDAITTGTRKRSSNINNNNNINNNINSNNNINSNGNRGESASGSSNGNAYKILEFL
TIYLPEMPYDLLKREKWKYEESNIHCNHDRRKRFSCNIQYEHTEYTGMMQNDTTNYNTHDVINNNRFNKKKNYPQRRSIP
EDFILLSKGNKNNNDDCYNDSIEHVSYINNNKFRGINEISRNSYITDSVYNTNNERASNYLVENDPRESSPYSSKGKYYH
VGEEARLHQRVHHRDHPQVHPQYEPSNYPYTHSNNRNFNYMRMRNEDVKELNMIHELLFKIDESIDLKTNQSIYMLKRDL
QNIQNSCLKKISDNNEIIKKNRSLRIQNIKFYFFKYMAIFFGFIISLLRYDLLVYFNFIKPELFFSIFSKYFLFLASYNK
NSLFIAVNMLLVVAYFALYIRYNRRNYFKSLDKSDLNKLKIILLFTQIIFDEINQLHLKLLGRTDKDVRR
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86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE

A0A1D3PB81 **A0A1D3PB81_PLAMA** (2587 aa)
B30.2/SPRY domain-containing protein. *Plasmodium malariae*

```
MIECFNAIYEDDESLIDDDCFTNNGKLNKLNDFFFNRYLFINFKKIIFYISQKRCLSFKFLEQNKICEQVGGKKIKYRRR
EKNRKELYKTVMYATKRNINEAFFFNLDRGKENINNPYFNKYEYYVKIKNLQKKKREFYNPLQWRVMYKNAYIVGHINKS
FFNNKIERKVRKLYLNIYILNEDVSTLLQNILRMKKNLFYTNYKVISLENWKALNLPFLIFLLKYNKKKLNKFQVILLIF
NSHYEYNKWKSVKITCRQQQLYLFTYANDSKNCEKTKEHNFFFCLFWCTIFKKYISYIVEGVNILKDIKKGMLIRGYHFA
NAFLKINEFICILCCHNIQDQKIKKIKKEKCAFLHILKQIFFKRINSKKELKCKNLDKGKYDVYNVDMCLLGQNIFQFIS
YNRNNMIIIKYKKGKHKMCMRKISEMDILFYLKLCNFQNFLFFFTFSKLQYIFKKYRMIYKWNGSHNFYRWLDVITILSK
PLFKYIIIMLFKILKIILIIKMIIKLILMISIIIMEVIKKEVLFFLQFTYTRIYKIYFPTNQLLLINILDFDKRASIKFG
CLRCSIAPHLDYNVIIYSFFVLLKNYKQFSALKIWKNDNLFYRLNIGVGNKCIATTHGREEVQTLKDISPFTDVRFNFHF
LRIFIDDSNFYLNNIDRIIIDCSSKVVRHYFPSTFSSVFRSGCNKDLFHLFVLLVFDYFPYSLYFYEKNKKREVLLYYFL
YIMINYLTSKLFYFLHILHFVFSSIKFCINALIIFLKYKVSTFFQIRIKKEEDNLLVFFKPEKIREFYMHNFNQAVQKGK
DIRDRINLSINKKKFLRNANMSSSCDESKMEKYNRRMSTNDPWIYGVHVNEDAKNYKNHKKRTCNYVDSEKSDEEPYNWT
NQLSPANIFSKKNDTLFRYTKWRVLKDYCKYKSNKNKKKIIYKRRVKIKKNGKIHVKHLLPLLFLNEVAYFRHAHEYKPC
QSLIMPFKLLVFSSDNSNNISSRRKKTESHSNRRKNKKNKINEQKENKEKERKKKNSSNDSDSDMDSDSDSDSDDDEVEE
EEEEEEEEDEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEDEEEGEGEEEKEDEEEGEGEEEKEDDEEG
DEFDNDDEDEEEEEEQDKDEEDKEDEDKEDEEDEGNEENEEDEEPRETEDTDDNEEEYKEDEVETDDEKDEDEGEDSFND
NERKNRKKKKKKIKNKNNNNKNRKRNRNKNKKCKYEHNGVENNASDEEIQKEEDSYYNKKKKLYLKRTNKRFKHNYIYLK
NLFKEHVCINTTNVSNFISVSKDKLTATYTAWGKHTDIACVQVNKCALRDCSIYYFEVEVLNCTNFSKIVIGMTSKNYTI
NKNPGSEYNSFGYKNDDGKKIIDGKIENYCNSYTKYDIIGCGINYFDNSAFFTKNGKFLGKACNINSKYDYYATVGLSTL
GDRIKFHLNNFYFDVYNLIYEENEKERKIIKSVYIQKDIFSDIIKSHLIKCGYLNTYKSFVNFLEKNKNSDDNNSVGSSS
NSKNEIDKFFMNKTDLPNVLEKKVVDESSQNISNNHEDKENKKNVTDETKKKMDIIIKSNNAKDNANIFVENTTAKCTPL
NVDNTKNSSNNDNISSVELKKEGLIHRENDNNTENTEEKCRTDHIKKEEDTFTPINSNSSIKNTVDVDVPKYVSLLSENI
PEKEGKVSKDEGSTKGDKNVLSTFLVKYLDAYEKCDEQGKSDKEKNDMEHIDNDSSKMEMTNKETTNKESTTKGTYNQEK
NEECTSATVEVKEDKKMSKLPDSPSSLNKKDESKLEEKSDTSEKLEKSENSSATLIVASDQAKGNNKLIVSETGKSGKDE
NVNSIKIPNEQKHSTEENVEKMEKNQIIDTTSSILKCYDFSQYSFAGGSIQNSLWVSRKNSLSNLINVRKDSSSTLLNRL
RNKRSLSTKDNLNILPTNFLSTKKESKKNDSDINKKIHLLLKDKSGIIKNEKKKLSKKEGSKNYSTDKEYITKYFMNLYL
SEDKLNKMVDSLETRYLIRNNVINGNIIDVLNILEEQYSDLFTNAHASFNIAMLYTQQLIEILKPHKIFIKKISSKKRRK
CKKSVAYDEEEDLLSESSYKTYNTLSDDRFYDDIKTDYNSSDSLFCDSSNNEENNYAAFNIEKLNKRRNQKKCSKINDEE
DRYSRDKNILASYRKNGKDKSSDSSRSNGSRSGSISSSSNKSANKLGRDSFDNGNVLPVCATKLKEKMSNIDNSYSNSNN
NNNFYNKHNNNKHLLNIGDKKGLEHGKYTRNDCQKTKVNCEEGATISPIKHTQLNHNDFLKEKKIEQMSLRSIRSNYNEE
FYKKNNMLEEYEDHYKKLSKEYEFFKEDNPYNNKCKKECYKTLYKEVEEEEKKRFYYMSSNDDITSDYDSNDSNFNEKFY
QFNDINFDKIYQYIYKNNFSPNKQLKFKKDHLYLALLWIKEKLSVFNKSPFVNVRQCILDSTSLIAYHKPYKQKLVRMFF
SKNRNLLTFNAVNEGILDICLKVPIYSPLEVMVKHLILCRNLLREKKGNVGVKYDCRYVCQPYKRYMVKIKNNKKKRRYF
KENTKQKNEKGSLNGKLIEDKRLSIFH
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1057 - 1076:	EEEEEEEEEEEEEEEEEEEE
1058 - 1077:	EEEEEEEEEEEEEEEEEEEE
1059 - 1078:	EEEEEEEEEEEEEEEEEEEE
1060 - 1079:	EEEEEEEEEEEEEEEEEEEE
1061 - 1080:	EEEEEEEEEEEEEEEEEEEE
1062 - 1081:	EEEEEEEEEEEEEEEEEEEE
1063 - 1082:	EEEEEEEEEEEEEEEEEEEE
1064 - 1083:	EEEEEEEEEEEEEEEEEEEE
1065 - 1084:	EEEEEEEEEEEEEEEEEEEE
1066 - 1085:	EEEEEEEEEEEEEEEEEEEE
1067 - 1086:	EEEEEEEEEEEEEEEEEEEE
1068 - 1087:	EEEEEEEEEEEEEEEEEEEE
1069 - 1088:	EEEEEEEEEEEEEEEEEEEE
1070 - 1089:	EEEEEEEEEEEEEEEEEEEE

A0A1D3PC52 **A0A1D3PC52_PLAMA** (1503 aa)
Calcium-dependent protein kinase 6, putative. *Plasmodium malariae*

```
MLVSAKRKKKKNSILEDESEKDIRFIESGNHEDSYNICELYGDIENNGNRTNTNYSFQNLNKKEHITKNSFKEFYINSKE
NMQYGTNENEIFTEDILENDNFDDINFVEDENIEYKTYSSYTNRDFKLFSKYPSESIKKKIVQPDRKYNQLDGKYKKYWY
NNERFKNNLNEEDSDKMEFLNKNKKSVEYNKQNGIHFKKGIARSSTRNNNYIQENYKKYKGNCIGSNNYEYFNRGDSSYY
EYEDDDEDAYEGDDDENNQEIKRKKNLENTGVVRQSRGNAENEDYEYEEYYNDTKEEVEYNEEEEEEEENEEENEEEEDE
EEEEEEEEEEEKEEDKEEEEEEEEEEEEEEEEEEEEEEEEEKAFRDSVRESEQKCTSALRNRRNNFNLKNEYKENENSNK
```

RENENFEKEIISYEKEENKMIVPMHNIINYNGKNNNKNYDVNVSIYEKDRYINNLRTMEKKQSEELATMYNANQNNLKKN
DLRKNIQSRVKSSNIENKSKSNIISAKYTNVCIDKNKYNTFNNMDDKTIMFNIIGSTASTPTSATTTITTAATSGNVKLK
YKDEMINNVEYMNNSLYKSTAYKDSNYIIKKMEAGYKELKYTGKYAREPIQDSNVEDKKKNKIKNFLEKIKHRKNNEENL
IKKEHRNYEQEQKKDKLKMKFIDILHTGTLGNFFHRSKSNYAKSLSPQRKRDNSFNSVSSSNDVYKISLDYSKKSKIMNT
LHHHESNNTPFQFSIKDEAKYYNRQELKREIYYNSNEESKVKNNLVYDSLSNERSQHIKDDIKYIELINKKDKIKYLQFS
NNLNDKEKSVKNGKCLRSEYSKYLEVNKKDYQDDFTKSRPTYTNNISLDVNNEQPNTSENIFPIHQHLSKKTIFWSDNEM
KELKQIQKENEINTKKLSTKEEDLEVKINQTLSKKMIENNELKKQNENNEDLIVTPFYIKSKIDKVLKNSEIFEKSARAT
FQQFDVKNKNFLHFSEIESLIQQMCYNLELPPVDKNILSIVYKDYDSSKNNSMNYTDFRQMYWDLLKQIKKKYYPTKNFK
IKRNCIISRKKLGGYDYSSIYNYLSFKKILGCGAFGEVHLVEDNICKLYKVVKILKKKNMKNIKINEEINVLIYLDHPNI
IKIFDVYENVDCTYIVMELCEGGELMSKIRKSENFNEAYIKNIMFQILCAIAYMHSNNIAHKDLKPENILFKTKEDDTLK
IIDFGLAELINKSEGVSKTAAGTVLYMAPEVFKKNITIKCDIWSAGVIMFFLFTKNLPFSGTTYEQVKHSVFKDEPNYKS
LKQKLSQPALHILKLMLEKDHKKRPMASVLLHHPWFQGYLDPVEISPGTMNNIKSYMKHSNIRNIIVNIMAHELSIINNN
VKYINELFFKIDTNHNGSLSHREIYTVLSNAGIKKWDINRIVQALDINDRGSITYTEFIAGCYRWKNIESTFLKAAFNKI
DKDEDGYISKSDIFSLVQDKDIDSNDIDNFFSSVFSIKRDLSKDKRINKISFPDFKEYLLSTF

337 - 356:	EEEEEEEEEEEEEEEEEEEE
338 - 357:	EEEEEEEEEEEEEEEEEEEE
339 - 358:	EEEEEEEEEEEEEEEEEEEE
340 - 359:	EEEEEEEEEEEEEEEEEEEE
341 - 360:	EEEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEEE

A0A1D3PCW9 **A0A1D3PCW9_PLAMA** (3145 aa)
Uncharacterized protein. *Plasmodium malariae*

MNKNYEFEYYQNLMQKELKEYETHSDISCKIGYSDSESEGVASIKEVPYYSYNNSLKNYKKEKLEKPVWKSLYDIEETAK
DSYSDYEYSKNDKSESEIESPRFGNSSEDEKGKEVDGLNGEDEQNEEDKLYEKDELNGGDEPYEMNERYEEGEHKEETAR
IKNFVNGVNNSENFFAFDKINDELKNSKSNDPFGNFSNKENISISSSINYNFREELENNMYNNLSMFKSIKNRYDDTTKH
FMKPKTCKDINGIYYDVSDEKVDIDLLKREHEKLKKGHILEKLSTSEYDYLTRGNSSNSHYRNVQYTSAKNSSKLKKGVL
DDNTLKKISKNFGISSDNSTSDTFDQILVDQNIAYKGKKLHERKITDYSNSVKKKNTRLRKIANRGVEQVEKEVEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEGEEKNEEEEDAQKNTDIKEDEDKEEEEQHNKV
GGNTEEEDEGNEEEDNAVLENSKCKRNTNKAASKIRTDNINSKNIPNFQKKNNETKKRNSNKKKIAKDKVFTCKKITEII
DEKNSSERVTTSSTTSESNDEIISYIHNKNIIINKTETEKQNDLVNEQIAKEMNFEWWKPNEKTVHTQMENLQNMKEDID
NKLNNEKRVIKSEKEILNKERILNRYEIPKDISYYVEKYQKRKEEHDKNSSNVHINVNNDANRKEVVNESENILAHNNTN
DILSEKKDLFNTRNSENKNQDIEAEKGLEHLYHDRFNRYDDSLKVPNNRTTIQDCNKEMIPISTNDQVDSLKSCNIIDEF
FSDKPKIKNDVNYENGANINNSNTFLKEEKVPYINSINMNQISNSNNTCEVHNNSFFNNDHKNKGKDLLGIPRNMLQNEI
CNGQISGDTYTIYDKIYDSIYDQINNYSEKNNEECFNKSTENNNNEKNLPFFQNIDESKENCMYIKEKGDTRIYSDEEKN
EKIKMFLKYLKCIDDNSLTKVFEHIVQRENDDKLKKQLEMYLIGKKNINKIENNECEQETRHILRSNQNTQTTDKHFKNE
EIQTSIKDTNKSDSCMQTEINDINNKLYVQNDMISKKTSIDSIFFRNLSKDSYPLDVDNCAVKNSHVESKERKYFASDRN
DDLNNDEYNELKKINDLKAKILEKIKSCYENTNENNDEAAAILMLQDKKEFKNNSNSCRIYDNNTCNSRSVEKRRSNNSS
KNSSSHIDNNRNNGNISGKSNKSVSTLETLESMKSFEKEMNLLISHNERLKRRIEKLYEEKEKIKNDYKKIEKIKESQDN
LFLATEKHIEKLHGELDNLSKQNESMKGDIKKKKMKIIALESQIDESNTNNDVNDSDDLTLKRHTHMIKDELTYIDINNR
LDEFKGQIIDKKKIKTQIDQLQKQLHILKDEIKKTEFLKLENEELKKLLTMKNSNINDYEKSTMKLEKHIEKLNEHNLRI
YKENFNLCENIVMLKKENTTVPYSSEEIHDKPTNIEKELHADGASIQTIGSKVNEKGARDLQKHGNIIKKLEKTVDLLNE
QNFHLNEKICDLKEQNMKLRKTALLSNKENGNILDSNKHIEMIQTETEKIYIDKINLLKCNLEASKNKINMLNILLKTSN
NQTTQLNKKVKYIIKENKTLQKKYEKCLTYLEKLKIKYDDEILKVNYEKSGISLYDSKDINNNKDEEAIHKMNKIHDMQL
LKEGEHINILEHKLYEKDEKSTEVFNDTKEEGNMGSIVQKRNINGKCSTGIGTLVGIKEENEDNKKKNKEVSKLLKFNDL
ISNNEDENIYQNWLDSENKYVHVNNIFEIDSITKDLQNMFCSDTENTSKKLLKDSMSDNDNSIINTRVNTQEGVKNIEST
NSISNERSLRNIEKRFVSDKIKKMNENINKYIDEKKNNIKNICYNDNFPYSKSHMKEDYQGHYSDIDPKNRIIKEQKGNE
QDINRMYNNKTDGNIIPMNSVDQTYNKKQLGNMNNADYKNNTNNTYSMNNSSYNNSLARSTNSYHMYKENVGDSLINNDS
DNFKSVLRTYQIYDDKEDMQIKNNGLNNEYPLQKCNATNLEKTNENDVKSNDYMNKLHLCNENNTSAHNNNNLVNNSFNN
YKLNSSENMYIAYNKQNDITIYGNPEYSNRNAPATSQNMNNGVEANDKYQNAKNEKKGEAWIIDIKNNEIMPYRKLQSTI
LTEEVERGTENRGKYGVKDGINRTKNKAKNREKNGMKNWLHQNRYMNNHTKLKPLLHHKKFSKGSAYNNGKNKDKLHLLV
NNISKLVKGKIEEELKSKNISKDILNFEITKIKKKKAVPNSSLKNKSQETTIILSDSMSLSSGTLNSTFETIDDHKNNQI
TPNFLRNMQESNLTFNTDCASNLSKNGKGRHVYIGKNNNSFVDHKDRDDKNNFQLTNMNKSIINGGTYVNEANYLYGGSY
LNNDTLLNNFIVNKNYMQDIGSLNENLFLNDQSVLPEVPLNNIGDIYYKQNLSCDYVGNVQLQHNIDYLNFSGLSNKNQL
NQSSLSNNRNNYKSNNIVVNEYINIKNNSTSSNNNNNNGSSSSNTNVNNGSNNNDALNSSIKNKAVNAEENANIMNSRNI
RKDEEAFIVDEDVNNSIENTNNNLNMNMVINNYQDINNNFINDPVSNVYDTNQCLLYNGVLSNKNGKEASTIFDVDKMNN
SYLFDINTIKQGMIPPFYDDASLNYNLIDRNDTNDMNDTNDVNDMDEGSKGGSLGNNLNSSSNKNDNSSSSNKIIGKSEH
NFKNADGSIAFFPEYCVDKNISNKTQKEVKVCEKINVNKKGNNQLLKENIVDEKHKTLERNTRRSKSVDIRRFETKNDLA
SKGDSTRNKMKTQIFNYSDYKNNGLRDMSTYADKVLQDMKSLIPSNVSNLINKANLKGKTGRSITKMVSNNSNISSSNNS
ISSSRSSSCNSCGSRGSCNSNTFNSANYKLCTKHEPGKLNKNKDKIHSNHGGTLLKSTSTKNLYQNYRYDETNNVSENIM
NNINILGLEKGDYINKCPSINKNETRIIYNDSNDSNNNNYLVGEGVNNIMIGKTNENALLSSRNSSSNNNENNIKKNLMS
MNAKNGEHTRLNAGINSNINNNMHYDLNNFNYNLNKFENILKEDQFKNYSNNAHNIIYKQVNSNQHLVKNSIILNRKEEG
NAFQSETRRSLSCFREALKKQGILG

395 - 414:	EEEEEEEEEEEEEEEEEEEE
396 - 415:	EEEEEEEEEEEEEEEEEEEE
397 - 416:	EEEEEEEEEEEEEEEEEEEE
398 - 417:	EEEEEEEEEEEEEEEEEEEE
399 - 418:	EEEEEEEEEEEEEEEEEEEE
400 - 419:	EEEEEEEEEEEEEEEEEEEE
401 - 420:	EEEEEEEEEEEEEEEEEEEE
402 - 421:	EEEEEEEEEEEEEEEEEEEE
403 - 422:	EEEEEEEEEEEEEEEEEEEE
404 - 423:	EEEEEEEEEEEEEEEEEEEE
405 - 424:	EEEEEEEEEEEEEEEEEEEE
406 - 425:	EEEEEEEEEEEEEEEEEEEE

407 - 426:	EEEEEEEEEEEEEEEEEEEE
408 - 427:	EEEEEEEEEEEEEEEEEEEE
409 - 428:	EEEEEEEEEEEEEEEEEEEE
410 - 429:	EEEEEEEEEEEEEEEEEEEE
411 - 430:	EEEEEEEEEEEEEEEEEEEE
412 - 431:	EEEEEEEEEEEEEEEEEEEE
413 - 432:	EEEEEEEEEEEEEEEEEEEE
414 - 433:	EEEEEEEEEEEEEEEEEEEE
415 - 434:	EEEEEEEEEEEEEEEEEEEE
416 - 435:	EEEEEEEEEEEEEEEEEEEE
417 - 436:	EEEEEEEEEEEEEEEEEEEE
418 - 437:	EEEEEEEEEEEEEEEEEEEE
419 - 438:	EEEEEEEEEEEEEEEEEEEE
420 - 439:	EEEEEEEEEEEEEEEEEEEE
421 - 440:	EEEEEEEEEEEEEEEEEEEE
422 - 441:	EEEEEEEEEEEEEEEEEEEE
423 - 442:	EEEEEEEEEEEEEEEEEEEE
424 - 443:	EEEEEEEEEEEEEEEEEEEE
425 - 444:	EEEEEEEEEEEEEEEEEEEE
426 - 445:	EEEEEEEEEEEEEEEEEEEE
427 - 446:	EEEEEEEEEEEEEEEEEEEE

A0A1D3RJB4 **A0A1D3RJB4_PLAMA** (763 aa)
Uncharacterized protein. *Plasmodium malariae*

```
MMHCTIKYRREFLTLFNVWMNRKNNYICTNIVKLFTTHSAESTRVDDNEDVLGNVYKSGVEEKEENKKSKSKQKDLKEGK
QQKEYERYNEYRQHNEHTQIPPQNLPPHDYKETSFVKPRSFVYGPRASNTLTSELYNKIVNEHKLCEEIPYDSGKKKKRH
AQTLSQSVIKTKYRTVGETKENPLYDMNKKYFNKGDNTGTPLNEEHMSTNSEHLMIENKRFTEGTMKCNDNPSVDDKKDE
VLHGKLNSDRNNDLIISSNIKMDAKSIIKNKGKNNMENKIIKRKGYDVVHNTVDKHINNMLMKSKDNQLSISEKKKNDHF
YKIFFSSKKVKIIKSQNHPVFIHLYKLATDRKYREKQEKILLTSKKIILERQKNYLCRIYTNSIDNLKDFHSFDNFILLS
NKLLKKLSFLYSFKNGVLAEVLHKFHFDNVGLPHLAFCFYNVNWGEEHQVGAEVKMNHVDEAKEEKEEEEEEEEEEEEE
EEEEEEEEEEEEEEEDGEDEWKERQKIPFEVKQSEQNLKIYDIHFEEKENANDRAVKRDDCSLNSESAQQYDIKNNVEYL
CNGDIGTIIRSCFLLKWQCIFNIENLKKKNKNKIASYKTLDINSIYNIDFFHPFTIRASSGYLLDIPYKNTDLNELHKYA
KENKILLLKYSSHSDLYINYKKNYSEHDHTFLNLVNKAKGVFLIMDNCNNIEKKYKSVHKNFINMSNNLHNKDEIFDNIY
YVNLKQNKDRPLGLVATYSIFMYILKTNFFKHLPQSSYVCIED
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467 - 486:	EEEEEEEEEEEEEEEEEEEE
468 - 487:	EEEEEEEEEEEEEEEEEEEE
469 - 488:	EEEEEEEEEEEEEEEEEEEE
470 - 489:	EEEEEEEEEEEEEEEEEEEE
471 - 490:	EEEEEEEEEEEEEEEEEEEE
472 - 491:	EEEEEEEEEEEEEEEEEEEE
473 - 492:	EEEEEEEEEEEEEEEEEEEE
474 - 493:	EEEEEEEEEEEEEEEEEEEE
475 - 494:	EEEEEEEEEEEEEEEEEEEE
476 - 495:	EEEEEEEEEEEEEEEEEEEE

A0A1D3S5F2 **A0A1D3S5F2_PLACH** (1495 aa)
Uncharacterized protein. *Plasmodium chabaudi chabaudi*

```
MKVQQKRNIKNKDEKYIIHSEKKTHTNSCDNNDTRHNKSSRLGGSNEISNKKNTEKDAKTDENMKSKTVSGSNNKSKMPE
KKTSSRNTTDTNTRDNAKMNKNEKGDTNDSKKRSVSNSKIKSSRHNYSNSSSNITKSSEDSNKKNKNGSSITSEDDTKEY
SEPITRNSLKRNSSLLKNVKKKNTSKNDSDDMLSDDNYEQSKSLKNSKNKNNKNSKNKNAKNANDSDSDSNNSNEGNFYN
LKKRTRLSNCDSETLKKQASKKDGTKKGLLNNKKNSKGKNENDYSSSEDGINKKGKNKRSGSSRYRGKSIVDSEEEEDDD
EEEEEEEEEEEEEEEEEEEEEEDESDEGYKRSRSSRLSRSKNIKNKKNGKNMINRNSRNSKLLKKNKNIKSGKDKGVSNN
KSGKNQIKNVKNEEEYSYFDDYIYSNEERKAILEEREKKRQIKEGYIKKMKLNKYADDETIEFINNPNYIMVLLFLTIYK
NIIKIDWNFKDIDEMFQNKENTEFGRNLILKLFFLLGRYFNSKSVFMYKYISRIFQDKQNALVKVVNFNELFPLLNEKQN
DKNGSGGTSKKRKDKRGKKNKNLVKTDEMDEELAEHDDANDDANDDGNEFDEDVLTHEEEGEEYDESEEEEHNNEIKENS
ENEQTLSEAEKDTNIVKEENNIDKKEDEVNCKDSLELEQNIKNEIENHGESKTEIVTNQVVKSEQNGEQVQDETGLSKKL
FLEWSDLSIISKLRIIRMLLNLVLCESSNLKKMLLTEEVNYNNGYLGKINNDKYWFIFNDTINIEFKLYVEKEEKGIFEF
VCDNDEVLYTIGYNMLRHADTKFMGDIIIEKYNKICRERRNRNRILKQQKKLFDDLNNEQLLYASKKRQHKQVEHFSFDN
DKMRKKKNENIITNPYSLQKNSYQKNDRSYRLATRNAQKENGGDDFESWKNGGNINGNGLGVDNNLNDNQIVGLNPMIDN
VNYQNVNDVNNLNGGVVVKVPLKRGRKKKSEKKKRGRKKKIIIEEGMDPNNPLPNEIKKPVKVKRAPYTKRASKPIVSIK
YGTRSNSLTKYEADQMQFGGYDMNNHALQNDEFYKNNNLDNSKFFNPNMHLNNFFNPNMPGAYNMHNNMINMRNQKTNPP
NNYNFPYIYNPPIYNQYYMYNGSMYMYNAGMNGNPSTVKDGKGESGYMNDTMGVNLRNGIGQNTNNNAIRSDNESGKVAI
SENGNANDVSGITTPGMNANGGELGSMANMGNVNRSNNENNTIDPNNNKNNENENNVNYNDSMNKYNSFMANRNNNPVNN
MNAPPMYNNMYNLKFPYVNNDMMNYNYNLNNYQNFNIDKMNKNMYKRYSNFIPNNFPPYNNMNMYPGFNSYNMNYQPGQV
```

```
MKNFGNEPGGFGEMHENNLTAPNNGGSDMMSGVENVSKMNEVSNLNRMGNMVSSPNVGTIPDMNQQENNPMNVNNEIMKN
DGILFGDETANKSSYILNNENGQMGDPNGINVDVTNNETNLSVENGTRDIDGNGI
```

321 - 340:	EEEEEEEEEEEEEEEEEEEE
322 - 341:	EEEEEEEEEEEEEEEEEEEE
323 - 342:	EEEEEEEEEEEEEEEEEEEE

A0A1D3SP11 **A0A1D3SP11_PLAMA** (372 aa)
Casein kinase II subunit beta (CK II beta). *Plasmodium malariae*

```
MEFMSYNESSNEIVQDENQEEGMNVSDESLCGKGAEHWEDVKYEIADDVFDGDANDYSNDYCNYGGGDNNVQRSDPILEE
AEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDDEEDDDDDDDDDDDDDDYDDDEYDEDDFNEATVSWIEWFCQLKQNIFLI
EVDEDFIRDEFNLIGLQNKVPHFKKLLKIILDEDDDDDDDDDEEDDYDEDDDEINRGSEEIYKNKDIYEQNAACLYGLIH
SRFILTSKGLALMREKYKSGIYGTCPSIYCDNAKLLPTAISEVPKFLSPLLYCPRCCETYYPHKNSLINQLDGSYFGTSF
ASFFALSFNIQSDKKKIYYTPQICGFTINRDIRETLYMDMNKDNSESSEEYS
```

82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE

A0A1D3TG31 **A0A1D3TG31_9APIC** (748 aa)
U3 small nucleolar ribonucleoprotein protein MPP10, putative. *Plasmodium ovale (malaria parasite P. ovale)*

```
MEQVNVKMYTDFISSFCKRSEEILSFGKVSEEDKNKLMEMIEYFCNILISYFYNDMNMDRISISESGFDCEQLWFFIECI
IKQKKLDSLLLFFNNFERKINETKNCKQEDRCRIIEEGDTKVRRKRKLEKASLRRNPGTKRTNRRGDQDDNAATEDGSAA
TEDGSATTEDGSATTEDESATTEDGDDAAMHEDDDAAMHEDDDAAMHEDDDAATDKDDDAATDEDDDAATDEGNGEEGDR
FFNRVEMETFIEEEEKKFLRAADESSSRGNSSGEESDGEYNLNDFECDYEGAHKLKYRDFYKGEGEQLEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
RELNEEEDEAVSAKTGEADRERIERELVATKHWSLTGEVFANQRPKNSMLELNVDIPKINTYNNDAFVSKTVGSIEGSEE
DTEEAAGRTRSSRQNLLNEEIELVVKQRIKNMLFDDVEKKTIEDLDAMYGVSEGDGGEVNFDSLNFTRSKLSLADEYAKK
IEDDIKNSHSMNKEISLQKIELMNMFKKIMHCCDALSNDYYIPNPVYINGKRSDINAKLHIEENIPIILSEKNKNAPEEN
YKPGFMKEIHEMSKKEKKALRKQKKNKRRKILLSQFKDNGGGISEWKNRNSHLLEKNKKKKEEKLNRMKYGVISKEKLTQ
GPGQHSKYNFSRDITKAIAYDKRRKGDS
```

309 - 328:	EEEEEEEEEEEEEEEEEEEE
310 - 329:	EEEEEEEEEEEEEEEEEEEE
311 - 330:	EEEEEEEEEEEEEEEEEEEE
312 - 331:	EEEEEEEEEEEEEEEEEEEE
313 - 332:	EEEEEEEEEEEEEEEEEEEE
314 - 333:	EEEEEEEEEEEEEEEEEEEE
315 - 334:	EEEEEEEEEEEEEEEEEEEE
316 - 335:	EEEEEEEEEEEEEEEEEEEE
317 - 336:	EEEEEEEEEEEEEEEEEEEE
318 - 337:	EEEEEEEEEEEEEEEEEEEE
319 - 338:	EEEEEEEEEEEEEEEEEEEE
320 - 339:	EEEEEEEEEEEEEEEEEEEE
321 - 340:	EEEEEEEEEEEEEEEEEEEE
322 - 341:	EEEEEEEEEEEEEEEEEEEE
323 - 342:	EEEEEEEEEEEEEEEEEEEE
324 - 343:	EEEEEEEEEEEEEEEEEEEE
325 - 344:	EEEEEEEEEEEEEEEEEEEE
326 - 345:	EEEEEEEEEEEEEEEEEEEE
327 - 346:	EEEEEEEEEEEEEEEEEEEE
328 - 347:	EEEEEEEEEEEEEEEEEEEE
329 - 348:	EEEEEEEEEEEEEEEEEEEE
330 - 349:	EEEEEEEEEEEEEEEEEEEE

331 - 350:	EEEEEEEEEEEEEEEEEEEE
332 - 351:	EEEEEEEEEEEEEEEEEEEE
333 - 352:	EEEEEEEEEEEEEEEEEEEE
334 - 353:	EEEEEEEEEEEEEEEEEEEE
335 - 354:	EEEEEEEEEEEEEEEEEEEE
336 - 355:	EEEEEEEEEEEEEEEEEEEE
337 - 356:	EEEEEEEEEEEEEEEEEEEE
338 - 357:	EEEEEEEEEEEEEEEEEEEE
339 - 358:	EEEEEEEEEEEEEEEEEEEE
340 - 359:	EEEEEEEEEEEEEEEEEEEE
341 - 360:	EEEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEEE
344 - 363:	EEEEEEEEEEEEEEEEEEEE

A0A1D3TGW4 **A0A1D3TGW4_9APIC** (2292 aa)
B30.2/SPRY domain-containing protein. *Plasmodium ovale (malaria parasite P. ovale)*

```
MNTKLVSHNCVEQYINCKDVVEGQKKELRIKENKQIGSAILYTRKGNTRMEELISILGGRRKDAKQIFFYNNCANKRYGK
INSLYKKKKEMKKNIYSVEEILERPAFNKTVEKKKNIFCFHRIPYIGYISEIIKSLIMRKKIYCSVSFNIIFSENGETFL
LRCLTFLLKYNKKNLSKSETFSLILKNECSSNKDRSFITRGVQYFLPHFNSKEGKYYEVKVVMEENIFLSLSHDNVLKIR
TYFFSKDVNFVENTPFANTYFELNYRGSTLFYDNIEIHNLKNHPIVRSVKDNFLEITVNCSEMKCNQCKKRKNEMGDSRY
SRAIRDAVSPLALLKNPFFSIIYKKENSKIGVNILEVHAFCCTKICTIQVFINVFTFPEIKTIFNYPSMKYGMSILYYVS
IFSYMINTHGVIFYHIVITEMVKVVLLMLFCTYICIMNLIFLRTRIYNNTHFSKHFTKKWEQREICVISLLCHTVVHIPF
SKKSYKEYITNRKNEHWSIGNPVLCLEKVPITFHFARRKMEKRRHFPIYSLPRYNTCHNGYFITTSFIDQFYHVLLEFYN
IVIYAVGMILHFFYIYMSTMISEFFCSLCCFLCLIIQGIVFFLNVMLNFVKYKMDLFLKMKNKKIEKYPTLFWIPREIRK
WNFPDLNQVTQEDTDENEDIKHQKWEEKIKTGNDYVARFDNKSELSHGCPRVGREVSGERLQRAACSSGFGNINNGRRRR
RRNVDSCGYLLPGIRNSVLCDAKKGVSKEYHESGNKKKRTFSSGRVVIKKKKNGTIHTKNGNMHCAIFSPVLYFKYSLYF
KETHEYNFAQFHGTPFQPLLLPSDSCSSHMSTGKKKSQRHANRRKNKKKKTNKEGKQQRGGKDKRNSNGSGSGSDSGSDS
GSDSGSDSDLESGSDEEEEEEEEEEEEEEEEEEEEEEEEDEEEEEEEEEKEPEDKFGDGEEEDDNDDDDNHNDDDDDNDN
DDDNDDDNDNDNDDDDDDGDDSYSERERKKRKQKNKKIKGRGMYGDDPSIESEGEKQKGDSYYDKKKNLYLKKKKKKFKH
NFIYLKNLFKENVCINTTNVSNFISISKDKLTATYTAWGKHTDIACVQVNKCALRDCSIYYFEVEVLNCTNFSKIVIGMT
SKNYTINKNPGTEYNSFGYKNDDGKKIIDGKVDNYCNGYTKNDIIGCGINYYDNSAFFTKNGKYLGKACTINAKYDYYAT
VGLSTLGDRIKFHLNSFHFDIYNLIYEESEKERKIIKSIYIQKDIFSDIIKSHLIKCGYFNTYQSFVNYLEKNKNSDDNN
SISNSSNCKNGINKIFEKNTDSIKAKDNNDHKLYDGKKLKDSEGMKKENLTISGINGKGENNEKNDNPNKGNNTDISGRM
KCIITITPEENNSVKFNEGNSKFKTEEGTCTEHGDVVGNIGEKHKNEHIEEDCFTSQIKSDTVKSAAEGEVVAAAEVVAT
AEVVAAAEVVAAAEVVAAAEAVATAETATGKKCESKEEKSNIDRNKDDKICDKSNDKSILNAFLVNYLDVYEKLNKEGNT
EKEVKDQGTIKTTEKKNDKGMNASDKSPHRPNKNGEGEGKYGEGEHGEKQETQIKTKSDEGKRSNKKTDCEDRKGRKEEN
VHLVKCPIEETAEEGRKSQVGGTDPQLDILKSYEFSPYNNYGGVSSQNIQLASRRNSLSNLINARKESSSLLLSRLRNKR
SLSTKDDLNILATNFLNTKKEAKKNDSDINKKIHLLRDKSNIVKNEKKKLNKKEGGKNYSNDKEYITKYFVNLYLSEEKL
RKMKESLEMRHIIRKNIINGNIINALNILEEQYTELFTNERASFHIAMLFTQQLIEILKPHKKFIKNISSRKIKYKNEGK
YEKQDDLSSESSYKSYNTLSDDHFYDDIKTEYDSSDSLFCDSSNGEESNFTISQLEKLGKIHISKRGNQAEVKIGNKFES
GHNDKAANSSAKGFLNNGNVMLPLDNDPSKEETVGKDQKPSPVLSESKNLDNNASTIDNPKTNAEDGGVSVSPMNITQLN
DIDFVKEKKIEHMIFKSMQCNYDEEFYKKNNLQEEYESHYNKLSKEYEFFKDDNPYNYKHKKKCYDKMHREDELGKDVKD
ICTSSTDDSTSDYDSNDSNFKRKYYEFNDINFDQIYQYIYKNNFSPNNQLKFKKDHLYLALLWIREKLSLFNKSPHVNVR
QCIQDSTSLIAYHKPYKQKLVRMFFSKNRNLLTFNSVNEGILDICLKAPIYSPLEIMVKHLILCRNLLREKKGNIGIKYD
CRYVCQPYKRYMIKIKNNKIKRRYFKETTKQKNEKGSLNGKLIADKRLSIFQ
```

896 - 915:	EEEEEEEEEEEEEEEEEEEE
897 - 916:	EEEEEEEEEEEEEEEEEEEE
898 - 917:	EEEEEEEEEEEEEEEEEEEE
899 - 918:	EEEEEEEEEEEEEEEEEEEE
900 - 919:	EEEEEEEEEEEEEEEEEEEE

A0A1D3TI57 **A0A1D3TI57_9APIC** (712 aa)
Serpentine receptor, putative. *Plasmodium ovale (malaria parasite P. ovale)*

```
MIKFVVGIICYYILYCSYNVYENIKTPIYDYSLEGSNLKKEKDNHVDGKYINKPFKNMLRKNDKINYHFYLSCIEEINLN
KYAKEKYIDNDKNFINVYNLTNVSYNWDYGHNLGDISKWLFFSGSKYPSVNLIIPQKLINKNKHIYLHIITYVNDELYRH
GFVTSLLTKSKNGRRDNVIKKKKKYLWKWLFDDEEEEEEEVEGIQIGEKTMEEDDRKGEEEEGEEEGEEEEEEEEEEEE
EEEEEEEEERSTSSKTTSGVTIGKTTSGATFGKTTSDATTGKATYGSTTGETKQKNEQQRSSVKNVRHNSLYIPRRVRFG
PIIEYNDINVNRIGFFSNVLLDKSTSTYLLPTYFNNYLTPEDEYQLLQGDYEEETDEDEFEAEKRKKKKERLKSASHGSS
NMIEGIRWNEVTVEYAPISYTHFNLFNIIIFNINHLKEKYSFSSYDLDSLAVHLCGNIYFSLFIYTICLVHIIIDLIALL
FDIKSWTQLNSLYSFLPNTIYLKFFFTSFILLYLKNKSDCKIVMVFCLVKMAVCICRLVSNYDIHFLPIYPYIYIGNNKI
GLDAKDSIVQQLEKTIKMKIQNVMICAMVILLTYNFLYNKYDSIYSLLIHTVGIYSYVFNFLFMCPQILRNYCDKRVQHI
PALYFFFLFLTALMDDLFALLLRMPIAHKFNALGDDIIFVIFLAQHLLYKKGGVLVSPAQVVNTSKESKKKK
```

228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE

A0A1D3TJQ6 **A0A1D3TJQ6_9APIC** (1735 aa)

Leucine-rich repeat protein. *Plasmodium ovale (malaria parasite P. ovale)*

```
MLLDLSKCNLQSLEDTDIILEKLIDLNCDYTSITYLDVSYNQLRCLKGLRHFENLKVLNISNNKLESLDGDYIPSSTEKI
LAGYNNLTDICFKGAHTSKTLCREIISDIVDGEDTSPVCSPIYHPFNSSTLNEKREYTNRNLPLNRLTYLDVSYNNIKRL
ITFEKYLHIMNKKRKNKKYESYLEDGYINNYIQSKTEKDVMILFFNSLQTLHLKGNKLTNLKGLSVFKNLKTLDLRSNMI
NHPVQLFYLLDNKNWLKRYQQRGGTSNRDTKKEMKNGTNNCSKGGRENRNGSYYSYFIYILKKYRNFKHLQNLLLLGNQK
CLRPKHLFMSVFNVLRNVNERGELLTDVTDGEALINTNGAVETDVQSTATTGQFKWEKESQGKCSHNDIKSSIRQVHRGI
SNAYPGCGENSTQDAPESSLHLGGVAERESVEADEDWEGEGEEWEEWEDKEEEIEEEEIEEEEIEEDDIEEDDIEEDDIE
EDDIEEDDIEEDDIEDDDIEDDKIENDKIENDEIEVQEVDDTEKAMRRKSDTGVHPKGGDEMVLNEGIKTKDQETGRDSD
EAKYWAPRSSERETLNECHVGGSNENQEEGETEEAEEETAEEDSEMDAKIWVQKAMQNVRENAAEMSPSLLSFYNKLRKN
ICGRSSNDDLYDPNGQRVLENMKKEFTKLTKGQFRDAEYETDCYDNEDEWVQMKNGNHDTLKVQEGEGMKSKKGEDLSST
GGAKALRKDEAHEKVNEEMHGEVHDEAHRETQKQAHKARDVANPEPVLTVQSSLDSQENKNDKLKFLPTKSLKRVSSHHS
GGNTTITASANLNNDEYHFHRCGQIKEKEVNTEENETSCSFTSILKRKRTNSLLREMLIGNKYPERYSLVNFSSMDSDVF
DSNSDDMSKTSLDEDSQAGGLQLLSGKKDGEGAVGGEDKEKEEKMEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEEVREE
EDEIVGEQMPHMPRAKGSLTQERPHQHNSNRRNEYNDDETRPSGRFGSISKKHNITQNSSNCGKGKNILHRDQTGNDVVK
EEGEGKKWREEVYRQSKNRRNNFENNDHLTGEENIMSLGRKNRTTRDSDKNGGMQNGGMNENKILEVRGGDRNHYTGKDK
GKEWKQKEKKEQKGQIDHTEKTKQTEQKNQSEHTEKTKQTEREKLMKLLRLNLCKEERPCPPNSKTNNLEEYNLKLKKSQ
NYSSSLKSESTDVTERNVHGHNIRSDKYAPKDFVYNHNKTGNMLNFDVQEMVKEVNICAYPVRITHNGAVNLGGGKEDNL
AFPGKGDSKEAYLVTEKGSNGSNRSSGGSEKGGCDEEGEGGNIDEDRSDTKQPITSADFFSKMCTPQLSNTKDLALSNTL
ALYLRDVCLKLGKEKQHSNMLLKEKKRLEIKIKLLNENKQLYKKKIKSLEKNCNEKMKMTRKYQIMKEKFKSMENIKMEM
PKDDINLQNEYIENAMEQLYNIFSDVFGENHIITKRIENLADVYIKKEKKIEIQMELDLLKNVEEIVKKKNEYHKELEKK
NDIINSLNNNLTKITRSVANMKCSIIENEKKSKSLLEELAKKDSLLKELDERSSQMAKEKEMAFQKERTQLLELLNDRDE
DRKRAKQYKEEIKGLEEKLKSYLDTNVHKIHDKNYEIMVDRLHDEQIKMHSLLTEKEKLINEKNLQIENLESQLQSWADE
ATNWIVVADKHTKLITNHNILKQNYEELKFKYIMDMKYIQTNKNEKVKELMRKFS
```

926 - 945:	EEEEEEEEEEEEEEEEEEEE
927 - 946:	EEEEEEEEEEEEEEEEEEEE
928 - 947:	EEEEEEEEEEEEEEEEEEEE
929 - 948:	EEEEEEEEEEEEEEEEEEEE
930 - 949:	EEEEEEEEEEEEEEEEEEEE
931 - 950:	EEEEEEEEEEEEEEEEEEEE
932 - 951:	EEEEEEEEEEEEEEEEEEEE
933 - 952:	EEEEEEEEEEEEEEEEEEEE
934 - 953:	EEEEEEEEEEEEEEEEEEEE

A0A1D3TK92 **A0A1D3TK92_9APIC** (383 aa)
Casein kinase II subunit beta (CK II beta). *Plasmodium ovale (malaria parasite P. ovale)*

```
MEFISNNESSNGVVEEENQEEDVELSAASLDEHARNDFKAEESEEAERDEVERDEIEKKEVGEEEVERDEVEKEAERNEV
EGAEVEGAEVEGAEAEGAEEEEEEEEEEEEEEEEEEEEEEDDDEEDEDDDDEDEEDDDDDYDDDEYDEDDFNEATVSWIEW
FCQLKQNIFLVEVDEDFIRDEFNLIGLQNKVPHFKKLLKIILDEDDDDDDDDDEEDDYDEEDDEINRDSEEMYKNKDLYE
QNAGCLYGLIHSRFILTSKGLALMREKYKSGIYGTCPSIYCDNSKLLPTAISEVPKFLSPLLYCPRCCETFYPHKTSLLN
QLDGAYFGTSFASFFALSFNIQSDKKKTFYTPQICGFTINRDIRETLYMDMNKDNSESSEEYS
```

99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE

A0A1D3TL87 **A0A1D3TL87_9APIC** (637 aa)
snRNA-activating protein complex subunit 3, putative. *Plasmodium ovale (malaria parasite P. ovale)*

```
MAERKYQSFTLPIPHFSPNLIFNPDEYDFYKIKHKEGHKASPNGNTLKKGANAKVEGSPKNRDGSDNERGSGSGSGSGEE
SENEKLFMRYLKHIGKKDVSRRGDNQASKSSPCSRDSGKDNASVAKDQPGGNSNKLDVVRKKVHLFEKYPHITIKEELKM
EWLYHMVPKSFVTRRVNISAFEEECRRVRDRLKVRPCHVRKEVDEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEAGMEEEEKEENEGEQERDNKRDETDDVGEEIVERAKSKIYSRLIRVLLSGVRTPSVEEIINHIVYHNCN
NWQYKIDMDVLKKVANTEKTRKVLNRTKCYLDWLPNMESNPFSKYEIIAKLKEKTISKTFKLVCDFNNTILKSLYINQNV
INIFYTLTEYPTYAKDSLKNLSSETIFIISVSFYHPIRGIKIAEYDILSNQTLAHLTDVFFCFDTSNYGFPKFAGSLYYI
DGILYPDLRKKEALDYSTCILNFYKKMKNNDFVRPPYKIPQHKAILRDIEIPLYERCCFLHQGNCEHRVVFTNVRQHNSY
RDKEFSQYPLRTFKPNITRKFCTCCHKNEAKKIVLDCYLLKENPSYVCNGCFDLFLLNESGDFVDPSMKQFDYINDV
```

209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE

221 - 240:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEEE
225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE

A0A1D3TM12 **A0A1D3TM12_9APIC** (430 aa)
Uncharacterized protein. *Plasmodium ovale (malaria parasite P. ovale)*

```
MNDSNASLSRKFSCPTNEKPEDGNKKRTKLIRLRNGHFRRIVDISNIDEKKILPNSCTFPCSTPRTEANGMLLALRGVQQ
TGARNMVATWSQHGHHISATCFASFLQFSYHPFSNYIHFSPVLILSSLDNKEKKWEEVSEVPSPNVYRKRRNSSMPPPSY
IVTVEEEKSSEQPSVRTISEFSLTCTSAKDEENESVKTQPEEEEVGEEQDEDVEEEEEEEEEEEEEEEEEEEEEAGKEEGE
EEGEEEGEEEDFMAEKEEEKVEEKEEEKEEVPPEDKQLIAPSKTLMRGIKTNIYFLSNKEKVQALMCYNYKCNAVVFEKD
TFLRYLYMKSINNIILNERMIEELCKQEELKYVLASNSIVVESTDFLKPLIIEFESSISKKIFVKHIKLNAKKEMDMKKF
DEYLYELDPNEKLRLRKVERFHSFNKLVAE
```

214 - 233:	EEEEEEEEEEEEEEEEEEEE

A0A1D3U879 **A0A1D3U879_9APIC** (1141 aa)
Vacuolar protein sorting-associated protein 33, putative. *Plasmodium ovale (malaria parasite P. ovale)*

```
MNTLNELKEQGRLLLLNILQSFSGVKCLFFEKSLHILLNVVLNDEDVNKEKIEHIFVVSNEMDVQTSKLDNISNILFFIR
PYFYEIENIFKIIEKIEKVKSSEKKYVFIFIPYMTYMCEQEILKNNIFEVSIKIIIYPLYFIPLYNDVFSLEIKNIFKDY
YVDNDFSNLIFCAFSLMFLQHLFNGVFKNIKSLGYLSHFISEQLIQLRKEIVASNFHIQAPNNFDEDFLDILSNIQHLQD
NQHFKNSTELAVVPVKYALHKIFLSEKKKNKSEQEKKSHKKGNVNKKEKNFKIASSFEQNEELPKRYVDAHRINSVTKKI
EGRGKTPNGELPVEEACGEEEVEEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEGEEEEGEEEEGEEEEEEEE
EEEEGEEEEEDDDVEENVKSESAEKRTGGREKREKRKHELGDEQYEEKEALKCAASMEQNVMGKESKAGIATPEEVQTKD
IVSTLGTNVDVTPNPNDKNSLCSDSPSGRSCSNISPFCEDVCKTEQEQFVEEEQEKENESQERNRQKGGEMDKQESEVYM
YVNPGVRKYTRKTTTKNKASSSKGGKELSITKGNKFRDCLSPDIQKRKMEPAHITVDAAADAGAEVGSEKKDPSEEPSRR
EKQKKEQQKRREGKGKTKWGSAHGRRHWDEAEVIYKKNRKQGVTRKEGKVSPGFMATMDNTKFLMKKKDREKAEREEKKE
KNYLLEKIGISSFQFLLNVCDKIDSCVIIDRRIDMVTPFCTPFTYEGLIDHLFCIENLQIEIPRYIIFNDQRGRNGTIAS
TPSVAVENNFSAGGSTGGGGDLRVRVKLRSSVDVLYNYIKDLSQNEIGSFLHKRASDIQKTYQEKDSLKDIGQINEYMRK
FKEKHYEHNSLSTHVNLASFILSVIKKEHNFSKLKLEDEIIQLNTNSSKSKIHNVVKKIQLLIYTKENIYEVYRILCLFS
VITNGFSDNYMNELKKDIIEQYGINEIVRLNKLHLCNILKYQPKQKFIWNCLKNNFNLLSNEENDISYVCNGYAPLSVRL
IEYMGILKNNVQVFPEFFNLLNGPTYDIIQNAVGYEHVQDKENHLDINNKKKFVILFYVGGISYAEIAAIRRLNRNNQDY
HYLIFTTEVTSSRKILQAMGA
```

348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE

A0A1D3U8Y1 **A0A1D3U8Y1_9APIC** (1636 aa)
SET domain protein, putative. *Plasmodium ovale (malaria parasite P. ovale)*

```
MFRVALLKNLERGGTGDEEEEEEEEEEEEEEEEEEEEEEEEKISEESNKVSRKEKEELLEVAKELPILYENNDKEVIEALI
SSFVERYPKSVDAYECFSNFYIKMKDYKSALSMLYAALYVEKKNKTIVRMLHECEGRLVSQVYKIPTRYKNWVSFPESRP
YKEDVYSWESNCGNYGRSGGENVRGRGDRTDNNQDDEFIERKSLGKKVHLVRQGQQYIALARTNLEPGEIIFQEKPLVLT
QHIFSNYFTYSTCYHCFRERNISQKSYACPVNPHTCSYIFCNWKCLVDNIKIHKIECNILPIIYAASKKCKLGYYNVLHI
FRVLIKTRIDRDYKDKDHNMLNDIFTFPSYYYAVKENQKDIFNSFNTLANIIILKFPCSFYLYLKQQELVEFMLIIWQYS
TFVKYYSPSSIIQQINPETTFGFVFSPQLAKLHHSCIPTCTFYYDDNGKITVRSLCTIPEGGKLCINILPDQYLPLKIRK
SFKAIPRIFTCGCARCSDPTENNLHLRSIKCPKCILGYICPMKTDSLVETLKLHWYGQKGMNEEEERAYSREEVIAKRSG
SPSKCSDSSTKRGGSPSNCSYSPAKRGGSPSNCSYSPAKRGDPSSNYYASPSRSKPLLTDKEKKILDRLEKEMERWVCSN
CGKLSIQGNKRCIMLENKIYMLYNKGENEYMRGNLISSRNILLQLYKEFCHVLHPNHYIIFNTNVLLAGLLRYNPNKEIY
ESLVCLRKAIIAAENVLSVCSLEKVHLYINLAHYTFNCLNVYKLHHKGIGISSEFVIDPIYTAIWNSSVVTGFNSTLTIV
LMQQLRMYAIYMNKFTPYMDIHFSIERKENFCTFYHKVTQKKSEPFRYIKKKTEDDPFYPIYMACQCFDLKFEKNKYFRN
IFKSFKNIPYFGNGLDALSLACSFGNINLVKLLLKLKYSIFLKNELHMNALLYMASSFLPEEKTSYHYNYYYTLLKEIEL
QNINFGHVEGNYLSQEMFTHEENKKSFLLPQNGLNYMNSCHIKNEIEKPFPFDIVLDEEFIYGEKCKEIDTNQKIILILF
```

```
LKHLHKIEVKKKKLYKKRLGLSERFHRFGNTNARFLKRAERRGKGGKRGKKKGMKKREKKGVEKREDKTELTPYNNLAGN
NEEEDGNWGSTRKKPDNTKRHGSHLKELSSSGSSLFSDNPSHGSSQTGESDFLNGSNLSEESDIPSRGSNLSEESNTSSG
SNLSEESDTSHGSNPSEESNLSSDNSEDVLNNKVKNYYSQKLLVQSVSHKLLGFNNVLHYACARGKRELAKQLIISGVPV
MLLNGEGSTPLHMASFGGHNEIVKTLITYKSDINFVSSHGETPLMLAIYGLHIDVVKSLIENGANIMTKRNNNMTVLHCL
VHGLLRTETIHYKNVITMDDIPYLSLHGFTELSSSKCNIQRLTNLNINVLNSHITIIEQMSHDFFLLPFKLLHRLKKAIT
ILKYIMSYCPIFIYEIKNVNGYNPFELLKTTWKKLCERRLEVLSMSDLKISSFSERQKNIISQAWTLITSLVNAILSILR
PDRSILTSIYKNLLHMRGTTTWGNQGNAQVADVKKPVEDTKKPVEDTKKPDEDMKKPDEDMKKPDEDMKKTDEDTKKSGE
DAKVPSESSNTVVAKASALKKVVLKKMKPPMLKNKG
```

18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE

A0A1D3UAN7 **A0A1D3UAN7_9APIC** (2498 aa)
Transcription factor with AP2 domain(S), putative. *Plasmodium ovale (malaria parasite P. ovale)*

```
MNDDMCAKEKLSKVEKLRKKKEGYNVSDNCKLSKNEHFDHEENLRYSKFCEHNNNAYDSYDLVNIPSTNRISDDEVKPSS
ISGRTISSAYAYVDDMRNISDSINSTNSNCNSTLYGNSSQGQNVEGSYKGASKDDQTNFNAGLNIPLMKLLSMRCSTNVD
LGNNTNCDSVSSKSIFKQGFERDSISKVNSAYTVHGENIDEDCDEKKDTMRSTNVMNQIMQNSEENEGNCEQSNNTMDSP
RFADTFSGEYQKSSVVYQQKEANIMSTIMDSKNMYDCSKTFDKVLTRKKKKQSKDNEDELNVSYGKIDYTNRIVQNMNMF
SMNGKKCINMVTSENDDISSENENILSNDIAKKFFDNMDLLHSLNKNADNDNAKSEQLSKFNSMNYVKNVLSDMSNMHSG
IGNSHNNAGRILGNVINSSEETNYINEQDSYINLVNMDRKNLKDSQNYLYSSDYLGIHNAKLGSKRSNKKGATLSTKNNE
NVITPHDAFTHNTYIGMNKDSCDMSLYNNGSSRNGVIQNGVAPNEVIQDGMSNKIVYRKQPSSDMHGETLKSAECMKINS
PLSTYDYDYDYDYCNFALNNFPNSGIELIKSQKKFMNTKCENTMAANSSSSNVCNINNKKSSNSKLETKDNAEFYGNVDN
DSYKKKTINDKFINVNKTNEDMDNSRNYAIPLVLKTSKDLGNSVKKNISSSVDVITNACGMSQSNNLSERKNINSGDMKM
SGKLINMNHHNRGNNTYENAGDSSSNYGNAFDKENFLLTCNQEDIDNFRIMNNSDGLMTGDTLLYNAQEMKHKEKLKNVC
YNDVFSSRMKKIPEEQFRYLSQKEESFSSHSFCPDVNVVAVSNGANVVGEAFLGNPKRRNQSIDFQTHRSFSCDEERAEN
DDFVDKVRRYQSFETHEEFGEKKNELDMYNVLRGGAPFISTTSSDIRTSYKSDNYCNKNETDIEEEYEDAPLLCERMQSN
NNERVNEQREIASEHAGEEEIEEASNNERKIFTEWNESFRGEIAGEKRKMRNSAKLKILKNDNTRSKKDMNNVEPSIISK
DKNNYISQYYDDLNKALFNIKNNSNIDELTKKKLLSRIENSFFPGKNPNMHFSNEEHDEQAQSSAVHANYMKQGRTNATQ
EVHRGSNNASHSGMRSTEHGEDCDPFEKCNDYDNSKRSRKCDLKPPRSSVRSEKAPRDIKMEKHREYFYKNSFASMGTST
SVVPNVTANANSCSSVNAQLLMGKQCEQGFLNKYNYAHDGSRICDVGINEDAKVFTVKERKNKKQKKIMNVLGEKNRADD
MLQQGVGVNEKYDTHDNCMNEEFYNDISNENNTNEVICVGDFKNRSMNNAGMEKFQMNILNAPFKKKGKVTLSCGDDMND
ELRKIIISKNELTKALEQNDRNIIENVEGRMFMYSSNSNNSNNNNSIGKSTSDVWKKGNNNDPMLRKGKMIMDEGSSRNF
SIMKDELNASMDTKKLLYKKNKEDMEEEEEEEEEEEEEEEEEEEEDEEGEEEEEEEEEDEEEDKLVNVRNGYEENADMGI
NGKKYDSDDLKSRKFGEIQNNEKKQKLCMSDVMKSNELQNNDNYFKFHSNLPSNLLSTSTSSSYSNDNLKVSSANYSMNE
LSSNACTNKYYTEESMPSNLNVNTQINKNNNISYEKKKKKNDKKYVTSSFNSATNYVSNVNYANGKITDNDANVDGFCQS
QKGKGQHLLNVLHRMDAESKVIPNGILIDECVKKELINSSKNQFMMKNHHVGEKQKQNQKQREREKEEEETEETEETDEA
DGADEGGEADEVDEKEHVDHAHHENVCSTGMSNNSHFGHHLGDSNLHDNSKKVVWGNANEINGVDVRRCYEDKFVENSQS
NYAKSDVQFRKNNLQKSKSHSENDKLLNLYLKRKMSVFSDYAESDETNLKKHKLYNNYGKEDNEFLLSRTNSLNINMSRM
KKEQLDCENEANSNLNNDNSGNKQVGGGRLYDPLVRVKGEQEMLSNITDSSKLLEEKFDLQKGSRNQFDDNKIGAQVKGE
NMVGEKGEKPNEPGNDASNRLEKDTSNGQENETLNGLENDTSNGLENDTSNETSNEASNAGGGTVKNEIDVSVCTLANCP
THNPQSYTRNVSRRGDSQGEGGMVKEENDELKRIPGVYYDKNSQRWFGEHKINGVKCAQSFAVKKHGCEEAKRLAIEWKK
ARIRGEVWDRFINKKKKSNNNSSCINKTNKTSRPSVEELRIKYLSMSKNMPKVRGVWFNSTPQRMGWVGQAYKKCKRIER
IFSVNKYGFEGARKLAIAFRNSQKPSNEDSDEDSWSKDDKGNIKNGDENLNSYEFKTGYSSCVTRTKSSHDDMNDANDMN
DINDGNDVNDINDTNDSNDNNDSHYGNDDNDGNDDRYNNDNSYSRPMSNNMNKIENKDTRINLCRDAILFILHDLETILE
LNIPMLNKNVNIYKICIKHHLNYLTLIKSEEQIIPYLNVFGDYIQRCILPTDLPYAELYVLIDSLIHNDILPSFDHKENF
AECSVAEDPGIITPSMLL
```

1466 - 1485:	EEEEEEEEEEEEEEEEEEEE

A0A1D5PV42 **A0A1D5PV42_CHICK** (1105 aa)
Uncharacterized protein. *Gallus gallus (Chicken)*

```
MSLENDDKRARTRSKSVRGEQLAVPDCPTPGCNGSGHIRGKYARHRSLQSCPLAKKRKLQDAEAEHLVSKRKSHPLKLAL
DEGYNVDSDGSEEAEVKEESGSEESEGTLEEDEAEVVEQEETRSPEPAEGRSPAKSAHYGQKPATSTSGPSKANYSNYQE
IIANSLLNLGQIAEETLLQVSKPPSNVVHLVHEDAGEEIVEEECDKEIIIQTEDAEEVIEVTSERSSELCPEHQDDTNCE
ESCKLQKAMQTEAEEEDEEDEDEDEDEDEEEEEEEEEEEEEEEEEEEEEEEMAPEVICEEAPHTSQDTQKSHCEGQFSPKPE
YSVIVEVRSDDDKDDDAHSQKSAVTDESEMYDMMTRGNLGLLEQAIALKAEQVKIVREPSRLPGEHVKHFQVDEKQSKPL
DSIRKSYYGKDPSRPEKREIKCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRIPPEILAMHENVLKCPTPGCTGQGHVNSN
RNTHRSLSGCPIAAAEKLAKSHEKQQTQSGDPSKPSSNSDRILRPMCFVKQLEIPQYGSYRPNMVPATPRANLAKELEKY
SKVTFDYASFDAQVFGKRMLAPKIQTSETSPKAFKCFDYSHDAEAAHMAATAILNLSTRCWEMPENLSTKQQEAPGKSMD
IEVDENGTLDLSMNKNRKRESTFPSSSSCSSSPSVKSPDVSQRQNSTSATSSTMTSPQSSQTSRQDEWDGPIDYTKPNRQ
REEEPEESEPAAHSFASSEADEQEVSEENFEERKYPGEVTLTNFKLKFLSKDIKKELLTCPTPGCDGSGHITGNYASHRS
LSGCPLADKSLRNLMAAHSADLKCPTPGCDGSGHITGNYASHRSLSGCPRAKKSGIKITPTKDDKEDPELMKCPVPGCVG
LGHISGKYASHRSASGCPLAARRQKEGSLNGSSFSWKSLKNEGPTCPTPGCDGSGHANGSFLTHRSLSGCPRATFAGKKG
KLSGDEILNTKFKTSDVLENDEEIKQLNKEISELNESNSEMEAAMVKLQSQISSMEKNLKNIEEENKIIEEQNEALFLEL
SGLSQALIQSLANIRLPHMEPISEQNFDAYVNTLTDMYTNQECYQNPENKDLLESIKQAVKGIQV
```

269 - 288:	EEEEEEEEEEEEEEEEEEEE
270 - 289:	EEEEEEEEEEEEEEEEEEEE

A0A1D5Q3J0 **A0A1D5Q3J0_MACMU** (1266 aa)
Euchromatic histone lysine methyltransferase 2. *Macaca mulatta (Rhesus macaque)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGA
LLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDESENLEGDGDLH
GGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGPEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEELGSARRSEVTLAKGDSGSLEEWET
VVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAKK
KWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEELP
LCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAG
TFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGAAAPAPPPLSQDAPGRADTSQPSAR
```

```
MRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQ
KVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCV
YSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHW
ASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLN
RKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGESCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSN
CLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFI
CEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDI
RTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE

A0A1D5QPG7 **A0A1D5QPG7_MACMU** (1499 aa)
Shroom family member 4. *Macaca mulatta (Rhesus macaque)*

```
MENRPGSFQYVPVQLQGGAPWGFTLKGGLEHCEPLTVSKIEDGGKAALSQKMRTGDELVNINGTPLYGSRQEALILIKGS
FRILKLIVRRRNAPVSRPHSWHVAKLLEGCPEAATTMHFPSEAFSLSWHSGCNTSDVCVQWCPLSRHCSTEKSSSIGSME
SLEQPGQATYESHLLPIDQNMYPNQRDSAYSSFSASSNASDCALSLRPEEAASTDCIMQGPGPTKAPSGRPNVAETSGGS
RRTNGGHLTPSSQMSSRPQEGHQSGPAKAVRGPPQPPVRRDSLQASRAQLLNGEQRRASEPVVPLPQKEKLSLETVLPAR
NPNRFCCLSGHDQVTSEGHQNCEFSQPPESSQQGSEHLLMQASTKAVGSPKACDKASSTDSNPLNEASAELAKASFGRPP
HLIGPTGHRHSAPEQLLASHLQHVHLDTRGSKGMELPPGQDGQQWTLSPLHSSHKGKKSPCPPAGGTHDQSSKERKTRQM
DDRSLVLGHQSQSSPPHGEADGHPSEKGLLDPNRTSRAGNELANQQPSASGSLVQKARDCSSTTKVAGGTEAGEEGDSEH
KECSRMGGRRSGGTRGRSIQNRRKSERFATNLRNEIQRRKAQLQKSKGPLSQLCDTKEPVEETQEPPESPPLTASNTSLL
SSCKKPPSPRDKLFNKSMMLRARSSECLSQAPESHESRTGLEGRISPGQRLGQSSLVLNTWWKAPDPSSSDPEKARAHCG
VHGGHWRWSREHNSQPLVAVAMEGPSNPGDNKELKASTAQAGEDAVLLPFADRRKFFEESSKSLSTSHLPGLTTHSNKTF
TQRPKPIDQNFQPVSSNYRELRRHPMDQSYHSADQPYHATDQSYHSMSPLQSETPTYSECFASRGLENSMCCKPLHCGDF
DYHRTCSYSCSVQGALVHDPCIYCSGEICPALLKRNMMPNCYNCRCHHHQCIRCSVCYHNPQHSTLEDSSLAPGNTWKPR
KPTVQEFPGDKWNPITGNRKTSQSGREMAHSKNSFSWATPFHPCLENPALDLSSYRAISSLDLLGDFKHALKKSEETSVY
EEGSSLASMPHPLRSRAFSESHISLDPQSTRAWGQHRRELFSKGDETQSDLLGARKKAFPPPRPPPPNWEKYRLFRAAQQ
QKQQQQQQQQQQKQQEEEEEEEEEEEEEEEEEEEEEEAEEEEEELPPQYFSSETSGSCALNPEEVLEQPQPLSLGHLEGS
GQGSQSVPAEQESFALHSSDFLPPIRGHLGSQPEQAQPPCYYGIGGLWRTSEQEAAESAKQEFQPFSPPPGAPAIPTSYS
AYYNISVAKAELLNKLKDQPEMAEIGLGEEEVDHELAQKKIQLIESISRKLSVLREAQRGLLEDINANSALGEEVEANLK
AVCKSNEFEKYRSFVGDLDKVVNLLLSLSGRLARVENALNSIDSEANQEKLVLIEKKQQLTGQLADAKELKEHVDRREKL
VFGMVSRYLPQDQLQDYQHFVKMKSALIIEQRELEEKIKLGEEQLKCLRESLLLGPSNF
```

1136 - 1155:	EEEEEEEEEEEEEEEEEEEE
1137 - 1156:	EEEEEEEEEEEEEEEEEEEE
1138 - 1157:	EEEEEEEEEEEEEEEEEEEE

A0A1D5QQM9 **A0A1D5QQM9_MACMU** (677 aa)
YTH domain containing 1. *Macaca mulatta (Rhesus macaque)*

```
MESTDTKRQKPSVHSRQLVSKPLSSSVSNNKRIVSTKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPE
KTCVRKRDPERRAKSPTPDGSERIGLEVDRRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEE
DEEVEEDAEEDEEVDEDGEEEEEEEEEEEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSG
TDGSDEKKKERKRARGISPIVFDRSGSSASESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSL
AKAKGVWSTLPVNEKKLNLAFRSARSVILIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICR
RELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVR
DVGRRRPEDYDIHNSRKKPRIDYPPEFHQRPGYLKDPRYQEVDRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPP
YPGMEQPPHHPYYQHHAPPPQAHPPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRP
RDNRRDRERDRGRDRERERERLCDRDRDRGERGRYRR
```

179 - 198:	EEEEEEEEEEEEEEEEEEEE
180 - 199:	EEEEEEEEEEEEEEEEEEEE

A0A1D5QTR4 **A0A1D5QTR4_MACMU** (214 aa)
Uncharacterized protein. *Macaca mulatta (Rhesus macaque)*

```
MAKGDPKKPKGKMSAYAFFVQTCREEHKKKNPEVPVNFAEFSKKCSERWKTMSGKEKSKFDEMAKADKVRYDREMKDYGP
AKGGKKKKDPNAPKRPPSGFFLFCSEFRRKIKSTNPGISIGDVAKKLGEMWNNLNDSEKQPYITKAAKLKEKYEKDVADY
KSKGKFDGAKGPAKVARKKVEEEDEEEEEEEEEEEEEEEEEEEEEVEEEEEEDE
```

185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE

A0A1D5R677 **A0A1D5R677_MACMU** (1175 aa)
Euchromatic histone lysine methyltransferase 2. *Macaca mulatta (Rhesus macaque)*

```
MAAAAGAAAAAAAEGEAPAEMGALLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGAD
TPVGATPLIGDESENLEGDGDLHGGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGA
AAAGPEPPPATTSPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEEL
GSARRSEVTLAKGDSGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEE
EEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAPKI
DRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRV
```

```
AHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGAAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRPP
CDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLD
PNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCL
HHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAE
VLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRA
IRTEKIICRDVARGYENVPIPCVNGVDGESCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCW
YDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDA
EADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYG
DRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

299 - 318:	EEEEEEEEEEEEEEEEEEEE
300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE

A0A1D9CF75 **A0A1D9CF75_CASFI** (3735 aa)
Dynein heavy chain domain 1. *Castor fiber (Eurasian beaver)*

```
MKPHQQFWLSSLPLPPTSLKPDEVQQQRAWNWQLEPELWARALRQQLNAQLLLFPADETSSNALESWHSADALDSKGQPR
AVFQRKHKLFLKAVTGPEQSTELELLLAELRSLFSAVLQDGSPAAWRYLHAVLGLLPPYRELLVGRLDLLPFLEQLYCWA
PKVQVQLQLDLLDAIDKAFPSDRSLLHRASHVDCSPWKRRAYHGPPCPACPFVQALWGEQQVQKELTTWLRPLTLPELQH
CLGIVGAEVALEETQWLDGLSLLPLALATDIPVQYESSGTDYAEEEPVESRQTKSQLYYEVPEGKAFHKRSIGFLHEASF
LGSQVRSILKTERYLKKIHFLYLNVAPSRYFKPYDLMVVPPKKVNPEHYIFSPFGILHIHPVEGSETMTLGTWHRHSVLW
QQLQFIPFFKYCLLRKALTCWKKKVRLQGLHRLHTFLGNRLLLAVPHFGTGLLHISRLLQELHCVSWIPKDRDKCYELLD
LKKALAKEKHKALRLLCHCLNLCTSILQLIHEDTYHMQQGLQERVQNSHRIRKGEGSIYLQRVLRQQLQQKLKQTETWLL
HLGKFARLINYMICQNLVSVLEDEITSFVANILQAPRQCPFLLSQLVFDDCGQLSPVPCIENMIQILTEGLQSIKVSALQ
VMQSAEQKTRKESLFYEEEDDEDDSDTEFLTPKFQGQPSDAVHMFCGPNVGLVLPWKSHTVTDILEVRGHRLRGQYLPPN
YNHLQEDLENSLQIQQALTIQQALLEGMLWEVQEFCREHHWITGIYEFLQTWGPQKLEDMRGCPIKDYIVLVNRLNVWQA
RVSNMPVELLTKGKLLLLSCREIHTELKSKLGNMRKDILAQIQNECWSRSQQLMRELTGFMKVFQTINSDIHAIAQCSQK
LNEANEQHIQLEMQVEYIRSLHEVLRNHFGLFTAENEALDISLLDMWEAFQFEKTQASEFLLSKQHAIVPKLQQLMAAAL
SELEGLLEKALSGPFMDPTEDQGTIEHQLISLEQQFENTVSHLCELHDAYATFTGDESPVPLPVCGTRPIVLQQRIWHLY
RGISENLSKWKCMAFGKFSLSVAQEKIDGWLTEAARMSTALGLHSPVLQRCMRMLEDFRTYLPLLTKLRNLQMQNLNCQS
LLRALGLDSLQSMELLTLGQLLTCPLLEFADRINQVWQRDKEQIYAQECLQQLQQHWEVRQLRLFNFILHVPYEPPTSER
SKKQVLRNPQWEVVGKDSGTFILSDYSSLQNSIQDSLQALFKILAIQKSGDFHKIALEWVTIMHGLGALLEVWVIFQQKW
IFLNKVLYEMKIQFPSADLNARFKAMDDQYRTLMRISLADPLVLSLIVPNAKRSPYFQGQQLQQLLQAGSMELEGIIIAL
ENVLYGVRAHFPRLFFLSNSELVALLAAPLEPCEAQLWLQRCFPHVRSVSFKSSPSDEKNMPDWESSSSRQSHVEALAVL
GAGGEEVRLQEPLLLYPDLPKWLASLEKCLRLTLVHLLQDCVASRLALGPFLCEAFQNLPQQSQLPLQNVLKWLDLIHAF
PWQCVLVAEEVVWWAEMEEALLKSGALAMTHTHVHKVEVLVQLMRTQRSIQGKQPLPSVRQASLLSALLVMAVTQRDIAQ
LLEKHQVSDVTDFHWARQLKYHLGSPHLIPNSPLQSLKTITSTEPSLSPVACWIDVLGRSVLYNYEYLGPRLGSLPGLLP
ERPVLALLLALEEVACGTLVGPDGVGKTEMVNSLARALGRQMVMIPCLSQIEAQCLSSYLNGALQSGAWLLLEAVHRLPP
GLLSALGQRLAELHLLYAPLCQEAFRRISTIDPTEPQLLGSGFFEKHHVCMRLGYGCLLTMHALSPTVPANLHLLLRPVA
LALPDLKRVAELTLLGAGVQEASHMATCLSKFFSLELELASGPLPCRLPLLKQILEDTIQTLNVTTEEFQSQQSHNFAAM
EEAALLRALLHSPLFNTLDGLRLQNLQELLCEIFPSARQLLAEPMIHKLVKMIVVEEMQQIGLLPSPDMLRSLEQLSQAL
SRSSGILLLGPAGSGKTTCWHSLFKIQNRLAAMESTSTYGCQPVEITHLYPSVLNSQEFLGWLEGPCWHHGIFPRLLRAT
PQCNSMGPKEQTKQSMGIQHWIVCDGASSAAWLDSITCLLSNPPQLSLPNGQQIARPPDTFFLMELADATGMSPTVVGQC
TLVWRGGEQTWQSMLSILMASLPHDYRLQLQTVTELNRLAEVLVPATFRFFTHKDFSSLLQVHGQRAVCPGVAEVTSLAR
ILRSLLDPHLRLYEEEKVPDPEDLNEPVAQSFKSSKSSSLNRSQVDSDDAPNKHREHLLAISSFLFALIWGFGAHLPSRL
WPLFDTFMRSSISCLSNYPEPPPSALVFDLHVNPEDGTLVPFTGQYLSSRIKETLGNFYPSTQTERLLYVVDLLLSRGQP
VLLAGEAATGKSTFVEVLVEPNHPYIYSPIHPAFGSTHLRLLLSRAVQGQAQASPWPGNNQDSKDSFLFVLEDLHLATSD
PQKSCQPVLETLRQAMDGTVYAHITLELQTLQPVVNFLATATVPGFCERPLCPRLFRLFTVLALDSMTQATMLSRHAPSI
QAWLEHFPSVERESILAKALVWASMEAWEAVCNCFMPSPLHPHYRFSLHSVSHLLGSLQLLPSKMGSRGFVDCCDHEEHL
RRVSGLRGTRLAVMMVMRSMVRLWMHEAQRTFCDRLDSPRERSYCAKLLLEVAQGIFCCGSWTQHSNKDREEEEEEEEEE
EEEEEEEEEEEERVPEVESEGELAQWEDLSNSNSEAEQEEDTYGFQPTTVSHCSEPTVALSIRSINRETTERKGHKIKQEE
ETRAPSSKKSKKSKICWKKALQADLISPLLLPVLLLRPREKPSDIVFSQELILGSDSENPNLYLEREWKNLEEQLATSAA
QLRLSPHLARCHSMVQHVARLVRVMARPRQHGLLLAGALGTGRRTAITLATSICQAHLFHLPSGSEEAIFQCLRDASWHA
GMLSQPVALLVPKSVALITLHRLVALATSGSFPDQYTEADLDNIEEHLPRENLSIKHNIKKETILQRFYQQVCSNLHMFF
LIGDDQTQKQLPSTLFLRLLQLATASIDRYEPWDQASLVRVAQYHLKDAHSPPLDDGPLKCPDLQASIPSVAKAMALIHL
SATYYYEHLCPGLPLVTPKTFLDFLDTFILQQQHMILQIKNSGQRIHNALENLRMLIEQHSVQSNLVFNLEEELKGSHKI
VSMFQQELEQSKLQHKQQLSECQHQESLIENLTKQRDALQAQRDAFQEQMGKAFLGPLSKLQVTDFEEIRSYRAPPESVV
QVTDALCDLFHRETGWASARQLLCTEDFYQELVFFPKEKLTDSELIKLNQALKAPGMSDAALRAVSIPAASLAGWLWAVL
HYGLAQRRGLPTGLLLRQVEATLTREQSRLGQYQFQAQEMFEHTLALTKKLEDAQASHRHLMETLSQAQYGQYHEWPVKS
ALLTPMHTWTTKLQKLRGQCITMFGDALLCSAAIIYLGPFPRLRRRELMDKWLALCRGCQEALGPDDIAQALKQNSVVMP
PKMPLLPTSCPFRILSLLSCESEQYQWDRDQKPQGKTARFVGLLLRSCSHYYSCRWPLLLDRSNQAPIWLNPLPLEDNRS
LAPVPIEDIGKGLTRNQNGDDKEWEDMEEDDDSEEESKDKDQTKEQKADKRENEKEKKQEEKKEEEKEVKENETESQGSN
VASETRSLPPLCLSVLSGADPELGPQLQEAAASGENCSLLSSPNFVTPQSSHFSV
```

2711 - 2730:	EEEEEEEEEEEEEEEEEEEE
2712 - 2731:	EEEEEEEEEEEEEEEEEEEE

A0A1E1K1W2 **A0A1E1K1W2_9HELO** (382 aa)
Uncharacterized protein. *Rhynchosporium agropyri*

```
MAEPPKPPASTTRKSRRRRSQKAKKKAALFRSNDSPTDSTPAMRPKPQITKPEIINRSIAFGLKFSDLILRDSIQLYSVG
STRGKHEEGKKGGEEEEEEEEEEEEEEEEEEEEEEEEEEEERLPAHKRITQHANLVLSQQARLPDRESQTINTTTTSPTTVV
AETNHTSTSTSKSKNTTRTTSPFPFSNLPPELRLTISTLILTSSSSSSRGQKPRFLWAVQRNAALYAEVKEAWCRVNEFH
FTLQESGPNRVREGMRRAMRGLVRRAVVRVHCTLAIHHIIPSLAHLTSITVHIHGPKRVIQGRVALNDAEFFRPFAEARS
MLDKMLSKVGKCVYVERRSQEWCWEAEKGQVFKPRGRKVHIKFDEEAREIGTEPVQDGGDAS
```

94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE

97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE

A0A1E1KGH7 **A0A1E1KGH7_9HELO** (579 aa)
Uncharacterized protein. *Rhynchosporium agropyri*

```
MERLSYKVKGRRFTSFVHIRYCETSFFGAIEIIASRFFAWLSYARLDYYIALREYGRPRREISLHRNHRVDVYLTFSKIL
LNMLARSCQNFSFSAHFVIQDLALPFGIDNKQQQTGLSEMITVFWKRERIVKTSLGGENKARYRKVEQKDLDTQPNIFRL
GYYSKVLDPPKEDPSILENYRTITIKCLYRYCNKTWRNLRVNESISNLFTYYKHSHKAINLRFLSDNNIALEDLVNIQLS
IEESFNREGSTTSTISQFTEENFKRLLLNFIILNNISFRAISSLSFNKLVNYLNNHFINFDLDLKSYLLSIVPLEIIYYS
RYIKKVLIKTLKDYNIKYNITSNILLIIIXEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEELEEEDLPRNINYSIWKRIX
TNIISLKYNQENRRLFEGQLLACKLESNRKPQLVPEVYIIYNRFDKFKEGSKDLLIIHAINKELAKLRKYYPKEGFIGDI
TRNRALYIALVLDPRIKREGLSNIGLSSGLESDIYTLRSDYLSSNPTILDTSNLYDTSDDDEYNIYTNTEEEEGIIDELD
TYLDEKRASRCNTSYLLES
```

351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE

A0A1E1KLG4 **A0A1E1KLG4_9HELO** (117 aa)
Uncharacterized protein. *Rhynchosporium agropyri*

```
MAIANLLLAVRESCPGEKLYRLGGMKSIPLPLPLPPLGPDGASRLASPRIAKSDSPIHPAESENNPRMTGRKETHRRSSS
VCGVYIMDPGKEGTAEEEEEEEEEEEEEEEEEEEEE
```

96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE

A0A1E1VXG9 **A0A1E1VXG9_PECGO** (383 aa)
Uncharacterized protein. *Pectinophora gossypiella (Cotton pink bollworm) (Depressaria gossypiella)*

```
MSDEEEYSGSEEEEVEEVVETKPAPKQEGEGDPEFIKRQDQKRSDLDEQLKEYINEWRKQRAKEEDELKRLKEKQAKRKV
SRAEEEKRLAQKKKEEEERRIREIEEKKQRDIEEKRQRLEEAEKKRQAMVQAMKESSKTGPNFTIQKKSDNFGLSNAQLE
RNKTKEQLEEEKKISLSIRIKPLSIENLSVDKLRVKAQELWDCIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKA
LKKGLDPEALTGKHPPKIQVASKYERRVDTRSYDDKKKLFEGDLEKLNKDFLEKVWSERTDQFKGRQKTRLPKWFGERPG
KKKDEPESPEGEEDVKAEEHEEDDEPAYEPEPEEEEEVVEEEEEEEEEEEEEEEEEEEEEEE
```

360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE

A0A1E1WM87 **A0A1E1WM87_PECGO** (389 aa)
Uncharacterized protein. *Pectinophora gossypiella (Cotton pink bollworm) (Depressaria gossypiella)*

```
MSDEEEYSGSEEEEVEEVVETKPAPKQESRPSIAGEGDPEFIKRQDQKRSDLDEQLKEYINEWRKQRAKEEDELKRLKEK
QAKRKVSRAEEEKRLAQKKKEEEERRIREIEEKKQRDIEEKRQRLEEAEKKRQAMVQAMKESSKTGPNFTIQKKSDNFGL
SNAQLERNKTKEQLEEEKKISLSIRIKPLSIENLSVDKLRVKAQELWDCIVKLETEKYDLEERQKRQDYDLKELKERQKQ
QLRHKALKKGLDPEALTGKHPPKIQVASKYERRVDTRSYDDKKKLFEGDLEKLNKDFLEKVWSERTDQFKGRQKTRLPKW
FGERPGKKKDEPESPEGEEDVKAEEHEEDDEPAYEPEPEEEEEVVEEEEEEEEEEEEEEEEEEEEEEE
```

366 - 385:	EEEEEEEEEEEEEEEEEEEE

367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE

A0A1E1XTW2 **A0A1E1XTW2_9ACAR** (391 aa)
Putative troponin t skeletal muscle-like isoform x5. *Amblyomma sculptum*

```
MTEAEMLMEEKLRKKKEEEEEMWAEYLEQRKKQRAKEEEELRKLKERQAKRKAQRAEQEAKLMEFKKKQEEQRIKEMEEK
KAREAEAKRKRLEEAERKRQAMQAAKEKREQEPVKPNFVITKREGEEMPGSALGGSGFDKFANIMYARGEMGKTKEQMEE
DKKAILSFRIKPLEIEGLTVEQLREKAKQLWEKIVTLESEKYDLEERQKRQDYDLKELAERQRQINRSKALKKGLDPEAL
QGKHPPKIQVASKYERRLDRRSFVDKRDLFSGGLEAMTDAELEKQWEERMLSFKESSRQGLPKWDPENPKNKQVSRARHV
DEDEEEEIEAPVFEPPKPEPPKPAPPKPAPVQQQEEEEEEEEEEEEEEDEEEEEEEEEEEEEEEEEEEEEE
```

370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE

A0A1E2XYM5 **A0A1E2XYM5_PARBR** (462 aa)
Uncharacterized protein. *Paracoccidioides brasiliensis*

```
MHGEGEFDLAILASQRNDNATMGVLSPIATATATMTEPARAKTTKTTTTTTTTTTTTTDSSMHLPFSDSAIDMDTESSGN
ADQTPETTTIPTTRDTMNATGKSHLQSLTTITTTMIKERLIHLTHLITDSDSHPKPDNRHNKDQNSRNEYSNSSPYHPLT
SHATSPSTSLSWSPQKSIAINRYLDGIEALLLALHITGFSSGASSEEEEEEEEEEEEEEEEEEEEEEEKEKEVKVDRGEN
ERKTNHCCTLSNNHHDPRLACISLEAGCQNANTKPHNQNQIQTKLDSQLDDVIRDLKVVTGSLEQRRAECLHLNAVFTMK
CEKLAQRILDLEEQMEELRAKKIENTIELEGLKGTVRGLEGWIKRWKMRQCEDEEGEEGRNSKHAWSETSDHGRGQWGKP
GRVLWGGDGDYDSNDGDVDDDTLMDGVSAWLRDWRDVEEGFRIRARLRERMKAVRRGPGKSE
```

206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE
208 - 227:	EEEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEEE

A0A1E2Y3H6 **A0A1E2Y3H6_PARBR** (321 aa)
Uncharacterized protein. *Paracoccidioides brasiliensis*

```
MREHDEEDDEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
G
```

12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE

A0A1E2Y3K4 **A0A1E2Y3K4_PARBR** (241 aa)
Uncharacterized protein. *Paracoccidioides brasiliensis*

```
MSTRKRARGDEEEELVALPSDESEEEEEYEESDAGDEDEEHESVSEDESEGGFENGEAEGMEPIKPTNELSRIFPKFPST
PASIHSTQSPTFGGFWIIADISISPPTAVHKKRKVVPGPNAEVTGEADGVAEEEEEEEEEEEEEEEEEEEEEEELDETENR
LEAEYEDGEGDAEADAETEAEKQKENGAASTVPTAKGAVASDVPEVPASAPAPAAKATANGAPAVASVTEVEGVGGAGDG
E
```

132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE

A0A1E3B4F2 **A0A1E3B4F2_9EURO** (225 aa)

Uncharacterized protein. *Aspergillus cristatus*

```
MNQKLRHQAEKNGKISEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDKRPSRRMGRQKDKASEYPTHFTAVRDNEVKRD
```

17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE

66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE

118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE

170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE

A0A1E3HEB7 **A0A1E3HEB7_9TREE** (1595 aa)
Uncharacterized protein. *Cryptococcus amylolentus CBS 6039*

```
MPHPPGPFDIFPPTDVHHWLTDLQLRIKNGINPPDSPGPSRSPSPLLNGHIDAFQDDGVNQQEQDKDSEADSESESDGSG
EEEEELDDINHQPQNTLAATNYLEVSSDDEDEDELQDDDGQYEEEGDYYEDDREANVAYDEQDELYDDDPRYGVEPEEDH
QAYVGSDGDVYADEYGTDESEDENEEEEEEEEDGQENEPSEEGNESDDSDGIEYVGQSQSPLPAPSPTLNPLDSPLQAAP
VPSAAASTSIYPGTGIYPAPASALPALSDLTYAPSPYADPGAPISTSTPDPTFSAQAPLPPSVDTQVYQSEMDIDPTLLG
SGYQIDTAFLNDLVQHVAQGGAPLSGMGQPGPSFGSFDPAQNQEVDGMPSLPSLDQPGECDYEMGDEYMDNEVILEEDEV
AGDQDVSGRDPSEPPKHDEDMEEADQEVAEQESLSSGDARANDEEGEEDSITVKTTTVREVIEFDSSSDDGEEEEDEAEQ
DNQAEDHEEDEDEDEDDDEEEEEEEEEEEEEGEEAGEGRISAAHAAFLQDDSIEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEWGRADGEDEEGSVGDEQPEDEPFVARDLTVDTDQVVEDVLVAGEEVIESVESRNEVTSSKSA
TPVESAPAESEIHEGVDEGLVETSAESAHEAKDLSDEGARTEHHQEAIEVQETEISQASPVDHGEQPEIFPDSEVISVAR
DRTPASNGSSSTPPDPARSPPPTSLLAPLSPHSLQPHPPRSPSVEAQIANDPRPSEVPEPPLSKDQSEREETPVEFPEPK
SAPPDSDFTAEFAYNPDPHPPSSPSLIVEPPADPRPDITFSRTVSRAATPSIGAAFSNGDGAVPGTPVEFPDPRLPPADA
HLDVPLTPHGLEPNDEGEQSPSLRVQVGASRKGSLSGPSSPPLESQEPEVSGDSRVEAHSDPEASKSSEPDEHCPRQSPT
YAAAEIEAEDATSLPLEDDIPMAPMDDYDVQGSILAEQEEEAGLGQELEPHVAADIVHDVEAPGIEGTDDKSEQVAADLP
LDAAELAEGNQRAAEEPIGEGPEQVADGNVDTGGEKPYASAYKGKGRALEIEPQDEERVLDERLPSDPASATASPERPPL
ATSNSAIERLRHHHGLGSSSHTRIPTQAREVSRNSLKSHRGRDEGSPSPPAPPVTRSHCYYEKLRLTYEGAVAVILAPHC
SLSNAQEIEHEECTVEGVPSEGEEQQARLGQMSHDNEVLQPAFSTKLRRIVGAQLFDEGCCYLLLADDNAKLPPPPSEAK
ESTPQSSSARGGPKSRTSLTASQVSPFKPAIGNPLTARTSKRLSASLEPSTPPRKRLSQEPEPSRGSPAGSVTDVGEDSA
TDSPEADPTPRRSTRLSLKREAKQAPPVREKRGGSSLRNLLATEESTTQNGQDTEGPTGSNERETTVQSEAVVRQGKRPV
LIDLRSVSPDSAQSFGSPTASTHSLQGADMSSSRALVGKKRRRDGDAYRPDEESEDEGHAENSDEEENEDEDRQNSPASL
EKGTKRKLDTGDGDVWEGGIEDEEDGERAAKRRALENIEESGTPVVEAPKAEGQEQDVGNETQRRHGFGKWFRWW
```

534 - 553:	EEEEEEEEEEEEEEEEEEEE
535 - 554:	EEEEEEEEEEEEEEEEEEEE
536 - 555:	EEEEEEEEEEEEEEEEEEEE
537 - 556:	EEEEEEEEEEEEEEEEEEEE
538 - 557:	EEEEEEEEEEEEEEEEEEEE
539 - 558:	EEEEEEEEEEEEEEEEEEEE
540 - 559:	EEEEEEEEEEEEEEEEEEEE
541 - 560:	EEEEEEEEEEEEEEEEEEEE
542 - 561:	EEEEEEEEEEEEEEEEEEEE
543 - 562:	EEEEEEEEEEEEEEEEEEEE
544 - 563:	EEEEEEEEEEEEEEEEEEEE
545 - 564:	EEEEEEEEEEEEEEEEEEEE
546 - 565:	EEEEEEEEEEEEEEEEEEEE
547 - 566:	EEEEEEEEEEEEEEEEEEEE
548 - 567:	EEEEEEEEEEEEEEEEEEEE
549 - 568:	EEEEEEEEEEEEEEEEEEEE
550 - 569:	EEEEEEEEEEEEEEEEEEEE
551 - 570:	EEEEEEEEEEEEEEEEEEEE
552 - 571:	EEEEEEEEEEEEEEEEEEEE
553 - 572:	EEEEEEEEEEEEEEEEEEEE
554 - 573:	EEEEEEEEEEEEEEEEEEEE
555 - 574:	EEEEEEEEEEEEEEEEEEEE
556 - 575:	EEEEEEEEEEEEEEEEEEEE
557 - 576:	EEEEEEEEEEEEEEEEEEEE
558 - 577:	EEEEEEEEEEEEEEEEEEEE
559 - 578:	EEEEEEEEEEEEEEEEEEEE

A0A1E3IAX3 **A0A1E3IAX3_9TREE** (1646 aa)
Uncharacterized protein. *Cryptococcus depauperatus CBS 7841*

```
MPRQGGSAAIRQPGPYDRFPPDQIHLWLDNLQNKIKKGINPSDSIDLLRSPSDIQAQKDEGVFGAHRILDECPVLERNVS
TTEGEVAIVQQSDSVQQADSELVFDGGAPVKGHHDHDEQRKTHESLYMGTDGSFTQNVWVEKQHLIKAEDRYDSRRDVTY
EKDCQAPISLPRHLHPNEHRYANTFHQRNGESKGHDKKEEHEMEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEDEEEDEEEDVGREESDNEIDKGHDKKEEHEMEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEDEEEDEEEDVGREESDNEIEYVNRSPSQPSFSLKTESNPSTNIYPFLPMHRTYQHAYPISLQQPVAPMLNQA
MNIDPTLLESDLLHNAPLLRHFSNEVVQVAQFNHQEGVNEASGNEMAESHESSDDEETYYMDEDDSAERSADTQPLEASV
TAKTTMDCEVIVIGSTDDEEYSDADEEENLEQDEEDDDHAPSEATQSQSVQEFDNDEQKFRKELKANLSPREDNIPAEKD
IDIPLLRSVEKKVDSFPELKNNILKSPTSSEHQSVGNVEIHDHQNEPIERTETEGVTGFTTNEPSSSTLNQKAEPLVTLK
IVEVTESLPDLRHASGIEEMNIPQSPNDPFRINVSVDQVKPNAQPLDKKEETHETLRDAQHSKREWLLNQHPQTPIVTSK
```

```
DLTTVPDVGNSLLRISKFPCHADTSLEENQSYEGVDGDNPSVTIAKMDRMSQGHDQKFVDSALSMEDVPDDEDRQFQNVS
VSHSDKSYHESAVDTQVPELDAFPDSPAPSNMTTQNESLSPYSHNPHPSTRLSPLAQNENGFSQAEVPSVAASGVIRNRS
PITLPDPKHAPVETDLASLYDVHHDRTIPPSSPSVITEDPSHPQSVENPSETFSNFGISSRTNTPVEFPNPQAAPRETNL
PQPINPSELEPHAPSSYSLIVEPSNEPDPIEQIATDPIPSVETAVELPDPHLPPVDSYLQTPLTPHGLGPPSGEISQSLK
VEPGDEVSREGTVETSSAPLSSEDKEEVAKDASKALAGKTPTPTGKQMNLDTDIPSASNDDHTRKTSDIDEEGYRDDEGA
EGYLIKCEAETHILKKKADKETEQRDVKPSIQSKGKGRTTVALGEGQILDDALSPSLQEIETSERPPLIMSDSAIQRMRH
HHTLAANSSISPKTRLSDHKKQQSRQKTESAANDITLPVTRSNCFYEKLCVNTDDQDSSTLKVIILAPHCSLSDAQNIDR
ENGRVEGIPTQAEEIEAMQCQLSHENQVLQPAISTKLRRIVGAQIFDEGCCYLLSANDQARLLPEDETKSATFDTSGSLR
GHRKRKSTSVLPGDGSANASPAKRSSYNSRAAIKRLSTASVEPDDGSTNTGSPAPRRSARLSLQREGTLEAQTTPVLKVE
ELPAVTEGEGDRGDEDGIEFQHGLGNMIKDADEDLEDCKGNEGMRADSSDEDGEAITADAFTSYQSKGPPSSYSVDDAAY
ESEEDRYEETEQEYEQQDDDTKSQRKPRRTLKPSRSLQPVVEVRSRKRRNRKELDEAQGVADRSGRENLDGQGSDVDTQR
TKKRAIEDESTGEPVPNSKENGDGEPAKREDDTCRRHGFGKWFRWW
```

204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE
208 - 227:	EEEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEEE
225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE
287 - 306:	EEEEEEEEEEEEEEEEEEEE
288 - 307:	EEEEEEEEEEEEEEEEEEEE
289 - 308:	EEEEEEEEEEEEEEEEEEEE
290 - 309:	EEEEEEEEEEEEEEEEEEEE
291 - 310:	EEEEEEEEEEEEEEEEEEEE
292 - 311:	EEEEEEEEEEEEEEEEEEEE
293 - 312:	EEEEEEEEEEEEEEEEEEEE
294 - 313:	EEEEEEEEEEEEEEEEEEEE
295 - 314:	EEEEEEEEEEEEEEEEEEEE
296 - 315:	EEEEEEEEEEEEEEEEEEEE
297 - 316:	EEEEEEEEEEEEEEEEEEEE
298 - 317:	EEEEEEEEEEEEEEEEEEEE

299 - 318:	EEEEEEEEEEEEEEEEEEEE
300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE
306 - 325:	EEEEEEEEEEEEEEEEEEEE
307 - 326:	EEEEEEEEEEEEEEEEEEEE
308 - 327:	EEEEEEEEEEEEEEEEEEEE
309 - 328:	EEEEEEEEEEEEEEEEEEEE

A0A1E3IP12 **A0A1E3IP12_9TREE** (288 aa)
Uncharacterized protein. *Cryptococcus wingfieldii CBS 7118*

```
METEEALPGPSSRPSTASTRPASTNTPPSKSKRRNSTSQGKGKGRAAPEPEAAESAEGQQEDKDNEGELEDRVALARREE
ASNKRPRSSNKATRRMKALRNAEKFVHIPPVPPPPNPSTDFLQSLHQLSSQFYSSHSLLHPPVKRQRAVPWASKKRLQLA
RDSNRLTEVRGGEMSEDGEEIEDILGDHEEAGGTPSMGAEDQDGQATRGVRGKYKVKDMYKAIEGEGLMAMGILVQEHII
QQLEQAGYQRPEKDASADEEIEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

262 - 281:	EEEEEEEEEEEEEEEEEEEE
263 - 282:	EEEEEEEEEEEEEEEEEEEE

A0A1E3J1N7 **A0A1E3J1N7_9TREE** (446 aa)
Uncharacterized protein. *Cryptococcus depauperatus CBS 7841*

```
MAGKRPYRDGLNFPQPVVITSGPAPSHSAHQDIQEFDYNDKEVAATQLEPIEDGIRKNSAYEVLPKHLAWREWNINPSGH
GPERIKHPPIFVKGQNVYDELGRMIDGVDVSVGIDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
TGESVRKWYLQLAKFKSEKTEAVPAADRTVELLDLSTPSPPCGSQLLPTAEPRLSMKEKTAQLSRPLRIHDSEWFIRRAL
TSSQSTSTQASRSTTPLYIPSLLKVPSAVPKRENVPNYVLGPGNKGYGLLQELGWEGGGLGKLEKRQNTCETRKDKDIIP
RVRDAQDTTIERNPVIDLTISSDEDSLVSEDESSHSANRSGPGRTDPIATALKLDRSGLGRNKSQSKITHTHKEIVRAQK
RAKYAQKRLKKGDAKGDMGKKEKADWKRRDKMDREERRRLLEVLNN
```

116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE

A0A1E3JRX1 **A0A1E3JRX1_9TREE** (486 aa)
Uncharacterized protein. *Cryptococcus wingfieldii CBS 7118*

```
MSPNLKPMIPSLLPLLLSTTPRIIALAAQPGGPLEREEYTMGIARGQIEDAMGLIRGELGKKEWKRVVKRVVQEEISEQE
```

```
DGGVGSDQDGQKEEQVPMAPTPSPSPSPSPSPLPSPSPSPPPPKHKPTTNKPKPPASSPPDISPISPKRPPASNSKRQPP
SPIGRKQEPTVIEILSSQPSHPFSPPPPPRYGKKHVVIVDDEDDGSEVEVIEVEEEEEEEEEEEEEEEEEEEEEEEEEE
EEGRGGGGGEAEQDAPSQMSSVYDTTSQARRAAKSKAGVTPSPSPSPVKKKKKKKRANRGDGDEKKSMGSDLEERKEKKE
GKGRKRKRTVEEDETPKKKPAPRSRAKKDPHEGLSAQEIKVVELKKIIVACGLRKRWSKELANYPTPSSQITHLQSMLRD
DLGMRGTPTLGKARSIRVRRELAQELDDVKAYEKERGRSADQRGNKSRSTSDDESTATEKASLHDKLTKEGVCADAIFGY
RVLWRP
```

214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE

A0A1E3JT72 **A0A1E3JT72_9TREE** (1554 aa)
Uncharacterized protein. *Cryptococcus depauperatus CBS 7855*

```
MPRQGAHAAIRQPGPYDRFPPDQIHLWLDNLQNKIKKGINPPDSIDLLRSPSDIQAQKDEDVFGAHRILDDCPVFERNVS
TTEGEVAIVQQSDSVQQADSELVFDGGAPVKGHHDHDEQRKTHESLYMGTDDTFTQNVWVEKQHLIKAEVKYDSRRDVTC
EKDCQAPISLPRHLHPNEHRYANTFHQINGESKGYDKKEEHEMEEEEEEEEEEEEEEEEEEEEEEEEEEDEEEDEEENE
EEDVGREESDNEIEYVNRSPSQPSFSLKTESNPSTNIYPFLPMHRTYQHAYPISLQQPVAPMLNQAMNIDPTLLESDLLH
NAPLLRHFANEVVQVAQFNHQEGVNEASGNEMAESHESSDDEETYYMDEDDSAERSDTQPLEASVTAKTTMDCEVIVIGS
TDDEEYSDADEEENLEQDEEDDDHAPSEATQSQSVQEFDNDEQKFRKELKANLSPREDNIPAEKDVDIPLLRSVEEKVDS
FPELRNNILKSPTSSEHQSIGNVETHDHQNEPIERTETEGVTGFTNILANEPFPSILNQKAEPLVTLKIVEVTESLPDLR
HASGNEEMNIPQSPNDPFRINVSVDQVKPNAQPLDKKEETHETLRDAQHSKREWLLNQHPQTPTVTSKDLTTVPDVGNSL
LRISKFPCHADTSLEENQSYEGVDGDNPSVTIAKMDRMSQGHDQKFVDSALSMEDVPDDEDRQFQNVSVSHSDKSYHESA
VDAQVPELDAFPDSPALSNMTTQNASLSPYSHNPHPSTRLSPLAQNENGFSQAEVPSAAASGVIRNRAPITLPDPKHAPV
ETDLASLYDVHHDRTIPPSSPSVITEDPSHPQSVENPSETFSNFGTSSRTNTPVEFPNPQAAPRETNLPQPINPSELEPQ
APSSYSLIVEPSNEPDPMEQIATDPIPSVETVVELPDPHLPPVDSYLQTPLTPHGLGPPSGEISQSLKVEPGDEVSREGT
VETSSAPLSSEDKEEVAKDASKALAGKTPTPTGKQMNLDTNIPSASNDDHTRKTSDIDEEGYRDDEGAEGYLIKCEAETH
ILKKKADKETEQRDVKPSIQSKGKGRTTVALGEGQILDDALSPSLQEIETSERPPLIMSDSAIQRMRHHHTVAANSSISP
KTRLSDHKKQQSRQKTESAANDITLPVTRSNCFYEKLCVNTDDQNSSTLKVIILAPHCSLSDAQNIDRENGRVEGIPTQA
EEIEAMQCQLSHENQVLQPAISTKLRRIVGAQIFDEGCCYLLSANDQARLLPEDETKSATFDTFGSLRGHRKRKSTSVLP
GDGSANASPAKRSSYNSRAALKRLSTASVEPDDGSTNTGSPAPRRSARLSLQREGTSEAQTTPVLKVEELPAVTEGEGDR
GEEDEIEFQHGLGNMIKDADEDLEDRKGNEGMRADSSDEDGEAITADAFISYQSKGPPSTYSVDDAAYESEEDRYEETEQ
EYEQQSDDTKSQRKPRKTSKPSRSLQPVVEVRSRKRRNRKELDEAQGVADRSGRENLDGQGSDVDTQRTKKRAIEDERTG
EPVPNSKENGDGEPAKREDDTCRRHGFGKWFRWW
```

204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE
208 - 227:	EEEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE

A0A1E3K202 **A0A1E3K202_9TREE** (750 aa)
Double-strand break repair protein. *Cryptococcus amylolentus CBS 6273*

```
MTQPRSQREYTEAIEEQPLPPSSDHGIDTDNCFRILVATDNHIGYAEKDPVRGQDSINTFREILQIAQKEQVDFILLAGD
LFHENRPSRTCMHQTIALLREYTLGDKAIPFELLSDPMDGATPGFNFPAVNYEDPNLNIAIPVFSIHGNHDDPQGTGPEG
ALCALDVLSVSGVLNYFGKVSLADEDAQSADPDKGIRIKPVLLRKGDTHLALYGCGNVRDQRMNFELRSNRVKMYVPTGG
EVADDEWFNILLVHQNRRVKHGPQQHVPEGMFDDSIRLVIWGHEHDCRLTPESVPGKPYYISQPGSSVATSLSAGEAIPK
HVGILSVQGEQFGIEEIPLKTVRPMAMGEVVLGDEAKDEAFSLDDRDEITMFLRGEVEKCIAQTKEEWDETHTPEDGEMM
LPLIRLKVETTDAKDVINPVRFGQEYIGRVANPRDLLQYYRRKKVAERKPKNNADLPDSDDIEEEPQSLLADDEASSKLR
MAHLVGQYLKAQELGVLVEGGLEEAVMRFVEKDDRDAIKDFVAKTTSFVSKTMLHNVEFDPDTVKEQMWEAKNEAVARHE
KEKGQFELNKNKGKGKSRDEDADSMAEEDDDDAMSVDSESDRPAPKKAPARGPGSRGGRGGATRGKAPAKSTGRGKSQAL
FDAASDDNDISDPEEEEEEEEEEEEEEEEEEEEPAPRKGRGRAAGSSTAAAKKAPAKKAPAKKAPAAKKAPARASARGGA
SQMTQSQLSFFQGGAGGGKKTVITLSDSDD
```

654 - 673:	EEEEEEEEEEEEEEEEEEEE

A0A1E3NIR0 **A0A1E3NIR0_9ASCO** (431 aa)
Uncharacterized protein. *Pichia membranifaciens NRRL Y-2026*

```
MAPDRDTKEIPSSDAETDRMEGVDERESQLEQLASTKTASTAELLSAPTATSSTEPSSTSSNNSVFSNTANNNDKKRSLE
ATDEVRNREGSDDTHKRVKMEENGNIEHDEDSAAQEAVADEVEGKENEEKKDEEEDEEEGGHEAEDEEEQEESAHVRETA
NNKIGEEEEEDVDANEEEEEEDEVEVEEEEEEEEEEEEEEEEEEEEEEEDEEQKLKKAQAEKEEEEEEAQKENSRVAAM
```

```
NRLKDIEILFAQLKDKLYETQLNKLEFELKLCQSNKHPELLDYMKMVDDDFQKKAERLMNLQKYQLKCLDNQTRAHRVAL
HQQFMKSRQDLKSKEVVKITTDWYDINKERRTMDMQTLELPEYYQYNETVNSANIEEYLPALVHQRNSVYKELSVLQGLI
DYKQMIPSSLNNLRGCSEEEINTDLQEMGLI
```

187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE
190 - 209:	EEEEEEEEEEEEEEEEEEEE
191 - 210:	EEEEEEEEEEEEEEEEEEEE

A0A1E3NJD9 **A0A1E3NJD9_9ASCO** (473 aa)
Uncharacterized protein. *Pichia membranifaciens NRRL Y-2026*

```
MARRARSFARAEEKKNEETGIEEFGMDEVDAFADARDKSLMEKAGLNEQPYDANNSEDEEAVEGVMDIDSDAEVEKYKKK
FQGPIDESDEEYFRAEDDSGAEGEDAEGRERWGGDYYGADEAEDEEDEKLLEEEALRLQKKHMEELNVEDFMLDEVEDWE
SEKEKKRKQKQVGAGDEGDELLTENDDKFAEMLKKGDKQSRTEMINKKYPEYLPLVLELKELQGVYESLKSSKSESVIKE
VQFKALSLYLGSIVSYLAVFASKLQSGDKFDMKDEDVMVSILGSRELWRQAKGLRKASHITVEEDQEYEEDAEDQESVES
EFAEESLSNKKPNKFAKEDLRGSDVSEEEEEEEEEEEEEEEEEEEEEEEEEEEEEATVSKPQEKTPDFTKLRSIKKSTRK
NLEDMDDLDVEDKQGRRKTLGFYTSKIDKRDIGKAAVDGDVDAAYEEESSNKNKHYAQKRRSQPSQRGRRRRH
```

347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE

A0A1E3NUX7 **A0A1E3NUX7_9ASCO** (870 aa)
Zn(2)-C6 fungal-type domain-containing protein. *Pichia membranifaciens NRRL Y-2026*

```
MCSELDSELKAHLVRIEVQETESQHVSSDEFRREIAVLAEAEDRSKEEGEGTKSMKKKEEDYEEEDEEEADEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDEGSQSSGSNRNKSSRAEGELGFKKFRRKHKNSKSGCAN
CKQRKIKCDEKLPICTFCKKRNIQCSYLTMTPFQIHKIVCSQTSNKKTHLIAEDSTDSIDGDDSAFFEEGDVLRQPTPSS
LSEDSREPTPDPPPVGFQYQPIREISLGNDGSPINSAVYHAYKIEGVMLPTSMGSQLIYDTFETNQYVPLRTKYQQAKHE
LVAGGGGSSGDVTKPKPLYSNFRISKRIFPLRSPAVVDALEEYAEQSLAVNKLLHKQDFEGIRRLLKGKSIDSYLQTDTI
WILSVVQIFKRLLRKSMILLAMDYYKNVLLKQSLLPAVNYKVKLSISCKCENESVVFIDDITNIIKCEYIPFFRDFSLAG
VNLFAGCFWVLNECLVYHFKNGLKYDLNYEEGNNAIKLLGIFSTGFYSIVMERTRVDLTITGSNIISSHLTSHFKKMLIR
NNSVDVFEEMKKALDKLGNTFINNVDYENLRLFYEEHARLLRANVHEHSLLGFNNGYIVRLLNSYASILPAHFSNLNPSF
DEHLRGQEQTVLTYLFYYATAHVLNATLPCIQAIAVNSFVGTSWELFEFDDPANLIRVFRLVQSPDLQLVAIYLIRTACF
FRCRNSYYQNHLGPLRIGPLLDDDGPLSLHDKYTKLLAMKEAGVMDELPVKSFALQKGQFFKRWNYPNTSRLKPKRGSKV
SLNKIANRLPTDADLVADFLTANNGFFTHDYDPASDLAGGHTLAQGATFIDGFEMKTLWKLEVYIRINNL
```

72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE

89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE

A0A1E3PFJ6 **A0A1E3PFJ6_9ASCO** (532 aa)
CobW-domain-containing protein. *Nadsonia fulvescens var. elongata DSM 6958*

```
MPSEVISAPLPVTLLSGFLGSGKTTLLEHILKSNHGYKIAVVINDMSTLNIDAELITAHKVTKKQEKIIQLQNGCICCTL
RGDLLEELATLAKSGKFQYVIIESTGISEPMQVAETFSTEFSDMLAQDDSGITGLEKEQDQDIIKDIVALGGLHKLATLD
TTVTVIDAVNFKANFETTEFLADRWGNNDAGEDERTITDLMVDQVEFADVIIINKISAVSKKVQKELRSIVKSLNPAAKI
IMTDYSKVDIKDIINTKSFDFQKAATNAGWLRSLHEMTLREGFGKKGSGSKLTPKPETEEYGINNFVYSARRPFHPERLY
SQLHDKFMIIESAYNEGEEXEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEXYPTISSEQLIENRRNSPFGRLLRAK
GFFWLASRCLLRGEWSSAGAMLTIRGGTPWFAVVTDADWPTDPEIVALMKRDFEGLWGDRRQELVFIGQKLDVKAITKAL
DSCLLNDEEMKEYKKIMTSSQNVITIENRLAKAFDDGFEEWPIGLPDDEKEE
```

341 - 360:	EEEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEEE
344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE

A0A1E3PNM2 **A0A1E3PNM2_9ASCO** (519 aa)
Uncharacterized protein. *Nadsonia fulvescens var. elongata DSM 6958*

```
MSSQPIKAVDTTVPVNEEPILQSLLALRAQLSSLKRDRSSYLKSADVNEVYERVIDQIRLINAIRSLPERSNEQNRLDVI
LDDLFQMLSLSFLTVGLTKAAPASYASLSTVRRLLEHLKESGIYTEGDIRPIRERLIEISTNLKQASEEDSESAEVLQLV
ERKLERCQQTFDQVEKSLVTTSPDLAPVINKLIGIKRRILAVRSKPKFDPTELKPLRDQIREFENSRVNGYFIMPDGSIP
EGQNVARTLLEDCHCLINDFMAHGDQVDPSLHGIYKQLIGIKATLENLLVTHRWTLRETDLYYYQKQLRALDDLRVNGIF
LPANKDNTVTNIPNDGRPPSGQSILLYLLRRCYAVMYKLLESSEPVSEALIPIHNQLTTVRRCLLEVKRMGGLSSTRELY
PYQMKLASIDNLRVDGKFMVGDSIPEGQGMLNALLAECFDICHELKVEMVENEATGNTGEDEIDDQDDEDDDGDDDDDDD
DDDDEEEEEEEEEEEEEEEEEEEEEEEYDDDENIDIGNN
```

485 - 504:	EEEEEEEEEEEEEEEEEEEE
486 - 505:	EEEEEEEEEEEEEEEEEEEE
487 - 506:	EEEEEEEEEEEEEEEEEEEE
488 - 507:	EEEEEEEEEEEEEEEEEEEE

A0A1E3QXN1 **A0A1E3QXN1_9ASCO** (534 aa)
WD_REPEATS_REGION domain-containing protein. *Babjeviella inositovora NRRL Y-12698*

```
MDAPSQPIDEEEDDEDEEEEEEEEEEEEEEEEEEEEEEETKVEGDESQLATAKDDVLKEDTDDADIAMEEPRKDEDLRGSP
ASDGETKLKATNYRDKLHLNAQLANGYEYTPTVAVAQSTAIQSLALSAGPKWLFTGGEDGFIRKIDFIGTIEGKSPLTVA
QRHSLVDSIVNAGVVTSYWENEQPILRGNLADTATYEPQVSPVYSLAVESNALWLLAGLRSGGITLQTVRHSEGSIQHYF
```

```
SRHKSTVSVLSLEGDEKSFLSGSWDSSIVQWDLNTGSEIRDFSGAGGQISSIKHRPTGSTALVLAPEDNATEEKKDDDLD
SLFGDSDKEDASDAEQVKLESEDKTPEDVKAAMESPQSVRLVDQNIFMSSSIDGAIDIWDIRTSQPVIHYAVPKNTPPWC
MSACWSGDGEFIYAGRRNSTIEEFSLKMPLKLNIPNVTKTLRFPLVSGAVSTVEIMPNNTHVLCGSQDNVRLYDLRRHLG
SKKTPFSIIPGHHGGVLSTLYVDPTCRFMISASGNRGWLGVSTELLLVYEINVL
```

17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE

A0A1E4RCJ2 **A0A1E4RCJ2_9ASCO** (881 aa)
DNA mismatch repair protein MutL. *Hyphopichia burtonii NRRL Y-1933*

```
MTIVNIGASDIHRITSGQVITDLVSVVKELVENSIDAGSNKIDITYSNYGLDLIEVTDDGRGIDPADFELVCLKHHTSKL
SDFKQLSEIGVSTLGFRGEAMSSLCSIASSVIVTTCTPKQYPRATQLEYNHMGVLKNKKVVVGGLKGTNVKITKMFDNLP
VRKKNLIKNLKKEFHKSVNFLMNYLIIYPNIRFTIFNTNSQGRKHLLMGTKGGPKTTILDNLISVYGTNGAYGLVPLDIE
MNLKFSGYISNSSFGLGRSSSDRQFLFVNQRPITMKKYLKTINEVYRSFNHIQNPVIVLNIELDYKYLDVNVTPDKRIVM
IHNEELINEVLRNELINFYQKQITVIPKNRNSEITINGEKILVLSQREDLLKKGGFKKEPTRTLHGVQVKKEKDDEKDDE
KDDENNENDERDDEESQEEEEEQTQKERKEVEQAEAEEEDGEDKEGEEEQLESEPEPEPEPEQVENKVKMEEEQEEEVQE
EVQDEVQEEVQEEEEEEEEEEEEEEEEEEEEEEEEEEEVQQQEEVQQEEEQEDELEKISSEELDDMLQTKKRSQGSTLDLS
QFISTSHETCECKHDNEEDKLRIEIGEHVEERQVKRPRIMKQRDDIAFGEDEIEAKLIIKKETSDEVYRLQSELRVDQDQ
WETMILPKLNGKTNINKVKVDDISHREEAEAKLSYTIKKEDFKEMQIIGQFNLGFILVTLNNLNNLFIIDQHASDEKYNY
ERYLKTITFDKNTQSLIKEQTIELNIIDEMIVLENVEIFKNNGFIIKFNQDDIPGQRIKLVSLPVLKHTTFDLSDFNEII
HLINEHKSSNIKCTKWERLLASRACRTSIMIGQSLSHKKMSKIVCNLSSLQKPWNCPHGRPTMRHLIELQQMPQFNQDYK
L
```

492 - 511:	EEEEEEEEEEEEEEEEEEEE
493 - 512:	EEEEEEEEEEEEEEEEEEEE
494 - 513:	EEEEEEEEEEEEEEEEEEEE
495 - 514:	EEEEEEEEEEEEEEEEEEEE
496 - 515:	EEEEEEEEEEEEEEEEEEEE
497 - 516:	EEEEEEEEEEEEEEEEEEEE
498 - 517:	EEEEEEEEEEEEEEEEEEEE

A0A1E4RJV2 **A0A1E4RJV2_9ASCO** (351 aa)
Uncharacterized protein. *Hyphopichia burtonii NRRL Y-1933*

```
MPTFHELYKDVQYRIRYWEISYRQKYYSTDKNPRVIQTKLPNQKLISLRILPHDKYLIKPGEFLSVSYEPDKSSAMVVEK
HNKSRFNIQPKDYENYLESRNGEKLFGGFDDTVIGSPMKSQPLRRVKSVTDLVSLRAQGEEEEEEEEEEEEEEEEEEED
ATAEDKILSASSLNTFSLLSPSLLPKIPSGKSIRRFIKSPWAKLTPLPEPNDPPGSPRKSDKILPPSRVHSIVSKLSAPS
CIERKTCPCTKCSARRPSSPANNENDQDPLLEIQPWTKIYNDISLTAARVSTGSLPSSRHDFDNLSSDFVRPKLVNKNLD
NIRKCSAKSNECSSFLDLYSDDTDLLSMYNY
```

140 - 159:	EEEEEEEEEEEEEEEEEEEE

A0A1E4SLY4 **A0A1E4SLY4_9ASCO** (674 aa)
DEAD-domain-containing protein (Fragment). *Suhomyces tanzawaensis NRRL Y-17324*

```
FKFSLDGFETTKFEGWDFKVKEDTPKLSKDVDLDGILRRKGGLVNLAGEEEEEEEEEEEEEEEEEEEEEEEEEEEGGDE
GSDDELAMDGFGMGAEQVDNTAEEDEDEAKVEEEEESDVEADMDEEHPGSDEESDAENDDEDSAEKMAEFYETPEATTTQ
AHQTFQSLQLSRPILKGLSQLGYTTPSPIQSASIPIALMGKDIVAGAVTGSGKTAAYMIPIIERLLYKPSKVSATRVIVL
TPTRELSIQVCDVGKKIGRFVNNLNFGLAVGGLNLRQQEQQLKTRPDIVIATPGRLIDHIRNSPSFNIDSLEILVIDEAD
RMLEEGFQVELTEILSLIPKHKRQTLLFSATMNTKIQDLIQLSLQKPVRIMIDPPKSTSNKLIQEFVRIRKRDHLKFALL
FQLLKDINPDQSSRIVVFVSRKETAHKLRIVLGLLGMKVSELHGSLSQEQRLKNVSDFKNLVVPVLICTDLASRGLDIPK
IEIVINFDMPKSHEIYLHRVGRTARAGRDGRSISFVGESTQDRAIVKDTIKVISEDPSNAKSKAVSRNVDWKQVEGLNKI
IEEKKETIEEVLDEEKQAKEILLAEMEINKAANIMNHEKEIQSRPKRTWFKAGAEDKKQTEVMKHLTKHGKKVNSKKRKA
IEVKKEDLGRSYKKTKNDRMDDQKRNPKAKIGKG
```

49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE

A0A1E4TDJ4 **A0A1E4TDJ4_9ASCO** (194 aa)
Uncharacterized protein (Fragment). *Tortispora caseinolytica NRRL Y-17796*

```
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEELEDSEMLDELEDDELEDDELEEELEDSDTLEELEEEL
EDSETLNETGEAEALAESETLNEPGKTEALAESEALNEPGEADALAEPEALNEPGKTDALAEEEALNETGKADSSVRADV
GVVVWGVCDPVGSTVTVTTIGTSIETSTSTDTDI
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE

A0A1E4TUU8 **A0A1E4TUU8_PACTA** (327 aa)
Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) (Fragment). *Pachysolen tannophilus NRRL Y-2460*

```
MSGLLPLSSYNLELKPFEPTPAIEDDFPVTIRITLAAIDPEDNDGEGVPSTLRILKRSAFIDDDDLSDYDSEDGSLDEDE
DEEEDEEKEVEEEEEKPKKGKKSKKAQKEEEEEEEEEEEEEEEEEEEEDAEDVDGEVKDDDEDDEEDDDLDIEDLDDGVE
EYVVCTLGPKFQYQQTLDLTITPEEEVFFVVTGSYAIHLTGNYVEHPYDGDSSDEEGDYDDYSDEDDLDSEDYDLTPDED
EVLSGEENYDLDDLEDVDDVEGKIEEILEQEEGEEEEEGSENKKQNKKRSLKETEQQPSKKSKKSKDEKRNVKFSENLEQ
GPSGSTL
```

109 - 128:	EEEEEEEEEEEEEEEEEEEE

A0A1E4TYM8 **A0A1E4TYM8_PACTA** (422 aa)
Uncharacterized protein. *Pachysolen tannophilus NRRL Y-2460*

```
MATQFVLDLGIKPEEIYSISNKSLKFDSLSDIQPYLDEMDKFKNLKKIDFSGNTIGVEASKYLALKIENFANTILEINFA
DFFTGRLKDEIPRSLEYLFPSLLKCSNLKVLNLSDNAFGLQTIDPVEDYLKKAISLEHLILSNNGMGPFAGARIGKALYV
LAHAKKLNGTCPPSLKTFYCGRNRLENGSINYLAIGLKNHQGLECVRLYQNGIRPSGIKKLILHGLKYNKNLKILDLQDN
TFTINGSVALASSLSSWEFLEEINVNDCLLNPKGSLEFVKALAELPANNNLKLLKLQYNELETNALSQLAITLTKNLKNL
KNLELNGNRFSEDEEVLDKIKEELESRSGELDELDDLEEPDSEEEEEEEEEEEEEEEEEEEEEVDLIQLEKQLAQDEKFI
SKPSKEEASVEDIAAAIEKTHI
```

363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE

A0A1E5R569 **A0A1E5R569_9ASCO** (299 aa)
Histone chaperone. *Hanseniaspora osmophila*

```
MSVISLLNIDVLNNPSKFTDPYEFEITFECLDHLAKDLEWKLTYVGSSKSLEHDQVLDSILVGPIPVGINKFKFVADPPS
AELIPNNELVSVTVILLSCSYDNREFVRVGYYVNNEYDNEEMKLEPPKKVDVQHVVRNILAEKPRVTRFNIVWDNKDEDN
DNEDQVALDKEINKRFEQENKRDLKKRKLNPDEDEEENDDEEEEEEEEEEEEEEEEEEEEEEDDEEDEDIDESEDIEDS
EGEEDAFDEQKELQAEEQGQAKQLQEQEREEADEELAEQNIDAQDTHNGDDDLVATPKD
```

201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE

203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE

A0A1E5R7A8 **A0A1E5R7A8_9ASCO** (1325 aa)
Uncharacterized protein. *Hanseniaspora osmophila*

```
MTESSNNLNFVKNGSKKTLMKRYTSPFDRGSKKKQISTCIQRSLYCVSKPWNDGHSSSLVFFPKTRDESKLSNAVPLLSE
NIEPLHNAVSWMEDLIKQGKQALGEVTTLEKEFVDSVNTIQLKELAHKSLLEKSLQALSSTEKCRIDDLDNKSKKSYVET
AGGSLSQDFGLEENQTDERLSGSNDDDEDMDNRVNKPLAQEEEEEEEEEEDDDDDDEEEEAEEDNVVIMIDSSEEESTQD
LLNSPAKSFEDTFEGSHVQTAIQDPSHKISSDYMQNKNDIKTTYDKVESPRIKKRIGPIITDSELEVSENEIPEPYLSFE
EQSEEYSEQSFYESDGSNEQKNEVPETLDNLQFQKTERASVGGKYPGKFPSVNHDQSLKESAAESFDDMNALHKEQKFEY
AQVSESSELEEEEEEEEEEEEEEEEEEEEESAELFEHSDSERGQLKQTVYYHLEPLSKKENNGQLTTATSFVAHDNDELK
VEHGNNVGQSAPFDSINSYTAKQDPTYDANFYSTPSFSTQNAPALMDDFAQNKADFQDGESSRTQSVFEISDSDESRTAS
RPSENVADEPMDDSNLTDLATSALLSMKMPVYEAYDRILPEKNKESQQSFIDPAFNELSAEISNTAHELNDSSQTHTEQS
YASAGSQNLHDLSNNVFASDDFVNAESLSKIETALNIEHENEGGTSNGKLNDIESTESEPFVKRVEEITNIDLFENPSDK
RGASSFTNTDTNNPSADTMALTLQAHEANETDSMSAHKLADSQTTTSQSPFPTFPPFENADGYKKNDENMKEASVSAQRN
AEYHLVYETSPVSSNNSTPKEVLIPSAHAGVFQTNPFDQTNVSVDLDVILATIQENISSSNANENVYVSPVNDLEPPTLE
EPAENYQVSAKPDLNADTEISQSNGEGTPNKNDALGGLTAIEKNKMNDLLLTNHKDSEPVNDPVVVNKSESSLLNIESMA
KQQNSSTTTEQNENAEKHASNANVVDKAFVARENHGAKSESDIGGLPTDNLISPLLAEQNNSTVDATETTLGHPAFQSVA
VDVAQSKTQISKSKEGFVQSEDVFDGTVNDAVLGPEVVTDLLALHNDSLDHFANIDSAQAPVAETVTEKVDAAPGKSFLE
IADPDVTELQVETDSRETNISNATSKENSNENSEYQERDINENNLSSSEKQEIQHSINDKNVQELPLDEDTTSDSFPHDK
AAVHDESIQTKGLDQSPPSAEDLAGTVKDDKATAKASEVGSSSHLDHSSLAGNQASLDDGIAEKSFEAGKEAPSAGPSPK
VPKSPKSSKKKKRAVRTKKRMIIEDHSSAPISKRLRSGNQKSKKE
```

410 - 429:	EEEEEEEEEEEEEEEEEEEE
411 - 430:	EEEEEEEEEEEEEEEEEEEE

A0A1E5REQ5 **A0A1E5REQ5_9ASCO** (1090 aa)
Guanine nucleotide-exchange factor SEC12. *Hanseniaspora osmophila*

```
MKFESTIYNVGYPIYGAKFISDRYLLTAGGGGEGANGIPNKLSVLKINFAKPQKPVKKFRELSLDDLDDSPTCLDFWLPE
DINNTALGNNNSNNSNGNGFSNDNNGIVLVGCNENSSNVKRGTNRHLRKFAWENEHLRFLASCDYNKSTDPSVYTKFLSM
SNDGXHAALASSELPSIIRVINPQDLSETYEIETGNEVKDLDFSPNGKVLAYITETSIDIISIVTGSFIVRKMDFDKNLA
LSKVKFLNEDKILVISSSASKGISLSILNVKSGSISVVKSKVLKNLKFKGVTAMAVDTKGTLLVLAGNDNSLSLIKLTKN
QSDFQVMKTFKDVHSFAITKVAISPNSKIIASVSAANTVNLIKLPENMANSLSVGEKLWKFFVNFVLIVLIAALLQLGYH
YNAHLFILEKTKNTIAQYRDSNDSSSYFTMSEDIMSPTILTKKTGSSSVSVKSSLSTPMSSYTTSLTTSNYRDEYYANEY
SSELISPSAETAKTLGITEKSDIVSETLNSKTKSVTKQRSPRTTKSMKXKKPKTKTYKKKLTKVSKNAKQTAVSXSLETS
LSHSALTTMTKKDEPLYTTAASSNVSAFVXLSSSINSLTSSPLDXSSSSQETQITKPLTASDAVTNNEEDLHSIIQNEYD
XLAXERQAAVNELEEMISLNSSEIADAKDEYSDLEKDLESAAEGVEDLESELSEIENVAHTQTTPTSENKLDLSRDEVQT
XXADATQVNNDXAEEPVSRPPQSVEEEYAEDAEEYEDAKEDEEYEEVEEVEDAKEDEEVEEVEDAKEDEEVGEAEDAEGA
EDVEDAEEVEEVEXAEXVEDAEDAEDVEDAEDSEEVEDAKDVGEVEAAEVVEDAEVVEDAEXVEDAEDAEDSEEXEDXEX
DEDAEESELENLEKIPKTQNSEDNXFDKPEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEAEDYAKNNIKEFSEVIEISVDNEANANVPQPEVTXTAFYKVYENVTETVEVTYPTPDPPLDEPLIAIETPLP
ESLEAENESTTAFSDETSIAYDEQISEPVPMDEPVETEPETEDIIEQDEL
```

910 - 929:	EEEEEEEEEEEEEEEEEEEE
911 - 930:	EEEEEEEEEEEEEEEEEEEE
912 - 931:	EEEEEEEEEEEEEEEEEEEE
913 - 932:	EEEEEEEEEEEEEEEEEEEE
914 - 933:	EEEEEEEEEEEEEEEEEEEE
915 - 934:	EEEEEEEEEEEEEEEEEEEE
916 - 935:	EEEEEEEEEEEEEEEEEEEE
917 - 936:	EEEEEEEEEEEEEEEEEEEE
918 - 937:	EEEEEEEEEEEEEEEEEEEE
919 - 938:	EEEEEEEEEEEEEEEEEEEE
920 - 939:	EEEEEEEEEEEEEEEEEEEE
921 - 940:	EEEEEEEEEEEEEEEEEEEE
922 - 941:	EEEEEEEEEEEEEEEEEEEE
923 - 942:	EEEEEEEEEEEEEEEEEEEE
924 - 943:	EEEEEEEEEEEEEEEEEEEE
925 - 944:	EEEEEEEEEEEEEEEEEEEE
926 - 945:	EEEEEEEEEEEEEEEEEEEE
927 - 946:	EEEEEEEEEEEEEEEEEEEE
928 - 947:	EEEEEEEEEEEEEEEEEEEE
929 - 948:	EEEEEEEEEEEEEEEEEEEE
930 - 949:	EEEEEEEEEEEEEEEEEEEE
931 - 950:	EEEEEEEEEEEEEEEEEEEE
932 - 951:	EEEEEEEEEEEEEEEEEEEE
933 - 952:	EEEEEEEEEEEEEEEEEEEE

934 - 953:	EEEEEEEEEEEEEEEEEEEE
935 - 954:	EEEEEEEEEEEEEEEEEEEE
936 - 955:	EEEEEEEEEEEEEEEEEEEE
937 - 956:	EEEEEEEEEEEEEEEEEEEE
938 - 957:	EEEEEEEEEEEEEEEEEEEE
939 - 958:	EEEEEEEEEEEEEEEEEEEE
940 - 959:	EEEEEEEEEEEEEEEEEEEE
941 - 960:	EEEEEEEEEEEEEEEEEEEE
942 - 961:	EEEEEEEEEEEEEEEEEEEE
943 - 962:	EEEEEEEEEEEEEEEEEEEE
944 - 963:	EEEEEEEEEEEEEEEEEEEE
945 - 964:	EEEEEEEEEEEEEEEEEEEE
946 - 965:	EEEEEEEEEEEEEEEEEEEE
947 - 966:	EEEEEEEEEEEEEEEEEEEE
948 - 967:	EEEEEEEEEEEEEEEEEEEE
949 - 968:	EEEEEEEEEEEEEEEEEEEE

A0A1F5LEE3 **A0A1F5LEE3_9EURO** (541 aa)
ANK_REP_REGION domain-containing protein. *Penicillium arizonense*

```
MPFQSLPLEVIRIIAWELPSDRDFLNLICTNSQLCSLLMRDLYKRNLETDPTNTALDWCATTGCMSALYKLAHWKPDFNR
PLRFWDDFSNKWKPTSALVKAVENNNAKTVLFLLKNGADPNYGNGISDHTIEKLTPLEIAAERCAYMSVERLLSHGAKMD
QSILYRAITSGGRYTWVCGERAGAKRRLQGEYIDPERTVRVILDHGAILNDPTTLWSPLHEAVESYHYPGNGVIKWLLDH
GADVNSRDALGRSPIFYAFKTEYRNPYQRSKKMVELLLEYGAEPSPEELGVHLFGSQYSFEMTKLLLDLGADVNILNHDD
MTPLHLLLSRPDSKGHFEQLEPEEKERLTKLFISHGADVLLKDREGNTPLHLALDPDLETMANANTVKQLLDAGAKVLCQ
SEDGFDPLLALLDHWCDLPYADDDFDASNPMDYWCQEWNRDWDLKRKEVNEMINSFVESGHPTDILVDIDPLVAQHFPAL
DPYIPEEAKKEAREAREEEERKARQEEEEEEEEEEEEEEEEEEEEEYTNENSASQKVTDVY
```

506 - 525:	EEEEEEEEEEEEEEEEEEEE
507 - 526:	EEEEEEEEEEEEEEEEEEEE

A0A1F7ZMD4 **A0A1F7ZMD4_9EURO** (344 aa)
Uncharacterized protein. *Aspergillus bombycis*

```
MAENETPKYRLKATAGPSYDPSTHQLVPVNEDQTLRIENEHAITSLCVRIQDYTGKSGPLSTNRQSTAAEREEEEEEEEE
EEEEEEEEEEEEETKTDLKHYQYSISFAIVFKRPVNANSLLFGNDFDRPIRDRLPPGFNAALRLVKWTIDPTLDGDAYAD
KPYLYSPAVASWNQFCIGEKVRKDDEVPGMHERVVEEGGEGSGLEVRDQMGVPTSVNERRKYFQSEEARTGFKFEEGRVY
WVDFGNPYLGFNDFSLHLPGITINVLPYINEDNHSLRYVLKNRDTDEVYLVVLFTLVLQGTDEEPWHKEEAERMRRESKE
HHEKNDGKLGRFEWEPEPSVDDVE
```

72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE

A0A1G2DWW2 **A0A1G2DWW2_9BACT** (803 aa)
Uncharacterized protein. *Candidatus Nealsonbacteria bacterium RBG_13_37_56*

```
MVNNLIKKFITKKILIGLILVILITLIVIIWAFWIKPEDNELIIEEPSEDGSSIEEKPSCFDSNQDPIPICNCEDLQKIE
QDLSANYKLENDINCSQTKNWNDGKGFNSLALGQPVPFSGTFDGQSHIIFNLFINRPDQNSIGLFSYSKGEIINLGLKGA
EITGKDNTGILVGSNFGGKVINSYVLGSIFGNDDIGGLAGRNEQDGEVINSYASVTVFNGGKDTGGLVGENEGIILNSYA
TGSVSSQKGSGGLVGENEGIVRDSYARGNVTGDENVGGFVGDNEGIITNCYATGIVSGNKDVGGFIGDNHGGTVENSFST
GNVIGFDRIGGFNGVNHKGNIINCYWNKQSGSLLSESGSIKQGIVKCSVIENNEQYFYDTNKAPMNLWEFPPWTKENNGK
AYPVLSPEESIEPPGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEIISIYNCEDLQAIQQDLSADYKLANN
IDCSDTQNWNNGKGFNPLGRDSDSLAEDHQGEKFTGDFNGQGYVISDLFINRPQEDYIGLFGISEGEITNLGLENFNITG
RDEAGILTGDNNGTINESYATGNLFGNKDVGGLAGDNDGTVINCYANVVIVNIPDENVGGLVGNNEGVIENSYAIGNISG
KKEDVGGLVGDNHAGVIKNCYATGKIVTVKNGGGFIGNNHEGSIENSYAIGNISGVKDVGGFIGDNHAGTIVNCFSTGEV
SGNERIGGFIGVNHGGSVTNAYAHRSTGNLPNCVGEVNFGVVECNTIQNNESYFYNLGKAPMNVWKFPPWSRTNDGKDYP
VLE
```

416 - 435:	EEEEEEEEEEEEEEEEEEEE
417 - 436:	EEEEEEEEEEEEEEEEEEEE
418 - 437:	EEEEEEEEEEEEEEEEEEEE
419 - 438:	EEEEEEEEEEEEEEEEEEEE
420 - 439:	EEEEEEEEEEEEEEEEEEEE
421 - 440:	EEEEEEEEEEEEEEEEEEEE

422 - 441:	EEEEEEEEEEEEEEEEEEEE
423 - 442:	EEEEEEEEEEEEEEEEEEEE
424 - 443:	EEEEEEEEEEEEEEEEEEEE
425 - 444:	EEEEEEEEEEEEEEEEEEEE
426 - 445:	EEEEEEEEEEEEEEEEEEEE
427 - 446:	EEEEEEEEEEEEEEEEEEEE
428 - 447:	EEEEEEEEEEEEEEEEEEEE
429 - 448:	EEEEEEEEEEEEEEEEEEEE
430 - 449:	EEEEEEEEEEEEEEEEEEEE
431 - 450:	EEEEEEEEEEEEEEEEEEEE
432 - 451:	EEEEEEEEEEEEEEEEEEEE
433 - 452:	EEEEEEEEEEEEEEEEEEEE
434 - 453:	EEEEEEEEEEEEEEEEEEEE
435 - 454:	EEEEEEEEEEEEEEEEEEEE

A0A1G2XHK4 **A0A1G2XHK4_9BACT** (103 aa)
Lipoyl-binding domain-containing protein. *Planctomycetes bacterium GWE2_41_14*

```
MRVEVELPEVGENNGAEATVSFWYVEEDEEVEEGEDLVEMLTEKTTFNVTAPVSGRLVEILAQEGDVVKIGDIVAILETE
EEEEEEEEEEEEEEEEEEEEE
```

80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE

A0A1G3CD97 **A0A1G3CD97_9BACT** (105 aa)
Lipoyl-binding domain-containing protein. *Planctomycetes bacterium RIFOXYC2_FULL_41_27*

```
MRVEVELPEVGENNGAEATVSFWYVEEDEEVEEGEDLVEMLTEKTTFNVTAPVSGRLVEILAQEGDVVKIGDIVAILETE
EEEEEEEEEEEEEEEEEEEEEEEEE
```

80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE

A0A1G3CJ27 **A0A1G3CJ27_9BACT** (103 aa)
Lipoyl-binding domain-containing protein. *Planctomycetes bacterium RIFOXYD2_FULL_41_16*

```
MRVEVELPEVGENNGAEATVSFWYVEEDEEVEEGEDLVEMLTEKTTFNVTAPVSGRLVEILAQEGDVVKIGDIVAILETE
EEEEEEEEEEEEEEEEEEEEE
```

80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE

A0A1G4AN21 **A0A1G4AN21_9PEZI** (2097 aa)
SH3 domain-containing protein. *Colletotrichum orchidophilum*

```
MPWQPLPRIAFAVATYPFAASGPADLPLELGDELYIIEETPDGNWLRGYLVAPPSLLAGLTSVKGQTLEARVFSGIFPRS
CVEVREVLGESDDTEELEDATSDDAAAAGDVQLGSDSGKSGLTPTATDNPKLKEGHKSLGSSRGSKGSRIEIKGRKPLRE
LPNGTQGRLSIPVKRDPDAPRPAAPVPMLKIGDETPTSAAEPLIDEIASCLREWHSTNLHGLLLSRQYPRLEKLSQLIQT
LNLSRQQFLHNVLTRHEYDKLREKTVWDLVRVNKLCGGEVIVRDPADRGRVLTGDDSVVDITKLQSVMSVLDAPPVPTVE
PTALHHLLVDVKGFAGASAEETSLVVYLVAKPLGGQAATLTECFIIDIPPGGTIGSLAKSGQTRTIFADLSAQDIGDVAS
```

```
AETDLYLVVKVRSSQQVIPSGKPDSRSGAKSQGGGYPKDPAQPPSSSGNKASRRSLMWGSKSGRSAFSRGNATPKLESLT
EQPEGRPPTQDESQDSAAPPSTAGSRPRGSFDGGSGFHMAERTVGIGVLKLNAVMKQDEDVEQVVSIWSPSPTLPTEKQG
FHEEWDTLIRDLMDSKSGHYEKSRRTERVQVHLKSFNHPDVDALVKITPTMLAGIRKTNKMGFSGAPTKARSDIYITLDT
AALSKQNLLSRYAGNPTTLSGSVHGNNLQVTLEVRRTGGEKIPNCIYSASNTEGITTWKSVVVEKGEHWSQTVRLAVPPE
DVFTSHIVMFLSDMPHAPFAVAHMPLWNQEAFVRDGAHALLLYKTDEFTSAAQAGPTGKGGYLSLQWSARGNDEHSSEVT
GPLAILRVDTYLCSTRFSQDRIVLGLLKWKEAPKEDIPMLLKHLIFVPEIEVVKLLSDVLDALFGVLVEHSGNDKYEDLV
FTALVRVLGIVHDRRFNLGPLVDHYAENRFNYPFATACLVRSFTRLLEKPTEAQTSRKLRSTFKVVRHILKFITHARGQQ
KAKEAGIGITTSHSAPGFTRELRNIFKALDSMMRSNAPVLVGSQTLAVQHFHTWLPELTGLLTTEEILHIAIDFLDSCSL
VKGKLVLYKLVLIINYSKLEIFSHPEQKSALTANTVRWIAPHWGHTEDVTDSWKEQVRLCCSILAGQIDNLGPEIPDYLP
KILDSYLSIVATPSKPCSRLSLLFPTSYPFPSKPIAEESTFDEALVELSAILSAISNSPSGMQLELTEGDLTALLENTLR
VHMSILMGEAFPHEWLSVYIYHHKSTMRTLQYLSSILLESFLPHPDEAENFNTELWKMFFTTMLKLVGSPSLALETFPEQ
KRRAVWKIAGDVREHGAELLRRTWEAIGWETSSDERARYGLSKMGGYQVQYVPTLVGPIVELCLSVHEGLRRMAVEVLQT
MIVSEWTLSEDLSVIQTEMIDCLDHYFKSKPLTESILQKLFVNEVLERFAPLSTAPDEPLYAGIRDLMETVDEFLDLLVA
VHSSDNTSEATHLINRLRLMEFLRDMQKEEIFIRYVHQLALLQGEARNHCEAGLALRLHADLYDWDPTKQVAALDDPEFP
IQTSFERKERIYFDMIKHFEEGEAWTSALAAYQELRIQYESNIFDFAKLARTERAIATIYETISKSDKLVPKYFKVVYKG
LGFPSSLRDKEFVYEGSPTERASAFTDRMQEQYPSAQIVTGGDVDDVEGQFLVVSAITPHRDLSHQVFQRARVAQVIRDY
LVSAHPQSFSVSSKRSTSGPVQEHFAEKMVFTTADPFPTILRRSEIVHTEEIKLSARQTGLERIVRKTQEMTVIEKRITE
GDEENAQLLVDAVSVSVNPDSENSVACYRQLLPSRAEPEEHEDDEDDDEEEEEEEEEEEEEEEEEEEEEEEEDEGAIELDPQ
DNAIKMALVDHAIMIKRCLATFSRSSNENLNERHEELQRYFESTFAPEIALFAPQQPSRESANASPTWRRSSPSTEQASP
QPQSIAGNMTNGVAAEEVSTVQPVAIRPGRGARLSFLGGRKKESPVLQQTNSDPQTTSETEDTVSHRSRSLSKTQDNANN
TSNTNRRSSFFRAPSSDIPRILGSNDAASEWVTDSGGRRSSDAGTNLAEKEREYKDERPADGLGIVKRGSVRKRLSMLKL
GKKSTKGNGTMISVHEE
```

1809 - 1828:	EEEEEEEEEEEEEEEEEEEE
1810 - 1829:	EEEEEEEEEEEEEEEEEEEE
1811 - 1830:	EEEEEEEEEEEEEEEEEEEE

A0A1G4AYR7 **A0A1G4AYR7_9PEZI** (297 aa)
Uncharacterized protein. *Colletotrichum orchidophilum*

```
MTSPVPSPEALSLLWRLQGPLAESIFVVRSWDTQDPPREPFAARDLTGNVAWHAISQQSLAEPKIKSISVHVDVLERWQR
DWIEWHERHASPDDDNCIYGELPDNDLYKSEGSSSEGEEEEEEGEEEEEEEEEEEEGEEEEEEEEEEEEEEEEEEEEEE
EEEEEEDGDDNDGDVGELLHCCNTDRPKRALPLVIEASNTEYITIHDYVSALHPWLMGLWQDIKRADNLLGDRKPEEYEH
LVVDITSPHYLSIVDEKRFLGLRYTGPPIPMPMSQERMDWLNNVLLRHDVPFWSVPR
```

138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE

A0A1G4GR17 **A0A1G4GR17_PLAVI** (1083 aa)
DNA repair and recombination protein RAD54, putative. *Plasmodium vivax*

```
MRKCPGRAKRSREDSPDRACITLVRATLLPILSIDKNEKTTLFHPFKSPLPGFVSDRRLYVQKTLGAKVRRTGWLNLMKN
SIPRRSDEAEASEQNKADEIKNEFVPLILYESENSKVEVDPILAQFLREHQREGVTFVFECLMNLRDDRISGCILADDMG
LGKTLQSISVLYTLLKQGIDKKPAVRRCLILCPASLINNWNDEINKWLPGRCNVTCVNDNAKEKIVSKLEGFKYDQKSTV
IICSYECFRINNDSLDKSSIDMIICDEAHRLKNDKTKTYMSIYKLAARKRLLLSGTPIQNDLSEFFALISLCNPDLFDDT
NSFRKKYANPILIGRDKDATEKEQEVASERLAELSTITNKFILRRTNNLLSKVLPVKYLINIFIKLNPIQEALYVLFLKD
KRILKNEQSTNKVNVLINIKKLEKICNHPLLLNPNDMKDVGHVSLAKLIEDAAKQHQGKRQAKQEKAERTEKPPLEGHPQ
GDRDRDRDRERDRDRRRAVEMDYDKPVKKLLEECRRDTHRCYYNMSCKFQLLHFLLKTIKQNTTDKVVIVSNYTQTLDYM
EILCKENFYKFVRLDGGISIKKRHKVISDFTHSSDIFIFLLSSKSGGCGINLISSNRLILLDPDWNPANDKQALARVWRE
GQKKICYIYRLFCTGTIDEKVYQRQISKDGLSSMIVTNTNLSKDQLSDENVKKLFNYKMNTLCETHDNIECTRCTIRNCT
EKEVENFSEQLEDFEEEDVNTWAHHQNVESVPDEILAKAVKAATDYKRNDMNNFPVLKKLSDLFVTFAMSCKIEFRDDLI
KQKAQKAQKGERTCRPGAAADGPVEQDEEADYEGEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEGDEAEEEDDEDDEAEEEDAPPKRADKTSKLEYQHKLMEIMEYQRARRREKGAGEARKRSDEGEGKRDGGAK
REGAAKLEDGAKREDGTTREDGATREDAQQQAPRETPRETPRETQPGQKQDAKVSGKAKSQEGAGEEEDPASKRVTRNMS
QKNLMELLSQDEESKVTLSMSEDPDADADASVENVSTDSSYFI
```

837 - 856:	EEEEEEEEEEEEEEEEEEEE
838 - 857:	EEEEEEEEEEEEEEEEEEEE
839 - 858:	EEEEEEEEEEEEEEEEEEEE
840 - 859:	EEEEEEEEEEEEEEEEEEEE
841 - 860:	EEEEEEEEEEEEEEEEEEEE
842 - 861:	EEEEEEEEEEEEEEEEEEEE
843 - 862:	EEEEEEEEEEEEEEEEEEEE
844 - 863:	EEEEEEEEEEEEEEEEEEEE
845 - 864:	EEEEEEEEEEEEEEEEEEEE

846 - 865:	EEEEEEEEEEEEEEEEEEEE
847 - 866:	EEEEEEEEEEEEEEEEEEEE
848 - 867:	EEEEEEEEEEEEEEEEEEEE
849 - 868:	EEEEEEEEEEEEEEEEEEEE
850 - 869:	EEEEEEEEEEEEEEEEEEEE
851 - 870:	EEEEEEEEEEEEEEEEEEEE
852 - 871:	EEEEEEEEEEEEEEEEEEEE
853 - 872:	EEEEEEEEEEEEEEEEEEEE
854 - 873:	EEEEEEEEEEEEEEEEEEEE
855 - 874:	EEEEEEEEEEEEEEEEEEEE
856 - 875:	EEEEEEEEEEEEEEEEEEEE
857 - 876:	EEEEEEEEEEEEEEEEEEEE
858 - 877:	EEEEEEEEEEEEEEEEEEEE
859 - 878:	EEEEEEEEEEEEEEEEEEEE
860 - 879:	EEEEEEEEEEEEEEEEEEEE
861 - 880:	EEEEEEEEEEEEEEEEEEEE
862 - 881:	EEEEEEEEEEEEEEEEEEEE
863 - 882:	EEEEEEEEEEEEEEEEEEEE
864 - 883:	EEEEEEEEEEEEEEEEEEEE
865 - 884:	EEEEEEEEEEEEEEEEEEEE
866 - 885:	EEEEEEEEEEEEEEEEEEEE
867 - 886:	EEEEEEEEEEEEEEEEEEEE
868 - 887:	EEEEEEEEEEEEEEEEEEEE
869 - 888:	EEEEEEEEEEEEEEEEEEEE
870 - 889:	EEEEEEEEEEEEEEEEEEEE

A0A1G4GRB4 **A0A1G4GRB4_PLAVI** (2098 aa)
Uncharacterized protein. *Plasmodium vivax*

```
MESYIRESKKLTFKGSKGKKLLRYVDISLNNKALHDSHIVELVNILKKYIKVVYNHFYCLNIDLSENYITCTGLKTLLKF
ILNYHDNIGVHILKLYKNNIKDDGVSLIKQLVYVQKIPMEELHLSHNFVQDDTCKELLLSFVQAKKENSYVYPRYEKYQS
HYKHLQIPVWIRLEYNCIQNPKEILKEVEEFAKKKRGYKSNLIICAALKSDKRCCPYKCLNATVRNTPIMHVYMFIHQKD
SPAYAISTNGKVGKEERKREFSSPSEVVDAGRMHASAHLQHKAQPEGVERQDGEAALPAKGEARSGAARSAAKSAAKGAA
KGAAKGAAKSGKDKKTAVRKGGANSGKRLSRGSLPHDVSADEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDD
DDDDDDDDDDDDDDDDDDYSEEEEEDDDDEEDDEDEDDDDDDDDDNDDDDNDYRHKRGKPLKGKEKNGQLPDAAPLYASK
NGAAIGAQTNGRDEEDYDEEAEEGEESPNAADPAKKKKGKKKKKKKKKKKKEQVEVSPLEGGCEEAKGSGERGEEGSAVG
GESGLGDGSGDESGDDNDNDNDNADRDDCDRRDHRYPREDLFRAVGGDPLRLDGGGEEDALPPELCPPRQDRLNLTSDAA
SSLPLYIILDCTAVLDMKELWKDSSFLPFSFPGLLYLYNNKLLRSNAEGASGGRGVNGVSQNDAFICLMCSYVANELKLV
CQKSEIIRQKMVNLKLNIWDKLSELGIIEFLSVPKDFKEKKKNFLNSSFLTEAQIKLANEYYDISQETLQMIQFSILWST
YIYKIGNKEIIIKNAAKEINKGGMKKSKKTIFTEVLYLTSSPNIYSFFEHLYGEDMNMILPLCVTVNQINKYIQDEHSCV
VELLSSGRPVGDKGGNFLLDKAFFKAFIKDKCARYLPDGEEGVASIGGATNGGTTNGGTTNGLPSNGGIANGGTSNGGIA
NGGSSKKKKKKGAPPKRSADKLKDGFPSAHDNGTPSMSSLSAATPNCTSRSDKLSPGGKRSDDECVRGSLPIGGTHINTN
AYDYLDIKSVKSFSNENISKLCQLESSIQGGPFGMVGINGGGRMAAPMGGDRHSHYNDPSGGANKVKTNVGGRASGEETH
KGAEKGNAAVGMYASPIDANNGGNGFGMMMVTPPSGSAKENPQGGKENKGSSLYSMLVNAFNGKKKGAQKGAERGADRAT
DRATDRATDRATDRGVASGQDKSGNNMFMGAGPNQSVRDSVDPLSSHAGGENSQNEGGHGNNAAAAAAVATRPQLNMSNG
KVKSTGADLLDQLMHGGSESAPSQGKAASGLGANGGAATSPQMGIPSNDKATYLGSNNNSGSNHPPAHSLFAFNSSMLKG
VAPSGKGDLSFQSQMGTEGGGSGKSGSGIGAGLLGGVNFPMNGAGMGTLANRTTQGNSKQLQKNAVETIIGSDLLNVNEV
ELNNFMGSIPKSFNDSLSMYLDSSNRNDSCYDGIARGENMMPFFNHSLLKGDAEQDLANLAARAEGHSRAEDHSRGADHS
RVTDHTRVADHNRVTDHNRVTDHNRVTDHNRVTDHNRVTDHTRLNEMKNVFELYKVDILNTSLLLEEMILNQNVCKYIPS
ELYNKILRCYERLDCLLAGLNRVGSLSGLSGLRGVSGIGGMSGIGGMGGIDAIGGMNQDILCEDFKSYWDYAFSKNESSP
LALLTSGGGSGIGGGGGAAHQDFTDGAGNISGNKSGNASNAMFYNTVSGNRGSKSALKSSMLNASSHSANGGIGGGSGPL
LASHLNSQNNGAVTPKKSRKKPPMNVSMGSGNNVELGINSMKNNSSQKKFMGGLSDGLDNTGFMNNSPGGNLSGSRNSQM
GRNANYGLGQSIPPNRSGNGNQAGARNSGSGSNNAKSKDMKNHNAGPKDRNLNSVETDEYKNVNKLLLLGGNAQNVKMNG
EKNPYDHGGGGSGGNAHTEHQEHFPHKMNPYNDGGGSGACDSNLLALIHMKKNIKNGVSSSAGPKAGVNSGGANGGGANS
GTANELNGLRNRSYKKLLNNESIGLFNSPANKNTVNEMNLKYLEVLNSQFNFSARENRKNECDPNALNSSVMNFQNDLDK
KYKNPLVDLCDKGSVKKL
```

362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE

371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE
379 - 398:	EEEEEEEEEEEEEEEEEEEE

A0A1G4GRV2 **A0A1G4GRV2_PLAVI** (841 aa)
RNase NYN domain-containing protein. *Plasmodium vivax*

```
MGERPEGEAKGEAHEETNEESHEEANEESHEEAKGLIFPSDIKLIYGSITTTDREKTPNVKKKMTALLSKNLYDVVLLYY
EMHFYNNIDSFQVDVNVYEIYNDLICLIDELYSMYIIDSEKKQSCYPYEDVAERYLSKELSGGWGERTQEELLQEYYILR
GDRNTLFINFKLMKMVYLSAVFDLEFFGDVCQESVFLPDGGSGVGWGSGVGWGSGVGWGSGVDGGSGIDGGSGVDGLGCV
DRVDYVDCVECVSRVRGCSCGADVCRVNCLSGVAPARTGDRRAGPPGRAVDRAVEAPRNDNRGDKKKSNKRKGISKRADR
RSDRREIPSPVLKSEVLRYRERKSAAAAAAAAAAAEEEAAVGQEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEVFPVEDATPFEEPPPVKEVFPFEEAPPFEEAYIREDQKLCYRILCDEQPYKALLIKDELNLSSSDDGEGYRGRARTPV
KEVPALRASSASRGAARNAAAALSVESSASLANLAVAPGLAVSPGVAVSPSLAVSPSTAALPNIATSAAESHQTSSENDR
DSIAQGRHSRVYTKSKWNQGILSYASQHEKSVSIPKDILNITSLLSTPILSMSNIKSLNQVNFSYGYSKTKKDLYNYCYA
YLLSIHNGYDVIPMEGYKFRPIIIDGANVSAKVIHKHISNVLDTDMSTIYDCFLLHEAYVFFKRKKVDDIIIVLNPVTKK
GEEYFLGNKKVCNYSYLENLIKQNAILICNEKYYHSYKGDVVKRRTYDDVLILELASHRNGCVISNDNYTDIEADTACEE
IKHVISHYVVKHHYDKQNGFGLDMTKKPLKFVLNSLFQKIN
```

370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE
379 - 398:	EEEEEEEEEEEEEEEEEEEE
380 - 399:	EEEEEEEEEEEEEEEEEEEE
381 - 400:	EEEEEEEEEEEEEEEEEEEE
382 - 401:	EEEEEEEEEEEEEEEEEEEE
383 - 402:	EEEEEEEEEEEEEEEEEEEE

A0A1G4GUG7 **A0A1G4GUG7_PLAVI** (1815 aa)
Uncharacterized protein. *Plasmodium vivax*

```
MPSKSSPKKDVHLGELPSEGMPSKGVPSKGVPSEGVHPGVHRGMHREAYAAQGEMPLNQWGGDSEGGPTNRTRTNLVDAL
QMIKTNEVTLLESLNDASCEGVKDRQVGLAQGGERPNGRALLNTIEEESNPIEKPNPAGDLYKHILSLYRRKHPEGQLPC
EVTSLQMMGGETHAEDTRVISRRDELEDATYGGAERDEAMSGIHSWGDYIVFGRGEEPQGHVETAFCLGRSDANCFARAA
GGEDSSDGERLPGGDTPPGEYCLRGAPPVGLPNKGEDATLNHLHKRECSFGPSERSPPPDGYDRRGCHCIGGGAPHVESP
LLKSPLLKGGGLYYGVKFDGEEEDEMGAAPKGGCFPPLANKCGGCSSSGALPGDCPEGGREKRFALNQLSSCEDKQVVYA
QTEATQMRLNLSGVPAGPKQSQPRQPQPPADGTALANAASCLHRRAKDPLYEDPSVGGSCKGESFLLGSRASQRGSADGD
PSKNRLNFPPFEGIHMSDANVMRRKQENGKMRLRGDLNEESAAGELMRLREKCFQNERLNHLYIGEQPFCRLRRDGGSNE
YPCGESKGGGPNAEGALDLQVSSLWGCASRASSFRGGQEARWKERGEQVSRGQNPRVMVDPLPLISGTNHAGKLPPADTL
HPNECLIVEAPYFVGDKIMATNPPVVKDPPKLIRCENLHWGESTLGRDPHNVQRDKTDRQHLIRVEKMFEEEAVGAVGRS
ERGGAPQLMLCDDEQGKPTWERPTWGEANLVTPPFPRSDTLKRHPFGGGRLHIPNEEATAGKRNTCPSVVTPVVPRQDGL
LPRVASNRANQSPPQWADIPTDQKISSAPMGRDLPGGSRMGKVPYEEISHCTEEERAVLVDPFFYNCRGENPWECQWKKD
TFADSRMGMERNELTHAERLFASPYHHEGEGTREGPGGGSARTEGGGRSVDGYRGDGYRGDGYRGGTASFAAPTARPVPI
STGEKPWGDTPLALSLPISKAIKGCSPGGQIHTSCSDPHREKNIPREAYARGAANVGEARNALKDTNVNLLKCFKLSFER
GRLAPLGRGACTGVPTVGRTPESRTPPLSGFPLREDSPAVSHKGNLFESVDAFFYNFKKSGASLRGESRQVEEHVGAKVV
ANVRAKVVANVRANDRENDRANDRANDRANDRANVRANDRAKVVANDRENDRENVRAKVVANDRENDRANTHPDCQSNSH
VRASSSGVAQLANPSGSVTTTTTTTTTTTTMGAASAASAANVVNAANVATASNATTTNCTTRSEPGKEGGEEEEKEKEKE
KENEEEEEEEEEEEEEEEEEEEEEEEEEEEEEENGEKLDEQKDDLLDEQKDDLLDEQKGGEELDDLLDDLPDDGGEGMKGRE
PPPWRREKTILTIQWNIKKISLLCSSDSHFVVSPEYKTETLINEFFILLNINKDMHVHLLGENSFGLLFSYTGFCDILFS
VTCGVYQKKFCAYDCSTLPWFGFNNWGILKNCMQNDSISITVDIHEIRRKDSLKEVFLSNVILSMRSSNGSFHFKEGASP
VSPSAVVEAEEEKKKKKAPSPTIATASATTAATTSPLDLGRHRRSAKCFFPQSAPATSDSCSRFAPPTVKRRHPGSVHMV
GSKHMAGNMHMAGNMHMAGSMHFAGTRANAPQWETKQTNASSWNGKVAKQQMIRANRETNPTQGNKLHKGIKKNLYAHNL
IDVCSPFEEHPGGNFIQLSQGLQEGTLAKCTSGSSAHRAAPCAVSGFANQPSVQQEGTPQMKKEGPFGRDPPRRGPTSVK
TFIGALPNDALPNEALPNEALPNEELPTEELPSREGKPRGGGATLEDRFSENGTP
```

1284 - 1303:	EEEEEEEEEEEEEEEEEEEE
1285 - 1304:	EEEEEEEEEEEEEEEEEEEE
1286 - 1305:	EEEEEEEEEEEEEEEEEEEE

1287 - 1306:	EEEEEEEEEEEEEEEEEEEE
1288 - 1307:	EEEEEEEEEEEEEEEEEEEE
1289 - 1308:	EEEEEEEEEEEEEEEEEEEE
1290 - 1309:	EEEEEEEEEEEEEEEEEEEE
1291 - 1310:	EEEEEEEEEEEEEEEEEEEE
1292 - 1311:	EEEEEEEEEEEEEEEEEEEE

A0A1G4H110 **A0A1G4H110_PLAVI** (384 aa)
Casein kinase II subunit beta (CK II beta). *Plasmodium vivax*

```
MDEEGLSNNESSNDVVDEENLEEERGLSDASFGHREEEEGGLHGGSGEGGDGEEGGDCEDGLDGCDCDHGVDGGLDVEDL
EGQAADAPGEEKDAEGGGNEEEEEEEEEEEEEEEEEEEEEEEEEEEDDDEDDDDEDDDDDDYDDDEYDEDDFNEATVSWIE
WFCQLKQNIFLVEVDEDFIRDEFNLIGLQTKVPHFKKLLKIILDEDDDDDDDDDEEDDYDEEDDEINRGSDELYKNKDIY
EQNAACLYGLIHSRFILTSKGLALMREKYKSSIYGTCPSIYCDNAKLLPTAISEVPKFLSPLLYCPRCCESFYPHKNSLL
NQLDGSYFGTSFASFFALSFNIQSDKKRIYYTPQICGFTINRDIRETLYVGMNKDNSESSEEYS
```

100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE

A0A1G4H2V7 **A0A1G4H2V7_PLAVI** (352 aa)
Uncharacterized protein. *Plasmodium vivax*

```
MNLSSPLLALPEEGKKRRTKLIRLRNGHYRRIVDISNTDERKLIPSMCRCACVTPRKDEVENEGKWEDAKKAKSSQEYDE
TSDYVESEKKESYMLAVNEEDQTEDMYSKTISFTSITPTSIRSEEPEPRRKLSLLDVKEEEEEEEEEEEEKEKEEEEEEE
EEEEEEEEEEEEEEEDEIESTAEEKEEEKKQVPPEGKKLIEPSKTLMRGTKTNIYFLSNKEMVQTLMCYNYNCNAVVFEK
DTFLRYLYMKSISNIILNERMIDELCKQEDLKYVLTSNAIVLESTDFLKPLIIEFESSISKRVFVRHLKHNARKEIDMKK
YHDYMGELNANEKIRLMKIERFHSFNKMIQCN
```

154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE

A0A1G4H6H8 **A0A1G4H6H8_PLAVI** (1076 aa)
DNA repair and recombination protein RAD54, putative. *Plasmodium vivax*

```
MRKCPGRAKRSREDSPDRACITLVRATLLPILSIDKNEKTTLFHPFKSPLPGFVSDRRLYVQKTLGAKVRRTGWLNLMKN
SIPRRSDEAEASEQNKADEIKNEFVPLILYESENSKVEVDPILAQFLREHQREGVTFVFECLMNLRDDRISGCILADDMG
LGKTLQSISVLYTLLKQGIDKKPAVRRCLILCPASLINNWNDEINKWLPGRCNVTCVNDNAKEKIVSKLEGFKYDQKSTV
IICSYECFRINNDSLDKSSIDMIICDEAHRLKNDKTKTYMSIYKLAARKRLLLSGTPIQNDLSEFFALISLCNPDLFDDT
NSFRKKYANPILIGRDKDATEKEQEVASERLAELSTITNKFILRRTNNLLSKVLPVKYLINIFIKLNPIQEALYVLFLKD
KRILKNEQSTNKVNVLINIKKLEKICNHPLLLNPNDMKDVGHVSLAKLIEDAAKQHQGKRQAKQEKAERTEKPPLEGHPQ
GDRDRDRDRERDRDRERDRDRRRAVEMDYDKPVKKLLEECRRDTHRCYYNMSCKFQLLHFLLKTIKQNTTDKVVIVSNYT
QTLDYMEILCKENFYKFVRLDGGISIKKRHKVISDFTHSSDIFIFLLSSKSGGCGINLISSNRLILLDPDWNPANDKQAL
ARVWREGQKKICYIYRLFCTGTIDEKVYQRQISKDGLSSMIVTNTNLSKDQLSDENVKKLFNYKMNTLCETHDNIECTRC
TIRNCTEKEVENFSEQLEDFEEEDVNTWAHHQNVESVPDEILAKAVKAATDYKRNDMNNFPVLKKLSDLFVTFAMSCKIE
FRDDLIKQKAQKAQKAQKGERTCRPGAAADGPVEQDEEADYEGEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEGDEAEEEDDEDDEAEEEDAPPKRADKTSKLEYQHKLMEIMEYQRARRREKGAGEARKRSDEGEGKRDGGAKREGAAKL
EDGAKREDGTTREDGATREDAQQQAPRETPRETPRETQPGQKQDAKVSGKAKSQEGAGEEEDPASKRVTRNMSQKNLMEL
LSQDEESKVTLSMSEDPDADADASVENVSTDSSYFI
```

846 - 865:	EEEEEEEEEEEEEEEEEEEE
847 - 866:	EEEEEEEEEEEEEEEEEEEE
848 - 867:	EEEEEEEEEEEEEEEEEEEE
849 - 868:	EEEEEEEEEEEEEEEEEEEE
850 - 869:	EEEEEEEEEEEEEEEEEEEE
851 - 870:	EEEEEEEEEEEEEEEEEEEE
852 - 871:	EEEEEEEEEEEEEEEEEEEE
853 - 872:	EEEEEEEEEEEEEEEEEEEE
854 - 873:	EEEEEEEEEEEEEEEEEEEE
855 - 874:	EEEEEEEEEEEEEEEEEEEE
856 - 875:	EEEEEEEEEEEEEEEEEEEE

857 - 876:	EEEEEEEEEEEEEEEEEEEE
858 - 877:	EEEEEEEEEEEEEEEEEEEE
859 - 878:	EEEEEEEEEEEEEEEEEEEE
860 - 879:	EEEEEEEEEEEEEEEEEEEE
861 - 880:	EEEEEEEEEEEEEEEEEEEE
862 - 881:	EEEEEEEEEEEEEEEEEEEE
863 - 882:	EEEEEEEEEEEEEEEEEEEE

A0A1G4H6T5 **A0A1G4H6T5_PLAVI** (2084 aa)
Uncharacterized protein. *Plasmodium vivax*

```
MESYIRESKKLTFKGSKGKKLLRYVDISLNNKALHDSHIVELVNILKKYIKVVYNHFYCLNIDLSENYITCTGLKTLLKF
ILNYHDNIGVHILKLYKNNIKDDGVSLIKQLVYVQKIPMEELHLSHNFVQDDTCKELLLSFVQAKKENSYVYPRYEKYQS
HYKHLQIPVWIRLEYNCIQNPKEILKEVEEFAKKKRGYKSNLIICAALKSDKRCCPYKCLNATVRNTPIMHVYMFIHQKD
SPAYAISTNGKVGKEERKREFSSPSEVVDAGRMHASAHLQHKAQPEGVERQDGEAALPAKGEARSGAARSAAKSAAKGAA
KGAAKGAAKSGKDKKTAVRKGGANSGKRLSRGSLPHDVSADEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDDDDDDD
DDDDDDDDDDDYSEEEEEDDDDEEDDEDEDDDDDDDDDNDDDDNDYRHKRGKPLKGKEKNGQLPDAAPLYASKNGAAIGA
QTNGRDEEDYDEEAEEGEESPNAADPAKKKKGKKKKKKKKKKKKKEQVEVSPLEGGCEEAKGSGERGEEGSAVGGESGLGD
GSGDESGDDNDNDNDNADRDDCDRRDHRYPREDLFRAVGGDPLRLDGGGEEDALPPELCPPRQDRLNLTSDAASSLPLYI
ILDCTAVLDMKELWKDSSFLPFSFPGLLYLYNNKLLRSNAEGASGGRGVNGVSQNDAFICLMCSYVANELKLVCQKSEII
RQKMVNLKLNIWDKLSELGIIEFLSVPKDFKEKKKNFLNSSFLTEAQIKLANEYYDISQETLQMIQFSILWSTYIYKIGN
KEIIIKNAAKEINKGGMKKSKKTIFTEVLYLTSSPNIYSFFEHLYGEDMNMILPLCVTVNQINKYIQDEHSCVVELLSSG
RPVGDKGGNFLLDKAFFKAFIKDKCARYLPDGEEGVASIGGATNGGTTNGGTTNGGTTNGGTTNGLPSNGGIANGGTSNG
GIANGGSSKKKKKKGAPPKRSADKLKDGFPSAHDNGTPSMSSLSAATPNCTSRSDKLSPGGKRSDDECVRGSLPIGGTHI
NTNAYDYLDIKSVKSFSNENISKLCQLESSIQGGPFGMVGINGGGRMAAPMGGDRHSHYNDPSGGANKVKTNVGGRASGE
ETHKGAEKGNAAVGMYASPIDANNGGNGFGMMMVTPPSGSAKENPQGGKENKGSSLYSMLVNAFNGKKKGAQKGAERGAD
RATDRATDRGVASGQDKSGNNMFMGAGPNQSVRDSVDPLSSHAGGENSQNEGGHGNNAAAAAAVATRPQLNMSNGKVKST
GADLLDQLMHGGSESAPSQGKAASGLGANGGAATSPQMGIPSNDKATYLGSNNNSGSNHSPAHSLFAFNSSMLKGVAPSG
KGDLSFQSQMGTEGGGSGKSGSGIGAGLLGGVNFPMNGAGMGTLANRTTQGNSKQLQKNAVETIIGSDLLNVNEVELNNF
MGSIPKSFNDSLSMYLDSSNRNDSCYDGIARGENMMPFFNHSLLKGDAEQDLANLAARAEGHSRAEDHSRGADHSRVTDH
TRVADHNRVTDHNRVTDHNRVTDHTRLNEMKNVFELYKVDILNTSLLLEEMILNQNVCKYIPSELYNKILRCYERLDCLL
AGLNRVGSLSGLSGLSGVSGMSGIGGMSGIGGIGGIDAIGGMNQDILCEDFKSYWDYAFSKNESSPLALLTSGGGSGIGG
GGGAAHQDFTDGAGNISGNKSGNASNAMFYNTVSGNRGSKSALKSSMLNASSHSANGGIGGGSGPLLASHLNSQNNGAVT
PKKSRKKPPMNVSMGSGNNVELGINSMKNNSSQKKFMGGLSDGLDNTGFMNNSPGGNLSGSRNSQMGRNANYGLGQSIPP
NRSGNGNQAGARNSGSGSNNAKSKDMKNHNAGPKDRNLNSVETDEYKNVNKLLLLGGNAQNVKMNGEKNPYDHGGGGSGG
NAHTEHQEHFPHKMNPYNDGGGSGACDSNLLALIHMKKNIKNGVSSSAGPKAGVNSGGANGGGANSGTANELNGLRNRSY
KKLLNNESIGLFNSPANKNTVNEMNLKYLEVLNSQFNFSARENRKNECDPNALNSSVMNFQNDLDKKYKNPLVDLCDKGS
VKKL
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362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE

A0A1G4H7C4 **A0A1G4H7C4_PLAVI** (832 aa)
RNase NYN domain-containing protein. *Plasmodium vivax*

```
MGERPEGEAKGEAHEETNEESHEEAKGLIFPSDIKLIYGSITTTDREKTPNVKKKMTALLSKNLYDVVVLYYEMHFYNNI
DSFQVDVNVYEIYNDLICLIDELYSMYIIDSEKKQSCYPYEDVAERYLSKELSGGWGERTQEELLQEYYILRGDRNTLFI
NFKLMKMVYLSAVFDLEFFGDVCQESVFLPDGGSGVGWGSGVDGGSGIDGGSGVGWGSGVGWGSGVDGGSGIDGGSGVDG
LGCVDRVDYVDCVECVSRVRGCSCGADVCRVNCLSGVAPARTGDRRAGPPGRAVDRAVEAPRNDNRGDKKKSNKRKGISK
RADRRSDRREIPSPVLKSEVLRYRERKSAAAAAEEAAVGQEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEV
FPVEDATPFEEPPPVKEVFPFEEAPPFEEAYIREDQKLCYRILCDEQPYKALLIKDELNLSSSDDGEGYRGRARTPVKEV
PALRASSASRGAARNAAAALSVESSASLANLAVAPGVAVSPSLAVSPSTAALPNIATSAAESHQTSSENDRDSIAQGRHS
RVYTKSKWNQGILSYASQHEKSVSIPKDILNITSLLSTPILSMSNIKSLNQVNFSYGYSKTKKDLYNYCYAYLLSIHNGY
DVIPMEGYKFRPIIIDGANVSAKVIHKHISNVLDTDMSTIYDCFLLHEAYVFFKRKKVDDIIIVLNPVTKKGEEYFLGNK
KVCNYSYLENLIKQNAILICNEKYYHSYKGDVVKRRTYDDVLILELASHRNGCVISNDNYTDIEADTACEEIKHVISHYV
VKHHYDKQNGFGLDMTKKPLKFVLNSLFQKIN
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367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE

372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE
379 - 398:	EEEEEEEEEEEEEEEEEEEE
380 - 399:	EEEEEEEEEEEEEEEEEEEE

A0A1G4H8N4 **A0A1G4H8N4_PLAVI** (8548 aa)
E3 ubiquitin-protein ligase, putative (EC 6.3.2.19). *Plasmodium vivax*

```
MKIQIPKDDNYILMLDKISEEEKFFIHVLSTCDEKNLIDHLFPFVDWVWLKSDLIAWAPVLNRFDDLLQRYIVHNKLSRE
ETSIARGAISGGVSEGVEAGESNTDKTSERKNERPNQKNRELLGDKTPELRGDKTPELRGENPPEPFVPPDLLVEQMLRF
TYHILDNCLSKSKYNSLDHLLVLLWSFNPKISILSAQILNIYYLFIKKTKKNENKINQIVNILSALINIPVPSFLHPYIN
SDIGRINDNNYISGLVLYYLHDSSDRRYMQNVYSKIDNRYLLDLIDYELNLDTVTINVEDHEIPFTSVLPKEVNYKNAKK
ALQQAYDTIVNKYQLDEKKTFDLRHKLRIYMGLICPKYRRKLFNLRYLIISGSLSINSILYPQIIPSNTIFLQEILYLLK
YHKFIAFNTLHIIFDLLTTAIEPHLHYQVVSDILGLRLHSGLFISVFKYYLNYFLSTYTVQKDICPLHIMNESPVEMYST
NDINTLYVKKIQEEKAVGTSSPSLQGGSVHTAGRNGAIIARASIYSSLSELLPNEGMEQQPPRQQQQQQSRPPPHEEAAT
HYANDHQDVPQEEGGIRPTAAQTANQMSGTDQLSGSNQFSGSNQMSPANQLNPANQLSGTNDSSLFSADAFRGEDDPAGV
IGAMPPFLNNPPIGGGISSVQNLNIFDYMSNEGDTNNEGDSTHVRGLPNVEDLPNVGNPPNVRNLNLFDFMNNMDEVDLL
GGGPADSRLSSHPRDRNRFKEETQYENYISEEVIVSNIKKCKKNGESEFIKISKKQFKDFKKKKKEVSMMLQLLTLYHTC
IMEPCPILTIAQQNTLKFFPLYLQDSYTNNLPIVHLLLRIMETLLDFTPNFYFTAKNEEELYKILLSRFQYEIFMMSDSF
YHLNREHFLRFYFEPFDYRGYDRAFVEAVGEVEAAKEVEAAGGADEANEGNAEVVTAGSAGCAAPPPQASLFSRRNAKLV
RLFQTYDINERASEETLLNRFAFWWKLHIYEERVKIIKMIIKALNLALKGYSPTDTLLDIFTNNYISVKIIKYILKYPHK
FGLCLYGYILGFIYEHIYEDPTILSTLLKEGLLNILLNSIVEDNLKDETVLIYVPSLLSLMFIHSIGKSAMRKLNYSPIY
NLFHYVIKIDYFFFDRFGDIAVSIGNIINELENYGFVMRDFLSFHVKLLKKLYLEGLNLGYWRCLDYDYVQKYVEASAKQ
LHHVQLKDLNIDRYKHRRDNFFLDRLSILCRCILSYMKTSWVKSFLKLNGLKFLMAYTNLISLPPNYIHIFEYHSIYTFV
MKIYLYASFKNVYNQFLYPLYNYSNFVSYVQYVSLLFRGCCYFDLGDNIVVVKRSALLAGELGRTTPMSEAPGSVGAAGK
PPQRGSKYQRTDYFAGPFIDRNQLLLCNITQLFNILYFLISAYTDAKGLYSNEEKLYDLSELSNRKILEIFSDVLVTIES
VFDFYFTLYFYQTNDSNQNMFLHLKDKVCIHEHIKRTLRNSQNKSDYLLYNLFGSSRSLFCYSINNNLYVLNQGQGKTHI
ICDHDSADDYKRTDHLSGLDNEDRVYKAIYRYTFSQVLIEFNTFVHKSMKLPSDIVTFKSKEKSKFQKYFSSSEDSLVGG
KTGRKRTASNLASSRNGINAAVAVHPLCNGAAAQCSAVKEARLLSGNPFEAASSGAEKSQLNAQSVANMYAAYRGGSCEE
CHVAEKNKQQGGNNDPSVGRNENDAAKSEYNDYYIEDKDIHLHTRLAYDSKYVLCESLRSLLVVIKKFFIMINLACHTRQ
LKLKPTPNYIFYNVIQQKHILCIIRCLTKCMMNVPVVSKPIQENPYLAGGAARNAAGGVNNLYSVLSDHITAEKVSYLSE
PSREHPQSPGLAATACKSGAKKWPKVGTKMDFPPCEGTAEANPTKEHLPHCGSANWGAERDAQQKDFNLYDYAYTPFTSH
HVEKIENFYPEPFYMEEILFKRYNFNFSLIEVVPNKDLHQSGGATAGVEASVRVNVAARRSPPEEVEEEEAHHCRDPQGD
LPSRDLSKYNKSYICTSVREADGTFRVVHHNGGFNFAKFAEEGANERGEGNQASRAASREGGGEGTGEMSHEGNHKTNVW
NNPTSSNAAPGENRRASETPKERKLSPVGISIEHYSPMKTVKYIAELINILHKLLADNKLEFISYFYFLDLLYKVGTFDF
IFNMFNYVMSVYISLLALYYRKKKEMREVKKNKQNARPNYVTYIPIHISKNFTCTNTFFVRYVIRVMEFYADADMSSLKI
YLQIVVKGISAFLDFFVNLINIGKFNLMLFCTKMLHPLTRLHNDFESLSPQGKAREAAVEAAAEGAAANTHSGDGAAPNG
KAEEVNPLLASGSVQTPNNGAGGEANLLTPHMEGPNELSESSVEAAALENSHVGAFPNSGEAKGKKKHDAAELSKGINSV
SAAKESKKGGDALPDGRNAKEESSSSTPPQSAKRASEHTFTYNNNFIFSLDYFDIVNTIRSVKCEITNNVFMWLTYINST
SVKIGNLGKNNIYINFNNNVVYTMLRIILKFIHHSVGVEPRIIDFWAKEKCRDKRSVGGKDKERDKDKEKDKDKDKDKERER
EKEKDKDKDKERERERERERKDAFNYPHVNILEEWGLMGFDEKTIYDCLNYSGTTDLDCTLNYLDKAKEKEFFLNIGRDKLPG
ERKNGVGRRPPYYDFDYNSSDENENSTAINRRVDNIRLGVNENASEEELNDAVQVAAERNPVDGSSTTGGGHPTDANTSP
PPLTPSDAPKNGNDKEDIFHKDDKYVLEKFPFMFEILKEAKAKSTHARVYYYQTVMDPNSKRNMIFYLQYYLKLLKKNLF
LTYEEKNEIKQFWDEENYLLLRQLIYKYIFNMLINIIITIPFNEGGYTNLYLSFLLVDIDKKSVKLLLDHYRKTIQDKNT
NKSRIFNHQDVKIIILYYFIENISKKIKMLKNDEAFPIEPFYHCHHLFMYVNKRKNKNVKNGDDGGGKPEKKDNKNGSKG
KFAQSRSGLPSDAGGVIPILAQTAEANVGSGGAIGAVGSGRQLGSDAGRAASSTAGMAPNVSQNVPHNVPHSAPQSIPTS
GGPSGGGALGSVRNMLVSSSNNPMSSANGRGRAGNPVSEFLAEYQLNSNYDVSNHSDDNTTTAFYPGSDIVDDKNSVTNN
HKKGKEHANHPDAELANDSNDPKNCIYGTKYIKGDLDVIYESQRDMEIYSYHFCLHMLFFTLCNIIDKYTIARNLILHID
RNILDYCIFFLHKFNGAYVKSVEANVNHFLAESISQHCFATPGSSDEQMLSNTHGGCCEASANDIDAGKRNQEKNKRKRK
FNKIGAASRIAPISNEQQNGLTNGDPCEQGALLTGQIPPLGSAHSNSVDGAPREDANECAQNGSHKKYAAHLCDERDNDY
VHPTCGGSTHVGDSGTAGNNCQAETPQKEQKIINHMYNKGLVINKNIKTYGMLIPYWNLADTDAAEVNQKTAINYSPQEN
EENKYVSLYSKPPCIYTPLFMCLYKIVINYSLHNFNDKSRKVVKKQKEERTNDEKCGSGLVRNVPSGKVEKATSQSEKKN
LGQSAPTSASVATVQAVQAVQAVQAGQTGQAGQTVQTTQAVQTMSENVRFISAEKQHNIIKICIDTLYFFKGYNAQLCMS
ILQIIEYLTTTYSNVIFFISYTPPNVYRNFRKVFELEERKMERMRAGGKNPLDNRGSAHGRPNAAGENPSEELFPSREEE
LSRGDLHKRETTISVGNVMEPPRDRSTEGMCSPPNVTMNEQQDNGGPFEQKCTPHVDVNELILNNISRSGLGILLTISKQ
AKFKDMLIILINILIQCFTDNYVIANRIEYSLKSYFLCHGIPVKCFMRKDDLKVLEDHKFSNALGVSLSELNEALYPFIF
KNPQMYEEILSCLCFFPNLKYVKKEEASDVQQQVGDAADFLSVNGFGETVGAHSAVGLASEQTREKRNGGNVHTGVCNGV
EVAKGAKRGKHGGKDYGKDSGKDCGKDLDQEGRSAFQSATSSGAPSGAAQLGKKKGKSARESSAQQGAPPDGEGSGKGGA
GSDNVGCGSGNGSGGGQFYLNLLPIPEHIKSIYMLSETANSTKYLRKYFLKNNFYNFYILAVLLDFLNLFTIIQSKTRLV
KLSEKEERLQFNKRLMEIYGTHADFDAELDYKVMYPFALTADNMLFIVNLIFKTFKHLIVYLVKVPNSFNQKIMKTFFLN
DYDELVQGCKGDAQQYSDAAAFAHPFQVNTTQGREAKMGSTVLAAAGINQGTSSRSKNCADVFSSSCGVVYLPNGNHNSC
GDDLNALIKGTPEQAANPPCGDNHVAVESSSAVLKLAKPELASNTPYTYREISEFYLQNYLQYYALFDLSKLTFRSCLFP
FLMERGSGSGSGSGSGSRERGKDRGREKEKHIEREKEKPTEREKELLAGHLLSANPPNNLVFTPLLIFLFKRILPQFICL
SHPSIHTTYSPKKLEEKSKCTDYHYQSLLNSNEFKNVNYVKHIANFVQLIFDIHSSSYDVHKKVVQEIMHLLKVYSIFQK
RKEQPSGKASPEWHNNVFATLIDVFSYAVSALLYKLVNEEQNIKIENSHLLEEKHLLGSGKYISKVLEFAQKGEEEQEAG
NGGGGPNRDDDSDDCGDCGAGGSGSGGNHRGNASGGNAGGGNASGGNPSGGNAGGGNHNRGNNNGGNHNGGSNNGGNHNG
GNHNGGGGGGSGGDGGGGGEDHDEEEKAEKKDDGNKAFTYSREQLALFRMALCSLLNKLDYTKEDFANTATSIIRCLSVL
TSAPILGYPIKTKNNKLYMLKLNKLNERKNKKIKKIKRNKRRKNLSCVTFLNPSYVRFRSDSSNNNSAGSDIPYSVDSDV
SYEEHFVFDNDDSNEEDDLRYEYEEEMDDDYVDMVDGEDTEEDADDADDAEDADDADDADDADDADDDDDEADDEVDDEV
DDEVDDEVDDEADDEVDDEADDEADDDGEEDAGDEADAAAHGEGEDDEVEEADDVDAVGEAEDRPRRRRRRGRRRRRRRR
NAELHNEREGHSEQRRNNNGSSNNPLSNAHLDTDENNENSPNEGANETEGDYTNEEVEEEEEEEEEEEEEEEEEEEEEE
EDIDEEDEDVEEDVEEEDEDVEEEEDDDDDMEDDDDDMEDDDDMEDDEEDDDEAMEEEEEYDEIDMEEEEDDGGRNGNEH
DANRGLHVHAYLVQDRNVIDEDNLYDHSNNLLLPHEVDENEENMSHMGDNNNNIVSNLELGSDSSNDMDEGQGVHRIREI
DETEDYDEDDEDDDEDDEDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDEEEEEIDEDEDEEEINGNNGAFRISQADDNVRAAN
NNADLIDTEMNVNNSLLTCNENQHEILDILMEEDGVYNINDDIDEYNDDYMDEGENNNRAASGTLNVGGAQLGGDDHVEN
AQLGGDNNGGSSSQNGSGGVDKNAHPDGAHRGDDKMGSGEAIQGDLIGTTPDGISNRLNIPHADSPSEVKKGACGMNGSS
AANMANVEDTADYPSGMTADAEVSTQNKGVCNELQNELATNGIHVGMNNGEDQNGAYNCIQGGNFNPLVSSDNVNSLVSS
DNVNPFVNARSDPGLPVPASDTPGETLFPPHMNQGTHKSVNAVANGNVIKSEMNSVAAINQQDGAGGAEGGADNKLAARS
TAAAITKQEENKKGGSPTGANASIAESGKKGESGGAFDKMQSPSAEATTSRTSVNENDINLIDLYYHFYNSNNRDVNTLL
GENNSILYLNETGTIHPSAVKSSASGLPSGATADQGDGAGAIGVDAPPSGFPTNGSLSNGVPTNGSLSNGVPTSGVSPNG
APPSVVPTNETSPMGLPPVEAAPMELIDREQGTLLSSRMENYGPVNYTPTSTNIFALMDNLCSNLLTLNRRRNERLNSML
GTSVHIPDGVRNNSINIPMGINEDFNISGSISNENAAYDPTNMLHESGCTYYHLNLDRVNSFYSPPMFNTSPSMRSNNVS
VRSINQTNHSLRNLFNIIRNYNISDNNINYTRNSSPTLNDLGRRGEGSAEAVSGSNSGVVSGAISGAICGANNGSNVMSA
ENGEAPVGDAFSERGSNDAPAEMNTLANKIKSGNTIKEKNEGVKEEKFCLADTVLDNDKKLKSSICNMMYNRLCKAIPKV
HINLPIENLLEEKKKIIQSMRRKEEEKKELGSKKEAQRGKAGKQEQAKRGGPQKGEAPLKGEEVENGVENDAEGHAEGPV
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EGPVEGPVEGHTEGHTEGEEKPRDNGAAPPEADSTPSQNAPAEIAPSGAADPPFEAVLYDGNSSPDVPSSDIMGAEQSNA
ADPNQAAEQNDHPGESIPNEEDYKNINYEEIFDNVLRIESLLIICCALGINEGQFFQLLNVDRSFLIELPNNLIDEIIVQ
HLKNITLAGVNELAQENTQNGKKISIELYKKYLKFQEFSRTHPGGQQAGAHNETADALTDQQNGSGSDPNASAIATAHVE
GNAAGNNGSGALSDQMGEAVVETVQGGANNGDATVEGNGLPVENAANVESAANMESATNVESAPREEAPPQGETTAHPEN
PAKSEGEKNLLIYNSIKKSYLEALPSSVRAEIKKRIIGNRSQRNETQDETNIAFIDSLTPELRRDVLSSASLRFIRTLTE
EMIEEARNLRFVVLNSRSNLLTGSNRPRQNAVANAVSEGDSADASANFRGSSSGNASGGGGISSGPNASGMNASEINASR
IGASETNAVGVSEGANRSNNNVSGSGASSANGQTDSAHVSSARLNTIRNDIQERITNTVLRNAVSNLNNMSSSENSNSNS
NSNSNSNSNSNSSSNNNVPVISSGSSRHARNNRTLFNVLSRANANNRRRLNASLRNPLTTGSQRNNFIRITYNENNNPII
MINTGHENYDSLTVSRFLDHFLGGRSFNGAISNLPLSDSGTISASFSLIPTNPGGEGGHGGASSGNLNGGMSGHSGSRGH
GGMGNHAVSRSHGGMSNHVVMSNHVGMSTHGGNNAGSSGNAGGSGHLNASHRSGNNNTGGGSANNGMNETRLFINQENRL
NYADPNFSLFTDDKFAEKEDDITLSRYLKNLFPTKNKADAESSKGNALYVCLEEPVSSQALIDICRLLFLKKEINKKIMF
TLFCNLTCSYQKTKICALQLFMSILWSASVDLHGKNNAPRVVALRQAVNFPPKMLYHNVNKKNYGLFSDNYFTTAYVSAE
RVLEQVQSLLITIPHITSFFSMLLVHPALFVPKDIIEHKVVGQKRGGNGESRKGPSGGAFPEEGSPEGAHSLAGKKEEQV
VSQQPVNPSQSNANKINDDEAAILQYELKRKRPKMDQKNSPHALALSAKMDHAKQGDKSKNEYPINILFKLLNSFIYLTS
KKLMSHLLSVIFNLLINCGKKWHTYSNFTKWVYTENLEELLDVENANNEEEVGAKKSEDVSNNDASNNNEGAALNNTSDS
RSGRSNNGNKRNTTTGKGKKQRQHSSNLREFYHSSSKINRELLMSIRNVKQNEPDSSSSGSRKDSTKRPFYLLEVISADA
LSNLSKLICNYKTNFLWINSNGSGGNSNANTPANSNNLEQVHKQDISSLTQIVVLFFSHYKLKKWHIQTLKYHTHVLIRR
IIYDLKKIIQSIHNRTFNVYAVDHSDSLEQKLIAFYRVITILFNAPSLIDNLINRSEVSRNSSAEEISTPPSKSVLDFSA
GSTTAPHNAGTISTGDAAPGGKEANLGDIPAGGGATRTDQAVHHAMEKKSADEETKFDICADFFLSINIDELWEEFNKAM
QVINNALIDKNYKFTYNNRSNMQFPAEEGKAEQHDGGAHLPSHIKGESNVVEGGAVPGAPTPPCTNGKNDRGEAPLGGEI
SQSFYELDSSSSETSEQGSPNSVTAGSPQQEEEPPLPRSGANAAENANSNPVEEKKKDNEDDPPPTILNYLLPLMEAYLF
IEEVILVSQYKLKKFKDLEKKVANLNIESIKINEKLAYDDSPFYISIYHKKEKRSASDSNTGGDLQSGKFNTGSRVSSNV
SNKMKRKKELSALSDEELQKEGQHKQPKKEDVSMAHLAEADASAAGFKQLGNDGGEKGQQGAGGGGGDGDGDGLISKREE
MTGYLASDAEEGKKEGVVEPKKSAKPGESPIGERNRGSSSPNGDHTEEAAQQRGGEVGPYADEYEGEDAEEEMLMRAFGD
ANEDGNNGDNGDSRYDRHDRYERRDLDDDEYIQIKLEDSAGSINGRHKKLIKFVYINRRVINSLIKQTPILLHHNFKSLI
KLTSSCINFENKRHYLRKKLKHLKSGVRSEPIRLNIRREKVFTDSYYQLRNKSGNDLKGKLVVTFKNEEGVDAGGLTREW
YSILAKEIFNPNYALFCREGKKSEFNHPNPLSYINPDHLHFFKFVGKFIAKAIYDGQVIDAYFCRSFYKHMLGRKILPAD
AESVDPEFYNSLIKIAEYKLEDLNLEINFSTEIDEFGKTKVIDLIPNGRNIPVTDENKHKYIELLCEMKVTNSIKEQLEA
FMDGFKELIQPKLISIFDDKELELLISGIPTIDLNDLKENVEYHNYSPNSIQIIWLWDVLQEFDENKKASFLQFVTGTSR
VPLGGFKNLMGMRGAQKMIIYRAYGEDRLPTAHTCFNQLDLPEYSSKELLRSKLIRAIMEGKEGFGFI
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5018 - 5037:	EEEEEEEEEEEEEEEEEEEE
5019 - 5038:	EEEEEEEEEEEEEEEEEEEE
5020 - 5039:	EEEEEEEEEEEEEEEEEEEE
5021 - 5040:	EEEEEEEEEEEEEEEEEEEE
5022 - 5041:	EEEEEEEEEEEEEEEEEEEE

A0A1G4H9D0 **A0A1G4H9D0_PLAVI** (1321 aa)
Histone acetyltransferase (EC 2.3.1.48). *Plasmodium vivax*

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MPHQAELPKGCLFLANNSAKMKPKCSHKPSLASAEESKNEEIDREYYSCIKNCATDLQNLSLNFFPSINTYTCIPKINAI
NSITFHPCISSRDYFNNTYSFKPLFTHHFFSDSEQVIGFDSLKIDFYYTCDNYEVFMKLSGSISDQYENSNYIMLMLLQN
LYITTPYPGGFIETEEEFLRILRRNEGVEGVEVVGPLERAGPVERNAQGRAKEKTKASGAKQSAALTQEQIYKPPGFIIY
EKRLSDDIYLQIRKCGFSSKYFKLESVSNADEEEEEEEEEEEEEEEEEEEEEEGEKPGEKPGEKLEANLGGTDGSVYQNG
FADMVQNENTPSKDQPCSPPKTDRSKHKRGSSVKETKSEHRKSSKGGEINSSCINQNDNHNIKRGLPNEPCEDDSKGEGN
EAATPKYVIHDDNCGSSTTSNEFNKEILRKKRDSKTSLVGSCTRSNEESLSSKEKIKKEKKTKEPPTHPVVDGADCGNDN
SPVELKKAKKNFTKHVTERDMSKLYRQYLRVVRAKRRNSLAARGDSLKEKTPARRKLERQKCSGGSARGGAAVPVEENAA
GNAAETAAETVAIPAAIPAAVPPAVSPAVSPAVPASIPAAVPPEMGAASESAAPLDSSSPKRGSPPKRGGSPKKACSPKR
GSSPKKGGSPNQRASPGKGGSANQAVEPPQGNAPHEKGTNSRRKKNVREELPGAKYDYTVKKNFELLHRKVEWFYHWFIE
SASNIEYDYRWSVILPYIVFKHDEEKKFTENNFIENLNVQLLKNRSANVSVLPSVKLEAAAPPSVAVSNEEVSPPMGKDV
ETGNKKKHKRGATAAVREKKQVKKRKKGQGGAAGEQTLECVGDRVGDRVGECFPEAANDLQSGREQPEGRVKKESSNKRE
NTQESHHDGHTEAVFDQNEYVLTSEIVIKAIENTLKDVRSQDEEEYYAFHKNHDVIYLYSDLEKGGGEAATKGEAAARGA
VQNTQAITDVKGERKTTGRKGSAAEGGKEIPLKEEEPMEDVNEQDGEKKRKKSKNKNEAKSEGKSEGKNEAQNEGTSETK
SETHNEGKHKSKDKRRDKQKSKAKRDAKGEDKKQSLYYFYLFGLATTYTFFTFQFDRNRISQFLIFPPMQSKGLGMKVLE
KIYHLSIVNSNVKEITVEDPAVSFTQLRDIITIKMCIDLRILSPTILYPSDYLKTKNIDKEYADLDKRKFMKVCKETHKQ
ITRMIETLLLAGVLPHPAPSYADIGEDKASGVRKKEKKNESPDSLNSMEHFESSDLCKDVRIKIKKRIKNDYIGNLINKN
MNCMASDVFQDYVKEELYKLWKKQCKVYYRTIKKLRSLYPL
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272 - 291:	EEEEEEEEEEEEEEEEEEEE
273 - 292:	EEEEEEEEEEEEEEEEEEEE
274 - 293:	EEEEEEEEEEEEEEEEEEEE

A0A1G4H9S2 **A0A1G4H9S2_PLAVI** (1752 aa)
Uncharacterized protein. *Plasmodium vivax*

```
MPSKSSPKKDVHLGELPSEGMPSKGVPSKGVPSEGVHPGVHRGMHREAYAAQGEMPLNQWGGDSEGGPTNRTRTNLVDAL
QMIKTNEVTLLESLNDASCEGVKDRQVGLAQGGERPNGRALLNTIEEESNPIEKPNPAGDLYKHILSLYRRKHPEGQLPC
EVTSLQMMGGETHAEDTRVLSRRDELEDATYGGAERDEAMSGIHSWGDYIVFGRGEEPQGHVETAFCLGRSDANCFARAA
GGEDSSDGERLPGGDTPPGEYCLRGAPPVGLPNKGEDATLNHLHKRECSFGPSERSPPPDGYDRRGCHCIGGGAPHVESP
LLKSPLLKGEGLYYGVKFDGEEEDEMGAAPKGGCFPPLANKCGGCSSSGALPGDCPEGGREKRFALNQLSSCEDKQVVYA
QTEATQMRLNLSGVPAGPKQPQQSQPRQPQPPADGTALANAASCLHRRAKDPLYEDPSVGGSCKGESFLLGSRASQRGSA
DGDPSKNRLNFPPFEGIHMSDANVMRRKQENGKMRLRGDLNEESAAGELMRLREKCFQNERLNHLYIGEQPFCRLRRDGG
SNEYPCGESKGGGPNAEGALDLQVSSLWGCASRASSFRGGQEARWKERGEQVSRGQNPRVMVDPLPLISGTNHAGKLPPA
DTLHPNECLIVEAPYFVGDKIMATNPPVVKDPPKLIRCENLHWGESTLGRDPHNVQRDKTDRQHLIRVEKMFEEEAVGAV
GRSERGGAPQLMLCDDEQGKPTWERPTWGEANLVTPPFPRSDTLKRHPFGGGRLHIPNEEATAGKRNTCPSVVTPVVPRQ
DGLLPRVASNRANQSPPQWADIPTDQKISSAPMGRDLPGGSRMGKVPYEQISHCTEEERAVLVDPFFYNCRGENPWECQW
KKDTFADSRMGMERNELTHAERLFASPYHHEGEGTREGPGGGSARTEGGGRSVDGYRGDGYRGGTASFAAPTARPVPIST
GEKPWGDTPLALSLPISKAIKGCSPGGQIHTSCSDPHREKKIPREAYARGAANVGEARNALKDTNVNLLNCFKLSFERGR
FAPLGRGGCTGVPTVGRTPESRTPPLSGFPLREASPAVSHKGNLFESVDAFFYNFKKSGASLRGESRQVEEHVGAKVVAN
VRAKVVANDRAKVVANDRENTHPDCQSNSHVRASSSGVAQLANPSGSVTTTTTTTTTTTTMGAASAASAANVVNVVNAAN
VATASNATTTNCTTRSEPGKEGGEEEEKEKEKEKENEEEEEEEEEEEEEEEEEEEEEEEENGEKLDEQKVDLLDEQKDDL
LDEQKGGEELDDLLDDLPDDGGEGMKGREPPPWRREKTILTIQWNIKKISLLCSSDSHFVVSPEYKTETLINEFFILLNI
NKDMHVHLLGENSFGLLFSYTGFCDILFSVTCGVYQKKFCAYDCSTLPWFGFNNWGILKNCMQNDSISITVDIHEIRRKD
SLKEVFLSNVILSMRSSNGSFHFKEGASPVSPSAVVEAEEEKKMEAPSPTIATASATTAATTSPLDLGRHRRSAKCFFPQ
SAPATSDSCSRFAPPTVKRRHPGSVHMVGSKHMAGNMHMAGSMHFAGTRANAPQWETKQTNASSWNGKVAKQQMIRANRE
TNPTQGNKLHKGIKKNLYAHNLIDVCSPFEEHPGGNFIQLSQGLQEGTLAKCTSGSSAHRAAPCAVSGFANQPSVQQEGT
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PQMKKEGPFGRDPPRRGPTSVKTFIGALPNDALPNEALPNEELPTEELPSREGKPRGGGATLEDRFSENGTP

1239 - 1258:	EEEEEEEEEEEEEEEEEEEE
1240 - 1259:	EEEEEEEEEEEEEEEEEEEE
1241 - 1260:	EEEEEEEEEEEEEEEEEEEE

A0A1G4HGC5 **A0A1G4HGC5_PLAVI** (378 aa)
Casein kinase II subunit beta (CK II beta). *Plasmodium vivax*

MDEEGLSNNESSNDVVDEENLEEERGLSDASFGHREEEEGGLHGGSGEGGDCEDGLDGCDCDHGVDGGLDVEDLEGQAAD
APGEEKDAEGGGNEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDDEDDDDEDDDDDDYDDDEYDEDDFNEATVSWIEWFCQLK
QNIFLVEVDEDFIRDEFNLIGLQTKVPHFKKLLKIILDEDDDDDDDDDEEDDYDEEDDEINRGSDELYKNKDIYEQNAAC
LYGLIHSRFILTSKGLALMREKYKSSIYGTCPSIYCDNAKLLPTAISEVPKFLSPLLYCPRCCESFYPHKNSLLNQLDGS
YFGTSFASFFALSFNIQSDKKRIYYTPQICGFTINRDIRETLYVGMNKDNSESSEEYS

94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE

A0A1G4I2Q3 **A0A1G4I2Q3_TRYEQ** (569 aa)
Uncharacterized protein. *Trypanosoma equiperdum*

MPPKKSELEAREEEEEEEEEEEEEEEEEEEEEEWEESNDLSQLEDGPSTFYVGGFSSMQKLQEALDAVTYREDLVIVYPGAY
LEKEVVIEESRLDGLRIMSVPVALGRKAGYRKKIHIPRDERRLGPWYAPYGGEAPATATVTPTAPDPQLFPVIEGRLIVR
HSRPFVSVDEDAEIPEGLQGIKHYDDEQDRVADGDEEEENADDAPEGSTEEAEMVHKAKDNHLEMQGLCFFGGIELNPLT
RSTFRHCVFGDYALQRKDPLATTEAVETTTCQPSTEPPVLPTVVAHPLSEALIEFCIIYGSAKQALYAYPRCSLQIHTSM
ILGPVEGTPTTYTADQFRAARHAQQSPLFRLKNRWKKVVSQPKIPTKAMCNVALYLDDADVSVRDCFIAHTDIGVMLVDG
CAGTELKFLRLESHSTVGILFTGECGAAKVKCCAIRWCGRECILVKGRVPPIPPDAEAVERVACERAQREAEENENEEVE
EEGEEEEDADVPRPPPIPAQHPSLQKNALEGTVRLEGDVSCGTMCDNVIYMEKDDTQPPLSGPSEERRFLLKGFHVHVRG
STPLESEDN

12 - 31:	EEEEEEEEEEEEEEEEEEEE

A0A1G4JI45 **A0A1G4JI45_9SACH** (1229 aa)
U3 small nucleolar RNA-associated protein 22. *Lachancea meyersii CBS 8951*

MAPLKRTASETLSAESPWQNAEGSIQKKALIEALGQAQGRNGDTEGKQGASSAPGNEGDEDEDEEEEEEEEEEEEEEEEE
EEEEETEHREKHRAGQISAQDVQVARATAELFKSNIFKLQIDELLQQIKLKDSRILKVEKFLHKLYDTIQMVPDWEPTAL
ADVESYFKGKIVAVPFADPKPAVSVQYKFNYKAPDVSLIGSFALKSATYDPKGSSVDVLLTMPAELFEKKDYLNFRCVHK
RSVYLAYFTHHLSVLFGKEQFSDFLQLSYEYLNNDPLCTILRLQCKPGGSSEYNFYKTNFSINIIVGFPHGLFDAKKLLP
NKNCIRVQEDKDTMTPLYNFSVLSSSTHEHYLKFLYKTKKQTEAFKDACMLGKLWLKQRGFSSKSAHSGGLGGFGAFEFA
TLMSALLCGGGVNGNKILLHGFSSYQLFKGVMRYLATMDLCSNGHLQFYSDLTPSSNLPTSRYIAEGFQTPTIFDKTTKV
NILTKMSVSSYQALQLHARETFVLLTDVVKDQFASIFLTNLNKFQEVKYDMTFDLEIPTQSVILEKFGPTEKIKFVSIEN
FVVNKISNVAKIALGDRIKSLQVELLNHKTWFPISKRKPSNTTNISYARIRILVNPAECEKLVTKGPLNSEEFAAEALVF
KNFWGKKASLRRFKDGSITNSCVWATSASEPVISQILTYIFKLHLAENAKLSNLTSRHFLELLPLPNLPASSSMSVLSLN
SFYNVRKSFDALSALLFKLDLPLAIKSVLPVGSAFRYTTTCHPVPFAYSNPDFLQDVILEFESSQKWPDEITSLEKAKTA
FLLKIQEALSSQHGQYKTFFARDELIPFNLDIVTLNILTPDGFGFKFRVLTERDEVLYLRAISNARMETKPELENVFLKF
TAKFLASPRHNRTLENLSHSFPLYPPVVRLFKKWLDCHLLLSHLSEELVELIAMKPFVDSAPYFAPASLENGFLKIIQYL
SQWNWREDPLILDLVKPEELDLGSDVGSASGLDLSAKLSKDLRENLTASQLKAIQGNFSALRKNDPQGLHIQFFVASRND
PSGILYSSGVPLPIATRLTALAKVAFNLIQAHGLNKQTVDLLFTPALKDYDFVVKLQMPISLKLPCGVLENNTFKNIDQQ
QRAFPQDLSHMSGKMDPSFQLVKYLNMKYKNSIIFSSHRYPGINGGGAGDRNVITGLIRPTYKSSVKFRANMDANVKPVN
NELAVLNKEAIFNEIAVFGDELITAFEFN

64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE

A0A1G4JQM9 **A0A1G4JQM9_9SACH** (1071 aa)
LAME_0F02542g1_1. *Lachancea meyersii CBS 8951*

MDGKGLSLSSLKEKVASKMKENQKPSKAGKKGSGKETKRESNKPASKNAAGTNSAKTEVIKSNKSAEKEAIRREALALGA
SEKDLDLINGLSDDDDVSEQEFGGSKDENDKKFDDDFQSFLKSAGIDAVTARQDVVEGQEDQDQESESSSEEEEEEEEEE
EEEEEEEEEEEEEDIPELVKTNEEELSLGSDSSEDEKSEAEEGPFLNQDSDPETTEEKKEDKNLISQTHLVTSDRLLLPA
DVIWHEIPLDPEANAQNDPLSADKIDALYQRAKEALEADNTLYYEEFTKNSSQRKFMSQILSDGTLNDKISALTLLIQES
PLHNTKSLDTLISFCGKKSRNSALQSLNALKDLLLNGLLPDRKLKYFKNQNLSMMLNKKTLAIFYFEDYLKNLYFQVLQV
VERLSHDPIIHVRMQVLSHIFELLTAKPEQEFNLLRLGVNKLGDIDNKVSSKTSFQLLKLEQAHPNMKSIVLDATVDVAL
RPSADYHTTYYSVLTLNQTILKRSEDKIANQLIKTYFTLFEKFLLSTDSSNAEGGDHAPQNKQASYENKRKKNFKRGKNG
GKSVKNEKTDKEVVDEKNSKLFSAILTGLNRALPFSNMPASVYETHLDTLFQITHSSNFNTAVQALMLIHQVTLKAELND
DRYYRTLYESLLDARLVTSSKQGIYMNLLYKSLKRDKHVARVEAFVKRILQVCSSWLNVGALAGMLFLLLQLGKSVPQIK
NLFTNTPADEEYASEDETTDKDSQKPAYDSGKRDPKFANADNTSVWEIRHFLNHYHPTVQTYAEAFLNSSEDVTKPDLGL
YTLAHFLDRFVYRNAKQKPTTRGNSIMQPLGGSHTGSLIVRASDAHATGLNVVPANTQDWLAKKVDQVNPDERFFHQYFS

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TKQTAIKRAEKDKKGGAKGDSNEFENESELDEDEVWDALVKSRPDVEDDSDDDESMDDLEAMSMSDESGDEEEDEEVEAE
AEAEAEAEAEEDEDDEDVFYSFADESANTNSKKRKREDGRADAGDSGSDDDDEEDAALAEAFQSESESESESDRESATPE
VPTAGQRLSRKKLKSLPVFASVDDYAEYMSE
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151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE

A0A1G4JRU1 **A0A1G4JRU1_9SACH** (1073 aa)
LAFA_0F16886g1_1. *Lachancea sp. CBS 6924*

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MVGNGLDLSSLKHKVASKMKDNKKKPSKSSKKDSGKHAQRSEEGKPVAKVDSKEKNAEKEAIRREALALGASEKDLNLIS
GLSDDDDLSEQEFGSTKQGKDKEFDDEFKQFLKSSGIDAVAPPQDAEEAEEDEQEEEEEEEEEEEEEEEEEEEEEEEEV
EEEEEEDSESESIPELVKGVESEMTEGPELSDDDKSFDEEGPFLNQDSDAETAEEKKEDKDLISQTHLVTSDKLLVPSDA
VWHEIPLDPQANAQNEPLSADKIETLYQRAKQALEADNTLYYDEFTKNSSQRKFMSQILSDGTLNDKISALTLLIQESPL
HNTKSLDTLISYCGKKSRNSALQSLNSLKDLLLNGLLPDRKLKFFKNQNLSMMLNKRTLAIFYFEDYLKTLFFQVLQVME
RLSHDPIIHVRMQVLSHIFDLLTAKPEQEFNLLRLGVNKLGDIDNKVSSKTSFQLLKLEQAHPNMKSIVIDATVDVALRP
SADYHTTYYSVLTLNQTILKRSEDKIANQLIKTYFTLFEKFLLSTDSENAEGGDHAPKNKQASYENKRKKNFKRGKKGGK
SVKNDKTEKEVVDEKNSKLFSAILTGINRALPFSNMPASVYEAHLDTLFKITHSSNFNTAVQALVLIHQVTLKAELNDDR
YYRTLYESLLDARLVTSSKQGIYMNLLYKSLKHDSNVARVEAFVKRILQVCSSWLNVGALAGMLFLLLQLGKAVPQIKNL
FTNTPADAEYASEEEEDGKTDSSRQRTYDSGKRDPKFANADHSSAWEMRHFLNHYHPTVQTYAEAFLTSSDEVTKPDLGL
YTLAHFLDRFVYRNAKQKPATRGSSIMQPLGGSHTGSLIVRASDARATGLDAVPANTQDWLAKKADQVSPDERFFHQYFS
TKQSAIKRAEKGKGSGASHEFDEGSDLDEDEVWDALVKSRPEVEDDSDDDESMDDLEAMSMSEASDEEEEEGAEAEGAEA
EAEKEEEEEEEEEDVFYSFADDSSVNAKKRTRDADLSDDDDSDDEALAKAFQSDSGSDSDSDSDVQQEQEQEQEQDQTKQL
GKDKDSSGRMSRKKLKALPVFASVDDYASYLSD
```

135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE

A0A1G4M890 **A0A1G4M890_LACFM** (999 aa)
LAFE_0B08482g1_1. *Lachancea fermentati (Zygosaccharomyces fermentati)*

```
MSKPHGIRIPGAILDVLKNTDYENDERFASKKRKKGSTVGRKEKRKQQRLAKKQRHQRNDLPRGENVQSSFKKPKSEKRK
QVKFVDDVVSEDDQESNELQEDNIGNFEQADSETEDLTEDDNFSEDEDTEMTVEETMEALKRAKSSKAARTEDHTVNYQQ
SGSKDEEELSDDLSGEEEEKEEEEEEEEEEEEEEEEEEEEMTVEETMAALKAAKEKKNGKDKKLQKIKSESKSKGSEKSH
QPAPLTPSERAQIERDEMDMSYYAKKLGLKGKTKKLKASDEFDAVGGLLEGLDFFENYGEDDAYDGKNSIAGVPSSDEYD
GTDEENLSNEGSHRNGEESSHDDSSEDDIQKAFSSDDELSSGDFDEFDENDLNEEELEQLRELEGDDSDVSSGKKENPYV
APNMDATEYIPPSLRRQQLSSNEPDNLIELRKKIKSSLNKVSESNISVIVAAINDLYESNPRQYVTDILSAQITEIICQK
NKLLDSFILNYAALIVSMWKLRGIEVGASFTQYLVQKFLDLYEAQQSVLQGANAHGNTSEPVIIPKNCSNLITLLSYCYN
LGLISCKLIYDMIALFIMTPNEFTTELLLRIVSVSGPLIRGDDPKALKEILSDLLKNVKSVSLTPRLKFLLETMSDLKNN
RLKPSVMATNHSSMKKTMSAFLKNSISSATDPLQVTLDDIKSIESKGKWWLVGASWKGNLETAFDDRSSLNENNSQGVSK
IVVEDNLLDDIPDWTVIAKQQRMNTDIRRAIFVSIMAAQDFMDAFAKIEKLNLKNKQSLEIPKVLIHCLSMEGKSNGYNP
YYGLLAAKLCEQNHHLLKSFQFIFWDIIKKFENDHDSDPEDDLNEDETDEAQRLKKISNQGRFFGYLISQGVFSLNVFKH
VPLMGGLNSDGILFVEILLFQILLSVARKSETKSKKDSQKVYEYKDDHLRGLISSQIKLENKPVILKAFKWFTTKKFKYE
KYVSSNAKSKEYEREKRRLQWAVPKFVELINQELAVISS
```

181 - 200:	EEEEEEEEEEEEEEEEEEEE

A0A1G4MJW8 **A0A1G4MJW8_LACFM** (241 aa)
Pre-mRNA-splicing factor CWC15. *Lachancea fermentati (Zygosaccharomyces fermentati)*

```
MTTSHRPQLEARNGAKGSYVPTSIEHARLLPSHTKLKYRKRKTHLPSERSRENNNEENKKRKHENGKLLLKVSGNLKENL
AEKTSASDEEDSSYKELNHGDNTSNLESDKSAADTVGSNSEDNISGSSSDEEEEEEEEEEEEEEEEEEEEIEDQEALLRE
LNKIRQERLMKKMEEQQAKGDAERESEPSFKTKSDWRSRTAFGRRRKVNSSSNRNKDDKSKYTSDLTKSQYHQEFLHKFV
K
```

131 - 150:	EEEEEEEEEEEEEEEEEEEE

A0A1H7FWS3 **A0A1H7FWS3_9EURY** (158 aa)
Uncharacterized protein. *Haloferax larsenii*

```
MSQSTLGDDDLFGEAAAEMRADVEEHLGEARAALPDADAVWDAEADNVLGVLNGLRSSLDVEGAAEHVRQAKKWYVIGER
ADAFDDPEDLEEAIEELQELLEMVEEAHELVGELTNTMPQLRGALTEAAEVADADDESEEEEEEEEEEEEEEEEEEEE
```

139 - 158:	EEEEEEEEEEEEEEEEEEEE

A0A1H8SIH1 **A0A1H8SIH1_9EURY** (83 aa)
X-linked retinitis pigmentosa GTPase regulator. *Halogranum amylolyticum*

```
MTERDVTVDLEVEVEVDTEELEIETSGKQEVEAELDAEGVSIEVEAEIAVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EED
```

51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE

A0A1I1MJY3 **A0A1I1MJY3_9BACI** (215 aa)
SMI1 / KNR4 family (SUKH-1) (Fragment). *Bacillus sp. 491mf*

```
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEKEEEEEIEGEEEIEGEENFYTKRRNRDINFEYSFESINKQHIKDFEM
KCNIALPDDYKNFLLLNNGGKTDRRRFTICNNKGATITSSIMLFFPLSLETENNLEGMYSLYNRENIVPNNFLPIGIDPV
DNLICLSIEGKDAGYVYFCDLGYFEEDNELREEYIILMAKSFGDFVNNLFFPPVS
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE

A0A1I1UKZ0 **A0A1I1UKZ0_9BACI** (174 aa)
SMI1 / KNR4 family (SUKH-1) (Fragment). *Bacillus sp. 491mf*

```
MGEITWLFTDKSVDEKTISKVEQSFGIKFPQDYKECVIKYNGGYPKPDNFDFSDEGEGGAVFNNLLSFTGDFSIEAIYEF
SKESLQKGIIPFARDPFGNLICFDYRQSNNEPTVVFFDHEEQGENSIELICNTFTELLNKLYSLEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEE
```

145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE

A0A1I7TLR1 **A0A1I7TLR1_9PELO** (559 aa)
Uncharacterized protein. *Caenorhabditis tropicalis*

```
MKQYREEERNEEEGEIEEMEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVNTTNELPTISQTTGHISEQPRTGNGYVINPEN
VLVPSGISTDSQVSGTKKRNFVLHKSENRNLIEFKKMRRLNAHFNGEEENNNMGRTEQHIGDRVIKQEAPDDYQSNEQSI
HLIPNPELNRPSNSHPNIVKIINYYDSEMMAKKDHSIFQLWNQFPGRLEKRMAAFVSRTDGTWLYEAIKADVVKIQQFQS
TTEQVPHAHNNAAEQVPRAHNTAAAQPQSSTSACRIQPARVMYYKKVNGMLYLYPEVPPTAAHVQPQQNEQHRQEQRQQM
PQQDPPQNPQHTQQILQHQIQPQQQHQQQQDLQQQNRNLQMILQALENQHNVRQENQPFWPHIKQFLCERLQQNQINQQL
QNLNDLRQKILQQKDLQPPHQQDLQKEHDQHVRHTLKLLEHQIQLQHQGYQPNQTQEDLHREQEQLNRSYARHLLKIIEQ
SSQPPKEYEQNQQQQQTTQQKPATDQLMTQVILLGYCSEVAKKLLVVHQLEFRTHWTSVLSMVNTHKTIEQQSVSNQNS
```

20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE

A0A1I7TLR2 **A0A1I7TLR2_9PELO** (645 aa)
Uncharacterized protein. *Caenorhabditis tropicalis*

```
MKQYREEERNEEEGEIEEMEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVNTTNELPTISQTTGHISEQPRTGNGYVINPEN
VLVPSGISTDSQVSGTKKRNFVLHKSENRNLIEFKKMRRLNAHFNGEEENNNMGRTEQHIGDRVIKQEAPDDYQSNEQSI
HLIPNPELNRPSNSHPNIVKIINYYDSEMMAKKDHSIFQLWNQFPGRLEKRMAAFVSRTDGTWLYEAIKADVVKIQQFQS
TTEQVPHAHNNAAEQVPRAHNTAAAQPQSSTSACRIQPARVMYYKKVNGMLYLYPEVPPTAAHVQPQQNEQHRQEQRQQM
PQQDPPQNPQHTQQILQHQIQPQQQHQQQQDLQQQNRNLQMILQALENQHNVRQENQPFWPHIKQFLCERLQQNQINQQL
QNLNDLRQKILQQKDLQPPHQQDLQKEHDQHVRHTLKLLEHQIQLQHQGYQPNQTQEDLHREQEQLNRSYARHLLKIIEQ
SSQPPKEYEQNQQQQQTTQQKPATDQLMTQVILLGYCSEVAKKLLVVHQLEFRTHWTSVLSMVNTHKTIIPEQRFCQELL
RGCSVASDRYISIMRSCADLLVRSPDPIVKVHSSEMETVTIEIPEGRTFDQTVREIATRFLATPRLYLELLTRIAEQQSV
SNQNS
```

20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE

A0A1I7TLR3 **A0A1I7TLR3_9PELO** (639 aa)
Uncharacterized protein. *Caenorhabditis tropicalis*

```
MKQYREEERNEEEGEIEEMEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVNTTNELPTISQTTGHISEQPRTGNGYVINPEN
VLVPSGISTDSQVSGTKKRNFVLHKSENRNLIEFKKMRRLNAHFNGEEENNNMGRTEQHIGDRVIKQEAPDDYQSNEQSI
HLIPNPELNRPSNSHPNIVKIINYYDSEMMAKKDHSIFQLWNQFPGRLEKRMAAFVSRTDGTWLYEAIKADVVKIQQFQS
TTEQVPHAHNNAAEQVPRAHNTAAAQPQSSTSACRIQPARVMYYKKVNGMLYLYPEVPPTAAHVQPQQNEQHRQEQRQQM
PQQDPPQNPQHTQQILQHQIQPQQQHQQQQDLQQQNRNLQMILQALENQHNVRQENQPFWPHIKQFLCERLQQNQINQQL
QNLNDLRQKILQQKDLQPPHQQDLQKEHDQHVRHTLKLLEHQIQLQHQGYQPNQTQEDLHREQEQLNRSYARHLLKIIEQ
SSQPPKEYEQNQQQQQTTQQKPATDQLMTQVILLGYCSEVAKKLLVVHQLEFRTHWTSVLSMVNTHKTIIPEQRFCQELL
RGCSVASDRYISIMRSCADLLVRSPDPIVKVHSSEMETVTIEIPEGRTFDQTVREIATRNNNQSQIRTHEHLLQYKHNR
```

20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE

A0A1I7VGP3 **A0A1I7VGP3_LOALO** (1156 aa)
Uncharacterized protein. *Loa loa (Eye worm) (Filaria loa)*

```
MAANLDAEMTSFFKICNTRKTGTTTEMDKMLIKNEVNDEQLEDEQEEEEEEKEDEEDDEEKEEEKEEEEEEEEEEEEEEE
EEEEEEEEVDEEEAEEKKKQNAINRKPPLLLVTQSSTQNSPNHLTTEFTFVDNINFNMMQTNDGDNDEEGNDAILNMQND
NFETDMTVTETIELQTENDKTERKPRDNHYPIVLSESRKHSLSPIPDYENDFNEEFIVEAPTRNNDNRGRVSEIMAIPAP
IFAASISYDDMDDWDSTQEESVELLSDYEDIDDFHSDEQYTRNRSCLENDEYCPSSSSIGIYFSPISSPTDDYDGIQYQD
SVNVGCTLKLVQKAALKCDDDEESSSECYDDSEYRLQYDEEEMYTNDEDDDEYTEDDETSEDLYTIDNISTEPLESAIDS
ISSISIPPLVVASMHEDDDIEIDEICDEIFDDAFSVPVAILSNVEKIEIEENEIPEKHREITYTDEIHLKQNAEEVLKLT
IKETNEDAAMEHIAEGATEIIVRKMVPQHVVPAEENVEIVEIDELEVQKPEQVVAIIKEHDNEKETKQIEVIPTYVWPTT
EDQPVDSVRSFIQRKPSTDWAKKAVVLAPKFETVKIQKVQVRFDEERLLKNEDMSSSSANTSTNSTSKTASAELSRPTSA
LSNTSSSSGQKEDKSAIRKSVLNMAKNETVTNCAPVDSTNKSANIEHSRPTSALSNTSSSSSQKEDKSALRKSTINMAKD
VAIKARALEEEKSKQNARRLGIVNALSAKFNLAEAQPNAYTYKRSRLLAKKDEERPKRTYGPIIKPVINDNFDKQIEEIR
MKMRTGNKILSSQFTELKQGIATVADDARRAILEQKHQQLLIEADATFGKIGDNFKKWKENRTAEQQKELIRREQEMHHA
KATNVEIAKTTTMAQPLVEPKKTVRQLKSSQETKMTNVMPSFVTECETINSGKNSSSKIKMEIQAKKNIEAIKENNHKNA
LNNHTSKIVATTATEVSMKLQSPTMDNYLTKLPNVENSSTTSVENSKKQGIKPDPVIPKTRKILGSTENREIRKYGTRNK
TQELMNFAKDAEMNDEIEESKIHRQNCIHRRNRYIRKPFDIDILLGYDKENSFEQFEARFAASGCDKRSIIDTDKNDKKS
KRRRKESKKIWISELRDIDKIYRTSELRDIINSVRI
```

66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE

A0A1I7VJW0 **A0A1I7VJW0_LOALO** (52 aa)
Uncharacterized protein. *Loa loa (Eye worm) (Filaria loa)*

```
MTQMIGVEKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEEEEDEKKKRDEQK
```

11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE

A0A1I8IE14 **A0A1I8IE14_9PLAT** (2087 aa)
Uncharacterized protein. *Macrostomum lignano*

```
MNLESSGRIWYVIKLSVTLSCEMDLKKYPLDTQMCPMMFESFGHTMDTVAFYWLQPPKRPDDRPDDLTMPQFDLREIHLK
SCDLNYTTGAYPCLQMTFELKRDFGYFLIQIYIPTMLIVILSWFAFWLNIDAVPARASGSKSSLPKVSYIKAIDVWMSAC
LGFVFASLLEFAVVNVYSRHGSGGGGGGGGRSGGRGRRAAAAGPAISGGKKSGRKSASAAASRRRLRGPWNNGGGGGSG
GCEPDGGDSPVFVRDPPAAMSPLQPPQQQEQHQQFHTELTVETSPQQPSPKPQLPSIAKRIDKFSRRFFPLTFLLFNVVY
WHCSASTSCHRLLHPATGFYILPPASTSCHRLLHPATGFYILPPASTSCHRLLHPATGFYILPPASTSCHGFYTGFYILP
PASTSCHRLLHPATGFYICHRFYICHRLLHSATGFYILPPASTSCHRLLHPVYLAMRKPGDCMVGCLVLGQASPHQPVPG
VAVSREDDDPPFAAGGAGSYSCTELLVMSNRTVGLADWLRARRLSLPLCIDAARRAVGRRGGALASAVTVAAAAAAAVVV
VELDVGWPSEAIGGRGFEPKPTAAVRGLAEDAGSSCCSLTAAAAVAAVAAAFFFRIDLICDGQQRLWLFSRSRIGRRGCR
SRSSWRCYRWSRSGGRDAGGFRLSVGWQQLGPRRCRSLWQSLLPLLLLLQILIGHAVQKVHNQCCRWSRWRRLAGASPLL
MAGDCRSAGQPVPPPPLPPQRSPLARRQWFDFAFGCEPPQCDAAAPPPPQMAAAAAVATGAPASLAAAPVDLLRSLMRGG
SGSGHHLWSDPAASGRRQVAALTGRRLRRRRPSVMTAGAPPGGAVCADGTTGAKWPPLLLLVMHSCKRPAVCQLHWQRQF
PTASWRLLEHPAGAADPRRRRRPGAPTASGACRSGGGLQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEGGAAPPIVAMGLPIAAVGILALSCCCGSFCSASGLRSRPVALAHDGPPFEYEQGQLMLNAPSNTTCYNEDRIRSNGT
DALQGRFFCPEEGGSAELTECCGSPEREYCCSPWDSVGVKWGIGIGITLAVIVLMALGYTVQLFRACDRCYHEFPILSQP
GWYSVSHEGNRYGVTFHSKSFASHFMELLESCYGPWNAANILRIRKDDQDFVVLHIFFNDFFTPWFYTQGPIKNDEEWIR
SDFKDLCYQTQFDLAVNFGPCCPRGKDSQVDGESGIQEEAFELMIVPAQEPSLSGPRQSQTGQQLSPQHLPTPPLSATQL
RLPPSVRRGTAVGGRPSITSDKKDHRPWTKHTFKIGLGQRTSAKSAARAGDAADRDSALDPPWHRRLPDAIEEVDAGDGG
NEKATQTLWVPATVLKGHQHHPPGFWAAAAGNPRQMTAPKLISIGVLNSIMFSAKTDINWSIEVDHFSAKTDINWSIEVD
HFSAKTDINWSIEVDHFSAKTDINWSIELDHHVYSNSRSFFGLSDAASSQRQQWQSSAVPEQLLKPSSSSDCRGSALMPI
SSMNIRPRRPLPPLRPTPRPLPLPAPPVTTCSSRRATAWLCSASTPGWSRGDKSLASGICGRCGWLIAMARSSANSVRSS
CISEILPTIRRRLFAVSVSSALVPLSSAAVSWRPRSLSRSSSGQAFRTRRSCSAGLSRAIPGWLRAQRTPICSRRLDRPS
ESACCGSGVDCGGGEAVPEAPPPPPSHSSAASASVLATLACGLAAEAAPRLPGSRRSRWLSAPLPPTLLPVVGVDSGVCG
SGGAGGRPVRKAHPLEAAAAAGSGCGVVQQQGGVQPVRSGERQREVRMRWLAVQQVPCQSPPLCLSASFCCPGGRRSRSS
GQPRRRPGHEYLIPGDGMKLLSVPTGTWIGNYGIKNSTAREGRPRAGARASLSTNLSTKFSSTVFSLIVLQLLLFGQNCQ
DCLRESAAASPLPVQTTEPGGEQPVKDASDAAADSSWRESASSGSSAAAASTAAAAAAVSEADRPACSEDQRVGAVLFGQ
AVASGSALVLHSWNRSRKAALPHLLEQPIVSVARVVAGDMPWTHFNCQQLLQRTKGRQQHRRRQARLWMLLEEGGLSGLA
GGAGEKI
```

920 - 939:	EEEEEEEEEEEEEEEEEEEE
921 - 940:	EEEEEEEEEEEEEEEEEEEE
922 - 941:	EEEEEEEEEEEEEEEEEEEE
923 - 942:	EEEEEEEEEEEEEEEEEEEE
924 - 943:	EEEEEEEEEEEEEEEEEEEE
925 - 944:	EEEEEEEEEEEEEEEEEEEE
926 - 945:	EEEEEEEEEEEEEEEEEEEE
927 - 946:	EEEEEEEEEEEEEEEEEEEE
928 - 947:	EEEEEEEEEEEEEEEEEEEE

929 - 948:	EEEEEEEEEEEEEEEEEEE
930 - 949:	EEEEEEEEEEEEEEEEEEE
931 - 950:	EEEEEEEEEEEEEEEEEEE
932 - 951:	EEEEEEEEEEEEEEEEEEE
933 - 952:	EEEEEEEEEEEEEEEEEEE
934 - 953:	EEEEEEEEEEEEEEEEEEE
935 - 954:	EEEEEEEEEEEEEEEEEEE
936 - 955:	EEEEEEEEEEEEEEEEEEE
937 - 956:	EEEEEEEEEEEEEEEEEEE
938 - 957:	EEEEEEEEEEEEEEEEEEE
939 - 958:	EEEEEEEEEEEEEEEEEEE
940 - 959:	EEEEEEEEEEEEEEEEEEE
941 - 960:	EEEEEEEEEEEEEEEEEEE
942 - 961:	EEEEEEEEEEEEEEEEEEE
943 - 962:	EEEEEEEEEEEEEEEEEEE
944 - 963:	EEEEEEEEEEEEEEEEEEE

A0A1I8MYM1 **A0A1I8MYM1_MUSDO** (376 aa)
Uncharacterized protein. *Musca domestica (House fly)*

```
MSDDEEYTGEGDPEFIKRQDQKRSDLDEQLKEYITEWRKQRAKEEDELKKLKEKQAKRKISRAEEEQKMAQRKKEEEERR
VREVEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDTGVLGLSSAAMERNKTKEQLEEEKKISLSFR
IKPLAIEGLSEDKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQ
VASKYERRVDTRSYDDKKKLFEGGYDTLYKETLEKVWQERQERFTQRSKSKLPKWFGERPGKKAGEPETPEGEEDAKADD
EIAEEDEEVEEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

335 - 354:	EEEEEEEEEEEEEEEEEEE
336 - 355:	EEEEEEEEEEEEEEEEEEE
337 - 356:	EEEEEEEEEEEEEEEEEEE
338 - 357:	EEEEEEEEEEEEEEEEEEE
339 - 358:	EEEEEEEEEEEEEEEEEEE
340 - 359:	EEEEEEEEEEEEEEEEEEE
341 - 360:	EEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEE
344 - 363:	EEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEE

A0A1I8MYM2 **A0A1I8MYM2_MUSDO** (375 aa)
Uncharacterized protein. *Musca domestica (House fly)*

```
MSDDEEYTGEGDPEFIKRQDQKRSDLDEQLKEYITEWRKQRAKEEDELKKLKEKQAKRKISRAEEEQKMAQRKKEEEERR
VREVEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDTGLGLSSAAMERNKTKEQLEEEKKISLSFRI
KPLAIEGLSEDKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQV
ASKYERRVDTRSYDDKKKLFEGGYDTLYKETLEKVWQERQERFTQRSKSKLPKWFGERPGKKAGEPETPEGEEDAKADDE
IAEEDEEVEEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

334 - 353:	EEEEEEEEEEEEEEEEEEEE
335 - 354:	EEEEEEEEEEEEEEEEEEEE
336 - 355:	EEEEEEEEEEEEEEEEEEEE
337 - 356:	EEEEEEEEEEEEEEEEEEEE
338 - 357:	EEEEEEEEEEEEEEEEEEEE
339 - 358:	EEEEEEEEEEEEEEEEEEEE
340 - 359:	EEEEEEEEEEEEEEEEEEEE
341 - 360:	EEEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEEE
344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE

A0A1I8MYM5 **A0A1I8MYM5_MUSDO** (398 aa)
Uncharacterized protein. *Musca domestica (House fly)*

```
MSDDEEYTSSEEEEEVVEEVKEKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYITEWRKQRAKEEDELKKLKEKQAKR
KISRAEEEQKMAQRKKEEEERRVREVEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDTGVLGLSSA
AMERNKTKEQLEEEKKISLSFRIKPLAIEGLSEDKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLR
HKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWEELGKEVNEKIWNEKKDQYAGRQKSKLPKWFGE
RPGKKAGEPETPEGEEDAKADDEIAEEDEEVEEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE
379 - 398:	EEEEEEEEEEEEEEEEEEEE

A0A1I8MYM6 **A0A1I8MYM6_MUSDO** (397 aa)
Uncharacterized protein. *Musca domestica (House fly)*

```
MSDDEEYTSSEEEEEVVEEVKEKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYITEWRKQRAKEEDELKKLKEKQAKR
KISRAEEEQKMAQRKKEEEERRVREVEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDTGLGLSSAA
MERNKTKEQLEEEKKISLSFRIKPLAIEGLSEDKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRH
KALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYDTLYKETLEKVWQERQERFTQRSKSKLPKWFGER
PGKKAGEPETPEGEEDAKADDEIAEEDEEVEEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE

A0A1I8MYM7 **A0A1I8MYM7_MUSDO** (388 aa)
Uncharacterized protein. *Musca domestica (House fly)*

```
MSDDEEYTSEEEEEVVEEVKEGEGDPEFIKRQDQKRSDLDEQLKEYITEWRKQRAKEEDELKKLKEKQAKRKISRAEEEQ
KMAQRKKEEEERRVREVEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDTGLGLSSAAMERNKTKEQ
LEEEKKISLSFRIKPLAIEGLSEDKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDP
EALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYDTLYKETLEKVWQERQERFTQRSKSKLPKWFGERPGKKAGEPE
TPEGEEDAKADDEIAEEDEEVEEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE

364 - 383:	EEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEE

A0A1I8MYM8 **A0A1I8MYM8_MUSDO** (376 aa)
Uncharacterized protein. *Musca domestica (House fly)*

```
MSDDEEYTGEGDPEFIKRQDQKRSDLDEQLKEYITEWRKQRAKEEDELKKLKEKQAKRKISRAEEEQKMAQRKKEEEERR
VREVEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDTGVLGLSSAAMERNKTKEQLEEEKKISLSFR
IKPLAIEGLSEDKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQ
VASKYERRVDTRSYDDKKKLFEGGWEELGKEVNEKIWNEKKDQYAGRQKSKLPKWFGERPGKKAGEPETPEGEEDAKADD
EIAEEDEEVEEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

335 - 354:	EEEEEEEEEEEEEEEEEEE
336 - 355:	EEEEEEEEEEEEEEEEEEE
337 - 356:	EEEEEEEEEEEEEEEEEEE
338 - 357:	EEEEEEEEEEEEEEEEEEE
339 - 358:	EEEEEEEEEEEEEEEEEEE
340 - 359:	EEEEEEEEEEEEEEEEEEE
341 - 360:	EEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEE
344 - 363:	EEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEE

A0A1I8MYM9 **A0A1I8MYM9_MUSDO** (397 aa)
Uncharacterized protein. *Musca domestica (House fly)*

```
MSDDEEYTSSEEEEEVVEEVKEKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYITEWRKQRAKEEDELKKLKEKQAKR
KISRAEEEQKMAQRKKEEEERRVREVEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDTGLGLSSAA
MERNKTKEQLEEEKKISLSFRIKPLAIEGLSEDKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRH
KALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWEELGKEVNEKIWNEKKDQYAGRQKSKLPKWFGER
PGKKAGEPETPEGEEDAKADDEIAEEDEEVEEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

356 - 375:	EEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEE

366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE

A0A1I8MYN0 **A0A1I8MYN0_MUSDO** (389 aa)
Uncharacterized protein. *Musca domestica (House fly)*

```
MSDDEEYTSEEEEEVVEEVKEGEGDPEFIKRQDQKRSDLDEQLKEYITEWRKQRAKEEDELKKLKEKQAKRKISRAEEEQ
KMAQRKKEEEERRVREVEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDTGVLGLSSAAMERNKTKE
QLEEEKKISLSFRIKPLAIEGLSEDKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLD
PEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYDTLYKETLEKVWQERQERFTQRSKSKLPKWFGERPGKKAGEP
ETPEGEEDAKADDEIAEEDEEVEEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE

A0A1I8MYN2 **A0A1I8MYN2_MUSDO** (388 aa)
Uncharacterized protein. *Musca domestica (House fly)*

```
MSDDEEYTSEEEEEVVEEVKEGEGDPEFIKRQDQKRSDLDEQLKEYITEWRKQRAKEEDELKKLKEKQAKRKISRAEEEQ
KMAQRKKEEEERRVREVEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDTGLGLSSAAMERNKTKEQ
LEEEKKISLSFRIKPLAIEGLSEDKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDP
EALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWEELGKEVNEKIWNEKKDQYAGRQKSKLPKWFGERPGKKAGEPE
TPEGEEDAKADDEIAEEDEEVEEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE

350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE

A0A1I8MYN3 **A0A1I8MYN3_MUSDO** (390 aa)
Uncharacterized protein. *Musca domestica (House fly)*

```
MSDDEEYTSSEEEEEEVVEEVKEGEGDPEFIKRQDQKRSDLDEQLKEYITEWRKQRAKEEDELKKLKEKQAKRKISRAEEE
QKMAQRKKEEEERRVREVEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDTGVLGLSSAAMERNKTK
EQLEEEKKISLSFRIKPLAIEGLSEDKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGL
DPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWEELGKEVNEKIWNEKKDQYAGRQKSKLPKWFGERPGKKAGE
PETPEGEEDAKADDEIAEEDEEVEEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE

A0A1I8MYN4 **A0A1I8MYN4_MUSDO** (397 aa)
Uncharacterized protein. *Musca domestica (House fly)*

```
MSDDEEYTSEEEEEVVEEVKEKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYITEWRKQRAKEEDELKKLKEKQAKRK
ISRAEEEQKMAQRKKEEEERRVREVEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDTGVLGLSSAA
MERNKTKEQLEEEKKISLSFRIKPLAIEGLSEDKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRH
KALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYDTLYKETLEKVWQERQERFTQRSKSKLPKWFGER
PGKKAGEPETPEGEEDAKADDEIAEEDEEVEEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE

A0A1I8MYN5 **A0A1I8MYN5_MUSDO** (375 aa)
Uncharacterized protein. *Musca domestica (House fly)*

```
MSDDEEYTGEGDPEFIKRQDQKRSDLDEQLKEYITEWRKQRAKEEDELKKLKEKQAKRKISRAEEEQKMAQRKKEEEERR
VREVEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDTGLGLSSAAMERNKTKEQLEEEKKISLSFRI
KPLAIEGLSEDKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQV
ASKYERRVDTRSYDDKKKLFEGGWEELGKEVNEKIWNEKKDQYAGRQKSKLPKWFGERPGKKAGEPETPEGEEDAKADDE
IAEEDEEVEEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

334 - 353:	EEEEEEEEEEEEEEEEEEEE
335 - 354:	EEEEEEEEEEEEEEEEEEEE
336 - 355:	EEEEEEEEEEEEEEEEEEEE
337 - 356:	EEEEEEEEEEEEEEEEEEEE
338 - 357:	EEEEEEEEEEEEEEEEEEEE
339 - 358:	EEEEEEEEEEEEEEEEEEEE
340 - 359:	EEEEEEEEEEEEEEEEEEEE
341 - 360:	EEEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEEE
344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE

353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE

A0A1I8MYP0 **A0A1I8MYP0_MUSDO** (395 aa)
Uncharacterized protein. *Musca domestica (House fly)*

```
MRSTPVPKRRRRLSRRSKSKKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYITEWRKQRAKEEDELKKLKEKQAKRKI
SRAEEEQKMAQRKKEEEERRVREVEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDTGLGLSSAAME
RNKTKEQLEEEKKISLSFRIKPLAIEGLSEDKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKA
LKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWEELGKEVNEKIWNEKKDQYAGRQKSKLPKWFGERPG
KKAGEPETPEGEEDAKADDEIAEEDEEVEEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE

A0A1I8NFU9 **A0A1I8NFU9_MUSDO** (1185 aa)
NRF domain-containing protein. *Musca domestica (House fly)*

```
MSRETFGYKKWSWCLVILLLVLTFLPPSQEFSFGWGDGDDDGKSREAAGTSASREGRKQPKRHLVEKKHKFHKIERIIPE
GYDEEADEDDDTGGDENASTNVEEDRTEENNGGGEDVDEDEATNENDGEEEEEEDVSRKERAASINSANNDDEEEEYRFK
KARRAEKPARSSKTKAASTESQEKSGSWFSSLFGGGGGSSNKEESSKQQESAEESATTTSKSNGIIDWILWLGERTGRLR
PDSTEDTSAPADSSGETWMDYLNRWPFNSLFPIGKPPKPIKMPKVAKKRSKDVSHDEAASTEPPMSQESFDNLLYSLPNF
IVKPQDIENDECREQLQIFQRQLRGHKLWTLQMLDATGKVGPGLLRGNINQFGDFNMCTDIKTIVKVTSNHPVRIRGKYC
LAHIETQTSVSELKIPVHMLHGRGLFNSHLGNPYHFIPRYGVANWGICVPNACDGDVVRQMLQSSLQDYNNTGVELHVEV
DDNDCYVKQNRKFLKILQKDKKFCATVLYILGLILISLSTMAWENWSRIQPMLERVVSLIKIVVDAIKTMIKKISELLKG
LMEKLKKKPESGEEEDNKDSNEDETRSDGEKKDKEENETNEADEQEEEAKTEEKEEESEPKVEEQAEAEEGDPTSDDLSF
NTLALEIFKSFSPKRSLDILLADDDTHDVPFPLFHVLKVVATLMLYLCLKFLMIGHLPITNRDQLVRTFDNPLSILIRSP
MIYADILLLISGFLTAYQLSEEMEQKSYIQLLKRLALKISRYLPTVYLLICFQTWILPHLNSGPLWENLVGHNSRLCDDQ
WWRNILSLQNAIDFEETCSPSTIQLALEVQLYLVGPLVVWLYYTDSDASFFVYGALHAMSVAARYARTNKEHLSMTLFHG
INVSKFYRTANILYSSPISRATTYLLGIGAGIFQRSNNGVLDLTPEMMKFGWALSSLGLFWCFWSPASSMRTDFIYTSSD
AASYASWCPLVFGLSLCWFIFMLPKESENVVLKFLTTSKVFLVLSRLIFPIQMVMYIVVLYGTAKVKETDKFHLTDLFNI
QEIAIILLGALAVSFLIDIPSQNIRRLIINRIFIERPHLEGDDHATSEGEPMSEASEENSEQVPTSDTPEPPDTVWGSDP
EEEEQKYIQRRRSSLVESDAKKVAESKKEEAEEEEEEEEEEEEEEEEEEEEEEDISEKEEVKKHP
```

1152 - 1171:	EEEEEEEEEEEEEEEEEEEE
1153 - 1172:	EEEEEEEEEEEEEEEEEEEE
1154 - 1173:	EEEEEEEEEEEEEEEEEEEE

A0A1I8QB00 **A0A1I8QB00_STOCA** (370 aa)
Uncharacterized protein. *Stomoxys calcitrans (Stable fly) (Conops calcitrans)*

```
MSDDEEYTGEGDPEFIKRQDQKRSDLDDQLKEYIAEWRKQRAKEEDELKKLKEKQAKRKISRAEEEQKMAQRKKEEEERR
```

```
VREVEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDTGLGLSSAAMERNKTKEQLEEEKKISLSFRI
KPLAIEGFSEDKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQV
ASKYERRVDTRSYDDKKKLFEGGYDTLYKETLEKVWQERQERFTQRSKSKLPKWFGERPGKKAGEPETPEGEEDAKADDE
IAEDEEEVEEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

334 - 353:	EEEEEEEEEEEEEEEEEEEE
335 - 354:	EEEEEEEEEEEEEEEEEEEE
336 - 355:	EEEEEEEEEEEEEEEEEEEE
337 - 356:	EEEEEEEEEEEEEEEEEEEE
338 - 357:	EEEEEEEEEEEEEEEEEEEE
339 - 358:	EEEEEEEEEEEEEEEEEEEE
340 - 359:	EEEEEEEEEEEEEEEEEEEE
341 - 360:	EEEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEEE
344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE

A0A1I8QB04 **A0A1I8QB04_STOCA** (392 aa)
Uncharacterized protein. *Stomoxys calcitrans (Stable fly) (Conops calcitrans)*

```
MSDDEEYTSEEEEEVVEEVKEKAPQTPAEGEGDPEFIKRQDQKRSDLDDQLKEYIAEWRKQRAKEEDELKKLKEKQAKRK
ISRAEEEQKMAQRKKEEEERRVREVEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDTGVLGLSSAA
MERNKTKEQLEEEKKISLSFRIKPLAIEGFSEDKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRH
KALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWEELGKEVNEKVWNEKKDQYSGRQKSKLPKWFGER
PGKKAGEPETPEGEEDAKADDEIAEDEEEVEEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE

A0A1I8QB06 **A0A1I8QB06_STOCA** (383 aa)
Uncharacterized protein. *Stomoxys calcitrans (Stable fly) (Conops calcitrans)*

```
MSDDEEYTSEEEEEVVEEVKEGEGDPEFIKRQDQKRSDLDDQLKEYIAEWRKQRAKEEDELKKLKEKQAKRKISRAEEEQ
KMAQRKKEEEERRVREVEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDTGLGLSSAAMERNKTKEQ
LEEEKKISLSFRIKPLAIEGFSEDKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDP
EALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYDTLYKETLEKVWQERQERFTQRSKSKLPKWFGERPGKKAGEPE
TPEGEEDAKADDEIAEDEEEVEEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE

A0A1I8QB09 **A0A1I8QB09_STOCA** (391 aa)
Uncharacterized protein. *Stomoxys calcitrans (Stable fly) (Conops calcitrans)*

```
MSDDEEYTSEEEEEVVEEVKEKAPQTPAEGEGDPEFIKRQDQKRSDLDDQLKEYIAEWRKQRAKEEDELKKLKEKQAKRK
ISRAEEEQKMAQRKKEEEERRVREVEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDTGLGLSSAAM
ERNKTKEQLEEEKKISLSFRIKPLAIEGFSEDKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHK
ALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYDTLYKETLEKVWQERQERFTQRSKSKLPKWFGERP
GKKAGEPETPEGEEDAKADDEIAEDEEEVEEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE

A0A1I8QB17 **A0A1I8QB17_STOCA** (383 aa)
Uncharacterized protein. *Stomoxys calcitrans (Stable fly) (Conops calcitrans)*

```
MSDDEEYTSEEEEEVVEEVKEGEGDPEFIKRQDQKRSDLDDQLKEYIAEWRKQRAKEEDELKKLKEKQAKRKISRAEEEQ
KMAQRKKEEEERRVREVEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDTGLGLSSAAMERNKTKEQ
LEEEKKISLSFRIKPLAIEGFSEDKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDP
EALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWEELGKEVNEKVWNEKKDQYSGRQKSKLPKWFGERPGKKAGEPE
TPEGEEDAKADDEIAEDEEEVEEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE

350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE

A0A1I8QB23 **A0A1I8QB23_STOCA** (370 aa)
Uncharacterized protein. *Stomoxys calcitrans (Stable fly) (Conops calcitrans)*

```
MSDDEEYTGEGDPEFIKRQDQKRSDLDDQLKEYIAEWRKQRAKEEDELKKLKEKQAKRKISRAEEEQKMAQRKKEEEERR
VREVEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDTGLGLSSAAMERNKTKEQLEEEKKISLSFRI
KPLAIEGFSEDKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQV
ASKYERRVDTRSYDDKKKLFEGGWEELGKEVNEKVWNEKKDQYSGRQKSKLPKWFGERPGKKAGEPETPEGEEDAKADDE
IAEDEEEVEEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

334 - 353:	EEEEEEEEEEEEEEEEEEEE
335 - 354:	EEEEEEEEEEEEEEEEEEEE
336 - 355:	EEEEEEEEEEEEEEEEEEEE
337 - 356:	EEEEEEEEEEEEEEEEEEEE
338 - 357:	EEEEEEEEEEEEEEEEEEEE
339 - 358:	EEEEEEEEEEEEEEEEEEEE
340 - 359:	EEEEEEEEEEEEEEEEEEEE
341 - 360:	EEEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEEE
344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE

A0A1I8QB44 **A0A1I8QB44_STOCA** (391 aa)
Uncharacterized protein. *Stomoxys calcitrans (Stable fly) (Conops calcitrans)*

```
MSDDEEYTSEEEEEVVEEVKEKAPQTPAEGEGDPEFIKRQDQKRSDLDDQLKEYIAEWRKQRAKEEDELKKLKEKQAKRK
ISRAEEEQKMAQRKKEEEERRVREVEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDTGLGLSSAAM
ERNKTKEQLEEEKKISLSFRIKPLAIEGFSEDKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHK
ALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWEELGKEVNEKVWNEKKDQYSGRQKSKLPKWFGERP
GKKAGEPETPEGEEDAKADDEIAEDEEEVEEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE

361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE

A0A1J1GN56 **A0A1J1GN56_PLAGA** (2077 aa)
Leucine-rich repeat protein, putative. *Plasmodium gallinaceum*

```
MLLDLSNCNLRSLEDCDIILEKLIELNSDYTSITYLNVSNNFIKSIKGLRAFENLKVLNISYNELTSLEDDYIPSSTEKI
IADHNYLTDICFKGIKKKKKKKKDSEDYDEHINKEKGEIKNQKEIEKGEDVNNLASCSNDSLNSSFYDTFNNNVLNEKSS
YTNKNLPLNRLTYLDVSYNNIKKLTTFEKYLHIMNKKMKKKNDCYLDDVNIKNYISNKTEQDVMILFFNSLETLYLRGNK
LTNLKGLSVFKNLKVLDLRSNLINHPVQLFYILDNKDWLKKYQEKKIHKKSNSYYSYFVYILKKYKNFKNLQNLFLQGNK
NALKPKYLFMNVFNVLRNINSKSKLITDVINENDSSSHTQNSTIQKEYSNNEKDKKKDSFDSIISTTSELNEEMHNDYVQ
LYLNNIQEKVGDTEDSNKKKNILREKKDVHEEEEDNVMEEKNEMSKHDTKEDHQDEEQLQQKRKIYLKRKPKDEEDENKH
EDEKEEENEETEEEEEEEDEEEDEDEDEEEEEEEEEEEDEDEDEEEEEEDEDEEEEEEEEEEEDEDEDEEEENEEEKLN
QYQKLTEKDEKQKKEKKKKINHYLKQRDKKNDRNSEEEKENENDYDEENIEEEDDEEEEEQEEKEEETEEQEEKEEETEE
QEEEEEETEEQEEEEEETEEEERDKERKEEEVEEEEQQQEQEEEEEEEEEEEEEEEEEEEEEYEETEVEEEQEGEKEEQQ
EEEQEGEEEEEEQEEEEEYEETEEEEQQEGEKEEEQEEEEQEGEEEEEEQEEEEEEQEEEEQEGEEEEEEQEEEEEEEEE
EEEKEEEEQEQEQEQEQEQEQEERERERERERERENENIRNANINKILYNDFKNKKKHDESIYTSLIENSSSHKGETLKEKTS
YNYVNEKLINNVKIKNNVNDDKSSMNRCSYIPVVTENVCHEENILNKKKKKERSLKTECSHKNEENRHKKIERENIGDIN
NDKTSMNNNFKKDKYTDDYDEDEEKIEKLIKNINLNVTKNSSYLVSFYNKLKEDMNIKNYDDTNNYNLKKNNVDIINKNS
KLKKLKLCNIDKLKELSVEINNSEKEKRICNEGKQISKLKMGKTKLVKSDYLKKHKETDEINNEIEVKEKGKIWNNEQNK
EKKSVIYDNENKSNITENIYTTKKGNENSTEIKKNSLLNESCFNSYQKKNNKLTKKNIKNNDKNSFYNTHNSKFNKLSNN
LKKKEVNGEGNEVIYCSSTLKNKKPNNILKTILNKNNDIDKSTLTSFSSIGSDIFDSDCEENDEPHENENKEISDVVKND
KNRNVVRNIISDTFLEKREKTFHKNNSNLKKFVFTRKDCYEFNKNKKSLNNDNVNCYNDKIINRKYNIINNNKEIKKKEK
MNSEKSEDKKGERNSIKYEYEDEEEYDYKDVQQKGEKNINNYMKDNILKKEKRTKDEIKNLSINNRNEIKICEKNKINET
NGDSKEKIENKIYEKDKNECKEYEEKEENVISSDIKKKEDIKNEKEKNKEIFKGLLKIDLYKDEKTENNNKNNKTNNCEL
LNSKTKKPNNCSSSLKSESTDVTERNTNRENIRKDKFLLKDYVYENNLGNTNNLNELKISKENNICAYPIILQNSNIKNI
NENLYNEIFINNKSNFLTNNHISSMNKTNLLDSRNVSIKNTDIINSKNKNDEGSENKKISIIPSNEKNCSLNSLDNSNKM
KSLENLNTKDINLTNNLALYLKDVCFKLGKEKQHSDILLRENKKLENEIKLLNENKQRYKKKIKNLEKNFNEKNKITKRY
QNMNEKLKSIEKIKIDLPKDDINLQNKYIENTMEQLYNIFSDTFGENHIITKKIENLADVYIKKEKKIEIQMIAQKKELD
LLKNVEEIVKKKDEYYKELLKKNEIIKSLNSNLTEITKSVSDMKNSIIENESKSKKLLMELSKKDTLLKDLEKKNSFIIT
EKEKKFEKERTHLLGLLNDKEEKIKCIELYKDEIKSLEEKLKNYLDKNVNKISDKNYEKIVDKLHDQQIKMHSLLTQKEK
IINEKNIQIENLESQLQSWADEATNWIVVADKHTKLIKNHNILKKNYEELKFKYIMDMKYVQSTKNEKVKELIQKFS
```

682 - 701:	EEEEEEEEEEEEEEEEEEEE
683 - 702:	EEEEEEEEEEEEEEEEEEEE

A0A1J1GNY7 **A0A1J1GNY7_PLAGA** (2620 aa)
B30.2/SPRY domain-containing protein. *Plasmodium gallinaceum*

```
MEMINRFNITHENEKNIDDYLIINGKLNILIDYLIKHSHINYKKVIFLLVNNIYESYICLEQNKKYEENVEEKCTYRNEQ
KKKYITKIYNIKRKSRLEFNFLKKKRIYKILKSDYLKINHLQKKKNIDNLKWKKICTMKNIKKKILNNKEKTLKKKLYLI
LFKGNKNMSEFEKNFKWKQNFYIYYKIIFSEKMKILFLRLLTFSLNYIHSKLNKHFQIFFSIFKNSYEQKWITSLFSQKY
FIFFSRKDNNYKKNLLLFFYIIKEYISSLISIKINKKKKLKNHFLDKCILELNNFNILFDIIQKNKIFLYILKQFFFLVS
SFYKKFINTSRWNNKNYLDNYTYSREKEFFIINYNSSIITIINLLYKILNESTEKNAFYKGVLNFQKFQVSNFPEFKNLL
KLHMNEVNITILLTFLDIINNLSNVVLMNSLIIDENFFLVFYIYIYRRHFLPNKLLLFSILNINRKLSKKYKESNNFTFL
KKSFTFFIFFVKLITYNENIIEYIFNNRTIHVTIIHNIFLNEENEVFNFFKNYIIYNSNFQITNHILRMKEIHKMQEHFT
QNNIKNNLFFPFVSLSYLYRKKYPNSFFVDKYKEFFFFMIYKFRDNNTFFLLFFENVSKILSFDELIKYGEFLYILNNIR
SIFNLLYFTYFIHFILLICHFIYRIVKFLKCKFLFFKLRHKKRENLLDYNELEKIKKFTLFNFNYFSKKKERKNKFLDKI
VLEKNRKISEYSEKKYHMENESDLFFNCESKLQKDIEIKEKKIQYEFPFVDTKKKIKKNNNNDKNRKEKKIEVKHDYENY
MYPVEINYMENGENNYFLNTEENTYENIYNDVKNNKVDSYINKKEEISYCKNRKAKKKNKKKVKSEIKLKKDIMIKTIKI
ILKGKIVIIKNEKIFNTKEIYYSNYLLSLLFINYILDLNICEDKYCKSSHSLSKSTIYSLGGSNNLSSQKKKSKSHSNRR
KNKKKKINNQKKSQEKERKKKDNISGSGSGSGSGSGSDSGSDSDSDFESDDEEEEEEDEEEEEEEEQKEKEKEDEEEEDD
DEDEDEEEDEEEEEEEEGEEEDDEYEEEEEEEEEEEEEEEEEDEDEEEVEEEEEEEEEEEEEEEEEEEEEEEEEEDD
EYEEEEEEEEGEEEEEEGEDDDEEEEEEEEDDEYEEEEEEEGEEEEDDEYEEEEEEEEEEEEEEENKKKKKEEKEEEEDDDD
NDDDDDNDNDDDDDDDDDDDDDDDYGDEEEESDEDEDEDNEDEEECKNEEGEDEENEKDDADINVSKDEECSDEYEDYEM
NSEDEDIDDENMEENVVDDDEEECDYENEEGEYEEETEELSNKSEYKYNEKEEEKGLDNKNKKRKKKKKRSRDEYAYEDN
DPGGQKSYKEDNYYNGKKNIYLKKKKKKFKHNYIYLKNLFKGNVYINTLNASNFISVSKDKLTATYTAWGKHTDVACVQV
NKCALRDCSIYYFEVEVLNCTNFSKIVIGMTSKNYSINKNPGSEYNSFGYKNDDGKKIIDGKIENYCSAYTKHDIIGCGI
NYFDNSAFFTKNGKYLGKVCNINSKYDYYATVGLSTLGDKIKFHLNSFCFDIYNLIYEENEKERKVIKSIYIQKDLFSDI
IKSHLIKCGYLKTYKCFVNYLEKNKLSDDNNSIGSSSDYKNELDKNFTTDINSKFLEKKSCFSSNDKTKKEDRDKKKEIN
EADKNITKNTDSNAFYACEDMKRKNVISTDIKESNDNNNSKLKKIISNKEDNVISLEKCEKEEKKEVIDSPLKNNNSMNE
TIEDAEKKNTNFLNFDKITMENNKDDKNLLNSFLINYLDVYDKLNKDNSTNVKKEECNNKNDEIKDYIKISSATNSSCNI
KKIDEKNEELKIDKVKSDFNEKKKDNHMEEKKCLKVIKEGIKDLSIEDNSKEKKNISDEKLKIKEELESEDRNDANIAKD
EHYINDEKDIKDESNIKNKKEIQEKDTNNEKDKNKKEEKKNVEDTEKNVYDENSSNILKRYDLIQYNYSNINLQNSLWGS
RKNSLSNLINLRKNSSSILMNRLRNKRSLTAKNDYSDLTYSIINTKKESKKSDNDSNKKIQYIPKEKTSIFKNEKKKLNK
KIGKNYSIDNEFITKYFVNLYLSDDKLNKMIDSLETRYMIRNSIINGNIINALNILEKKYSELFTKENASFSIAMLYTQQ
LIEILKPHKKFIKKISSKKRCKKLIHSEDDLLSDSSYKTYNTLSDNHYYDDIKTEYNSSDSLFCDNSNVEKNNFKTLKLE
ELYKRDKHKIDDKMEKTNKYCSDKKSFKNNKVINNSLTTYLEDVKSISLDTCESKGKVTNKNNENVLTQNDKIVYQKEDT
SENTKTNLDKYDNDISLKKKELKIEKIIYENINSNFDEEFLKKNNLQEEYNTHYNKLREQYKFFNDDNPYNNKFNNKIYK
NTYKEEKNIFSDSNGDNISDYDSNDSNFKEKYYEYNDINFDEIYQYLYKNEVFPSNQLKYKKDHLYLALMWIKEKLSLFN
KSKLANVRQCILDTTSLIAYNKPYKEKHVCMFFSKNRNLLTYNSVNEAILSICLNVPVYSPLEIIVKHLILCRNLLREKK
GNVGIKYDCCYVCQPYKRYIIKIKHRKIKRRYFKENTKLHNEKCPLNGKFSEDKRLSIFQ
```

1066 - 1085:	EEEEEEEEEEEEEEEEEEEE

A0A1J1GQ50 **A0A1J1GQ50_PLAGA** (3380 aa)
Uncharacterized protein. *Plasmodium gallinaceum*

```
MDYKFILKKQELYVNIDMNNKVIEGNTVMNISLNLPIYYLYDEIDFMKNNYDLKRIKIIKGEKKEKEEKEENEEKEENEE
KEEKEEKENKRNTKEIFLEDDEAYINFQKKKKDKKLFMVVHIPNNIHSSKYYDIKLNEKDEKRYYIIYNSLKENLHVFEK
KNENNEYDNDGNIKPLTKKKKNSKLIKMNKNKKIISSFQEKDSSYSKDLSINEKMSLKNKMNSNNYLTNITDSGEEINNE
NICPYNESVNIKSFKYHHIETRKEQSTKKEVEQTYTGDHYENDIVKNEYIGEKKKKKKDINEYVLKQDNMCNNKYKIVKN
EENMCREEQPELYFKEKGSKTEDIKEKKLIIDRKKKYKEKKTKRKNEIEDKERDKDNKKFNEKDTDEDEKENYERKKGEG
SREDEEEDEEEEEEEEEEEKDEDEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVEEEEEEEDEEEEE
EEDEEEEEEEEEDEEEEEEDEEEEEEEDEDEDEEEGEEAEEEKEEDEDDNKNNNGEKNCNINDYINVKSLGEEELEEY
RNNEIGENKYERYHKAESNRSEKKSKFYYNENYEKNKIKKDKKKKRKKKNNFDIIDFLSLNKYIDENNLKEDSYMFIAIN
EEIFNREKERNYEKFQDFCKNDTILINKKEQYNIKINITVNINFKFFNLTSYYNKVYFKNNDNLLITLQNYAKGNTWFPT
LSKFDSVYSRCSWLCVFKISKPYFVISSNSLINIYEMFDKNCFVYKTTNKKSKLFPDQIGLFAGNFIFLHLNNLNFKDFQ
KIDYEFLYKNEFFSKSGKIHSTEQYSKSKNKSNANKNNPDMLKNKKMNFSEHHKQNVNSSLKRKYSSLNNLSNDYYKDIN
DMGIDKDENNDENNDENREKKKKKKILLNENDIYNKNNYRDNVTNEEYYNVKKNFYLNDYELEENCNSISTTYDYLIKNN
IKEEKYNYYEKINNKIVPNIFVFSIKNYENELIYSNLHIGHILKCFFDISKESFPYDNLIILFIPLNFSNFEKYYNSENI
ECSINSHTYDDIKNGYNLFSNSNILNYKITEPYVYLKNNKYFIFGNVIIFSTQILHNIYDVLFNINIYSYKIIIAEGILS
LWFEYYSNLLKNENIYFIYMLKCFALQKYIENIFGIVELNAIFYEIRERYCSLVEIFGDVNLYHFYEKNKNNVSENFISH
YVFNNIFFLKCFLCVRIFFNILKNFPFCNSIHQYCFSLFFTYFKNKKKVIQSTKFWKKVFNECTRRYIENYKQMPKNKFK
MKKVDLNISELKNEEHEQYQLFEKYFYYFFKTYIKGYGVCQYILTFNVHLQRKGTSMDSFNFLISQNSINPFYFVDENFH
SNYFLSDISSMTVYDLLELNKYIELKNFINDFNKDKKMNKYLDKIYFDKLFEIPYIIDFYNLEENFLSFLKKNYYHIDHF
YEYPIKEFSKKYVKYIKKHIVKKNKNYFFIKERIKKKSNTKYTHINKMNHIKNINKKMEIKERDMDTNIKSDADFGNTDS
YHNNMSKSDKRENSMEEITLKESDKKDNVDNNKKNILKEKNEVTEENINQRKKEKKRKVQLVKKKKIFKKKKIKRSIKNN
NKSVEIRKEKLSKYIKINKNYILKKKKELINLPYSNFDSLDLIGRDGNFYLGFGYVGSDDLTLSTGRGNLYNNIIAFQKL
KNCNIQKLSELCIDKHNIYEYNSSPFYTDCIYPQWRIVLRLYYYLQLLNKIYKKKKIINKGYSLKLKNNEIDIFNDVKKN
KLYELKKKDKKKKKKKKKMKKDKKNKKKEINEDNDDNNNDFLSSYTKDNFSTFNSYQHKCSHNTENILVDEKKKKSINMI
KNVTYENEKSEICTHSDNKEKHQEYDKKSNEECDESSYEVYGNNEYEDYGGRHKYDEHSEKVYDKYDSGTEKLKKKKKKK
KKKKKKKKEKKEKKNIKDILNNKKYVESYLNPFVSNNVPSSVDENKFFFCHLKIEIIEDDGVRIVRKNLINNITPTRFSV
NARPEKGRKKVAFKHEAFINKSEEYISRNSIDMPNNFINKNVKFVGVTNDSDKFMIEYCKQKIIKKDKSLLCLDNRKLVA
KICSKNKIPILWIRIDNDFFILGRIRRSQSISMWIQQLFNDNNIFSQLESSFALAYIPFFYLNKSFSTNFSEYKNNDNSQ
NDNNNKKDNIGESSIHFIKSVLNKSKLKNKKSNLNFNNINANISSNDALNNDLLNDSFNLEEDTSKRHLLNNNNDSLILG
KKKNANKSTKKLMNNIIDSNFIDQNNLEINNDKEKLINNLQNDFPSDLLKDGNLSSQTSSSGSESGSYFSNLTTSTIDDF
NEEYSSSLYNYTNINNKRKMYKKKWKNYISITNIPINVEVIKCLYKSLTCDYLHYLVKIRCVYSLCFIHNKYLCTQKIIQ
NLFCEYLCYFYGNNLNQKKFMHAFYIAMSLLRNKNNRTPKIIIFLLTQKCANFVFSLNLDDKHKINKDWENEKKLRIQQH
YTSYNKDDIICDKTVDTNLPYNLNPNIYAESNSLNDYENKINYKNILNINDKENDLENENKYILNNFVDKEDNEMNIKTK
KLQNCVDENHIEKNSIKINDVESCYNQKVFANSENIDPSKTKKNAHNSENSSIDLNEYLKENKKKRFSISSFTNNSDEFI
DNNNVINKIIKITHEYSYDTNNYSYDNNNNNNNNNNNNNNNNNNNNGYLNINKLEKKVAFKKKNKISYVKETIIEKEEEED
IKMVLECLGNIKYKQRNIYKDFNNLYELSNYYRSNNKENLFYKYFCNLTSKNSSYNKKKKKKGYDAYDFYDINIYDKKKL
ENHFLKLKKTKKEYIEELINLIFIIYQLKKMSPYLHISDWIIIILIRTISRNKNILDSFKKKLYFENKEYFDLCNYIPSF
SISTKIHPSISLKNSSFFFVEILRALLHLILEGNIRVYQIFYKNTKEDLKEKKCTFLNKNINKNNSLSRINKKNFDITCE
KVKEKVINESDIFTNKNYDEKYELFNSGNNDDYFFISTYTNYVEKKMICSHILNIYSAFEFSYKIINKFHDCELEMQIWN
HMYQILLIFQQKYPFFFLPFSKNFDKYFKEYQKKNLTIFEFYYLLYGLNKINSFEKFNFGETKKNLCDNNYDSEIFYDFN
IQNIFTTKNNINLFFLKNKSYGIYKYNIIGYVKLVDILKSIKNSNKLRKNFIQITYIKYLVKYIHNFLRKLIINISNTNT
NYFKNSILYDLKNIFLFFYGYGIPPFNSKKNAKVYKPHYSQLSNITSKGVQINDLIKFLRTYYDNNKLLEWKKVASEFVN
VLMNMKELELFIDNPTISLHNYNFVKENTWLTLISAKLRNDIYKLPMDLKRDIVLLLKNIRSVDMCSGTNHYEYVNNIFT
VCWFIIVKIFQNYEKSKRNT
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432 - 451:	EEEEEEEEEEEEEEEEEEEE
433 - 452:	EEEEEEEEEEEEEEEEEEEE
434 - 453:	EEEEEEEEEEEEEEEEEEEE
435 - 454:	EEEEEEEEEEEEEEEEEEEE

436 - 455:	EEEEEEEEEEEEEEEEEEEE
437 - 456:	EEEEEEEEEEEEEEEEEEEE
438 - 457:	EEEEEEEEEEEEEEEEEEEE
439 - 458:	EEEEEEEEEEEEEEEEEEEE
440 - 459:	EEEEEEEEEEEEEEEEEEEE
441 - 460:	EEEEEEEEEEEEEEEEEEEE
442 - 461:	EEEEEEEEEEEEEEEEEEEE
443 - 462:	EEEEEEEEEEEEEEEEEEEE
444 - 463:	EEEEEEEEEEEEEEEEEEEE
445 - 464:	EEEEEEEEEEEEEEEEEEEE
446 - 465:	EEEEEEEEEEEEEEEEEEEE

A0A1J1GQX0 **A0A1J1GQX0_PLAGA** (2647 aa)
RGS domain-containing protein. *Plasmodium gallinaceum*

```
MILHSRKRKNYEKAENRKEKTIDKEIIYEQIFSTPKKNKPRCLVAADNKNNLLNYFTSILNFENDEKEFKKKWYIHLYKI
CLYNERLYVNNNKDKNSDKESSDYNIEEVLTKLQYLIERKLDCENLYYQKILITICLLFDYFQNKKNTNIKKLKSLEENE
EKRKIESCYDMTSKQNKESKKRSLTSAVYSNNIDDDDETHKEEIENVKNKEEIKKEKEDLNFHKNYYIIEFKNILYNEKK
KFNNLEIFYHITNFIIHKYWYSQEYSHYNIFIWFLNYMNSKLDVKKAISKINEHLEVFINLHPKVFNISHAKKKRKKNVQ
YHNTSSSHYFENGVLDYPFVKNRFKQTGGGFSDLADLEKKNKQNIENLNKINNFSNFQSSTNSFFNNTMTNMKNANNSSL
NNFNSSFKGFDQNNNIFNNKNTENSLFKKNINSSSLFGNTLNNNQSNNNLIPNYRAGFSNDLNAQNMNNFNLSMNKTNNV
SPANIFNVKNNLNNNLENSANSNLNLLDNSQNKNVSIFGLKNNTSLNISNVNASNNNFFGFNKTGFNTLFGNASNNDKNI
YSLNNSQKNSIFENKQINSLDKNKDLLNASQSNTTTSIFSPKNKEETPFSLLSGNRINSNMNNSSISLNSKSIFDNNVNT
SKPNIFSNSKTDDSIFSKNSSGHVNIFGNQMNGMQQSPFSKSTSNYNNNNILNTNNNNLSNNLNNNMSNNLSQVNSTTQS
FNPLNKAQNENQLATLFNNENGSKELFKDLKFSNDNGPKFSVNKKPLFSRRTKNTLLSSNTLNQENNIFSSSYISKDNLL
NSQDKPLKVIFGQNNNNNNNISSTNNTIFSTPSNNNISGNTNKNIFNQNCNMLKSTNQSIFGTITNNSSNNNNSHFGNNI
FFNGNDINKGEINKSQNLSIPVKKLTLEERKKKTIKNNMLSLFSNNNNSNDSHNVDSSLATTSKNIISANNTNSSSLFNF
NPSNNNTMTLFNLNKNDNFNTNNKQQNTNDSKIIFGSNNNLLGCQKNKNNDNEKNILSNNSENNNIKNNLFLGKTFKEET
EKEKIKEKEKDNNCELKTKNIFGFVEKDQKKSNTRIDTKTLLMNIDKDSPNYKLKNNKLEQNGDSLSKDDKNTFKGFNNI
HQNDSETNVKKIKDDEKDKSKTSIFGLNNKEEEKNKTSIFGINNKEEEKNKTSIFGLNKEEKEKDNKTSIFGFNNKEEEK
NKTSIFGLNNKEEEKNKTSIFGLNKEEKEKDNKTSIFGFNNKEEEKNKTSIFGVNNKEEEKNKTSIFGVNNKEEEKNKTS
IFGLNNNKEEKDNKTSIFGLNKEEKEKDNKTSIFGFNKEEKEKDNKTSIFGLNNKEEEKNKTSIFGLNKEEKENYISKSD
ESLFAMNNNNNNVTLNMKDLDENKTRDNINYDDVKNRKRRRNFDIDEVDNAFINDEKKDKIVNSETILFDKESKLNEKSDL
KELNTKNLNDNNIQSNDKNMNNDENIFFKKSRIGNALNDAKNILNTLKFNSLSSNDINNDTFSENKKNELMNEKSLTTKD
TNLTGINVLNANDETHKDIYNTILSNDDKCFNNNKINNLKNNDFNLKQNPIEDFNCTKKNVNIEKMKESSINNNLNLKNL
ESNKIETEKSTMLQVNCNLKNHINENMININQKEKTYQENEMNKIRVMKRQREDILDDDEKILMHEYLIHEKSSLNDIKN
ARKENIFTYKKTIDRIVEYNKKISFDNIEVDLDKDMLDIQDLKQNLLLCALNFHLNYWAEKVILFYPHNEKINKFCNKLI
KIKNEFDETYNFTLFEQIHELSKKLLKSLDKNCCIYESVLFLSTENINVLKNVKLSLFDAFNIYHFWYQKNSGDIKKNFQ
NFMYTNKIYPCYINYYMDLYKNNKSFNYKYSDLKQKFNQEKSKKRKKKKNTKINVFSLYSSPSFHNDYYTPYSNYKSVIT
NLKRKKKIIEQSKNDFSYYSNVSCDIYKNNNKDKKRRYDGNIGNKKDEDELEEKKENEYKNIDEHENKEEEEEKEEEEEE
EDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEDEQPKNKDKKKKTDEDEIHLKENSLINVLNSNSSDISDVLDNNYKD
EPLNINIKEKYIYFAKVKSRKSKFQLPSHIKIKKLSVCECILLELMLKNNILNVLKKYKIFKMEKYEYLYINLLAMLKHY
NYFTMDKVENVNDKKKTNNFSNLNETDNNVKKSVDNLEVNSMNSKNEKINILKKLCDKNLLYYLNIQLKNISHLMTYNEI
EIACAFLNHIKNNLYVMFQMPILLFNVLFDKIIHSYNDYIILEKFFNNSYLFNDFRYEYIFKTKIAYMLFKKFYSMNDIE
NSIKFALYFERYRAKAQKNNIYNDYIFHKNLINSYIQIHENIIPSEWINLQKSNGELNNLNDSEYLDYYSFFFKDISKYI
KFNIIEKIISFNIFSLHKEDYNTKIKASVNNEERKFSCYFLYMVNKSLLDDIVNIYSLKGEYFYKRISTSLINHTLVKDY
EKIHNKHFHLFVQVADINDFMKIHFFEYINFFKKKELYHIDKTKNEDQIMDNLVNVIKVNGKKVNEVINTLVEIIMKIEK
KIINDINIYIIINLRNVIIDTLYLFKYIFNNKEFSLNIVEDLYRNLLEFNNIIYSTFSDDSHIYPKEQIKKLFTSIKHKF
TNQHLIN
```

2003 - 2022:	EEEEEEEEEEEEEEEEEEEE
2004 - 2023:	EEEEEEEEEEEEEEEEEEEE
2005 - 2024:	EEEEEEEEEEEEEEEEEEEE
2006 - 2025:	EEEEEEEEEEEEEEEEEEEE
2007 - 2026:	EEEEEEEEEEEEEEEEEEEE
2008 - 2027:	EEEEEEEEEEEEEEEEEEEE
2009 - 2028:	EEEEEEEEEEEEEEEEEEEE
2010 - 2029:	EEEEEEEEEEEEEEEEEEEE
2011 - 2030:	EEEEEEEEEEEEEEEEEEEE
2012 - 2031:	EEEEEEEEEEEEEEEEEEEE
2013 - 2032:	EEEEEEEEEEEEEEEEEEEE

A0A1J1GR38 **A0A1J1GR38_PLAGA** (2640 aa)
Ribonuclease, putative (EC 3.1.13.1). *Plasmodium gallinaceum*

```
MKENNNINKKLKKKRKRKNREFSYLSLKKEIANLYEKEKKILLQNQNGNILTENTDINSLIENPKYQATLFNKNEMLNNL
NSNEVIKENLNFRQKKKKKKKKKVLYNRKNSMQKKNVNGLIKLFSNENKDVSKICISNNNIKNEKGSIIYNSNVESKCKK
KNNSKKSSKEDNNLINELLHIIITKSKIKKIKKKLLENCLVNFVSSNMVRYVIRKSKKDIDLHILKTFLVNNVDIKNLNC
TIVSRRKVEKLTNYIFPKKKIKSIEIVLSQIFKTNSIKKNFLEEFKKIIISENDYLSSVKMVSFYLLKNEKKNTDSYKKI
TKIYETSIELLKKKIENKENTETIENRNDNSKKKKNDKIIKYHDYIYENNEELVDKKSEQEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEKEEEEEEEEEEEEKEEEEEEEEEEEKEEEEEEEEEEEEEEEEEEEEKEEEEGDEKVEQKHEKVEEQKHE
KVEEQKHEKEKEQKHEKQKEQKHEKQKEQKHEKDKEQKQEKKNKKIFYSENQTQINNLLSNINNYKNTIDVKQSLKNKID
ISYILKLVNEEINEKDMQIKNLKNHVNLIENDIKLLFEKNKIMEKKIEEMEMNAKKNSLQNILEKSKKDMFVKQSDIIFN
IYEKAHLHFSDIKELNDKTDYTSNLNAKINKNPFNFAENVSFDHINENSLKILSVNDIVNLKKKMNKFMKLLKLSTSKNS
DTIDTKMKKELNLDCINNEIDKLIYLLENDKNVIERNKISKSLKNDYILGIKKNKSESTIIKGKKKNSTQIQKVIEHIDK
```

```
KEEEKNNKIQKVTEIKKKKKKLEKNSIINNEKNSKNYNDVNSLNYSLKKNENIFEIQKKNKSNNIKNNKKYISISSSSEH
VDEHLKNEYNDNKKEYKRNNLLNNLNFFMNSVDNKIHKKIISLDNINKKEKKYLKSDISDDSSFNNEKTYKRKNYFQKFM
SYCNDSEQDKNKENLNNEKHNKLNNKYLDSNESSDDKINEKLNSSNLKNNLYNESVSDINKNVSNEISYSNKKQKGKKKN
KIKGKKKRKNKKKNKRYEKYEENISKIIHLNKKNKRNKEDIRKDKLIIYANKKNDRYEKNIEKDKHIAYINKKNKRNEEN
IENDKHMIHLNKLSENVTDDSGDSVVYNYNLYNAIDDLNAQFSNVVKNIRLDRNIQKVKSIYQSDKAKKNEKNLTINSSP
TRDDIDNFRFQFNQVKNDYNFIEVLPNDKKREKKKNIYDEYITQEKAIEGIIKKKYIRGILSVRKHDYGFIIYNNQKIHI
RSKKDMNRAIDGDSVVVKLKKDKENEISGKIVYIEEHHGSNIQYVCIFRDKIKNQKFNFAIPFKKNIPLIKVLNEHIIEF
MKKYHIEDISNQLVYIKVFRWNSNETFPEGKIVEILGQNDIFHNMQNAILLNHNLNFNLKDALEDQHLRELKDKNTYKNI
ISNEIKKRIDLTKKCIFTIDPETARDLDDAINISKISRKKIINCNYYIQIIHNLIVHNGEIEECILKKNLSLFVKDDNNF
FDNLKSNKYIKEMEHIKHDNFMKEKTGEENKKKKKKSDKTAFKILTKKYEKKIKAHQNINYDINNESFEKNKLCREVKKK
KRESSDENNNSINIMNHIMNEKSIKMNNYSEDTNKDNNNSKNSNDEGFFHISNDCVNTESDTDNILDDIYELKGTRKRKH
KISKNEKRQKKKIYTENFCNIFSEDSGDDIYDRYRENEDFFYCKIKSESDTDNEKKKNNNNKRKKKKENKIDIFNYVSKS
NNDSGEEQKKEESEEGKEEDEEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEDEEEEEEEDEEEEEEEDEEEEEEEEE
EEEEEEKEIEEEEQKQKGKIQKKEKYKKKKELLNNNKAEKNKKIYEEKNKMKKFQKIFLDNSDYECFFNSEIKGKRKNKK
EKFSENYEFFFKKECDKDIGYNLFDNHDLFCEKCKQIIKLDDIIKEMKEEKWRKYNLYEVGVHITDVSFFIKENSSLDID
ARNRAMTIYLTHTCFPMISKILSEELCSLDPLNNRLCLSIFFYMDSTGKIDHNSFFIKESIINSKVKFTYEEVYLIIRNY
IKLKKIVNNLKKEQFELFKNKKNNNSILEDVDKNTKNNDNKNDHDNDNDNNNDNNNDNNNYNNKDKDNDNNNDNDNNNDN
DKREYINKKNNIYKKFLNTHFYNNINNNDSYIYHSKEDLTTILKKEFNEDKKTNSDFNFCKNFHLNEKNNSLDNLGNKQE
AKYDNNNVILKSVNSLINEKILKNSKVKKNIKILIKIFKNLSNSKHNLSNKEIFTIIKNLYEMHKITKGAREIRRKNGSL
LFNNDKINFILSDACNPIGIVRKQYTFSNYMIEELMLSANKLIAIRQYFSKYRDISVFRSHSLDNAIEVSDIIELLKKHG
IHFKVCDLRHILKFLDDNKKIFKHEKKNIFDVVCTYVKKKMIRAEYHTFKFIKDNNMSTYHYALSFLLYTHFTSPIRRYP
DILVHRIIKKIIYDEDKLKKNIHTEEEILKTVETSDIGIIEKICENCNNCKAKSKKAQIDCEIAFFCLYLQKLDYPGYNR
GIIMDIYKEKSSIYFKSFSFENNLYHSNHEKHFHKMNKEHIKYVTNYVIHPNITKQEFTLVLYNKNTNKVRLRRVYKVFK
```

381 - 400:	EEEEEEEEEEEEEEEEEEEE
382 - 401:	EEEEEEEEEEEEEEEEEEEE
383 - 402:	EEEEEEEEEEEEEEEEEEEE
384 - 403:	EEEEEEEEEEEEEEEEEEEE
385 - 404:	EEEEEEEEEEEEEEEEEEEE
386 - 405:	EEEEEEEEEEEEEEEEEEEE
387 - 406:	EEEEEEEEEEEEEEEEEEEE
388 - 407:	EEEEEEEEEEEEEEEEEEEE
389 - 408:	EEEEEEEEEEEEEEEEEEEE
390 - 409:	EEEEEEEEEEEEEEEEEEEE
391 - 410:	EEEEEEEEEEEEEEEEEEEE
437 - 456:	EEEEEEEEEEEEEEEEEEEE
438 - 457:	EEEEEEEEEEEEEEEEEEEE
1790 - 1809:	EEEEEEEEEEEEEEEEEEEE
1791 - 1810:	EEEEEEEEEEEEEEEEEEEE
1792 - 1811:	EEEEEEEEEEEEEEEEEEEE
1793 - 1812:	EEEEEEEEEEEEEEEEEEEE
1794 - 1813:	EEEEEEEEEEEEEEEEEEEE
1795 - 1814:	EEEEEEEEEEEEEEEEEEEE

A0A1J1GRS5 **A0A1J1GRS5_PLAGA** (357 aa)
Casein kinase II subunit beta (CK II beta). *Plasmodium gallinaceum*

```
MEYISNDESSNEILQENMAGEIELSDTSFCNAIKNDDFKEAEYIKEENEENYILDGEKQKEKEDENEEEEEEEEEEEEEE
EEEEEEEEEEEEEEDDDDDDDDDDDDDDDDDDDDDDDDEYDEDDFNEATVSWIEWFCQLKQNIFLVEVDEDFIRDEFNLIG
LQNKVPHFKKLLKIILDEDDDEDDDDDEDDDYDEDDDEINRGSEELYKNKDIYEQNAACLYGLIHSRFILTSKGLALMRE
KYKAGIYGTCPSIYCDNAKLLPTAISEVPKFLSPLLYCPRCCETYYPHKNSLLNQLDGSYFGTSFASFFALSFNITSDKK
KVYYTPQICGFTINRDMRETLYMDVNKDNSESSEEYS
```

67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE

A0A1J1GS45 **A0A1J1GS45_PLAGA** (1353 aa)
Serine/threonine protein kinase, putative (EC 2.7.11.1). *Plasmodium gallinaceum*

```
MSFSNSRSPSNNNSSQDATSGKLQYTESDDEGSEEYCKGGYHPVKINEIYNERYRIEGKLGWGHFSTVWVATDLKSKPLK
FVAIKIQKGSETYTESAKCEINYLKTVKVNSFDSSWVELKEQQREKLLHYNMTKGVVSLIDHFEHKGPNGTHICMVFEFM
GPNLLSLIKHYDYKGIPLNLVRKIATHVLIGLQYLHDVCKIIHSDIKPENVLVSPLSNIPKPKDYSKDKLIKINENEENK
```

```
ETKSEIKENKLIAKDGIEKCEIEQEQEQEQEQENEIEKEINKNEWDLIDWNKLSKNEKKKLKKKKKNFLKRERLKQELLD
KNREMNQPTTNTSSDKLNNNEKNIIHLNNVNKNDDNQFKKEDIEKLNNNQLNENEHSKKTVENYCKNTYNKNHMNVTSDI
NIKCNSNKSNVIESFNDNNIYSSSIIHNNAIKNEKIEKSEYVEDKYDNLNNAILDQSTPCNQEMKKYTKEHILLEDKEKN
LNNKIDEQSLNKYKIFNEPPYIKHMLKPSNSDPSLLTSYNNVHALQEALTKKPYHFNNYFLYNPEKYGDNKMSLFLHRLP
NDYLKKNAINDDVEGLQNSESDICDDEELLENDINKFPLYCDMFNHLIHPEALKLHELYKKNKKNKISEYPVNAVDSNEN
THKVVYIKTEDGDYCIRPYDPSVYCHEKSCYKICDLGNSLWIDESRFAEIQTRQYRAPEVILKSGFNETADIWSFACMIF
ELVTGDFLFNPQKTDRYDKNEEHLSFIIEVLGNIPKHMIDSGFNSHKYFNKDTYKLKNITNIKRYGLHKILKCKYRIPEK
EINPLCSFLLPMLSIDPQTRPSASTMLQHPWLNMVALEDDEIYIKNSSPSFNNIYIKNNLNYDIYESSNKSINSSNNQNI
HEDFRDFNNSTFVHLEQESRKGEDYDSEYEYPFFYQKSYNYDASELSKVNYDTKYAKNVKKKLTIKSKNKKENYSKLRDS
SINTDDYILNSEYISNAIDHNSYNKLLKNTAPYKKDKIKDYKRINIHNETMQNEENNYRHYYEQGDGCKREEYADKSENV
KQKEEDEDEDEEDGEEDDEEEEEEEEEDEEEEDEEEEEEEGDEEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEDENEYQDK
NEKYDVNKYDNKSGDNNQYEYENNDNYQYENENNFDACCDDKNIYEQEDIEIDTDEGEQKEQKQKLERELKTEVLCEIEG
RSIINNKMKENIDNKEKKVKDNNKLYEKISNNLEHKKEENKTMNDEIINEKKKLIESKEIEQHNKFTKNVSNIMLNCNAS
TSLNKCDHIEKNQMTIKKQQEKILHEENKILDNRDEEKANKINCKIINKNTFCDISKKINFLEAKNSLEFMNQ
```

1091 - 1110:	EEEEEEEEEEEEEEEEEEEE
1092 - 1111:	EEEEEEEEEEEEEEEEEEEE
1093 - 1112:	EEEEEEEEEEEEEEEEEEEE

A0A1J1GTC0 **A0A1J1GTC0_PLAGA** (4245 aa)
HSA domain-containing protein. *Plasmodium gallinaceum*

```
MNLNNKFVNFHRYYWVNDNEDKILRYNDYTFNENNITVFKHINKKNIIETITNNKRSLNIMNFFIKLLNYKKYENDIFLI
NLIYLQVTRRMVLFFIKIYTFIYIYIQQIIKLHFLLLFNCLNYITKRCKYYIFDEATKKNKYIYVSEIKKVGLENYEEKD
RKKRIHVINNFVHNGFCYFKIEKKKHKKLQEKIYNNYFVSIKICIDISFMKKFLIFLLINNRNIKFSKAFINNFNLIFNK
NNEMNNRSNKNKSKYGNNNCNNNSKKIIKFKYKIKNNKIQLITIYVNKLLKLNYKKSSKSIFKKRKRKKNYKNVHYIIYN
IIYKNTRYFNKRSNSIINLDIKESKHFYQIYYEEKYICTINNYIDIFKIFLKEEKIRNDLFIHKIQKKIKSLCSSFFKKI
NKYNKIIYLISFKKNGNFNQAKQNSFINMLNKIRFLTNNNIIYYKKILMNNVSDSNKRKQEYKQFLYFDLREITHIVEIF
LFLKMLKYYLINLIVMDKNSLFLFLEFKFNYITLYIILNNQYFLNANKYSFLILKKRNRNFYIFELFFDSSYIIILCTKI
IKFFKYINKDLRGNFLIVSKCKGIFSSEYVGNIDKNQIELLKINHINNKSNIYYKKVIESLTNKIKIKVLKISKVFKRRK
SFRKNEIIKVNIKRVKNYYIDERFFKYKYFKNVIKKKFIISYKSLLKYCKHFLFNYKILNIKQCVKYKGKRNRNSNEIFL
GDSFMKSCSNDKYSSSSSNNNGNDNSNSNNNNSNSNNNNSNSNNNNSNSNNNNSNANNNNSNANNNNNNNENSNNNDNND
NSNNSNNNDNNDNNDYSNNSNNNDNNDNNDNSNNNDNNENSNNNDNNDNNDNNDNNDNSNNNDNNENSNNNDNNENSNNN
DNNDNNDNNDNNDNDKNKKIQNDKDYKNNNDESNDKKRKNEKNKSKNKVKTESVNGCINHIALQKIEKLSSNNDESFLNI
EKKEINKKKKVSKTGKKNYPNEKNDKYAMNILIAENAYKIIKNGRLYKQAEPINNFQTHNNFMLKEMMWMSIDYYEEKRW
KKNVSKRFGYLMNNHFEEKKKNDKYFISSQISNDIKMFWFFILNEIRPDLVPVELDHKIKNKSVLKKNFFDSFQKNLQIE
ENNLHINKNNLFCDDYNRNNEHLMHINSENKHNNSEVVNKLSINNVGASENILSLNSFHNKNIVNNNIDYVISIHNENNN
NNNNFFSTNDRLNQEYLNINENNIYYNKNNLYLDKNVLKNSEMEFDEQIITSYINYEHSLINLRENINKDLLNKHEFNKK
EHITENRKYDEFTYLDVLHYKDNNDFYSNNSNYLDLSNHLYIYCLLFISISLIEVNESVFYKDDNAINEKKASILNDDSL
EQMENKLNHCYNETHVNQINMDKSQIEINKKIKKEFEDFRKYKKKKKINPYDGECLNSFTNDSKVMLEENEIKEEIFDFQ
NNKKKINKYNDDGTEDEDEEAKKKPEFEEMEKMQILKTKNRNEMDEYDDYKEYKLKKKEYKKLYHNNNNHDFYIINKNHI
DHYEDMKHNSIFTSSPLNIDVKELIVIPYSVDNINKEIHNSIIEKNINEYFNEIKQKNVDVYINNMELHGGKIYPFEFRY
IDGYYNDINLPLMNLSEYDEYTFFLYLFYLKNSSYILKKQIKRDKKKRKKDFSDILSSKKKILKRKLSENYKGVEIIDET
EKLSLNEKILINIDENIELNEVNCNDSEGQCPSPKRENKIYNFFEKSNLKNESNVLKREFLFNEKNDENFKKWKEKREEW
TNDEMNFLLILTKTYMNYINVDEIKKKENNSMLCFEESKELIYKNDNNLDKNNVNDLDKLRNETNNCKETKSDKLDNYNK
VDEVNYENTSTNEKFESECNNENYKDEFVDGINNDMKHHNNKINYIDYINWDIISLALGSYNKINNIYEKNRSPDECKNK
FFSLIKDDLYNDIVSYNLHYENYSNGTKTFKKRSKKLKFLPIFSSNVNTLINTLKKYFNEKIQNYKSKKKKNTNSSEHNS
YDKIKNDIESEKCDKNLKEMKKNPYDENNLEGENIKCFYGNKKKRNDFLKKLSKDSKLLNFKSFMNNRKNKSQNNFHMVN
EMDEANNPFKYKKKIHIDNLKRKKDFFNDLFNDFSCASKETSEEDTDCGKDSFFSCSDVENSTLKLDDLRKKSFNYKNKI
IKNEKETLLNIDNIKGNEGNENEKIEEKKEKDIDEKKYEEEEEKGKEKEKENEEEIGEKEEEDEDEEDEEEEEEEEEEED
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEAEEEEEEEEDEEEEEEEEAEEEEEEEEEEGEGEEGEGEEEEEEFDGEEDAN
IDLEKNKDENKDKKEGKKEEKNCNEKDKNGYLEKEKKLEEEDIRNLEINKEDENSQSQERKEQEKVEIKNEEKNKDKNEM
KQNEDVSYADQQNIREAKKEIIVIEKEKINDITRNGLMKENIFVDKNISDSSNIGSSLLLKDKHINKKIKKNCELNYILK
NCDGIKKLLNSVCNNKKNVKEFLSIINKGSNVENKHIYKIIQKFYKSIKPVIGYEDNFLDSLNNEVSHKFISNSNNIKNS
ENKNNLFLNKIDEEFLKYITKIIQHDKRKKSESLGKLNNLLNNESFKVNELYIYSPNESYKRVNEFAQQILNYVPFVDDK
KKINIKKIKKRFHCKNLISQILLADYILDKLRNFPVNGSLLSSKNNKAIENLLSETRLRAYRKYINENFNGNYNELKAEK
CHNKIFLEKNEEIYKMSLSNNKNLTDSNNKNENISHDKLIKENNVNNDFNDEKKNLYFDKNKELNYAKINENNMINSLNS
NNNGNIENLNIKKKNNSFLSNSCSTDLLSKNTNKEECENNNKAKFSITIEKQLKQNKEDMMKEENNPLNKRPENLNDSCN
LPFNPNDTSLYDHIKEEVPKNENFINFSLNNNNDNNKVFNNSNNLSNIKDQNMKTNKETTKTKRQTISLIKSYNEYLNDS
PLSDKQIKYSSKTTHLSGSRQKSQPIKNTDHANNMTKSKTSISMSNLLSDELKNINVSNNTHNLNTYISYRKHAKTHIPD
SNKINNIHVKEKGSYFQRDINLEKNNSLIDKELINEHNINDQIPFNFPNNHLINDKLNIPNKKYILSDNTNNIPNNSINE
NINNSINNQQAPTKNIQDCYISNQSPNKIQKSTSNTESIKSNSSAILYQQTQITSEKNYNVSDSLHNMKALQPTNKLNLS
NNSNNLNNKLCIFSFQNKEDDNFTSPIHVSSQHSKHISMNHSNNHISYNKTPLYESVELPPKQITSNVLNNSRQLEISSN
ASTKQLQNSLSNSLNSEKKMYSMYLENQVRPSSMNKINDDSFSIKSASPGNYPSSYTANSQLIQDNQNKLIFQEKILNQD
IDDSLNFIDANNKNIQNLNYVPTNYPSNNIKNFNTIHNEGRTNLLSNYKQTNYNSFNVNYAPNIIQNINTSNNVKKVISF
PNHQVENFVNINNTNVDNLEHIPYPSESVNKNINYISQNSVKNEINEENKNMSTNSKSIIDNSQNFQNVFQMKQQNEIQN
KLLDNNKIQQNYANSNSFVNNDQSKLPSVESNTFRQTYIHMNDQKTNSIYNMNERNINQRNFNGQNNNLQSLNQQNMNLH
NLNNQSMKYNNVNFQNRKQMNLNQYVNQMNFILQVLSQLNMNSKGYSQQNMSQQNLNQPNINQQNLNQPNISQSNMNQPS
MNQPNINQPNMNHPNINQPNINQPNISQTNMNQSNMNHPNINQSNINQPNINQPNMNQPIMNHPNMNHPNMNHPNTNHPN
MNHPNMNHPNVNHPNLNHPNINHPNINHPNINQPNINHPNINQPNINQPNVNQPIMNRPIMNQPNGNQPILSHSNGNQPI
VNQSNGNQPNVNAQIFNQSNITPQNVSKTCIPSFRSPNLKQQNVKSTFNDHNINNSNMISTGLNNNLTKNMLQKLPKKNV
FSSQEMIQQKLIQQELLQQKLQQQKMQQELFQKAYNDKESQQNSPSSFQQMHNQCTQENQIKNDQIRQQKLLQKLQQQQL
QKQLQQLQSQQISHQLQTQIQPQMQSQLHSQQLQMQLHPQLQPQQLQQIHMQKYQFHQQELKKQMEQLQQQIPLPQQKLQ
QIYALKKNVLINEENEKKQKQRQITMPVNSQVPNLHNLRQINNNNDEIITKENLNNNLNENTLFMLNKNVSNNINKFTNQ
DKFFTYDSFQQVMPSNNVNIMELRNIDKNVNENNILLKASQPTDISNNIPPHILPNNMASYISQNSPYQITHNKNINHTQ
QKNNC
```

2241 - 2260:	EEEEEEEEEEEEEEEEEEEE
2242 - 2261:	EEEEEEEEEEEEEEEEEEEE
2243 - 2262:	EEEEEEEEEEEEEEEEEEEE
2244 - 2263:	EEEEEEEEEEEEEEEEEEEE
2245 - 2264:	EEEEEEEEEEEEEEEEEEEE
2246 - 2265:	EEEEEEEEEEEEEEEEEEEE
2247 - 2266:	EEEEEEEEEEEEEEEEEEEE
2248 - 2267:	EEEEEEEEEEEEEEEEEEEE

2249 - 2268:	EEEEEEEEEEEEEEEEEEEE
2250 - 2269:	EEEEEEEEEEEEEEEEEEEE

A0A1J1GTY5 **A0A1J1GTY5_PLAGA** (642 aa)
Uncharacterized protein. *Plasmodium gallinaceum*

```
MNKKKKKNLKKPIDLKVLENKLNIINFIKNDFDKNLEKENEKYFKVSNKHNSKVENTLNEKERINIILEELILSCDENKN
NLDNYVKVVKEIINMNNDIIEKEKLEIEKMHSEKNKEICVIQEKIDYVKKSHDDLNSSIMHIFNNLNLFLMNKINVKLNI
DQLNESNTPKKDINIGIEDIKKEEIKNIKGQEIYDEYKKELYESMSEYNRKLYNVKLFIKENKLDELQESSYLKKYEVML
SREDQKDNTSAIRNNNYYDNCSKTCNNNNMNNKNTYVKEIEKNEINKKRETNAFIERLISEDNKIYENYFAKEKNSETIR
DNEGNENKKNEEEMVDKRSENLENEEENGDKEREEKNDEEIEKEKSDVEREEEEKEEENADKEREEKNDQEVEKEKSDEE
REEEEKEDENGDKEREEKNEQEKNDEEIEKEKNDEEIEKEKSEEEREEEEEEEEEEEEEEEEEEEEEDEEEKEEEEEEEE
EEKAKEEKENEDEEEDEDEDEEDEDEEDEEDEEEVEDEEEVEDEEEEEEEEVEEEEEVEEIGEREKKVSMYNKIKYNSREI
DKYEKEVIENKTKNYNYKSQKKAENGNYKTNEVFILNEKEDINNFSSQTHKIISNDNMNVLIDKIKKIDFDYISYFKQKL
RN
```

447 - 466:	EEEEEEEEEEEEEEEEEEEE
448 - 467:	EEEEEEEEEEEEEEEEEEEE

A0A1J1GU94 **A0A1J1GU94_PLAGA** (502 aa)
FACT complex subunit SSRP1. *Plasmodium gallinaceum*

```
MGDNNGTNSNNNSVISIGNIRGFGGGDYGSFRMSNEFLGWKNKKTNNVYQYKFSDISEGEWIKTSYNNNRLHLKLIESKD
NLIVYFDGFPDRNINEITQHFQKYFNIRLSNRKITTKGWNWGEFKFENSNLLFDIDKKYAFNIPTNNINQLNVQIKTDIA
MELKNEENQTNEDSLAEIRFYYPHENDENQTFQNLKNDLLEKVNIGDSKSESIASLTNIPLLVPRGRYEIEMYIRTFKLH
GKSYDFTIQYTNINKMILVPKSNSNQYVLIFSLNNKMKQGQTEYPFILIQLNNDDDMDININANEEIIKKYKLEKTISGK
PYDVVTRLFTSLVKKSVIIPGDFRTAKNQYGITCSYRAASGQLYPLNKYFLFIIKPVILISFEDIVTLSFQRTGNINQHR
FFSLIIKHKRGISYEYTNIDKNEYVPLLNFLKSKNLNIQDDANNTENKQDFRDELSESDEEEYVEDEDEEDYVAEEEEEE
EEEEEEEEEEEEEEEEEDDENK
```

475 - 494:	EEEEEEEEEEEEEEEEEEEE
476 - 495:	EEEEEEEEEEEEEEEEEEEE
477 - 496:	EEEEEEEEEEEEEEEEEEEE
478 - 497:	EEEEEEEEEEEEEEEEEEEE

A0A1J1GVQ4 **A0A1J1GVQ4_PLAGA** (1025 aa)
Regulator of chromosome condensation, putative. *Plasmodium gallinaceum*

```
MGQGNGKNKLIIQGTNEFLIDKKKKFCSLNIRSSVNIKNIYNGPNNIIIIYENDDFEIVGLNNYGQLGLGDKINRNKLTI
NSILSKQKIRKISCGYEHIIALMCNHNIFVWGNNHYGQLGIGENTVEIYTPLLIYFNEKVIDIACGKNHSLFLTESECES
CNYSNISEVKKADIPYNFIKKKKNDRQNCLSKSEININDEVNSKLNDEFIENYSSESEEIQNIKKENKEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEKEKEKEKEEDEDENKTDEENNKEEEYDNNIYVEKEEKEKKKYKHGNNDEINNK
KYCKTDNLNDTIKILKENEKKNRNGKILNFNIYSCGSGINGKLGFKSEENIYFPKKIIMKKKLKISSIYSSYDHNALLTK
TGKLYTWGYNKNGELGINNNKSSHKLKKINLKNDIIVKVCLSKLYSACLTKNNNFYIWGNNILKMKKINFLNFQISDFCC
NEDNIIILTKDQKLFLLDSFKKIQNLNKLIQTKLLNDAKNANNIQYNFIGNGYNYLYAHISINKDINNKNILEKKYYENS
TLCETKTNIKIEKENISLLDNSELESYNMNKKKKNIEIDEFSVIPNNKDILNEIKKNVNINNVNKEKKENIKDGVYKKME
IKEMDRNLWKIMNKCEEKKQTNSIKENKEQEEERKEKEITKEERITEEIEEEGNTNLCMPKVNSNNDKNYINTIDNFKKD
KNKLKTECANFSDLSENIKFHSFSNDILHIEKREEKEKNNKNIKSFNEKQIENVAIQNDVEKKMKNKIDIEYLINNIDNI
NLDIINIEDVYIDNNFLLNRTSDIIKRNVNHIDYLSTNNEKIEKCNNLTKKENSFCFNLEDKYVNLNIILLKELKKQKKI
NVFYNHLLNKLLNESIYLKEEKKNLKKKISLLLKIKNSKQNTDLNEKKKKKNVNSCLKKKHTFPLSLIPNDYQSKEKSDK
HISSSSNISTFSLNKNNKLINRKKKNIYNQSNDLLVLDDLTSDLFNKKNEEQNKINNIPIFFLNN
```

229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE
239 - 258:	EEEEEEEEEEEEEEEEEEEE
240 - 259:	EEEEEEEEEEEEEEEEEEEE
241 - 260:	EEEEEEEEEEEEEEEEEEEE
242 - 261:	EEEEEEEEEEEEEEEEEEEE
243 - 262:	EEEEEEEEEEEEEEEEEEEE
244 - 263:	EEEEEEEEEEEEEEEEEEEE

245 - 264:	EEEEEEEEEEEEEEEEEEEE
246 - 265:	EEEEEEEEEEEEEEEEEEEE
247 - 266:	EEEEEEEEEEEEEEEEEEEE
248 - 267:	EEEEEEEEEEEEEEEEEEEE

A0A1J1GVR7 **A0A1J1GVR7_PLAGA** (2308 aa)
Uncharacterized protein. *Plasmodium gallinaceum*

```
MYNSPRPEVTKGNFNFFGSFYSKYANRNVNDGISSCDKSATNKKSSNKNKVTSNQNISKKNELFKEAEKFYDYTKNLYKS
LKSFYNTPLKHNEGNRDKFLDNEYFSSEHSSASIECISNAKNKKYNKKILNNEDDRNNRCINNLNGIEDNKSSKNKNLKK
HQKIIKENYKTENSRNFDNTDLVRITKHMKKRENVNLYKNKKENNENEKKKKERNSESNKDKDDINEVEKKEKDDGKGED
EDGEIDQDKGKEKDIEEDPIEQKTDEASEKEQDVEEENICENEKNRYRNIEKNLYDEKVFYYEKFLLKNYFTKMLSGISN
NHEEHSNCKKKTIQNDNIVFNFTKPDTCINSCNSLYGMKGHFDSTKINSDNMKSNPNNIKLKKTVDRYPHLMNNILDENV
NFGNCTINEDNCIYELGNKYLKSDSLINNNVYPHMKKINDENISKENKKNSNSSINRQYFTDLDKTNEDKCDDSEISNIQ
KNCSILANKEKYMNLNRKSENEEKRFNNNLSNKNNYYINDYINDKKLINNQKYFFNKNYVNNNNSSHIPCIKGNTPTYYS
SVHKLQKKKKICLNDNISGSPLTNNFLLENCLLNKNITENDNFYLKKNYFYNKLCYDSNIGKVNNNKVNNFNYSFKKNYF
FNKGLSRFYKNRYNNFNYTKEYVHSKSRRYNPFVNKMTIKKQFFKNQYGEMCKINKRCVNFNYKMFHNEKSMFNYNKEKN
MKIINEKKCLCYNLSNNNIKRAKIVKNVFKDNENDDVLVAISRYEHFNIANFKENFNFCNNNNNNFYIKYNENNINGNLS
DEVKRNENLLNAINNKNVTLNNIHNMNKENTLKFYKKANNNFIKNEENIRSESYENKINRNYINVKLEETNDSITRNLSE
NMKSFNDNFVTSSINEYMQDNSNKNIIYYCNQKEEGDKNNFKNVLNESNYIDTINDANWKHRHKLSVSEKIEIVRKNEIN
KKIINGTNDERKIIINSRTTLPNARFQPINNTNFQNNLYVSLPNINNIDKFNKIKNLNSQNKTNDLIQKESKKGVRNKME
LEKKHGKFFNNVIDLDKINEIKYIIYNKVHLENRSKKSTNNIIDLDDLYEKNCVIYNEVELENKNENIKNKNTIKNLYNE
KENINNNTLSSEKKKEKIINYIIDVDKVYENKYVIYNDAELEKKNETTNNNNNSIIDLDRERVSTNNDKFTTDKIREDIF
MNTLEFSNKHENAKKEKKNEIICEYNIFNQSELEKKNEAENVIPNKKISEKRNKNDNINEDVLCNKSELEKINEIENIIC
KKINLEKMNDSENESDIYNKIEFEKIKDDANIITGTIELENKDEGIISNILELERRKYTINCIMEKLSRRENENESENDD
EDEIKKKINSYIYDLYSDKSTYNIYNTKMCVNYLHEEKIHSSENKEYIKNFLIEKHSKNIYFVEIFKKKKNKNKKLFNCD
GKNTVHNYSKEELNKTNEKKKDTYYLRSDQLYIEEKGGKESHISKKNIFEAKCIEEGKYKKVKEKYKNEVNYFNDKTPII
KRKLNNFERDQKKKTKIILNKKGKKKRFNKEFKEKMEIIDGKIVYVIDESITNISENEKNKMEEIEKKKNEQRYYDKREV
NKETKVTKIEEQENGKEKNLENKFKKYNEEYTDVSRNNDEGTYDCDYGDEDDDEDYEEEEERHLNEEIIEIEEEQDGFRE
SEEYYGKELRGKENGDYEEQSNEEIIEIEERKYKKNQNWDKTNEEVVEMEQKKYKKEEDEEEGKIKEEIEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEIEEEEEIEEEEEEEEEIEEEEEEEEIEEEEEEEIEEEEEEEEEKEEEEEKE
EEKEEKEKEEEEEEIEEEAREEEEREERVKREQIVKREQIVKREQIVKREEREEEEEEEEEEEEGEEEEDEEEEEDEEEED
EEEEEEEEEDEEEEDEEEDEEEEEEEEEEEDEEEDEEENYGGKQEKQEFEDKRGEELKNEKKKEGYKEEYKEKEIIKIDEE
EENEKEYQEELGKINEEIIIEIDEEGQYQIKGESKLENKKEQIGKKKMVENIYNTKNRNTYARNIINENYYIDEKYYDKI
GKEYEYENKETYIENSKKNEYEIEKYIYKQDIKNKNFKNDNYEDNYSMENEELNKIVYNNYGNKKGKNIFLKDMLNENNQ
YIHDYCDFEENIKYKLLGKKRKKRIEKIKRKIKKNKKLTKEDLKLLSELLHHKFLLNEINAVGNYDIKCNNSFDLLSLDE
YKLRKDSLNMYCECLSIGLTTYEQDFLKVFQIFMPDTNIMDDKNILYVLRHSKNEKKCIFKNFLNDKE
```

1750 - 1769:	EEEEEEEEEEEEEEEEEEEE
1751 - 1770:	EEEEEEEEEEEEEEEEEEEE
1752 - 1771:	EEEEEEEEEEEEEEEEEEEE
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1757 - 1776:	EEEEEEEEEEEEEEEEEEEE
1758 - 1777:	EEEEEEEEEEEEEEEEEEEE
1759 - 1778:	EEEEEEEEEEEEEEEEEEEE
1760 - 1779:	EEEEEEEEEEEEEEEEEEEE
1761 - 1780:	EEEEEEEEEEEEEEEEEEEE
1762 - 1781:	EEEEEEEEEEEEEEEEEEEE
1763 - 1782:	EEEEEEEEEEEEEEEEEEEE
1764 - 1783:	EEEEEEEEEEEEEEEEEEEE
1765 - 1784:	EEEEEEEEEEEEEEEEEEEE
1766 - 1785:	EEEEEEEEEEEEEEEEEEEE
1767 - 1786:	EEEEEEEEEEEEEEEEEEEE
1768 - 1787:	EEEEEEEEEEEEEEEEEEEE
1769 - 1788:	EEEEEEEEEEEEEEEEEEEE
1770 - 1789:	EEEEEEEEEEEEEEEEEEEE
1771 - 1790:	EEEEEEEEEEEEEEEEEEEE

A0A1J1GWR0 **A0A1J1GWR0_PLAGA** (3145 aa)
Bromo domain-containing protein. *Plasmodium gallinaceum*

```
MKFSNSINLKDIKKKKKKKEKNKQKQKQENGYFIYDNEEIDKSNEKKHSIKKVENNVQMNQEDLLLYILDMNKKYIEENE
RMKINDVNLNSYIIIEDTYNKREMKTYYELYNLTKYKNVDKNYEKNNLINFYNDQNVCYYSKNDIKVHKNDLKSINKKNK
KEYKKKIDVTTSDILNITNIKWKNGLSKNYLFECCNSIDGIDLNIHNTDFIEIQDIFDENRLNKIKNKSFCFYRNFKIKR
KKKSKNIINCESIKNKKEDKNNCEIEKKNFNYNIKNYNIKKKKEEFFFSELENENDKKYNNVNNIENDESYINKEEINFS
EKINDLIDLKENKSSIEQINSKSHSSDDFINLDIDKEFNFNDESKSDNIEEGIEIGESEKENKKENLNILSNIKEQSDNI
FSDFSFDCNNSEEDNKIKSSKTKKKEKLDNIKHDKLKSNEDLSEKYDFNNNDRIIELIGDDDNDLEENIFDENYAFSKNK
NQNKDFENEDNNINLKENNGGFTKINDLFNNNYSNLDGKEIKKKNSLLYDSNYDEKNDLIDDQNNIDNLNNINLHSNDEK
EIIKDFNLDKRRNDSLNNIYSYGNYANKKNDFYFHEENDDKSKKDKNEYDFFKNIYTDYKNYPLYNELNLFGYNIINNIY
```

IFMLLNYKYIRNYNYNNYIYPLNTEDYSEYIFKNKYSDKNILYDENIINEIFSLNNKNSLSEDDKKKRKKKTKNEYDNVI
INDDEYNHKDDECSVSMLSNHNFHMINNNSSNLINNDLFYMNIRNYVDNINENYEDNIYLDNFATIMKDLNINNIRRENK
NTILQRINRNLLFELKKNNHISYILKNLFLKEKSISDLLYKSLIYRYDEYKFLKNEYNKDILKVSDNVEKKNTFDINQSF
IEKSRADYAKDNLFSHNKKLRLKCLENTLSKTKNIMFFSNLKLDNYYKKRNPHEIENMLIASNNVYIHTRMTNDYYYNYE
LSNKRGIIAFSRFHKLDFRTNIEKYFYNYTYETLKKQDNEGKSDLLNLNKIKCEIKLYSEKEAKNFIYKYNHKIDKHNYL
ANINNNNDITKPFNIINILLDDHFDFNPYIINRWQVENNFDNSVTSEYKHNKDADNHSFLFFNNSCLLLSDDSPLVILEY
LEKDPLVMLKIGMNSKLNHYFMCKDEENLYSFDYKNKLKRNVEPFGEINVINNSINYFGVSIKLKKSKQKLTFLENELFK
AFLFTIPIYQTNNKEEQKLNETDNLNESINRNNNLSDNNILNDKSSNYYENNIANEDNEVVNDKTNNSSIVNANCDLEEY
QKIQNNDINFVSDFNKKIKLNNNSMQNNCDSDLNQENYFYYTDFLLIRNFSNNKSKFFLKPLYVDLNMYNEENVRNEIKK
EINGRNYENNNNYPFNIIDSYNNCNIEEKKDINNEDIDNLCEINNIRTFNNNYFNCIFYNVGFLDINIDMINPLYKKYIG
EKRNYIRSWLIKLIIKHKIKDIKKIKEILKKKLSAFINEKDINAIVKSLDFNFLLNKNYIDDVDQKNYYKIKNVCMIECI
YHYLQLFKYEGINFKNILEKEEKLNKLITILKIEKERAANNIINAKKKMHYIYEKYCYKKEAKAIDFNIKKEDIHITLIN
NYNFVGNYFFDKNMLNYLFYIKYLISYSPWNLLKDYNNVYNLKKKENYKYEKKKKKKKYKNKKEINYDEDNDIQEEEEGE
EEGEEGEEEQEEKEGEKEEGEEEQEEEEEEEEEGEEEEEEEEEEEEEEKEKEKEEEVEEEEVEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEGGGEEDEEEEEEKEKEKEVEEEEEVEEENEDGEEEEEEEKEEEEVEEENEGEEEEEEEEEEEKEEGEEEKE
EKEEEENEEGEEEEEEEEEKEEEEKKKKIKEEEKEKEELKKRKKKLESKLKGKEETEEDKNEEERESEDLEDSEEPEEKI
YGRKETDEESDKNEKEESEKNGKEEEEEEEESEYEDEEKENENENEKEDKEENNSDEYKDENEKKKKKKVKYNEEIENEE
KKEKDIDMKIKCNTNNVNNDEDFISDNIHKNKKESSCTNKKKIKKNYIYARYLFNHILHNEKLQYNILSKNSKNNYTINN
SIDLKKHKNNLKNIKKKIFMQSNSILKRKINKRGYKLEKNKMNHNFIKNKKSSFFNTKMKYNFSYFYTKKHLSQDIDEIE
NKKKENKKKYNQYDDERSKGDYNEDYQDKDKDDEDENYDFDMDDSINLNKKKTTVNTYKINKYEIKKQKRYNDNMLTDRY
DNENKFNKNFKNIKEFNKNYDLLNNMKSIVNLKLKDLTKTLLQIGYNLNDIKKMNRNEQISTIKKYLKKGTINSENKIIY
ITMIKKIIYEQFKNLHYPVCLRYNNNILYINEKKSLLNDKKTYNLHNNGNHNKMYTLIKKKKKVEKNRIKLIKSFFCDSS
SDNHSSCSSSSSSSSFSSSSSSKRLHYNKEKEEKKKKKENNNNEGKYEDDEEEEKKHLEVIREIQTKKDNFEDHENNYKL
IHCLKWTRIYIRRNDNSISICEFENFEDNNFDENANKMKSSFIYSNENLQKLKEDEKKNYFENLKNKNNILLKNSFKNIE
KYLVNENSKVENVQTLYIYGEKNINTFLKWKHFRSILKRYFTLLSNKKEENKDADEEYLKENIENKLNSYNEDIMNNENI
CFSQFKKKKNKNKNKGISASFKNILNIFPTIGEDIKTWNVSKSVSEKNSLKIEKKKKNKHDENTDSKDKKRKINEIYGDN
KNVLNKKFVNTNYSMNNKKHNKNLHNIMKDSSLTAPIKITTKKNKISNAKSKNQANYNKNNSIKGHENEKKGDEKCNEEK
KSQKNQIKKTSSINTDGKENEEDKKKKKKRKKSKEEKEEKKNKKKSHEHNIVINLADKSIRKTTSLSEGSANSNIYNKNV
EEKKRKKMKKGNTYNNIKEIIEKFNENLLIIMNEISEVAHYKPFLNEVNETYAPMYYSVIKKPMYINKIIFRCRKRKYNN
LNLFFDDVNLIVNNCKLYNTPTSLSSYLCVIVDNMFKEIVNKVKNDDNLQNYNNILTEHFYKNKNFYNTWESFNIDKNDI
SNYSSNSFKKLNDLVISNAKQEGFSNNSVFSVDMLSDETNKNSNILDVEMTSNILNFMNSNNSVNMKSCTLTDKLNVSNI
SYHDNTEDKNDQENIENKDDIKNVQ

1742 - 1761:	EEEEEEEEEEEEEEEEEEEE
1743 - 1762:	EEEEEEEEEEEEEEEEEEEE
1744 - 1763:	EEEEEEEEEEEEEEEEEEEE
1745 - 1764:	EEEEEEEEEEEEEEEEEEEE
1746 - 1765:	EEEEEEEEEEEEEEEEEEEE
1747 - 1766:	EEEEEEEEEEEEEEEEEEEE
1748 - 1767:	EEEEEEEEEEEEEEEEEEEE
1749 - 1768:	EEEEEEEEEEEEEEEEEEEE
1750 - 1769:	EEEEEEEEEEEEEEEEEEEE

A0A1J1GXG8 **A0A1J1GXG8_PLAGA** (1414 aa)
CCR4-NOT transcription complex subunit 4, putative. *Plasmodium gallinaceum*

MRRGGGNDKRFLRRSFNRSYYYKKNEKEKVEEINNRKSKNFEREEEEDEGDEEEDGEEKEGEDEYNSEEEEKNRKKKIKK
IKNKEKKELFDEERDALKSIEESNEKNQDKNNIICPLCVEVLDETDRNFFPCDCGYQICLWCLYYIRDHMSNKCPACRRS
YNEKKFIYNRETHEKLFKKQKNQHKNKNENTNLSKCDLYKNANIYNIHEYDNLLEIIKGIRVVQRNLVFVIGITSAFAKK
AILKKSEYFGKYGKILNIIINKSQAYNPNYNGPSFSAYITYSNEKEAINAIYFIDGMTLDNKILKASFGTTKYCSSFLKN
SSCSNEECFYLHELGNVVDSFSKDDIHGPKHLYHDLLYFYFKKLPEKKNEQNYDSSNNLTKYNKKILDPNKTSKNSGVDI
KKKIDSNEELINNKKAISNNPENKMMYKIYNEWKKKSIESSKDAGGKIVEEMKKEKKMNEINNKKESILEEKKKKWNSEE
KVNIKSGMNEELEEENINKNKKKKKKNKSEEMLNCDIIKDNNNSSYNYCKEKNYLSSLQNISYIKENDNSKNEEKGINKK
NNNSEIEDTYYLDEISENYPLINDVRFEKERRKKIKKKLEQNKGEYVNMKEKDKFKEKNKNYQQSRENKEQKEIKKQKRK
NIYDNPIDNNKDTNQIELHHKITGTTKERGKSNELQDNDIKKMYYRIDNYFDELLDKNKKREQTKTSIENILNEKKKIVG
IDKKDIYCTEYNDDIEKSKKREVTNLREDNSEYKKIKECEEKEKKNGKLKENKEKEEKNKIDQKEIEKIEENETENRSNV
KEKKEDNVGFYEKNIYRDKYRKGKYNDYEKSEKIKKGVEIEGDKEDEGDDEYEDDEEEFEGNEEGIKEEYEEDEGEEEEE
EEEEEEEEEEEGEEEEEEEEEEEEEIEEDEEEEEEEEEEEEEEEEEEEEEIEEDEEEEEEEVEEEEEEEDEEEEEEEEDE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEEEEEEEGEEEEYINVELKEEEKKKDKQNKKKQKYN
DNLDDEEIQKMTNIENIIKMKNNASITSHDVIGEYIKKINNNEKKENAEFDTYDNIVNNYFNESECLESMDEKNIYIENS
KKTTKKNEIINGEFLEKKNKNEIKKIKTKLDNEDSNIKEIINMEENKMVLSNKEKKKKKKKNTFKKILYHEEIENDVMNI
IRDMMMYQVKLKSKKNSNKRNCEKIALFNDLEIFIRNLCIAKSKSIQNNPVDEGTVYLIEDIISKKDKSAKKNDYLLYSN
DENVFLKSYKGIIEYILKRNSSFKIKKNFNEHTFDAYKELILSKDDNMITDQNNLFDKIFNEQINFVQQLCKSDYNISSS
DIHSSKKKSIYNFYEDNNLKDKEKSLLKSIPNLWVNFNNSFNSEEVNDKVNLSA

910 - 929:	EEEEEEEEEEEEEEEEEEEE
911 - 930:	EEEEEEEEEEEEEEEEEEEE
960 - 979:	EEEEEEEEEEEEEEEEEEEE
961 - 980:	EEEEEEEEEEEEEEEEEEEE
962 - 981:	EEEEEEEEEEEEEEEEEEEE
963 - 982:	EEEEEEEEEEEEEEEEEEEE
964 - 983:	EEEEEEEEEEEEEEEEEEEE
965 - 984:	EEEEEEEEEEEEEEEEEEEE
966 - 985:	EEEEEEEEEEEEEEEEEEEE
967 - 986:	EEEEEEEEEEEEEEEEEEEE
968 - 987:	EEEEEEEEEEEEEEEEEEEE
969 - 988:	EEEEEEEEEEEEEEEEEEEE

970 - 989:	EEEEEEEEEEEEEEEEEEEE
971 - 990:	EEEEEEEEEEEEEEEEEEEE
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975 - 994:	EEEEEEEEEEEEEEEEEEEE
976 - 995:	EEEEEEEEEEEEEEEEEEEE
977 - 996:	EEEEEEEEEEEEEEEEEEEE
978 - 997:	EEEEEEEEEEEEEEEEEEEE
979 - 998:	EEEEEEEEEEEEEEEEEEEE
980 - 999:	EEEEEEEEEEEEEEEEEEEE
981 - 1000:	EEEEEEEEEEEEEEEEEEEE

A0A1J1GXS1 **A0A1J1GXS1_PLAGA** (3133 aa)
CCR4-NOT transcription complex subunit 1, putative. *Plasmodium gallinaceum*

```
MNNNFNINVQVDEAALNKHEVEVNGYFAKLYTGEITVNTMLDIMKNLSYSPKGSKNNEVYKSMLLILFNECRFFPKYPVE
ELDVTAQLFGKLIKHNLLISYGNTLAVALKCILEALKKGKDSKMFNFGITALEQFEDSLICYPSFLSSLISIPNLRQYNA
QYIIHCRNLLNSLPEHMRNLPYIDSSTILKIKHFSEMSTNNSSNINISQLLNSDLNNNLKNVNNLMLNFNKNRNNNTSSI
GNVNNNDFSRGSSCSSNNNNNNNNLSNALGNLLNNGCNNNNINNDNLLLYINDILPNCTNKEQSIHNVNDISSINRNDNI
FKNNNVNDNLNNNLNLNNFSSINNLNNQLNINILNNDKSNNTSSTNQLYLNRSFLTLNESNQLNRNRNINIVGNNSNVSR
EINSRNSSCLNENIVDTNITNFIDNPVKVNINENIKCEDNEDNNNSFKEKEQLYGIIGSFYDQPQKSLPSHLNLSNISGF
GLGQIECLMDGTDFTKNIIVPSSFIVGEVYSIFNTLCLFNIDEKVKILKNVMQPEYYSWLAFYIVKSRASKEVNLHNLFL
EFIDKLSYPLFIDTIINMTYDCILILFKYINELKEVSAFRTVLKNLGSWLGYITLGRNRPLKSKILDLKLVLFEAYEKGC
LVCILPMVCKILESVKLSKNFKPPNPWTTTVLCLLTEIHELPNVKTYIIFEVEVLFKNLSINIQDYQNKTALLSKRIPYN
KKNDFVISRNNNISSINTEIKNISLKDNITNINSLHREENLNENFKLEELENAGKNLLTNNRMNTDKIQQMNQNNQQNIN
LKNIASQWNQNNANRIDPLMNDTTLVSSFSPPDLNLINSHFTKKSVNNLNKNPNIMNDLNTNNLKVSDFSNDNISNNKIN
NSKFLQSLNNAVIISPSIALFQIQPSLKKVVPIAVDRAIREIISAILERSVAISCVTTREIIFKDFCLEKDENLIRKASH
IMIASLAGSLALATCKEPLRISLTQHLRQLLQPTSTKDCNDQVLIEQVVQILSADNLELGCNLIEQAVIEKAIKDINEAL
APSFLARQVASENSITFNDSSYAINTKKIQMEFAEVLKLDSPITNHQLQIYKDFLNIAPLKKLHAAAKALSLIYKNVNEN
NTENQHQNFQGNVSFSKENLQNNQEKIAYSKNMSQAHLNEQQNNISKSDIKINKVNNVDYNMNNNIKNQQSFASKANINE
NNTQSNIPLSIPSASNVQFHKVLKKLELATGQLKEAIKDIIMLPPMLFNLNKEKSYCNISKMSLYILYSLSVDGNIFNLI
KSIPEIAALTHHKNETIISYSNKIYKFLFEITPYNSKTQLNYRLNDPAGIYLEVFLCILEKLKKKCPLLKKHISNFIMPN
NIYSSNKNNTENRNTSFLNMNESPKENEINNESKDEINNVVKNTCLNNNSDTNNESKDEMNKKNNEDLYKYNVNVISGLI
RYNLVDIEKYKQYLERELIEEKCFNCTEFVVLLLKNILLDFQIFRYNDFENIFSILNTFKEQNIVPNKIIYTNNWTPMTI
NSAIKKLTEESKKIQEKEDSIFFSDLLDFCEEYMNSDDEYDEENEEEKKKEKLKKGQENEGENEEDIKKKEEIKEEKKEK
EIKTHDNKKNKIEQYIQSDNIIENVNEEKLDKVDLNEKEKENFSKIENDLINNKNKHEIEKSKSSNEISLNLKREHNLNI
DNLIGVNEKNIGENNNSDNLGLLNEKRTKENNISEDMQINNENEQSENLSGNICINRLNNDINNAKKKEIKYNKNNKKKD
FKRYLKILMDPKNLTTLTQIIDFCLNTDWNILQKKKNKKYFKDKGVGGVRIVPKPQKVSKEYEKIISIVFFQWIKLSNLR
NTDNSNKNYVQFFQKISNQGLLRIDNNTDKFFTVCINKAVERACNILNPHSHENEKENITNTLDEESLSNKTNSNITIQV
NENDIKDNTSYHKINAKSHTNDNYNKNNVETDETSKHIINGINKEYVNCSEIKNEKSHKKEEKDVILECVKDSNENLNDK
KKENEEIIEKNENNNNLMKGGKEKPSLHLEAHNNDHIDKINENLLDNERTFTNNEYSGDSDDNFSDISSTNLTFYSNISN
CDNSFSEDERCHSFSIKNDSNAKQMKERKNEILKKLSSDINESIGIDISSESDKNINKKESELEYKKYTKKDEEKTKSHL
NKSSTFLEYDENDKKNNEEKQSDDDKEEEVEEEEEEEEEEEEEGEEEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEDEI
EEEEDEIEEEEDEIEEEEDEIEEEEEIEEEEEEDIEEDEEDIEEEEEEEEEEEEEIEEEEEEEEIEEEEEEEEIEEEEEEE
EEEIEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVEEEEVEEEEVEEEVEEEEEEEEVEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEEEKEEEEKEKEKEKEGEKNNTKSNRQKKNIYLN
LEENSLLSDTLDTSSVDSLAKMIMCMMKLVDSQQISPFILFQKAMNVFCRIVVYESRKNKRNFNQRPYFRLFLSLLVEIS
KNEKGFEHSYNKCILAMGYYLSILNPLRVPMFVFAWLELISHKLFLPKILKTSKGWCIYNKLLIYLLEFLYIFLKNSYLT
PCIKILYRGTLRTLLILLHDFPEFLCVYNFSFCNSIPLNCVQLRNLVLSAFPRNLKLPHPFYPNLKVDLLPEMKIVPVIL
NNFTFILIDYKIKKDVDNYFVTRNINCLKKIHKKLMIKNKMKALYLKTKYNIALINALVLYIGMSLPSQILMIDKASETH
PALEIILYLTYKLDMEGRYYLLSSIANHLRYPNAHTHYFSCLLLWIFSISKVEIINEQITGILLERLIVHRPHPWGLLIT
FIELIKNPIFKFWQCSFVHVAPEIENLFQSIAHSCLVNQMEHLNNKQLNTNINSTNVNVNINNINNMNNLNIKNKNVNNN
RNSNLKNIINIDDVHSNKIPNINYNNINDANIYNNLKNFNINNIHMNNNGSFSNSDIIRKAMDNNLNNYNLKNTILENHY
ASLKVNNNIPKNYTDYNDNIVNTENSNLNKNIFNNYIISNSVDMNISDKHFNVQLHDKNKILEDMENKYIEMKMNIKNSN
IMGNEVNKNISGN
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2212 - 2231:	EEEEEEEEEEEEEEEEEEEE
2213 - 2232:	EEEEEEEEEEEEEEEEEEEE
2214 - 2233:	EEEEEEEEEEEEEEEEEEEE
2215 - 2234:	EEEEEEEEEEEEEEEEEEEE
2216 - 2235:	EEEEEEEEEEEEEEEEEEEE
2217 - 2236:	EEEEEEEEEEEEEEEEEEEE
2218 - 2237:	EEEEEEEEEEEEEEEEEEEE
2325 - 2344:	EEEEEEEEEEEEEEEEEEEE
2326 - 2345:	EEEEEEEEEEEEEEEEEEEE
2327 - 2346:	EEEEEEEEEEEEEEEEEEEE
2328 - 2347:	EEEEEEEEEEEEEEEEEEEE
2329 - 2348:	EEEEEEEEEEEEEEEEEEEE
2330 - 2349:	EEEEEEEEEEEEEEEEEEEE
2331 - 2350:	EEEEEEEEEEEEEEEEEEEE
2332 - 2351:	EEEEEEEEEEEEEEEEEEEE

2333 - 2352:	EEEEEEEEEEEEEEEEEEEE
2334 - 2353:	EEEEEEEEEEEEEEEEEEEE
2335 - 2354:	EEEEEEEEEEEEEEEEEEEE
2336 - 2355:	EEEEEEEEEEEEEEEEEEEE
2337 - 2356:	EEEEEEEEEEEEEEEEEEEE
2338 - 2357:	EEEEEEEEEEEEEEEEEEEE
2339 - 2358:	EEEEEEEEEEEEEEEEEEEE
2383 - 2402:	EEEEEEEEEEEEEEEEEEEE
2384 - 2403:	EEEEEEEEEEEEEEEEEEEE
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2394 - 2413:	EEEEEEEEEEEEEEEEEEEE
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2419 - 2438:	EEEEEEEEEEEEEEEEEEEE
2420 - 2439:	EEEEEEEEEEEEEEEEEEEE
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2422 - 2441:	EEEEEEEEEEEEEEEEEEEE
2423 - 2442:	EEEEEEEEEEEEEEEEEEEE
2424 - 2443:	EEEEEEEEEEEEEEEEEEEE
2425 - 2444:	EEEEEEEEEEEEEEEEEEEE
2426 - 2445:	EEEEEEEEEEEEEEEEEEEE

A0A1J1GYA9 **A0A1J1GYA9_PLAGA** (5012 aa)
Uncharacterized protein. *Plasmodium gallinaceum*

```
MIPKGVIQKKLKKKRLKRLINKNKKRKKSTIFFNNNELNYIYKDDFTIIDGEKINVSKEKEKKSMNKYVIKLQNLYKELK
LEECLRYGLENLEKLKKKDFIGKIEFLKTIGNAYFYFENYKYSSFTYILLSKYLNKVNEKYKIEICYNAGIAFIKYFLES
NDIEYFLNAKTSFMCCLLYNDKESEYFNPTIYESTVKILRNNFLTDIKQNSVNTENVDFENSSHESIFLKNYLNLSSIEI
RKEESNTESTYLKSISNIEEDLKEKTHRKNIEDNINFDSNYLDNIQIYDSSFDKKDLSAKKKYLLQRERKKNNINDINNV
NNRKEQIYNNDISTEDNLMKKKLEENNPSNFDNFFMKKKVSDDKGDMKSLSKNDEKNDGKNDEENDGKNDGKNDGKNDGK
NNENDLINIYSSTECNFFNKNKLNENIQFKKKRKITCQSIVSAVHYNSNEFLNNYNSSQNENYILENYSEDISDSLINKL
DDFLLENVKKKKKKIKTQRMKLLNDNIHGNDNASYSINKIKKIYKEYEFNLLKEYYYIYDLKKKKKEMKEVLKNKKILDF
FNTIYKICKYKKFNTLIKFVNNFSHNSMVPDESHCKVVNIKGYSRKNENEENKNKIVEEITYKDKHTNENINIKELEKKK
FEEIYSLSSIEKRYKENNEMDNKESKEGNKTEEEKIEKNKEIKNKRHKNETNYNNIIEIYSDIRNSIKQNGLIYNKCNEK
YYEEKREIEETIILNINKINKKRIRDKVKKLSSHNNYLLPNVGDKIIDDMDKLFLMNNYSIVLKSIKKNKNIKHIYHLYE
SMYAIDKFDSINSSNFFNISHFIIDILLLKQVQEKDDLKKKIKKIKYSYRKYYTRHTESNSNILFKNIIKNVPSNDIEAN
FDKYEEFTFFNLRKRRKIIKSNENNLVNNDTKINPTIIAYSNDSEICMNNKRKTLNNTYENLGNDKYHNINNIILDGSLN
SENIKRMENRESNQMENKEKFNEMEEKEKDNMEKKEQNKNFINDRNMSSNEMSCELKLKKKNILFHSYNYEKEKIFAEIK
KSEKEFFDIETLFDCLNSMNENNCIKDKIEEIILILFYHYCDKENNIKNTLLKIFFFFTNNNIINKKNVHCYLSFLRLYN
LYMYDYKCKSLNIFYHNIENDSEKIRNEKNDISIDSNLEFDNYEDLIHFHLYMLKLLYKCYLNKLKKKHTFDNINLEKMI
NCTFAILNFLLIKYSYDQQNGKIRRRIIFLFLEFLYINSKYYFKNIKFFMDTYDINYLIKKENAKIRETNIEEKVYNNLY
EKFTQKDTLKEQEKNEGKVDEEEKKKENEEKYSERKEYELNDENREHNEKYDENEKKENENQEVIDEEEIEAEAEIRKYE
KKEVEGYEENEKEVRIREKVEEKEEKKNERNKIKENVDNHEVEEEEEEEEEEEEEDGEEEEEEEDGEEEEEEEEEEEEE
EEEEEEEEEEEDEEEEEREVEKEEEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGSEEEEEEGSEEEEEEEEEEE
VEEEENAEGEEEEEEEEEEEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EGVEKEKDEEEEEEEEEEEEEEEEDEEEEDEEEEEEREVEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
NEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
FSSFLKCYNKCFFILNLKLYENKFFKKNIMKKIKKIVYYCNSLYSMVKVKKLPIYKVYNFTLNELNCNLYNENIFSKPHF
FKILKEDKYVKKIYTHKQDYISKMNAYNISNMFNRNITKKNDLMSILVSFTRRVKKKYEKKKLSKKKKQFIILTYSYKYV
KNCICKEIKKNSILCLYEKAKALDKNFTLNIDSLHSLFDTRLCILTLNYELQNIIIQFINDCMNFIMKNKKKAYFILIRK
VMNIYNMIFSIFYLRLNSFSEFHTNKLYKVLSQNKDIFSYDDKINSNMLNFFNFINFRYGCSYDFLNHVFTSFHVLMNFI
VKINVNIKIDKKFIGVQKKTKGNKQNTQKKVENISHEIQKYIKKKKDTEQLIKRKKSTINCIYLKKEKIYKIIKEIKRKV
GINGQFKIKNNLLERKLGKKINKCYSYFVKDKKRVKEKRNKQQKKINIKKYSQLKRSNRKLYYLARNESYKISKKVGNKN
IRKKKLCSLKKSSKLNKNSTNLSYTRRRFRYIERNNRYKIRKDNYKKKENIIEKNLYKYKNKYKSILNSYKKLKKIKRKL
KKTVDNTSFFKYISIINKSDHKIYTSLYPLFSHILFILISILYIENYNILHLRKSQDFFMINDIYNTYYIFLHISSSIIL
LISSPLKTHLHFYPFLKSKQGCFIKRKNIKENIEYNNNEIENLDKKYVISASEDKNHQNILNFSKNKLEIESNTSKLKNN
SNLIKCGNKVELNRKCNNKYEIYLQTLLNFSLVDVLLVSKKKNNTKRKIKKNKYIYIFCNLVENLLQINMFYVDLFNNCK
RSNVLQMNEIFLKLNKLCKDNNIMDDFTQMKQTLINHALFKFVLQDKYLIYFDLNKNELYNINKCSMNLFYFSLNILLTS
FNTDISIHLERNIYNINLYHQKNLYYELILNNIKRTILYINNSNKSSFNCIFPCVIYYLNKYKKRKKTNKKKKNNIITSS
LSHVSLSDVKSKSCISLGNDANENKKKIRIDTILNKKEKNQIREVIDIDNIEYADNQHLSYNKCINYINNSNIMINQTRN
DTFENKKKKFRKNKIISKIIFDMIMPYTDIKNIKIQNKIYRNNHSINGLINICFSFLFNNFLFLKTVYPFDIIPKDKNEN
ESDDKKIKITKYTLDIFNMKMNEIKSVELFLSLYIHKYMQSICLDIKKLVDYNTYLNQFFWISKKSHINISHNDYIYLNY
KYRNIYYKFNDYNVLQFLINFKKSKTEGKEFMMSFVKIFEKLISIDDETITNFIDPLIYNIFIDYMKDLFLNDDYYYVCF
YEYIKNVYLEEKKKTFKIENFDCYIGELNELNPYKIKKNMKNKLKENIDKSCLMLIVKRKIYKSLNYNNYYEIESNVDII
KNGHINSEGNLILNKLDKNFTNKDTFNSLRKHKNINDHSTNENDDDKNINASNISKNTIERLNKNESVTITLNNDPYYFK
KIHIYYKSKLFSIINKKNIDYLELTKVINEKHYNHFSNIFYSFFIHIMSEVKYDYNKQYNFNILKIIDKLNIGLKASFYN
SKNIFLYYYIFQQYFHLYKFLEDKYFSELVLSEYLLLNITTKLVDNSLYNTDLYKMYYFLKFLYLKYTLKHTDILINFLI
YVYYKYFFYHYKGKDNYFNYFIDLFISIHEESYNNSIFTSEYKNKENNAYMNFTKEVFFTKNFFINYGSNSSLKNTLNND
NDNNKITNDGHKKMNNYYLVLSNSQNRYIQILFFKILTNFIRSKISLLNAKHLFDNLNFYISSYIKYTLFYSFEEKSNCF
VNSLRYKYFFYDFKTIKKNIKLCVYLKNIYLKQDLFNSNILSFLNIECKRDKKRLNNKKHLYNQNKNNSEKSFIDSQNLK
NYNNENSKKNSIDVNIQNFTNVKNNNINIKETTFSENENNSKNKNKGANAKRLRYEEEKNSKVKTKKKKVLEENKYLEQE
KGIKVDKKDETHIKGVKVEVEANLENSEVARNSNADHSHNYNNKKINEKYKSNIELDIEKNLKNYNLKVINQNSDDKNEN
DKKKIRVNIKTEEFSDVDINPLDALDQSEILKNKFYKKINNNKKISIKYYIRILKFYLKNKVHGYSIKSLESLKLHDKSI
YLIFLFLGKLFNFLFNSLLSYNGEEDNIKKKTNTKLNNEKKLSKVDSNSYSYDKLLLYFMLISMCYYSDSLIFSSVNFLD
FQNICSINEVTCLNKKKEDNIRNVSEKTSVEKRDENEKERIKGDNKKVKEEKNKIEEYVNNIKNITLEENMINAKNIIEE
KNEDLKKNKFPLNPSFLNTNSYYIFRSKANDIINSDKESIKIIIPLYKLLVTRLKICLYYPRYFFIACLFNFKNETMLSN
NLLNYIKEEKFLNENIKYIYQVDKDPQNVEKDYKVTKCDTIVDEFNKIEHFDNLNTPDLKNLVDVTESINYKNMENFVES
LKIKEENYNTSNNFIKKNPSTNENGSLSNIKNVPCNNKKKENNVSKYINYYNDYYENCNLNSSVLYDLSNSQNNLKNEEL
IDNIKLYENEQNSCKLLKENCIKNNDCYIIEKDTHISEKYNVTNDTHEKEIDINEINKFNYNLNKLKVIIKNIEIKYSDV
INDIIEGLKFISENKNCNNYNSQAAYYVCIYYFMKRNYAKCIQYIKIFVVKGVFKIWQNDTFNQDYYNLYCKRIQRNEFC
SIKYFTVVLEVSKSVLKKTLTKINDEMCNEKKKLLENIYNNKLEDEINKILVEVKILDKIKESNENEKLIIENKDNHDNN
LNSNNNNKDDEEVKANNNRGIMTDLDIKEKLNSNENTTNINTYVLNSDSMNDKKENQYSTKENKWIFLGFDHLDHLNETY
EILKILFEIYLNLGKTMKKFNDCKILEEATSSYGYNLSIINILFKMLTEHLCFILEVLCYFTPHILIYPIILLFSNNHDK
YFYLKDASINEEIIYNRESSSIDLRIFKLFRELLANKSVVLPSYLSTRMHNIFLIICKKLLYYQRCEEDMLKNMNDDSNK
GNKKKKKGIIQFVINALNNVNKTNLSYFVKLFKNTKLLNCTNYLNCESVKFLTSKLVYDSTYSDINKNPPLIELDEDIVD
KTNYPINKDIVMDTLNKLSNNFYDITDKGTLNNTDQLDSEKNKKNALFYIRLNNEKYICLYDDFDILSNIKTKHEALNSV
YSLLSHKNSLSKKTDNSNLKKKKTSDLIIPEVKNSVRERDLRRLNREKSKVM
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1427 - 1446:	EEEEEEEEEEEEEEEEEEEE
1428 - 1447:	EEEEEEEEEEEEEEEEEEEE
1429 - 1448:	EEEEEEEEEEEEEEEEEEEE
1430 - 1449:	EEEEEEEEEEEEEEEEEEEE
1431 - 1450:	EEEEEEEEEEEEEEEEEEEE
1432 - 1451:	EEEEEEEEEEEEEEEEEEEE
1470 - 1489:	EEEEEEEEEEEEEEEEEEEE
1471 - 1490:	EEEEEEEEEEEEEEEEEEEE
1472 - 1491:	EEEEEEEEEEEEEEEEEEEE
1473 - 1492:	EEEEEEEEEEEEEEEEEEEE
1474 - 1493:	EEEEEEEEEEEEEEEEEEEE
1475 - 1494:	EEEEEEEEEEEEEEEEEEEE
1705 - 1724:	EEEEEEEEEEEEEEEEEEEE
1706 - 1725:	EEEEEEEEEEEEEEEEEEEE
1707 - 1726:	EEEEEEEEEEEEEEEEEEEE

A0A1J1GYQ6 **A0A1J1GYQ6_PLAGA** (3247 aa)
Uncharacterized protein. *Plasmodium gallinaceum*

```
MNKNHEFDFYQKLMKKRLNDYETHSDVSCKIGYSDSESEGVASIKEAPYYSYNHNLKNYKKEKLEKPIWKSFHDIEETAK
SSYSDDEHIKNDKSENEIESPRFGNSSEDEKEKEEEIEENEYKRIHKNTENLYIFDDVNEDVKTLEENESLDNYTQHNIS
SNINYNFREELKNNMYNNLSMFRSIKDNYDDATKHFLKPKTFKDVNGLYNDINDERVDIDILKKEHERLKKVNKLGNIEQ
AYFPVTSLYNDEDMEKINKQNISKFKNIKNKKLEEKEFKNSISIFNKIYNKYDEINMNKKHFKNNNVCEQKMMDNKQGKA
KKKTILKKIKNNADEKYYEVKETKLINNELYTDEEKYERKNEGENKCNMINGKNKEMHNEKQQTSEEEDIEEKREDVEEE
EVEVEEDMEEEEEEEEEEEEEEEEEEEEEEEEEVEEEEEEEEEEEEEEEEEDMEDEEGKDYIDEEKEAENQKENNDDKEINE
DGCKYEENKINNKNDNIDEETDYMYNEGYDKENDEKETGLSGKLKNKFSKKQKFLENNNSENIINNFYNKKKNSNIKKKK
KYKKQIPLQKGNTSDNNRKVEVVTYKKKYSKINENFIRDPNINNKTEDENYKINDNINNNKKKIYDNFEKDDDLMNEHIA
KEINFEWWKSNENINDLQNKNNDIDEKINNECNLINSESKTLKREKILNRYEIPKDISYYAEKYQNNKNKKEKSNEIMHN
AIHEEINMNSTATECKNINENVVLPNDTSGDIHFYKNNDLINSKNDFNNRYLNNNILLNSKKDLYNKDMNNNNDSEFNKI
IENMNIDSFNNKNRTKFSSNIQSEMLKDSCSVEMIQSYPYNYLGSLNNYNLVNEFYSPNIRTDKCEKHDNNTELNDSHVL
KSINIPFNEKMKNNDINHSNNKNIIFNSFMNNDNINKGNELILTHNNCIEKKMYIDENGNLSNFYDKINLYNEKVNEKGL
NNKKEDYIKNNVNENNSRGNVNENIDMVEKIEEEKNKKINFFLNYLKSISLDSVNNIFEYFVENEKNSTVKEIMEKTLLK
KDNQNKKIKLEEYVNDLSKSDQNTQTVDKNLKNEEIQTNNTRKVENFMQTNIKDINNELYIKKDVLSKKTSIDSVFFKNL
SKDLNSFNNESKEKKNDNSKNNLNLESKNDSYVDTKNNLSVDEYNEVKKIHDLKEKILEKIKSCYDNFSENNDETAILML
KDKYECTNNNNYYSNKVKDNTNYNANSKRKNKRNMSVITVETTESLKSFEKEMSLLKSHNERLKRRIEKLYDEKEKIKND
YIKIEKLKESQDNLFLATEKHIEKLHEELNNLSKENEDMKNDLKKKNIKIIALESQIDNNEFSISSRSTHKKDELTYIDL
NNKLEEFKCQITDKKKVKEQINLLHTQLHILKDEIKKAESLKLENEELRKLLNKKSSTINEHENSIMKLEKSVDNLNKQN
IHLSKENVDLNKKSLEFKKGNIILSSYDENIDTNKMNEMLSIRNKTMDLYSDKINLLKSNIEEKENQIRDLERNVNILKE
QNFQLNEEILDLKENNIKLKKISLSPNNENDLYNNNENIEIMQREIEKVYLDKINILKSNLEEKKKKIDLLNALLETSNN
QTSQLNDKVKNILKENKKLQKKYEKCLNYLEKLKIKYDEHILKKNEKSVISFDELNNCNHNKADYQSTKSNDQMSENLCL
KNNKEKIILSNNSEENEMKNLNNMYHSDDEDIREHNKGEYEEEYEEEYEEETNEDSECIIKYGNEETSEKEENSIDFKEK
ISNDILTKEVKMNTLKKHTNNVNSNEEDAYNVSYVDRNNMEKNVNKKNKNVCKVLKYNDLEHEKSKLLDKKGKNLYKNLL
DNENKYVNINNIFEIENITQDLQNMFYKKQYSNEKLDNTIINNNLNNKILKSFNNNLSNENHNALYENGFHRNREQFYQK
RNENFIHNDSNDINYNNENNFNNNIMSENMSNLEFINYTLNEMNLKNMEKSYVTNKIKTFNDNVSNYIEKKKKIDEMCNR
NNLLYNNTNQKCNNSSYSNFDTNNIKIGETENDIYKELYNKNIMDNINNINKMNITSNMNNNGNINNMNNMSSRININDI
DNTNKMNNINDMNNLNNINDMNNLNNINDMNNMNNINDMNNLNNINNMNNMSNINNMNNMSNINNMNNLNNINDMNNMSN
INNMNNMSNINNMNVNNINGMNYMNNVNRINNANNMNNMSNKNTSNSVDNIIRNNSNNLRNLYINNLDNQKVREQIENNN
VNRFSLNTNETNLKNINSNNLKSNECMSNIKKIENEDSDRTNKLSNENNIYNFNNELKNNIVNLNTSSNVNNNEIYCDRK
EIKNVNTPENNNIINNNSNNIYEIETKENLNKEGNKKGEAWIIDLKNNEVFPYIKLKNTLLEEEKQRKNSRKKDIYDKNS
RKKDIYDKNNKKNSIFDKKNFYKKDKNYKSILQKKYTNRILDMRNKDKLNLLVSNISKLVKSKIAEEMHKKKLPKDILNF
EITKIKKGNSSKKNTYKCYDNKRQETKMILSDSISISSGTFNNTLETIEDDNSDINSQNLLKNINENIFRYNIANSNVSK
NEIKSANRKNVYHPNVDNSSLNNFIPKEKSKSVLNDGNLLNNDILLNNFLLNQNYVNDIRDINEKIMNNNLFSSKNSLKN
LGDTHFYQNLNNNGLGNVPLTGNMNYCNLVDSNCNYNKLNFLNKNINRNNNNIGNDLEINISKNLNNNNISNILNSDLKV
DIENNKDKNITNNKNIDIMNKSNQNICNNFNNDMKNNNQNVYNNVNIDMLNNNENICNNLNIDMINNNENICNNLNNDIE
NSIRVVNPFVFSNDILNNNNISNTIFEVNKLNNSYLFDINALEPKENSISHNNTVLNYNVLDRKDINIPNNEIILNDDLN
KNNINNKNIFNEIQRDNKVYEESNINEKTSNHIYKENKIENKNNIFKNSVKRSISVDIKKNETKKNSANECTELKPKMNT
QIFNYSENKKNGLRDMSAYADKVLEDMKSLIPFKVNSVINKINKGDKKECEVKKTLNIKKNNSKSYNEVILNKLNNNINK
SDYCNKGTILKNNYTNNSVTNYKYKRINEKSEKMMEALKNKENKKIDYAKENSHSNSINSKKIDNSNYNKKKKYKVIAPN
TTNKNKKYALNEHTSDDICINNEFGFLNENKSNKLSLGLNENRDINFNEVSNLHYNSFKYEDYIKEAQLNNCVSDGNNIF
NNSNRNKNIIQDPLIFNRREESNLFQSQARKSLTSFRESLKKQGILG
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409 - 428:	EEEEEEEEEEEEEEEEEEEE
410 - 429:	EEEEEEEEEEEEEEEEEEEE
411 - 430:	EEEEEEEEEEEEEEEEEEEE
412 - 431:	EEEEEEEEEEEEEEEEEEEE

A0A1J1GZL5 **A0A1J1GZL5_PLAGA** (3358 aa)
Ubiquitin transferase, putative (EC 6.3.2.19). *Plasmodium gallinaceum*

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MKKYLVFENSQYSYIINSIKNGNESEMLAGLNDFYEQLNLSADGGLSNSNLEEYINVLIHVIKNPHISYNSVYGKSDNNK
KISKSSLNDKKVSSDKINEVVGGGINSFFKIIQEHIGVYASDFDNNDSDSDYSDNKKKKKKKKKKDTEKNKNSNDKERKK
FEIFNTKDEEKDKEKGSIKKEVIIESDEESSELDTYSDQSSSSSVTSECSIESNNEKLFLNDANPIDVKYINIIYTATCC
IYTILDIYPNSIKYLINNKDGVYILNRKLNDIEYIDVAEVILKIFEKLVEKDPMFILKKKSIKYMLMHIDFYNVNIQKKI
FFCIIQMINNITKYKHITKYITPYCSIFVNFFHFHYIHILNIICTLWRSLLDKMITLRLEDENKLRKKEKHLSKKTTKEA
SYLSKLIDKKEKKKKIESSNLTEENKKKIDASYKIEEEKNIKDQKNKKTKVEHEEEEVIEISDEEYTNDLHYKKSINLID
EQDNKKINKEQKKKKENSNKKNKKKTKNFTKDEEEKKENSDEEIIKIRKDSSGCDYDKINNSSSTKKNNLSENNKKSIKN
EQSDIDNLNAYDKDNSHIISKSNNSNENINILTSFLKSTIDDLKGDFVYKDSVCNGKESNYFVLENKKALKDKNNNSNSI
NSKENNLWDISNYEETCKDGNKMRENYSSSNYYNKLLLNMINLNNNDNTYFKLSSEIESVYNINIRNNIIKLLIECQIED
NLYAFMETFYIISIFVHYSNNILENFCNSDFLNKFNEFFQNKKFQNNSFLIIYILFTLYSFLPICTYDGLLIYEYEKKKN
INDNIFIENVNFDKDKNIDIDKEKDKNTDNANSKKKNLYPFFNYEKCGYIIYKFPIDVKKHKLEFYKNNFNYLMTLIKII
IPNIYSIYEGALYFDIKYLCIVISLSLFISLYKISFFYYNNSDFVECIDYIFSFYKELYSFIKSIISNNLSESSVISGII
LCKIIEHFNMLICKEPIFSSINKKINKNNNYIVNFYTSNKIGNSLNDISTLNNFEEPYLFVLTSIINKILLKKKEEIYEL
EKNECICTNKKIYNIIFLYFYDIFNAKSSYNCENNFLFFHHDREMKNVALEFTTLFLNYENYNDCKKEHSSSYTICNLIV
DETTCYNNIVLCYYYLINLFYNLSLMNENSSIYFYQYNIAKRLYFFLFQKLFHCDSGEKEEKNKKDFNFAFDLTKEKNKK
NIFNLLKSIDRNIRLYIFLYALLFTNDNKKEELVNNLFLNSIKALYNIFCNILKKNVEDIDENEFKKIESLVIEIFDSYH
YYLIMNNLSFNNCLLLINLTKECLNIYDNLPIYFFRENNDIEQDQGREDNILGWMKSYDDFPSLKNNSFFNLKSKKSYDT
IVKNVKQKKKKGKEDSNSKECPIENTVEKKINSSENNEKNELKKNKSLKKGHEAEKENIKNKTEDSIAKEKEERVLKDKG
KEDVEKGKIKEKEVEIIKETKEVSKEKEKYNSIPYTKLNKEKKKVLKINNKKEYNFHDYFNSSNYKNDFDYIQKDSFYDY
IFNDSNIRNNKKKNKSIYNNYNCHFPIHLRRNGLYIDNISVFNSLNKGIPISLCAEQIKSDKNEEEKLEKEINYLDDKKS
SNNKEELYIPSKINKTNYKKSTDNTILLNKISKNLTFKNALSGENIYANDHFIRNIIDRRRNLQGSFNIFESFNKIENFI
RKNINKNNKNFYSKYDSKSEDLIILSINGIDVHSDSCLSEYLIKLDNVYYINKNSLCLTEENIFYNMENFYVYNDVVENF
ETNYYNLKNKIKYLWDSSNNSHNINYKIIKKRKNDERCSDVIDDEINNKNNLFVTLKKKKTTTDYNEEKKYCERNENEKD
IYTYVDVNTYKKIKSSIDTPLYCKVINEKYNFYNISFDLVEYLYNSNSHDDINNQYDEKKDKISFYNSLKTNINDDKMQK
GEINYCETDHLLYKYNSSKEDEESILCYKSEEEKSSCLIDYLKNRYKNKKIEFSFSHCNFVENDSIYLSNYLKKEMTKAT
ELIFFDDHYINKDIMLSTHLHNINFLMHKGKGNILKRKNCVDQIEVTRKKEKCLFEKYKKENFFKIEDNKEIRNNYEYTS
FLLKENVTEKEKEEFYLLYNYMPIYSEMIKKNNIKKEEQKGRTNSEKEDKYQIEKNEEKDIFIENVYNFLLFKFLFLLCK
YFKQCDISSLLSFYINNNQENKMIKSNNENNIVLTEYTKGEISKMKHIFENRSEKENNVSVENIKKKNFLLNSINNKIIY
YLNNPLFIFSEKLPSWIYKIFYLFNFVVDIDIRLLFFEIIYFGNYRGFYNYKQKIKELVEKFNEKVNFGNRILTEEHLLS
VCSNYTYNYDKKKLFNFLSDNTTLTLPRTKIKLHRNKMIDSSFRIFNHLHFINSNYITPSYLDIEFFNEEGTGIGPSLEF
YNEVIEELKKEKLKLFKIEDDYLFPLSYKINLDNFDFDLLKKPKSSDLMGINKSYNSFHSNSYQSSSSNKRINVISEGSN
ANNYSSVNNLINHFLFSMNSNVFQKNTKNLNKYDDISEIELLDTKIRNKKNKKFFKNISDNSKKNSKKYKSGKSYKKKCS
SNMESNRNSNDKKKKKEVNEEKNKHALTHLGSKGTKQKGKDNNNIQKKESYNKNHNIALEKSNIFDLKEQTELDEEYINS
DKNKKKRIRRYVDEDTKEKKNEEENKKKIISSDKKHENKEKGKVAIDDNKEKEGENDKVEIDEEEEEEEEEEEEEEEEEE
EEDEEEEIIDDYEEEEDEEEEGEEIDDYEEEEDEEEEEIIDDYEDEEEYEDDDETDDHLEDEEIYDEIDYDNEDEIEEDNR
EENEYEEIEKEEEKEKNCAKKKKKNDKSNLQKLSEIKEPLISSSNNPSLEKIADISDISNKPKRKNSINLKEKNRKNCCK
LLDKGMDAKRINEDIDKKKKIEKKEKEKEKEEKVKDKEENKNIEKEKIKEEIKMKENEEIIDNEKKEIDGKENKKVQIKK
YKLFTKDFEENFLKEENNLNLKKKNETKKINLNNQIKLNQSVTHNIINSLFSEIENKTVNKILEKEEDKSIDKKDNENKN
ENSNKKINENDDMKTNENINKKSNEKNKKKSVNINQDTIENRLFKYFKLLGQLCAKILTDNRNVNINLHPLFWYMVMNNS
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GYINLSKFHHYQAIDRVNMNSINKLLEYRKENKNIEDLHLDFTLLGSDPPVELIPNGSNISVNNENLNMFINKTIEYSLY
EGIKFQIWAFRFGFSTIAPLICTNIFDEEEICDYLFGSNIENDAYWTKSHLSTYIKPDHGYTNDSITFITLIEILSEFNN
EERRMFVKFCTGTSSLPNNGFSALKPLMKVVKKEDNNDLPSVMTCTNYLKIPDYKDKEKLKNRLLYAIREGQKNFSLS

2703 - 2722:	EEEEEEEEEEEEEEEEEEE

A0A1J1GZZ1 **A0A1J1GZZ1_PLAGA** (2725 aa)
Uncharacterized protein. *Plasmodium gallinaceum*

MSIHNNIAELVKNKKEIIKEEKKRQRAKSCACANSVSEDNNNVLDKNLLINNFLNSQKIIKEIQQLNNVSLRTATYLLNV
EIKKIEKIKQCIKWKNVPYIYQKSADEILLKKNEYMKKLQEKINEKKKKNRKCGITKEKGDISTFRSKSVFDEKKKKNNN
KNNNNNNNNNTVINNESLRVCSVQNTKNVSARKLKKTEKHDEKKNEKIEIKEFSLKTYKGEELINIDNIKMENRNVQNNY
KDNEKIINYEGCCYANNNSVNENYFYYYDDEKDKVSDEYKNESLLCCLREKNKNEEDNNVINDESFVNKMPHNCRINDHN
CFLISNINDQNKKGCTNLYDFSYRNNLNNIIDIKRKTAMCVDNEYSNLKISEEKKTKKTIPNFERHTVSSFIKNLSTHKT
LQEKNYSEKMNKKNKKNTINSSKRALSACNYSTKSKINKLNILKSKNVKEEIDKNNQNNNNEISENEQAFEKLWNFVINS
PDAGRNKNISLNKKVDLFNIDSLNEDYSWVNNLRNYSNSENKKLKKLQMKNNFRNSYSKISCRNKVIYNNKNKNEFNNN
FLNKKFGTHLTNDNLTKDKNIHLYNSIFCCKNDYYDKIDDKEMNNDKYFLYVNKDYNNDENCNFHNKYMNNYINNEGKKV
VKENYKTKKFLEQEEKIPLDKIKERKTYGRTEDNNNNNMNILEGKKVYYMNENIPNNFKILINGTNGNVIEYNGNKVESR
FDVIKKKEIIQEKTDQENPILCGYINNVFNDCKENDNYINIRSNNDNISKCIKLKNNQENTFLNNELNNHKTINLRVKCM
NNSNQNLCNNVNNSNLHNVNNDNYIYNNNVDGSLSNINNRDKNSLFNRLKNKISCQYSKNNSIEDNCDTLSIKEKIKTDE
NANNYEDICNRNDSIREKNENLGEMDIEDNHCFKTLCVYNNFILKKQCNEDENNEVNSCTEEKELGVNETKKKKLNKQKK
RNSNKISNKDSMEDSTRSDMTYYNSDSFDSSQKLKHFCCISERYNESKNEDKDNEETPKYNKVRYSCNTDTTKKGSIINE
KDIYSVSKEIHNDMPILKCKNLNEILHKNCNLNFNKNMDLNYEEDNKNNEISKIEYVKPVYDNIDFKNGKIIEMNRKSSN
FTCFSLNNNINNEKISSSLDNYVKIKDKILIPKLKLDKIQNKNGQNFNSYEIQEVYALNESNSNKNNLNKNDLKKKNYTE
NGFFNINPKCCYSFVNCNNTNNNNFAINNFVNNDEFSEYNLHNSNSLNFESKYLEVPYNSKNLSESKVRNFSNINNKDVI
KKNIYYNNIPKEGKEKNLRSLTVDCNYYKPNTICGLNNLERNSIVMNNFTSNQMHLSKNKNENTSLNYAITKNVFNNRCT
SHIVNKTSGHHSKRKFFLNDYEDLRCDAGNCQSIKPNLNCIKINDMTNRGNQFLQNKHSSNCVDIYVYSNNLKNINISDN
KKDNFQVKNKKTNIDDNINNNNNNYFDDNNNDDNNNNDNNNNNNNNDNNNNNNNNNDNNNNNNNNNNNNDNNNNNNNDN
NNNNNNNSNNNNNNNNDNNNNNNNNDNNNNNNNNNNNNNNNNNNNSNNNENNNNNNNNNNNNNNNNNNNNNNNNNNSN
NNENNNNNNNKLHKNNYNSNSKNNSSCVYNRSSSYNIRQNNSSIKSYTSKFLNFFRKSNNKDETKINNKSKLENKVNRLN
SNYTRNKIINISSFTKNNFQNINTYNSINNLNYLNNNKNNFIPVFKDNFIPPTMTFIRNSKKKERSKTTPLNKNSFLSVN
NSRHNALVDYKIDSQISNFNLLEKRKTCNFSSVPCDNNNLYNSYQNGISSKMNLNINDFSNLTNKKTNNNYNEKIAHGEV
KIGYIEDNCNTNSNKYNYVDKENILKDISLNNLNYCNENDILFNKRNYHNISPTKQNEIKYYDANNDNNNNASNLFEKNV
NNNVFYNNNNNNNIGYHDINQNNFTISNNDNFLCKNNNNENYKIDKNTLDKNKNETYSDQYSTDISDRISVNHSGRLSKN
EKQMDDQNVYEKSNFQTNMPNEIYCGYAREQTFNEIFKNPGILYNKDTNEKNINQIIYNELHPITKLNGEYKNNMYINKE
ICGSNSIDKLHKNELFTQNTKDHLIYKELESFHIPVKENILNNQILKNENSNYQSNYAKNFAFNVKGNQKINKNLEQNFD
IIEENNQGVNGNKYVKIDEVDGKKDNKLYINDEIYPKIEKENERINEKIEDNEEEKNSEVVNEYEEVEKEKKHMMIKKEEK
EEENKEEEVEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEEVEEDEEEEEEVEEEEEEEEEGEEEEEEEEVEEEEEEE
EEVEEEEVEEEEDEDEEEEEEDEDEEEEEEEDEDEEEEEEEEVDEDGVKEEKNKANNSVNINKNKIPFCKKSIVNEKELK
NINKIDDLLNVKLEKNMYNSIKLTNFDNSKDDNLDESLCKNNNIFKFPTRKDINSKEKIIKTYEDIVENKIIPLINSEVK
NVIQEKLLSKKDIIVNNSDKNYDSLNYTNSSQNNASMEKTCDNSETKHSKNNIDTQENYDPNYYMNRIPSSINENKKEKV
STLIKNSKKSLNSPYSRLSSTNNKNFLSTPVPNGNYSSRIFSFDKKKENNLNTIDKKNNINKEKDDISLKYKNMDNFSKN
SLSNAVLSSNVSDNYTNLTHKNLDEIEKQIIRSKRNNEDLKKKLQEQIIIQQGLLKIKEQQQIYIEMLKQNEMEKQKEKT
YIKNI

2255 - 2274:	EEEEEEEEEEEEEEEEEEE
2256 - 2275:	EEEEEEEEEEEEEEEEEEE
2257 - 2276:	EEEEEEEEEEEEEEEEEEE
2258 - 2277:	EEEEEEEEEEEEEEEEEEE
2259 - 2278:	EEEEEEEEEEEEEEEEEEE
2260 - 2279:	EEEEEEEEEEEEEEEEEEE

A0A1J1H141 **A0A1J1H141_PLARL** (3406 aa)
Ubiquitin transferase, putative. *Plasmodium relictum*

MKKYLVFENSQYSYIINSIKNGNESEMLAGLNDFYEQLNLSADGGLSNSNLEEYINVLIHVIKNPHISYNSVYGKNDNNN
NNNKKISKSSLNDKKVSSDKINEVVGSGINSFFKIIQEHIGVYASDFDDNYSDLDYSDNEKKKKKKKKKKKKKKKKKKK
KYRKKNNNDKERKKNSETLSSKDEEKDEKSSNKREVIIESDEKSSELDTYSDSSSNSSVTSECSLESDNEKLFLNDANPI
DVKYINIIYTATCCIYTILDIYPNSIKYLINNKEGVYILNKKLNDIEYIDVAEVILKIFEKLVEKDPMFILKKKSIKYML
MHIDFYNVNIQKKIFFCIIQMINNITKYKHITKYITPYCSIFINFFHFHYIHILNIICTLWRSLLDKMITLRLEDENKLR
KKEKNEKSISNLEEKHFSKKNSKEVSYLSKVVEKKEKKKKIESSNLIDVDKKKMGSSYKIEDKKNIKDQKNKKIEVSEEV
EEVIEISDEEYANDLINKKDIHIIDDDKDDKKINKEQRKKKENSNKKNKKKTKNYIKDEEEKKGKSDEELIKIRKDNSKC
DYDKINSSNNIKKNYLNENNKKIYKKEQSDIEDLYICDKEYSNIKCKSNNSNENINILTSLLKNTVDNLKDDYIDNNLVC
NGKESNSYVLENKKVNKNKNNNSNFINSKENNIWNISNCDETYSKENKMKDNCSSSTDYANKLLKNIINLNNNDNTYFKL
SSEIESVYNINIRDNIIKLLIECQIEDNLYAFMETFYIISIFVHYSNNILENFCNSDFLNKFNEFFQNKKFQNNSFLIIY
ILFTLYSFLPICTYDGSIIYEYEKKKNINDNIFVENIEYCKGKNIDIDKEKEKNTDNDDDKKKSLDNFFSYEKYGYIIYK
FPIDVKKHKLEFYKNNFNYLMTLIKIIIPNIYNIYESALYFDIKYLCIVISLSLFISLYKISFFYYNNSDFVDCLDYIFS
FYKEMYSFIKSIVSNNLSESSVISGIIMCKIIEHFSILISKEVSFSSLNEKINKNNNDIFNKYLCNKIGNSLNEINSLYN
SKKPYLFVLTNIINKILLKKKEEIDESEKDNCICSNKKVYNIIFLYFYDMFNAKSIYNYENSFLFFHHEREMKNVAIEFT
SLFLNYKNYNDCKKNSSSSISIHNIIVNEVTCFNNIVLCYYYLINLFFNLSLMHENSSIYFYQYNIAKRLYFFLFQKLFH
CDSEKKEKKNTEQDNFVFDLTKEKNKRNIFNLLKNIDRNIRLYIFLYALLFTNNKKMEEIVINIFLNSVRTLYNIFYDIF
KKNIEEIDDNEFKKIESLVTEIFDSYHYYLIMNNLSFNNCSLLIKLTKECLNIYDNLPIYFFKENNNIEQCQEREDSDTR
WIKSYDDFPSLKNDNSFFNLKSKKNNDTTTKSVKQNKKKKGKEDSNSKECFIENIVEKKINSNENNEKNESKKNKSLRKG
HEADKEKIKNKTEESKIKEKEVGILKGKGKEDKDIEQGKVKEKEVEIIEKIEENKEKEKEKEKEIVKDNSISNSKLNKEK
KKVLKINNKKEYSFYDYFNSSNYKNDFDYMQKDSFYDNLFNDSNNKNNKKKSKSIYNNYNCHFPMHLRRNGLYIDNISVF
NSLNKGIPISLHVEQMKSDKNEEKLEKETDYLHDGTNSNYKEGLYIPSKINKTNYKKSLTDNTNVLNKISKNLTYRNTFS
RENIYTNNYFVRSFIDRKRNLQGSFNIFESFNKVENFIRKNINKNNKSFYSKYDHKNEDLIVLSINGIDVHSDSCLSEYL
IKLDDVYYINKNSLCLTEENIFYNTENFYVYNDVVENFETDYYNLKNKIKYLWDSNNNAHNINYKIIKKRKNDERCSDPL
EDEINKKSNFFVTLKKKKTTDYNEEKKYCQINENEEDIYTYVDLSTYKKMKSSIDTPLYCKVINEKYNFYNISFDLVKYL
YNSNSQNDINSQYDEKEDISFFNSLKKDINNDVKKKGEMNYSEMENLLYKYDSRREDEEEVVFYKSEEEKSSHLLDYLKN
RYKNKKIEFLFSQSNFVENDSMYLSNYMKKEMKKATELIFFDDHYINKDIMLSTHLHNINFLMNNEKNSNNSKRKNRIDQ
IEVMREKERCLFEKYKKENFFKALNTKEERNSYECESLLLKENFTLKEKEFYLLYNYMPAYSEIIKKKILDKEEKEGEN
ISSQKRDKHEIEKNKEKYIFIDNVYNFLLFKFLFLLCKYFKRCDTSSLLNFYINNNQDNKINKVNSEVNVVLTEDTKEEI
NKMKYIFENMNEKENNLTVDDIKKKNFILNSINNKIIYYLNNPLFIFSEKLPSWIYKIFYLFNFVVDIDIRLLFFEITYF
GNYRGFYNYKQKIKELVEKFNEKVNFGNRILTEEHLLSVCSNYTYNYDKKKLFNFLSDNTTLTLPRTKIKLHRNKMIDSS
FRIFNHLHFINSNYITPSFLDIEFFNEEGTGIGPSLEFYNEVIEELKKEKLKLFKIEDGYLFPISYKIDLNNFDFDLLKK
PKNSDLMGINKSYNSHNSLNFNSYQSSSVNKRINVISEGSNANNYNSVNNLINHFLFSMNSNVFQKNTKNLNKYDDISEV

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ELLDAKMRNKKNKKYFKNISDNSKKNSKKYKNVRSHKKKYLSNIESSQDSNDNKKKKEEKVQENEEKKKSVLANVRSKET
KQKKKDNNIQKKESSNITLNTALEKSNIFDIKEEQTELDEEYINSDKNKKKRIRRYVEVDTKEKKNEEENKKKSISSEKC
GIKEKEEIVYSNEENDKLEEIIDELEEEGKENEEEEEEEEEEEEEEEEEEEEEEGEEEEEEEGEEEEEEEEEEEEGEEDEDE
DEEDEEEEREIDDYNDYEEDEDEEDDDDEIDDHLEDEIYDEIDFENEDEQIEEENKEDEYEVEGGEGEEEKENEKKCIKR
KNKNDKSNIYKLSEIKESLISSSNNHPPLEKVEDISDISDKPKRKSSINLKEKNRKNCCKLLDKNMNSKRTSEDISKKKK
IEKKEKEEKIKNKENKDTVNQKITEEIEMKRKEEIEDNEKKEIEGKENKKVQIKKYKLFTKDFEENFLKEENNLNLKKKN
EAKKKINLNNQIKLTQSVTHNIINSLFSEIENKNPVKEENKYVDKKDSENANKKINENNDKKTNENITKKSNEKDKKKYV
NINQDTLENRLFKYFKLLGQLCAKILTDNRNVNINLHPLFWYLVMNNSGYVNLSKFHHYQAIDRVNMNSINKLLEYRKEN
KNIEDLHLDFTLLGSDPPVELIPNGSNISVNNENLNLFINKTIEHSLYEGIKFQIWAFRFGFSTIAPLICTNIFDEEEIC
EYLFGSNIENDAYWTKSHLSTYIKPDHGYTNDSITFITLIEILSEFNNEERRMFVKFCTGTSSLPNNGFSALKPLMKVVK
KEDNNDLPSVMTCTNYLKIPDYKDKEKLRDRLLYAIREGQKNFSLS
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2753 - 2772:	EEEEEEEEEEEEEEEEEEEE
2754 - 2773:	EEEEEEEEEEEEEEEEEEEE

A0A1J1H1W1 **A0A1J1H1W1_PLARL** (3238 aa)
Uncharacterized protein. *Plasmodium relictum*

```
MDYKFILKKQELYVSIDMNNEVIEGNTIMNISLNLPIYYLYDEIDFLKNNFDLKRIKIIKEEKENKRNLKEILLEDDESY
INFRKRKKERKIFMVLHIPNNIHSSKYSDIKLNEKDENRYYIIYNSLRENLHIPEKKNKNNDFDNNRNKKVLSKKKKYIK
SIKLNKNKKVTSSLQENDSNYSKDYYLNKRNSLKSKINYNGCVTYISNNEERIKSEEHIPSESENIKSFECYNIKSEKKK
SIEKEMEMKKEGDYYQNYVIKNEYIEEKKNKEKENKKNLEEYIFKQGNLYDNEYKVYENEEDIYRGKQPDLDHKEKKAET
KNIKEKMMLNKKKRCKEKESKTQYKIDDKEIDDGNEKYNKEDEEEEEEEEEEEEEEEEEEEEEEEEEEDEDGDEEKENY
VEEEDNDNDDEDEDDDKEENEEEYEEEEEEDEDENDNKSNNGKKNGDKNDYIDEKHSKEEETEEYRSIEIGENKYRYDK
KGSNRNEKKSENYYNENYGKNKFFSAKNKIKKKKKKKRKKKNNFDILDFVSLNKYIDENNLKEDSYMFIAINEEIFNKEK
EKNYEKFQDFCKNDTIVINKKEQYNIKINMTVNVNFKFFNLNSYYNKTYFKKDENLLITLQNYTKGNTWFPTLSKFDSVY
SRCSWLCIYKIAKPYFVISSNSLINIYEMFDKNCFVYKTTNKQSKLFPEQIGLFAGNFNFLHLNNLNFKDFQKIDYDFLY
KSEFFSKNSKIYSSEQFNKSKNKNSPNKNNSDMLKNEKISHSESFKKNTNTPLKRKYSYINNLSNDYCRDFDGSDDDEDE
DENEKKKKKKNMLLNENDMENKNNYELEENCNSISTSYDYLIKNDIKEEKYNYYEKINNKIVPNIFVFSQKNYESELVYS
NLHIGHILKYFFDISKESFPYDNLIILFIPLNFSNLDKYYNSENIECSINSHIYDDVKNGYNLFSNSNILNYKITEPYIY
LKNNKYFIFGNVIVFSTQILHNIYDVLFSINIYSYKMIIAEGIISLWFGYYVNSLKNENIYFIYMLKCFALQKYIENMFG
IIELNAIFYELRERYCSLVEMYGDVNLFHYYEKDKNNTSEKFISHYIFNNLFFLKCFLCVRIFFNILKNFSFCNSIHQYC
FSLFFSYFKNKKKVIQSTKFWKKVFNECTRRYIENYKQIPKNKFKMKKIDLNINMSELRNEEHEQYQLFEKYFYYFFKTY
IKGYGVCQYILTFNVHLQRKGTSMDSFNFLISQNSINPFSFVDENFYSNYFLSDISSMTVYDLLELNKYIDLKNNNDSNR
DQKMNKHLDKIYFEKLFEIPYINDFFNIEENFLLFLKKSFCQIDHFFEYSEEEFSKRYVKYIKKYIVKKNKNYFLIKDKM
KKKSNTKCTFTNKINSIKSRKNINKEMNINETDIDADIKSDSNIQNSDTDHNNMIINRRENNLEYIPFEERNMKDNFHND
KKDSVKERNVFIEEKTNQKKKEKKRKVQLAKKEKIFKKKKKNIKKDIQHNRKSVEIKKEKLPKYVKINKSYILKKKKELI
NLPYSNFDSLDLIGRDGNFYLGFGYVGSEDLTLSTGRGNLYNNIIAFQKLKNCNLQKLSELCIDKHNIYEYNTSPFYTDC
IYPQWKIIFRLYYYLQLLNKIYKKKKIINRCNILKLKNNEIDIFNDDKEKSLYELKKKDKKKKKKKSKIRKDKRNKKNEI
NEDNNDIDNGFLSSYTKDNCSQYNSYQNKCLYNTENILIDEKKKKDINMIENITYEDEKSETSKFFDNKERHEEYDKKSN
EECGEHKYEEYDENIYNKYDSETEKLKNKKKKRKKKKKKKKEKKNIKDILNNKKYIESYLNPYVSNNIPSSVDENKFFFC
HLKIEIIEDDGVRIVKKNLINNITPTRFSVNARPEKGRKKVAFKHEAFINKSEEYISKNSLDIPNNFINKNVKFVGITND
SDKYMIEYCKQKIIKKDKSLLCLDNRKLVAKICSKSKIPILWIRVDNDFFILGRIRRSQSISMWIQQLFNDNNIFSQLES
SFALAFIPFFYLNKKFSTNFSEYKNNDNSQNDNNKENIGESSIHFIKSVLNKNKIKNKKSNLNFNNINTNISSNDALNND
ILNDSFNFQDETTKRHLLNNDNSSLIPEKKINTKKISKKMLNNIIDSNFIDQNHLEINNDKEKLISNLQNDLQSDLLKDG
NLSSQTSSSASESDSYFCNLTTSTIDDFNEEYNDSLQNYSTTNNKKIIYKKRWRSNLSVTNIPINVEVIKCLYKSITCNY
LHYLVKIRCIYSLCFIHNKYLCTQKIIQNLFCEYLSYFYGNNLNQKKFMHAFYIAMSLLRNKCNRTPKIIIFLLTQKFAN
FVFSLNLDDKYKINKELEDDEEKQIEQSYNFYNKNDVICNKATHTNVPYSYYSSNINAQSPSLNESKNRNKINCEHNLNS
NDEKSDLANDNKDILNNYLINKEEQKYIKTENSQDLVNPNDTKNSSIKINDTDSCHNQKNFTNLENIDNNKIKKNDHISE
NSSIDLNEYLKDNKKKSVSISSYTENSEEFINNNNVINKIIKITNEYSNDTNNFSYDNNSNNDYLSNNKLEKKTALKKKK
DIYEKEAIIQIEEEEDIKMVLECLGNIKFKKRNIYKNFNNMPELINYYKTNNKENLFYKYFSTLTSKNGNNKKKKKKKNY
DTYDYYDINIYDKKKLENHFLKLKKTKKEYVEDLINLIFIIYQLKKMSPYINISDWIIIILIRTISRNKNILDSFKKKLY
FENKEYFDLCNYIPNFFFSSKIYPFISLKNSSFFFVEILRALLHLILEGSIRIYQIFYRSTKENLKEKNCIFLNKNYQKN
NTLDIINKKISNIACEEIKENDMNESNKFTNKNYEEKLESFNSDKNDNYFFISTYTNYVEQKMICSHLLNIYSTLEFCDK
IISKFQDCQLEMQIWNNLYQILLIFQQKYPFFYLPFSKNFDKYFKEYQKRNFTIFEFYYLLYGLNKINEYEKNNLGISRT
NLFDNNNDYAIFNDFNIQNIFNTKNNSNFLYALKNKSFEIYKYNVLGYVKLVNVLKSIKNPNKLRKNFIQITYIKYLVKY
IHNFLRKLIINISITNTNYFKNSILFDLRNIFLFFYGYGIPPFNLKKKNTKVYKPHYSQLSNITSRGVQINDLIKFLRTY
YDNNKLLEWKKVASEFVNILKHMKELELFIDSPTVSLHNYNFVKENTWLTLISAKLRNDIYKLPMDLKRDIILLLKNIRS
VDMCSGTNHYEYVNNIFTVCWFIIVKIFQNYEKSKRNT
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363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE

A0A1J1H2W4 **A0A1J1H2W4_PLARL** (1658 aa)
Exoribonuclease II, putative. *Plasmodium relictum*

```
MFFFNNIRRYCFYTKIYNNIKIIRRLRLEKENKEKTENHEESLSINIIETNKNTNLQYTINKDEKHFYEEIFNKIKQKGI
NNNAKNVVIANISDEIKLNKNSINSIVFGKENREEKLKKNYFIKKDNEKKVDYDYAFQKDNEYQEKKIKEEVNEEKYKYF
KEQNDSLKKDKNKNNYNKIAKNEKYLKEKNKYLKRKDMYLKVKDEHIKKNRILKKDEKSNSYIKNEIFKNTFIKKKKEEE
KKKEEEEEEEEEEEEEEEEEEEEEEEEEDEKKEKEKEKEKNLIDKNKDNFNSVDENNIYNKNSIINIHDLNNKKKLIKNIE
KDKKRYGDYSDELKNFNIGNNKISHINNEIVDKNYILVEYEKYWDNEKIDNLLQLQKTTKDLKNKLFKGVLYVSPFDTSK
CFVVNEESSPSSKSSFYFVYGYISRNRALNNDIVYAYTARRKIRQVESKENENEALNKHINENEDENEKFCRVVNIVERR
NLEIVGILNYLNVKEKINNNFGKKEKTNKLKNVNCIYSKNYYSEIKNNNNEKINKINENFVKKDDIIVLKKEKELTKTEN
ENENEYFFAKIQPNDPRLPCFIYNSSNSIINKILYHIKKKKINLCVLVKFKEWKQNEINPLGNISKILGNEKNFFGIIYL
LLHFYKINFHIYNESDMLYLNSRITVNERIISNFIKRKKNALLLDNRNKKIVDNIEQYDKKIDYLKNIQEKNKSLEKYMI
KCFLKNRDIITHLDIFTIDPLNAKDLDDALSIEFIKNKNNLTSKFQYKIGIHISDVSFFVSPNSYYDNIASKICNTIYMD
FLVIHMLPSILSEEICSLNTKSEKLSFSIFFYLDDISNPYNLTENGNLENVEIKKCLIKSHYKLNYDIVEDFLDDIYFKI
KQNNETVKEQEEKLLINGHLHLNHFVNDFQELCKKYNLSIKIGSDIFRLYLLSKMLKEKTRRKNIYQKYSLLFSFNNTNN
KNDEKKVIPMSIEEITKEYMLSSSTTKISLEKFLESEKYKNLLNETNIRNVNMETFDYKKKSHMLIEEMMILTNFLVANK
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```
ISYNNTLGILRVHQDTSEEIKKNFLKIIDYNTYNKINNIININENSINDILLVCEKILNENQLLCLHYNILKYYKEAIYI
PTEENKNNSDHFGLLLNKYIHFTSPIRRYIDIVIHRILNNIIENEKICYNYEELKKICDHCNYQKRKTDEAQIHMKNFFL
NKYLVYLNDLYKCTLKKKKKTKLKNEVHKLNEEDQTINKKENKICKNEKIEMSTGKIKILNKNEKCDIHKNVICEKKEKK
IEKTNYLINNKNIKTENCKPVKKYFYLNRGSVCFLTEAYIQEIIITKSIKENICLNILKDNYIYVNENECTDINNIIYTC
FTLDSSKSIHITDNLVDSRNINYNDIRLFSDIDKSDYKNLNNNNEENFKSKLKKNSNENGKLKNAIVFYVPLLETEKSMS
DNLLNLQFEFILLSYNECTFIYNIAKDILYKINMNYYNINETFENYLSYEKEKNEDLNSEHEKKMNEYLCNIFKIINELK
LEVKYKILELEHKKKFQKIYDDLYIHDVFIKKNKDAHEQDMFKENINNENINEENILVDTNEDISEKGINEKDLDEEYLN
EHINDYIINKNNQNYFKEYIYDKNMKYKYCNKYEKVSRFQKIKIFIIPGSQMWTLSLF
```

244 - 263:	EEEEEEEEEEEEEEEEEEEE
245 - 264:	EEEEEEEEEEEEEEEEEEEE
246 - 265:	EEEEEEEEEEEEEEEEEEEE
247 - 266:	EEEEEEEEEEEEEEEEEEEE
248 - 267:	EEEEEEEEEEEEEEEEEEEE

A0A1J1H3T9 **A0A1J1H3T9_PLARL** (1214 aa)
Vacuolar protein sorting-associated protein 33, putative. *Plasmodium relictum*

```
MNKLNELKEEERIILLNILKKFKGKKCIFFEKSLHIILNVLLNEEDLNKEQIESIFLVCNEKDVNVKKLENIPNILFIIR
PYFYEIENIFKIIEKIEKVKTTNKKYSFIFIPYMTYLCEQEIFKYNIPDVFIKIIIFPLYFIPLYNDVYSLEIKSIFKEY
YVDNDFTNLIFCSFSLMFLQFLFNGVFKNIKSLGYLSQFVCEHLIQLRKEIVSNNFSIQSPNNFEDDFFDILNNLQNIQD
LNNFKKSNESVVPVKYAIHKIFMSEQSHKKFIKKKKKSINEINIKLTSSSEENWEENKNSRNIKIYENIKKEKEENKEKV
KEEIEIEKDNKKQEQGKRQKHRLKGEDNEGGKEKEEYEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EDDEEEEEEEDGEEKKEEEEEDEEEDDEEEEEEEGEEKKKEEEKEEEEEKEREDEEEGEEEEEGEDEEKVGEEEKEKEEKE
KEEEKEKEEEKEKEKEEEGEEQNEVEEKDEEEKKDNEKEKKEDNEKEKEKEEKKKLDEDKDYIEDEILKNEVEKKVEENY
LYQKNEYEKKDVREYGEEREQQEIKEKLKKEEDKEDERKKNAKYNVINVSKNSLYYLDSNNSYQITYNTHDKSINTCDND
NNINETDFNNDINKTENMNCSEKRNSKIEYTNINKEKKKKNELQKYCEKKKKENKNAKSQEHKYLNDNMIEYTNNISSKN
NTCSDKNIKKIYKSKEKNYNYINKNKLKKKKKRQKEEMKEVTEKEEKKKIKKKIKGFATITHNFMTKMDNTKYFMKKKDR
KKMEKECKKEKNYLLEKIGITNFNFLLNTCCNIDSCIIIDRKIDMITPFCIPFTYEGLIDHLFCIDNLQIEIPRYIIFND
EKSISKKKEKSFEDVNSMKVRIKLKSSVDVLYDDIKDLSQNDIGRFLHKKASEIQKTYEEKDKLKDIEQINEYMRKFKVK
HYEHNSLSTHVNIASFILNTIKREQSFNKLKLEDEIIQLNSNTNKSNLLDIVKKIQSLIYTGEDIYEVYRIFCLFSIITN
GFNENYMNDLKKDIIEQYGINELTRLNNLHTCNILKYQSKNKFIWNNLKNHFNLLSNEINDISYVCNGYAPLSVRLIEYM
SVLKNNLQIIPEIFNFLNGPTLDIIQNSVGYENFEVKQKKISKKKNVILFYIGGISYAEIASIRKLNEKSENYNYLIFTT
EIISSKKILQSMNL
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358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE

A0A1J1H4R6 **A0A1J1H4R6_PLARL** (1341 aa)
Serine/threonine protein kinase, putative. *Plasmodium relictum*

```
MSFSNSRSPSNNSSSQDATSGKLQYTESDDEGSEEYCKGGYHPVKVNEIYNGRYRIEGKLGWGHFSTVWVATDLKSKPLK
FVAIKIQKGSETYTESAKCEINYLKTVKVNSFDSSWVELKEQQREKLLHYNMTKGVVSFIDNFEHKGPNGTHICMVFEFM
GPNLLSLIKHYDYKGIPLNLVRKIATHVLIGLQYLHDVCKIIHSDIKPENVLVSPLSNIPRPKDYSKDKLIKKNDSKENN
ETKNEIEENSSITKECIEKCEIEQEKQENEVEELNESEIRLNEWDSIDWNKLSKNEKKKLKKKKKNFLKRERLKQELLNK
NKENNQSTINEPSGKLIINEQNIKNLSDTDQNGENQFKKEDTENLNINQLNKNELQKKILETCNDSHVNITPNININCNS
IENNIMKSFNDNKYSSNTNHNHVNTNEKIEEPEYVKNKHCNLDQNNLSIRDMETCTKEHELYKDKENNLHNKIDEKSLNR
KKIIDEPPYVKHTLKPSNSDPSLLTSYYNVHALQETLTKKPYHFNNYFLYNLEKYGNNKMPLFLHRLPNDYLKKNAINDD
EEDLRNSESDICDDEFLENDINKFPLYCDIFNHLIHPEALKLHEIYKKKKNNKISNYPINSGGSNENVRKVVYIKTEDGD
YCIRPYDPSVYCHAKSCYKICDLGNSLWIDESRYAEIQTRQYRAPEVILKSGFNETADIWSFACMIFELVTGDFLFNPQK
TDRYDKNEEHLSFIIEVLGNIPKHMIDSGFNSHKYFNKDTYKLKNITNIKRYGLHKILKYKYRIPEKEINPLCSFLLPML
SIDPQTRPSASVMLQHPWLNMVALEDDETYMKNRSFSINSIYMKNNSNYNIYENSSKSINSSNNRNIHTTFKDYNNNTFV
QLEQESCKSADYDSEYEYPFFYEKRYDYNCVGDRFSKMNYDTMYTKNVKNKLDCKSKNKKENYSNLKDNSINIEDYILNS
DYISNTIDHDPYNKQILKNTTNYKIGKIRDYKRISIHNETMQNEEDTFENYNEQGDEYKHEEEHENNSENLMKKGDDEDE
EEEDNGEEEEEEEEEEEEEEEEEEEEEEEDDEEEDDEEEEEEEEEEEEEEEEEEEEDDDGNEYDDKKEKYDTNKYDNKNDDNN
QHENDDNYQYGNENDFDACCDNENIYEQEDIEIYTNEREKKEQKRKKEIERGMKTEKLSVTEGKNIIKNEIKEDKKNEEY
KIEGNNKFCENAKKKYEKRISNFKHKKEENKMSAEIIKKKNTSTESKEMEQNKCTKNVSNILLDCNTNKEFNKYDHSEKN
QTAIKREQEQMFYEGSKMLENHVEEKVNKINCKVINKKTYCAISKKINFLEAKNPLEFMNK
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1047 - 1066:	EEEEEEEEEEEEEEEEEEEE
1048 - 1067:	EEEEEEEEEEEEEEEEEEEE

A0A1J1H580 **A0A1J1H580_PLARL** (2833 aa)
CCR4-NOT transcription complex subunit 1, putative. *Plasmodium relictum*

```
MRSLPYIDSSTILKIKHLSEMSTNSSSNINISQLLNNDVKKFSTTNANNNLKNMNNLSVNLSKKKNNNTSSIGNINNISS
CSNNNNNNLSNALGNLLNNGCNNNNINNDNLLLYINDILPNCANVEQSLHKVNNMSSLNRNDNIFKNKNVNENLSNNLNL
NNFSSVNNINNQLNMNILNNDKSNNTSSINNLYLNRSFLTANENNQLNKNTNVAGNNSYINREMNYRNSSCLNENTANSN
IASYIDNAIKINTNENVKYANNENDNNSIKEKEQLYGIIDSFYDQTQKGLPSHLNLNNISGFGLGQIECLIDNTDFTKNI
VVPSSFIVGEVFSIFNTLCLFNIDEKTKILKDVMQPEYYNWLAFYIVKSRASKEVNLHNVFLEFIDKLSYPLFIDTIINM
TYDCILILFKYINELKEVSAFRTVLKNLGSWLGFITLGRNRPLKSKILDLKLVLFEAYEKGCLVCILPMVCKILESVKLS
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KNFKPPNPWTTAILCLLTEIHELPNVKTYIIFEVEVLFKNLSLDIQDYQNKTSLLSKRVSYNKKCDFVVSRNNNISSANV
DMKNVSLKDNITNINTSQREENNLNENLKLEELENSAKNILTNNRISTDKIQQMNQNNQRNINLKNIVSQWNQNNTNRID
PLMNDTTLVSSFSPPDLNLINSHFSKKSMNNLNKKPNIMNDLNTNNLNYNNNMNVSGVSGDSISNNKMNNSKFLQSLNNA
VIISPSIALFQIQPSLKKVVPIAVDRAIREIISAILERSVAISCVTTREIIFKDFCLEKDENLIRKASHIMIASLAGSLA
LATCKEPLRISLTQHLRQLLQPTSTKDCNDQVLIEQVVQILSADNLELGCNLIEQAVIEKAIKDINEALAPSFLARQVAN
ENSIAFNDSSYAVNTKKIQLEFADILKLGSPITNHQLQIYKDFLNIAPLKKLHAAAKALSLIYKNVNENNTENQNQNSQV
NVSFSNENLQNNQEKIVYAKNMSQTRLNEQQNHISKNDFKINNTVNNIDYNLNNNIKNQQNFPSKTNVNENNTQSNIPIT
IPLGANVQFHKVLKKLELATGQLKEAIKDIIMLPPILFNINREKSYCNINKLSLYILYSLSVDGNIFNLIKSIPEIAALT
QHKNETIISYSNKIYKFLFEITPYNDKTQLGCRLNDPVGIYLEVFLCILEKLKKKCPLLKKHISNLITPNNSNVSNKNNT
ENNNVSFLNMNDSPKENEVVDDESKDNTKVEVKNSSCLNNNLDACNENKSEENKKNNEDLYKYNVNVISGLIRYNLVDIE
KYKHYLEKELDNGRCVNCVEFVVLLLKSILLDFQIFRYNDFENIFSILNTIKEKNILPNKIIYTSNWIPMNINSAIEKLI
EESKKIQEKEDTIFFSDLLEFCDEYMKSDDEFDIENEEAEKKEKLGKEKENRDENKEDIKKDEEIKEKEEKENEKKIQNH
EKEKIKQDIQLDKIIENGDEEKDKVDINEKEKKNCSEMKNELINNQKRHETENSEPLNEISLNLKREHDLNVDNLTDTNK
KQNEKNIEKNNSNNIGLLNEKGKKENNISEDMQMSYKNEQNKHTGTSACINDLNNDINNSKKKEIKYENNKKKDYKKYLK
ILMDPKNLTTLTQIIDFCLNTDWNILQKKKNKKYFKDKGVGGVRIVPKPQKFSKEYEQIISIVFFQWIKLSNLRNTDNPN
QNYVQFFQKISNQGLLRIDNNTDKFFTVCIYKAVERACNILNPYAQRNEKENITNSLDELLSNKINSNFVIQVNENDIND
NVSKQKRNANSPTNDTDYKDVIEVKEKNKSIVNGINKENVNYTENENEESYKREDKHAIKESMKDFTENLNDKKKEEIIE
HNENDNNVEKEREQKIPICQEVHNNDHMYNMNEKFLKNEKTFTNIEYSRDSDDNYSDVSSTNLTFYSNISNYDKSSSEDE
KSHIYSIENDNNAKHMKQRKDEILKKLSSDINESIGIDVSESDEELDKKETKLKQKKYLKKDEKIKIDHKKGNKQRIKNK
KENIIFLGKSEKEGEEVEEEEDEVEEEDEVEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEDEEEELEEEEEEEEEEEEEEKEEEKKIEVKGKNITKNNRQKKNIYLNLEENALLTDTLDTSS
VDALAKMIICMMKLVDSQQISPFILFQKAMNVLCRIVVYESRKNKRNFNQRPYFRLFLSLLIEISKNEKGSENSYNKCIL
ALGYYLSILNPLRVPMFVFAWLELISHKLFLPKILKTSKGWCIYNKLLIYLLEFLYIFLKNAYLTPCIKILYRGILRTLL
ILLHDFPEFLCVYNFSFCNSIPLNCVQLRNLILSAFPRNLKLPHPFYPNLKVDLLPEMKVVPVILNNFTFILIDYKIKKD
VDNYFVTRNINCLKKIHKKLMIKNKLKALYLKTKYNIALINALVLYIGMSLPSQILMIDKASETHPALEIILYLTYKLDM
EGRYYLLSSITNHLRYPNAHTHYFSCLLLWIFNISKIEIINEQITGILLERLIVHRPHPWGLLITFIELIKNPIFKFWQC
SFVHVAPEIENLFQSIAHSCLVNQMEHLNNKQMNNNNANNTNVNINVSNINSMNNLNVKNKNVSNDRNSDIKNIINMDDV
NSIKNPNINYNNINNANMYNLKNFNINNVNFNNTGSFSNSDIIRKAMDKNLNKYIVKNNILGNNASLNINNIPKNYNNYN
DNIVSTENSNFNKNIFSNYIMSNSVDNSENDKYFNTQFRDNKNLDIDVENKYGEIKMDIKNANFTSNENSKNISANKNIN
SNNKNINNLINVSNFYNLKNITNNSNIMDKNFD

2035 - 2054:	EEEEEEEEEEEEEEEEEEEE
2036 - 2055:	EEEEEEEEEEEEEEEEEEEE
2037 - 2056:	EEEEEEEEEEEEEEEEEEEE
2038 - 2057:	EEEEEEEEEEEEEEEEEEEE
2039 - 2058:	EEEEEEEEEEEEEEEEEEEE
2040 - 2059:	EEEEEEEEEEEEEEEEEEEE
2041 - 2060:	EEEEEEEEEEEEEEEEEEEE
2042 - 2061:	EEEEEEEEEEEEEEEEEEEE
2043 - 2062:	EEEEEEEEEEEEEEEEEEEE
2044 - 2063:	EEEEEEEEEEEEEEEEEEEE
2045 - 2064:	EEEEEEEEEEEEEEEEEEEE
2046 - 2065:	EEEEEEEEEEEEEEEEEEEE
2047 - 2066:	EEEEEEEEEEEEEEEEEEEE
2048 - 2067:	EEEEEEEEEEEEEEEEEEEE
2049 - 2068:	EEEEEEEEEEEEEEEEEEEE
2050 - 2069:	EEEEEEEEEEEEEEEEEEEE
2051 - 2070:	EEEEEEEEEEEEEEEEEEEE
2052 - 2071:	EEEEEEEEEEEEEEEEEEEE
2053 - 2072:	EEEEEEEEEEEEEEEEEEEE
2054 - 2073:	EEEEEEEEEEEEEEEEEEEE
2055 - 2074:	EEEEEEEEEEEEEEEEEEEE
2056 - 2075:	EEEEEEEEEEEEEEEEEEEE
2057 - 2076:	EEEEEEEEEEEEEEEEEEEE
2058 - 2077:	EEEEEEEEEEEEEEEEEEEE
2059 - 2078:	EEEEEEEEEEEEEEEEEEEE
2060 - 2079:	EEEEEEEEEEEEEEEEEEEE
2061 - 2080:	EEEEEEEEEEEEEEEEEEEE
2062 - 2081:	EEEEEEEEEEEEEEEEEEEE
2063 - 2082:	EEEEEEEEEEEEEEEEEEEE
2064 - 2083:	EEEEEEEEEEEEEEEEEEEE
2065 - 2084:	EEEEEEEEEEEEEEEEEEEE
2066 - 2085:	EEEEEEEEEEEEEEEEEEEE
2067 - 2086:	EEEEEEEEEEEEEEEEEEEE
2068 - 2087:	EEEEEEEEEEEEEEEEEEEE
2069 - 2088:	EEEEEEEEEEEEEEEEEEEE

2070 - 2089:	EEEEEEEEEEEEEEEEEEEE
2071 - 2090:	EEEEEEEEEEEEEEEEEEEE
2072 - 2091:	EEEEEEEEEEEEEEEEEEEE
2073 - 2092:	EEEEEEEEEEEEEEEEEEEE
2074 - 2093:	EEEEEEEEEEEEEEEEEEEE
2075 - 2094:	EEEEEEEEEEEEEEEEEEEE
2076 - 2095:	EEEEEEEEEEEEEEEEEEEE
2077 - 2096:	EEEEEEEEEEEEEEEEEEEE
2078 - 2097:	EEEEEEEEEEEEEEEEEEEE
2079 - 2098:	EEEEEEEEEEEEEEEEEEEE

A0A1J1H5Q0 **A0A1J1H5Q0_PLARL** (3204 aa)
Uncharacterized protein. *Plasmodium relictum*

```
MNKNYEFDFYQKVMKKRLNDYETHSDVSCKIGYSDSESEGVVSIKEAPYYAYNHNLKNFKKEKLEKPMWKSFHDIEETAK
SSHSEDEYIKNDESEKEIGSPRFGNSSEEDEKEKIEETEEKEYKRLHKSTENLYIFDDINEDVKTLEENESLENFTQNNI
SSNINYNFREELTNNMYNNLSVFRSIKDNYDDATKHFLKPKTFKDMNGLYYDINDEKVDIDTLKKEHERLKQVNKLNKLG
NMKQDYFANNSFYNNEDVENMNIQNKNKFKNTKHKKLKGKEIKNSVSLINKISDECDEINLNEKINFINNNIYEQGMIDY
RRGKIKKKTTLKKIKNNTDKKYDNAKEKKRISNESYRNGEKNEKKDEGEDECNTYKDKEELCKEELHLSKEEEERVEEEE
VEDEEEKEVEEEEEEEEVEEEEEDEGVEEEGEEEKEVEEEEEEDEGVEEEGEEEKEEVEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEERKEFDEDMYAKQDECEYEENEINNKSDNNINQRVDNYMYNKNNDKDKKENEFLGKLKNESSKKQKFSKRNN
KENDTNNFYINSQKKNRNMRKEKIFKKQISSEKGNNNKNKKKEVINYKKKYFKINENSNNDFNNKKKDANYKISDDIHNN
NKKINAYVEKDDDSLNEYIAKEINFEWWKTDEKINDFQNENLKNNDNDINGKLNIICDVKKSENENLEKEKILNRYEIPK
DISYYAEKYQKNKEGKEKYNENMHKEVHEEININKTVNECKKANGNVVLHNDISENSNFCKNYDSIRSKNDFNNINLNNN
IFINSKKDIYNKDINNNSDTELNGTSENLNIDSFNIKNRTKLLSNIQNEMLKDSCNIEMIQKYPYNDLGALKNYNSANEF
YSHNIRTEMCGKYENNTKLNDSYISIGTNIPFNDKLKINDINHSNNENVLFNSFVNSDNINKGNEFFSNHKNCLDRKSCI
GEDSSISNIYDKINLYNEKFNEEILNKNRENYIKNNLNENERKYDINKYFEKKEKEKEKIIEDEEEKNKKINFFLNYLKS
INLSSINEILEYFVENEKNITKRKDMMEITSLKKENQNQKIKFEECANDLLKNDQNTQTVDKNFRNEEIQTKNARKIENF
IQTDIKDINTDLYIKKDMLSKKTSIDSVFFKNLSKDMDSFNSEGKEKKVDNSKNNLNFESKNDLCSDTKNNLSIDEYNEV
KKIHDLKEKILEKIKSCHDNFSESNDETAILMLKDKYEYTNNNHSYFNKIDDTNLSANSKKKKRTISVTTVETAESLKSF
EKEMLLLKSHNERLRRRIEKLYNEKEKIKNDYIKIEKLKESQDNLFLATERHIEKLHEELNNMSKENENMKNDLKKKNIK
IIALESQIDKNEFSLSSNNTHKKDELTYIDLNNKLEEFKCQIPDKKKVKEQINLLQTQLHILKDEIKKAESLKLENEELK
KLLNKKNSAIDEYEHIIMKLEKNVDNLNEQNIHLCKENSNLNENNAKLKEGNIILSNNGENMDTNQMNEMLLTGNKKNIH
SDKINLLKSNIKEKENQIRDLERSVDELKEENFHLNEEILNLKENNIKLKKISLLSNKRNDIRNSNENVGMMQEEAEKVY
LDKINILKNNLEEKKKKINLLNTLLKTSNNQTIQLNDKIKNIIKENKKLQKKYEKCLNYLEKLKIKYDEQILRKNKQSDI
SLDELKNHNHNNADYESTKSNEENSENLCLKNNKEEIIFLNKREEKEFKDLSSEYDYEEKDSQDDKEEYDEEHEKEYEEE
IDDYSEGSIEYQDKETSEEEEKITNVKEKSINDTITKEIKKKIIKKCSSNISHAEEDTCNMTYDKSTCSFDNRNNMGKNI
YKKSKIKRIIKTNDKPNFKEQSFIKDTENGYNSNANKISMIKKNKRGACKILKYDGSQYEKNNSLKNEKKNIYENLLDNE
NEYVNINNIFEIENVTQDIQSMFYKKKCSNEKIDNIVINNNLNDEIVNNFSNNLANEKRNTLNQSVLYRNKGEQYYQIKS
EKFTHNDQSHINNNKNNLNTNIINDRISNLENINYASNEMNLKNLEKLYISNKIRVFNNNANNYIEKKKQIDEFCNERSL
HNNNIHQKNSKMSFLSYDTNNVTVGGNENNIYNELYNKNIMNNISNINKMNTLSNVNNINNMNNMNNIDNIINMNDINNI
DNIDNINSINNINSMNNIGNINSMNNINNMNNINSMNNINSTNNTNNMSNMNTSNIVDNLIKSNSSNLRNSFINNLDDKI
VQSQIENNNVSKFSLNNNEGNFKNINANSLKSNECINGIKKIESEDSNKIHKLSNENNISIFNSEFKNNTFEKLNSNSYD
NKNETYYKREGMKEIHILENSNIIESSTNNIYGIEKRDNLNKEENKKGEAWIIDLKNNEIFPYIKLKNTLLEEEKSKKSN
KKKGIHDKNNKKKNIFDKNSCHKKSKNYKSFLQKKYIRTPYIRNNDKLNLLVNSISKLVKSKIEEELHNKKLSKDISNLD
ITKIKKGNSSKNNIHKCYNNKRQETKMILSDSISLSSGTFNNTLETIEDDNSDNNSQKFLKNIKENIYGHNADDNNVDKN
EISYANIKNKDYAYANRSNVSNFIPNEKNNFLFCEKSKSIVNNGNYLSDDILLNTFLLNQNYVNEIEDVNQNIIVNNKFS
SQNALNKLGGSLINQNLNNNLENGQLTNNVNYYNFGHSNNSYNKLNLLNENININNNNNNNHNIVNDLDINISNSINNNI
IGNIINNDLKIDLENNKDKNIMNNFNNDVMNNDLNDDSARNIRAVNPLMFSNNISNNNNSNTISEINKLNNSYLFDINAL
KQKEYSPSYNNAFLNYNLLDRENINITNNENIINNDLNKNNISNNIFNEIQQDAKVYEKNNINKKSSNHIFKENRINNKE
SILKNSMKKSNSMNIKKNETNKSLTNGCTELRPKMSTQIFNYSGNKKNGLRDMSTYADKVLEDMKSLIPFNANNLINKTN
KSNKKGCEIKKILNNNNNNLRLHNESESNILNKNIGKSDDFNKNTILNNSTTDNLVTNYNRIKGKSEKSMEDLKNKKKKK
IDHAKENFLNNSVNGTKKVDNSNCNKKKKCEEATSNIINKNKKNILNGNTSSDTYINQNLNFLNENNNNFTMLDIDLNKN
GDINFDDSSNLHYNSLKYQNNLKETKLNNCLSNASNIFNSSNIIQGTVQDPLCFNRREKSNIFQSQARKSLTSFRESLKK
QGIL
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459 - 478:	EEEEEEEEEEEEEEEEEEEE
460 - 479:	EEEEEEEEEEEEEEEEEEEE
461 - 480:	EEEEEEEEEEEEEEEEEEEE
462 - 481:	EEEEEEEEEEEEEEEEEEEE
463 - 482:	EEEEEEEEEEEEEEEEEEEE
464 - 483:	EEEEEEEEEEEEEEEEEEEE
465 - 484:	EEEEEEEEEEEEEEEEEEEE
466 - 485:	EEEEEEEEEEEEEEEEEEEE
467 - 486:	EEEEEEEEEEEEEEEEEEEE
468 - 487:	EEEEEEEEEEEEEEEEEEEE
469 - 488:	EEEEEEEEEEEEEEEEEEEE
470 - 489:	EEEEEEEEEEEEEEEEEEEE

A0A1J1H773 **A0A1J1H773_PLARL** (920 aa)
Uncharacterized protein. *Plasmodium relictum*

```
MHENNKKNSLKKGWIEDIRGKYSSFMSSGNKSTTYLNSLNNESNKDVNDNLNNIKEEKKKNIKVTNSMKEEKNEINKKKK
DKKKNSSLVDDIDLHEKKKVCFEIYKKYYFIEMTEYHKSRENCTNNFLNFLERIFEKMLEVLKHGSENINNLNKFFKEFL
KNDIAYFKNVSYGNSRISNLTHSFLNISNENNLSNQHIDIDKKDEPKMNDKRDYIMEDGINDDNTFSCASKEINCDMNNR
```

ERRDSFLKYDNICTNSNEKKNINKRDSNNNMKYIDNDINEQNPHFLNQNSSRNSVNKINEIVDNIIDVNSEKSNLNHNVI
DEWINYGFMNYIKIMRSMKISCDLIDNKIYQKKLVLLKETYMKEQENLIELFKKKKNDFLKQLDICKNCWKYFENSYSNS
EKIRSNGIKDSKKIKCSWLCQRKYLKNVKDLLVIQNEYLEIIYKCVKTFFQLIEWKKNTVRDILGSYILLYKSFMSFYLN
NMNILYESILQEKNIEKSQIDNLNSATMMEDDIIKPVSEFYFDENCDSIPILNNALNLIKKSVIFFNNQINVKSILCLFS
SNIKGYLTSVGIFNKYVEGVIVISWDKFIHFFTNVEDTSPQWSYYIGDIEFKMVKSKKYQKKGSKDKNKKDIDANDNKSY
TNNSIKSNNEESKNEDNNKHISSKNDEDDVRVKNLKNEFSANFSTNCSTTNENEDMEIQMKEKRKTLLINGWSFTFKCST
EHLTNVCFELLRNHLYSEYFKDETSFSHFTNIISNGEVKNDLLCDDEIANFYNVNLEKTQSDTQGIFKYKSCFEKSIYMN
YEKEDKRLSYADDDNNLKDDIINLEKKSLREGNHSNNYDNKRKMILIKDEKKHKEELEKRGDDDDNEDEEEEDEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEENEDEDETNKYNEKK

874 - 893:	EEEEEEEEEEEEEEEEEEEE
875 - 894:	EEEEEEEEEEEEEEEEEEEE
876 - 895:	EEEEEEEEEEEEEEEEEEEE
877 - 896:	EEEEEEEEEEEEEEEEEEEE
878 - 897:	EEEEEEEEEEEEEEEEEEEE
879 - 898:	EEEEEEEEEEEEEEEEEEEE
880 - 899:	EEEEEEEEEEEEEEEEEEEE
881 - 900:	EEEEEEEEEEEEEEEEEEEE
882 - 901:	EEEEEEEEEEEEEEEEEEEE
883 - 902:	EEEEEEEEEEEEEEEEEEEE
884 - 903:	EEEEEEEEEEEEEEEEEEEE
885 - 904:	EEEEEEEEEEEEEEEEEEEE
886 - 905:	EEEEEEEEEEEEEEEEEEEE
887 - 906:	EEEEEEEEEEEEEEEEEEEE

A0A1J1H7H1 **A0A1J1H7H1_PLARL** (767 aa)
Uncharacterized protein. *Plasmodium relictum*

MQGMRGKTIANIKYNNNMNDGKIIKKKSTISFRKSVNPNKQNKSILDDPYEKKKTLNENIVKLKKTYKKKNSVVHEPTLK
KIKSKHLNIIGNALGIKYYEDLEKKSKRKIMKENSDYFALKKNIFSKNSMKKSRSKIKVMRKKKAERRNNEKINEYEERG
EREDDKEEEEEEEKEEEEEEKEVDEEEEEEEEEEKEEKEVDEEEEEEEEEKEVNEEEEEEEEEEEEEEEEEKEVNEEEEE
EEEEEEEEEEEEEEEEEEDEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDKEKKEESDEE
IEEDTIEDEYEGGERYEEKQKDYKKEQELKKQEHHKKYAKMQKQEKKAMKENEKKKRVIDRGNLFQKITVIKKINDYNKN
ANEKLKKNFTENIDSIMKNMPKKSLSMRIDKNVVDTSLIPYNKTRKLNMEKKLSIMKTRSQILKIAERYMSIDQINSLKN
IERKNTQSLLKNKKNNSDKLKVSGPFLPKKKEEVKLLRKPGYIPNYLKKKLKNKSNGTLFLKKNLKMILTKQNSLHGFTL
FQNMLALDNSGKLHVWSGYRWKYINILYEIFISVCTNKKGYILCINSNFKPGYLMNNKYFQKIDTYKEVFFLKIVINTKS
QIWGINLRGDLLKWNRYEWVKAKKAYGISKLKSLAFDRNHRLWVLDQHNYFYIFDTENKNWMLKNINGLNIKDFDFNENN
YLVAVTNEGVLKIHRHKRWIKYGILAEMRISSLHFLREISNSTKEND

236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE
239 - 258:	EEEEEEEEEEEEEEEEEEEE
262 - 281:	EEEEEEEEEEEEEEEEEEEE
263 - 282:	EEEEEEEEEEEEEEEEEEEE
264 - 283:	EEEEEEEEEEEEEEEEEEEE
265 - 284:	EEEEEEEEEEEEEEEEEEEE
266 - 285:	EEEEEEEEEEEEEEEEEEEE
267 - 286:	EEEEEEEEEEEEEEEEEEEE
268 - 287:	EEEEEEEEEEEEEEEEEEEE
269 - 288:	EEEEEEEEEEEEEEEEEEEE
270 - 289:	EEEEEEEEEEEEEEEEEEEE
271 - 290:	EEEEEEEEEEEEEEEEEEEE
272 - 291:	EEEEEEEEEEEEEEEEEEEE
273 - 292:	EEEEEEEEEEEEEEEEEEEE
274 - 293:	EEEEEEEEEEEEEEEEEEEE
275 - 294:	EEEEEEEEEEEEEEEEEEEE
276 - 295:	EEEEEEEEEEEEEEEEEEEE
277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE

281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE
287 - 306:	EEEEEEEEEEEEEEEEEEEE
288 - 307:	EEEEEEEEEEEEEEEEEEEE
289 - 308:	EEEEEEEEEEEEEEEEEEEE
290 - 309:	EEEEEEEEEEEEEEEEEEEE

A0A1J1H7U0 **A0A1J1H7U0_PLARL** (2564 aa)
Ribonuclease, putative. *Plasmodium relictum*

```
MKEDNNNISKKLRKRKKRKSRKFSYLSFKKEIANLYEKEKNILMQMQNGNSLPDNKKINNLISIPEDKSLTILNKNEIPN
NLKNKTIKENLNCRQGKKKKKKNVLYNSKNNMQEKNLNSLINIFFNERKGISKIGNSNHNVKNKKGSITEYSSVESICKK
KKGNSKKSNKENDDLINELLHIIITKDKITKIKKKLLDNCLVNFVSSNMMKYVIRKTKKDIDFNILKTLLVINVDAKNID
YTLISRRKIEMLTNCIFPKEKLRIIKRVLSQIFKTVSIKKNFSEEFKEIIISKSDYISCVKAVSSYLLKSEKKNTNNYKK
FKKIYELSVKLLKQEIENIDNIKTIENKKNNSKKEKNDKIIRSLDYIYEEQKGQTNKNSEQEEEKEKEEEEEEEEEEEEE
EEEEEEEEEKEEEEEKEEEEETEKENEEDEEHAEEGGEESDEKEAENNAYNEDEEKEKEGKEKEQEKEYKHIFCNEKQI
HINDLLTNLNNYKSTLDAEYSLNNNINNSNILKLVNEEINKRDMQIKSLKTYINLMENDIKLLFENNKIMKKKIEEMEMN
IKKNSFQNILEESKKGIFVKQSDIILNIYEKAHLNFSDIKELKDKRDYMSILNVKIDKNPFNFTNNVSFDNINKNSSKSS
DMNETDNLKKKLKKLIKLLNLNMFSKNNDGVYINKMKKELNLDCINKEIDKLIYVMKNNKIANEENQKNKILKIKNDSAL
DKKKKESELTMTKNNKKNSTQVQKIMEQEDKKEQEKSKNKIQKILEKKKKKLEKNPIINNKTYSKNCDDPNFLIYTKQKS
EKTFEILKNNKSNKIKNKKDIITNSFSEHVEKHLKNDSNENKNEHKKNSLLSNLNSYMNSIDYKIHKILSLDTIKKKGEN
NLKGDVSDDSFFKNEKTNKRKNYFQKFMNYCNDSEEDENKKNSNDEEHIKLCNESLSNGNRDDKIKKKLNSNNLKNNLCN
KNVLDLKKKVTSEILSNNNKQKKGKSKNKIKSKKKRKNKKKSKGYKKNEENSNLIIHSNKKNKENEDIKSGKRMSYINKQ
NKRNEKNIENDKHITYINKKNKRNGKDAEKNKLVNHLNKINENVTDSGDSVVYNYNLYNAIDDLNAQFSNVVKNIRIDGS
FQKVESIYESDKEKNEKSETVNSSTREDIDNFSFHFKTVKNDYNFIEVLSNDKKREKKKNIYDEYITQEKAIDGIIKKKY
IRGILNVRKHDYGFIIYNNKKIHIRSKKDMNRAIDGDSVVVKLKKNIKNEIIGKIVYIEEHHGSDIQYVCIFRDKIKNQK
FNFAIPFKKNIPLIKVLNEHIIEYMKKYHIRDISNQLVYIKVFRWNSNETFPEGKIVEILGQNDIFHNMQNAILLNHNLN
FNLKDALEDQHIRELKDKNTYANIISQEIKKRIDLTKKCIFTIDPETARDLDDAISISKISRKKIISCNYYIQVIHNLIV
HNGEIEENILKKNLSLFVKDDSNFFNILKSNKYVKEMEDIKYDNFMKEKIEEEKKKKIITEKKAFKILTKKCGKQTKTHQ
NITSDVNNENFEKNKIHDEVKSKNKESSNENNNSIKFMNHIMNDKSIKMNDNSENSNDNNSNSENNGDDFFQISNDYINT
ESDTDNILDDIYEIKGTHKKRRKISRNEKKQKKKIYTENFYNIFTEDSGYDNYKYRENEEDFFYCKIKSEDGTDNEKKKS
NKKKKNEKKKEIKKEKKKIDMLNYASKSDDAFEKGQKKEDSEEENNTYNGDEEEDEEEEEEEEDEEEEEEDEEEEEEDEE
EEEEEEDEEEEEEEEEEEEENEEENEEEEKQKVEIQKEEIKKEIFNNNNVEKKKIDEEKNKMIKFQKIFLDNSDYECFFKN
ERKDVKKNKKRKFSDSYEFFFKKEYNKDIGYSVYDNHNLFCEKCKKFITLDDIIKEMKEEKWKKYNLYEVGVHITDVSFF
IKENSSLDIDARNRAMTIYLTHTCFPMISKILSEELCSLDPVNNRLCLSIFFYMDSTGKIDHNSFFIKESIINSKVKFTY
EEVYLIIRNYTKLKKMVNKLKKKQHEFFNNQKSSNSIFEDIDKNSKGKDSNSNNISSSSKNKKEYIDRKNNIYKKFLNTH
FYNNSNNNDSCKYHSAEDLSTILKKKFDEDKKAHSDFNFDKFNHLNEKNNSMNNLGCKEETKYNSNNIILKSANHLINEK
ILKNSKVKKSIEALIKIFKNLSNSKHNLSNKEIFTIIKNLYDMHKITKKAREIRRKNGSLLFNNDKINFILSDACNPIGI
VRKQYTFSNYMIEELMLSANKLIAIRQYFSKYRDISVFRSHSLKNAIELTDIIELLKKHGIHFKVWDLHHILKYLDDNKK
NFKHEKKNIFDIVCTYVKKKMIRAEYHTFKYIKDNNMSTYHYALSFLLYTHFTSPIRRYPDILVHRIIKKIICDEDKLNK
KICTEQEILKTVETSDIGIIEKICENCNNCKAKSKKAQMDCEIAFFCLYLQKLDYPGYNRGIIMDIYKEKSSIYFKSFSF
ENNLYHSNHEKHFHKMNKEHIKYVSNYVIYPNITKQEFTLVLYNKNTKKVRLRRVYKRFDYIPLYFIPLNSMPPSYFLAV
AFNK
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388 - 407:	EEEEEEEEEEEEEEEEEEEE
389 - 408:	EEEEEEEEEEEEEEEEEEEE
390 - 409:	EEEEEEEEEEEEEEEEEEEE

A0A1J1H8M6 **A0A1J1H8M6_PLARL** (1873 aa)
Leucine-rich repeat protein, putative. *Plasmodium relictum*

```
MLLDLSNCNLRSLEDCDIILEKLIELNSDYTSITYLNVSNNFIKSIKGLRAFENLKVLNISYNELTSLEDDYIPSSTEKI
IADHNYLTDICFKSIKKKKKKKDSEEEEDYNEQINRDRDEIKNKKEIEKKDDVNNLVNCFNDSLNSSFYNTFNNNIINEK
SFYTNKNLPLNRLTYLDVSYNNIKKLTTFEKYLHVMNKKMKNKNDCYSDDVNIKNYISNKTEQDVMILFFNSLETLYLRG
NKLTNLKGLSVFKNLKVLDLRSNLINHPVQLFYILDNKNWLKKYQEKKIQKKSNSYYSYFVYILKKYKNLKNLQNIFLQG
NKNVLKPKYLFMNVFNVLRNINTKNKLVTDVINDSSSFHTKDSTIQKEYSNDEKRKKKDSFDSLASTTSELNEEMKDNYV
QLYLNKIQEKVEDDEDNDEKKDKLRQKKKNEHEENEDNAIKGKVETSEYDTEEDAQEEKHYQQKRKQYINRKQKDKNEGS
NKEEEEEEEEEKEEKEEEGEEEEEEEEEEEEEEEEEEEEEEEEDEDEDEDEDEEEKEKEKDKDKKDKEEEDEVEEEEEEE
EEEEEDEEEEEDEEEEEDEEEEKDKEDEEDEEDEEDEEDEDEDEEEEEEEEEEEDEDEDEDEEEEKEENEKQETKEYKEGKE
EKQEREKKQKIKNKIKKKDEDEDESEDEEDTNYDEEDNKEYEKEDKDKDKDKDKNEDENNDYDEGKNGLTFNLKKESYET
LIPQKYSNENIKNYNTNKILYHDLKNKKKREISIKMESSHKNKEKLNKKIEREDNGDINDDKTSMNDDFKKKLYTDEYDE
DNEKIEKLIQNINLNVTKNSSYLVSFYNKLKKNMNIKNYNDSNNYNLKKNNVDTINKNSKLKKLNFNNIKKLDKLDVKLN
KYEKEKGIFNERKEINEFRKKKLKLFKSDDTKKYKETDDIYSKSEVKEKKSIMNNNENKNFIDENIYNEKNRNENSTEIK
YNSKLNESCYTSYAKKDNKLAKIIKKRDKKSYCNTHNDEYNNLNNSLEEKEMNTEGNELSYHFSSTLKNKIPNNVLKTIL
NKNNDIDKSTLTNFSSIDSDVFDSECEENSHPYKNENKEISEGVNNDKIKNVAKNINSDKFLEKGEKNFYKNNTNSKNSI
FDRKYCYKYRGSVINDNTSFCNNETINKKYNVINNNREVKKKESINYTDKYEDKKGKRNSIECEYEDVQKRETNIKEYVK
DDILKERRKKKEIQNLIINNRNEIKMYDKEENETNEKNKNSNEKIEKMFEKSENECKKDEKKENIIVNIKRKEDIKNEKE
KNKEVFRDILKIDLYKNEKAENSCKNNKNNKCEFFNSKTRKLNNCSSSIKSESTDVTERNANKENVRKDKFLLKDNYVDE
NNFENVNNLNELEISKENNICTYPVHLQNYEIKNMNESVYNETFINRKSNYLLSNNDVSCINKDNLLENKSINSKNTYLI
NNKTKNDENNENKKICIISTNEKNESLSSLNNSNKMKSLENSNTKDSNLTNNLALYLKDVCFKLGKEKQHSNILLKEKKK
LENEIKLLNENKLRYKKKIKNLEKNYNEKNKITKKYQNMNEKLKSIEKIKMDMPKDDINLQNKYIENTMEQLYNIFYDTF
GGKHIITKKIENLADVYIKKEKKMEIQMIAQKKELDLLKNVEEIVKKKNEYYKELLKKNEIIKSLNSNLTEITKSVADMK
NSIIENENKSKKLLIELSRKDTLLKDLETKSSLIISEKEKKFEKERTHLLELINDKEEKIKCVEQYKDEIKNLEEKLKNY
LDKNVNKINDKNYEKIVDKLHDQQIKMHSLLTQKEKIINEKNIQIENLESQLQSWADEATNWIVVADKHTKLIKNHNILK
KNYEELKFKYIMDMKYVQSTKNEKVKELIQKFS
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500 - 519:	EEEEEEEEEEEEEEEEEEEE

501 - 520:	EEEEEEEEEEEEEEEEEEEE
502 - 521:	EEEEEEEEEEEEEEEEEEEE
503 - 522:	EEEEEEEEEEEEEEEEEEEE
504 - 523:	EEEEEEEEEEEEEEEEEEEE

A0A1J1H8Y0 **A0A1J1H8Y0_PLARL** (597 aa)
Box C/D snoRNP rRNA 2'-O-methylation factor, putative. *Plasmodium relictum*

```
MKKLYLLFECSAGYFLLKVEEWDQIGTNENIEKKILDPDIFHQIVRFCSFISFETAERALDNLININEGKATEFLLNFLE
QNLPNNKSKYELGVTDLNLGKFLSNIGFNVIHNNNILELFRACRLFYLKKISTYVNNIDIDIKNFNIGLGHSYSRSKLKL
DPRKQDKSIINSIATIESLDKNINLFSMRVIEWYSWHFPELKKIVTDVCMYCKLVNLIKIKENFDFENNREKINEITQNE
EMTENISKVANLSIGQELTEEDLNNIINFSKEVINLSNTRNILWNYLDKKLNIVSPNLKELLGNTLSARLISHAGSLVNL
AKCPSSSIQIFGSEKALFNSLKGNKKTPKYGILYNSSYISKTPLALKGRMSRYLSCKSAMAARIDSFSDYPTNSYGLIFK
KQLEHKILHMIKGVKLSKNIDYMNEAEQIYQKEISIIEKDKELKKVKKELKKKEKKEKKKEKKEKKKEKKEKKEKIK
KEDTNEKEGENQKLNEIVEEKKKKKKEKKKGKEEEKEKEKEKEEEKEKEEEKEKEKEEEEEEEEEEEEEEEEEEEEEEEKKK
VEKKLKKKELKKIKKEGKKKKKKEKKDKKKKEKKSEK
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537 - 556:	EEEEEEEEEEEEEEEEEEEE
538 - 557:	EEEEEEEEEEEEEEEEEEEE

A0A1J1H9J5 **A0A1J1H9J5_PLARL** (861 aa)
Splicing factor 1, putative. *Plasmodium relictum*

```
MEDHLYFDAVEKLLENKNPNININGNIINEINENKDINNIVNNQYHNEKIENDENNYENSTREDETYILKNNSNKKYINE
KKKKNKEEKIKVSDDNKKENEKKKMKKKMEEKTLQNISSESFKNNDNKIEDNIMINKLNEKNEVYEINSSSESNNESVVY
IKKNIDKNIDVSIEKYDSLENRIHKLDERKSEIKEKIDKSQKKSKKNYKNSDDEDNKIMDPENSNLSNEEKREHTNKNEK
WKYDKDLHQSSGSKGNEKMKDHKEEEKEEEEEEEEEEEEEEEEEEEEEEEEDKNKKEKGEKKKKKRKKKSYSSDERSSSSQVY
SDNDDSFSEERNKRKRKSKNGTYYEKKMVEEYSSSSEYSSSSHEDSHNKRKRSYSSSKSYFSDDDHYCRSRSSKRRKYNK
HDKLKRRDRERERRRERERERKEKEKIKRERIRERIRRERERERERLRRERERERERERERMEREKERMLREKKREERRLKEEM
EEAKRDDLTVLVLNLSLKADERDIYEFFSEVAGKVRDIQCIKDQRSGKSKGVAYVEFYTQESVIKALAANGYMLKNKPIK
IQSSQAEKNRAAKAAKHQPIDPNDIPLKLYIGGLLGPLSNISEQELKQLFNPFGEILDVEIHRDPYTGKSKGFGFIQFHK
ASEAIEAMTVMNGMEVAGREIKVGYAQDSKYLLACDNTQENLLQKHQMIKKVKNEDIELDNEKIDNDDDDGGGLIAGAGS
KIALMQKLQRDNIIDNNIPNKYGPGPNALINKNSLAPINPLSNVTPNLVLSNMFSPNDNNIGSDPDFFNDIIEDVKEECK
KYGTIVKIWLDTKNIDGKIYIKYSNQEESLKAFQFLNGRYFGGSLINAYFITNSIWDTTCL
```

268 - 287:	EEEEEEEEEEEEEEEEEEEE
269 - 288:	EEEEEEEEEEEEEEEEEEEE

A0A1J1H9W3 **A0A1J1H9W3_PLARL** (967 aa)
Regulator of chromosome condensation, putative. *Plasmodium relictum*

```
MGQGNGKNKLIIQGTNEFLVDKKKEFCLLNIRNSINIKNIYNGPNNIIIIYENDDFEIVGLNNYGQLGLGDKINRNKLTI
NSILSKQKISKISCGYEHIIALMYNHNIFVWGNNDHGQLGIGENTVEIYTPLLIYFNEKVIDIACGKNHSIFLTESECEN
YNYCNNFKIKKNGNLDNSVTKKKDRQNYLSKLEININDEMDSKMKSKFTEDYSVEFEVQNIRKENKEESEEEEEEEEEE
EEEEEEEEEEKNNGEEEENEDADKEKYKHEKNNEINDKKNFKINYVNDVIKIIKTNKKKFVNRKISNFNIYSCGSGING
KLGFKSEENVYFPKKMEIKKKLKISSIYSSYEHNALLTKNGKLYTWGYNKNGELGINNNISSHKLKKINLENDIIIKVCL
SKLYSACLTKNNNFYIWGNNILKLKKINFSNLQISDFCCNEDNIIILTKDHKLFLLDSLKKIQNLNKLIQTKLSNDAKNI
NNIQYNFIGNGYNYLYAHISINKDINNMNNLNKKDYANSNPRETKQNINVEKETSLFLDNNELRNYDMNKDMQNLKTIIN
DINEEEKGKFKEGTHKKIEIKEVEKNPWIIKNKCDEKKQKNLIKENEEEKQEIKKKEEKEITKEERAKEEIEKEEYVDLY
MLRTNSDNNKNYININDNFKRSKNNLKKECENSNDLKENIKFHSFSNNGLHIEKREGKKINNKSIKSCSDEQIENILIHN
DTEKSMKNKMDIKYLISNIDYINLDLINIEDIYIDNNFLLNRASGIINSNINYIDYLTINNEQIGKCNNLNMKQNCFCSN
SGDKYINLNIMLLKELKKQKKINIFYNHLLNKLLNESICLREEKKNLKKKISCLLKINNSKQNTDAYEKKKKKNLNFCLK
KKYTFPLSLNPRDYNCQEKNSKYISSSSNISTSSLNNINKLINTEKKNVHKESNNLLVLDDLNPDLFSNTNEDKNTINSI
PIFFLNN
```

230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE

A0A1J1HA64 **A0A1J1HA64_PLARL** (913 aa)
LisH domain-containing protein. *Plasmodium relictum*

```
MKIHLSSDEINLLVYRYLVENGFIHTSFGFFNEANISKNPYYISHGEKLPTNALVSFLQKAMIYIYIEYHTDNNDGKKIV
CEEPFSFFRRHECWNNENNLSEDKIEINKNEKNLTNNINSATSSNVFDNKSNLNNKTNNYRNSFTNFASLNYNDSNISFK
DIKRNYANIFAQGKNSKKSSNKKKSNTEYINLNEKDESYSTIKKRKKSKIFKTQNKTNKLINEKSNNILNSEKKIEQNHV
IETKSEINETDNINISNKEYINKNNQNDLNTSNKESDNSNKKDSIISSNLQNDTIKKKKKKKKKKKEFYNLNDNKKIIKI
PIKKEKKNNSKNILKQKKQLKNISDEHMEKCSLMNKDDSNLFIYNNSDNNKSQNNEQNNNENVNKNNVIITNENPNKIDA
NLKRNSSISCYSVENNHDVKEVKEKNTFYSDSMYNSLDKKQKYKFSNSVKSYNYKNKLDNHLHTKRISDLNNRKINYINR
NDFNFSFSNYINNRKNYIFNKNKIFKVNKDLKKGKVKRERIKDSINQKNELNNNNNKEKLKKNIKKREMNKILESHHDKS
CQYNNKNKDNIEKKHIEENKIIQVNSDLKLKNKEKSIMISKFNYNQLINKKEYEQSSPKQEIRREVKEIEEQKEKDDNTK
KEKKEDNDNKNTNMEIEDEKKEEQGDLEEKKKDKCLYEEDYKNEINNLLLKKIILKTLKNGKKKFKINNRIKKKEKIKKK
NENNQDKDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDDEDEEDEEEEEDEEEEEEEEEENEEEDNENEDQEDNNDVDEYED
NNNEVDNDDKEDSNDEKELQFIQKRNEEKQAEGDENNDNEEKHKEKRKKQKQGKEEEGEDEENNNDRKDDAHKEWNNKKN
KEDDLCNKDNLYNEKNEREKYNHENSSENKEIE
```

729 - 748:	EEEEEEEEEEEEEEEEEEEE

730 - 749:	EEEEEEEEEEEEEEEEEEEE
731 - 750:	EEEEEEEEEEEEEEEEEEEE
732 - 751:	EEEEEEEEEEEEEEEEEEEE
733 - 752:	EEEEEEEEEEEEEEEEEEEE
734 - 753:	EEEEEEEEEEEEEEEEEEEE
735 - 754:	EEEEEEEEEEEEEEEEEEEE
736 - 755:	EEEEEEEEEEEEEEEEEEEE

A0A1J1HCS5 **A0A1J1HCS5_PLARL** (1508 aa)
Uncharacterized protein. *Plasmodium relictum*

```
MEECLNLKKTILTNLNQSFLTTIQDCESSAIYQNEYLDNNKYINKENDTKNFCEDEKKYIHEFDNIEKKEKKKNGLSFVA
TNNEYRTIIHPSYIREHNFENDKKYIDLSFVNDLIKIPKDEIRFRNKNSSDRKYNYTYNDKNNKKNYEFINATNEYYITK
NVQEKMSNTGITTEHFFCDNDLLIYEDDMKAWNDKSRYLYFIDKEKENIGNKKKTKFKNVHFKDSVLVDKYERAAYKNDV
FSDKIKIENLILDILNNNFDDIESDEDKKSQASLKIDHLEEDKLEIKKKTEELNIIKKKRIKDNKTNILDYLHYDNFFFD
ENADRISESSTSDNSYRFQNQKNISLKNYTFEKTEEEEIKNNVNNLLTKVKNDLNIKNFTNFIPEQFDTEIFLSDSEKFN
KYETSYSQKFDQVLTQKKIELNKEKMKQESELLQKYNYVDSLYSPGYYTRITQNLNKKLKEEKINIYDLKKKKIYDKIRE
DIMEDEKMNKEEENLTKLRLENINIYEEDLIIEKPASSDNNEEQSIKLSKNEREKDEIHEEDDDIDEEVSEIEDSIKTNS
SLNFEYLDHRSIDNLKKKYKVMKKSDRVYEDDLRRLKFYICNRLNKKKYIHKSKQTEKIIKKKKKNVKKAMKFSKAGYNL
LAKIHKDNQNNEEEEEEEEEEEEEEEEEEEEEEEEGKSEESELFEDEDKNSSDLNSSEYTYSSLTISSYEYFNIRNVYYND
NAIEKVFYYKDPKINITYLYSYVDFFLINKDTRISKGNFFIEILIYHIKLYENSTHISEDSLLYSFIINENTTAKIEKKY
NNISEILLRVANEGNIIINCCLSGNADQINLIFNSIMKRVLLVKYNIYLNSIYSCTYENAVHYFLLEENLLNLKNITYDS
NADKIICSYKKKMKNINVVNFSNRNMNILNLSEFLSFSNINQCNTLIMTKNPLFLDLSFEVIKKDIDDTIIFLKSINLTE
LVLDFIDLSNSSAEYFISNLILNTNISFLSLMKCELNEDNITNIIKIIKEKKGNMSSTINYLNVEFNNLKYFDILSLIKI
LFELNNDFKKLYIYGNFIQRDIFDTSFEFKRKKKAIEMDKYFKQIPNIFSFNNIYEIKNYFYCNLRGFAQLYEGDKSMHI
FFELYSIYLYILRPEIKLYIIKNISVMKKDDLSFVLIGALFNNKEIKFSLKLFKHNITSLFYNTVNDSLLGKLYYYEQIN
SNREVNENILNYFIMRSENEINFYHYKINKEEIDFILKLCKDGVVKNINLSYCYLTNEDILYFNSIKGSKYGIKTYKLSL
SNNFINSNLPMEELINFLLNFSVYFKINLSDLKIGKSPNIHELFFYLLNNTKCKIISLDNCNLGNNFLINVNKNIKKLNE
NRYINLLSLQCNSFNNKRELINFLNNLISKCKSLDKIKIYSNSLHKENCENIINYVSKKQKVSFQNTYDTPMYKRNLKKK
VSKLKKNKINNDIEYNTELTENEMNIIKQFFEKKQNKEGIIGKKDFKIKSRYNLMDLKNRKIKYNFKK
```

652 - 671:	EEEEEEEEEEEEEEEEEEEE
653 - 672:	EEEEEEEEEEEEEEEEEEEE
654 - 673:	EEEEEEEEEEEEEEEEEEEE
655 - 674:	EEEEEEEEEEEEEEEEEEEE

A0A1J1HI06 **A0A1J1HI06_PLARL** (1657 aa)
Uncharacterized protein. *Plasmodium relictum*

```
MSKVVDELKLFLTNLSRGSDTVDTDDLLNSGIADKSVILNIKAKLGESPWNIQNLIDLGIDIIQKDNENELELKHDSSDN
IISEIENESESDIESDDDFYIKNIKFETCENIEETLKVMIQENAINLHPIIKEFILLLVFLFSCIRKSNKNNLENANKFF
EKITNKEYNNDEIMNKRSFKNENKTKIKYTNIKCENNEAFYTNIRSKNNALNDDISDNILIESFYKNSISNKFYCDINNK
DNFNSNENLYCKDVYSIFLNLNEKSIYEYNIEDVKQAFSIENLNKVCETFYRHLHKVRKMKNDQLIKKGINIIMVLLYLT
YVYFGIFFLKTKNLYVKLYCIDKEFRENKIKNEEIKNNLNKKVEELLNQLKISEKYFEEYEKYKENFNEIKKENEKLKNT
NIIIQKLKKKISLMETEKLMIIKKKEELEFIIKQKNLLIESNKAKKNEKEIKKPELKRTKLVLKNDHNNFNRMKSITTKS
ENNNVKSVYLLEEKNNTEIQQNIKNKEEDYEHIIKKKSILTTDKDTQTLNHKKEKITKDKETETMSEIKKNKISRGVQTL
KCEDFKKINRHVLNNQLSEDKKKKKIINKLYEHIKEKEENEEEGEEEEEEEEEEEEEEEEEEKEKEEEEEEEEEEEEEEE
EEEEEEKEKEKEKDRYKEQKEKENNNNKKSKELEGEIRKEAKDKIKNEVENKERKKSKEHKETIYKKEREILLFEENNKE
RKVYKNIKSNNKYNDIYALKDINEPFKQSSCLLNIKVKEKTENKSILNYVNHFFILSDIINIKRKKEKLIKNSYKKYYLY
LNTNGFKTNDYIIQNIVNMNREILIESMYDYLINKYDIFNRLFEKIFFYECIYIFSNFFLNEEIIDSQRLIDNNFYNIIS
SCFNYFDELSKLTYSIKRNIYLSEALVNSHHVDLNNIFNFNFFEKTKFLNIRNDNSNFLLEFFYESLAFIDVKEESNLSE
ELNHFSIFTNEMDLPNLRNNFRTSDFLNDNFNGINEFNKLNKERKIKKCNVLNKISYSNNCIFFSKYSSSHDYYCSNYNY
IFHEENESILIYNKIDKLSENKINIEKENTELLKKQWNNPKLFNSSNRKIVGIFNEKYKHKKNNLLFKKKIYSKKKKFHK
YYKHKNKINFYSFNEKINNSYNKNGNNDYLLNENLSRDNLNIKFTNFFINLNNQILYASLSHYYNIFYLFKNNNSNVENY
NENYKKRKRCKFKSNIYKKKKNIKIILPNKRENEETKVIKLVNNYLYKKRKASLKKKNILFRRINCKNKANGSIHKNDGK
NENNNDAYKQHNRRNIMKELKKKYFIISKKNLNIPESKASKELEGMCKGYIYKSYNKEKKIEELFLRKYNIKKHKKKRRF
KRKMIEHFNHNYKFHTIQNARKKLTFNICINLLKNTSHLFKEVFLSNIKNYSYLSSDDNIITIKNYDLKKKSVCSKINEF
LNKKYNTYNLKDYDSLLYCSQFSRIYNTLISLKKRNYEYLKFNKYIDTMSAYKSNVLSEHKLKKKKEVILGKYDKCVINN
KYSEKRKEKNEKTKRISNKFIIRKKCFDKNTNTNYSYYLLLTNSIYILALSFFLVFLFLIDVYFFNNFIFSCFVYILCFF
LLFIVSLFRGIIYTINIFLKKKVISQDLLDFFSIHFVEMINNIRFYIYENSNNIDYT
```

626 - 645:	EEEEEEEEEEEEEEEEEEEE
627 - 646:	EEEEEEEEEEEEEEEEEEEE

A0A1J4MCS5 **A0A1J4MCS5_9CRYT** (604 aa)
SET domain-containing protein. *Cryptosporidium ubiquitum*

```
MSSYYESNTGTKLRPVVDFGDDRWVTLSTAEYKKTLIRKGEQNIESDYEEEDGYEYHEEDLEDEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEVEEEEGTDEEESFHQEFNDGSEGYYRGTKSNNDVSIYPEMIRYHFKEAFSINEGVEAREFGFNEDDAE
LEELVVEEEGEITTDGHNIDEAEVVPDELTQPWDLESIRENVEVKYTESKGRCLYARKCFNPGDIIFAESPLLVVTPELA
PELSEFLEDMNSKETFTLPPLWHVAALCTLTMLEDEDKAICLDKWVPDPAAEPSYDVKKIIENTGIDVDPHLYERTLNAW
RFNSFNHTSNNGIVLYNVISMMAHNCGASCCWHYGVDNTFVLRAKTRLEVGDEITISYISDDDLFKCSKTRRELLSNWLF
YCRCERCSNPTDLSRGLKCASCGVGSMFFKEDENGVTKSSKCSVCRSQPDREIIDSYTDLESQYIARLEETHKSDVEDVE
AVYQEAQKVFTQHWIMYELDTMLFEAYKESQQFSFALSCLYNRLNFVRNVLPDCTYTLAWITEELGDILSILQDERHEGK
SKTNQEVSAIQRYYYDTWCYLSILTGPNHHFTIAAKNKYEAITD
```

64 - 83:	EEEEEEEEEEEEEEEEEEEE

65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE

A0A1J4MEP9 **A0A1J4MEP9_9CRYT** (1058 aa)
CRAL-TRIO domain-containing protein. *Cryptosporidium ubiquitum*

```
MVKEDIIVKCELKNNTMKEFSDSSSQEKIEVGDLNEIELVLEKQNLSINNTSGYPEIFDQLSNTPLNWDLKIYEQFFNLS
KNCIKEVYNYKDIQIPNETVENCFKAMLSPLRLLRFLIGFNFNINNAFHAFNKHIKWRKEFNMDNVVRPYVITNMVPNNN
IEMAPLHNIITRYYPCNLLLRESTHEKTPLKDFYGNIICIERFGLLDETRLLGAVKVEELLLWYSYHMEYRSILLDNLSY
EVKSLVRATCIIDLFGLSISQVHSSHMITILRRMIQLASDNYPEGMSYVIFVNSPKFFSIVWNSFKSLLAARTVEKILVL
DEDYKTKLINIVPISNLPQFLGGLTTDQFSTVPNTGTLLLDCFGLGDDRQTLHIKRMKKEKVSISISKPNTKVFWTWGVL
DGEISFSAKYFTDKIFTSLSNEKTRNDFCHSGDIDKQFSSNNNFLSENYDNHPEFKINISSTNDLNNTYNFNTSKRSSKN
SKRLSSNNITSPVTSMQNLMNQEITLVPMSKFDSTKAYGGSYFSESPGYLVLQWDNSWSLFSAKTVHFVIKTSNTALPED
HNDNNSNTNNNDNDNDNNSGNNNDDINVNNIDSNINDLSDISNLVSHNVALTNITKKRPSKSHKSVEKKKINSKRNSKVS
NKSIALVKMDDNISMPNMDKSNNDYLMSKPIKKGKQKHKSREGNTHNISDYKKNNVFNENDKMAITSILNDKDQILDSSL
NYDIDSNSECQTNYSFMTAYSGVDEILDLFEYNKNSLMNLNTYKKKINQTDENNSKDKELFDKPLKTSVNYKLTELNSNI
IESRISVKDLNRDDDNDDNGEDDDVNDEEEDKNEVDNDDEEEEEEEEEEEEEEEEEEEEDDDEKQAEEESNSEFTSSQLS
VDETGECDLIVDSLNSSNCSNSSKESFNREFNLGNKCLNVRNRNLLSKNQISLETSINIFGFENFGFESSQEYKRRYDEL
LDYINSTLMLESTKNQEFYSPQSSFIFTDKPKKASSPIFECKFGHLHHKFANIFIRSRKNNNRVNNSSTSVKNNNKNIGS
LLKNTLFTRLRNKFKREK
```

840 - 859:	EEEEEEEEEEEEEEEEEEEE

A0A1J4MFU0 **A0A1J4MFU0_9CRYT** (6474 aa)
Uncharacterized protein. *Cryptosporidium ubiquitum*

```
MLGSTIIKSLIGNLLEKLGSDLLGTWNLAENIEINSFSPLDIELKNLPIPQIIFELADLPFIIVYSNIRLVKVFLRTDQM
PSEENPLNIEAWDVDLQIRLASLDEWDSKKWCKRLLKSKRKKILRWYKYVSPWSTNKVANQISQSLETSIVNSLNIKLHN
IHCMLIDDHLGPNPFVIEIVSDSFFIDSVNDSKVLSQEELQGKKSNLLQFLWIRFYGFKVIFRKFDHLLLTSVPKNVVTK
LVDIEGDTTTALGEDDETGFSNSNQHDSSSNNHNQSGFFSKIKSLLPVFFSSDKTEKQKINFMSNFLCNYARQDSSQFEI
FRELTDISVGSKDYSQTEFPKHTQNGNSKFIKLPEDPCSCVQVTKDQGIELHILFKRWDIRALNAPHTMFGALFKDEEQY
NKYISSREWKASKLIFLPNSEKHLVRPPSVDDFPDETFELKCTEDIISVLYNFINYFNQWSSFLKASQYIYNNRKTHQQL
EKYLSLIISYNKGSKGNAGPKNIPKNLLSEIETEISIRDVIALNMSANEFLKESYSSKGNEFWGSLNKNYNIDPKVLHDF
VVEKVLLNKIQDHDQEKGTQDHKNWIPESKHVDSMKFSTFNKWFSSEGKLHVNIPKARISVIMSDVSSISSKITPVPDWM
RPLLFTKTSNESLVGKISGLVMEFDLNMISDKISFYHRQTLIDIFRFEIFENEFGLVCGLIKKCKPGLENSNSNSISLMK
IPSHTIKIFPITFLPSIRVLEIGVREKSFSKMSHNNSRIGNENDHSYGNSMETFANKRFKEVTKISKLKLVDLDYKEISL
NEKKNHEKMQVRAGLHIQIHQLFGCTVFKDNKKQDFTQIPGFSTDLDYYIIWDEYLPHFNLTTLKISDFNLHDLKSIWKI
GNLIPNVTSNINSIISRSQKEEEITLVKSLMAMMNLSSKDNMIFSVELHQINISSRFPNTINSMSRYSTKNLCLDKHLHD
TLSHPKCLGCNISPKGRRKSTANNIKETPDLGLITFKVENDLTKLNGVEENVEKKVTRIISEILTSPEDFLQSLKTYRVM
ESSQSIFRGVTGLTLNSSFGNLASYDYEEEEINHISESLLYNEILRYLLQNEYFIEENVSFTGTKILVSGLSFQIWTSTR
TLSLEIEGLFISMLANNIKVVTHDLRRDKIDDDEKLMMTIKQVDNIKEDQLKFRKEKEQIIEFFSLKNVSFNLFDNKMDL
NLSKTSLNVFPAIVTLINGYELLIFPKKSPLSDMKKVFENILSFNKNKMKKTNNTKAESGFLESLKSLNLKLGEISIQIY
DTECLLYQFCLFNLRFKYISNLNNRNRAIIDFSLGEIFIQSINNIILKDQNMGYQQIRKDFSGKHFFTPSVIFSKLSGHL
IPTSQIHSKKNSKNHFPYVLVYPDAFKNNANRLGTELNASQDPVFHLEIRIRVKEVNLDDEEKENKDLSLGKIEYTGGED
KDGGANKYVIIMNSKICNGHFFFTDDEIIRLKSVLYLYKRIFNKFKEEKNILWNSDFVLERESPLEAYKLAKLNDTDCSN
NININNSKQPDKQLVSESSDFCQKCGGIDSNLMGEPKNKDEYFVEFILSFENFYTHLLVNSDKLYKSRLLNNEILEIHRE
AVEFSNESLTLVRPLYCFNDQIFDSKRCNPRTAVLTAESIGLRLNFCIQTSVFTQCVSRDKLLESRSGFMIPQIEDQNSC
VREWKIKTGFREMNIMVIRNGTWGMLDFSLKKMNLKLVIYLSNIFEYKNNKQSEDILRRLFECIKLILKKKATRIVKIKF
KIRDICIWSILYERIKSNGSSKQSNGTITTSSTVDMYLTKTSSSLDYVCLSPLKNSLSEYSSSMLPEYITVDRKKHLSKE
SIEEELFPSWEYGLSLPLPVPFNHPDLLLNCKPKIFPVFGKRPIEGGDFELENRYKKCFKSGKEVYIIPIITLKSNEVDF
GNSMNSPISIEITISPTFLSIVPLVFRQLIDISFMYSKFKTVNLDESLLGSKKSGRSYLSFKAIQDQKTLKSQSIFLNTQ
KTQEEPKNEDTVTNILKSFKNIPFASLEIKSKFNTMVIIFPEFNDLEMSDSISSRYFESYSMKIGQFKEGMDFLLGSKAE
ESSEKKSENSIKSNSNIKNDDYYISVFSNSYHPAIAFSHNLNFLFALDTEEGEESLDHESLKISLEFSQLRVQLPFVKNI
GGNYVMDGMSGRIRSKDYFKIGSEDNIEGRDPILDIFIPSVTSCFVLSRNIQIEKDTDFQPSDTYGMLFGMINIPIVFAI
DGARIPVMDDTFILRKYALRKNGGENNLSLLVKDREQVQEEGMELKGDLNSEEDSCFANCMMNRPELLGIIINALGDHYL
QIQANMNNFRFIFSLTTFSVSAPYIQRIKSWWNDIWLIRMRYPRCKGSTMRYFFVDTRSDTINISSFGLTVKNNKLDYLQ
EDLDQESLDHENNVEDKEFKWRYIKGTNEIYNINRFDYSNYEITSPLFFPLDESIPIVLALPVTAWLEDNVRPWNSLEFR
AQDNSVIQFDDRLKSFNLGILQEERKNLLSKSKSFVKGNSSISSVHDLVQDHLDLSQNITNHISDTKFQSVLKLDPFLVC
QCMQENNSSQMRSNHSESNMVHNDLAEFNSDEDNLARLDYRFSVNMMEVVGAGGRRRRSMNSEDIQLLHHDGSFEYFNSA
YPNKISKSQRKGGGLFNGWNTFKQRLSSNSSVGLLPKEDLNFDQFEFNNNYENSRAIRGRQSTSLNSHLSHSSKRRSFSL
FKRRSSNEVRNNSQNGYHPNLSPINENNPHHNNSKNDLRSGKDLKQNIGIEEEKIFKFQISLSNLEIWFHRDNTKENMSV
ISRENLTKDEIEQLTLEEVAVDWMSKAVYCVPASKSKREKKQNKDVFKIQILDHHEREVGNADPTFNSHDYKPEGEEEEE
EEEEEEEEEEEEEEEEEEEFIENEQNFDKVYDEFEDVYEAGEESLVVKVKRPGENENNQVKSDLPIKNKEVHFFDLEEEG
DEIKSKKKRRFRLNGKDHGESLRSRKLFTNSYEIFAFRKSISTYDQADYDYIIKSNRYGKRQELAVHRYLKLSYSNYYIP
SIGIDNKLIKAVESEPRQEFGSGSEPKRRQEALRYKIRRQDMGIRGSGKKESQFMSGTAFSILLSFEINTEMMNETFQLS
GECNEMRILPGFPVKIKEETLVQFGVLPDISGDKKDLKKNCLCNYCRITSLRRYLYLHTLNGRNIYLGLSKTVPNYIKKD
FLLFINHLKIFSSPNGIKKSNISKHWTSYQTEIEIVIDEVTISISMDILQEIKLFINYYNDIKDSILYYSLAYSKSGKSY
ITPEAILNPYLIQQLSSLNRIEDQVNTTYCRRSILNQVLPTITSINRLGSNLKSSYKDGENDISDEKDTYIESRDVSSDE
FSVSSSQSSKSSRSSNSMQENQVILLYYLGFPLPHSNINFIPESVKRHLKQERLNYLNKSRRYGIYATKNDSRIPYSAGD
FGRDSELIDPVIGEKVDSKDDSEQNKVLLSENIIYSIITNLIKYTSLSLEWIFKGLKDQSYDSIPNIFDRYQFLSLLKLP
KSHFEKIRQIIFEYRLSSFNIVIHNDNIDILKLSIDNTRCQIKFPEQISCKLAGVVSAITHDPIMDCMITIVRPFPYTLE
MSLSKQKENFEGNIVNYKNISLSEIDLANYYLSSRSLLDLSPILEVDFCTESISLELTSGFLQNLRLILSDLKNPHLLGL
VHAYERRINSVRIINDIGQQSFLIIQPVSVLVYNRESNDKELMEEESTRKGKIKKRNMREEIRGLRKFFLKSGDYCTVSIK
LPVYMAVEKFTHRKGQKTAARIQANRNSDYNRMAFSLKNQYHNNNRLLHIDDHEQHLNGFLNITSATMNGGKIDYRKKVK
DEKDNHVINFERLLDKRGRDLDSLETKNEKNLKNSSGVILSDIVNELCTLGIPKRKKKLGVKYLWLEDKKSELLYGSTGL
AESELRQLAEQLELTTPALGMASEGVEMMIHRFLISQSTWSSIGKLKDDTLYRRAYRLGILGFLLVLEPESGTSPNEWIW
TLGTCVQIENATNTVFRVTANWRHGIRHLCGAIFTEPSKRNKEKEYSSMDNQHNHRNDLIFSKNDNLNNGIGTDINTVGT
NKQYGVKYKGNERKDHDSSSNRYFPYIDIPPYSRRSIPLSWFLLSDMEPSIIPILDYNDIDDYDDDNVDENDHHIHSNEE
NIKRDFSYKSFGEDEEIGGSVNNGGRLRSQNDHNDKKFFSSVNKQKHIHKNKNKNKDTSEDCGAGTGAVTGAGAGAGTGA
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GARKKIPVDKKSVKRIQSRLHSIPFTILKMLIHEIMATQPGNVTKAKLVNEVSSLTFESLMAFNCQVECMDIPTSDKYVT
SYSYSIKLTPFLKLTNSLPFPIQIRLKMAGGLNLPALVGAVHDKVEFDIPNMADFTENRLRSLGLLNSPSLPSVAIPNGS
LTTGEFGSKFCSGDWKSHSVNKNSDSNYSRLRRVYQREFAALIQFLSGKSVDYIIQSQQELELPICRQKINLVIYVNGSP
LEYCSYPLFTNTHESTDYIQSCNAQISEFIYRSEHISISFPFGSTISHNVSLRRVSGNPFNAWNPFYSQLLQEFFSNIGD
SGREKLADAISNFTISVSTSTKRILFSALSRVENTTDSIICLFFNDITNTNNSNNINSNNGIIRKEGVIKIKNANHNNKL
MEEQEKQEQEILDLEKGYEEGLKGQVEVEKDDKNDIYSKMDRSEIVSLLSTNYKIVPLPPMYRFFTSLETLKNMRIGSFT
LDFFTKNLRITTRVRKGSISGWTEFNKMVSSNLLINYISKLSSKYDFSYLGTSYSIKLPLNPISESKKQNKEEEQQTVSI
GVITHNNDLLSQLNCPLVSFYNKYEFVSQLPFPIVIHKFTNSKEMHQTIRTKHSKPLDLESDMRDASIIFFRNSKEAEDY
DGNHYENDDHLNNGSNNLNQNQNTAFGGENLVKDQITGNLDSSYISRKFESKPQKASKSKKKYHRFSSKDLKLPPKTSLS
CDGVLLRPNERRPYHGNDPNVWICKPIIEGSSEPLQASKEFSLFSGHKLEYTPQLNKFQIILHPQQIYPNHQKHDHHSTI
GTNQTLSSGTHSTVGNSKSIHQTQTIGSGGTTITQINASNPLTTTSALNELENKNPLLITIQIIPAILGNTTSGSTSLRD
SAYFVIFSVAEAPFFEICNLSNYYIAYDTPEISKSHNYYYRSKKAVLEAVSVGTSQLEDFSRTMTNNNNDRNSANGVLNQ
IKSKKKTYVNHTYGTGYVYPDIFSAKSADISVIPPKTRIPYIPKNWDCEFVGIRPFNVRKSAWTTHSVTSIKDQISVISF
IKLNEKITKMNSNQINVKHLSGVNQSHNQSQLQDSKISNRFQNPFTSMNIVSNTGLNSMQSKPKTGKLYVFLMVNSKGTR
VLTIMDSRKYAEKLLNGNILSTSNSSFWDSNIENLLSLNSNQYGTNEENDKRIRKDVKDQIISKQIQSENGFEADFNPRR
KYQKTNQLPSVRQSRNLSNINSTDTKSRDNLRENAYTNVISNSSGNKLISGRWRKISCIGFKVSFFIPRISISWIHQNEL
VLVTHGSLFHVSANILPQNIYPMSVMNIVCDSLMNICYKLVGFSENKDYHKNPKIDSKIEKLRIISQDHLNSNKASISNQ
KKNIMALFTDRVNNLFNNTNKKKQIFGKTIQLDGDSDSQLLYNNSGEHNRIDYIWRKGHKIKKMLMNRLLNGENNEHINN
FNTELDEENYEIQKKQSEGIGREGEEVGEVGRELMSIYTGSNIYSHDIRNTRNNMSFPSTSYNSYNKGMSSLNDISEERQ
FELLSENIKEIYQFLSRNLNSIGGSVSPKENPTLNNVLKLLRKVYKNCVSNEKYIKKKLSSSRFYGDEVNEGVDDGLVSL
RSEFRTSIVGTLDQLYKDNDETDHLGNTYDQDLSLKYYEIYDGVLISLIHIVVLISNYMEETLLTSGKIILNLGLSSIHI
DHFLPGDIPVILKTSTNNQISDRTESIRQIKDSEMKDYDGNENLNINLEYDKQEEKLGKSNKEKKNNIKGGNNKKLNSVN
LRDLNEENIIENEINVISDGGGDDDLGYEEFGSNSEDFMLKYSKHNGNFDDKIVNINNGKNLESKFFSLTISRSLMSPMY
APIFDEINITVSQICCNLERLVVQTLYFMISKEIENMNNITYSRQKTLWMHSSRQKMVKKKSHREMNYLGSLVCYVSGGY
GLPMYITRTPWDQLKIGKPLYIRTLKISDIIVTITIRTSDDTIDIDTLTPEALLFMNILPLDTPHMILNVNSLNKNALVV
DIAEFFHFLVSSYSRQLKRRVLPSLGVTHLVAIYSGIKRGFKALFIEIKRGVTDDDLTFVEGFIQGFRVGLIHFFRYFLG
GAFQTASVIFNFGHKLLGGRRPRPKSILDAIWNGIVGMFMDTFITPWILLYRDPTESFRKTNKKSLFILTLIFSIIRIAL
SSLFGALNLLASITESLATTLIGDFEQFVHVKSRAELMSEIEKDRILSQGKEEKKFMEHNTEDQDFSDFESDKE
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2876 - 2895:	EEEEEEEEEEEEEEEEEEEE
2877 - 2896:	EEEEEEEEEEEEEEEEEEEE
2878 - 2897:	EEEEEEEEEEEEEEEEEEEE
2879 - 2898:	EEEEEEEEEEEEEEEEEEEE
2880 - 2899:	EEEEEEEEEEEEEEEEEEEE

A0A1J4MNT1 **A0A1J4MNT1_9CRYT** (105 aa)
Uncharacterized protein. *Cryptosporidium andersoni*

```
MAGDKRKRDIESENADSESSEVETTNKKHSHQDDDNFDGLPEEEEDYEDEDEEGGDDDDDDDDDDDDDDDEEQEFDEVED
NEEEEEEEEEEEEEEEEEEEEEDE
```

82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE

A0A1J6ING5 **A0A1J6ING5_NICAT** (168 aa)
Uncharacterized protein (Fragment). *Nicotiana attenuata (Coyote tobacco)*

```
ISFKLITLKWYHDGVLVLGNFARYERGSQTLTLDVDVDLLSFFELMNYTKLYKFKNMVELYSCPMDRTDKLVNILIDKDI
LDICNELEDEDSLDIYVTHVVPLNVVDINETSKGVGWSNSGAFKSTIVLEEEEEEEEEEEEEEEEEEEEEVEDSEPEPEP
APAPAPVP
```

130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE

A0A1J6K2V9 **A0A1J6K2V9_NICAT** (394 aa)
Uncharacterized protein. *Nicotiana attenuata (Coyote tobacco)*

```
MILESFDGSFSDEYNKLKAYAIELRDNNPDNDVVINLSKNALEERRRRFLRMYICFQSLKMGFKLGLRPFIGLYGSFLKG
KNHFYPLTWAVVEKDKEYMKLVPTFASTFSVPNDGEGITFMSDMQKIYNTGESKKLLWKCVWSTYEEDFKEQLKNLEELK
KDAATGLAYLDTMCKNQSIDNNLTESFNKVMNLLREHEDEVRSWRHDFSPKSMELYSEYMQIAQSAYRVNANGENGYEVS
EGSDKHCVNMAMKKLKKKLTVQPLQSVNQVKIVTLGSCLHLELGVLANGARNWRLIKMLYQKVPISTGRRSINFTGDHTS
VSDPTNLPYSPPSLSWKGKPGTIAKQLEKQRQQRIEKLRLKLEEEEEEEEEEEEEEEEEEEEEEEEEDILHKL
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363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
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369 - 388:	EEEEEEEEEEEEEEEEEEEE

A0A1J7G4C8 **A0A1J7G4C8_LUPAN** (401 aa)
Uncharacterized protein. *Lupinus angustifolius (Narrow-leaved blue lupine)*

```
MRVRQGEEKKFLPILVCALLQFWTEKSRKELGIREIEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
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EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDVLESCLFITLIYTLLSGSTFTFTFSEKIVFGILSNIKVGF
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37 - 56:	EEEEEEEEEEEEEEEEEEEE
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A0A1J7G572 **A0A1J7G572_LUPAN** (1405 aa)
Uncharacterized protein. *Lupinus angustifolius (Narrow-leaved blue lupine)*

```
MRMRRRRRRRRMRIGLDDDEDEDEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
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A0A1J7GBY8 **A0A1J7GBY8_LUPAN** (112 aa)
Uncharacterized protein. *Lupinus angustifolius (Narrow-leaved blue lupine)*

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MSRWMNGPINGRRCEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEACGRRCEDEDEPMKTRLDGDRRCRWKI
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A0A1J7GSH9 **A0A1J7GSH9_LUPAN** (336 aa)
Inositol-tetrakisphosphate 1-kinase (EC 2.7.1.134). *Lupinus angustifolius (Narrow-leaved blue lupine)*

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DVVLHKLSGKEWREIIEDYRQKHPEVPILDPPDAIQHLHNRQSMLQDVADLNLYDCYGKVGVPRQMVITKNPSTIPYEVT
KAGMKLPLVAKPLVVDGTAKSHELYLAYDEFSLSELEPPLVLQEFVNHGGLLFKIYIVGETIKVVRRFSLPNISKHELLK
VDGLFRFPRVSCAAASAEDADLDPNIAEHPPRPLLERLARELRRRLGLRLFNIDMIREHGTKDVFYVIDINYFPGNSLAN
ADVANAAIACHAIYCD
```

8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE

A0A1J7HA65 **A0A1J7HA65_LUPAN** (63 aa)
Uncharacterized protein. *Lupinus angustifolius (Narrow-leaved blue lupine)*

```
MEQKEKIRKEKEKKKRKRRKRRKRRKNEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEGEEEGKN
```

25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE

A0A1J7IQY0 **A0A1J7IQY0_LUPAN** (313 aa)
Uncharacterized protein. *Lupinus angustifolius (Narrow-leaved blue lupine)*

```
MRDEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEDEDKDEDEAEEEEDEAEEEEDEAEEEEDEAEEEEDEAEEEEDEAEEEEDEAEEEEDE
AEEEEDEAEEEEDEAEEEEDEAEEEEDEAEEEEDEAEEEEDEAEEEEDEDEDGDEDRMRMKRRVEEEDEDDERGGGGGGG
GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
```

6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE

15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE

67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE

A0A1J9PFW5 **A0A1J9PFW5_9EURO** (1014 aa)
Fungal_trans domain-containing protein. *Emergomyces pasteurianus Ep9510*

```
MATAAAIKPPPTSRPLASTSAPPTTLPPPTTAAAPNSLSSNYHNNNKTITPSTTNAPASNTAFTSTSGPGASAGVSACAG
ASALGGIPPRSAARPANYIITSRQQLQQQAIMNNSVSNGYSVAVRAASPITTTTTAALSSTTGSPAANSARPICDACYGR
KIRGATDEAADKSYLCEFHRQDCTFNYPTQTRVQTASQLGKRKFQEESRVGPSTEEDANEDEGIKRHATEQPLSPTTAFS
MSVSRRQHPHPFSTATSIGATPGSSSLEDSFATSQHIGMTTELEPLLLDFLTLDHNNESPLATSRVRKLAPDGTFMRVID
SSLARQELHTSSIEAIENAVHPFGPILVDKFFQHAHPAFPLLKEHTFRHSYQTRQNLSPVLLAAMYFITLKWLEPGTETG
PGSDMQTLRKPDATHLEAMATRLLNESLSQPHISTIQAGLLLSQKWNFNTPTLIAQLVTVGHDLGLHQDCSSWNIPACEK
GLRKRLAWALYVQDKWCALVHGRPSHIFATNWAVKELSAEDFSSTGPGALLFRHFVTLTAILSEILDTFYTLQATSEFSA
AGPQRTRIILERAKPIQIRLKEWFTRLPDQLRMDHHQYFSSRSDSSSSSSSSSSNAIANSMGVDAITNTNTTPNKPDHPN
FNGGLHLAYFATEITLHRSIIRSLGPDSADPYLSHICRSAAKTRLISAMDFVNRLRPAHLRAFWPSASRTNFALISSFGI
LLRATALTREEEEFYRMRLGEYRWTLSVSCKDAKFLAGAIEGLDVGMCLLSNVPPKKGLDEVVADGYAYGDGNGNGKGKG
KGTGNRDVITIPGGGDEINIAEDEEGLDVDPELEEEMEQLEEMEEREQEEEEEEEEEEEEEEEEEEEEEEEEEVEGVDVYSF
SSGEYSEEYPHSGHPKPSPVGALGGGQGDRLGQRRGHGGLGSQGSYQPGFLDNTDVDPSATMNNSRRPQGTRELASRKLN
GRRSGNRNLGQSNRNANGGDRRSSSLPSVVSGLASPVTSMEGKRERERAAQGGR
```

849 - 868:	EEEEEEEEEEEEEEEEEEEE
850 - 869:	EEEEEEEEEEEEEEEEEEEE
851 - 870:	EEEEEEEEEEEEEEEEEEEE
852 - 871:	EEEEEEEEEEEEEEEEEEEE

A0A1J9PQ52 **A0A1J9PQ52_9EURO** (1059 aa)
Nuclear pore complex protein. *Emergomyces pasteurianus Ep9510*

```
MAPLTYSSGFPLGQHNVSASPTQAPPSRLHDVEIIEIEDDDEEEEEEEEEEEEEEEEEEEEEDNLDDNLEEEEEDEDEDEE
ADEEGDDENEQDDDDMTGTDSMEDRSSDFEESEQDAITISSGLASPGLLTTSDIQQVLNPLRNTANRVTNQIEAFAQSLN
QFKQHCHGRPGDPETFREACKLVKKYQKIAATAAEELSRTNNLRKVKQSAINRDTGAGQGPNRGKLDEQIRRWQLEAETW
ELLLQMLSNDDPESRSRSQRAQHTVLQSLHRYSSDQEVWNKFLEADHFALENVVVLKWLEKTARSSTQDIDGLISELETQ
AERGQGLWAHGWLYTKEAIKGAKRLRSWPQPLEPEDPGLSISLLSSEKQEPLVTQLDPDAVTRQQHGLQKQDQFYEQAAW
LTCWKMLRQGQSWKKIQEWSHERLENWRAISVCGTPTEDENNAADSSLTRLMSCRSQESWRSACLALANNPVTSNFERAV
YALICGETEPCYAICQGWGDYIYVFFNHSILARYREFCKQFHRKLSFSPTTDMTLSLEPPAYDNIYTFLDTVKQNDRTAV
EARNPYRTIQAAILSKNYDPFFFHQANAISKAASLSNKATLVPKTVIANVDDASLIAARDEDAIRIICHLFLILQSLGYV
RSDSHFVQTASVNVIGYINLLRKAGKLEFVPLYASLLPQNTAHVVLGNVLIDIVEPEDRERQVTIMKRLNINLSAIVESQ
WQLVTSQADAKEDKTTTIRLKRSVIQQAKGPGRIGPIKKNLIGRRISNEDEYLIRCLEWHRYTDDQLPNICPRGTHLYKR
FMGAGRLAAARELFNRVRVDMVPGDISGLGHSAHEILANGSENGFDEPPSPVKASPTKSPMKSGIQRRRPLSSNLRAELF
LQSHTMRDLEYLIAAFDSLETWAGQMDQYEHLSDKQQAKEFRKKLQVTIDTITERIEPLCGEWLSYPKDDAEATELEFIK
STYLPEVILAYHSALFFAGHTIGREVLAQCMMLSSVIASSPSLTNSFMASGRMCELVDALALSSIAMMSAKDSKLKKKLE
DGASLDIWRIKPHQDGEMV
```

42 - 61:	EEEEEEEEEEEEEEEEEEEE

A0A1J9RF31 **A0A1J9RF31_9PEZI** (151 aa)
Uncharacterized protein. *Diplodia corticola*

```
MVVFCFGALFEQFAGPSGTYVTRSLWPGREPTPDSIPSPPPPSPPSSPSRSRSRSRSPLPDPPKRKRAVDDDDDDNDDDD
AAAATSTPSPPRAVKRRRRVVVDDDDDDEEEEEEEEEEEEEEEEEEEEEEAPPPQPGQLPEVVVISSDSAQ
```

109 - 128:	EEEEEEEEEEEEEEEEEEEE

110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE

A0A1J9RF50 **A0A1J9RF50_9PEZI** (101 aa)
Uncharacterized protein. *Diplodia corticola*

```
MEAAMLAAMAVVRVEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDDAEAAWAGTVELAAGEAVVGVSHWRKNGRGHWRLAEKR
WWPLVSGKAVVDAAAGVLAVV
```

15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE

A0A1J9RWS0 **A0A1J9RWS0_9PEZI** (742 aa)
Uncharacterized protein. *Diplodia corticola*

```
MGQALPKQHWHDADSFFVAAQLHVLPDQQDIARKGDDHHPRQHQHQQKQNSHHRDRHDGSHHRHDSHSHSHSQPPPNGLK
LTTTTTTALQPAPPPSIPSSKSKSSSSLSSSSSSSPAPSPTTSSSSSDEASSDDEAADDAADDSPSASPSLSSSEQDQDQ
DQDHTAIPPPPHLHPRLDPPTNVSANANVSAPAPAPARTLAAQHWVGVVREARGFQRVYARALEAWVVGVAEGKGEAEAE
VVEVEDEEAAEDEVMGNGGRMGRRGSGSSSSSGGSWGGSDSDSGSSSGSGSGNWSTKVARRARGRGRGRGRGHGHGRVGS
GSGGVVVDAGGGGEGGNWVALDVMERKGKGMDEGEDEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDKAVEPLN
GRANAIDATKGNWLLRSTAATLHDTRTKCRTDVSSWTAADLVDLATRGGPLRCYRWHSDGDGREGKERSRRQLTEDAAKL
GWCGRWLVRNYYRGSTTTAPDTSRARGDEQGEAAQTEREATTVIDDETGLCSITVRVPMHNRPRDDTSSSSHTTLVTIPP
TTFLLIKLLTILYPSGAPWSSPPSPTDPDTDIDAPPSTNPATAITAEKASRNRRVWLAMCLGWAWALQAYLAAHPPPRTT
TNGSIIDGSDASDGDSDDNGDDLDADAYLLDRSDDDEGLLDGDGDDDSDGQEEWEGMSEVGIEDADVLAALARVGLGGGT
GGQRRRSLVPSDGDDEDEIGGG
```

360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE

A0A1K0G2G1 **A0A1K0G2G1_9BASI** (968 aa)
Uncharacterized protein. *Ustilago bromivora*

```
MPTITFVTPPGRPSVLRAHTIQPALPQDDQPQASTSKLPSQTMPVPTTNKEDERSKPTPLVFQKRILPQLTTSPEPAQES
FGTPQPRPRVSLDESRSPTGEKKKPSLLSTAISGSSRLPPRSASTTNLGILRRAELDDAHFSSTELPRPRLHFVEPHKQA
APVMSAKPEPTAEQQSTSSTQAASEQPRKRSLVIQEHADVLERAAERAARNNLSTQALEQHGRSRQHCTFSGGEETASTR
SSWALRSSSRGSSIATSPTYASERSDGEVGKPQAEETHVVSIFNHNTTAASEAAPSRKLTFIDPAPSRKRSPPRPSRALS
PTSHSSPSDRKPSDEETHREPSHRVLAFAACPKPERARAARKQKAKLSASPAPHKLAYPQRLRGIRGTDPIRSPAPEFAA
LQMGQNWDFRGEDVDEEGSGYSEDEEDSDEEDDEEDEASSEGGRSDIQSLQQSDEEEDAVDMQLTGQDLRSTWSAPNDVK
LAPTQRRASTPGLTITNTAFSNQRSPPRTQIQSPRSTQISPLSVPSTRKLKPKEFFSSHPMCFLPDAFEDSAPPTPTEPD
SEGYEPPRATLLSGWLSEGGGGGGSGASSRRTSWQHPHPNPSLRSPVGEEGLAMPITLPPFRRTRERTPQYGVTSDGEQS
SRSLGGNVAFIRESAGFGRSPNWGASPSQHLGISVPINPNPTQHDRPSTALAGYRRASHSVEPQIKVNSAFTSPIGSYSH
QQPGRRPGMGKQRAVSTCSHIRSFASVKTSINGDVVVATSPPREAGSALECLKHQLEAHSPKCRSGRTTPGWLSDGPGLG
AGKYRSERLSSLAQAMSVGGAKATGFVDGDGGEAHRRSKSVPLQIAPSPVPPVEVEGTLELVKPTPIAITPTTANSETTA
NSKWTAERDGETLPPPPSSTKRGDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKSFQFAKQELGEDGKLRMVVI
HTSSERKA
```

905 - 924:	EEEEEEEEEEEEEEEEEEEE
906 - 925:	EEEEEEEEEEEEEEEEEEEE
907 - 926:	EEEEEEEEEEEEEEEEEEEE

908 - 927:	EEEEEEEEEEEEEEEEEEEE
909 - 928:	EEEEEEEEEEEEEEEEEEEE
910 - 929:	EEEEEEEEEEEEEEEEEEEE
911 - 930:	EEEEEEEEEEEEEEEEEEEE
912 - 931:	EEEEEEEEEEEEEEEEEEEE
913 - 932:	EEEEEEEEEEEEEEEEEEEE
914 - 933:	EEEEEEEEEEEEEEEEEEEE
915 - 934:	EEEEEEEEEEEEEEEEEEEE
916 - 935:	EEEEEEEEEEEEEEEEEEEE
917 - 936:	EEEEEEEEEEEEEEEEEEEE
918 - 937:	EEEEEEEEEEEEEEEEEEEE
919 - 938:	EEEEEEEEEEEEEEEEEEEE
920 - 939:	EEEEEEEEEEEEEEEEEEEE

A0A1K0G603 **A0A1K0G603_9BASI** (1791 aa)
Lipase_3 domain-containing protein. *Ustilago bromivora*

```
MSPSVRIDDDKPAVASSGPEAVFLRRPELLDLDLDELSPLPPAQGFSSNSRPASIERLSSLKRDAASRPEPLHAVAPSPA
LSAAPSSFRLEGSPASSSHPVDTFDELPSRARTSSNYQEKPTAPPAEARQSRPELDINTNLESEQVQQQHPSLYPTSPPS
ARYVTVSAILSRSEMYYAPETSDQWDILRSPHALPTDARQSHDPYTSEQFGSSRRRRSQRKRPSNGSAIEALGALLLRKD
SSGRVANLSFVRENDDSGVTLDKSRDRSQSQSTRSKRGTASKQGLQVWTSALGSFGKKKLRLQLPQSASSQASSSRSGAT
IAERRAQMWHQVLTRQGAVVEGNHDGFSKVRSRRGGLSFEVGKVNRKQTPSSLLQLNNYTPHARGKQRLDSSEGKGQDEP
QSEKHLDTNGASSPGFGFGRLPDTIVLKAGRRPKLTQTSKSEFGIGSAYHDHTLPEAPPSPVAMPGAWQDGSSWRSKPGD
GYEEGALVLPPPLLDDHGSDASSFEGLLGVRRMREREKVRKQAEKLAARNRPAHKVGPLTALTNFVKAAHAAETSAKRAR
GYRRFDQPPAFLRSYTEPAQLVRSRSGSAGSASRIKIEKSPVAGPNGILDGDASFPLTANGAGAIQAAETDTPMQIRLDA
SPAAVASDVEVRKSPAVTSASPFLSAAARRAVLSRRGSRNNSVDAAGRQLNTVFESEPLDPSQIPDDELASPDLPPISSP
LLRPSSRGSSKSNAFRDFPAAPRLLPVQLSMPSSPFTPLAPDHRSMGPPTTANGDYLSARYIHSAPRTPQLPPTMLSLPP
SPWTPYGEPSGLHAPPMVHLHLNTSSSSLRLPPGTPRLVPTHIEVLPSPFPTSAASRRGSLTYDSPSGLRAIGSARSPLT
GATTDFTAFSALRDAETADAASKSATEVSKAADAKRGKSNGSLRLTPSSMLIAAQSRHDFDTASGQRDAGDAETPTSSGP
KAARKISDGAIDPQKQHRPSQSTIHVDSSGRTRSFVLWFLIGDLGLRNRSPAISETVATSNGADAEADYGGLVAIVSHTF
GLVVFILAHLVDLAYATYERVSLVLWFLRWMVYNLTGRTVLAQCVIEAYGFIQAEWATVAVEDHEEKGPKKKADSQGHRK
PKGLSQWQVMRGLLELYCLHSVTRERYLAEGAGLQALEGWTRPSRQDHNDRVHKPRGPDRVDIGAHRAASRAALGEKRRS
WAQQNETSALSDDNDDNDVHGHPNVQDWAGNGRGWSSRVANGGNRDDNGFNHNEDNEAYDDDDEEEEEEEEEEEEEEEE
EEEEEEEDESSDGEMVVTNRGDDILEFAKTPRLDAARPGQASTGYFGRAYDFMTSPQVGASQPGATHHDLRAFKESNRDL
VRTIKWCGRLAISAYGLHVHIVDLPPTFTPSGDRFSRQTFAYLSRLNADDVLHADIQTLDADADYSPTFYVVRDYIRKVV
CVAVRGTQSFSDIIVDLELQTEEIELPQVQPTPGEEFRCHAGIWRAAKALVSSQSKLFATLRQALAENEGFGVMFCGHSL
GGAIASAAALLLAEYFIPDGAEPDSGTWVTNMSSGLPARRPIRAVSFASPVTMTADLATRAAMGSVPLVTTVVLGSDVIP
RVGHGQVRELRRVLGALARVRRRHAMASSEGQDDAHIHILRSYWDWRSISMAEDADDVMLHRKERIEEQLWSLRREVESD
LYAAIKARLDTDSTAGSRIPPSPWVGPQQRDEAPLHALATRRQELDSATLRSEAAQGGPLIPPGRCIWINNKQVYHVESP
LAFFSLPELRSDMFAAHFPAAYEEAILELRT
```

1264 - 1283:	EEEEEEEEEEEEEEEEEEEE
1265 - 1284:	EEEEEEEEEEEEEEEEEEEE
1266 - 1285:	EEEEEEEEEEEEEEEEEEEE
1267 - 1286:	EEEEEEEEEEEEEEEEEEEE
1268 - 1287:	EEEEEEEEEEEEEEEEEEEE

A0A1K0GCD6 **A0A1K0GCD6_9BASI** (1481 aa)
Uncharacterized protein. *Ustilago bromivora*

```
MTAATAPSPSPAPSAPPLARTPARQSSTDAAVHHVTADGGSTRRHDPSSASASTSKVTSAPPASSSSSSSTTTNNAASST
GLGTLAKPIDLASPPASPTSTATTPNVVASESTRPLNQPSPSPSGTESQAASTSAPQTGTSNAAASISTAADAASLPSSV
QKGPPYGNALNTPNRLLPPTPLGNTSDRASATSPSAASSTPSKTVQLPAPYKAPRIAKSGASESFATAYPTQETRQKYAS
PSKPLAFGSGLASSHKRSWQSSRSFDLSNKKFRTSSLASPSPAAASTSLTAPTASASPSPSATAARPLASAPTISRPLLA
TPTAGRATSASSGVTLTNIPMPGSSLSNQAGVGPLNLIPAVSGTDLPASLRDEYLSLLQKSELIDLVKQLERQLNDLIAA
PVGSSTLYRQAHIYPSQIHTQIDRLKARQRVEAAKTTTSSDLSLKDVYSLLNASTSTSGTPTFTRPAGVPTRPTASNPLL
TGRPAFTPSTAPRRPYATNPMPISNTGAARGTARQEQASKDTAQNASLVNLINSINAIVRQQAQPARGPNGAPLPPAQAP
SGTSATPPATTATGKGGSSAPSITPAALRSIVGDGPMPSNAALAAAIAAHFGNNLPGRATATASRPANASATSASPSANT
SAERTGAASSQAPAAPPTAASASGPGKDISDKIATILGSTSSLQTTMLGPQGLPLAPAAQTPGAGAGSSPLPIGNIAAML
SSFSDQLNQSNPSAGSAKSGTPAASEGQENALSSLLQQLEEAKKRLPSQATASSASANAPSLPAVPSASNLSALQDPIAI
LTGASANPVFTPTYSAGGASATTSTGIGGASGSAWSPEAESVIVQGPLGTSTLPSYEEMIVEGLRIHGQAPPRELFNWMQ
STYPLMKKFRPSAHQALQKAAKRGRLLKTGSRYRLNPNWKEPADSRKPTRRPQVGRDHPMLAPGLNGEVLAVSPLKDSQA
YRNVGDSGLRTPGKGTLQKPRPYGQPGAAPLANPASSIFQNGSAASIILEYQKRTGKKLDADSVKQLYQLIRSGPSDGPA
EEILAHLLTQAGYHDAAAQATAAAAAQTAAAAMPASMPSYPPSSTSMSAMASGPSASGTSAPVSALGRAGAAAASTAARG
RMPTRPVPKGPTSLPLATTSEPTMMQQLASMLNDLSSPINPVLANSLLGQLSSNAAAAARAANMPGMSTAPPLPATPART
MASATSAPTSASSQLATALSSLAGQTPQQDLDSAVSETLAAALQQIGAAPTSTAAPSTAESARKEKETVSEAATTAPKQP
AESQAAEKQSKKGAAAAAAGESGEAAEEGIDLAEYEDAIRALISAFGKSNEDTEEGDSDDESDVEADERAIAAAEAEPDS
VEDSAAESTDAAGQADKADATQEAQHEQQQQQQDEAEEGGEEEGGEEGEEDEEGDEDEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEDGEQMDLSAVLRQLTASLQAHQQTDSET
```

1420 - 1439:	EEEEEEEEEEEEEEEEEEEE
1421 - 1440:	EEEEEEEEEEEEEEEEEEEE
1422 - 1441:	EEEEEEEEEEEEEEEEEEEE
1423 - 1442:	EEEEEEEEEEEEEEEEEEEE

1424 - 1443:	EEEEEEEEEEEEEEEEEEEE
1425 - 1444:	EEEEEEEEEEEEEEEEEEEE
1426 - 1445:	EEEEEEEEEEEEEEEEEEEE
1427 - 1446:	EEEEEEEEEEEEEEEEEEEE
1428 - 1447:	EEEEEEEEEEEEEEEEEEEE
1429 - 1448:	EEEEEEEEEEEEEEEEEEEE
1430 - 1449:	EEEEEEEEEEEEEEEEEEEE
1431 - 1450:	EEEEEEEEEEEEEEEEEEEE
1432 - 1451:	EEEEEEEEEEEEEEEEEEEE
1433 - 1452:	EEEEEEEEEEEEEEEEEEEE
1434 - 1453:	EEEEEEEEEEEEEEEEEEEE

A0A1K0GCG0 **A0A1K0GCG0_9BASI** (1890 aa)
Uncharacterized protein. *Ustilago bromivora*

```
MVSPTKRAPSRRAALTSRPTIINDENVSPYREASLSLQPSEPPSSPLISNSFLYNLPDPTLGFPAASSSILPSPFKRSAI
ASLNKPLPREQTQELPKSAPAPSSSTDVAKLMQANLNAPGGLPTPPSSSEALTTTPAGPGKHTLAALPREPVSPSPSRTR
NAVLSPARGSPAKVSQDGPATPSNRRLLSSNNQGTDEDEDDVFKGSSTDRTPTRLNAFSEVESEEEDEEEEEEIQLVGIR
RGGPDATFIREIKENGWDQPLPPSPIKFTYLQPDPPRTRRQSSVGSRPRSKTPSVSAPSRASSMAVEEEGEGVSDESIKS
STSQLTSLSRISRSRRGGRVSVARSSAQTPVMADLTRDHPSLPDSPGDDPLLLTGPDTFIVYHEGTPSAKQHARVARAKG
DASMSLTHSTPLPTAAAGQRRDSNGSDTSSGSQRSLYAHMSGRTAAAAEGQVSFNDAEEEEGATASPFLPFDDAGFASES
DDEAGPLVAEDATAVQEEGVLREIASMSDISPSFADESALRKEQVEVEASIRMVNEKVLAEGPDQSMDASVGEQSLDASA
TVDSEAEDQDEEDEATTHNTSMVASMDANPDHTDESEDHKSEETEGQQVAADVSLAGQTLDSGQTLDSEPNETADFDDSA
RADTTRDVAEDAVGVSQSNEVSEEEEGPEASHAADESQMHADASASLDVDQSMDSSMTSHASTHADESGDVDVSHQVADE
SMASSTLSNPGEELDESRQEGAETSVIVDESMASSDHSKASDQGVDESLQVDASQQIDPSLRSEAAGESSMASTDLSEAE
ASFDSSDLGKDNEGAAEESQVAHDVSVVDDSLIYDESHVADDSASHQDPIDQHDEQKTVSFADTDSPVPTSPQFVEAIRA
FPAIHGHPIISPPHPVVLIDALPREPQACFAGGEQSEDVEIEFSTSNVAVESLGMRHSESVSSELSALSSIADLGEGEDE
EEMRKKYESKGGSRNTVVDRSRRLSLSTDSEPDLSRKEEGKSDGEWEDVETGRGTKTNRSSTIATPAAEEESDEEEEADD
LSSSSNSAVEQGGSDAEEHDSHDEQEEESDNEEEGSEEEKDESSQLDEEEPSAASLQEAVIISSSSPSAHSDSESDEEEE
EGYVVEAVVRDSRDRFSTTHSVFDETDSALIHTLSLRQPHHPSTSQLDVTGDASHSRSRVMKLNQPTSTPIVEISSLDPR
AAARATAILKLFHKYVDEGYIAGGGEMGEVTEGRMRRVVDAIRDADRRRQEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEGEEEEGEGGRDLTTLLMDAELSLAREDERAESGSLIGGSIGMRSPATPFLPGGFRGTPVQTSP
SVSRTMLGKRKEPHALPVGTRDRSTHSRRRSSTIPQISIGTLDPRSWDTSDWARLEKYFTSSIKTSAQMGEHSASRTDKA
RRYVDALLSTNLEGAASALLSELHIPSSLRTHEWSVEKLEYRLQALQRKYLRKVEAKYPDAFQSNHLEERREEGEETLPS
GDLDWSLTTNITAATAPPPQGAKGRVSFGTPFRMGMHSTPAVGLLKRATQNAAQASSRQQAERLYPELPVSPSPATPSQG
DDGVIRKAGRLISRLSGSFAGLVSSPRPSQEEQRGDKGKGKRKATEAELTAASPSVSTRRRVVEEADVSASTNASLSSGG
DSFVDSLLVGSVTNATSIQPDTTACPPPTKQSRLPIATSTGAQPAEERRTVVARRVIVDLPEPRPQHIAGQKGFTSSLNL
AGGSSGVSHTPLSLLSPNTHRAAAKKADELRQSRRERGWVSPRKQRLQQPTRTRSIAAGQITRTTWNGGKESGRRGTRQQ
QVERADISGSGREASTGDGSTSCSSLADVISCRAAVEAVQQRRRGQLSRR
```

1251 - 1270:	EEEEEEEEEEEEEEEEEEEE
1252 - 1271:	EEEEEEEEEEEEEEEEEEEE
1253 - 1272:	EEEEEEEEEEEEEEEEEEEE
1254 - 1273:	EEEEEEEEEEEEEEEEEEEE
1255 - 1274:	EEEEEEEEEEEEEEEEEEEE
1256 - 1275:	EEEEEEEEEEEEEEEEEEEE
1257 - 1276:	EEEEEEEEEEEEEEEEEEEE
1258 - 1277:	EEEEEEEEEEEEEEEEEEEE
1259 - 1278:	EEEEEEEEEEEEEEEEEEEE
1260 - 1279:	EEEEEEEEEEEEEEEEEEEE
1261 - 1280:	EEEEEEEEEEEEEEEEEEEE
1262 - 1281:	EEEEEEEEEEEEEEEEEEEE
1263 - 1282:	EEEEEEEEEEEEEEEEEEEE
1264 - 1283:	EEEEEEEEEEEEEEEEEEEE
1265 - 1284:	EEEEEEEEEEEEEEEEEEEE
1266 - 1285:	EEEEEEEEEEEEEEEEEEEE
1267 - 1286:	EEEEEEEEEEEEEEEEEEEE
1268 - 1287:	EEEEEEEEEEEEEEEEEEEE
1269 - 1288:	EEEEEEEEEEEEEEEEEEEE
1270 - 1289:	EEEEEEEEEEEEEEEEEEEE
1271 - 1290:	EEEEEEEEEEEEEEEEEEEE
1272 - 1291:	EEEEEEEEEEEEEEEEEEEE
1273 - 1292:	EEEEEEEEEEEEEEEEEEEE
1274 - 1293:	EEEEEEEEEEEEEEEEEEEE

1275 - 1294:	EEEEEEEEEEEEEEEEEEEE
1276 - 1295:	EEEEEEEEEEEEEEEEEEEE
1277 - 1296:	EEEEEEEEEEEEEEEEEEEE
1278 - 1297:	EEEEEEEEEEEEEEEEEEEE

A0A1L7VW12 **A0A1L7VW12_FUSPR** (992 aa)
Uncharacterized protein. *Fusarium proliferatum (strain ET1) (Orchid endophyte fungus)*

```
MSWIVENFQIPVPVGDCSIHFLVNKQRKSVEYAFIMDGGTGKDHSASEAIVQTLKCAKDYLKSTWKIKKEIKFNLWVVTH
WDDDHFRGVMDLITGKTIHGDGWMTENFVKSPKLYCGRSEKPSEQTFVLQASARGFSSTAGKMVLGLDMFSGSKIFNDKG
NLERSDLDKSRPRFCIVGANGHGILVPRFQQVVTPNQSSILAVLFWPGNVWQCCFYAGGDGNPELERAIISKFLNKKKNI
ELGDGLDLIKLDHHGSSQENIYGGDLRKVKAERKLKLAEMPIGLFKPKNILVTPGNLHGHPTFDVVHCLFDLLGTTTGLA
KDTGKPIGRVWTTRSPYWANKQSPTTKDLNPSHNQDLKDIHKKELQAYQDPTKKYLDTGMLMAVEAEGSEKRLKRAKGLK
AWKKKIRQQEIIEGGHNPTDYRVKAKANTELIELVSVPIRVRGSQYVPSTNVVLLELDIVERHIPKNKKQPKSASAIEEE
EEEEEEEEEEEEEEEEEEDYYDLEIDEEKDKKEEEPAASAQFDYDYVSYDDIMNLRFSGIMMWNLICDQGIVLETEDPFF
IIHFSWDNGKFRGVKCLGMDGVERKDYKTEPLVPRRYSKRLAVIKEAQKQRMIKLLNQKAEELKMAEESKRTKRKGLFYT
DSGRGKDQDNDIDFSGFELLGKYNTQDFKKQNVFTHISQSNVSTTRKNFTGTGLGGFSTRPLGNISLQANLSLGIPPSTS
GDKMFSLHGLTFGDFSSTVSGNPLLESWWAASHHYNFIKGLEPGFKLKYGHDSGSSAEVDESFQAVDDKETGDEDFLAAD
SIEEEDVEDEVLDDAWEDGDEEIDLALETLNGLQQRWQTAWKDSQSEVSKKRQTREEKERIEAAIASMKSIKEEAEQAVA
DLDPTLFTGKDDVTSLLEIQKRLVLAITYISPDFEAKFKQGNDGGTKNNKVQEKKSRATVKETKAEKQKREAKAQEKHKE
DKELNTEGKRQTRSGTVYGINDQPTGQKRLHK
```

478 - 497:	EEEEEEEEEEEEEEEEEEEE
479 - 498:	EEEEEEEEEEEEEEEEEEEE

A0A1L7WSW9 **A0A1L7WSW9_9HELO** (1215 aa)
Uncharacterized protein. *Phialocephala subalpina*

```
MSYRLQKSRAHRFTRDDPRALTSRSSFGPSSSQPGRMNERSRLSGPTQNIVDLTGDDAPTKTFYDLTADSDDDDPPPPAR
GQSTPPVASSASALPATATAPKDAPGASSSKAPTPPTEKNVSETSSSKTPPTAVANDVPPASSSMAPPAQKNVSEAPRSK
APPTAIGKDVPVASSSKPPPPKHQSRDIPKVASPKVTPASPPKAVNAIQTTPPPQIKLSPHSSKGKAPPINEPPQSGSKR
TIIQHSDLQPGPSNVTKSTPQPSSSSSSSEAEDIIPLSPVKNVKASPGTPSKSSTRGKGASQKSSTIDSSSPLVPRLKAR
KAIARQSNPPVERDESPESAMTRQRASREQDISAEQSQEDQATVESIAASLRSMEQSMRYDHAMSTRWLLQDAREAAQSS
PSMTVDKVSPFASMSGVQQRAGEKIPNGCVAEKLESWTMSKSGNKMTKSKSVQNAKQIYGDTPRVPRYSSHTNISRNILS
ADSEKLKYVPYMGDVGGSTNKETNFKKLLKELEEAYSPRRIESTRECEKASRVRAYVEAWFEENHLECDQRTLVQYMMAE
ENANELGLRDAEREMLLASFGEPLSKQTKDAAEQFWEAFDSVFKELDIRLPNVLLPTELLKDMVESVRKKTHSTPEKAAN
IPGDRLGTYTTLTCLICAAVDCQTHADYSHDEIQRVGGEDDENHEPEYLVQRQPLVLPYNDTLRRFDLRKKNEAEVPRRS
SKHHQPCSEECWRIIDYSEKEILWEQHDLDALHDMLISITDKDNRACYIAFALHLPCWQVHGVIADYEARVDTTRTVPEP
TGRAKRPDWYFNKTKTLHRDWQEMTKAHLHQERSQANPCTHEGYCTNKCPCFEANILCESFCGCSDDCPRKFTGCSCLGN
GLICVSETCICIQMNRECGPECISCGAIPRINPANKHEDDLFTHGCQNVCLQRGVLKASVMGESQLEGVGFGLYLAEPVR
KGDFLSEYTGEVISSQEAERRGIIYDRKFLSFLFDLNKDYVIDAARLGNNTRFINHADNEKDGLNCEAKIILVNGEHRIK
FVALRDIAVGEELLFNYGKKFAEKHGLSKKLPKAKEGGKKGVLVGEEALDALDGVDQRQKSARVKVEQTRATRGRPRGSR
GRGGGGGGSRGGSKMRKTAPARQLIEEDLEVPIVEPLSQEQEDDLYTASPDVDEDEEEEEEEEEEEEEEEEEEEEASLAS
GRPKRKTTLTKRYTR
```

1176 - 1195:	EEEEEEEEEEEEEEEEEEEE

A0A1L7XP08 **A0A1L7XP08_9HELO** (550 aa)
Uncharacterized protein. *Phialocephala subalpina*

```
MAPLRRQSSRGGKSKDLGSSGSAHNNPSDTPTPDTSAQDVYAHGTAQGATNPPPNVIGGANDSHSELLPVNEDGDSDVKG
TENNKGDNSDHGHADDADEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEDNDD
GQQPNAGASIPAKMFKPRCKQCIKKGKDCGRIWYKGQECDLCRNSMKNFKKKHEACVPEDKKPAGAIYGRDKSNEKKRVP
KPKKAEPKSKEAASESESSPSPPENPQGLPDNASAGPSSSSVPTILPEDPPRPNIAGDEDLAQSLRRQEIEHVNRTCKRK
RVRFEGHTRDEDELGGPAREEDISFMGTSSAPPDFNQTHNLGNMRSASERMARSRAPAPLRFEPHPEHGNQAIARQEAST
YHPFTQSLTQPLARSGNGWTLDTTAARGDTCRGSGDHANTRGSVATPLGMHGRSERGGRGSPIPPIRTSQTREQVSRLQR
LISTHEQTLDHLRRLQIADEDFAEAMPRIPAEVVVVRTWIRDRAIMIARLQRRLAQKKAEHDHLKEELGG
```

101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE

115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE

A0A1L7XVR5 **A0A1L7XVR5_9HELO** (267 aa)
ANK_REP_REGION domain-containing protein. *Phialocephala subalpina*

```
MRLLLDHGANIHARGGRSGTLLQVARAFKRHSIVQLLLDKGAGAGEEEEEEEEEEEEEEEEEEEEEEEEEEGEETRIPH
SIEQFPSQQIDKARSVVFEDVFAAEDAQQVIVATRGDPISATRVTAGVRASQWFGQMSDDVLRRLLQDRGVDSFSGTDKA
RSVVFEDVFAAEDAQQVIVATRGDPISATRVTAGVRASQWFGQMSDDVLRRLLQDRGVDSFSGTEEQPYRNLLPGGACKP
SGACKPGGVQKPSGVQKPSGGQIILFG
```

46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE

A0A1L8E5N6 **A0A1L8E5N6_9DIPT** (380 aa)
Putative troponin t skeletal muscle (Fragment). *Nyssomyia neivai*

```
DDEEYSSEEEEVVEETHEQKGEAGDPEFVKRQDQKRSELDEQLKEYISEWRKQRSKEEDELKKLKEKQAKRKVTRAEEEQ
RMAQRKKEEEERRVREVEEKKQREIEEKRMRLEEAEKKRQAMVQAMKDKDKKGPNFTITKRDTSSKTIGDINMSAQMDRN
KSKEQLEEEKKISLSFRIKPLDLAGLGESKLRTKAQELWETIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALK
KGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYITMMDEQRNEKWQKRHDRFAKRRRPKLPKWFGERPGKK
PGDAETPEGEEEGKVDDIEDEEVEEVAIEEIEEEVVEEEEEEEEEEEEEEEEEEEEEEE
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE

A0A1L8E5W2 **A0A1L8E5W2_9DIPT** (382 aa)
Putative troponin t skeletal muscle. *Nyssomyia neivai*

```
MSDDEEYSSEEEEVVEETHEQKGEAGDPEFVKRQDQKRSELDEQLKEYISEWRKQRSKEEDELKKLKEKQAKRKVTRAEE
EQRMAQRKKEEEERRVREVEEKKQREIEEKRMRLEEAEKKRQAMVQAMKDKDKKGPNFTITKRDTSSKTIGDINMSAQMD
RNKSKEQLEEEKKISLSFRIKPLDLAGLGESKLRTKAQELWETIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKA
LKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGFETLNKEFLEKTWHDKKDEFGGRQKSKLPKWFGERPG
```

KKPGDAETPEGEEEGKVDDIEDEEVEEVAIEEIEEEVVEEEEEEEEEEEEEEEEEEEEEEE

359 - 378:	EEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEE

A0A1L8E5X9 **A0A1L8E5X9_9DIPT** (383 aa)
Putative troponin t skeletal muscle. *Nyssomyia neivai*

MSDDEEYSSEEEEVVEETHEQKPAAKSEGEAGDPEFVKRQDQKRSELDEQLKEYISEWRKQRSKEEDELKKLKEKQAKRK
VTRAEEEQRMAQRKKEEEERRVREVEEKKQREIEEKRMRLEEAEKKRQAMVQAMKDKDKKGPNFTITKRDTSSINMSAQM
DRNKSKEQLEEEKKISLSFRIKPLDLAGLGESKLRTKAQELWETIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHK
ALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGFETLNKEFLEKTWHDKKDEFGGRQKSKLPKWFGERP
GKKPGDAETPEGEEEGKVDDIEDEEVEEVAIEEIEEEVVEEEEEEEEEEEEEEEEEEEEEEE

360 - 379:	EEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEE

A0A1L8E600 **A0A1L8E600_9DIPT** (388 aa)
Putative troponin t skeletal muscle. *Nyssomyia neivai*

MSDDEEYSSEEEEVVEETHEQKPAAKSEGEAGDPEFVKRQDQKRSELDEQLKEYISEWRKQRSKEEDELKKLKEKQAKRK
VTRAEEEQRMAQRKKEEEERRVREVEEKKQREIEEKRMRLEEAEKKRQAMVQAMKDKDKKGPNFTITKRDTSSKTIGDIN
MSAQMDRNKSKEQLEEEKKISLSFRIKPLDLAGLGESKLRTKAQELWETIVKLETEKYDLEERQKRQDYDLKELKERQKQ
QLRHKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGFETLNKEFLEKTWHDKKDEFGGRQKSKLPKW
FGERPGKKPGDAETPEGEEEGKVDDIEDEEVEEVAIEEIEEEVVEEEEEEEEEEEEEEEEEEEEEEE

365 - 384:	EEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEE

A0A1L8E664 **A0A1L8E664_9DIPT** (364 aa)
Putative troponin t skeletal muscle isoform x10. *Nyssomyia neivai*

MSDDEEYSKGEAGDPEFVKRQDQKRSELDEQLKEYISEWRKQRSKEEDELKKLKEKQAKRKVTRAEEEQRMAQRKKEEEE
RRVREVEEKKQREIEEKRMRLEEAEKKRQAMVQAMKDKDKKGPNFTITKRDTSSINMSAQMDRNKSKEQLEEEKKISLSF
RIKPLDLAGLGESKLRTKAQELWETIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKI
QVASKYERRVDTRSYDDKKKLFEGGYITMMDEQRNEKWQKRHDRFAKRRRPKLPKWFGERPGKKPGDAETPEGEEEGKVD
DIEDEEVEEVAIEEIEEEVVEEEEEEEEEEEEEEEEEEEEEEE

341 - 360:	EEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEE
344 - 363:	EEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEE

A0A1L8E675 **A0A1L8E675_9DIPT** (382 aa)
Putative troponin t skeletal muscle. *Nyssomyia neivai*

MSDDEEYSSEEEEVVEETHEQPAAKSEGEAGDPEFVKRQDQKRSELDEQLKEYISEWRKQRSKEEDELKKLKEKQAKRKV
TRAEEEQRMAQRKKEEEERRVREVEEKKQREIEEKRMRLEEAEKKRQAMVQAMKDKDKKGPNFTITKRDTSSINMSAQMD
RNKSKEQLEEEKKISLSFRIKPLDLAGLGESKLRTKAQELWETIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKA
LKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGFETLNKEFLEKTWHDKKDEFGGRQKSKLPKWFGERPG
KKPGDAETPEGEEEGKVDDIEDEEVEEVAIEEIEEEVVEEEEEEEEEEEEEEEEEEEEEEE

359 - 378:	EEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEE

362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE

A0A1L8ECN3 **A0A1L8ECN3_HAEIR** (373 aa)
Putative troponin t skeletal muscle. *Haematobia irritans (Horn fly) (Conops irritans)*

```
MSDDEEYTGEGDPEFIKRQDQKRSDLDDQLKEYISEWRKQRAKEEDELKKLKEKQAKRKVSRAEEEQKMAQRKKEEEERR
VREVEEKKQREIEEKRQRLEEAEKKRQAMLQAMKDKDKPGPTFTIAKKDTGVLGLSSAAMERNKTKEQLEEEKKISLSFR
IKPLAIEGFSEDKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQ
VASKYERRVDTRSYDDKKKLFEGGWEELGKEVNEKVWNEKKDQYSGRQKSKLPKWFGERPGKKAGEPETPEGEEDAKADD
EIAEDDEEVEEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

335 - 354:	EEEEEEEEEEEEEEEEEEEE
336 - 355:	EEEEEEEEEEEEEEEEEEEE
337 - 356:	EEEEEEEEEEEEEEEEEEEE
338 - 357:	EEEEEEEEEEEEEEEEEEEE
339 - 358:	EEEEEEEEEEEEEEEEEEEE
340 - 359:	EEEEEEEEEEEEEEEEEEEE
341 - 360:	EEEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEEE
344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE

A0A1L8G7Q4 **A0A1L8G7Q4_XENLA** (710 aa)
Uncharacterized protein. *Xenopus laevis (African clawed frog)*

```
MVTLAQEARFDNPVGRCRCATVCILHHNVYWPVGTHLSTTGKDEPSSYTCTTCKQPFSSAWFLLQHAQNTHGFRIYLESE
HGSPLTPRVGIPSGLGAECPSQPPLHGIHIADNNPFNLLRIPGSVSREASGLTEGRFPPTPPLFSPPPRHHLDPHRIERL
GAEEMALATHHPSAFDRVLRLNPLAMEPPAMDFSRRLRELAGNTGSSPPLSPNRPSPMQRLMQPFPSGNKPPFLATPPLP
PLQSVPPPSQPPVKSKSCEFCGKTFKFQSNLVVHRRSHTGEKPYKCNLCDHACTQASKLKRHMKTHIHKSSPMTVKSDDG
LSTASSPEPGTSDLLGSASSRLKSVVAKFKSENDANMIPENGDEEEEEEEEEEEEEEEEEEEEDLTETDSRPDYSFGLNL
EAARHHENNSRSVEERSMPEVMQSMGLGGMHHFSDAFHQVLVEKHKRGHLSEPEVQRDTCDEDSVAGESDRIESGTVNGR
GCSPGESASGGLSKKLLLGSPSSLSPFSKRIKLEKEFDLPASAMPNTENVYSQWLAGYAASRQLKDPFLTFGDSRQSPFA
SSSEHSSENGSLRFSTPPGEMDGGISGRSGTGSGGSTPHISGPGPGRPSSKESRRSDTCEYCGKIFKNCSNLTVHRRSHT
GERPYKCELCNYACAQSSKLTRHMKTHGQVGKDVYKCEICQMPFSVYSTLEKHMKKWHSDRVLNNDIKTE
```

364 - 383:	EEEEEEEEEEEEEEEEEEEE

A0A1L9AKV2 **A0A1L9AKV2_ARMVU** (533 aa)
CDC45-like protein. *Armadillidium vulgare (Pillbug) (Pill woodlouse)*

```
MASPVHFFKDYISNIYGIEKENIKTRNSCFKKSREEYDEIYALSKKPLGRASKPFSKQDRPFQILYDECLRDYKNYIDSI
KRSGGGGENAENVAAAAAAAAVVDPRCMKTVFINLNLKRIDAFRKFFYSGFDTYSNSEKEKKKEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEKEKIEKSKEIKKRMSKLFTKFVKRIRKERKTEKCKKCDFGGEYDEDPDSDLEFDEFDDVSDIW
KNDILFIKMKRTPFEEIPSIFEDIKKESERRFPYLNPHHKESSKSKKTTTTTTTTTKKSKKKNDNNNSLPRSKIISSAPV
KSSQKGEQSKSNNNNNNNTPDLGKKIVNSVVVGDDEETTTTTTIHHRPDKLIKKMRELEEGEIIDSDDEDVEIVDNNDEK
ENKKKYHQQERQLERKSSKQHDLNQKNKEQVLNNQVLQDKMMLDLKRTLKERALKLQMEKEEALKKIKSPDTMKRKRDSK
EDEINKENHLGGDQPPNLKKKKYDIEGEEEEEEEKGDIEEEGKTKKKNKKRLF
```

144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE

150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE

A0A1L9N8U0 **A0A1L9N8U0_ASPTC** (424 aa)
Uncharacterized protein. *Aspergillus tubingensis (strain CBS 134.48)*

```
MAPPKVFSIEGKGLKLDSAEDIESHIKPLLEATDYTEIRFGGNTLGVPACERLAAVLSTQKSLEVAELADIFTSRLLSEI
PDALTFLLNALLEITTLHTVNLSDNAFGANTQKPLVDFLARHTPLRHLILNNNGMGPEAGSNIAKALTELAQRKEEARKE
GKEVPLLESIVCGRNRLENGSMAAWARAYEVHAAGMRSVKMTQNGIRQEGISMLLKDGLRHCSALEVLDLQDNTFTIMGS
TALAGVVSSWPSLRELGVSDCLLSGRGGVKVAQALAEAKNQKVQTLRLQYNEITAEGVKQFLHATKTALPALRRIELNGN
IFNEDDNNVTELREILEARQEEHGQDDDPEDMWGVDELDELEEEESEEEEEEEEEEEEEEEEEEEEKAEKLVKDDEAAE
NEKVSQKKDEDVDKLADVLGKTGL
```

367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE

A0A1L9PGC6 **A0A1L9PGC6_ASPVE** (417 aa)
Uncharacterized protein. *Aspergillus versicolor CBS 583.65*

```
MAPPKIFSLEGKGLKLDSAEDIDAYIKPLTESTDYTEIRLGGNTLGVPASERLAAVLSTQKSLEVAELADIFTSRLLSEI
PAALTFLLNALLEASTLHTINLSDNAFGANTQKPLVDFLSRHTPLRHLILNNNGMGPEAGSNIANALTELAERKEEARKG
GKEVPLLESIVCGRNRLENGSMAAWARAYQMHAAGIRSVKMTQNGIRQEGISHLLKEGLRHARALEVLDLQDNTFTVTGS
TALATVLSGWPSLRELGVGDCLLSARGGVKVAQALAEAKNQKVETLRLQYNEISAEGVKQFLHAAKTALPSLRRIELNGN
KFQEEDNNILELSELLDARKEEHGKDDDPEDMWGVDELDELEEESEEEEEEEEEEEEEEEEEEEEEEEEKAETEKVAQK
EDKEVDKLAEVLGKTGI
```

366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE

A0A1L9PVH3 **A0A1L9PVH3_ASPVE** (131 aa)
Uncharacterized protein. *Aspergillus versicolor CBS 583.65*

```
MWPSPESLIHEWIQGLKNGRTDDASADEEDYYTDDSDRRGDCGCGLCNQEDLPDQDEEEESADSTEDEETETDSDGSEAG
EEEEEEEEDEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEESEEESSDED
```

92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE

A0A1L9RL34 **A0A1L9RL34_ASPWE** (478 aa)
HET domain-containing protein. *Aspergillus wentii DTO 134E9*

```
MKYSVLEFPIQAEPTDPCAKWLGIRRRRIPRNALSELGLANIRAMIERATLDIEEEEEEEEEEEEEEEEEEEEEEEEEE
```

```
EEPYLPKRLVYVGDESHNPRLVISNEHIQPSTRYIALSYCWGSLEEAKSQLKTTTDSLEAHLREIDSNALPQTLWDAILV
CRALGVNYIWIDALCIIQGDLKDWERESSQIAEIYSHAFLTVCAAQGTSCQSGFLERDLDEVQVSFRSSLGPSTTGRFLI
SEYQPKYKHYLSPYDNEKKLAISDVNAHWNSRGWTFQEAEFASRLLLFGENMAYLCVNGLWVCENGACFRGDGNVLPWGE
RLFKSNRKLLSPEETHQDWYSLVERYSERHLTFPSDKLTAISALARRFGKNIKGQYLAGMWSDNLHHGLLWRTKSGRSYA
EYTAPSWSWASQDGGVSVEYSKKAEFHLLDAKTVVGEDPYGQVTGGYISLSARVIKFPSHYFEIHKFDGRSIKNPSRV
```

54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE

A0A1L9SFL6 **A0A1L9SFL6_9EURO** (1112 aa)
Cytokin_check_N domain-containing protein. *Penicilliopsis zonata CBS 506.65*

```
MVFLRLTVKVFPREQVQTSSSFSLRSLIGDSSRDDSSRGAATSATGKPVSFLLVLEQPEEVTLGALAGMIQEKWAKLRPD
AGPLEIKKLLDDSHDADDLDAEMTVADVFVDIGKGLRDGLDQRGAVRVIQKPAPYAPVRFPSVTQDWDAAAEDYERLKDI
KKEAMESMQKLATIEEEPSQSQASISESIASEPLDAFHQRTPTSTSGHSRRDVSLPSVEREEALPLPRWGQPQSTLLEED
SQNRRTSAIASTPPPRRLMSQELGDSPASARTRNTRWIDSNAKPRSQPVSVSGQSAARNGSESHLAVPSQQSGNASGSES
PLGTRKALPKHIPEPEPILLDESSDEERRADGDVQMADADPDADLVPLPPTKVTTPLPTTSPMVVIESPTAKQPTSAKTN
DHASEPRTRKRKKSLEPPTPNKEPRLASQSPTKPADTSKESTPKAPELPNGGASVFRRPSFSEPGRRPSLTDQSKGGGLG
LGITRSPPGKKTVPFDHSPDSTLSTEAANKPNPPPLFTTPAFSSSAPDTQHDLSTQEMITPSKVLTPAIENVKRLSSALR
KDSPGDKHGERRSVSFAEDNDVFISQPTSAPPKSTPKSTTTPVSKLAKATPAAGTPSSATDSARKTSSTPSRMVFPEDVS
PTKLAQYEREAQEKVQKIQEEKEEWEQRIASAAEAGKPSEYVQLLRDVYTASTQVGELERSHRQKDKSKLKKLKGELEKK
CKELETYETSLANADNGPPTPTSATKITKTNGTLADKPTPVKSTPSKKTVPTKPVPTVNGKASLSTAKYPGIATTVATKS
TPVKDISTSAATAQSKPAIPTPAAKARSISSTSSTSASKVNGVNASQTNQVPPSAQGKAVDPVRQNKLNRGSSQDEPLDL
STSDEEDEGSKSGNSESEPEPDSPPSLEVSSLVDVEAEEEEEEEEEEEEEEKEEEEEEEEEEEEEEEEEEEEKEEEEEE
EEEEEEEEEGSEGDAPTVSKADILARVARSSSQPTKQPVLASPSPSFIFPQNANGRPTLKLMRAVKHQEQAERALKKKPD
PNASLAARKDIFEGPDSDSSDEESSESESESDSDSDSESDNSDSQTNSRIGDDHGDILPSGSANKLRTARRV
```

934 - 953:	EEEEEEEEEEEEEEEEEEEE

A0A1L9SWL3 **A0A1L9SWL3_9EURO** (1235 aa)
Stress response protein NST1. *Penicilliopsis zonata CBS 506.65*

```
MAPSHVPRATPAAAKAERATPTTTTPAHLTNGQASPPPVSVNRKKQKRRQKQAARLAAEQQQQPPPPPPQVHSGYMTSDV
AQQNGRPAAGYDVDEEPDDYEDAEPDHQVNGDGYYDGDHAHHGLAASSQPPTGKKSKKKRGKKGRSGSQTLPEEGSTPLS
TPSLSLSHTLPHAAPPPHVAPRSAPKSTKDRSIWNTSTQEERENIKTFWLELGEDERRQLVKVEKDAVLKKMKEQQKHSC
SCTVCGRKRTAIEEELEVLYDAYYEELEQYANTNQGVFDKGSPIVPPPRLYQHSLRSPGLYTRTQAQFHPSRGRVQELPE
EEEGDLEEEYDEDEEEEEEEEEEEEEEEEEEEEEEGEGEGEEGIEGEENDAYSDDGVEDEETRAARADFFAFGNSLTVKDG
ILTVADDLLKNDGKHFIDMMEQLAERRMQREEDTQYGMVAAHQSLHAGHNHGPLDEDDYDDEEEEEEDDDYDSQEEEEYE
DDEMDAMTEEQRMEEGRRMFQIFAARMFEQRVLTAYREKVAEQRQQKLIEELMEEQTRNEQRSAKKAREAQKKKDKKKIQ
RQAKEEEKARREAEKAAEEAAAKAEQEKKLEEQRRKREEQRKKKEAEKKAQEEERARKEAEKQRRLKEERDRQAEAERKQ
REQKEQERKRREEARRKEREERESREKKAKEDRERRAREEQQAKKKDKAEQGSKDRDKRDPPHVAPQLVPTAIAKRTSNP
GPVPIPSGLQHAPSPHFQVATPIVAKASTPVRPRQHSQHGSHTSSPRSQPGSTEPSQLSISPRSVPLSQSSGTSSVTSLK
GAAAQQPILYHPQPSAPLSPLGAAGRMHPHGFPAINGLPSNPPGLSGMVPRPPPMGHDLPMYPPHTGPLVNQYRGFPAPN
GIPIPPGMNGARPIPSGRGGFPLEPGQGLPFHGQQAISGAFSAQPGVHSRQPSSSFERSPLQSHAQPFPISRPSPIKRPS
SSAQDQQHKENGHATQRDVDDLSAHLGSSALLDDTDIPAPSSLSQSLPGATVAEPFHGPTRASFGGPSLFTDPLGVVPKP
PNFSISPGVGGATWGMQIPFGSPAFPGAPTWGGSSGGGWSNNAFGTSGHHRAHTSRPVAIRLLVIQACKQLNTMSPGKTS
SAGGHFHDANLVLRQVEQLRPSNEPAISLKEMLDICDTEGNPQNGGGSFLVRDDADEGKFVKFEPDSNSATPGHHRGSIV
PGEIGSPIPSNSLPAFGGIGMSSVLRQFSSPPTGF
```

334 - 353:	EEEEEEEEEEEEEEEEEEEE
335 - 354:	EEEEEEEEEEEEEEEEEEEE

A0A1L9VFR3 **A0A1L9VFR3_ASPGL** (1052 aa)
Probable E3 ubiquitin ligase complex SCF subunit sconB (Sulfur controller B) (Sulfur metabolite repression control protein B). *Aspergillus glaucus CBS 516.65*

```
MDNGDNSQMDGSFGQFSFAPATQTTVVTTTTTTTTTFPPLIIKPPRATRNLDTKLYPLAASPTPDSLRNIKFELGGKSVV
FNEPEDTLSAVNETRERNDALKTSNGLLRSVASFTTSNDAGHPRRNAHPRLSSQPSSHPSSSKRRPVSPVSIPEAQPSVP
RTRSRVPSEPALRSSRTRAPAVDGLATPETENNSFSAGSAFSRRRIHSAALPRRASNLRSPLSSEVESQGTLQGSNPKSF
LGKDAARARFGALGKSPRLDRGKQVLQDDLSARVDNEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAPTSKLSDN
VSVQIPQQRKLLDTNTQRTAADNVAAQDMCLPSPSLSPVAAMNAMNADSSFDSTEDAGVDTDSSLDNNVPRFSKSADVPR
STASLMDMPNVLDFFDSVPEGFKTYLMYQLLRRCPKPTLRFVANVVNPALKCDFLSMLPLELSLNIVKYFDAPTMCRAAQ
VSKKWRHIINSDEKTWKELLDRDGYVLPEGELERAIREGWGWQFPNGDEDFEKDLTTYLPLKSGPGSSASASLPAAGHND
RMLVTRQSKRKAATRTSTRKHAKRKISSSGTDRSETPDWRVDIATAEGPYAAASAAAAAVPYPDVGLSSLRSLHLYKSLY
QRHHCIHKGWMKPDVRPKHFAFRAHDRHVVTCLQFDTDKILTGSDDTNINVYDTKTGALRNTLEGHEGGVWALEYYGNTL
VSGSTDRSVRVWDIERARCTQIFHGHTSTVRCLQIVLPSEVGKRADGTAEMMPKVPLIITGSRDSNLRVWKLPRPGDQVY
FQSGPQVDDADCPYFVRALTGHQHSVRAIAAHGDTLVSGSYDCTVRVWRISTGETVHRLQGHTSKVYSVVLDHERNRCIS
GSMDNLVKVWSLETGSLLYNLEGHTSLVGLLDLKCDRLVSAAADSTLRIWDPETGRCKSMLSAHTGAITCFQHDGQKVIS
GSDQTLKMWDVQTGEHVRNLLTDLSGVWQVKFNDRRCVAAVQRDSLTYIEVLDFGASRDGEPPEKLGKRIVVNRRGLETG
DYAEEDYDMSDG
```

277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE
287 - 306:	EEEEEEEEEEEEEEEEEEEE
288 - 307:	EEEEEEEEEEEEEEEEEEEE
289 - 308:	EEEEEEEEEEEEEEEEEEEE
290 - 309:	EEEEEEEEEEEEEEEEEEEE
291 - 310:	EEEEEEEEEEEEEEEEEEEE
292 - 311:	EEEEEEEEEEEEEEEEEEEE

A0A1M3T9W1 **A0A1M3T9W1_ASPLC** (400 aa)
Uncharacterized protein. *Aspergillus luchuensis (strain CBS 106.47)*

```
MIISFLLRCHDSIWAFLHATILNIPPSRLYIFPTLAGSVWFLTLASLLLTWLARGMPVYPGQSNPDVAFISDIASFELKP
LFLIGASMTAVGFVFTVAAVHVMRYEPGFALVKCPVISEETSNNQGNNNTYTQSSDHNHRNAYNHITGGGHSEEEEEEEE
EEEEEEEEEEEEEEEEEDQETTRTLKVISLLSILAAGTASTALILLGVMDTFRYKFAHHIFLRICFGCLAIQSAGTAIVY
STEVLSFVSYLYHWGVWGNDWGRKRSNRVRIFASLSTILILIQLFLGVAFISLTIPEDANDYRTAGILEWIIAFLGTIYL
WLFCGFFDRTSFEGYVPSILYNATPHGKFLGRPALPGVGVAEAESSYNPADDTLDVDPERAPLLPQSQYQSEGGPRTRYT
```

153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE

A0A1Q2YFV8 **A0A1Q2YFV8_9ASCO** (239 aa)
Zn(2)-C6 fungal-type domain-containing protein. *Pichia membranifaciens*

```
MFSELSSKPKTDFMRVKAQQTGHQHAPLDDYRRDVAALAAAEEREMEKDEAEEDDKMGVEAEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEDEEREGDDEEEDEGSESSGSNRNKSSRLEGKLGFKKFRRKHKNSKSGCANCKQRKIKCDEKLPICTFYQP
VRTVAHEVPAGEARDAGWRRRRYGETEAAILELPNIEEKVHTEVARCAERDRGVCKAVAGGEQAIAQARFSRDCAGLEG
```

62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE

68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE

A0A1Q2YKP2 **A0A1Q2YKP2_9ASCO** (1101 aa)
CBF domain-containing protein. *Pichia membranifaciens*

```
MEGTLSNLASLKEKVSNALSKKEKASKTNKKKNSKSNSSNKESSDKPTKKLLDKKTVTDDEQEILRREALNLGATEEDLK
LVKDLDVEDESEQEFDDVDSSKNSPNKELVNELSDFMKTIGFKSHKAEDFEVSDEENLDAADAKEAEKEEEKSAKEEGRV
ENDSDEEAEEVLQKKSEEEEEEEEEEEEEEEEEEEEEEESKLADAPDQAKNEPDNTATQSKSSDKILNLQSVISDRLTVESRS
DWYNIPQNLDHSVADRSMKQSDIDELYEKAKRLIEAENQVYDEEFNKSSSQKRFLSQILTGGTLSDKISALTLLVQEAPL
HNLRALDNLFNMCQKKSRTAALQCVDAIVDLLVNTILPPDRKLKTFKKQPLSKSLSDDQLILMYFEDHLKTMYFQFISLL
EKLSHDSILYVRMKIVSHIFSLLKAKPEQEANLLRLGVNKLGDIDNKVSSKTSYQILLLEQEHPAMKQVVCESVIDVVFR
SNNDHHALYYSVNTLNQTILTRQDEALANKLVDAYFALFEKLLIKTDDENVGAFKESEHQKEGRRKKNVKRGRKGGKSVK
NVKDENEILEEKNSKMFAAILTGLNRAFPFSNFPTNIFENHLNILYKITHSLNFNTSVQALILIQTITAKFSDDKYKDRY
FRTLYESLWDERLLNSSKQGIYLNLLFKSLKDDENIDRVLAFVKRISQVCLNWLNIGTISGMIFLLIQLEREIPQVRNLF
LNTPMDDEINEKLEQEESLDEVASQNKEVRLYDPRKRDPKFVNADKSSIWEIGFFLKHYHPTIKTYAENFLKFDELSKAE
RRTINKPDLGLYSLSHFLDRFVYKKPKSKANLKGSSIMQPLGGAHTGNLLVRATGVESNDIPANTEDWLSKKASQIKPED
DFFYQYFSTKQEKVMRSKFDKELDHKAKNGDEDEDSELDDDAVWNALVASNPNVEGEDDDLDDELSDLNMSDFSEAEDDD
ETSVTGIDLEAEDAEGNSDEDEEDEEEGEGLVRLKTLGDFDDEEGVEDESNDEISGAKEESDSSDGEDIKMLLEEDAEDE
LYDSEDDSIVPKADLTTTKKSKKRGSQPEDSKKNKKIKLSSLPTFASAEDYAEYLQSSDEE
```

177 - 196:	EEEEEEEEEEEEEEEEEEEE

A0A1Q2YKS4 **A0A1Q2YKS4_9ASCO** (1286 aa)
Uncharacterized protein. *Pichia membranifaciens*

```
MAAKKARHHKTKNKSKTGGNKPAAKETAIGTGNGIGINHTETISVPDGHEMGVGSLQVMSGMDDPFDEVVARAMNFSYSD
SINFKGGNFALLKSIRNMVSTMEENKFLSYMEDIRTGKTGIEDIVQLLDSFRIEGSESSKILYENGHGAAPSTINSNNDH
HINSTKAANKIRELEPKQSDRVSHISNEEDEVEVEVEVEVEEEEEEEEEEEEEEEEEEEEEEEKEERERKQEEEDAYLSS
NEIESDNDSGEEYSFDLELSNNFFDPYKFHDALFKLLRITTPNAKGVSSGEKQRIKSLFSILATFCDPYTQPSSTGEHNE
MILSADLISDLVISLIYKDYIKSSNGQTMNLPAFDMAYDIAVIIEKIMIILNADDETNLIYINNDEEHWERELPKWLPHS
ALSNIVNIASDFHHMMLLYTIVTAGLLIIQKLYRNMGNICLNPFLSMYLQLWKNQTRIIYLGIEIDRRDEDNGFPGYPEV
IRYMIKGASAVRSMISLILNDNLEKRLHDLKHESLINFMRPWGRKFTNGSITRDIRVFVAALLALGSELDGVTELLFNFD
PEDRYDEDIKYMFEMELEDMEDENAPAISADGTVAESKDDGSGIEELQGASATHENGHYHDHHKENVRRYVGKNGILEIE
RHDEEVDESGDNEDAMFMNQTSASPAYDLHPDCDCVFEDFESDFEEEGEYEEMNGEDEISAKENEARLKQLKHFDNDKLL
NDFESLSRLSHIDLKDLDMETIQNLHLEAVRNINNGPSAVRATGSKHTEIDSKGRDWRDIPRGDNVMLTTRFVNLLKSSI
EDSSIFLTPMENLLSSLQSMASETLNSQTCEKIVRSIAWVVQYEHESKLMSDEEVKMNNDPNVNADVIYNFLKLNDNFVK
MMNHNPSSAFFIIDELLMAEGYRRVLIWFLTHLPLNQWIINYFHDLLIGQRGNPTKDGNDANTRFSFSRQGPLVLSEVEQ
SMLLHEFLSNAVIYLSRGSSYELEDIMWNQIEEGKPGHDEKSGTTPSNNVSSFITNRSNAQKLIKVICLMLKSLETHKVI
NPKNTEYRVEIQTLLVQWVGVGFVPEARELFFRYSSTENTEHELSDNVDEKPDAKKVEEKENEKSTGENILSRLFQSKFS
KLMSYLENFSSFDLFIITLNMAQHYRTEKETCFDFMKDLNSIAHVYATEEELLKSFDEFYLALNEALSTGDEERIIEIMY
ASKFLTTETNIIHARRAIKIFIEGGELTNEAKTIQTLQLPGKNQLTDYVEREKTQGSLDDSSPPKPTALQNNIKKTKKKT
KHGKHK
```

201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE

A0A1Q2YL81 **A0A1Q2YL81_9ASCO** (625 aa)
Uncharacterized protein. *Pichia membranifaciens*

```
MAKGERGMDDPRFSKVFSDPRFRTVKKKDLKVTLDDRFNKKDLKKEFSLLKSTAKVDKYGRAISKDDGSSVIDNLDKYYK
EEHGEEEEEEEEEEEEEEEEEEEEEGERKADDDDDDDDDDESGFSLSSSEGEEAETDPLAKARGLAEDNTSASELDSSDEE
VSELEETLSSDVPETEDIPEQDPTTRIAAVNLDWDHLNSTDLFATFSSFLPQDGHIKCVTIYKSEYGKQRIADEELNGPP
REIFKESLDNNEDEDDEDEDDEELDLAKASKKLIQENNGEEEGFDSSELRKYQLQRLRYYYAIVELNSLSSAKEIYEKCD
NTEYESSGNFFDLRYVPTDMEFDDADIRDLCEKLPPNYQPIEFSTDSLRNSKPKLTWDETPIERVQILSKSFKKGELDDL
DLKNYLASDSDEEAQDENISKYKQLVGGSGLDKVGKAGEEDSDSSDVDMEFTFTPGKAKTEDSSEKENGKGEKSTIEKLR
EKEKERRRARKQKVKELKRDAQSNRNKGKKNRPNTDEHKEDDLEIEQIGTEGKELHHFNIKDFEKLEKLKAKKNKFKNKR
QRELQKELESRMEDSNQGNLEVDDRFAEMIDSHAFVGGSKLLQQERKKRKKMSNKVKKKIDASTD
```

85 - 104:	EEEEEEEEEEEEEEEEEEEE

A0A1Q3ABJ2 **A0A1Q3ABJ2_ZYGRO** (275 aa)
18S rRNA aminocarboxypropyltransferase (EC 2.5.1.-). *Zygosaccharomyces rouxii (Candida mogii)*

```
MGKGKNKNHEFRGSRPSRGANGHNSKQNHKHMEMKHGGSSSSNKTKFPVKLAMWDFDHCDPKRCSGKKLERLGLIRSLRV
GQKFQGIVVTPNGTGVVCPNDKSIVEEHGASVVECSWARLNEVPFNRIGGRHERLLPYLVAANQVNYGRPWKLNCVEALA
ACFAIVGRTDWASELLSNFSYGPSFLEINAELLGIYQQCTDADSVKSAESAWLDKIEKEIQDRKTQSKNEDIWMTGNVNR
MPAASQESDEEEEEEEEEEEEEEEEEEEEEGEQKMT
```

250 - 269:	EEEEEEEEEEEEEEEEEEEE

A0A1Q3AR80 **A0A1Q3AR80_CEPFO** (643 aa)

Zf-C3HC4_2 domain-containing protein. *Cephalotus follicularis (Albany pitcher plant)*

```
MANPLPSNLENLQSEEVYEEPEQIFLQQESEDDADDVDYIPIEVSQSPPRVTRVVVAVEEEEEEEEEEEEEEEEEEEEE
REKRRRRVEKGAESCSLSGEESCQGALWNRSDIDGLFCPICLDAWTNGGDHHLCCLPCGHMYGFSCITKWARQKSGRSGK
CPQCNKKYTLKDVRKLFASSITAVDEESQKRIQSLEVKCASIKKKEADLCMKEIDLQKREAALHLKFDQLTERTSYLERI
LVDLQSRSSGLVSGSEACQGFSASGNYFLGDNFGSKFCRREFPADFLLQGEMQLDGARLFDVNASRQILLIVRRLPGICG
THVLTKMSLIPPHESEDILLPSCTKAIRDVQISPFNDSLALFASLGKKLLVFSMESNNAILTYDLPAAAWSCSWDINSSH
YIYTGLQNGMLLVFDMRQTGRPMESVKGLTCNPIHSIRSLNSAPGVRTILSASSIGLCEWNFGGNEERPFLVPETANQGV
CISFACCPRSDDIVASYRPRVEISNESTVSQPPLTPSPVAGQGIIGSHVLLKRVGTKCYQKRSYSHANVPDVRLPKSMII
DMNQKRLFVSSDEFTRGLVLQEVPSLTVTRHLKSHKHPILDVRYTHALGQGLLGCLSEDRLQLFSIKVSCKVQTSQKATF
EIL
```

59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE

A0A1Q3DVK6 **A0A1Q3DVK6_LENED** (770 aa)
Uncharacterized protein. *Lentinula edodes (Shiitake mushroom) (Lentinus edodes)*

```
MANPDFSEAKVDVLQQSPDQTEEALYIDSATSPLSSPSAYLSSLPPSSPPTSEAQLSPLMHGNDLSVTTATPLTDVMNLT
AEPRVDVDCLGLQGIESHKSLNPVSDEVSQLEDNSSPTSALTQDLIVTNFAVEADDDDDHPFSPAGAIDLESNKVAATLV
TEESAPELNQNTESQHSPSQVIDDCGPYKSSSNKDEPPPASIFSESKLLSISADSAQVLPVAPYPSTSISALKASPKQLP
AKSKNKTKMKSTSSAPSISSSAPRVTVTVVKRMRPVPKIHHIVNEASVKKGTSMSIKGKEKGSSKTKPLDSHSSSSKRGR
TSQTASKDQTNTASNSLPSSLAEAICTSFDTSNTSITDSLSIVPAKRKASHEIPSPEISNSSAHSPTISSKHSPAFPSHS
SNPQKKLRTVPVEVPVPSKDKSSSPTDNNTWVDENWVDAVAAAYGSPHHSPQTLRRKTAAKTMPEIGSIEDEDEDDNERR
SLKVKFLRSPHKRIVIESESEDEDDEVEKRLPLRQSSRQMVDSDSEPEQDVEIERRSKSHTSHPALSNDVESSESELTDS
DEKEEEEEEEEEEEEEEEEEEEEEVPTKEKNALGSNHQKPRSSLSSISPFDRELVGIIVETMSLSRSSSHLAFSLYKTVR
ETRNSVFAQLMKANWAHLDVVTRELRSKGLCGHVPGNQDDLPRRGRPKRNTSMNEEGGTADRYGMFGMVESSFRNESRNL
PLPFSSRFFYVPDCDPDVERAQLIRLTMPGSGKRSETKKYKQYYWKPVGK
```

564 - 583:	EEEEEEEEEEEEEEEEEEEE
565 - 584:	EEEEEEEEEEEEEEEEEEEE

A0A1Q3DVT0 **A0A1Q3DVT0_LENED** (773 aa)
Uncharacterized protein. *Lentinula edodes (Shiitake mushroom) (Lentinus edodes)*

```
MANPDFSEAKVDVLQQSPDQTEEALYIDSATSPLSSPSAYLSSLPPSSPPTSEAQLSPLMHGNDLSVTTATPLTDVMNLT
AEPRVDVDCLGLQGIESHKSLNPVSDEVSQLEDNSSPTSALTQDLIVTNFAVEADDDDDHPFSPAGAIDLESNKVAATLV
TEESAPELNQNTESQHSPSQVIDDCGPYKSSSNKDEPPPASIFSESKLLSISADSAQVLPVAPYPSTSISALKASPKQLP
AKSKNKTKMKSTSSAPSISSSAPRVTVTVVKRMRPVPKIHHIVNEASVKKGTSMSIKGKEKGSSKTKPLDSHSSSSKRGR
TSQTASKDQTNTASNSLPSSLAEAICTSFDTSNTSITDSLSIVPAKRKASHEIPSPEISNSSAHSPTISSKHSPAFPSHS
SNPQKKLRTVPVEVPVPSKDKSSSPTDNNTWVDENWVDAVAAAYGSPHHSPQTLRRKTAAKTMPEIGSIEDEDEDDNERR
SLKVKFLRSPHKRIVIESESEDEDDEVEKRLPLRQSSRQMVDSDSEPEQDVEIERRSKSHTSHPALSNDVESSESELTDS
DEKEEEEEEEEEEEEEEEEEEEEEVPTKEKNALGSNHQKPRSSLSSISPFDRELVGIIVETMSLSRSSSHLAFSLYKTVR
ETRNSVFAQLMKANWAHLDVVTRELRSKGLCGHVPGNQDDLPRRGRPKRNTSMNEEGGTAESADRYGMFGMVESSFRNES
RNLPLPFSSRFFYVPDCDPDVERAQLIRLTMPGSGKRSETKKYKQYYWKPVGK
```

564 - 583:	EEEEEEEEEEEEEEEEEEEE
565 - 584:	EEEEEEEEEEEEEEEEEEEE

A0A1Q3FUW6 **A0A1Q3FUW6_CULTA** (457 aa)
Putative troponin t isoform 5 (Fragment). *Culex tarsalis (Encephalitis mosquito)*

```
GDDPEFIKRQDQKRSDLDEQLKDYINEWRKQRAKEEDELKRLKDKQAKRKVSRAEEEQRMAQRKKEEEERRVREIEEKKQ
REIDEKRRRLEEAEKKRQAMLQAMKDKDKKGPNFTITKKDSNFGMSNAQMERNKTKEQLEEEKKISLSFRIKPLEIDGLS
ADTLRARATELWETIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQVASKYERRVD
TRSYDDKKKLFEGGYSAYYLEKMDKKWAQRQELWMARTKSKLPKWFGERPGKKAGDPETPEGEDEVKADDEEIEVEEVVE
EVVEEEEEEEEEEEEEEEDEEKKAEKVAKRLNREVNMLSARLIRLKEKQEEKHAERQALKYAMKTNQYALKNEQKKYKKL
QKEGDKMAAMMKLEDEDEDGDGEPKEPPPEEPEEEEEEEEEEEEEEEEEEEEEEE
```

433 - 452:	EEEEEEEEEEEEEEEEEEEE
434 - 453:	EEEEEEEEEEEEEEEEEEEE
435 - 454:	EEEEEEEEEEEEEEEEEEEE
436 - 455:	EEEEEEEEEEEEEEEEEEEE
437 - 456:	EEEEEEEEEEEEEEEEEEEE
438 - 457:	EEEEEEEEEEEEEEEEEEEE

A0A1Q3FYY5 **A0A1Q3FYY5_CULTA** (384 aa)
Putative troponin t skeletal muscle (Fragment). *Culex tarsalis (Encephalitis mosquito)*

```
SVSKRFFSSEEEEEVVVEEQQQETKPAAEAKGDDPEFIKRQDQKRSDLDEQLKDYINEWRKQRAKEEDELKRLKDKQAKR
KVSRAEEEQRMAQRKKEEEERRVREIEEKKQREIDEKRRRLEEAEKKRQAMLQAMKDKDKKGPNFTITKKDSNFGMSNAQ
MERNKTKEQLEEEKKISLSFRIKPLEIDGLSADTLRARATELWETIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRH
KALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGFDALTKESLEKQWSERKEQYVGRQKSKLPKWFGER
PGKKAGDPETPEGEDEVKADDEEIEVEEVVEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE

A0A1Q3NPN9 **A0A1Q3NPN9_9GAMM** (115 aa)
Uncharacterized protein. *Acinetobacter sp. 38-8*

```
MYNHKIIFFKIKKNIFINLIKDSISAHHYTLKNNQLLSFEEEEEEEEEEEEEEEEEEEEEEELIYQFQKNKLKFITNTIIK
KLKLFDFYLFTQTNFGIFIFFNLNLKNVFQYWLNL
```

40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE

A0A1Q5UH12 **A0A1Q5UH12_9EURO** (399 aa)
Uncharacterized protein. *Penicillium subrubescens*

```
MCHEKARIKIQKGLDQLTTHSRNAEEVIVHIEKFSAHEEIVGAKESLKPSNDAPKGNTISTSITVTSASKVSDTLNLSQL
ERVAPTASSTIWVTAIDLDYPRPPRVANGAHTFRCPCCCEVLPAENADKTDGATIPLDKIQVLLEFSQKNTPTEIRHCAL
CNWLEEEEEEEEEEEEEEEEEEEEEEEEERVEMDKDGDREESKERIRDSSEKVYEWLVKNKIQPNPGMEPISPRREKEVRQC
GYFRQNGYFAGSSKASSFSEIDSVGSRDNELEELRALGEPVVHDGPLESEPAFLEEKDVEEDTQQLSGSATADLKSPQDY
TVACVCALPIELIALQTFLEEMHECPLGIRSDDPYDYGFGKIGSHNMVISVVPWSEDGRVLEDIYGFCHSKSEPKLSES
```

165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE

A0A1Q5UM53 **A0A1Q5UM53_9EURO** (181 aa)
Uncharacterized protein. *Penicillium subrubescens*

```
MPIIHDSAHGAADTGIEEEREENESIGLSRTRERRRLEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGNKEGPTRPQAQRKGEVLAIPGHHLARAKKTTN
PTNPLRSKGIDVKGDQIINTV
```

38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE

49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE

101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE

A0A1Q6UB99 **A0A1Q6UB99_9PROT** (84 aa)
Uncharacterized protein. *Azospirillum sp. 51_20*

```
MSPTEKHYFTQKNTAKFQTSRSSETSVRKAWQEGTEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEADRKMQVRKRKQ
MWKK
```

36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE

A0A1Q9C3X2 **A0A1Q9C3X2_SYMMI** (482 aa)
Uncharacterized protein (Fragment). *Symbiodinium microadriaticum (Dinoflagellate) (Zooxanthella microadriatica)*

```
MRLPTIVTSYFVKKPNSSHKEQGAVAAEPATTSSAGANGSSLAVSTSHEPEQQELQEEAGSLQEEQEEEEEQEEEEEEEE
EEEEEEEEEEEEEEEEVEESEQSTRAEEPQVPQHGSSTVAEDETEHTRLESLKDLQACVSSRHDQIEALQHRLQSAGQQR
QRQQGGELNSSERGERGELQGLRDRLQRTEHHRAGLRPSELELRSIREQHRAVRGEVASFQYGGGDGDGPSHDQVAYLTW
QCESLRGSISAAEKDAAEEHRHISKLEAEMSNEHRAGDEYSLALKYQLAETARLEAAEKVAANELADLTDRYWDYAPFSA
GSYGFTALAIDQEMLQLRQRVGFEQEEVARLEGKLIQARAACKSAGDAAATAVHLAHVLREQSKAVDVDQDEAAHSNLQK
VAAVQARPCHQAEDELPGRKPNPCIKLVRRIVDTVASEHVLKQKLGEVRRRNKELERQVQAAKTRLAGKTHIHFKPVNSI
TE
```

73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE

A0A1Q9DAE3 **A0A1Q9DAE3_SYMMI** (408 aa)
Uncharacterized protein. *Symbiodinium microadriaticum (Dinoflagellate) (Zooxanthella microadriatica)*

```
MGPATDGESSRKHQPRPFSRYRRSVLSAASLCEDDEDDANDEEVVAVMMMMMMMMMMMIMMVVVVVVVVVVXLRTNTSL
LPVAVAVAVGGGGGGGGGGGGGDDDDDDDRDDDDEEEEKEEEEEEEDMAGAGCGGGTMVKEEEEEEEEEEEEEEDIRAE
EEEEEEEEALQRAGQWYSHAAAIQEEEEEEEEEEEEEEEEEEEEEEEEMWKPSWTFQLQRGGMLQEEEEEEEEEEEEE
EEEEEEEEGVRCTEAGQEEEEEEEEEIQEEEEEEEELWVEEEEEEEEEEEEEEEDDREEEEEEEEEEEEEEEEHRLLQSLAC
QWQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDTALRMWNLAEEEEEEEECLAVVAVLAVAVGGSCQPQAQTFLRG
SVLAMLRP
```

185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE

190 - 209:	EEEEEEEEEEEEEEEEEEEE
191 - 210:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
324 - 343:	EEEEEEEEEEEEEEEEEEEE
325 - 344:	EEEEEEEEEEEEEEEEEEEE
326 - 345:	EEEEEEEEEEEEEEEEEEEE
327 - 346:	EEEEEEEEEEEEEEEEEEEE
328 - 347:	EEEEEEEEEEEEEEEEEEEE
329 - 348:	EEEEEEEEEEEEEEEEEEEE
330 - 349:	EEEEEEEEEEEEEEEEEEEE
331 - 350:	EEEEEEEEEEEEEEEEEEEE
332 - 351:	EEEEEEEEEEEEEEEEEEEE
333 - 352:	EEEEEEEEEEEEEEEEEEEE
334 - 353:	EEEEEEEEEEEEEEEEEEEE
335 - 354:	EEEEEEEEEEEEEEEEEEEE
336 - 355:	EEEEEEEEEEEEEEEEEEEE

A0A1Q9DAN7 **A0A1Q9DAN7_SYMMI** (3728 aa)
3-phosphoinositide-dependent protein kinase 2. *Symbiodinium microadriaticum (Dinoflagellate) (Zooxanthella microadriatica)*

```
MRSVVDVLLPTKMRKLTEDLSLPASDLSPAPIVHFTVRREVPLEHLVDLCFDELFRIRLTQRRMPFWLKLIEFAAAKELR
EIDGAAILAPVTTDANDDEAEIVENVTRDDVYAKLEEMQKTVARRSLGDDDNAGQADHLIAWPESEIRARSLWPRAVPWL
DSCAYPGRHRRPDLDPKQAKMPGCGHGANVLEPTMSVRDVDWEWSLVFPLESVGDSHGKKTIVDGSKKEATSTSGKASDH
FVMDCIHVVHWLMAAVATRDPIPGAGSDPGNRHPKQPLCADRSRYLGKAERRNRVDHPQGGRHQGPPPAKGATQGMALPS
CEAGQGMVCQQSRHLWDVMELMLLLHRNGCTRAPSYVKRDFHRWADEVTPVTHPDCQNFSPDRRLRVSRPLGGLESGWEI
SKDVLLTPVARRLAHAWSALSHHGQRLQLYFVHARSAHFNRRAGSMRRAGDWTCDKCGDLQFARNAICRRCGAPKSSGAY
AGSGAQAPAAPNQDGTRAGDWTCPLCNGLVFASRSQCRKCGTNRPASSAAAPPTPAEAPSGGKSGDWTCPTCGDLVFSSR
GHCRKCGASKPGTSTSPGDGKDWSCPQCGDLVFGSRSSCRKCGAERLVTAKPTVQMHTGDWRCPKCNDHQFARNERCRSC
GEARPSASWLGTAVGLAPPCYWTSKEGDGPPWRIVPADAAEIEALRLAMDPGGSLGGRDQRAAGKHQGAVLWGPSKVHKG
MTVAELASTLDRPSTSPGLKIACKESMLEPGADLSQLADPSELFVHFDPPKPFDHSFVKELIELAQECEDNEFLAPRRME
ALWENHQSKLVREGVTFETHPQEAADELNRLVEELKEKSAKDYHPGTDEIVRDLVHPSLYPFVEGVSQTAGTDDVTPAVT
VQGLQQDMWGRPYETSKYQWLPSEVSVAADGTCKFQTYINNLDQEKYGELCGALERLLTRCLPHLEAAWSHGQQVKGLDD
ENEDMFDSDCSAGEPENIEIQSLRGRSIQVITKIVDYELPPGGTHEGVWHVEGMSHENIVATAELILKKDAALVGGGLQF
QRTFRVHERDAMIAGFPECRAAQMDEVVKAGLVPLGQLPLPHRRLAAWPNSHIHKVENISNTSESLAVRRIVVFWLVNPG
VRIISTQHVPKQQGVMPLEEAQNHRLSLMEERKLHKQNWRSPSIVVIAICKGTATGFQLHGAWRLQHPGLWGKYAMEREN
LRQIDMKSISSAVPSVQLRRQYVEMAEKLPAALFTDVNEVFLSHGTVPDSVLPILSGGLNERFSGGLFGNGTYLAEDIGK
NDQYCRAHFPGQHPELEKLLYGDSGISHPGDVFYMFVCRTLLGYSIRTRDGRSDVDNKGRSIWSSEKRELAAIPSSSPPV
LHHSLVAETGGVIANRAELPKQRHEGQERFVLCVRNPFDFASSLLSHMSLDTFVTSEEEQIFSWVAGRLPKHFSRGKQQY
LDVALSGLRYSGYVDAVVQRWVLVVDEYLQCPQEFVLVRYEDFSSDPVQETRNLLHALGFAHLWGQGAEERVRQVAEVQY
QTKGQHGRNPEEVFGPRMLARVVVAVQTRAELLGYGSLLPAVKAVPEDWPAIDVPPTPVVFELHAEELWGPGKQIPAFEV
VKAPVPPPAPEAEETKRPTPVPPDITSLRFRAGDWKPGQPGGGKQPPLTTTGVAPWAFKGGAGSKQPPVTVTGVAPWAFK
KDAAPPPPPPKLNSLEETPEEEEEQKPVSGLDRVHKYMKLLLPAAPAEGPTSWEAALMEEAPTLLPTLKFHNLVYGAEDI
GQGAFSVVRYARAIQQEKTQSQWPEYAVKVINTKTMEELGYEASVNREICVLKMLSHPGIARMVAAFRYRDGAYLVLEYA
HKGDLHNILVGAGKLEEDVVRFLVGEVVAALCAIHDIGFMYGDLKPENIVVTSSNHAKLTDFGGCRPITDEALALAAGHG
QLTVPTVRGDSLGRRESHEQRAPVYTLDGNRGGYSPTSMRCHDFNPDSDGPKTTLQAGSSFDVTWTMEAGHPGDCYFYVS
YDPDPSNVANFFKIAAFPGCGAPDGLNIPSSVSTSVLLPAELPACEHCVLRWEWTGHQQVVNIEFYVQCADIKIASSAQP
VLPSPMTPISGIEHLPQGAEGYRKVYNGQGPEEQYLVGPAIATYSSCDANTPGCLGLGIAPIPTDSTSPSAVTSTTSETS
VVTSPSEAGCTCTPSTEWTGDFSQYASDQDFCSQNFGGSNPWISAGGGPGTSGGFSGAGPCTSGQYNFQEDGSWHILAGQ
EALGVMPYRAFAYAQFCNGKAYSECWTTGAAAFSFSLMVRGVSQTGAFVKVLFWTDSGNILGLVPPSHPKGEGKLRLVAF
MTDDYPNSWDFELEISESTWYHIQVAFQASTGAAEISVNGVVLGSGTLPVNMLAATTGPQIGIYSFDYGTSWPAEGVVLS
LADVCIGEVAGSCRSGVIASPTETVASTALSTTAAGATSGFAITRHDGIMDAKDTVCQVAMLSIRSEDMLAYYTADQFAT
GFKKRPAFQLRGITWNSGSSCEGIWITKRQPGSSCPSPDVMAFVGSKDMLCRVAILNIGWEDTLAQFTIEESATGFKKSL
AFQPDGIKQSKVPSGEGIWTTNRQPGSSYTSPDVLVLMGSKDTLCKVVMLSIGVEDTLAHITMAAGFKKMLAFQPCGIKP
SRGSSGEGIWITTRHRSCAIFDFVVGTGQLFRLLVTSHPCLVSAYYAYRFLRHRTSANEAAGTTTSAAQSAGALPGADSS
GADSCPLEGFGLPSFVSQCYCGFVGPDGAGCGPDDGTACWCKCCCHHVAGGSCRYRMTEMEAMDELSSHAVGASIGAMSM
GTLGVMLTVLAAVRCRQALLKRLRDGDWQAQDVPEATPAECEEEELVAEDDRVEGTMLYLPPETAARIPFLSGMADFQQF
LSHGLLSFLCPKTCTSVMRLDFECARHLLLHEHGFFSMQASIPPNALSLEDVTLVEGDRSGYWQELQAVLNSHSVGLPIA
GTHSVASLIKIASTSGKEPARELVFQMAAVAEKDRGNSFFKACSYEKALASYSRAMALLGLLSGKIIADGTTEASASLDL
SVSLCNNRSLCFLKLGRTLPAMKDAEKALGMLGGHSKNIAAWSKAMHRLASACTRAGLFKEAGTRLDTIEKATRSRAATA
ELRQVLRSLRENCSVACSGHKFLLDHLKEQRAGLSEALDDADVAVAWFVIREHFASFPLLFLLDMPELRQRCRKLPGKML
NLMAMIQRSQDPLNPYTGGKMTEFNVEKLRSMIEGAYLQTENERKRRQSLLELANSAKRAFPAEQIAEELGVDLEEHPDQ
EEVHQQLILLMRWVLAYLELDDFQFDAARESLHRLIFHVTVHPKAAKYFPDHINRLKSPMRTDFKNPYVGSQELDIVPFP
KWYLAALLHLLAVCECGRGDWRSCGSAIESYFDLVPKSFRDRNWESALFLRAWAELKPLQLERDSEEFHRIREKRLERLL
KETTPVWKELQGLYGKDFAAAFETETWVEARFYTDLGFSLPGSFQDIQDQLQRHQDKMPRLAQDDPFSCSLETFVGRAQG
VTVRFRTSLEEKARQAQRSRGPSRYGAFAMPDVENELYEMQQNLFASVMGGFGLNGLGNALGGESDSDGEGEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEQEQEQEQEQEQEQEQEQEQEQEQEQEQEQMELEDLGEEVVRGARPSLAS
DAWALGCLVYQLLTGRPPIWADSEMEEDIRRCIISFKLDDVTACYNTA
```

3592 - 3611:	EEEEEEEEEEEEEEEEEEEE
3593 - 3612:	EEEEEEEEEEEEEEEEEEEE
3594 - 3613:	EEEEEEEEEEEEEEEEEEEE
3595 - 3614:	EEEEEEEEEEEEEEEEEEEE
3596 - 3615:	EEEEEEEEEEEEEEEEEEEE
3597 - 3616:	EEEEEEEEEEEEEEEEEEEE

3598 - 3617:	EEEEEEEEEEEEEEEEEEEE
3599 - 3618:	EEEEEEEEEEEEEEEEEEEE
3600 - 3619:	EEEEEEEEEEEEEEEEEEEE
3601 - 3620:	EEEEEEEEEEEEEEEEEEEE
3602 - 3621:	EEEEEEEEEEEEEEEEEEEE
3603 - 3622:	EEEEEEEEEEEEEEEEEEEE
3604 - 3623:	EEEEEEEEEEEEEEEEEEEE
3605 - 3624:	EEEEEEEEEEEEEEEEEEEE
3606 - 3625:	EEEEEEEEEEEEEEEEEEEE
3607 - 3626:	EEEEEEEEEEEEEEEEEEEE
3608 - 3627:	EEEEEEEEEEEEEEEEEEEE
3609 - 3628:	EEEEEEEEEEEEEEEEEEEE
3610 - 3629:	EEEEEEEEEEEEEEEEEEEE
3611 - 3630:	EEEEEEEEEEEEEEEEEEEE
3612 - 3631:	EEEEEEEEEEEEEEEEEEEE
3613 - 3632:	EEEEEEEEEEEEEEEEEEEE
3614 - 3633:	EEEEEEEEEEEEEEEEEEEE
3615 - 3634:	EEEEEEEEEEEEEEEEEEEE
3616 - 3635:	EEEEEEEEEEEEEEEEEEEE
3617 - 3636:	EEEEEEEEEEEEEEEEEEEE
3618 - 3637:	EEEEEEEEEEEEEEEEEEEE
3619 - 3638:	EEEEEEEEEEEEEEEEEEEE

A0A1Q9DU64 **A0A1Q9DU64_SYMMI** (1413 aa)
Replicase polyprotein 1a. *Symbiodinium microadriaticum (Dinoflagellate) (Zooxanthella microadriatica)*

```
MWLLPVAGVQQLALAPRGLKRSAHRIMEVSKSVEGQARRVVEFHQAHISAPWTVERFGKAVANALTVIFDLAQAAVLVQL
PQALTAPGGAAPAPSVEGITCSVTVAESPVRWTCAAGRRRYFDSAGLAAAAPVSFVVMSEPERASAHEFDVVGVDDDDDD
DDDDADADDGDGHHHHLPRLVKLAGRLAVVDVDVRQKNLTGTCHLHRSFLLHALLLRGKRQPPTQTDTGDKESNPALGGW
EESSEVGPKDDEAFREEASAPSEQKENEAEEAATSQSRLQAAALGLGDVAPRQQSFRCLSLFGSISQEVFDPPLRARGLY
VLAGAEKTEWRPCEATAIRRRAEAESRRDTVEAMMLEQVVVEELRSVAGNRRQTSARPPLRGEILRNASRLFAPSRQDDD
EDDGGDGDDDDDVDGVYDDDDDDDDDDDDDDDVVVDSVYDDDDDADADADTGDDADDDDADDDDDDADADADTGDDADDD
DADDDDDDDDDDGDDDDDDDDNDDDNDGILDLAQLTRYEASDEVVQALVREAAESYSRSQEYLGIKPVPLPEKSPWWSPR
RSFGAETVSGCFGNRRGASGEALPSATAEGEARGGSLGDLPLLQNRATQRLAMPAVVLTTVALAGVVIDCAAAAAAAAAA
AAAAAAAPAAAYDDVDDDKLTKEQRQQQQEEQRGEPPPRSAERGGNLAPNRKFRNLPSPLVVQKSQAVAAQRLAAVSLIG
ESDPQSRLLQVSCAKASHQELGGKREPYSLQSFSRSMSDGFSRSASFYRITWPEWAKGKGESITLFYMSETGVVSPWRPE
IWAMMLIQCWTQRSSGLIARLMEALRVLGSIPRITGYAACAMLEREEEEEEEEEEEEEEEEEEEEEWQRRVLLAFLTAQ
LAQLAWAIRNQGHSAQEEAASYVDGVVPFPGDMISGVSEWKCIRFGHGVYDKESGQCLQNLKSLLTLMEGYAKLSKARYE
GLLELTPPLVYQRMALVSYEQHPLFRIQVIVERSATWLSVLRNICIDGRGSQEAKLNLDYALCPFCRGEEERLRHPAKRR
SLYFYDPFVQSVVQKHLSEIAKVILQTDKVPDSSEGGAPSANHLAIQKNIVHWAAQLASGAQQAAEDAEESEVVKLTAHP
KEFRGVLGEHFRKIVDLTERFTRIDGSLEQDGEALPSGVRPKGGQGISTMAGASTASTAVQGEGQGAPGAPGAPGAQLLL
SDISIRFEDGTVLRVDALASATLMTASPVFHKMLTHDMKEKERSEIELPGKDPKQFETLLKFLMPSAGRKQKLSDENVGF
LRKLCEEYMIETLREECVDFIRTAEPSTKVLVAAHALNLDDNVRRGIDELLGRGIRDWGECYGDSALMQKIIERTMTFLQ
GKESQLRLKESEVQAGMDQLRLMKKKLDGSQSRLQQAENQLRERDAHLMRTYR
```

846 - 865:	EEEEEEEEEEEEEEEEEEEE
847 - 866:	EEEEEEEEEEEEEEEEEEEE
848 - 867:	EEEEEEEEEEEEEEEEEEEE

A0A1Q9E4C6 **A0A1Q9E4C6_SYMMI** (4808 aa)
Autophagy-related protein 18. *Symbiodinium microadriaticum (Dinoflagellate) (Zooxanthella microadriatica)*

```
MAADDARRSPEPGPISSDFEFRSAIAATAMRAVALLQAAVVWFLAHPAAAESTPALDVCQNEATCEHLPLAGDEMSALQS
DMSALTKPEKVHEKVNKKKHKKAVIKQVRKRKLKKSLKNAWKHRLDDDVSALQSDSSASTNPEKIHKKMNKKTAKKEVIK
RARKRNLKNGLKKAWKHRNKDSRPFSRLPIGANLCNNTYARGDGCIPEAQTPKEILCLAFNQDGSCLAIGRARGFDIFST
ETAALLHREDCGMVRLVEMLFRTSLVAVVSFSRSRQLTMWNTRARTGICALQFPSEICNVKMNQRRAVVLLRQKVHIFDL
RTMKALHVLDRSEPAPGLDPSLASLCCDSELTQRAQIALGVGTARLLDSSGVVLDGYAEIRNSRIQNGDSLSLHVNTVQI
QATDVACAAILGDGSVVTWGRSGDGGDSSAVQGQLKNVQQIQANGSAFAAILGNGSVVTWGAAGDGGDSRAVQDQLKNVH
QIQASDGAFAAILGDESVVTWGRSGDGGDSSAVQGQLKNVQQIQATGSAFAAILGDGSVVTWGAAGDGGDSSAVQCQLKN
VQQIQASQFGAFAAILGDGSVVTWGDAGYGGDSSSVQDQLKNVLQIQATREAFAAILGDGSVVTWGRSVLGGDSSAVQEQ
LKNVQQIQATGCAFAAILGNGSVVTWGAAGDGGDSSAVQDQLKNVQKIQADTAFAAILGDGSVVTWGHPVASDSRAVQGQ
LKDVQQIQATGWAFAAILGNGSVVTWGAADNGGDSSAVQDQLKNVQQIRAAHKAFVAIRGDGSVVTWGVAANGGDSTAVQ
ERAASGITAPGGLRGLLAAPLVAGSQGAPPDARAGLIGLVDTYTLQPAGAVMAHRTPIRAMALNASGQLLATASARGTVV
PGYGFGTATQGAFGASLSEAVPSLTMLCSFRRGASECCIHGVGFAADSKHLLASTANAMIHVFRCPKQAVEGISPTSLAR
AIGNIDSKYKYSSNMRSLILKAPDVKKPEVEEDDDLSDWNIVDCDRAGRETRRVETGGLQGHVHKVKSILTQLWKPCRDY
LDGPSAVAWVHQGPEESNIAPKANPPRSPGLGPLLPLPPAMLEVFTTCSMSINVEVGLLSGKTVSVQVNLSEDAEVLIQR
ARIALGVGKGRLLDPYGGVLDGCTPIKKARIQNGDSLTLHISKVQVQTTGHAFAAILGDGAVVTWGVDIRGGDSGALQGQ
LKNVQQIQASGFGAFAAILEDGSVVTWGARGDSSSVQDQLKNVRQIQASSRAFAAILGNGSVVTWDAAAFGGDSSAVRDR
LKTVQQIQASYSAFAAILGDDSVVTWGAADCGGDSSAVQGQLKNVQQIQASHGAFAAILVDGSVVTWGHAAYGGDSSAVQ
LKNVQQIQASIDAFAAILGDGSVVTWGRADCGGDSSSVQDQLRNVQRIQASAYAFAAILGDGSVVTWGAAADDGGDCSAV
RDQLKTVQQIQASYSAFAAVLGDGSVVTWGSAAYGGDCSAVQLQLKKVQQIQSSGRAFAAILGDGSVVTWGAAAFGGDSS
AVQGQLKNVQQIQASRYGAFAAILGDGSVVTWGHATSGSNSIALQEQGFEKSCRTVDNCRPLQLPLHLRRRAKRADDLWW
```

```
RRAVDGSPPSIGAVAPPCRHHGRTATVKAYVHESVLDVDAPIKRAGLQNAILVDGSVVTWGDARYGGDSSAVQDQLQNVQ
QIQASDGAFAAILGDGSVVTWGDADFGGDSSAVQEQLKNVQQIQAIQASDGRAFRLFEGGAFAAILADGSVVTWGFAMYG
GDSSAVQDQLQNVQQIQASDDAFAAILADGSVVTWGDARYGGDSSAVQDQLQNVQQIQASDGAFAAILADGSVVTWGDAG
DSRAVQNQLKNVQQIQASDDAFAAILGDGSVVTWGRSDCGGDSSSVQALTSDATLPAPAPSFLPRQMQHGLDLLETPTIK
PVPSPLLIEACSESSSTAKTPVKTVGARAGYRPEQGVLEIPALPSILEGEVAGPTYGAADDRGSNGWKRPWFADTGRVTE
FSVALSALTAWNTDGPFDEPGDEAGYDFLDGKVVMEEVRKQVKAALDERESEMKRLHDENQELRQVVMALSEREFSGEGG
GQNSGVLMEGSIGPRGGEPRGNPTLERRDAVAVGRAPPGLSAQSPVPGGEPFTGASLEAPPGLQRQVEYPVSSVGRMSRL
LAPTGLSAQSPVPGGDPVRCAPSDGHGGFQGQWLAGDVGGAEPPLAPAGLLAQSPVPGGNPSGDGSKSADPESQNGLLGT
SGHGEGILGDEHEGPGTGAAIGEDNAMVDHLHLLVQGMRQLQQLQMNKKDHPEAEAVKGSVELQKMPEPGDAAVEFNDWM
YVTEQMLGALTDNASAWFGQCLQCAREAYAKYQDASALERLSITPSLTDSLRDPKWFRLERRVLSLLLSAMPKAVKEDTI
THRIETVAGVLYRLHVIYQPGGTLERTAILKHLEGTVGSEDPGEVVAQLRRWRRHLARAEEMAIALPDASLQLKGLEAIT
SKVLEKLPDVKFRLALAKNELRLASTPTAETVLKFYQHLLAELQQVTPTVKTENAKLKGATTGTSTGQGTGGSGTPGGSP
KKGKNPCKFFQSEGGCKRGTSCNYAHEFASKADRKQRCWSCGATGHRQQECPTASGGGKGNGKSNGAASTSSTTPTPKAT
ASAAQVHLPTGDAANLEGTAPPEATTSSSTTTATADEAVAQKEEMKKLLREASSMLSKIQLMTMRAAETDQATENLELLL
RSAGVDQHGLALLDSGASHPFRSAANPTEFEQASSVGVELADGQTVKLKQTNTGTLLKVEDGSPQAPIVPLGALVQQLGC
SISWSKRQGLKVYHPVHGDLKVKMKGTCPFVSELEALKLISEIEDKNLERLQQTTIRSLWASTPSTAPLPWTSNLEIYAS
TGKRGNALAATMDPSFPVYLETATQRFNFVGPADIDLSDESGWNYLKSLPVNRKNRRRLHGSRWMVHLYDGKNELATQEL
KKLETEDIAVLEIDVQRSKMYNLKGWNNVLRALLWAGCRGQLEGVLGGPPRNGDDELRQKLMYVWMVAENGADIRDLKRP
FLFMEYPGQKPWWKSTEWRNFRDEYQLSHVSLGQTQHQVFHAVSNMNFVNHVMEPGVDSTTPTTWTSGLLKAIVDGVKEW
KRWPDQVRQAQLLCKMEGCLEEMTEKELKQWAKHVRDGHVPFNKRCRTCVINAGSGRPHRKVITPSAYVLSVDVAGPFRA
KGVDADGKYRYALIGSYCMPRLDGYQEASIPQDFLPQPDPDEERDLDPLQPDPNEGRDPDPLQPDPSEGPDSGRVCHDDD
GKGVGVILDEDENFLDEEEAIEHPPSPEDQVDMDQKNDDYRKFYDDVYKEVGDPLEYQTLLYVVPLRSRQKVDVNAAMRR
MYLQLRQEGHPVVRVHSDRARELKSAALRQWLYEKDVWITTDEAQTPQQNGRAEAAVKNLKKYTKVLLGSTRLPRECWPL
AMAFAAQKQRKRALGQPSDKDPAFGVKVAVKSKVFGTGGSYDLDPRWREGRFVGYSSDVKNGLVVRYDDGTFVTSCHVRE
GLVEAEAIVDEEPIEVGLPVPSRRMRTKARLALITSVYEDVEAYAKDLRSEEMYDLETVLRLWERIKRVPRPTRRGAKAM
STKDDGGAFYAGCYVHGGVCGVMKLAKQSPNTTAYLVEAAKRITGRDHFGSVAIVENVAMGPHRDSHNHRGTSNIVTALS
NFTNGEIWVEALEDEYDYSDVWRQVTPGQWRRGKLHRLQPGRPVVFSPGQWHQTEPWEGDRVALLTYTPRLTNLSKEDKE
EFMSLGFNLPEQQGDQDEPEREEGARGSIFEPPDEEKDMVWFKCVAGLNEDQRDLLEELQERSLSLRRLLEEEEILLEEY
RRMAKQVTEEANNTHQVLIDMMEQTAEAITGQEEDNAINILKGIQVEQPETDGIDDIEKHLSELTSDLQVVLNVPLDQVK
SNLPLWVPAIDKELETLFKNGDSGTLRRITMKDARERERRGELVIVPSKLVFTCKPPNQGAAPKAQDVSKGKEARAKWRR
KCRLVLCGNFAERPEGQSQAELYAAGASADSMRVALVLASACYWAGAGSDIQGAFLLAPWPKPMRRYAIVPPKTLILAER
ATETEAWEVDRALYGLRESPAVWSDFRRQRLKKAKAPWKDGFLTLRASIVDPEVWMILYTTEDGPDVLTGVLVTYVDDLL
YLAENQVIIAMHSWLCEDWPSSPLEWTVDGTRYLGVEIEQADDGHFLISQRGYLESLVRGYDLEPGEHARLPCPREWLVD
DEGADEVTAQEDYTPEELKRAQKITGELLWVTRSRPDVLFVVTMMASALARRPCHVYRVGLKVMAYLAASVNVQLQLGGA
LTVNHINGQRQLADLPTKLHSRVRMSELMSAAQEELDKEALRRELEAETASLPPSLEINAETTDGGADASKLRVLRDTPP
DASQGEEMTETVRSQEQAEGDLEEPPKPAAEEELEVPAPASNSEEPSLAVPPVAPMEDDQDAASAEAETVSVGHEPVQDE
SDGEASLASCAEEMPLQEPEDSDAEEVASGRPLETAEEQVQRVPSKDQDLGPPEEEDEELQLPEEVEEVEEEDQEEEEEE
EEEEEEEEEEEEEEELQEEEEEELADGEEPEEATATKSADDAEDPLSAAARTLLVVPVETAPAILPAPFNRTAPVRSRQED
LDEDFAAGNRREKRRQRREARRSLAVTPGAREEEDSDGLRPRKGRKGRRRSEDRQAPEAPQAPVEDAPRRAKRAAKRAAK
AAAAKDSPDSDEVFRKRPRDCTHDRPAIDLVDGVCRRQLAMTICGLERLLERRPLDAVDGRRPARAEWPNSYLRQLLIRS
VQHPGVCT
```

4555 - 4574:	EEEEEEEEEEEEEEEEEEEE

A0A1Q9E4T2 **A0A1Q9E4T2_SYMMI** (715 aa)
FAD_binding_3 domain-containing protein. *Symbiodinium microadriaticum (Dinoflagellate) (Zooxanthella microadriatica)*

```
MGSRVIILSPIISLINLFYMFKFGIFLLAIAAIFGLQWYFEATTTEGQCPGCGVLQRGSNTEPFNCGMCGLELEVKDGQF
VRYMKSGQAPQTPFEQIRDFAKQAAETKPPPKASPKASSAGKKKSSSSEVVDVEGPEGSLSYCRQNMQDMAASEESAVHG
RICILGAGPAGLGLALGIARRGFSGGVVVYDQAEDHETAPRYNPDRSYTIDITGHGARALDYLGVVHRFDEQLIKFRGIR
ILPLGKEEPWTGPGWTGSRGDICRALMRECREKYPGKVKFVFGTTAEVQDAYTGTVVLKDGSGGVLEKSFDLIVACDGAG
STARTKVMADVPGFKSEKTSLTNFCTMVHFDQNTEELDPSWLYVLNIDPPAVAGAINGDGGPRDPKWFCQIGFRCKNEFK
DVPDAIRYIKKTEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEAEEEEEGMCLTKSWQPSPSGSVCTLDGLWSATPSMQASKLLSSRGSGQSGSMT
KMTLWLVPRSLLLGLGLRLTPGGPLLPGLAGAGPSVIKDAETTRMRVPISPCGSLSWAHQPAFEEAAGMDGWAGAELVHL
PDGAFQFASDLFALQLLVPPFLTAARVHGRLVLLGDAGNPFPPVGQGINAALESAMVLDQCLAIRCRLIMDTITT
```

413 - 432:	EEEEEEEEEEEEEEEEEEEE
414 - 433:	EEEEEEEEEEEEEEEEEEEE
415 - 434:	EEEEEEEEEEEEEEEEEEEE
416 - 435:	EEEEEEEEEEEEEEEEEEEE
417 - 436:	EEEEEEEEEEEEEEEEEEEE
418 - 437:	EEEEEEEEEEEEEEEEEEEE
419 - 438:	EEEEEEEEEEEEEEEEEEEE
420 - 439:	EEEEEEEEEEEEEEEEEEEE
421 - 440:	EEEEEEEEEEEEEEEEEEEE
422 - 441:	EEEEEEEEEEEEEEEEEEEE
423 - 442:	EEEEEEEEEEEEEEEEEEEE
424 - 443:	EEEEEEEEEEEEEEEEEEEE
425 - 444:	EEEEEEEEEEEEEEEEEEEE
426 - 445:	EEEEEEEEEEEEEEEEEEEE
427 - 446:	EEEEEEEEEEEEEEEEEEEE
428 - 447:	EEEEEEEEEEEEEEEEEEEE
429 - 448:	EEEEEEEEEEEEEEEEEEEE
430 - 449:	EEEEEEEEEEEEEEEEEEEE
431 - 450:	EEEEEEEEEEEEEEEEEEEE
432 - 451:	EEEEEEEEEEEEEEEEEEEE

433 - 452:	EEEEEEEEEEEEEEEEEEEE
434 - 453:	EEEEEEEEEEEEEEEEEEEE
435 - 454:	EEEEEEEEEEEEEEEEEEEE
436 - 455:	EEEEEEEEEEEEEEEEEEEE
437 - 456:	EEEEEEEEEEEEEEEEEEEE
438 - 457:	EEEEEEEEEEEEEEEEEEEE
439 - 458:	EEEEEEEEEEEEEEEEEEEE
440 - 459:	EEEEEEEEEEEEEEEEEEEE
441 - 460:	EEEEEEEEEEEEEEEEEEEE
442 - 461:	EEEEEEEEEEEEEEEEEEEE
443 - 462:	EEEEEEEEEEEEEEEEEEEE
444 - 463:	EEEEEEEEEEEEEEEEEEEE
445 - 464:	EEEEEEEEEEEEEEEEEEEE
446 - 465:	EEEEEEEEEEEEEEEEEEEE
447 - 466:	EEEEEEEEEEEEEEEEEEEE
448 - 467:	EEEEEEEEEEEEEEEEEEEE
449 - 468:	EEEEEEEEEEEEEEEEEEEE
450 - 469:	EEEEEEEEEEEEEEEEEEEE
451 - 470:	EEEEEEEEEEEEEEEEEEEE
452 - 471:	EEEEEEEEEEEEEEEEEEEE
453 - 472:	EEEEEEEEEEEEEEEEEEEE
454 - 473:	EEEEEEEEEEEEEEEEEEEE
455 - 474:	EEEEEEEEEEEEEEEEEEEE
456 - 475:	EEEEEEEEEEEEEEEEEEEE
457 - 476:	EEEEEEEEEEEEEEEEEEEE
458 - 477:	EEEEEEEEEEEEEEEEEEEE
459 - 478:	EEEEEEEEEEEEEEEEEEEE
460 - 479:	EEEEEEEEEEEEEEEEEEEE
461 - 480:	EEEEEEEEEEEEEEEEEEEE
462 - 481:	EEEEEEEEEEEEEEEEEEEE
463 - 482:	EEEEEEEEEEEEEEEEEEEE
464 - 483:	EEEEEEEEEEEEEEEEEEEE
465 - 484:	EEEEEEEEEEEEEEEEEEEE
466 - 485:	EEEEEEEEEEEEEEEEEEEE
467 - 486:	EEEEEEEEEEEEEEEEEEEE
468 - 487:	EEEEEEEEEEEEEEEEEEEE
469 - 488:	EEEEEEEEEEEEEEEEEEEE
470 - 489:	EEEEEEEEEEEEEEEEEEEE
471 - 490:	EEEEEEEEEEEEEEEEEEEE
472 - 491:	EEEEEEEEEEEEEEEEEEEE
473 - 492:	EEEEEEEEEEEEEEEEEEEE
474 - 493:	EEEEEEEEEEEEEEEEEEEE
475 - 494:	EEEEEEEEEEEEEEEEEEEE
476 - 495:	EEEEEEEEEEEEEEEEEEEE
477 - 496:	EEEEEEEEEEEEEEEEEEEE
478 - 497:	EEEEEEEEEEEEEEEEEEEE
479 - 498:	EEEEEEEEEEEEEEEEEEEE
480 - 499:	EEEEEEEEEEEEEEEEEEEE
481 - 500:	EEEEEEEEEEEEEEEEEEEE
482 - 501:	EEEEEEEEEEEEEEEEEEEE
483 - 502:	EEEEEEEEEEEEEEEEEEEE
484 - 503:	EEEEEEEEEEEEEEEEEEEE

485 - 504:	EEEEEEEEEEEEEEEEEEEE
486 - 505:	EEEEEEEEEEEEEEEEEEEE
487 - 506:	EEEEEEEEEEEEEEEEEEEE
488 - 507:	EEEEEEEEEEEEEEEEEEEE

A0A1R1PG67 **A0A1R1PG67_ZANCU** (991 aa)
Uncharacterized protein. *Zancudomyces culisetae (Gut fungus) (Smittium culisetae)*

```
MSSVVIAKTLDREPESRVGVCTYSGANEAEEHNACAQRDVSGEESSGVGGISEQIPEDEETEDEQEEVSEDQQEEESEDE
QEQVSEDEEEEGSEEEEEEEEEEEEEEEEEEEEENSKLEINSRYENSEETETEGITYLTKEQAAVMAQNVAYKLDTNLEDN
HWSEQEQTRLRASLEGGKRSTSVQNDANAVVDSEKLYGSEYQAAGYERRMSNVSNQLQEIFDSSSATESAFEAESPKQVS
KIKVEAMNMDDGDECVYIENHNQLNGSKSTVGSLDEKKTLTFGTEGEGRVFDVQNKKKENFRRETNGAKAEPNLVSVVEN
ERIRAEGKGKKMFGTSKDLEKMVGNAEKGTDRYTRKTGTTGYNSSRVDTEKLSNKTKIANIRDARLQGYEAAGDKAEQHH
SHKNRRHTSNAELNDTAIGKSQSYISGVDGQIQENRATKQRENESINTHGLGIGYGKGRLFRSRTHHNSNTNFDSSSRDQ
PLLSKGDSIDTRQFVTNRNEDSYVRSDGSGSGGGGIEVGSSQSHTDNEGGGIYTAHNGSEPEHILSFRKSTGTVNATTDS
TLVSSPDPFASFTENNSIQQPFSSRSSIMGIPGGSNLPQNSNSNSNNNNNNNNNNNNNNNVNNSSNLTNTPYYFKNSNL
STFEFNSPSSTMLKRTSTIGNRFNLSNIPSMHTQNHSGFSSLINDSYERDILRNVTRSEEEMFGSRVRRSPQSSTSSCSI
PHLKDGLFANSNSPDSNPGYQNSKYYDSRFGLNKLDTGRELLHSNDYYDALFDISSKNRATNNDASTNDSYTTFSKAYTQ
NQCANRRPFDKLQAYTPNRLSAHYGAGSQNTHIDSMGRSSFAPSGGGWYLPENQPISSTTGFSSPISQRNDGAGSTPLGP
RSFDNDARNSHFFYESYPSSLSNPAFASLSPNEQITNHVTAPNGSTYSVLNDKHLIDYFNSSSSSSSSRSAVRNPNADYQ
RRNINHSPPKNSLNSAKLSSKSVKKSSFATP
```

94 - 113:	EEEEEEEEEEEEEEEEEEEE

A0A1R1PP44 **A0A1R1PP44_ZANCU** (607 aa)
Putative serine/threonine-protein kinase iksA. *Zancudomyces culisetae (Gut fungus) (Smittium culisetae)*

```
MFDGRVRSSSEEMIRFGTSDVMTTELESRRNIQSGRARDMGGLRGRRGSGRRMRDELGSGEPGYRYQSFERHGGGNAGES
GIGGIGGIGNLHSGRYCPTCFREFEEEDLWYESGGGNHLIMNKEYFTYLLKAYNTSKKLGLPYKSTEEQPTELGVEVDME
TTEINNGGNLYEFVEGGGDRNRSGGGNGSGDNYGVRKRGRGESGIDVEDGVSRKARKSLRVKRMLERENKMGSGLNKGGN
KKKKRNYLTEEYIWAFFSDICEGLLFLHKKGIIYRDLKPQNLLLKAESKYGKDNSERVSGIQCDKIKPDGTGEFGSGDRG
GGEKNSVGDSIPRVLLSDFGECEILTGFGSTKESRRQQGKRTGATGTLEYMAPELLRVNEQGKYYDEYSTKADMWSLGTI
LYFLCYSTVPFVRKLKKTDKKIDKKSSRDSVDNRDDNGNEINGLVINEEDGDGDGDGDYEKRYEEEEEEEEEEEEEEEE
EEEDYDKIRSQILGFKKVRFPKVKDRGGKGPISDELKELIKRLLSVDKEKRPDVEEIIEQVSKKRYESAKASKMMAFTPI
KSRGVNSRDEIMKGYEIGEDSGRDAAGMMWDDGRYKKIGTESGCLDL
```

464 - 483:	EEEEEEEEEEEEEEEEEEEE

A0A1R2B558 **A0A1R2B558_9CILI** (246 aa)
Uncharacterized protein. *Stentor coeruleus*

```
MPKGKKSKKKVQEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEEEEEEGEEDEDEDEEEEDEEEEGEEEDDEEEEEEEEEEE
EIRSNQSHDKEQPEPSFYQMPRFGGVDAIKSINYDLECISDEIDKLFNLQLKLSQRELKSPLPAISQHEYSDYRVPYLTK
EPDKASNPFSNHNEYEHTPKSNYSEDIGNFAIPSKYFTNPQRPCAQPRSIEEFYNNPRKNDEPISLVKETKPRGLGFFNR
NAPPYY
```

13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE

A0A1R2C4T0 **A0A1R2C4T0_9CILI** (1277 aa)
Uncharacterized protein. *Stentor coeruleus*

```
MMISGLLLLYSSFLSFVLAEVLIEYHLFENFGDRLYDYSQNANYGYNGKSTDSFSFKDTIFTDKGAYFKGTNTAIILPDK
NNAVNYFLFPQEFSIAFWVNLKNYNEYDNEGDGDGDGEADGEGDEEGDEEGDGEGDGDGEGEGDGEGDEEGEADGDGDGE
ADGDGDGEGDEEGDEEGDEEGEADGEADGEEEEETDGEEEEETDGEEEEADGEEEEEEEEEEEEEEEEEEEEEEEEEED
GGGDGDGEGDGDGDGDGDGDGDGEGDGDGDGDGEGEGDDKNSDDLLLFIRYLDEANYFYISATKDNQLKLYVKGSSKANS
MILNELVPNSWQYIVLTLDKTSTFILEVLNEAKSSLTLDYDYSEESTDFIWFIGSNLLDKSCIQGFVWFFAFLSDYESIS
DYYAHASNNCWYNEAECISSCEPAFKYKGSDYCIDGDINANDDKCIDTCNNGCKDNICLDCDSDCDSESCIIIDNKVSCI
CLEDSTGDDDKCNYSLCSDLCKYCTLGICYECISTLMHPVEDTCVCNDNYFLDGKECKSAQCSELCKTCIDAKCILCNDE
NSLPIDDTCECDSGYYLEGDKCLPYQCGDLCLKCDLNVCLECANEHMHSVGTYCICDDDYNLNEITCYEKPCGNLCSNCK
LGECQECIDQNMYTINDNCKCKTGYYLDDNKCLSEPCGSLCSDCNLGVCYDCVDENMHIANNDCECNDKFYLDKTSCFPC
SSNCIKCNSQGCEICDSEKGYNLVDYKCVCPAGFIDSNGCYSGAFSVVISITSANQISLSFSEMLLSNLNVEDLEIIIDN
VSYKIESITSTDSQTFVITVDADFNNIKAANVEVNFLSAIKSSSGNILIVSPESKVENKIIIAKKYSQTYIDHISSSAKT
ISRSFIGASAILGLITGFSSLWILLNTLQIISLMPLNSINYPPTTIQFLASFNNMNLIPNILVYIFGSGNDATAYLESRR
YGFQTSIIIINSTTYIVSMVISVIIIPFLYFGTKLSNITISKKCSERLADYRYNYFIRFWIQGFLDLVTLSLVQIKSEFT
FEVLWMIGAVASISILTLAFLTVPAFMRWTNNHYYKIIGNGNREFLLRWGSFYEEFKNNRSFWSTQYYTIFFLRRIQFAL
TQAFMNSNLKLQAGINIVASIFQFGYVIYYSPQKERKLYYSEIIGEICTIEVMFVSTLFLSYTDDATRNVLENIIIISVI
ATIIIQVGISIYSAISPLKNLFGSSNSNISINPNASLSVAPKSAKVQPIKNDTIITDLAENTNDSIITGNSLKNKHY
```

213 - 232:	EEEEEEEEEEEEEEEEEEEE

214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE

A0A1R2CA83 **A0A1R2CA83_9CILI** (387 aa)
Uncharacterized protein. *Stentor coeruleus*

```
MLIFVFLLITQALSRNFYDSASFIQMRLALKMMDDEEDNLSEFIIDVLEDDSDDSTIEDDILNDIMLVDDSDDITLEDMV
ILALEANEEDEATDEAAVEESEEEESDNNDANEDDADDEEDEDEEDDEDEEEEAEEDEDDEDEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEDEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVVE
EEVVEEEVVEEEVVEEEVVEEEVVEEEVVEEEVVEEEEDLAAKALSGWFLELNDEEIQNDLDSDGTVETEVPDESVADMEIPNDA
EVTDMEMPDDAEIPDDTEIEEYSEEEAESDVPEEFREVEPSEYLPFDPQEKFTDMAKEEGLEELGLV
```

143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
184 - 203:	EEEEEEEEEEEEEEEEEEEE
185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE
190 - 209:	EEEEEEEEEEEEEEEEEEEE
191 - 210:	EEEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE
194 - 213:	EEEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEEE
196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE

207 - 226:	EEEEEEEEEEEEEEEEEEE
208 - 227:	EEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEE

A0A1R2CYI4 **A0A1R2CYI4_9CILI** (549 aa)
Uncharacterized protein. *Stentor coeruleus*

```
MEPKLSSSAEDKIKSIKTIKEGKYLFENAFIRYTDEISMLILKEQDQESLSKSDSALKIFTRAVYKDIKGFQSGLEVFSN
SLNKVGICNKEKHLKKCFSVLNRMACIEESTHGNLEIDFKSWQITISIVGEKIKRQLNDLKSMNDDDKLSQEKKGEINKN
LKQIGENKKVVKGVKKLCSKNKRSSAVKKSKLSKNNATSRLSKGSKGLLSQKGKSKAKKENIKKQKNVKGEEELKDKIEG
LKEENKDVEGEEDEEYEDEDYDDEDYDYDEDEEEEEEEEEEEELEEVKKVELVEEKLGAVKSQESNSLTNKDESKNNQVG
KEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEVNENERKILDENKASDIEAKTSTNAGAKEQTETTNKN
DLNQGKEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDKKEDKSEDKNIINDKDKAIVNAGIKENTE
IIQIKPDEEEEDEDEDEEEEEDEEEDEEEEDEEDEEEEEEEEEDEDDEEVVDQKEVKNEIKEEKDSNKS
```

322 - 341:	EEEEEEEEEEEEEEEEEEE
323 - 342:	EEEEEEEEEEEEEEEEEEE
324 - 343:	EEEEEEEEEEEEEEEEEEE
325 - 344:	EEEEEEEEEEEEEEEEEEE
326 - 345:	EEEEEEEEEEEEEEEEEEE
327 - 346:	EEEEEEEEEEEEEEEEEEE
328 - 347:	EEEEEEEEEEEEEEEEEEE
329 - 348:	EEEEEEEEEEEEEEEEEEE
330 - 349:	EEEEEEEEEEEEEEEEEEE
331 - 350:	EEEEEEEEEEEEEEEEEEE
332 - 351:	EEEEEEEEEEEEEEEEEEE
333 - 352:	EEEEEEEEEEEEEEEEEEE
334 - 353:	EEEEEEEEEEEEEEEEEEE
335 - 354:	EEEEEEEEEEEEEEEEEEE
336 - 355:	EEEEEEEEEEEEEEEEEEE
337 - 356:	EEEEEEEEEEEEEEEEEEE
338 - 357:	EEEEEEEEEEEEEEEEEEE
339 - 358:	EEEEEEEEEEEEEEEEEEE
340 - 359:	EEEEEEEEEEEEEEEEEEE
341 - 360:	EEEEEEEEEEEEEEEEEEE
409 - 428:	EEEEEEEEEEEEEEEEEEE
410 - 429:	EEEEEEEEEEEEEEEEEEE
411 - 430:	EEEEEEEEEEEEEEEEEEE
412 - 431:	EEEEEEEEEEEEEEEEEEE
413 - 432:	EEEEEEEEEEEEEEEEEEE
414 - 433:	EEEEEEEEEEEEEEEEEEE
415 - 434:	EEEEEEEEEEEEEEEEEEE
416 - 435:	EEEEEEEEEEEEEEEEEEE
417 - 436:	EEEEEEEEEEEEEEEEEEE
418 - 437:	EEEEEEEEEEEEEEEEEEE
419 - 438:	EEEEEEEEEEEEEEEEEEE
420 - 439:	EEEEEEEEEEEEEEEEEEE

421 - 440:	EEEEEEEEEEEEEEEEEEEE
422 - 441:	EEEEEEEEEEEEEEEEEEEE
423 - 442:	EEEEEEEEEEEEEEEEEEEE
424 - 443:	EEEEEEEEEEEEEEEEEEEE
425 - 444:	EEEEEEEEEEEEEEEEEEEE
426 - 445:	EEEEEEEEEEEEEEEEEEEE
427 - 446:	EEEEEEEEEEEEEEEEEEEE
428 - 447:	EEEEEEEEEEEEEEEEEEEE
429 - 448:	EEEEEEEEEEEEEEEEEEEE
430 - 449:	EEEEEEEEEEEEEEEEEEEE

A0A1R2D3F3 **A0A1R2D3F3_9CILI** (881 aa)
Uncharacterized protein. *Stentor coeruleus*

```
MLPKGIAFMLLLLTIQGAQIAMQSKLSAQDQLSSSSSVSFIQQDDEIDNTEIDDNTDVEGEGDGEGDDLTETEDEGEDED
EDEEEDEEEAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAEEEEPAVDDAADDGASSGVTDDKPE
DEETTDETTDETTDETTEETTEEVVDEGEPLEEEPGEGEEVPELEEVVETETGDTGDEKPEDEVEEETEDGEETETQTPD
DVADDEVEEDENPTNDEEVEEIIDEAEEEPGEVEEDIEEVPLDQSEDPAEDEDEPLSTTEEVTVNVDDDETQDTLNEAAE
DEIDAAEEIEEETTTVNLDDSDDVDNENPAVPDDTEEAEVDSDVAINEEDIEDDGDFDIEETTTAETNVDDDETQDTLNA
AAEDEVEAAEEAEATEVTANVDDDESADTLNDDAEDEVEEETVTVSTEELEEGDDYDSETETVESNPDEVDGELEDETED
LTFDTDVDESADSENPAVIEEEVVEVVEVTVSTDELEEADDTYEIEETEEIEANTDGDDAEDNLNPGAEDEIEDAEEEDI
AMNDDTSDDADTNNQDAEDVEEEVLVPISETELAEGDDYDTAEDDEAEVNLDDDAAADTLNSDAEDEVEAAEDAEEETVT
ADTDTSDAADSDNPAADGAVEEVELSVTPVTEEEEDVADDATVNVDGDAATDLSNPAAEDEVADAEDDADEAEDSAGSDD
IALDSDVSADADTENPAAATVVETETDDLPIDPESADGVDEDEAEDLPVNPDGETDDVETDNVEDTVDSLAPLAEDEQEA
SDEEVAVSPDEQDDATAVVVDEFEEDEITPVSTDDVLEAEDEIEEIVEDEEADDIDWEFNIDLGVICCDPEPTGFLSINQ
E
```

91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE

A0A1S0UED7 **A0A1S0UED7_LOALO** (578 aa)
Uncharacterized protein. *Loa loa (Eye worm) (Filaria loa)*

```
MDKMLIKNEVNDEQLEDEQEEEEEEKEDEEDDEEKEEEKEEEEEEEEEEEEEEEEEEEEEEEVDEEEAEEKKKQNAINR
KPPLLLVTQSSTQNSPNHLTTEFTFVDNINFNMMQTNDGDNDEEGNDAILNMQNDNFETDMTVTETIELQTENDKTERKP
RDNHYPIVLSESRKHSLSPIPDYENDFNEEFIVEAPTRNNDNRGRVSEIMAIPAPIFAASISYDDMDDWDSTQEESVELL
SDYEDIDDFHSDEQYTRNRSCLENDEYCPSSSSIGIYFSPISSPTDDYDGIQYQDSVNVGCTLKLVQKAALKCDDDEESS
SECYDDSEYDEEEMYTNDEDDDEYTEDDETSEDLYTIDNISTEPLESAIDSISSISIPPLVVASMHEDDDIEIDEICDEI
FDDAFSVPVAILSNVEKIEIEENEIPEKHREITYTDEIHLKQNAEEVLKLTIKETNEDAAMEHIAEGATEIIVRKMVPQH
VVPAEENVEIVEIDELEVQKPEQVVAIIKEHDNEKETKQIEVIPTYVWPTTEDQPVDSVRSFIQRKPSTDWAKKAVVLAP
KFETVKIQKVQVRFDEER
```

40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE

A0A1S0UID6 **A0A1S0UID6_LOALO** (53 aa)
Uncharacterized protein. *Loa loa (Eye worm) (Filaria loa)*

```
MTQMIGVEKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEEEEDEKKKRDEQK
```

11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE

A0A1S2ZMJ1 **A0A1S2ZMJ1_ERIEU** (1140 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Erinaceus europaeus (Western European hedgehog)*

```
MAAAVLSGPSAGSAAGVPGGTGGLSAVNSGPRLRLLLLESVSGLLQPRAGSAVASVHPPARSAPHLPGLMCLLRLHGTVG
GAQNLSAVGALVGLSNARLGSIKTRFEGLCLLSLLVGESPTEMFQQHCVSWLRSIQQVLQSQDPPPTMELAVAVLKDLLR
YAAQLPTLFREISMNHLPGLLTSLLGLRLECELSALEGMKACMTYFPRACGSLKGKLASFFLSRIDALSPQLQQLACECY
SKLPSLGAGFSQGLKHTESWEQELHNLLTSLHSLLGALYEGAEAVPMQHEGPGVEMLLSPSEDGDAHVLLRLRQRFSGLA
HCLGLMLSSEFVAPVSVPVQEILDVICRTLSISAKNISLLGDGPLRLLLLPSIHLEALDLLSALILACGSRLLRFGSLII
RLLPQVLNAWSIGRDNLSPGQEKPYSTLRTKVYTVLELWVQVCGASAGMLQGGAPGEALLTHLLSDISPPADTLKLRSPR
GSPDGGLQTGKPSAPKKLKLDMGEAMAPPSHRKGDSNANSDVCAAALRGLSRTILMCGPLIKEETHRKLHDLVLPLLMGF
QQGDVLGTSPYTSSRCRQELYRLLLALLLAPSPRCPPPLTCALQAFSLGQREDSLEVSSFCSEALVTCAALTHPRVPPLQ
PMGSTCPTPAPVPPPEAQSPFRAPPFHPPGPIPSAGPMPSAGPVASTAPMPSAAPMPSAGPMPSVGPMPPTRPGPPATAN
HLGLSVPGLVSVPPRLLPGAENHRAGSNEDPVLAPSGTPPPIPSDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDSV
VIVPEGLPPLPPQPPSGATPPPVAPAGPPAASPPVPAKEEPEELPAAPGPLPLPPLPPVPGPVTLPPPQLVPEGTPGGGG
ATAMEEDLTVININSSDEEEEEEEEEEEEEEEEEEEEEEEEDFEEEEEDEEEYFEEEEEEFEEEFEEEEGELEEEEEEEED
EEEEELEEVEELEFGSAVGEAEEGGPPAPSLPAALPPAESPKVQPEPEPEPGLLLEVEEPGAEEEQGAEMAPTLAPEVLP
SQGQAEREAGSPPASSPPPQELVEEEPSAPPALLEEAAESGDDKKPPLPEPSAAEEEMEMETEAADLPEKEQDDTAAMLA
DFIDCPPDDDKPPPDTEPDS
```

898 - 917:	EEEEEEEEEEEEEEEEEEEE
899 - 918:	EEEEEEEEEEEEEEEEEEEE
900 - 919:	EEEEEEEEEEEEEEEEEEEE
901 - 920:	EEEEEEEEEEEEEEEEEEEE

A0A1S2ZTG9 **A0A1S2ZTG9_ERIEU** (394 aa)
coiled-coil domain-containing glutamate-rich protein 1. *Erinaceus europaeus (Western European hedgehog)*

```
MSQTLYTKEDPLNLGGGWTQAAAQASSSSSSCPRRRRGAPVFKRRYHCASKAKREPPRKHPQPQYGHGPWFQPAPRSSWS
MHPPWGPWGGPCHPASMGFWNPPSPVQVVWVYGLHPVCHLCCCCSCMHGSCNPGWVSPPGIKKRWGRWGRRGRQPRRTSK
KNPQVDLSTLLRPVNLYGWRAPGMRAPRNTTQFIMNQIYEDMRQQEKLERQQEALQEQQAQEGGEVAQTHVSPRGGEEEL
QETLYNFMQDPSLLFSQGPEEQEENKSPNLQMGEEEGEKNHKEVLEEEEEEEEEEEEEEEEEEEEEGSEAHYEEEVEEAG
NMLEGEKEEKIGEDQMEEEQRAEENHLPLEMPLSFLLGAEEERECFMDCSYLNPEEIMPNVSQDALLMVQDINC
```

286 - 305:	EEEEEEEEEEEEEEEEEEEE
287 - 306:	EEEEEEEEEEEEEEEEEEEE

A0A1S3AL89 **A0A1S3AL89_ERIEU** (1283 aa)
apoptotic chromatin condensation inducer in the nucleus isoform X1. *Erinaceus europaeus (Western European hedgehog)*

```
MPEAVGTDPSTSRKMAELEEVTLDGKPLQALRVTDLKAALEQRGLAKSGQKSTLVKRLKGALMLENLQKHSTPHAAFQPN
SQIGEEMSQNSFIKQYLEKQQELLRQRLEREAREAAELEEASAESEDEMIHPEGVASLLPPDFQSSLERPELDLSRHSPR
RGSSVSEEKGESDDEKPRKGERRSSRVRQARAAKLSECSQAAEEEEDQEAPSRNLRVRADRNVKTEEEEEEEEEEEEEEE
EEEEEDDDDEGQKSGAAPVLKQIEEEVGGELPRTKPEDVMDEKPQSVKSQEQEGLERGGRVTRSQEEARRSHLAKLQQEK
EIKIVSPLEEEEKEVKPSKALEEKSKSPSPPRLMEDLEKTPHALQPEQTISEEETPPPLLTKEASSPPNTRFQSEEVEPM
EGPAPPVLSQLSPPNTEAEAKESVAQHTVQLVGDLSPLSSPADTKAESPAEKEESALPPVQKDTLIESTQKSLETESEKS
AQPLPPKTVELALAKEIGEESLRQPSSEQMKNRRASPALLPSHRLERSADSSPSRSSSSSSSSRSRSRSPDSSGSQSHSP
PRAKQKDSSQPQTLGNPCGRSKMGSRSTSESRSPSPSRSASSNSRKSLSPGVSRDSSTSYTETKDPSSGQEVTAPAVPQL
HILEPKEKTSVSSSVQVRRMSQPEPAGKHMTQGLQPEPGSPKKCEAEDAEPPAATQPQTSETQSSHLPESERTHHTVEEK
EEVTMDTSENRPENEVPESPMPIADQVSNDDRPEGNTEDEEKKESSTPKSFKRKISVVSTKGVPAGNSDTEGGQPGRKRR
WGASTATTQKKPSISITTDSLKEAVVDLHADDSRISEDETERNGDDGTHDKGLKICRTVTQVVPAEGQENGQREEEEEEE
EKEPEAEPPVPPQVSVEVALPPPVEHEVKKVTLGDTLTRRSISQQKSGVSITIDDPVRTAQVPSPPRGKISNIVHISNLV
RPFTLGQLKELLGRTGTLVEEAFWIDKIKSHCYVTYSTVEEAVATRTALHGVKWPQSNPKFLCADYAEQDELDYHRGLLV
DRPSETKAEEQGVPRPLHPPPPPPAQPPQHPRTEQREQERAVREQWAEREREMERRERTRSEREWDRDKVREGPRSRSRS
RDRRRKERAKSKEKKSEKKEKTQEEPPAKLLDDLFRKTKAAPCIYWLPLTDSQIVQKEAERAERAKEREKRRKEQEEEEQ
KEREKEAERERNRQLEREKRREHSRERDRDRERDRERDRGDRDRERDRDRDRDRGRERDRRDAKRHSRSRSRSTPVRDRG
GRR
```

226 - 245:	EEEEEEEEEEEEEEEEEEEE

A0A1S3AL90 **A0A1S3AL90_ERIEU** (1256 aa)
apoptotic chromatin condensation inducer in the nucleus isoform X2. *Erinaceus europaeus (Western European hedgehog)*

```
MPEAVGTDPSTSRKMAELEEVTLDGKPLQALRVTDLKAALEQRGLAKSGQKSTLVKRLKGALMLENLQKHSTPHAAFQPN
SQIGEEMSQNSFIKQYLEKQQELLRQRLEREAREAAELEGRGSSVSEEKGESDDEKPRKGERRSSRVRQARAAKLSECSQ
AAEEEEDQEAPSRNLRVRADRNVKTEEEEEEEEEEEEEEEEEEEEEDDDDEGQKSGAAPVLKQIEEEVGGELPRTKPEDVM
DEKPQSVKSQEQEGLERGGRVTRSQEEARRSHLAKLQQEKEIKIVSPLEEEEKEVKPSKALEEKSKSPSPPRLMEDLEKT
PHALQPEQTISEEETPPPLLTKEASSPPNTRFQSEEVEPMEGPAPPVLSQLSPPNTEAEAKESVAQHTVQLVGDLSPLSS
PADTKAESPAEKEESALPPVQKDTLIESTQKSLETESEKSAQPLPPKTVELALAKEIGEESLRQPSSEQMKNRRASPALL
PSHRLERSADSSPSRSSSSSSSSRSRSRSPDSSGSQSHSPPRAKQKDSSQPQTLGNPCGRSKMGSRSTSESRSPSPSRSA
SSNSRKSLSPGVSRDSSTSYTETKDPSSGQEVTAPAVPQLHILEPKEKTSVSSSVQVRRMSQPEPAGKHMTQGLQPEPGS
PKKCEAEDAEPPAATQPQTSETQSSHLPESERTHHTVEEKEEVTMDTSENRPENEVPESPMPIADQVSNDDRPEGNTEDE
EKKESSTPKSFKRKISVVSATKGVPAGNSDTEGGQPGRKRRWGASTATTQKKPSISITTDSLKSLIPDIKPLAGQEAVVD
LHADDSRISEDETERNGDDGTHDKGLKICRTVTQVVPAEGQENGQREEEEEEEEKEPEAEPPVPPQVSVEVALPPPVEHE
VKKVTLGDTLTRRSISQQKSGVSITIDDPVRTAQVPSPPRGKISNIVHISNLVRPFTLGQLKELLGRTGTLVEEAFWIDK
IKSHCYVTYSTVEEAVATRTALHGVKWPQSNPKFLCADYAEQDELDYHRGLLVDRPSETKAEEQGVPRPLHPPPPPPAQP
PQHPRTEQREQERAVREQWAEREREMERRERTRSEREWDRDKVREGPRSRSRSRDRRRKERAKSKEKKSEKKEKTQEEPP
AKLLDDLFRKTKAAPCIYWLPLTDSQIVQKEAERAERAKEREKRRKEQEEEEQKEREKEAERERNRQLEREKRREHSRER
DRDRERDRERDRGDRDRERDRDRDRDRGRERDRRDAKRHSRSRSRSTPVRDRGGRR
```

186 - 205:	EEEEEEEEEEEEEEEEEEEE

A0A1S3AQB7 **A0A1S3AQB7_ERIEU** (1266 aa)
histone-lysine N-methyltransferase EHMT2 isoform X1. *Erinaceus europaeus (Western European hedgehog)*

```
MRGLPRGRGLMRARGRGRAAPTGSRGRGRGGPHRGRGRPRSLLSLPRAQASWPPQLPTGLTSPPIPCVPSQGEAPAEMGA
LMLEKEPRGATERLHGSLGDAPRSEETLPKANPNTLEPAGPSSPASVTVTVGDEGADTPVGPTPIIGDEPENVEGDSDLH
GGRILLGHATKSFPSSPSKGGACPSRAKMSMTGAAKSPPSVQSLAMKLLSMPGTQGTAALGAEPPPATASPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDIHSLGKVNSDLSKRRKLNPGGGLSEELGSARGSGEVTLEKGHPGSLEEWE
TVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAKK
KWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEELP
LCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAG
TFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDAGTLPVGSAAPAPPPLAQDAPGRADTSQPSAR
MRGQGEPRRPPSDPLADTIDSSGPSLTLPSGGCLSAVGLPPGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQ
KVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCV
YNKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHW
ASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLN
RKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSN
CLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFI
CEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDI
RTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNP
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE

A0A1S3AQU4 **A0A1S3AQU4_ERIEU** (1232 aa)
histone-lysine N-methyltransferase EHMT2 isoform X2. *Erinaceus europaeus (Western European hedgehog)*

```
MRGLPRGRGLMRARGRGRAAPTGSRGRGRGGPHRGRGRPRSLLSLPRAQASWPPQLPTGLTSPPIPCVPSQGEAPAEMGA
LMLEKEPRGATERLHGSLGDAPRSEETLPKANPNTLEPAGPSSPASVTVTVGDEGADTPVGPTPIIGDEPENVEGDSDLH
GGRILLGHATKSFPSSPSKGGACPSRAKMSMTGAAKSPPSVQSLAMKLLSMPGTQGTAALGAEPPPATASPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDIHSLGKVNSDLSKRRKLNPGGGLSEELGSARGSGEVTLEKGHPGSLEEWE
TVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAKK
KWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSG
CNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGE
DASEAQEVTIPRGDAGTLPVGSAAPAPPPLAQDAPGRADTSQPSARMRGQGEPRRPPSDPLADTIDSSGPSLTLPSGGCL
SAVGLPPGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSV
EICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYNKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDV
NAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIA
```

```
ARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCV
NGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECN
QACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYC
IDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHS
AEAIALEQSRLARLDPHPELLPELGSLPPVNP
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE

A0A1S3ASW6 **A0A1S3ASW6_ERIEU** (1894 aa)
Histone-lysine N-methyltransferase SETD1B (EC 2.1.1.354) (SET domain-containing protein 1B). *Erinaceus europaeus (Western European hedgehog)*

```
MENSHPHHHHHHQQPPPQPGPSGERRNHHWRSYKLMIDPALKKGHHKLYRYDGQHFSLAMSSNRPVEIVEDPRVVGIWTK
NKELELSVPKFKIDEFYVGPVPPKQVTFAKLNDNIRENFLRDMCKKYGEVEEVEILYNPKTKKHLGIAKVVFATVRGAKE
AVQHLHSTSVMGNIIHVELDTKGETRMRFYELLVTGRYTPQTLPVGELDSVSPIVSETLQLSDALKRLKDGGLSAGCGSG
SSSVTPNSGGTPFSQDTAYSSCRLDTPNSYGPGTPLTPRLGTPFSQDSNYSSRQPTPSYLFSQDPTVTFKAQARRHEPKF
ESKFADAYNRRHEHHYVHNSSAVSAVAGATSAFRGSSDLTFGAVSGSSGPPFKAQPQDSATFAHTPPSAQTTPTAGVSFK
SAFSPYQTPVPPFPPAPEEPPTTPTFGTRDSGEFRRAPVPPPLPPTESLTKEKPGTPPGPPPPDASGMELGGRPTFGWSP
EPCDSPGTPTLESSPAGLEKPHDSLDSRIEMLLKEQRTKLPFLREQDSDTELQMEGSPISSSSSQLSPLASFGANSQPGF
RGATPPSSPPSSTGLEDISPTPLPDSDEDEELDMGLGLRPPPKPGPPDPSGLLGQTAEMRLDLTGDRTPTSEKMDEGQQS
SGEDMEISDDEMPSAPITSADCPKPMVVTPGAGAAPSVLAPIPAPPGVPPPPILPPLPPFPPGLFPVMQVDMSHVLGGQW
GGMPMSFQMQTQMLSRLMTGQGACPYPPFMAAAAAAAASAGLQFVNLPPYRGPFSLSNAGPGRGQPWPPLPKFDPSVPPPG
YVPRQEDPHKATVDGVLLVVLKELKAIMKRDLNRKMVEVVAFRAFDEWWDKKERMAKASLTPVKSGEHKDEDRPKPKDRI
ASCLLESWGKGEGLGYEGLGLGIGLRGAIRLPSFKVKRKEPPDTASSGDQKRLRPSTSVDEEDEESERERERDRDVADTP
CELAKRDPKGVGVRRRPGRPLELDSGGEEDEKESLSEERESTEEEEGGEEEEEVPQDDDDSDAQDESENEDDNLALSEA
SEKEEGNSDGEETVSIATSKAGPGTSSESSESSEFESSSESSSSSSSSEDEEEQVVDEEEEEEEEEEEEEEEEEEEEVEE
EEIEEDEEEAESMAPTAPQDLEEDMSLEIPELESSGMEEEVDIEAEEEAPEEQTPMLEEPPSPVGVKEVTRCKEPPEELG
LNQEGVARLKSPEPPTREMEPRPPPSPEPIPEDDLEAEPEPPPVASLSAQPPLPPTQPPRPPSPPPEPETPEPPLPPAPL
EPPPEEQPPRTPGLCGSLAKSQSTETIPATPSGEPPLSGGSSGLSLSSPQVPGSPFSYPAQSPGLGSGGLPRTPGRDFSF
TPTFPDPGGPLLLPVCPLPAGRRDERAGPLASPVLLETGLPLPLPLPLPLPLALPVPVLRAQTRPPSQLPPLLPAPLAPC
PSPMKRKPGRPRRSPPAVLSLDGPLVRPPTGSTLSRDLLLLPGQPQTPVFPSTHDPRAVTLDFRNTGIPAPPPPLPPQPP
PPLPPPPVEPTKLPFKELENQWPSEAIPPGPRGREEVTEEFTDLTKVHGPWRRPPKKRHEDLVTSASPELSPPQPLFRPR
SEFEEMTILYDIWNGGIDEEDIRFLCVTYERLLQQDNGMDWLNDTLWVYHPSTSLSSAKKKKRDDGIREHVTGCARSEGF
YTIDKKDKLRYLNSSRASTDEPPTDTQGMSIPAQPHASTRAGSERRSEQRRLLSSFTGSCDSDLLKFNQLKFRKKKLKFC
KSHIHDWGLFAMEPIAADEMVIEYVGQNIRQVIADMREKRYEDEGIGSSYMFRVDHDTIIDATKCGNFARFINHSCNPNC
YAKVITVEAQKKIVIYSKQHISVNEEITYDYKFPIEDVKIPCLCGSENCRGTLN
```

1098 - 1117:	EEEEEEEEEEEEEEEEEEEE

A0A1S3B395 **A0A1S3B395_CUCME** (235 aa)
VID27-like protein. *Cucumis melo (Muskmelon)*

```
SSSSSSSSSSSLSIFSHPLFSALLSFFTLILLFFPPFLWTSLLSPSLLLAGFLFLSLLRLGATQREHQPITITNPQSIKL
TQPPEHWSGSPISSCFEESFVQWNVRAPLEVIYEVYEEEEEEEEEEEEEEEEEEEEEGEGEDQVKDDGTVVHMRSNPMERY
PSLSLYYPETDSDSSSAAAADEMENVCFMWDDEDRDEELIEIALDKKRVSSECFQLEEENLIEINISPTAFPTFV
```

117 - 136:	EEEEEEEEEEEEEEEEEEEE

A0A1S3BKG3 **A0A1S3BKG3_CUCME** (350 aa)
coiled-coil domain-containing protein 97. *Cucumis melo (Muskmelon)*

```
METAETVAAKGLSCEAMDCLSERLSLQEDLYFPRALQSTASNPSQRKAILLDLLSRDVAVFLERYGSQLTSNELHEFDAL
KDDYEINWHLKHLRSIKSPTSDELHTRSVIVKNRRRAYLSKLIYDGQYFSEDAMREREPFLHHEYVGKFQDPSGRGMARP
GERWSETLMRRSEEAMLVAKIRGEQRRLGVAERDLVGNNVNQGEEEEEEEEEEEEEEEEEEEEEEKEKEEEKEKEEEEEEK
EKEEEGEDNNKPENGVDSMEVTRAMDDQHERPATENSEGAEGGSNHVATLSEADMQDQMDQFTYIMHQKFLLGEDSEHLD
YSKIDNDETLDDHWMREANDDAEEKYFDED
```

204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE

A0A1S3C2S1 **A0A1S3C2S1_CUCME** (817 aa)
DNA ligase 1. *Cucumis melo (Muskmelon)*

```
MAIPALSPSQSHSEDQEEEDPISPFQNPNSMDHQQPGEAAEAPVDVQQNHFDPPQSSQTLTLDLPDPQQNSPQPDPQDSE
LQLNENFINDHDPSDQGEPTALSPRIADINALVSPSSVSRRGPKRKKSWMKLRSFQEKSQKKLEILIATFKPIPFVPAKS
LDFSSHEKLLNRLGLWDFVHTKFDTPLRQDLLMQLVANFNNTQRCSYVNGNRIMVNRADLARALRLPVRRTTSVDNGKKE
PVASEESIAFIEDFVSNWLLLHEDTWMMPNEIMHWTKVIKDGKFERVDWAGLIWFMVEKELMQSPQLVNCYYASHLQCLI
RSQREDILKEEAPKVEENEHKEKVEQEPEQGQRQEQEQEQEQEQEQEQEREQDDEDGVCNESPKIVGNDDSMVKELEEHN
IELCLGQDNVEKVDDHKEKDSLGDMMDLMENKVEEDDEHEQEEQEQGQWLLDGKGRAPELLFRRCNTNEFKEFDLGDEKK
VELEEGDGQGKEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEFRLLPRSNAIDGFPPSQFIQEMETEPINFNSEFDLQG
HSSVEFLPPPRDDNRMSSGGCIPFVSNNKRVIDPDIDNPAQSLNGGNKRLRSEGPLDYDKCMDNVQQWLDKARMMYAEKE
QVHQQATMNQQYLLHELQQRETFIEHLRKTKFEEQQKMQSDIYRLERELYVMGNLLDGYRKALRETNKAFADYRTRCPQS
DEPLYKDVAGSGGLVLSTMELERIRLKQAEEDRLSRLVIEKKFKALEDKFVDIFHAHLQQVSSLDSRLLEFGNEVKTLRE
SLANKKASETSEPISNE
```

495 - 514:	EEEEEEEEEEEEEEEEEEEE
496 - 515:	EEEEEEEEEEEEEEEEEEEE
497 - 516:	EEEEEEEEEEEEEEEEEEEE
498 - 517:	EEEEEEEEEEEEEEEEEEEE
499 - 518:	EEEEEEEEEEEEEEEEEEEE
500 - 519:	EEEEEEEEEEEEEEEEEEEE
501 - 520:	EEEEEEEEEEEEEEEEEEEE
502 - 521:	EEEEEEEEEEEEEEEEEEEE
503 - 522:	EEEEEEEEEEEEEEEEEEEE
504 - 523:	EEEEEEEEEEEEEEEEEEEE

A0A1S3C2T2 **A0A1S3C2T2_CUCME** (1957 aa)
uncharacterized protein LOC103496212. *Cucumis melo (Muskmelon)*

```
MLHIWFLGFCNWTNNRILQRLCACRLIICLGPRLCSRFLFLIFVMRLSSGSVSSSLKQSGNRSGPRLKKKHKRLDAICEK
EYSRNHGDVNENVTRLGTLEADPGLRRSSRVRRAPVLLDASPMPRKKRRIVRGNGTLGVKTSANTLPLFSDDLKGETEGN
WRSRLRSRNRNLGIRVDKGARASRKRKLFDEIIDVKVRNGGMRIDLDEEKRKMEFGESMVGRSNRTSRRFGVTNDPIKIE
EEVKSPRIKDDYCKEEMLIIDIDDEEEEGEGEGEEEEEEEEEEEEEERERGGGGGGGEXEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEAVEGKEVVTAKDEKGEDVLPLENEMDEENVKVVDDVTPQVVEKLDKETSSSLHVDEACSGDHNEELANAGE
IQLEESTQLNEGVNETQDVEAAVVSTNEVVGGRSCNEKAVDLGKFTEKSRQHGDDLNLKKFTDSSTGMLGKARIKEGRRC
GLCGGGIDGKPPKKMAQDSGESGNEACSGSSASEEPNYDKWDGFGDEPGWLGRLLGPINDRYGIAGIWVHQHCAVWSPEV
YFAGLGCLKNVRAALCRGRALKCTRCGRPGATIGCRVDRCPKTYHLPCARANGCIFDHRKFLIACTDHRHIFQPHGNQYL
ARIKRLKAKKMKLEIKKQSNDAWRRDIEAEEKWLENCGEDEEFLKRESKRLHRDLVRIAPVYIGGSNSEGENLFHGWESV
AGLQGVIQCMKEVVFLPLLYPELFDRFGITPPRGVLLHGYPGTGKTHVVRALIGSCARGDKRIAYFARKGADCLGKYVGD
AERQLRLLFQVAERCQPSIIFFDEIDGLAPCRTRQQDQTHNSVVSTLLALLDGLKSRGSVVVIGATNRPEAVDPALRRPG
RFDREIYFPLPSVEDRAAILSLHTQKWPKPIDGPLLQWIARRTAGFAGADLQALCTQAAMSALKRNFPLKEVLSASGEQV
LRVNRPPLPSILVEERDWLEALLYSPPPCSRREAGMAANDVASSPLPFHLIPCLLQPLSTLLVSLYLDERITLPTNLLKA
ATSIKSVIVSALDGKNIVTSCWWSHVHDFVQDADIANEIEIKLQGSGVLVEDSTFGSSGVLNIDTGNESSKFENLGHCGG
RPATMVEHTSFTLGNKSGFRILIAGNTRSGPRHLASCLIHCYIQHVEVRKVDIATISQEGHGDLVHGISQILLNCSSMGA
CLVFMPRIDLWAIETQSQTSEECGFYLNEDEHVEDGIIVKDEGQLGERDDCRYPDQSKSSERTGLQDECLSSASYAWGSF
VEQVESLSTPLMILATSEVPFLLLPQEIREFFRNDLSMCRPTTSEHSVPRFSVQIDGVFDHDMVINQSAAELSRDIVKLL
VHLIHQKSHTKTSTCTKYQIPVIQGENNAENQQIDKETASEHNGEMKSPDVSSLRIAPLPGSRTMKVKSNLISVISTFGH
QILRYPHFAELCWVTSKLKEGPYADVSGPWKGWPFNSCIIRPMSTLEKGASSSLSNGKSKEISGLVRGLIAVGLSAIRGA
YTSLRKVSLDVRLVLELLVEQINAKINSGKDRYQYFRLLSQVAYLEDVVNSWAFTLQSLEHDSRTIETSKNHTSGGSEIQ
CEKNEPIISNKGSLANEIPEVSCQEPVEEKTVRIDSLIDGNLNHSSSKDTTIVPEEHGERNFGISNLVSNESYDNAAVID
DQLADNIPLKHGEATIPQQDSLDNERNGTSVKTPLDLGTESIVNLEHHHRNSSVLCGDGIPSGTKPCSISNGGCSALENG
CKRDDSQLDTNDREVNVHSSPSRSGHSTNPALICSIQCCSGCLNVLYNMSKNILCNELGSNQNNWTVEDVHDVVVALSVD
LLATVRRAFLDENNDTRVFDDRQMGGNDRFKSPDWRTCDCKSSKDMVFKGVECICHLSEKVSPSPYSEMGIDPNFIFRDG
VLVSVDPKKNVSFHCKLETLCLCSLTELIVMAKKPLN
```

299 - 318:	EEEEEEEEEEEEEEEEEEEE
300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE
306 - 325:	EEEEEEEEEEEEEEEEEEEE
307 - 326:	EEEEEEEEEEEEEEEEEEEE
308 - 327:	EEEEEEEEEEEEEEEEEEEE
309 - 328:	EEEEEEEEEEEEEEEEEEEE
310 - 329:	EEEEEEEEEEEEEEEEEEEE

A0A1S3F5E2 **A0A1S3F5E2_DIPOR** (353 aa)
protein PROCA1 isoform X2. *Dipodomys ordii (Ord's kangaroo rat)*

```
MWVRTTVTIKRWIERKSDVWDDSESGEYKETNRCCWKHKQCAGHIIHPFVNYGHHNLHLHAVNHCNCDPRLKDCTEKINS
SSSEYMGPTCSRDRGPTCYDVFQTPCFELIPDEDCVERRLWYSWCKSYRPVSVAVIHHPIHHECRADEEEQEEEEEEEEE
EEEEEEEEEEEEEEASQPPIPIQVGPSALTTDQETCTANGSPDSAAPITIWRSESPTGKGQGSKVIKKVKKKEKEKEEEET
TLDEKTKLKKKVKKGKLTKKKSPVKSESSPPDLSPRELTRMSGESSQESREEQESEESYRGQEEPSSEDIAESSPKKREK
NNTAQAKKTGTKTSPVRKVSKRKSPPVSNPNLS
```

152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE

A0A1S3F5I4 **A0A1S3F5I4_DIPOR** (382 aa)
protein PROCA1 isoform X1. *Dipodomys ordii (Ord's kangaroo rat)*

```
MWVRTTVTIKRWIERKSDVWDDSESDISSLPSWESGPLLAGVDSTTDFSSFSSEGEYKETNRCCWKHKQCAGHIIHPFVN
YGHHNLHLHAVNHCNCDPRLKDCTEKINSSSSEYMGPTCSRDRGPTCYDVFQTPCFELIPDEDCVERRLWYSWCKSYRPV
SVAVIHHPIHHECRADEEEQEEEEEEEEEEEEEEEEEEEEEEASQPPIPIQVGPSALTTDQETCTANGSPDSAAPITIWR
SESPTGKGQGSKVIKKVKKKEKEKEEEETTLDEKTKLKKKVKKGKLTKKKSPVKSESSPPDLSPRELTRMSGESSQESRE
EQESEESYRGQEEPSSEDIAESSPKKREKNNTAQAKKTGTKTSPVRKVSKRKSPPVSNPNLS
```

181 - 200:	EEEEEEEEEEEEEEEEEEEE
182 - 201:	EEEEEEEEEEEEEEEEEEEE
183 - 202:	EEEEEEEEEEEEEEEEEEEE

A0A1S3F746 **A0A1S3F746_DIPOR** (343 aa)
protein PROCA1 isoform X3. *Dipodomys ordii (Ord's kangaroo rat)*

```
MAEGLPVVVWSPKQRGEYKETNRCCWKHKQCAGHIIHPFVNYGHHNLHLHAVNHCNCDPRLKDCTEKINSSSSEYMGPTC
SRDRGPTCYDVFQTPCFELIPDEDCVERRLWYSWCKSYRPVSVAVIHHPIHHECRADEEEQEEEEEEEEEEEEEEEEEEE
EEEASQPPIPIQVGPSALTTDQETCTANGSPDSAAPITIWRSESPTGKGQGSKVIKKVKKKEKEKEEEETTLDEKTKLKK
KVKKGKLTKKKSPVKSESSPPDLSPRELTRMSGESSQESREEQESEESYRGQEEPSSEDIAESSPKKREKNNTAQAKKTG
TKTSPVRKVSKRKSPPVSNPNLS
```

142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE

A0A1S3G2T7 **A0A1S3G2T7_DIPOR** (1297 aa)
splicing factor, arginine/serine-rich 19. *Dipodomys ordii (Ord's kangaroo rat)*

```
MEEEDESRGKTEESGEDRGGDGPPDRDPTLSPSAFILRAIQQAVRSSLQGDLPSDKDGSRCHGLPWRRCRSPRSESRPQE
SGGTDTATVLDMATDSFLAGLVSILDPPDTWVPSRLDLRPGESEDMLELVAEVRIGDRDPIPLPVPSLLPRLRAWRTGKT
VSPQSHSSPPACAHHLLTLGTGDGGPAPPPAPSSASSSPSPSPSSSPSPPPPPPPPAPPAPPAPRFDIYDPFHPTDEAYS
PPPAPEQKYDPFEPTGSNPSSSAGTPSPEEEEEEEEEEEEEEEEEEEEGLSQSISRISETLAGIYDDNSLSQDFPGDESP
RPEPPPPAAGPGTPPQADSTRAEGATRRRVFVVGAEAEACREGKVSVEVVTAGAALPPALLPPADSEIEEGEIVQPEEEP
RLALPLFRGGRPARPPPAPAATAAPAPPPPPPAAAAAAAAAARAPEGDDFLSLHAESDGEGALQVDLGEPAPAPPAADAR
WGGLDLRRKILTQRRERYRQRSPSPAAAPAPAPGAGPPARKKSRRERKRSSEAKEAAPGPGAPPAPASPWDSKKRRSRDR
KPSSHAAASARRRSRSRSRSARRRSRSSDRRRGGRRSRSREKRRRRRRSASPPPATSSSSSSRRERHRGKHRDGGGKKKK
KRSRSRGEKRAADGGEKAAGGGGPAASSAEREGRRRGAVPPSIQDLTDHDLFAIKRTITVGRPDKPSPRGPSPGPAASPR
REVLYDSEGLSADERGKGGDKERRRAGPAAAASSSSSSRDKGSRRKGPDAAERERERDRDRPSKKVRPKEAAAPPAGPPK
SAASSGSGSSSSSSSCSSRKVKLQSKVAVLIREGVSSTTPAKDTAGPGSIAVKFSRDRESRSPFLKADERAPADAAKAAA
GSAKPKKTKAKAKAGAKKAKGTKAKTKPSKTRKKARSGGSGAAGGPGALKKSKADSCSQPAGPKGAEETSWSGEERAAKA
PSTPPPKAAPPPPALTPDSQTVDSSCKTPEVSFLPEEAAEEAGGRGGEEEEEEEEEEEEEEEEEEQQPATTTATSTAAAAP
STAPSAGSTAGDSGAEDGPAARVSQLPTLPPPMPWNLPAGVDCTTSGVLALTALLFKMEEANLASRAKAQELIQATNQIL
SHRKPPSSLGMTPAPVPTSLGLPPGPSSYLLPGSLPLGGCGSTPPTPTGLAAASDKREGSSSSEGRGDTDKYLKKLHTQE
RAVEEVKLAIKPYYQKKDITKEEYKDILRKAVHKICHSKSGEINPVKVSNLVRAYVQRYRYFRKHGRKPGDPPGPPRPSK
EPGPPDKGGPGLPLPPL
```

269 - 288:	EEEEEEEEEEEEEEEEEEEE

A0A1S3G4Q1 **A0A1S3G4Q1_DIPOR** (1737 aa)
protein unc-13 homolog A. *Dipodomys ordii (Ord's kangaroo rat)*

```
MDRQNLCGKALFPGSRWCGLHPGLPWHSRCFSMRQDTVKKAKFDGAQEKFNTYVTLKVQNVKSTTIAVRGSQPSWEQDFM
FEINRLDLGLTVEVWNKGLIWDTMVGTVWIPLRTIRQSNEEGPGEWLTLDSQVIMADNEICGTKDPTCHCILLDTRFELP
LDIPEEEARYWAKKLEQLNAMRDQDEYPFRDEPDKPLPVPSSQCCNWNYFGWNEQNDDPDSAVDDRDSDYRSETSNSIPP
PYYTTSQPNASVHQYAVRPPPLGSRESYSDSMHSYEEFSEPRALSPTGSSRYASSGELSQGSSQLSEDFDQDEQSLQGSE
LEDERDRDSYHSCHSSVSYHKDSPHWDQDEEDLEDLEDEELPEEEEEEEEEEEEEEEEEEEEEIPDDLGSYAQLEEVAV
DEPKDFKRISLPPAAPEKVDTAPMPPTEGSEVTKGAPKPATPEEAPRAERTPESEPPKAEESFRQGEDEEGHEGQDSMSR
AKANWLRAFNKVRMQLQEARGEGEMSKSLWFKGGPGGGLIIIDSMPDIRKRKPIPLVSDLAMSLVQSRKAGITSALTSST
LNNEELKNHVYKKTLQALIYPISCTTPHNFEVWTATTPTYCYECEGLLWGIARQGMRCTECGVKCHEKCQDLLNADCLQR
AAEKSSKHGAEDRTQNIIMVLKDRMKIRERNKPEIFELIQEIFAVTKTAHTQQMKAVKQSVLDGTSKWSAKISITVVCAQ
GLQAKDKTGSSDPYVTVQVGKTKKRTKTIYGNLNPVWEENFHFECHNSSDRIKVRVWDEDDDIKSRVKQRFKRESDDFLG
QTIIEVRTLSGEMDVWYNLDKRTDKSAVSGAIRLHISVEIKGEEKVAPYHVQYTCLHENLFHFVTDVQNNGVVKIPDAKG
DDAWKVYYDETAQEIVDEFAMRYGVESIYQAMTHFACLSSKYMCPGVPAVMSTLLANINAYYAHTTASTNVSASDRFAAS
NFGKERFVKLLDQLHNSLRIDLSMYRNNFPASSPERLQDLKSTVDLLTSITFFRMKVQELQSPPRASQVVKDCVKACLNS
TYEYIFNNCHELYSREYQTDPAKKGEVPPEEQGPSIKNLDFWSKLITLIVSIIEEDKNSYTPCLNQFPQELNVGKISAEV
MWNLFAQDMKYAMEEHDKHRLCKSADYMNLHFKVKWLYNEYVAELPAFKDRVPEYPAWFEPFVIQWLDENEEVSRDFLHG
ALERDKKDGFQQTSEHALFSCSVVDVFSQLNQSFEIIKKLECPDPQIVGHYMRRFAKTISNVLLQYADIISKDFASYCSK
EKEKVPCILMNNTQQLRVQLEKMFEAMGGKQLDTEASDTLKELQVKLNNVLDELSRVFATSFQPHIEECVKQMGDILSQV
KGTGNVPASACSSVAQDADNVLQPIMDLLDSNLTLFAKICEKTVLKRVLKELWKLVMNTMERTIVLPPLTDQTMIGTLLR
KHGKGLEKGRVKLPSHSDGTQMIFNAAKELGQLSKLKDHMVREEAKSLTPKQCAVVELALDTIKQYFHAGGVGLKKTFLE
KSPDLQSLRYALSLYTQATDLLIKTFVQTQSAQGSGVEDPVGEVSVHVELFTHPGTGEQKVTVKVVAANDLKWQTSGIFR
PFIEVNIIGPQLSDKKRKFATKSKNNSWAPKYNESVQFTLSADAGPECYELQVCVKDYCFAREDRTVGLAVLQLRELAQR
GSAACWLPLGRRIHMDDTGLTVLRILSQRSNDEVAKEFVKLKSDTRSAEEGGAAPAP
```

363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE

A0A1S3G7T6 **A0A1S3G7T6_DIPOR** (1215 aa)
myelin transcription factor 1-like protein. *Dipodomys ordii (Ord's kangaroo rat)*

```
MDLDAEEKRHRTRSKGVRVPVEPAIQELFSCPTPGCDGSGHVSGKYARHRSVYGCPLAKKRKSQDKQPQEPAPKRKPLTV
KADSSSVDECYESDVSEDMDEKEEEEEEEEEEEEEEFSEDNDDEQGDEDDEDEEVDREEEEDEDEEEEEEEEIDEEDDDD
DDEDGDDVEEEEEEEEEEEEEEEEEEEEEEEENDEHPVSCHSSRVGQDPEKDDNNNDEYENYDELVAKSLLNLGKIAEDAAHR
ARTESEMNSSTSNSLEGDSDKNDSLGRKGELSLDLDSDVVRETVDSLKLLAQGHGVVLSENLGERSYADGAAPQDGRNLN
YVMLGKPMSNGLMEKMVEESDEEVCLSSLECLRNQCFDLARKLSETNPQDRSQPAGAGLRQHGRPEEDFPGRTPDRSYSD
MMNLMRLEEQLSPRSRTFSSCAKEDGCPDREDDAASVNSDRSEEVFDMTKGNLTLLEKAIALETERAKAMREKMALDAGR
RDAMRPFEDQSPRQPSGEDRRPKSSDSHVKKPYYGKDPSRTEKKESKCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRVPP
EILAMHENVLKCPTPGCTGRGHVNSNRNSHRSLSGCPIAAAEKLAKAQEKHQSCEVSKSNQASDRVLRPMCFVKQLEIPQ
YGYRNNVPTTTPRSNLAKELEKYSKTSFEYNSYDNHTYGKRAIAPKVQTRDISPRGCDDAKRYCKNASPSSSTTSSYAPS
SSSNLSCGGGSSASSTCSKSSFDYTHDMEAAHMAATAILNLSTRCREMPQNLSTKPQDLCATRNPDMEVDENGTLDLSMN
KQRPRDSCCPVLTPLEPMSPQQQAVMGSRCFQLSEGDCWDLPVDYTKMKPRRVDEDNPKDITKQNVEKHLPSEVFGGDGS
KAPACLVPFFFNLHCVCPPAAPDPRAQEHRQLGFWPRLLTPPTGTRLSGCPLADKSIRSMLATSSQELKCPTPGCDGSGH
ITGNYASHRSLSGCPRAKKSGIRIAQSKEDKEDQEPIRCPVPGCDGQGHITGKYASHRSASGCPLAAKRQKDGYLNGSQF
SWKSVKTEGMSCPTPGCDGSGHVSGSFLTHRSLSGCPRATSAMKKAKLSGEQMLTIKQRASNDPHEVAFSLEEHEWHLSA
LITTMESNLKTIEEENKVIEQQNESLLHELASLSQSLIHSLANIQLPHMDPINEQNFDAYVTTLTEMYTNQDRYQSPENK
ALLENVKQAVRGIQV
```

169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE

A0A1S3G8N5 **A0A1S3G8N5_DIPOR** (223 aa)
cysteine-rich hydrophobic domain-containing protein 1. *Dipodomys ordii (Ord's kangaroo rat)*

```
MSILLPNMAEFDTISELEEEEEEAATSSSSSPSSSLVSGPEDDEEDEEEEEEEEEEEEEEEEEEEEEVPPPPRVVSEEHL
RRYAPDPVLVRGAGHITVFGLSNKFDTEFPSVLTGKVAPEEFKTSIGRVNACLKKALPVNVKWLLCGCLCCCCTLGCSLW
PVICLNKRTRRSIQKLLEWENNRLYHKLALHWKLTKRKCETSNMMEYVILIEFLPKYPIFRPD
```

47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE

A0A1S3GCS6 **A0A1S3GCS6_DIPOR** (1172 aa)
myelin transcription factor 1. *Dipodomys ordii (Ord's kangaroo rat)*

```
MALCRSFLENEFRGKLLTQRWTHGDKASSCTTSRNLLDQHSKMSLENDDKRARTRSKALRGPPETTSADLSCPTPGCTGS
GHVRGKYSRHRSLQSCPLAKKRKQEGTEAEHLVSKRKSHPLRLALDESYRVDSDGSEDAGVKEASVSDESEGPLEEADAE
MSGQEQIHRLEPAEGRSPIKPHFGSNPTSSPSGPSKSSYSSYQGIIATSLLNLGQIAEETLVGEDLVQVAKPVPSVVHLL
QEETTEGATSDESEKELFIQPEDAEEVIEVTSDRSQEPCPQSLEDVAREEFSNQKGVLSQEEDEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEDREEEAGPDVIFREAISHTSAQKGPEPQCPEPHSPKPEYSVIVEVRSDDDKD
EDARSQKSVVTDESEMYDMMTRGNLGLLEQAIALKAEQVRAVCEPGCPPVEQSQLGPSEPGKVVKTLDAVRKSCYSKDSS
RTEKREIKCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRIPPEILAMHENVLKCPTPGCTGQGHVNSNRNTHRSLSGCPIA
AAEKLAKSHEKQQPQAGDPSKNSSNSDRILRPMCFVKQLEVPPYGSYRPNVAPTTPRANLAKELEKFSKVTFDYASFDAQ
VFGKRMLAPKIQTSETSPKAFQCFDYSHDAEAAHMAATAILNLSTRCWEMPENLSTKPQDFPSKSVDIEVDENGTLDLSM
HKHRKRENAFPSSSSCSSSPGLKSPDVSQRQSSTSAPSSSMTSPQSSQASRPDEWDRPLDYTKPSRQREEEVEESEPAAH
SFASSEADDQEVSEENFEERKYPGEVTLTNFKLKFLSKDIKKELLTCPTPGCDGSGHITGNYASHRSLSGCPLADKSLRN
LMAAHSADLKCPTPGCDGSGHITGNYASHRSLSGCPRAKKSGLKVTPAKDDKEDPELMKCPVPGCVGLGHISGKYASHRS
ASGCPLAARRQKEGSLNGSSFSWKSLKNEGPTCPTPGCDGSGHANGGFLTHRSLSGCPRATFAGKKGKLSGDEVLNPKFK
TSEVLENDEEIKQLNQEIRDLNESNSEMEAAMVQLQSQISSMERNLKNIEEENKLIEEQNEALFLELSGLSQALIQSLAN
IRLPHMEPICEQNFDAYVSTLTDMYSNQDCYQNPENKGLLETIKQAVRGIQV
```

304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE
306 - 325:	EEEEEEEEEEEEEEEEEEEE
307 - 326:	EEEEEEEEEEEEEEEEEEEE
308 - 327:	EEEEEEEEEEEEEEEEEEEE
309 - 328:	EEEEEEEEEEEEEEEEEEEE
310 - 329:	EEEEEEEEEEEEEEEEEEEE
311 - 330:	EEEEEEEEEEEEEEEEEEEE
312 - 331:	EEEEEEEEEEEEEEEEEEEE
313 - 332:	EEEEEEEEEEEEEEEEEEEE
314 - 333:	EEEEEEEEEEEEEEEEEEEE
315 - 334:	EEEEEEEEEEEEEEEEEEEE
316 - 335:	EEEEEEEEEEEEEEEEEEEE
317 - 336:	EEEEEEEEEEEEEEEEEEEE
318 - 337:	EEEEEEEEEEEEEEEEEEEE
319 - 338:	EEEEEEEEEEEEEEEEEEEE
320 - 339:	EEEEEEEEEEEEEEEEEEEE
321 - 340:	EEEEEEEEEEEEEEEEEEEE
322 - 341:	EEEEEEEEEEEEEEEEEEEE
323 - 342:	EEEEEEEEEEEEEEEEEEEE
324 - 343:	EEEEEEEEEEEEEEEEEEEE

325 - 344:	EEEEEEEEEEEEEEEEEEEE
326 - 345:	EEEEEEEEEEEEEEEEEEEE
327 - 346:	EEEEEEEEEEEEEEEEEEEE
328 - 347:	EEEEEEEEEEEEEEEEEEEE
329 - 348:	EEEEEEEEEEEEEEEEEEEE

A0A1S3GEN5 **A0A1S3GEN5_DIPOR** (321 aa)
Protein-serine/threonine phosphatase (EC 3.1.3.16). *Dipodomys ordii (Ord's kangaroo rat)*

```
MASELLFCEPTKLYNILNQATKLSRLTEPNYLYLFDVRSKKEYDESHVITAILVKKKENQYLVPESVDLDCVRYCVVYDK
NTTSLEVLDEEEEEEEEEEEEEEEEEEEEEEEKLEPGPAVQFGRVLIHLTRYPVYVLRGGYEHFTSLYHFLRTQKIIWMPQ
ELEAFEPYPIEIVPGHIYLGSYKQACDPKIKKDLKIKAHVNVSMESTPFFQEDPDYLLHVKIEDDPEANIIPFLRPICHF
LEIHVQLKSAILVFSTLGISRSCAAVVAYLMHRNTETLRRSWNHVKQCKPTMRPNQGLVSQLLEWESTILGVFITDITEF
F
```

90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE

A0A1S3GNR2 **A0A1S3GNR2_DIPOR** (1002 aa)
histone-lysine N-methyltransferase EHMT2. *Dipodomys ordii (Ord's kangaroo rat)*

```
MSDDVHSLGKVTSEVAKRRKLNSAGGLSEELNSARGSGEVSLDKGHPRSLEEWETVVGDDFSLYYDSYSVDERVDSDSKS
EVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAK
ELRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMA
TESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLN
GMVFCPHCGEDASEAQEVTIPRGDGGTPPAGTVAPAPPPLAQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGP
SLTLPNGGCLSAVGLPPGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTA
LHAAAQKGSLEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLDVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVS
LLLSTGQVDVNAQDSGGWTPIIWAAEHKHIDVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVN
YHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVAR
GYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNK
IEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFD
LDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTC
QCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPANT
```

91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE

A0A1S3GT24 **A0A1S3GT24_DIPOR** (180 aa)
Transcription elongation factor A protein-like 1 (Transcription elongation factor S-II protein-like 1). *Dipodomys ordii (Ord's kangaroo rat)*

```
MEKSCQEKKEEPQSAPKANEGQPPMEQPPEKQSSDEDQTSEDCSSEEEEEEEEEEEEEEEEEEEEEEEFFPEELLPELLP
ELLLSQERPQRQCLSVKALLEERPPMEQPPCGVGKHKLEEGSFKERLARSRPQFRGDIHGRNLSNEEMIQAADDMEEMKR
VRNKLMIMHWKAKRSRPYPI
```

46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE

A0A1S3GVV8 **A0A1S3GVV8_DIPOR** (625 aa)
huntingtin-associated protein 1. *Dipodomys ordii (Ord's kangaroo rat)*

```
MLCGHPWCPLASFLITVTADIRPKVQAGSKTGAPRSSGRSVLDHSEAPWTRFVFQGPYGPRATGLGTGKAADIWKTPAAY
IGRRPGVTGPERAAFIRELQEALCPNPPPTKKITQDDIKVMLYLLEEKERDLSTAARIGQSLVKQNSVLMEENSKLEAML
GSAREEILHLRHQVNLRDDLLQLYSDSDDEDEDEEEEEEEEEEEEEEEEEEEEEEEEEFGREEDRPCDHPYDVSKPAPQE
ESLHHCPQLEVLQRKLRLLEEENDQLREEASHLDTLEDEEQMLILECVEQFSEASQQMAELSEVLVLRLENYERQQKEIT
QLQAQIAKLQQRCQSYGAETEKLQQQLASEKGIHVQLQAENLRAGSQMPDPREKYTDCGGMMRERQEEAKHLRQHPRAPA
GSVTHYAYSVPLEVLPSFPETLAEELRTSLRKIISDPAYFMDRCSNLRYREEQKQEPEEFRAEQGFKLPPDMDPAEELVP
EEELEAREEREPSEEGLAEESELMSEDTEAWEELEPEVDEATRMNVVTSALEASGLGPSHLDMKYVLQQLANWQDAHCKR
QQQQKVAQKGSPNLQQWQTQAKTNMGGGIEEQQPRVPTQDFPRLEEERASPPPKAWEEEGPSGAT
```

194 - 213:	EEEEEEEEEEEEEEEEEEEE

195 - 214:	EEEEEEEEEEEEEEEEEEEE
196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE

A0A1S3LQK2 **A0A1S3LQK2_SALSA** (536 aa)
protein POF1B-like isoform X2. *Salmo salar (Atlantic salmon)*

```
MSIHNTSTSYRTVNVSSDPATTVLSSGQYIDGYRTMSVSHAPVQYGIDNGYETVRYLMPVQQPMQQQQMQYVLVNQAPQV
MQQMVSPVYLQSMQRVSVSSLEESDIYRQQNVENFNGKTPSVFSQASSSIKSPEPGVGEAEEEEEEEEEEEEEEEEEEE
EEVEEESVEERVVERVIENVSQVKIKCKVREVQPVVKMDTRFFGELLAEVYRKNCDIHTCISEHVAKIRGRKHLLDPSND
YKMEREDIETLIPKGASELTKQQIRYLLQTRMTADKTMRLLLTTFSSLREELIHMSEDLRRLESEKETLERDLSFKADQA
EQYDRLLEAVRENNRQLQMSLKESSSSQRTLETQLLSSHSTDSDREFRIRELEGSYRALEKENEMLKQKLAGQSSSSTIQ
FKTEELSRQYSEQLAALRQEKDKELQSLRTQLTRITTEYTTERSGDKSLQLRITQLLTTLEQREVVIKRQEEEIWRLQQK
KSDSAKNVTTTTVTKRYSNRYPLLGLLSEDFQSTLPVKDAKTIIIESRTGEIIKQE
```

141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE

A0A1S3LQT1 **A0A1S3LQT1_SALSA** (537 aa)
protein POF1B-like isoform X1. *Salmo salar (Atlantic salmon)*

```
MSIHNTSTSYRTVNVSSDPATTVLSSGQYIDGYRTMSVSHAPVQYGIDNGYETVRYLMPVQQPMQQQQMQYVLVNQAPQV
MQQMVSPVYLQSMQRVSVSSLEESDIYRQQNVENFNGKTPSVFSQASSSIKSPEPGVGEAEEEEEEEEEEEEEEEEEEE
EEVEEESVEERVVERVIENVSQVKIKCKVREVQPVVKMDTRFFGELLAEVYRKNCDIHTCISEHVAKIRGRKHLLDPSND
YKMEREDIETLIPKGASELTKQQIRYLLQTRMTADKTMRLLLTTFSSLREELIHMSEDLRRLESEKETLERDLSFKADQA
EQYDRLLEAVRENNRQLQMSLKESSSSQRTLETQLLSSHSTDSDREFRIRELEGSYRALEKENEMLKQKLAGQSSSSTIQ
FKTEELSRQYSEQLAALRQEKDKELQSLRTQLTRITTEYTTERSGDKSLQLRITQLLTTLEQREVVIKRQEEEIWRLQQK
KSDSAKNVTTTTVTKRYSNRYPLLGLLSEDFQSTLPVKDAKTIIIESRTGEIIKQVE
```

141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE

A0A1S3PFL7 **A0A1S3PFL7_SALSA** (1066 aa)
MORC family CW-type zinc finger protein 2A-like. *Salmo salar (Atlantic salmon)*

```
MAYSNYSTLNRAQLTFEYLHTNSTTHEFLFGALAELVDNSRDANATRIDIYTEKRQDLRGGYMLCFLDDGTGMDPSEATH
VIQFGKSTKRTPDSTHIGQYGNGLKSGSMRIGKDFVLFTKKDNTLSCLFLSRTFHEEEGLDEVIVPLPTWDLLTRQPITG
DPEKFAIETELIYKYSPFKNEQQLMEQFNKIEGSSGTLVIIYNLKLMDTREPELDVETDHQDILMAGTPSEGVKPERRSF
RAYAAVLYIDPRMRIFIQGHKVRTKRLSCCLYKPRVYKYTSTRFKTRAEQEVKKADHLAKIAEEKAREAESKSLSLEAKL
GDDLSKESRVMLRKAQEGAMMLRREAEVKKMIQESKQKALKEPKELSFIFGVNIEQRDLDGMFVYNCSRLIKMYEKTGPQ
LEGGMACGGVVGVVDVPYLVLEPTHNKQDFADAKEYRHLLRAMGEHLAQYWKDSNIAQKGIVKFWDEFGYLSASWSSLPS
AEQRYKRRRAMEIPLTIQCDKCLKWRTLPFQMDAVDKRYPDSWVCLMNPDSTQDRCDAAEQKQNLPCGVLKKDRQTAEDK
QKELTEKIRQQQEKLEALQKTSTIKSAADVKKLPLDVSMRPMNDSSSQATRSSERVSRPRSPPLPALLKNAPSQPPALNR
KLTNSPRPTARPAAPASRVDQSRARAAAKPSPPPAKPAPKAPAKIPAKPTPPSRSSRIQAKSSLAKATTPASSQRKRVME
QEESEEEEEEEEEEEEEEEEEEEEEEKEPQPKKSKMAAAVGNRGKAVEKTPLKRGKVAEVPTPPLSTKPPLPEKRSATIPT
RLPPATPPPAKPIPTPPKPSAGARAKVTGSAEDEHPENEPKNAQKDKGMLVEVRVNKEWFTGKVVAVETSKQSVRWKVKF
DYVPRSTPKDRWVFKGSEEVRLMRPPSPLSQTPDTQQGEGTEKGPAPMEPDTTQPGTSREVTDNLVNMMRTLLRYFFPPD
FRIPKDDVNSMTAEELVAFPMKEYFQQYELGLQSLCNSYQSRADARAKAVEEKSTSAETKLREADEKLQKLRTNIVQLLQ
KVQEDIDINTDDELDAYIEDLLTKGD
```

725 - 744:	EEEEEEEEEEEEEEEEEEEE
726 - 745:	EEEEEEEEEEEEEEEEEEEE

A0A1S3QSF7 **A0A1S3QSF7_SALSA** (949 aa)
zinc finger protein 850-like. *Salmo salar (Atlantic salmon)*

```
MLHQRTHTGEKPYECMVCGKGFSQAANLKTHQKVHSGEKPYPCSDCGSRFTHMGDLKRHQLLHSGEKPYSCPECGKSFSQ
LAHLKSHQQTHTGEKPFLCAHCEKTFSTAAKLKNHERVHTGERPYCCSYCPKRFALSGTLVKHERLHTGETPYQCGECGK
GFAQLVSLKIHAQSHTGVNFYNCFHCDQSFSTSTKLKEHQRIHTGENLYQCTECGKSFTIESKLLKHQRVHTGEKPYQCS
SCGMRFSLSENLLRHQRNSSGICGAVSLNQATGSGILLLQDAAVFQNILVKAGHKPTESLPSDQSHSEASTQTAGMTVNV
KEEDRTLGLKIKTEELEEEEEEEEEEEEEEEEEEEEEFAGLINSDGEEMDWDPSLLGYNPNQSSDIEESPSTSGVPEHHQ
ENHTAKSSHCCSVCGKDCQKLSALQKHMRIHTGEKPYPCTLCGNQFREKGHLKAHLKTHTGEKPYHCPTCGMKFAHLGAM
KIHLLTHTGEKPYPCSVCGKSFTQSSRLKQHFRTHTGEKPYSCSVCRKSFARPADLKVHHRDHTGEKPYTCAECGQSFTS
SHNLWKHQKTHLPPGLPPPVEFDNHNQTPEMNAKNEGLKEEDEEEEEIGVLINSDGEEVGLDLDPPRLNPLSSEEEESPS
TSGETEQHQVNHNTALRYSCHVCGKQFNHKGHLRRHESVHSVEKPYGCSDCDKMFGSTIALNRHKKLHREEKPHTCTVCG
KGFVQLSRLKEHYPTHSGEKPHCCSVCGKRFTTASYLKTHSKVHLGESPYTCNICRRDCQKLSAFKLHMRIHTGEKPFSC
SVCEKQFTQKRHLQDHQKVHTGEKPYPCPHCDKRFSFSSALKRHQQLHTGEKPHCCFVCGNSFSQAGRLKEHLRTHSGER
PFSCSVCEKTFRKASELTIHIRSHTGERPYSCAECGKSFTSSMKLGRHKKIHQNTNTEENLTKDVKKIP
```

337 - 356:	EEEEEEEEEEEEEEEEEEEE

338 - 357:	EEEEEEEEEEEEEEEEEEEE

A0A1S3QTI3 **A0A1S3QTI3_SALSA** (340 aa)
piezo-type mechanosensitive ion channel component 2-like isoform X1. *Salmo salar (Atlantic salmon)*

```
MASEMVCGLIFRLLLPICLATACLFRYNGLSFIYLIFLLLIPLFSEPTSTTMQGHTGRLLMSLCFSSLSFLLFHIIYQIT
VNSLLAGNNIDPAFNCSRWERSIRQIGFESVIGADAGNGIRVFLPDIGMFLTGLGCWLLCHSLVQKRPPEDVVYDFEPEE
GVEEEDLSLDDNVLLDENFEAGYEGGEEEEEEEEEEMEEEEEEEEEEEEEEEEEEEESTKMKILGRVAAVASKVKEIIG
NLISTAGKVVVTILLGLTGIILPSMTSAVYFFVFLFLCTWWSFCRTFDTLIFSCMCVLMAIFSAGHLVVLYLYQFQFFHE
FIPPKDSYIRLDTGTFFLFK
```

198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE

A0A1S3QTJ3 **A0A1S3QTJ3_SALSA** (289 aa)
piezo-type mechanosensitive ion channel component 2-like isoform X2. *Salmo salar (Atlantic salmon)*

```
MQGHTGRLLMSLCFSSLSFLLFHIIYQITVNSLLAGNNIDPAFNCSRWERSIRQIGFESVIGADAGNGIRVFLPDIGMFL
TGLGCWLLCHSLVQKRPPEDVVYDFEPEEGVEEEDLSLDDNVLLDENFEAGYEGGEEEEEEEEEEMEEEEEEEEEEEEE
EEEEEEESTKMKILGRVAAVASKVKEIIGNLISTAGKVVVTILLGLTGIILPSMTSAVYFFVFLFLCTWWSFCRTFDTLI
FSCMCVLMAIFSAGHLVVLYLYQFQFFHEFIPPKDSYIRLDTGTFFLFK
```

147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE

A0A1S3RRD2 **A0A1S3RRD2_SALSA** (633 aa)
calnexin-like isoform X2. *Salmo salar (Atlantic salmon)*

```
MELNVRCVVLLAVALCSTLLLTTVAAHQEEEEPIMELAEDMGVEDELEDLGLGEELLDGEVEPEDADTPPGPPPAPKVTY
KAPEPMGEHFFAESFDRGTLDSWVLSKAKKEDIDEDIAKYDGKWEVEDMKDSKLPGDKGLVLKSRAKHHAISAQLLRPFI
FDTKPLIIQYEVNFQQGIDCGGAYVKLLSQTPDLNLDEFVDKTPYTIMFGPDKCGEDYKLHFIFRHKNPKTGEYEEKHAK
KPDADLRTYYTDKKTHLYTLVVNPDNSFEVLVDQTVVNSGNLLTDMTPPINPAAEIEDPDDHKPEDWDERPKIQDPDAVK
PEDWDEDAPKQIPDEDAVKPDGWLDDQPEYTSDPDAVKPEDWDEDMDGEWEAPQIPNALCETAPGCGAWQRPMIDNPNYK
GKWKAPMIDNPNYQGVWKPRKIANPDFFEDLHPFRMTPFNAVGLELWSMSSDIFFDNFFITNERHTAERWANDGWGLKKA
AEGAAEPGLVNQMMTAADERPWLWVVYVLTVAVPLILIVVFFCTGKKAAAPAAADYKKTDEPQPDVKEEEEKAEEDQVKE
EKSQPAAEKKSDAEDSPAEKEEEEEEEEEEEEEEEEEEEEEAAVNEEEEAATDQKQQQDDVLRRSPRNTKGRKD
```

581 - 600:	EEEEEEEEEEEEEEEEEEEE

A0A1S3RSJ5 **A0A1S3RSJ5_SALSA** (634 aa)
calnexin-like isoform X1. *Salmo salar (Atlantic salmon)*

```
MELNVRCVVLLAVALCSTLLLTTVAAHQEEEEPIMELAEDMGVEDELEDLGLGEELLDGEVEPEDADTPPGPPPAPKVTY
KAPEPMGEHFFAESFDRGTLDSWVLSKAKKEDIDEDIAKYDGKWEVEDMKDSKLPGDKGLVLKSRAKHHAISAQLLRPFI
FDTKPLIIQYEVNFQQGIDCGGAYVKLLSQTPDLNLDEFVDKTPYTIMFGPDKCGEDYKLHFIFRHKNPKTGEYEEKHAK
KPDADLRTYYTDKKTHLYTLVVNPDNSFEVLVDQTVVNSGNLLTDMTPPINPAAEIEDPDDHKPEDWDERPKIQDPDAVK
PEDWDEDAPKQIPDEDAVKPDGWLDDQPEYTSDPDAVKPEDWDEDMDGEWEAPQIPNALCETAPGCGAWQRPMIDNPNYK
GKWKAPMIDNPNYQGVWKPRKIANPDFFEDLHPFRMTPFNAVGLELWSMSSDIFFDNFFITNERHTAERWANDGWGLKKA
AEGAAEPGLVNQMMTAADERPWLWVVYVLTVAVPLILIVVFFCTGKKAAAPAAADYKKTDEPQPDVKEEEEKAEEDQVKE
EKSQPAAEKKSDAEDSPAEKEEEEEEEEEEEEEEEEEEEEEAAVNEEEEAATDQKQQQDDVLRRSPRNTKGRKD
```

582 - 601:	EEEEEEEEEEEEEEEEEEEE

A0A1S3RSV8 **A0A1S3RSV8_SALSA** (622 aa)
calnexin-like isoform X3. *Salmo salar (Atlantic salmon)*

```
MELNVRCVVLLAVALCSTLLLTTVAAHQEEEEPIMELAEDMGVEDELEDLGLGEELLDGEVEPEDADTPPGPPPAPKVTY
KAPEPMGEHFFAESFDRGTLDSWVLSKAKKEDIDEDIAKYDGKWEVEDMKDSKLPGDKGLVLKSRAKHHAISAQLLRPFI
FDTKPLIIQYEVNFQQGIDCGGAYVKLLSQTPDLNLDEFVDKTPYTIMFGPDKCGEDYKLHFIFRHKNPKTGEYEEKHAK
KPDADLRTYYTDKKTHLYTLVVNPDNSFEVLVDQTVVNSGNLLTDMTPPINPAAEIEDPDDHKPEDWDERPKIQDPDAVK
PEDWDEDAPKQIPDEDAVKPDGWLDDQPEYTSDPDAVKPEDWDEDMDGEWEAPQIPNALCETAPGCGAWQRPMIDNPNYK
GKWKAPMIDNPNYQGVWKPRKIANPDFFEDLHPFRMTPFNAVGLELWSMSSDIFFDNFFITNERHTAERWANDGWGLKKA
AEGAAEPGLVNQMMTAADERPWLWVVYVLTVAVPLILIVVFFCTGKKAAAPAAADYKKTDEPQPDVKEEEEKAEEDQVKE
EKSQPAAEKKSDAEDSPAEKEEEEEEEEEEEEEEEEEEEEEAAVNEEEEAATDQVRDKTTTR
```

582 - 601:	EEEEEEEEEEEEEEEEEEEE

A0A1S3S5A0 **A0A1S3S5A0_SALSA** (729 aa)
zinc finger protein 652-like. *Salmo salar (Atlantic salmon)*

```
MPCLNLGDAFFPSSFLSPQWREGWGIASVPPAPPYNIARVLSQFKNTNTANKSLAVLQLALLQSPPPPHMKSCQSLKGEV
SSPGGMSQEGRRTQQVAQSYYHSPTPDLDLAGKLYKREGGGKPYSVLVDNKMAAKTPMGDQTPSQMSPQHVTSSQQQFFR
EGTVGQEGGAQGPQAGNGGTSEDSEEEEEEEESFKREQIIVEVNLNNQTLNVSKGDKSAPQTDASERHCSEEEEEEEEEE
EEEEEEEEEEDLEEEEEEIESRRTRAKRARRGVAPATSQPRRKTQCTALSTTGMTTRGRRKKTTQPPKRTRRTAREGKGT
PSSAGSATGDKADGDERETLACEKCPRVFNTRWYLEKHMNVTHRRMQICDKCGKKFVLESELALHQQTDCEKNIQCVSCN
```

```
KSFKKLWSLHEHIKIVHGYAEKKFACEICDKKFYTMAHVRKHMVAHTKDMPFTCETCGKSFKRSMSLKVHSLQHSGEKPF
RCENCAERFQYKYQLRSHMSVHIGHKQFMCQWCGKDFNMKQYFDEHMKTHTGEKPFICEICGKSFTSRPNMKRHRRTHTG
EKPYPCELCSQRFRFSNMLKAHKEKCFRVTSPVTLQASSLPLHLSAPSSSGPGPALAPSAAATSAPLGLSPAGGALPPRA
PVGHATFSHLHMTPSHHLPHHHTSQQQQHHPGTPLPPPPLPHHHLPVPPVSPPPALFKSEPLTHCGQEDSSYLRYMAPQD
KGPGAPQHH
```

231 - 250:	EEEEEEEEEEEEEEEEEEEE

A0A1S3W6X4 **A0A1S3W6X4_ERIEU** (1850 aa)
coiled-coil domain-containing protein 108. *Erinaceus europaeus (Western European hedgehog)*

```
MQSAVSSASRPQDSKEWVMYSASFLSASTMVVPTITGNSTAMSACSNSNGSSCSFFLPTEQSACPEVTNKCFPVKTERVK
KKVFWGIKVPELLKWKGWHLGMEVSKNLVLKNLSLSTQKIKYRPPKTKFFFTVIPQPIFLSPGITFTLPIIFRPLEKKEY
ADQLWFEKEEGAFCVDLRATLPCHTLSCPQSLQLPACAVGDLTEAWFCLDNVGELPTFFTWETSSPFQMLPSTGLLEPSQ
SCRVKVTFQPTEAGILEVQATCWYGEDSKQRSSLELRAVAKCAQLLVRMKKKRPEDQDAEGAPKLLHFGRVPVGHTTVRQ
IQLYNPTSVSTSFRIEMAPDVLAGDRTFWCPTEQGTVCAGETKALSVFFRPESLDARTMDYLTVMPCGPASQTLLKLVGF
STGPAVTLQRSCVNFGCVNLGKRSEQPLWIENQSDSVAAFQFALDWQESVFSISPASGMLGARTRLTLYCAFRPCHPIIY
FLRVACLLHHQEPVFLDLMGTCHSDSTRPALLRPQHLTWYRTHLARGLSLHPPDVLAIMLKEKKLEQDKDGALMIAAEDA
EDTPALQYPLIPPMAEYFFDGTADLTIFPPPVSVEPGEVDFGDCSGSECPNPVPLCLTNHTKGKITVVWTCRDGCPFWVT
PQTCDVPPLKSTALRLHFQPPHRNGLFSSQLEAFALYKVLQSYSNIEEDCTVCPSWHLAVQAHGHSYQDSMEHHVPQYSL
DAPKLFPAVPPGDLSYRSLLLTNKGSLLLTFTLASQSSSDIFLRPSSGLVAPGAHQILIVSTYPKGTAWKQHSLYLQFNL
CPQYLKKVILQSREEPLQLQLDTCKNIFFKPTWVGCSSTSVSTLSNPSRLPLDFEWRVSEQHRKLLAVQPARGRIQPNEN
LTLTWTFSPLEETKYLFHVGAWVWDGGLPPQVKPPATTHYKLRLVGLGISSSLSTKEKELDFGNVLVNSQETRSLVLQND
GNCVLYYRLSLDAEGSCNESQALKLDRTEGSMPPRSQDTIYVTACPLCRARFTWTISYSLISPRDNKVGAKQELCRVLLV
AVYPLLSVLDICAMGSAQGITRKQLWRLFSLDLLNSYLERGPTPGELTYKVPTRNSTSQVPSIFTPLKLDFNFGAAPLEA
QPSVVLLGLKNKGVVPLDWAFLFPSDQQIHMELWAEQMELDPTELHQMRAQDNRIFSIHPKEGKLSPGQEQVVELKYRHL
FVGTDRLPVLLKVSHGREILLNFIGVTVKLEQKYVHFISTSHQFIPVPIGNKLPPRQVYELYNGGSVPVTYKIQTSILSQ
VQEKNFDHPVFTCLNPYGEIPPGTTAPVLWIFSPIEARTYTVDVPIHIVGWNSAIIRFQGVGYDPHMMGDTAFFHNISSL
DSSSTHSRLTVPGQTVFLSQSNISLGNIPVQSKCSRLLFFNNVSKKETIFFVWKLKPVYLGEVSISPITGKVAPGETLPI
VVTLKASVHASFYSLEFICKVYQLELLQQFQQELQKWNEEKARQEVEFTITDKKVKKRMTCTACEPVRRYKTLPPIKNQE
PINRPASWNAQNAQEEAVWPCPNPPKPAMLCLSLTARTHPIDYFLASFSDFPCYFLHQELPLRKTSGEEPDGFVDNSTVS
WVPVSRQEKQVLVDCLTTIIRSLLEDRTFHEAMGQSLVEQIPYFSQFWNEEVPNIKTQNLFFGAPHYSTSSSCEYRIGLE
RQERKHRKEGLELLKEEEEEEEEEEEEEEEEEEEEELQEEEAEEGEDQQSLPEGDLLQPRPQDSLRWQQQLKVMVKEQQEK
QEKEAIRRLPSFTSLQEALLENMLQNILVEASRGEVVLTSRPRVIALPPQGHARNTDQLLTVPLGSQPLEGPYPWQQASS
EEYVDFGAQP
```

1696 - 1715:	EEEEEEEEEEEEEEEEEEEE

A0A1S3X7T3 **A0A1S3X7T3_TOBAC** (328 aa)
troponin T, skeletal muscle-like. *Nicotiana tabacum (Common tobacco)*

```
MKNSRKGKGPPSADLLVCFPSRAHLSLMPKPICSPVRPSDSIKRHQNHDLKKISTRIGGGAAQSSPLLWSKSKNSEIISE
PTSPKVTCAGQIKVRPKPGSSCKNWQSVMEEIEKLHNRKAQKKNWMEAIGIKKDVMQFLTCLRNIRFEFRCFGSFPTTAH
DITSDEDDDEEENYVVGREIKDEEDNEENSRTVFSKWFMVLQDENQKTEKDNSNDDNSDVPNCAPPPNALLLMRCRSAPP
KNWLVEEEEEEEEEEEEEEEEEEEEEGINEEEKKATLALEEMENKRKNESLVVMRCGSDFHKLSADIAKETWVVGGVRDQL
TRSRSWKR
```

246 - 265:	EEEEEEEEEEEEEEEEEEEE

A0A1S3XB32 **A0A1S3XB32_TOBAC** (277 aa)
PHD finger protein ALFIN-LIKE 4-like. *Nicotiana tabacum (Common tobacco)*

```
MEGGGKLGGEQNNTLSVKDVFQDFKGRRAALIKALTTEVEEFFKQCDPEKENLCLFGLPNEQWEVNMPAEEVPPELPEPV
LGINFARDGMQEKEWLSLVAVHSDAWLLSVAFFYAARFGFDKSDRKRLFNMINDLPTVYEVVTGATKKQQKEKSTVSNHR
SNKSKPNSKKKAAESQGKFTKLLQKYEEEEEEEEEEEEEEEEEEEEEEGLDEKEDEEVQGETLCGACGEKYAEDEFWICC
DICEMWFHGKCVKITPARAEFIKQYKCPPCSNKRART
```

187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE

A0A1S3Z6B8 **A0A1S3Z6B8_TOBAC** (427 aa)
histone H3.v1-like. *Nicotiana tabacum (Common tobacco)*

```
MRCFTACFGNCKHKKIIKPCTDSYKSNSISPKTLKNLLKTHKNGEASVAIKNATKEEAQHGDVTNTINIIQESKNKEEEE
EKELNISSRKKVTFDDVNISSIINERGLANQESAYCLEEICNKEKEKEKGNVKEEEEEEEEEEEEEEEEEEEEEEEGTTL
SDSSASSYISFPPSHRYHCCRKSDDEFEAIDLNDNDLENDDDVEVSGNAMIEQEQSSDSSLFSLSIDSRKRNPKPELGEK
EVNSPLKLSAKDRSQLSVLNPIQEKENINILNLPNFRTSTTYCVQQDPSLKQSTKQTKRLEENQITVDTSLSSWLIESQD
DDTPNSKNNVGDLVGNYSSTPSIRVEDRPVLVELKHIANSSCVIGTVGSYLRHTGQATDSDSASSCKGISSNKTYALLRE
DKNYICSHSTPFQVRLVRALDSDLAQA
```

134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE

A0A1S4A4F1 **A0A1S4A4F1_TOBAC** (698 aa)
FRIGIDA-like protein. *Nicotiana tabacum (Common tobacco)*

```
MNKMVKPADSAAAAGAMPRSEPLEIHSQESIFVNLRKLSDGLSAFQRCLTDLEQHIDSVRTSIGSSMLLLRNNEQSTNNT
PSAAALTPPQPEPEPEPSCESDPSEVEDEDEDEEEEEEEEEEEEEEEEEEEEEEAKSPCRSELEILCETMNSIGLKEYMIT
HLSDINGLREQVPKALKLSPNPARLVSECINKGESERYVNSSRSLASVLALECLLLAAVENDKGAKEDAELAALAWRERM
ICQGGVIKAHEMDARGLLLLIGCFGIPQAFTNLDIRYLVTVSDAWVIAGALRRSSVLMEKIPEIIEWMLKQNIVVEAVDI
AYTFGMEGRFNPRRHLTSFLHNSEVSLLNNAKGLEQGITVRSDKKKHLSHLKSVSECLGRHKIDPSKLLPGWQINTRIMN
LEKEIAELNKHIGEKELAELTMRIGDQKMAQKRKNDEIESSSSGSFSNKEMRHSHFPNPNPWPPQQQRVVNHVADSNNTL
LGGGGTAGHIYGYSLSPSVLHGTVAGSIHENVVGSLAGPVGGVVAMDGAGAGKSVQGGLGVDHIPGQIGGHIGQLYGSHG
DAAVYDKLASHSYAYRPSSYLEGSSSTGLPSTIPGDAYRPTYTESSKAFPNTISGDANRPPPYLGGSAGLPNTIAGDAYR
PPPYLEGSIGLPNTIPAPYQFADTVPATEIHRSSGSRAVDHVPSAAVAHPSSYLYWKR
```

113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE

A0A1S4B6G3 **A0A1S4B6G3_TOBAC** (292 aa)
DNA ligase 1. *Nicotiana tabacum (Common tobacco)*

```
MAMSRPNLIENPIKLSKFRNNNQAQQRNRLSFWAFIFSIFMYISIFYIFNLSPSTLLNTTKFWFFISNTLILIIAADFGS
FSSSSDQEYSFEEYMKKCHQEKSVNISTSSFNYSPYTIKSIEYKETNPQEEVVMIKEEEEEEEEEEEEEEEEEEEEEEE
EEDDDDEEENIKDVVFVEKNKKEKQIININDKDKVDHEDKKKNKKKGEAKCERSNSEKAMIKVANNNGNIEKKIHGIQRS
KSERYNFVNKGDEENEEFSDMSVEELNRRVEEFIQRFNRQIRLQAVARNRQT
```

137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE

A0A1S4BS85 **A0A1S4BS85_TOBAC** (348 aa)
protein IFH1-like. *Nicotiana tabacum (Common tobacco)*

```
YTSIIRISFEKIHLGRQVQQEKRKTDAFKITVAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGGGGEDDMNIAMLFK
VITNMMKKNRYSRRGKSNFRNDKMNNDNDKNDERCCECEKHGHIQAGCPELKKKLSRNFQKKKSFGAWSDEEESDQEEIA
YICFMVINDDSNEDSGELGLMADEGTSEEQRKRNRKGKWYLDRTCSSHMTGDKQVFKTVTKFDEGTITFGDKSKGNIIGV
GRVHLSSTCDVDEVYLVDELGYNLLSISQLCDNDYEARFKKSGWLIEDELGKVILSENRDKNVYTICNMDSLDTNTHLRN
VKLPEDEEISIVPKFVVAGKDSQYQSTD
```

34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE

A0A1S4DLQ3 **A0A1S4DLQ3_TOBAC** (408 aa)
WD repeat-containing protein RUP2-like. *Nicotiana tabacum (Common tobacco)*

```
MTDISSRQEAIVEIQVAEGEEKLGSELVVVVEEEEEEEEEEEEEEEEEEEEEEEEARCEWDFHLSTFISNSCNNSLNGSAC
DTLGVLEFDASGNFLASGGIARKIRIYNVNSLLQEEREGGGLVSLDHGNACNFYMCTPAKLSSLKWKPGWGSRVIGSGDY
DGVVLEYDLEKKMPVFERDEHGGRRIWSIDYSHSDPVLGASGSDDGTMQMWDPRCGDDGKYLAKVQPSKQCNPVCCVEFN
PFKGPIVAVGCADRRVYAYDVRRMTDPLFVLDGHQKAVTYIRFLDEHTIVSSSVDGCLKMWDAENQHVIRTYKGHDNSRR
FVGLSVWRPGGLICCGSESNQVYVYDKRWGEPIWVYGREPMGVTGYNPGFISSVCWQQKEENRCTLVAGDSDGVLRVFSG
KRRCLAEL
```

32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE

34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE

A0A1S4DZ28 **A0A1S4DZ28_CUCME** (374 aa)
dihydroflavonol-4-reductase isoform X1. *Cucumis melo (Muskmelon)*

```
MEEEEEEEEEEEEEEEEEEEEEEEEEEEEDFVSKELGPKTYCVTGATGFIGSWLVNLLLLNGYKVHATARDPAKFLKLLSSW
TVTDRLRLFKADLREEGSFDEAVKGCDGVFHVAASMIFNVDQQDNIEEYVRKNVIDPEIKGTISLLKSCLKSESVKRVVL
TSTISTLTGKDADGERRRLVDESCQTSVDQVWKNKPSGWIYSLLKRLSEDAAFNFASENSIDIVSVITSTVSGPFLTSYI
PSSIRVFTAPITGDSDFLRILSNVNERMGSVAVVHTNDICRAHIFLMEHENAKGRYLCCVESCALSELVKRLSRHCAVNF
QRSVDEKKNWMPSEVSNKKLKDLGFRFEHGIDDIINETIDACVECGFISRRFQF
```

2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE

A0A1S4DZ33 **A0A1S4DZ33_CUCME** (369 aa)
dihydroflavonol-4-reductase isoform X6. *Cucumis melo (Muskmelon)*

```
MEEEEEEEEEEEEEEEEEEEEEEDFVSKELGPKTYCVTGATGFIGSWLVNLLLLNGYKVHATARDPAKFLKLLSSWTVTDR
LRLFKADLREEGSFDEAVKGCDGVFHVAASMIFNVDQQDNIEEYVRKNVIDPEIKGTISLLKSCLKSESVKRVVLTSTIS
TLTGKDADGERRRLVDESCQTSVDQVWKNKPSGWIYSLLKRLSEDAAFNFASENSIDIVSVITSTVSGPFLTSYIPSSIR
VFTAPITGDSDFLRILSNVNERMGSVAVVHTNDICRAHIFLMEHENAKGRYLCCVESCALSELVKRLSRHCAVNFQRSVD
EKKNWMPSEVSNKKLKDLGFRFEHGIDDIINETIDACVECGFISRRFQF
```

2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE

A0A1S4DZ42 **A0A1S4DZ42_CUCME** (371 aa)
dihydroflavonol-4-reductase isoform X4. *Cucumis melo (Muskmelon)*

```
MEEEEEEEEEEEEEEEEEEEEEEEEDFVSKELGPKTYCVTGATGFIGSWLVNLLLLNGYKVHATARDPAKFLKLLSSWTVT
DRLRLFKADLREEGSFDEAVKGCDGVFHVAASMIFNVDQQDNIEEYVRKNVIDPEIKGTISLLKSCLKSESVKRVVLTST
ISTLTGKDADGERRRLVDESCQTSVDQVWKNKPSGWIYSLLKRLSEDAAFNFASENSIDIVSVITSTVSGPFLTSYIPSS
IRVFTAPITGDSDFLRILSNVNERMGSVAVVHTNDICRAHIFLMEHENAKGRYLCCVESCALSELVKRLSRHCAVNFQRS
VDEKKNWMPSEVSNKKLKDLGFRFEHGIDDIINETIDACVECGFISRRFQF
```

2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE

A0A1S4DZ45 **A0A1S4DZ45_CUCME** (373 aa)
dihydroflavonol-4-reductase isoform X2. *Cucumis melo (Muskmelon)*

```
MEEEEEEEEEEEEEEEEEEEEEEEEEEEEDFVSKELGPKTYCVTGATGFIGSWLVNLLLLNGYKVHATARDPAKFLKLLSSW
TVTDRLRLFKADLREEGSFDEAVKGCDGVFHVAASMIFNVDQQDNIEEYVRKNVIDPEIKGTISLLKSCLKSESVKRVVL
TSTISTLTGKDADGERRRLVDESCQTSVDQVWKNKPSGWIYSLLKRLSEDAAFNFASENSIDIVSVITSTVSGPFLTSYI
PSSIRVFTAPITGDSDFLRILSNVNERMGSVAVVHTNDICRAHIFLMEHENAKGRYLCCVESCALSELVKRLSRHCAVNF
QSVDEKKNWMPSEVSNKKLKDLGFRFEHGIDDIINETIDACVECGFISRRFQF
```

2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE

A0A1S4DZ50 **A0A1S4DZ50_CUCME** (368 aa)
dihydroflavonol-4-reductase isoform X7. *Cucumis melo (Muskmelon)*

```
MEEEEEEEEEEEEEEEEEEEEEDFVSKELGPKTYCVTGATGFIGSWLVNLLLLNGYKVHATARDPAKFLKLLSSWTVTDRL
RLFKADLREEGSFDEAVKGCDGVFHVAASMIFNVDQQDNIEEYVRKNVIDPEIKGTISLLKSCLKSESVKRVVLTSTIST
LTGKDADGERRRLVDESCQTSVDQVWKNKPSGWIYSLLKRLSEDAAFNFASENSIDIVSVITSTVSGPFLTSYIPSSIRV
FTAPITGDSDFLRILSNVNERMGSVAVVHTNDICRAHIFLMEHENAKGRYLCCVESCALSELVKRLSRHCAVNFQRSVDE
KKNWMPSEVSNKKLKDLGFRFEHGIDDIINETIDACVECGFISRRFQF
```

2 - 21:	EEEEEEEEEEEEEEEEEEEE

A0A1S4DZ52 **A0A1S4DZ52_CUCME** (372 aa)
dihydroflavonol-4-reductase isoform X3. *Cucumis melo (Muskmelon)*

```
MEEEEEEEEEEEEEEEEEEEEEEEEEDFVSKELGPKTYCVTGATGFIGSWLVNLLLLNGYKVHATARDPAKFLKLLSSWTV
TDRLRLFKADLREEGSFDEAVKGCDGVFHVAASMIFNVDQQDNIEEYVRKNVIDPEIKGTISLLKSCLKSESVKRVVLTS
TISTLTGKDADGERRRLVDESCQTSVDQVWKNKPSGWIYSLLKRLSEDAAFNFASENSIDIVSVITSTVSGPFLTSYIPS
SIRVFTAPITGDSDFLRILSNVNERMGSVAVVHTNDICRAHIFLMEHENAKGRYLCCVESCALSELVKRLSRHCAVNFQR
SVDEKKNWMPSEVSNKKLKDLGFRFEHGIDDIINETIDACVECGFISRRFQF
```

2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE

A0A1S4DZU0 **A0A1S4DZU0_CUCME** (370 aa)
dihydroflavonol-4-reductase isoform X5. *Cucumis melo (Muskmelon)*

```
MEEEEEEEEEEEEEEEEEEEEEEEDFVSKELGPKTYCVTGATGFIGSWLVNLLLLNGYKVHATARDPAKFLKLLSSWTVTD
RLRLFKADLREEGSFDEAVKGCDGVFHVAASMIFNVDQQDNIEEYVRKNVIDPEIKGTISLLKSCLKSESVKRVVLTSTI
STLTGKDADGERRRLVDESCQTSVDQVWKNKPSGWIYSLLKRLSEDAAFNFASENSIDIVSVITSTVSGPFLTSYIPSSI
RVFTAPITGDSDFLRILSNVNERMGSVAVVHTNDICRAHIFLMEHENAKGRYLCCVESCALSELVKRLSRHCAVNFQRSV
DEKKNWMPSEVSNKKLKDLGFRFEHGIDDIINETIDACVECGFISRRFQF
```

2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE

A0A1S4GEL7 **A0A1S4GEL7_ANOGA** (380 aa)
Troponin T, fast skeletal muscle. *Anopheles gambiae (African malaria mosquito)*

```
MSDDEEYSSEEEVVEETREEQPAAKSEGDDPEFIKRQDQKRSDLDEQLKEYINEWRKQRAKEEDELKKLKDKQAKRKVSR
AEEEQRMAQRKKEEEERRVREVEEKKQREIDEKRKRLEEAEKKRQAMLQAMKDKDKKGPNFTITKKDSSFGMSNAQMERN
KTKEQLEEEKKISLSFRIKPLEVDGLSADSLRARATELWETIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALK
KGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYSAYYQEKINKKWAQRQELFMARTKTKLPKWFGERPGKK
SGDPETPEGEDEVKPDDEEVEEVEEVVEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE

A0A1S4GFA2 **A0A1S4GFA2_ANOGA** (380 aa)
Troponin T, fast skeletal muscle. *Anopheles gambiae (African malaria mosquito)*

```
MSDDEEYSSEEEVVEETREEQPAAKSEGDDPEFIKRQDQKRSDLDEQLKEYINEWRKQRAKEEDELKKLKDKQAKRKVSR
AEEEQRMAQRKKEEEERRVREVEEKKQREIDEKRKRLEEAEKKRQAMLQAMKDKDKKGPNFTITKKDSSFGMSNAQMERN
KTKEQLEEEKKISLSFRIKPLEVDGLSADSLRARATELWETIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALK
KGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGFDTLNKEVLEKQWAERKEQFGGRQKSKLPKWFGERPGKK
SGDPETPEGEDEVKPDDEEVEEVEEVVEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE

354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE

A0A1S4GFA8 **A0A1S4GFA8_ANOGA** (374 aa)
Troponin T, fast skeletal muscle. *Anopheles gambiae (African malaria mosquito)*

```
MSDDEEYSSEEEVVEETREEQGDDPEFIKRQDQKRSDLDEQLKEYINEWRKQRAKEEDELKKLKDKQAKRKVSRAEEEQR
MAQRKKEEEERRVREVEEKKQREIDEKRKRLEEAEKKRQAMLQAMKDKDKKGPNFTITKKDSSFGMSNAQMERNKTKEQL
EEEKKISLSFRIKPLEVDGLSADSLRARATELWETIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPE
ALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYSAYYQEKINKKWAQRQELFMARTKTKLPKWFGERPGKKSGDPET
PEGEDEVKPDDEEVEEVEEVVEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE

A0A1S9D680 **A0A1S9D680_ASPOZ** (570 aa)
Protein BFR2. *Aspergillus oryzae (Yellow koji mold)*

```
MGPKSLAEQIAELEDPTPKDFDPEDLERGGSDSEDEGGRAADSSAGREHYQAVGKAKLRKQDPVDLGKQYAGARVSRDAL
DADSDDDPFKARSGDEEEGSEDEDEDEDMSDEGDEEQPQKSKAAQKKGHGARIVDDMRSDDSEEIGSDEDSEDFDEDDMD
EMPSDGDEDEDEDEDEDEDEDDDEEDDDDDDEEEEEEEEEEEEEEEEEEEEEESSARRVKFAKTAKSDDREELRRLMASDQKTI
TATISQAAKADAVKGKAVKQQRATFDALLNTRIKLQKGLTAINQLSVAAKEEEDLDGEAIKSAESAALALWSTLEDLRLA
LADAQTQDESKKRKRPSAVSPSTSTASLWKRMADLESDSVAHRRAILDKWSLKVRGSNATIPNSRGKLLGSAASGQQSIT
AVLDAQIASETDRAAKRARTANGNSTDEDQEPIYDDTIFYQSLLRDVVEQRMSSSDAITNGVDTLHIQLPSRGLSIHPVT
GMRKDKVKRDVDTRASKGRKMRFDVHEKLQNFMAPEDRGTWTTHAREEFFASLLGKTASGMLREGDDEDASAAEESDSDR
EEGGLKLFRS
```

190 - 209:	EEEEEEEEEEEEEEEEEEEE

A0A1U7EI29 **A0A1U7EI29_9SPER** (1120 aa)
DNA-directed RNA polymerase subunit beta (EC 2.7.7.6) (PEP) (Plastid-encoded RNA polymerase subunit beta) (RNA polymerase subunit beta). *Callitropsis vietnamensis*

```
MRLEENKGIFTIPQFGKIQLEGFFRFINQGLIEEINNFSKIESSNKKIKIILFGSEYKLTEPFIKERDAVYMSLTYNCQL
YVPARLIKKTKKTCEIQDQILYLGDIPLMNSKGTFVITGNYRVVVNQIVRSPGIYYTWERKPSGNIIWIGTIISDWGGRS
RLELNKKKEKIWIRIKKKKISVLLFLLAMGLNSEDIFNYKNVKAFFQYSKEYYTYKYDWYGGKRKAILKLYKKLYISDEN
EEEGEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEELDFESIYEKVTTFFRTKCLLGKIGRRNLNKKLSLDIPENEI
LLLPHDILAAVDYLIKVQFGAGTPDDIDHLQNRYIRSVADLLQEQLRLALYDFREAVEKTILPVSINAKKRITLIKLETF
ISLTDTFHNFFGLHPLSQFLDQTNPLAEIVHSRKVSSLGPGGLTSRTSTFRTRDIHPSHYGRICPITTSEGINVGLIGSL
SIYATLGHYGSLQSPFYRLSERSNKDHMVYLLPGEDEYYRIAIGNSLALNQGVPEEQLTAARFQQEFLFFAWDQIHFRSI
FPSQYFSVGVCLIPFIEHNDANRALMGSNMQRQALPLVQPEKCIVGTGLEGQVALDSGSVAIAKQGGKIKYIDGENIIIT
SSVARDNIETELILYQRSNSDTCMHQKPRVRQGEYVKRGQIIADSAATAGGELSLGKNILVAYMPWEGYNFEDAILISER
LVYEDIFTSFQIVRYEIGVYFTDQGPEVITREIPHLNAYLLRHLDENGIVMIGSWIETGDILVGKLILEAEEDSLINTPE
GKLLQALFDIKAPTGKENCFRVPKGVKGRVIDVRCFQEFEEEEDDYLGDIIEKVHVYILQKRKIQVGDKVAGRHGNKGII
SKILPRQDMPYLQNGTPVDMVLNPLGVPSRMNVGQIFECLLGLAGKLMNKHYRLPPFDERYEREASRKLVFSELYKASEQ
TANPWVFETDNPGKHRLIDGRTGKVFEQPVTIGIAYISKLCHQVDDKIHARSRGPYALVTQQPLKGKSSRGGQRVGEMEV
WALEGFGVAYILHEILTLKSDHMDTREKIFGAIFNGEPMPKPTTFTESFRLLSRELRSLALELNHTILSEIDFQIDKKEV
```

249 - 268:	EEEEEEEEEEEEEEEEEEEE
250 - 269:	EEEEEEEEEEEEEEEEEEEE
251 - 270:	EEEEEEEEEEEEEEEEEEEE
252 - 271:	EEEEEEEEEEEEEEEEEEEE
253 - 272:	EEEEEEEEEEEEEEEEEEEE
254 - 273:	EEEEEEEEEEEEEEEEEEEE

255 - 274:	EEEEEEEEEEEEEEEEEEEE
256 - 275:	EEEEEEEEEEEEEEEEEEEE
257 - 276:	EEEEEEEEEEEEEEEEEEEE
258 - 277:	EEEEEEEEEEEEEEEEEEEE
259 - 278:	EEEEEEEEEEEEEEEEEEEE
260 - 279:	EEEEEEEEEEEEEEEEEEEE

A0A1U7QK39 **A0A1U7QK39_MESAU** (1071 aa)
sodium/potassium/calcium exchanger 1 isoform X2. *Mesocricetus auratus (Golden hamster)*

```
MGKLIRIGTRERRLFRRPKRLHWSRLLFLLGMLIIGSTYQHLRRPQNSPSMWTKVSSQQPIKLAGRDLPSDEMTVVGSDP
PEASSEVDGEILAPQNTVIRDEATPSITMEDTPNPPRTTKITPTSPKNDYSPIAAGTERKKEKPPPTSSRASNHFISTSG
RERIKNYTPIPRGERRNSTPAHSREKGRKYTPSPAGAPSATTPITTEKDSKTMATYRLLETRPPERIVEETTAASFRRVV
PNTPTFLTREAETSLLTTPSLVEENTLGSPGREEQNSSTSLQGTVPQHTPATSEEQVTVRARMGSNPATVGASTAAWRIS
NLLSRTSAPTIRIASVTNREGAKRPSTAPVTSKVKAILTTQVHRCVVMEPVPAVPMTPSPSITNILFPGAPSPSPSASPP
GWPKLHAKAEYPPDLFSVEDRRQGWVALHIFGMMYVFVALAIVCDEYFVPALGVITDKLQISEDVAGATFMAAGGSAPEL
FTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCALFSREILNLTWWPLFRDVSFYILDLSMLIVFFLDSLIAWWESLLL
LLAYALYVFTMKWNKQIELWVKEQLSRRPVAKVMALGDLSKPSEGAIEENESQDNKKLKLPSVLTRGSSSASLHNSIIRS
TIYHLMLHSLDPLGEARPSKDKQESLNQEARAHPQTKAESSPDEEEPAQLPEVTVTPAPAPDVKGDQEEDPGCQEEVGEA
DRTGETQPGERETEAEGNEDEEGETEAEGKEDEGETEAEGKGDEQEGETEAEGKGDEQEGETEAEGKEDELKRQGEIQAD
DTEVKDGDDETEANAENQCETTQGEKGADDEGGSDGGDSGEEEDEEEEEEEEEEEEEEEEEEEENEEPLSLEWPESRQKQ
ALYLFLLPIVFPLWLTVPDVRRQESRKFFVITFLGSIIWIAMFSYLMVWWAHQVGETIGISEEIMGLTILAAGTSIPDLI
TSVIVARKGLGDMAVSSSVGSNIFDITVGLPVPWLLFSLINTLQPVPVSSNGLFCAIVLLFLMLLFVIFSIASCKWRMNK
ILGFTMFLLYFVFLVISVMLEDRIIACPVSV
```

845 - 864:	EEEEEEEEEEEEEEEEEEEE

A0A1U7QTY3 **A0A1U7QTY3_MESAU** (1134 aa)
myelin transcription factor 1 isoform X1. *Mesocricetus auratus (Golden hamster)*

```
MSLESDDKRARTRSKTLRGPPETTGADLSCPTPGCTGSGHVRGKYSRHRSLQSCPLAKKRKLEDAEAEHLVSKRKSHPLR
LALDEGYRMDSDGSEDAEVKDASVSDESEGPLEETEAEMSGQEEIHHPQPAEGKNLIKPHFGSNPTSSPSGFSKGSYSSY
QGIIATSLLNLGQIAEETLVQEDSVPVAKLDPAVVHQLRDEAAIGATNEEDEKDLFIHPEDVEEVIEVTSERSQEPCPQS
LEDMISKESSKQKGVLGHEEEGEEEEEEEEEEEEEEEEGEEVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEETTPNLI
FGEDTSHTSAQKSSSEFRSPELSSPKPEYSVIVEVRSDDDKDEDSHSQKSAVTDESEMYDMMTRGNLGLLEQAIALKAEQ
VRAVCEPGCLPAEQGHLGPGEPGKVAKPLDVVRKSCYSKDPSRVEKREIKCPTPGCDGTGHVTGLYPHHRSLSGCPHKDR
IPPEILAMHENVLKCPTPGCTGQGHVNSNRNTHRSLSGCPIAAAEKLAKSHEKQQLQTGDPPKNNSNSDRILRPMCFVKQ
LEVPPYGSYRPNVAPATPRANLAKELEKFSKVTFDYASFDAQVFGKRMLAPKIQTSETSPKAFQCFDYSHDAEAAHMAAT
AILNLSTRCWEMPENLSTKPQDLPSKAVDIEVDENGTLDLSMHKHRKRENAFPSSSSCSSSPGVKSPDVSQRQNTTSAPS
SSMTSPQSSQASRQDEWDRPLDYTKPSRLREEEPEESEPAAHSFASSEADDQEVSEENFEERKYPGEVTLTNFKLKFLSK
DIKKELLTCPTPGCDGSGHITGNYASHRSLSGCPLADKSLRNLMAAHSADLKCPTPGCDGSGHITGNYASHRSLSGCPRA
KKSGLKVAPTKDDKEDPELMKCPVPGCVGLGHISGKYASHRSASGCPLAARRQKEGALNGSSFSWKSLKNEGPTCPTPGC
DGSGHANGSFLTHRSLSGCPRATFAGKKGKLSGDEILSPKFKTSDVLENDEEIKQLNQEIRDLNESNSEMEAAMVQLQSQ
ISSMEKNLKNIEEENKLIEEQNEALFLELSGLSQALIQSLANIRLPHMEPICEQNFDAYVNTLTDMYSNQDCYQNPENKG
LLETIKQAVRGIQV
```

283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE
287 - 306:	EEEEEEEEEEEEEEEEEEEE
288 - 307:	EEEEEEEEEEEEEEEEEEEE
289 - 308:	EEEEEEEEEEEEEEEEEEEE
290 - 309:	EEEEEEEEEEEEEEEEEEEE
291 - 310:	EEEEEEEEEEEEEEEEEEEE
292 - 311:	EEEEEEEEEEEEEEEEEEEE
293 - 312:	EEEEEEEEEEEEEEEEEEEE
294 - 313:	EEEEEEEEEEEEEEEEEEEE
295 - 314:	EEEEEEEEEEEEEEEEEEEE

A0A1U7QVK6 **A0A1U7QVK6_MESAU** (1053 aa)
sodium/potassium/calcium exchanger 1 isoform X3. *Mesocricetus auratus (Golden hamster)*

```
MGKLIRIGTRERRLFRRPKRLHWSRLLFLLGMLIIGSTYQHLRRPQNSPSMWTKVSSQQPIKLAGRDLPSDEMTVVGSDP
PEASSEVDGEILAPQNTVIRDEATPSITMEDTPNPPRTTKITPTSPKNDYSPIAAGTERKKEKPPPTSSRASNHFISTSG
RERIKNYTPIPRGERRNSTPAHSREKGRKYTPSPAGAPSATTPITTEKDSKTMATYRLLETRPPERIVEETTAASFRRVV
PNTPTFLTREAETSLLTTPSLVEENTLGSPGREEQNSSTSLQGTVPQHTPATSEEQVTVRARMGSNPATVGASTAAWRIS
NLLSRTSAPTIRIASVTNREGAKRPSTAPVTSKVKAILTTQVHRCVVMEPVPAVPMTPSPSITNILFPGAPSPSPSASPP
GWPKLHAKAEYPPDLFSVEDRRQGWVALHIFGMMYVFVALAIVCDEYFVPALGVITDKLQISEDVAGATFMAAGGSAPEL
FTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCALFSREILNLTWWPLFRDVSFYILDLSMLIVFFLDSLIAWWESLLL
LLAYALYVFTMKWNKQIELWVKEQLSRRPVAKVMALGDLSKLPSVLTRGSSSASLHNSIIRSTIYHLMLHSLDPLGEARP
SKDKQESLNQEARAHPQTKAESSPDEEEPAQLPEVTVTPAPAPDVKGDQEEDPGCQEEVGEADRTGETQPGERETEAEGN
EDEEGETEAEGKEDEGETEAEGKGDEQEGETEAEGKGDEQEGETEAEGKEDELKRQGEIQADDTEVKDGDDETEANAENQ
CETTQGEKGADDEGGSDGGDSGEEEDEEEEEEEEEEEEEEEEEEEENEEPLSLEWPESRQKQALYLFLLPIVFPLWLTVP
```

```
DVRRQESRKFFVITFLGSIIWIAMFSYLMVWWAHQVGETIGISEEIMGLTILAAGTSIPDLITSVIVARKGLGDMAVSSS
VGSNIFDITVGLPVPWLLFSLINTLQPVPVSSNGLFCAIVLLFLMLLFVIFSIASCKWRMNKILGFTMFLLYFVFLVISV
MLEDRIIACPVSV
```

827 - 846:	EEEEEEEEEEEEEEEEEEE

A0A1U7RE61 **A0A1U7RE61_MESAU** (1190 aa)
histone-lysine N-methyltransferase EHMT2 isoform X2. *Mesocricetus auratus (Golden hamster)*

```
MGALLLEKEPRGAAAERVHGPLGDTPHAEETLPKADPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDEPESLEGD
GGRALLGHATKSFPSSPSKGGACPSRAKMSVTGAGKSPPSVQSLAMRLLSMPGAQGAATAGPEPPPAAATTTGQEGQPKV
HRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHPLGKVTSDAAKRRKLNSGSLTEDFGSARGSGDMALEKGEPRPLEE
WETVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEDEEEDEESGNQSDRSGSSGRR
KAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGF
EELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCEAHRARMVKHHCCPGCGYF
CTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGGTPPAGTAAPAPLPLAQDAPGRADTSQ
PSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGSCLSAVGLPPGPGREALEKALVIQESERRKKLRFHPRQLYVSVKQ
GELQKVILMLLDNLDPNVQNDQQSKRTPLHAAAQKGFVEICHVLLQAGANINAVDKQQRTPLMEAVVHNRLEVARYMVQL
GGCVYSKEEDGSTCLHHAAKMGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIDVIRMLLTRGADVTLTDNEENI
CLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFA
LQLNRKLRLGVGNRAVRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDC
SSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRSCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQ
GTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFS
SRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELSALPPMNA
```

279 - 298:	EEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEE

A0A1U7RG75 **A0A1U7RG75_MESAU** (225 aa)
cysteine-rich hydrophobic domain-containing protein 1. *Mesocricetus auratus (Golden hamster)*

```
MSILLPNMAEFDTISELEEEEEEAATSSSSSPSSSSSSVSGPDEDEEDEEEEEEEEEEEEEEEEEEEEVPPPPRVVSEE
HLRRYAPDPVLVRGAGHITVFGLSNKFDTEFPSVLTGKVAPEEFKTSIGRVNSCLKKALPVNVKWLLCGCLCCCCTLGCS
LWPVICLNKRTRRSIQKLLEWENNRLYHKLALHWKLTKRKCETSNMMEYVILIEFLPKYPIFRPD
```

49 - 68:	EEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEE

A0A1U7TJC4 **A0A1U7TJC4_CARSF** (1122 aa)
myelin transcription factor 1. *Carlito syrichta (Philippine tarsier) (Tarsius syrichta)*

```
MSLENEDKRARTRSKALRGPPETTAADLSCPTPGCTGSGHVRGKYSRHRSLQSCPLAKKRKLECAGAEHLVSKRKSHPLK
LALDEGYGVDSDGSEDAEVKEASVSDESEGTLEGAEAEMSGQEEIHHPEPAEGRSPIKFHFGSNPISSPTGSSKGSYGSY
QGIIATSLLNLGQIAEETLVGEDLGQAAKPNPGIVHLLQEEAAEGATSDEGEKELFIQPEDAEEVVEVTSERSQELCPQS
LEDAASEESSKQKGILGHEEEDEEDEEDEEDEEEEEEEEEEEEEEEEEEEEEEEDEEEEEEGEEAAPDVIFEEDASHSSAQ
KAPELRRPEPPSPKPEYSVIVEVRSDDDKDEDARSQKSAVTDESEMHDMMTRGNLGLLEQAIALKAEQVRTVCEPGCPPA
EQGPLGLGEPGKAAKSLDTVRKSYYSKDPSRAEKREIKCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRIPPEILAMHENV
LKCPTPGCTGQGHVNSNRNTHRSLSGCPIAAAEKLAKSHEKQQPQAGDTSKNSSNSDRILRPMCFVKQLEVPPYGSYRPN
VAPATPRANLAKELEKFSKVTFDYASFDAQVFGKRMLAPKIQTSETSPKAFQCFDYSHDAEAAHMAATAILNLSTRCWEM
PENLSTKPQDLPNKSVDIEVDENGTLDLSMHKHRRRESTFPGGSSCSSSPGVKSPDVSQRQSSASAPSSSMTSPQSSQAS
RQDEWDRPLDYTKPSRLREEEPEESEPAAHSFASSEADDQEVSEENFEERKYPGEVTLTNFKLKFLSKDIKKELLTCPTP
GCDGSGHITGNYASHRSLSGCPLADKSLRNLMAAHSADLKCPTPGCDGSGHITGNYASHRSLSGCPRAKKSGVKVAPAKD
DKEDPELMKCPVPGCVGLGHISGKYASHRSASGCPLAARRQKEGSLNGSSLSWKSLKNEGPTCPTPGCDGSGHANGSFLT
HRSLSGCPRATFAGKKGKLSGDEVLNPKFKTSDVLENDEEIKQLNQEIRDLNESNSEMEAAMVQLQSQISSMEKNLKNIE
EENKLIEEQNEALFLELSGLSQALIQSLANIRLPHMEPICEQNFDAYVSTLTDMYSNQECYQNPENKDLLESIKQAVRGI
QV
```

272 - 291:	EEEEEEEEEEEEEEEEEEE
273 - 292:	EEEEEEEEEEEEEEEEEEE
274 - 293:	EEEEEEEEEEEEEEEEEEE

A0A1U7U0J0 **A0A1U7U0J0_CARSF** (727 aa)
YTH domain-containing protein 1 isoform X2. *Carlito syrichta (Philippine tarsier) (Tarsius syrichta)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLISKPLSSSVSN
NKRIVSTKGKSVTEYKNEEYQRSERNKRIDADRKIRLSSSASREPYKSQPEKTCLRKRDPERRAKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDPEEDEEVDEDGEEEEEEEEEE
EEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSAS
ESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNVAFRSARSVILI
FSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEI
ELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQR
PGYLKDPRYQEVDRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHH
PVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDRG
ERGRYRR
```

230 - 249:	EEEEEEEEEEEEEEEEEEE

A0A1U7UA40 **A0A1U7UA40_CARSF** (1268 aa)
histone-lysine N-methyltransferase EHMT2 isoform X1. *Carlito syrichta (Philippine tarsier) (Tarsius syrichta)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGAHRGRGRPRSLLSLPRAQASWAPQLPTGLTSPPVPCLPSQGEVPAEMGA
LLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDERADTPVGATPLIGDEPEILEGDGDLH
GGRILLGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGTAATGPEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTTDVAKRRKLNSGGVLSEELGSARGSGEVTLEKGDPGSLEEWE
TVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKA
KKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEE
LPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCT
AGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLAQDAPGRTDTSQPS
ARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGE
LQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGG
CVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICL
HWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQ
LNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSS
SNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGT
FICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSR
DIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELSSLPPVNT
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE

A0A1U7UEM9 **A0A1U7UEM9_CARSF** (585 aa)
ran GTPase-activating protein 1 isoform X2. *Carlito syrichta (Philippine tarsier) (Tarsius syrichta)*

```
MASEDIAKLAETLAKTQVAGGQLSFKGKSLKLNTAEDAKDVIKEIEDFDSLEALRLEGNTVGVEAAKVIAKALEKKSELK
RCHWSDMFTGRLRSEIPPALISLGEGLITAGAQLVELDLSDNAFGPDGVKGFEALLKSSACFTLHELKLNNCGMGIGGGK
ILAAALTECHRKSSAQGKPLTLKVFVAGRNRLENDGATALAEAFGIIGTLEEVHMPQNGINHPGITALAQAFAINPLLRV
INLNDNTFTEKGAVAMAETLKTLRQVEVINFGDCLVRSKGAVAIADAIRGGLPKLKELNLSFCEIKRDAALAVAEAMADK
AELEKLDLNGNTLGEEGCEQLQEMLDGFNMTKVLASLSDDEDEEEEEGEEEEEEGEEEEEEEEEEEEEEEEEEEEPQQRR
QGEESCTPSRKILDPNSTEPAPVLSSPPPVDVSTFLAFPSPEKLLRLGPKSSVLIAQQTDTSDPEKVVSAFLKVSSVFKE
EATVRTAVQDAVDALMKKAFSSSSFNSNAFLTRLLVHMGLLKSEDKIKAIANLYGPLMALNHMVQQDYFPKSLAPLLLAF
MTKPNGALESCSFARHNLLQTLYKV
```

376 - 395:	EEEEEEEEEEEEEEEEEEEE

A0A1U7UG89 **A0A1U7UG89_CARSF** (1325 aa)
tau-tubulin kinase 1. *Carlito syrichta (Philippine tarsier) (Tarsius syrichta)*

```
MQCLAAALKDETNMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTRENVALKVESAQQPKQVLKMEVAV
LKKLQGKDHVCRFIGCGRNEKFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESIEAIHSVGFLHRDIKPSNF
AMGRLPSTYRKCYMLDFGLARQYTNTTGDVRPPRNVAGFRGTVRYASVNAHKNREMGRHDDLWSLFYMLVEFAVGQLPWR
KIKDKEQVGMIKEKYEHRMLLKHMPSEFHLFLDHIASLDYFTKPDYQLIMSVFENSMKERGIAENEAFDWEKAGTDALLS
TSTSTPPQQNTRQTAAMFGVVNVTPVPGDLLRENTEDVLQGEHLSDQENAPPILPGRPSEGLSPSPHLVPHPGGPEAEVW
EETDVNRNKLRINIGKTPCVEEEQSRGVGVPSSPVRAPPDSPTTPVRSLRYRRVNSPESERLSTADGRVELHERRSRMDL
PGSPSRQACSSQPAQMLSVDTGHADRQASGRMDVSASVEQEALSNAFRSVPLAEEEDFDSKEWVIIDKETELKDFPPGAE
PSTSGTTDEEPEELRPLPEEGEERRRPGAEPTVRPRGRSMQMLAEEDLRQMPSQPPPPQLSQTDGRSETSQPPTPGSPSH
SPLHSGPRPRRRESDPTGPQRQVFSVAPPFEVNGLPRAVPLSLPYQDFKRDLSDYRERARLLNRVRRVGFSHMLLTTPQV
PLAPVQPQANGKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVAVALGEVLGPRSGSSSEGSERS
TDRSQEGAPSTLLADDQKESRGRASVADGDLEPEEGSKTLVLVSPGDMKKSPVTAELVPDPDLGTLAALTPQHERPQPTG
SQLDVSEPGTLSSVLKSEPKPPGPGAGPGAGAGTTGAGGVAVTSSPFTKVERTFVHIAEKTHLNVMSSGGQATRPEEFSA
GGELGLEVPSEGGAAEQGAPGPLENGVALSGLDGAEMESCALSGPPGEAPSEVAMDSLPNGPAFADAPSPACPLEPGPEK
MATISPSRHAMPGPRPRSRIPVLLSEEDTGSEPSGSLSAKERWSKRARPQQDLARLVMEKRQGRLLLRLASGASSSSSEE
QRRASETLSGTGSEEDTPASEPGGALPRKTGRAAAARSRIPRPISIRMPTPAATQQPPSRSHVATPASDTAITSRLPLQK
PPGSATAADLRPKQPPGRSTGPGRAQAGARPPAPRSPGLPASTSAARHPSASPRSQSLSRKESPSPSHQARPGVAPSRGV
PQARAQPDGTPSQGDPKKGPRGKLQAQRAATKGRAGDAEGRAGAR
```

733 - 752:	EEEEEEEEEEEEEEEEEEEE
734 - 753:	EEEEEEEEEEEEEEEEEEEE
735 - 754:	EEEEEEEEEEEEEEEEEEEE
736 - 755:	EEEEEEEEEEEEEEEEEEEE
737 - 756:	EEEEEEEEEEEEEEEEEEEE
738 - 757:	EEEEEEEEEEEEEEEEEEEE
739 - 758:	EEEEEEEEEEEEEEEEEEEE
740 - 759:	EEEEEEEEEEEEEEEEEEEE
741 - 760:	EEEEEEEEEEEEEEEEEEEE
742 - 761:	EEEEEEEEEEEEEEEEEEEE
743 - 762:	EEEEEEEEEEEEEEEEEEEE
744 - 763:	EEEEEEEEEEEEEEEEEEEE

745 - 764:	EEEEEEEEEEEEEEEEEEEE
746 - 765:	EEEEEEEEEEEEEEEEEEEE
747 - 766:	EEEEEEEEEEEEEEEEEEEE
748 - 767:	EEEEEEEEEEEEEEEEEEEE
749 - 768:	EEEEEEEEEEEEEEEEEEEE
750 - 769:	EEEEEEEEEEEEEEEEEEEE
751 - 770:	EEEEEEEEEEEEEEEEEEEE
752 - 771:	EEEEEEEEEEEEEEEEEEEE
753 - 772:	EEEEEEEEEEEEEEEEEEEE
754 - 773:	EEEEEEEEEEEEEEEEEEEE
755 - 774:	EEEEEEEEEEEEEEEEEEEE
756 - 775:	EEEEEEEEEEEEEEEEEEEE
757 - 776:	EEEEEEEEEEEEEEEEEEEE
758 - 777:	EEEEEEEEEEEEEEEEEEEE

A0A1U7UM71 **A0A1U7UM71_CARSF** (1234 aa)
histone-lysine N-methyltransferase EHMT2 isoform X2. *Carlito syrichta (Philippine tarsier) (Tarsius syrichta)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGAHRGRGRPRSLLSLPRAQASWAPQLPTGLTSPPVPCLPSQGEVPAEMGA
LLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDERADTPVGATPLIGDEPEILEGDGDLH
GGRILLGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGTAATGPEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTTDVAKRRKLNSGGVLSEELGSARGSGEVTLEKGDPGSLEEWE
TVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKA
KKKWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGEL
SGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHC
GEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLAQDAPGRTDTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGG
CLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKG
SVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQV
DVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLH
IAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIP
CVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFE
CNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEV
YCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCK
HSAEAIALEQSRLARLDPHPELLPELSSLPPVNT
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE

A0A1U7YNC5 **A0A1U7YNC5_NELNU** (448 aa)
probable transcription factor At3g04930. *Nelumbo nucifera (Sacred lotus)*

```
MASKEEEQNICQKGEGKELDEEESEEDEDDLTTHQLEDDDEDDDEEEDEEEEEEEEEEEEEEEEEEEEEEEEEDLHSPSP
PSTSSSSQHNTNKGTPSTAPIENPTTSTSVPAPAPAPTATTITGTFPNCSVLETPPVTDTSPDPKRQRTTEASAATKEKK
PAVFDDSRRLFQRLWTDEDEIGLLQGFLEYTIQRGKQNSSHHHDTAPFYDQIKTRLQLDFNKNQLVEKLRRLKKKYRNVV
SRISSGKDFSFKSPHDQATFEISRKIWSGVAARRGGVDEGGLEDDEGNPHNNNNNHHNNKNIRNLDDNSNTNNNGLDTNN
SEKAVPTPRSRKRSRKRGPEDNLANYQGTSSVHNVIEDTVRSCLSPLFKELLYCAISGPSNAGGYAGQALNPLPLSFVGN
SINISKEDMVDEKWRKQQILELEVYLKRIELIQDQIKSVIEELKSMGS
```

49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE

A0A1U7ZID4 **A0A1U7ZID4_NELNU** (426 aa)
F-box/kelch-repeat protein At5g60570-like. *Nelumbo nucifera (Sacred lotus)*

```
MLPETDRSKELLKLPYLAQFASDNFSKKREEEEEEEEEEEEEEEEEEEEEEEEEAVMKIRSSGGGYDCSKRCSREGSYDS
SLIPGLHDDIALTCLARTRQSDHASLACLNRRFRSLMSSGYLYGLRKQLGIIEHRVYVVCDPRGWEAFDPMRKKWMRLPK
IPCDDCFNHADKESLAVGSELLVFGRELLDFATWKYNLVSRNWIKCQGMNLPRCLFGSGSYGSIAIVAGGSDKHGTVLKS
AELYDLESGRWDLLPNMISPRKLCSGFFMDGKFYVIGGISSPNVVLTCGEEFNLQTRKWRKIEGMYPNVINASQAPPLVA
VVNNQLYAVEHSTNMVKKYDKEKNTWSVLGRLPLRVDSSNGWGLAFKAYGDELLVVGGQRSREGEGILLSSWSPMLGLKN
GILNWKVLDVKEHVGLFVYNCAVMGC
```

30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE

A0A1U7ZZK6 **A0A1U7ZZK6_NELNU** (394 aa)
trihelix transcription factor ASIL2. *Nelumbo nucifera (Sacred lotus)*

```
MDDTEDDARYPPNPYPGNHHQSYGSSHRPKLPVRNASYPQTVGNEYGDEDEEEEEEEEEEEEEEEEEEEEEAGVQRVTEEA
EEDEDEEEEDDDDEDDDDGGNYRRRIEVDEESERHRKKRKLKNLGYEFAPRIAAPSAAAAAPKPSFGGRNSPADWTEHAT
FVLLDAWGDRFLQLGRKSLRSDEWHEVANKVSEESNTIRTDTQCRNRLDTLKKKYKKEKMKLAETGNTTSKWVYFKKMDM
LMTSSARQPGLSCGLDSGEYVFMNPRVYLNRANGLDEMRDSPGNSESSEGDEDDSDGLPPNRPRFGDDTGGSSSFRLLAD
SIQKFGEIYEKIENSKRQQMLELEKMRMEFHRDLELQKRQILERAQAEIAKIRQGDRDDDDEDDIDVSTENISG
```

51 - 70:	EEEEEEEEEEEEEEEEEEEE

A0A1U8A6T6 **A0A1U8A6T6_NELNU** (712 aa)
Exocyst subunit Exo70 family protein. *Nelumbo nucifera (Sacred lotus)*

```
MIDRWMDQANWSANFGQLFSSAQSNGVLIPEEEEEEEEEEEEEEEEEEEEEEEEEEGRNQMGVPLPMETLSERAAFMREAL
QKSQTITDNMVTILGSFDHRLSALETAMRPTQIRTHSIRRAHENIDKTLKAAEVILSQFDLCRQAEAKILKGPHDDLENY
LGAVDQLRSNVHFFSSNKSFKSSDAVLNHANNLLAKAILKLEEEFKQILVSYSKPVEPDRLFEGLPNSLRPGSGSGSPGH
QADSTWKNPSSNNHHEHQNKGLESYTPPTLIPPRILPLLHDLAQQMVQAGHQQQLLIIYRDARSSVLEQSLRKLGVEKLS
KDDVQKMQWEVLEAKIGNWIHYMRIAVKLLFAGEWKVCDQIFEGIDSLRDHCFAEVTENSVAMLLSFGEAIAKSKRSPEK
LFVLLDMYEIMRELQSEIETLFEGKACSEMRESALSLTKKLAQTAQETFGDFEEAVEKDATKTAVLDGTVHPLTSYVINY
VKFLFDYQSTLKQLFQEFENGAETNSQLASVTMRIMQALQTNLDGKSKQYKDPALTYLFLMNNIHYMVRSVRRSEAKDLL
GDDWVQRQRRIVQQHANQYKRVAWGKILQCLSVQGLTSSGGGSNSAMGGDGGNSSGVSRAVVKERLKTFNVQFEELHQRQ
SQWAVPDSELRESLRLAVAEVLLPAYRSFIKRFGPLVENGKNPQKYVRYSPEDLDRMLNEFFEGTILNEQKR
```

31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE

A0A1U8AAP4 **A0A1U8AAP4_NELNU** (700 aa)
BTB/POZ domain-containing protein At5g66560-like. *Nelumbo nucifera (Sacred lotus)*

```
MENSSSKGQAWFCTTGLPSDIVIEADDMTFHLHKFPLMAKSRKLHLMITEQEANVARSREELEGNDAEVDVEIEEEPCYI
SLPDFPGGSETFETAVKFCYGVKIDLTSWNVAPLRCAGEYLMMTEDFSEDNLISKTERFLSQLVLRNIKESVRTLKSCEA
LIPLAEELSIPQRCIDSIVARWSVNEGASTGSTRSSNQNILNGIDTGTRRKSKSKNTAASNAEPWFEDLCILSLPVYMQV
ISAMKARDINSEIIESSLLSYAKKSIPGLSRSNRKPSSASIASEAEQRELLETIITNLPQERSSRSRSGSSSSTMTRFLF
GLLRAANILNASDDCRAALERKIASQLEQATLDDLLIPSYSYLIETLYDVDCVGRILGYFLEGLEERPEIGVDGHGDNGV
DGARSSGVNPVMLVGKLIDGYLSEIASDANLKPEKFWELAVALPDHARLYDDGLYRAVDVYLKAHPWITEEERDKICGVM
DSQKLTLEACTHAAQNERLPLRAVVQFLFFEQLQLRNAIAGSILTADIIPPDSAGAGSSVLQHQQEEVEEEEEEEEEEE
EEEEEEEEEEQRQQQQQHWQQLQLALAAPGGESSNTWRTAIRENQVLRLDMDTMRSRVHELERECSTMKKAIAKIDKVGP
QGASGSGSGSGSGGWRNSLTKKLGCKFKTQVCDSHERTVIESRKQGKQHHHQHQQPTNFL
```

549 - 568:	EEEEEEEEEEEEEEEEEEEE
550 - 569:	EEEEEEEEEEEEEEEEEEEE
551 - 570:	EEEEEEEEEEEEEEEEEEEE

A0A1U8AK33 **A0A1U8AK33_NELNU** (1118 aa)
histone-lysine N-methyltransferase ATX5-like. *Nelumbo nucifera (Sacred lotus)*

```
MIIKRSLKSRMPYLKRCKAEQPGCEDDESSGNKKKRKTNGYYPLDILGEVAAGRIPLTGFGFRRRLGNDGEEFSSVAASW
CTEVSYCPGELDSESKRQDALKVKNHIADVFRPPLVKTSRGRVQVLPSRFNDSVLDPWKKEKAKPSVRESGFHTEIGTSK
KEKFSCKTTKFSSRLTKKLCKDDKFSYDSPKCFPLLKEECEEEEEEEEEEEEEEEEEEEEEEEEEEEGGNLLFKNLDIR
KYSSSRSSLTSLHEPIIEVEKSGPLVEFQKSPRNFELTGVPKSSKENTEKRKGFYRPEDFVLGDIVWAKSGKRYPAWPAI
```

```
VIDPMLQAPDTVLNSCVAGAICVMFFGYSRNGKERDYAWVKHGMIFPFIDYLDRFQGQTQLHKSKPSDFRMAIEEAFLAE
HGFMELPAEEMNAVVGQPAYNHSIPRGVQEATDSNQDQECYSQNQDAFEKKKGTQPCDGCGLSLTFKTTKKVKGSTPKGQ
FLCKHCTKLLKSKQYCGICKKIWHHSDGGSWVRCDGCKVWVHAECDKISSNLFKDLEDTDYYCPECKAKFNFELSDSEKS
QQRNRSDKITGQFVLPDKITVVCTGMEGVYFPSLHLVVCNCGSCGKEKRSLSEWERHTGSKKKNWKTSVKVKGSMLPLEQ
WMLQMAEYHERGLVSANPLKRPSPKLRKQKLLDFLQEKYEPVYAKWTTERCAICRWVEDWDYNKIIICNRCQIAVHQECY
GARNVRDFTSWVCRACETPDVKRECCLCPVKGGALKPSDVDTLWVHVTCAWFQPEVSFSSDETMEPAVGILRIPSNSFVK
VCVICKQMHGSCTQCCKCSTYYHAMCASRAGYRMELHCLEKNGRQITKMVSYCAFHRAPNPDTVLVIQTPIGIFSAKSLL
RNKKQTGSRLISSKRSDLQEDSTSEADQFEPSSAARCRIYKRSKNKRTGEEAIAHRVMGPCHHPLDAIECLNTFKEDKDV
KSFSSFRERLYHLQRTENERVCFGRSGIHGWGLFARRNIQEGEMVLEYRGEQVRRSVADLREASYRLEGKDCYLFKISEE
VVVDATDKGNIARLINHSCMPNCYARIMSVGDDESRIVLIAKTNVSAGDELTYDYLFDPDECKVPCLCKAPNCRKFMN
```

201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE
208 - 227:	EEEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEEE

A0A1U8B1J2 **A0A1U8B1J2_NELNU** (324 aa)
coiled-coil domain-containing protein 97. *Nelumbo nucifera (Sacred lotus)*

```
MQEKRALSSSVMEGITNRLSSLEDLYFPRAVQATAVNPSQRKSILLDLLSRDAAVFLERYGPHLTSEELHEFDTLNNDYE
VNWHLKHLRSVLSPTSEEVRSRSVTVKNRRRAYLDKLIRDGNYFSEDAMREREPYLHHEYVGKFQDPSGRRMARPGERWS
ETLLRRSEEAILVAKIRGEQQRLGVVEKDWVGNERELEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEESDDYEEAEKLE
VVADQATENGSQKINSNVHEGSTLSSAEMQDRMEQFTYMMQQKFLSGEDSQHLDYSKIDNDETLDDHWLREANHDAEEKY
FAED
```

198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE

A0A1U8BV75 **A0A1U8BV75_MESAU** (295 aa)
LOW QUALITY PROTEIN: protein SET-like. *Mesocricetus auratus (Golden hamster)*

```
MAILNFAEESGANAIHPLPWCHGPPKRRSGLLLQSKKPKSVPAAKLEDKSVSLDLLNGEKEQQEAIEHIDKVQNEIDXNE
QASKGILKVEQNYDKLRQPFFQKRSELIAQIPNFWVITFVSHPQVSALLGEEDEEALHYLTRAEVTEFEDIKSGYRIDFY
FDENPYFENQILSKEFHLNESGDPSSKSTEIKWKSGKDLTKCSSQTQNKASRKRQPEESESFLTWFTDHSDAGADELGEV
IQDHIWGANPLQYYLVPDMDDEEGEAEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

267 - 286:	EEEEEEEEEEEEEEEEEEEE
268 - 287:	EEEEEEEEEEEEEEEEEEEE
269 - 288:	EEEEEEEEEEEEEEEEEEEE
270 - 289:	EEEEEEEEEEEEEEEEEEEE
271 - 290:	EEEEEEEEEEEEEEEEEEEE
272 - 291:	EEEEEEEEEEEEEEEEEEEE
273 - 292:	EEEEEEEEEEEEEEEEEEEE
274 - 293:	EEEEEEEEEEEEEEEEEEEE
275 - 294:	EEEEEEEEEEEEEEEEEEEE
276 - 295:	EEEEEEEEEEEEEEEEEEEE

A0A1U8C054 **A0A1U8C054_MESAU** (1041 aa)
sodium/potassium/calcium exchanger 1 isoform X4. *Mesocricetus auratus (Golden hamster)*

```
MGKLIRIGTRERRLFRRPKRLHWSRLLFLLGMLIIGSTYQHLRRPQNSPSMWTKVSSQQPIKLAGRDLPSDEMTVVGSDP
PEASSEVDGEILAPQNTVIRDEATPSITMEDTPNPPRTTKITPTSPKNDYSPIAAGTERKKEKPPPTSSRASNHFISTSG
```

```
RERIKNYTPIPRGERRNSTPAHSREKGRKYTPSPAGAPSATTPITTEKDSKTMATYRLLETRPPERIVEETTAASFRRVV
PNTPTFLTREAETSLLTTPSLVEENTLGSPGREEQNSSTSLQGTVPQHTPATSEEQVTVRARMGSNPATVGASTAAWRIS
NLLSRTSAPTIRIASVTNREGAKRPSTAPVTSKVKAILTTQVHRCVVMEPVPAVPMTPSPSITNILFPGAPSPSPSASPP
GWPKLHAKAEYPPDLFSVEDRRQGWVALHIFGMMYVFVALAIVCDEYFVPALGVITDKLQISEDVAGATFMAAGGSAPEL
FTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCALFSREILNLTWWPLFRDVSFYILDLSMLIVFFLDSLIAWWESLLL
LLAYALYVFTMKWNKQIELWVKEQLSRRPVAKVMALGDLSKPSEGAIEENESQDNKKLKLPSVLTRGSSSASLHNSIIRS
TIYHLMLHSLDPLGEARPSKDKQESLNQEARAHPQTKAESSPDEEEPAQLPEVTVTPAPAPDVKGDQEEDPGCQEEVGEA
DRTGETQPGERETEAEGNEDEEGETEAEGKEDEGETEAEGKGDEQEGETEAEGKGDEQEGETEAEGKEDELKRQGEIQAD
DTEVKDGDDETEANAENQCETTQGEKGADDEGGSDGGDSGEEEDEEEEEEEEEEEEEEEEEEEEEENEEPLSLEWPESRQKQ
ALYLFLLPIVFPLWLTVPDVRRQVGETIGISEEIMGLTILAAGTSIPDLITSVIVARKGLGDMAVSSSVGSNIFDITVGL
PVPWLLFSLINTLQPVPVSSNGLFCAIVLLFLMLLFVIFSIASCKWRMNKILGFTMFLLYFVFLVISVMLEDRIIACPVS
V
```

845 - 864:	EEEEEEEEEEEEEEEEEEEE

A0A1U8C0X6 **A0A1U8C0X6_MESAU** (1111 aa)
myelin transcription factor 1 isoform X2. *Mesocricetus auratus (Golden hamster)*

```
MSLESDDKRARTRSKTLRGPPETTGADLSCPTPGCTGSGHVRGKYSRHRSLQSCPLAKKRKLEDAEAEHLVSKRKSHPLR
LALDEGYRMDSDGSEDAEVKDASVSDESEGPLEETEAEMSGQEEIHHPQPAEGKNLIKPHFGSNPTSSPSGFSKGSYSSY
QGIIATSLLNLGQIAEETLVQEDSVPVAKLDPAVVHQLRDEAAIGATNEEDEKDLFIHPEDVEEVIEVTSERSQEPCPQS
LEDMISKESSKQKGVLGHEEEGEEEEEEEEEEEEEEEEGEEVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEETTPNLI
FGEDTSHTSAQKSSSEFRSPELSSPKPEYSVIVEVRSDDDKDEDSHSQKSAVTDESEMYDMMTRGNLGLLEQAIALKAEQ
VRAVCEPGCLPAEQGHLGPGEPGKVAKPLDVVRKSCYSKDPSRVEKREIKCPTPGCDGTGHVTGLYPHHRSLSGCPHKDR
IPPEILAMHENVLKCPTPGCTGQGHVNSNRNTHRSLSGCPIAAAEKLAKSHEKQQLQTGDPPKNNSNSDRILRPMCFVKQ
LEVPPYGSYRPNVAPATPRANLAKELEKFSKVTFDYASFDAQVFGKRMLAPKIQTSETSPKAFQCFDYSHDAEAAHMAAT
AILNLSTRCWEMPENLSTKPQDLPSKAVDIEVDENGTLDLSMHKHRKRENAFPSSSSCSSSPGVKSPDVSQRQNTTSAPS
SSMTSPQSSQASRQDEWDRPLDYTKPSRLREEEPEESEPAAHSFASSEADDQEVSEENFEERKYPGEVTLTNFKLKFLSK
DIKKELLTCPTPGCDGSGHITGNYASHRRCPTPGCDGSGHITGNYASHRSLSGCPRAKKSGLKVAPTKDDKEDPELMKCP
VPGCVGLGHISGKYASHRSASGCPLAARRQKEGALNGSSFSWKSLKNEGPTCPTPGCDGSGHANGSFLTHRSLSGCPRAT
FAGKKGKLSGDEILSPKFKTSDVLENDEEIKQLNQEIRDLNESNSEMEAAMVQLQSQISSMEKNLKNIEEENKLIEEQNE
ALFLELSGLSQALIQSLANIRLPHMEPICEQNFDAYVNTLTDMYSNQDCYQNPENKGLLETIKQAVRGIQV
```

283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE
287 - 306:	EEEEEEEEEEEEEEEEEEEE
288 - 307:	EEEEEEEEEEEEEEEEEEEE
289 - 308:	EEEEEEEEEEEEEEEEEEEE
290 - 309:	EEEEEEEEEEEEEEEEEEEE
291 - 310:	EEEEEEEEEEEEEEEEEEEE
292 - 311:	EEEEEEEEEEEEEEEEEEEE
293 - 312:	EEEEEEEEEEEEEEEEEEEE
294 - 313:	EEEEEEEEEEEEEEEEEEEE
295 - 314:	EEEEEEEEEEEEEEEEEEEE

A0A1U8C4K0 **A0A1U8C4K0_MESAU** (1308 aa)
tau-tubulin kinase 1 isoform X2. *Mesocricetus auratus (Golden hamster)*

```
MQCLAAALKDETNMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTRENVALKVESAQQPKQVLKMEVAV
LKKLQGKDHVCRFIGCGRNEKFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESIEAIHSVGFLHRDIKPSNF
AMGRLPSTYRKCYMLDFGLARQYTNTTGDVRPPRNVAGFRGTVRYASVNAHKNREMGRHDDLWSLFYMLVEFAVGQLPWR
KIKDKEQVGMIKEKYEHRMLLKHMPSEFHLFLDHIASLDYFTKPDYQLIMSVFENSMKERGIAENEAFDWEKAGTDTLLS
TSTSTPPQQNTRQTAAMFGVVNVTPVPGDLLRENTEDVLQGEHLSDQENAPPILPGRPPEGLGPSPHLVPHPGGPEAEVW
EETDVNRNKLRINIGKTPCVEEEQSRGVGVPSSPVRAPPDSPTTPVRSLRYRRVNSPESERLSTAADGRIELHERRSRMD
LPGSPSRQACSSQPAQMLSVDTGHADRQASGRMDVSASVEQEALSNAFRSVPLAEEEDFDSKEWVIIDKETELKDFPPGA
EPSTSGTTDEEPEELRPLPEEGEERRRLGTEPSVRPRGRGMQTLAEEDLRQGLPQPAPPLLSQADGRSETSQPPTPGSLS
HSPLHSGPRPRRRESDPTGPQRQVFSVAPPFEVNGLPRAVPLGLPYQDFKRDASDYGERARLLTRVRRVGFSHMLLTTAQ
VPLTPFQPQANGKEGEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEGEAGALGEVLGPRSLSSSEGSERSTERSQEGAPS
TLLADDQRDTRGRASMADGDLEPEEGSKTLVLVSPGDVKKSPVTAELAPDPDLGTLAALTPQHEQPQPTGSQLDVSEPGT
LSSVLKSEPKPSGPGTGLGAGLVAAGGAGAVTSSPFTKVERTFVHIAEKTHLNVMSSGGQASRPEGSGTGGELGLEMLSE
GGAAEERGPVPLENGMALSGLDGTETESCALSGPPGETPSEVVTDSLPNGPALADGPAPATPLEPVTKKGTAISPSRHAM
PGSRPRSRIPVLLSEEDTGSEPSGSLSAKERWSKRARPQQDLARLVMEKRQGRLLLRLASGASSSSSEEQRRASETLSGT
GSEEDTPASEPTAALPRKVGRAATTRSRIPRPIGVSASAEGQQLPGRPHGAASASDLAITSRLQLQKPSGSTTTADLRPK
HSASRGPGPGRAQVSRSAAPRSPGLPASTARHPSGSPRSQSLSRKESSSPSHQARSGVPPPRGVLQARSQPEASPGAPKK
GPRGKQQQTQRAATKGRGAVSEGRPGTR
```

744 - 763:	EEEEEEEEEEEEEEEEEEEE
745 - 764:	EEEEEEEEEEEEEEEEEEEE
746 - 765:	EEEEEEEEEEEEEEEEEEEE
747 - 766:	EEEEEEEEEEEEEEEEEEEE

A0A1U8FN61 **A0A1U8FN61_CAPAN** (1281 aa)

lysine-specific demethylase JMJ25-like. *Capsicum annuum (Capsicum pepper)*

```
MATLVAKQGPLSSQNQHTPRMRNQSKVFRKRKFVLNLDEEKLEKDNAASAPDVTDLPNKKKKLCSESGALRGKRTVSEHV
NVAIRKEEALLSGGSAEKIKTAEKPKRNMIKSRLRTKTVAKQTMTVKESEGSHRRITSKEHHRSAEKKLSSKIWDEMVSN
DEEEEEEEEEEEEEEEEEEEEEEEEDEEYFPGPLTKFQMPLKEALNSLRTSTKGKVLRNGRMRNKGNDEEKDKPSQCRD
RLKLSTSTKNFLLSGNSQTKRMPDKVNLEQHPGTSRKKMAGTREIQGSKNKRRAPAILNEQCLGRSKKRKIPQGERTMDN
VDESEEEWSMSKEKPSLSKDVENRRTSVRHATGSFKRYGDFYVGEWEDDTDDYEVFPLSDGHHIPSNTRSQGSDVSPESK
PKNSPKDMRKISGKLSACSSLPSWAPAKLNGEQCLGMSSKKKRPRADRTMDKVDGSEDEWNVCKEKSSLSKDGKKKQRIY
EKDAENKRTSVRRAAASLKRYDHNYFVGEWEDDAEEYEVLPISDGHHTPSNPRSQRSEVSHESKPKDSPKDSINNSGKLS
ACSSLPSTSSSSGSTISRNGIDGSKNMKVNCHQCRRSDRRTVVPCTKCKEKFYCIKCIKEWYPELEEEEVSELCPYCRGK
CNCNLCLHSRVMLKTSRKDLTDREKIEHLHYLIFTLLPFLKEIHHEQIQEIETESSTRGVSSSSVEIKQSLCHNDERVYC
NNCSTSIVDLHRSCPDCSYELCLSCCRELRGGMFRGNSCKAVYKYSDRGCDYMHGGEPLPESFHNVEIPQDQNKPITWVA
NCDGNIICAPVEMGGCGKCVLELKHLLPRNWISTLKAKAERILIQCNFSQMISQPICRTDDPELLHRAASRVGSDDNCLY
STTAKDAMEDEALLRFRRHWAKGEPVIVRNVLEHTSGLSWEPMVMWRALCETTDSKILTSMSEVKAIDCLADCQVQINTR
KFFKGYTEGRSYENLWPEMLKLKDWPPSDKFENLLPRHCDEFISALPFQEYSDPRTGILNLAVKLPAGVLKPDLGPKTYI
AYGVTKELGRGDSVTKLHCDMSDAINILTHTAEVAVTDEQQSAIEILKQRHRAQDERERLEREGNEFPMKMSSDIGREEK
TSDDSETTGGALWDIFRREDVPKLKDYLLKHAKEFRHTYCYPVDEVFHPIHDQIFYLTLEHKRKLKEEYGVEPWTFEQRL
GEAVFIPAGCPHQVRNLKSCTKVAADFVSPENIRECFNLTDEFRKLPKGHKAREDKLEIKKMVIHAINQVVTDLEQLTYI
V
```

162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE

A0A1U8GFU9 **A0A1U8GFU9_CAPAN** (406 aa)
RING-type E3 ubiquitin transferase (EC 2.3.2.27). *Capsicum annuum (Capsicum pepper)*

```
MARFSVGREEEDDNEDGDSEGPARGGGGGGPVPKRRRTFGGTFSCSSVRRQQEQEQQQERERERERREMVVDEEIEEEEEE
EEEEEEEEEEEEEEWESESEEEESEEGRLGGVGDAEGSRGSGSIARGNGSIARGNGSMAVDEQDNDVEGLRGNGSISVTL
SDPDVLDCPICLEHLSVPVFQCENGHIACASCCIKIANKCPSCCWPIGYNRCRAIEKVLESVKVSCMNKSYGCKEVLSYS
KKTVHENTCIYVPCSCPFRGCDFVGAATKVYAHFSDKHASSAVHMLFNAVHPIFIEKHRRYQILQMSTKDVLFIINHASD
RVGSSVNIICVGPAMQKRRFMYEIVATDGESTFKLESVAESVPNWSENTPLKKYLLVPRDIVNCGARLKLDVFIKERECI
GSGSTT
```

75 - 94:	EEEEEEEEEEEEEEEEEEEE

A0A1U8GII4 **A0A1U8GII4_CAPAN** (106 aa)
histone H3.v1-like. *Capsicum annuum (Capsicum pepper)*

```
MARFSVGREEEDDNEDGDSEGPARGGGGGGPVPKRRRTFGGTFSCSSVRRQQEQEQQQERERERERREMVVDEEIEEEEEE
EEEEEEEEEEEEEEWESESEEEESEE
```

75 - 94:	EEEEEEEEEEEEEEEEEEEE

A0A1U8KRY3 **A0A1U8KRY3_GOSHI** (652 aa)
neurofilament medium polypeptide-like. *Gossypium hirsutum (Upland cotton) (Gossypium mexicanum)*

```
MDDRELEWEIQESSTEDSENGKLSWLMRLGRKIFVTGIVISSAPLVFPPIMAISAIGFVCSVPYGVLLVSYVCTKTLMSR
LLPMPSRSAPLLLEYGKACNDEEEEEEEEEEEEEEEEEEEEEETNGVQNEVIKGDISIEREEEELKEDIIEEIEARIELV
DKRNEEPDKGDILQKGAYQKDGVQNDVKRSAGDDSEFMNERPSQSFEEVKEITGMQTEQPMIGECRNKPPAEKGQGIEAV
VQRDEKCSSNLVNETPLGSGNVKEKDEYVQLIRAIDALVNEKFRGTTREQQKEKEVPGINEVKEEEYVRDKQPIEETCNV
VIEFVEDEKNGNNKENEKQFLMEKVDVHFTQSTDIEEDEELVRETRGLLEKIRDQGERGYMDAKPSTEKVHVGTEKDDKQ
ILQISANAVADYGMEMPTSESETEVEKNKADSKEQMKGSVEMDIQKREQPVGPVSETANDDSITKGLTVEIAASIVGQAK
DENIVDPSYQLNKEKKDVVFSNEDEREISEEQGLDLSENLSSVSLQGSPQEVNTEESWPSSSYSLHQDASDSSDLPVSTK
AQEADNTKIPVENATDAPSNEAIHCEEKIWEQMNALRTIVGYKAARRETCIEELKALYVFTGIEPPASLKDTCDPAEVDA
KLGFLKSVVGVK
```

102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE

A0A1U8NA89 **A0A1U8NA89_GOSHI** (1010 aa)
glutamic acid-rich protein-like. *Gossypium hirsutum (Upland cotton) (Gossypium mexicanum)*

```
MASSQLEIVPSSPFGCVLRDHNRKERCRDSNVSSVQTVFDKNFNDLVRDHINGCISLSSPKSPQNHNNVASWVSAEQGNA
NANANANANRHNLPSFSNKNHHNKKKGDPSPINPKQSPVLDRWVTRQSQDVAVSTIDKQVNEAAEQVLAPSHSNPVSPPP
PPPPMASSSTTKNAQTRSENASVTHNLAASSLVQIWEARLNRSNSINSYQNQSMDSNTSRTSSGVSSNENNASPMEESST
SEPFEEKMENRTNNVDSLIELESPSDRTAAGEAASSSSSSCSKTFDAGEIERVRIVDIIKKLKNCREDADDHEHTGSHSQ
CKEPKHCSKPNESLRRCFSLVINSPLIRGRQAFQDFLIRIERDKKRELDSLVKRQAVSKFPQRGRVQSMLRLKSLQRCLT
IQDKCRPQLNRSQGSTIMHLREKFSTGAEQGMTAQNVSATPRYICKDKSSTCKPPQREDTHCQKGQQSSSPVDSLTTNKN
GDVKEQAKPPSDAVQQKTSLEAKSPESPKIAKETKPLEGPSENDVAKKEDLSSQQLILGSQETAETVTQNEVAKAEQEKD
QHQLILDSQETMETTTTTATSVVSSIENEIVEEDIGDQQHICVDPQSQDIVDNTSTSCINDRNENEVTEEEEDHYQQYFD
ETDDYDWFSNISRPRSYWEGLRQAWYEEVLNTTSNNEEIRQLLERGRVSTLLGSDFRDTMDRLMTSRVQMQADGAESQQE
VDDKEGIICRGRVSTLLGSDFRDTMDRLMTSRVQMQADVAESQQEVEDKEGMVQPVSYEEEEEEEEEEEEEEEEEEEEE
```

```
EEEEEEEEEEYDDEEERSLSSRQCQEVNNYFNNSSPSIQMPSPSAMMTRSWSFQDDNETSNDERGASLYSPPPQPSQAER
YQDARQSASSINRPSLEMELICDLRGHIEQLHSEISELRKSVMTCMDMQMKWQHYSLNREVHSVEGEGKNSADRTPWKRR
CCICYEMQVDSLLYRCGHMCTCLKCGNELQWRSGKCPICRAPILDVVPAK
```

779 - 798:	EEEEEEEEEEEEEEEEEEEE
780 - 799:	EEEEEEEEEEEEEEEEEEEE
781 - 800:	EEEEEEEEEEEEEEEEEEEE
782 - 801:	EEEEEEEEEEEEEEEEEEEE
783 - 802:	EEEEEEEEEEEEEEEEEEEE
784 - 803:	EEEEEEEEEEEEEEEEEEEE
785 - 804:	EEEEEEEEEEEEEEEEEEEE
786 - 805:	EEEEEEEEEEEEEEEEEEEE
787 - 806:	EEEEEEEEEEEEEEEEEEEE
788 - 807:	EEEEEEEEEEEEEEEEEEEE
789 - 808:	EEEEEEEEEEEEEEEEEEEE
790 - 809:	EEEEEEEEEEEEEEEEEEEE
791 - 810:	EEEEEEEEEEEEEEEEEEEE

A0A1U8QTE0 **A0A1U8QTE0_EMENI** (774 aa)
Uncharacterized protein. *Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) (Aspergillus nidulans)*

```
MAGSQKKSTKKFEKKHLKDVLERRKAAAKIKQRNQLKEKRKSDNTKSRAERKDDSEDDAEQVKKQNAFAEMNVDDFFAGG
FDIADPAANKKKVKKDVSPKIGKRKRSETQEEEEEELSSGDEDFAESQDGDGGSEASELDDAETHKKDIEALKEKDPEFY
KYLQENDAELLEFGDLAEVDALSEGEDEQDEEPAKKKKKAAKEEEPASNLTVASVQKWQKLMEEQHSIRAMRQAVLAFRA
AAYLDDPDAQEQKYSISDSNVYHQVLVTALNNVPKVLSHHLPVKETASGKVRVSLDSKKFKTLTPLIKSHTSSVQKMLAN
LSDEQTLKLTLSSIEPMLPYLLQFRKLLKVLIKTIVGIWADASTTEATRIVGFLLLRRLMVIGDSGLKESVLKASYEGVV
KGSRNTTVHTLPGVNLMKNSAAELWGIDQNVSYTTGFNFIRQLAMHLRSSITNTSKESYKTIYNWQYVHSLDFWSRVLSQ
HCDGLVEAKIGKQSALRPLIYPVVQITLGASRLIPTAQYLPLRFQLTRSLLRLSRASGTYIPLAPLLLEPLNLTELRKAP
KQATLRPLDFTTTIRAPKSYLRTRVYQDGAAEQIAELLSEFFVLWSKHISFPELSVPIVVALKRWLKQVSSRSGGNRNQK
LNQMILLLVQKVEANAKWIEERRAHVTFAPRNKTEVEAFLKDVDWESTPLGAFVKVQRKLREEKAALLEEGRREEEKRRQ
EERDGGDDVVMDDVASENDHSGDDEEEEEEEEEEEEEEEEEEEEEISEEEEDDD
```

745 - 764:	EEEEEEEEEEEEEEEEEEEE
746 - 765:	EEEEEEEEEEEEEEEEEEEE

A0A1U9X7P8 **A0A1U9X7P8_HUMAN** (1210 aa)
EHMT2. *Homo sapiens (Human)*

```
MAAAAGAAAAAAAAEGEAPAEMGALLLEKETRGATERVHGSLGDTPRSEETLPKANPDSLEPAGPSSPASVTVTVGDEGAD
TPVGATPLIGDESENLEGDGDLRGGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGA
AAAGSEPPPATTSPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEIQHFRMSDDVHSLGKVTSDLAKRRKLNSGGGLSEEL
GSARRSGEVTLTKGDPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEE
EEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTL
SPNHAGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVL
CETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGT
AAPAPPPLSQDVPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQE
SERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRT
PLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEV
IRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELR
NKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETS
TMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRL
QLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNII
PVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLP
ELGSLPPVNT
```

300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE

A0A1V2LDV0 **A0A1V2LDV0_CYBFA** (1814 aa)
Intracellular protein transport protein USO1. *Cyberlindnera fabianii (Yeast) (Hansenula fabianii)*

```
MELIQGLMAQQKTQSAEEIIPTLCDRLAHARLASDKRAAILTLKGFARQYRESVISNGLRALISTLREFAVDTDIIKASL
ETILVLFIRGESEEDQTRAWISQQSRTQNGKYPSPLLMKQEDETSAFDHFSLWIADEITQSEENISVIVSLLENNDFYVR
LYTLQLLEALVAMRPNKTKDSLLNAPLGIPALISVLDDLHDPVKNEAVLLLMAVANDNSNIQKLVAFGDTFDKLFEIIHE
EGDIRGSIVVQDCLTLLTNLLKYNVSNQKLFLETYCLPKLAFLIAEPLEDDDILWNDQRLQNIIIALEIIGLFVIEGNES
TLKNQNSLHNAGIFVTVLRLAFSPSTDNKIRPHALRTVAVLMSNNPDIQQTFSEIDVPYIDPSLPKQLQRFKDPVPAVVA
LLNWCLFVNSVHVFDIRITALDVLTAYFEGNNDNKLAFLQDQISDFYNEDRDDEVEDAEEEEEEEEEEEEEEEEEEEEK
EEAKTVVPEQNGSRTDIPHTSDDSNGSETNPATNDSAGTNGTTSALEMKETPIANIFQALLEYDPELKLNPYKVWFSAVI
```

```
LINLIQHNDDLKALVRGVHTGDEDAGEEKISAIQAMSGLLVTTLTNQYQRVSVGYLQLLIVLLYEDFESVDDFLGDVSNV
KSLLQYLAQPSSDGIVHGLMTVLIGVAFEFSSQSSPLSRVDFHSLIVKMLGKDSYGFKVLQFREDEAFANFSEDDILKLT
WDETGLPKVYFVRTVVSLIKDNYYRIKNTLNQDPELESNGRISYEKFEELNDHYHQLQKTHSEYMEKSTTTHKEITANLE
KTTADLSKITEAHDSTQKELDALRVTHAELEAKFESTSTALANLEKLHADLTDSSDKQSKDIESTTQQLATKETLIINLK
QELKQVQEQKKKAENDVSKMSRDLFQLNTKKEELERTVKKLEKDVQKNVKHQEKLEQSLKQKEAEASDLKTRLGEAMKEL
KTAESTKTTLQRSIDEHKSKGSENKMLIDQMTEKLRSIATTCNELASAKAALEEESATLKATSSRELELYKSKVADLEAS
SKDLQSLTDKLSADKDQLESTLQATKSEHVSAIQKLEGENQELQKNISDLKAELETSKDLSGKHEEQINSLTTQLKSTKD
ELSGLKEAHSISVKETADSHHKALSAVQKELSSHKETHKSKIGELQTRIAELTKAEEAATKELDSHKNDIAQAKKDLEKK
NSKLESLEKQLGERKTEIEVLKSSNAALETKLKDSDEKSKNKLSELQQTVDQLTKTKTDLETELDELALELESKESESKN
EIRNLSEKIKSVEEEKKSLSSTLEIISQRIETKDMESQSLNKSLKAKTSEIEEVTKSKNALETEKKSMEQSLEKSQEQVE
TLQVEIGTLQENLETTTEKLSKSEAALKAANQRLEDQKKSWSEKVTVLEREIKTLKESIEKKNTEFEKERTLLSENSSST
TKEYSEKVTKLEEELQKLQTSSGTKTEELEKAKQNLEETIADLRSGNESLTSDLKSKDAKVTELKTNIKELEKKIKDLER
KHIEALKDTANVATLEANLKEKDGTIQGLKSDLKEKEDEAKDLKKKLDTSVGVIEKLERDAERLEKEAESETTKSSSIKA
TLEAKVKTLETELSSLKKQNAKLTADIDGASSKSVTEIEQKQNEIEELKKRASTTEADLKTAKASLIKAEESENASKKKL
LEVMESAKSEKESMQTEISTLKKSVEESEKLTKDIEAVKEKNANLSRDLESAKSSSTDIDKFKKENDELKQKLEDFKKTM
VARSELDDLMLVLDDLDDKKKKYKEKVKSLGGDVSSDEEDEEDDDDDDDDSDEE
```

459 - 478:	EEEEEEEEEEEEEEEEEEEE
460 - 479:	EEEEEEEEEEEEEEEEEEEE

A0A1V2LJP5 **A0A1V2LJP5_PICKU** (372 aa)
U3 small nucleolar ribonucleoprotein LCP5. *Pichia kudriavzevii (Yeast) (Issatchenkia orientalis)*

```
MSLTNQESLDDLLLSISESVDSTASVLGKIENDFDLNNTEIQNELVNSLVKTLDSSSNPLDSLSLLSLKNSALLGYVTDL
ALLMALRLKSLKEQDKNSLNQERDNLLKSTVTNRVVLEKGVKSLENKMSYQLEKMVNAYHRREKEQDDVEKKINENNASD
VGDVGSSSEGSDGGEEEEEEEEEEEEEEEEEEEEEGLNFKPNPSALLNRKNQNVNSGKTMAGGDDNEGEAKSNEKYRPPKI
SATAINDPDKQVKGRKQRNLQSMDEYLQDISEAPSMEKSIGSTIINNGRDMKSRKQMEKEAEIQRYEEENFTRLPATKTK
EDKRARAKRMRNEFMGEDWSMFDNNMNPDEASGAKKRKRLSAWERAKRKIDH
```

175 - 194:	EEEEEEEEEEEEEEEEEEEE

A0A1V2LNK5 **A0A1V2LNK5_PICKU** (2845 aa)
Histidine biosynthesis trifunctional protein (EC 1.1.1.23) (EC 3.5.4.19) (EC 3.6.1.31) (Histidinol dehydrogenase) (Phosphoribosyl-AMP cyclohydrolase) (Phosphoribosyl-ATP pyrophosphohydrolase). *Pichia kudriavzevii (Yeast) (Issatchenkia orientalis)*

```
MDGANQGFQPNQQQQQQQQQQQQQQQQQQQQFRMQISQNDRIQFIKVLITSLQKIQGPSFNIQKIKPVADEFEKYAFANSS
SKGQYVEFLKNKITSLTQAKRNQSQQVSQQMMQAQQAQQAQGQPQRMPQIQQPLQQPMQNPQQKFTMLQQQQQQQQQQQQ
QQQQQAQAPSQQLDSKSISFQNIPIPRELLMKLPKVFPTHLNTWHQIMPYLRNNQLSQNDLEIIRKVHMAHLNYFKQNFA
NQSQTPQQLQLQQKHQQQQQQQQQQPQQLQPQPQSQPQSKSNVALNPQQILMMKQQSHQQQQQQQAAMAQAEAARNAQAAA
QAHAQMKAQAQAQAAAQAQIQAQMQAQLQAQNIQNQNKMNPNMQASQQQMSKMKQAQINAYKAQAVQVIRKLQSAGKLPV
TLTPEQEANYVKKYLLHILQNSNKEQQKQAHQNLQQQQQQQQQQQTQQQTHQNNQSNQQLQHPQISPNMGFNQTMDNMSP
MNRRNVSMGMNSGNVDMTKMSSPVVPMSNLNTSVLNNNQQMNNFSSPTIPNPQMIMNNQIANQQQPQLSQSVDSQFSLQQ
TAQQSSTKRTGGIVNQQLPTNQNNFGNTINNQIGKPTSASSIGAKLLPGLKATPEDWESLKKIYMETIQSPIVLKDVTNQ
LLDEEKARIIGLAKQSKQLMILCQTMIIPNFYFITKQRVPTEKIIYNELMLRQFLEKLTSSRVFVANEELLIKIHDHIKK
YLQFVRDQSNKIIKAQVLEQQSRVNKLQQQQQLQQQYADNMNGPPKGTFNQMPANLTPTMMQVNMQQQMMKGNQESVVTG
QPIGFTPQQIPSSTVPTPTAGPNPSLKAASPPKQAKKPRKKATPKSTVSGNGKTSASNTPNSTTPGSKPATENTSATTHQ
MKSSLSNKSQDSSASMTNEIQNILKTNNELIEKEELRLKNIDIARARRRALVPVPTTNAKSTPASASSPAKSAATATNSS
ITGAAAYFLATLNDTLGLESEEKAIVTNATSKSTLPKSKSSSLRDHPKVLTPSAVLATPVGLNVKTPVNKSTITDEENKV
TQWKGKISANLISNAFRPVIHINTSISPKMLQSGKFFTKSTPSMSGGKNLSFLDVVKERTANKRALELIIPTTEGSNWTG
NSSNIWSFGNNENNRKDVSKIYPTPPEDANEAKRRKLNNNSSVDCDIFWDFDHMGGSESDTEVQGGFLVSKGAKEISRER
KRTRSGTRQLRHMNNQTPSSSSTRNTRSRIRRSGLAVEEESYGEDQGEKEEEEEEEEEEEEEEEEEEEDDDGDEDYVED
DVVITGFNEKGEKGDPVELSDDSNDDVIITEGRDFKSDFREISELQDEINELQKESNGNSNNEELVDGGFIKESNGSTKK
KSSRKKPTKSPRKKKEPKPKLTPFERRTNRLYEAHPELRDIFPSLEEQGPKKVILADQPPDLAVTLLNFQREGLSWMVRQ
EDESPYNGGILADEMGMGKTIQMIALMMHDRSKGPNLVVAPTVALIQWKTEIETHTNNALKVAIFHGANRATSLEELEDI
DVVLTSYAVVESSYRKEKYGFTKKHKKVREKSILHLKKFYRVILDEAHNIKDRTSSTAKACDVLNCEKRWCLSGTPLQNR
IGELYSLIRFLDIAPFCQYFCTKCPCKSKEWNFPDYKVCAQCGHAPMVHSNFFNHFMLKNIQKYGLQFEGEESFHRIQLL
LRQIMIRRTKVERADDLGLPPKLVEIRRDYFNPEEKDLYQSLYTDSKRQFDDYVAEGVVLNNYANIFTLITRMRQLADHP
DLVLKRMKLPSSANGGNEGVVELPPGVIVCQICDDEAEEPIESKCHHKFCRICVSEYVESFNGDTSKLKCPVCHIGLSID
LEAPAIEMDLDAVDKTSIVNRIDMAGNWKSSTKVEALMEELYKSRSDRVTTKSIVFSQFTSMLDLVEWRLKRAGFSTVKL
QGSMTPSQRQSSIKYFLETPSVEVFLVSLKAGGVALNLVEANQVFILDSWWNPSLDTGQAADRIHRIGQHRPIRIVKLVI
EDSIESRIIELQEKKANMSTGKPLLSVVGQALYRFNGSNTDAIVQISKYTPNLNVFVELAVNEISDAIVEQLLSLYNNGV
CSVLATPEQGSVILEKIPNARITYTASENKQYQSIAYVLGSSLPQTIDEKITAFVYVEDTLSLEELQKLVKSGYIPIVKS
DLLTNEYEDVKGQYPLVDFIIPKIVTDRADGLYTTLVVDSSNQSLGLVYSSVTSISESIRTGTGVYQSRKHGLWYKGKTS
GATQKLISFDLDCDSDCLKAIVEQSGSGFCHLSTNSCFGNFTGLKALEATLFQRKTDAPEGSYTKRLFDDESLLNAKIKE
EAEELADAKTKEEIAWEAADLFYFALARCAKYNVTLADIEKNLDMKALKVSRRKGDAKPKFIEKKQSTEKSEINERHIGP
DDKIYLNRINAATASKEEVEACLERPIQKSADIMSLVTPIVENVKANGDKALLELTAKFDRVQLDSPVLFAPYKPDMMQI
SEKLKKAIDVSFENIRIFHEAQNQKDILTVETSPGVYCSRFARPIEKVGCYIPGGTAVLPSTSLMLSVPALVAGCKEIIF
ASPPGKDGKLTPEVVYVAHKVGAKCIVMAGGAQAVAAMAYGTESVPKCDKIMGPGNQFVTAAKMLVSNDSNALCAIDMPA
GPSEVLVIADKHADPDFVASDLLSQAEHGIDSQVILLAVDMTDAEVDAIDEAVHRQALALPRVDIVRKCIAHSTTIVVKT
LDEAFEMSNKYAPEHLILQIENAEEWVPKVDNAGSVFVGALSPESCGDYSSGTNHTLPTYGYARMYSGVNTATFQKFITS
QVVTREGLKNIGPAVMDLAEVEGLDGHRNAVRVRMDKLGMLPEGY
```

1250 - 1269:	EEEEEEEEEEEEEEEEEEEE

A0A1V2LR27 **A0A1V2LR27_PICKU** (893 aa)
Ribosome assembly protein 1. *Pichia kudriavzevii (Yeast) (Issatchenkia orientalis)*

```
MAGKVRYLDSRPDEQLRGITMESSAISLFFKTINQNKEISQFLINLIDSPGHIDFSSEVSSVSRLCDGAIVLVDVVEGVC
SQTITVLRQAWIDNLKPILVLNKIDRLILELQLSAEDAYDHLQRLIDQTNTIMASFYQGDVIGTHYNWDGTADTWIEHND
DDIYFDPNLQNVIFTSAYDGWGFNLNQFASILSKKTQIDQSEFTGKLWGNFTIDMKNKKMVEIPKKSKAKPLFISFILDS
IWKIYNSVSDRDIDSITKITNSLSIKISAKELNSKDSKQLIQSIMSQFLPISSSVLSAIIDKLPSPSVSQETKMNSFLKS
IPNSQLIDDNLKDGLFHCDKNGISCGYISKMLSIPGSEMPENQPAVLSQDEIMERGRLARLKAAKAAELAAMADSDNTRA
QKAESDTEEAGVASEEFEFEDPFEYEEEEEEEEEEEEEEEEEEEETNPEVLIAFTRIFSGTVKRGDTLSILSPLYDVSKP
DDEENKKHIHSIEVDNLYILMGRDMTAVDAAPAGTIIGISSSSFKSIILKSGTIIDPNYFDKCINFAQSLTIIDVPPIVR
VTLEPAQLRNMDKLLKGIKRLNLADPCVRGYMNEVGEVVLETAGELHLERCVRDLEDRFAQVAITVGKPIVPFRETILES
```

```
YEFEVSISGSTIKMQVKPWDGSSNGGSETLLESKKYKDILTKNTTIDITLLDSTLKSGFSLAIKEGPVIAEPLEGVEVHI
ASIEKNDSVENHENGLSKIRDSIQNAILKASPRIKLAMYVVDIQTSAELLGKVYTVIQKQRGSIISEEMKEGTPFFTVEA
KLPVLTSFGFSNEIRKKTSGGAIPQLVFDGFETVDEDPFWVPTNEEEIEEFGETGDRENWMRTIMNEVRKSKGLFVDELV
VKDGEKQRTLKKD
```

426 - 445:	EEEEEEEEEEEEEEEEEEE

A0A1V4L1X9 **A0A1V4L1X9_PATFA** (3983 aa)
Cardiomyopathy-associated protein 5. *Patagioenas fasciata monilis*

```
MEGYRGAECDRASETSSFVEDEEEEEEEEEEEEEEEEEEEEEEEEEEEAVDPEEAEELTNSLKDIIQSEDVKPKLQYIMTN
PSFSMVTVQSEDSGITWETSSSRCSTPWTSETSTTSDLYSMESSPVGSPPGKVIFIMDEGKIVRKRKRKSSNRVPMATRL
KGGQGNKKRDSSGMQRQEPRTVLGDVQASMLNVEQVEAQNTDEEMLDDKEDLENIAEEPVKRAPIPSIFRESRLRKVGPI
LGGPVQARIQLFNSIFGGTGPAPETLEKTRIRRSSSVSGDSEQLLETSVKEKLQKFSSLSERTDLKAFQRLSRDLTTPSE
RKREIREQLAAQSYQTYTSPTMPLKKRLTTKDVSIKPTKMKCKTSRFSSFGAETTPQHEERKDSLLETPDQVSGQSRKSC
LPEEARKHQSYSPAEKTSMTEQSASILLESDDKPGKQVPLSSAETANQESDRSLLTASGLLDEPKKQEIQPNSAPQSVSI
DSELGRQSTQPILPRASMSEHPEREAQKSAVQSFLPGAPSAKHKYSTLSETRQEDIILQPSETAQTESEHVLLPHSVGET
EKQETECHSTTVLSETEPPGLLSSVKKEEGQKTSPQETKDINLEKQTESEQDFSSSLQEAEEQGIKLTTPIPEKIDSKYF
SISYPDHTKPQETQKTSPVGKAVDLGHIEKNKQTESAQMEIEHPGFSYSRREVGQSERTKMETEHPDSFFFNKGTEELEC
AQMEMERPDFSFSREEMEEPGSAQLETEHPDFSYSGDEVEESESAKLEAEHPDFLYSRDEVEESESAKLETECSEILFFT
KETEESESSQLEREHSDFFSKGETEESESTQLEIEHPDFSFSREEVEELESAQLETEHPDFSYSREEMAESESAQLVMEQ
PDFSFFREETEKQKSVPFQREQPESYSHEEAEQEETAQPALVPSDLSCLTEEAETEGTAELQLVHPHIPDSTIRAETQQI
GYLETEHLPYPTSETKQQAFTQADVGNSLTSYFCDKREEPQPVQQDSQPGGKLYYRAEGVQGESAELQSEHPVLSHPAGK
EQQHKTSQLRIEQPETPYSTGKTKNQEILQPKLKQEDLPYSQGETAQEAVQRDLEGPEPSHFISKEEQHENVQLASENMD
FSFTTGEAVQEGVEAGSLGSSYLTDTAKPQEMAQMEQEQPLTSCSAAGSQRQETSSLDVAQPDISYSFGRIEQQDTLQRE
LEQQETAQHKVIQMEMEYSDLSESWRKEEPQVTDQINLSEQEIAQPASLHPSLLYSFSEQMQEEMQIEPAHPEETFDLST
DMQEKMTQRKSEILHPELEQTFLSSSSRKEAPLETEISSEYPDLSYSFHEAEQQKKLKHPTLPFRSKRQETAPLVMECPD
FSRDTGEAKPRDIMEQELGHPELSYSMGETQGQSEHLDSPGTLGETAQVESMEVESKYLNLSCSDDQKKQQESSQLDSKY
PDLSFSFGKAKEQSTQEFESKHQELPKMARKRASPATAQMESKHPDFMYPPGKANEPEVAPWETKHPDLSHSTDETSKQE
VVVLDQKHRKISVGRENEQQTAKQQLEPEKLSHSPGKTEQLKHVQEDLEQPGLSFSVNRLDDKTAPPEAQHADVIYPLDI
TKGLQRVEETEQAYLFGKSEHKTVQLEAEIPHVADAVGTVGEETAEPGQGHPDLSYSVSKAGGLQTAQVKRKHPGLMCSH
DKVQETTQLGLEQLDALSVHAKTPSQPELGQADLASPADKVGQQGMEHTASGHPDEGQSVSRAEHPQATKENLGAPEAST
RSGKKEQRQMEKTEPKHPDISCFTDKTQTPESTQLVLGKTALSSWPGETERAQTAQEEQPGFLHSFEKAAQGEKVQPELG
HSRLSYSVSEAEQETALVKSNRPALSAGRLEHYEIVQPEAEVMDLSWSVGETQQPQMAEADLEYSDLLHSTGTVQGQVKI
QPVQEQSGDFSSSLGKEEQWEGMQVEHPELQCSRRKTEELQNFQTKSEHVDLSFSVGTAEPHKTAQPELKEHNLLHSFVK
TKPSLAAPWELERPDVSDAMGKVPHPDLSSSVSEEKRSAELEVTQERGSFTVHPEETVQLRMEQSMFSSSRGTAEQPDRA
PLEQEFPDFLYSSGKKQQQEVAKQELKHSHSSYSTDKTQQQETAQHVLEEPDLSSCPGKTWQPQTVQVEAEHHDLLHFTG
KTEWRGTAQPEAEHPDLLYSSDKAEQPPATEWKSEQPITPHPTGKTEQHSEWELPSLSFSVSKTLSQEATQIDFGQQDLT
CPLGNTHEMQTVQSELEHTGSLYSSDKREQEMVLPELRHPQLSYLVRESEEKATHQKSNYPDSSYYFGQQEHHDIEKPEV
EEMDLSYLSGKSEHLQPAQEILRQPELLESFGKREEKQVAQPGFLHSLGEETQKPAAQLELVQAGLSHLLGKTEHQETAQ
TQLTSSDFSYSTEKAEQSQTERLKLKCPDLSYSHGTKPADLLHSYGKAEQPQSAQMEHPETSYFMEQEEKASVSYTFGGT
EKPATVKLDFEQSDLLSATDKAEKHEMALLRARHSEKRDIGAASSLTAQLESEKQNSSPVTGGLSPKHSDKVETLESQDY
LTVPSKLESEPSVPFYSADKTCQQEIPPYSKPASEYLVPTWSLAEQERQSLQPLIARSAQPECKRVIPPHDEEELQKIQL
YSPKKASLKAVQLETVSLPLTQGQDEQEPQDHLLNTKYLSSEQLRGPPKLTADQDKQDTQSDVQTVPRLVTADSEMTPVA
EQQGVSSDSFVPFHTLREKSVSVAVTGDEEKQNIPSSVSDAVGMLGRQSDVVSGIYTEGEGRHEMQPYFADQKHTSLEHL
RVVSSDLAYETVTQKTQRYSGEQGNLSSTKMKSVSSSSEEKQNPDIPSFGLATWLAEEVKARSISPVRATEADRQRIQLF
PNEASDFGSKQIPAGSCTELTVHGATKNTSHTAQRHDLASLGGDKPGPDKVPGSETSIGNPTKIEAMQHLEVDKVSEVRE
HYLRGEEEMEHVSTVEDKESKQMTDKLEYLETNPSLKRKLADDGHRALASETTTEISESSVVGNPSSHELKEVVKNDDVE
ETGETQQENPMLPVNNAMLDPNNDPDDPVEETTSLKESTEVDTLEEEFSLLEDLDEVFYGTVKGESKMQSYADAPKPLPL
QQSIDISINPELLEEPPALSFLYKDLYSEAVGEKTKDETPSDEESDEIPSKALGPPTEEIPEGKGVVHKEKVRVDSDIQA
TICKPMHAIPFGSKLTLSGARSDATEQREEDNVPIETTEELPEQTSHQAYSQLVDYQGAAYQEAGNKQEEQHNITAVPRM
EKYVPYVRTPVEDSEDDRYTQENLSCVPTIQQTEKPDLERAEQHPDVYGDLAESMDYDVITQEELLQDEISSQFTHEELL
FEDRDSFEHAGDSYEFVNKPEQRTPVEIEDSGFVVMYPEKSATNIPQVESPQRELKKVQADTYCYHCKCPISAIDKLFGE
HKDHEVTTLDDAATKMKNQLNELLIAVEEKSMKTEEFVSDIESLFKSVEENCKKNAELLEKQNEEMLKKMVAQYDEKSEN
FEELKKMKMEYLYEQMVNFQQTVDSAKETLETTLKEMEELDGFVFLNSSKELNKRLLSAMDTALSLEKVPRAFSLFEHYA
DSPGQSNQHSLKHVAVPQTPTVVPQEPNSATSTSIAIYWVVNDGDAIDCFQVYCMEELQASKDAGALVEEYRVTVKESHC
ILEDLEPDRCYSVWVMAVNGTGCSLPSEKAIFKTAPAVPTIKAEDCTVCWDVATVRWCAGSASAESFTVEYCRQHSLEGE
GLRSFAGIKRPELKVSLEPNVNYFFYLRAVSPFGTSEQSEAALISTKGTRFCLLSDTAHPALQISCNATVIHLPEKATFT
EFPSVLGELLPARGRHYWEIIVSACRSYRIGICYEAISQSNVLGLSDTSWCMRCCPTQTSFLYRFLHTGVMGDVCVTEQL
ARIGILLDYSTDRLLFFNAERGLVLFAIQHKFTGAAHPAFALEKAGMLTLRTGMELPEFVKHS
```

22 - 41:	EEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEE

A0A1V5PQC3 **A0A1V5PQC3_9BACT** (468 aa)
Uncharacterized protein. *bacterium ADurb.Bin363*

```
MHNGEREKPDSEKELLLEKWLVAKKEKKLAEKTKVSPESEKDTEKIKIQEITVEEKNQEYNNKSDSIKIDIKSNVETKLY
TKDTEFKDILDEDMELINQEKLFKKLEEDEEISLLREIENELKMIDSKKTIEEEKEQIIEIEQEIRNKEAVEEEIIDEEM
EKIIQEELKKVKEELEEQELIDKELEKIIQEELKKVKEELEEQEVIEEEQEVIEEEQEVIEEEQEVIEEEQEVIEEEQEV
IEEEQEVIEEEQEVIEEEQEVIEEEEMEQEESIQEKLEIKEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EKIKKEIPKVIVEQEKKVEKIIICSVCHRKNPSKNRICSYCFNYIEESQSEIIEEPVLIEKVENIIEKIIEQSQQKIIEK
VEENFSEDLSQKVIIKATEKVEEKILKESPEKKIKQSQEDEIIICPVCQRKNSKKNKACSYCSNYLGR
```

285 - 304:	EEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEE
287 - 306:	EEEEEEEEEEEEEEEEEEE

288 - 307:	EEEEEEEEEEEEEEEEEEEE
289 - 308:	EEEEEEEEEEEEEEEEEEEE
290 - 309:	EEEEEEEEEEEEEEEEEEEE
291 - 310:	EEEEEEEEEEEEEEEEEEEE
292 - 311:	EEEEEEEEEEEEEEEEEEEE
293 - 312:	EEEEEEEEEEEEEEEEEEEE
294 - 313:	EEEEEEEEEEEEEEEEEEEE
295 - 314:	EEEEEEEEEEEEEEEEEEEE
296 - 315:	EEEEEEEEEEEEEEEEEEEE
297 - 316:	EEEEEEEEEEEEEEEEEEEE
298 - 317:	EEEEEEEEEEEEEEEEEEEE
299 - 318:	EEEEEEEEEEEEEEEEEEEE
300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE

A0A1V6QNS5 **A0A1V6QNS5_9EURO** (1418 aa)
PH domain-containing protein. *Penicillium antarcticum*

```
MGNGSGQRPLSEVSPMAQRRNSPSWNQVTKMPNGESPSYDVSSLNSKASPRLFWKGRETPSPFSKGTENKKPYDPEGSYF
PTRRPSLENLKRVSKVKNHSMFLEGGTEYDPAAVAVPQRPLARDRSPQRDSQMNVAKSQFDDEDDSYIPRPQSPSKDQAS
PSKSSLSKGSRYGKGFDPQHDIWSEYGSAGHRHAKSVTFDHAPPQVNEYEMTTPDPSSVASESRENSYESEEEEGDISFE
HESSIERDDSFDASLEDIEKTPVVLPEDWRFMSPGTDDEGDVFSEHVESRNTEDRPVSRERDSSAHKRVESLDSNGERRP
LPPLPSVNRLSAARPSSPGKLGAAFELGSAGQRNLPAPPAAASYNKSDIGGVVSLEDRLRLMMLHEKEENNETHEDHAED
TEEPEKKLVAAPEPASKTNDAEEEEDPKENFFSPPRISRDSILRDMRKGDSYDEDDDDSFDASSQIDSSPRHYDHYDPDV
PIPSLETDDDDASSVIIKQEENDEDMFSITDYYQNMSDNSLSSRDQRAKYDEDSNYSLRSAAEAAERARNDNHSQGSGQS
TPTAEEKGTAQKTTQINETQDEQEEEEEEEEEEEEEEEEEEEEEGEAPSKDQRLDMTSIRQSLGRPVTPEMHEDQESEP
STPDSVIRHPVEDDEDFEKEQEDEHQPEEEREELQEEVESSSDESVPEPVATIRAPGAGLKTRPSLTPADMQSMAATRRK
ISGQHIPPVPPLTKQVSRETDPSDQENKHADSPPKLTLPTDFNQRQSSLMKLDIPFSIQEESLGSGLNKEFDRVIESQKV
AFHALSPIPRLAPSQAKYLQTPVTRGYRSIPADSCFSVQRGYLMRQNTKVIIASSRNEEEPMPSPEQTPQDPRGTRSAGS
SPRKPSQQTWTTVPWNGSPRRSSIKPATGIPKKKPVPGAGPVPPLPGQASNVQEAPATVEENEPATAESFEDGEERGRLF
VKVVGLKYLDMPLPRGERSYFALTLDNGLHCVTTSWLEMGKTAPIGQEFELIVQNDLEFQLTLQMKIDENKFQTPEPAAS
PSRQKASALSRVFASPRRRKELDMKQQMQSQQQKAKDVNAPVYDRLRNLVARDGSFGRAYVALSDHEQEAFGRPHVVDVA
CFNEWAVEDQMSSVKSKKSATSVNAQRRPPYKIGKLEVQLLFVPKPKGSKDEDMPKSMNACIREMRDAESVAARSWEGFL
SQQGGDCPFWRRRFFKLQGSKLTAYHETTRQPRATINLAKASKLIDDRSSLLQKETSTKNGGRRKSAFAEEEDGYMFVEE
GFRIRFGNGEVIDFYADSAADKDGWLRVMSEAVGKGSASGNGAIKPWADLVLKRERSMMAKQETSRPTSGTSRPSSGIPV
PPASPSRNRNSAMMGPPSSAGSGAPASQPPRSRHKHTYSQPEMGGAEARRQKTRSLMF
```

584 - 603:	EEEEEEEEEEEEEEEEEEEE
585 - 604:	EEEEEEEEEEEEEEEEEEEE
586 - 605:	EEEEEEEEEEEEEEEEEEEE

A0A1V6QZZ5 **A0A1V6QZZ5_9EURO** (1134 aa)
Uncharacterized protein. *Penicillium solitum*

```
MARESTAPMEPLTPGGKPNTQPHPAHVQEPEFGKPSPIGPPQHRSNHLFNIPKPNQSRAEHHRPAPRPQPQQQPQSRHQG
QSSATPHAYRQPGTSGAPFATPSVKRSEPWDPFKPVAPSAYNNPRGGFQHGAVSIKRPENVTWSTPRAPRPIYQSKPVPP
RVGGASNIQKFIDLTRDDTDPVPKASAHATPSFGAMDMNGYVDTAMANENIKALLEGAFEDEEDKAEPKPKGKKKKGGKK
SKKTSLKKQKDEVVVDKKKEQAIDDLDDLAAQLQGVTVNDPKENDAKSEDDSSAKVEQDDKVAKLDEEDEEEEEEEEEEE
EEEEEEEEEGDSDDEDKGVIEGLKVTLLPHQIEGVRWMSDKETGRKTSKGIFPKGGILADDMGLGKTVQTIALLLKNRKS
DHEDSENTESEGKTTKLPPNCIASTLVIAPLALIKQWEAEIKDKVEPSHKLRVCIYHGTTRAKTSTTLDKYDVVITTYGT
LTSEFNSSASDKAKKAGIFAVHWYRIILDEAHTIKNRNAKATQSAYALDAQYRWCLTGTPLQNNLDELQSLIKFLRVKPY
DDLAAWRDQISRPLNNGRGGLAIQRLQVYLKAFMKRRTKDVLRLNDNVKPGEEGEDGKPKKSSNGFHITKREVIKVSPEF
MPGELNFYKRLEQRTDNSLEKMMGGSKVDYAGALVLLLRLRQSCNHPDLVKGDLAKDKDILLQNGSTSSQSTKSKPDDLD
SIADLFGAMSVVAKKCDVCQTDLSPNEIKDGGSRCSECEADLNTNVMGTDKKKKKKSKKSHKELDIPDSPSARKSKAQIA
RSRKNRRVIIDSDDEDEEGDWVVPDDQRKMPNLGKAGGSDDETAEGGGEWLVSDDETDDEIESPSRRKSKPIVLSDSEDE
SDSEADDIYNDEGENGELPSTKIRHLMRILNSEAPDFKFIVFSVFTSMLDKIEPFLKSSNIGFARYDGGMTNNHREASLE
KLRNNSGTRVLLCSLRAGALGLNLTAASRVVILEPFWNPFVEEQAIDRVHRLNQTVDVKIYKMVIKGTVEERIVALQDRK
RELANATIEGKTGAGKLTMRDMMALFGRDAESRFTDNQSTLDFNQPTRLLNTGDETEPVHSSSQESTQSAPRSRGNEAQA
NRLRNEDSVYGRRW
```

310 - 329:	EEEEEEEEEEEEEEEEEEEE

A0A1V6UKT2 **A0A1V6UKT2_9EURO** (574 aa)
F-box domain-containing protein. *Penicillium coprophilum*

```
MLLQLPTELIQLVLRNCDTPTYFQAAFSSRRLYEIASGSREVIIHHLHNTPGWNDGIETYQTKRLFGELMRRSYEHLDGA
EHYANPTYEYQDRIIDYHASTIEALEDSVRALLVFKGHSTVHLVDMSDGNRTEVQLKAPGQDIGKIEVIQTAFDENGGVY
VLHRFKPFLDQELDTDHPFVKHALESHPNGSIHLACHRLNRRKNTIRMCDFPEFRDYRPLALSVTNRKIVISWQNTLDPF
DHYVVLYTQLYDEEEEEEEEEEEEEEEEEEEEEEEEEEEDEDEDEDEDESSQGRVIEQGKGDNPCRIIYAALEAYILTSS
DYQDPSVRSSQKTGPAMRLAFNDRGFQLLYYYRAQHIYGAFQRLHRLSGLPGEPKPHVNENACTVQFSPSLSLQFSIAIP
FFGTHELGDINQGEQCHWQYLAFGIATHRVEKWAVACLLKSEAYTGPRCTHVLNLDRGRRFDHWRIMAQLGGFREVSTSH
GSPVATSGRGTRVAVANWKTIYVWTLNPSELIEDNDNGFYPSSWESSTGVIELRPVVLQLEVVCSQLRFTKEDELVAITD
RGMMFLNLGYSGKG
```

253 - 272:	EEEEEEEEEEEEEEEEEEEE
254 - 273:	EEEEEEEEEEEEEEEEEEEE
255 - 274:	EEEEEEEEEEEEEEEEEEEE
256 - 275:	EEEEEEEEEEEEEEEEEEEE
257 - 276:	EEEEEEEEEEEEEEEEEEEE
258 - 277:	EEEEEEEEEEEEEEEEEEEE
259 - 278:	EEEEEEEEEEEEEEEEEEEE
260 - 279:	EEEEEEEEEEEEEEEEEEEE

A0A1V6V5Z4 **A0A1V6V5Z4_9EURO** (1336 aa)
Uncharacterized protein. *Penicillium coprophilum*

```
MNPVTPWIAALADQCLSFYLDQNDQDDIQVEDFEGCLIFIIRRPTLNTAVVVSWGEGEDSHRATFTDSKNQIDAIILRGS
PDAQEETSPCPPSVKGGPRHLVELSDTKLIFTYSASVPDVYLHVNRFTIHPNAVPKGDVPKPKLKKTPTLRTLMTMACEK
IKKAQAQTGSNSQSDVGLTVSFVSQRDQPMPPHYSQNNKASQLLFSQPPSNMCHVAPESNLTTDRVFITESSDLLGLLAP
SRPIQKGGPATRELPEADGLSLGERKSRRSPLPNERKSVAPQEFDTSPTGTQPSFRSLSGNTADARRASNSVTNVSFANL
SEDVDNLIAECRSQAAQSSTEPDDHGPAHTVATGDNQHFSKKRHRGSTDAPLHEARDDNLDLQGLQNPHTSPSRKRQRVD
TGKAMPTDTTEAEQVQIKAMPSLPRVQIVSTKTDSVCPPTTNPWEGMIQIPLSEVEIPKDQAELLEGLKWIPQDPGVSAP
LCHVPPHLLRQWNSIARKRQHLNKEEEEEEEEEEEEEEEEEEEEEEEEEGGEEEQVFDRAFTPTPQDIQTSPIPWSPSPNR
TPARDLLPRDTASPPRYTRPIRKNPTPSGTQCSVYQSADHADMDMLNGSSSASSQPGQGDIAASKDNTKTAGQQYTQFPE
KVTTKQINPVSLDHDPGDSSSQEHNTPTSLDVIDNQPLGVIQEDPHDEQPTRNPPLTFELRDESSGDESDEPEMETYVPF
ALGGSLPLSSQPEKEFTSSGLSLPRFAGNNIQVVETPAVHTTRLNSGNLNKQRVGLELQSSQHPSSQAAKTSSSSRILNT
YHSQDSHGRSIPSQEAPNPSLPILEGGSLRVDVLGTQTQTSSIHALPKATVQSSSDVVFDSSRPAQRQRGSSIFGLDILD
DPSSFPYARCHSLPMSQLHEPSQDSLREYFSLDGASQLPDLSPMEFTTWVAANGESPSRYSRPLRRESADTGRKVSPSPN
AELVARRRGFIGKSDKYAEAQTIYEKFCNDYSPYSGDFAHFVEMCSKLQTMRQRGQLQRSFLWDDFVIQHLEEYPRYFAE
RTSQDSKPLGYEDFFCLKFLRPQHKKRSLTAHGVDIVASQFAAPTVEGEVTQDKAVQSETAHTSFTASLVGESSTRHTRS
FGDVPIPNVYMPTATQSSSSSTDTDSDSVEVKFEDDSSDGSTDCQTPTRSNDQQPVLFGLDEEIVNATQCDAKNTLIAPD
SNNVGVAETSMDEVDDTEEGDSTHHETASIELGDDTDDRHISAFLAPPDPPAALGSLNGAAMEPPRQRKPWFRSLRNIYP
TGPVWSDDPDTPFKRWARHDQNVLQELNRRGGVRVLLDEKGVIRRPIYNHGNNPGF
```

505 - 524:	EEEEEEEEEEEEEEEEEEEE
506 - 525:	EEEEEEEEEEEEEEEEEEEE
507 - 526:	EEEEEEEEEEEEEEEEEEEE
508 - 527:	EEEEEEEEEEEEEEEEEEEE
509 - 528:	EEEEEEEEEEEEEEEEEEEE

A0A1V6XBY2 **A0A1V6XBY2_PENNA** (611 aa)
F-box domain-containing protein. *Penicillium nalgiovense*

```
MGKAASHYRRPENELIKHAGWSEARCQFCGVSFDIARKRKVGEPEVASWRFEGDSLWGYEQPVEDLDQSECLKQGCALAV
IDPEEEKEEEDDPVNDPDFVPKSEDCDEYDRLYEYDPGYESNSGDHDDDDSLHISDNGDTVGNEEDEEEEEEEEEEEEEE
EEEEEEEEEALYRNFLTQTIYNQPHFTGEPVGPFVYASTSVSFQKDILVPLPCDSLPDGYSFEDLEHIPGPKCPMEDAYPG
SGISLAEMRGCRTVQFLVHKSLAQDGPWQADALHEPWEDFEEWFLSGLSDGMESRDGGLQLVCPARGGLKEIWDADTINF
DPERLGSTGLAMPFHPWCFDIFSRQSKLHFGNKVNIAGLINWRNAECSFDANRDFPRHPDVANAQQQVWMHDPDAAYLVA
NPLHIIGLTEFLLDAAQEEGDFDMELAGKESDAVLFKNNPTDRLSALPPELRLHVVSFLDSGSIMSLRQASKTFMDLTNN
VWYRIVRGQMPWLWEAWEEGEIKHSPSPWTFMTANEVKAVEELKRRYTAVLSDEYEYAMTPDKVIDYLLPRPTAVLDQGL
LPKGDTNWYRVFRQIRTHWPRVKGLRNRARIWTDVEEVIRRIRMHDSVELS
```

147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE

A0A1W0VV42 **A0A1W0VV42_SORBI** (252 aa)
Uncharacterized protein. *Sorghum bicolor (Sorghum) (Sorghum vulgare)*

```
MPSIWEEEEEEEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEWFFRKSERELSNSRKKQIQKQEKAEEVESCIPDQFQF
ARFIQETMLRMLAFVDFLVALDPNTICEFSVANGSGVPAPALYQKISILLRVLDALSNACFEVEVLLLSMPSEIEEVKRI
RGEIINLLYAKDNKATEAVWGTMEEIWALIMDSMEEDGQDSVMTTQGSSDIHKLTLSVTDHIRNFKLHTAATSCIHTSQP
LIAESRTTYRPI
```

19 - 38:	EEEEEEEEEEEEEEEEEEEE

20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE

A0A1W0VV67 **A0A1W0VV67_SORBI** (352 aa)
Exocyst subunit Exo70 family protein. *Sorghum bicolor (Sorghum) (Sorghum vulgare)*

```
MPSIWEEEEEEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEWFFRKSERELSNSRKKQIQKQEKAEEVESCIPDQFQF
ARFIQETMLRMLAFVDFLVALDPNTICEFSVANGSGVPAPALYQKISILLRVLDALSNACFEVEVLLLSMPSEIEEVKRI
RGEIINLLYAKDNKATEAVWGTMEEIWALIMDSMEEDGQDSVMTTQGSSDIHKLTLSVTDHIRYLWANYWSVTSVVFCLG
NGKQHVTETAGNTITNPLANLTTEMVSCLDEKLAEMSQSFADQGIKYLFLINNSTYILQELQTTYGSNFLHSYFAALDRR
IEDYIQAYLKLCWVPVLSENLYHPKVVEGPGS
```

19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE

A0A1W0WMU7 **A0A1W0WMU7_HYPDU** (150 aa)
Uncharacterized protein. *Hypsibius dujardini (Water bear) (Macrobiotus dujardini)*

```
MDVDYCLTVSSLAQERFITFFHYFSSGNNGRRRRRRRRRSEGEVEEVEEEDEEEEEEEEVEEVEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEERRRREEEERRRRRRREEEEEEEEEEEEEEEEEEEEEEEEEGGGERRRGGGGRNFKLE
```

64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE

A0A1W4W243 **A0A1W4W243_DROFC** (397 aa)
troponin T, skeletal muscle isoform X1. *Drosophila ficusphila (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETKPPQTPAEGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAK
RKVTRAEEEQKMAQRKKEEEERRVREVEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSS
AAMERNKTKEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQL
RHKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWETISKDSNEKIWNEKKEQYTGRQKSKLPKWFG
ERPGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE

373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE

A0A1W4W249 **A0A1W4W249_DROFC** (395 aa)
troponin T, skeletal muscle isoform X6. *Drosophila ficusphila (Fruit fly)*

```
MKSTPAPRRRRLSRRPARRRKKPPQTPAEGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAKRK
VTRAEEEQKMAQRKKEEEERRVREVEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSSAA
MERNKTKEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRH
KALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWETISKDSNEKIWNEKKEQYTGRQKSKLPKWFGER
PGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE

A0A1W4W251 **A0A1W4W251_DROFC** (396 aa)
troponin T, skeletal muscle isoform X4. *Drosophila ficusphila (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETKPPQTPAEGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAK
RKVTRAEEEQKMAQRKKEEEERRVREVEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGLGLSSA
AMERNKTKEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLR
HKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWETISKDSNEKIWNEKKEQYTGRQKSKLPKWFGE
RPGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE

A0A1W4W255 **A0A1W4W255_DROFC** (388 aa)
troponin T, skeletal muscle isoform X11. *Drosophila ficusphila (Fruit fly)*

```
MSDDEEYTSEEEEVVEETREETGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAKRKVTRAEEE
QKMAQRKKEEEERRVREVEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSSAAMERNKTK
EQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGL
DPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWETISKDSNEKIWNEKKEQYTGRQKSKLPKWFGERPGKKAGE
PETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE

363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE

A0A1W4W256 **A0A1W4W256_DROFC** (389 aa)
troponin T, skeletal muscle isoform X9. *Drosophila ficusphila (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAKRKVTRAEE
EQKMAQRKKEEEERRVREVEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSSAAMERNKT
KEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKG
LDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWETISKDSNEKIWNEKKEQYTGRQKSKLPKWFGERPGKKAG
EPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE

A0A1W4W259 **A0A1W4W259_DROFC** (374 aa)
troponin T, skeletal muscle isoform X14. *Drosophila ficusphila (Fruit fly)*

```
MSDDEEYTGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAKRKVTRAEEEQKMAQRKKEEEERR
VREVEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSSAAMERNKTKEQLEEEKKISLSFR
IKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQ
VASKYERRVDTRSYDDKKKLFEGGWETISKDSNEKIWNEKKEQYTGRQKSKLPKWFGERPGKKAGEPETPEGEEDAKADE
DIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE

A0A1W4W266 **A0A1W4W266_DROFC** (395 aa)
troponin T, skeletal muscle isoform X18. *Drosophila ficusphila (Fruit fly)*

```
MSDDEEYTSEEEEVVEETREETKPPQTPAEGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAKR
KVTRAEEEQKMAQRKKEEEERRVREVEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGLGLSSAA
MERNKTKEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRH
KALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWETISKDSNEKIWNEKKEQYTGRQKSKLPKWFGER
PGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE

369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE

A0A1W4WCS4 **A0A1W4WCS4_DROFC** (397 aa)
troponin T, skeletal muscle isoform X2. *Drosophila ficusphila (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETKPPQTPAEGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAK
RKVTRAEEEQKMAQRKKEEEERRVREVEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSS
AAMERNKTKEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQL
RHKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYNTVYAETLEKTWQERQERFTQRTKSKLPKWFG
ERPGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE

A0A1W4WCS9 **A0A1W4WCS9_DROFC** (394 aa)
troponin T, skeletal muscle isoform X7. *Drosophila ficusphila (Fruit fly)*

```
MKSTPPRRRRLSRRPARRRKKPPQTPAEGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAKRKV
TRAEEEQKMAQRKKEEEERRVREVEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSSAAM
ERNKTKEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHK
ALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWETISKDSNEKIWNEKKEQYTGRQKSKLPKWFGERP
GKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE

A0A1W4WCT5 **A0A1W4WCT5_DROFC** (388 aa)
troponin T, skeletal muscle isoform X12. *Drosophila ficusphila (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAKRKVTRAEE
EQKMAQRKKEEEERRVREVEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGLGLSSAAMERNKTK
EQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGL
DPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWETISKDSNEKIWNEKKEQYTGRQKSKLPKWFGERPGKKAGE
PETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE

361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE

A0A1W4WCU0 **A0A1W4WCU0_DROFC** (373 aa)
troponin T, skeletal muscle isoform X16. *Drosophila ficusphila (Fruit fly)*

```
MSDDEEYTGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAKRKVTRAEEEQKMAQRKKEEEERR
VREVEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGLGLSSAAMERNKTKEQLEEEKKISLSFRI
KPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQV
ASKYERRVDTRSYDDKKKLFEGGWETISKDSNEKIWNEKKEQYTGRQKSKLPKWFGERPGKKAGEPETPEGEEDAKADED
IVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE

A0A1W4WDQ4 **A0A1W4WDQ4_DROFC** (396 aa)
troponin T, skeletal muscle isoform X3. *Drosophila ficusphila (Fruit fly)*

```
MSDDEEYTSEEEEVVEETREETKPPQTPAEGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAKR
KVTRAEEEQKMAQRKKEEEERRVREVEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSSA
AMERNKTKEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLR
HKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWETISKDSNEKIWNEKKEQYTGRQKSKLPKWFGE
RPGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE

A0A1W4WDQ9 **A0A1W4WDQ9_DROFC** (394 aa)
troponin T, skeletal muscle isoform X8. *Drosophila ficusphila (Fruit fly)*

```
MKSTPAPRRRRLSRRPARRRKKPPQTPAEGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAKRK
VTRAEEEQKMAQRKKEEEERRVREVEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGLGLSSAAM
ERNKTKEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHK
ALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWETISKDSNEKIWNEKKEQYTGRQKSKLPKWFGERP
GKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

365 - 384:	EEEEEEEEEEEEEEEEEEEE

366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE

A0A1W4WDR4 **A0A1W4WDR4_DROFC** (388 aa)
troponin T, skeletal muscle isoform X13. *Drosophila ficusphila (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAKRKVTRAEE
EQKMAQRKKEEEERRVREVEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGLGLSSAAMERNKTK
EQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGL
DPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYNTVYAETLEKTWQERQERFTQRTKSKLPKWFGERPGKKAGE
PETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE

A0A1W4WDR9 **A0A1W4WDR9_DROFC** (373 aa)
troponin T, skeletal muscle isoform X17. *Drosophila ficusphila (Fruit fly)*

```
MSDDEEYTGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAKRKVTRAEEEQKMAQRKKEEEERR
VREVEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGLGLSSAAMERNKTKEQLEEEKKISLSFRI
KPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQV
ASKYERRVDTRSYDDKKKLFEGGYNTVYAETLEKTWQERQERFTQRTKSKLPKWFGERPGKKAGEPETPEGEEDAKADED
IVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE

A0A1W4WE30 **A0A1W4WE30_DROFC** (396 aa)
troponin T, skeletal muscle isoform X5. *Drosophila ficusphila (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETKPPQTPAEGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAK
RKVTRAEEEQKMAQRKKEEEERRVREVEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGLGLSSA
AMERNKTKEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLR
HKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYNTVYAETLEKTWQERQERFTQRTKSKLPKWFGE
RPGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

367 - 386:	EEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEE

A0A1W4WE35 **A0A1W4WE35_DROFC** (389 aa)
troponin T, skeletal muscle isoform X10. *Drosophila ficusphila (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAKRKVTRAEE
EQKMAQRKKEEEERRVREVEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSSAAMERNKT
KEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKG
LDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYNTVYAETLEKTWQERQERFTQRTKSKLPKWFGERPGKKAG
EPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

360 - 379:	EEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEE

A0A1W4WE40 **A0A1W4WE40_DROFC** (374 aa)
troponin T, skeletal muscle isoform X15. *Drosophila ficusphila (Fruit fly)*

```
MSDDEEYTGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAKRKVTRAEEEQKMAQRKKEEEERR
VREVEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSSAAMERNKTKEQLEEEKKISLSFR
IKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQ
VASKYERRVDTRSYDDKKKLFEGGYNTVYAETLEKTWQERQERFTQRTKSKLPKWFGERPGKKAGEPETPEGEEDAKADE
DIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

345 - 364:	EEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEE

A0A1W4WE45 **A0A1W4WE45_DROFC** (396 aa)
troponin T, skeletal muscle isoform X19. *Drosophila ficusphila (Fruit fly)*

```
MSDDEEYTSEEEEVVEETREETKPPQTPAEGEGDPEFIKRQDQKRSDLDDQLKEYITEWRKQRSKEEDELKKLKEKQAKR
KVTRAEEEQKMAQRKKEEEERRVREVEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSSA
AMERNKTKEQLEEEKKISLSFRIKPLAIEGFGEAKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLR
HKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYNTVYAETLEKTWQERQERFTQRTKSKLPKWFGE
RPGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE

A0A1W4WRI6 **A0A1W4WRI6_AGRPL** (367 aa)
troponin T isoform X5. *Agrilus planipennis (Emerald ash borer) (Agrilus marcopoli)*

```
MSDEEEVYSESGDPEFIKRQDQKRSDLDEQLREYIAEWRKQRAKEEDELKKLKEKQAKRKVTRADEERKMAERKKQEEER
RVRELEEKKQREQEEKRQRLEEAEKKRQVMMQAMKDQSAKKGPNFTITKKDASAALSPAQLERNKTKEQLEEEKKISLSI
RIKPLQLDGLNVDALKKKAIELWDCIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKI
QVASKYERRVDTRSYDDKKKLFEGGFNSLSMEVLEKVWQTKMEQFMNRTRTRLPKWFGERPGKKSGDPETPEGEEEGKHA
GDDDEDIREPTFEPEPEEEEEEEVEVDEEEEEEEEEEEEEEEEEEE
```

348 - 367:	EEEEEEEEEEEEEEEEEEEE

A0A1W4WRI7 **A0A1W4WRI7_AGRPL** (388 aa)
troponin T isoform X2. *Agrilus planipennis (Emerald ash borer) (Agrilus marcopoli)*

```
MSDEEEVYSEEEEEEEVVETKPVERKVEVEESGDPEFIKRQDQKRSDLDEQLREYIAEWRKQRAKEEDELKKLKEKQAKR
KVTRADEERKMAERKKQEEERRVRELEEKKQREQEEKRQRLEEAEKKRQVMMQAMKDQSAKKGPNFTITKKDASAALSPA
QLERNKTKEQLEEEKKISLSIRIKPLQLDGLNVDALKKKAIELWDCIVKLETEKYDLEERQKRQDYDLKELKERQKQQLR
HKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGFNSLSMEVLEKVWQTKMEQFMNRTRTRLPKWFGE
RPGKKSGDPETPEGEEEGKHAGDDDEDIREPTFEPEPEEEEEEEVEVDEEEEEEEEEEEEEEEEEEE
```

369 - 388:	EEEEEEEEEEEEEEEEEEEE

A0A1W4X171 **A0A1W4X171_AGRPL** (379 aa)
troponin T isoform X3. *Agrilus planipennis (Emerald ash borer) (Agrilus marcopoli)*

```
MSDEEEVYSEEEEEEEVVETKESGDPEFIKRQDQKRSDLDEQLREYIAEWRKQRAKEEDELKKLKEKQAKRKVTRADEER
KMAERKKQEEERRVRELEEKKQREQEEKRQRLEEAEKKRQVMMQAMKDQSAKKGPNFTITKKDASAALSPAQLERNKTKE
QLEEEKKISLSIRIKPLQLDGLNVDALKKKAIELWDCIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLD
PEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGLEEIIKEVSEKTWKDRSGQWESRQKARLPKWFGERPGKKSGDP
ETPEGEEEGKHAGDDDEDIREPTFEPEPEEEEEEEVEVDEEEEEEEEEEEEEEEEEEE
```

360 - 379:	EEEEEEEEEEEEEEEEEEEE

A0A1W4X299 **A0A1W4X299_AGRPL** (367 aa)
troponin T isoform X4. *Agrilus planipennis (Emerald ash borer) (Agrilus marcopoli)*

```
MSDEEEVYSESGDPEFIKRQDQKRSDLDEQLREYIAEWRKQRAKEEDELKKLKEKQAKRKVTRADEERKMAERKKQEEER
RVRELEEKKQREQEEKRQRLEEAEKKRQVMMQAMKDQSAKKGPNFTITKKDASAALSPAQLERNKTKEQLEEEKKISLSI
RIKPLQLDGLNVDALKKKAIELWDCIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKI
QVASKYERRVDTRSYDDKKKLFEGGLEEIIKEVSEKTWKDRSGQWESRQKARLPKWFGERPGKKSGDPETPEGEEEGKHA
GDDDEDIREPTFEPEPEEEEEEEVEVDEEEEEEEEEEEEEEEEEEE
```

348 - 367:	EEEEEEEEEEEEEEEEEEEE

A0A1W4X2H1 **A0A1W4X2H1_AGRPL** (388 aa)
troponin T isoform X1. *Agrilus planipennis (Emerald ash borer) (Agrilus marcopoli)*

```
MSDEEEVYSEEEEEEEVVETKPVERKVEVEESGDPEFIKRQDQKRSDLDEQLREYIAEWRKQRAKEEDELKKLKEKQAKR
KVTRADEERKMAERKKQEEERRVRELEEKKQREQEEKRQRLEEAEKKRQVMMQAMKDQSAKKGPNFTITKKDASAALSPA
```

QLERNKTKEQLEEEKKISLSIRIKPLQLDGLNVDALKKKAIELWDCIVKLETEKYDLEERQKRQDYDLKELKERQKQQLR
HKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGLEEIIKEVSEKTWKDRSGQWESRQKARLPKWFGE
RPGKKSGDPETPEGEEEGKHAGDDDEDIREPTFEPEPEEEEEEEEVEVDEEEEEEEEEEEEEEEEEEEE

369 - 388:	EEEEEEEEEEEEEEEEEEEE

A0A1W7RE92 **A0A1W7RE92_AGKCO** (587 aa)
Ran GTPase-activating protein 1-like protein. *Agkistrodon contortrix contortrix (Southern copperhead)*

MASEDITKLAESLAKTQVGGGQLSFKGKSLKLNTAEDAEEVIKEIEEFDGLEALRLEGNTVGVEAAKVIAKALENKSQLK
RCHWSDMFTGRLRSEIPPALISLGEALISAGCQLVELDLSDNAFGPDGVRGFEALLKSPTCFTLQELKLNNCGMGIGGGK
ILAGALKECHRKSTARSKPLALKVFMAGRNRLENDGATALAEAFAVIGTLEDVHMPQNGITHPGITALAEAFAVNPLLRV
INLNDNTFTEKGALAMAETLKKLRQVETINFGDCLVRSKGAVAIAEAVSEGLHKLKELNLSFCEIKLDAALIIAEATEDK
SMLEKLDLNGNYFGGEGCEQLQEILESFNMADVLGSLSDDDGENGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEPLQVQE
RGQGEQEPLTPKKILKEHDSTPPLSSPSLPPVDVGTFLAFPSPEKLLRLGPKCSTLITQQTDTSDTEKVVTVFLKISSVF
KDETVVKTAVTETTDALMREAFSSANFNSDAFITSVLIHMGLLKSEEKIRAVPSLYGPLMTLNHVVQQDYFPKSLVPILL
AFVTKPNRALDSCSFARHLLLQTLHQL

366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE

A0A1X0NHD2 **A0A1X0NHD2_9TRYP** (1663 aa)
Exocyst complex component Sec8. *Trypanosoma theileri*

MAWRYGSGTGNSAPNTNTGNTFTFGTNQNSLAGHAATGSGIFSNTPNAIFNAGAFLRSNAAPVLDPKQREEAEGEDETEF
NDEVSSSRRGSTSVLEHSKGTINNHMVESSQGQPVFGRANTSIKPLGGAFLRNIAQQGNASDTTNSTNKTSWGKSVSNIQ
PRKLFERSVLPTDAAEYEDDYYEEDGEEGDREFLRNTKALFAEVDADLLSDSFIPYEHVLQIISSDDGTEATAGDIDDRL
LPYYELQEELDDLLGKYIEVHHDEFNEAISGFSELILAVSGSDEMLARLKQQLIMATASLHNRSEQLQVLRMRAAKALLM
TESLKGLESSLSCESAVKQLIATHHYLAALRLLKKHKERLEMPEFTDIRATQTLRDYVNGTLETLHNTIIDDLMSTVFRQ
GKLNEADAQLVDRMLADGASEKPSGTMDNLERMCEEAQMRGSDMDKSIVTFSGFLGDIHDDPTDEDMIRNYLRFIPLCVR
ALKELDKLDLCYEAFFSHAASNIEQTISHFLRLYGVWRRRALSANSVAGCSDASTVRATRVQGRERASTIISTDEAAAVI
QAPELRAMLNALFAEMGKVVRNADYLIRVILTIHFPFLASFVIQPGGFDPEQSYENWDILHAPIRDLKDFHEMVASAFST
ALSMREGLQRHVGDESQQSIDDDDNTDIVSLKRLMVKFDVDGTFEKFESSGKAVCFQDVRNAINVAGEAVKHDFPEEGEE
LGACCSEVDSLILSSLLQYFRHNVKEMYEQWDLRVLSSQVSYYIELIFHVLCDAKEVEEDTSDEIALKAFLKHRNLVRRV
QRTAEMMNSGNVESFPSLEKMLSAQDASGMLTVVEQTGRVSFSLVAAVKCAQRDLRRFNEGQVRQYGGDPALAMGEGNIN
IKSGDNRGGLLVLKQAGTLKNWFVLTPMNLLTCYECTRRFFQSCSERVPRLSNAFQNELREFFRHFLQTTYIPTLFMFHA
QQLRQLCAGVSEGDGLMGSETVSTGERDKTTSTWSSEQATSIEPLVHHQKGQQSGIKWPTVDVRQSNGTTNIGKNTTTNN
NNNNNNNNNNNNNNNNIDTNSNNTNTSYPVLACVYYVGQVLYKVSRICRLFPDVLAEGIQQNIAETLLTELTMFLKKKQH
LITQGSLHHRLLSANFEDAFYDNPDARWKALSDETQLHSAHSAVDADIFQYYAYNNEQRTSGHQYIRTTPSNIHEIFGVA
GGESTTGSVDKTILEPSIGSSSAAELALKGDSIIVALAILCHSMEWLCDVALSTLGPDDWQLEDSSKSLVPGTVFFQRYA
QWSESPAAAAALAMTTGTGDTARWVRLSGILKQMYSLSQVCLFSLSIEARFVAFQFIPQLRDESYNIVATASSADTFIQA
YNRRITSFFALLKLHLSENKLKYIGITIAKPLSDLIMVELSHLRDKSISPAGLARLNVNLLSIETALLLLLPIDDEVRVA
VKQQLKRPATFLKYLPNKDVTNDLMTSGDYRQFSTEEMEELLRLVFRQEKNQEIVTQQIELLHEKLRSVVSTLAAAQRPA
LNAITPSQSLSLTSVPPVAGKREQKPQEKQPPKVQEKVQQKEEEEEEEEEESEEEEESEDNDGDADKIVPKTVEREGPRY
VDPNSAMASPRGPAAAQGAKQGEMRGQVPQHSKNESEEEEEEEEEEEEEEEEEEEEVGDFSRH

1637 - 1656:	EEEEEEEEEEEEEEEEEEEE

A0A1X0NQC0 **A0A1X0NQC0_9TRYP** (1170 aa)
Putative glutamic acid rich protein. *Trypanosoma theileri*

MLRRRLIFSTSTQTTFAGALSATVEAHATYKSDAITTLTHSTITNISSSPSHSLGKSKGNSNGNGCPTPIFISCRAHFTT
LPLLAPSTTRTLPASPHQCSVEQVLLPNIQTNESGIRTETLRGMVQLLLEPDATDVEDVSMLDFVVMVPKRQLAALRGRK
EWLEVVLSSERYQACKDARALRLAGITTLGRWDENRERVPVSPYSRGLLEDAFAAIARQPVESQKDQVITWLTKTIQKAV
IEEFAANKGNRKVLAPLITGMQALPETVAAAAATIKEDESQQRLEGTKEENDTAETSEWESSNQKTTKATKNRGKKQAKH
VEEDHAEGAEATTKAVESEDVSKKDNATASMEDDEDAEIARLLKETEQEFAPTPYVRGSNDTNKTSSSTTTASTGGAAAK
TDSDDYSRSGKLKKKKGSEALTKKAELQKQQQEQELELPDEDDDMEMDEATEKGQKTRGVTAADTVPSDAKQNRSLARLA
ELMLTQFNSADGYLHMSDIKDDEKKGFVIVVEGDMAQVDPFALYSTFSAAKVTDGDSREILALKQVCSAYNTYTEAHDAA
NDEATAKFYKEKGVEALVHGAVLLRAISREHPVTLEPRDIPAYGFPLLSSDRRPHRVRRNKGATDMTAEKVEEAVKAYTS
FFATKSKRFTPIRPTIDFNSGCSVVALMGTTLHLYETSLKETVREDDIRCRFAESMLGVLHVLERKVLNRVNVVHYHILA
TSISGGGGANGMDMMPTSIVSIDTTGSFTSAEKTRLHQLAEPLGMTSTIAECSSVSDLVDAIESLGVSVVHDILTNREDL
EALLTPTLVQLLPEAEEEEEVEEMDKKPPAKRVSATVGKEVTSKSGSGGGGGSSNSTTAAAAAAAKVAMAAATATSKDEE
EEEEEEEEEEEKTPKKKGKGKKKEEVEEEPEEEEVEEEEEEEEEEEEEEEEEEEEEEEEEVRTPPVNNNGNKKNLPPAK
NRSARGRAQATEELTLEKDDEEEDEEEEQYHHHHQKSRAPPTRKATQGGKRAPPPAAVEDDEDEDEDDEEEELVEKAPPP
PPPPAAAGNKKGHMVKKTSSPPPPAAVDEDEDEDDEEIEETPRTPPPPPPPPSAKKGAHARRAPPTPPTPPVAAAASEDE
DSKSLEDEQEEQVVVTSRPRNRTRRMARALPPRVDNDDDDDDRWFQKTRR

917 - 936:	EEEEEEEEEEEEEEEEEEEE
918 - 937:	EEEEEEEEEEEEEEEEEEEE

919 - 938:	EEEEEEEEEEEEEEEEEEEE
920 - 939:	EEEEEEEEEEEEEEEEEEEE
921 - 940:	EEEEEEEEEEEEEEEEEEEE
922 - 941:	EEEEEEEEEEEEEEEEEEEE

A0A1X0NTQ8 **A0A1X0NTQ8_9TRYP** (597 aa)
Uncharacterized protein. *Trypanosoma theileri*

```
MAREKNDKDARKKEEQEEEEEEEEEEEEEEEEEEEEEDEEWTELVELEEYQDGPSTYYVGGFSTLKNLQDVLEIVTYREDL
VLVYPGSYTEKEVKMDETRLDGLHIMGVPVAMGLKYGYPKKLRIPTDQRRIGPWYAPFGAEAPKPITVTPTKSDPSCFPV
FNGKLVVVNSGPFIATGKEDSTEPVLKPIKHYDPREDAMDDEEEDEEHERENEDQDEDEEEANKKNTVVSRLEVQGLCFL
GGVSFESLSRATIRHCVFGNQIIQKLSEVNGVTSSSSSSTPPPQQDQSSSSQDQTSPLVTTLVGHPLTAVQVEFCVIYGG
KEHAVYAFPRCGLRIHNSLILAPQEGQKAESEGLLYRAARHAQQSPILRLAHRWQHILDQAKIPKTTTTAVGVYLDDADV
SIQDCFIAHSGIGMLLLNGCTGTEVCATRMESHSTVGILASGSGGSAKIKRCAVRWCGRECLLIKGPVPPLLPDPLPEET
LLQESMNAKEKEEEEEEEEEEEEEEEDAKEKALNVVPQPPLIPTQHLTLRGNAFEGGVRLEGDISCLSMCDNVIYIGKDD
STTAIPPFVTPAEDKHFAVKGFEIHLRGATPAPSEAE
```

17 - 36:	EEEEEEEEEEEEEEEEEEEE

A0A1X0NUA5 **A0A1X0NUA5_9TRYP** (281 aa)
18S rRNA aminocarboxypropyltransferase (EC 2.5.1.-). *Trypanosoma theileri*

```
MGKPRGDHRGPGRCGVPLAMWDFGQCDPNACSGRRLHRLRALRLLQLREPFHGVVLTPNASQVVSPADAGIIAQYGAAVV
DCSWNQLDAVPWTRMRMGAPRLLPLLIAANPVNYGRPSKLNCAEALAGALAIVGRMEDARVVMAHFPWGESFFDVNAELL
RGYVTCADANEVIAFQEQFVEAEVQASAERRQIDFNNLDLMDVVPLNAKRGKLRNQKAWQQEYESSTEEEEEEEEEEEEE
EEEEEEEEKQACGDDSDGEKVDDTGVVEAERVQKIKADDGE
```

228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE

A0A1X0P2J4 **A0A1X0P2J4_9TRYP** (1040 aa)
Protein kinase. *Trypanosoma theileri*

```
MAWLILTQLNGELQSFSLKDAELLWSTKLHGGPLLYCGERKSTEAESRLWTHRPSLSTCSRCPLTLRRSCEDVLMSKPKT
QETESVPLDFQENENMKCCLVSSTHTDDAVSTPSQKWCFYLDSLVTPSLHDDSDNDNNSDNNDNDNGKAVGMYVDELLQQ
WNDNSCPLHRAVELLHKEMLYVELDLFTGRLLSCFSNADSYCNNDLKIARDDNVSLRLLLKRTNISRSVMFPPQRVPTPS
LINSNYSEESITSHTWYVLNSKVELELLETSINNDFPYEPWLHAADHSFFYINQIPTSEGVNAYLRSSCELEKFTELKFT
VTSPIISAYLLWADQSTNASMDDGAGMMSSVHCQEIPVVLSEGFPGKKILVKSPNLQEQNNNNNNNNETKEILSGFLDSD
SRVLFVESNEMKITLTSPHKLLFPHPNEDMDSQSSQDENTEEEEEEEEEEEEEEEEEEEEEERMFLLNGDDSDTTEESPSK
SGTSENAMVVYRGIPSKQGNRSDTNALLSTHVESSFFDENFEVKSLLGRGASGVVLLVRHRVTGVLYAVKVMLARDYFTE
NDVLREVRLHAHLHNRNLVRYFACWSEAITPFRVLQLARIGLCSGKDVRKICGKNNSNCMHLVNTQRETPLNVEEKINWM
LPPLPPTTTAAATKTTKRSTSTVPLSANNRNLLLGPPPVEKDATAYLVGDESMDESSATSCSSEDDKSMGDESSEVTSSE
NSISNFLGRVVFLQLEYCQTTLAHRLGSRTEIDRLENIIIALQLFSGLRYIHKCGCLHRDIKPTNIFLDYRSQMGIVDDN
SDDMSDDDSDYDNSMEEENEKEEEETVVRNGCTREKELTDGKHLPDLFVPSPSAFDFLKKNIRVGSLAVYLRQLRDAKCE
RKKEKILRSVRVWLKRRLVQVRIGDFGLSKPLSDQRMDIASYFDNSTINTVGIGSPIYSSPEQLNGDICTPATDNFAAGV
VLAEMYFLPKTISERLVELRRVREGTFPNPHLLKRYPELQVVQSLTHSNPEKRMKLRDATRMLAKTANDLLLSFFQSHGY
```

441 - 460:	EEEEEEEEEEEEEEEEEEEE
442 - 461:	EEEEEEEEEEEEEEEEEEEE

A0A1X0P466 **A0A1X0P466_9TRYP** (882 aa)
Multidrug resistance protein, MATE family. *Trypanosoma theileri*

```
MDPHSTRSSPNQRKERERERERGGGAEGHHEGSGLLGLRQEVGVRRRRQHYGATVRSISVPVTRTRRVVIIRRSGARYAEL
TVSQQTTKLAEEARKTLFHGSFTSSHGATFCVPPLRRPDRTPKHSSKGHSDAATSTSTNTTINTTTTAVAVEMSELEIKT
TTTEQGSNYRFDKDLVAPQSAFKKEKKVSHDNQGEVRGNTSFLHEYIILKPRSNSADMRHSIDRENSSQTSREHLPKTSI
DVIGLERIRDNFSPRGKLSSYNIEKTNEALATYKEKCTQINKNKISPPPKEEESIGSNSYKSTVPVENNKLQEGTSSHID
NRRVSFSNHINLTTDKKQSEEEYSDDVHEESGESIKLSYWEAAVQIISFAAPAAVTIGLTFALSVVPLAFVGTHLGERYL
SGASVGFFILSIVGLYPIIGMTFAMDTLCSHEYGRDPNSQDLGLLLQRGILINLFFLVPDCLLFYQLRPLLIKIYGLEVS
DVAMDFLLYMPFFLLPLTVFIAFNKFLSNQMQPQMPMIALIAGFIITPFVQRFLTPMGVRYTMIGMSITAWFQLCVLVIM
TLNKPQTRHTLGTLRLKEALQLSDVKEYLKLAIPSAIFVAAEASAFDLSILICAHFGEQQGAAWSGIMNALFIFASISGG
LSAGACANIGRSVGSNEPVNARTFVEVTVFISVLISLIDCVILYNFFDFIMSLFGTKGSTLQLARSTINILPFFHIADAV
QFAFQGIFSGLGKNHLGALILLLSLWVVGIPSALFFGIFMNYQIYGVGLGLTIGLCIEAPTMVAATFSLDYNAVCDAFIQ
NNEVEEEEEEEEEEEEEEEEEEEEEVNRLYDEGEEVKESYAINDDVMRRSGIPTTPAQFGRRLSHKSRHQLHIPPHPKSQ
ID
```

805 - 824:	EEEEEEEEEEEEEEEEEEEE
806 - 825:	EEEEEEEEEEEEEEEEEEEE

A0A1X0P6K8 **A0A1X0P6K8_9TRYP** (690 aa)
Uncharacterized protein. *Trypanosoma theileri*

```
MPKVRTGPSKRMTSRQRHKIERKKREHKRDLRKAAKALKKSGLGPKRSKKSREMAKLALRVSNAHPDKEAILKSVLQARE
NARVEKANRLKKKSEDDNNLESVSEEVSCIPPSQVGKKALTYIPVRESNNFTYQFNKVLSEMVFPPSGSLMELPSAAFVV
TLDARCAVQCIPWGLLDAIINESNLYGKNGGKRKVLILFAITKVDLVSSPAIVSQISLVAHALSERYGTSANGKVLLEPS
ENVCIAFCPFSNQFEKTTRHFIRIMRQFLNSDNCAQSNKHCNVEGKLSSFVIGLPNTGRRTLCRAILQYGGDSCVSIVPV
```

```
SSAQIQVMSKEDNNEEEINLKLAFPNAKEITLLQFPEDAHLMRDISSPIGGDVVFKSFSFVERITDPELIGCMLFAGAID
KVALAQGFCQSAEGFNESLDEEKTLKAGERFLRGLGHTVRREKGFYVSPLFVSNAGTMGKVCSSSLTASVNFTSRQQSTQ
TTLLDASFSNATPNKLVRISSVVASSRGKKKSNLNVKRIDSHNAFKLGARTFVREFCQGKNIPWAVMRPPMKKCLTKAEV
EQASTLFDLSLCCGKRLGTLETKKSSDEHLAALLEHLASLLKQYLIFMPNNVVEFDPDCIVAPIHNLDVSEINGKGDKKK
MNEEEEGEGEGEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEEEEEEESD
```

652 - 671:	EEEEEEEEEEEEEEEEEEEE
653 - 672:	EEEEEEEEEEEEEEEEEEEE
654 - 673:	EEEEEEEEEEEEEEEEEEEE
655 - 674:	EEEEEEEEEEEEEEEEEEEE
656 - 675:	EEEEEEEEEEEEEEEEEEEE
657 - 676:	EEEEEEEEEEEEEEEEEEEE
658 - 677:	EEEEEEEEEEEEEEEEEEEE

A0A1X0P9U3 **A0A1X0P9U3_9TRYP** (1129 aa)
Putative eukaryotic translation initiation factor 2-alpha kinase. *Trypanosoma theileri*

```
MTNGYHRITALLLFVCLCALAFLATDVSISADSGAPIPTSVHLYDVMPQTTETTTTKTPTPTTPTNVVNDESTTVPTQGS
TDLGLMPLYGFRLPSLVLLLHMEGNLSAHLLDSGIQLWSVDTGGSVMHAKYEQHPTDKILKEDPLSQPFLIEGDMLFTRR
RFTPNLSNRRLPLNDAGNNEGIDYSGDSDDGEEENIGNIPLTPLHPNYFMNLSTLIRRRHVHVGDTDVFVTSSAQLMDVN
SYNGEPVKSKNTLWPYLHIVRYNITIHVQCHEEYSWQMSLAQYKLRKRSPPQSSGSSLEYNNPHYFSRLLQELLQNKDPN
NEHKLPLFPETIVKETKNFKSLLNGNQKNIFKDVLSVREVKPKKYVLWNSMAGNSLWTNTVGSLNGFAAAYVWITEQSGV
QRVPVYPIIPSSYTTTCGSRGSTTNNNNNAIITTTSTATVKLIDEEAGTSIKNINELVNIPPFIEDRQCSEQPSIGFSFG
DIWEYDIDAEERENRELHDSFQQCSWFYGYSNPYGPLLNRSLMGSNQSMEMSQFFSTISLLWSYGATRRTAFIGFHFLCL
IISFTLLSLGVGQRPRLRNAWAQSDALRDKVRNSSRSSSDKLLPEDMRTNGDKVESISNISKGMTPFMLNGRNDNLMSFP
SLSLKSDTRTEGIKETNSDQRDLTDDWWKNSGGDDSSVSEKQTSDTLIEKNVNSPPQLFQQHFEVLRKIGRGAEGSVHCV
EHRVTGKVYAIKAICIDEKVQERYIREAVLHSSLDCPNVVRFFYSWIENVPTHVAETYGIIHHRGTRDSISTLYKEESSR
SWSITNSISSDFLRRVLFIQMEYFERGTLADFFRQRNRFTRRQNLKYLLQISEGLRYLHSQKIVHRDLKPTNIFLTDSGI
VKIGDFGLAKQSVANPNSQGTINDDYASQKCINDRESSIVGGTPLYCSPEQKIGKPATAASDIYSLGVIAVEFYSLFTTD
HERLDTLGEARLGKLPAALAAAFPEEAALIRQMLSEQREKRPTLDEVLRELRRIIGTILNKKKQWVHKEEQEQEEKEEEE
EEEEEEEEEEEEEEEEEEEEEEEDEEEGSPHQHQHQHQHHNGTNHYDHGQNQGPESGSSLHSTSDRKIQSYIFKSNAGDS
ETSLDSKKL
```

1037 - 1056:	EEEEEEEEEEEEEEEEEEEE
1038 - 1057:	EEEEEEEEEEEEEEEEEEEE
1039 - 1058:	EEEEEEEEEEEEEEEEEEEE
1040 - 1059:	EEEEEEEEEEEEEEEEEEEE
1041 - 1060:	EEEEEEEEEEEEEEEEEEEE
1042 - 1061:	EEEEEEEEEEEEEEEEEEEE
1043 - 1062:	EEEEEEEEEEEEEEEEEEEE
1044 - 1063:	EEEEEEEEEEEEEEEEEEEE

A0A1X0QY26 **A0A1X0QY26_RHIZD** (296 aa)
Uncharacterized protein. *Rhizopus microsporus var. microsporus*

```
MRYNILSLGLIAATLIASISARALPVGSLPDTTSSIDSAVAADEDVVTTALGRHPLYTSNKKRATVSFQRREEEGEEEEE
EEEEEEEEEEEEEEEEEEEEEEEDDDDEESGGGEEGAADQPSLARRHWQKDKETSNDDAGAANDGDTEDEDAVTEELEPV
TEELDTATEDIDTIYPDDTDAAEDEVAYGGEDDEDDDEDSDDDSDSDDDSDSDDDSDSDEDEDEEDSKLARRQNTEEAAV
NQPVDTSAVDTTEQPADPANGEGEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDE
```

76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
266 - 285:	EEEEEEEEEEEEEEEEEEEE
267 - 286:	EEEEEEEEEEEEEEEEEEEE
268 - 287:	EEEEEEEEEEEEEEEEEEEE
269 - 288:	EEEEEEEEEEEEEEEEEEEE
270 - 289:	EEEEEEEEEEEEEEEEEEEE
271 - 290:	EEEEEEEEEEEEEEEEEEEE

272 - 291:	EEEEEEEEEEEEEEEEEEEE
273 - 292:	EEEEEEEEEEEEEEEEEEEE
274 - 293:	EEEEEEEEEEEEEEEEEEEE

A0A1X0RPY2 **A0A1X0RPY2_RHIZD** (2829 aa)
Uncharacterized protein. *Rhizopus microsporus*

```
MSLKNRKSVYSKKHSTSDNEATLLKEDDPEIMKRNNTRLSRRYTQRKPLPSVTEFMTEFEQERRPSPPPTPLPQEEEEIT
FEDEVFSDTARLTVNASNMSGFKHPLDASPELPAIYKPASVDPEIDRKKVNRLIQYDRHKFFRDLVKAVRGVAERVVNLH
QYAINHKAAVDENKELQERRQEQWQKYSEEDQESDASSVVDENIPMKRTATISNPDQVKDDSTSDVESFSYLSGNSLKLF
SPQNPFRVFLYHALCWKWMETLIMFLIVFHTITLFIVGWGSDPFPNPPSTWGQVWYQYVLLVIFILYTIIAICRIIVLGL
FFNPPSPQSPRAYLRHSWNRIDFISILSYWVDFILLMTHQEINEDQGRRILVFKMLSALVLLRLLNITDGSKVILNSLKR
AAPLLVNVLFFVFFFFVIFAGSFQRHCVWHDPNNASHTEELQQYCGGYINETGYKVPYKLKSGQTALWSKGFICEQGLIC
EETENPYGGTISFDSIFSSMLIVMIITGVQSWTDRMYDMMDAEYVVAALYFIVIVIVMNFWLINLFIAVITEMFAKVRED
SQHSAFTNATAKPILADMNEEGGWEFAENEEQEQQQKVSSLTWLVTFMRPFWIFLIAVDLVCMATKHNDMSTAQLDGLDL
AETIFSLAFLVEMVLRLLAQRRDLKAFFKDKMNTTDLLIAVVTCIIQLPWIKQHRLIYIWFTGFQVLRIYRVIVAIPRLR
NLMSRVVGSMYGLINLTFFIVLSTLLCAIIAYQLFEGVINETGEEMRFFSIYNSFAALYQLFSGEDWTTVLYNVLQAGST
NRNSAIYALFLVFWFCFSNFVLVNMFIAVLMENFEIAEEDKLKNQVLFFMKKTESELNRKTVVSRWNIYRYFKPQPKGLD
LTNIPNHLVLSVQKNVVREFMNETTQEIAEERQVETTRHGMMSKAMNFISRLFPSPDLAHAQRPVLQTHARQSMHFDQVG
TFYDLKGRGSTDEPRALRYLIDPTLRDTVANRYQQETTDLDIEERKALKRDFIAAHPSYDRALFIFSSNNPIRRFCQRIV
PPSRGERTFGVPASRWISLSFSAFITACVVANVVLTIQNSPVYQYQHRNDPEKIMRFVYTDWAFTVVFSIEFVIKIIADG
FVMTPNAYLLNGWNMLDLFVLVTLYMSNFDKFAGATGIERGFRAFKALRVLRLINLLGPAKDTFTAILFTGLPRLLESAA
LGLCLIVPFALYGKNVFMGLFYQCNDDSSTGKSDCLFENMLGTQEPMPEDTSIYLPRRWANPYDYNFDSFWRSLLILFEI
ASGEGWVDVMETSMGITGKDLSPEQDASQLWGIFFMVYNLAGSVFVISLFLGVVMENFTRRNGSAYLTSDQRRWLDLKKF
LNQVRPAKRPKSPPTNKLRKWCFDLTVEKQGFFYKLMTVVVTLNIVFLCADNVSSSDPGSGDVTSWDNAKVDVYLTFIVI
YWLEIIIKILGLGWSSFRKNLWNLYDVVMVFGGSVTTFIHYGSPGLQWNVELQKLFVTALCFKLVQRSDSLNQLFTTMAA
STYQILNVMAVWFIVMTTYAIMFMQIFGLTKYGPSVSNEHVNFRTFSSTMISLIRYSTGEGWNNVMHDFTVEYPNCVVSD
NYLDSDCGSLRWAYFLFLSFNIISMYIFTSIFVAVVADNFSYVYQTRANFSLVNRDEIRKYKMTWASVDTDRTGYVKPSE
YMTFWRRLEGIFTIRIFEPEYSYKNLVTQFKKNVKTDKYDHDLDLKGLSEKLNELNSQELHKRRHDLERIYWETALIESG
SKGVSFNQMLLMLSQRKLIVPEHSLVLEDLLEYQKKEEAIHTLISIDRVRGLMETIALRKKFLRHLEKQKKVPAIMVDNE
VVQQSSASYTPLSPHHLNTNSVYDLTSEDESGDEDHVKSMLAVSSEESAVVEDNPSHTIWQADHKKNKKTVEKSKNVAKS
DDAFEQAVLELGGTKGDIKYLKDIDDDNEEDLQTTATKDEEALKNELKSFMANIGLSASTYEQDIDTDEEQPEDKEDEEE
DVSSEEEEEEEEEEEEEEEEEEEEEEEEEPMKIHTPKSSSGLLIEPTPFWYNVSLPAISIENVQRLSTLQTQEKLNYAKQL
LKDENAKAETHPMLTSSNRSFMSNIIQSGTLNDKVSALTLMFRESPLHGIKTLDTLISMSRKKGRNEAVMAITSLKDLFI
GSVLPDRKLIYFADRPLAAKEVSDTHLLVWAFEDYLKKTFLEYLRIIEELSRDTLMYVRNNMVTCIHDLLANKPEQEQNL
LKLLVNKLGDSDNKVAAKTSQLIIELLIQHPGMKMIVIRELEQLLFLPSTNEKAQYYAMITMNQTILTAKEKDVANKLIE
IYFIFFKKLLKIQEKEDNSKKNEENEEVKVEEENDKKKSKKQMKKEKQQEQKKLELDDHKTKMIAAVLTGVNRAFHFADI
SDKIVEDHLETLFKITHASTFNAAIQALSLIFTISISKPNIADRFYRVLYESLLDPRIHQSSKQSMYLNLLFKAIRADND
MRRVMAFVKRLVQIAARHQPAFVCGIFFLISQLMESKPGLKTLLMPPEDDEEEHFEDVEEDDAPKKEDNKSSRVEYDGRK
RDPRFSNAEKSCLWELLPFKLHYHPSVVKYVESLFAGELITNQPDLHQFTLMHFLDRFVYKNPKKESVPKGQSIMQPLSG
SRRDGGVLFTKSAINEIPVNSEQFIRKKEEEVAADEVFFHKYFTQKAASQPAKAKKEKSGEDSEEEEDEVWRAMMASIPG
GLDDEDDNDEDAALYDDDDEDDEEMKALLAENEEEEENEGDEDEEDIEFGSDEEDIELLNASDMEEELQAKRELSDDEEE
EQPKKKKSKKERLPTFATYEDYAKLIEQE
```

2005 - 2024:	EEEEEEEEEEEEEEEEEEEE
2006 - 2025:	EEEEEEEEEEEEEEEEEEEE
2007 - 2026:	EEEEEEEEEEEEEEEEEEEE
2008 - 2027:	EEEEEEEEEEEEEEEEEEEE
2009 - 2028:	EEEEEEEEEEEEEEEEEEEE

A0A1X0RTK4 **A0A1X0RTK4_RHIZD** (883 aa)
MI domain-containing protein. *Rhizopus microsporus*

```
MAPTFHKSKMPHKRGPTPGSVLPKAMKEEVDAAEKDDRKFGKKFVNKIANRKELRKQKRAEKGKRKAIHQQTRDQQNKKR
LLSEKQPQPNKRQKKEDLPKDQSKDQPKKQVTNSEEAEKRLSKKNPALYKMLAADNLVGKNSTTDEDFEEDDKEIAYWEK
KLGLNKKKKKKLGKEFENDGLLDVLGNVDNVNNEMDDIEYLKQKRSKQAQLKEQKSLEENAERAVDQLFEDFPSDEDDDD
MDASVDEDMSDILNDEQESGEEEEVSDALEDEQDDDDDDDEEEEEEEEEEEEEEEEEEEEEEEEEENDEENDEENKKEEQVVV
KEPPKSSVLTKYVPPHLRKPVSTGKSEQQLRLQKQLQGQLNRLSELNIESILVEIEKCYGTYPRHDVTSTITELIINSIS
QRSNLLDSFVITYATIVASLYRLVGVEFAAHFVQTVIEMFETEHKKYKKAKQQTIDDEQEGYKETRNLLTLILELYNFQV
ISCILVYDIVRMLINELDEGNVELLLRIIRTAGAELRNDDPTSLKHIIDEIQKETAKRDPSTISLRHKFMLETIANVKNN
KIKNKQTAAGHGDKELVQKMKKFIQGLSKKRSTRSTEALRVSLDDIHNVHTKGKWWLVGASWKDNLVGTESKYKTTNVPE
DLKKDQSMQEALLKLARKQGMNTDIRRTIFITIMSAEDYLDAFEKLMKLGLNEVQQREICRVMLQCTGNEKTFNPYYMLV
SRRLCEIDHSFKVTFQYCLWDFLRECGESEVGGLERSASESFSGSKEVRLSKIVNMAKFYASLITEGALTLAVLKSINFM
NLQKNGRIFLELLFVNILLQLHAGGAQAIANVFGKIRDQRILAQGCIFFIVGTVTHCKHSGLEEDDIEKVQWGCKIAKEV
LNK
```

281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE

A0A1X0SA93 **A0A1X0SA93_RHIZD** (281 aa)
Uncharacterized protein. *Rhizopus microsporus*

```
MRYNILSLGLIATTLIASISARALPVGSLPDTTSSVGNAVAADGDVVTTALGRRSLYTNDKKRAAVSFQRREEEEEEEEE
DEEEEEEEEEEEDEEEEDEEEEEEEEEEEGGEGNAADQSSLARRHWQKNKGTSNDDTEAANDGDAEELEPVTEELDTATE
DIDNIYPDDTDAAEDEVVYGGEDDDEDDEDEDDDDSDDDSDSDDDSDSEDEDEEDSKLARRQNTEEAAVDQPTDTSAVNT
TEQPVDATSGEGEGEEEEEEEEEEEEEEEEEEEEEEEEEDE
```

255 - 274:	EEEEEEEEEEEEEEEEEEEE
256 - 275:	EEEEEEEEEEEEEEEEEEEE
257 - 276:	EEEEEEEEEEEEEEEEEEEE
258 - 277:	EEEEEEEEEEEEEEEEEEEE
259 - 278:	EEEEEEEEEEEEEEEEEEEE
260 - 279:	EEEEEEEEEEEEEEEEEEEE

A0A1X2HUX9 **A0A1X2HUX9_SYNRA** (414 aa)
Leo1-like protein-domain-containing protein. *Syncephalastrum racemosum (Filamentous fungus)*

```
MSDDERNEHDFGDLFGSEDEQSDLAPESDVSDDEQQQDTQVASSGFDASPEQTQAQSERTTSEQEEQEEGDEQVDEDLQ
YGHDGAIGYDDEEPTPVRRPVAPVGLELPLLPTPTADDNKFTLARIPHYIDFDPAHYDPDTFAVELDPDWSPEDKRQAIR
HQIENTIRWRQTPTGMQSNARIVEWEDGTKSLVVANQCFDIVEKPLREDEHSYLLAHQTDSGVLESHLLLTHHMNFHPAD
AAAFAHQNLITADVKKARTKMVLTEDNPEQAQKEEEARANERLRLQRKLEGARRKADSFGPGTSSRRFYDYSDSPSYTQR
TRADDRYEDDFVVEDEEDEDFMDEERLTSAQHSYKRQRDTYEEEEEEEEEEEEEEEEEEEEQAGQEEDDEEQVYIKRQK
RQRRHHISDDEDEE
```

362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE

A0A1X7QXL1 **A0A1X7QXL1_9SACH** (1171 aa)
Similar to Saccharomyces cerevisiae YPR104C FHL1 Regulator of ribosomal protein transcription. *Kazachstania saulgeensis*

```
MSFNTTHSVAEGLSQPHNDLDDLESKPIIPSTNDTSVHKGDLSSHVQEQFTFLPEKVITESPRAPNNEDEHLEIETTTLE
DSTNKQSNDNTGLTGEIQSKIDELPAEVETTILEEVLTKAIQEEENEVEDDDGKESELYDHDIQMANEPDFENTGHVQDV
LKNTSTQPDELKIDVNDDPIDNEAFSKLLEFDSKNDKELFSTNDISEETISKENRDTNEIEITETIDQQNDSTKDIEDKT
RESTVKLEDSKKKEDSSISPYPTLPKDSKQTLSAYTNTPEILLSPTNNDKDRVIVKPEDVVNGESNLVQKLFMEKSMEQQ
QRKNSIIPGMFHTNDLHPQSNQLENISQHGGTLSRIGNGISPMDVGDSNAIGGVHQGMPGVPDEQPTIFAYARLDFQNFT
FYVQTLHAIIGRRSENDTTHKVDVNLGPSKSISRRHAQIFYNFGTGRFELSIIGKNGAFVDDNFVERGKTVPLMNKTKIQ
IGQIPFQFVLPDQENNMIEDDHKEKASNDSKSIKSASNKTKKTPAKKSTIKKETTKKQSSVKKEAAVKKEISKKKESATK
KEPTPKKKTTKPAIKKDKKTVKVPKKVYTLEEIPEEYRTKPAFSYSAMLTTCIRKNSTEKGMSLSEIYAGIRELYPFYKY
CPDGWQSSVRHNLSLNKSFRKVSKEGKGWLWGLDEAYIAEREQQKQKQAEAAKAKAEAAQARQEQQQQQKAKKATTAKTT
STKKQSISQTLAANRATTNNANKLTDHQRTMKYLQGQLMILTKDRKGLSKQVIANILTQALAMTINQVTQAAKNKGISGN
PLTALMDKNPKHLNLILAAAVNAATAKVTNGKIKSLVSMTPPTIEKPKITTQQPNIQRPATVDTTSSSQKIKTEKHELSS
SSSSSKDTSRLEADSESIDTSFDPTSLSRFFQPRQQIRVPPSSNSKPTTSITPQKRPLEDNSDESSDESTSSGESESDSN
NDEEEEEEEEEEEEEEEEEDEDDEEEEEEEEEEEEEEEEEEEEGDEEEEEEDDEEEEEGDEEDDDEENDDDDEEEEEEEE
AAEEEEDTATRDNGDSENTNGVAEENVEGNTIEQEENDKVIKHAEDGAENNLPTTLLSEEDNADEVEEKPRNENDHSNEI
ISENTNPLTEHNETHDTADGDGDIEMKDASEDITKTVEEANTAIVNEDASI
```

983 - 1002:	EEEEEEEEEEEEEEEEEEEE
984 - 1003:	EEEEEEEEEEEEEEEEEEEE

A0A1X7R3M6 **A0A1X7R3M6_9SACH** (585 aa)
Similar to Saccharomyces cerevisiae YBR030W RKM3 Ribosomal lysine methyltransferase specific for monomethylation of Rpl42ap and Rpl42bp (Lysine 40). *Kazachstania saulgeensis*

```
MSSTVSSDLDDIFQFVKNAEGKFTHDLCEVKESPLGGQGVFAKQDIPKGTTLLQLHKNSIFSASNSTIANLLNDEEIDGI
LALNIAFIYETTVFMDKSDWYPYLKSIKIQDENTGIVKLPPAYWDEQDKKLLHGTTLDTLFDALTPQDEVQRGFEIAIDL
AEKWNEEFGLEIPKGYLDVNIQDEGDIRTKFNKFVAVAYAISARVFEIDAFHESALVPIADLFNHHVVTPDLKFISLFDV
CDLCGEPGMCKHMLAEELEEAKELEKEKTHQNEINKTSKKSKGGLTKIDESIIAKLEKDLQKEMQEQILEKEKENSKEKE
LDPDECIDMTTTRDLTVGDEIFNSYGELSNIFLLTRYGFTIPKNPYDVVHLGSRILDLVRNDKNLKERALWWSETGYGKY
IDWFKEQFPEELEHEHDENCDHDHDEHEEGGEDEIEEEDEEIEEDDIDEEGQEEEEEEEEEEEEEEEEEEEDKPWLSEL
EIDYHGEPTPALLATCNLFSMEPEKFEQFSTKINTEPQQMEVLLALDNTKTNNLFKKLAQEYRESLQDPSKIEATSIIQE
QKDCVKALIEAELNILGKFTSTLKE
```

453 - 472:	EEEEEEEEEEEEEEEEEEEE

A0A1X7RB72 **A0A1X7RB72_9SACH** (1634 aa)
Similar to Saccharomyces cerevisiae YOR191W ULS1 RING finger protein involved in proteolytic control of sumoylated substrates. *Kazachstania saulgeensis*

```
MTSGMPTIDLTLEDSDEEMNLPNVNENGSTSNETPNANSSYHSISGKLDELFEEDNKQIPSPTSSDEPNDYDEKHIQHAT
TADEKLKNLASLQRSRFINIDTDNNNNSNNNIDSKLIWKLSNDTTSKILTPKAPEMERMESTSSSDELDEVDDDSSIFQR
KEEEEEEEEEEEEEEEEEEEEIEKNLELSSHTEESTELPIKNESIIEQHQDNSPEKVRKDIIIPNPGILTPKQEIIERSQ
ISETDNNLSDISNDKNNSNSPVETSNNVESLETSNDNNLLDTQKDDNQILDLKSENSSFQHKTTEHNSLETSNNEIVQNI
PVIENNQLEIPTNFDISSDIKNEANDENIKISRTGHINDNSKELSKPDPEVTQSTPPILTKSEITSTIEPADINDNPQKR
KAVEEIHDTNTFKKKFLETSSQSENPSIQDQIIILSSDEEEELENAKAIPDQSQKVTNAEKIETIDIPNNITETESLSEN
IELTQKEYQKLEKEFTTKENSLRNKLDSLKSSSMILERKLEKRNERLKQTTTKLESFEKMQTLSSSRRLLIADTKRTVES
LTVQRDMTLMKYKRVQSSLEKTKITLNLLISEKTDKLGKAKNNLIMAERDFEIKSIVKQRKELLEQKDTLNFMLSEGTIS
QSAHRTAMNEVQSQLTNLSVQNRSAPAVQDPQKVINGMNNNLNNQPDYFVKSIEAAKKLILESTTRTGLTKQMLVQHLDV
LLKYKDHFESGRTIAAFMMGTCLDSAELLFTNGVKMPVVYNLLQDYGLKYRKEGLIPVDRRSQYFKSIAIAKQLVNESSR
YADIKRSILSHLDLIDLFRKNIDNGTPPVPETRIMVTRSVIFLLKQGLKMTKLYENLKVYQVGSTEDELRTLIQRSNNHQ
NFNIFDSHDDKGLTKWQLSQQTHSNIQQNKLQGNDAFPSGGISNIHDVQDKEYIRELLANVKETENQIEGEEMTPDELTV
NLLRHQRIGLRWLLNVEKSKRKAGLLADDMGLGKTVQALALMMANKSDDRRQKTNLIVAPVSVLRVWQGEMETKIKKNVG
FTSFIFNGAKGKLKTWDEMKSYDAVLVSYQTLANEFKKHWPDALSIDQKKIPSIPDIKAMNKLKRHNEYWSPFYRDDSTF
YRIILDEAQNIKNKKTQAAKACCTLYSTYRWVLSGTPIQNSMEELYSLIRFLRIPPYNREERFQADIGRPFGKNKKFEYD
SEDRKKALQKVQVLLKAIMLRRSKTDKIDGKPILELPPKNVEVDETSLKGEELEFYTDLESKNQKLAKRLLARKAKGNYS
SVLTLLLRLRQACIHSELVIIGEKKSETTKVVNGKNFERDWNRLFEVVNRMNMIKRNTVTESLDRMTCLWCMEQLELENS
```

```
SVLTGCGHMICDACIEPLTEEATLDSSARIVNDAMMLPCHDCRLLTSDKEIVSYKLYNQTVNLNYTRADLRREYELAMDS
RRSRPEYRPDMTKLKPSQKMTQCMDLIKKVFENSTTEKIIIFSQFTAFFDIFGYFLTNLMNVGYLRYTGDMNAQKRSDVI
SQFYRDASKRILLISMKAGNSGLTLTCANHVIIVDPFWNPYVEEQAQDRCYRISQTREVFIHRLFVKNSVEDRIAELQKR
KREMVDAAMDPSKLKQINGLGTRELGFLFGLNSL
```

162 - 181:	EEEEEEEEEEEEEEEEEEEE

A0A1X7S2F6 **A0A1X7S2F6_ZYMTR** (93 aa)
Uncharacterized protein. *Zymoseptoria tritici ST99CH_3D7*

```
MRGGLLLRFGVGRKVVMKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDCWRSGWVRRKRG
MGVGMVEGGRDLV
```

19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE

A0A1X7TTB4 **A0A1X7TTB4_AMPQE** (816 aa)
Peptidylprolyl isomerase (EC 5.2.1.8). *Amphimedon queenslandica (Sponge)*

```
MDEDDFIGPGGGSGLASIFGASVAMDGSHGNESLTYKAPKQPKKQKGSGSGQESQQVLAAVSVDCQKHVDGRYQPQGKLG
CALIGLHSSRDYKMLLYLSNNKHVTSVKVDTSFNMTIQASNYASFYDDARQAWSLHFTSTEDAVKLAKEIAVCKANSVGP
AFSQLLKQDLVLGEGQPVDKGDSVEVVYTGSLLENNGIGKVFDSNDKGFRFKVGAGKVIRGWDEGTVGLCKGGIDTPPID
RKSSDTVRDRTQSFEDQLVQSGEGGGEEGGANRSEILSRISKMGQSMLPVATTVASTSEPTVAPVSQATPPVASEPVPVQ
PQPVPQVVQPQAPPIAQPSPFQQQPQVMTSVGPQIIQPMGGVMGGVVGGVPGSTMPGTMNGVIGGGMMGGAMGGAPANQL
ALYQPPSSQFGYNPATGYYGQQPGGFGQNMYGQPIPPPGMAPPPAPPPAPPQQQDSSSGTNTTLWKVEKKEEEEEEEEEE
EEEEEEEEEEEEEEEEEEKEETKEEEETKEEEEEEEEEEEEEEEEEEEKEEEEKEEEEEETKEEEEEEKKDETGTDDDKDPKE
VPEINIREETNGRQSPPPLEEEEEEEEEEEEEEEEEEEATVVVVKEETDGDTKVEPPPLPEEEEEEEEEEEEEEEEEEEEE
EEEEEDKQEVPPADKFSKEEVDHHEATPPVQTPPTDRPESPIIKDPSPQPSPSPPPRSPVQPAKQTPKKGGGLFDDDDDD
DDFFSITSNDKATSSSTKETVKHDKEKIDSSIFGASSDFAFGQDEDDNLFLSPSAPEPAAKQDEPTKDSPETTKAKPPPN
PLFGDDDDDDKDEWWN
```

471 - 490:	EEEEEEEEEEEEEEEEEEEE
472 - 491:	EEEEEEEEEEEEEEEEEEEE
473 - 492:	EEEEEEEEEEEEEEEEEEEE

474 - 493:	EEEEEEEEEEEEEEEEEEEE
475 - 494:	EEEEEEEEEEEEEEEEEEEE
476 - 495:	EEEEEEEEEEEEEEEEEEEE
477 - 496:	EEEEEEEEEEEEEEEEEEEE
478 - 497:	EEEEEEEEEEEEEEEEEEEE
619 - 638:	EEEEEEEEEEEEEEEEEEEE
620 - 639:	EEEEEEEEEEEEEEEEEEEE
621 - 640:	EEEEEEEEEEEEEEEEEEEE
622 - 641:	EEEEEEEEEEEEEEEEEEEE
623 - 642:	EEEEEEEEEEEEEEEEEEEE
624 - 643:	EEEEEEEEEEEEEEEEEEEE
625 - 644:	EEEEEEEEEEEEEEEEEEEE
626 - 645:	EEEEEEEEEEEEEEEEEEEE

A0A1X7VC60 **A0A1X7VC60_AMPQE** (1099 aa)
Uncharacterized protein. *Amphimedon queenslandica (Sponge)*

```
MQRPTRMITRLDLVNTWILNSILKEIQWEVSYQLVSNRKSRVNYQSTGEQNFHIFFQLLCGTDEDFLGMLHLQKDFSKYR
YLVSTDVDRPDGFLQQQAKEFETTLKAMEVIGFTAEEISSVLELLAAILNLGNVTFKGYALPNGTNACEMQNNMEAATFA
CDMLGCSLELLEQCLTKKSVETSKEVVLTPLSQAESEFARDGLCKAIYERLFKWLVSRINDKIKPQARGKRKSIGVLDIY
GFEVFKSNSFEQFMINYCNEKLQQLFVDLTIGSEQKEYIIEGIEWETVEFFDNSVVCEIIEDPKQGVIALLDEECLRPGE
VNDLTFLDGLNRRYVKNENFISRASHDHRSDTTLERNQFRLRHYAGMVTYDVTGFMDKNRDHLLKDLSQAMFACERALLK
TMFPEGDPESRHLKRPSTTGFKFKASVNDMMKNLLAKNPNYVRCVKPNDLKKSKMFEAQLVETQIRYMNLLENVRVRRSG
YAYRQSYEQALQRYKMLTSKTWPTWKKSPRDGVKTILKECKRKDEEYSFGRTKIFIRNPQTVMDLEEMRKKRMHDLATLI
SKRYRGWIKRKKFLQIRNSQITISKHLRGSKVRKQYLIKRNATIVIQSYFRGWQVRDTLAKVRVLSRQLYVSSVIRRYYY
AWKLRKVINDRIHSKKYLPAAIVIQKYYRGWKVRRKDTKSPQVQVPLTMDSESTDTPAGTNTNGVLPEANTESVSDDSEE
EEEEEEEESEEETEGEETEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGGREEEGEREEEGEGEEGESEE
SEEEVKVKVAAQVSKVPKEVTVDTDSAGLLVLKFIRRSVQYKFLLTLLYNLPSRSPIDKKWPRCSPLFKKTSILLRNIYH
KWRCKLVRDYYNANPMVKHKLSEKSRASTLFKGKKSVYQASIPVAFISDRLRIKSDERWKKLINDVSDTRIVWADSVQKM
NRSDAKLCSRAIVLTYKSLYILDSKNYRLLYLLPLSDVTGVSLSPFNDGFLIIHIRPHDGQDKSRPKGDLVLLTKHIVEG
VTKLSVVIRQLQVNFKTEIETQLKFGELSTIVFKGISGDNGSPVCQRRGGNTILIHVEQ
```

739 - 758:	EEEEEEEEEEEEEEEEEEEE
740 - 759:	EEEEEEEEEEEEEEEEEEEE
741 - 760:	EEEEEEEEEEEEEEEEEEEE
742 - 761:	EEEEEEEEEEEEEEEEEEEE
743 - 762:	EEEEEEEEEEEEEEEEEEEE
744 - 763:	EEEEEEEEEEEEEEEEEEEE
745 - 764:	EEEEEEEEEEEEEEEEEEEE
746 - 765:	EEEEEEEEEEEEEEEEEEEE
747 - 766:	EEEEEEEEEEEEEEEEEEEE
748 - 767:	EEEEEEEEEEEEEEEEEEEE
749 - 768:	EEEEEEEEEEEEEEEEEEEE
750 - 769:	EEEEEEEEEEEEEEEEEEEE
751 - 770:	EEEEEEEEEEEEEEEEEEEE
752 - 771:	EEEEEEEEEEEEEEEEEEEE
753 - 772:	EEEEEEEEEEEEEEEEEEEE
754 - 773:	EEEEEEEEEEEEEEEEEEEE
755 - 774:	EEEEEEEEEEEEEEEEEEEE
756 - 775:	EEEEEEEEEEEEEEEEEEEE
757 - 776:	EEEEEEEEEEEEEEEEEEEE
758 - 777:	EEEEEEEEEEEEEEEEEEEE
759 - 778:	EEEEEEEEEEEEEEEEEEEE

A0A1X7VC91 **A0A1X7VC91_AMPQE** (462 aa)
Arf-GAP domain-containing protein. *Amphimedon queenslandica (Sponge)*

```
MASPETKRALQALRGKQDNNACFECGAVNPQWVSVSYGIFICLECSGKHRSLGTHVSFVRSTTMDKWKDSELEKMKVGGN
KKARQFFDSHGEVQRGMSLSDKYNTRTAALYRDKILCLSEGGEWSEEKSAARHQKKKSSRKQKQAEPDPVPSSRLESIDL
EGDQDLEDFLNDTDSSQKVGRKQRSSERRREEDPASLSSYQTGNGSEESTTASKYVGFGNPNYERRTEEEQGSDFWNTLQ
SGWSSFSSGASSLASQTGQGLSKFGSTVNQNVLKPSAAQASKFGHYVNDSVIQPTRQKAQEGHLWTDMSSSASQFATKVK
VSGEKGWTGFSNWIQSSFKTEEGRENQQEEDNHEEREEEEEEEEEEEEEEEEEEEEEEEEEERVQSTKKNLLIDFDEEDTPV
IKNEPTQDLLIDFNSDAPPSDSTTSKKSSKGKKETVSSGGGDWDGWGDNWGWDSSSSNRKSD
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE

A0A1Y1I0U0 **A0A1Y1I0U0_KLENI** (679 aa)
Plus3 domain-containing protein. *Klebsormidium nitens (Green alga) (Ulothrix nitens)*

```
MSDLEDELLMVAGHSKAGGKRGGSSRRQSKPSKRRRVARDESDEESEEEEEEEEEEEEEEEEEEEDSDADVKGKKGKGG
SKMPLKKRFADKDDEEEEEEEEDGERKDDGYDSELSFGEDLFKDDEDRAKLMAMTELEREMLLAERSERRDEVLERRALR
DQARQRDEAAEKAQKAKQRSRAAPPTRSKLSTTREAPRSKEKASALEELVARRNRAVEGGNRRRAEQDRRRREESMSPKR
KGRESDEGSSSDSDRSDEEDERARSDDDDEDARSDDDVRRGRRRPDPDAMDEELDKIVVKRVWLEQHCYEPYFDDLIRNC
LLRLSIGQGPSGQNVYRIVEVVDVDSNPANKPYKFGKGSIARRLTCKWGVAERSWPMDQVSNQRPSSKEWNEWRNELEKR
AIRKMSKREVAEKREALMSAMTFQYTSEAVRNMVLEKQKLRRTPVNAAAEKARLEKQVQAAKDQGRLDDIPELKAKIAEL
ELFIKNREGGDRLTKMLDLNKRNRQKNFNQDGLKASTDASAGGEYDPFSRRWTRSQNYWQTRAAAEVDETALLTMGEVAE
ALPQAGDPGVVSLEDGLAITKAQVAQAANGDLLVQTEAPVDPKANALRVHSFDLPIDLEGLAKWQPVGAGQGATAGAAAA
AVLARKQRIEAKYGAPIGVPRDGRRSLKITDYKRRRGLT
```

47 - 66:	EEEEEEEEEEEEEEEEEEEE

A0A1Y1J9Q5 **A0A1Y1J9Q5_PLAGO** (1094 aa)
DNA repair protein RAD54. *Plasmodium gonderi*

```
MRKCTQRLKRSREESPDRTCITLVRATLLPILSIGKNEKTTLFHPFKNPLPGFVSDKSLYVKKTLGVKVRRTGWINLMKN
SIPRRSDEREIDDQDKNKIDEIKKDFEPLILYENENTKIEVDPILAQFLREHQREGVTFVFECLMNLKDDNISGCILADD
MGLGKTLQSISVLYTLLKQGIHKKPAVRRCLILCPASLINNWNDEINKWLPGRCNVTCVNDNAKEKIVSKLEGFKYDQKS
TVIICSYECFRINNEALDKSSIDMIICDEAHRLKNDKTKTYISIYQLAAKKRLLLSGTPIQNDLGEFFALISLCNPDVFH
DTNLFRKKFANPILIGRDKDATEKEQQIASERLAELSNITNKFILRRTNNLLSKVLPLKYLINIFIKLNPIQEALYVLFL
KNKKILKNENSNNKVNVLINIKKLEKICNHPLLLNGNDMKDAGHIPLSKLIEDVVKEVEKKKTERGSKRRNNSTSGSCNP
VQGKPLTMSVGEDNTTWRDRDRDRRKPVEMDYDKPVKRLLEECKRDIYHSYYNMSCKFQLLHFLLKTIKQETTDKVVIVS
NYTQTLDYMEILCKENFYKFVRLDGGISIKKRHKVINDFTHSSDIFIFLLSSKSGGCGINLISSNRLILLDPDWNPANDK
QALARVWREGQKKICYIYRLFCTGTIDEKVYQRQISKDGLSSMIVTNTNLSKDQMSDENVKKLFNYKMNTICETHDNIEC
TRCNFKNPQGNYSEQLEDFEEEDVNTWAHHQNIETVPDPILVKAVQAATEFKSNDMSNFPLLKKLSNLFITFAMSCKIEF
RDDLIKQKAKQMQIKTEAGKDPTLPGVYSEEGEAEEEEEVEEEEEEEEEEEEEEEEEEEEEEEEMEEEEEEEEEEEEEEEE
EEEEEEEEEEEEVDDEEEDDEKAEEEAEAEDEEADDEEEDDEEADDEEAEEDDPSERTLKKDYKHKIMEIMEYQRIRKKE
KGTNEPKKRIQEENFDIETETKGEEKEKQAHARSRSLPEKDDDKREDHEELSIVRKEANQNNDSRMNNHTKSKSDERIID
QEEQHSSKRITRNMTQKNLMELLSQDEESKVTLSMSEDVDASVENVSTDSSYFI
```

841 - 860:	EEEEEEEEEEEEEEEEEEEE
842 - 861:	EEEEEEEEEEEEEEEEEEEE
843 - 862:	EEEEEEEEEEEEEEEEEEEE
864 - 883:	EEEEEEEEEEEEEEEEEEEE
865 - 884:	EEEEEEEEEEEEEEEEEEEE
866 - 885:	EEEEEEEEEEEEEEEEEEEE
867 - 886:	EEEEEEEEEEEEEEEEEEEE
868 - 887:	EEEEEEEEEEEEEEEEEEEE
869 - 888:	EEEEEEEEEEEEEEEEEEEE
870 - 889:	EEEEEEEEEEEEEEEEEEEE
871 - 890:	EEEEEEEEEEEEEEEEEEEE
872 - 891:	EEEEEEEEEEEEEEEEEEEE
873 - 892:	EEEEEEEEEEEEEEEEEEEE

A0A1Y1JG29 **A0A1Y1JG29_PLAGO** (3091 aa)
Uncharacterized protein. *Plasmodium gonderi*

```
MSIYNNIVDLVRNKKEVIKEEKKQRGLSIGCSKSGVKEKNARGSSCGKRRSGTSERSRQNSKINNVESQLGRNALINNFL
SAEKLIKEIQTLKNVSLGTALYLLNVEISKIEKMKKCEKWENIPYIYQKTANEILLNRKEYIKKIQKLYSQDEKEMTQRK
NPLEKSSNKSVRSRSVHNKKFNEKPSVHFNDLVRSYSHGQVSGRKFVTNFKTSNDTSHNSQMGGKVRNIKYKTKKTSQDT
TACESISRKVNNTVGVEFRKVKKDSRDVTPSEINSSIGRVVKYRGCFYDSCKAEIGPNDSESGPNGFSPNGFSPNGFAPN
GFAPNGFAPNGFASNGFAPNGFSSTGFAKDDSKNKDPSDERRNRSGNCLFYYEQTDKEEIKNKISKEVENKKGEITNGGS
KQKKESRKNILKKKNERNDEDSMKKDVVQGTTCGMQRYNCFSTRKENLHSDSNNKKSSNIYNFGNAGNTLHDGCNLRRMS
QYECFNLKSQSCVNTKKVIPNFERHTVSSFIKNLSTQKKYMQEKKKITQKGKKQKTMKDEEIRLHKSKRALSDFNGLEKY
KLSKVQMMHKFSTMDKLHKLSLLNEFRKFKNLEKLSDTKDKEEDLHMEKAQPYHNSLLGRASPNRGTSSNRGTSSNDRTS
YNCRTPYNCRVSHNSNTSYDEDAAFEELWNSLIDRKTSIMRKLSSSINNKFDLYHIECLNENYSWVKNLRNYNNPMCKTR
QVSFKKDSWITSFSKPVITTMNNRFDHSRKKTKIRKTNTPQSSIIPLTRGGSQSRRKSMSRLMHVGSAPCGNAPHLTERV
CTTDPADGGGDDSDDNDDGGDDNDNDDGGDDNDNDDGGDAHADELSLTMQANREKKTNAPWEEADVEYLKANEATIQKDH
VRHSLNIEDKTPLEKIQKRKSLVKMEQNIMKKLNEEEDLGKSTQNLCSLRHNPPRVYEILINVPKKDNNIGYTESQYYAE
DESDNSSYMIQNNEGEYHANPSRNHMFCTDENYNNSQSKCISLKLKGRQVFQNGLDCNWHKYVNEKLRKVDDTSKEHKII
YERVLPSASTCFGATGRNKSCSMFKVMENNGEVKNAASTNSNLNYNLNTMRNKSLSNIGRGTVQDKFLDNADSLERKYHA
DSLERKYHANSLERKYHADSLERKYHADSLERKYHADSLEKKYHADSLEKKYHADSLERKYHADSLEKKYHVDSLEKKYH
ADSLERKYLEKRQVSQEREEGNTSFTKTMNVYNNFLLRSGNDEELKMVKFGSKEFDQSKIGSVQLHFPKLDASKLDAEKP
YKLSHEGSLNHITKHAAPEGDIFNNLLKSSTEMNNVSRKKNLYDTHKSVERYTNNDSREKARKMESSFLREKYTSSAASQ
ENAKNSEFGTESSADIDMVKGNGLTHQPTLSKTKKGCVLNTHTGIAPSNGNFPGKAESIPYENMKLLMHESCEMEKDHQD
NVVREVYLDEMNRKPTTYSFPIFKNENEKSREKTTISFAEPMSDNYVMIKNKIPIPRLKLGEIQNKKNYNSYEIQEIYQN
```

RNKILDKDATNQLNLMNSRSISKNRLQIHNPARFPIITCNNIAVKGFMNPFINSMNCLTSNNHNPIKQSEDKEDIDTNEL
YLESKYTGKNSKCTHLNENKSISHLHQLDSLPFDVSKENKIKTYPRSFTTDLDIHKENLNENLNKNFNRSRTNLVYPRKK
ASFNRNCSKKVNLPKEEGTGTNISENHMSMKCINNGEIISQKGSKVFNYHSLSMEKKNIPEEEFAHVSASIVSSSIPVLT
KPSINLSKKKKKFFMNGCEDVRCSSIHFEDIQNGGAIQNGEAIQKREPIEKVETDETDTVGDTCTNAMVLNSTSGCTNVC
FCSGNVEGLINKSSEDHEFYDDSSGEPGNDSSYESGGESPYDLDDDPGNEEIMRTNKYVQKCKLSHEEIHSGSFHCKEKH
HQGEERRKFREKEEGGEEDIKCGGNADKKTGSKVWDEDNNTDFKRFDRNVHANEKETKRMQNTSMIMAPPNTCGTLDKAH
ENNTETKKNKSYTRMIMEFFGITSLSKKVETDETGGSKFNGGTCQNGKKTPRSSFVANRGICTLPPMRKTFIRNTKKRDT
NQAVPSNVSRTDNQSKVSPFDNNFCQNVSRMSEKGRRSFSTHCTNFNIIQGTDLCNFRFIPKDAKKIGGNVHMNRYNYNE
ADLRNRIVDLHVSPMHYMRNRTQMKENCNVDVGNHIDRLQSVKFSKKNTALPLINTNRYSIDEWRKSSKCCENINMEERN
LIALNNFSTMIPCKNNEVMMLRAGNKTFLQENENKYINSRFTNFNMNERRPAEEIPHSNFALQSSNIGNGSSITLANHSN
NRTTREASTQQYQFESNRTRTRNETYNDQNLTDISDRSPLHLSSQMKNIQNGSNIDEINNHNFDLKNIDIQNMEAIPSPS
PPIEFGITQSKQNPFVHEPIIMPYKQINLTKELKKYTNDVVISNMDYTNDEFSMNLNSKPFPMHGFNAGMNGINENSPAN
GFKNRCEEANHFIQKDMKGGIQPINASSMQAHQDVQKKNDEPRMEFSSNGPVIPRVHNCQIAQAQVREEAEYVEDVEDEE
EEEVEDVEDEEEEDVEDEEEEDVEDVEDEEEEEVEDVEDEEEEEVEDVEDEEAEEEVDEEVEEEVDEEAEEEEDEEVEEE
VDEEEEEEVDEEEEEEEDEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEEE
EEVDEEVEEEVDEEEEEEVDEEVEEEVDEEVEEEVDEEEEEVEDVEDEEEGDVEDEEAEEEVDEEAEEEVDEEAEEVDEE
AEEEVDEEVEEEVDEESEEEVDEESEEEVDEELEEEVDEELEEVEDVEDEEAEEVELEIDVEDSEIEGSGKESKVDYDMK
ANGGPQIDNNSSFYNNVSIQNIFHQKSTKSVQENGDLDLYPKGSLHTINSNDAMKRINGALTLHDDGNFISSSNESNSDN
DKHVLYKDMSNKIPRSETFHNDYVTEANNYEDLNKDYKGEKHINVKSVNENNYHHAETLNVCNTTSSHKYMNDIAKQMKM
EKENNKELKKKLQKQILIQRDLVRMKEQQQVYLELLKKNDAQNQMEKEPIV

2667 - 2686:	EEEEEEEEEEEEEEEEEEEE
2668 - 2687:	EEEEEEEEEEEEEEEEEEEE
2669 - 2688:	EEEEEEEEEEEEEEEEEEEE
2670 - 2689:	EEEEEEEEEEEEEEEEEEEE
2671 - 2690:	EEEEEEEEEEEEEEEEEEEE
2672 - 2691:	EEEEEEEEEEEEEEEEEEEE
2673 - 2692:	EEEEEEEEEEEEEEEEEEEE
2674 - 2693:	EEEEEEEEEEEEEEEEEEEE
2675 - 2694:	EEEEEEEEEEEEEEEEEEEE
2676 - 2695:	EEEEEEEEEEEEEEEEEEEE
2677 - 2696:	EEEEEEEEEEEEEEEEEEEE
2678 - 2697:	EEEEEEEEEEEEEEEEEEEE
2679 - 2698:	EEEEEEEEEEEEEEEEEEEE
2680 - 2699:	EEEEEEEEEEEEEEEEEEEE
2681 - 2700:	EEEEEEEEEEEEEEEEEEEE
2682 - 2701:	EEEEEEEEEEEEEEEEEEEE
2683 - 2702:	EEEEEEEEEEEEEEEEEEEE
2684 - 2703:	EEEEEEEEEEEEEEEEEEEE
2685 - 2704:	EEEEEEEEEEEEEEEEEEEE
2686 - 2705:	EEEEEEEEEEEEEEEEEEEE
2687 - 2706:	EEEEEEEEEEEEEEEEEEEE
2688 - 2707:	EEEEEEEEEEEEEEEEEEEE
2689 - 2708:	EEEEEEEEEEEEEEEEEEEE
2690 - 2709:	EEEEEEEEEEEEEEEEEEEE
2691 - 2710:	EEEEEEEEEEEEEEEEEEEE
2692 - 2711:	EEEEEEEEEEEEEEEEEEEE
2693 - 2712:	EEEEEEEEEEEEEEEEEEEE
2694 - 2713:	EEEEEEEEEEEEEEEEEEEE
2695 - 2714:	EEEEEEEEEEEEEEEEEEEE
2696 - 2715:	EEEEEEEEEEEEEEEEEEEE

A0A1Y1JI19 **A0A1Y1JI19_PLAGO** (388 aa)
Casein kinase II subunit beta (CK II beta). *Plasmodium gonderi*

MEEGMSNNESSNGVLDEESQEDERDLSYSTFCNQEEGRDLSYDSFCNQEERGNISDNSSYNQEEEIKCQKNEDHDGCANA
GNYLDDCNEPKGDVRDKENDADGGQNEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDDDDDDDDDDYDDDEYDEDDFNEATV
SWIEWFCQLKQNVFLVEVDEDFIRDEFNLIGLQTKVPHFKKLLKIILDEDDDDDDDDDEEDDYDEDDDEINRGSDELYKN
KDIYEQNAACLYGLIHSRFILTSKGLALMREKYKSSIYGTCPSIYCDNAKLLPTAISEVPKFLSPLLYCPRCCETYYPHK
NSLLNELDGSYFGTSFASFFALSFNIQSDKKRIYYTPQIFGFTINRDIRENLFLDMNKENTESLEEYS

107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE

111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE

A0A1Y1JIX7 **A0A1Y1JIX7_PLAGO** (4503 aa)
Uncharacterized protein. *Plasmodium gonderi*

```
MNELNPPYVSSITFINSNGVIITTEIKKANKRIQGNFINDNEGNYVFCEKDIDHIKNVVLTLKPFHKEYESNILFRIKKK
EDKYRCEWVLLLKTLKEDLIKQKIDTFIDIDRKNNYEKQVLDQVYVRDPEPISDKEEVEEKTFDCCDIKDIVLKYVYCIT
YFDNYIINLRNEIGIIYNSDNDNFLNQLIKINNDFTKKNNKRKDDSLHTNVNIHHDKKFINHHDVNENGNKLNLYNYTFK
SSQNKHMELAHSTQTSNHARSTSGSGPSGGNGCNKINNCSRDNYENYESYENYESYENYESCENYESYENYENYDNYENY
DNYENYNNYENYDNFDNFDSVNSCNNLINTNVKSNICDGLSNLTIHNRSNDTSVVDMARANCDNSDNELNEKLCSKSNTE
KCSLIKSASEHSNENWNVSTYTEESVPSIANSSLNSSARTDMNADINTDINTDINADINLDINADINADINADMNADMNA
DMNADINADMNADINADINADINADMNADINADINADINADINTNYDYENYLATPEPFKKDNDHRAQDHEKTLKNDNKEE
LEEEGEKEKHLCFLKKFFYSKFGFEKSNKQKDKNKNVNSRNLSVKNENNNYSLKKVEDEIRDYAGANSFVHGEKKETINM
NPHEKDRNYKGDKTSQRLEDEGDDEDENNNIIINRDQNNNSSSSSSSSSSSSSSRSHSSNSIKNRNSQCNSNNDDDNNNN
NNNRINNSNISSDNKSHSNNRDNNKEKGAIFNKGKRDDETTAINVQNGAEGNFYVLKEKKKKTNNNTFTNVEDIRTELVN
FLKENEINEKTNGGKTNKNDNLRERYYLQRSSNENCVHNENINMLDKISSDKLLNILNKKNCSSVKYDFFHQENMHSSIP
SLVNFQKFSDGSVGTNKKWNKGSNSGNSNGRTLDRRRSRNDKGIGGSINNNNDIMHREICRTQDGTDPIVNSEDDADVKL
IKLIMQKQMKNKCTRGEGEDTIKHCKNMLSEHISGNGNKRKVFFEKGYKEEEEKDNLYMNDELVKDTTRSDDKCYNHDHH
PQHLHYPHHQFGEIVEMKKKGFANTTVSTNDKIKDSFFNVKDYINNNSSKGMSSTIINSKMSNDINALVSHNGDGNFNKS
KDDFRIRKRRDYYNSEQNDFIHYNIIKQKKEFTENKDEKRSKDFPYENSTTEILKFMLQLIENCRSTKADMNEFTNSSSV
SNDNNDRNDCYVNNDYNDTLNNLLTTLIKNISPMEMNNLVINKEDAFSKISNSSKIAKDRKTNVKCDNEQSYINVNKKEI
PWSFSPLCNNTDTTDNGNNNGNNNGNNNGNNNGNNNGNNNGNNNSNNNSNNNGNNNSNNNGSNNSNNNSNNNGNNNSNNN
GSNNSSNNSSNNSSMLNTLNKSNIINNDYESDFCNNINMENASLNNICKQEIDHKFLNNSVRNEIELENEHCSGIVNIMN
FIRDTMKNNFGDIECVNDFLQQSSSSSNSSSSNISNKAKVEEDNSKRYVPPSGSACIAESFNPLHGYDGSEMKEVLLKGK
TQSNSVEIKRIDDIVSVSDVKNNSSSDFEKNSNSDVNENNAHSNIVDSTINDSSRNRNNSSNNNSNNYITCGRYPNVCEE
LCSKNCNNLCCNSIDSKDSCNIPQEYNVSNSCEAHNNTKQTFNISDENMDLLYNYYLQACKSCMENTKKNTHNDKNDGIA
RVDTENGEHRNREKHMNITSCNNKGFIYRESKKVLSSRCSNSIHCDNNNHNKKGIKNTIDNTKENMNYSVQNVCNNVNAN
NSVCDNNNFDMNLSDNYKNQKNVTDQVNSFFHNCLFNLKNMNDIAVCDSSTNPENDENIIDNSSSNNGSHHSSNYSNSSS
NNKTHGEIDGRIKSNPKINNNLKKSNENLNEISNINDKHYLNQNNYKGEENNLIRPGDLQNIQSSNFLKDIRMKETFDNT
KKVVRTDESSGLMHTGNGKIILNEVNDVDHFNDLNSLDYTMDTEKMDIYHNFDSDFSALMNNYENNENPLHYQKSIMKIV
EHFSTQKKSNIHSFQTSMGAGSGCNTADKHSDEHILKTILINMIKDFSNSKNENCLTRNTFTSKNSKGEKGSNRNNTNAQ
HKGYNNQHKSHDDCDRHHCHNEHKGDMDHNNHEGYIDHMDYIDNNGYNIHNGHNMHSSCSSHLSNENNESSNRCSNICSN
DCSNICGNECSNLFLSSCESRKRNESSLPPKKSASKNNRNASKNNRNASKNNRSASKNNRSASQNNRRASQNNRSASQNN
RSASQNNRSASQNNRSASQNNSSANTAYNNFQNNMSSNINFQTSVDAFNNIYNNLVIRNNINNSNNYYSNYCQNNIININ
NCGGNNYFYNNSRDNKSDNNMLKEGNEMLDAINIQEGMMCNSNNNMDFTAPSNIIRRIQKKNVSAFHMSEYKDSLSDDPS
LLYQNKSYDSDKSNGNDEKDVIFSNASTDETNVEKQNNDNIISDDRFSAEHPSVDMSNDSKININEDNDDDTNIDETNID
EPNIYEPNIYDPNIDESNIYDPNIDDPNIDDPNIDDPNIDDPNIDDPNIDDANSYEENIFETNIVSSNISDINIDIVNTF
NGNECSAKLYDRDIYGDNSYTGNTYSNENLYLVDNNNEDTNNYEANNDDTKYDENNNITTNDILEEEEEEEEETLLVQGE
NMLLQNVKEIEMGKNEIISNMNTEKQEFHKTKGIGNDNWKNENIRDEENNKIADSMLSSFYYGDISMCSNMSGNKFDNQR
ENNNTAVLVEDDLDPNKSSHIEMKKKEIFDEFQMKNKKKYSFIFNSCIEDYSPISDVSNYAFSSSILNDKYRNKNCILDK
LCSGLKDEEATKLRETRLGEIKYSCFNNSAENSFFREDEKNCKFLVDLKNLNESYLKDLLHQKMWYRTAMKSDEEEEGRE
KQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEQSHQPHQLQQHDKSKIESSNMHSTKRKLKEYIDHDLH
YDSMNLNTNLEVNIKNNIYNHFSSYSSLNINFFCLFDDMYDNFFRENFEDREKMLKILNLNKDLCYNQLLMFYKKKIFFK
CKNENNSNLPVCPYPFFNHLPTIVNTKGSNRSNNSDSNNHYENNAMIHYPSDFMNNVLINKERHYSHESKQLDYTTSMYR
CISTEVGSGGICEGERDNNINSTNNSSNNSSNNSSNSSNNNNSNNSSNNSSNNSSNNSSNNNSRDQSDVIYNSIEE
HSVNEKKTCVDFPLQIKEEMSCFKKVINELKDFQNIINNKSQLKSNNCMDCIKDESINETDDMTDIPNNEEIDTDEKKGR
NSVSLDIANTTEGDYRDMLQKEQKNLNTSIRNEEFSTDTMMMNKQRLFQAEINAPSGEQISKNELDIEFDKVNKVTSINK
VIKPKEEKMKTETKEEITETKKSSDTYAGYVSDNSFDSDFAHEQVESVLEPVLRTSYNCDDNSGNGRRDSNGSNDNNDGG
DQCVGSSHKSQDETSPSSNAFMEFEINIDCSEEENDAMFKFIYHKINCIRNNMWMQSIDELQNKEIKETLLKVREKNCSR
KGSDIYNDKELSKNEIEQEGGVEGRGMLHLRTQEEMEQIENDNNIPNDIYYFNIYTNLWENVDLNVSHKLLETLKLKKKR
INRYYKNNYYKNMNFITFTEWNLYNLIISKIYKSFDLKKYEDYQLKIYNMDKFQYELKKRSTYNFGIKIIGDSNGTRRTV
SHNNNGKENGSKVKNKQNNTKSRRASKKSEEYSDFNNDDDYYMEEEEEEEEEGDGEYELHGLEDDVKEEVDEEILPHDED
EVEEQNDCTELEEQGNDSKDFLLISERGGGGIGSSREIRREKGSRSSGKDTMIIKDTNNLNHEDTENNTASTTKNLRSNI
TKNYSSGSRTFCKSKNKNVNRLCVSDKDYQMYNNCADQKGIKEAREDNITIDPCEEDPWNKRIKNAFNSSEVKQHVADKV
NDNRMSTGMSLRRKKRNSTLSGNSTENGIITTNKRKIKKLKVSAKVDRYNEKKITEPNSRHMNICSDGGGDTDGINNMNS
IYIHRNSSGNKGSNTGYSKLKRVQIFKKRLSQKRNLNPFMDKKQNVYHLIQLPDYVSHKELIKSKNDCLPTYILQYEQLK
KNECIYFNIQNHYNNFINNVYHFAISYEQSLKHNEYLNNTLNNVKARLYIKRLYLKKNVTLKDNIFDVCNTYFNDLYTYD
TLSNTYVIYKTKKLRMNKLEKTINNQDYYSMYVNDYIESELLNKRKRGKKNYTSNLLCKDDSNKLANADGNDPMLKQLTN
MHEIENTYEQKNVYEDATSCEQDNAFEMVNNYANSHDNVREIQHQNEVVGNQDMDIGRNNNTDSVHCTHSTFNIQYIQEN
NENNKNGDTGNGGRDHVDHGVNKNDNRRRNAYGEDNLIQKDHELCNQLDCLNYFVDNVEDDYECNGGTCKNVMSFSDRTI
EEELGDMEQDHLEEKNMFKVKQNGSIAPDILSTYTNHFDDGNDKSHFNKTNETFFNYHNQSNNRTFFQESDNGKSKNYNN
KNKEFYFNGNINHDDIIQYIDIQ
```

2883 - 2902:	EEEEEEEEEEEEEEEEEEEE
2884 - 2903:	EEEEEEEEEEEEEEEEEEEE
2885 - 2904:	EEEEEEEEEEEEEEEEEEEE
2886 - 2905:	EEEEEEEEEEEEEEEEEEEE
2887 - 2906:	EEEEEEEEEEEEEEEEEEEE
2888 - 2907:	EEEEEEEEEEEEEEEEEEEE
2889 - 2908:	EEEEEEEEEEEEEEEEEEEE
2890 - 2909:	EEEEEEEEEEEEEEEEEEEE
2891 - 2910:	EEEEEEEEEEEEEEEEEEEE
2892 - 2911:	EEEEEEEEEEEEEEEEEEEE
2893 - 2912:	EEEEEEEEEEEEEEEEEEEE
2894 - 2913:	EEEEEEEEEEEEEEEEEEEE
2895 - 2914:	EEEEEEEEEEEEEEEEEEEE
2896 - 2915:	EEEEEEEEEEEEEEEEEEEE

2897 - 2916:	EEEEEEEEEEEEEEEEEEEE
2898 - 2917:	EEEEEEEEEEEEEEEEEEEE
2899 - 2918:	EEEEEEEEEEEEEEEEEEEE
2900 - 2919:	EEEEEEEEEEEEEEEEEEEE
2901 - 2920:	EEEEEEEEEEEEEEEEEEEE
2902 - 2921:	EEEEEEEEEEEEEEEEEEEE
2903 - 2922:	EEEEEEEEEEEEEEEEEEEE
2904 - 2923:	EEEEEEEEEEEEEEEEEEEE

A0A1Y1JNM0 **A0A1Y1JNM0_PLAGO** (2073 aa)
Uncharacterized protein. *Plasmodium gonderi*

```
MNKMKSDEKRNTHDTNLKNKSSGKQALASVEKKKNANNDHSNIDDSKNNGKQKLEGNSESDMKKKNEKNVEKGGHKNSEK
NVEKGGQVKNKSPSSSNSRSKLDNARTIEKKESIKGFSNDSLKVKSSNSRESIKSFKSNKNEKGRDEGGTEGEYKKEKIL
TNGDKKKKDHSTDKHVVKVSNKLISKNSNSKSASNSDTVTTQNSNGSSKGSDEKVKKNLFASSSKEKMKNITSFTNHSNN
SNNRNTTNATNSRNTSNTSNISNNRNNSNSSSNQNSSSKGGSIKGESKNDVSKSGSSKSGSSKNDASKSIPSKSAFSKNG
SSKNDTSKNASSKIDAQRSDSLKCDSSKNEVPPPINKSSKSCLSRNDSIKSSSSKNLTSKNDSLKSNSTKNLSKSSSHET
INNENHKKVKKSETSSNNNKVVRKSSETAKEIVSNNRSNSKEGNSKTSKSSKDVKKNIKTEKEKNGKSVSESDDNLNVHE
SSKKKKSNASSRESETMKNKNSKSSKSFVVTDSNRKKDLTKKGSSGQQKNNKKSNSVKDLRTHTKSSKSKTSMKEKKKSA
KYKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDIEEEEEEDVEVEADEKEGEEEEEAEETEEEEEEEEEEEDDDDDDD
EYHEGKKRRLSTSSSKQTMKKKINATKTKKKKKRSSFSLKKKKKKYLKVNEQESSKSKVVKKEEVKKEEKKKKKSKKSVK
NENVSLKDVEEEENSYFDDNEYSENARKIALEERERKRQLKENYIKQMKLPTYADDESILFINNPNYVMVLLFLTVYKDV
LKMSWNFKDIDEMFQNKETTEFGRNFILKLFFFLGRYFNSKSIFMYKYISRIFEDKQSSLMRVVNFNELFPVIEGRKEKK
NKSGSGGFLGGSSGVNSKKKKDKKKKKAKAVIAKAEELFDAETIEHAYVNEFDGEEKDENDENDEIDDNDENDENGENDE
NGENDENGENDENDDHDDGEERTEDENRVGRVDRENKKINKTRPSDANEKSMNQYKDEQSAVLASEDEEDEEEEEEEEEE
DEERKSDKNNLSDELNEKRRDIYASNFSNKTENDPFEKELGDDKLKGATKNIGNFDIGDEEEDNVENDASEMTKGVDSMK
MVNSNGTASLEEMIKGDNNNPCGEDEKYKEASNEKYGYRDSLNSVRSEIKKNDVNGVNCENEENVENGENANKDGLSKKL
FFEWDDLNVTSKLRIIRMLLNLVLCESNNLKKMLIAEKIDYNNGYLGKINNDKYWFILNDTVNIEFKLYIEKEEKGIFEF
LCDDDDVLYNIGYNLLKDSETKIMGQTIIDRYNKICRERRNRSRILKQQKKLSTDFNMNNDLLLTSKKRQHKQVEYFNFD
NDKMRKKKNENGAYNSSGMHNNSGSYNSYTSNTNNPYSVQKNNYQKNDRSFRLAARNAQKGDSLVADFDASENQDFFNNG
NPMAGLEGIINKGVGGVIIGNGADGVTGVGEAAIAGVAGVAGEGGVVLSSLNSVNSNIGSGTIFSTSGTTAGMNNPGAIP
IMGENNVVVKVPQKRGRKKKSEKKKRGRKKKILPEAEMGLAAGGLGTDPNNPLGIMSSKETKKSLSSTPRVRKTPYTKRN
IKPTVSIKYGTRSHSISKNESDPIQFNDFSLTHSLNNEHFYKNENMMDSKFFNPNISNPYNMQNNLLNMRGNKLAGTPGS
YNFPYMYNPQLYNQYYMYNGNMYMLNNNPGGNHLFSQKSAPPPLGAGSNIPIGGSNVPIGGSNIPSEGSNVARSGTSMNS
LGSFNSAIGSIGNGQGGNNSSSTDNGKDIKNECTFMTKRSTLKGTTTTTSSLNSMNGTGTKGAMSSNDPDNQMYNEMNGA
ERDVAVAMNGPMSSPLKGSSSNPLSNPINNHLNMINSVNAMEGGGGGGINNSMKYMDPMVNNNNHLNKYNPYIMNRNAMN
NIASNPMYNNMYNLKFPYLNNDMMNYNYNLNNFQNMNFEKMNKSGMYKRYPNFMGSSFPIPYGNMNSNPYANLNTYNLNY
QRNDQFGLIPLPGGSGQSGGAGGVGNFKNKITRPLPSDNGTLTETLNDSIPIPLMGNENNHMVDVKGKSSDHS
```

564 - 583:	EEEEEEEEEEEEEEEEEEEE
565 - 584:	EEEEEEEEEEEEEEEEEEEE
566 - 585:	EEEEEEEEEEEEEEEEEEEE
567 - 586:	EEEEEEEEEEEEEEEEEEEE
568 - 587:	EEEEEEEEEEEEEEEEEEEE
569 - 588:	EEEEEEEEEEEEEEEEEEEE
570 - 589:	EEEEEEEEEEEEEEEEEEEE
571 - 590:	EEEEEEEEEEEEEEEEEEEE
572 - 591:	EEEEEEEEEEEEEEEEEEEE
573 - 592:	EEEEEEEEEEEEEEEEEEEE
574 - 593:	EEEEEEEEEEEEEEEEEEEE
575 - 594:	EEEEEEEEEEEEEEEEEEEE

A0A1Y1MV05 **A0A1Y1MV05_PHOPY** (391 aa)
Uncharacterized protein (Fragment). *Photinus pyralis (Common eastern firefly) (Lampyris pyralis)*

```
MSDDEEVYSEEEEEEEEVVEVKETGDPEFVKRQDQKRSDLDEQLREYITEWRKQRAKEEDDLKKLKEKQAKRKVTRAEEER
KLAERKKAEEERRVREIEEKKQREQEEKRQRLEDAEKKRQMMMQALKDQSSKKGPNFTIQKRDPNSALSPVQLERNKTKE
QLEEEKRISLSIRIKPLNVDHLSVDKLREKAVELWDLIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLD
PEALTGKYPPKIQVASKYERRVDTRSYGDKKKLFEGGYEEQIKETHDKTWNDRSGQWDARLKARLPKWFGERPGKKAGEP
ETPEGEEEGKHIEEEEDLKEPVFEPEPADEEEDEEIEVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE

367 - 386:	EEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEE

A0A1Y1MV06 **A0A1Y1MV06_PHOPY** (379 aa)
Uncharacterized protein (Fragment). *Photinus pyralis (Common eastern firefly) (Lampyris pyralis)*

```
MSDDEEVYSETGDPEFVKRQDQKRSDLDEQLREYITEWRKQRAKEEDDLKKLKEKQAKRKVTRAEEERKLAERKKAEEER
RVREIEEKKQREQEEKRQRLEDAEKKRQMMMQALKDQSSKKGPNFTIQKRDPNSALSPVQLERNKTKEQLEEEKRISLSI
RIKPLNVDHLSVDKLREKAVELWDLIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKI
QVASKYERRVDTRSYGDKKKLFEGGYEEQIKETHDKTWNDRSGQWDARLKARLPKWFGERPGKKAGEPETPEGEEEGKHI
EEEEDLKEPVFEPEPADEEEDEEIEVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

347 - 366:	EEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEE

A0A1Y1MV09 **A0A1Y1MV09_PHOPY** (398 aa)
Uncharacterized protein (Fragment). *Photinus pyralis (Common eastern firefly) (Lampyris pyralis)*

```
MSDDEEVYSEEEEEEEVVEVKKVEKKVEETGDPEFVKRQDQKRSDLDEQLREYITEWRKQRAKEEDDLKKLKEKQAKRKV
TRAEEERKLAERKKAEEERRVREIEEKKQREQEEKRQRLEDAEKKRQMMMQALKDQSSKKGPNFTIQKRDPNSALSPVQL
ERNKTKEQLEEEKRISLSIRIKPLNVDHLSVDKLREKAVELWDLIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHK
ALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYGDKKKLFEGGYEEQIKETHDKTWNDRSGQWDARLKARLPKWFGERP
GKKAGEPETPEGEEEGKHIEEEEDLKEPVFEPEPADEEEDEEIEVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

366 - 385:	EEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEE
379 - 398:	EEEEEEEEEEEEEEEEEEE

A0A1Y1MV21 **A0A1Y1MV21_PHOPY** (398 aa)
Uncharacterized protein (Fragment). *Photinus pyralis (Common eastern firefly) (Lampyris pyralis)*

```
MSDDEEVYSEEEEEEEVVEVKKVEKKVEETGDPEFVKRQDQKRSDLDEQLREYITEWRKQRAKEEDDLKKLKEKQAKRKV
TRAEEERKLAERKKAEEERRVREIEEKKQREQEEKRQRLEDAEKKRQMMMQALKDQSSKKGPNFTIQKRDPNSALSPVQL
ERNKTKEQLEEEKRISLSIRIKPLNVDHLSVDKLREKAVELWDLIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHK
```

```
ALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYGDKKKLFEGGYEHLLMENVEKSWQTKMDEFMSRSRSRLPKWFGERP
GKKAGEPETPEGEEEGKHIEEEEDLKEPVFEPEPADEEEDEEIEVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE
379 - 398:	EEEEEEEEEEEEEEEEEEEE

A0A1Y1MY72 **A0A1Y1MY72_PHOPY** (379 aa)
Uncharacterized protein (Fragment). *Photinus pyralis (Common eastern firefly) (Lampyris pyralis)*

```
MSDDEEVYSETGDPEFVKRQDQKRSDLDEQLREYITEWRKQRAKEEDDLKKLKEKQAKRKVTRAEEERKLAERKKAEEER
RVREIEEKKQREQEEKRQRLEDAEKKRQMMMQALKDQSSKKGPNFTIQKRDPNSALSPVQLERNKTKEQLEEEKRISLSI
RIKPLNVDHLSVDKLREKAVELWDLIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKI
QVASKYERRVDTRSYGDKKKLFEGGYEHLLMENVEKSWQTKMDEFMSRSRSRLPKWFGERPGKKAGEPETPEGEEEGKHI
EEEEDLKEPVFEPEPADEEEDEEIEVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE

A0A1Y1MYN7 **A0A1Y1MYN7_PHOPY** (391 aa)
Uncharacterized protein (Fragment). *Photinus pyralis (Common eastern firefly) (Lampyris pyralis)*

```
MSDDEEVYSEEEEEEEVVEVKETGDPEFVKRQDQKRSDLDEQLREYITEWRKQRAKEEDDLKKLKEKQAKRKVTRAEEER
KLAERKKAEEERRVREIEEKKQREQEEKRQRLEDAEKKRQMMMQALKDQSSKKGPNFTIQKRDPNSALSPVQLERNKTKE
QLEEEKRISLSIRIKPLNVDHLSVDKLREKAVELWDLIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLD
PEALTGKYPPKIQVASKYERRVDTRSYGDKKKLFEGGYEHLLMENVEKSWQTKMDEFMSRSRSRLPKWFGERPGKKAGEP
ETPEGEEEGKHIEEEEDLKEPVFEPEPADEEEDEEIEVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE

367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE

A0A1Y1WVY6 **A0A1Y1WVY6_9FUNG** (1495 aa)
Uncharacterized protein. *Anaeromyces robustus*

```
MTLNEDNINSTSHPLKRKFETIISNINNDNDINQNPFKPKDEQFIKRLESFKSSTWYLKPKQLNSLACALHGWWNISENK
LECSECKARLFITLNLNDKDIDSHLINKYHKQLKLSHAKSCKMHWHSCNESIYRFPTLPSIRAFNFFKNRINSLLTIEQY
LPKIKKSIMIFNEEKLDKLIYILDLPKTYSKDVIEMVIYLSIFGWQGYSIKGKGYIQCLFCRRLVGLWNFENHNHLSNET
LITDKHQTDRPKHIINLKRLNEILLKRKANENDENINKKLKIEREYSELSNKDDSIIHNNESYCENSEKDIILTDNENSL
DSNNINSIKCNIEYENNSNNKINDINDNNNIADVDQREENHLSDAISSLNEQNFELQINTENVNQEQGETSIKNICDITP
ISNNSENIEAGDISKMEEIINTQRNEINDLIERHDFTIDNSFVSLSEEISDISENHTSGQITISDINIESTNRPEIQSSI
NKKKLIIDNKSIIKDNLQIKNSLNAINVINNNNNVLDSDTIININNDESLNNQNENKNKNKNEIRNSSLKLNNNSMNLEN
SSTLEKSKETNDDMMKLDGNSPFNENAEKNENNLIKNEIKSGKEIDEEIKNELTSNSNKILNSALGIISNFNLNVDDDNK
NKDKSMKNNEDSKTTKENISKQIENVPKLKSNDKNNNERKEIKENIIFGENNSQKEEEKNKINQNKMINIEYQPKFEVEL
VKNKNELDNDIKNNNQINKNENDILNDSLSEKNDKIDDKIVITESIKEMKQESNESGKFNNDKEFKNEIKDDQNEIEVLD
DGDKENIIDNNDSSNQVLSEDKDEDDAILYENDIKKDSNSMQIQINSESEEEINSDNTSESKSESENISDSESENEVNSK
NLNENESGNESLSENEISESGTESEIEIENENESENVSESENESENESENDSENESVSGNGSENESENENESESDFEMES
GIEESGHEIKVIKDNNRKSQYESLKRDESVNISNRKNENDNEDETVSESESENDSGDEIISESESENDNGDETVSESESE
NDFPKNNLHNNNNNNKNNIHIINSSEADSNSEDELNTYNNSSLYSNEDDDENESSDIDTNDNHSNLYQHNNDSNDIILIE
SDSNTDNLHNSSNEEEEEEEEEEEEEEEEEEEEEEDYSDSMKDDSQNISSDIDNNDHCDNINYRHMFTFKNPIDDNNYRSHD
FNEDEEMLYHNNQNENDIFQEKYENKEDKENDNESENVNKNYEEDNNNYGTMEDNYEENVSISKISKENEKNRNDCDVNI
NEKKKSNKDDKIKKNNTTNNNMEEYNEDNLLDISNQSGLNQNETRFISLIENNDLSSKPESSLNLNGNNNKTSKEKKKEK
EKEKEKEKEKEKEKQKQKEKEKQKQKEIEIEYVDDSKLNEIKKDMENTSKFLNIEKEHRSYCPWINKNDNNEMAGWEITV
NSIIAQLEPKSLLPDDKKMFSMKDTHGLLKHIKSTLSSSIHKPMTSITNKKQKLW
```

1134 - 1153:	EEEEEEEEEEEEEEEEEEEE

A0A1Y1XDY2 **A0A1Y1XDY2_9FUNG** (671 aa)
Uncharacterized protein (Fragment). *Anaeromyces robustus*

```
FNNSNNNNNNNNQYNNSNKVPTNNSYYQKDYNSSNNNSNNNYGRNNNNMNRNDNSYYQENYNNSDNNNMNRNNSYYQKGF
NNNNNNMQINNNDDDDNNNLFYQKKFNDNNMKINNNNNNNNDLFSNNNNYNQKMNYNNQNRNIKYENIDQKQLNRNNDSF
NNDYLDKADKFNNNNYYNNSNFNNSRNNFNTNNNYENNISNNNNNNNNNNNNNNNNNRNEIGMILNNDENDDINKNNMNQ
LITRNNNNNNNNIKNEFLSNDNQKIQPYEDNRYNINKERKDNKTSIANIVNENENVNGDIEKNTTIEKINNKYNEETENI
MITEMKESLNQNLKSKNNQSIDKETKTKNRDSKTSIKMNIDEEDINKNINENENGDEKINENKDENENENENENDNDNEN
EDINVVDNEDDNENEDEDEDEDEDGDENEDENEDENENENENENENEGEDENEDENKNENEVEIEENKNENEKVIEEYEY
SLDENEDESGKSLNDEIESKKGKTKKKSKSKHSKEKIDEKLSSKKKDKKRNKRKSKKHSKNKKYSFNSEDNDEEEKEDIQ
TINESDDIDEIEEEEENSNEEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEKEEEDIQNKKKLSKKNKKDKKKKLKEKHMK
YVEEENEVDEDEVEDDDDEEKKEKSKRSKFR
```

589 - 608:	EEEEEEEEEEEEEEEEEEEE
590 - 609:	EEEEEEEEEEEEEEEEEEEE
591 - 610:	EEEEEEEEEEEEEEEEEEEE

A0A1Y1YL03 **A0A1Y1YL03_9PLEO** (134 aa)
Uncharacterized protein. *Clohesyomyces aquaticus*

```
MITGSALGIKIATLGLACRYVAKAPRDDGPVPPHPMPLDAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEESAREEDEGIENLEEDEDGEDEGGAEKEEDEDEEDEEDEQ
```

41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE

55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE

A0A1Y1YVX1 **A0A1Y1YVX1_9FUNG** (332 aa)
Nucleotide-binding domain-containing protein. *Basidiobolus meristosporus CBS 931.73*

```
MTAVVLGAGVIGLSSALVLQKAGYKVHIVAAQLPGEFHPDYTSPWAGANWNSFAEKDDLKLHEFERVAFNKFKELEQYPD
SGIKSFLGINYYDKKPSDWCNPWFSTFCKEFRNMDKSELPEGTELGFEFQTLCVNTQQYLVWLQKRFQENGGTIEQRKLD
DIRDAFEAAEQVNIVINCTGLQARYLGGVKDGLVYPTRGQVVIVDAPQVNATVIRFGEKEITYVIPRNNGHVILGGTMQA
HNNDEKHDEETAKKIMERACKVYPLLGKPENLKVVKHCVGFRPSRQGGIRIESQLYESLIGTDMWGGEEEEEEEEEEEE
EEEEEEEEEEDK
```

308 - 327:	EEEEEEEEEEEEEEEEEEEE
309 - 328:	EEEEEEEEEEEEEEEEEEEE
310 - 329:	EEEEEEEEEEEEEEEEEEEE
311 - 330:	EEEEEEEEEEEEEEEEEEEE

A0A1Y1ZQ06 **A0A1Y1ZQ06_9FUNG** (163 aa)
Uncharacterized protein (Fragment). *Neocallimastix californiae*

```
MFHVNRCITNIFLTLLYNVSNEKLFLKDIMLVLIMGTVIVKNVKSCNEKLDENFKLNKKQCTDLEKNEKEKRDVKEEENE
EEEEEEEEEEEEEEAVEEEEEEKEETIEEEEEEEEEEEEEEEEEEEEEEEEEAVEEEEEEEEEEEEAVEEEEEEEEEEE
EET
```

108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE

A0A1Y2A4X1 **A0A1Y2A4X1_9PLEO** (87 aa)
Uncharacterized protein. *Clohesyomyces aquaticus*

```
MRRQTEEEATEKDDKEDAGTPVKMRVEARKRRTTTTRRRRRREEEEEEEEEEEEEEEEEEEEEEEEEEEEEGADKAWFR
EKWDNAQ
```

43 - 62:	EEEEEEEEEEEEEEEEEEEE

44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE

A0A1Y2F1G1 **A0A1Y2F1G1_9FUNG** (1218 aa)
TPR-like protein. *Neocallimastix californiae*

```
MKLRDRKKIAKPKVDDTHTVTRRRKRRVPLKKKLKQEKIDEIKIPKIEPIDSENEDKSYVRNSIINRFVKESIEDSVKEL
VGIKTEIEETEESTELSNSNNLNLNINYNTFNNNNNDNKEEKKNNENNENSISSNNQNINLMKDSKKGKEIENDQENIIN
ELINGPYDDTYGADEPSNDMDDNDNEDNLSENEDLIDEEEFSEYYDSDENDFYREKKVKNKRKNSRKGKAPMNSDEEEEE
EEEEEEEEEEEEEEEEEEGDNEYSGNRDEDEDLENENTQIPQKVGEWLFEANKSVGGRNGQFTEYSKDFWIDEDEMDQDQ
EDDLKDLEEEMEEEGKRKRKRKKRSGKDSKLSDENGKLLGKANVAYSNKQYQEAIQYLHSIIQSAPNANQAWFLLAIIHE
ELGEELKAFQFYLVAAHITKKDGSLWKRLGLMAKNLNQIEEAIYCYTKAIHTDNKDFDAVWDRSYLYYEQGNYKKAINGY
IYILKYCPNNTHVIKELSKLYLKTNNVEKAIILFENAIKASDEEQELYKQHLLKKERLKAEKANEVSTSTQETEKGFFDD
DPNKLQPIITSDDEEDDFQFECSIGYEEINMLAELYMEINEYEKAINTIRKRCRILQGREIPEKENMMDDSEFDEDENTP
EHLRLPMELRVRLGICRLYLNQINLAVHHFYYLYKYEVQYYPELYFDVGEAYIERKLYTKALAIFNVMEECEQTNVPITW
SKLAYCYHQLGNLETAVNLYKHVLKYLPDNHDLKLSLAEVYGDLGEEEKALALINEVDAATSKDNNEEKEEPEKNESERL
SIFVDTQKTQVKKQEDESVKIRDNKLYYQKIGLLYPKIGKDEIAQNEFLNTAFKLVQRFQNTKEFYPSDRQKKFTGTKNR
KKRILPSFMDHDEIISHENKEKLPESFQGLSFNEWFEVIVKYAIGLAKTGSANEAQEVLWNASKANVYYHNKERSKALRY
YMLGIALYSKNYIKVCEICRWFINTYPDDLDSYRLYMVTFTSGNSIIQAYASSSSQKFFSRFIKNLKHDENSGKFNNPLV
YVIYGHILHSARSYMQALNYYSKAFKIAPEDPIINLSLGLVHLHRAMQRQADNRHLQIIQGLTFIFRYFKIMKGNQEACY
NVARAFHQIGLLYLAVQYYEKVLEMPSRKELEVKRYLREKQRKLKDGINEVDEEFELYMKQEDDTDLKSEAAYNLSLIYV
ASGSYGLSQQLLRKYCTF
```

236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE
239 - 258:	EEEEEEEEEEEEEEEEEEEE

A0A1Y2G8A3 **A0A1Y2G8A3_9FUNG** (1038 aa)
Vacuolar protein sorting-associated protein 41. *Lobosporangium transversale*

```
MSSIPELGGISATSNDSVTQKQPNVFTSHSDLNKHDEHAADSRNSEEDDGEKEKEKKEEDKEEDEQEKEEEEEEEEEEEE
EEEEEEEEEEEEEEQGEEEEDEEEEEEEEEEEDEEEEEEEDEEEEEEEDEEPKLNYQRLGAGIGDMLKKDSASATTVSERF
LAMGTHWGVVHIMDFEGNENQKFQAHQATVNDLSVDLDGEYIASASDDGKVVINGLFQSENQVFNYKRPVKAVALEPHYA
RSNSRQFVSGGMAGQLILNEKGWLGNRDVILHSGEGPIYAIKWRGNLIAWSNDLGVKIYDTTTEQRITFIDRPGSSPRAD
LFKCRLCWRNDVELLIGWAALVKIAVVKSRPKDQIKAGFPAQYVEITTMFQTDFIVCGIAPFKDMLLLMAYVVDDIDEIA
HVTGAERNVRKLAKRPELRIINAYNEEISSDALTLHGYAHYQANDYMFEYLTSQDMFYIGSPKDLVVAKERDLDDHIEWL
MERERYEEALGHAREAQVYGGSKRFNASEIGQKYLGWLLDRNEYGKAAEQCPSILGQDAELWEHWIYAFAGARQLKAIAG
YIPFKEPTLSSTIYELVLNHFLLHDHQSLFKTVKSFPPGLYNIQNVIAAVEDRLKKDKDNVLLMESLAELYTRDGRADRA
LEYFLRLRRPNVFDLIRGHDLFSAVRDKAVLLMEFDQYLYDQEKKKREEARAKESDKAKDMSEKAEIPQPHDPTAEEELV
KGPAVQLMVQHTEEIPIKRVVPQLKSHPRLLHIYLDALFLRDPHLSFEFHDLQVVLYADYAPGKLIDFLRASNYYSLEKA
YRACEQRDLVPEMVFLLGRMGNNKKALMLIIERLGDVERAINFAKEQNDDDLWEDLLKYSMDKPHFIRGLLQNVGTEIDP
IRLIRRIPNGLAIPDLRPALLKILQDFNLQMSLREGCRRILVSDSVAMADQLQRSQKRGISCSEETLCARCQEPIFIAGE
NRLPGTSISTFVMFFCRHAYHDRCLFMDDQDTMPKMKSTLAKVTLRAKANHAALVRSKRGRTPCPLCVDQAKVDISAR
```

69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE

A0A1Y2GGF2 **A0A1Y2GGF2_9FUNG** (968 aa)
Uncharacterized protein. *Lobosporangium transversale*

```
MADSPTEKPSQAASSLAPGGMGREEEGGGGRVADSTQELQPIIMDTINKLSCTLSFEQISSIEETLQHIKWHKQRHQQHS
PYQQQQQQQQQSQLQLPPQQLQDYDTSIQPEPSGSAQASQQSLLVSSSQQLQRQRPPSLPRTTMPAMRHFMSVMTSASEE
AVTLLPTAPLIKLAEDGVPWLTFAYNTRTSRTLCKIRADIDSIQDITVMDTPADFRSLNCIYVNANGPENCYKGAKARRD
FERECNEQGWKLAYLNPQVLAGKKGLLQQAVNSLRNATVKQRSRRARRREKNLRLAMDTIIASQGSLPNQYQYQHQYQHQ
EKTWKQASEQGLDLAQGLARVGPQREQPQSSPEFHPPSAAQRALQWRPLLVPSLLPQEERQVTMDTTSRSDTAEEPSSLL
PSPKTILVSPTLPQQNLPNLGYFKHVPPYTVTTADLDYYLEFDGFFDGRFQKVHVLHYGIEQVQVDELSLEFKRANAVFP
RSFSDDSQKSGNTRKNRRNNNNKDENEDEDENENDNGGLSGSQQWKVSNARQAEESYLNELGWKLCSLNQAVLGGRRLLL
QQALNAYRRRFLHATCHPRARVAPTLLSRWTIAPSSSSSLSPLLSRLRASQLSTTRTFDDHNAFTRYRLKASRPLQQYIP
DRRVRLKGYSDKKYITVAKARPKFVSPKYGMDCNSFKRKNLTDIKTNGNLGDEEGDGDGYGSEIEDETNFYHDNDDDEDE
```

```
DNIGGGSDGSDGDNSHSQMSLLTFTGNIRTYNLGSGSGSARSRPRINTSNTKLKSFSCTHSPLQRSSERHHYNKIEVASS
MSRPSRRSHRQEHQEDTFRPRKKVRRNDFNELRASQDNDSGERPSKDPSGTDAARTQIGEVENDNISGNDDDEEDNWWMS
RLQNSSYPEDHNFVSMTTEELIDALTTGYSNEVEDEEDEEGEEREEEEEEEEEEEEEEEEEEEEEQEEEEEEEEEEEEE
KVSETDYE
```

925 - 944:	EEEEEEEEEEEEEEEEEEEE
926 - 945:	EEEEEEEEEEEEEEEEEEEE
927 - 946:	EEEEEEEEEEEEEEEEEEEE

A0A1Y2GGS5 **A0A1Y2GGS5_9FUNG** (303 aa)
Uncharacterized protein. *Lobosporangium transversale*

```
MFFIKHCTLTFAIFLATSFVAQAAPVPTTEAPVPVVTSIVQEGALWIDNNTEHIPVINAAEASEGSHGYRRAVNSQPYYP
PGYPVSQAAENALPRIYPGHPVTAAPKSVVALVSKPQEGSKDLVKRRMPVYKDYNEGDEDEDKVKKDEEEQEEDQEEEQE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
PSNEQGHPKKGQSGGKREKRAEEKVGKKGKVHEDTKAGKKEKKYESFLDKIRMNWCYVMFCKY
```

160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE
180 - 199:	EEEEEEEEEEEEEEEEEEEE
181 - 200:	EEEEEEEEEEEEEEEEEEEE
182 - 201:	EEEEEEEEEEEEEEEEEEEE
183 - 202:	EEEEEEEEEEEEEEEEEEEE
184 - 203:	EEEEEEEEEEEEEEEEEEEE
185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE

A0A1Y2GIH3 **A0A1Y2GIH3_9FUNG** (281 aa)
RING-type domain-containing protein. *Lobosporangium transversale*

```
MEDQYFPLVILIEATKEYRASGPTRSLPTPIADSPGLYLVENQAISTFACFNISSEGGFEIKVMKQKVWINSTNYLIQEI
YGFTDSVTSASSKPESSAKQRQKQRHEEKIKAEKKRLSRTMSGVSRAESIANRVDELTMDRPKKMKTRHSSASSMMISKR
SEGSFNSRSTSKPRTRSGTEVDDISDYEEEGRVEGNEEEEEEEEEEEEEEEEEEEEEEEEQNLVLLDAPECVICLSDVK
DTIVLPCRHFCICNECGEVLRRRVPQRCPICRQEKKRRKTH
```

197 - 216:	EEEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE

202 - 221:	EEEEEEEEEEEEEEEEEEEE

A0A1Y2HFN5 **A0A1Y2HFN5_9FUNG** (349 aa)
Caspase domain-domain-containing protein. *Catenaria anguillulae PL171*

```
MPSAAVCVGMTYPPEHETGASELKGCIVDAMRMSNFARSLGIDNVEVLTDRLGFPLVKDQVRSALAKMIVNAEAGDFLLF
YYSGHGGSIDAEDCDEEDGKDECIFLSDGPMVDNEIKEWLLEIPEGVRVLLIFDSCHSGTVADLETGAQTAAEIVCLSSA
TDEQVCLGGMDGSKFTNALIHVILEHTNESWRQLMKRVDAIDGQQSANVTASHPELLDSTWFTTQGSGHALQDYESYESQ
RISRKKPAAGKKPSGAKKPAGEGRNKRQQGSVAAAAESVGRMRISRESDEEEYEEEYYEEYEEVVEEEEYEEEEEEEEEE
EEEEEEEEEEEEEEEEEEQEFDEEEEEDE
```

311 - 330:	EEEEEEEEEEEEEEEEEEEE
312 - 331:	EEEEEEEEEEEEEEEEEEEE
313 - 332:	EEEEEEEEEEEEEEEEEEEE
314 - 333:	EEEEEEEEEEEEEEEEEEEE
315 - 334:	EEEEEEEEEEEEEEEEEEEE
316 - 335:	EEEEEEEEEEEEEEEEEEEE
317 - 336:	EEEEEEEEEEEEEEEEEEEE
318 - 337:	EEEEEEEEEEEEEEEEEEEE
319 - 338:	EEEEEEEEEEEEEEEEEEEE

A0A1Y2LKF1 **A0A1Y2LKF1_EPING** (497 aa)
Uncharacterized protein. *Epicoccum nigrum (Soil fungus) (Epicoccum purpurascens)*

```
MPSYWDIKPQRHNAFTSSTPDSVEIQETDYSNRKHTNWTQHWHNYLNGYYCDIQQPLLLPYSPYPEYSQDAMHHAYTREY
LQWLEDRRRHPPSPPPPPSTPVQEHFDGHLRCILGARPWAPVSTQSEPSPVGSSFWGRPSRLVDLFREPAWASAPASPIC
TLRQALNEDSKPNAEGGAQVLAHTREQQWRDQWGHEPGQSPQYYAAFFRDREPAYSRSEREMWEERERYVFEEEVRRKDR
LRKIREQVQLGPWHGMTRDEKRRGKNKAKRARQRERERAKREARRAADMAEEGEGGRGEERGEESGKGDNGKKVEGNGDE
EGEGEGKEDEVKLKEEEEEEEEEEEEEEEEEEEEEEEEEEKVKQEEAKEDANQDKEGEQERAASDQQGDNPTQEPLHPNP
PPSPPPAPWPPHYCTCFSHLQCAAHSDIPDSCHLCASFYFAGYWCGMEKGWCNFVRFVEESAVKGWGLKVIGPGEGEREW
AVVGWDEEAVGGRGGWV
```

335 - 354:	EEEEEEEEEEEEEEEEEEEE
336 - 355:	EEEEEEEEEEEEEEEEEEEE
337 - 356:	EEEEEEEEEEEEEEEEEEEE
338 - 357:	EEEEEEEEEEEEEEEEEEEE
339 - 358:	EEEEEEEEEEEEEEEEEEEE
340 - 359:	EEEEEEEEEEEEEEEEEEEE
341 - 360:	EEEEEEEEEEEEEEEEEEEE

A0A1Y2MCF2 **A0A1Y2MCF2_EPING** (384 aa)
Uncharacterized protein. *Epicoccum nigrum (Soil fungus) (Epicoccum purpurascens)*

```
MSHNEDTLGDITGTNDNLPQVAVRYPMYVRDGDSILPYGRDPILWGPQDPLDLIGPAGPFDDEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEGGEFWIVSGDGRFIWTGETHAHSRKSHKAQQERQTKFWEFCDAQKAQGTTIVLVDRPV
QEDVGESQFPDALPEYPQSEEVLPMFVTIPTRLPEPALTQAAAVGNTTPYDLHNSKQPRHAQGFATPQSSVPPGTSRPFV
SSYTPRPIILPAAPRPFISPATPPPTESPNTPPPFTSSVPNKVSAIHNDPTPTPPRSTFPSSSPSETSPARNVNDWTDDS
LLRLWISKVVRKKGNEPVLKLFPGHTVDTLQEIWKARRPRCEELGAMWDKAERPKGPIAGWWRE
```

63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE

77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE

A0A1Y2MFM7 **A0A1Y2MFM7_EPING** (553 aa)
MFS domain-containing protein. *Epicoccum nigrum (Soil fungus) (Epicoccum purpurascens)*

```
MTPSEPKAESGQMVANIGTNETPTFRPTPDPTQAGFLTEEEEEEEEEEEEEEEEEEEEEEISRWDKVYNVLTYCPPRCRWN
PDKPPQFSMSMNVLFAFAAGFTVANLYYNHPILNILARDFGVRYEQVAQIPTVMQAGYAAGLLFLCPLGDLVPRRPFVCG
LVFFTATLWLGLCITSNLGVFTAISFITAVTTVTPQLMLPLVGDLAPPNRRAAALSIVVSGLMLGVLVARVLSGTISNFV
TWRAVYWMSLGLQYLIFILLWLFMPNYPATNPGMNYFRILWDILLMIPRHPVLVQACLAGMFCSAPFTSFWTTLTFLLAG
SPYHYDSLTIGLFGLIGIAGMLISPIWARHMTDRFVPHFSILFGLTCSLIAVCLGTYIGTFNVAGPVLQALLLDFGNQTA
QIAQRSAIYTIEPKRRNGVNTAFMVSTFCGQLIGTAAGNHIYAAAGWIGSGSASVGFISAALLVMIVRGPWEEGWVGWTG
GWSLKKKNKDSADGKTSEKTHFGADGKIRDEEEGAVEKVLEEIAAEDGNENPLHADARSEKSSKEDVIRPVQK
```

39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE

A0A1Y2VDS1 **A0A1Y2VDS1_9PEZI** (310 aa)
Nudix hydrolase domain-containing protein. *Hypoxylon sp. CO27-5*

```
MSSPPKTYLDLIKACDKYAIPPRIGMLPVQVLDTSNGADPSSACNAAFLSLIDKAFSFRTFASLTRRRPTEEYRVMGAKY
YPPVRMKRAAAPLLGIACRGAHMTVYTRTAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGKLKIWVPRRSAHLHTYPGKL
DSTIAGGIRADESPFECIVHEADEEASLPESLVRQRARPCGAITYVCTSDAGSGLEDGLMASGILYLYDMEVDHTVVPKP
RDEEVQEFYLLDVQQIKEAMLRGEFKPNCASVMIDFFIRHGIITEDNEPDYLDIITRLHRTLPVPTTPGV
```

111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE

A0A1Y2VX38 **A0A1Y2VX38_9PEZI** (922 aa)
Uncharacterized protein. *Hypoxylon sp. CI-4A*

```
MVDPDNLRTASLYINNQLMSRGLLRDGHNIDFANPEASEGGLQDTMGKIMSVINDLILRRDRDAENRESLSTTLRTLRAD
SQRQTTEFSRQTEKLADTQRRLDSADATERAVRQQLKTAEQTIHRLKDESAKMKTLLSQARAACATEIRKRDRQIDSLKK
AVSDAGRVRGGGRNRDVLSISVTGEIGGDERGLPAGATEAEGYSLRLETNGFLTELARGLSEENEGLLALVKRTVDGLRD
MSGLERSAAVECGNADRRLDRGGADVIVMASQKSADELAAELEGIMEHLRTILTNPSFVPIEEVEVREEAINRLRAGLET
MESRWKDAVQMMDGWRKRMVSDGKSIDMDDLRMGLRLSPVRVRDVEETENVAPMKLSYIQEEEEEEEEEEEEEEEEEEEE
EEEEEYGDESEAGGDNYDQAYGQEQEQEEQRLRSPSPVESLHLVPAPGYENENENEDDSDSSIFQDDIDIDDLDAEEPNV
QVLQESTYATSMDSPPLPAPPQISPLKDSYASGNRGVAGNEYRKRPGDFSTIVEENTRELAAEEEKAPAVPPHLINPQSP
RTQKKSTTSSKRSPTWQDVGAGSTSSYDSPLFGRSGERPSQSDPSRKLFSKPAVNLIQQIQTKSQPEPGNTSNAQSPTKP
KRPLSSPDALGAAAEIKRNSPSPTSSSARQQEGVSTPRSQRTTATQSRPGSASSIRQTIITVPQQSQQLTLMQQPPRSPT
RLNGANSSSRLPRPNTTNPAPQQSPLTMATIAAKLAASEREADAARVRAKLRAVRGGGPRRNPALAAPTTAVSTADSSGS
PSKEVKKEDDKDSNEHSSVDPVKRDREVPTPAAPSSARKQRAARRNQREREATIKEDDRSADELVEPAHNERNGNGTLPS
PGGIHVTKRRRDRGERRTSKVASRRRSTLNPWELEALIQGNA
```

381 - 400:	EEEEEEEEEEEEEEEEEEEE
382 - 401:	EEEEEEEEEEEEEEEEEEEE
383 - 402:	EEEEEEEEEEEEEEEEEEEE
384 - 403:	EEEEEEEEEEEEEEEEEEEE
385 - 404:	EEEEEEEEEEEEEEEEEEEE
386 - 405:	EEEEEEEEEEEEEEEEEEEE

A0A1Y3AX59 **A0A1Y3AX59_EURMA** (238 aa)
Troponin T-like protein. *Euroglyphus maynei (Mayne's house dust mite)*

```
MGKSKEQLLEDKRIAMSFRVKPLDIDGLPVEDLKKKASQLWDMIVQLESEKYDLEERKKRQDYDLKELAERQRQINRNKA
LKRGLDPDALSGKFPPKILTASKYERQVDRRTFNDKKSLFEGGYDAMVEAQLEKMWQERVKEFKEKDKSLPKWDPEHPKN
KETYEPGARTYDVNDEDDLDLLDAFIKPPGFDSAGGEEDSAPTPASKPAPPPAQEEEEEEEEEEEEEEEEEEEEEEEE
```

215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE

A0A1Y3DH02 **A0A1Y3DH02_PLAKN** (1904 aa)
Uncharacterized protein. *Plasmodium knowlesi*

```
MHVLCAYKDRNTPFGNASPLEGRLSTKERVKSKNKDVYRGIMKKMKNQERRSSNDSSVKSKSGGRLGGNSWNIEGEVTHS
RTESLSRRKSEKGGDKNIEEGKSKSSSNTRSKMDTAKMNEKKEDLKNVKMFKNNTSESLKNKGSNSRESVKSNRSRSEKG
ATIEDKKKDESSHSNGEKKRKDSYNEKQEKNDLKVNNKLISKGTKSKNVNGKGNSSSASSTNHSRISASRAGDEKGASSK
GLPSKGSSLKNTPSKSSSAKSTPSKSGSSRSIASRNDTLKNDTPKNEARRNNSTRSLSKNASQESVNSENVKKEKRASTS
SSSSKGAQRSSEDASELMSNHTASSKEEGSRISRSVGKTEKKVKSERYKKGEREKSISGSDSEESKQKSSKKKSGADTRR
SDVVKNSLSGRGKSGVSETTKRKDITKKGSADQKKKKNNSKGGSGKDRQADSKSRKSKGGSRSKGGKDDEEDDDEDDEED
EEEEEVVEEEEEEEEEEEEEEEEEEEEEDDDDDNDDEDEEDDEDDDDDDEDDDEEDEESDPKRRSSSSSKKVTKGSVTKKK
KKRMSFSLKKRNRNRKGTQEDGKKGGNKNSGKSVNKSISKSTSKTSGKSSSKSKKAVKNEKKKNNNNSSNRNSKNNVKDE
NASEDEEEENPYFDPNDYTVDARRSVLEERERKRNLKESYIKQMKVPTYADDESILFINNPNYVMVLLFLTVYKDVLKMS
WNFKDIDEMFQNKETTEFGRNFILKLFFFLGRYFNSKSIFMYRYISRIFEDKQSSLMRVINFNELFPVMEIKRGKKSKSG
GGGGTSGGGNSFKKKKKNDKRKRKGKAEEDVNADAIDDANDDAIDDANDDVNEEVIDEVIDDVNEEVIDDAIDEEEEPDP
EDDENDSENENEVDETIEGDDAEDPPLNEANEVRKKSRNHGKAEQLSSDKLVKEGEEPQGMEEAPLGVAKDGAKREDSGT
TFIVRNENPDGSSTQQGVTTIANTSVADGANTFGGTEENDESANNPNGDHLIDSVKNEELQENRRLSKKLFLEWDDLSVI
SKLRIIRMLLNLVLCESNNLKKMLMEEKVDYSSGYLGKVNKEKYWLILNDTINIEFKLYVEKEEEGTFEFLCDNDDVLYT
IGYNLLKDTETKVMGETIIERYNKICRERRNRSRILKQQKKLCSDFNLNGGSLVTSKKRQHKQVEHFNFDNDKIRRKKNE
GANMHGVGASGYTSGLNASNPYALQKNNYQKNDRSFRLAARNAQKGNGLLVGELLDGMGNQEYVQGGGSVVGVEGALLNN
VDGTGVGGVVGTLSNLQGQNAGALGAGGVVVKVPQKRGRKKKSEKKKRGRKKKILTEGGALIPGASLGGEGGSLAAGLVV
DPNNPLATITQGKETKKATSTSTRGRRAPYAKRNTKPTVSIKYGTRSHSISKNRNETSDFSDFALTHGVNSETLYKNGNL
DEKYFNPNMHVNNFIPPSMNTPYGMQTNVLTMRRNKMEAPPGGYNFPYMYNPQMYGQYYMYNGSMYMLNNGGGGMFNQSG
ASGGGSGGGNGKEMKNEGVFMAKGGGSSGSGTTINNANNLNKNSVGPGGSGGSKGPVSGKDAEGEGSNEMSGSGVAGQMS
GPMTMMNSVGGPDGGLNSGMGGGLNYMDPMNKYQSYVLNRNAMNNMPTNPMYNNLYNIKFPYMNNDMMNYNYNMNNFQNM
NYEKMNKVGPGGPTGQSGGASSSPPSGGGMFKRYPNFLGGAFPPSYNNMNNPYANFNAYNMGYPRNEGGYASIPPGGTGT
GASPSSGGTSGASSFKSKLVDLNASESSSGVTGGTTGTVHSSGAGVSGYHMGNVKSRSGNNDVHGASAIYEKPTQLISSG
ASSGVNPGTGEANQKGETHRIDNLMNYMIMHSGSNADIHHGSNGKNNSSMANTENNVVQNGLNG
```

488 - 507:	EEEEEEEEEEEEEEEEEEEE

A0A1Y5IAD3 **A0A1Y5IAD3_OSTTA** (632 aa)
Calcium channel, voltage-dependent, T type, alpha 1G subunit (Fragment). *Ostreococcus tauri*

```
MAEDSAREENSDDSDDGARASRSIASFERAFERWRKNPRSLLVFAPNSGFREGCRKVVESSAFETAIAGCIVASSVAVAV
VKPKRDGTSEEMWLTIMGYVLTAVFGLEAILKIIARGFAFGEETYLSARWNQFDFFLVTVSLILLPIGGNSVMVFRLLRA
LHVFKIFNRYRSARLVMRTIFRALPLLGDVCLFLLWFVIFFAVSGVTVFGGRLTGRLYGTPPAQEGNASYALPTGTGKEV
CAKLVAEWLGNESLGAAGTYPDAYNSTCNFASWNTNQSVEEYCCDSGVAPYDGFLDFDDAFRSAIVTLNGMTIDGWNELL
NPAAYGVGFVNAFIWFIAVVIVGGFFMMELFTSVICATLQSIVDDDSQEEKEGEEEEEEEEEEEEEEEEEEEEEEEENK
VKDSWNALRERCFIACKSDRFNNVVTGVIMLNTLLMMAQHANASSTFTSTSNILEYTFLAVFGMEMIFKHMAYGIIDYWR
SKENALDGVIVVTGVFSSAMTSQGVSVSFLRLLRVGRAFRTFRVIRRNREFRRIISSSVLGFQDMWPFLVVWMLFSVIFA
IFGFQLFSGLGTLDEERLTFKTFLRSTLTLFVISSGEDSFTVAWSTMVAYGNNFIVFYTIGWILISTVILSL
```

374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE
379 - 398:	EEEEEEEEEEEEEEEEEEEE

A0A1Y5IDZ9 **A0A1Y5IDZ9_OSTTA** (374 aa)
DEK C terminal domain-domain-containing protein (Fragment). *Ostreococcus tauri*

```
KRARKAVETFVVDVAPARASKVEIGRGKGTKLSEIPNVAFRLSKISRKEDILKFIYRVLYKGTPRQLTVKRDIGEFSGWT
FESDGERAVKEDLLMRAYKETLHEILDLFEVPRGSGAEAKKESQVARLMAFLDAPKASGKKSLAEAAEKKKKAKDRQRTT
KSATSAKKDAASGGGLAKHVALIKKLRAENAALKKKIVELTGKEEAEEDGDDEEEEEQEEEEEEEEEEEEEEEEEEEEEE
EESEDEEDSDEEFTAKNPAPKKPKPTPAPAKEAPKSSDAPKPAPPTPKSAPVEPAQPKPLEQTPQPEQAAQQPTKPAPSA
EDLASAIRTMLASADMSEVSMKTIRKDMEAKFGISFADRKEEIKTVVTSFIENQ
```

219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE

A0A1Y5YQA5 **A0A1Y5YQA5_BACCE** (178 aa)
Uncharacterized protein. *Bacillus cereus*

```
MADVKRAKIKLDVENGFSVNSDGDLQEVLKALAEIIQSGTHNGVEVEIQYVDETEVIFTDEEEDDDEDEEEEDEEEEEEE
EEEEEEEEEEEDEEEEDEEDEDEDEDEDEDEDEEEEEEEEEEEEEEEEEEEEEEEEEEEDEDEDEDEDEDEDEDEDEDEDD
EDDEDDDDEDDDGEEEDA
```

112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE

A0A1Y6M2U4 **A0A1Y6M2U4_ZYMTR** (216 aa)
Uncharacterized protein. *Zymoseptoria tritici ST99CH_1A5*

```
MGPNGLPPAMNESSESWAPTAFRVLREELSAQQTRDERIGRCHEEDEEDKGSSPRTWLLPGERGGSRSSSESSTDTDNDN
KERRRKEKTMVMVVRGRGRREKSPAGRRERIPTAGRDDDDDEEEEEEEEEEEEEEEEEEEEKKDPRRPRAKAKANEAPPP
PQRPQHHRRRRRHHHHRSRQEAHEASSSSAANSVAVQVACGLERLDLYHGNRWHSN
```

122 - 141:	EEEEEEEEEEEEEEEEEEEE

A0A1Y6M5M0 **A0A1Y6M5M0_ZYMTR** (147 aa)
Uncharacterized protein. *Zymoseptoria tritici ST99CH_1A5*

```
MDTTKVLSAAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGAVLPRQRSTARLKISSVPRPRAFWTRWRPLREQ
EEEEKRRKNRRLAQTLSDAITRLVCRMVDRSKRIHRSVSQRCPSHPFSHSSRSSRRLLRQEGGARTG
```

11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE

A0A1Z2QRY2 **A0A1Z2QRY2_9ASTR** (2481 aa)
Protein TIC 214 (Translocon at the inner envelope membrane of chloroplasts 214). *Centropogon granulosus*

```
MLFQSFVNLCMKITNSVVGIGLYYGFLTTFSIRPAYLFLFVEEPEQKAAAITGLIMGQLVRFMSIYNRPLHRLLWTPHIL
TVLFLPYLLLYFAADNWDYTITTSTRSNFLIFLNTFIFQLANQILLPNSTLARLVNVYMFRCNNKMLFVTSSFVGWLIGH
ICFLLLTKRLFDWIRIYLLSRSKKELVSALDKYIYKYLGAKFQVRFSHFQYRVAELNKYIKSELNKYKKKIYQYLVRSLG
EEFEFLMRTFQWVVSEIQYLLLINLRRNTGRFVNIFLFVTCAYYLGRIPLFIFPHPLTSVQAPQLQPNWLARQGREADTY
WEDEDEEKEEEKEEEKKEEIARKKVLFKEEIPPQSWGRDLDEEKDQKDPIVVESILASDFFQFQWTRPVRYISNQHFFGA
VRKEASQYFFDTCRSDGKKRISFTDPPSFSSFKELTKGMISSSTVERLSFDKLDKDWLYKNKQRQNNLNNEFIKRIEALD
MGFLFLDILDKRTRVCIEKMNETCLCLPKRYDPLLNGPSRGRIKKFSKVIEDPEEKEKSEEKEKSEEKEKSEEKEKSEEK
EKSEEKEKSEEKEKSEEKAPKSKEQEKREEKARLREEARLREEARLREEARLRDERALLQLGEFREKVYNVIQSRKSRGI
KKNEMQSREKVQNAMQSRRRKKNEMQSREKVQNAMQSRRRKKNGTTKSRERIDDGTTKSRERIDDGTTKSRERIDAEPTE
SRERIDAEPTESRERIDAEPTESRERIDAEPTESRERIDAEPTATEFQLKQILALNQIHETLLPGFIFESPKYEERIFAI
LKSKTLKLRAEGKLYYNPLAKFFSKPWEKGGGSIDWNQRKLKKLQQLRTYKVGERAGRAHIRQRVPRWSYVLLREVVYDL
DEPFVTKRGDDECFDIISAQYKYEIILNQDTQNLLIKNFDKDSNKIDPEIAKEINKKVMKDLIKSGGDPYSIDFEKSLAH
VHVGSLTTNIEWKTENKDVWRTSLRAVRDQFWHQDDIKGVASVLRRKNGVVVRQIEMFPHSPLFLGFLKSTLSSSFRVVK
PLVLKMQNLMHRFGIKKGDLFTLKGPKKEQTKTKRKTKRKTKRKTKRKTKRKTKRKTKRKIDEKKSKALKERKKLKRIKK
```

```
DKIELDPEEELFRMDGIDAWNELYYGLGVRGIVLILNSYLRRYIALPLAIIAKNIGRILFLQQPEWAEDRKDWENETHLL
CNDDGFAIGVISIRNFPEEWWEYGLQVKVLWPLELKPWHTADDRQRITNDYAFIRSFWGLADYPWGGVRPNRSFSIFWGP
IFKELGKKSQRFAAEKLEGSAFRLIRSVFNPKIKQNFVRVLGNAKESIKRLNESIKRLKERVLVLKSTILKIIKKNTRLK
GIGVDESSETQKEKDSIISNEIINESFSQIRSTASTNSEEKIQNLINRTSTIKNQIERITKEKKKVTPGLNNSPNNKKQN
NNVESPKNIWKIVKRRNVRLISKWNYFQNIFIEKIYKIYLDIFLCIIKIPRINLTKKFFEKDISNTETNQKRITFSSTIK
NINKRKSQIVPKFASLPNLSSLSQAYVFYKLSQTLVSDKLRSVLQYRGTSFFLKTAIKDSFERQGIFHSELKHKKLRNFG
TNPWKNWLRGQSQYNLSKVHWERVGAQAWRNKVNRRHTPQNNDLNKGDSYEKDPLLHSKKQDDSEVYSLVRNQKTKFKKN
YKYDLLAYKYISSETKKDSSISKLPLQVNKSQEIDLFDIPEEIVFKTYFKNWILDKKFLDKLYRDSTYLHLHNYLDNTYV
DKDYHKGYQDYLDKSFLDKVYFKDSIDQLYLETDYYEDYLDEVYLDKNSLDNYLDKVYMSLKKMRKKKPERKYMDFDWKF
LEKYLVNLEAGKKIDPNHNTNTKIETKNSQIIETKNSEIIETKNSEIIENENSEIIENENSEIIENENSEIIENENRGLI
YDIVPKMLLDPEIEKDPELKEDPELKEDKKSFFNWMGMNEEILKAPRANSNEEDSNQEDWFFPEFMLRKRTYQMNPWLRP
MKLLLLNFKGKEEEEEEEEEEEEEEEEEEEEEVSQGKEEVSQGKEEVSQGKENVSQKKENVSQGKETKGKATKGKETKGKA
TKGKETKGKETKGKATKGKETKGKATKGKETKGKATKGKETKGKATKGKATKGKETKGKETKGKETKGKATKGKETKGKE
TKGKETKGKENVSQNIEDIDIEDIDIEDIDIEDIDIEDIDIEDIDIEDIDIEDIQEVIREDYEKGFRKKKTQYRSDSPRL
VDFVDLQEKYLGFSIHTERLVEEDMLERLSLMQMVGNTKGRLQSKRRLLAYLKMGDLPVDRIVSHYSKESTLFNWAEFGL
MKFQPLLTSSIKDLEEFLMYQAIGISLVHKSKQQTNQRYGKQKDVDKDHFDLLVPEMILSSRRRRELRILNSLNFNLKNR
NGVDRNPVFCKENNIKSWGQFLDESKHLDRDKNELIKLKFFLWPNFRFEDLACMNRYWFDTNNGSRFSMLRIYMYPRFKI
R
```

2012 - 2031:	EEEEEEEEEEEEEEEEEEEE

A0A1Z5JI28 **A0A1Z5JI28_FISSO** (559 aa)
Uncharacterized protein. *Fistulifera solaris (Oleaginous diatom)*

```
MVQAEPPVKKRKRATTAAKTKTAPTTTTTSTTSTIPTTAPTRILILDNGGDSIKFGWTTDTEPRRMPNITARLPQQWTIL
AGDLVTDVQNPTHLLHLTRSTERSLIVNLGNQIQVWKRVLDVLQVVIPGATAQALGWKKNLEAKIAPQHCAILLTVPPFC
PRVLLDQITTIWMDDFQFGHVGFVVAPLCAALQPHSTYQTSCVVDLGWSQTTVVPTFQHQLIQESSIRRMAVGGRHLQQI
WKYQASYRQWNLMDQEFLLQQVLEETAFVSLQWDQDMKIAQKLPAGRRPYDREFVLPDYQTTFRGRVQLPPYLRREAAMK
AMGKVLEDDNDDDDSEDDDDFNEQDVEEEDEDFDENLGEVNDSPDDDDEEEEEEEEEEEEEEEEEEEEEEEEESLEQIKAR
LLVQRQEEERTRWEAEAQQQILNLSVERFAIPETLFRPSDAGLPVEWANLPETIHQSIEDCPILYRAALYRSIRLVGGLS
QLSNLKERLQQELRCLVGCQHEIEIETSETATIDAWLGAKQLCIEKSFEKWSFSRMEWEQSSRKGAWARLLSSSGGRFV
```

369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE

A0A1Z5RJB9 **A0A1Z5RJB9_SORBI** (214 aa)
Uncharacterized protein. *Sorghum bicolor (Sorghum) (Sorghum vulgare)*

```
MAGYAEANQSPPKKNISAPEQLHPMAGAGGEVKSDECPLAAAAAAAPSYLVRSAAPDEEEITTRLSNGFVEWILNRKWVS
FEEDPDEHYDQMINDPDRPEEYTQEYLEEERDMMRELVAHNERSRACFEKFQQWVRRQLVEKGYVEVGEAYIAQCAINRR
SVSPEQWSALMGGLKLEEEEEEEEEEEEEEEEEEEEEDDDDDDDDDDEGVVESN
```

177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE

A0A1Z5SA63 **A0A1Z5SA63_SORBI** (820 aa)
Uncharacterized protein (Fragment). *Sorghum bicolor (Sorghum) (Sorghum vulgare)*

```
NATAFASSLVVIVLVLILSVLHDSGAGVTLLAPLLGVLRAVMVLDLLSLMGAYAAGAFRDTLTAVYSLVVLSAGVVGYLV
AHLVLASRSSAEEDKYKRGKSAPERLRKVLMLLATFAASVTYVAGLSAPGGFWDHAEDGHNPAMRSSREGPTTRASRRSS
SQHHGKKLCFSQKVRSYEIYGFIAVTLISLLAAYAAGSSRKIDTTIYVSALVGAVGVCILIQVVFVLLFQQANSMSVMSV
NRLKVRKLAVTTMAGTDGRTYCPLSLYMLCKLLELEYEQQQQQTQSPQTGNGTGSGSDEHEKQQNQALEKARSLVLLLAT
LATAITYQAGLNPPGGLWQSDGGGGGGIYKTGDPILLTTNPRRYKAFYYCNSIAFVASLVAVVLVRMKTLHHHNALEAAM
VLDLFGLIGAYAAGSCRDVSTSIYAMALAGLVLVYVVIHVILLTLDHKDGGSASARGNGETSGEEKNDAELVEKRRKRLL
LFAILAATITYQAGLTPPGGFLDQDDSRTGRHAGDPVLLNNYPRRYTAFFYCNSVSFMLSIALIILLVNPNLYRPAIRSN
ALSVCTAAGLIGIMGGYAAGCTQHLKTSIYIFALAAVVLSTVVLLAAVFLEEEEEEEEEEEEEEEEEEEEEEEEEEASTGARR
KEKRVHAKRKYLMLLGILVASVTYQAGLAPPGGAWQSNDGTHTAGDPVMHDYRRARYLAFFYSNSTSFVASVVVIVLLLP
ESLQGWWLRVMNTTIVLDLLGLLIAYAAGSCRTWQTSVYVSALVLAVLAYFAIHVLLSSCVRRRKKTAPDSASQENGEGN
KAATTEVELQLAETECAVRS
```

611 - 630:	EEEEEEEEEEEEEEEEEEEE
612 - 631:	EEEEEEEEEEEEEEEEEEEE
613 - 632:	EEEEEEEEEEEEEEEEEEEE
614 - 633:	EEEEEEEEEEEEEEEEEEEE

A0A1Z5T6S7 **A0A1Z5T6S7_HORWE** (962 aa)
Uncharacterized protein. *Hortaea werneckii EXF-2000*

```
MSTERSSSAVRNLRSIFENKGSDNSPDGRGRSTSGLSSEASNSSRPTSRIRANFVSVEPPKMSALAPEEGVGKGSAEGKR
ESTADIRRGSFTANTDEEALTLKKTISEEAHRREEESRIAQPIPEAAVESSGQTSAQTSGAGTPQMQAKHDTKVEPVAVD
PSPEQETKGKEDKEPANPDKPTTAAEEEPVEMRPAEPANEEAVSGGQALPPVTEDLRHSEIQESAAAPPAAAGTPEQKAP
KRNQRRRRLHRPRRLRLRPLPQDKAAQSAKKPEAKETASTKSPSTAAKASPKPTQSVPTARTSTGGSRSPAATRKQAPAP
SEAPKQKQPVKKPSRTSLTAPTASSMSKAHGSDRTSSTSSKPSTAAKPEASKPKTTKPIDLPSRLTAPTASSRAKHEPES
AQAPAPRPSATTSKPSAAPKPKPKPATTASSARPTPRSSLAPSQRPESRTSGTSAPQKKPAPADGSFLERMMRPTAASAN
```

```
KSHDKHDKTEMKSEETRTGYGNRCPDKTQLKTQYRQIRGSEKASSLLSSSAVDAAPAAEQTNGSHEFTPAPEPQPAAVKG
TLPQEPSAAVATQPVPPPEQQHSGLETPPTQLSNGAPASSLLQEQEQRQDKQQGAGTTLEATPAAIGEELSGGGGEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEGGGRRISEVDSCGGQHSPLLALPKELRLMIYDELFTPLIQRPEHFDTYVLPSEWP
KIDFTPYRALLLTCKEVNEEATTHFEGHFLRDVMVFFDNVADLASFYFKIEKTRSGKRFANMQACLHTWPWRMRDHIDPE
AMTKPNFGRANSETFLCCLDMFVFDRSRLATAKARELYGVDLLADICKAIHGPFEHPNPNSNRTHSMRGATKVDVLVRTD
RSKLSQATLEISSRQLCSNVRTMYTQMAAPVGCLGSNEWIQLLYADLRERDPDEVRRETGGTFWPGIKEYERHLKEEYGL
NA
```

636 - 655:	EEEEEEEEEEEEEEEEEEEE
637 - 656:	EEEEEEEEEEEEEEEEEEEE
638 - 657:	EEEEEEEEEEEEEEEEEEEE
639 - 658:	EEEEEEEEEEEEEEEEEEEE
640 - 659:	EEEEEEEEEEEEEEEEEEEE
641 - 660:	EEEEEEEEEEEEEEEEEEEE
642 - 661:	EEEEEEEEEEEEEEEEEEEE
643 - 662:	EEEEEEEEEEEEEEEEEEEE
644 - 663:	EEEEEEEEEEEEEEEEEEEE
645 - 664:	EEEEEEEEEEEEEEEEEEEE
646 - 665:	EEEEEEEEEEEEEEEEEEEE

A0A1Z7ZN17 **A0A1Z7ZN17_9FLAO** (1420 aa)
OmpA-like domain-containing protein. *Flavobacteriales bacterium 33_180_T64*

```
MKNQNNLLFGQRINYFIGIVVLSILIPTRMAFTNFSFKILLLFFWVTTLSLIVFIVLDGYMKLQNLGEDADKKPREGLLN
HILISSKAVTGIVLLLICFTVFIQFFVGLFSYRYGVEFKLFLPVVLLAVFGSWFLRDMETSNWIESNARWLLPIIRKQSE
NMASKAKKVAVWIGSKRYLVGGIAITVLLGFLLAVLLRPPELFVKEITITGISSDPWMTRSVVADSLTIDHDFDQNLVID
VKNTGIDTIAVFLRATSLAGKDNLILGFTGEGSDFDEIHPSNIYPNTTRQYELIIHADNAKLDKYKIMVQLFKYDSFSPD
TAEPIDDKTFTIKIRTTPIQIKFTKKGEDENTLSQHYLLQNTGETISNFSLLEDEQLKGKIRMVPQINNFRFQKGSVISI
QVKPHLHVGFDSLVGNLIASGGDSKPIEQPLLFQTPTGKKVFLAVARCGSKNHKLSSNCINRKNVKDNISKPPGFMGETH
EYSPPGVAKLGLVEIEEEEEEEEEEEEEEEEEEEEEEEEESEPSLTLLPPDGDYIDGVPSELVLKDVATLEELLDNLMDEF
TSRGAQLRISNTKEEHLTTIRNLIGDKETLDDTDIEVVNKHMNDALDTYYLMTSEVVWNKRKSTFIEELLPDITGVGNLR
MNKEWLKFNNAHAPNIYYGENAVHFSWHYRAPTSSGKQFILYSAHTKQGAVLNETTDLTPDGEYGQWPFILEGTQSKTFL
AWQGSKHDEKPEIKLRVSLDSGVTWEAPLSITNHGQGAYSPQLVYRNNTLYAIWHEMLDQDNQLKLAYSSNDGKTFSSPI
TLASNVTPNSVSKFDVSSKSLHFVHTTLSEGDQNKLIYGSLFLNQLNVFQPVITTEILGNGYQAVIKSDEQNVHLSYVTG
EGNQSEIFYRYSIDEGRSWAAPFQLTEDSAYSISPSICFDVNKKVRIFYHSNKADSESFLDHIYYSDQQTYENWTTALRL
PSFSSNAKKAFLTVKFKIPWDRNKYGEYNVKIRFNGYLVDNIKGFVPEGTLLYPIDPSWIRVDGSNTVNLDADHFNPAHY
LTTYGFSLISDMEFIEQKVFARDEKEADSLLRADPLFNHDYPDLGLFATTENKIPLLVEKDEKITIKLNLWNLGQAVSNN
SIIDIYGGPTVLSDNPYQDRYLLGQKKIAELKPMHNIKINFPITYWNGLEKIFFRVRTQEKDFDETNNVHEISLLGVNTT
YSDQGALRVAIFDEPGELSDDVEMKIYYAGSNIPIQSGNENPQIWWLNAGNYDVFVKDRSSNKVEQWIRGGSIVPENNNT
ISFDILTQRIDETIRSLGAVVSDKQITFQLPSAILFHSGEFEISTYSIDYLKKIQVLLKSYPQSVLTIIGHTDNVGDPSD
NLKLSEKRAESVKNWLVSLEGITEERLKTIGMGENDPIIETDTEEGRLKNRRVNFILNRN
```

496 - 515:	EEEEEEEEEEEEEEEEEEEE
497 - 516:	EEEEEEEEEEEEEEEEEEEE
498 - 517:	EEEEEEEEEEEEEEEEEEEE
499 - 518:	EEEEEEEEEEEEEEEEEEEE
500 - 519:	EEEEEEEEEEEEEEEEEEEE

A0A1Z8JQG9 **A0A1Z8JQG9_PICKU** (473 aa)
PWWP domain-containing protein. *Pichia kudriavzevii (Yeast) (Issatchenkia orientalis)*

```
MFEPKQLVLAKIKGFPDWPAIIVPIESIPAKLSSSRYQRQIDAYLKNDVCVKFYFDDQYSWTKLTNLKPLSLDMVEAFLL
QDHGGRRKKRIVEAFEKVKEVPVDEFLKWGSWGEPKPVVEDVEDVFEDGLDNKGGRKRKNNNGSKQTGKGKGKGKGKGKD
KDKDQDKDLGRETKRRRSGRATKVTEETSTPEFTEEEQIVDDEDVEYVEPEDEDLEEEEEEEEEEEEEEEEEEEQTVEP
PAIVDDLSSKQPPDFNVDFSVIPHSSALTTEVQEMSQWCHDLRMELQTLIFPLRKQQPGEMEEEAVVPNEANGADNASNT
SVEVTGTNVDDAHQQHNESEVKAEDVEQVQPNYKDLNKQIEELISPLLNADLSKSIVKSTGLSKIILIILSKPEFSSACT
KRLSKWWVSNFDFSIKPDHHWSDEFTIADHLQEEKQRKAMEEERRRKKKEERRLASMSAVSQTPETEPQSSNV
```

216 - 235:	EEEEEEEEEEEEEEEEEEEE

A0A1Z8Y2R0 **A0A1Z8Y2R0_9BACT** (92 aa)
Uncharacterized protein. *Verrucomicrobiaceae bacterium TMED76*

```
MPKRSSEEDIKEEGNLNFNFGSEKKDIDEKEESVINSANDEGLDSVKIYRGSDRTFGQLIEEEEEEEEEEEEEEEEEEEE
EEEEEXVLLTKS
```

61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE

65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE

A0A1Z8YZG6 **A0A1Z8YZG6_9ACTN** (765 aa)
Penicillin-insensitive transglycosylase (EC 2.4.1.129) (Peptidoglycan TGase). *Acidimicrobiaceae bacterium TMED77*

```
MRQITVLFRLAIVLILAGLVVGIVGVLSGPQIKEIGTSGEWSHSPVALASTGTRSLVYDQNGELMATFFDENRSPILLDL
IPVEVREAILAIEDSNFYGHQGVDLKATARALIENVDAGGISQGGSTITQQLIKNLVLTPEQTVERKVQEAALAVRLEDQ
LTKNEIYEIYLNTVFFGSTAYGIKAAAEVYFGLDLANKTPEEVKRTLDDGLGWPEAALLASLISNPSVNDPTVNPQIATY
QRRIVLDRLAELGYFSQAKAEEYALTPLPTQRFQPSLPSADDFFVAEVRRSLLEDPTFLGGGVESRLEDLLGINGGIRVY
TTFDPTTQQMALDARDEVLREQWGVDPFFTVSIASIDPDSGAVRAMIGGESFDSESQFNLATQGRRQPGSSFKTIVLVAA
LQRGIQTDDKINGEGPCEFPEETEPDGIYEANNFANDDGEIAEVRDLLXSSSNCGFLKLGQLTGINNIIDTAKLLGIKSE
MSPVISLPLGVEEVSPMEMANSYATLASGGLRREPYFIERIERLIENEWVSIYEHENDERYLPERVLTETVSCWATETLW
ANVRGGTGVRAGWPMGSQPAAGKTGTTENFEDAWFVGYTPYLATAVWMGNPDEKVSMRGIYPHGNVTGGSFPAEVWGSFN
SKYHANLPERTFPYCRPFAQEGEYLRTIDDPQAGTDPCPDQIALDYFGDEEIDVCEDEIPEEFIECEYEYDFLDIEAVRV
TVYCGDPPXEEEEEEEEEEEEEEEEEEEEPSQETESGSDEEEQED
```

730 - 749:	EEEEEEEEEEEEEEEEEEEE

A0A1Z9QG75 **A0A1Z9QG75_9BACT** (70 aa)
Uncharacterized protein (Fragment). *Phycisphaeraceae bacterium TMED231*

```
MFIGLVLGSPGEPLVREAARKILRIPAAFEPEAVQPHLFGGDEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE

A0A200Q139 **A0A200Q139_9MAGN** (922 aa)
Uncharacterized protein. *Macleaya cordata*

```
MEETNFCKEFENRPGERRTTGTGIKYYSKRHEISFVEADKQEDPPLEKHIPLPTTDCSSLLPCNYNNGCLEHIKVGCFYE
LNHTKLPPKSPIQLKSVRAVMVMEKTELNVSVKFPSALSLRTYFTSVDETSDYQPQMMMNLREKMHPELDEQFVMGSKLA
QEVLIQQILPSDFAKQKHLQSFWLLPPPPAGAASCGTRMISTSSPGMVDAMERLSNTRRRYDNNLVRRGGTCWSELINSD
GLVHWGIRRRVAFMGSHDNHGKADTIVKQNSSNKKTPLVPLDHHRHQSLLTTLVAAREEDDEEEKVEVEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAKRSLRETKINEKNQQQQQKKNKVTSYDRWSKERYKTAEVKM
LEIMKERGAVFGKPMLRRTLRMEARKHIGDTGLLDHLLKHMAGKVGPNGEDRFRRRHNAEGEMEYWLESADLVNIRREAG
VKDPFWTPPPGWMPGDNPSQDPICARELKLLKQEMSTLKRNVEQIMEAHRQQQQQRCGGRGSSGGGRDGGDQALLPNVIT
TNPAAVVSSSNNCGNKLDQSQSTNTTIVVDQHQLKESYENLMKRKAQLEQQLIEISNSLNGIQEDVLRLTASRVEAETTG
KSVSVVVAEEKEETNNNPKQQKEENNRIMGGVGGNRHSGKEGGEEEEDRRGTTGDDHVDDYHKKGTDKAEAAAAAAAKET
TAEKRQRLRSGFRICKPQGTFLWPNMAMAHTAAGAAGSSSTASCSNTKLLSPHDPQHQHHQAVVVPTPPSVTSAPNRNFL
LLQAPPHPPPVTRQQQPTSPVKPLAERRAVSVSTVTSFVNLNVLPPPPVQPENRYSECETTDHQRDFGDNISSTTTTSSF
LHYHHRLSDTNNNRELCGTPTSVPRQQQQQQPRTLLLLPHKM
```

309 - 328:	EEEEEEEEEEEEEEEEEEEE
310 - 329:	EEEEEEEEEEEEEEEEEEEE
311 - 330:	EEEEEEEEEEEEEEEEEEEE
312 - 331:	EEEEEEEEEEEEEEEEEEEE
313 - 332:	EEEEEEEEEEEEEEEEEEEE
314 - 333:	EEEEEEEEEEEEEEEEEEEE
315 - 334:	EEEEEEEEEEEEEEEEEEEE
316 - 335:	EEEEEEEEEEEEEEEEEEEE
317 - 336:	EEEEEEEEEEEEEEEEEEEE
318 - 337:	EEEEEEEEEEEEEEEEEEEE
319 - 338:	EEEEEEEEEEEEEEEEEEEE
320 - 339:	EEEEEEEEEEEEEEEEEEEE
321 - 340:	EEEEEEEEEEEEEEEEEEEE
322 - 341:	EEEEEEEEEEEEEEEEEEEE
323 - 342:	EEEEEEEEEEEEEEEEEEEE

324 - 343:	EEEEEEEEEEEEEEEEEEEE
325 - 344:	EEEEEEEEEEEEEEEEEEEE
326 - 345:	EEEEEEEEEEEEEEEEEEEE
327 - 346:	EEEEEEEEEEEEEEEEEEEE
328 - 347:	EEEEEEEEEEEEEEEEEEEE
329 - 348:	EEEEEEEEEEEEEEEEEEEE
330 - 349:	EEEEEEEEEEEEEEEEEEEE
331 - 350:	EEEEEEEEEEEEEEEEEEEE
332 - 351:	EEEEEEEEEEEEEEEEEEEE
333 - 352:	EEEEEEEEEEEEEEEEEEEE
334 - 353:	EEEEEEEEEEEEEEEEEEEE
335 - 354:	EEEEEEEEEEEEEEEEEEEE
336 - 355:	EEEEEEEEEEEEEEEEEEEE
337 - 356:	EEEEEEEEEEEEEEEEEEEE
338 - 357:	EEEEEEEEEEEEEEEEEEEE
339 - 358:	EEEEEEEEEEEEEEEEEEEE

A0A200Q483 **A0A200Q483_9MAGN** (1493 aa)
MATH. *Macleaya cordata*

```
MSGSLSEDSSVGRLSEGISSGHRYQSGEALAEWRSCEQVENGTPSTSPPYWDIDDDDDCGPKPAELYGKFTWKIENFSQI
SKRELRSNAFEVGGYKWYILIYPQGCDVCNHLSLFLCVANHDKLLPGWSHFAQFTIAVVNKDPKKSKYSDTLHRFWKKEH
DWGWKKFMELSKVLDGFIVSDTLVIKAQVQVIREKSDRPFRCLDCQYRRELVRVYLTNVEQICRRFVEDRRGKLGKLIED
KARWSSFCAFWLGVDQNIRRRMSREKTDVILKVVVKHFFIEKEVTSTLVMDSLYSGLKALECQSKSKTAREKVLYTEESP
SPIVRVENDMFTLVDDVLLLLERAALEPLPPKDEKGPQNRTKDGSSGEDVNKDSIERDERRLTELGRRTVEIFVLTHIFS
NRIEVAYQEAVALKRQEELIREEEEAWQAENEQKAKRGTSEKEKRAKKKQSKQRRSSRKGKDKGRNEKLEVLLQDKPQSE
GPIDRAMEGLSMKQALSVLEKPDTLEDVSDVTDAADDVAETLQPDLEDRDASPVNWDTDTSEVHPATETSSSGVSGLPIQ
NGRVDKKSTSVMDDSSSTCSTDSVPSVVMNGPPYKGNSLPYYKRQASATRGKNQRGKETLDRSGWVHDMDSHPSESAPDA
GRLHDLSGTCTAAEPDSLHTLKDRIHWLEQHLVEKEEEVSTLQKKLIVKDVDVVTDQKKNLVDVERPDQRMAEEASSGST
SLSTNLPSSLQPKLVAESTIRDQPFPVKVTSPNSPRQTEKVVPVRTPSPQIPAISKPESHIPAAPLKPTATPSEKPTTHQ
VSAMSRPLSAPLVPGPRPTAAVVSMVQTAPLLARSLSAAGRLGTDPSPATQSYAPPQSYRNAIMGKTMAPTPASFTIRPC
SAVSPSPTHSQSTSPLVSTQMHLPQNSARRDQNMVRPGFTFGSVTPDILQNRPQWMEGSQQDCNPSSLNGGIQNLDFYGT
SGSSTSTTQGVSSDEFPHLDIINYLLDEEQSMGKAAKANAVFSTTNNGYHHHPLNRQFTFPGDITMSGEVGPSINSCRFH
RQESYHDDGLQQVYGSSSGGSSYDGFREVYPVVGLPYADGQIVDGMIENQWPVGGADRSLLSMRSTAGDGYLYHHHHHHH
QQQHHPLPDYSNLACDVNGYPVFRPSNGLDNMTQNLQLDLSEATARSRQILDSSPCPPLCFFFLLLPFLGQSLPALSLEF
NEVQRKKETLRISFKENEEEEEEEEEEEEEEEEEEEEEEEEEGLRTCNEGLLGDDVDDGTEKEEGKNEVAVVQKDVDRIEIV
GNADDLGMQISNEDSELVGKYERKNVRKIQFKNVGMKTRVLDDEMGEKSKVDDESELGVQSNVDETKIEGGTDDDMGILQ
STEYDNLVGGVDEQGKEGNQEKNPTQKKNRAVEEMVSNLRGLMKSLEDERELTEGMIGRVHGGVVEMSQEEILQQMMKHL
SFKVEQDRRRSSFLTTQIESLSLWNTTTIGGADNDDDDQTNRDGAGESEGDNN
```

1218 - 1237:	EEEEEEEEEEEEEEEEEEEE
1219 - 1238:	EEEEEEEEEEEEEEEEEEEE
1220 - 1239:	EEEEEEEEEEEEEEEEEEEE
1221 - 1240:	EEEEEEEEEEEEEEEEEEEE

A0A200QHM9 **A0A200QHM9_9MAGN** (298 aa)
The fantastic four family. *Macleaya cordata*

```
MASCGSLQQIFEKPLPENPTLIESLSRWNQIKSIKPIEVSSFTEIFGELHFKENSELLSSSPHTPSSFKDLNSQLENEKI
DDNDSFSPSSFLGTPRHQYRGSSKSSDGFSPRSSESLQLCTEGLGVESFDGVEESMNENGDDSDNREKDKVSVLKHQSYN
IPCQEFRRSRTGGRSFPPPISSIGRSGKPWVCFKSYRQDGRFVLKEIRIPTQEFLHAFREDGRLKLHFVHPNQEILEEEE
KEEEEEEEEEEEEEEEEEEEEEEEEEEGEEDDEESASKERNEGTEEQKAEISDAEIVS
```

242 - 261:	EEEEEEEEEEEEEEEEEEEE
243 - 262:	EEEEEEEEEEEEEEEEEEEE
244 - 263:	EEEEEEEEEEEEEEEEEEEE
245 - 264:	EEEEEEEEEEEEEEEEEEEE
246 - 265:	EEEEEEEEEEEEEEEEEEEE
247 - 266:	EEEEEEEEEEEEEEEEEEEE
248 - 267:	EEEEEEEEEEEEEEEEEEEE

A0A200QQJ2 **A0A200QQJ2_9MAGN** (330 aa)
DUF2052 domain-containing protein. *Macleaya cordata*

```
MVETRRALSRSVMEGIAERLSSLDNLYFPRSIQDTAINPLERKTILFDLLSRDTAVFLERYGSQLTSEELHEFDALKDDY
EINWHFNHLRTLLSPTSEEVRSRSVTVKNRRRAYLNKLMSDGNYFSEDAMREREPYLHHEYVGKFQDPTVRSMARPGERW
SETLMRRSEEAILVAKIRGEQQRLGVDQKDWIGNVREEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAMEGRE
NPHSSEVLADQKSAGGGQCTGMDHQEGTTLSDAEMQDQMEQFTHIMQQKFLSGEDSQHLDYSKIDNDETLDDHWFREASH
```

DAEEKYFAED

197 - 216:	EEEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE
208 - 227:	EEEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE

A0A200QRT9 **A0A200QRT9_9MAGN** (638 aa)
Bromo adjacent homology (BAH) domain. *Macleaya cordata*

MGNRRFVSTSDSEDEDKGRGKRKAAEEDQKKKTKKKKITEEEEEEEESEEISKDEEVEVKEEDENEEEEDKEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEVEEEEGEEEAPKPMGEVIRVSGKGKSRRNHYKAFDYDGNTFELEDPVLLTPEDTGQKP
YVAIIKEITQDKDGTMMVTGQWFYRPEEAEKRGGGTWEAHDTRELFYSFHRDEVPAESVMHKCVVHFVPLHKQLPRRSEH
PGFIVQKVYDTVERKLWRLTDKDYEDGKQHEIDLLVQKTRERLGELPNIETEEALADLEYQLKNKRLFRRKIMSPIDVSR
EDATTRSDQHLTAETPGSCTGDASEYYTILANFKALTGDTIRDKWLEKLLQGIQFVCDSKDSMKVEHTGKGGSVSLDNNA
SANDRPENSTNGSREKGCGTTQWPDAAVSAIVALEGASHDALSCDFQKYNQKMRQLQFNLKNNARLARRLVKRELEASVI
FNMSPNELKDGLTAEETATKEPEESERMQQMTDARCSRCTEKKVGLTDIIQAGGRGDRYQLECIACGNTWYASRDEASTL
TIDAPSVVTNVGTAPWATAKFEDVEKKLLSPRETEKPSAADVFKKKTAAYMPVLETQKSFNKAKPEDLPGSTTSNTAE

72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE

A0A200QWF4 **A0A200QWF4_9MAGN** (322 aa)
RNA recognition motif domain. *Macleaya cordata*

MAAAARATIGSCFSTAATTTTCTCRITSKQYAPASDFVLLRMTYTGNVRIPALQTGASSKSHSQYSPLDSLCRITTSAPP
PPHKLSRVAFRISATIEQEEVSAATEIESSVEEEEEEEEEEEEEEEEEEEEEEEEEESNEKEKEVEVKVSGDQVGEAST
EGATNTKLYFGNLPYNCDSAQLAGIIQEHGSPEMVEVLYDRDTGRSRGFAFVTMSSIEDANAVIENLDGSEYGGRTLKVN
FSDKPKPKEPLYPESDYKLFVGNLSWSVTSESLIQAFQEYGNVVGARVLYDGETGQSRGYGFVCYSSKEEMDAALVSLNG
MV

112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE

116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE

A0A200R2H1 **A0A200R2H1_9MAGN** (969 aa)
Nucleolar protein 14. *Macleaya cordata*

```
MAKQKTQSDPNKSNSKKKKKITSKKLLSGPNAVAMKSKTPKDNPFETIWTRRKFDILGKKRKGEEKRIVDIGMLFWQQRK
NTLLKEYQQSGKSSVFMDKRIGEQNGELGEFDKAILRFQRERQLKLNKKSKYNLSDGEEDDYEIHGGGSFPERDDFEDDM
SPDDDADGDETEKKSAVLKQLSAHNAQNPLESGLMEGDEHKQKSKKEVMDEIILKSKFFKAQKAKEKEENEQLMEDLDSK
FASLVQSKALLSLTQPGKMNALKSLLNKGNSKQSVNVDELSAQMEPTNLDRPDAYDKLVKEMVLDMRARPSDRTKTPDEI
AQEERERLEQLEEERQKRMLGMDDSSDEGSDGYEDFNKSSSQKVRSISGDDLGDSFSLDEEVGHKKGWVDEILEREGRSI
QDEYGVSSEDSDEDGDEDESDQEDESDEDIDEPGKKMSLKDWEQSDDDNLSTDLEEEEEEEEEEEEEEEEEEEEEEKEDD
EREEIGDNDTRKVEDYVKPKTKNQLADPSTVKKTKSSLKQPPTKQDSLPFVIEAPNSLVELSTLLENRSDDEIIEAINRI
RACNGVRLAVENRKKMQVFYGILLQYFAVLATKKPLNFKLLNLLVKPLVEMSMDTPFFAAMCARQRIHRIRNQLCEDIKN
PEKSCWPSLKTLFLLRLWSIIFPCSDFRHVVMTPAILLMCEYLMRCPITSGRDIAIGSFVCSMVLSVTRQSQKFCPEALI
FLQTVLMSALKMEKNLPKRLQVSYFSELKMLKPWLRLSHHVSEIHPLDFLTVVDMPEDSPFFSSDNFRASVLVSVIETLQ
GFVQIYEGYNSFPQIFLPISTLLHQVLEQKNIPDLLQDKMKDVAQLIGKKVDEHHLLRRPLQMRKRKLVPIKQSTPKFEE
NFVKGRDYDPDRVRSESKKLRKLLKRESKGAASEVRKDRVFLAGEREKRKTQVEEEQAEKYGKAKAFLQDQQHAFNSGQL
GGSRKRRKR
```

455 - 474:	EEEEEEEEEEEEEEEEEEEE
456 - 475:	EEEEEEEEEEEEEEEEEEEE
457 - 476:	EEEEEEEEEEEEEEEEEEEE

A0A200R4N4 **A0A200R4N4_9MAGN** (643 aa)
Uncharacterized protein family UPF0503. *Macleaya cordata*

```
MNLEQPQPFFSSSRLTICDRHPDEPLTGFCASCLRERLAGLDSSTSSSTSSLRKTNITTTTTTTTSALKAIFRGSNAAVA
DNNNLLNKDPASSSSSSSFFPELRRCKSFSGRKAEGLSGAFEPQRKSCDVRGRNTLWCLFNKDDDRKLGKSEICAEIEVE
TRNLGFLGVGDPELETREEERENREEIRVPVASNVVEVIEEEEGEEEEEEEEEEEEEEEEEEEEKELRMKDHIDQESQNK
KPAGRDLKEIAGSFWFAASVFSKKLQKWRRKQKMKKSETSTSGLSTMRVDKPHSEIADYGYGRRSCDVDPRFSLDIGRMS
FDDPRYSLEEPRASWDGYLIGRTFPRLAPMVSVVEDVAVPVRRSDNQIPVEEPLNSVNGDDTTPGGTAQTRDYYSDSSQR
RRKSFDRSSSLRKKAAAVGAEMDDSKSGSNSKVSPTSVDLFHGAKLIGTDRDLRDSKSNSLRDDRSESFESAFRESASVS
CSVDQKGLKKSSRWSKAWNIWGLINRRSVSTKDEEEERYSRGNVVERSFSESWQDLRKDANGESKSGCNRVLRSNSSVSS
RNSINTGGAFGGMRNVSEINGFGKKKREEIVLERTRSARYSSADADNGLLRFYLTPLRNKRSLSGNGRPKNPQSIARRVL
RLY
```

205 - 224:	EEEEEEEEEEEEEEEEEEEE

A0A212C3C2 **A0A212C3C2_CEREH** (1614 aa)
Histone acetyltransferase (EC 2.3.1.48). *Cervus elaphus hippelaphus (European red deer)*

```
MCKQLYWSWVSTFTSGIRLEERQAADGKALQQQVMSQQKVGVTGPPDPQVRCPSVIEFGKYEIHTWYSSPYPQEYSRMVR
MNVLADALKSINSAEKRGKCQVLIRPCSKVIVRFLTVMMKHGYIGEFEIIDDHRAGKIVVNLTGRLNKCGVISPRFDVQL
KDLEKWQNNLLPSRQLPKLYLCEFCLKYMKSRTILQQHMKKCGWFHPPANEIYRKNNISVFEVDGNVSTIYCQNLCLLAK
LFLDHKTLYYDVEPFLFYVLTQNDVKGCHLVGYFSKEKHCQQKYNVSCIMILPQYQRKGYGRFLIDFSYLLSKREGQAGS
PEKPLSDLGRLSYMAYWKSVILECLYHQNDKQISIKKLSKLTGICPQDITSTLHHLRMLDFRSDQFVIIRREKLIQDHMA
KLQLNLRPVDVDPECLRWTPVIVSNSVVSEEEEEEEEEEEEEEEEEEEEEREREERQSQEGELEPSVGKSASRENKEQDSY
TSVESEKKPEVPTPASTTRLSKQALPRDSLPANSQPPRRGRWARKNRKAQERFGDKDPKLLLEETSAPQEQYGDCEEKSE
PSQEQYLESEEPSAASQEQPSQDGKPDGPKRRPSEGLELWRGPPKKSPEPLKCGLPDAHDRLPRRYSEGRYCEGRYADGD
RPALRGCSESSEEDGEPESPRSSSPPVLTKPTLKRKKPILHRRRRVRKRKHHNSSVVTETISETTEVLDEPFEDSDSERP
MPRLEPTFEIDEEEEEEEESELFSRGYFHRLASQDILRCRSDSKRKSKDEDDDEESDDADDTPVLKPVSLLRKCDVKDAP
LEPDTSTPMKKKKGWPKGKSRKPVHWKKRPGRKPGFKLSREMVPVSAQESVVEPIVSLPKAGRKSKMEESEEIVEPKEDL
PLTEERKEDEELPLEAEEVEEGEEEDTTSSDVRAASPADASSPEAEAKEPEAGEDEEKPRVPAEQRPTEEAPQELARQEP
EEEEDTAAETNQSEDHDADDEDDGHLEPAKKEEEPGEPPAREGVKEEPGGREAFLDPNVQGSGENPKDKEETEPDSEEEQ
TSHDASVVSEHMPGSEDDHEEDSRSKEELLELKEEEEIPHSELDLETVQAVQSLTQEERGEQEGAYQDCEETLAACQTLQ
SYTQADEDPPLALVEDCHASEHNSPLSSVQSHPSQSVRSVSSPSVPALEGGYTQISPEQGSLSAPSMQNMETSPMMDVPS
VSDHSQQVVDSGFSDLGSIESTTENYENPSSYDSTMGGSICGNSSSQSSCSYGLSSSSSLTQNSCVVTQQMAGMGGGCSL
MPQSSVPPAANCGIKSPQSCAVERPPSTQQPPPPQPMNNSFTPAPMIMEIPEAGSAGNISIYERIPGDFGAGSYSQPSAT
FSLAKLQQLTNTIMDPHAMPYSHSPAVTSYATSVSLSNTGLAQLAPSHPLAGTAQAQATMTPPPNLASTTMNLTSPLLQC
NMSATNIGIPHTQRLQGQMPVKGHISIRSKSAPLPSAAAHQQQLYGRSPPAVAMQAGPRALAVQRGMNMGVNLMPTPAYN
VNSMNMNTLNAMNSYRMTQPMMNSSYHSNPAYMNQTAQYPMQMQMGVMGGQAYPQQPMQPSPHGNVMYTGPSHHSYMNAA
GVPKQSLNGPYMRR
```

430 - 449:	EEEEEEEEEEEEEEEEEEEE

A0A212CP30 **A0A212CP30_CEREH** (1177 aa)
Histone acetyltransferase (EC 2.3.1.48) (Fragment). *Cervus elaphus hippelaphus (European red deer)*

```
YLLSRREGQAGSPEKPLSDLGRLSYLAYWKSVILEYLYHHHERHISIKAISRATGMCPHDIATTLQHLHMIDKRDGRFVI
IRREKLILGHMEKLKTCSRTNELDPESLRWTPILISNAAVSEEEREAEKEAERLMEQASCWEKEEQEILSSRANSRQSPA
KVQSKNKYLHSPESRPVAGERGQLMELSKESSEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDNIQSSPPRLTKPQSVAIKRK
RPFVLKKKRGRKRRRINSSVTTETISETTEVLNEPFDNSDEERPMPQLEPTCEIEVEEDGRKPVLRKAFQPQPGKKRQTE
EEEGKDNHCFKNTDPCRNNMDDGANNLKEASRDNPEPLKCKQWPKGTKRGLSKWRPNKERKTGFKLNLYTPPETPMEPDD
QVTVEGQKETPADRTSPTSTRIEEGVKEAVEPLLPQDKNGREETCAPVSPIKSPGGKPEDDSIKPEEEEEEEEEEEEEE
GNVEKDPSGAKSQEKVEPEVCMDKDDALHLDDHEEEEEEDEEPSHNEGHDADDEDDSHMESAEAEKEEHPREAFKEVLEN
QEAFLDLSVQPSHSNPEVLMDCGVDLPASCNSEPKELAGATETAPESDEEPPGEQAQKQDQKNNEEVDSEFKEGNTATLE
IDSETVQAVQSLTQENSEQDDTFQDCAETQEACRSLQNYTHADQSPQISATLDDCQQSDHSSPVSSVHSHPGQSVRSVNS
PSVPALENSYAQISPDQSAISVPSLQNMETSPMMDVPSVSDHSQQVVDSGFSDLGSIESTTENYENPSSYDSTMGGSICG
```

```
NGSSQNSCSYSSLTSSNLTQSSCAVTQQMSNISGSCSMLQQTSISSPPTCGVKSPQGCVVERPPSSSQQLAQCSMAANFT
PPMQLAEIPETGNANLGLYERMGQSDFGAGHYPQPSATFSLAKLQQLTNTLIDHSLPYSHSAAVTSYANSASLSTPLSNT
GLVQLSQSPHSVPGGPQAQATMTPPPNLTPPPMNLPPPLLQRNMAASNIGISHSQRLQTQIASKGHVSMRTKSASLSPAA
ATHQSQIYGRSQTVAMQGPARTLTMQRGMNMSVNLMPSPAYNVNSVNMNMNTLNAMNGYSMSQPMMNSGYHSNHGYMNQT
PQYPMQVQMGMMGTQPYAQQPMQTPPHSNMMYTAPGHHGYMNTGMSKQSLNGSYMRR
```

193 - 212:	EEEEEEEEEEEEEEEEEEEE
194 - 213:	EEEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEEE
196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE

A0A212D4K9 **A0A212D4K9_CEREH** (650 aa)
Uncharacterized protein (Fragment). *Cervus elaphus hippelaphus (European red deer)*

```
VFSVAPPFEVNGLPRAVPLSLPYQDFKKDLSDYRERARLLNRVRRVGFSHMLLTPPQVPLAPVQPQTNGKEEEEEEEEEE
EEEEEEEEEEEEDEEEEEEDEEEEEEEDEEEAVALGEVLGPHSGSSSEGSERSTDRSQEGAPSTLLADDQKESRGRASMA
DGDLEPEEGSKTLVLVSPGDMKKSPVTADLAPDPDLGTLAALTPQQERPQPTGSQLDVSEPGTLSSVLKSEPKPPGPVAG
QGTGAVAIGAGGVAVTSSPFTKVERTFVHIAEKTHLNVMSSGGQASRSEELSSGGELGLEVPSDGRVAEEGAAAHLENGI
ALSGLESCVMSAPPGSGPLEVTTDSLPNGPALADGPAPVSLLEPGPEKLATISPSRHAMPGPRPRSRIPVLLSEEDTGSE
PSGSLSAKERWGKRARPQQDLARLVMEKRQGRLLLRLASGASSSSSEEQRRASETLSGTGSEEDTPASEPAVPRKAGRAA
ATRSRIPRPISVRMPTPATAQQPPDRPQGAAPASDTAITSRLQLQKPPGTAIAADLRPKQPSGRGPGPGRAPAGTRPPAP
RSPGLPASSAHHPSASPRSRSLSRKESPSPSHQARPGPAPPRGAPQARAQPEGTPSPLGGPKKGPRGKVQTQRAATKGRA
GVAESRAGAR
```

71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE

A0A212D576 **A0A212D576_CEREH** (1011 aa)
EHMT2. *Cervus elaphus hippelaphus (European red deer)*

```
MGALVLEKEPRGATERVHGSLGDTPRSEETLPKASPDSLETAGPSSPASVTVTVGDEGADTPVGATPLIGDEPENLEGDG
DLHGGRILLGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAPAAGPEPPPATASPEGQPKV
HRARKTMSKPGNGQFSPRASCGLGGATALPLFQSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRS
GSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSL
ETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCC
PGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPPGPGREALEK
ALVIQESERRKKLRFHPRQLYLSSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLDVARY
MVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDN
EENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSD
VWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSNCLCGQLSIRCWYDKD
GRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADV
REDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRAGEELGFDYGDRFW
DIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELSSLPPVNP
```

205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE
208 - 227:	EEEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE

A0A212D5N7 **A0A212D5N7_CEREH** (285 aa)
Uncharacterized protein (Fragment). *Cervus elaphus hippelaphus (European red deer)*

```
GELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLISKPLSSSVNNNKRMVSTKGK
SVTEYKNEEYQRSERNKRLEADRKIRLSSSASREPYKSQPDKTCLRKRDPERRVKSPTPDDSERIGLEVDRRASRSSQSS
KEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEEEEEEEEEEEE
YEQDERDQKEEGNDYDTRSEASDSDSESVTFTDGSVRSGSGTDGS
```

219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE

A0A212ME26 **A0A212ME26_ZYGBA** (175 aa)

Pre-mRNA-splicing factor CWC15. *Zygosaccharomyces bailii*

```
MTTSHRPQLEARSGAKAASYVPTSTQHARLLPGHKMLKYKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
DDDGEDSDDQKALLQELNQIKHERMVKKIREEQKQHSNVDLTRSTPQSSTSNWRKTTFGRGKISKQKPNDIKAQGYVNDM
TKTAYHEDFMRRFVK
```

41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE

A0A212MEC6 **A0A212MEC6_ZYGBA** (779 aa)
Histone acetyltransferase (EC 2.3.1.48). *Zygosaccharomyces bailii*

```
MKKDKTDPKEANDKSLAIKGSGRPPDQVAHRKRRVNSLLKELELTDNIYSKCAKEARDHPDEIRGKRRSRSLENENDNRK
NWKMPEDLAVANSLNSYVQFLPNEKPTREGSYDYSCNRILIRYQPAKLLGFQRLLSDPGGTLGAANRHTDCYRHDFDIYE
SEDLINMLDNDSTVPYRSAISQKKDYSTAKTIPTIKDREFFQQLLDQSSTARYFNANIFLADHDEEESSSNTKSPKKRAQ
LKKTIPNQDSRTSSIEYIYLRDYEIKTWYTTPYPEEYNRNKILYICEYCLKYMNSRYIYYRHQLKCSYFRPPGNEIYRDG
KISVWEIDGRENVIYCQNLCLLAKLFLNSKTLYYDVEPFIFYVLTEREDEQGEPRKFHLVGYFSKEKLNSTDYNLSCILT
LPIYQRRGYGHFLMEFSYLLSRREFKWGTPEKPLSDLGLLSYRNFWKVKCAQVLMKLKIFLDQGLPSLQVSLEDISNLTG
MIPTDVVFGLEQLHVLVRRRTKEGNIQYAIKIDSWERIEWIFHNWNKKGYCKLDASKLVWKPMIFGPSCGVNAVGTMIET
TTGATRNTSGINDLQEDFFKKSMSMLVNFLKDDIADPRSMEDAAFEQIKQRKHNITEEVASSSDWEVCSQETLLQENGKT
GKKIKSNGGSYTNVETSELNTENARGKENHSHGKVNYSCGVLSEKQNGRGGVLHPARETDDEQQEEIEDEEEEQEEDEDE
EEAEEEEEEEEEEEEEEEEEEEGDAISTRRSKRLRQLREPQPFRHHLRGRGTKYNDNM
```

724 - 743:	EEEEEEEEEEEEEEEEEEEE

A0A218UBI5 **A0A218UBI5_9PASE** (1379 aa)
Metalloendopeptidase (EC 3.4.24.-). *Lonchura striata domestica (Bengalese finch)*

```
MDDSSKEALMEEAPPRYTESPRLPCIPHELKSLLLMVALVVVALVVVNVAFLLLGLRLSESHAETVLRMTTHGLDGDGSP
QQLAVSKKERSGTFAVRDGHNGSAAVVYDYGKLPAVGLGWEWEEEEEEEEEEEAAMESSMKQVVLEEEDPANGCCLSCAT
CCGKCCARCSMCCARCCTKCSWCCAKCCCLPKCCKCPKCPKCAKCPGCGSCSGCLKKSLCFVPRLLCYLPRKLLSCGRLR
CLLIAVVLLVLLALRDELRAGPAREDDAVTFYLDNGDGNAATVIYDYQNLLVSYRARLHRACFVTRVDKDDIPGLDTVVE
TFQRRQRGEEEEEEEFQERRRTRRGGVPREEKRKRRRSSKRGEEEEEEEFQERRTRRGGVPREGKKKRRSSKRGEDLRGE
EEEEEEEEEEEEEEEEEEEEEEEVGEEEEEFQERRRGGGGVSREKKRRRRRTAFLGDIALDEEDLQLFQVERVVDLARHT
ITRLPSNSSGSNATVPRPGHAGHRGRQRARSRRAATSRPERVWPDGVIPYVISGNFSGSQRAIFRQAMRHWEKHTCVTFL
ERNDEDSYIVFTYRPCGCCSYVGRRGGGPQAISIGKNCDKFGIVVHELGHVIGFWHEHTRPDRDDHVSIIRENIQPGQEY
NFLKMEPEEVESLGETYDFDSIMHYARNTFSRGIFLDTILPKYDVNGIRPAIGQRTRLSKGDIAQARKLYRCPACGETLQ
DSQGNFSSPEFPNGYSAHMHCVWRISVTPGEKIILNFTTLDLYRSRLCWYDYVEVRDGFWRKATLRGRFCGNKLPEPIIS
TDSRLWVEFRSSSNWVGKGFFAVYEAICGGDVRKDNGHIQSPNYPDDYRPSKVCVWRITVSEGYHVGLTFQSFEIERHDS
CAYDYLEIRDGSSDSSSLIGRYCGYDKPDDIKSTSNKLWMKFVSDGSINKAGFAVNFFKEMDECSRPNNGGCEQRCVNTL
GSYKCACDPGYELAADKRRCEAACGGFLTKLNGSITSPGWPKEYPPNKNCIWQLVAPTQYRISLQFDFFETEGNDVCKYD
FVEVRSGLTADSKLHGKFCGAEKPDVITSQYNNMRIEFKSDNTVSKKGFKAHFFSDKDECSKNNGGCQHECLNSFGSYEC
QCRSGFVLHDNKHDCKEAGCDHKVTSTSGSITSPNWPDKYPSKKECTWAISTTPGHRIKLTFSELDVEAQQECTYDHLEI
FDGKDAKAPALGRFCGAKEPEPVVSSGNKMFLKFVSDNSIQKKGFEATHSTVCGGQVRAEVKTKDLYSHAQFGDNNYPGG
SDCEWVIMAEEGFGVELIFQTFEIEEEADCGYDYMELFDGYDGTAPRLGRFCGSGPPEEVYSAGDSVMIRFHSDDTINKK
GFHLRYTSTKFQDTLHTRK
```

400 - 419:	EEEEEEEEEEEEEEEEEEEE
401 - 420:	EEEEEEEEEEEEEEEEEEEE
402 - 421:	EEEEEEEEEEEEEEEEEEEE

403 - 422:	EEEEEEEEEEEEEEEEEEEE
404 - 423:	EEEEEEEEEEEEEEEEEEEE

A0A218UEW3 **A0A218UEW3_9PASE** (731 aa)
Kin of IRRE-like protein 1. *Lonchura striata domestica (Bengalese finch)*

```
MGQGLKAWPRYRIVGTADSGQYNLEIRDAELSDDAVYECQATEAALRSRRAKLTVLIPPEDPTIDGAPEILLRAGTPYNL
TCRARSAKPAATIAWFRDGLQQDGAVTSTLSPCPQPLWSCPLPVSPPVSPAQELLADGKRESTTSLLAINPTDLDIGRVF
SCRSSNEAAPAGKETFVRLNVHRGSGACGRDLLEEEEEEEEEEEEEEEEEEEEEEEEEEEEAGPGLAGCCGQGRPPADPP
TVTLSIQPQTVQEGERVVFTCMATANPEIKGYRWAKGGVIIEEAKENRYDTQVDYTFFTEPVSCEVHNDIGSTNVSTLVD
VLSNSNQLYLKSVTQADAGQYVCKAIVPRIGVGEREVTLFVNGPPIISSRPVQFAARGGRGSVECFIGSTPPPDRIAWAW
QENVLEAGTLERYTVERSSTGSGVLSTLTINNVVDADFQTRYNCTAWNSFGPGTAIIQLEEKVSEEFPEFRVTTWGRAPL
GDPTNLLGAALWGRRDEGPGATPSSRVPAEVLPVGIIAGATIGASVLLICCLVALACFLYRRRKGSDGHSMSFKDDVDLK
QDLRCDTIDTREEYELKDPTNGYYNVRAHEERPASRSVLYGDYRVPGPGRFEARPPSRLSHSSGYAQLSSYPRGGPEFPA
EAAAPAPAPAPGDTASQLSYENFAGGGGGFAGGAAFPPYRLGFGGAAAGLERGAYEPFDVAGKFGGAARFSYTSQHSDYG
QRFQQRMQTHV
```

194 - 213:	EEEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEEE
196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE

A0A218V972 **A0A218V972_9PASE** (634 aa)
F-box/WD repeat-containing protein 4. *Lonchura striata domestica (Bengalese finch)*

```
MGRKGSPRSPQAEGGSRAASPPSPLWALPEELLLLICSYLDAQALGRLAQVCRRLRFLSSRDVLWRRIARGCLNSGFTQL
GTDLAPGIPVKERVKVSQNWRHGRCRRETVLKWKCKQVVSSSFSLLFVHYDVTRLICFVFFSSLLHAPNLLSVCSLMPWM
ELDGEYLYLSQAENIQAYHLCAGGSGLECHPQAIFSGHQEDVCRFVLVNSHIVSGGGDGSVVLHKIHGSYSVKFSAHEQE
VNCVDFQGGLIVSGSRDRTAKVWSLSAGRVGQCLHTVQTEDRVWSIAISPLLRDQGKPKCSGLVQMCKVRQTWEFLVEQW
NLHALWFTEVAVAREEKGEVYKGRKNLLNCEIPEWTCNVSVSALRRGWGEEKKGEEEEEEEEEEEEEEEEEEEEEEEEE
EEKSILCSDVWYAINKSSHYALLTVLAILFGICTIQLILPESIAFLNLSVKDQDALGRSGTAQIIQRSAVRIELSNGRRG
LRDISRAAFGEREWRRIGVDTGGQLLTCLGTDFHRGAGVLDVFYETPSLLLSCGYDTYIRYWDIRTSTRKCVQEWEEPHD
SALYCIRSDKNYMIASGSSYYGVVRLWDKRQTRCLQSFHLSSPTSSPVYCLRFSTTHLYAALASALHVLDFTAL
```

375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE
379 - 398:	EEEEEEEEEEEEEEEEEEEE
380 - 399:	EEEEEEEEEEEEEEEEEEEE
381 - 400:	EEEEEEEEEEEEEEEEEEEE
382 - 401:	EEEEEEEEEEEEEEEEEEEE
383 - 402:	EEEEEEEEEEEEEEEEEEEE

A0A218WML3 **A0A218WML3_PUNGR** (1167 aa)
Uncharacterized protein. *Punica granatum (Pomegranate)*

```
MQMAPLPSENGIDGDDEREDEEEEEEEEEEEEEEEEEEEEEEEEEEEPRLKYQRMGGSIPSLLSNDAASCIAVAERMIALGTH
DGTVHILDFLGNQVKEFAAHSATVNDLSFDIEGEYIGSCSDDGSVVINGLFIEERMKFDYHRPMKAIALDPEYSRKASRR
FVTGGLAGHLYFNSKKWLGYRDQVLHSGEGPIHTVKWRTSLIAWANDAGVKVYDTANDQRITFIERPRGSPRPELLLPHL
VWQDDTLLVIGWGTSVKIASIRTNTQNGANGTYSRIPVSSMNQVDIVASFQTSYYISGIAPFGDSLVVLAYIPGEEDGEK
DFSSSLPSRQGNAQRPEVRVVTWNNDELATDALPVLGFEHYKAKDYSLAHAPFSGSSYAGGQWAAGDEPLYYIVSPKDVV
IAKPRDAEDHISWLLQHGWHEKALAAVEAGQGRSELLDEVGSRYLDHLIVERKYAEAASLCPKLLRGSASAWERWVFHFA
HLRQLPVLVPYIPTENPRLRDTAYEVALVALATNPSFHKELLSTVKSWPSTIYSALPVISAIEPQLNTSSMTDALKEALA
ELYVIDGQYEKAFSLYADLMKPDIFDFIEKHDLQDAIREKVVQLMMLDPKRAVPLFIQNRDLITPSEVVLQLMSAQDKCD
SRYFLHLYLHVLFEVNPHAGRDFQDMQVELYADCDPKMLLPFLRSSQHYTLEKAYDICVKRDLVKEQAVEFVTMQHDDDL
WEELIKQCLNKPEMVGMLLEHTVGNLDPLYIVNMVPNGLEIPKLRDRLVKIITDYRTETSLRHGCNDILKADCVNLLVKY
YKEARHGVYLSSEEGEARAKRDDHRASSQDTVKPLTLKNSEVKSRTRGPARCCICFDPFSIQGLSVVVFFCCHAYHEACL
LDSLYTIDSKKGSKDGSSQRTMSDYGYDDGNDEEDEDEDESATNRMRMKKGKGSGLSVGDLDPTTEWHAPTEDVDDHRGG
VRAIDWRSSSRIDRDLEFEIAVDLGLFNKEAIEKERARLKDEMNRGYFADISEFKLHGGKVAAANKIIIPAMAAKKFPDI
EVTRYDRGSFKLPISCKGNMADANTPTVPKVSLVCLSFRANSQPMVDSWTVPFANAFNDPENVHLYEVSLIDQWLLCLRP
IKWLLLRVVRKTKHDGGKDALERQIVYSFGDHYYFRKELKILNLLTA
```

21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE

23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE

A0A218WV51 **A0A218WV51_PUNGR** (106 aa)
Uncharacterized protein. *Punica granatum (Pomegranate)*

```
MTTISLPLNKKRKEKKKKKKKKKKKKKKKKKRSIIVREEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEHM
SKSNICRIAFQRITTVPRKTSDNTFK
```

37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE

A0A218XUN9 **A0A218XUN9_PUNGR** (327 aa)
DUF2052 domain-containing protein. *Punica granatum (Pomegranate)*

```
MAEAAETSGGAGGRRELTSETKENIAERLSSLENLYFPRALHSSASDPSQRKSIFLDLLSRDVAVFLERYGSQLTNGELQ
EFDGLKDDYEINWHLNHLRSIKSPTSAELRSRSITVKNRRRAYLNKLMHDGQYFSEDAMREREPYLHHEYVGKFQDPSSR
SMARPGEKWSETLIRRSEEAFLVSEIRREQQRLGVAERDWVGNERRQEQEDMEEEEEEEEEEEEEEEEEEEEQKNMEAEK
GEQAMKMNGSSHVESTSRGNEGPSTALSDLEMQDQMDQFVYIMQQKFLTGEDHEHLDYSKIDDDETLDDHWLREASHDAE
EKYFAED
```

213 - 232:	EEEEEEEEEEEEEEEEEEEE

A0A225XMT5 **A0A225XMT5_CRYNV** (1309 aa)
ATP-dependent RNA helicase DHX37/DHR1. *Cryptococcus neoformans var. grubii c45*

```
MAGPPVRQRYNAKARGSVAGGSSHKKRKNITKERTEEDAQDNEADQHGAVFEDPTAGMSSKKRKRFESYMAKKLKSEQRL
ETFKLLQSLAPSSSTSASLLSASTLGQNPLNPTSARERQEKREDRFVRRGIDRLSKRFGEGDDDSGESENDAPSRKGKGK
AKEVMVEIIRDGQAEETEEVKTTVIPSKGERKAEIKAAEKGKRKGKLPKKAGWNPNLLSTQAPNSSSSEFDSSDSGNDTS
DEEEPKKAAEPSPTIEPELVSETIKSPISAPSAPTVLGGALKKSTDGQVVKPRVEIRRKRGFVYGMFGRRGIDHREDSDD
EDEDDEDEDDEDDDEEDDEMDSNEEASDEEDEGDSEGEGSEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVAPPKKKRS
LGFKDWALKQMGQTSQPSAPDLLAVDTATTLYKSHPLPAARVGEYIGPLGQELVMPTTSLLDQSKDSDKSKVRPNITRRP
SVSEARMGLPILAEEQSIIESILMHPVVIICGETGSGKTTQVPQMLYEAGFGYKGSDNPGMVAVTQPRRVAAVSLAERVR
SELNLPQNSSLVAHQIRYSSTTSPDTAIKFMTDGVLLRELASDFLLSRYSVVVVDEAHERGVNTDVLVGVLSRVAKLREK
LWREGKQDVKPLRIVVMSATLRVSDFAENPTLFSKPPPVIHIAARQHPVTVHFSRRTVSDYVTEAYKKVSKIHARLPPGG
ILVFMTGQSEIQALCRKLEKKYGAKKSSQKPQIINDNSLPPEEREAEEVEFGKDEDLAADVDDGAAESDPEALDTDDEIE
GIPGLEFDEPADAPLHVLPLYSLLPNDQQMLVFKPPPEGHRLVIISTNVAETSLTIPGIRYVVDSGRAKERHYDPTNGVQ
SFQVSWISKASASQRAGRAGRTGPGHCYRLYSSALFEDHFEQFSKPEILRMPIEGVVLQMKSMNIDAVINFPFPTPPDRA
ALRRAENLLTNLGALSLPTLTKMINGVQHKGSAGGQITDLGKAMAGFPVSPRFAKMLAIGTQHDCMSYIIAIVAGMSVSD
PFIHEQSLEVDEEEDEAAEISHIKSEEIKEKEQRKETRRRFFKAQQQFLALGKGTSDMFKLLAAIGAYEYDPSPAFCAKT
FIRLKAMQEIHQLRAQISSIAKVPLSKLLPPNDTQLKVLRQILAAGFIDQVAVREDLVLKKGVSYESTRGVAYRAVGLGS
EPVFIHPSSALFHRAPPDFVVFSEIVRTSKPWMKGVTKINPAWLPSLGKGLCTFSKPMEMPTKGFARKSGLKDDEREVFV
TPHFKDLGVDLPVMKKKQRREGTRWILVD
```

361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE

A0A225XPH2 **A0A225XPH2_CRYNV** (541 aa)
Non-specific serine/threonine protein kinase (EC 2.7.11.1). *Cryptococcus neoformans var. grubii c45*

```
MKLDATDLRYISADEFRVLTAVEMGSKNHEVVPSQLVAELSQIRGGNVKKALGDLAKRNLVARVQNVKYDGFRLTYGGLD
YLALRTFSRRKPPSVHSVGTRIGVGKESDIYVVADERGEKRVLKMHRLGRISFRAIKSKRDYLGKRKSASWMYMSRLSAQ
KEFAFMKALYQHGFPVPVPIDQARHCVVMSLVDGYPLRSVEAVDDPADLYSKLMELIVRLAHAGLIHGDFNEFNVMLLRK
TGEPVVIDFPQMVSTRHENAEYFFNRDVNCIRRFFRRRFRYEATSWPTWKNVLEIETGNVENAVQGGVNDGLTDLPVAQN
RVRIDLEVEASGFGRALQRELEDYMIEVQDIPGSESDEEEDEEEKEEEEEEEEEEEEEEEEEEEEEEEEEALSSHVQGND
EKEFSDEAAVAARLEALRLHRALGNDVSDEDADPDSEHSLTDFTSDDDSDDSDDSTGVAQTDFTTYTPSMRNQPRHHTRL
PVKEFENRGGARSAIAKQVERERHQTERKVNAGKTSVKLGKQKGHKWKSSDKYVVGKDSGW
```

366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE

A0A225XQJ0 **A0A225XQJ0_CRYNV** (1603 aa)
Uncharacterized protein. *Cryptococcus neoformans var. grubii c45*

```
MPPKKKARRLAKSQSATKEEVTEKPSRPRKARDLSGGAGTSRSDIDPRAAIALVKVSRDNRSVTFESASDGYAPRRKASR
QKNGRHLMRSSLIGPTVLTMTILDRVEILANVAGDCLLTLLTNGYPPRNRRDSAVDEGKRAWDGLYALKQSYIFSPYSPP
FPLPEDVLSSLSPTTSASLRRNPLALNRAVYLSNLATFVWLILRPDEAGDIMAPLDVDEGNDRRITRSQQGINAERETIK
GRVRRRNALMVAAWKKYWTAIIPKGQHGKEIALRLWLDLVTQIDITYRLQTITSSTKSEFLPHIDEVLHDDMFSASSISR
FGFPSDQDTSSGEGEDGEDHKLYLHDLWGDLCVEREEELPKLEQEEARTAYPWEDFQRGMLRFVKDEVLGESGEESLLTP
GRRGALAGTQTRTNQTASESELDSERQESPEQSQMTAQTPNSPLHSFAAQPARDNPNTDDDPIDFDLLDEIARELAAEES
NQADPASPPLDGDRNGNGNGDNSNSRNSPETSSTWAINESTPVPSRPSSSRPLSHENQSTKAKGKERGPLNLFGKKLEKN
GFEWNKRQEGAERIEWESQSQSQVSTPRASRQAQEEIGKAIQKQLEETQEEVEPILYEAYDPSDLLPDARQFQSINPRPD
EANEEGYLEGEVLLDPRQLNHLQQPVGEEEEDYQEDIMFDPRQLNAKRETEDGEEGYEEDEGLMPDPRQFARTTRSQSKR
TEKAGTPAGMKTEEAETQIAKEEEEEQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDQ
EDHDYNELLGSLEENPTSAQPEQPAQIPARDGDFIFHSSPDFPFDDLPPQAEMDDYDVEDVARAERQAELEAENAWKGSG
DDNDDADTNIERHGMPEEKEAEQKEEEEEEKEEEEEEEEEEEEEEEEEESTPRGKRPYSSAFAPISSSEDEADRQRIFSH
GRKSSRTLTSQKKSTQPQSLQTALFSPPTSPDRFPPNRQASAGPGPSTLQNRHAAAQPSSSAQSLFFENDENPPEREDDS
EDASTIIEERDPFLVDEDGNSLTPNKEFTLPDDRNKQYVFFESKLHGQTSQKGSRYVRLSGPRRWTKEEELLLWRTVQRI
PATQVYPLRVVWYLHGDGGRLSEKLKWFSVQHMKDKMRTTVMRRLRAGERVEGNARAWAPLGSKEREDWDEEQSDRMHER
ALLAIQLERRKFEKKKEATRLREEERERRKEEKRRNQEEKKRAREEKERKCQDEKRRLQEDKRKCKEERKKKKEEEKRRE
EEEKQRKKEEREKKAEIKGKGKQHSESEDEESEEHENEEQQDEPQEEEDGLESSVDGSDENESSSSRPSPKRRATRGKPS
SDNPEHNTKKRSKVQKGADAAAATRTSSHTNTKRPSLRSKRLMMEARKSHAAANSSSEEEDDALENEAEQTTSQSPVRSA
PFKTTAARKTASQPAKHSQGAVTVRAARKTTSSADDVTSRPINPTHTSTGLSSSDITNQSTAKRIQSDQERDLTTETGGK
TDRGSESEIDELQQELELELDSESEVSPPESKEEMVEDDDVHPPLGQGSHATTDWPEQIDSSAQVTHVSGTQYADDAEPA
ESQ
```

748 - 767:	EEEEEEEEEEEEEEEEEEEE
749 - 768:	EEEEEEEEEEEEEEEEEEEE
750 - 769:	EEEEEEEEEEEEEEEEEEEE
751 - 770:	EEEEEEEEEEEEEEEEEEEE
752 - 771:	EEEEEEEEEEEEEEEEEEEE
753 - 772:	EEEEEEEEEEEEEEEEEEEE
754 - 773:	EEEEEEEEEEEEEEEEEEEE
755 - 774:	EEEEEEEEEEEEEEEEEEEE
756 - 775:	EEEEEEEEEEEEEEEEEEEE
757 - 776:	EEEEEEEEEEEEEEEEEEEE
758 - 777:	EEEEEEEEEEEEEEEEEEEE

759 - 778:	EEEEEEEEEEEEEEEEEEEE
760 - 779:	EEEEEEEEEEEEEEEEEEEE
761 - 780:	EEEEEEEEEEEEEEEEEEEE
762 - 781:	EEEEEEEEEEEEEEEEEEEE
763 - 782:	EEEEEEEEEEEEEEEEEEEE
764 - 783:	EEEEEEEEEEEEEEEEEEEE
765 - 784:	EEEEEEEEEEEEEEEEEEEE
766 - 785:	EEEEEEEEEEEEEEEEEEEE
767 - 786:	EEEEEEEEEEEEEEEEEEEE
768 - 787:	EEEEEEEEEEEEEEEEEEEE
769 - 788:	EEEEEEEEEEEEEEEEEEEE
770 - 789:	EEEEEEEEEEEEEEEEEEEE
771 - 790:	EEEEEEEEEEEEEEEEEEEE
772 - 791:	EEEEEEEEEEEEEEEEEEEE
773 - 792:	EEEEEEEEEEEEEEEEEEEE
774 - 793:	EEEEEEEEEEEEEEEEEEEE
775 - 794:	EEEEEEEEEEEEEEEEEEEE
776 - 795:	EEEEEEEEEEEEEEEEEEEE
777 - 796:	EEEEEEEEEEEEEEEEEEEE
778 - 797:	EEEEEEEEEEEEEEEEEEEE
779 - 798:	EEEEEEEEEEEEEEEEEEEE

A0A225YN53 **A0A225YN53_CRYNV** (844 aa)
Uncharacterized protein. *Cryptococcus neoformans var. grubii c45*

```
MMYATELISKSQSSASITANCSRSVPSPRKTLTERTTFLQFYTYRNDQNPRAQIEGSIGDRTHRVKVIFEVEETDKFEQP
DPDTGYKHSLTSQLRSIFQIKEFYIRIGPPSLLAGTEIPLVTFFVTKWDVVSGNHDEPVYWLDTCKIGEGNNDGKVREVL
KKWWCGESNSEPSQNRSSQNILSQGNIPDMSITAASPKGEKDVIYYHRTTVALGDIVSIEEAKASRVGEWDAQSALAWLE
RNQDTVLNTCAQYRNHPSNNVETIKSLQHFQGKTAPKEPSGNGHPPKSQPTDAVNSRSPHLSNNKRSPSGSSQSHHISSS
SLLRASPTKGQFSREKITDPLSFPSSPATNMSPGNTDEELLSPYEREERRKRGRKSKGVRGDGSKKMEQRSPSSSQLSQL
SWMSPSSPTMAMPRKSGAELSQADCPLPELTTSGNATISNARDKWKRPRESLNSRRQSRVVVWDEDEDIAEEPLIKNASK
RKIILSSSEAPSQVIEIQGSSDEENFAQTSSSSTPKRSTRGDTGQTVIAQQGATLRTREATKPIKPPSGSNVLNEITVGQ
RTSKEGDKREENRRGKGGNELEGKEKATEEEKEERETEKEDEEEEEEEDEGNRKEMKEEEEEEEEEIEEEEEEIEEEEE
EIEEEEEEIEEEEEEIEEEEEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDREMKEKKEKGLQVKLGEKRAEEEEE
EVRGRTMKKTEISVKEDNDGANDSRAQRRLENERLARMDIPGMGKEMGKAHTPPLVLEGGSEIPPKKRKHRAEDPTSSQH
VPKFGGFKLDMTLREGGLDEARVLQMLGWAREKRQEIAKRVKKP
```

665 - 684:	EEEEEEEEEEEEEEEEEEEE
666 - 685:	EEEEEEEEEEEEEEEEEEEE
667 - 686:	EEEEEEEEEEEEEEEEEEEE
668 - 687:	EEEEEEEEEEEEEEEEEEEE
669 - 688:	EEEEEEEEEEEEEEEEEEEE
670 - 689:	EEEEEEEEEEEEEEEEEEEE
671 - 690:	EEEEEEEEEEEEEEEEEEEE
672 - 691:	EEEEEEEEEEEEEEEEEEEE
673 - 692:	EEEEEEEEEEEEEEEEEEEE
674 - 693:	EEEEEEEEEEEEEEEEEEEE
675 - 694:	EEEEEEEEEEEEEEEEEEEE

A0A226A0W5 **A0A226A0W5_CRYNV** (30 aa)
Uncharacterized protein (Fragment). *Cryptococcus neoformans var. grubii c45*

```
EEEEEEEEEEEEEEEEEEEEEEEEEEEEDS
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE

7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE

A0A226BAF5 **A0A226BAF5_CRYNV** (1617 aa)
Uncharacterized protein. *Cryptococcus neoformans var. grubii Bt85*

```
MPPKKKARRLAKSQSATKEEVTEKPSRPRRARDLSGGAGTSRSNIDPRAATALVKVSRDNRSVTFESASDGYAPRRKASR
QKNGRHLMRSSLIGPTVLTMTILDRVEILANVAGDCLLTLLTNGYPPRNRRDSAVDEGKRAWDGLYALKQSYIFSPYSPP
FPLPGDVLSSLSPTTSASLRRNPLALNRAVYLSNLATFVWLILRPDEAGDIMAPLDVDEGNDRRITRSQQGINTERETIK
GRVRRRNALMVAAWKKYWTAIIPKGQHGKEIALRLWLDLVTQIDITYRLQTITSSTESEFLPHIDEVLHDDMFSASSISR
FGLPSDQDTSSGEGEDGEDHKLYLHDLWGDLCVEREEELPKLEQEEARTAYPWEDFQRGMLRLVKDEVLGESGEESLLTP
GRRGALARTQTRTNQTASESELDSERQESPEQSQMTAQTPNSPLHSFAAQPARDNPNTDDDPIDFDLLDEIARELAAEES
NQADPASPPLDGDRNGNGNGDNSNSRNSPETSSTWAINESTPVPSRPSSSRPLSHENQSTKAKGKERGPLNLFGKKLEKN
GFEWNKRQEGAERIEWESQSQSQVSTPRASRQAQEEIGKAIQKQLEETQEVVEPILYEAYDPPDLLPDARRFQSTNPRPD
EANEEEGYLEGEVLLDPRQLNHLQQPVGEEEEDYQEDIMFDPRQLNAKRETEDGEEGYEDDEDLMPDPRQFARTTRSQSK
RTEKAGIPAGMKTEEAETQIAKEEEEEHEEEEEEEEEEEEEEEEEEEEEEEEGEKEEEEEEGEKEEEEEEDHDYNELLGS
LEENPTSAQPEQPGQIPARDGDFIFHPSPDFPFDDLPPQAEMDDYDVEDVARAERQAELEAENARKGSGDDNDDADTNIE
RHGMPEEKEAEQKEEEKEEEEEEKEEEVEEEEEEEEEEVEEEEEEEEEEESTPKGKRPYSSAFAPISSSEDEADRQRIFS
HRRKSSRTLASQKKSTQPQSLQTALFSPPTSPDRFPPNRQASAGPGPSTLQNRHAVAQPSSSAQSLFFENDENPPEREDD
SEDASTIIEERDPFLVDEDGNSLTPNKEFTLPDDRNKQYVFFESKLHGQTSQKGSRYVRLSGPRRWTREEELLLWRTVQR
VPATQVYPLRVVWYLHGDGGRLSEKLKWFSVQHMKDKMRTTVMRRLRAGERVEGNARAWAPLGSKEREDWDEEQSDRMHE
RELLAIQLERREFEKRMEATRLREEERERRKEEKRRNQEEKKRAREEKERKCQDEKRRLQEDKRKCKEERKKKKEEEKRR
EEEEKQREKEEGEKKAEIKGKGKQHNESEDEESEEHENEEQQDEPQEEEDGLESSVDGSDVRDGLESSVDGSDENESSLS
RPSPKRRATRGKPSSDNPEHNTKKRLKVQKGADAAAATRTSSHTNTKRPSLRSKRLMMEARKSHAAANSSSEEEDDALEN
EAEQTTSQSPVRSAPFKTTAARKTASQPAKHSQGAVTVRAARKTTSSADGVTSGPVNPTHTSTGLSSSDITNQSTAKPIQ
SDQERDLAAETGGKTDRGSESEIDELQQELELELDSESEVSPPESKEEMVEDDDVHPPLGQGSHATTDWPEQIDSSAQVT
HVSGTQYADDAEPAESQ
```

749 - 768:	EEEEEEEEEEEEEEEEEEEE
750 - 769:	EEEEEEEEEEEEEEEEEEEE
751 - 770:	EEEEEEEEEEEEEEEEEEEE
752 - 771:	EEEEEEEEEEEEEEEEEEEE
753 - 772:	EEEEEEEEEEEEEEEEEEEE

A0A226BAJ3 **A0A226BAJ3_CRYNV** (1294 aa)
ATP-dependent RNA helicase DHX37/DHR1. *Cryptococcus neoformans var. grubii Bt85*

```
MAGPPVRQRYNAKARGSVAGGSSHKKRKNITKERTEEDAQDNEADQHGAVFENPTAGMSSKKRKRFESYMAKKLKSEQRL
ETFKLLQSLAPSSSTSASLLSASTLGQNPLNPTSAKERQEKREDRFVRRGIDRLSKRFGEGDDDSGESENDAPSRKGKGK
AKEVMVEIIRDGQAEETEEVKTTVIPSKGERKAEIKAAEQGKRKGKLPKKAGWNPNLLSTQAPNSSSSEFDSSDSGNDTS
DEEPNKAAEPSPTVEPEPVSETIKSPISAPSAPTVLGGALKKSTDGQVVKPRVEIRRKKGFVYGMFGRRGIDHREDSDDE
DEDSDDEDDDEEDDEMDSNEESSDEEDEEDSEEEGNEEEEEEEEEEEEEEEEEEEEEVAPPKKKRSLGFKDWALKQMGQTS
QPSAPDLLAVDTTTTLYKSQPLPAARVGEYIGPLGQELVMPTMSLLDQSKDSDKSKVRPNITRRPSVSEARMGLPILAEE
QSIIESILMHPVVIICGETGSGKTTQVPQMLYEAGFGYKGSDNPGMVAVTQPRRVAAVSLAERVRSELNLPQNSSLVAHQ
IRYSSTTSPDTAIKFMTDGVLLRELASDFLLSRYSVVVVDEAHERGVNTDVLVGVLSRVAKLREKLWREGKQGAKPLRIV
VMSATLRVSDFAENPALFSKPPPVIHIAARQHPVTVHFSRRTVSDYVTEAYKKVSKIHARLPPGGILVFMTGQSEIQALC
RKLEKKYGAKKSSQKTQAINDNSLPPGEREAEEVEFGKDEDLAADVDDGAAESDPEALDTDDEVEGIPGLEFDEPADAPL
HVLPLYSLLPNDQQMLVFKPPPEGHRLVIISTNVAETSLTIPGIRYVVDSGRAKERHYDPTNGVQSFQVSWISKASASQR
AGRAGRTGPGHCYRLYSSALFEDHFEQFSKPEILRMPIEGVVLQMKSMNIDAVINFPFPTPPDRAALRRAENLLTNLGAL
SLPTLTKMINGVQHKGSAGGQITDLGKAMAGFPVSPRFAKMLAIGIQHDCMSYIIAIVAGMSVGDPFIHEQSLEVDEEED
EAAEISHIKSEEIKEKEQRKETRRRFFKAQQQFLALGQGTSDMFKLLAAIGAYEYDPSPAFCAKTFIRLKAMQEIHQLRA
QISSIAKVPLSKLLPPNDTQLKVLRQILAAGFIDQVAVREDLVLKKGVSYESTRGVAYRAVGLGSEPVFIHPSSALFHRA
PPDFVVFSEIVRTSKPWMKGVTKINPAWLPSLGKGLCTFSKPMEMPTKGFARKSVLKDDEREVFVTPHFKDLGVDLPVMK
KKQRREGTRWILVD
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE

A0A226BGN5 **A0A226BGN5_CRYNV** (617 aa)
Uncharacterized protein. *Cryptococcus neoformans var. grubii Bt85*

```
MEVSFGISSTCRPDPDTGYKHSLTSQLRSIFQIKEFYIRIGPPSLLAGTEIPLVTFFVTKWDVVSGNHDEPVYWLDTCKI
GEGNNDGKVREVLKKWWCGESNSEPSQNRSSQNILSQGNIPDMSITAASHKGEKDVAYYPRTTVALGDIVSIEEAKASRV
GEWDARSALAWLERNQDTVLNTCAQYRNHPSNNVETIKSLQHSQGKTAPKEPSGNGHPPKSQPTDAVNSRSPHLSNNRRS
PSGSSQSHHIPSSSLLRASPTKGQFSREKITDPLSFPSSPATNMSPGNTDEELLSPYEREERRKRGRKSKGVRGDGSKKM
EQGSPSSSQLSQLSWMSPSSPTMAMPRRSGAELSQADYPFPELATSGNATTSNARDKWKRPRESLNSRRQSRVVVWDEDE
DIAEEPLIKNASKRKITLSSSEAPSQVIEIQGSSDEENFAQTSNSSTPKRSTRGDTGQTVIAQQGATLRTREATKLIKPP
SGSNVLNEINVGQRTSEEGDKREENRRGKGGNALEGKEKATEEEKKERETEKEDEEEEEDEGNRKEMKEEEEEEEEEEI
EEEEEEEEEEEEEEEEEEEEKEEEEEEEEEEEEEEEEERRKRRRRKRRRRKRRTGR
```

561 - 580:	EEEEEEEEEEEEEEEEEEEE
562 - 581:	EEEEEEEEEEEEEEEEEEEE

A0A226MXX7 **A0A226MXX7_CALSU** (736 aa)
Ski_Sno domain-containing protein. *Callipepla squamata (Scaled quail)*

```
MGDLKSGFEEVDGVRLGYLIIKGKQMFALSQVFTDLLKNIPRTTVHKRMDHLKVKKHHCDLEELRKLKAINSIAFHAAKC
TLISREDVEALYTSCKTERVLRTKRRKLGRALAGGELRPERAPADPFRGFWKENKLWLGLNDSPRPLLPIRRKALRPGAA
ALLPASHLPHLFSKYTGHGYPELARAPRKAPGSYETATGGCSGSSDSESSCCSGRAAHDSDCGSSLSSSSEGSSEEEDEE
```

```
EEDEEGSGGSDSSEGSSEEEEEEEEEEEEEEEEEEEEEEDSTSDSDSSSVSSQVSVQSIRFRRTSFCSPPAVVHANFLYHL
AAAAAAPRPPAPAPTDPGGPPALRRAAGCVKPELPEEWGRPGWGPALRCPGGPGSCFAEIRERRAAEITFPHSEFPNNAK
STDLTINCVAKGASSPSPKTNNAFPQQRILREARKCLPATTTHCADNNTIAARILNNDSSSAAANSEKDSQIPHCIEFAT
DLPSLRTDPAEDAASPGAAELRSAEPGNEGLPFPPRVRIKTEEEASGEDGPDPPPHEPRCECNDPEEERRRVTEGSEQDA
LGTAKEDSACTEKETTSFPPLTQSQGLSCTLGTPKPEDGEYKFGARVRKNYRTLVLGKRPALQPPPLKPNLKSARSPRPA
GKAEPEGTLDDLTANNRRRRVAGNVASAVKRPFNFMANFPCPPSLIIGHDGDLLPAYSLSTTKDSQAPHRAHPVWKWQLG
GSAIPLPPSHKFRKFN
```

258 - 277:	EEEEEEEEEEEEEEEEEEEE
259 - 278:	EEEEEEEEEEEEEEEEEEEE

A0A226N1M3 **A0A226N1M3_CALSU** (140 aa)
Uncharacterized protein. *Callipepla squamata (Scaled quail)*

```
MSKCTNFERHKMHGHDTVELKNFWEKAIQEQTRQRESEESRLSKSALNKEEKEEEEKRRRGEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEKRREEKRREEKRREEKRREEKRREEKRREEKRREEKKDM
```

62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE

A0A226N1Z7 **A0A226N1Z7_CALSU** (303 aa)
Uncharacterized protein. *Callipepla squamata (Scaled quail)*

```
MKLQAVMENLQRQQRARLQQALEARQQEQQQQRSTPPPAQPPPASGQTPARGRGPDVAPAPLEEGTEPESAHIQRAQMAA
LAAMRAAAAGLSHSSSPGLSEESQEEEERGEEEEEEDEDGGGYQQEMASEEEEDLKGKWDEEDFEEDLGEEEEEEEEEE
EEEEEEEEEDYEEEEEMGEEGLGSAEAVRTGTGSLLLRKPPAPQHCRGEAQRLPGAQERLPAGLGPQGHAQLPQPAPDHG
DWTYEEQFKQVGAEGTWGLAPCVWLGLSLLRNRRVPLGVRVGCRENCWEQRGKKRRPGFANVK
```

150 - 169:	EEEEEEEEEEEEEEEEEEEE

A0A226NKB2 **A0A226NKB2_CALSU** (1094 aa)
MYT1 domain-containing protein. *Callipepla squamata (Scaled quail)*

```
MSGVGVPELSAAVVLTRWKDVGRSDPETLCENEFRGELLNQRWTCGEKISSCEGAASLHGTCIKMSLENDDKRARTRSKS
VRAKKRKLQDAEAEHLVSKRKSHPLKLALDEGYNVDSDGSEEAEAKEESGSEESEGTLEEDEAEAVEQEETRSPEPAEER
SPAKSAHYGQKPATSTSGPSKANYSNYQEIIANSLLNLGQIAEETLAIEGQLPEAELQVSKPPSNVVHLVHEDAGEEIVE
EECDKEIIIQTEDAEEVIEVTSERSSELCPEHQDDTNCEESCKLQKAMQAEAEEEDEEDEDEDEDEEEEEEEEEEEEEE
EEEEEEEMAPEVICEEAPHTSQDTQKSHCEGQFSPKPEYSVIVEVRSDDDKDDDVHSQKSAVTDESEMYDMMTRGNLGLLE
QAIALKAEQVKIVREPSRLPGEHVKHFQVDEKQSKPLDSIRKSYYGKGGILQDLRSEKSNVRRLAAMGLAMSQDSTLTTA
ASLAVRTKTGSPLRIFIVSVSLSFFPSPACSKVLAMHENVLKCPTPGCTGQGHVNSNRNTHRSLSGCPIAAAEKLAKSHE
KQQTQSGDPSKPSSNSDRILRPMCFVKQLEIPQYGSYRPNMVPATPRANLAKELEKYSKVTFDYASFDAQVFGKRMLAPK
IQTSETSPKAFKSKPFPKASSPSHSPSSSYVKSTSSSSTGFDYSHDAEAAHMAATAILNLSTRCWEMPENLSTKQQEAPG
KSMDIEVDENGTLDLSMNKNRKRESTFPSSSSCSSSPSVKSPDVSQRQNSTSATSSTMTSPQSSQTSRQDEWDGPIDYTK
PNRQREEEPEESEPAAHSFASSEADEQEVSEENFEERKYPGEVTLTNFKLKFLSKDIKKELLTCPTPGCDGSGHITGNYA
SHRSLSGCPLADKSLRNLMAAHSADLKCPTPGCDGSGHITGNYASHRSLSGCPRAKKSGIKITPTKDDKEDPELMNLSGC
PRATFAGKKGKLSGDEILNTKFKTSDVLENDEEIKQLNKEISELNESNSEMEAAMVKLQSQISSMEKNLKNIEEENKIIE
EQNEALFLELSGEQNFDAYVNTLTDMYTNQECYQNPENKDLLETIKQAVKGIQV
```

306 - 325:	EEEEEEEEEEEEEEEEEEEE
307 - 326:	EEEEEEEEEEEEEEEEEEEE

A0A226NQV6 **A0A226NQV6_COLVI** (173 aa)
Uncharacterized protein (Fragment). *Colinus virginianus (Northern bobwhite) (Tetrao virginianus)*

```
MAALAAMRAAAAGLSHSSSPGLSDESQEEEERGEEEEEDEEDGGGYQQEMASEEEEDLKGKWDEEDFEEDLGEEEEEEEE
EEEEEEEEEEEEDYEEEEEMGEEGLGSAEAVRTGTGSLLLRKPPAPQHCRGEAQRLPGAQERLPAGLGPQGHAQLPQPAP
DHGDWTYEEQFKQ
```

73 - 92:	EEEEEEEEEEEEEEEEEEEE

A0A226P4A7 **A0A226P4A7_COLVI** (480 aa)
Uncharacterized protein. *Colinus virginianus (Northern bobwhite) (Tetrao virginianus)*

```
MIKHLQNIEYASRTKLFTREKVRHFTFNFTLENQIHQGGEYFNDNYYGLTVWFPDMIKHLQNIEYASRTKLFTREKVRHF
TFNFTLENQIHQGGEYFNDKWSCQAEVTQWIAACSGLLQTAVVQGQCRRMLHGVFLRRKVGQFQMPKAYGGLTQANGTKM
HQNRLIYSTNKQLSSKDSVQTSEEKVGPFTRIIEAMGFTGPLKYSRWKIKVAALRMYTCCVEKTDYEEFFNTSKGAPETT
LMWVLHAYTIALFRTPKNSNVVAKDPAQEEVEEEDEEKDEEEEEEEVEDEEEEKEKEEEEEEEVEDEEEDEEEEEEEEDD
KEEEEEEEEEEEEEEEEEEEEKEEEEEEEEEEEEVEEEEEEEKEEEEEEEEEEEKEEVEEEEEEEEEEEEEEEEEEEEEK
EEEDEEEEEEVEDEEEDKEEEEEEVEDEEEEKEKEEEEEEEEEEEEVEDEEEEEEEDDEEEEEEEEDEEVEDEEEEEEEE
```

322 - 341:	EEEEEEEEEEEEEEEEEEEE
379 - 398:	EEEEEEEEEEEEEEEEEEEE
380 - 399:	EEEEEEEEEEEEEEEEEEEE

A0A226PFN7 **A0A226PFN7_COLVI** (1120 aa)
MYT1 domain-containing protein. *Colinus virginianus (Northern bobwhite) (Tetrao virginianus)*

```
MPTTLAIISALRNLILTYSNASLPQQQGNFVHPLRYVESPGFLGLWTKEQDDRSQYCQQLCATLAKLLGSLREEEDDSAW
YLSKPPGFNSSPIEEHATENEFRGELLNQRWTCGEKISSCEGAASLHGTCIKMSLENDDKRARTRSKSVRAKKRKLQDAE
AEHLVSKRKSHPLKLALDEGYNVDSDGSEEAEAKEESGSEESEGTLEEDEAEAVEQEETRSPEPAEERSPAKSAHYGQKP
ATSTSGPSKANYSNYQEIIANSLLNLGQIAEETLAIEGQLPETELQVSKPPSNVVHLVHEDAGEEIVEEECDKEIIIQTE
DAEEVIEVTSERSSELCPEHQDDTNCEESCKLQKAMQAEAEEEDEEDEDEDEDEEEEEEEEEEEEEEEEEEEEEEMAPEVI
CEEAPHTSQDTQKSHCEGQFSPKPEYSVIVEVRSDDDKDDDVHSQKSAVTDESEMYDMMTRGNLGLLEQAIALKAEQVKI
VREPSRLPGEHVKHFQVDEKQSKPLDSIRKSYYGKGGIPQDLRSEKSNVRRLAAMGLAMSQDSTLTTAASLAVRTKTGSP
LRIFVVSVSLSFFPSPACSEVLAMHENVLKCPTPGCTGQGHVNSNRNTHRSLSGCPIAAAEKLAKSHEKQQTQSGDPSKP
SSNSDRILRPMCFVKQLEIPQYGSYRPNMVPATPRANLAKELEKYSKVTFDYASFDAQVFGKRMLAPKIQTSETSPKAFK
SKPFPKASSPSHSPSSSYVKSTSSSSTGFDYSHDAEAAHMAATAILNLSTRCWEMPENLSTKQQEAPGKSMDIEVDENGT
LDLSMNKNRKRESTFPSSSSCSSSPSVKSPDVSQRQNSTSATSSTMTSPQSSQTSRQDEWDGPIDYTKPNRQREEEPEES
EPAAHSFASSEADEQEVSEENFEERKYPGEVTLTNFKLKFLSKDIKKELLTLSGCPLADKSLRNLMAAHSADLNLSGCPR
AKKSGIKITPTKDDKEDPELMNLSGCPRATFAGKKGKLSGDEILNTKFKTSDVLENDEEIKQLNKEISELNESNSEMEAA
MVKLQSQISSMEKNLKNIEEENKIIEEQNEALFLELSGEQNFDAYVNTLTDMYTNQECYQNPENKDLLETIKQAVKGIQV
```

374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE

A0A226PYT7 **A0A226PYT7_COLVI** (577 aa)
Ski_Sno domain-containing protein. *Colinus virginianus (Northern bobwhite) (Tetrao virginianus)*

```
MGDLKSGFEEVDGVRLGYLIIKGKQMFALSQVFTDLLKNIPRTTVHKRMDHLKVKKHHCDLEELRKLKAINSIAFHAAKC
TLISREDVEALYTSCKTEREEEEEEEEEEEEEEEEEEEEEDSTSDSDSSSVSSQVSVQSIRFRRTSFCSPPAVVHANFLYH
LAAAAAAPRPPAPAPADPGGPPALRRAAGCVKPELPEEWGRPGWGPALRCPGGPGSCFAEIRERRAAEITFPHSEFPNNA
KSTDLTINCVAKGASSPSPKTNNAFPQQRILREARKCLPATTTHCADNNTIAARILNNDSSSAAANSEKDSQIPHCIEFA
TDLPSLRTDPAEDAASPGAAELRSAEPGNEGLPFPPRVRIKTEEEASGEDGPDPPPHEPRCECNDPEEERRGVTEGSEQD
ALGTAKEDSACTEKETTSFPPLTQSQGLSCTLGTPKPEDGEYKFGARVRKNYRTLVLGKRPALQPPPLKPNLKSARSPRP
AGKAEPEGTLDDLTANNRRRRVAGNVASAVKRPFNFMANFPCPPSLIIGHDGDLLPAYSLSTTKDSQAPHRAHPVWKWQL
GGSAIPLPPSHKFRKFN
```

100 - 119:	EEEEEEEEEEEEEEEEEEEE

A0A229XUY4 **A0A229XUY4_ASPFM** (862 aa)
Uncharacterized protein. *Neosartorya fumigata (Aspergillus fumigatus)*

```
MATASSLAFTNMEVPGLDDTMEMASPYQGHVDDFDIDLDVMEDQASNADKDMTAADDYPDTLHDEDINQDGPRDADMIDD
VAEPTMVDADDQYQEASHNVEMQYGIEESHEEEMLEDEYVDDADTAAPEYQDVQVCDNTDKPGTEEAGSAEYPVAGDHAQ
EPAVGAHLEAKPKYHDGNGHELQGALDQRNDDADQPPDTHQPEIAVDTINSTNETDQVDSALKPLDAAKTRPDPGHPEGS
DDYNEGSDEHASQISQPVEEHGAAGDEGTDEQAAQDLGLQGPEQLSEHEPDTTGQVALHPVKVYYQENEISLFPPHEGDS
SETFFLEDESLAYEPLGKLFESCREVLYEHVGENETLVLDIESLNLQLMEDSTHISKVTLHQIIDVYLRLCHNDGIESPE
PLYLTLSTKSTISAEVSNLLLAASEGKGLSEINLWDDYQEVDEQLGEVSEAHDEGAHDEEEEEEEEEEEEEEEEEEEEEE
EKEEAQGQEEEPISPNRPMTNQNVDARELQAASDEDESHHDIQDNGEAFKAQELVGNDTASLAKRSSSVAPATDVQEDEL
NEEGEVEDANDPEFDKGTASNEEAAHEESNDSEEQQTDTTVTMTHLPGADMNDELENKDGSASPVHNDQTDRDLGNEHSE
IDKSGEENLERTGPVELEVPEGPGVSDDERQDSGSVKPVVGDSRTEQSLAGHGGPSIDDAVDNVEEHSQDLEESSTAGDD
DYLHKDSESVPTLQVSERQERDTPDPANDTLGFVEDLFESPSKGSKNKDGNLDDTSEFGKNHDEFEDDTPAEILRQHDDE
LPLDDEEYIDLGFADGPDTVDESPVSGLRSLDNRASKRIRDPEDEFDIAENASPDLKRSRSS
```

459 - 478:	EEEEEEEEEEEEEEEEEEEE
460 - 479:	EEEEEEEEEEEEEEEEEEEE
461 - 480:	EEEEEEEEEEEEEEEEEEEE
462 - 481:	EEEEEEEEEEEEEEEEEEEE

A0A229XWL6 **A0A229XWL6_ASPFM** (788 aa)
Uncharacterized protein. *Neosartorya fumigata (Aspergillus fumigatus)*

```
MAGSQKKSTKKFEKKHLKDVLERRKANAKIKQRIHLKEKRRADNARGRENGDVEEESPEERKKQNAFAEMNVDDFFAGGF
EIADADTDKGKSRRKDVTPKIGKRKRSEEQKEEDEEASSVASSEEEEDGGVSDDDAASQASSAPDDFEAHKNQLQALKDK
DPEFYKYLKENDSELLDFGEHGDLTEVLELSEDEAEEGPAKKKKKAAKDEGEEAADNTLTIAMVKKWQKLMEEQNSIRAM
RQAVLAFRCAAYINEAETQEQKYSISDPDVYHQVLVTALGTVPKVLAHHLPVKETASGKVRVSLDSKKFKTLTPLIKSHT
SSVHQLLVNLSDASTLKLTLSSIEPMLPYLLQFRKLLKVLIKTIVGIWADVSTTEATRITGFLLLRKLMVIGDSGLKETV
LKASYEGVVKGSRNTTVHTLSGVNLMKNSAAELWGIDQNISYTTGFSFIRQLAMHLRSSITNASKESYKTIYNWQYTHSL
DFWSRVLSQHCDGLVEAKAGKQSALRPLIYPVVQITLGAMRLIPTATYFPLRFQLTRALLRLSRATGTYVPLAPALLEVL
NAAEMRKPPKSSTLKQLDFSTAIRAPKSYLRTRIYQDGVGEQVAELLSEFFVLWTKHIAFPELSVPIVVALKRWLKQVGS
RTTGNKNAKVNQAILLLVQKVEANARWIEEKRLNVTYTPRNRAEVESFLKDVDWESTPLGAFVKTQRKLREEKAAILEQG
RREEEKRRAAEKKADEDEMMEDAPSDDDGSEASSGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEFEEE
```

756 - 775:	EEEEEEEEEEEEEEEEEEEE
757 - 776:	EEEEEEEEEEEEEEEEEEEE
758 - 777:	EEEEEEEEEEEEEEEEEEEE
759 - 778:	EEEEEEEEEEEEEEEEEEEE
760 - 779:	EEEEEEEEEEEEEEEEEEEE
761 - 780:	EEEEEEEEEEEEEEEEEEEE
762 - 781:	EEEEEEEEEEEEEEEEEEEE
763 - 782:	EEEEEEEEEEEEEEEEEEEE
764 - 783:	EEEEEEEEEEEEEEEEEEEE
765 - 784:	EEEEEEEEEEEEEEEEEEEE

A0A229XXK9 **A0A229XXK9_ASPFM** (821 aa)
Diphthamide synthase (EC 6.3.1.14) (Diphthamide synthetase) (Diphthine--ammonia ligase). *Neosartorya fumigata (Aspergillus fumigatus)*

```
MSPPTQTPPATPGLNVIALISGGKDSLYSILHCIRNGHKVVALANLYPSTSRQAASTAAKDSHEDLKKEEGTEDEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEDIDSFMYQTIGHSVIPLYEAALGIPLYRAPITGDAVDTSRIYRHNAADQMAEGS
ESANEENKQHRQDETESLVPLLRRIKAAHPEANAVSAGAILSTYQRTRIENVASRLGLVPLAWLWQYPVLPAPVERSALS
AESSLLGDAGLLEDMAACGCEARIIKVASGGLDERFLWGNVSSADGALRRRIVNGMRRFAAPGDLRGAVLGEGGEYESLA
LDGPGFLWRSRIEVCETEVRTGEGGVGYVWLKGARCVPKTATEGDTITPESVRRPMLLDEAFARVLADVRSASGSYGGEV
LAKSISAGGIKCEPRQLRNGRIWHICNITAPEAGTEAAEQMKGIVEEIRTILQSSSNIPRGTEDIVFATVLLRSMADFAS
MNGSYVSLFKKPNPPARATVACGDELPEGVNVMVSFIVDLGDRDARQGLHVQSRSYWAPANIGPYSQAMSIPLRGAEHIV
YIAGQIPLEPASMQMVCDSAPTEERSWLSDYSLRAVLSLQHMWRIGVTMHVDWWLGAVAFITGAENIAAKAQVAWHIWET
MNRKRDDESIDEEESSFDVWDIKYGRRTEEQTPKATVSASIPNFEVLRSSGVTPPFLAVQVEELPRASDIEWQGLGYRCD
GLELNAEETDQGRITRTVTEQKAGYTIIEIDMEKPESDLKSALQRILAAHTVTSALTHAVIYTTKAFPLMTWPGEVVPCK
SVWGRKGRRLAAGIIFQSLES
```

75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE

A0A232ER23 **A0A232ER23_9HYME** (263 aa)
SWIB domain-containing protein. *Trichomalopsis sarcophagae*

```
MADISKDELRKEITAILKDADLTSMSAKKVRQQIEEKLDVDLTERKKEIDDLVMECLQEKQDSGKKKKTTSDESEDGEEE
EEEEEEEEEEEEEEEEEKKPAKRGPPKKTAAKRKKGSSDEEDSASDEDASDEEYSPKKAKPAAKKGKAGKKGKKGKGGDS
DSDSDWGKSKKSSGGPKKGGGGKGSGYTRAITLSPELAALVGAKQMPRYEVVKKLWSIIKERKLYDPKNKQFAICDDDLF
KVIGVKRFRTFGMMKYLKDHFVD
```

78 - 97:	EEEEEEEEEEEEEEEEEEEE

A0A238FIC1 **A0A238FIC1_9BASI** (1511 aa)
BQ2448_4585 protein. *Microbotryum intermedium*

```
MALVGFHSNAALDFKFLADADDICTRVLLDVCVFEEDRVSGRRTGKIDRHQRAETRLRQPDIDDVLNVVKRLRKAELTAT
EATEELCTINVFKNFMNKYEDDDYDIFKTHLKRYAAALRPDTGIAFHETNRYAKKQRKTNNTFSAFRSLLPTNAAGVVAL
PRLSPADSSIALNLLQPSTSHGPTPPKNDLIEVGVFATRAFQKGDIIRLQGGIADLTDEDDDEMRENGGRSDFSILWSER
KKCFCLLLGPARFVNHDCRNNVEFYLVGNVMSFKVVEDIQPDEEIFTHYGQQCSWLGVKEGVWVMLNPSPWCVRSGIHYF
ERDNMGCMCATCEKFKRGFFTPKPTRGSKKVSSHPAQQNPIVNPSVLPLSKLSSTTAIVSDHEGRRGRGGSDSSTTSPHP
VSASPRPESPYGTRRRSSIRVSEAASAHATSSSSSSSLMGNGVVQPPTSVTHQLMNALKARSSTRIRLSSFPLTLHHGKR
TPNGVKGTFTPPMTQFSSSSSSTIPNLNLNPNRLLTDLELRSGPRLVHPKLKPPPIYKDDYSWDERKKIAVYKGMVRAPQ
KPKKKVLTAREKRRERERLEERRKEEEEKRRSHRKRVVRVEEVDGAGGKGKQKGEVKREVKRGRVRSTRSRASTNASTNA
RPKRERKAKVLEEEEDADEEEEGEGEDEDEEEGEEEDEEEEEEEEEEEEEEEEEEEEEVKKPAPRKRIRATRTVPVTKPK
PARNRKAPTLAAAKSKLRRPASKRRKVRSESEDQQFVGVVVVDQSPVRSGSRRRSKKEVNGDDREVELGRFVPIGLSMDE
AVIESSGGMSAFEEDAYGRVPETPFDASSVASPYEKVGSEPMPPSRERPKDSVGSKGRQSLPPRDPTPLPPYLRRSTSIT
TRASIPPRDSTATELDSEMDTESRSDKDVVRATISTSSFFGVPIPIPKLRAFVTTHTTDPSGSSTTTTNGAGTSSSGSSS
THACTSSSSSSFAAGASATQSFRLGSRPRKGGGGAGQHDDEDDDDDEDERRRRQNGLHGEKVDDVIMEDIKPKVEEREEG
GEAVADGDAAMMVVDTPDEAMLGLGDEQAIDALDLRDTDTQEAAALLLMLNSPHSSANQDLSTNSAHSSNVSTPSAPGSS
ASGSSAQANRRPRVSTTSTKAVASTSMQRKRSRMSVDGTPSTSSASISTSKAPVASANPRSTRRHSQLDQGQSPVASTSG
STSKPNVKSVKSVAELKPVIQPQPIKPGERGTRRSAPLAGNLSDILATPAVLRVSGGYDAEKGRYIAKGAPVDIEGPLFA
LAPSKPNPSPKQTPSQSMSASTSSSSSGAPRRSLPGRLIINEPKQRRYSDSKLADRKPHNLARTASVPRASTSRGATSTS
AAQLVAPVVPPPRPRSVPTHSRATRFAAPLEGDLRALLDSESVGAVTGIYDPTKGKYVSQKYVAAAAAKQAPSSTSTSTS
TNETAESNGPEPIVVVDVGVGGSERARGTRASRPIAGSVADLLASPTVANVTGRFDAEKGKYVAGTTARKG
```

678 - 697:	EEEEEEEEEEEEEEEEEEEE
679 - 698:	EEEEEEEEEEEEEEEEEEEE

A0A250X9K8 **A0A250X9K8_9CHLO** (783 aa)
Uncharacterized protein. *Chlamydomonas eustigma*

```
MENPVLQSVIVESEGDIASNTNATPQSAEGENHAMTGSDSAAQAAEKDSRQEQEKDEEEYESEYETDEEEEEDEEDEEEE
EEEEEEEEEEEEEEEEENQKVTASVPVAHLAASTSDAKSSAPEEASDSHAPPPSSSPEATTTAAATPAPNETTHSTSSENV
NTEGDTAVGMITLPASLPDAPVKDENDSSLPTTHASAEDIPRGTSSNTLEEPPLTASQQLGSDPSALPAVAAAQEPEGSV
EAVPAASTAQDLECSIEAAPAASAPEETRSPADDIDTPAGHRLVEQSEDVHMSESSQTEVVPEIARGACGNREQSNHVQK
EKDAGRSADEKDQRKDSLPRLSPLAPEASTREEHQVVLSKEGEVYNQAVESEAHDLPQSSMLVEEGEVLMSGSSELPYHV
ANADSDPGLASNADSEPGLASNADSDPGQPAAKMLGSAPLQYTVGGAVTDEDEDEELEDLLVSSASTVALTDRHQAASEG
VASTENAYRGLNAQTQSATGSQMKALNPHKQPAMVPVRKVPQHAGGKPLSSRPGAKDLPRSAASTSPAGERYTHREEPRA
VPPSSHKQAGPEGLLRYHHWKPKEEVSSPTNKPPRAKHPLVNVDKDYIESVSYVVRPGVGQVYDWRSHHKKNEILARHRQ
EQKRAQIIIEAAKKEIAYRTESEKAFQAWLASKQKERKTFIKVQKRFAQMAAAVIPNSEMASAHPEDLSLKEHHWRDNFG
MPAHVSPTFSSFKPEAPWSEVADIDKETAMLERVVGEEQQDHAGQGDDKVSMRHRKLRLVNVN
```

77 - 96:	EEEEEEEEEEEEEEEEEEEE

A0A251NNU8 **A0A251NNU8_PRUPE** (804 aa)
Vacuolar protein sorting-associated protein 41 homolog. *Prunus persica (Peach) (Amygdalus persica)*

```
MAPIPPDNGVEGDDEREEGEEEEEEEEEEEEEEEEEEEEEEEEEEEPRLKYQRMGGSIPTLLTSDVATCIAVAERMIALGTH
GGTVHILDFLGNQVKEFPAHTAAVNDLSFDIEGEYIGSCSDDGSVVINSLFTDEKMRFEYHRPMKAIALDPDYAKKSSRR
FAAGGLAGHLYYNTKRWLGFRDQVLHSGEGPIHAVKWRASLIAWANDAGVKVYDTANDQRITFIERPRGSPRPELLLPHL
VWQDDTLLVIGWGTSIKIASIKTNQSRAANGTVKHVSMSMSNMNQVDIVASFQTSYFISGIAPFGDSLVVLAYIPGEEDG
EKEFSSSVPSRQGNAQRPEVRIVTWNNDELSTDALPVHGFEHYKAKDYSLAHAPFSGSSYAGGQWAEGDEPLYYIVSPKD
VVIAKPRDAEDHIAWLLQHGWHEKALAAVEAGQGRSELLDEVGSRYLDHLIVERKYAEAASLCPKLLRGSASAWERWVFH
FAHLRQLPVLVPYIPTENPRLRDTAYEVALVALATNPSFHMELLSTVKSWPPVIYSSLPVISAIEPQLNTSSMTDALKEA
LAELYVIDGQYEKAFSLYADLLKPDIFSFIEKHNLYDSIREKVVQLMMLDCKQAVPLLIQNKDLITPSEVVKQLLNASDK
CDSRYFLHAYLHSLFEANPHAGKDFHDVQVELYADYDSKMLLPFLRSSQHYKLEKAYEICIGRGLLREQVFILGRMGNAK
QALSVIINNLGDIEEAVEFVNMQHDDELWEELIQQCLHKPEMVGVLLEHTVGNLDPLYIVNMVPNGLEIPRSGSPSENHH
QLQD
```

21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE

A0A251P0S5 **A0A251P0S5_PRUPE** (667 aa)
Kri1_C domain-containing protein. *Prunus persica (Peach) (Amygdalus persica)*

```
MCGLQLFDGGSDSENEMEIEIENENDDIPQIKINEEYARRYEHNKKREDLQRYEELKKRGLVADPSRQSDSDSESSSSED
EDDILLANSKKKDLEFLEALIKVKNRDPSLKNKDVELFKSDGTEKTRAKGEGNGKAKKKMYLKDVVAKHLIEDGPELKED
```

```
DNNTKVYDEEQEQRRKEFLSAVAEDEEDDNGELLVEKDKNAVGDDDDDDSVVNAEYDQKLNECFPDEDENARFLRDFIKF
RQWKEDKRSKGSSPDVKEEDLEMVSEDEMEIERQEEYEHRFQENAGDRILGHSRQVEGSVRKKVKARKEQRKSKEDRMEI
ARLEREEELRHLKNLKKKENDENLKKIMEIAGIKEGEVSSFDAKELEKEFNPQEYDRMMKKAFGEEYYEAEDADFAFGSD
MDEDGGEIEKPDFDKEDELLGLPKGWDSVGSGDGFLAAREKVLKLKKENVGDHEEEEEEEEEEEEEEEEEEEEETVSEEG
KQEKKRKLALLERAKKEMMDEYYKLDYEDTIGDLKTRFKYAKIKPNRYGLSTAEILVMDEKELNQYVSLKKLAPYAEKEW
KVPNNKRNEIKQKVKEIFKQGKPGNKKNRKKQKISDAKDLNLSMDAAGQSSTGAPEHEKKLVDSNGDKGNPSRSARRRRN
QAARKLPASRLMAYGLMPVKSKKKGKH
```

454 - 473:	EEEEEEEEEEEEEEEEEEEE
455 - 474:	EEEEEEEEEEEEEEEEEEEE

A0A251PH19 **A0A251PH19_PRUPE** (478 aa)
Protein kinase domain-containing protein (Fragment). *Prunus persica (Peach) (Amygdalus persica)*

```
LHKLDPPVIHRDLKCDNIFVNGHLGQVKIGDLGLAAVLRGSHHAHCVIGTPEFMAPELYEEEYNELVDIYAFGMCVLEML
TSEYPYSECSNPAQIYKKVTSGKLPNAFYKIEDLEAQRFVGKCLENASKMLPAHELLLDPFLASDDRELLSTPRIPFQNL
MPNDDSAVVEEEEEEEEEEEEEEEEEEEEEELPLDLGVDLKRSTNMIITGKMNPEDDTIFLQVRISDQDGQNARNIYFPFD
IVNDTAIAVATEMVKELEISDWEPSEIAEMIEKEISSLIPGHKKWGTPQDYHPHQHSFKYEDEDDDHDHGHHPFYYFPSY
SSSQNSLHAFSSHCKTQFHCGENISNDQDWLQGDLFINDDASSQSSFSSCNYSNINYFSGTEDDHHDLISCFGKSHKSRF
CPSESRAANCYKHCNSQLHHQRPHELNHPLCHHQRKLPRIQSLIDVRSQLLHRSLVEEINKRRLFKTVGAVENIGVCK
```

170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE

A0A251TCF4 **A0A251TCF4_HELAN** (773 aa)
Uncharacterized protein. *Helianthus annuus (Common sunflower)*

```
MIVIEMLMCIQVNKLEHLMIPLTHIQSATNDFSETYKIDSGIPCSLYRAKVDNSDKKNHSSKRHDTVLIKRYPSGHHLYY
GEKQFLKEIEVLSSVKHPNIVSLLGFCVEASEMILVNENFSNGFLGEYLGNFRDKSILTWEKRLKICIDVAHALRYIHYE
MDLVNREVHSFNIGLDDNWGAKIAHFWWSVFLPPNQQDRAFYHNNNFIRDCCVEPEYEKTRNLNRESDVFGFGVVLLETL
CGRLVSDQIYLKESDKGLPNIARQRFHMGTLEDMIDPVIKEETGENHFVLNKGPNKESLHTFIKIALKCVAETQDKRPTM
KVVVKELEKALFFQKNNKDNPKMSFEDIKRATQNFHNDNCIGGGGFGKVYKGNLEDGDGFKIIVAKRLDTRFGQGEQQFL
GELQILLDYKHENVIGLVGYCDEKDEKVIVYEYAPKGSLERYLNDASLTWVKRLNICIDVARALDFLHGGVGKQAKVIHR
DIKTANILLSDDWKAKLADFGLSLISPLIQETDYVIDHACGTLGYLDPLYKKSGFLTIESDIYSFGVVLFEILCGRSTFE
IHKNEGHYLPEFIKNIFEAGKHDEVVFKHIREEIVPKSLTTFQEIACQCLHHEREKRPTTKEILRELKKALEFQEGCSGM
AKTVEQISMKYSETGKQIQETESSMQHTEQDYVSPTDRKATVIPLRSKQRVLEHLKQEVILGEHQVRMLKEELHKVEMAN
KSRLALIQALEEEEEEEEEEEEEEEEEEEEELFFLITISNIFLFIIWYICSFL
```

731 - 750:	EEEEEEEEEEEEEEEEEEEE
732 - 751:	EEEEEEEEEEEEEEEEEEEE

A0A258HKG2 **A0A258HKG2_9CAUL** (137 aa)
Uncharacterized protein. *Brevundimonas subvibrioides*

```
MKTKLFMAASTAAILFATGAMAQATMTVTNDGEVAITELAISGTSVEDFGDNLLDEEIAPGDGVEVTFDVGDDCVQDVQA
TYEDGDTEEVYDVDLCEGGGFEVEDDDADEEDPSEDEEEEEEEEEEEEEEEEEEEE
```

117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE

A0A260YPK6 **A0A260YPK6_CAERE** (119 aa)
Uncharacterized protein (Fragment). *Caenorhabditis remanei (Caenorhabditis vulgaris)*

```
MWLRVGEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEGETKTVITWLKCATATEVPHEALVVTYRTVTLVQNGGDDGSIIVTS
SLPRLIQRLTNNEKQRKTTTDQPICVIKNFEPSEIITCD
```

7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE

A0A286UQE2 **A0A286UQE2_9AGAM** (430 aa)
Pkinase_fungal domain-containing protein. *Pyrrhoderma noxium*

```
MSYTKSTKKTDASATAGYLNTETPNQDVPTKNIRPGTTLVRKQEGIVVPTFKKYKGEHPNRTNEVSSGHVVKIVSTSSRM
RIEQNAVATVRAILVKAEANIEKDNMDKSNETNKGKGRQVKLSQSLPNIYCTGTMETSRVLRDFLGPERRESRLAQMIFC
ERLDPAYTLTSTKEFKNVIRDIADASDERGWKHQNINCNNVMFRRLQDGSVQGVLTDWECVSALNIRFKSQLDDTRTTAF
MALGLLENNPPNEYLERFDYESLFYVIFLVCLGYPFQTPDNSLLPHDFLLTYNQWNSLDLDVARMSKFNYISNNFLEDSP
```

```
SNLLEKHHSLYMDWIAPLKSMFAWGYMNSKEPICESSDNSSESESETDSESGTETEEEEEEEEEEEEEEEEEEEEEEEE
EEEDALWNEDGWPTFGGSVTYEKTLLFSTT
```

376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE
379 - 398:	EEEEEEEEEEEEEEEEEEEE
380 - 399:	EEEEEEEEEEEEEEEEEEEE
381 - 400:	EEEEEEEEEEEEEEEEEEEE
382 - 401:	EEEEEEEEEEEEEEEEEEEE
383 - 402:	EEEEEEEEEEEEEEEEEEEE
384 - 403:	EEEEEEEEEEEEEEEEEEEE

A0A286XGR1 **A0A286XGR1_CAVPO** (1079 aa)
Myelin transcription factor 1. *Cavia porcellus (Guinea pig)*

```
MSLESDDKRARTRSKALRGPPETTGADLSCPTPGCTGSGHVRGKYSRHRSLQSCPLAKKRKLEGPEAEHLLSKRKSHPLK
LALDEGYGVDSDGSEDGEVKDASVSDESEGTLDEAETEMSGQEEIHRLEPAEGRSPIKSHFGSNPISSPTGSSKGSYSSY
QGIIATSLLNLGQIAEETLVGEDSGQVAKLGPSIVHLLQEEAAEEATSDEGEKDLYIQPEDAEEVIEVTSERSQEQCSQS
MEVLAREGSSKQKGVLGQEEEEEEEEEEEEEEEEEEEEEEVEEEEEDEDEEEEEEGEEATPNVHFEEDATHTSALKGPEL
RCPGSSSPKPEYSVIVEVRSDDDKDEDMHSQKSTITDESEMYDMMTRGNLGLLEQAIALKAEQVHTVCEPGRPPSESGQP
APGEPGKVVKPLDTARKSCYSKDPSRAEKREIKCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRIPPEILAMHENVLKCPT
PGCTGQGHVNSNRNTHRRPMCFVKQLEVPPFGSYRPSVAPATPRANLAKELEKFSKVTFDYASFDAQVFGKRMLAPKIQT
SETSPKAFQCFDYSHDAEAAHMAATAILNLSTRCWEMPENLSTKPQDLPSKSVDIEVDENGTLDLSMHKHRKRENALPSS
SSCSSSPGVKSPDVTQRQSNTSAPSSSMTSPQSSQASRQDEWDRPLDYTKPSRLREEEPEESEPAAHSFASSEADDQEVS
EENFEERKYPGEVTLTNFKLKFLSKDIKKELLTCPTPGCDGSGHITGNYASHRSLSGCPLADKSLRNLMAAHSADLKCPT
PGCDGSGHITGNYASHRSLSGCPRAKKSGLKVAPTKDDKEDPELMKCPVPGCVGLGHISGKYASHRSASGCPLAARRQKE
GSLNGSSFSWKSLKSEGPTCPTPGCDGSGHANGSFLTHRSLSGCPRATFAGKKGKLSGDEVLSPKFKTSDVLENDEEIKQ
LNQEIRDLNESNSEMEAAMVQLQSQISSMEKNLKNIEEENKLIEEQNEALFLELSGLSQALIQSLANIRLPHMDPICEQN
FDAYVNTLTDMYSNRDCYQNPENKGLLETIKQAVRGIQV
```

259 - 278:	EEEEEEEEEEEEEEEEEEEE
260 - 279:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE

A0A286XXN5 **A0A286XXN5_CAVPO** (514 aa)
Thyroid hormone receptor alpha. *Cavia porcellus (Guinea pig)*

```
MEQKPSKVECGSDPEENSARSPDGKRKRKNGQCSLKTSMSGYIPSYLDKDEQCVVCGDKATGYHYRCITCEGCKGFFRRT
IQKNLHPTYSCKYDSCCVIDKITRNQCQLCRFKKCIAVGMAMDLVLDDSKRVAKRKLIEQNRERRRKEEMIRSLQQRPEP
TPEEWDLIHVATEAHRSTNAQGSHWKQRRKFLPDDIGQSPIVSMPDGDKVDLEAFSEFTKIITPAITRVVDFAKKLPMFS
ELPCEDQIILLKGCCMEIMSLRAAVRYDPESDTLTLSGEMAVKREQLKNGGLGVVSDAIFELGKSLSAFNLDDTEVALLQ
AVLLMSTDRSGLLCVDKIEKSQEAYLLAFEHYVNHRKHNIPHFWPKLLMKEREVQSSILYKGAAAEGRPGGSLGVHPEGQ
QLLGMHVVQGPQVRQLEQQLGEAGRLRGPVLQHQSPKSPQQRLLEVLHRSGVLHARAVCGDDDSSEAGSPSASEEEEEEE
EEEEEEEEEEEEEEEEEEESPEGCMDPAGSAASP
```

474 - 493:	EEEEEEEEEEEEEEEEEEEE
475 - 494:	EEEEEEEEEEEEEEEEEEEE
476 - 495:	EEEEEEEEEEEEEEEEEEEE
477 - 496:	EEEEEEEEEEEEEEEEEEEE
478 - 497:	EEEEEEEEEEEEEEEEEEEE
479 - 498:	EEEEEEEEEEEEEEEEEEEE
480 - 499:	EEEEEEEEEEEEEEEEEEEE

A0A286Y0T3 **A0A286Y0T3_CAVPO** (1117 aa)
Myelin transcription factor 1. *Cavia porcellus (Guinea pig)*

```
MSLESDDKRARTRSKALRGPPETTGADLSCPTPGCTGSGHVRGKYSRHRSLQSCPLAKKRKLEGPEAEHLLSKRKSHPLK
LALDEGYGVDSDGSEDGEVKDASVSDESEGTLDEAETEMSGQEEIHRLEPAEGRSPIKSHFGSNPISSPTGSSKGSYSSY
QGIIATSLLNLGQIAEETLVGEDSGQVAKLGPSIVHLLQEEAAEEATSDEGEKDLYIQPEDAEEVIEVTSERSQEQCSQS
MEVLAREGSSKQKGVLGQEEEEEEEEEEEEEEEEEEEEEEVEEEEEDEDEEEEEEGEEATPNVHFEEDATHTSALKGPEL
RCPGSSSPKPEYSVIVEVRSDDDKDEDMHSQKSTITDESEMYDMMTRGNLGLLEQAIALKAEQVHTVCEPGRPPSESGQP
APGEPGKVVKPLDTARKSCYSKDPSRAEKREIKCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRIPPEILAMHENVLKCPT
PGCTGQGHVNSNRNTHRSLSGCPIAAAEKLAKSHEKQQPQTGDPSKNSSNSDRILRPMCFVKQLEVPPFGSYRPSVAPAT
PRANLAKELEKFSKVTFDYASFDAQVFGKRMLAPKIQTSETSPKAFQCFDYSHDAEAAHMAATAILNLSTRCWEMPENLS
TKPQDLPSKSVDIEVDENGTLDLSMHKHRKRENALPSSSSCSSSPGVKSPDVTQRQSNTSAPSSSMTSPQSSQASRQDEW
DRPLDYTKPSRLREEEPEESEPAAHSFASSEADDQEVSEENFEERKYPGEVTLTNFKLKFLSKDIKKELLTCPTPGCDGS
GHITGNYASHRSLSGCPLADKSLRNLMAAHSADLKCPTPGCDGSGHITGNYASHRSLSGCPRAKKSGLKVAPTKDDKEDP
ELMKCPVPGCVGLGHISGKYASHRSASGCPLAARRQKEGSLNGSSFSWKSLKSEGPTCPTPGCDGSGHANGSFLTHRSLS
GCPRATFAGKKGKLSGDEVLSPKFKTSDVLENDEEIKQLNQEIRDLNESNSEMEAAMVQLQSQISSMEKNLKNIEEENKL
IEEQNEALFLELSGLSQALIQSLANIRLPHMDPICEQNFDAYVNTLTDMYSNRDCYQNPENKGLLETIKQAVRGIQV
```

259 - 278:	EEEEEEEEEEEEEEEEEEEE
260 - 279:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE

A0A286Y2S6 **A0A286Y2S6_CAVPO** (3669 aa)
Zinc finger homeobox 3. *Cavia porcellus (Guinea pig)*

```
MEGCDSPVVSGKDNGCGIPQHRQWTELNSTHLPDKPSSMEQPTGESHGPLDSLRAPFNERLAESSAPSAGPPAEPAAASK
EVSCNECSASFASLQTYMEHPCPGARAPAAPSASDTSERSDLSQLTPPSGGACAGGSGGPVPSLFLNSVPGAGGKQGDPS
CAAPVYPQIINTFHIASSFGKWFEGSDQAFPNTSALAGLSPVLHSFRVFDVRHKSNKDYLNSDGSAKSSCVSKDVPNNVD
LSKFDGFVLYGKRKPILMCFLCKLSFGYVRSFVTHAVHDHRMTLSEDERKILSNKNISAIIQGIGKDKEPLVSFLEPKNK
NFQHPLVSTANLIGPGHSFYGKFSGIRMEGEEALPAGSAAGPEQPQAGLLTPSTLLNLGGLTSSVLKTPITSVPLGPLAS
SPTKSSEGKDSGAADGEKREAGDPDCFSEKAEPAEEEEAEEEEEEEEEEEEEEEEEEEEEDEGCKGLFPSELDEELEDR
PSEESGAAAGGSSKKDLALSNQSISNSPLMPNVLQTLSRGTASTSSNSASSFVVFDGANRRNRLSFNSEGVRANVAEGGR
RLDFTDESANKDNATAPEPNESTEGDDGGFVPHHQHAGSLCELGVGECPSGSGVECPKCDTVLGSSRSLGGHMTMMHSRN
SCKTLKCPKCNWHYKYQQTLEAHMKEKHPEPGGSCVYCKSGQPHPRLARGESYTCGYKPFRCEVCNYSTTTKGNLSIHMQ
SDKHLNNMQNLQNGGGEQVFSHTAGAAAAAAAAAAAAANISSSCGAPSPTKPKTKPTWRCEVCDYETNVARNLRIHMTSE
KHMHNMMLLQQNMTQIQHNRHLGLGSLPSPAEAELYQYYLAQNMNLPNLKMDSAASDAQFMMSGFQLDPAGPMAAMTPAL
VGGEIPLDMRLGGGQLVSEELMNLGESFIQTNDPSLKLFQCAVCNKFTTDNLDMLGLHMNVERSLAEDEWKAVMGDSYQC
KLCRYNTQLKANFQLHCKTDKHVQKYQLVAHIKEGGKANEWRLKCVAIGNPVHLKCNACDYYTNSLEKLRLHTVNSRHEA
SLKLYKHLQQHESGVEGESCYYHCVLCNYSTKAKLNLIQHVRSMKHQRSESLRKLQRLQKGLPEEDEDLGQIFTIRKCPS
TDPEEAIEDVEGPSETAADPEEIAKEQESAGEKDQSKWTASSSQAEKELTDSPAASKRISFPGSSESLLSSKRPKTSEEV
KPEQMYQCPYCKYSNADVNRLRVHAMTQHSVQPMLRCPLCQDMLNNKIHLQLHLTHLHSVAPDCVEKLIMTVTTPEMVMP
SSMFLPAAVPDRDGNSNLEEAGKQPDTSEDLGKNILPSASTEHSGDLKPSSADPGSVREDSGFLCWKKGCNQVFKTSAAL
QTHFNEVHAKRPQLPVSDRHVYKYRCNQCSLAFKTIEKLQLHSQYHVIRAATMCCLCQRSFRTFQALKKHLETSHLELSE
ADIQQLYGGLLANGDLLAMGDPTLAEDHTIIVEEDKEEESDLEDKQSPTGSDSGSVQEDSGSEPKRALPFRKGPNFTMEK
FLDPSRPYKCTVCKESFTQKNILLVHYNSVSHLHKLKRALQESATGQPEPTSSPDNKPFKCNTCNVAYSQSSTLEIHMRS
VLHQTKARAAKLEAASGSSNGTGNSSGVSLSSSTPSPVSTSGSNTFTTTNPSSAGIAPSSNLLSQVPTDSVGMPPLGNPI
AANIASPSEPKEANRKKLADMIASRQQQQQQQQQQQQQQQQQQQQQQAQTLAQAQAQVQAHLQQELQQQAALIQSQLFNPT
LLPHFPMTTETLLQLQQQQHLLFPFYIPSAEFQLNPEVSLPVTSGALTLTGTGPGLLEDLKAQVQIPQQSHQQMLQQQQQ
QQQQSQLSLSQSHSALLQPGQHPEKKNKLVIKEKEKESQREREGVEGGESNTGPKELLPDALKAKEKKELAPVGGSEPSM
LPPRIASDARGNATKALLENFGFELVIQYNENKQKVQKKNGKTEQGENLEKLECDSCGKLFSNILILKSHQEHVHQNYFP
FKQLERFAKQYREHYDKLYPLRPQTPEPPPPPPPPPPPLPAAPPQPASAPAIPASAPPITSPTIAPAQPSVPLTQLSMP
MELPIFSPLMMQTMPLQTLPAQLPPQLGPVEPLPADLAQLYQHQLNPTLLQQQNKRPRTRITDDQLRVLRQYFDINNSPS
EEQIKEMADKSGLPQKVIKHWFRNTLFKERQRNKDSPYNFSNPPITSLEELKIDSRPPSPEPQKQEYWGSKRSSRTRFTD
YQLRVLQDFFDANAYPKDDEFEQLSNLLNLPTRVIVVWFQNARQKARKNYENQGEGKDGERRELTNDRYIRTSNLNYQCK
KCSLVFQRIFDLIKHQKKLCYKDEDEEGQDDSQNEDSMDAMEILTPTSSSCSTPMPSQAYSAPAPSANPAPSAFLQLTPE
ADELATFNSKTESSDEKPKQAEPPSAQPNQTQEKQGQPKPELQQQDQPEQKTNVPQQKLPQLAAPPSLPQPPPQAPPPQC
PLPQSSPSPSQLSHLPLKPLHTSTPQQLANLPPQLIPYQCDQCKLAFPSFEHWQEHQQLHFLSAQNQFIHPQFLDRSLDM
PFMLFDPSNPLLASQLLSGAIPQIPASSATSPSTPTSTMNTLKRKLEEKASASPGENDSGTGGEEPQRDKRLRTTITPEQ
LEILYQKYLLDSNPTRKMLDHIAHEVGLKKRVVQVWFQNTRARERKGQFRAVGPAQAHRRCPFCRALFKAKTALEAHIRS
RHWHEAKRAGYNLTLSAMLLDCDGGLQMKGDIFDGTSFSHLPPSSSDGQGVPLSPVSKTMELSPRTLLSPSSIKVEGIED
FESPSMSSVNLNFDQTKLDNDDCSSVNTAITDTTTGDEGNADNDSATGIATETKSSAPNEGLTKAAMMAMSEYEDRLSSG
LVSPAPSFYSKEYDNEGTVDYSETSSLADPCSPSPGASGSAGKSGDSGDRPGQKRFRTQMTNLQLKVLKSCFNDYRTPTM
LECEVLGNDIGLPKRVVQVWFQNARAKEKKSKLSMAKHFGINQTSYEGPKTECTLCGIKYSARLSVRDHIFSQQHISKVK
DTIGSQLDKEKEYFDPATVRQLMAQQELDRIKKANEVLGLAAQQQGMFDNAPLQALNLPTAYPALQGIPPVLLPGLNSPS
LPGFTPSNTALTSPKPNLMGLPSTTVPSPGLPTSGLPNKPSSASLSSPTPAQATMALAPQQHPQPQQQQQQPQVQQPPPP
PAAQPPPTPQLPQQQRKDSEKVKEKEKAHKGKGEPLPVPKKEKGEAPTAAAATISAPLPSMEYAVDPAQLQALQAALTSD
PTALLTSQFLPYFVPGFSPYYAPQIPGALQSGYLQPMYGMEGLFPYSPALSQALMGLSPGSLLQQYQQYQQSLQEAIQQQ
QQRQLQQQQQQQQQQQQQQQQKVQQPKASQTPVPQGAASPDKDPAKESPKPEEQKNAPREVSPLLPKPPEEPEAESKSAD
SLYDPFIVPKVQYKLVCRKCQAGFGDEEAARSHLKSLCFFGQSVANLQEMVGSYHCLACESALCGEEALSQHLESALHKH
RTITRAARNAKEHPSLLPHSACFPDPSTASTSQSAAHSNDSPPPPAPPAAPPAPPHAASRKSWPPAAPRAPAAKPPSFPP
LSSSSTVTSSSCSTSGVQPSMPTDDYSEESDTDLSQKSDGPASPVEGPKDPSCPKDSGLTSVGTDTFRL
```

440 - 459:	EEEEEEEEEEEEEEEEEEEE
441 - 460:	EEEEEEEEEEEEEEEEEEEE
442 - 461:	EEEEEEEEEEEEEEEEEEEE

A0A286ZID3 **A0A286ZID3_PIG** (1710 aa)
Histone acetyltransferase (EC 2.3.1.48). *Sus scrofa (Pig)*

```
MVKLANPLYTEWILEAIQKIKKQKQRPSEERICHAVSTSHGLDKKTVSEQLELSVQDGSVLKVTNKGLASYKDPDNPGRF
SSVKPGTFPKSTKGSRGSCNDLRNVDWNKLLRRAIEGLEEPNGSSLKNIEKYLRSQSDLSGTTTNPAFQQRLRLGAKRAV
NNGRLLKDGPQYRVNYGGLDGKGAPKYPSAFPSSLPPVSLLPHEKDQPRADPIPICSFCLGTKESNREKKPEELLSCADC
GSSGHPSCLKFCPELTTNVKALRWQCIECKTCSACRIQGKNADNMLFCDSCDRGFHMECCDPPLSRMPKDTEIKISIKQE
STDINVIGNKDTVTEEDLDVFKQAQELSWEKIECESGVEDCGRYPSVIEFGKYEIQTWYSSPYPQEYARLPKLYLCEFCL
KYMKSKNILLRHSKKCGWFHPPANEIYRRKDLSVFEVDGNMSKIYCQNLCLLAKLFLDHKTLYYDVEPFLFYVLTKNDEK
GCHLVGYFSKEKLCQQKYNVSCIMIMPQHQRQGFGRFLIDFSYLLSRREGQAGSPEKPLSDLGRLSYLAYWKSVILEYLY
HHHERHISIKAISRATGMCPHDIATTLQHLHMIDKRDGRFVIIRREKLILGHMEKLKTCSRTNELDPESLRWTPILISNA
AVSEEEREAEKEAERLMEQASCWEKEEQEILSSRANSRQSPAKVQSKNKYLHSPESRPVAGERGQLMELSKESSEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEENIQSSPPRLTKPQSVAIKRKRPFVLKKKRGRKRRRINSSVTTETISETTEVLNE
PFDNSDEERPMPQLEPTCEIEVEEDGGKPVLRKAFQHQPGKKRQTEEEEGKDNHCFKNADPCRNNMDGDANNLKEASRDN
PEPLKCKQWPKGAKRGLSKWRPNKERKTGFKLNLYTPPETPMEPDDQVTVEEQKETPEDKSSPTPTRIEEEVKEAMEPLL
PQDENRREETCAPISPNKSPCEKPEDGIIKPEEEEEEEEEEEEEEEEEEEEEANVEKDPAGAKSQEKEEPPEACTDKEDPV
RLDDREEEEEEDEEPSHNEGHDADDEDDSHTESAEAEKEERPREAFKEVLENQEAFLDLSVQPSHSNPEVLMDCGVEDLT
ASCSSDPKELAGATETAPESDEEPPGDPAQKQDQKSSEDVDPEFKEGNAATLEIDSETVQAVQSLTQENREQDDTFQDCA
ETQEACRSLQNYNHADQSPQIATALDDCQQSDHSSPVSSVHSHPGQSVRSVSSPSVPALENSYAQISPDQSAISVPSLQN
METSPMMDVPSVSDHSQQVVDSGFSDLGSIESTTENYENPSSYDSTMGGSICGNGSSQNSCSYSNLTSSNLTQSSCAVTQ
QMSNISGSCSMLQQTSISSPPTCSVKSPQGCVVERPPSSSQQLAQCSMAANFTPPMQLAEIPETGNANLGLYERMGQSDF
GAGHYPQPSATFSLAKLQQLTNTLIDHSLPYSHSAAVTSYANSASLSTPLSNTGLVQLSQSPHSVPGGPQAQATMTPPPN
LTPPPMNLPPPLLQRNMAASNIGISHSQRLQTQIASKGHVSMRTKSASLSPAAATHQSQIYGRSQTVAMQGPARTLTMQR
GMNMSVNLMPSPAYNVNSVNMNMNTLNAMNGYSMSQPMMNSGYHSNHGYMNQTPQYPMQMQMGMMGTQPYAQQPMQTPPH
SNMMYTAPGHHGYMNTGMSKQSLNGSYMRR
```

715 - 734:	EEEEEEEEEEEEEEEEEEEE
716 - 735:	EEEEEEEEEEEEEEEEEEEE

717 - 736:	EEEEEEEEEEEEEEEEEEEE
718 - 737:	EEEEEEEEEEEEEEEEEEEE
719 - 738:	EEEEEEEEEEEEEEEEEEEE
720 - 739:	EEEEEEEEEEEEEEEEEEEE
721 - 740:	EEEEEEEEEEEEEEEEEEEE
722 - 741:	EEEEEEEEEEEEEEEEEEEE
723 - 742:	EEEEEEEEEEEEEEEEEEEE
724 - 743:	EEEEEEEEEEEEEEEEEEEE
725 - 744:	EEEEEEEEEEEEEEEEEEEE
726 - 745:	EEEEEEEEEEEEEEEEEEEE
727 - 746:	EEEEEEEEEEEEEEEEEEEE
992 - 1011:	EEEEEEEEEEEEEEEEEEEE

A0A286ZKW1 **A0A286ZKW1_PIG** (2011 aa)
Histone acetyltransferase (EC 2.3.1.48). *Sus scrofa (Pig)*

```
MVKLANPLYTEWILEAIQKIKKQKQRPSEERICHAVSTSHGLDKKTVSEQLELSVQDGSVLKVTNKGLASYKDPDNPGRF
SSVKPGTFPKSTKGSRGSCNDLRNVDWNKLLRRAIEGLEEPNGSSLKNIEKYLRSQSDLSGTTTNPAFQQRLRLGAKRAV
NNGRLLKDGPQYRVNYGGLDGKGAPKYPSAFPSSLPPVSLLPHEKDQPRADPIPICSFCLGTKESNREKKPEELLSCADC
GSSGHPSCLKFCPELTTNVKALRWQCIECKTCSACRIQGKNADNMLFCDSCDRGFHMECCDPPLSRMPKGMWICQVCRPK
KKGRKLLHEKAAQIKRRYAKPIGRPKNKLKQRLLSVTSDEGSMNAFTGRGSPGRGQKTKVCTTPSSGHAASGKDSSSRLA
VTDPTRPGATTKITTTSTYISASTLKVNKKTKGLIDGLTKFFTPSPDGRRSRGEIIDFSKHYRPRKKVSQKQSCTSHVLA
PGTTQKLKPPPSSLPPPTPMSGQSPSSQKSSTSASSTSPQSSSSQSSVPSFSSLTNNSQLKALFDGLSHIYTTQGQSRKK
GHPSYAPPKRMRRKTEFSSTAKSKAHFFGKRDIRSRFISHSSSSSWGMARGRIFKAIAHFKRTTFLKKHRMLGRLKYKVT
PQMGTPSPGKGSLTDGRIKPDQDDDTEIKISIKQESTDINVIGNKDTVTEEDLDVFKQAQELSWEKIECESGVEDCGRYP
SVIEFGKYEIQTWYSSPYPQEYARLPKLYLCEFCLKYMKSKNILLRHSKKCGWFHPPANEIYRRKDLSVFEEKLCQQKYN
VSCIMIMPQHQRQGFGRFLIDFSYLLSRREGQAGSPEKPLSDLGRLSYLAYWKSVILEYLYHHHERHISIKAISRATGMC
PHDIATTLQHLHMIDKRDGRFVIIRREKLILGHMEKLKTCSRTNELDPESLRWTPILISNAAVSEEEREAEKEAERLMEQ
ASCWEKEEQEILSSRANSRQSPAKVQSKNKYLHSPESRPVAGERGQLMELSKESSEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEENIQSSPPRLTKPQSVAIKRKRPFVLKKKRGRKRRRINSSVTTETISETTEVLNEPFDNSDEERPMPQLEPTCE
IEVEEDGGKPVLRKAFQHQPGKKRQTEEEEGKDNHCFKNADPCRNNMDGDANNLKEASRDNPEPLKCKQWPKGAKRGLSK
WRPNKERKTGFKLNLYTPPETPMEPDDQVTVEEQKETPEDKSSPTPTRIEEEVKEAMEPLLPQDENRREETCAPISPNKS
PCEKPEDGIIKPEEEEEEEEEEEEEEEEEEEEEANVEKDPAGAKSQEKEEPPEACTDKEDPVRLDDREEEEEEDEEPSHNE
GHDADDEDDSHTESAEAEKEERPREAFKEVLENQEAFLDLSVQPSHSNPEVLMDCGVEDLTASCSSDPKELAGATETAPE
SDEEPPGDPAQKQDQKSSEDVDPEFKEGNAATLEIDSETVQAVQSLTQENREQDDTFQDCAETQEACRSLQNYNHADQSP
QIATALDDCQQSDHSSPVSSVHSHPGQSVRSVSSPSVPALENSYAQISPDQSAISVPSLQNMETSPMMDVPSVSDHSQQV
VDSGFSDLGSIESTTENYENPSSYDSTMGGSICGNGSSQNSCSYSNLTSSNLTQSSCAVTQQMSNISGSCSMLQQTSISS
PPTCSVKSPQGCVVERPPSSSQQLAQCSMAANFTPPMQLAEIPETGNANLGLYERMGQSDFGAGHYPQPSATFSLAKLQQ
LTNTLIDHSLPYSHSAAVTSYANSASLSTPLSNTGLVQLSQSPHSVPGGPQAQATMTPPPNLTPPPMNLPPPLLQRNMAA
SNIGISHSQRLQTQIASKGHVSMRTKSASLSPAAATHQSQIYGRSQTVAMQGPARTLTMQRGMNMSVNLMPSPAYNVNSV
NMNMNTLNAMNGYSMSQPMMNSGYHSNHGYMNQTPQYPMQMQMGMMGTQPYAQQPMQTPPHSNMMYTAPGHHGYMNTGMS
KQSLNGSYMRR
```

1016 - 1035:	EEEEEEEEEEEEEEEEEEEE
1017 - 1036:	EEEEEEEEEEEEEEEEEEEE
1018 - 1037:	EEEEEEEEEEEEEEEEEEEE
1019 - 1038:	EEEEEEEEEEEEEEEEEEEE
1020 - 1039:	EEEEEEEEEEEEEEEEEEEE
1021 - 1040:	EEEEEEEEEEEEEEEEEEEE
1022 - 1041:	EEEEEEEEEEEEEEEEEEEE
1023 - 1042:	EEEEEEEEEEEEEEEEEEEE
1024 - 1043:	EEEEEEEEEEEEEEEEEEEE
1025 - 1044:	EEEEEEEEEEEEEEEEEEEE
1026 - 1045:	EEEEEEEEEEEEEEEEEEEE
1027 - 1046:	EEEEEEEEEEEEEEEEEEEE
1028 - 1047:	EEEEEEEEEEEEEEEEEEEE
1293 - 1312:	EEEEEEEEEEEEEEEEEEEE

A0A287A3X4 **A0A287A3X4_PIG** (739 aa)
YTH domain containing 1. *Sus scrofa (Pig)*

```
MLAVHLLQKKGDAYSRHGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLISKP
LSSSVSNNKRMASTKGKSVTEYKNEEYQRSERNKRIEADRKIRLSSSASREPYKSQPEKTCLRKRDSERRVKSPTPDGSE
RIGLEVDRRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEEE
EEEEEEEEEEEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGIS
PIIFDRSGSSASESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLN
AAFRSARSVILIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEH
KPVKIGRDGQEIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEEYDIHNSRKK
PRIDYAPEFHQRPGYLKDPRYQEVDRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMTPYPGMEQPPHHPYYQHHAP
PPQAHPPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERE
RERLCDRDRDRGERGRYRR
```

236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE
239 - 258:	EEEEEEEEEEEEEEEEEEEE
240 - 259:	EEEEEEEEEEEEEEEEEEEE
241 - 260:	EEEEEEEEEEEEEEEEEEEE
242 - 261:	EEEEEEEEEEEEEEEEEEEE

A0A287A973 **A0A287A973_PIG** (1270 aa)
Tau tubulin kinase 1. *Sus scrofa (Pig)*

```
MQCLAAALKDETNMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTRENVALKVESAQQPKQVLKMEVAV
LKKLQGKDHVCRFIGCGRNEKFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESIEAIHSVGFLHRDIKPPRN
VAGFRGTVRYASVNAHKNREMGRHDDLWSLFYMLVEFAVGQLPWRKIKDKEQVGMIKEKYEHRMLLKHMPSEFHLFLDHI
ASLDYFTKPDYQLIMSVFENSMKERGIAENEAFDWEKAGTDALLSTSTSTPPQQNTRQTAAMFGVVNVTPVPGDLLRENT
EDVLQGEHLSDQENAPPILPGRPPEGLMPSPHLAPHTGGPEAEVWEETDVNRNKLRINIGKTPCVVEEEQSRGVGVPSSP
VRAPPDSPTTPVRSLRYRRVNSPESERLSTADGRVELHERRSRMDLPGSPSRQACSSQPAQMLSVDTGHADRQASGRMDV
SASVEQEALSNAFRSVPLAEEEDFDSKEWVIIDKETELKDFPPGAEPSTSGTTDEEPEELRPLPEEGEEQRRRPGPEPVV
RPRGRGMHTLAEEDLRPTPAQPPPQMSQADGRSETSQPPTPGSPSHSPLHSGPRPRRRESDPTGPQRQVFSVAPPFEVNG
LPRAVPLSLPYQDFKKDLSDYRERARLLNRVRRVGFSHMLLTAPQVPLAPVQPQTNGKEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEDEEEEEVVALGEVLGPHSGSSSEGSERSTDRSQEGAPSTLLADDQKESRGRASMADGDLEPEEGSK
TLVLVSPGDMKKSPVTADLAPDPDLGTLAALTPQHERPQPAGSQLDMSEPGTLSSVLKSEPKPPGAGMGPGAGAVTTGAG
GVAVTSSPFTKVERTFVHIAEKTHLNVMSSGGQASRSEELSAEGELGLEVPSDGRVVEEGASVPLENGIALSGPLGDSPL
EVATDSLPNGPALADGPAPASLPELGPEKLATISPSRHAMPGPRPRSRIPVLLSEEDTGSEPSGSLSAKERWGKRARPQQ
DLARLVMEKRQGRLLLRLASGASSSSSEEQRRASETLSGTGSEEDTPASEPAVPRKAGRAAATRSRIPRPISIRMPTPAA
AQQPPDRLHGATPASDTAITSRLQLQKPPGTATAADLRPKQPPGRGPGPGRAQVGARPPAPRSPGLPASAVHHPSASPRS
RSLSRKESPSPSHQARPGVPPPRGAPQARAQPDGTPSTGAPKKGPRGKLQTQRSATKGRAGVAEGRAGAR
```

699 - 718:	EEEEEEEEEEEEEEEEEEEE
700 - 719:	EEEEEEEEEEEEEEEEEEEE
701 - 720:	EEEEEEEEEEEEEEEEEEEE
702 - 721:	EEEEEEEEEEEEEEEEEEEE
703 - 722:	EEEEEEEEEEEEEEEEEEEE
704 - 723:	EEEEEEEEEEEEEEEEEEEE
705 - 724:	EEEEEEEEEEEEEEEEEEEE
706 - 725:	EEEEEEEEEEEEEEEEEEEE
707 - 726:	EEEEEEEEEEEEEEEEEEEE
708 - 727:	EEEEEEEEEEEEEEEEEEEE
709 - 728:	EEEEEEEEEEEEEEEEEEEE
710 - 729:	EEEEEEEEEEEEEEEEEEEE
711 - 730:	EEEEEEEEEEEEEEEEEEEE
712 - 731:	EEEEEEEEEEEEEEEEEEEE
713 - 732:	EEEEEEEEEEEEEEEEEEEE
714 - 733:	EEEEEEEEEEEEEEEEEEEE
715 - 734:	EEEEEEEEEEEEEEEEEEEE

A0A287AB29 **A0A287AB29_PIG** (732 aa)
YTH domain containing 1. *Sus scrofa (Pig)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLISKPLSSSVSN
NKRMASTKGKSVTEYKNEEYQRSERNKRIEADRKIRLSSSASREPYKSQPEKTCLRKRDSERRVKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEE
EEEEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIIFDRS
GSSASESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSAR
SVILIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGR
DGQEIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEEYDIHNSRKKPRIDYAP
EFHQRPGYLKDPRYQEVDRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMTPYPGMEQPPHHPYYQHHAPPPQAHPP
```

YSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDR
DRDRGERGRYRR

229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE

A0A287AGG6 **A0A287AGG6_PIG** (1773 aa)
Histone acetyltransferase (EC 2.3.1.48). *Sus scrofa (Pig)*

MVKLANPLYTEWILEAIQKIKKQKQRPSEERICHAVSTSHGLDKKTVSEQLELSVQDGSVLKVTNKGLASYKDPDNPGRF
SSVKPGTFPKSTKGSRGSCNDLRNVDWNKLLRRAIEGLEEPNGSSLKNIEKYLRSQSDLSGTTTNPAFQQRLRLGAKRAV
NNGRLLKDGPQYRVNYGGLDGKGAPKYPSAFPSSLPPVSLLPHEKDQPRADPIPICSFCLGTKESNREKKPEELLSCADC
GSSGHPSCLKFCPELTTNVKALRWQCIECKTCSACRIQGKNADNMLFCDSCDRGFHMECCDPPLSRMPKGMWICQVCRPK
KKGRKLLHEKAAQIKRRYAKPIGRPKNKLKQRLLSVTSDEGSMNAFTGRGSPDTEIKISIKQESTDINVIGNKDTVTEED
LDVFKQAQELSWEKIECESGVEDCGRYPSVIEFGKYEIQTWYSSPYPQEYARLPKLYLCEFCLKYMKSKNILLRHSKKCG
WFHPPANEIYRRKDLSVFEVDGNMSKIYCQNLCLLAKLFLDHKTLYYDVEPFLFYVLTKNDEKGCHLVGYFSKEKLCQQK
YNVSCIMIMPQHQRQGFGRFLIDFSYLLSRREGQAGSPEKPLSDLGRLSYLAYWKSVILEYLYHHHERHISIKAISRATG
MCPHDIATTLQHLHMIDKRDGRFVIIRREKLILGHMEKLKTCSRTNELDPESLRWTPILISNAAVSEEEREAEKEAERLM
EQASCWEKEEQEILSSRANSRQSPAKVQSKNKYLHSPESRPVAGERGQLMELSKESSEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEENIQSSPPRLTKPQSVAIKRKRPFVLKKKRGRKRRRINSSVTTETISETTEVLNEPFDNSDEERPMPQLEPT
CEIEVEEDGGKPVLRKAFQHQPGKKRQTEEEEGKDNHCFKNADPCRNNMDGDANNLKEASRDNPEPLKCKQWPKGAKRGL
SKWRPNKERKTGFKLNLYTPPETPMEPDDQVTVEEQKETPEDKSSPTPTRIEEEVKEAMEPLLPQDENRREETCAPISPN
KSPCEKPEDGIIKPEEEEEEEEEEEEEEEEEEEEEANVEKDPAGAKSQEKEEPPEACTDKEDPVRLDDREEEEEEDEEPSH
NEGHDADDEDDSHTESAEAEKEERPREAFKEVLENQEAFLDLSVQPSHSNPEVLMDCGVEDLTASCSSDPKELAGATETA
PESDEEPPGDPAQKQDQKSSEDVDPEFKEGNAATLEIDSETVQAVQSLTQENREQDDTFQDCAETQEACRSLQNYNHADQ
SPQIATALDDCQQSDHSSPVSSVHSHPGQSVRSVSSPSVPALENSYAQISPDQSAISVPSLQNMETSPMMDVPSVSDHSQ
QVVDSGFSDLGSIESTTENYENPSSYDSTMGGSICGNGSSQNSCSYSNLTSSNLTQSSCAVTQQMSNISGSCSMLQQTSI
SSPPTCSVKSPQGCVVERPPSSSQQLAQCSMAANFTPPMQLAEIPETGNANLGLYERMGQSDFGAGHYPQPSATFSLAKL
QQLTNTLIDHSLPYSHSAAVTSYANSASLSTPLSNTGLVQLSQSPHSVPGGPQAQATMTPPPNLTPPPMNLPPPLLQRNM
AASNIGISHSQRLQTQIASKGHVSMRTKSASLSPAAATHQSQIYGRSQTVAMQGPARTLTMQRGMNMSVNLMPSPAYNVN
SVNMNMNTLNAMNGYSMSQPMMNSGYHSNHGYMNQTPQYPMQMQMGMMGTQPYAQQPMQTPPHSNMMYTAPGHHGYMNTG
MSKQSLNGSYMRR

778 - 797:	EEEEEEEEEEEEEEEEEEEE
779 - 798:	EEEEEEEEEEEEEEEEEEEE
780 - 799:	EEEEEEEEEEEEEEEEEEEE
781 - 800:	EEEEEEEEEEEEEEEEEEEE
782 - 801:	EEEEEEEEEEEEEEEEEEEE
783 - 802:	EEEEEEEEEEEEEEEEEEEE
784 - 803:	EEEEEEEEEEEEEEEEEEEE
785 - 804:	EEEEEEEEEEEEEEEEEEEE
786 - 805:	EEEEEEEEEEEEEEEEEEEE
787 - 806:	EEEEEEEEEEEEEEEEEEEE
788 - 807:	EEEEEEEEEEEEEEEEEEEE
789 - 808:	EEEEEEEEEEEEEEEEEEEE
790 - 809:	EEEEEEEEEEEEEEEEEEEE
1055 - 1074:	EEEEEEEEEEEEEEEEEEEE

A0A287AIB6 **A0A287AIB6_PIG** (722 aa)
YTH domain containing 1. *Sus scrofa (Pig)*

MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLISKPLSSSVSN
NKRMASTKGKSVTEYKNEEYQRSERNKRIEADRKIRLSSSASREPYKSQPEKTCLRKRDSERRVKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEEE
EEEEEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIIFDRS
GSSASESYADQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSARSVILIFSVRESGKFQGFA
RLSSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLLFP
PDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEEYDIHNSRKKPRIDYAPEFHQRPGYLKDPRYQEVD
SFTNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMTPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHHPVPHE
ARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDRGERGRY
RR

229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE

232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE

A0A287AZ94 **A0A287AZ94_PIG** (743 aa)
YTH domain containing 1. *Sus scrofa (Pig)*

```
MNYLPPVPNLVNDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLISKPLSSS
VSNNKRMASTKGKSVTEYKNEEYQRSERNKRIEADRKIRLSSSASREPYKSQPEKTCLRKRDSERRVKSPTPDGSERIGL
EVDRRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEE
EEEEEEEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIIF
DRSGSSASESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFR
SARSVILIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVK
IGRDGQEIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEEYDIHNSRKKPRID
YAPEFHQRPGYLKDPRYQEVDSFTNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMTPYPGMEQPPHHPYYQ
HHAPPPQAHPPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRD
RERERERLCDRDRDRGERGRYRR
```

232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE

A0A287DAD7 **A0A287DAD7_ICTTR** (718 aa)
YTH domain containing 1. *Ictidomys tridecemlineatus (Thirteen-lined ground squirrel) (Spermophilus tridecemlineatus)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSN
NKRIVSTKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSTSREPYKSQPEKTCLRKRDPERRGKSPTPDGSERIGLEVD
RRPSRSSQSSKEEVNSEEYGSDHETGSSGSSDGQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEE
EEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSA
SESYADQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVILIFSVRESGKFQGFARLSS
ESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLLFPPDES
IDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQRPGYLKDPRYQEVDSFTN
LIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHHPVPHEARYR
DKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDRGERGRYRR
```

230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE

A0A287DAG9 **A0A287DAG9_ICTTR** (1220 aa)
Euchromatic histone lysine methyltransferase 2. *Ictidomys tridecemlineatus (Thirteen-lined ground squirrel) (Spermophilus tridecemlineatus)*

```
MRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWAPQLPTGLTSPPVPCLPSQGEAPAEMGALLLEKEPRGA
TERVHGSLGDTSHSEDTLPKANTDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDEPENLEGDGGRILLGHATKSFP
SSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGTAAAGPEPPPATTSPEGQPKVHRARKTMSKPGNGQPPV
PEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGNGLSEELGSARGSGEVTLEKGNPRSLEEWETVVGDDFSLYYDSY
SVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPT
RKRRKREPARAKEPRGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESIDGELSGCNAAILKRETMR
PSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPR
GDGGTPPAGTAAPAPPPLAQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPPGPGRE
ALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGAN
INAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPII
WAAEHKHIDVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLF
LSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDY
KYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNR
VVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRF
INHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLA
RLDPHPELLPELGSLPPVNS
```

343 - 362:	EEEEEEEEEEEEEEEEEEEE
344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE

A0A287DCS3 **A0A287DCS3_ICTTR** (1677 aa)
Histone acetyltransferase (EC 2.3.1.48). *Ictidomys tridecemlineatus (Thirteen-lined ground squirrel) (Spermophilus tridecemlineatus)*

```
ISPNINILPHFFSLSYSPRADPIPICSFCLGTKESNREKKPEELLSCADCGSSGHPSCLKFCPELTTNVKALRWQCIECK
TCSACRIQGKNADNMLFCDSCDRGFHMECCDPPLSRMPKGMWICQVCRPKKKGRKLLHEKAAQIKRRYAKPIGRPKNKLK
QRLLSVTSDEGSMNAFTGRGSPGRGQKTKVCTTPSSGHAASGKDSSSRLAVTDPTRPGATTKITTTSTYISASTLKVNKK
TKGLIDGLTKFFTPSPDGRRSRGEIIDFSKHYRPRKKVSQKQSCTSHVLATDTEIKISIKQESTDVNVIGNKDVVTEEDL
DVFKQAQELSWEKIECESGVEDCGRYPSVIEFGKYEIQTWYSSPYPQEYARLPKLYLCEFCLKYMKSKNILLRHSKKCGW
FHPPANEIYRRKDLSVFEVDGNMSKIYCQNLCLLAKLFLDHKTLYYDVEPFLFYVLTKNDEKGCHLVGYFSKEKLCQQKY
NVSCIMIMPQHQRQGFGRFLIDFSYLLSRREGQAGSPEKPLSDLGRLSYLAYWKSVILEYLYHHHERHISIKAISRATGM
CPHDIATTLQHLHMIDKRDGRFVIIRREKLILGHMEKLKTCSRTNELDPESLRWTPILISNAAVSEEEREAEKEAERLME
QASCWEKEEQEILSSRANSRQSPAKVQSKNKYLHSPESRPVAGERGQLMELSKESSEEEEEEEEEEEEEEEEEEEEEDE
EEEEEDEEEEEENIQSSPPRLTKPQSKKRGRKRRRINSSVTTETISETTEVLNEPFDNSDEERPMPQLEPTCEIEVEEDG
RKPVLRKAFQHQPGKKRQTEEEEGKDNHCFKNADPCRNKIDDDASNLKEGSKDNPEPLKCKQVWPKGTKRGLSKWRQNKE
RKTGFKLNLYTPPETPMEPDDQVTVEEQKEISEDKTSPTPIRIGEEVRETVEALLPRDGNRKEEVCAPVSPNKSPEEEEE
EEEEEEEEEEEEEEEEEEEEEETIEKNQDSAKSQEKEEPGIAMDKEDTVHLDDHEEEEEEDEEPSHNEDHDADDEDDSHM
ESAEVEKEELPRETFKEVLENQEAFLDLSVQPSHSNPEVLMDCGVDLAASCNSEPKELAGDTENAPESDEEPPEEQTQKQ
DQKNSEVDSEFKEGNTATMEIDSETVQAVQSLTQENREQDDTFQDCAETQEACRSLQNYTHADQSPQIAATLDDCQQSDH
SSPVSSVHSHPGQSVRSVNSPSVPALESSYAQISPDQSAISVPSLQNMETSPMMDVPSVSDHSQQVVDSGFSDLGSIEST
TENYENPSSYDSTMGGSICGNGSSQNSCSYSNLTSSNLTQSSCAVTQQMSNISGSCSMLQQTSISSPPTCSVKSPQGCVV
ERPPSSSQQLAQCSMAANFTPPMQLADIPETGNANIGLYERMGQSDFGAGHYPQPSATFSLAKLQQLTNTLIDHSLPYSH
SAAVTSYANSASLSTPLSNTGLVQLSQSPHSVPGGPQAQATMTPPPNLTPPPMNLPPPLLQRNMAASNIGISHSQRLQTQ
IASKGHVSMRTKSASLSPAAATHQSQIYGRSQTVAMQGPARTLTMQRGMNMSVNLMPAPAYNVNSVNMNMNTLNAMNGYS
MSQPMMNSGYHSNHGYMNQTPQYPMQMQMGMMGTQPYAQQPMQTPPHSNMMYTAPGHHGYMNTGMSKQSLNGSYMRR
```

697 - 716:	EEEEEEEEEEEEEEEEEEEE
698 - 717:	EEEEEEEEEEEEEEEEEEEE
699 - 718:	EEEEEEEEEEEEEEEEEEEE
956 - 975:	EEEEEEEEEEEEEEEEEEEE
957 - 976:	EEEEEEEEEEEEEEEEEEEE
958 - 977:	EEEEEEEEEEEEEEEEEEEE
959 - 978:	EEEEEEEEEEEEEEEEEEEE
960 - 979:	EEEEEEEEEEEEEEEEEEEE
961 - 980:	EEEEEEEEEEEEEEEEEEEE
962 - 981:	EEEEEEEEEEEEEEEEEEEE
963 - 982:	EEEEEEEEEEEEEEEEEEEE

A0A287DE52 **A0A287DE52_ICTTR** (1152 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Ictidomys tridecemlineatus (Thirteen-lined ground squirrel) (Spermophilus tridecemlineatus)*

```
MAAAVLSGPSAGSPAGVPGGTGGLSAMNSGPRLRLLLLESVSGLLQPRTGSTIAPVHPPVCSVPHLPGLMCLLRLHGTVG
GAQNLSALGALVSLSNARLGSIKTRFEGLCLLSLLVGESPTEMFQQHCVSWLRSIQQVLQSQDPPPTMELAVAVLRDLLR
YAAQLPTLFRDISINHLPGLLTSLLGLRPECEQSALEGMKACMTYFPRACGSLKGKLASFFLSRVDALSPQLQQLACECY
SRLPSLGAGFSQGLKHTESWEQELHSLLASLHSLLGALYEGAETAPVQNEGPGVETLLSPSEDGDAHVLLRLRQRFSGLA
RCLGLMLSSEFGAPVSVPVQEVLDLICRTLSVSGKNISLLGDGPLRLLLLPSIHLEALDLLSALILACGGRLLRFGALIS
RLLPQVLNAWSIGRDTLSPGQERPYSTIRTKVYAILELWVQVCGASAGVLQGGASGEALLTHLLSDISPPSDALKLRSPR
GSPDGGLQTGKPSAPKKIKLDVGEAMAPPSHRKGENNANSDVCAAALRGLSRTILMCGPLIKEETHRRLHDLILPLVMGV
QQGEVLGSSPYTSSCCRRELYRLLLALLLAPSPRCPPPLACALQAFSLGQREDSLEVSSFCSEALVTCAALTHPRVPPLQ
AMGPTCPTPAPVPPPEAPSPFRAPPFQPPGPMPSVGPMPSAGPMPSAGPLTSSGSMPSVGPMPSAGPMPSAGPIPSAGPV
PSARPGPPATANHLGLSVPGLVSVPPRLLPGPENHRAGSSEDPVLAPSGTPPPTIPPDETFGGRVPRPAFVHYDKEEASD
VEISLESDSDDSVVIVPEGLPPLPPPPPSGTTPPPVAPTGPPTASPPVPAKEEPEELPAAPGPLPPPPPPPVPGPVTLPP
PQLVPEGTPGGGGPPALEEDLTVININSSDEEEEEEEEEEEEEEEEEEEEEEEFEEEEEEEEEYFEEEEEEEEEFEEEFEE
EEGELEEEEEEEEEEEEEELEEVEELEFGSAGGEVEEGGPPPPTLPPALPPPESPKEHPEPEPEPGLLLEVEEPGSEEQH
GTETAPTLAPEVLPSQGEEEREGRSPEAGPPPQELVEEEPSAPPTLLEEGTEGGGDNVPPPPETAAEEEMETETEAAVLQ
EKEQDDTAAMLADFIDCPPDDEKPPPTTEPDT
```

911 - 930:	EEEEEEEEEEEEEEEEEEEE
912 - 931:	EEEEEEEEEEEEEEEEEEEE
913 - 932:	EEEEEEEEEEEEEEEEEEEE

A0A291FI63 **A0A291FI63_9FABA** (248 aa)
30S ribosomal protein S3, chloroplastic. *Tibetia liangshanensis*

```
MGQKINPLGFRLGTTQSHDSIWFAQPTNYSENLKEDKIIRDCIKNYIQKMIRISSGIDGIEGIGRIKINKRIDMIHVLIY
LGFPNLLEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGKPRIIEELETNVQKKVNCVNRKLEIEITRIPNAYGDPNILAEF
IGVQLKNRISFRKAMKKAIELAEEAGTKGVQVQIAGRIDGNEIARVEWIREGRVPLQTIRAKIDYCSYTVRTIYGVLGIK
VWIFLNKE
```

88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE

92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE

A0A293N7M3 **A0A293N7M3_ORNER** (109 aa)
Scaffold attachment factor B2 (Fragment). *Ornithodoros erraticus (European soft tick) (Alectorobius erraticus)*

```
MASSETSSQPRKTLSDLKVVELRSELEKRGLEKTGCKAALVERLSKVLEEDGEDPDTYEFETASDVNTSKNSSHVVEETT
TEQAAVEEEEEEEEEEEEEEEEEEEEEEE
```

87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE

A0A2A2KIU1 **A0A2A2KIU1_9BILA** (133 aa)
Uncharacterized protein. *Diploscapter pachys*

```
MMPSPFHSSSVRCMPPPEEEAKRDLKFTFSSNSKLNMKVQEKVLQRDELYNSSTACSKYENDTGATRAEKTGKGKKAEGK
YREEEEEEEEEEEEEEEEEEEEEQEEEEVEEEEEEEEEEEEEEEEEEERESEP
```

83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE

A0A2A3E1B4 **A0A2A3E1B4_APICC** (2425 aa)
PHD and RING finger domain-containing protein. *Apis cerana cerana (Oriental honeybee)*

```
MSSDSNQTSQSAKRKKLVKLDSEDSDESIVQSRRRKKTFKFISEGETSDEDSDVQRPIIQTKNHRIIAKDELNYESSSSN
TSKYKQFGESSETSEWQSDWSSSSELEKKSPVRRKVLGKPKAKKPPKIVSDTDSDNNDDQVEKCPICLLPFKRQQLGTPS
SCEHCFCLECLIEWSKNINTCPVDRQTFTIIHVRDKLGGQIIRCVPVEVASSEEENLDDLTFCEVCHQSNREDRMLLCDG
CDCGYHLECLTPPLNEVPIEEWFCPECSQNREINAKVVRINMNEIIDPIEEARRLGVTYGRIRINALDSYPRIIPRTRHT
ERVRATIRRRNRLDDHIQLTRQIPFDPNQPSTSSGLESFGDKSQSRSPSNASSSLGSGDRNCSNRYFRKSRKYRSSSSDS
SNESISRKSRKRINNKNNSENSNSNKSKKKNNNNKQSGDNSRKNETRNNSRKSGKSKNVSNKEALLREVRIVEHNENGEE
EEIITHVRVASITLRKRRRTKRRKRRNRRHRARTLSNVLTNTKKRLAVALGICKPIKNVSNLLPSVRNRQVISDRSALTI
ARYNAGISRLSIFGESLHLDYTPPESDTEDYHAIVGPTISVQRHSIISSRRRLRLKNIVTPQQPQPDLLSNIIKDQEIWH
SNNNNVTIKANGLLLIEKKETLNDLKKEKSEEKGLLKNEEIESIVENRVSRVDTSLEVSRIDTPLEISRINPESIVQAPM
YNNPCGGGNRGNFRGNYRDNTRHSHGGQNYGRDSLSGSGRHSYGGSGGNFGRDFGPPPFYNPNFEHCGPPMFGGNPPFRN
RNPQHFRNERFRFMPSGRPQFNFAEGLSEHHTFSERYNRPRSPQVSNERPQNNMPPNLPEDTPRNESVEQQSQDIENIST
RQEEDCDIYCDIETKSDGELQDQQNSSMVLLPPPEPPSGLLDFEENSKSDKDSDQELVIDDSQKEDTPKNDKYDPFSVDS
DSDSEIKKNEGIMEKEKEEQIVKDITQAETLDTSIRLSTYDDEEEEDFQADCPNFSIYSSQTIDVARHTEQQLSQQIGPL
QPPPLPPSIPDDDDVIVGDVQACDLTEIPEPSDPYVEALRKERQTLSKIPPKKISHDSRGKITFKIGTKLKINNRLLGLQ
EEEKESNDDKKKEIELIKEEETSVDREEERKRITKSKYEEEIQLKGDKEQNIKEILIPIIPLNLKEKNTNKEEKEKEWIE
KSKDNTTENDSNAIITTEVTRLSPKRLENEIISECLSKEGSKTFTLFHKPSKIDLEKKDSKEESKNKEEYITNKIKNLYD
YKSEKDDKHDKGEEENDDDDDDDDDDDGDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERFPIEKEKFSKKN
IIEKDIDKNTWESDGAYTPCRDELPLKESKSSSEQLPFIESGLEPITPTKDKPDDLDSCRTPVDYNVLGTEAISETDEAM
NFEDELTLLSLRKEKEMEDGEIIEEKIMKEGEVEKEKEEEKKRKKKEKKEKSKETEKNKENIASENQVAWKKLSKNTKER
SYRDKEKRSKSKEREKLKKKKEVVKKKEKRKELPRYDVRKIVAERPSRPRKDEYGRDIREKSRQRSKSRSCSSSKRSRSY
SKIRSRSRSRTRLQRSWSRDRRSYSKSLSRRRSLSRGRRKSPKRRSTSRRRSSSRKRSLSRRRSRSVSRKRRSLSRRRSR
RSISRSRQRRSISRSRRSLSRSRDRRKDKKKYKSRSRSRNRKKSRSKSPRKSSKSRERKHSKRKAQSRSRSKGRSCSRNW
EQVDKIVEQEFSREREERESWSAQWTPSWSRSRSKTPQHVQQEPITSREWSPMLDNVSVPPKNLTVILTNKEAIKKKKKE
RRKESKKKDEKKRKGKRNRTPPPSKEVFASGDNILVSVCFNKDNETDQTVVPELPETIPLISPLKRRRRESLQTDPPKRS
KKEKSKDKRSKSPKPKKDKKKKSKAAEIAATKKPVAVIDLDQSPFREQTPSPRDVIVLSDDDDKQIQQITSDQCQPSQNS
PPREQFISQGPKTPPEPQIKFSINKQSSNLRPSMLNPLLDEEEEEEMDERVEEELEMRAQEELELRLKIGPNTPPEPPTS
PPTSPDAYDPFDPTKSRSPTPDVSQEANSSDERRRSPRKHDSVDDSILEEENQNQERQSQEKQLEKPKIISMVTIKRASP
QRDDVNDNDSNNDITVSAGNLEIQQNQQNVQNQNNPFTVMNPVLATVAAAVQRSGVFNAPNSNNNQRNLLQSNRISPTNQ
QKQRSSDRSQAPSVFTNSGKSSRGSKSGQTKTNGQNGNDAGTETMDNVDMSSPYSPGSTLSDGIFDPPSPTNYNSPNAGT
GSGAGPIGTQITKNSNSKAIKTTEKKDAFDALFGSLPITKTSTKSNRNKKSEKDKKKKSTNPKVGVRMDENQLQILDDLP
SSAVEMQVKDKVWVLYIFISFCFLI
```

1310 - 1329:	EEEEEEEEEEEEEEEEEEEE
1311 - 1330:	EEEEEEEEEEEEEEEEEEEE
1312 - 1331:	EEEEEEEEEEEEEEEEEEEE
1313 - 1332:	EEEEEEEEEEEEEEEEEEEE
1314 - 1333:	EEEEEEEEEEEEEEEEEEEE
1315 - 1334:	EEEEEEEEEEEEEEEEEEEE
1316 - 1335:	EEEEEEEEEEEEEEEEEEEE
1317 - 1336:	EEEEEEEEEEEEEEEEEEEE
1318 - 1337:	EEEEEEEEEEEEEEEEEEEE

1319 - 1338:	EEEEEEEEEEEEEEEEEEEE
1320 - 1339:	EEEEEEEEEEEEEEEEEEEE
1321 - 1340:	EEEEEEEEEEEEEEEEEEEE
1322 - 1341:	EEEEEEEEEEEEEEEEEEEE
1323 - 1342:	EEEEEEEEEEEEEEEEEEEE
1324 - 1343:	EEEEEEEEEEEEEEEEEEEE
1325 - 1344:	EEEEEEEEEEEEEEEEEEEE
1326 - 1345:	EEEEEEEEEEEEEEEEEEEE
1327 - 1346:	EEEEEEEEEEEEEEEEEEEE
1328 - 1347:	EEEEEEEEEEEEEEEEEEEE

A0A2A3E2A9 **A0A2A3E2A9_APICC** (507 aa)
Uncharacterized protein. *Apis cerana cerana (Oriental honeybee)*

```
MSGDVQARKRKEKKRKKDEEDNIIPSPTLGNINENLTDNVTIHIYKESTTGGHWCARIIFFIILTMLMGLIGIVIFEHRG
TTDISTPLESSRWAFIFEGWVDDSALLSNEESHDNEQETKEIKKETKNDEDNKEITEIKISNEEEIQEDEISNEHTEEEK
ETINENESNEEQNIFQSKEEELSHESEYEDREQQEDILEEDITPEEFDNINVLEEIYSISTEKFSDEKNILYETDSQFDK
IIKMTRNEDEKFENFLDIPGINEINDDNLEPLEEVENIEPEEYVNDIDVKPEIEEIEEESANVAMKFGVGVALIVAAHFV
LVKRWNNEVIFVQNQSKLISSEKKDVEEKVTPKNKLIIQVEEYETGEQNKNKKIETKEEKRKIEIIKEQISLQQNDKIED
EEEEEIEDKDEREEEEEKELMEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVKDEEEEDEEKEEEEDKYKSNEKYDKI
DDKEKEQRRILEIENEKLIKIRRRRSS
```

422 - 441:	EEEEEEEEEEEEEEEEEEEE
423 - 442:	EEEEEEEEEEEEEEEEEEEE
424 - 443:	EEEEEEEEEEEEEEEEEEEE
425 - 444:	EEEEEEEEEEEEEEEEEEEE
426 - 445:	EEEEEEEEEEEEEEEEEEEE
427 - 446:	EEEEEEEEEEEEEEEEEEEE
428 - 447:	EEEEEEEEEEEEEEEEEEEE
429 - 448:	EEEEEEEEEEEEEEEEEEEE
430 - 449:	EEEEEEEEEEEEEEEEEEEE
431 - 450:	EEEEEEEEEEEEEEEEEEEE
432 - 451:	EEEEEEEEEEEEEEEEEEEE
433 - 452:	EEEEEEEEEEEEEEEEEEEE
434 - 453:	EEEEEEEEEEEEEEEEEEEE

A0A2A3ECU3 **A0A2A3ECU3_APICC** (415 aa)
Troponin T. *Apis cerana cerana (Oriental honeybee)*

```
MTPYRACDVELAARGVWGEYRVYEGEETNAESLRYSVRHVFTFLLPFAQRQEQKRSDLDEQLKEYIAEWRKQRAKEEEEL
KRLKEKQAKRKITRADEEKRLAQKKKEEEERRQREIEEKKQRDMEEKRKRLEESEKKRQAMMQAMKEQASKKGPNFTITR
KDLAGNLTSAQLERNKTKEQLEEEKKISLSIRIKPLEIDGFSIEKLRSKANELWDTIVKLETEKYDLEERQKRQDYDLKE
LKERQKQQLRHKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGLTEQQKEFIEKQWAQQKEQFLGRQ
KTKLPKWFGERPGKKPGDPESPEGEEDVKAAAEDEELEEPQFEEEEEEEEEEEEEEEEEGEKKEGEGEGEEEEEEEEEE
EEEEEEEEEEEEEE
```

390 - 409:	EEEEEEEEEEEEEEEEEEEE
391 - 410:	EEEEEEEEEEEEEEEEEEEE
392 - 411:	EEEEEEEEEEEEEEEEEEEE
393 - 412:	EEEEEEEEEEEEEEEEEEEE
394 - 413:	EEEEEEEEEEEEEEEEEEEE
395 - 414:	EEEEEEEEEEEEEEEEEEEE
396 - 415:	EEEEEEEEEEEEEEEEEEEE

A0A2A3EHV4 **A0A2A3EHV4_APICC** (406 aa)
Uncharacterized protein. *Apis cerana cerana (Oriental honeybee)*

```
MFIQDKNEDKEKKREKEVEEEEEEDEEEEEEDEDEEEEEEEEEKEEEEKEEEEEEEEVVVVMVVATTGGQGGRYWRPEEE
EEEEGEEEEEEEEEEEEEEEEEEEEEKEEEEEEEEEEEVEEEEEEKEGEGDEEGRWCSKGREEPAWKSSSGGCGGGDGDG
DGGGGGGVVANRGARFSSHWNEAWTYEEEAARNGTAFLPSLADETWKEVEVATNSSSETITRDKLLVISTLSSCSTRKRT
AWHGVVQGRRREKFGQIGKKSTEDIECNGSFELINWYTMTNLQGGNETLKRTLTRLDGSFKRSKGSTEDPRCRDLPVPVH
GFLWSSLRLVFFSFFGISLRNEEAFLSSLTTLSMILSERFNVEIARFSYLKLIFGIECRAASIDLDILYKKVLHHLQQKT
YSLGNN
```

86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE

A0A2A3EQ25 **A0A2A3EQ25_APICC** (1912 aa)
Uncharacterized protein. *Apis cerana cerana (Oriental honeybee)*

```
MNDEIILKGLTGGGNIPFADEDGTALDHVGARSRTEVRRKEAHTFGTFGGPSRIDQEGRSCSSMLERNASMLVGQQQQQQ
RQQYKQSPGPRRIGARNEAIEGSGENPLQRYENAVLKYQRRQGSRDRQNHGCSSSDESVARNKSKSISSIDTQSVNNILD
EYEDLDYGRSSDLSDVGSISVSNFEAVMMDQRKKQQQQERSRALAATRIQPKWPGAREKSQPVARASEPMQARQRSRERQ
KESSRHPQSPIEDGTRPSSCVPVTVDPGRARVPEVLLRKGEVQKRVDEWLNQTQSQNFAGAREKALTRSNSSADQKSQRR
YRQDSRSRSIDEGRDKSNGTSSSYDDLSRAEKKVERKPNVDKVNVGVNTSRGTYKEYLASKSGGGGNGRSGKQQDYGFSA
SSCGATIGRTRDMSPSTAGSRIPQRGPLGSSFRSRRFESSGNEASQADNSGGGEQPSQFYQGEKNCRARNAADSRPTNLV
KTRNESDHGRISGVVVVVSGVTGGSTTSASASVASVIPCRKASFKRSQSHDQSAAGASRPLVKEETGQRGGRGGSGISKG
PANLGDQGEPISPNKDGESRRPALTTDSSRTAGDKAADVACKSIEVPRDRPTRVTGGESGGESRRCYPQDSKRDNKMDQQ
TVVYGAVGARVRTLQGHQESRVTRPRNLQAGFAPPEARKPPPNSRVYAALQQLNEQNSAKSRSTGNGPADKSPARPHYSS
PNHAVEKIYERSLQPQVIHVDDLQSILRPSLQVSAYGEGGTAARSDRKSPPKEVVMLGQRNEKEAEEEEEEEEEEEEEE
EEEEEEEEEEEEEEAEVYERVGELRYEHLETIEEDDQKSEASVCGYPEIGLSRCSKIEQGLANGRSQERRKKRRKKEGLTQ
CSKPDQANEAGRTFVTFCSSSSPQGIKANLQSRPAATGLSECNEQQEKREVAAAEEPPRIMIVHDTEIPYDSGNPADRSE
PCHSRENSNLSTATIPVDELESERQAAKFKVEDACLGSNEMSDHRTMEARFQKEDAKEVGCQKVDRWESEKERASSREME
ERGSVVNEVLVKNLQFEQDLPKDSVEHIVSGGGGGGGSGCSDTFGKIIEHVGQQRAMGYHNVLCDNYENVQNARYKESKVY
VTKEEMERQRLMELLRKGDYELAKALKSSVTIGCLQSSGSRGSEAEEGGGAVGGGGGSGTSMCCVLQGAERVFPSNGGKH
GSGTGSSSRGMGTSVGTQDLPLESLWAAGLDEGMGFPQRCSYANHHTTLANTATGHTTTNPEELWKERNLSYRTPTTSTG
IDSSITDEIWTSANEAKFFRTSTTSTGIGSSLNLHENNRSLESRDADFYSTDIEDSKDTYRRFFPNTPTTSGLGSSSDRQ
SVETRRGSKDLPDHLWAAAMEDGFSRFNAMKSLQTITRQPRPNHDWVKTERISRFTKHRTIGQSPQREEEIWTSKLNESN
VSTYATQRMNGPHKCHHQTRRSFSTSIVADLAVTPDGSQQSLGSGEFLDSGSLPTETSALVQAAVKCIVKRSLDPPVPYN
EEIPGHCRKRLEDFGKVSLAALREGRCCYTEAELRARGGGIEVTRLGFLTKGLTFGQRRKPDLYTPIHMAVAEFLAAYYL
TSVAQYANILRRELEGLPSGIISHLAGLLGPKTHLILNQLCPLEVPPRAVFSLLKAAGASDGNISAVCRLVGAGPGFGPA
PNERPPAPLVHTSPLELEGWARILESAACTLEALEVVFQVERGSDPRYLDDFFEALAGNESVKLVRITSLLGQEFPADEA
QKLAGHLKSVLGKKKLNDFELVITCLEEAAHDRLECVVNALCRGLSHASTSLARLVLDMNLSGEQVSRVCDALRDCVQVQ
ALHLPHLGCGCEGLASVAELLKERPLLALNLAGSWGAKNEDPSSSGISMGKTLNRTVWRCFPSYSDTRASAN
```

786 - 805:	EEEEEEEEEEEEEEEEEEEE
787 - 806:	EEEEEEEEEEEEEEEEEEEE
788 - 807:	EEEEEEEEEEEEEEEEEEEE
789 - 808:	EEEEEEEEEEEEEEEEEEEE
790 - 809:	EEEEEEEEEEEEEEEEEEEE
791 - 810:	EEEEEEEEEEEEEEEEEEEE
792 - 811:	EEEEEEEEEEEEEEEEEEEE
793 - 812:	EEEEEEEEEEEEEEEEEEEE
794 - 813:	EEEEEEEEEEEEEEEEEEEE

A0A2A3EQJ1 **A0A2A3EQJ1_APICC** (1423 aa)
Tetratricopeptide repeat protein. *Apis cerana cerana (Oriental honeybee)*

```
MEEEGPLFFRDGIVYREWGYIFTRLEKFHLAELYFDKAIKQTQSNDLRTYLGLVKAQLAYARFKRALKTEEKCVELDPTY
SHVKHIQLQTLFAIGEFEYSLIHAHQGFQKHPTTDLEHGILQGNETIEDCIGIDTSPITLQLLYPWIRELQEYRKFLVEK
LKEEVDELAGIEEEQSKFKVNDPIAQEELWFKKLQLIFSQIYMGHLAKDKEFLQFLAENPEKYDSPNKESSILLNEMIWR
NYNRCLRRQNVLRMRQPLYVMLFKRRLKPEGFRRALEAEKKLKKNLIIVQADFLLNRLHEIRMKKDYIEFFRMVDWIKDK
LDSFSSKMFPLKEKCLNVLYNMIAWTYIDSRNVTNIQDLNLKKIYLKHHLGIRVAELPRDIDIGWIKAIDRKEALKTYRR
RLAMASEPLELAWLFHELCKYLIDIRRYDLARFYGKKARDMGQEAQNEQWMLNSQHLFIRIEICQNYRNEAKEAALIALA
SSKKLGLDFLVDFYKRAVEIIDDIDMEKLLAFDAIAARQQLILNLMPEDMKAEVDFLWRRMEAVPAKRRMSVMPGCKPVD
KKFKLPCKRKTIMLQPPKDPVIEMRRAMLAHGDYESALVLYHRAANLYPKDSSHGVAARRTAATISSCNNPSKAVRKVSP
LISGEQLTAALCPETAAIIANEKLKKSPEPATIPEVLSIDADVNRDVKSPEIQRDVSMRTTTYESNCALFEISNVTISNP
TIQCDSDRGEFPFPELRNSYFDNHKSYWKTQPSPRVSSNQLAKSKMAHKQMNNLAETSLKNLQASFDSGKMSSALKIAQD
LLLVSGGFHDPTRYQIAAYHYLSLIHVALGRHDRAVCSVARLIRLSKSTADVNLICRSLVTLGKVHLSFGHLEAAAKAWE
HLAKDLKKPIPVAWIRHEIGRCYLETGKYERAMEMGFRCVDAATKGNSKKWMLNGRLLIGQSLAKLGRFVESLEELQVAA
KITEEEGDTPMMSYIRDLIDQVAHALRMIPFENGSYEIVASAISQDQATAKQNVNLFVSEQTVITTVFSQRKMITGGRRE
DESGNEGRITVDDSSKEASTYADFQEEQEKEEEGGGGNSTFRVKKSSSSDRKKRTISPSKSSSLSSSPFYSPKIKEVREK
RVMKPRERGRKKIEGNMGGGKSKNDEGEQGDEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVEEEEEVEEEEEEEELKN
ESSKTSLKSGNTMGTYVIEEGAAEKAAEEVSDNEEEVVDGVVARTTGGRPPIRLSEFGDKMAQRGDMLDALRVIEELGEK
NEVELLEMLKEMLFSTDNDKGRDFGDSGGDGFRNPRSGQDRQNTNTRSINAAVEETIRKVEILNLASPSFVCIHFFLISF
WFSLFSVIPRMETVSKSNSIVKLDEPWVFENLMAPRESPEVSSRIVMGREGKCQRGSYIRVNI
```

1154 - 1173:	EEEEEEEEEEEEEEEEEEEE
1155 - 1174:	EEEEEEEEEEEEEEEEEEEE
1156 - 1175:	EEEEEEEEEEEEEEEEEEEE
1157 - 1176:	EEEEEEEEEEEEEEEEEEEE
1158 - 1177:	EEEEEEEEEEEEEEEEEEEE
1159 - 1178:	EEEEEEEEEEEEEEEEEEEE
1160 - 1179:	EEEEEEEEEEEEEEEEEEEE
1161 - 1180:	EEEEEEEEEEEEEEEEEEEE
1162 - 1181:	EEEEEEEEEEEEEEEEEEEE
1163 - 1182:	EEEEEEEEEEEEEEEEEEEE

A0A2A3EUJ7 **A0A2A3EUJ7_APICC** (1012 aa)
DNA damage-regulated autophagy modulator protein. *Apis cerana cerana (Oriental honeybee)*

```
MLGHVEAGFPYISDTATYAPESCIFSQFINMFAMLMSFVVYIRYSQVKECSSTFRLQTSLPKWNHWALIFGLLSTFGLSV
VANFQETSVLVVHFIGALLCFGGGTAYFWTQAVCTFYLHPLGCSLRLAHIRTALSTFCTVCFVVTLITGVLARLAYKGTN
PRKWYREDGGWELHVASTITEWLCAGAFAVYILTFSEEFRDVKVIHPKIVCTLSRTRLSNETLNESQDSMGRGAGGYVNL
LSHSPVNTPCPGYRYRESREPLLDEAAPLIATTPPAACDVEGRTDVLCPVQIHVHDPSARERRRQMDEEDETERVQKWGG
NHRSRNWIDLDENVLDGYILIDDSCLESGVIPDETKELPYPEGGVEVDEENEDADSHGKDDGSIYSIAKRGISRRGPRGE
EFDLSSTYPLANSHGNAYKESSSHTRYTELYSELAVKNYLEGNREEMGNYSVANSHGDHSVSSENRERSLRENAETDQSV
WDTRQHTNYEVANSHSNYRVFYDSQTQQRELLRTSGWSIESWREHLMANNYVVEERKQKSENAGQLVRDDESTKTSRSEA
KSDPGSEPACDIEQCLVQIEESLLNIEQNLLHVQDLDIPELRNLLYKSPSIEKSLYEVQDLLYADGIVPVINKRKSSTLI
SEDEEEDEEEEEEEEEEEEEEEEEEEEEEEVWVGRNITVKDNDNEDDDAAIGTFDASNEESSDTANIDENNRSGSVDNCS
TTDCTNGSTIFHEDVPVDPNCNEKTMNFIPNSLNKTLPRRIILDGAKENIRLCSSEPEESTTVDYNLNTTCAEKKLFCRD
KCHSRTNSLDENSTFSNFDSFDKRETGKSSLQNLLFESANGNLFDRSGKARSEEMLPRTPRNRCFNASRKKSKEKQAKTE
DFRRKLEPVSSSRRFANASNEQKRAKISKESVNANAPRPIREKSPNRTRRGTISADKVQEKDKEKCTDNKRKRKKISSRS
QSSSENALVPSKLISLSLSLLLAALLQAVRCLTDLVEDAFRSVNCDRSGLLQ
```

648 - 667:	EEEEEEEEEEEEEEEEEEEE
649 - 668:	EEEEEEEEEEEEEEEEEEEE
650 - 669:	EEEEEEEEEEEEEEEEEEEE
651 - 670:	EEEEEEEEEEEEEEEEEEEE

A0A2A4JRD0 **A0A2A4JRD0_HELVI** (384 aa)
Uncharacterized protein. *Heliothis virescens (Tobacco budworm moth)*

```
MSDEEEYSGSEEEEVEEEVPETKPAPKPEGEGDPEFIKRQDQKRSDLDEQLKEYINEWRKQRAKEEDELKRLKEKQAKRK
VSRAEEEKRLAQKKKEEEERRVREVEEKKQRDIEEKRQRLEEAEKKRQAMLQAMKDSSKTGPNFTIQKKSDNFGLSNAQL
ERNKTKEQLEEEKKISLSIRIKPLNIENLSVDKLRQKATELWECIIKLETEKYDLEERQKRQDYDLKELKERQKQQLRHK
ALKKGLDPEALTGKHPPKIQVASKYERRVDTRSYDDKKKLFEGDLEKLNKDFLEKVWQERADQFGGRQKTRLPKWFGERP
GKKKGDLESPEGEEDVKAEVEEDDEPQYEPEPEEEEEIVEEVEEEEEEEEEEEEEEEEEEEEE
```

363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE

A0A2A4JS46 **A0A2A4JS46_HELVI** (389 aa)
Uncharacterized protein. *Heliothis virescens (Tobacco budworm moth)*

```
MSDEEEYSGSEEEEVEEEVPETPAPKPESRPSIAGEGDPEFIKRQDQKRSDLDEQLKEYINEWRKQRAKEEDELKRLKEK
QAKRKVSRAEEEKRLAQKKKEEEERRVREVEEKKQRDIEEKRQRLEEAEKKRQAMLQAMKDSSKTGPNFTIQKKSDNFGL
SNAQLERNKTKEQLEEEKKISLSIRIKPLNIENLSVDKLRQKATELWECIIKLETEKYDLEERQKRQDYDLKELKERQKQ
QLRHKALKKGLDPEALTGKHPPKIQVASKYERRVDTRSYDDKKKLFEGDLEKLNKDFLEKVWQERADQFGGRQKTRLPKW
FGERPGKKKGDLESPEGEEDVKAEVEEDDEPQYEPEPEEEEEIVEEVEEEEEEEEEEEEEEEEEEEEE
```

368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE

A0A2A4JT65 **A0A2A4JT65_HELVI** (390 aa)
Uncharacterized protein. *Heliothis virescens (Tobacco budworm moth)*

```
MSDEEEYSGSEEEEVEEEVPETKPAPKPESRPSIAGEGDPEFIKRQDQKRSDLDEQLKEYINEWRKQRAKEEDELKRLKE
KQAKRKVSRAEEEKRLAQKKKEEEERRVREVEEKKQRDIEEKRQRLEEAEKKRQAMLQAMKDSSKTGPNFTIQKKSDNFG
LSNAQLERNKTKEQLEEEKKISLSIRIKPLNIENLSVDKLRQKATELWECIIKLETEKYDLEERQKRQDYDLKELKERQK
QQLRHKALKKGLDPEALTGKHPPKIQVASKYERRVDTRSYDDKKKLFEGDLEKLNKDFLEKVWQERADQFGGRQKTRLPK
WFGERPGKKKGDLESPEGEEDVKAEVEEDDEPQYEPEPEEEEEIVEEVEEEEEEEEEEEEEEEEEEEEE
```

369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE

A0A2A4JT68 **A0A2A4JT68_HELVI** (383 aa)
Uncharacterized protein. *Heliothis virescens (Tobacco budworm moth)*

```
MSDEEEYSGSEEEEVEEEVPETPAPKPEGEGDPEFIKRQDQKRSDLDEQLKEYINEWRKQRAKEEDELKRLKEKQAKRKV
SRAEEEKRLAQKKKEEEERRVREVEEKKQRDIEEKRQRLEEAEKKRQAMLQAMKDSSKTGPNFTIQKKSDNFGLSNAQLE
RNKTKEQLEEEKKISLSIRIKPLNIENLSVDKLRQKATELWECIIKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKA
LKKGLDPEALTGKHPPKIQVASKYERRVDTRSYDDKKKLFEGDLEKLNKDFLEKVWQERADQFGGRQKTRLPKWFGERPG
KKKGDLESPEGEEDVKAEVEEDDEPQYEPEPEEEEEIVEEVEEEEEEEEEEEEEEEEEEEEE
```

362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE

364 - 383:	EEEEEEEEEEEEEEEEEEEE

A0A2A6C6N6 **A0A2A6C6N6_PRIPA** (388 aa)
Uncharacterized protein. *Pristionchus pacificus (Parasitic nematode)*

```
MSDDYGYDDTPAPRKKWNLEQLKGGHTFLSMQAGTNKFETQRGMTGLGMPRLNVTKDKKLGFLEHDRQSENVLRTQCGTN
QYASQKGETPMGANRMQVPKISYKKEWETVLDKEGEKILPKQCGDFGYASQAGEVSMGGHRNQVPMIRGRMPHDRRTHGI
LCYQSGTNLFASQQGMCAPPGVGAVRQATTEIEYAGFSEDLARKGTEITPWYSGQNKFATQRGTGGFLKVRDVLPHVTGG
KDIDADIKQRSEGIVPLQSGTNKLATQRGMTGFGTPRNTSMRAGWKKEWVEEYEAALRDWEENRPPGSASSADPFTRKKM
DEKLDEAIKANKVVEEPEEEAEAEAEEEQKVEEPVAEEAAEEAEEEEEEEEEEEEEEEEEEEEEEEE
```

364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE

A0A2A6RIG3 **A0A2A6RIG3_9CHLR** (2244 aa)
Uncharacterized protein. *Candidatus Viridilinea mediisalina*

```
MNANTNWFTRIAISLLSITLLLAALWPPAVPRAYAQTPIYVTPNGSGSQNGTSWANSMTLSNALQSATAGQEVWVTAGTY
RPGTSGNRSATFTLRTDVAVYGGFAGTETSREQRNWVINVTILSGDLNSNNTIDDSDAYHVVTGSNDAILDGFTITGGNA
NGSGDNGYGGGVFNSGTTPTLRNIIISGNHASLRGGGIYNHNSSPRLENVDIRGNRANDGGGIYNNSNSNATLINVVITG
NLADNGDGGGMYNQGSHPILTNVTISGNAAARPSGMLSWPPAYAGIYTPTTTLSDTRQATFHLQENAALYGGFAGTETIR
DQRDWTANPVILNGDLGAPGNSYQVVTLGANTILDGLNITGGNADGSAPYHRGAGIYSAVTGVSTIRISNTNIYNNSAQN
VGGGMYAEGSNLVLHTVTFTNNQTLAGDGGALYQSSGTLIFTNGNLSNNRANGTGRGGAIYQQNVGATTLLTVTMTNNTA
GGAGGALYQANSGATMLTSGNLNNNTAGGAGGAIFQSSVSSNLTISDASLNENQAGGDGGAIFQSSLSGDLIINAGSLNQ
NQASGAGGAIFQSSLSGDLTISGGSLNQNEAGDDGGAIFQSSASGNLTISDASLNQNQASGDGGVIFQSNVLGGNPNLTI
SGGSLNQNQAGGAGGAIYQEGAGLTTLTTVTMDGNRADGGAGGAFYQRNAGAVNLDRVTLNQNRASGAGGAFYQLNSQAT
TLTNGSLSNNTAGGAGGAIFRESTGDLTISNTPLNNNTAGGAGGAIFNESSSGDFALSALLLNENTAQGDGGAVYSNNGS
SGNTSITSVQLNRNTASGAGGALFLETNNLTLFNARINNNTATGGAGGAISYSGGNDTTDLNDVSLDENRAGSAGGAFYQ
SGGGSTSLISVTLNRNIAEDGDGGAFYQAEAGATTLTMVTMDGNTASLAGGAFYQTDAGVTTLTTVTMDGNRADGGTGGA
FCQLHGQATTLTNGSLSNNTASGAGGAIFRESTGALTISNVLLNDNTAQGNGGAVFNNSSSGSTSLSSVQLNRNRANGGA
GGALFLNTLGLTLHDATLEQNQASGGNGGAIRYVGASGPTSLSNVSMSSNTASLAGGAFYQENGGNTTLTNASMISNTAT
GGAGGAYYHTANGPTTLINVTLNENRARAYGGALYQTSASPQSFRLEDATLNHNRATQSGNGPGIIAARGGAIYLTNSQA
SIRRATLEGNQLSSSAESPIASAESHGGAIYTRHSELTIADLTLNGNEISSSASGGEAYAYSHGAGLYLRDGSVLLSYAT
ITNNEMTAHATATTGNTLPNSRALGGGIYTIDSYVELVNSTISGNFTDSSAENRGSSKLTHAMGQGGGIYNFYSVVTLTN
VLISGNAAISSAEGPVTSAPSAGGGMYNWDSGLLLTNVTISGNHVNNRGGGLYNYKSDLEIYNSIIWGNHAPGDVSIANE
VMQSMAISHSLLEGSFAGTGNLNSDPLFVSAVATAPSTGGDLRLRGNSPAINQGSLDRLPADVADLNGNNNRSEALPWDL
ARNPRVIGGSVDMGAYEALPNVSTITRRQPNPTNAAQIEFEISFNMPVTGFRAENLRLITSHGQSNASISAVRASGANWL
VTVNTVANTSGNIRLDLINTSNIQSSVAPYLTLTSTGEGYGEASEATYLVDHMPPSTFIEFRPPSLSNQTHAQFTFRGND
IFSGIGSGIASFECSVNNVAFSACTSPHNPGEFDAGEHTFRVRAIDQAGNIDPNPASYTWRIDTTPPIVTLITHPLSLTN
QSEASFTFSGPDGNNEAIQRFECAHNHGDFILCTSPFTLSNIADGLHHFVVQAVDHAGNRTSDPPSYTWEVDTSMPILNI
NSLINSPTNQSPITVTARFDKPVENFNPTAIELGNARVAQISGSGSDYTMLLLPQAQGMVSITVAAAAAHDAAGNPSLGS
NSITWLYDSVPPTTTITSGPISPTIATEATFSFIGNDGDGSGIVSFACALNDEPFTPCSSPHQLTGLGEGLQTFRVRALD
QAGNLESAPASHSWMVTTLPPTTSIEPLAPINAANVHRYNIRGDCATEKGPVTIYVADEERVIACVDGRYSATFDLYNLP
EGGPIEVRARQDEFSGLPGVTRAITFKDTEPPQVSLSAPTTSFTVTNPITITISFSEAVRGFSSESISLTNGLLSNFTVI
DDATYQFLLTAAQAGPISIYLAPGVAHDAADNPNPAATLSLEAQAEPEEEEEEEEEEEEEEEEEEEEEEEEDPVQRVFLP
LVVR
```

2208 - 2227:	EEEEEEEEEEEEEEEEEEEE
2209 - 2228:	EEEEEEEEEEEEEEEEEEEE
2210 - 2229:	EEEEEEEEEEEEEEEEEEEE
2211 - 2230:	EEEEEEEEEEEEEEEEEEEE
2212 - 2231:	EEEEEEEEEEEEEEEEEEEE

A0A2A9CGD1 **A0A2A9CGD1_9BACI** (75 aa)
Uncharacterized protein. *Bacillus sp. es.036*

```
MAENAKHQEVLAKLQELLATNEVEEIGLKFEMVNGEEHKFEFDLTEDEEEEEEEEEEEEEEEEEEEEEEEEEDEDE
```

48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE

A0A2A9P4I8 **A0A2A9P4I8_9HYPO** (160 aa)
UCR_hinge domain-containing protein. *Ophiocordyceps unilateralis*

```
MTIWEAITDIVEAAKPWAVAEAEAPAEELKEEISAEDKDKKEQAATEDKAESEAVEEEEEEAEETEEEEEKEEEEEEEEE
EEEEEEEEEEEIVDPKDVLEEECKNSAQCSPAKHHFDDCVERVKKQESDGGAKEDCVEEFFHLAHCATTCAAPRLWSKLK
```

72 - 91:	EEEEEEEEEEEEEEEEEEEE

A0A2A9P6Q7 **A0A2A9P6Q7_9HYPO** (94 aa)
Uncharacterized protein. *Ophiocordyceps unilateralis*

```
MRRPFLEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEAEEEEAQDEEAGAESPPRRSSGRTRPSRTSTE
PSLHSVVSIAAPPV
```

7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE

A0A2A9PA42 **A0A2A9PA42_9HYPO** (995 aa)
TPR_REGION domain-containing protein. *Ophiocordyceps unilateralis*

```
MTLMPSPFTLLVHGQVAGELINAHVSHVAASQTDASPSLGIEAEAIDILAVALAAFDAFLQINVTGPVIPAHILSAIESR
FIDAWSSSRQEAIGDVTRLRKACLAHLDVDGVSPYTYISHLELFSLARFLLFHLLSDSGHDVIDPSSSYPARTERVSIAW
WRLRINVWHYKLLTQPSLDSGSNLTKSSQWTDVPSLTSNILDTLDALYGSICGREVWSSTGAWDRQDQVHFLVEAATNYI
LLGCHDKAKERIQEAAQASGFQYALSGALGKRTRYQEKSTSQLLVLARSRLDPISVDGASRPNALRLDDDTLLEEIDFAG
DRTEAGADGLPLGLAELSPDHQPQLASLDQMLLLAEATFKDAFSPADMLTLEEVLPFAVRVLADKRTNWQIYTQALLVRS
RIELHRSRTVQRGVLQLQAVADQVIADTSPSADDAEAGHDVPVIRVSAAPTTFLPPPKASESAPAEVRLRYIHALSSPPR
WHLESELAHAWAGVGSLASALDIFKRLRLWAEVALCLAAAAASNDEDGRGAGGEEKAKAIIRWRLFHRTGAHVRDGDDED
DEEEEEEEEEEEEEEEEEEEEEEDVDDVARRGPEAYTGPRRKPSPPNAPRLWCILGDLEDDADHYERAWHVSHGRYARAQ
RGLGEYHLRRRDWARAEEAYRLATAVNRLSPDMWSRLGDVSLRRGMFAEAAEAFHRAIGCASAQAGGEDAKTWSNLGTSL
WSLYCRETDKEDDASPDVDSDDDGASRRSPATLLAQALSAYKRAASISHDNWRMWENVLTMASRTQPPSIPDMVQAMSNV
IRIRQSEEAIDADMLAAILQHSLLDTRRGPQQLTTSPSNEIGGSTAPGQITTLVESSIVPLITHRSRLWSLVARFRTWRG
DLVAAADASEKAWRAALASLDQHDDDDDDDDDDDDDDDDNDNGGGGGGGGTAWKEAVKTTGQLVDSLESLGADRWRLRA
ASAVRALLRRLADRSSGELGPDLVCLAERVGVDVG
```

562 - 581:	EEEEEEEEEEEEEEEEEEEE
563 - 582:	EEEEEEEEEEEEEEEEEEEE
564 - 583:	EEEEEEEEEEEEEEEEEEEE

A0A2B4R7X8 **A0A2B4R7X8_STYPI** (554 aa)
Uncharacterized protein. *Stylophora pistillata (Smooth cauliflower coral)*

```
MSNMENEDMQYDDTDLIQGQPTPIQVPHQKLVEPTTSILQRVIQEDSIPKEDLRKRWNNMKSEREKLRKQWNKSKDQMRY
WTLKTKEFEYQLNRNSEELERLKGINTVQHITNMKLTSLKEINKDNIIFEEATEICDHKHIKIKAKHACGENKAGPLVIA
SPLFPHSYLEQNLSVDGDIMGYSMPAFLDPERKEFADFYDAMKELKNLCYEHLRVVYGKDKAESMKFPLVEKEGKTPVLY
PKLIFSESIQKIHTLFYTGKTKVDPLDCLGRYCQVKMAIVVDGIYFSGDNISVQLQLHDAYVSPSWVRRRRYATFEEDSF
EVKYGWATSFAIDLEKLKQLPPPPSWPTTFVATFYEEPTAGRKLKQIIKKIKEENLKQLETDPAADREEEDLDELKEEEE
KEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEALPKSGQTFPGVKYLGPLRFDEKTGKLLHPVTGKILNIRNSLTGDVV
TRHNLTPTGDVAKLLSIDPNNVPFYPSPMDEEVEEEDEEEEDEEKASPFICSPKIEDKPLSLNPKSYPFYPSPF
```

402 - 421:	EEEEEEEEEEEEEEEEEEEE
403 - 422:	EEEEEEEEEEEEEEEEEEEE
404 - 423:	EEEEEEEEEEEEEEEEEEEE
405 - 424:	EEEEEEEEEEEEEEEEEEEE
406 - 425:	EEEEEEEEEEEEEEEEEEEE
407 - 426:	EEEEEEEEEEEEEEEEEEEE
408 - 427:	EEEEEEEEEEEEEEEEEEEE
409 - 428:	EEEEEEEEEEEEEEEEEEEE
410 - 429:	EEEEEEEEEEEEEEEEEEEE
411 - 430:	EEEEEEEEEEEEEEEEEEEE
412 - 431:	EEEEEEEEEEEEEEEEEEEE

A0A2B4RA48 **A0A2B4RA48_STYPI** (1052 aa)
Uncharacterized protein. *Stylophora pistillata (Smooth cauliflower coral)*

```
MGAIFLLVNTTKLYGSKTPTASKRESKTWPEEEPGLTQEFRTSSNSTKILQGPIESCAQSPIRQNVTLRGGINAGSFKKL
AQFVAMQLCIRLCCEEKGCDVALMSGKNCYGVQCFSEELCTAVPAKKAPSSLMISHVTIKGEEGNSRRIHPVPQNLKCTE
SKAEEGVTLKGGISAGHFTDVGTVESVDSCTRLCCVSEKCDLALVIKRHCFLVSCFTKELCKTVKSQTKNYRPTVAFVRR
WVTNVTEDTAITLSNLPATNSKLMCKNSDIKYNSTLKGGIKAGNFTDLGKISEISTCIRMCCGRKDCDVALMLEANCYAV
NCYNEDLCHPVLARKSGLLTNLSPRLSYITSRDEEALPQEIAIGNGMFCKPSVVSYDVTLRGGLSAGKFTPVGHVDSMEA
CVNLCCKRNACDIALMLRDSCYAIKCANEELCEEVPAPSSDFYPRLSYVRKEIGSQHKKEHPQVKSETTHQTNDTREDLD
TKEEGYCTNSEIMTNVTLRGGISTGHFRDRGKVPNMRACVEICCISKSCDVAFMLKNNCFSVTCFNEKLCEAVRARSSIY
APRIVYIYARTKSEVFTSQSVRKRRSENLKSNNFRDQLYDVPLTDSRQESLVTEITNVKPLKCQHGAILSNVTLRHELRA
GKFSRLGRAEDMKTCIQMCCDKDDCEMAFMPGTHCYGVDCFSQKHCEITTVKPSNVTVKIAAVRPIVVNPSKDQIAVSVE
DPSTQEELHCTQSPILKNVTLRGGIKAGNFSDLGDEKNMHMCIALCCERKTCDLAFMIGGTCIAVDCFSEELCQAVKARP
TIYDPQIAFIRRRELQRPARKELLEDEGADYTAIPKCTRSHILYNHTLLGGLRAGNFTHIAEVDSIETCAALCCAEQTCD
LALVLGENCYAGDCASKELCVPVPVHPTANKGSQIAYITSRKKVEEPGTGDPKCIKNGPMFLSDSESDSDEDAEVPRRSR
IPSLETQSIKKSIGYNGPPPPYIVERLNGPSVIKEEEEEEEEEEEEEEEEEEEEEKKTFRADGRNAEKFQKLMTRPDSFL
AIIASSIIELKS
```

995 - 1014:	EEEEEEEEEEEEEEEEEEEE
996 - 1015:	EEEEEEEEEEEEEEEEEEEE

A0A2B4RB92 **A0A2B4RB92_STYPI** (205 aa)
Uncharacterized protein. *Stylophora pistillata (Smooth cauliflower coral)*

```
MLGETCYSVACKSIELCEHSKAPPTDYNPQLSYVRPMKTSDNKRKDFCIPVSVKASKRSPLISAMVMKGEPKEETDLSGV
ASSPEDSTTTELASSSATCMLDSRISNDIKLRPGTKVSNFTALDLDKTIEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEPLLIYSAQGSPFRCKKLSIINKNPEPNDVLQL
```

130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE

145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE

A0A2B4RDL7 **A0A2B4RDL7_STYPI** (128 aa)
Uncharacterized protein. *Stylophora pistillata (Smooth cauliflower coral)*

```
MTITLWPMKKQNLKIATTYAMDQTKNVLECAGRNAGAGTGCVAIVVCTKVVCSTMHVAVMQIPSIYRHIAFFRFFTDLTV
KMVIMATQLVCIEEEEEEEEEEEEEEEEEEEEEEEESRAHHSLGFIFPR
```

93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE

A0A2B4RHV6 **A0A2B4RHV6_STYPI** (185 aa)
Uncharacterized protein. *Stylophora pistillata (Smooth cauliflower coral)*

```
MASKAFVLMCFLALLGQLSGFKLTRPVDLERFGQELEDVKKYIESLESPASDEGEEGEEENGEEESGEEEEGGEEEEEEE
EEEEEDDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEESGEEEEAADDEGEDXXXXRRGRRGRGRRG
RGRRRRRGRRGRGRKWRRRGRRRRG
```

88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE

A0A2B4RMI2 **A0A2B4RMI2_STYPI** (90 aa)
Uncharacterized protein. *Stylophora pistillata (Smooth cauliflower coral)*

```
MIFLRVMLSFDPVGTSKDNAVHHVSKGMSLNSRSPKIVKEEEEEEEEEEEEEEEEEEKEEEEEEEEEEEEEEEEEEEEEE
EEEEEQEEEE
```

59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE

A0A2B4RSD8 **A0A2B4RSD8_STYPI** (153 aa)
Uncharacterized protein. *Stylophora pistillata (Smooth cauliflower coral)*

```
MHHEVDYPTCYTPRDIKTVNFMSEQLMVNVVKSFAVVKQDHPDCRSRAISCTRPVMEHGRQSYGRGGLRRRRRGRRRRRG
EEEEQEEEKEEEQEEEEEKEKKEEQEEEKEEEEEVEDEEEEEEEEEEEEEEEKEEEEEEEEEEEEEEEEEEEEEL
```

133 - 152:	EEEEEEEEEEEEEEEEEEEE

A0A2B4RZU2 **A0A2B4RZU2_STYPI** (222 aa)
Uncharacterized protein. *Stylophora pistillata (Smooth cauliflower coral)*

```
MGVIRFAAVLLFVVSLSYIHSVVSVIFLGPRRDNFLLNKRFFPQAEEKHPRKRAPMFDPQAEKPQPGEAVKTKRLASQAD
AEKSENGAPLGNLFDPQAERPKKNKKSPSRSKRLAARSEHYDKMPPPAENMFDSQVQQDQDACRWRCQEWCRQRCQSSAY
EECLDGCLNVRGHRWRSCINKCKRGDMDRPGGDNEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

195 - 214:	EEEEEEEEEEEEEEEEEEEE
196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE

A0A2B4S7B7 **A0A2B4S7B7_STYPI** (1015 aa)
SEA domain-containing protein. *Stylophora pistillata (Smooth cauliflower coral)*

```
MEKLHWLLWNVAIFLLILFRGVTAFGREGSLVSYSHLVLIESKSGQLGKYSQIQSTSQLTRSSTPSPPPDHSEELMFVSS
AFRSSSVKTTNFDNDGFIPKSSLTARPIKGYELFATSRSTQINQIESLAKKSDWQTSGTTSAEVKATYPSFIFTSSSSLS
SSSTPKLLSSSSLSPLRSFLFTNPVSSSSSASSLSTSLSSSPSSLSSIFLSSSSSFSRPSFPFYFSSVSSDTSLSSTLSS
SLSPSPSSSHPSTSLKPSSSFSSLVSSSTSSRSSSSSPSPLPSLSLTTPSFSSSTIFSSTPASSLFLFSNSSSTSSSSSS
PLPFLALSLSPSLSLYSTRTSSSSSLSFDSFSSSSLSSSSTFSSSSSFGPLSPLSSLSPSLSPSLSSYSLSFPSLSSSFL
PSSSTLSSYFSSPFFFSSSSSFSLLLFPSSSPSSPSLSSYSPSSSTSSSSSSLSTSSSSSFSTSSSSSSLSSSSSSSSPS
SSFSLSSYFSFSSTSSSSSSLSSSSSSSSSSTPSSSSSLSTYSSSSSSSYSASSSLSFSSIYSSSSSLSSSSLSLSSTSS
QSLSSSLPSFSSLFLLLPPSSSFSSSSLSSSASSSSSSYSSSSSLSLSLALSSSTSLSLSSSSSSLLSSSLPYSSSSSSS
LSMSSSLPISSSSPSSSSSSSPSSSSSSSSSSLSASPSSIMSISARSSFSSSSSLPLSLLQPLPTSARSSSSSTAPLTKF
VSSSSLSSTTSMYLESTKKVIPTSGPEKPTSPTPGKTWRATLTIQNMEFTEGLTDPSSEEFMKLANELEDVLDDIFKPEI
SGFLSVEVVNFKKGSIVCDFLIYTELESSATADNFSDVLSAAINKGEAKKFKITYFTIEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEDVDVKSVIGTKERKNEFPLKVFAAAAFGALVVLVIGFVLYKRVSRKRREREGFKNTR
DIIPLNDFNSPNNNEEGEGELASQKIRISNYEDKEEDEDEVTPFCKPGVKKMSPV
```

859 - 878:	EEEEEEEEEEEEEEEEEEEE
860 - 879:	EEEEEEEEEEEEEEEEEEEE
861 - 880:	EEEEEEEEEEEEEEEEEEEE
862 - 881:	EEEEEEEEEEEEEEEEEEEE
863 - 882:	EEEEEEEEEEEEEEEEEEEE
864 - 883:	EEEEEEEEEEEEEEEEEEEE
865 - 884:	EEEEEEEEEEEEEEEEEEEE
866 - 885:	EEEEEEEEEEEEEEEEEEEE
867 - 886:	EEEEEEEEEEEEEEEEEEEE
868 - 887:	EEEEEEEEEEEEEEEEEEEE
869 - 888:	EEEEEEEEEEEEEEEEEEEE
870 - 889:	EEEEEEEEEEEEEEEEEEEE

871 - 890:	EEEEEEEEEEEEEEEEEEEE
872 - 891:	EEEEEEEEEEEEEEEEEEEE
873 - 892:	EEEEEEEEEEEEEEEEEEEE
874 - 893:	EEEEEEEEEEEEEEEEEEEE
875 - 894:	EEEEEEEEEEEEEEEEEEEE
876 - 895:	EEEEEEEEEEEEEEEEEEEE
877 - 896:	EEEEEEEEEEEEEEEEEEEE
878 - 897:	EEEEEEEEEEEEEEEEEEEE
879 - 898:	EEEEEEEEEEEEEEEEEEEE
880 - 899:	EEEEEEEEEEEEEEEEEEEE
881 - 900:	EEEEEEEEEEEEEEEEEEEE
882 - 901:	EEEEEEEEEEEEEEEEEEEE
883 - 902:	EEEEEEEEEEEEEEEEEEEE
884 - 903:	EEEEEEEEEEEEEEEEEEEE

A0A2B4SGJ1 **A0A2B4SGJ1_STYPI** (127 aa)
Uncharacterized protein. *Stylophora pistillata (Smooth cauliflower coral)*

```
MTKKIKGKAKREGERSAPELKETVLTYCEEEEEEEEEEEEKEEEEEEEEEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEAIQNYIVEIESSNIAPRIAFFSSYQKSFRK
```

53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE

A0A2B4SK69 **A0A2B4SK69_STYPI** (167 aa)
Uncharacterized protein. *Stylophora pistillata (Smooth cauliflower coral)*

```
MKAGPWGYTLDPIAGFYRSPGFKSLIFNPTELIGDAARFTKQVAKTALKRPLATKRLRKKFPVEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEERRRKKKKEERRRKKKKEERRRKKKKEERRRKKKKEERRRKKKEERRKKKEERRKKKDERRRRSSIRRRGRRR
GRRRRRN
```

64 - 83:	EEEEEEEEEEEEEEEEEEEE

65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE

A0A2B4SW02 **A0A2B4SW02_STYPI** (81 aa)
Uncharacterized protein. *Stylophora pistillata (Smooth cauliflower coral)*

```
MLLKSGCLKVPPAPLAIVERKSKLKLLGVTFEDDPVNWDSHINHVLEDEEEEEDEEEEEEEEEEEEEEEEEEEEGEEEEE
E
```

55 - 74:	EEEEEEEEEEEEEEEEEEEE

A0A2B4SW15 **A0A2B4SW15_STYPI** (358 aa)
Angiopoietin-related protein 7. *Stylophora pistillata (Smooth cauliflower coral)*

```
MTKTGGISLCEYICKQHQQKYNEGHRHGIGFATLFLALCVTFRIVPSTCAAPIDGQKNHALYSKKTTMEGTQDSTSLRCM
IKNCAELYKSGQKISGVYTIDPDGSDAFDVYCDQTTAGGGWEVFQKRFNGFVDFNRTWDDYKHGFGNFTGEFWLGLDKIY
RLTRNETKNMLRVDLGKATGETVHVEYSWFGIGSETAMYRLYIGNVTITLDYKTLIMLLKQRAGDAKKYINELCKQGLDT
ECCVFCKVIKSNREEKEEEEEEEEEEEEEEEQKDEEEEEEEEEEEEEEEEEEEEEEEDEEKEEESLSSFRLQNHERESLSQ
LHGGSTIGVLKSRFPASFSSQPAIPPLFMPGSRSRPIF
```

275 - 294:	EEEEEEEEEEEEEEEEEEEE
276 - 295:	EEEEEEEEEEEEEEEEEEEE
277 - 296:	EEEEEEEEEEEEEEEEEEEE

A0A2B7WG23 **A0A2B7WG23_9EURO** (473 aa)
Uncharacterized protein. *Helicocarpus griseus UAMH5409*

```
MSAEGTLQRNLNQSKQTPTFLSLPLEIRLRIYDGLHDPESNPQHACLMYLTCVCRQLRDEAFPLLFPERKCFRDRIKFTE
WASRVDPKWLSYTKELSLNLLSDLGEEFQPSVAGIGRAKKQRMRDGLDLETPKTGEWWEMKYLELLGKDIPTVDQVVMDE
EEEEEEEEEEEEEEEEEEEEREAAGPSSSRPIPQLWDILCSFSHLGALEINLSPYAREMVNGRPPPFGIQLDTMVPEHYL
IAQMLPHAIPSLTSLSFFSTPIHLYFLSNFENLQHLTLIYTSLTDPHTTLSILSSLKFLTSLGLSCPEPHAFIYKAPGKR
QSITSQVLTGLPNPLTSFEISNLPHNCFYPITVEFLLALFETHGSSLRHLRIGERCYETYERDVLDLLLGYLPRLDRLES
VKLNLLAKYDPEEVKNNKYYAGSGSGSDSRIRGLLDVGPRLHFGRTERPGFLNYVSDCSWGNVRWVLEWEKMG
```

160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE

A0A2B7YS13 **A0A2B7YS13_9EURO** (704 aa)
CP-type G domain-containing protein. *Polytolypa hystricis UAMH7299*

```
MVLAKSKNAVGLGNSLMNDRFGKGKASNRKKTSHNAATGIKRTGPTGETYITNASEEASWVKMRSITEQGALDEFLSTAE
LAGTDFTAEKLNNLKIIHTDQKNPYLLSAADERAAVKKHYKNRDRLTVPRRPKWDQRTTPQELDTMERQSLLEWRRGLAE
LQENQDLLMTPFERNLEVWRQLWRVIERSDLIVQIVDARNPLLFRSEDLEKYVKEVDPRKSNLLLVNKADMMTEAQREVW
ADYFEENGINYKFFSAELAKESNEAKLLEDESSEYDSEEEEEEEEEEEEEEEEEEEEEEEEEELAEDTKKMDLRDQDEETD
EDDESEDDGGLQLPNTSGSSRTNILTVEELEELFLQATPTSKSHNRDPSKPPITSIGLVGYPNVGKSSTINALLGAKKVS
VSATPGKTKHFQTLYLSPTLLLCDCPGLVFPNFASTKAELVVNGILPIDQLREFIGPAGIVAHRIPGRFLEAVYGMKIRM
RPLEEGGTGVPTAAEVLRAYARARGFSTTGLGQPDESRAARYVLKDYVKGKLLFCHPPPVSEAAYAEGKKPIDEAEFNRG
LYDISHLPPRRQEAMLKEASSITSHETTDDNESDVVSITSATPTATPTLPQGPLSRTIDSGFFAAGGAGARGHLVMPFNH
QYTEQGAVQRHKEPSGRKQRTMIALEKGVDVSEVRGPGKKHFKGGKRKLRSQEKAGAKPEDDGY
```

278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE

A0A2B7ZCD6 **A0A2B7ZCD6_9EURO** (663 aa)
Uncharacterized protein. *Emmonsia crescens*

```
MNPFAFSPFGFNFRRQPATYTRGAGPYVSRDCPNTPQIHTASKPLSRPEPNEQGMFRPPAILSTLFPAEVENDAEPEPED
TEMEDGEVIDLICDNESSNHPGQNSRQVPDNVTRVQSSFLQRRQSGKYPEPKIENGTSHCSTRRAPAEVDDNDAAESWLR
LRLQQEEDLKSRTRVITDLPVNSGTSKRGRFQNHSQVKQDSQAKKRFNQSAANLKKTREDLDGYLAKDPQHKKALEERQL
CQIYMKKVDRGETFTAGETDRLRRIRRNISRRECSFESKMKSDLDLCRKSRQLNELPKVGVDAESNPSYTKLENDSFEPH
SRCSSSTLSEATPGLSQRKTISGKTIRGGKFPSGYSRNAPPRILSSSAKNCLDGIGDRGGGKEETGEEDGEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEQSSEDDEDEGKMGECGQGETFWRYSVYQSTEGDFQDEEEPKCLETYLSRAKAEAKIRRQIL
RLQAAASIQERKKIECRIILEDNGLHAQVICFASSGRTVTVYMEKEVVEAAELSKTAQQNLSILPCRVYSVVEQVIDPLN
TDVPIGSPVWSECFVLRQHANEQANRRLLSYFTSYSENDETYNRIAGGTLEVDQGRYLQDLEDGERLFDRKISLPAGSGG
NTNTQRKQVVLRVVEQLLRGPRN
```

391 - 410:	EEEEEEEEEEEEEEEEEEEE
392 - 411:	EEEEEEEEEEEEEEEEEEEE
393 - 412:	EEEEEEEEEEEEEEEEEEEE
394 - 413:	EEEEEEEEEEEEEEEEEEEE
395 - 414:	EEEEEEEEEEEEEEEEEEEE
396 - 415:	EEEEEEEEEEEEEEEEEEEE
397 - 416:	EEEEEEEEEEEEEEEEEEEE
398 - 417:	EEEEEEEEEEEEEEEEEEEE
399 - 418:	EEEEEEEEEEEEEEEEEEEE
400 - 419:	EEEEEEEEEEEEEEEEEEEE

A0A2B7ZKY7 **A0A2B7ZKY7_9EURO** (816 aa)
Uncharacterized protein. *Emmonsia crescens*

```
MGSFDIFCALCSGSLCQVDIGSKSKRQRQVRQRFIAEKIKELETSRGEHKSPNVSYESSEEQWEMAEETQDIQSEDEQEL
ESEEEEEEEEEEEEEEEEEEEEDGCQSYDPDIVNTESIEWLRIVHVLGYNPRAAGPSKAYISGEGMYFDYGGVDISPGDD
PNAPGDPNSPQMINSVSCYGSGAFPFHWCCFEILTQVLTGSTDIGKVDKDILYNVMLGLSPEYASRLAIYYGEIIGVDQF
WESVPGEEYSVTHPTIIPGFEEVLRKLISEKTFKATCTGRLQLAGKVKWDPFNKLPYDIIYYVLRFLPGDSTRAFMAASW
AVYNATRHPTLWKQLMYWGMPWFWELHKLVDEHSTDLDYKNLYLWLDKATMPVYGMDGPFLGIANRRRIWGACTQLAEIY
FSSFHQRDQTTDEDLNSVLQESQIMQLPMVKYPQPNMEVRTISKQWLRTLEEFDSRSAVLETLWTSNEYLMGLSVIFGTS
RRVFGRAAATDGVIKRIILIASDDWITGLVLYVPGMDLLDKHACTAVRGIEIIFKSGKQVIIGDNQGNHRPFIVSEDHYL
VGLVGQTGEDEIISRFGILESPITKSNEFSVHDVKLVPVSERPFSQQLLWGPGVSLLESSTASRCGKRPIWNHPNIHVLS
SNGTGDMRHGVPGDLVPYQPLIWALHDHELQKLTQISAYVKTEITSSGPRECVLGLRAAYTRRYWEPKRYVGEFPGQDNE
DVVQEASDGEIRHFEIDGPNSEYVVGVDIAMGDSLKAIKEYSNMISSEPIGEEKCVLVIRIKMTGKFRVRQAEICLLGWR
LLFGLLLDTRRFRRRL
```

83 - 102:	EEEEEEEEEEEEEEEEEEEE

A0A2C5XMX3 **A0A2C5XMX3_9HYPO** (95 aa)
Uncharacterized protein. *Ophiocordyceps australis*

```
MCNRSRRRRRRWRRRREGGEGQRRTRRRRRRRRTKKKDKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
KEKEKEEEEEEEKEQ
```

40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE

58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE

A0A2C5Y8N4 **A0A2C5Y8N4_9HYPO** (556 aa)
Uncharacterized protein. *Ophiocordyceps australis*

```
MLFWTTICFSVACACSSVVPRALLGNVDLAKLINDSPQVAGHKANIIQAIKNDVPYTESRLKIDQASGMKHVKEEQRHCF
YVRRVMDPKSIETEIHVVANVDQSDEVTGDYEVPISISSSTATVDTERLGWNKEVMEETGGSVSVSAQLGLSFFASSVSA
TVFGSQRWSGGQSGDAMKQKEYRLDVTNVRTCPRFSICRVVTWTYTRKLSGNCFVLPILDTQCIDRQQTMGNASLRLFSG
CPPIDKLAHQFFESHLFWTKQFGPVLHGVTMHVPESVKRNKYQARCAFSHALTWDDGTPVRAQALITESLGPQYVKKGKD
LEEEEEEEEEEEEEVEVGEEAEEEEEEEEEEEEEEEEEEEEVEEAEEAEEQAVSIPHNIPQALEWRVRKNSKFGYCRLDN
NWAWEPDSWFYIPKPEGGSGAWQEQPSWPRPKYVDSKCRQHTWTRKSKRAKRNVEAVDKDMGTSRHVVVNMTINELPSYL
DQYKSALPDTSSQIESLSRRWGGSEFGWMSCPPGKRRDSRGKCRQVFGTELCQELDCPVRQYAVNKCLSLLQGPRI
```

342 - 361:	EEEEEEEEEEEEEEEEEEEE

A0A2C5ZHV1 **A0A2C5ZHV1_9HYPO** (129 aa)
Uncharacterized protein. *Ophiocordyceps australis*

```
MRLSTLIFAVFAAAATADKTAESEPYLLRGGSVSSVEFHKPGITCGIYVHAKCSDTIRGDIRESVADLGNTATIVSADCR
KIKDEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKGEKEEKENEGEEL
```

88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE

A0A2C5ZUL3 **A0A2C5ZUL3_9HYPO** (468 aa)
Uncharacterized protein. *Ophiocordyceps australis*

```
MAKKSKLRLAIAAEKGIDFKKLKLEKKHKETLKRKRAKQEALQPPNESQEVKDENDQEEEEEEEEKEEEEEEAEEEEEEE
EEEEEEEEEEEEEEEEEDDDEKEWEDEAGQDTDTMNLDAVDESDTSDSSIEFEAKLPHKASDQKSRPKLATKPNDQDDEQD
EDDEDDEDDEDDEDDEDDEDVPVSDLEDLEDEEKEDLIPHTRLTINNTSALHAALDRIALPTGPANPFAPHQSIVSAAPT
ADSIPDVADDLTREVAFYAQCLDAVQRARVLLRNEDVPFSRPGDYFAEMVKEDAHMEKIKAKLVEEAAAKKAATEARRLR
DLKKFGKQVQVAKLQERQKAKRETLDKIKTLKRKRQESGAQLGTNEADLFDVGVDAELAKHSQPHTASGSRNAPHKPNAK
RQRKAEKFGFGGKKRHAKSGDAISSGDLSGFNVKKMRAGRNADAAKAKMNSSKASRPGKARRKALANR
```

74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE

A0A2C6L610 **A0A2C6L610_9APIC** (1245 aa)
Sufb sufd domain-containing protein (Fragment). *Cystoisospora suis*

```
SSRLDCVPSRLSPSSSLSSLSSSFASGSLLERRGRTRRRRRRGKVKLLSPESFEQEEEEDSPPSCSFLECTDTPFQWFHT
FFRVFLSFLFSLFFLLSSCRRFKAPHFPQWLQSPFILAKKCVFTSLRQVAEEKKTPREYTNLFFFFSFFFFFLFSLFLCP
ILPRCLSRFFSLTCMESFRRQMSSLLFCPFFFLFLCLFSFPLPFQDEKEEKRKFFSISSFRSSKPTRRRRATCNEERIQS
KREEEEEEEEEEEEEEEEEEEETATLPPTYTPYRHFLSSFPSSSCSSLPSPSSSSPSPTSPSSSSFFFFSSVLTSLCCLQ
SMSSLSHPKKRHLASPRTNLSSYSCSFSFFFSSSSSFSYFSFFRSFPSFISVGFFSFFSPRPYLSLYHLFFSILVVLSLI
NPSLAGPSSHSHSSSFSSSSSTLSIPFQVPLHPLSPSSSPAFSDSPCSSSFLFARMQNKKRRGMKKRKKAKKEEREEDAL
REDHESTEASCRSPPEYKRMSKEMKKKKKELQSSTTDHKTYEQRRRRGRDRVSSFISFLPSSPFSPIPSTLDLAISSSSP
AHRLSSSSSVLFPLSLPRNFPSVVDPSRSAGPSLLPSHDFSLLPPLSSSFLSFAPSLSHQSYPFSFFSSSSPFPLGNLLG
GPSSREREARRRERTRRLTSAPYDRNPLLYHTLLPHPLLLHRHRARSNTSSPPFLSSSSLFARPFPSRVSQNAFFFSGEK
MKEISPLLSSLDNSSVPPRLTRRRTSMLATHQNVEELAMRKSIQKERKEEEEGDEERHGVESKERLRSSFSSSSKDGKEE
KRKIKQTTMRKKKEKSLSMGFREDMSSSSSSVHTAVGDRDGYNEEETEEEEEGGEKDGGGEEEERNEEIMLISEEEKKKL
FSFFQEAEASSPRLSLEGEEMTNESYDMFTEIFSLPPSSSSSSSSSSSFHDQFPTNSTSLRTASLPSPPSFSSSSSPPVD
EGLSSTRHAEWYLLKDFKPSFPTLIEPDPSYTSSSSPPPSSSSPPSSSSSPPSSSSSSSSSTPPSTTLRDIEPFAVTKRH
EASLRPNAQESLTPWKRIIARKFVETATDTFLPRHSDFEFSRFSRDFAYETAEMGVDLPMIRQAVSAAVKEAEIRRHKDL
LQEEKEKAIKEKEDEDSEAFLYKELGLETSRRGAGEEPNKKKKNEKGEDNERYKREILKREIERKVIEQMRSLLEGGGGG
TTESDFKETDEKFNSVWLGKESFEDISAEPRFIPETWTDVPRPCR
```

243 - 262:	EEEEEEEEEEEEEEEEEEEE

A0A2C9DX81 **A0A2C9DX81_9GAMA** (1324 aa)
ORF73. *Alcelaphine gammaherpesvirus 1 (wildebeest herpesvirus)*

```
MVLLRSGLGTRPGEEDCDGGPSTRTRGHGPLGPNIKSAAGIGGKFPPSPQGRKRKKGPKKSGGKKKKRKVTGEGPGGGEG
PGGGEGPGGGEGPGGGEGPGGGEGPGGGEGPGGGEGPGGGEGPGGGEGPGGGEGPGGGEGPGGGEGPGGGEGPGGGEGPG
GGEGPGGNSRKRKRGDGSKKHGGKKKKKTTVTGEGGSGPEGPERDDPDGPGSQEGPKREEGPLGPDGPEGPEGPEGEGPE
GLEGPKGEGPEGPEGPEGDSPDGPGAQEGPEGLEGPEGDEGPEGPEGPEGEGPEGPEGPKGDSPDGPGAQEGPEGPGGPD
EDEGPEEPEGPEGEGPEGPEGEGPEGLEGPEGEGPEGPEGPEGDSPDGPDAQEGPEGPGGPDEDEGPEEPEGPEGEGPEG
PEGPEGEGPEGPEGPEGEGPEGLEGPEGEGPEGPEGPEGDSPDGPGAQEGPEGPEGPEGEGPEGLEGPEGEGPEGPEGPE
GEGPEGPEGPEGEGPERPEGPEGEGPEGPEGPEGEGPEGPEGPERDSPDGPGAQEGPEGPEGPEGEGPEGLEGPEGEGPE
GPEGPEGEGPEGPEGPEGEGPEGPEGPERDSPDGPGAQEGPEGPEGPEEDEGPEGPEGPEGEGPEGPEGEGPEGLEGPEG
DEGPEEPEGPEGDSPDGPGAQEVPEGPKGPEGECQSGPSSCEGQQVPKGPDGPEEGSSGPGSSEGEGPSGPGSSEGQQVP
KGAEGSEGEGPCRPGGPDEDGDPEGPDGTEGEGPCGPGGPDEDGDPEGPDGTEGEGPCGPGGPDEDGDPEESEGTEDDIK
VGLTELLGSMKLDSSDSDSDNSSDSANRRALEGVCGSHSSSKDSDDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDEE
EEEDDEEEEEDDEEEEEDDEEEEEEEVIIITSSGEDGCGSSDVVCVGEEKGEGEKGKGREEDGGEGGEGGEGGEGGEGGE
GGEGGEGGEGGEGGEGGEGGEGGEGGEGGEGGEGGEGGEGGEGGEGGEGGEGGEGGEGGEGGEGGEGGEGGEGGEGGERG
KGGEGGEGGEGGEGGEGSEEDKKPFPCPRSPGVSGFYDLTWSSSDRSTEGSRGSPGPDDLDGRPGSQGPPTLSPQGFPGS
GYGSNYDDDREPPVLSPQCGGPSGNEGDESDPDSSREPPDLSPQNPPEGDNGNESDSDPSYQPLGGSSSSSEDDDPGEGT
SQGPPKRPPKHHPQTKRAQGKTLGLDPLYDPRQKAATFSLHLGCPTKDPLVRLSRMIRTLHPEGPHSSIFFTGGQYVVVF
YVTSYFEAKKLKDFIIREQNRNPLQGRVNVSLARHYPPFPFPHE
```

847 - 866:	EEEEEEEEEEEEEEEEEEEE
848 - 867:	EEEEEEEEEEEEEEEEEEEE
849 - 868:	EEEEEEEEEEEEEEEEEEEE
850 - 869:	EEEEEEEEEEEEEEEEEEEE
851 - 870:	EEEEEEEEEEEEEEEEEEEE
852 - 871:	EEEEEEEEEEEEEEEEEEEE
853 - 872:	EEEEEEEEEEEEEEEEEEEE
854 - 873:	EEEEEEEEEEEEEEEEEEEE
855 - 874:	EEEEEEEEEEEEEEEEEEEE
856 - 875:	EEEEEEEEEEEEEEEEEEEE
857 - 876:	EEEEEEEEEEEEEEEEEEEE

A0A2C9U5L1 **A0A2C9U5L1_MANES** (165 aa)
Uncharacterized protein. *Manihot esculenta (Cassava) (Jatropha manihot)*

```
MTTIFTAARDAFVHAKFEAQTTSGDSAIESATTQVLVVPHSNDSDWTRYEGKWISKAEAEKKEEEEEGGGDRKREEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKGERMENRRSPGKRFDSDTQQIDREGRKEIDRERFVQQIDGK
KVDDR
```

75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE

98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE

A0A2C9U986 **A0A2C9U986_MANES** (841 aa)
C3H1-type domain-containing protein. *Manihot esculenta (Cassava) (Jatropha manihot)*

```
MPPSSSTAARTAEYNDDHSPPSSDSPAEISDSDLDNREQEEPEIEVEEQEEVHNGNVDEEDMEEEEEYEEIEVEEEEEIE
EEIEVEEEEEEEEEEEEEEEEEEEEEEEVVEVEEEEEEEEEDDDDDDDDKLDSSKESNVELNDVGQHKEVEGQLVLSSTL
GRSELGLQSNSHIQDSISNPKLSGPLDESLTFQEKVHVNYEDSECCKSGDCLLTTGGNESQQFAVEKDVEAFVKKNSQEL
SKHNGDCKVHLCNDKSISDETTSPSIARNEVSNALAIKDCLSMDTNGILDSEVEVKPMEMQPEDKEQTASRFSRVVTSEI
RAQSPSPSAEFKDWNKRPAVICNFFAKGWCIRGSSCRFLHINNKADNAKEQLEGDAAVSHLSKGDQFDEGLKNIMEKPKL
SGFPDLVASSIGNGSAFPSRFSSEKILPFENGESQLFHQLDEQQKSSSLPREDLSRGVHLHPDTQQFPSSKGDLGVSSSL
KDLGKENLRQSWPASDYGRYASAINRGPSFSLTSSMNISPLGSQKLLGNDRDFCASRSSPILQTASPRSGSELENVPLTS
VSKDPLCYTEHKAKIFSNDWEPSIPFRPSFFITHTMTSSPGSQYDPLRDSIDLPTAGYKLPFKFSFVSQVTSNLNSSHLP
TYGNSVSQILGPECDNDKSTVSSHSRFHENVLGQNCFTPGKVVGGTSAVNVQKETKPKEENTSSSSHLNNVPNKRKIDID
CDSRQTNDGPRRKKDLKVDRVRQKNEMDVEQKTDGESRTLRHFRAALVDFVKELLRPTWREGHLSKDAHNKIVKKTVEKV
LCTLQPHQIPTTIESIKQYLSSCQPKIAKLIEGYCTKYGKS
```

86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE

A0A2C9UEC4 **A0A2C9UEC4_MANES** (951 aa)
Uncharacterized protein. *Manihot esculenta (Cassava) (Jatropha manihot)*

```
MSRNSRNCHKDASQEEEEEEEEEEEEEEEEEEEEEEHFYESLDRIASSSCSCSASNSDSDPDPNPTRSNSISNSPGNNNDPP
FSVSKLPLGVSKYAVWISEPASVSERRQRLLHQMGLTSDPSLSRAKPEGDFHFNRSVSSDHLSQEKPGPSTSGGIVRSKS
DGAGPRTDRDGGDDKCNDDFNSCSSPSSLLSVYSPRILSHDLMDVNNCNSNCDKNNKDNNNVVVSGSKKKTNVSSPKSTA
LSLNKPPSGKYGRKMDSYRSDSTNSSGNLNGSYSNTSMGELVEELDSNGVGGIDTTATAAENQVCTIKNLDNGKEFVVNE
IREDGTWNKLKEVGTGRQLTMEEFEMCVGHSPIVQELMRRQNEEDSSRENLDSTPNGGVGGGVSKLKKKGSWLRSIRSVA
SSVKGRKERSSSDDRDTGSDRGGRRSSSATDDSQDVSFHGPERVRVRQYGKSFKELSALYKSQEILAHNGSIWSIKFSLD
GRYLASAGEDCVIHIWKVIESKRKGDLLNDKQEDGNFNFLLTANGSPEPSLFSPTADGHHEKKRRGRTSISRKSLSLDHI
VVPETVFALTDKPICSFKGHVDDVLDLSWSKSQHLLSSSMDKTVRLWHLSTKTCLKIFAHSDYVTCIQFNPVDDRYFISG
SLDAKVRIWSIPDRQVVDWNDLHEMVTAACYTPDGQGALVGSYKGSCRLYSTSENKLQQKCQINLQNKKKKAHLKKITGF
QFARGSSSEVLITSADSRVRVIDGVDLVHKFKGFRNTNSQISASLTANGKYVVSASEDSYVYVWKHESDSQPCRSKGITV
TRSYEHFQCQDVSVAIPWPGLSDTWGLQDAYSGEQNGVDNHLDEVSVANHPPTPVDESSCNEGSQSLSGCTNSPLNGIIC
SATNGYFFDRISATWPEEKLKVATRSWSPRTSVDFSDGMNQNMSAYGMVIVTAGIRGEIRTFQNFGLPVRI
```

15 - 34:	EEEEEEEEEEEEEEEEEEEE

A0A2C9UWG2 **A0A2C9UWG2_MANES** (206 aa)
RING-type domain-containing protein. *Manihot esculenta (Cassava) (Jatropha manihot)*

```
MASQSQLAEVSSAFERMLRRRDLSLFLPLILGVTGTNPDQERIILINPFTQGMVMIEGAGDLGSLLRELATKNGQPPASK
ASIEALPSVEISEIGDRDCECVICLEEWELGGLAKEMPCNHRFHAHCINKWLEIHGSCPVCRYTMHVDEVDLGKQREEEE
EEEEEEEEEEEEEEEEEEEERRERRRFEREIWVGFSFNSNRRKMR
```

157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE

A0A2C9VKL9 **A0A2C9VKL9_MANES** (192 aa)
Uncharacterized protein. *Manihot esculenta (Cassava) (Jatropha manihot)*

```
MLLILLMMFMAYIFAGSFERFRGIFHEGEIDKRVQFLIEGLFAIRKAKFQGYPAVRPELDLVEQEDQLTHEISLQEDIDT
KITLDIFKLDPNFLENEKRYEELRKNILGEESADEEGSDAASGDEDDDEEEDDDDDDDDEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEDRKDEKEEEEEEGERMEGRKVAFH
```

140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE

147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE

A0A2D0QNN8 **A0A2D0QNN8_ICTPU** (789 aa)
B-cell lymphoma/leukemia 11A isoform X2. *Ictalurus punctatus (Channel catfish) (Silurus punctatus)*

```
MFFLWMQSFSALYVRSSAEKRGQDVDETMTAQKEYRSVWKRLYATVPSLPEPPSFVCINRIIPQALGGSGLPPFHTAGSP
CYMLCWLLKTSEKPPLRKTKEEMKEGKDEPSSYTCTTCKQPFNSAWFLLQHAQNTHGFRIYLESERGSPLTPRVGAPSGM
GADHASQPPLHGIHLPEGSPFNLLRIPNSGRDGPPLREGRFPPTPPLFSPPPRHHLDPHRMEHLSPEELALATHHPSAFD
RVLRLNPMPLDPPAMDFSRRLRELAGNTSGSTPPHSPNRPSPMQRLLQPFQSGSKPPFLSTPPLPSMQSPSGSQSTPTPL
PQQPNTPMKTKACEFCGKTFKFQSNLIVHRRSHTGEKPYKCHLCDHACTQASKLKRHMKTHMQKTSPTTVKSDDGLSTAS
SPEPGTSELVGSASNALKSVVAKFKSENDRLIPENGEEEEEEEEEEEEEEEEEEEEEGEEEEELEREGTRNNFHFGLNLE
ATRHHENNGGRLGLAEDGIPRSLPEVMQGMGLAASMQHYSEAFHQHKRGVLNSDSNAHRDICDEDSAMESDRVQEGSTIN
GRGSSPNESASVGLSKKLLLGSPSSLSPLSKRIKLEKDFDLPTPTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSP
FASSSEHSSENGSLRFSTPPGELDGGVSGRSGTGSGGSTPHLGPGRPSSKDGRRSDTCEFCGKVFKNCSNLTVHRRSHTG
ERPYKCELCNYACAQSSKLTRHMKTHGQVGKDVYKCEICQMPFSVYSTLEKHMKKWHSDRALNNEIKTE
```

437 - 456:	EEEEEEEEEEEEEEEEEEEE
438 - 457:	EEEEEEEEEEEEEEEEEEEE

A0A2D3UZF9 **A0A2D3UZF9_9PEZI** (234 aa)
Uncharacterized protein. *Ramularia collo-cygni*

```
MQRDPWVDEMLNLAGVPDNNEEEEEEEEEEEEEEEEEEEEEEEEEEEEDNTPLPPMEEEEEEEEEEAAAAPSIEKSPRATGKL
PSLRALPPRPPRTPARDSSVFSFRSDDDEDDNAAARGQMLPPPPLTPGSAKKSGPKVGSHNKGTTFRRPENTSSEVYYGL
SVRPESFDLKALDRQKALVHVARIEETSDGEVRPRCERCTERGYPICRQYTAQLKKDTKVVRCARCLXDAKPCT
```

21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE

A0A2D3V920 **A0A2D3V920_9PEZI** (1323 aa)
Copper transport protein 86. *Ramularia collo-cygni*

```
MGAAKAHAVFIRLVLPPYTAHFKSPSYIRDSTLTLLDQKVSKPTLTTTASRADVRHAIGTSESFWLDLATLLKAAIPSLE
RRSFSIWDPSSVDYESTSGALIAGHYPGLWKDLERLNDLVSICRNVLTAGEVVQDLAAGFGIDGEVFRLINCCVRVTARG
YDGEAGTGEEEKWQWIVNGYKKLLITGLQFLNNFVARNERRKLMLWVALFDGDASAVGGGGGGGGGGIGGGGGGVMAPE
DVPETSAASLTDVPSNPTSRPTSPLNKRDLLLAFGRNGSEELDLTGEAKPLYEEVSSFEEHPLPPEAIEGREKLVGNGYA
FFFKRISEFCKQDYQKIHGRMPTPLELHLEMPRRWAECDQEDKDYWQSLFDDAVAKWRQDLAVYEAKMLVLTEQQPVLRN
DASTIRSDASSVRQVERKIAMLEEQLAAKYQSEGIDMPSMDSNSSKLYGREGHLTFDSDMLQSKPVVADDMRMLFTAEAG
TKILESGKMELMKRLEGYEATHDAHLPPSRHPDGVTTRPCMVDKYGDAAERTASMEREEQGRNVEAPRRVQRRYPVEVEP
PSHEATQEEGSVRDTREQGVEEEDVDDEDEEDDEEEDDDEEEEEDDEEEEEEEEEEEEEEEEEEEEEEEEEEDYPGSTEDGR
GLLTDVPLILGPSEIEVLPMLIMSGIVPPLNISPTLTPAERNALINMHTVRTHLLLSQSNGRNLLRELLIFVAAWDLREE
ELYFKFMVKIMEAILKTGLMPYAYHAFRDRSRSKDIISPAQAVMMKLLTCIFRARGEAAKAAATGHPSKNNLPIPATGIP
VRSGTGIPIKTEFVKVDGKGPPILLAKEPSRVDLHILNFIFTEFRQHIIPQTCALIFLQGQIHAERASPEDFPLNLWDME
RMYEGVYQYLEFFAVLTEEGVWKGILGEWEMASELVTLLRELEGGIPKAGMQGGGNGGGGGGGGKRVGRTMSADAAIPLT
TNHPPPALSKGAEGDHQTLPPLPLPQPLAGGAEMEQPPPAAVPASTSTTATTALPSTHPPLPHDQDEPSDFEWRNLKKLT
VLVLSSLIWKNRIVQDQVREYGGLQALVSCCRNDEHNPYIREHAIMCLRFAVEGCERNAAVIRGMAGRRGGGGGVQQQSQ
QQQGSQQKDARGEEEEEEGEEEEGRVDAKEDLRVRERGGGGGGGGELSLVARGVTSVPREVLDTQGYETFMDGKGQVGL
RRKEGGNLHSLPLNHKGGSGRNVTTPSTGMGGSAATTTTTSTAALSAERAAELMSSALSSLPLGERSVAGSSAGNGSGSG
GGSGSGSGGERLLFSEEQKAEALAKLDRAFESTEILLGRSPRD
```

607 - 626:	EEEEEEEEEEEEEEEEEEEE
608 - 627:	EEEEEEEEEEEEEEEEEEEE
609 - 628:	EEEEEEEEEEEEEEEEEEEE
610 - 629:	EEEEEEEEEEEEEEEEEEEE
611 - 630:	EEEEEEEEEEEEEEEEEEEE

A0A2D4BRB1 **A0A2D4BRB1_PYTIN** (1429 aa)
Histone acetyltransferase (EC 2.3.1.48). *Pythium insidiosum (Pythiosis disease agent)*

```
MHESRARAAKKRARARMEVAAAAAAHPIGVSWSESRSANGRVFIHISDSSSDDDXEDDDDGSGDASGGGDSELEANDAIA
TRLRPLARASMAATRRGGGAMKMEITDEDKDDAEEEEEEEEEEEEEEEEEEEEEEVVLEDEEGEEGDDDDDVEIVVRPSSS
SSSSSSASAQQHRRTFKRLKRPEPPTASVVREETLGDRIIYCLDSDDESAEEQEQEQQQERQRDLIKREVIDDDTPEDVA
XGFDQPHQQNGAAENDSVVESDDTALHVSPVPEAHVAPLLTPRKTPIVVRRRRLDEEHAAFLLFHGERETPSAAVLRLVI
ELISRGVGANAIAMQQWVSYLLWCKFNTVVDRIQNHERERYSEWMKIVLGADEPPPTQVSRRRETESLLPQPIQHTLRAV
QYVLPPKSASHHQRHDSSSSKNESKSTGKKRQSSSSWLERKAAEVQNGASRLKIDIPAGQPRRRASVGTPTSPSPVFARN
AARKRKRERDADVAPALSRRALLYSPDVXRGRAASLQSQSDGIDYSPSTVSAVSSAPGPRRGTSVPLCFDLTNDDHTSGT
```

```
NRSMPVGWGPDDVQGVAPARRPAAMNPLWSMSLEDLKRHINAVRVEGRSKSYEKLSDVLSKLMTHPRNRHGVFNYPVDPV
AQNLPTYLEVIKRPMDFGTIKGRLDEGLYVAVDDFIADVELVFTNARTFNPPNHYIHVDAGVLLARFREMMGGDSDRSAS
LKRQRQHSCDVCRGNACALCEQGCLPFAQPHLQCSASCGTDIRKGSVYYITRDGTRVLCVKCRNRHVRALEENGLMSHDN
ASLHGHGHKKSPGTGGDKKKNDSKLKKKAKKTAPTELSTADAVLVHGELLKRKCDIDVEPWVKCGQCSRWLHQVCGLYNP
VAGVYAADNDYVCPLCIWKQRAPACESKTDLHSLLNPVAPPQTRSSSCQEIPSCELXEFIEKFLRRGLRDLSELEAADSL
HVRVLSFPNERVHVPEGVVQTFDSNASLLEQVCESSEPRRLPHEIAFTSRGIYLFQRHEGCDVCLFTLFVQEFGDDCALP
SNRRSVYVAYLDSIRYLSPPSARTASYHLVMMAYFDYIRRHGFERVHIWSCPPQRRISYVFWCRPPFQKTPSAEHLRAWY
KRLLTKAQDANIVRSWTTTYDRYFSSSSPLPAAALSGGSGVVPXSDXSXTDGVTCNGASSSTVATRGSTSRSIDPNELHW
PAPELPPIFEGDFLPAELERILGYIAAKNAKCRRASKKSGGKSSLVGSTGGKLAVGEVVTRLKEDPPAAAARVEIKLREV
FVRCQQAVQRLRNDLLVVDLVVPEHRPCDPTRLVPAWWSQVPRFFGSRFMFHQLCATASYQFDSLRRAKHSTMMVLHHFF
NERVCQLNVFCHECCLLITHIEXWTCVQCEPAVALCDTCYERQRRPATSTTLSPLPPHGHAMVYRRQSE
```

114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE

A0A2D4BVY2 **A0A2D4BVY2_PYTIN** (1142 aa)
Calmodulin. *Pythium insidiosum (Pythiosis disease agent)*

```
MDSSSHARARGTALSSSSWSEAARSRRSGARRGQAVAASKPSRNVSGRSSRGGVSDEEEEEEEEEEEEEEEEEEEEEIEE
EEEEAEPEEAEEEGGVGEEEGAEPSGRDPASARAADVLAFEKGSMVCIVRTPDVEQRVPHTIGKIGLIEDVPQHPNTWFR
VRIRDGDVVYKYRPSALRLTEEEAGEEDAEEGEQQEQQEEEEEEEEEEAPQDSDAKDIAEENSVEEDAEEHQEDADEEAE
EDAEPALDIDTRVRVQLGTLSRRERDLRKYQGKLGVIIAHEADGFKVQLDSEDILTIRSKHLVAAPDAPLAPASDGDQDG
EEEEEEDTPTSNGSKLPKGQLLSDLDPDMWIDRKCRINVGKFKGLHGRVLRSGNGWVQLRLENSNENTAKRAYELTLLED
MDTIQALYAKSLAHRREAGDGEEEEEEEEDDVRSGAEDNTTAEQTEDSQGEDNGKRTRRLSTRGSYGISWIEKKVLLPNR
KGYGIVKKADRETCTVEIVTSRVLKVFKKKDLELVEEDSTRGGRGSRSRNAAAKAKDRLGLPDGVVLMGTTPARYALFQD
QVKKFAMRRREKVKKRPYLLSWKYELEMYQRSSEFRDSQDPSVVDLLVVAQCEICGVEKEEIQGECWNAQCPRSIHFDVE
VYDHKTNEERASDIARLPIAPLPNDHITSTLCLKAVADVPRKRKRRHSSSPHAAEGAKSAGDATPPPQRHAKRQYSDESV
ASIKHDTKKPKKDTKSSKKNATADDKKGKKRPQKSASLDSAGGEGKSSKRGKDVAGAGAGGGPEPSDRRPSERPLLRKSS
STGLLDTEQTAADGSVPPKLRRKSSSLRDLTPEESAALQAXEKDKARKKSRRSARNSILRTGTDVDASALPPVTPKTGRV
DSQQQLQQHRESKATLPTQETFKRPKRRRRAGDIELHRQATVDIVVKYEIGQSELKKLKQCFHQIDLDQSGXIDYDEFFE
FIDERKTPFSEGLFRMIDADSNGTIDFEEFVHAMVLYCMYTRDEILQFAFDTFDPNKTGAIGEKEFKRLXSVVNDGKPAF
PGNFKNALXEFDRNKDGVLDFEEFKMLNKRYPLLXFPCFRLQDRMQKATLGENHWLKLHRRLYDRLKLEIYQRKNNGALP
ALGLFGSIRKFLGLDAMDVYQP
```

57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE

A0A2D4EVS4 **A0A2D4EVS4_MICCO** (114 aa)
Uncharacterized protein (Fragment). *Micrurus corallinus (Brazilian coral snake)*

```
VYPLCENNVYMLSPNASVCLYSPLAEEFSSQFPGHDLPAVLSKFSWPVSLSELKDPLAPAIQETHLIRMVAWMLQHRLLI
QLHSYACLMIPPKEEEEEEEEEEEEEEEEEEEEE
```

94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE

A0A2D4F8W8 **A0A2D4F8W8_MICCO** (174 aa)
Histone acetyltransferase (EC 2.3.1.48) (Fragment). *Micrurus corallinus (Brazilian coral snake)*

```
EEEEEEEEEEEEEEEEEEEEEEEEEEEESELFSRGYLRRLSPQDSLRHKPPLKRGSQEEEESDDTADSPTLKPVSLLRKC
DSLDSPLQPGTSTPMKKKKGWPKGKSRKPIHWKKRPGRKPSFQLRRGKVRAPASEETTELMEPCSRSGRKTKVQDEEEPA
EEKEELLPSAEERK
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE

A0A2D4F8Z2 **A0A2D4F8Z2_MICCO** (155 aa)
Histone acetyltransferase (EC 2.3.1.48) (Fragment). *Micrurus corallinus (Brazilian coral snake)*

```
EEEEEEEEEEEEEEEEEEEEEEEEEEEESELFSRGYLRRLSPQDSLRHKPPLKRGSQEEEESDDTADSPTLKPVSLLRKC
DSLDSPLQPGTSTPMKKKKGWPKGKSRKPIHWKKRPEHAKTYIPVPVKIYVYIHTHTHTHIHVFTKIFSILHGKG
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE

3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE

A0A2D4FDY7 **A0A2D4FDY7_MICCO** (257 aa)
Uncharacterized protein (Fragment). *Micrurus corallinus (Brazilian coral snake)*

```
EEEEEEEEEEEEEEEEEEEEEEDPVNLENRGLFSSHAEPPCSLTCNVEVLREEQRVTKPPRPTVGICAPLCERDNSVETRP
VTLQQRNRTRERPYICPDCGKSFMLRINYIIHQRNHLKEGPYECHACDLSFRIKQQYLLHQRLHTTRRGVAPPPRRGQTY
PNKRSFKQQPQPPPPPGKPYKCSECDSSFSHKSSLSKHQITHVGERPYSCGECRKSFRLQISLAMHQRVHAGKTELSFIC
PQCGKAFSRPSHLLRHQ
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE

A0A2D4FVX8 **A0A2D4FVX8_MICCO** (120 aa)
Uncharacterized protein (Fragment). *Micrurus corallinus (Brazilian coral snake)*

```
KKRKKEKEKEGEEEEEEEEEEEEEEEEEEEEEEKMIYVPRLCSSWMDAKTLDCKALCYVFWSPVKSQGLLGFCNKKIGVSEA
NQGGKKKKKKEPGLPFFFFKANGFSPYAFILQTEANRSGPG
```

12 - 31:	EEEEEEEEEEEEEEEEEEEE

A0A2D4G862 **A0A2D4G862_MICCO** (196 aa)
SAP domain-containing protein (Fragment). *Micrurus corallinus (Brazilian coral snake)*

```
MADGEEVTLDGRPLQALRVADLKAALEQRGLPKSGQKSALIKRLRGALMLENLQKHSTPHTTFQPNSQIGEEMSQNTIIK
QYLEKQQELLRQRLEREAREAADLESKSCVISRKRDESDEEETRKPEEHLSRVRQARAVKTTGGSHALMSEERETSLRSR
RAAQRVPVKEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE

A0A2D4GD76 **A0A2D4GD76_MICCO** (100 aa)
Uncharacterized protein (Fragment). *Micrurus corallinus (Brazilian coral snake)*

```
LQSKEKQGTGTAQTGDFRLPKAGRRAKRSSGLNCGVLGALRAWWISCRCFVTQLRNPNSARREWGGEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEE
```

67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE

79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE

A0A2D4HXM8 **A0A2D4HXM8_MICLE** (225 aa)
Uncharacterized protein (Fragment). *Micrurus lemniscatus lemniscatus*

```
FLCTGFTLNYGVCSIGLEHMAYILTAYGISSAVGSTLVLTMLRLPRQVPLLTGASIHAIILIALFCWKPQAKNLAEAPII
YLVAAFWGLGSALNKTGLSTLLGMLYEDKERQDFIFTIYHWWQACAMFVVYCWSGMPMKAKLSILLVTLVAAVFSYVWME
HKIAQSVPHRLPKIPKPRHKMRGYRYLEEDNSDATDSEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE

A0A2D4MJ48 **A0A2D4MJ48_9SAUR** (156 aa)
Uncharacterized protein (Fragment). *Micrurus spixii (Amazon coral snake)*

```
LRSRRAAQHMPVKEEEEEEEEEEEEEEEEEEEEEEDAPPLLVGQTPMRPEEPGMPAPQEPGMFQASLPIVLQAQQTEARSQ
TPDSLSGEATMPILAHLQRSEDEEAQLWATDPGEKQQAALTPGESPMEKDPLPDPPKEVGPQLPEALKMETEEDPG
```

14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE

A0A2D4MKP2 **A0A2D4MKP2_9SAUR** (155 aa)
Uncharacterized protein (Fragment). *Micrurus spixii (Amazon coral snake)*

```
LRSRRAAQHMPVKEEEEEEEEEEEEEEEEEEEEEDAPYLLVGQKPMRPEEPGVPAPQETGMFQASLPIVLQAQQTEARSQT
PDSLSGEATMPILAHLQRSEDEEAQLWATDPGEKQQAALTPGESPMEKDPLPDPPKEVGPQLPEALKMETEEDPG
```

14 - 33:	EEEEEEEEEEEEEEEEEEEE

A0A2D4MYM7 **A0A2D4MYM7_9SAUR** (531 aa)
HTH CENPB-type domain-containing protein (Fragment). *Micrurus spixii (Amazon coral snake)*

```
MYRSRQYTVLCNWLLFWLEMSSKGKRKSSTSIKEGRKKQRKTINLDLKMKIIKAHDEGKKVNIIAQEEGLAHSTISTILK
DKERIKKAIKGASGTDAIITRHRTGLIHETEKLLLLWIEDQIQKRIPISLSLIQAKARSIFTTLKDRAGQECTEVFTASR
GWFMRFQRRFNYHSTRKPRKGVSVDEAAKRFLDELDDIIAKGSYLPEQIFNVEETWLFWKKMPEQTYIHKEAKAMPGYKT
FKERVILLLGGNVSGFKLKPFLVHKSGNHHAFKNICKRTLPIYYRSNQKAWMTQVLFEDWCMNCFIPQVKEYCLQEKIPF
KILLLLDNRPGHPPHLHNIYPDVKVVYLPKNTMPLLQPMDQGAITIFKAYYLRAMFAKAVDAMEAEKRVTLREFWKNYNI
LHCIKNIEAAWQDVTVKCMQGIWKKCLKCYPVLVNNFQGFDHNKDLDEINKEILTLVKSLDLEVSAEDVKSLITYTEGEL
SNEDLIELKEELEARRVKEEEEEEEEEEEEEEEEEEEEEPEEEPEVEPEEE
```

499 - 518:	EEEEEEEEEEEEEEEEEEEE
500 - 519:	EEEEEEEEEEEEEEEEEEEE

A0A2D4MYP5 **A0A2D4MYP5_9SAUR** (512 aa)
HTH CENPB-type domain-containing protein (Fragment). *Micrurus spixii (Amazon coral snake)*

```
MSSKGKRKSSTSIKEGRKKQRKTINLDLKMKIIKAHDEGKKVNIIAQEEGLAHSTISTILKDKERIKKAIKGASGTDAII
TRHRTGLIHETEKLLLLWIEDQIQKRIPISLSLIQAKARSIFTTLKDRAGQECTEVFTASRGWFMRFQRRFNYHSTRKPR
KGVSVDEAAKRFLDELDDIIAKGSYLPEQIFNVEETWLFWKKMPEQTYIHKEAKAMPGYKTFKERVILLLGGNVSGFKLK
PFLVHKSGNHHAFKNICKRTLPIYYRSNQKAWMTQVLFEDWCMNCFIPQVKEYCLQEKIPFKILLLLDNRPGHPPHLHNI
YPDVKVVYLPKNTMPLLQPMDQGAITIFKAYYLRAMFAKAVDAMEAEKRVTLREFWKNYNILHCIKNIEAAWQDVTVKCM
QGIWKKCLKCYPVLVNNFQGFDHNKDLDEINKEILTLVKSLDLEVSAEDVKSLITYTEGELSNEDLIELKEELEARRVKE
EEEEEEEEEEEEEEEEEEEEPEEEPEVEPEEE
```

480 - 499:	EEEEEEEEEEEEEEEEEEEE
481 - 500:	EEEEEEEEEEEEEEEEEEEE

A0A2D4NQP0 **A0A2D4NQP0_MICSU** (507 aa)
RanGAP1_C domain-containing protein (Fragment). *Micrurus surinamensis (Surinam coral snake)*

```
LKRCHWSDMFTGRLRSEIPPALISLGEALISAGCQLVELDLSDNAFGPDGVSGFAALLKSPTCFTLQELKLNNCGMGIGG
GKILAGALKECHRKSTAQGKPLALKVFMAGRNRLENDGATALAEAFTVIGTLEDVHMPQNGINHPGITALAEAFAVNPLL
RVINLNDNTFTEKGAVAMAETLKKLRQVETINFGDCLVRSEGAVAIAEAVSEGLHKLKELNLAFCEIKIDAALIVVGATE
DKSELEKLDLNGNCFGEEGCEQLQDILEGFNMGEVLGSLSDDDGEDDEEEEEEEEEEEEEEEEEEEEEDEDEEEEEPLQV
QERGQGEQEPLTPKKILEEHDSTPLSSPLPPVDVGTFLAFPSPEKLLRLGPKCSTLIMQQTDTSDTEKVVTVFLKISSVF
NDETVVKTAVCETTDALMREAFSSANFNSDAFITSLLIHMGLLKSEDKIRAVPSLYGPLMTLNHMVQQDYFPKSLAPMLL
AFVTKPNRALDSCSFARHSLLQTLHEL
```

288 - 307:	EEEEEEEEEEEEEEEEEEEE
289 - 308:	EEEEEEEEEEEEEEEEEEEE

A0A2D4NQP4 **A0A2D4NQP4_MICSU** (356 aa)
Uncharacterized protein (Fragment). *Micrurus surinamensis (Surinam coral snake)*

```
LKRCHWSDMFTGRLRSEIPPALISLGEALISAGCQLVELDLSDNAFGPDGVSGFAALLKSPTCFTLQELKLNNCGMGIGG
GKILAGALKECHRKSTAQGKPLALKVFMAGRNRLENDGATALAEAFTVIGTLEDVHMPQNGINHPGITALAEAFAVNPLL
RVINLNDNTFTEKGAVAMAETLKKLRQVETINFGDCLVRSEGAVAIAEAVSEGLHKLKELNLAFCEIKIDAALIVVGATE
DKSELEKLDLNGNCFGEEGCEQLQDILEGFNMGEVLGSLSDDDGEDDEEEEEEEEEEEEEEEEEEEEEDEDEEEEEPLQV
QERGQGEQEPLTPKKILEEHVRYKHTFPLLNKKNNC
```

288 - 307:	EEEEEEEEEEEEEEEEEEEE
289 - 308:	EEEEEEEEEEEEEEEEEEEE

A0A2D4NXR7 **A0A2D4NXR7_MICSU** (167 aa)
Uncharacterized protein (Fragment). *Micrurus surinamensis (Surinam coral snake)*

```
CCLPKSGQKSALIKRLRGALMLENLQKHSTPHTTFQPNSQIGEEMSQNTIIKQYLEKQQELLRQRLEREAREAADLESKS
CVISRKRDESDEEETRKPEEHLSRVRQARAVKTAGSGHALMSEERETSLRSRRAAQRVPVKEEEEEEEEEEEEEEEEEEE
EEEEEEE
```

142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE

A0A2D4TK95 **A0A2D4TK95_9DELT** (274 aa)
FecR domain-containing protein (Fragment). *Deltaproteobacteria bacterium*

```
MMFRHLLTLILFFVAGYVLASEVKLSLETGRVKIKKQGNIRFISHSDPLNPLIVELELGEQILTGKNTRATIKMRGKEEE
IRLRVDTLFRVNSLEPNQTEVEMPTGKARFKIKRKLNRKKKRKRQFNVRTVTALIGVRGTEFVMGTSGASTSLLTLDGSV
EMAAAAAPQIKVEVSVGQASKMEVGKAPTPPITVPPALQSSIVESDSSETFGEVSFPPAQDLEEAVAEQKEKEEKEKEEQ
KEEKQEEEEEEEEEEEEEEEEEEEEEEEDEEEEEE
```

246 - 265:	EEEEEEEEEEEEEEEEEEEE
247 - 266:	EEEEEEEEEEEEEEEEEEEE
248 - 267:	EEEEEEEEEEEEEEEEEEEE

A0A2D4Z7W4 **A0A2D4Z7W4_9BACT** (337 aa)
Uncharacterized protein (Fragment). *Verrucomicrobiales bacterium*

```
EEEEEEEEEEEEEEEEEEEEEEEEEEEESPFDEKLSLNQVEEINVSGASINKDNLPIGMVLEPIHLDNRVGVQTWFKWVLLL
VITVIAIVFMVTKCSSTSKVPVLGRVENEIVNYKIKPLPRSNDESLFDLEDRVRDTIEKFLSVTSSSDLYGIIRSPSRCA
ELIENFYSRNEFVFPRLKSIDSIEKIDGDLEGFWLVNITVDDLIQARSVILEDTDRGFLMDWEEFVRFGEKNWDDFIESK
STEVSIFRVRCTLDTNPEFAFPDRSKWLCVRISDWISNEDLYGYVERKSDVGVRIAKLLDDEWERPCILKLTFPEDRKGG
ANQVEIIEIVNENWVLK
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE

6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE

A0A2D4Z9L8 **A0A2D4Z9L8_9BACT** (88 aa)
Uncharacterized protein (Fragment). *Verrucomicrobiales bacterium*

```
MPKRSSEEDFKEEGNLNFDFSSDKTDVTKNEEEKTEDDIDESFDNVNIYRGSDRTFGQLINEEEEEEEEEEEEEEEEEEE
EEEEEEEE
```

62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE

A0A2D4ZDE6 **A0A2D4ZDE6_9BACT** (209 aa)
Uncharacterized protein (Fragment). *Verrucomicrobiales bacterium*

```
EEEEEEEEEEEEEEEEEEEEESLKKSKDGSDGAVILFADSDMLFDALSVGRDMFGRMTYRNHNIPLLENAVEQASGGGSLM
SIRTRGSGRRPFTKFKELRAEASEKFSEELEKVTQKEQELASKISELMQEQDNDQMVVIGPEAANSIKDLREQEVIASRK
KRELSRELRKDIRKIENKIKNWNIAGIPALVIILGILHLFVRRSKISAR
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE

A0A2D5AWN6 **A0A2D5AWN6_9BACT** (870 aa)
DNA translocase FtsK. *Planctomycetes bacterium*

```
MMQMARARRKAKASHTPTFATRLRGFASSFVRDSDSGEETANHIQEIKGLVLAGWTLWLLVSLLSYEADPQAAGSHNWGG
QAGWYLADWAYIAFGWSAYLLAFLGFTWGAVLVARKEIGRPLLRAFGGISFLLASAFMFQLGFGDEHGFELPFGPGGYLA
LELVGPGVGYDQVPPVLVEKLGRPGLWILLWLSALIAFMLATEMAFYPALRALQDWLEERQEGRGESIPTVLSGWLGRLV
SGLWSFLRGDDLELRTAAASAVLTPATARGRRKAARIETPELPELFGAEGEEEEEEEEEEEEEEEEEEEEEEEEEDEDE
WEEEEEEDEDEASLEGKDEELTPAPKKASPRGKKRVQTAPAQTQIYEPPTPPPGDWELPSLEILEPPSAHSQEDNRKLEI
QANRLENVLASFKVEARVVGAKVGPAVTLFELEVVQGTRMNKVTQLSQEIAAALRAKGVRIIAPIPGRATIGIEVPNEHR
RLVLLSELITQDAYDKKHMALPLFLGMDAEGNAIVEDLARMPHLLIAGTTGSGKSVCINCILASFLLTRSPHDVQLILVD
PKMVELQMFSTVPHLMLPVVSDMRQATNVLLWACEKMEGRYDLFKNAGVRNIKNYNALGEDALRERMGEDFHEERTPRHV
PFIVIVIDEMADLMMISKKEAELSITRLAQKSRAVGIHVIVATQRPSTDVITGVLKGNLPTRIAFQVASKVDSRVILDQM
GAEKLLGQGDMLYTPPQSSQIRRLQGALVEDHEIQAIVDFVARESVPNFNQELAQTAGGASSAAARSGSEQDELFDEAVR
VVLKSRRGSASLLQRALGVGYTRASRLIDIMTAEGIVGEHKGSKAREVLMSLADWEENQSAIAKAESNHE
```

291 - 310:	EEEEEEEEEEEEEEEEEEEE
292 - 311:	EEEEEEEEEEEEEEEEEEEE
293 - 312:	EEEEEEEEEEEEEEEEEEEE
294 - 313:	EEEEEEEEEEEEEEEEEEEE
295 - 314:	EEEEEEEEEEEEEEEEEEEE
296 - 315:	EEEEEEEEEEEEEEEEEEEE
297 - 316:	EEEEEEEEEEEEEEEEEEEE

A0A2D5IQX1 **A0A2D5IQX1_9BACT** (881 aa)
DNA translocase FtsK. *Phycisphaerae bacterium*

```
MPRKKSPSRTRPSTRSTGRRAKATAEATEPNLLRRILWLLAAAAWVFVAVSLAGFDIADWPSTSVARHAEPASNPAGIVG
SLIAWWSYVTLGWGAWLVLGMAAVALVTIVRGYQITHPLVRTLGTLLAAVMVGGLHDAWIVSMWPQAGAIPGLEAGLVPA
ELDIALATRFGPVGASLILLTGLLLGLLVAADELLLRVPAAMVRSLEAARGIDLDPVRAAISAPFRGIXNLTERFAARRS
TLQPAGVPPEMVEAWLNDEARNEXEEEEEEEDDEDAWYGDDAEGEEEEEEEEEEEEEEEEEEEEEEEEETLVDETPAPRA
SAEELRRKIEKLPVRMAAASTEVVRDEDIPREENFEGYQFPTLDQLEDPEGDYSASMETTVREQAGILEEALRTFQIDAX
VAGIESGPVVTLYAILLAPGTRVARLNAISSDIARALQAQNIRIIPNMAGKSTVGIEVPNTKKEKVRLKELMSSGRSREM
MLPMFLGKDSAGDPLVADLAKMPHMLIAGTTGSGKSVCMNTIIMSWLYTKRPDELKLCLVDPKMVEMXQFSDIPHLMCPV
ITEMGKAAAILEWAVGKMEERYELLREAGVRDIRGYNDLTEEXLREAFEPSNDVEWAKLPKKLPYMVFVIDELADLMMTN
KEVEHSIVRIAQKARAVGMHLILATQRPQANVVTGLIKSNMPCRVSFKVASGMDSRIVLDQKGAELLLGMGDMMIVTPDS
TEIRRGQGTLVTDRETRQVAKFLKTVAGPTFERSLLQVKAPSSGGDADAGGEGGERDPLFDQAVEIMIETGRGSVSLLQR
RMAIGYSRASRLVDQMGLAGILSDHKGSVAREVLITLEDWHRMKRLEDGLDASNAAEDLDGDFGDDDAGGVPAELPGEHR
Y
```

285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE
287 - 306:	EEEEEEEEEEEEEEEEEEEE

288 - 307:	EEEEEEEEEEEEEEEEEEEE
289 - 308:	EEEEEEEEEEEEEEEEEEEE
290 - 309:	EEEEEEEEEEEEEEEEEEEE

A0A2D5XYT5 **A0A2D5XYT5_9ARCH** (1819 aa)
Uncharacterized protein (Fragment). *Candidatus Pacearchaeota archaeon*

```
MKERGMVIVLALVLLVLIFSVPWSTGRAVLELEHVSSGDVLGGQLRLSLEAGELLPVGSVVQLEVGNVSKSLVLSELVSE
RSVEGVHYVKGFELEGDGRGYGVAGVKNVSKEVTFDLLVSGPSVFSDEVGSSSAEINGDVNVSEGNETGEKVEGNVSLGN
ETEVSVNETEIEVNETVVNETDSSENETSADQEEEDVSEVNETVGVVSEEEEEEEEEEEEEEEEEEEETEKEKEEEEDFE
DDSVVEQDVEEDLGGEAVVEEESEKEVSEGENLEGSVLTGQAVAEGMRIVAGSVQKGEVYTYELGETESVTLNVGTVEVH
GIAVDAGVLSLEEDEGEVKVTTEYVVEEEGFGKGYGRNESLQLVVDLAQFGLVVEDTADVQVVLLVDEEEILSVSGEAPL
ATSAEEDVEEVNLSIVQGIGTQRVGVGDSFVLDLSEYFAGAQAYEIELMNFSASFEEHVVTLVADSGFSGARRGKVTALA
GEQRVEGDVFNVLVSNGAVHIQRAKKGTIRVGEPVKWVENVSLGVQENVSVELPSGAENVGVTKVDVLVVEGVEGAVLTG
QVIHADVNAELDLRPDFSRWLRDVFTGRVISGAVTAELEETEGVEVVLDGAEXLVYEIEYETEAPVAFEEEVLIGKKVVI
SGPDGLNYTDVLSFAEIDEKYAVGEEGAIRIVWVENETEVAKDAYDLDGNGLLDYVEWITPHLSNQTFEIILITRAEHLD
SERSFVADVYDEVSVLDEVSYSVGAGEYVRVWFEQNLSNGKDITIWGRANGSVGGVTVYEAGRNVSLMEFEIGSYGKYRK
LFDSLESEHDKFDLLVTEGAVEFDLIIDPTDDAPDLAYLDPTLANASTDADGYVEINMSIHDVDLDNVTLDWNGTDYAIF
DSDVVLFMNFDNRSELGENSSKIADLSRNGNNGTTFGHAIPNATGKYGSALNLDGDGDIVDIPYNWNNFGDITVSTWVYF
DTIGDMMIMASQDQTSNYFFYYNTLTRLQWEVGGTQIVPDWTPVADTWYHIVATKEGSTGKLFIDGGLLGSGAVGSSFAS
GLMRIGSYYDGLYDFNGLIDDVMVWNRSLTVVEINQLYTTSLTKFNSTDWELSVNQSLNSTDGLVAGDYWYSVDATDGSG
NLNTSEERLVSVDAVDTVLPLLEYADPTLANASTDTDGYVDVNVSIVEANLDNVTLDWNGTDYAIYDSDVLLFLNFDNRS
DLGENASDFTDLSSYGANGTGISFDSDEIVAGKYGGGVDFDGSNDYIAFGTPVHLKTTGSITISAWVNPDADESFGLVNY
DDVTGTRGYGLTPGTDGTNNKWRFSLANTGNSLIKRYSTKRILNSIGEWNHIVGVYDAGAQTMDIYVNGIEDNGVLQGTV
PTEQQITGGQFRIGNFINFDADFNGQIDDVTIWNRSLSAAEVNQLYMSSLTKFNSTDWELSINQSLNITDRLVDGDYWYS
VDGTDEEGNLNTSEERKVTVQGNTAPDVTINVPANSTYSSASFDFNVTLNENGSVVTHRFVSETENYTMTTEDNQDFNYT
NSSILDGSYQFLVYANDTSGNVNDTESVHFAVDATTPALTVDSPTNTSYASTNVTVNLTSSDAGVLDTTWWYNGTDNVTY
SSVTSHTYTAGTTNDFFGYANDSAGNVNETKVVFSVDSSGNEYTRLGDTSWDAISRQDGLLADGTSYSTDQFVDFNDSGN
GTRLTVQALFSTVTVNVSNLTIEASVGKTAVNITEVSGLAGNHTIYVQNLSDEGVYVCPDATDLAGVSATCANVIKFTKA
QVDSGTWVSGVKASMNGSLIMIENLTGSGGGDDGMAPRMVYVSPTLANASTDTDGYVDV
```

209 - 228:	EEEEEEEEEEEEEEEEEEEE

A0A2D6QCM1 **A0A2D6QCM1_9ARCH** (539 aa)
Ftsk_gamma domain-containing protein. *Candidatus Woesearchaeota archaeon*

```
MGLALCTVFAFPFVLAVLTFLRPAEADVTGTGALARQLVGAFGAWPTMLLSGGFAAVGAVLFFAGKEVEIDVGRHLCGIL
FTAIGLGICLGVISPTLGGEFGANTGGALKASIATWAGLALGLAVLFSAVWLTWLRDPSSFSGNSRRDLTISDALSEKDA
DGVSQAEARALVPDPATVAYMDQALQEAGEVGSQIQPLPPSPYPEDVRIHGEVPEGAQSLKPDNDPSDSERTHEVDSDKW
SSSDSQDGPQLGPGEDLAAPEVGGSEGAESGGGLDADSSSQIEVREPVDPSLESPPDPSEEDSEALSEEVLPAPGPSVSW
EQPDLFEEPEGEEEGEEGDLTESEASELEEEEEESAELEEEEEEEESAELEEEEEEEEEEEEEESAELEEEEEEEEEEEE
EEEEEESAELEEEEEEEEEEEEEEEEEEEEEEESAELEEEEEEEEDGDEPDSLLTPAAPPVKDQLEPAELLHEAGSLFL
REGRVAVSLLQRGFSLDFDMACAVLDELQDAGLIGPYKGGQKRDILLTSEEWDAQAASR
```

411 - 430:	EEEEEEEEEEEEEEEEEEEE
412 - 431:	EEEEEEEEEEEEEEEEEEEE
413 - 432:	EEEEEEEEEEEEEEEEEEEE
414 - 433:	EEEEEEEEEEEEEEEEEEEE
415 - 434:	EEEEEEEEEEEEEEEEEEEE

A0A2D7PL56 **A0A2D7PL56_9DELT** (166 aa)
Uncharacterized protein. *Deltaproteobacteria bacterium*

```
MASAFAFLLVATVCGWSPERWLPQVFDEAVTATSTSEPTSSPDAESTTVTRQRFTVRSLGFMAFGMAVTLLIGASNRRIR
TGTLLASAMTMLGLAGGGVFTIVQDGFPGWELAVVIGVTAILGLWSFWNLILGERAIDAGEEEEEEEEEEEEEEEEEEE
EEEEEE
```

141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE

A0A2D8AMA3 **A0A2D8AMA3_9EURY** (173 aa)
Thioredoxin domain-containing protein. *Euryarchaeota archaeon*

```
MAPYMQTLARTAEFKRIRFMRVDIEQVPAVAERCNVKALPTYQLYKNGEKLEEMSGALPSKLVTMLKEHNIKASGGGVLK
VLGVVLGIAGALFGVIALKHAVERGELKEAEEKKAREAAELARARKESEERRRRRARALGGAKEEEEEEEEEEEEEEEEE
EEEEEEDFFDDDE
```

144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE

A0A2D9H8T5 **A0A2D9H8T5_9DELT** (768 aa)
Guanylate cyclase domain-containing protein (Fragment). *Myxococcales bacterium*

```
EEEEEEEEEEEEEEEEEEEEEEEEEEEDTKADGGGLLLPPVETPLGRWLQGHPDDPAAPAIQAAYEDLTRQFREEIALWSN
PDEALEKSIDKYSDKVILGYTVLWEQTDEGLTVGKAPQWMVDMPNPDSLFREPRDQDFRIGVDDEGNETKIKLPAVPVAS
DLPGWESMDEDAREAAAKATLARVYLPEAEGGLVSPLTKFIEPSEYLAYFSVNPDTDGKLRGIHLLARVHDVVVPSLSLL
CAAVHFTSSYYPMANPAPGFEDRIAGIRLASEDYGVKDLPTDVMGRLMVNYYGGPGEVFDYLSISDIVYAMQPKEIKAKA
AAENWKEERIKAEMARWQHLTNTVHNKVVLFGTTAIGTYDQRVTPFSAFSPGVEVHATAVQNMIDGQYLQRPWQLLSYEL
LAMILMALLLAILTPNVSIPFSIGAAVMMTGFWYLIDTQMLFPSGWWVHGVLPNMMVGSIWASLTVFGYLSEGRERAKTR
KVLEGYVSPSVAAEVMDDPSMLDLGGEERELSVLFADIRGFTTMSEQFTANELTQFLNEYFTPMTAIIFETGGTLDKYMG
DAIMAFYGAPTTLDDHAVRSCRASLQMVRKLEDLNAQWTERGLLTIDIGIGCNSGPMRVGNMGSKQRMDYTVMGDNVNLG
SRLEGINKAYGTRICVSEYTVELAKEDIHFRELDAVRVKGKTEPVRIFEVVGEGQEPSADDGPWIKAYEDGLALYRQQSF
DEAIQCFEKVLSLKSDDFAARVFVDRCQALKDDSPGEGWDGVFVMKTK
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE

A0A2D9H9I0 **A0A2D9H9I0_9DELT** (173 aa)
CHASE2 domain-containing protein (Fragment). *Myxococcales bacterium*

```
MKLRLSYIAISLVVAFSFGAVHYLKDARNWGQTSNLVATFDGLETAFLDHKFRQRGKVGVNPSVVIAAVDEKAIRDLGVW
GSWERSVYATMTKNLVHAGASVVAYDMVWADESKSATRAAANRMVKALNTLGLAPSHLLPKPASEGDDEEDWEEEEEEEE
EEEEEEEEEEEEE
```

153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE

A0A2E0GG20 **A0A2E0GG20_9PROT** (443 aa)
Uncharacterized protein. *Rhodospirillaceae bacterium*

```
MARRKNDDRLEKITEDDISDEGDTSSSIIQDTDKSNDDNSHEIEDKISPEEEEEEEEEEEEEEEEEEEEEEEEEEKKKKFF
AFRSPLLSLLLLLIIILGGYLGWLHYNYKPPTEKDVASKPSNSVSFSLKKKKVNEGKTSNLIIKEKPTQQKKIKKKKVEK
GIPPNAPVKMASTPDPDLITESDFGPLPKISEDGKEPWIIYARPYDTKNKRPKIAILLAGLGLSEGATNTAIQKLPGSVT
LSFTPYAPRLEEWIDLSRAAGHEVILELPMESYDYPSSDPGPHTLLTTLEPEKNIERLNFLLSRFTGYVGVTNFLGDKFS
EDPNSLKPILEEIRKRGLLLLESKINNTSNTSLIASEISLPHAMNNHFLDIKASRVSIDSKLLELEKIAQDNGLAVGIGF
SYPVTMERISVWSDSLSDKGIDLVPVSSIASIKLSDKKSKQNE
```

50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE

A0A2E3IEX0 **A0A2E3IEX0_9BACT** (338 aa)
Uncharacterized protein (Fragment). *Roseibacillus sp.*

```
EEEEEEEEEEEEEEEEEEEEEEEEEEEISPINQKLGFNQVEEINVPGTSVKKDNLPIGMVLEPIHLGKSIGVKIWIKMVLLL
VMAVGAIVFMAIKCSPEPKISAASKSDNEIVNYEVNPLPRSIDESFIQLENRITDTITKFLSVTNKSQLNGIIRSPSRCV
ELIDDFYSRNEFVFPKLKSVDSIEKIEGDLQGFWLVNITVDDLIQARSVILEDTDRGFLMDWEEFVRFGEINWEDFVESK
STEVSYFRVRGTLDTNSEFAFSDSVKWLCVKISDWISNEDLYGYVDRESELGIKIKNLLNDEWQKPCILELSFPEDRKGG
VNQVQIIELVNENWVLKK
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE

5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE

A0A2E4XK67 **A0A2E4XK67_9ACTN** (223 aa)
Uncharacterized protein. *Acidimicrobiaceae bacterium*

```
MYWILILVVFILILCNKDNIEAFTSGKCDINEEKFRLLEKRIKSQEEEQPIIINNKLCDDNSKVAREIPAPRPSNERDNQ
TTIMLLKEQMNENRRKEQEYNSKLNELNTKIDLLNKKEKEEEEEEEEEEEEEEEEEEEEESEFYKIINMMNDPIGSNNL
INNIIIVIGGIFILITIYYTIVTLFTMFKRKPGDDIELINLSFDGAKKEVLLKKLKKKYKIKD
```

120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE

A0A2E4Y4J6 **A0A2E4Y4J6_9PROT** (404 aa)
Uncharacterized protein (Fragment). *Halobacteriovoraceae bacterium*

```
EEEEEEEEEEEEEEEEEEEEETLTVDTKLQRKINRIRENKKWRVDYFKKIEKEDESLVSDYQKAHKVPVSVMVLLAFFCL
VLSSLFIFVSFDFSTSEPSFEDLYVRDLQRLRSVASSINKEKPLVGLALEKNGKGLWLALNYAEPYSLLLRFESIQKKIL
SSESVVFSGKCIVVDHWCDINNLLIEEGTNIFPGFYKVKVKGFYLSEKESIQKRLVQLLRKSGMKGGGTKSFSFEGDAFL
FKGTPSHFNKRLKERERRHLEENTQFLREKLEEYRTLKALVSKMMDIYAEVLRKINIGRKVSRFEGKYAVTVGPLLRSLI
LSNKDAYEKEKLTNPFRAKFSKNAFFFGRQIGNLASDMVVLTSKKKKLGPRTKVKLQGLFKRKVEQLLSQGSNYVKEIES
LLKI
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE

A0A2E6RT97 **A0A2E6RT97_9PROT** (2124 aa)
FecR domain-containing protein. *Rhodospirillaceae bacterium*

```
MVESLTFGEGELGDVRSGTPASPAQDYNLVVDASNQTSLTIPFGVLLLKADFVREGPDLLLVGPNGEQILVRDYFTMDPP
PDLLTEGGAMLTADTVEALAGPVAPGLFAQAEEGAEAAPIGSVESVEGEVTVTRADGTEAQLNEGDPVFQGDVLETGEEG
TVGIVFVDDSTFALDEDGRMVLDELIFDPESTEGKSSLTVVQGAFTFVSGKIAQSGPDSMKVSTPVATLGIRGTKVAGQA
AQEGEENTIVLLEGEILVTNQSGVALTLNQPNQSVQVTSAFTPPQAVQLTPDQVQQRFGGVLESLPPSPAATQETQETEG
PAATEEAAEEEEEEEEEGEEEEGEGEEGAAEEGEEEEEEEEEEEEEEEEEEEEEEADADVRSPFGDYDNGESDIVHTYPNE
DLYTNFDPSLLKASGDIPYKHYEPSPDKIPSCDSWIGMFPDELEEHELVPVRAMAFNIPAEMFAQGANTYRDLIEWGNAP
TRSKALASLLGILFQGHYQGIPSGNHEEIHQERGGAPEDDNGNNDNDETAKEKGKSIKEVYRYMSLLRGQPGEPSKIQPM
FQVGSEELMCKDHKTVVAIRVWIFVYDEDHSHSHLVSTVMRNTNALQKASMASAQQPSRRKTSETTEVARQEKGGINVMR
LDDSFESTTGFQYMRITDEDRLLFWLRVHGGGTDKTSNANARSFVPNINEHVSGQPGMRRLTGDVRGGHGGIHPLAPEFV
FNAKRADALAYGLIHRDGQPIEVCDEQLDPNTYFRMGSTSFSLPKLNTPVGHTAFFLAVKSGARETILNMRLPRAFTGNV
VPGDTITRMYREIRLLDKANDDLRASHSDVSVSRNTHNNDIENALKRDVEETWSESYNVTIQDRMALQNMLEGNDEIVRE
QESRARADAYTHDTLAALAAQTGIVGSSIDRKNDGKCIIRIEKPTDVKRRGIQRIYSNVLERWLNHKRQKKDEDDAEVQK
RYHTGKRELTEYYLRLLEGCFASARDKSKLPPGWVAMYQQLCTGVQENGGSANIGFNENRQLSALDLTTFGELQNWLGNF
WMHDCKIQGRDRRIMDEMYMTMFETYTDLTYVLIIASMKGKGKSVRTERLAAVMPPGWCAFNSESSAKAGMNGNMSPSNG
KCVIYDEMPQDLKGHDSGPRIEYWKTMVTTRSFSIERTINIKSQDGTDAHTTFSIETDHHESFIIVCNKGQTFTDGPEEP
TEGKKAMVNRTICLQARSEADRDSPDGEFRAHIDNGHGRKNVATFRLFTALCGFIRLAIKGVSWLQPDLSYAEAIFRHGD
EMLQKEYGMPVPEPRRLAKRVQNLVTLCVLEAVAKVYFFKQTAVFFPAGNPIRLSNGQLVGKPFEIGHLWDVLRTMHPTR
EMILSAWSASLEYSIGTSSHGLHLMSALAEKVGFICGNPATAFMAMPPRKDDMLKKDGDGNFLIAGDDSDWAIAMREAGH
ADRLLSTKKVHSSATEQNEILGGCVKTIAERQRELDTTRVIRQQFRQQQKREVVGDTPLQAITEALGASEAKKYTDALFP
TAMEASLYYDSQALYKWATGHSAACRIGHGTGGGNSRDGSITLGSSSEMLSNDDQVIKYLDLEADNGNNSRSSTARMAKK
YDFAWLVLPGTRPHNTAPLRWKEVAKIIEHAPSCQLFDMHLDGIADGLLTLASEENMRTLALMPRLAPLHVPTQAFVTSD
NNTALYAVEDSTQHDAVAIRGVGGIAAHERVTGSPITRMTDGQRNDPIHKTFDMLIGRARLPALTPHVSTKTSYEPPLRR
HQGGVVVSSVALFEHVALVVGASLACSTIPGMHNQHEHFVNGNRPPDAFSASPSRPPLEGENDKSFVTKLPYSYDLVHIS
WTRDLQRRFYNTKTAEALNAFNTNKSDENASRGEWKQWLRLADLPQMTIRYPAYASVTGGSYKTLLSLNIANERPPDVPD
SNIATANGQNATLDATALLQEVSMNIGRPATDDDVHNYRRAQMGRSYLYDVDGDVYDFATFEHHMYASLAARGNISTTGD
QALSLLMDCETMLCVRNIERSMVHNGESKMNLSPPQYYALGNAEKQAELQRVLQERAMERMRRSESHANQRGEQSATPAK
RTRTDYEDALREKARLVDAVSRHMMDLADVSGGEEGGGAGASLV
```

354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE

A0A2E9EXP6 **A0A2E9EXP6_9BACT** (472 aa)
ABC_transp_aux domain-containing protein (Fragment). *Verrucomicrobiales bacterium*

```
MSSENENLAKSKSLVWLYSGIGVVLSFVILVVLNLIISTSIPMKLDLTEDKVHTLSKGTKDLLSELDTPVVMSFFVSKDK
DNMPPELIPFTKRVESLLKQYERGANKKSIEIERIDPSPDSEAEDRAKLNNLQEIPGRMNEPAYLGLTVTCLDRKSTIPF
IHPQREQMLEYDISRAIVEVTRENSPKVGIISALPVQGGPAAPFPQPGQGQQNRPWQFYTQLKRDYDPDPTEFGSNLIDL
GMDVEEIPEDMDVVLLIHPAGISDQAQFALDQFLLSGGQVIAFLDSFSAVAAQSQPQRPQFGGAPQAPGIPTSSNMSKLL
SAWGVSFESNQVLADRAYETAQSQTSSNPAILTITSEGVDEDSTLTTSIRDLLMYFAGTFYXNDKDGVEVETLVKSSTKS
QLVDSQAAQFNPDQIVQTFSSSGKEYPLAIRLTGNFNTAFPEGDPKEEEEEEEEEEEEEEEEEEEEEEEE
```

447 - 466:	EEEEEEEEEEEEEEEEEEEE
448 - 467:	EEEEEEEEEEEEEEEEEEEE
449 - 468:	EEEEEEEEEEEEEEEEEEEE
450 - 469:	EEEEEEEEEEEEEEEEEEEE

451 - 470:	EEEEEEEEEEEEEEEEEEEE
452 - 471:	EEEEEEEEEEEEEEEEEEEE
453 - 472:	EEEEEEEEEEEEEEEEEEEE

A0A2E9LCD2 **A0A2E9LCD2_9ACTN** (301 aa)
Uncharacterized protein (Fragment). *Acidimicrobiaceae bacterium*

```
MFISRVFQSLGRGLVILGGLTLLFVAYQLWGTGVLTDRYQEDLEKDFSELVETAESSPSVDSATDSDDVEKLDYATLLWR
PEGQAMAQLVIPKMGLTSTIVSGVSSESLKRGPGHFPDTPMPGMPGNTAIAGHRTTWGAPFGDIDKLEPGDEIKIQTIQG
SFTYIVLEQNGGRGNFIVSPKRFDVLDQTFESYPNRLTLVSCHPKLTARNRIIVVAELVGEPAEPFKRPDYLSKPTFVFA
FDEEVVAEALGESSGKEVLSNNTKENLDKEFIEEQEEEEEEEEEEEEEEEEEEEEEEEE
```

276 - 295:	EEEEEEEEEEEEEEEEEEEE
277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE

A0A2G2VMR9 **A0A2G2VMR9_CAPBA** (1174 aa)
Lipoxygenase (EC 1.13.11.-). *Capsicum baccatum (Peruvian pepper)*

```
MMFTAQPRSTPLSSEIQHVFTVRSPVEIMTTRRKISSQISRFKVKAVIQSGNEEKKKTVESGKLVEKSGEESNGFSGKGV
RDVKAVITLRKKMKEKISDKIEDQWVSLMNGIGRGILIQLISQDIDPVTKSGKYAESYVRGWFSKPSDHPYIVEYAANFT
VPHDFGCPGAIIITNLLDKEIHLVQIVVHGFNEGPLFFSVNTWIHSQKDSPESRIIFQNQAYLPSQTPPGIKDLRREDLL
SIRGNGKGERKLHERVYDYDVYNDLGNPDKSEDLARPLIGGQERPYPRRCRTGRGPTKKDPLAERRIEKPHPVYVPRDET
FEEIKQNTFSAGRLKALLHNLVPLIAATLSSSDIPFTNFTDIDKLYNDGFVLNDDKDLKKNKFLSDTLDKVFSVSKRLLK
YEIPAIIKRDRFAWLRDNEFSRQALAGVNPVNIELLREFPIVSKLDPAVYGPPDSAVTRDLIEQELNGLSVEKAIEEKRL
FILDYHDMLLPFIGKMNSLLGRKAYASRTLFFYTSRGVLKPIIIELSLPPTPSSPRNKRIFSHGHDATNHWIWNLAKAHV
CSNDAGIHQLVNHWLRTHACMEPYIIATHRHLSSMHPIYKLLHPHMRYTLEINALARQSLINGGGVIEACFSPGKYSMEI
SSAAYKSMWQFDMEALPADLIRRGMAVEDPSMPLGVKLVIEDYPYAADGLLIWSAIKEYVESYVEHYYSEPNSVTSDVEL
QGWWNEIKNKGHPDKKNEPWWPKLVTKEDLSGILTTMIWIASGQHAAINFGQYPFGGYVPNRPTLMRKLIPHEDDPSYEN
FILHPEYTFLASLPTQLQATKVMAVQDTLSTHSADEEYMCQLHEIQRFSIYDHEVLKVFERFSAKLKEIENTINQRNKDI
RLKNRSGAGVPPYELLLPTSGPGVTCREEESEEEEEEEEEEEEEEEEEEEEEEEDDEEEEDEEGRRGGRGGGRGGRRTL
DCGRLTQDDLKFVSMPIQSKKAVNIEEILKAEIIFGKYPMCITMSDIVIDNDDFDADDMTIECYDFVELSELAVAVVSNV
EYLPVVNVDSEELISNCYNSVVKVNQKFQLNEIPCTHAIAILKSKHVKEMKSHYSDYYKNEALVKTYEISLCPMPDKQDR
HIPPEVLEDVVLPPKYKYPPGSPKKGRQKKSSEKFSSTTNRCGKCGYVRVNEEC
```

912 - 931:	EEEEEEEEEEEEEEEEEEEE
913 - 932:	EEEEEEEEEEEEEEEEEEEE
914 - 933:	EEEEEEEEEEEEEEEEEEEE
915 - 934:	EEEEEEEEEEEEEEEEEEEE
916 - 935:	EEEEEEEEEEEEEEEEEEEE

A0A2G2WYW6 **A0A2G2WYW6_CAPBA** (436 aa)
RING-type E3 ubiquitin transferase (EC 2.3.2.27). *Capsicum baccatum (Peruvian pepper)*

```
MIRVNHRCSCRIRQEQLLQQREEQQGGGEMARFSVGREEEDDNEDGDSEGPTRGGGGGGPVPKRRRTFGGTFSCSSVRRQ
QEQEQQQERERERERERMAVDEEIEEEEEEEEEEEEEEEEEEEEEWESESGEEESEEGRLGGVGDAEGSRGSGSIARGNGS
IARGNGSMAVDEQDNDVEGLRGNGSISVTLSDPDVLDCPICLEHLSVPVFQCENGHIACASCCIKIANKCPSCCWPIGYN
RCRAIEKVLESVKVSCMNKSYGCKEVLSYSKKTDHENTCIYVPCSCPFRGCDFVGAATKVYAHFSDKHASSAVHMLFNAV
HPIYIEKHRRYQILQMSTKDVLFIINHASDRVGSSVNIICVGPAMQKRRFMYEIVATDGESTFKLESVAESVPNWSENTP
LKKYLLVPRDIVNSGARLKLDVFIKERECIGSGSTT
```

104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE

A0A2G2XLZ7 **A0A2G2XLZ7_CAPBA** (442 aa)
Putative carotenoid cleavage dioxygenase 4, chloroplastic. *Capsicum baccatum (Peruvian pepper)*

```
MKKKKKRKKKKRKRKRKKKKKKKKKKKKKEKKEKKKKEKKKKKKKKKKKKKKRKKRKRRRNRRRKRRKKRRKKKRKKRKR
KKKKKRKEEEGEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEETEKEAAAGEKEESEKEKESRMKNLR
KKKKMRKKNLRKKYVLSDNFALVDELPPVECEVVEGSLPHCLDGAYIRNGPNPQYLPRGPYHLFDGDGMLHSIRISEGKA
TFCSRFVRTYKYNIEHESGSPVLPNVFSGFNGLIASAARGAITIARVIAGQFNPSKGIGLANNALLGGRLFALDESDLPY
MQYIYAAIGDRPPKLKGIAKLDISIAEVDRRDCIVACRLFGEGCFGGEPFFVAKNPDDPTANEDDGYVMSYVHNEKTGES
KFLVMDAKSPNLDIVAAVKLPRRVPCGFHGLFVKENDLTKMK
```

96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE

98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE

A0A2G2XPB5 **A0A2G2XPB5_CAPBA** (481 aa)
Protein transport protein Sec61 subunit alpha isoform 1. *Capsicum baccatum (Peruvian pepper)*

```
MIVKAATTTRMHKTNCRQFAQNLKLIENLLEQLKITELKRYPKTQEPLEHLEHALRRVAVTKSSGTFAVGQHQKKPNLRP
DTKPDNAPSGDKVAETLNKDLRTRTLEEDEKDKSLDVGSNGHSLFTSTTSISELTKKDACTYMKFRREELESVLPERIPT
GMLKEFNDSVRDALLIRQSFLDLRDNFRRVFDPNLQSNAKAPSIWHTLYNWRRKIFYWMRVILASNRGTVVELGITSITT
SGMVMQLLAGSKIIQVDNNVREDQALLNNAQKLLGILVAISESVAYVLSGCSHRRIASMGHHHLAEKKLSSKIWDEMVSN
DEEEESEEEEEEEEEEEEEEEEEEEEEDEEYFPRPLTKFQMPLKEALNSLRTSTEGKVLRNGRMRTTGNDEEKDEPSQCR
DRLKLSTSTKNILLCGNSQTKRMPDQVNLQQCPGTSSKKMIHKGDNTMNKVEFRSEEKWDVCKKKTSSSKVGKKMPGTRE
I
```

327 - 346:	EEEEEEEEEEEEEEEEEEEE
328 - 347:	EEEEEEEEEEEEEEEEEEEE

A0A2G2ZQK0 **A0A2G2ZQK0_CAPAN** (340 aa)
Uncharacterized protein. *Capsicum annuum (Capsicum pepper)*

```
MNRLLHWKEDSKIFDLIEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEENKMIEATFWGEFALQIHPRLDGSIDKHVIVVMQLVQAHKFKGKYFVRNSWTASKLWINLQLPEVAEFISRM
EDVRGDKFERISQMSYQNNSSTSDELSSGSLEVKTIKQLIECIDNVGVVRVPSYPFQLDYILDREVMFKVAVKKDNIDKH
DEVYIVLKFSDDKDLIKQYRPPPSEDTCTCPEFNHEHLASGDDELTDSVAENDVISISNTPTKRSISENESYVVEIDDDP
NAQLSTNKVKRVEKGRKSHE
```

18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE

35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE

A0A2G3D2X3 **A0A2G3D2X3_CAPCH** (466 aa)
Aspartic proteinase PCS1. *Capsicum chinense (Scotch bonnet) (Bonnet pepper)*

```
MILMPEPINVVLGDEKDDKLVLDAIDEFLKFLVCEKEEEEEEEEEEEEEEEEEEEEEEKIEGKQSLILPLTAKKISSVSIP
KPPNRVAFHHNVSLTVSLSVGSPPQQVTMVLDTGSELSWLHCKKTTATPSVFNPLVSKSYSAIPCSSATCRTKTRDFSVP
VSCDPKKLCHATLSYADASSVEGNLALETFRIDNLNLPGMVFGCMDAGSSSNPEDAKTTGLVGMNRGGLSLVSQMGYPKF
SYCISGRDSNGVLLFGEVDLPWLRPRKYTPLVQMSTPLPYFDRVAYTVQLEGIKVGGTILPLPKSVFVPDHTGAGQTMVD
SGTQFTFLLGPAYTALKNEFMKQTKGVLRNLNDPNFVFQGAMDLCYQVESTRTTLPPLPPVTLMFPGVEMSVTGEKLLYK
LAGATRGKDQVYCFTIGNSDLLGVEAYIIGHHHQQNFWMEFDLANSRVGLAEVSCELASQKLGLGL
```

37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE

A0A2G4T8B4 **A0A2G4T8B4_RHIZD** (290 aa)
Uncharacterized protein. *Rhizopus microsporus ATCC 52813*

```
MRYNILSLGLIAATLIASISARALPVGSLPDTTSSIDSAVAADEDVVTTALGRHPLYTSNKKRATVSFQRREEEGEEEEE
EEEEEEEEEEEEEEEEEDDDDEESGGGEEGAADQPSLARRHWQKDKETSNDDAGAANDGDTEDEDAVTEELEPVTEELDT
ATEDIDTIYPDDTDAAEDEVAYGGEDDEDDDEDSDDDSDSDDDSDSDDDSDSDEDEDEEDSKLARRQNTEEAAVNQPVDT
SAVDTTEQPADPANGEGEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDE
```

76 - 95:	EEEEEEEEEEEEEEEEEEEE

77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
260 - 279:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE
262 - 281:	EEEEEEEEEEEEEEEEEEEE
263 - 282:	EEEEEEEEEEEEEEEEEEEE
264 - 283:	EEEEEEEEEEEEEEEEEEEE
265 - 284:	EEEEEEEEEEEEEEEEEEEE
266 - 285:	EEEEEEEEEEEEEEEEEEEE
267 - 286:	EEEEEEEEEEEEEEEEEEEE
268 - 287:	EEEEEEEEEEEEEEEEEEEE

A0A2G5CK32 **A0A2G5CK32_AQUCA** (435 aa)
F-box domain-containing protein. *Aquilegia coerulea (Rocky mountain columbine)*

```
MVKDQKMGNEEHLTNNQEEEEEEEEEEEEEEEEEEEEEDDDDEEEDYDYDDDDELLEEDEEENFEEDGFEDVLQTSGMMAK
LPVEIFFEILSRVPVKSLSQCRKVCIAWYNSIQHPLFIKMQHNRAIKSNSHFVILYELRTKQYYLVDYESLDGLEITQIS
QIPKMPYVYANLDSCNGLIYRREQTSFVMNPITGDFMLLPDSPKYYLEDIKRKEIEKYGCSLGRKCQCCEMETEIYTFSS
GTWETIYDVPYNLEYNDTNAFVNGAFHWIGVDRGKPKAPQVIVSFRLCTEDFQEIALPHGVHLNKDCQLCVLGGCLCLNC
DFSDWRAEIWVMKDYGIPGSWSREYVIENMKPWSEPYVPLKLMDNGEILLMSDDSIMGYYDPEKGTYKLINLYEFLPDRR
HIGQSLIHVGSLISPQNISRLLFIEHITRSPRLIL
```

18 - 37:	EEEEEEEEEEEEEEEEEEEE

A0A2G5VC72 **A0A2G5VC72_9PELO** (279 aa)
Uncharacterized protein. *Caenorhabditis nigoni*

```
MVENSVQIEGKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERRRRRRRRRRRRRRKKKKKEEEKKKKKKKKRRRRRRKKKKK
KKKKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKKKKKKKKKKKKKKKEEEEEEEEEEEEEEEEEERRRRRRRRRR
RRRRRRKKKKKKKKKKKKKKKKKKEEEEEEEEEERRRRRRRRRKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
KKKKKKKKKKKKKKKKKKKKKKKKNKDSSPFPSSFRVMAH
```

12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE

A0A2G5VG47 **A0A2G5VG47_9PELO** (189 aa)

Uncharacterized protein. *Caenorhabditis nigoni*

```
MGVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERRRRRRRRRRRRRRRRRRRRRRRRRKKKKKKKKKKKK
KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKEEEEEEEEEEEEEEEEEEEEEEEEEEKTSGHS
GVKEKEKRRRSRVAECVSMKSALFQESKV
```

4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE

A0A2G7G1W4 **A0A2G7G1W4_9EURO** (1300 aa)
Telo_bind domain-containing protein. *Aspergillus arachidicola*

```
MDANEQFPTSEPLRASRIPIAQLSPTLEHFSESSIHASVTLLWPYSSSTKSLSLLLAEPDFRLRHSNGQVKAVFHGHIAE
SVAQSQIGIGDSIYLSLNGARLSDNVTAPGTPGRSVAWDIHFDDRVFLEIWRSLNHVSTVKVDPPTPSPNDTTDAPPATP
IAKGYDRSDRNLLIDGLSSWQSPAFLGRSRTSLGGLADSVLDQFAEEDGFVPGKGRKRPRFSMRSSEWRVIDEPESPGER
GEVPDWTHIFDEDWGSEPEPGPEDLSEKEERPPDATKIKNTGIDSEEGSLTVPASEADVAMENASLASSRTSPERHIAQT
VDGIRLPPHGISGIAEFSRKRGVLNCSAHLPIETPRLHPIPSPGLPVPSPLVTMSNSPQGYFTPAAATAHSHTSQIPTTL
SREVTDLENEMPVAQPDTPQTPDCKETAITSGTKDRAIGVPEFTSESNATKITLKATSQPHTMANTELKGLLPDEDSKAA
AGPAQVHQFTPHISEKDTGKLDGHLGDPDQLRSLNRVGKEFELDETCIDAQMKAESEKDKGETHQEQEVVKEDKLEDNGH
IITRTSKGLVPGDTRASGVANVVEYGTDGSGEEDTEAPKRSRHYHDLATESEADTPETDREHPTEAALEGENKWEGKESE
GESEKELEEEEESEEEQAQGIKETDREGDADNEEMERDDLEAEWDDEEGWYEEEEEEEEEEEEEEEEEEEEEEEEEEEEA
EDRYEDEYGDGAESEIVSDQMSIDTPTQPPAMKNVHPEVIVLDSDSEDEATPASQAYPMTTSRDEANTQEIESSEPEASA
SEEGSLRSRRSDNSESSEDEEGEDWSDENSEDEQLLDKNGGEMMEDELGRANGEQQRAGHAVDELSDNGSTRGEKVDEDS
VDAHEEYEADNEAMEEQPETKRGQVSVSQPMDIRDAALPIGTYDWGPSHDSEQRNLDYHACTMASAQEPHSDSRTTLQEF
ETVIDPELQNIGLAKEQENKDVEEEHRSDSIYAEPRTDVSAKIPEAVQDIDQGLFLDGTSSSQASHDSREAVSEKPLQLQ
HLIPMDTQLAEVGQPSMDFTTTGILPTSEQVQRKTTVQSQGQMPPAIQIRTIAPTERHLNVAEDVEHEARLVPPQREGEH
ELEEFSADGVVGTPASFSGDQAQADELYSDDESVGDLDEVHLIGIDRHYPGLHSQLSYLAPLATLVDHYNALVDTISVVS
EVQPVFRAIFRPSKVALPSVEEGNAVLLRNFRVKSFNRSIMLISLDTSAWAVFKGLDDKALIHDPPVEYGSEEEACATDL
RQWYQETGMAMVQITNYKPP
```

692 - 711:	EEEEEEEEEEEEEEEEEEEE
693 - 712:	EEEEEEEEEEEEEEEEEEEE
694 - 713:	EEEEEEEEEEEEEEEEEEEE
695 - 714:	EEEEEEEEEEEEEEEEEEEE
696 - 715:	EEEEEEEEEEEEEEEEEEEE
697 - 716:	EEEEEEEEEEEEEEEEEEEE
698 - 717:	EEEEEEEEEEEEEEEEEEEE

699 - 718:	EEEEEEEEEEEEEEEEEEEE
700 - 719:	EEEEEEEEEEEEEEEEEEEE

A0A2G8K3B3 **A0A2G8K3B3_STIJA** (214 aa)
Uncharacterized protein. *Stichopus japonicus (Sea cucumber)*

```
MRSQVVEYSYLKEISKKYSDGQAIAQRVGKQIKISSASIKGLIQTYNGIFRLDQPITFAQVADLSNNLYHYLDDAHSTDK
QKIPMSVKRKAVCALNMLDRANEEENITTKEMKNTIEFYEVQASILHNLISNLELHQPRSLKEEGLLVHYRGKKSSIDSL
SPILKSQFAIARRGNIDIPVNQLTLSEDEEEEEEEEEEEEEEEEEEEEEEEHE
```

189 - 208:	EEEEEEEEEEEEEEEEEEEE
190 - 209:	EEEEEEEEEEEEEEEEEEEE
191 - 210:	EEEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE

A0A2G8K562 **A0A2G8K562_STIJA** (695 aa)
Putative WD repeat-containing protein on Y chromosome isoform X6. *Stichopus japonicus (Sea cucumber)*

```
MDRSVRMWNPYVTTKATAVMKGHTSAVTHIVVNGHHGQIISVGKDKGIKVWDMRDQTCLQNINPRSINIGPHGINTVCFH
AKTGSLILGSNQLALLEHKWESESEDDEAVSHTKPVTCALYNSLFNQVVSSCHESVVSVWDLETGTKTIQFSKAHTYTEK
GIEKSAEITAMTFDPSLRRLITGGRDGTVKVWNFNNGACLRELEVFDYVEVTGIVCSKLRIVTTGWNRRITTYIDSDEDE
DSRQWAVKHSEDILSIDHYDSVLATSSYDGEIWVWSLETAHPLCKLSANEGLKPQTGSHIVNLDTDFIHKPPAKVLLEPA
QSGNGVESKVSSNIQHQLSDEQIKNSYTSSEKFSIDRNGNMRRKSNDESRSKLPAINLAKRPSLVDNSYEAKQDTTGSKT
FFTESMTNFRKRIDVEEQEEEAEEEEENEARENGEHQEADDPNNNRERESLSKLGLLENKHESAVDKVLFLQSRPNDKDT
ATLMASGAEGWVRAWSIHHKGGLLGQFNAAQKPRESILTMATDSKNEFLFTGDTLGYVKVWDISDYCISESKKEQQPEED
AAEKIPREKQFAFLKGNEKLKTLTQKMIEKSRGRRRRRSRRRRRRSREEGGVGVGGGGGGRGGGVGVGVEEEEEEEEEEE
EEEEEEEEEEEEEERRRRRRRRRRRRRRRRRRRRRRREEEEEEEEEGRSYNIFKIYREHE
```

630 - 649:	EEEEEEEEEEEEEEEEEEEE
631 - 650:	EEEEEEEEEEEEEEEEEEEE
632 - 651:	EEEEEEEEEEEEEEEEEEEE
633 - 652:	EEEEEEEEEEEEEEEEEEEE
634 - 653:	EEEEEEEEEEEEEEEEEEEE

A0A2G8RR70 **A0A2G8RR70_9APHY** (392 aa)
Uncharacterized protein. *Ganoderma sinense ZZ0214-1*

```
MLRGRDGNVNERQAAPSREVNNLLHTLRGEQFRHSQNLRRSKAHLEILRSRTAYNNPSLPFSDIYKYANAPAEDAVHDDD
RILPLPPLPVLREGHLEHGYPRGAVPGPPPPKSWSGLFRSHQPRGQQTESRDTVAFRKQALSLVFSHTPWSFGSSDVPLL
PVSPPTEAGCGSGGVDSDPPNGELETDAGVPALTQICVRVLLEMFPDAAGFREELLEVLPSMFRRDVLRYTVVHDPLPNG
KLYALFEPEGHADGEVIVVGPQATLQRDLFAILSSSLEAQEEAGDDEAKDAQEGPSGIRQVVRGPSEPKVDVAEEEEEEE
EEEEEEEEEEEEEEEEEEEEEYKGDAGGSWEEESLASQDQPPPLHTLIVLNAQSPDSSQPTDPSLAQDMPSA
```

314 - 333:	EEEEEEEEEEEEEEEEEEEE
315 - 334:	EEEEEEEEEEEEEEEEEEEE
316 - 335:	EEEEEEEEEEEEEEEEEEEE
317 - 336:	EEEEEEEEEEEEEEEEEEEE
318 - 337:	EEEEEEEEEEEEEEEEEEEE
319 - 338:	EEEEEEEEEEEEEEEEEEEE
320 - 339:	EEEEEEEEEEEEEEEEEEEE
321 - 340:	EEEEEEEEEEEEEEEEEEEE
322 - 341:	EEEEEEEEEEEEEEEEEEEE

A0A2G8XLE0 **A0A2G8XLE0_TOXGO** (1885 aa)
IgA-specific metalloendopeptidase (EC 3.4.24.13) (Fragment). *Toxoplasma gondii COUG*

```
MTSARTREGLVGAEAPLGEGEEDLQDSTACSVPRAPTNSFEEGYEVECVDECPYIKFQHASKLPLSPLLFDASSSPAPLP
ERLLAARCTDSLCLLHCCGVLLLPGLDSILAVDATEAACGSPISRGRLPLHASKEGETKDAFPSLLLLSPDARFLAVAVD
CQVKLVQLGGCGGPSCSKSAGEASREGNAEARLGGQQGGDSCISEKTQVLSLAGFASRVKDISWIWPSGDRTETWCEGDT
QGDAERLIGVAVLTESGEAFILSSRGAQAFPLPAHGLAIHALPRRSPAAAKSEGAGPGGLAPLTAVVSCCAPASLWLVAL
QETALLPEGSGQGESLYDFGHRRPDVSRETANEEKRKGRRKIRVEGLADIPGYEDEAQALHKGRGRFVGVHCLGASLDSA
AGESPLPLALAWFVPDADLSTGEDDWEKPELESDSAEPRLDPLRQAPASAEDCGDSWSCFILFGFLARRPYTPSDARALP
GDIGEAESADEKEELVFRVYAASRNEMFLRSVAASTVCRFRWIPQWHCLWVFSNACTQVICFALPHSFSRNGDPLPSPRS
SSFLGSGEVPWRCFTMPEGRALETADEDAFPQGLALFFNFKESMFREHSTTDTPPLEHPPVFFLLQSDGQVCVHLADCCE
CYVDDAGIGKEKRLLPRLEWTPVSPPSSFLLTSWTETRRRACGEQPATPVPKVSPPALSPSSSSLASPLFASLQQGKPTP
SLFGTPSTNAASAPLFSSSSGTSLFPSSASSASSLFTPAKSEEEARKTGWVVPTTHLKVTSASSAANDPSASNGASASNN
LSALDGSSPRPLSSSRKDCVDQARPAAKETREEAPTRRLPAKSSSRDPQRRGHCLHCGAVDVGDRRGGREAERRRREKKL
RRRVEAKNASLRQAAAAANEVIEATLQAARGTKAEPAREKNAKKRIRLTEEQSEVKALLDEFDEKKHAFCSFSRFLPSSL
FRPLLLSARCFENALRHEERRDVLLESSPVSSSASSSASSSASSSSSSSSSSPGSLFVSRCGEKDAPVDCGAEQEKSTAA
```

```
LLPAAAAGLARTGRLADKLKDEQRNVRTKQETETEVVETLQEAQQHLVAWRSCLEAVRDQLLLRMQFAEKKSENPTERNG
EQTDAAGREEGRGDREADGREEKRERQAERGNSVTDEDVIACMQKIQSESGARRNLFEALQTLLPADSEHAQLNTDTHTK
CVLTHLESGLLRAERRLLLLLQRFRFYTSFQTRFPSSLDPESGSSVRRLAASGWPGSWKIDSGLSSLSSYGDKGVSSLPL
AHGKDSDRDARTKRGSVHTPDTACGRGRPGGCYGLRFEWLEEDEFPDKREESVVDSHRRVSSTTHPVSEGTPGARPSLAF
SLSASPPSAFHLSLFGSPGGAGDSRIACSQGPGGSVKDGGLAGSRSGAASGDFLLDMHAEHRAAGLVAELEAAVSEFLSS
VRQLEIDLAKLEWKATDLQSPARQSPSSSSSTSSFAASLSLLSSSVFGEPLPPSGPSGLPDVAGAEKPAKDGEQRFPVSS
LREQRERFDERRKLRRQLLEVWRATTSTDPQQEGEEETETDADEEEEEEEEEEEEEEEEEEEEEEEEEDEEEEEEDESDAFE
VLEDSSSVSYDEESDEWEPVGSASPENPQTPPRQSVVSRRLGASLRSGRRTSRSKQRAKFAPLSGDEDSSENACSSSPSS
PDDVSPRRPGAELSDSEGAPEDGASRSNSHDESASLPVCGVPAETHSISHSSLFSIKPEDVTQPPQSASFQFASSLAPRR
ASGLGHTLFSFASNSSSLPPDPTKPSSASSALLPPDPTKPSSASSALLPPDPTKPSSSTSALLPPDSTKPSLFTSAPLPP
DPTKPSLFTSAPLPPDPTKPSLLRQLLFLLIPQSLLLLPQLLFLL
```

1564 - 1583:	EEEEEEEEEEEEEEEEEEEE
1565 - 1584:	EEEEEEEEEEEEEEEEEEEE
1566 - 1585:	EEEEEEEEEEEEEEEEEEEE
1567 - 1586:	EEEEEEEEEEEEEEEEEEEE

A0A2G8XWQ0 **A0A2G8XWQ0_TOXGO** (1238 aa)
Daxx family protein. *Toxoplasma gondii COUG*

```
MRGRRPSQQRKKAASLGASSLLSSFPSSLPPSLFSRGDSVGRRLGKRRGIEEEGGKRKRARGGRSARHNFPEVDQQGGSD
LDELPSSEADPREAQQDGEGSFGHEQELAETLKKSKRAVLERKRRRHEERRQKKQIHRKQQQLWKLERQKALLERQLDMQ
KAAISGIRVNQGTGSGVRTPCGPEADSEDEEEDVSPRREKKTPSSLSSSLSSSLSSLDVRGSVLSALSAKDKKHTVSGEV
LLLSGVSSRSTEEHRKAEERRLALDAAGRQLDAELAFLESKLGIGKDSSKAGEKKKKKLAQELLDDGFDEDLQTLLDDIL
GGKAENRKRKTKTDYDHDEGEMEGEETQEGAHEELGRVEAEEDEEDEEEEDDEEDEEDDEEENEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEDEGDEEDEEEGEDLKLKTEQYSTCASASAGKYLPPHLRNRAQRELSNEAEFDGDNPGRNSTRQHGAAP
ASEASDKANFVASKLPLSCLEKARQTATDAGRGLTQRLRGSLNRVSEGNVEVILQQISQEVKAALTQVLSGALPVPATSP
ALTPRDVRGLRREQEISFFQEVNCIIVRLLMQSMVESKFSTASLVATQTALCCGLSCLLDASLCSQLLAALGEAFRKFFP
LALAQADRRTETGEPVGLYVRHTLMALCFLFDFNVVQPAVFLGLLQRLSGKVATTKEKGEAKNGERNEPLVEFQVECLLM
VLRLGGGKLRNDNPVLFKEAWNFLMTRVKGGEGEREVQVHSGREERPFEEQTREEQRARLARVSTSFSGALRQRQEGEQP
ATTGRLHYLARELEELKNNKGNTIHLASKASQEAMRRWLQTSPLLAQSPLRQCAGEGKSVLVGVSSWQEVEDGVVSVSPS
SHRPPVSPHKSVRVEKEKQSCLGDTGSEKALLDLAAKLRLHSEEQKKIFLAIMSAESPNDAVKRLLQLVPRTNKKKNFVT
TAVAVLLHISLQQSAFNPFYALVIARLCARCSCASWGRLEAEAEQPPLLGPLGSGRASVNQRRARGPCACLLPPDKEGKV
FRRVTQRGLAAQNSAAHGFPLRRLLHLARLEAFLIRIGVVELRVTRFVSFEGEKGQADAHMGLSGKLGVFLKELCTELLC
SPAFASVPLPGPSTASPLLPFLSLSALPDVREAFLLVLEDVLLPEARKNACSENGKGAKESVNAACMPGRQGKCVRAKGA
MCTPACGIRKDVISRVIWFMKKQERYEEEDPNTFAFDA
```

384 - 403:	EEEEEEEEEEEEEEEEEEEE
385 - 404:	EEEEEEEEEEEEEEEEEEEE
386 - 405:	EEEEEEEEEEEEEEEEEEEE
387 - 406:	EEEEEEEEEEEEEEEEEEEE
388 - 407:	EEEEEEEEEEEEEEEEEEEE
389 - 408:	EEEEEEEEEEEEEEEEEEEE
390 - 409:	EEEEEEEEEEEEEEEEEEEE
391 - 410:	EEEEEEEEEEEEEEEEEEEE
392 - 411:	EEEEEEEEEEEEEEEEEEEE
393 - 412:	EEEEEEEEEEEEEEEEEEEE

A0A2G8Y540 **A0A2G8Y540_TOXGO** (877 aa)
Utp14 (Fragment). *Toxoplasma gondii COUG*

```
MALERRTARRVPPRSQKEQEELTPWLTAGPQADDNEEEEKEEEEEDEEEEEEEKEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEGEANASKARVLKQRGKAMISAQKKSRDKDASDALSICRLMKDLVSDSWDGLRAEEEAEEEEDEEESEE
EEAEEEEEGEEGGEEEGLPSKLLKSLQRAQRTEEEEVDPFEGVSEHSLSLLKSEGDRRRAAASSQADSGEEGGDAGTREV
DAQLDAASADALSFSSLLTSLSTTTSRSGLRKQLESLARPRAASAAASSVRGSDETAVDADVVQEPLGPTQQKALLRSAA
YAEAKETAKKWTRVVQRNQQAVQLQLGVSTARSRGGDGRGEAPTEVRSLSHALSDFKANDAFEDALLAAVNADGVSDQKL
KASGGLGPANAIKRQAEQRQVARLKFLLFTEQRRARRLKRIKSKVSRKKRKQAERREEEKIMEKLEVGNPALAEELRKKF
EEKRAKMRLLRQQNARAKWAALAARFGGRDVQQEISRQMQREADERRTVERLARRRPGSSDGSESESAESAESAESEEEQ
SAGDKARLLRTLSRETADLQEALPDKGLLALPFMRRGLEKRRERNRQEIERLRRHGESEEDSEGADEALEAGRKPSGDED
ASDLESTLDETEAREARDAVAEAEVERRPTQTGRRKRAVDLDPKAVEAAEQELEGKFQFFELNEADGSETQASPKDAGKA
GAGEQRAFASSAAARAFFQAELEKEEKRREEAATKRSREAHATAWAQAERSGGSERERQRELERSAEAANPWLRPQKKRK
VSMAGTQVEETAQQLQKLLNDEESSASEAEGARPASNLRGKTEREAQRELIQQAFVCDEDAEEEFIQEQEEENKKEE
```

55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE

64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE

A0A2G8Y6M3 **A0A2G8Y6M3_TOXGO** (94 aa)
Uncharacterized protein. *Toxoplasma gondii COUG*

```
MQAEGDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDP
FRIGKCVSLWGRRQ
```

7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE

44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE

A0A2G9FYK2 **A0A2G9FYK2_9LAMI** (452 aa)
Splicing factor 3b, subunit 4. *Handroanthus impetiginosus*

```
MSASSISVAAAAIGTSSSHSVSSSTSIERVSLHLLPYKPNSIKTPLKLEAFHKPNPIKTPLKLKAFHNYSPFSSLSRSSV
FCFSTAFDRVELNQEEEQEKEKEEDEKKDDGNEDEKEEEEEEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEDDDDDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDEQSGIQGTVSEAEGVENEVPESGE
AGRLYVGNLPFSMTSAELSEIFAEAGRVDSVEMIYNKVTGRSRGFAFVTMGSVEEAKEAIRLFDGAQIGGRTTKVNFPEV
PRGGEKEVMSPKIRSSNQGFVDSPHKIYVGNLSWNLTSKGLREAFQEQPGFLSAKVIYGRDTGRCRGFGFVTFSSAEELE
SAMNAMNGVEVEGRPLRLRLAEQGPPGSPPPAVENTLEDNPENSEMLSNVST
```

131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
183 - 202:	EEEEEEEEEEEEEEEEEEEE

184 - 203:	EEEEEEEEEEEEEEEEEEEE
185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE
190 - 209:	EEEEEEEEEEEEEEEEEEEE
191 - 210:	EEEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE
194 - 213:	EEEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEEE

A0A2H0N6J3 **A0A2H0N6J3_9BACT** (877 aa)
Cell division protein FtsK. *Candidatus Magasanikbacteria bacterium CG11_big_fil_rev_8_21_14_0_20_39_34*

```
MGRRKKEEQHVLDATLSQGIIAILLVVFAFIITLSFFGKAGAVGEMLSNWVLSFLFGKIRYVTPLIVLLIAWFFIKDNDY
DYRPTHGLGAILFLLAAASLFHISFTPDEMWRQALEGNGGGVFGMLSWPLKTYLGFAASLAVLIGLVLISLLLMFNTLIT
HFVMLNRKLFYGLGLLGQSIFLVIRKLFVKNEDLPFDPEDTEDDFDEDEEEEEERQFSHKSLHEDEEEDLDIEDDELEEE
DDDDDEEDEDDEEQAHPNVHKIPFTPQATPTTDEGPWSLPVIIKNPPALSLLSNKKGKPTSGDIQRNQEVIQETLKEFRI
NVTMGEARVGPTVTQFTCKPAKGVKLTKITSLANDLALALAAHPIRIEAPIPGKSLVGIEIPNSKAALVGLRELLESKTF
KKREHNLMMALGRDVAGKPWFADLPKMPHLLIAGATGSGKTVCMNTIILSLLYQNTAETLRMIMVDPKRVELTPYNGIPH
LLTPVITNATQTVNALKWTINEMDRRFDLLSKAGNRNIDTYNANHPDNKLPYLLFIIDELADLMAMAANEVEAGIIRLAQ
MARAVGIHLIVATQRPSVDVITGLMKANIPARIAFSVASLTDSRTILDSSGAEKLLGRGDMLFQTADLSKPVRIQGAFIS
EQEMKRIIKYLRGNEKPEYDESIISKAGNNSGGTMSMFGGPTDERDSLFNDSKIAILEAGKASASFLQRKLKVGYARAAR
ILDELEEAGIIGPADGAKPREILVTEYEEVPLSESRVNVFDSTFPKDTNTEDETAEEEEENDEIEEEFEDNNDDSEEEDH
YEYEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEANQHKKEDDTDMDLRYN
```

804 - 823:	EEEEEEEEEEEEEEEEEEEE
805 - 824:	EEEEEEEEEEEEEEEEEEEE
806 - 825:	EEEEEEEEEEEEEEEEEEEE
807 - 826:	EEEEEEEEEEEEEEEEEEEE
808 - 827:	EEEEEEEEEEEEEEEEEEEE
809 - 828:	EEEEEEEEEEEEEEEEEEEE
810 - 829:	EEEEEEEEEEEEEEEEEEEE
811 - 830:	EEEEEEEEEEEEEEEEEEEE
812 - 831:	EEEEEEEEEEEEEEEEEEEE
813 - 832:	EEEEEEEEEEEEEEEEEEEE
814 - 833:	EEEEEEEEEEEEEEEEEEEE
815 - 834:	EEEEEEEEEEEEEEEEEEEE
816 - 835:	EEEEEEEEEEEEEEEEEEEE
817 - 836:	EEEEEEEEEEEEEEEEEEEE
818 - 837:	EEEEEEEEEEEEEEEEEEEE
819 - 838:	EEEEEEEEEEEEEEEEEEEE
820 - 839:	EEEEEEEEEEEEEEEEEEEE
821 - 840:	EEEEEEEEEEEEEEEEEEEE
822 - 841:	EEEEEEEEEEEEEEEEEEEE
823 - 842:	EEEEEEEEEEEEEEEEEEEE
824 - 843:	EEEEEEEEEEEEEEEEEEEE
825 - 844:	EEEEEEEEEEEEEEEEEEEE
826 - 845:	EEEEEEEEEEEEEEEEEEEE
827 - 846:	EEEEEEEEEEEEEEEEEEEE
828 - 847:	EEEEEEEEEEEEEEEEEEEE
829 - 848:	EEEEEEEEEEEEEEEEEEEE
830 - 849:	EEEEEEEEEEEEEEEEEEEE
831 - 850:	EEEEEEEEEEEEEEEEEEEE
832 - 851:	EEEEEEEEEEEEEEEEEEEE
833 - 852:	EEEEEEEEEEEEEEEEEEEE

834 - 853:	EEEEEEEEEEEEEEEEEEEE
835 - 854:	EEEEEEEEEEEEEEEEEEEE
836 - 855:	EEEEEEEEEEEEEEEEEEEE
837 - 856:	EEEEEEEEEEEEEEEEEEEE
838 - 857:	EEEEEEEEEEEEEEEEEEEE
839 - 858:	EEEEEEEEEEEEEEEEEEEE
840 - 859:	EEEEEEEEEEEEEEEEEEEE
841 - 860:	EEEEEEEEEEEEEEEEEEEE

A0A2H1H8R9 **A0A2H1H8R9_ZYMTR** (237 aa)
Uncharacterized protein. *Zymoseptoria tritici ST99CH_1E4*

```
MGPNGLPPAMNESSESWAPTAFRVLREELSAQQTRDERIGRCHEEDEEDKASSPRTWLLPGERGGSRSSSESSTDTDNDN
KERRRKEKTMVMVVRGRGRREKSPAGKRERIPTAGRDDDDDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKK
DPRRPRAKAKAKAKANEAPPPPQRPQHHRRRRRHHHHRSRQEAHEASSSSAANSVAVQVACGLERLDLYHGNRWHSN
```

122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE

A0A2H1H9L5 **A0A2H1H9L5_ZYMTR** (136 aa)
Uncharacterized protein. *Zymoseptoria tritici ST99CH_1E4*

```
MYMEVMSKCGDFECHIFFTRRTPHTPDTSHRRPLHTADHFTPPPTSHRRPLEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEGAVLPRQRSTARSKYVFHVPSMLMRVCTNF
```

52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE

67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE

A0A2H1X2W0 **A0A2H1X2W0_SPOFR** (442 aa)
SFRICE_003013. *Spodoptera frugiperda (Fall armyworm)*

```
MSDEEEYSGSEEEEVEEEVQETGEGDPEFIKRQDQKRSDLDEQLKEYINEWRKQRAKEEDELKRLKEKQAKRKVSRAEEE
KRLAQKKKEEEERRVREVEEKKQRDIEEKRQRLEEAEKKRQAMLQAMKESSKTGPNFTIQKKSDNFGLSNAQLERNKTKE
QLEEEKKISLSIRIKPLNIENLSVEKLRQKATELWECIIKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLD
PEALTGKHPPKIQVASKYERRVDTRSYDDKKKLFEGGLDTQLAEFMDKVWNEKMEEFMNRTKSKRRAPRVAVVSPMLPHD
ACLHGMLCSMSDPQLPDSAVEIYRDLEKLNKDFLEKVWQERADQFGGRQKTRLPKWFGERPGKKKGDLDSPEGEEDVKAE
VEEDEEPQYEPEPEEEEEVVEEEEEEEEEEEEEEEEEEEEE
```

421 - 440:	EEEEEEEEEEEEEEEEEEEE
422 - 441:	EEEEEEEEEEEEEEEEEEEE
423 - 442:	EEEEEEEEEEEEEEEEEEEE

A0A2H3IMU6 **A0A2H3IMU6_9EURO** (350 aa)
Protein-lysine N-methyltransferase EFM4 (EC 2.1.1.-) (Elongation factor methyltransferase 4). *Penicillium sp. 'occitanis'*

```
METQHPQYLEPSELGTKEYWETYYERSLEHIASKTKTRTNDTTPTNNEDDEDGERDEEEDDDDDPGTSWFSEHDAPQKIL
RFLTSRKFPLSPRNVHRRKGGAEPSILDLGTGNGSMLALLRKRGGFGGIMVGVDYSEQSVRLARELQRLRLHSAYESGDD
SDDEEEEEEEEEEEEEEEEEEEEEEEEDVVVATSTENGGEDSVQREEGIPLKNQDIQFEEWDILDPANETILTNNNDATKK
ISWFPYESQGFDIVLDKGTFDAISLSGETTASANAHICQQYPIIASKLVRPGGYLIVTSCNWTEDELVHWFTTATKTAEL
EVWHRLEYPRFRFGGMEGQGVCTVCFRRKE
```

164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE

A0A2H3JDF1 **A0A2H3JDF1_WOLCO** (248 aa)
Uncharacterized protein. *Wolfiporia cocos (strain MD-104) (Brown rot fungus)*

```
MSVPLTHEEEEEEEEEEEEEEEEEEEEEEEEEEEEIEHDEEIKDACAEFTAAWPLLVTCYEDVKRAKWNTPYIDKKLTTSM
QENRTQQPTLQNCENLTDMVESVKAAIDTQPITLPPPPTDETDEKGWVDWLIELNKILPPTEYQEGDDEAEGEKQTKDIF
IKDCPPVMESALMCKDLEIDILQIDCDILHQHLAVIVVAPELEQLQWLEWKSHMPWFEYEAGMLTSRKDKYQCPVVACDY
KCIDATTL
```

8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE

12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE

A0A2H3JHC9 **A0A2H3JHC9_WOLCO** (197 aa)
Uncharacterized protein. *Wolfiporia cocos (strain MD-104) (Brown rot fungus)*

```
MLVCGDGSYTPFQFGAHAPKSHCQRCKHLDSIFSVMKHRPAHECIHATCPQLGQITLEDLFPDNNTSTDRYVWPFADTLT
RLMGLSRVDVDIHIRKCKNFADDSDEDENDEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEDKDEEEEEEDEDEDEDEEDEED
EDEDEDEVEMEVDEDEDEDEVDEDEDEVDEDEGEVGE
```

111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE

A0A2H3RNV1 **A0A2H3RNV1_GIBFU** (1936 aa)
Protein transport protein sec16. *Gibberella fujikuroi (Bakanae and foot rot disease fungus) (Fusarium fujikuroi)*

```
MASESPKATDLATMPNHPDPTSSTQAPAHATSSTTPDAVVQADVPTSPDVSSQQDQKSSEQDGAANAWPSHEDDGHDSND
WLASDDAVPNQTQEETASNEPELDVASQPKAPVSQHSSSMSFARTVSHEISFGDEEEGEWNLSRTDTDPFKFMPPTDRTN
SFPPVPPAHTNSEVEDQQPLASNQALDVLEEIEKEADAEEELYQREETTDGLEAPRRGHSSSISIGGDLKSPEGQDSDER
YEEGMPLIPPPEEERHKVPSEQPNHTLSDSFDDKAEEGDDFFSQVQGSEQPSDEKPTPALERKSTMQVLDSMNAGAISNK
SALEGTPEEEEEEEEEKEEEEEEEEEEEEEEEEEEEEEDDDSSDEDDDSDEDSEEDKKAAQPAPTPASSNPAAAAPDSSPA
KKEDLASKWEQAFADDEDDDFLLEENAGDDKQVDPAAFFGSDDEGFLEDEEPASAPAPAPAPAPASRQPSGSNPYMPQAP
APHPAPSPYAPSIQVPAAAGSQISAYNTPAPVVTPFGTSPQYGQPLPARPDMSKAQSFADKSKGGYHSPYDLPTDLVTNL
VKPRKRASMQQLSQANQLHAPVQPPPRSASVGMPAPPTRLTPPSSSHGLPSHQQSTAPPKPTTPGAQHKENFFEELPLTS
RPRPSSRTSQRALSPARNAPPMAHVPHIPSPLAPAAPNHMVPPPFPATTVTPGEPHSDSTGQPALVPGAGLVAPERVSPY
AALTTSANHMPPPASTSTSRYSPAPGTSHTAPPAPASSRYSPAPPVPKSHGSYGAVATAGPGPVLPHQPRTSSPLTHSES
AHFEPRMSRVSSLPPTREVDEEDEQQTPTRSASATHAIPHYDSRYNPASPPKSTQTPPPPSYAGQLTLSPPKQSGPYVPH
APPTAQAGFVPPPRAQTQSPSASFGHKQAQRSSDSARRPSSAHSHSYPSPVGGKPAPSPYAPVAPTAPMAPAPGVSTVRT
RGQSITMNMVAPTDGRENDELQRWKGVPIISWGVGGTVVTSFPKSVPRYGMNQAVPMIVRTPGEVKVQSVKDIEPLHEHV
AKFPGPLRGKSKKKETIGWLSAGIELLEKDLPDVSFHSQLSLEAKRAVERLLLWKIMLIFIENDGILESNPAVEAAVRDV
LSPGENTSSASDDALFPAAASFDTGVPSVTSMQADGVDVSSMDQIRHHLLRGDRDKAVWALVDKRLWGHAMLISHTVEGD
LYKRVAQEFVRKEVNYPGHANESMAALYKILSGNLEDCVDELVPVHARAGLQLVSTGGGSGPTKDTLDGLDKWRETLSLV
LSNRSTDDIQGLNALGNLLSSYGRAEAAHICFIFGRHASIFGGLDDPNANFVLIGADHRQQSDQFAKETEALQLSEVYEY
GLSLAGGALAAAGTPHLAAYKLEHAMTLAEYGHRDKAMQYCDAILTAMSSQTKRSPYHHHVLETAVEDFMLRLKQAPKEE
SGSWISKPSMNKVSDSMWNRFNKFVAGDDNEENNGGTGEAGPFNRPSGEFSRSPSVSNFDIYGQQSPSFGMTPAQPSASI
AASKYAPNASTPAASANLYSPTSQYTPGRSSTEYAPNSYEPSYPGAASTDRGEGYTPSVPPSEPTSAGLSGPAGLAPAAQ
ITQGYSPAGYQPYGMPASTPMGNDETPADSSSQGFQPLSYGYEPPQVSSNPPEQAGEHNTGESGNGGYEPPSFQPYGYEP
PSYEPQSTAEGDDEQPKPKKKSFMDDDDDDFPSMKPAEKSKADKDRENDEMFRKAAEEDAKRAAAQQSSKKGWGFGGWFG
GSKKAPLEQTSSGDSSPGKPIRAKLGEASSFVYDPELKRWVNKKPGAENTPAKTATPPPPRAGPRSVSGTPPPPTATPPP
PLVTSNSAPPPLMPPKVRAGTPELSKQVSTESLGLAPPAMVRSVSNTSNASAPPSRPTTSMSNASSIDDLLSVAPRKASD
KKKPRKGGRYVDVMAK
```

338 - 357:	EEEEEEEEEEEEEEEEEEEE

A0A2H3RT40 **A0A2H3RT40_GIBFU** (3208 aa)
Uncharacterized protein. *Gibberella fujikuroi (Bakanae and foot rot disease fungus) (Fusarium fujikuroi)*

```
MPLNGTSRYARMRAPAWLNPSPQPPSDAQKERRQPNDALLNDPNSDILIDFNSHQGFYEAAKKKKTKTPSAPPPPPPPPA
APPADDGQKDDNTGGDGGASGGDAAGGAGDGNGDDNSNSSPKPPTTFENINLGDNKLDLGLSPPESKGISSSWGAKLGFG
GGGWGWGGGGKSETAPAPAPAPAPPPQETKAEENPWDKPHDKIGGIEDDDDGWGFGAKKEKKKGSTLWGAEPDEGPKDGD
DPWGWSGQKKKGKAGGILEELALDSDTAPPNGKKDIWDTWGISKKDRAKKKGIMEEVALAAAPEPPSMEDQWGGWSGKKE
HSQSSLWGAQDSIPAPAPDPPSFEDKDGDDFWSTFGTGKAKPPPEETSGWGPFGIGKKEPPKKEDDGWDLWGTGKKKKKA
GDLIQIEDDIPPPAPDPVEAVGTDDFLDSWGFGKKPKKPAADPFDFKTSGADDPNDAFWGSIDNKKPNAHEFLIHTTGDP
EQAAREAEEQAAREAEEAEAAREDEEIANLLDKKSKRGGRLLKSDRERLALLEGNATRRAEARATREAEMAAAAEAAQAA
ADAQAAADAEAAALQAAEDVEAAKENEELAALLAKKQKRNGKLLKKDQERLALLEGNVSRRAEAQAAREAEAIAAAAAAP
AAPPNEFLSQETDQDGLATEAAAEADTALATEIAQEEAEMESLQSKKAKKGKLLKKEQERLNLLINNAAKRAEEQAAKEA
EEQAAAAAEAEAAAQAAADAEAAVQAAADAEAEVAAKEEEEMAVLKAKKAKKVKLTKNETARLMTLVGNSVKRAQEKSVK
EAEEAAAAQAAKEAEEAAAREADALAAREAEATAAHEAEAVIAAEEEKELADLTAKKIKRGGNLIKKKDVERFNVLTQRA
AERAERVAKQAEAIGAVEAQGELTEATHGNVEVVAEAQPEPEPEQPLVDMDAASVDPDPDPAPDAAIIAEEEAELASLDA
KKIRKGKLGKKDTERHNILTENAAQRLAAKEAEEVAGAAAAEAKAAKEAEEAAAEAAAAEAEAVTASEAEAILIADEEAE
LATLAAKKAKRGKLVKKDADRFNILTENAAQRQTAKEAEDAAAAAAAAEAEEQAAKEAEVAAAAAREAEDAAIAEEEAEL
AVLTAKKAKKGKLVKKDADRFTVLSENAERRAQEIAQTTEQPEDPTPEPETEVNEPSPEPATDELSAEVNDPDAIAAAEA
EAAAIADEETELAALIAKKERKGKLGKKDTDRYNLLTANSTARAEKAAQEEAAAQATADAEAAAQAEAEQAAAAEAAALE
EAAAREAAEAEALLIAEEEDELAALTAKKNRKGKLGKKDSDRFAILTENATQRAEKAVEAEVMKEAVLEVEDLPAEIPAD
AEADAEVDAEAAEAAAIEAEAAAIAATIAAEEEEELTALIAKKEKKGKLGKKDSDRFAFLTENAAQRARNAAHEVAAEED
QEAAIADSADTNDRPDDIEDSLFENAPEPPVVEEEAPPEDDGAAAETMALVAAEEQEIADLEAKKARKGKLGKRDMERYN
LLIENAAQRAEERATKEAELAAAAEEEAVARETAEIEAAAVIAQEEEELAALEAKKQRKGKLGRKDTDRFEYLLGNKVAR
EAQVAEERAAKEAEEQAEEQALHEAAAAEAAEAAATAEAEETAAREAAEAEAAAVANAEDEELAILAAKKAKKGKLGRKD
TERFEQLSSNAEKRAEEQAAREVEAATDEAPAVEELLVEELEEPTPEPEETVEEAPDAPIPDIDDDGVAEAAAIAAEEEA
ELASLEAKKARKGRLGNKDTQRFTFLTGIVSRRAEEQAAKDAAAQALAQTTPEDVAEEEEEDIPDQEDAETAAIEAEAAA
IAATIAAEEEEELAALTLKKTRKGKLGRKDTERFDLLMQNAAIRAEERAIKEAEPDGQAEELVPEEVDDIPEPEPKENHD
AEEVAAQEAADAEAIELAALNKKKAKKGKLGRSDTERFNILVDNAAKRAEAEAAKEAGEGLGDVPRAEEEEDDEFVDAED
GEEDELAEELEPEGEELAEPDLQEDEPAIAEAMVAEAAAQAALIAEEEAELAALMKKKHKKGKLGRKDTERFQALTENSA
KRAEEAAIRDTEDAVAEVEVELGEPEPESEAAEPKPEDNCLEEAEQVVIAEEKAELAALMKKKAKKGKLGRKDTERFIIL
```

```
SENATRREQERAAVEAQTEAVQEEPDIEGVGETGVEEQEQEQEQEPLETQEEEAAAREAEEAAIAKEEEDELEALQAKKV
RKGRLGRKDTERFAILEENVARRAEERAAAEAAIVNQPEEDDEGEGEEEEEEEEEEEEEEEEEEEEEEEEEGEEGEEEP
DADEEELAIQEAEEAAAREAEEAAIAKEEDELEVLQAKKSRKGRLGRKDTERLRILEDNAAKRAEERAAKEAAAVEADLG
AEDAEEKEQEDDDDEEEEEEEEEGEEEDKDDDEDKDAEDEDIDNGEVGKGRDDADAEEAAAAAREAEEAAAKEATEAAAR
EVVTKELEELDSLQFKKARKGRLGRKDTERLRVLEENATQRAAELAAKEEAAAAAEGEEADVVEFGNPPEEEESDIKAED
NDEDQEADAEDTANKESSDVENEAIFGEDEEKEAEVLPKDQVPEAPADDEIVEVIDLSPKKERKSRKSKSRRDAPPPPPV
PDPPLTPPPESKQSRRPKIHREGTSFGRWAATPHEERDEPQEKSTRHRRREEKTSSKGSSSDKVEKTPSRSRGTALFSKP
PLTRSATMREKKDGISSKRRHSTNARGLVSPPPEDVLMGEDELSNRRKSRKPRSREDEDAMMSGAAPVPDKYERRRSNKP
RSHEDDDLVMIDPELAPDRRERRRSHKPRSREEEEVAVVDTERRRRAKRSRDEEPVMVEPDVPFDAPPRSSKKSSGFAGL
FSGLRTPKTERPDPLRRRSTYATTDDEALRSAKMDGDAVLVDADREARRAARRAKRAAESGPDPEEAARRARDEIRRERR
RQREEEADSTRQDKEARRAERRRQRDEDARRAQEERQAQEEQQRLQEEKEAQRAERRRLRREQEAVAAAEQIEDEEARRA
AKRERRRRDTKRAARGAEEEEGRQRRSQQSADEYNQRRSHRREERPQAPAWPHSGTSSWVKEHSDAPPPPDLGDGGEANG
GQTEDEMARREARRAHRSKYEEEPTEETEDRRRRRARRDDRERGGRDRERHRDRRSEGSDERHHSRRASTFMEAATTPRT
SWWKKIAG
```

2287 - 2306:	EEEEEEEEEEEEEEEEEEEE
2288 - 2307:	EEEEEEEEEEEEEEEEEEEE
2289 - 2308:	EEEEEEEEEEEEEEEEEEEE
2290 - 2309:	EEEEEEEEEEEEEEEEEEEE
2291 - 2310:	EEEEEEEEEEEEEEEEEEEE
2292 - 2311:	EEEEEEEEEEEEEEEEEEEE
2293 - 2312:	EEEEEEEEEEEEEEEEEEEE

A0A2H3T5X5 **A0A2H3T5X5_FUSOX** (3267 aa)
Uncharacterized protein. *Fusarium oxysporum (Fusarium vascular wilt)*

```
MPLNGTSRYAHMRTPAWLNPSPQPPSDAQKERRRPNDALLNDPNSDILIDFNSNQGFYEAAKKKKTKTPSAPPPPPPPPA
APPADDGQKDDNTGGDGGASGGDAAGGAGDGNGDGNSNSPPKPPTTFENINLGDNKPDLGLSPPENKGISSSWGAKLGFG
GGGWGWGGGGKSETAPAPAPAPAPAPPPPQETKAEENPWDKPKDKIGGIEEDDDGWGFGAKKEKKKGSTLWGAEPDEEPK
DGDDPWGWSGQKKKGKAGGILEELALDSDTAPPNGKKDIWDTWGISKKDRAKKKGIMEEVALAAAPDPPSMEDQWGGWSG
KKEHSQSSLWGAQDSIPAPAPDPPSFEDKDGDDFWSTFGTGKAKPPPEETSGWGSWGIGKKGEDETSESNFFKAHQIPEP
PKTEDDGWDLWGTGKKKKKAGDLIQIEDDIPPPAPDPVEAVGTDDFLDSWGFGKKPKKPAADPFDFKTSGADDPNDAFWG
SIDNKKPNAHEFLIDATGDSEQAAREAEEQAAREAEEAEAAREDEEIASLLDKKSKRGGRLLKSDRERLALLEGNATRRA
EARATREAEAAAAAEAAQAAADAQAAADAEAAALQAAEDAEAAKENEEVATLLAKKQKRGGKLLKKDQERLTLLEGNVSR
RAEAQAAREAEAIAAAPVAPAAPADEPLYQETDRDGLATQAAAEADTALTTEIAQEEAEMESLKSKKAKKGKLLKKEQER
LNFLIDNAAKRAEEQAAKEAEEQAAKEATDAAAAAAAAAAEAEAEAQAAADAEAAVQAAADAEAEVAAKEEEEMAVLKAK
KAKKVKLTKNETTRLMTLVGNSVKRAQEKSVKEAEEAAAAQAAKEAEETAAREADALAAREAEATAAREAEAVIAAEEEK
ELADLTAKKIKRGGNLIKKKDVERFNVLTQRAAERAERAAKQAEKIAAVEAQGELGEAAHGNAEVVVEAQPEPEPEQPLV
DIDAAFADPEPVTAPDAAIIAEEEAELASLDAKKTRKGKLGKKDTERYNILTENAAQRLAAKEAEEAAGAAAAEAEAEAA
KEAEEAAAAAEEAATAAAAAAAEAEAITASEAEAILIADEEAELATLAAKKAKRGKLVKKDADRFNILTENAAQRQAAKE
AEEAAAAAAAAEAEEQIAKEAEAAAAAESAAAIEAAEAEAAAVREAEDAAIAEEEAELAVLTTKKAKKGKLAKKDADRFA
ILSENAERRAREVAQIIEQPEDQTPEPETEVNEPSPEPAIDELSAEADDPDAIAAAEAEAAAIADEESELTALIAKKERK
GKLGKKDTDRFNLLTVNSTARAEKAAQEEAAAQATAEAEAAAQAEAEQAAAAEAAALEEAAAREAAEAELLIAEEEDEL
AALTAKKNRKGKLGKKDSDRFAILTENATQRAEKAAASEVMKEAVLEVEDLPAENPADTEADAEAAEAAAIEAEAAAIAA
TIAAEEEEELAALITKKDKKGKLGKKDSDRFAFLTENATQRARNAMHEEAAEEDQEAAIAESEDINDHPADIEDSLFENA
LEPPVVEEEAPPEEDDAAAAEAMALVAAEEQEIADLEAKKARKGKLGKRDMERYTLLIENAAKRAEEQATKEAELAAAAE
LVAIESAEAEAAAAEEEAVAREAAEIEAAAVIAQEEEELAALEAKKQRKGKLGRKDTDRFDYLLGNKVAREAQVAEERAA
KEAEEQALQEAEEAAAAAAAAATEAEEIAAREAAEAEAAAVADAEDEELAMLAAKKVKKGKLGRKDTERFEQLSSNVAKR
AEKQAAREVEAAAEEAPAVEELLGEEELEEPNPEPEETVEEAPEAPVPDIDDEAAAEAAAIAAEEEAELASLEAKKARKG
RLGNKDTQRFTFLTENISRRAEEQAAKDAAAAAQALAQTTPEDVAEEKDITGQEDAEAAAIEAEAAAIAATIAAEEEEEL
AALTLKKARKGKLGRKDTERFDLLMHNAAIRAEERAIKGAEPDGQAEELIPEEVDDIPEPEPEENPDAEEVAAQEAAEAE
ARAIAAEEEAELAALNKKKAKKGKLGRSDTERFNILVDNAAKRAEAQAAKEAEENLGDVPRAEEEEDDEFVDAEDGEEDE
LAEELEPEAEELAEPEPEEDETATAEAMSAEAAAQAAVIAEEEAELAALTKKRLKKGKLGRKDTERFQALTENSAKRAEE
AATRDTEDAAAEVEAELGEPEPEPEPEAAEPEPEDDGLKEAEQAVIAEEEAELAALMKKKAKKGKLGRKDTERFIVLSEN
ATRREQERAAVEAETEAVQEEPDIEGVEETGGEHGEEGGEEQEQEQEPSEGQDEEAAAREAEEAAIAREEEDELEALKAK
KARKGRLGRKDTERFAILEENAARRAEEHAAAEAATANPPEEDGEGEEEEEEEEEEEPEADDEDKADEEELAIQEAEEAA
AREAEEAAIAEEEDELEALQAKKSRKGRLGRKDTERLRVLEDNAAKRAEERAAKEAAAVDENLGVDDAEEEEEEEEEEEE
EEEEEEEEEGDEEDEEEEDIDNGEEGRGKDDADAEEAAAAAAREAEEAAAKEAAEAAAREVIAKELEELDSLQFKKARKG
RLGRKDTERLRVLEENAAQRAAELAAKEEAAAAAEDEEEDVVEFGNPPEEEKSEIEAEDDDEEKEAEAEDTADKESSDVE
NEAAVGEDEEKEPEVLPKDQVPEAPADDEIVEVIDLSPKKERKSRKSKSRRDAPPPPPVPDPPLTPPPEPKQSRRPKIHR
EGTSFGRWAATPHEERDEPQEKSSRHRRREEKTSSKGSSSDKVEKTPSRSRGTALFSKPPLTRSATMREKKDGISSKRRH
STNARGLVSPPPEDMLMGEDELSNRRKSRKPRSREDEDAMMSGAAPVPDRYERRRSHKPRSHEDDDLVMVDPDLAPDRRE
RRRSHKPRSREEEEVAVADTERRRRARRSRDEEPVMVEPDVPFDAPPRSSKKSSGFAGLFSGLRTPKTERPDPLRRRSTY
ATTDDEALRSAKMDGDAVLVDADREARRAARRAKRAAEGGPDPEEAARRARDEIRRERRRQREEEADPLRQDKEARRAER
RRQRDEDARRAQEERQVQEEQQRLQEEKEAQRAERRRLRREQEAAAAAEQAEDEEARRAAKRERRRRDTKRAARGAEEEE
GRQRRSQQSTDEYNQRRSHRREERPQAPAWPHSGTSSWVKEHSDAPPPPDLGDGGEANGGQTEDEMARREARRAHRSKYE
EEPTEEAEDRRRRRARRDDRERGGRDKERHRDRRSEGSDERHHSRRASTFMEATATPRTSWWKKIAG
```

2469 - 2488:	EEEEEEEEEEEEEEEEEEEE
2470 - 2489:	EEEEEEEEEEEEEEEEEEEE

A0A2H4SJ69 **A0A2H4SJ69_CORMI** (407 aa)
PAPA-1-like conserved region. *Cordyceps militaris (Caterpillar fungus) (Clavaria militaris)*

```
MVSRPKRSAATKATENISVQSKWTDNERTGDSPVPSRRSGRSTVFRDAPSSPESGSMPSRSRQSARAGRRSEQFDGGEIV
TGKRNRGTKKSYVVESSPDDDEDDMEDEVEVDLDDEDAEGEDEVDMDAEGEDLDADGDVDMDAAPPPRRNKVTTIRVSRS
AKPRNAARAAASRIVADDDDDDDDELSEPGSDLADETMGVREVEEDAEGEEIEVAGDGEEEEEEEEEEEEEEEEEEEEE
QEEEEDAEGEADVRELDSDEDGSRAGTPDLAKMTKRQRARFDEQPQEYMKLSDEVQAKKVFTAEELSMRRQEMARRRRNL
SEKRNEEVKMETINKLLKKQAPKTKKGARGNSPGADVRPAATLIRWVSSKGGSKIAVPEEIMGGPVGNVFGPAGKGSSGT
KMVEEVA
```

219 - 238:	EEEEEEEEEEEEEEEEEEEE

220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE

A0A2H4SS84 **A0A2H4SS84_CORMI** (363 aa)
HLH transcription factor. *Cordyceps militaris (Caterpillar fungus) (Clavaria militaris)*

```
MYSSTTQFGQIGWPPSCTVMPCPDNGPNPLPITLVDDRGTPFIAFVQDPYEAHGLYYEMSLNNQNFDANSCASQKYIEAP
SDVGQNPGFYPIPPHSLLKSDVSAVVGQLGNADGSPPSHLLHQTSLDFKEEMLRNRHINNNENTFMEWVYPPTKGSPARS
FSENTVQWGSDAMFDAETRTARRRVGVRQLTQFRLQLMPEEEEEEEEEEEEEEEEEEEEEQDGDAEDATSPGARSSQARS
PASSVRKGPSGRSRRNIPKKVYTDSPAASVARPLMSRREPKGQRKKLTIEQKRSNHIRHEKKRRGLIRDGFNDLTELVPE
LRGGTWSRSRILFKGVEFLTTLLEKNASLQAELDALKTGEQAK
```

200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE

A0A2H5SZW3 **A0A2H5SZW3_RHIID** (248 aa)
Uncharacterized protein. *Rhizophagus irregularis (strain DAOM 181602 / DAOM 197198 / MUCL 43194) (Arbuscular mycorrhizal fungus) (Glomus intraradices)*

```
METTKTADAGSKNWLKERAAISAAHRRQKTDPAAARLIEKADQLHKERTQKNLRETVDEDDEAVDEVPETTVKKNEAEDE
DLEDIDAIVSVPPPEEIVVKIAQKPAEEDTIASNHGKETSEDVYRSFAESVLEQGLTTKSELELSFDLKPEDIKIKEEEE
EEEEEEEEEEEEEEEEEEEEKGEEETQEDLNEADITEEKVQEKLKDADVEINHNEENKGDVKDQEDDKSEESTLTKEVDV
DTVPKNND
```

157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE

A0A2H6MWI2 **A0A2H6MWI2_MICLE** (216 aa)
RanGAP1_C domain-containing protein (Fragment). *Micrurus lemniscatus carvalhoi*

```
EEEEEEEEEEEEEEEEEEEEEEEEEEPLQVQERGQGEQEPLTPKKILEEYDSTPLSSPLPPVDVGTFLAFPSPEKLLRLGP
KCSTLIMQQTDTSDTEKVVTVFLKISSVFKDETVVKTAVCETTDALMREAFSSANFNSDAFITSLLIHMGLLKSEDKIRA
VPSLYGPLMTLNHMVQQDYFPKSLAPILLAFVTKPNRALDSCSFARHSLLQTLHQL
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE

A0A2H6NHQ2 **A0A2H6NHQ2_MICLE** (231 aa)
Uncharacterized protein (Fragment). *Micrurus lemniscatus carvalhoi*

```
GIGGGKILAGALKECHRKSTAQGKPLALKVFMAGRNRLENDGATALAEAFTVIGTLEDVHMPQNGINHPGITALAEAFAV
NPLLRVINLNDNTFTEKGAVAMAETLKKLRQVETINFGDCLVRSEGAVAIAEAVSEGLHKLKELNLAFCEIKIDAALIVV
GATEDKSELEKLDLNGNCFGEEGCEQLQDILEGFNMGEVLGSLSDDDGEDDEEEEEEEEEEEEEEEEEEE
```

212 - 231:	EEEEEEEEEEEEEEEEEEEE

A0A2H8TTU5 **A0A2H8TTU5_9HEMI** (367 aa)
Troponin T. *Melanaphis sacchari*

```
MLNYFYNLPIIFDFNQRQELKSSALDEQLKEYIQEWRKQRSKEEDDLKKLKEKQAKRKVMRAEEEKRMAERKKQEEERRQ
REVEEKKQKDIEEKRKRLEEAEKKRQAMMAALKEQTNKSKGPNFTISKKEGALSMTSAQLERNKTREQIEEEKKISLSFR
IKPLTIEGFSVQKLQFKATELWDQIIKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQ
VASKYERRVDTRSYDDKKKLFEGGLMETSKESMEKQWTEKSDQFGGRAKGRLPKWFGERPGKKKDDPDTPEEEELKKNEE
DEEPFGLDDEEAEEEVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

337 - 356:	EEEEEEEEEEEEEEEEEEEE
338 - 357:	EEEEEEEEEEEEEEEEEEEE
339 - 358:	EEEEEEEEEEEEEEEEEEEE
340 - 359:	EEEEEEEEEEEEEEEEEEEE

341 - 360:	EEEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEEE
344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE

A0A2I0A2H4 **A0A2I0A2H4_9ASPA** (439 aa)
Uncharacterized protein. *Apostasia shenzhenica*

```
MPLPFSVALQSDYVASQPISFWRQQDTAMHKLISVYSENAQSVGFGGKLASRDNDFHQNMIPDYCDRDIQGSDGLYADLK
QLSEPSFMRTKRARHEYDNLEVSTSQLISNPNAHDLESSKQQNNKRISEKTLQHPTSENTRKCLVDAINVNSSASFTDAL
SSSEFSTPNFCGKVASLIDLEAPLSTQEEEEEEEEEEEEEEEEEEEEEEEEEDITEIEEESKELSKEQQTDSSNEAPI
REAAENLVALSFDTLRWFAELASSIEIGIKEDDAQSLDLFEYMTLQLKEINETELLGQQKEKQSYEESGNAQAMPTKVRR
GQLGRRQPRDFQKEILPGLASLSRHEVTEDLHSFVDFMRVSSRPWQTGSSRRCSSRKEVTCLERASRRPRSLAITVSEIH
TSSLAKEQVSTPGILGWGRTTRRCRRQRVLPGNVSVSLV
```

188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE
190 - 209:	EEEEEEEEEEEEEEEEEEEE
191 - 210:	EEEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE
194 - 213:	EEEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEEE

A0A2I0AY05 **A0A2I0AY05_9ASPA** (825 aa)
Protein Mut11. *Apostasia shenzhenica*

```
MSNLAEGEEEEEEEEEEEEEEEEEEEEEEEEEEQEFYYESLDRILSSSCSSTSASDDEGDYGYQLHDRSRFGCTPPSVGSLD
VWLSEPESVEERRRRLLQQMGLAGDPFLARRKHEGWKSEAEMGRSVSCDGLWPRPNPPSVNSAAGAMGRSRSEGSVEPGL
VHRQHPSAAGKPPLVGRSRTSVGGDAEVLDGDVASCLGGRGRGGDGDDEQKCTIKDLDNGKEFVVKEFREDGMWNKLREV
GTGRHITMEEFEMSVGCSPIVQELMRRQSVEEGYNGSAGDQSKSSTDSSGGGGSKRRSSWFWNFKSVMAGGNQRERRSSD
EKDTSSDKGGRRSSSATDDSQDTPKSVHRVPERMKVRQYGKSHKELTGLFLNQEIQAHNGSIWTIKFSLDGRYMASAGED
RVIHVWQVLENDRKPEFLVDRGGEEINNGNLLAVTICNGFPAEQMLALVPIEGNQWENRRRAKGGRRSVSSDHLMVPEQV
FALSERPVCSFRGHLCDVLDLSWSKAQYLLSSSMDKTVRLWHLSSNCCLKIFSHNDFVTCIQFNPIDDKYFISGSLDAKV
RLWSIPDRQVVDWSDLHEMITAVCYTPDGQGAFVGSHKGNCYLYDTSDNKLLQKSKIDLQNKKKKSSQKKITGFQFASGS
SSEVLITSADSRIRVVDGNNLIHKFKGFRNTSSQISACLTANNKYVICASEDSHIYVWRYDANSRQSRSKSTVAITQSHE
HFQCLDVTVAVPWPNFSFMSGGASTPNENNTDLHLEANHFGDRVSATWPEEKLLSTSGRHSRQNSSDTGTDGFSAQNRAW
GMAIVAASRGGEIRAYQNFGFPIRA
```

8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE

A0A2I0BV47 **A0A2I0BV47_PLAFO** (3135 aa)
6-cysteine protein. *Plasmodium falciparum (isolate NF54)*

```
MKKIITLKNLFLIILVYIFSEKKDLRCNVIKGNNIKDDEDKRFHLFYYSHNLFKTPETKEKKNKKECFYKNGGIYNLSKE
IRMRKDTSVKIKQRTCPFHKEGSSFEMGSKNITCFYPIVGKKERKTLDTIIIKKNVTNDHVVSSDMHSNVQEKNMILIRN
IDKENKNDIQNVEEKIQRDTYENKDYESDDTLIEWFDDNTNEENFLLTFLKRCLMKIFSSPKRKKTVVQKKHKSNFFINS
SLKYIYMYLTPSDSFNLVRRNRNLDEEDMSPRDNFVIDDEEEEEEEEEEEEEEEEEEEEEEEEYDDYVYEESGDETEEQ
LQEEHQEEVGAESSEESFNDEDEDSVEARDGDMIRVDEYYEDQDGDTYDSTIKNEDVDEEVGEEVGEEVGEEVGEEVGEE
VGEEVGEEVGEEVGEEEGEEVGEGVGEEVGEEEGEEVGEEEGEYVDEKERQGEIYPFGDEEEKDEGGESFTYEKSEVDKT
DLFKFIEGGEGDDVYKVDGSKVLLDDDTISRVSKKHTARDGEYGEYGEAVEDGENVIKIIRSVLQSGALPSVGVDELDKI
DLSYETTESGDTAVSEDSYDKYASNNTNKEYVCDFTDQLKPTESGPKVKKCEVKVNEPLIKVKIICPLKGSVEKLYDNIE
YVPKKSPYYVLTKEETKLKEKLLSKLIYGLLISPTVNEKENNFKEGVIEFTLPPVVHKATVFYFICDNSKTEDDNKKGNR
GIVEVYVEPYGNKINGCAFLDEDEEEEKYGNQIEEDEHNEKIKMKTFFTQNIYKKNNIYPCYMKLYSGDIGGILFPKNIK
STTCFEEMIPYNKEIKWNKENKSLGNLVNNSVVYNKEMNAKYFNVQYVHIPTSYKDTLNLFCSIILKEEESNLISTSYLV
YVSINEELNFSLFDFYESFVPIKKTIQVAQKNVNNKEHDYTCDFTDKLDKTVPSTANGKKLFICRKHLKEFDTFTLKCNV
NKTQYPNIEIFPKTLKDKKEVLKLDLDIQYQMFSKFFKFNTQNAKYLNLYPYYLIFPFNHIGKKELKNNPTYKNHKDVKY
FEQSSVLSPLSSADSLGKLLNFLDTQETVCLTEKIRYLNLSINELGSDNNTFSVTFQVPPYIDIKEPFYFMFGCNNNKGE
GNIGIVELLISKQEEKIKGCNFHESKLDYFNENISSDTHECTLHAYENDIIGFNCLETTHPNEVEVEVEDAEIYLQPENC
FNNVYKGLNSVDITTILKNAQTYNINNKKTPTFLKIPPYNLLEDVEISCQCTIKQVVKKIKVIITKNDTVLLKREVQSES
TLDDKIYKCEHENFINPRVNKTFDENVEYTCNIKIENFFNYIQIFCPAKDLGIYKNIQMYYDIVKPTRVPQFKKFNNEEL
HKLIPNSEMLHKTKEMLILYNEEKVDLLHFYVFLPIYIKDIYEFNIVCDNSKTMWKNQLGGKVIYHITVSKREQKVKGCS
FDNEHAHMFSYNKTNVKNCIIDAKPKDLIGFVCPSGTLKLTNCFKDAIVHTNLTNINGILYLKNNLANFTYKHQFNYMEI
PALMDNDISFKCICVDLKKKKYNVKSPLGPKVLRALYKKLNIKFDNYVTGTDQNKYLMTYMDLHLSHKRNYLKELFHDLG
KKKPADTDANPESIIESLSINESNESGPFPTGDVDAEHLILEGYDTWESLYDEQLEEVIYNDIESLELKDIEQYVLQVNL
```

```
KAPKLMMSAQIHNNRHVCDFSKNNLIVPESLKKKEELGGNPVNIHCYALLKPLDTLYVKCPTSKDNYEAAKVNISENDNE
YELQVISLIEKRFHNFETLESKKPGNGDVVVHNGVVDTGPVLDNSTFEKYFKNIKIKPDKFFEKVINEYDDTEEEKDLES
ILPGAIVSPMKVLKKKDPFTSYAAFVVPPIVPKDLHFKVECNNTEYKDENQYISGYNGIIHIDISNSNRKINGCDFSTNN
SSILTSSVKLVNGETKNCEINININNNEVFGIICDNETNLDPEKCFHEIYSKDNKTVKKFREVIPNIDIFSLHNSNKKKVAY
AKVPLDYINKLLFSCSCKTSHTNTIGTMKVTLNKDEKEEEDFKTAQGIKHNNVHLCNFFDNPELTFDNNKIVLCKIDAEL
FSEVIIQLPIFGTKNVEEGVQNEEYKKFSLKPSLVFDDNNNDIKVIGKEKNEVSISLALKGVYGNRIFTFDKNGKKGEGI
SFFIPPIKQDTDLKFIINETIDNSNIKQRGLIYIFVRKNVSENSFKLCDFTTGSTSLMELNSQVKEKKCTVKIKKGDIFG
LKCPKGFAIFPQACFSNVLLEYYKSDYEDSEHINYYIHKDKKYNLKPKDVIELMDENFRELQNIQQYTGISNITDVLHFK
NFNLGNLPLNFKNHYSTAYAKVPDTFNSIINFSCNCYNPEKHVYGTMQVESDNRNFDNIKKNENVIKNFLLPNIEKYALL
LDDEERQKKIKQQQEEEQQEQILKDQDDRLSRHDDYNKNHTYILYDSNEHICDYEKNESLISTLPNDTKKIQKSICKINA
KALDVVTIKCPHTKNFTPKDYFPNSSLITNDKKIVITFDKKNFVTYIDPTKKTFSLKDIYIQSFYGVSLDHLNQIKKIHE
EWDDVHLFYPPHNVLHNVVLNNHIVNLSSALEGVLFMKSKVTGDETATKKNTTLPTDGVSSILIPPYVKEDITFHLFCGK
STTKKPNKKNTSLALIHIHISSNRNIIHGCDFLYLENQTNDAISNNNNNSYSIFTHNKNTENNLICDISLIPKTVIGIKC
PNKKLNPQTCFDEVYYVKQEDVPSKTITADKYNTFSKDKIGNILKNAISINNPDEKDNTYTYLILPEKFEEELIDTKKVL
ACTCDNKYIIHMKIEKSTMDKIKIDEKKTIGKDICKYDVTTKVATCEIIDTIDSSVLKEHHTVHYSITLSRWDKLIIKYP
TNEKTHFENFFVNPFNLKDKVLYNYNKPINIEHILPGAITTDIYDTRTKIKQYILRIPPYVHKDIHFSLEFNNSLSLTKQ
NQNIIYGNVAKIFIHINQGYKEIHGCDFTGKYSHLFTYSKKPLPNDDDICNVTIGNNTFSGFACLSHFELKPNNCFSSVY
DYNEANKVKKLFDLSTKVELDHIKQNTSGYTLSYIIFNKESTKLKFSCTCSSNYSNYTIRITFDPNYIIPEPQSRAIIKY
VDLQDKNFAKYLRKL
```

280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE

A0A2I0BW39 **A0A2I0BW39_PLAFO** (385 aa)
Casein kinase II subunit beta (CK II beta). *Plasmodium falciparum (isolate NF54)*

```
MEFVSNDESADDIIQDESNEGEVELTDADFYDLTVINDKIDEEIIEDDEEEADNDDQENDNVQEVYNIDDEDNDIHNDKL
LLDQQRDNDVNEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEDDDDDDDDDDDDDDDDDDDYDDDDEYDEDDFNEATVS
WIEWFCQLKQNLFLVEVDEDFIRDEFNLIGLQTKVPHFKKLLKIILDEDDDDDDDDDDDYDDEDDEINRDSEEMYKNKDM
HEQNAACLYGLIHSRFILTSKGLALMREKYKSGIYGTCPSIYCENAKLLPTAISEIPKFLSPLLYCPRCCETYYPSKNSL
LNQLDGCYFGTSFASFFALSFNIASDKKKVYYTPQICGFTINRNIRETLYMDVNKDNTESSEECQ
```

92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE

A0A2I0BXY4 **A0A2I0BXY4_PLAFO** (673 aa)
Glutamic acid-rich protein. *Plasmodium falciparum (isolate NF54)*

```
MNVLFLSYNICILFFVVCTLNFSTKCFSNGLLKNQNILNKSFDSITGRLLNETELEKNKDDNSKSETLLKEEKDEKDDVP
TTSNDNLKNAHNNNEISSSTDPTNIINVNDKDNENSVDKKKDKKEKKHKKDKKEKKEKKDKKEKKDKKEKKHKKEKKHKK
DKKKEENSEVMSLYKTGQHKPKNATEHGEENLYEEMVSEINNNAQGGLLLSSPYQYREQGGCGIISSVHETSNDTKDNDK
ENISEDKKEDHQQEEMLKTLDKKERKQKEKEMKEQEKIEKKKKKQEEKEKKKQEKERKKQEKKERKQKEKEMKKQKKIEK
ERKKKEEKEKKKKKHDKENEETMQQPDQTSEETNNEIMVPLPSPLTDVTTPEEHKEGEHKEEEHKEGEHKEGEHKEEEHK
EEEHKKEEHKSKEHKSKGKKDKGKKDKGKHKKAKKEKVKKHVVKNVIEDEDKDGVEIINLEDKEACEEQHITVESRPLSQ
PQCKLIDEPEQLTLMDKSKVEEKNLSIQEQLIGTIGRVNVVPRRDNHKKKMAKIEEAELQKQKHVDKEEDKKEESKEVEE
ESKEVQEDEEEVEEDEEEEEEEEEEEEEEEEEEEEEEDEVEEDEDDAEEDEDDAEEDEDDAEEDDDDAEEDDDDAEEDDD
EDEDEDEEEEEDEEEEEESEKKIKRNLRKNAKI
```

576 - 595:	EEEEEEEEEEEEEEEEEEEE
577 - 596:	EEEEEEEEEEEEEEEEEEEE
578 - 597:	EEEEEEEEEEEEEEEEEEEE

A0A2I0BYA7 **A0A2I0BYA7_PLAFO** (1988 aa)
Uncharacterized protein. *Plasmodium falciparum (isolate NF54)*

```
MNVCKMKVQQKKNLKDCNLKSKNTILTSFEKKKNEKDENNLLKFSKLIDNKNKVVNSKLLKNDNYKFNERKESLTRCSTN
ESLKLKNIKTLTKDFDYNNNNNNNNINNNNDYNNNNNNNNNNNNNNNNNNNNNNNKNNNNNNNGHSKLVFKKNDKDIESKV
REEDGKKSEKKNNDLINNKNEFKVNNKLILKSKEFKSNNNNNNNICKLNNIDDKNKKQQMDTYSPKENEEDNSNNMKKSS
SLKNIKKNQINEMEIISNSVEENHDTHSKGDKENNGVSTKNVKRMNTMSKEINHKNNNLKKHVSKSNSLELKKGKKGEKS
KDKLSNNVSGKKGMNKEKEVVQSSSVRRNSSRYSIDYGRRDSSRRGSVKQEKGKERRGSKNVSKKVSNSKYTRKKSKRIK
EESDESDDDDEEEEEEDDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVEEDNDNSDNNDESDE
```

VYTNRSRRSTRCSIVKRKSSLCIGKKNSKIIKKSTSKTKNNKKKKGSVIKLVKKKEKLSKKGILKKTNKKTKGKLRKNSK
LYHRKKNIKNEKDGIDEEDIDEEDIEEEEEPSYFDEYNLSYEERKKDLEEKEKKKEIKEKYIKQIKLPKYADDESIIFIN
NPNYVMVLLFLTVYKDVLKMNWNFKDIEEMFQNKETTEFGRNFLLKLFFFLGRYFNSKSIFMYKYISRIFEDKEESLSRV
VNFHELFPVLETKKEIKNSGVGSKRKKDKRGKKMKIHQKEDELLYDEEVIGNEDVHIFEEEEDNEHSNDDEDEEEEDNEH
SNDDEDEEEEDNEHSNDDEEKEDVHYNDEEEKKSDLNNDSTKNTVIKEEKDGLHISEGSHNLVNIVNDSMKREESCKNGH
IGDNERSGDINTNDDKNNADNNDDVDGEKIVDSKNNIENKLDNTVEGKHDINSTEGIIKSENVDDEKGLLTNKLFLEWDD
LSVISKLRIIRMLLNLVLCESNNLKKMLGDEKLNYNNGYLGKINNEKYWFIFNDTINIEYKLYLEREEEGSFIFICDDDD
MLYTIGYNFLRNSDTKFMGEALIERYNKVCRERRNRSRMLKQQKKLLCADINLNDPLLGTKKRQHKQVEYFNFDNNEKMR
RKKSDMNNNNPYSVPPTKSYQKNDRSFRLAARNAQKGSVDDLEAWKLNEGSLGIENQGATSGNYNIANDGTNMTETNNIN
DNHNNDNNNNNDGVVNADGNNIYGPNNNNVIGSDGNVNNANNTTTNNNNNNNNNNLGTVKIPLKRGRKKKSEKKKRGRKK
KILSVDGIGEIANNLSALNVDENRRKSMPNIGRGRRGTYTKRNTKPSVSIKYGTRSHSINKYKNDVMSFNEYSLNPGLSM
DDFYKNMVMDPKFFHANMNMNNYMNGGFNMPNNNNSMMNMRNGSKMGNMNNIGGYNFPYMCTPPPMYNQYYMYNGNNMYL
PNGGPNNNMNMSNANNGASVVMGGNVVSNQNTVKDVKAENMHMAKNSIMENRNSIIVNNMNNMNNINMNSMPHKNSFMGN
DGINNMNSMNNNNNNNNNVNNNNNNVSNNNNNNVSNNNNNNVNFMDNMGNNNNNNNNNNPMNKYNNYMMNRNVLNNMGG
TNPLYNNMYNMKFPYMNNDMMNYNYNINSFQNMNYDKMNKSMFKRYPNFMGGYPYNNMNPYNNFNAFNMNYQQNDQMNQL
PNMQGGYKSKLMNDNLSNYQSFNNNNVKQNHHDNNNNDNNNNKNNSEGGNKNMDDSNKNNDINKNDILDSTKLTEQPVGG
VVPNNDCITRGEDNHRIDLKGDIAEALVGNNNEKMNSSDHNLNSLKNLPNINNTYNMDHMSHMRNSVSASSIGMINPGHM
NSSHSGSIMNKDKFRDLQLNSNNNNNNNNNNNYVKVNPFDHPMKNMPNLMDDKYPKDNNNMMMMMMNSVYNMMGSDHFH
MNNSHMMDPMGSPKMNDNMYNHNNMNFENTNTNHNNHNNHNNHNNLNNLNNLNNHNNHNNRIQDKLPE

419 - 438:	EEEEEEEEEEEEEEEEEEEE
420 - 439:	EEEEEEEEEEEEEEEEEEEE
421 - 440:	EEEEEEEEEEEEEEEEEEEE
422 - 441:	EEEEEEEEEEEEEEEEEEEE
423 - 442:	EEEEEEEEEEEEEEEEEEEE
424 - 443:	EEEEEEEEEEEEEEEEEEEE
425 - 444:	EEEEEEEEEEEEEEEEEEEE
426 - 445:	EEEEEEEEEEEEEEEEEEEE
427 - 446:	EEEEEEEEEEEEEEEEEEEE
428 - 447:	EEEEEEEEEEEEEEEEEEEE
429 - 448:	EEEEEEEEEEEEEEEEEEEE
430 - 449:	EEEEEEEEEEEEEEEEEEEE
431 - 450:	EEEEEEEEEEEEEEEEEEEE
432 - 451:	EEEEEEEEEEEEEEEEEEEE
433 - 452:	EEEEEEEEEEEEEEEEEEEE
434 - 453:	EEEEEEEEEEEEEEEEEEEE
435 - 454:	EEEEEEEEEEEEEEEEEEEE
436 - 455:	EEEEEEEEEEEEEEEEEEEE
437 - 456:	EEEEEEEEEEEEEEEEEEEE
438 - 457:	EEEEEEEEEEEEEEEEEEEE
439 - 458:	EEEEEEEEEEEEEEEEEEEE
440 - 459:	EEEEEEEEEEEEEEEEEEEE
441 - 460:	EEEEEEEEEEEEEEEEEEEE
442 - 461:	EEEEEEEEEEEEEEEEEEEE
443 - 462:	EEEEEEEEEEEEEEEEEEEE
444 - 463:	EEEEEEEEEEEEEEEEEEEE
445 - 464:	EEEEEEEEEEEEEEEEEEEE

A0A2I0C0V6 **A0A2I0C0V6_PLAFO** (773 aa)
Serpentine receptor. *Plasmodium falciparum (isolate NF54)*

MIKIIIGVIGYYILYSSYHIYENIKSPIFNDGNVIKNNEGDKNEQLVIPKEGKKRNSINEEEEEYINKPFKNVLKKDDII
DYHLYFSCEEDIDINKHMQDKYLEKDERFISVYKILNGKYSWNNNVDLLDEKRKKNSFFFLFEKVHPSFDISIPKELIDQ
RKDIYLHILTYVNKELYRYGSRTVVITKRKEKTTTRGKKKFLWKSLIDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEKKYQHGNYEKGGSYKVHKNISNNKPNNKNPNDKRDIKHNNNNNNNKMKKDNFIKSNQNSLNIHKKKKKRKHKD
FLFYIPKKIRFGPVIEYNDFHISKLGFFSNMHVDKDTNTYLLPIYINNDLTPDDEYRMIKMKNSDDMMKKKLKKKRSSEK
NDPYYKENVRNDNNNNNNNNNIKNNYLEIYDLSKRTYEMRNERNKKIYEKNSSINNNVHKLEHELMDYIINIEYVPINYN
YYNLLNMLKFNVSYVKKKYNFISFDMDSITTFLCCHITCSMIIYILCIIYIIMEITYLLFDIKMWKRWNNLYTFTYNNDI
VMNITLLFFILLYLRNIDYGRVIMIYYIMKMMVLIFKIIYNYDICILNDYPYICMNKKSLKEMNKEMIMDEEFEKKIKKK
VNIFMIFSIILIFIYNYFYTKYDSYYSYVIHTLGFSSYLYKFILMLPQIITNIYTRTVQRMSFPFFLFLLVNVLINDLFI
IFLRMPKVHKYYLFADDFILFLFIIQYCIYKKENKIFGAREKLVLLKNAKKNK

209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE

214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEEE
225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE

A0A2I0I7J3 **A0A2I0I7J3_PUNGR** (95 aa)
Uncharacterized protein. *Punica granatum (Pomegranate)*

```
MEGGCANVGQLSRRDHLVTGRVLNKKKKKKKKKKKKKKKKKKKKQCDEEEEEEEEEEEEEEEEEEEEGKGLLALHNAQPK
QKKQKVRSCDQQSMS
```

48 - 67:	EEEEEEEEEEEEEEEEEEEE

A0A2I0K0F6 **A0A2I0K0F6_PUNGR** (505 aa)
Uncharacterized protein (Fragment). *Punica granatum (Pomegranate)*

```
MQMAPLPSENGIDGDDEREDEEEEEEEEEEEEEEEEEEEEEEEEEPRLKYQRMGGSIPSLLSNDAASCIAVAERMIALGTH
DGTVHILDFLGNQVKEFAAHSATVNDLSFDIEGEYIGSCSDDGSVVINGLFIEERMKFDYHRPMKAIALDPEYSRKASRR
FVTGGLAGHLDFNSKKWLGYRDQVLHSGEGPIHTVKWRTSLIAWANDAGVKVYDTANDQRITFIERPRGSPRPELLLPHL
VWQDDTLLVIGWGTSVKIASIRTNTQNGANGTYSRIPVSSMNQVDIVASFQTSYYISGIAPFGDSLVVLAYIPGEEDGEK
DFSSSLPSRQGNAQRPEVRVVTWNNDELATDALPVLGFEHYKAKDYSLAHAPFSGSSYAGGQWAAGDEPLYYIVSPKDVV
IAKPRDAEDHISWLLQHGWHEKALAAVEAGQGRSELLDEVGSRYLDHLIVERKYAEAASLCPKLLRGSASAWERWVFHFA
HLRQLPVLVPYIPTENPRLRDTAYE
```

21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE

A0A2I0M194 **A0A2I0M194_COLLI** (1999 aa)
Cardiomyopathy associated 5. *Columba livia (Rock dove)*

```
MEGYRGAECDRASETSSFVEDEEEEEEEEEEEEEEEEEEEEEEEEAVDPEEAEELTNSLKDIIQSEDVKPKLQYIMTNPSFS
MVTVQSEDSGITWETSSSRCSTPWTSETSTTSDLYSMESSPVGSPPGKVIFIMDEGKIVRKRKRKSSNRVPMATRLKGGQ
GNKKRDSSGMQRQEPRTVLGDVQASMLNVEQVEAQNTDEEMLDDKEDLENIAEEPVKRAPIPSIFRESRLRKVGPILGGP
VQARIQLFNSIFGGTGPDPETLEKIRVRRSSSVSGDSEQLLETSVKEKLQKFSSLSERTDLKAFQRLSRDLTTPSERKKE
IREKLAAQSYQIYTSPTTPLKKQLTTKDVSIKPTKMKGKTSRFSSFGAKTTPQHEERKDSLLETPDQVLGQSRKSCLPEE
ARKHQSYSPAEKTSLTEESASILLESDDNPEKQVPFPSAETANQKSDQSLLTASGLLDEPKEQEIQPNSAPQSVSVDSEL
GRQSTQPILRRASMSEHPEREAQKSAVQSFLPGAPSAKHKYSTLSETRQEDIIPQSSETAQTESEHVLLPHSVGETEKQE
TECHSSTTVLSETEPPGLLSSVKKEEGEKTSPQETKNIHLEKQTESERDFSSSLQEAEEQGIKLNTPIPEKIDSKYFSIS
YPDRTKPQETQKTSPVGKAVDLGHIGKNKQTESAQMEMEHPGFSYSRKEVGQSERTKMETEHPDFSFFKKETEELECAQM
EMERPDFSFSRGEMEEPDSAQLETEHPDFSYSRDEVEESETAKLETECSEMLFSTKETGESESAQLETEHSDFSYSRDEV
EESETAKLETECSKMLFSTKETEESESSQLEIEHPDFSSKEETEESESIQLEMEHPDFSFSREEVEESESAQLETEHPDF
SYSREEMAESESAQLEMEHPDFSFFREETEKQKSAPFQLEQPESYSPEDAEQKEAAQPALVPTDLSCLTEEAETESTAEL
QLVHPDIPDSTIRAETQQIGYLETEHLPGPTSETKQQEFTQADVDNSLTSYFCDKREEPQPVQQESQPGGKLYYRAEGVQ
GETAQLQSEHPVLSQHETSQLRAEQPETPYSTGKTKKQEILQPKLEQEDLPCSQGETAQEAVQRDLEGPEPSRFISEEEQ
HENAQLASENMDFSFTTGEAVQEGVEAGSLGSSYLTDTAKPWEMAQMEQEQTLPSCSTAGGQQQETSLLDVAQPDISYSF
GKMEQQDTLQRELEQQETAQHKAMQMEMEYSDLSESWRKEEPQVTDQINLAEQEIAQPASVHPSLSYSFSEQMQEEMQTE
PAYPEETFYVSTDMQEKMTQHKSEILHPELEQTFLSSSSRKEAPLETEISSEYPDLSYSFQEAEQQKKLKHPTLPFRSKK
QETAPLVMERPDFSHDSEEKPGDIMEQELGHPEFSYSMGETQGQSEHPDSPGTLGETAQVKSMEVESKYLNLSCSGDQKN
QQEGSQLDSKYTDLSFSFGKAKEQSTQEFESKHQELPKMARKRASPATTQMESKHPDFMYSPGKANEPEVALWETKHPDL
SHSTDESTKQEVVLLDQKHRKISVGRENQQQTAKQQLEQEKLSHSPGKTEQLKHVQEDLEQPGLSFSVNRLDDKTAPPEA
QHADVIYPLDITEGLQRAEETEQAYLFGKAEHKTVQLEAEIPHVVDAVGTAGEETAEPGQGHPDLSYSVSKAGGLQTAQV
KHKHPGLMCSRDKVQETTQLELEQPDALPVHAKTPSEPELRQVDLASPADKVGQRGMEHTASGHLDERQSVSRAEHPQAT
KEKLGAPEVSTHSRKEEQREMEKTEPKHHDISYFTDKTQTQEYTQLVLGKTAPSSWPGETERAQTAQEEQPGFLHSFIKA
AQGEKGQPELGHSQLSYSVSEAEQETALVKSNRPALSAGRLEHYEIVQPEAEVMDLSCSIGETQKPQMAEADLEYPDLLH
STGTVQGQVKIQPAQEQPADFSSSLGTEEQXXXXXXXTLSCSALGGKQKNCKISRQNQNMWICHSLLAQQNLIKQHSQS
```

22 - 41:	EEEEEEEEEEEEEEEEEEEE

23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE

A0A2I0MGY3 **A0A2I0MGY3_COLLI** (263 aa)
Bone sialoprotein 2 (Bone sialoprotein II) (Cell-binding sialoprotein) (Integrin-binding sialoprotein). *Columba livia (Rock dove)*

```
MRTALVFVCLVGMACAFSVKSWLRRAKSDDSEENAVFKNRHRYYLYRYAYLHPPQRWYQNSDSSEEEGDGSEEEDAGGKG
CQGPQNGGRNGAVGKGGDSENEDSDENEEEEEEEEEVAENENSINGTSTNTTKGADGPHNNGTAVAEEEEEEEEEEEEEE
EEEEEEEETEATTVASTTVEEGLSQATTVGDQAPTDATTAGEQWEYEVTAGVHGRGDEGATDGSYGEQDEYARGDSYRAY
EDEYGYYKGHGYDMYGQDYYYNQ
```

147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE

A0A2I0RRH2 **A0A2I0RRH2_9PEZI** (516 aa)
Uncharacterized protein. *Cercospora zeina*

```
MPPADVNLKDVLSRLVGGDLHKPHPDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDGGAPISLLDSRGSTASTL
SPSLAASVSGDTFSDASIQERAAARPGLVYIESVVSSEAAESRKPPQHALLGAPSARLRVPSDVPACLDVKFSPGLRPPQ
YGLVVRNPGVDAGGGFINVTFVNCRFDPHLPTIFDKCCISNTTFKNCDFRHAALEGVVMSGNTFMACTFSCAWRNRKLAV
DFPCHGETFIDQCFNDDEPDEIVALNRARKEAEDAIIVGPPPSDRHSSRWGNIKGFASAANDNENYDFMEPIVMSTEPYQ
IPLGLGKSLTFDDTPVAGLFITDGYGCKFENVHFIRCDFQNTAFDNCHLVNVVFKNCHFRDASFKEVAIKDRTYDNSWFD
GCAWQWRVLQFCKAPIEDETFRQGGLDGTHFPEIMRQHGTAQVKKATFRQRQAIIQRSPTKSQSKPKRRDFSVKDNMEIK
REGLGAGEMLRETIEPGAKREGRKDIGTIFVTPSFD
```

27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE

A0A2I0S338 **A0A2I0S338_9PEZI** (673 aa)
Uncharacterized protein. *Cercospora zeina*

```
MARKLQQVLAVWCLLFLSTFAFPWNISRFHIARQDDPDDITRGGLGPPPGPPPPGPPLTRTVTLRQTTTVGRTTITVVTT
SVRTSTRTFTETSTVARLSAVTFTEPASPPRTITRNRTLPGQTITEQGEVTTFYDTATVTRVATITVDGEPSTIYETLPA
ETSTVTEDGELSTTTIVEIAPVQTVTIDSGEEASTVTFTEPPTTQTVTIPDAAATLTATVYVTLDPEVSTTTEAGSTVTV
TETPDALPASTQTITQTVQTTMTEQLPATETVPVDSEPTPTSTEVPPEATTTASPEIEDGEEVLTSSTEDSAEPQTTLPE
DASVTVAPEVTTTDEAAEATITSSEDLVTATTAAEAGPILTEDVQSDLPTEAPTPIEETVLPAGTTVPVPEETAEVPEVP
SIPNPEEQTDLPTETPTAEEGPEETAAPTIPDAPEPTEEIAEPIVVGPEETTVPSTPQPTEESSVPVEESTPADEINQPT
EPTPEEATGNPADPDTTRPISTPTPTDEPEDPIFSILPFPEDIEPQPTAELEDPIFSILPFPNDSTDDVPSEEPSIPSAD
GEEEEITTPATTPVGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
GVEAEAGVGGGVEREGIQLKKRFTGLFGGILAA
```

576 - 595:	EEEEEEEEEEEEEEEEEEEE
577 - 596:	EEEEEEEEEEEEEEEEEEEE
578 - 597:	EEEEEEEEEEEEEEEEEEEE
579 - 598:	EEEEEEEEEEEEEEEEEEEE
580 - 599:	EEEEEEEEEEEEEEEEEEEE
581 - 600:	EEEEEEEEEEEEEEEEEEEE

A0A2I0U269 **A0A2I0U269_LIMLA** (88 aa)

Uncharacterized protein. *Limosa lapponica baueri*

```
MLSLETAGHSEVGEGIYYAAQEKKKKKKKKKKKKKKKKKKKXXXXREEEEEEEEEEEEEEEEEEEEEEEEERRTEPFSDCLL
LASVPPGT
```

47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE

A0A2I1C7U3 **A0A2I1C7U3_ASPN1** (758 aa)
Noc2-domain-containing protein. *Aspergillus novofumigatus (strain IBT 16806)*

```
MAGSQKKSTKKFEKKHLKDNGDAEEESPEERKKQDAFAEMNVDDFFAGGFEIADADTDKAKKARRKDVTPKIGKRKRSEE
QKEEEEEEEEASSAALSEGEEDGGVFDDDAESQASSAPDDFEAHKDQLQSLKEKDPEFYKYLKENDSELLDFGEHGDLTE
VLELSEDEEEEGPAKKKKKKKAAKDEDEEAADNTLTIAMVKKWQKLMEEQNSIRAMRQAVLAFRCAAYINEAETQEQKYS
ISDPDVYHQVLVTALGTVPKVLAHHLPVKEAASGKVRVSLDSKKFKTLTPLIKSHTSSLHQLLVNLSDASTLKLTLSSIE
PMLPYLLQFRKLLKVLIKTIVGIWADVSTTEATRITGFLLLRKLMVIGDSGLKETVLKASYEGVVKGSRNTTVHTLSGVN
LMKNSAAELWGIDQNISYTTGFSFIRQLAMHLRSSITNTSKESYKTIYNWQYTHSLDFWSRVLSQHCDGLAEAKAGKQSA
LRPLIYPVVQITLGAMRLIPTATYFPLRFQLTRALLRLSRATGTYVPLAPALLEVLNAAEMRKPPKSSTLKQLDFSTAIR
APKSYLRTRIYQDGVGEQVAELLSEFFVLWTKHIAFPELSVPIVVALKRWLKQVGSRTSGNKNAKVNQAILLLVQKVEAN
VRWIEEKRLNVTYTPRNRAEVESFLKDVDWESTPLGAFVKTQRKLREEKAAILEQGRREEEKRRAAEKKADEDEMMEDAP
SDDGSEESSGEEEEEEEEEEEEEEEEEEEEEEEEFEEE
```

731 - 750:	EEEEEEEEEEEEEEEEEEEE
732 - 751:	EEEEEEEEEEEEEEEEEEEE
733 - 752:	EEEEEEEEEEEEEEEEEEEE
734 - 753:	EEEEEEEEEEEEEEEEEEEE
735 - 754:	EEEEEEEEEEEEEEEEEEEE

A0A2I1DCH3 **A0A2I1DCH3_9EURO** (326 aa)
Uncharacterized protein. *Aspergillus campestris IBT 28561*

```
MPFMSTSSSIMSTTSTMTTQNLLLIISHKDGIFIPENLPGLPISSTSAIINNGMTGLISVDFLIALTDILRDEAFDGYSF
QTAWIDPEGYYHVILTRDDTPEERPTTPFTSFSSSSTASSSSSSTTPSIIINSDDTNHTEQPTEWYTGEESHFQNFEEEE
EEEEEEEEEEEEEEEEEEEEQVNGLSSTLVWDPTTNHTTGTNPSARWYTYALDGTALDADTESDLDFDSASEGSMGSLPA
LVSPILESASEGSIDSLPALVPALSDFASEGSIDSRPVLIPSHLHGWEVVNYDEDKLLARLEQLSVSLRPPLVDKGRLVP
LADLFR
```

157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE

A0A2I2GP99 **A0A2I2GP99_9EURO** (1503 aa)
Dipeptidyl-peptidase IV (EC 3.4.14.5). *Aspergillus steynii IBT 23096*

```
MANNCQSAALLLLLGLTQAIEVPRKPYAPTGGGKKRLTFNETVVSRAIAPSSISVEWIATAQDGEYVYQDADGSLKIESI
VTNKTTTLVPADKVPDDSYTYWIKPDLSSVLWATNYTKQYRHSFFADYYIQDVDSLESKPLVSDQVGDIQYAQWSPVGNT
IAFVRDNNLFTWINGTTTAITEDGGPDQFHGVPDWIYEEEILGGRFSLWFSPDGEYLAYLSFNETGVPTFTVPYYMDNQE
VAPPYPRELDIRYPKVSQTNPTVQLSLLELGSKDSSVVPIDAFDASELIIGEVAWVTDAHAKLAVKAFNRVQDEQKVVAV
DVASSRTSVINERDGTDGWLDNLLSITYIGPINSKNASSSYFLDISDKSGWAHLWLFPISGGEPIALTKGEWEVTSIVSI
DKKRQLVYYLSTQHHSTERHLYSVSYRTFKITPLVDDTVPAYWSASFSSKSSYYILSYSGPDVPYQELYSINQTKPLRTI
TSNSAVIDVIKNYALPNISYFELEIPSGEKLNVMQRLPVNFSPEKKYPILFTPYGGPGAQEVTKSWQSVGFNAYIASDPE
LEYVTWTVDNRGTGYKGRKFRSAVTRQLGLLEAEDQVYAAKQAAKLPFIDADHIGIWGWSYGGYLSSKVLETNSGAFSLG
LITAPVADWRFYDSMYTERYMKTLSTNADGYNTSAVHNADGFKSVTGGFLIQHGTGDDNVHFQNSAALLDLLVGEGVTPD
KLQAQWFTDSDHGIRYHGGSLFLYRQLSKKLLFTADSSTMAAFSTKEVLIADIPTKSVTFTTDQVTVAREILTTVQPGQN
EVTIYGLDPNVDVDSIRIEGSGPATITDIQTQIIPRRESSTDVYPDDSDIEDDSDEEPDDIDYGFDESELQATREKIARG
RAKKSKATDNKAAAAAKLQFLDKYGRSMSPETADLLKVNDFLQLYTRQRSEAAEASHAAEVELREVEDELKELQKKLLQL
ESKQRKAKKTALKDFYRVREERQRERRQRRQQRDRERAERRRFWTSMVGQVRVSLDSNSEPTPESSRRNSVADDDSAMEN
TGHAKPEADVTILLTYVLPGGKWAPRYELSINTPSSTAQMACLAEFRNSSSETWRDTHVALSTSKASFSGLRERVPSLEA
WHIQLDPDSQTNKPSWHNILKGGAPQQAAPGGLFGSAPGPRANSLFGSSQSVPESQPVRSLFGGFGPRTNVAPPTADSMD
TQQPTLLMAASAPAPMAMSSNPNAESDEYEEEEEEEEEEEEEEEEEEEEEEEEEEDDENDDLALPPANLDHQDSITQQYGL
TTTHKLPGRRTVIPSSVNRRHTLAELELDSMSLSYLIVPKHRTAAFLRARIQNTSSAHMLRGKVGLSVDGTFLGAIPMPS
TPPNEFFSLSLGSDPAILVKYPKPTVRPSSGSFFVKEEAAVFRRTCWIKNTKNTAVDLNVMDQVPLSENDKLRVNILEPE
GLGEEGSETDLELSEDVGEGTAVMGKTGEIKWSIRLEPGKEVRTVLEYEARVPSGSEVGTSYG
```

1230 - 1249:	EEEEEEEEEEEEEEEEEEEE
1231 - 1250:	EEEEEEEEEEEEEEEEEEEE
1232 - 1251:	EEEEEEEEEEEEEEEEEEEE
1233 - 1252:	EEEEEEEEEEEEEEEEEEEE

1234 - 1253:	EEEEEEEEEEEEEEEEEEEE
1235 - 1254:	EEEEEEEEEEEEEEEEEEEE

A0A2I2U7G7 **A0A2I2U7G7_FELCA** (195 aa)
Uncharacterized protein. *Felis catus (Cat) (Felis silvestris catus)*

```
MAKGDPKKPKGKMSAYTFFVQTCREEHKKNPEVPVNFAEFSKKCSERWKTMSGKEKSKFDEMAKADRVCYDREMKDYGPA
KEGKKKKDPNAPKRPPSGFFLFCSEFHAKIKSTNPGISRCGKEAGEMWNNLSDSEKQPYNKAAKLKDKYEKDVARAGGGE
GEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE

A0A2I2UBC0 **A0A2I2UBC0_FELCA** (737 aa)
YTH domain containing 1. *Felis catus (Cat) (Felis silvestris catus)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDIKRQKPSLHSRQLISKPLSSSVSN
NKRIVSTKGKSVAEYKNEEYQRSERSKRLEADRKIRLSSSASREPYKSQPEKTCLRKRDPERRTKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDDDGEEEEEEEEEEE
EEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSS
ASESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSARSVI
LIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQ
EIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYAPEFH
QRPGYLKDPRYQEVDSFTNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMAPYPGMEQPPHHPYYQHHAPPP
QAHPPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERE
RLCDRDRDRGERGRYRR
```

229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE

A0A2I2UBP5 **A0A2I2UBP5_FELCA** (1381 aa)
Shroom family member 4. *Felis catus (Cat) (Felis silvestris catus)*

```
MHFPSEAFSLSWHSGCNTSDVCVQWCPLSRHCSTEKSSSIGSMESLEQPGQASYEGHLLPMDQNMYPNQRDSAYSSFSAS
SNASDCALSLKPEEPGSADCIMLGPGPTKAASGRPNVTETSGGSRRTTNGGHLTPSSQMSSRPQEAHHSVPAKAIRGPPQ
PPVRRDSLQASRAQLLNGEQHWTSEHVDSLQQKEIVSLDTVLSPRNPNRFCCLSGQDQVTNEGHQNCELSQGPESGQQDS
EHLLMEASAKAVGFPKVYDKASSIDSSPLKKASAEPTKAASLGSPPHLTGPTGHRHSAPEQLLESHLQHVHLDMRGSKGM
ELPTGEDGHEWTLSPLHSSHTGKKSPCSSTGRTQDQPSKERKTRQVDDRSLGSGHQSPNSSPHGEADGHPPEISFRDPNR
ACRASSELASQQPSASGSLVQQARDCYSTTKVAGSMEATEEGDTEPKECGQVGERRNRGPRGRSIQNRRKSERFATNLRN
EIQRRKAQLQKSKNPLSQLCDTKEPVEETEEPLESTPRSASNSCLLSSYKKPPSPRDKLFNKSMILKARSSECLTQATES
HESRTGLEGQISPGQRPGQPSFGLNTWWKASDLSSSDSEKTNVHRGVCGGHWRWSPENNLQPHVALSMEGPSNPSDSKEL
KVSTAQAGEEAILLPFADRRKFFEESSKSLSTSHLPGLTTHSNKTFTQRPKPIDQNFQPMSSSYRELRRHPMDQSYHSTD
QPYHATDKSYHSVSPLQSETPTYSECFASKGLEPSMCCKSLHCGDFDYHRTCSYSCSVQGAIVHDPCMYCSGEICPALRK
RNMMPNCYNCRCHHHQCIRCSACYHNPQHSSPEDGSLAPSNTWKPRKLTVQEFSGDKWKPITGNRKTSQSGREMAHSKAS
FSWATPFNPCLENPALGLSSYRAVSSLDLLEDFKHSSKKPEETSVYEEGSSMASMPHPLRNRAFSESHISLEPQSSLAWR
QHRKELFTKVETQPDPLGARKKAFPPPRPPPPNWEKYRLFRAAQQQQKQQQQQQKEEEEEEEEEEEEEEEEEEEEEEEE
GEEEEELPPQYFSSETTGTSALNPEEVLEQPQPPGFGHLEDSRQGSESLSAEQESFGLHSSNFLPPIRGHLGSQPEKAQP
PCYYGIGGLWRTSEKETTDSPKQEFQHFSPPPGAPGIPTSYSAYYNISVAKAELLNKLKDQPEMAETGLGEEEVDHELAQ
KKIQLIESIGRKLSVLREAQRGLLEDISANSALGEEVEANLKAVCKSNEFEKYRLFIGDLDKVVNLLLSLSGRLARVENA
LNSIDSEASQEKLVLIEKKQQLTGQLADAKELKEHVDRREKLVFGMVSRYLPQDQLQDYQHFVKMKSALIIEQRELEEKI
KLGEEQLKCLRESLLLGPSNF
```

1016 - 1035:	EEEEEEEEEEEEEEEEEEEE
1017 - 1036:	EEEEEEEEEEEEEEEEEEEE

1018 - 1037:	EEEEEEEEEEEEEEEEEEEE
1019 - 1038:	EEEEEEEEEEEEEEEEEEEE
1020 - 1039:	EEEEEEEEEEEEEEEEEEEE
1021 - 1040:	EEEEEEEEEEEEEEEEEEEE

A0A2I2UT26 **A0A2I2UT26_FELCA** (1274 aa)
Myelin transcription factor 1. *Felis catus (Cat) (Felis silvestris catus)*

```
MMLCGTFLENEFRGELLSQRWTQGDKASNCKTSRLLLGRRSKMSLEHEDKRARTRSKALRVPPEPTGADLSCPTPGCTGS
GHIRGKYSRHRSLQSCPLAKKRKLEGAQPEHLVSKRKSHPLKLALDEGYSVDTDGSEDAEVKDASVSDESEGTLEEDEAE
MSGQEEIHRPEPAEGRSPVKPHFGSNPISSPTGPTKGSYSSYQEIIATSLLNLGQIAVETLVGEDLGQVAKPGPGVVHLV
QEEAEEGATSDEGEKDVFIRPEDTEEVMEVTRERSQELGPQSGEGMVSEESSKMKVNLGNEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVAAPDVICQEDAPHAPTQKAPEPRHPASPSPKPEYSVIVEV
RSDDGKDEDSRSQKSAVTDESEMYDMMTRGNLGLLEQAIALKAEQVQAVCEPGCPPTEQGQPGPGEPGKVVRPLDAARKN
YCSKDPSRAEKREIKCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRIPPEILAMHENVLKCPTPGCTGQGHVNSNRNTHRS
LSGCPIAAAEKLAKSHEKQQPQGGDPSKNSSNSDRILRPMCFVKQLEVPPYGSYRPSVAPATPRANLAKELEKFSKVTFD
YASFDAQVFGKRMLAPKIQTSETSPKAFKSRPFPKASSPRHSPSTSSSSAGFDYTHDAEAAHMAATAILNLSTRCWEMPE
NLSTKPQDLPGKAADIEVDENGTLDLSMRKHRKRDSAFPSSGSSGSSPGVKSPDASQRHSSTSAPSGSMTSLPSSQASRQ
DEWDRPLDYTKPSRQREEEPEESEPAAHSFASSEADDQEVSEESFEERKYPGEVTLANFKMKFLSKDIKKELLTCPTPGC
DGSGHITGNYASHRSLSGCPLADKSLRNLMAAHSADLKCPTPGCDGSGHITGNYASHRSLSGCPRAKKSGARVTPTKDDK
EDPELMKCPVPGCVGLGHISGKYASHRSASGCPLAARRQKEGSLNGSPFSWKSLKNEGPTCPTPGCDGSGHANGSFLTHR
SLSGCPRATFAGKKGKVSGDEVLSTKFKTSDVLENDEEIKQLNQEIRDLNESNSEMEAAMVQLQSQISSMEKSLKNIEEE
NKLIEEQNEALFLELSGLSQALIQSLANIRLPHMEPICEQNFDAYVSTLTDMYSNQECYQNPENKDLLESIKRAVRGIQK
SEEQLKVSSESSWTRFSGKFWSLQPQYSFVCRGWEGSRGHGAGGACDSVSLEHVPLGTRLLSEVNVASVFSVFI
```

301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE
306 - 325:	EEEEEEEEEEEEEEEEEEEE
307 - 326:	EEEEEEEEEEEEEEEEEEEE
308 - 327:	EEEEEEEEEEEEEEEEEEEE
309 - 328:	EEEEEEEEEEEEEEEEEEEE
310 - 329:	EEEEEEEEEEEEEEEEEEEE
311 - 330:	EEEEEEEEEEEEEEEEEEEE
312 - 331:	EEEEEEEEEEEEEEEEEEEE
313 - 332:	EEEEEEEEEEEEEEEEEEEE
314 - 333:	EEEEEEEEEEEEEEEEEEEE
315 - 334:	EEEEEEEEEEEEEEEEEEEE
316 - 335:	EEEEEEEEEEEEEEEEEEEE
317 - 336:	EEEEEEEEEEEEEEEEEEEE
318 - 337:	EEEEEEEEEEEEEEEEEEEE
319 - 338:	EEEEEEEEEEEEEEEEEEEE
320 - 339:	EEEEEEEEEEEEEEEEEEEE
321 - 340:	EEEEEEEEEEEEEEEEEEEE
322 - 341:	EEEEEEEEEEEEEEEEEEEE
323 - 342:	EEEEEEEEEEEEEEEEEEEE
324 - 343:	EEEEEEEEEEEEEEEEEEEE
325 - 344:	EEEEEEEEEEEEEEEEEEEE
326 - 345:	EEEEEEEEEEEEEEEEEEEE
327 - 346:	EEEEEEEEEEEEEEEEEEEE
328 - 347:	EEEEEEEEEEEEEEEEEEEE
329 - 348:	EEEEEEEEEEEEEEEEEEEE
330 - 349:	EEEEEEEEEEEEEEEEEEEE
331 - 350:	EEEEEEEEEEEEEEEEEEEE
332 - 351:	EEEEEEEEEEEEEEEEEEEE
333 - 352:	EEEEEEEEEEEEEEEEEEEE
334 - 353:	EEEEEEEEEEEEEEEEEEEE
335 - 354:	EEEEEEEEEEEEEEEEEEEE
336 - 355:	EEEEEEEEEEEEEEEEEEEE

337 - 356:	EEEEEEEEEEEEEEEEEEEE
338 - 357:	EEEEEEEEEEEEEEEEEEEE
339 - 358:	EEEEEEEEEEEEEEEEEEEE
340 - 359:	EEEEEEEEEEEEEEEEEEEE

A0A2I2V1C0 **A0A2I2V1C0_FELCA** (1135 aa)
Myelin transcription factor 1. *Felis catus (Cat) (Felis silvestris catus)*

```
MSLEHEDKRARTRSKALRVPPEPTGADLSCPTPGCTGSGHIRGKYSRHRSLQSCPLAKKRKLEGAQPEHLVSKRKSHPLK
LALDEGYSVDTDGSEDAEVKDASVSDESEGTLEEDEAEMSGQEEIHRPEPAEGRSPVKPHFGSNPISSPTGPTKGSYSSY
QEIIATSLLNLGQIAVETLVGEDLGQVAKPGPGVVHLVQEEAEEGATSDEGEKDVFIRPEDTEEVMEVTRERSQELGPQS
GEGMVSEESSKMKVNLGNEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVAA
PDVICQEDAPHAPTQKAPEPRHPASPSPKPEYSVIVEVRSDDGKDEDSRSQKSAVTDESEMYDMMTRGNLGLLEQAIALK
AEQVQAVCEPGCPPTEQGQPGPGEPGKVVRPLDAARKNYCSKDPSRAEKREIKCPTPGCDGTGHVTGLYPHHRSLSGCPH
KDRIPPEILAMHENVLKCPTPGCTGQGHVNSNRNTHRSLSGCPIAAAEKLAKSHEKQQPQGGDPSKNSSNSDRILRPMCF
VKQLEVPPYGSYRPSVAPATPRANLAKELEKFSKVTFDYASFDAQVFGKRMLAPKIQTSETSPKAFKSRPFPKASSPRHS
PSTSSSSAGFDYTHDAEAAHMAATAILNLSTRCWEMPENLSTKPQDLPGKAADIEVDENGTLDLSMRKHRKRDSAFPSSG
SSGSSPGVKSPDASQRHSSTSAPSGSMTSLPSSQASRQDEWDRPLDYTKPSRQREEEPEESEPAAHSFASSEADDQEVSE
ESFEERKYPGEVTLANFKMKFLSKDIKKELLTCPTPGCDGSGHITGNYASHRRCPTPGCDGSGHITGNYASHRSLSGCPR
AKKSGARVTPTKDDKEDPELMKCPVPGCVGLGHISGKYASHRSASGCPLAARRQKEGSLNGSPFSWKSLKNEGPTCPTPG
CDGSGHANGSFLTHRSLSGCPRATFAGKKGKVSGDEVLSTKFKTSDVLENDEEIKQLNQEIRDLNESNSEMEAAMVQLQS
QISSMEKSLKNIEEENKLIEEQNEALFLELSGLSQALIQSLANIRLPHMEPICEQNFDAYVSTLTDMYSNQECYQNPENK
DLLESIKRAVRGIQV
```

259 - 278:	EEEEEEEEEEEEEEEEEEEE
260 - 279:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE
262 - 281:	EEEEEEEEEEEEEEEEEEEE
263 - 282:	EEEEEEEEEEEEEEEEEEEE
264 - 283:	EEEEEEEEEEEEEEEEEEEE
265 - 284:	EEEEEEEEEEEEEEEEEEEE
266 - 285:	EEEEEEEEEEEEEEEEEEEE
267 - 286:	EEEEEEEEEEEEEEEEEEEE
268 - 287:	EEEEEEEEEEEEEEEEEEEE
269 - 288:	EEEEEEEEEEEEEEEEEEEE
270 - 289:	EEEEEEEEEEEEEEEEEEEE
271 - 290:	EEEEEEEEEEEEEEEEEEEE
272 - 291:	EEEEEEEEEEEEEEEEEEEE
273 - 292:	EEEEEEEEEEEEEEEEEEEE
274 - 293:	EEEEEEEEEEEEEEEEEEEE
275 - 294:	EEEEEEEEEEEEEEEEEEEE
276 - 295:	EEEEEEEEEEEEEEEEEEEE
277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE
287 - 306:	EEEEEEEEEEEEEEEEEEEE
288 - 307:	EEEEEEEEEEEEEEEEEEEE
289 - 308:	EEEEEEEEEEEEEEEEEEEE
290 - 309:	EEEEEEEEEEEEEEEEEEEE
291 - 310:	EEEEEEEEEEEEEEEEEEEE
292 - 311:	EEEEEEEEEEEEEEEEEEEE
293 - 312:	EEEEEEEEEEEEEEEEEEEE
294 - 313:	EEEEEEEEEEEEEEEEEEEE

295 - 314:	EEEEEEEEEEEEEEEEEEEE
296 - 315:	EEEEEEEEEEEEEEEEEEEE
297 - 316:	EEEEEEEEEEEEEEEEEEEE
298 - 317:	EEEEEEEEEEEEEEEEEEEE

A0A2I2YA39 **A0A2I2YA39_GORGO** (1233 aa)
Euchromatic histone lysine methyltransferase 2. *Gorilla gorilla gorilla (Western lowland gorilla)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGA
LLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDESENLEGDGDLR
GGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGSEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDLAKRRKLNSGGGLSEELGSARRSGEVTLTKGDPGSLEEWE
TVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAK
KKWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELS
GCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCG
EDASEAQEVTIPRGDGVTPPAGTAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGC
LSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGS
VEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVD
VNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHI
AARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPC
VNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFEC
NQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVY
CIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKH
SAEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE

A0A2I2YI89 **A0A2I2YI89_GORGO** (1192 aa)
Euchromatic histone lysine methyltransferase 2. *Gorilla gorilla gorilla (Western lowland gorilla)*

```
MAAAAGAAAAAAAEGEAPAEMGALLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGAD
TPVGATPLIGDESENLEGDGDLRGGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGA
AAAGSEPPPATTSPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDLAKRRKLNSGGGLSEEL
GSARRSGEVTLTKGDPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEE
EEEDEESGNQSDRRSGRLWGWRSGPEGVGGAPGGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETER
GFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCG
YFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLSQDAPGRADT
SQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSV
KQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMV
QRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEE
NICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVW
FALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVD
DCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTI
PQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAF
FSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE

A0A2I2YWX5 **A0A2I2YWX5_GORGO** (906 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Gorilla gorilla gorilla (Western lowland gorilla)*

```
MELAVAVLRDLLRYAAQLPALFRDISMNHLPGLLTSLLGLRPECEQSALEGMKACMTYFPRACGSLKGKLASFFLSRVDA
LSPQLQQLACECYSRLPSLGAGFSQGLKHTESWEQELHSLLASLHTLLGALYEGAETAPVQNEGPGVEMLLSSEDGDAHV
LLQLRQRFSGLACCLGLMLSSEFGAPVSVPVQEILDFICRTLSVSSKNISLHGDGPLRLLLLPSIHLEALDLLSALILAC
GSRLLRFGILISRLLPQVLNSWSIGRDSLSPGQERPYSTVRTKVYAILELWVQVCGASAGMLQGGASGEALLTHLLSDIS
PPADALKLRSPRGSPDGSLQTGKPSAPKKLKLDVGEAMAPPSHRKGDSNANSDVCAAALRGLSRTILMCGPLIKEETHRR
LHDLVLPLVMGVQQGEVLGSSPYTSSRCRRELYCLLLALLLAPSPRCPPPLACALQAFSLGQREDSLEVSSFCSEALVTC
AALTHPRVPPLQPMGPTCPTPAPVPPPEAPSPFRAPPFHPPGPMPSVGSMPSAGPMPSAGPMPSAGPVPSARPGPPTTAN
HLGLSVPGLVSVPPRLLPGPENHRAGSNEDPILAPSGTPPPTIPPDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDS
VVIVPEGLPPLPPPPPSGATPPPIAPTGPPTASPPVPAKEEPEELPAAPGPLPPPPPPPPPVPGPVTLPPPQLVPEGTPG
GGGPPALEEDLTVININSSDEEEEEEEEEEEEEEEEEEEEEDFEEEEEDEEEYFEEEEEEEEEFEEEFEEEEGELEEEEE
EEDEEEEEELEEVEREGESPAAGPPPQELVEEEPSAPPTLLEEETEDGSDKVQPPPETPAEEEMETETEAEALQEKEQDD
TAAMLADFIDCPPDDEKPPPPTEPDS
```

741 - 760:	EEEEEEEEEEEEEEEEEEEE
742 - 761:	EEEEEEEEEEEEEEEEEEEE

A0A2I2ZJ54 **A0A2I2ZJ54_GORGO** (728 aa)
YTH domain containing 1. *Gorilla gorilla gorilla (Western lowland gorilla)*

```
KYGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSNNKRIVSTK
GKSATEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVDRRASRSSQ
SSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEEEEEEEEEE
EEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSASESYAGSE
KKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVILIFSVRESG
KFQGFARLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQ
LCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQRPGYLKDP
RYQEVDSFTNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQAHPPYSGH
HPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDR
GERGRYRR
```

222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE

A0A2I2ZPS7 **A0A2I2ZPS7_GORGO** (1209 aa)
Euchromatic histone lysine methyltransferase 2. *Gorilla gorilla gorilla (Western lowland gorilla)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGA
LLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDESENLEGDGDLR
GGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGSEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDLAKRRKLNSGGGLSEELGSARRSGEVTLTKGDPGSLEEWE
TVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRVRDGEPQLLF
SSIQGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLC
ETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTA
APAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQES
ERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTP
LMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVI
RMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRN
KEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETST
MNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQ
LYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIP
VRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPE
LGSLPPVNT
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE

A0A2I2ZS57 **A0A2I2ZS57_GORGO** (1267 aa)
Euchromatic histone lysine methyltransferase 2. *Gorilla gorilla gorilla (Western lowland gorilla)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGA
LLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDESENLEGDGDLR
GGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGSEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDLAKRRKLNSGGGLSEELGSARRSGEVTLTKGDPGSLEEWE
TVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAK
KKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEEL
PLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTA
GTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLSQDAPGRADTSQPSA
RMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGEL
QKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGC
VYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLH
WASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQL
NRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSS
NCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTF
ICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRD
IRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE

A0A2I2ZW06 **A0A2I2ZW06_GORGO** (710 aa)
YTH domain containing 1. *Gorilla gorilla gorilla (Western lowland gorilla)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSN
NKRIVSTKGKSATEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEE
EEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSA
SESYADQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVILIFSVRESGKFQGFARLSS
ESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLLFPPDES
IDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQRPGYLKDPRYQEVDRRFS
```

```
GVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHHPVPHEARYRDKRVHDYD
MRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDRGERGRYRR
```

230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE

A0A2I3G6C7 **A0A2I3G6C7_NOMLE** (1096 aa)
Uncharacterized protein. *Nomascus leucogenys (Northern white-cheeked gibbon) (Hylobates leucogenys)*

```
HGSLGDTPRSEETLPKATPDSVAPAGPSSPASVTVTVGDEGADTPVGATPLIGDESENLEGDGDLHGGRILLGHATKSFP
SSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGPEPPPATTSPEGQPKVHRARKTMSKPGNGQPPV
PEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEELGSARRSGEVTLAKGDTGSLEEWETVVGDDFSLYYDSY
SVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSR
KRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRP
SSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRG
DGVTPPAGTAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREA
LEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLEPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANI
NAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKVCAQAMVSLLLITRQVEINAQDSGGWTPIIWAAEHKHIEVIRML
LTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEG
DTPLLPIFCRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRC
WYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISD
AEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDY
GDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELSSLPPVNT
```

263 - 282:	EEEEEEEEEEEEEEEEEEEE
264 - 283:	EEEEEEEEEEEEEEEEEEEE
265 - 284:	EEEEEEEEEEEEEEEEEEEE
266 - 285:	EEEEEEEEEEEEEEEEEEEE
267 - 286:	EEEEEEEEEEEEEEEEEEEE

A0A2I3GIN7 **A0A2I3GIN7_NOMLE** (534 aa)
YTH domain-containing protein. *Nomascus leucogenys (Northern white-cheeked gibbon) (Hylobates leucogenys)*

```
LKSDNGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSNNKRIV
STKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVDRRASR
SSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEEEEEEEEEEEEEEEEEEEEYE
QDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSASESYAGSEKKHE
KLSSSVRAVRKDQTSKLKYVFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVILIFSVRESGKFQGFARLS
SESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLLFPPDE
SIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRLETFFGLIIGTCIRIT
```

217 - 236:	EEEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE

A0A2I3GZR5 **A0A2I3GZR5_NOMLE** (225 aa)
Erf4 domain-containing protein. *Nomascus leucogenys (Northern white-cheeked gibbon) (Hylobates leucogenys)*

```
MSILLPNMAEFDTISELEEEEEEEAATSSSSPSSSSSVSGPDDDEEDEEEEEEEEEEEEEEEEEEEEEEEAPPPPRVVSEE
HLRRYAPDPVLVRGAGHITVFGLSNKFDAEFPSVLTGKVAPEEFKTSIGRVNACLKKALPVNVKWLLCGCLCCCCTLGCS
LWPVICLNKRTRRSIQKLIEWENNRLYHKLALHWKLTKRKCETSNMMEYVILIEFLPKYPIFRPD
```

48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE

A0A2I3HA58 **A0A2I3HA58_NOMLE** (205 aa)
Erf4 domain-containing protein. *Nomascus leucogenys (Northern white-cheeked gibbon) (Hylobates leucogenys)*

```
MSILLPNMAEFDTISELEEEEEEEAATSSSSPSSSSSVSGPDDDEEDEEEEEEEEEEEEEEEEEEEEEEEAPPPPRVVSEE
HLRRYAPDPVLVRGAGHITVFGLSNKFDAEFPSVLTGKVAPEEFKTSIGRVNACLKKALPVNVKWLLCGCLCCCCTLGCS
LWPVICLNKRTRRSIQKLIEWENNRLYHKVILIEFLPKYPIFRPD
```

48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE

A0A2I3HDJ9 **A0A2I3HDJ9_NOMLE** (1186 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Nomascus leucogenys (Northern white-cheeked gibbon) (Hylobates leucogenys)*

```
MLLFSLSPRVQPAFTQCAGPQPPPHAPSPVGGRRGVFASSRHAITGARGKMAAAVLSGPSAGSAAGVPGGTGGLSAVSSG
PRLRLLLLESVSGLLQPRTGSAVAPVHPPNRSAPHLPGLMCLLRLHGSVGGAQNLSALGALVSLSNARLSSIKTRFEGLC
LLSLLVGESPTELFQQHCVAWLRSIQQVLQTQDPPATMELAVAVLRDLLRYAAQLPALFRDISMNHLPGLLTSLLGLRPE
CEQSALEGMKACMTYFPRACGSLKVSIYALFSPPVFLSFLPQLACECYSRLPSLGAGFSQGLKHTESWEQELHSLLASLH
TLLGALYEGAETAPVQNEGPGVQMLLSSEDGDAHVLLQLRQRFSGLARCLGLMLSSEFGAPVSVPVQEILDFICRTLSVS
SKNISLHGDGPLRLLLLPSIHLEALDLLSALILACGSRLLRFGILISRLLPQVLNSWSIGRDSLSPGQERPYSTVRTKVY
AILELWVQVCGASAGMLQGGASGEALLTHLLSDISPPADALKLRSPRGSPDGSLQTGKPSAPKKLKLDVGEAMAPPSHRK
GDSNANSDVCAAALRGLSRTILMCGPLIKEETHRGPLLCTHWGRLHDLVLPLVMGVQQGEVLGSSPYTSSRCRRELYCLL
LALLLAPSPRCPPPLACALQAFSLGQREDSLEVSSFCSEALVTCAALTHPRVPALQPMGPTCPTPAPVPPPEAPSPFRAP
PFHPPGPMPSVGSMPSAGPMPSAGPMPSAGPVPSARPGPPTTANHLGLSVPGLVSVPPRLLPGPENHRAGSNEDPILAPR
GTPPPTIPPDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDSVVIVPEGLPPLPPPPPSGATPPPIAPTGPPTASPPV
PAKEEPEELPAAPGPLPPPPPPPPPVPGPVTLPPPQLVPEGTPGGGGPSALEEDLTVININSSDEEEEEEEEEEEEEEEE
EEEEEDFEEEEEDEEEYFEEEEEEEEEFEEEFEEEEGELEEEEEEDEEEEEELEEVEELEFGTAGGEVEEGGPPPPTLPP
ALPPPESPPKVQPEPEPEPGLLLEVEEPGTEEEHGADTAPTLAPEVLPSQGEVEREGGSPAAGPPPQELVEEEPSAPPTL
LEEETEDGSDKVQPPPETPAEEEMETETEAEALQEKEQDDTAAMLADFIDCPPDDEKPPPPTEPDS
```

945 - 964:	EEEEEEEEEEEEEEEEEEEE
946 - 965:	EEEEEEEEEEEEEEEEEEEE

A0A2I3HFV0 **A0A2I3HFV0_NOMLE** (885 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Nomascus leucogenys (Northern white-cheeked gibbon) (Hylobates leucogenys)*

```
MELAVAVLRDLLRYAAQLPALFRDISMNHLPGLLTSLLGLRPECEQSALEGMKACMTYFPRACGSLKLACECYSRLPSLG
AGFSQGLKHTESWEQELHSLLASLHTLLGALYEGAETAPVQNEGPGVQMLLSSEDGDAHVLLQLRQRFSGLARCLGLMLS
SEFGAPVSVPVQEILDFICRTLSVSSKNISLHGDGPLRLLLLPSIHLEALDLLSALILACGSRLLRFGILISRLLPQVLN
SWSIGRDSLSPGQERPYSTVRTKVYAILELWVQVCGASAGMLQGGASGEALLTHLLSDISPPADALKLRSPRGSPDGSLQ
TGKPSAPKKLKLDVGEAMAPPSHRKGDSNANSDVCAAALRGLSRTILMCGPLIKEETHRRLHDLVLPLVMGVQQGEVLGS
SPYTSSRCRRELYCLLLALLLAPSPRCPPPLACALQAFSLGQREDSLEVSSFCSEALVTCAALTHPRVPALQPMGPTCPT
PAPVPPPEAPSPFRAPPFHPPGPMPSVGSMPSAGPMPSAGPMPSAGPVPSARPGPPTTANHLGLSVPGLVSVPPRLLPGP
ENHRAGSNEDPILAPRGTPPPTIPPDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDSVVIVPEGLPPLPPPPPSGAT
PPPIAPTGPPTASPPVPAKEEPEELPAAPGPLPPPPPPPPPVPGPVTLPPPQLVPEGTPGGGGPSALEEDLTVININSSD
EEEEEEEEEEEEEEEEEEEEEDFEEEEEDEEEYFEEEEEEEEEFEEEFEEEEGELEEEEEEDEEEEEELEEVEREGGSPA
AGPPPQELVEEEPSAPPTLLEEETEDGSDKVQPPPETPAEEEMETETEAEALQEKEQDDTAAMLADFIDCPPDDEKPPPP
TEPDS
```

721 - 740:	EEEEEEEEEEEEEEEEEEEE
722 - 741:	EEEEEEEEEEEEEEEEEEEE

A0A2I3HUT1 **A0A2I3HUT1_NOMLE** (1122 aa)
Uncharacterized protein. *Nomascus leucogenys (Northern white-cheeked gibbon) (Hylobates leucogenys)*

```
HGSLGDTPRSEETLPKATPDSVAPAGPSSPASVTVTVGDEGADTPVGATPLIGDESENLEGDGDLHGGRILLGHATKSFP
SSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGPEPPPATTSPEGQPKVHRARKTMSKPGNGQPPV
PEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEELGSARRSGEVTLAKGDTGSLEEWETVVGDDFSLYYDSY
SVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSR
KRRKREPPRAKEPRGENGVGSSVQGGASGSREGTLSPNHAGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHK
CMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVS
QLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDS
SGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLEPNFQSDQQSK
RTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKVCAQAMVSLLLITRQVEI
NAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIA
ARESYHDCVLLFLSRGANPELRNKEGDTPLLPIFCRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNI
THLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKM
GWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLH
QDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELSSLPPV
NT
```

263 - 282:	EEEEEEEEEEEEEEEEEEEE
264 - 283:	EEEEEEEEEEEEEEEEEEEE
265 - 284:	EEEEEEEEEEEEEEEEEEEE
266 - 285:	EEEEEEEEEEEEEEEEEEEE
267 - 286:	EEEEEEEEEEEEEEEEEEEE

A0A2I3LQY6 **A0A2I3LQY6_PAPAN** (1209 aa)
Euchromatic histone lysine methyltransferase 2. *Papio anubis (Olive baboon)*

```
MAAAAGAAAAAAAAEGEAPAEMGALLLEKETRGASERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGAD
TPVGATPLIGDESENLEGDGDLHGGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGA
AAAGPEPPPATTSPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEEL
GSARRSEVTLAKGDPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEE
EEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLS
PNHAGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLC
ETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGAA
APAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQES
ERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTP
LMEAVVTNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVI
RMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRN
KEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGESCPEDYKYISENCETST
MNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQ
LYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIP
VRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPE
```

LGSLPPVNT

299 - 318:	EEEEEEEEEEEEEEEEEEEE
300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE

A0A2I3LUL1 **A0A2I3LUL1_PAPAN** (1232 aa)
Euchromatic histone lysine methyltransferase 2. *Papio anubis (Olive baboon)*

MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGA
LLLEKETRGASERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDESENLEGDGDLH
GGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGPEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEELGSARRSEVTLAKGDPGSLEEWET
VVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAKK
KWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSG
CNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGE
DASEAQEVTIPRGDGVTPPAGAAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCL
SAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSV
EICHVLLQAGANINAVDKQQRTPLMEAVVTNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDV
NAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIA
ARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCV
NGVDGESCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECN
QACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYC
IDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHS
AEAIALEQSRLARLDPHPELLPELGSLPPVNT

356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE

A0A2I3LUZ2 **A0A2I3LUZ2_PAPAN** (906 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Papio anubis (Olive baboon)*

MELAVAVLRDLLRYAAQLPALFRDISMNHLPGLLTSLLGLRPECEQSALEGMKACMTYFPRACGSLKGKLASFFLSRVDA
LSPQLQQLACECYSRLPSLGAGFSQGLKHTESWEQELHSLLASLHTLLGALYEGAETAPVQNEGPGVEMLLSSEDGDAHI
LLRLRQRFSGLARCLGLMLSSEFGAPVSVPVQEILDFICRTLSVSSKNISLHGDGPLRLLLLPSIHLEALDLLSALILAC
GSRLLRFGILISRLLPQVLNSWSIGRDSLSPGQERPYSTVRTKVYAVLELWVQVCGASAGMLQGGASGEALLTHLLSDIS
PPADALKLRSPRGSPDGSLQTGKPSAPKKLKLDVGEAMAPPSHRKGDSNANSDVCAAALKGLSRTILMCGPLIKEETHRR
LHDLVLPLVMGVQQGEVLGSSPYTSSRCRRELYCLLLALLLAPSPRCPPPLACALQAFSLGQREDSLEVSSFCSEALVTC
AALTHPRVPPLQPMGPTCPTPAPVPPPEAPSPFRAPPFHPPGPMPSVGPMPSAGPMPSAGPMPSAGPVPSARPGPPTTAN
HLGLSVSGLVSVPPRLLPGPENHRAGSNEDPILAPSGTPPPAIPPDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDS
VVIVPEGLPPLPPPPPSGATPPPIAPTGPPTASPPVPAKEEPEELPAAPGPLPPPPPPPPPVPGPVTLPPPQLVPEGTPG
GGGPPALEEDLTVININSSDEEEEEEEEEEEEEEEEEEEEEDFEEEEEDEEEYFEEEEEEEEEFEEEFEEEEGELEEEEE
EEDEEEEEEELEEVEREEGSPSAGPPPQELVEEEPSAPPTLLEEGTEDGGDRVQPPPETPAEEEMETETEAEALQEKEQDD
TAAMLADFIDCPPDDEKPPPPTEPDS

741 - 760:	EEEEEEEEEEEEEEEEEEEE
742 - 761:	EEEEEEEEEEEEEEEEEEEE

A0A2I3M2L8 **A0A2I3M2L8_PAPAN** (1006 aa)
Solute carrier family 24 member 1. *Papio anubis (Olive baboon)*

MGKLIRMGPQDRRLLRTKRLPWSRLLFLLGMLIISSTYQHLRGPRGLSSLWAAVSSHQPVKLASRDLPSEEMMMVSSNPP
KPSSEMGGEMLVPQASVGSDEATLSMTVENIPDIPKRTAKMIPTTTKNNYSPTAAGTERRKEDTPTSSRTLTYYTSTSSR
QIVKKYTPTPTGEMKSYSPTQVREKVKYTPSPRGRRVGTYASSTFMTTETSHAITPRTTVKDSDITTTYKILETNSLKRI
MEETTPTTLKGMVDSTPTFLTHEVETNVLTSPRSIVEKNNLSPPRRVESNSSAHPWGLVGKNNLKTPQGTVLTHTPATSE
GQVTISTMTGSNPSETKAFTAAWSVRNPSPRTSVSAIETAPTTVWRLAKKPYIAPSTSTTPTVRAKLTTQVHHCVVVKPT
PAMPTTPSPSLTTALLPEELSPSPSVLPPILPDLPPKGEYPPDLFSVEERRQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLIMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKQIEAWVKEQLSRRPAAKVMALGDLSKLPSLLTRGSS
STSLHNSTIRSTIYQLMLHSLDPLREVCLAEEKEEESLNQEARAQPQAKSESKPEDEEPAKLPAVTVTPAPAPDIKGDQK
ENPGGQEDVAEAESTGEMTGEEGETAGEGETEEKSGGETQPEGEGETGTQGKGEEREKENEAEGKGDNEGEGEGEIHAED
GEMKGIEGETESQELSAENHGEAKSDEKGVEDGGGSDGGDNEEEEEEEEEEEEEEEEEEEEEEEEEEGNEEPLSLHWPET
RQKQAIYLFLLPIVFPLWLTVPDVRRQESRKFFVFTFLGSIVWIAMFSYLMVWWAHQVGETIGISEEIMGLTILAAGTSI
PDLITSVIVARKGLGDMAVSSSVGSNIFDITVGVESCEMFQLGAIH

842 - 861:	EEEEEEEEEEEEEEEEEEEE
843 - 862:	EEEEEEEEEEEEEEEEEEEE
844 - 863:	EEEEEEEEEEEEEEEEEEEE
845 - 864:	EEEEEEEEEEEEEEEEEEEE

846 - 865:	EEEEEEEEEEEEEEEEEEEE
847 - 866:	EEEEEEEEEEEEEEEEEEEE
848 - 867:	EEEEEEEEEEEEEEEEEEEE

A0A2I3MBH7 **A0A2I3MBH7_PAPAN** (1075 aa)
Solute carrier family 24 member 1. *Papio anubis (Olive baboon)*

```
MGKLIRMGPQDRRLLRTKRLPWSRLLFLLGMLIISSTYQHLRGPRGLSSLWAAVSSHQPVKLASRDLPSEEMMMVSSNPP
KPSSEMGGEMLVPQASVGSDEATLSMTVENIPDIPKRTAKMIPTTTKNNYSPTAAGTERRKEDTPTSSRTLTYYTSTSSR
QIVKKYTPTPTGEMKSYSPTQVREKVKYTPSPRGRRVGTYASSTFMTTETSHAITPRTTVKDSDITTTYKILETNSLKRI
MEETTPTTLKGMVDSTPTFLTHEVETNVLTSPRSIVEKNNLSPPRRVESNSSAHPWGLVGKNNLKTPQGTVLTHTPATSE
GQVTISTMTGSNPSETKAFTAAWSVRNPSPRTSVSAIETAPTTVWRLAKKPYIAPSTSTTPTVRAKLTTQVHHCVVVKPT
PAMPTTPSPSLTTALLPEELSPSPSVLPPILPDLPPKGEYPPDLFSVEERRQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLIMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKQIEAWVKEQLSRRPAAKVMALGDLSKLPSLLTRGSS
STSLHNSTIRSTIYQLMLHSLDPLREVCLAEEKEEESLNQEARAQPQAKSESKPEDEEPAKLPAVTVTPAPAPDIKGDQK
ENPGGQEDVAEAESTGEMTGEEGETAGEGETEEKSGGETQPEGEGETGTQGKGEEREKENEAEGKGDNEGEGEGEIHAED
GEMKGIEGETESQELSAENHGEAKSDEKGVEDGGGSDGGDNEEEEEEEEEEEEEEEEEEEEEEEEEEGNEEPLSLHWPET
RQKQAIYLFLLPIVFPLWLTVPDVRRQESRKFFVFTFLGSIVWIAMFSYLMVWWAHQVGETIGISEEIMGLTILAAGTSI
PDLITSVIVARKGLGDMAVSSSVGSNIFDITVGLPVPWLLFCLINGLQPVPVSSNGLFCAIVLLFLMLLFVISSIASCKW
RMNKILGFTMFLLYFVFLIISVMLEDRIISCPVSV
```

842 - 861:	EEEEEEEEEEEEEEEEEEEE
843 - 862:	EEEEEEEEEEEEEEEEEEEE
844 - 863:	EEEEEEEEEEEEEEEEEEEE
845 - 864:	EEEEEEEEEEEEEEEEEEEE
846 - 865:	EEEEEEEEEEEEEEEEEEEE
847 - 866:	EEEEEEEEEEEEEEEEEEEE
848 - 867:	EEEEEEEEEEEEEEEEEEEE

A0A2I3MDJ1 **A0A2I3MDJ1_PAPAN** (1216 aa)
Euchromatic histone lysine methyltransferase 2. *Papio anubis (Olive baboon)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGA
LLLEKETRGASERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDESENLEGDGDLH
GGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGPEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEELGSARRSEVTLAKGDPGSLEEWET
VVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRDPPGVPVGEVQ
GLPQLLFFSVQGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSR
VALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGV
TPPAGAAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEK
ALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAV
DKQQRTPLMEAVVTNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAE
HKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRG
ANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGESCPEDYKYIS
ENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQS
GIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHL
CDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDP
HPELLPELGSLPPVNT
```

356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE

A0A2I3MF08 **A0A2I3MF08_PAPAN** (1252 aa)
Euchromatic histone lysine methyltransferase 2. *Papio anubis (Olive baboon)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGA
LLLEKETRGASERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDESENLEGDGDLH
GGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGPEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEELGSARRSEVTLAKGDPGSLEEWET
VVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRVRDGATRGRPQ
GRREREGGEPRQSRGVHGVLGHGGEDPPGVPVGEVQGLPQLLFFSVQGVSNDTSSLETERGFEELPLCSCRMEAPKIDRI
SERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHR
FHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGAAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDP
LADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNF
QSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVTNHLEVARYMVQRGGCVYSKEEDGSTCLHHA
AKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLL
NARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRT
EKIICRDVARGYENVPIPCVNGVDGESCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDK
DGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEAD
VREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRF
WDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE

A0A2I3MJM3 **A0A2I3MJM3_PAPAN** (544 aa)
YTH domain containing 1. *Papio anubis (Olive baboon)*

```
LKSDSDKEDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSNN
KRIVSTKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVDR
RASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEEEEEEEEEEEEEEEEEE
EEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSASESYAGS
EKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVILIFSVRES
GKFQGFARLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGT
QLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRLETFFGLIIGTCIRIT
```

222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEEE

A0A2I3MR30 **A0A2I3MR30_PAPAN** (1063 aa)
Solute carrier family 24 member 1. *Papio anubis (Olive baboon)*

```
MGKLIRMGPQDRRLLRTKRLPWSRLLFLLGMLIISSTYQHLRGPRGLSSLWAAVSSHQPVKLASRDLPSEEMMMVSSNPP
KPSSEMGGEMLVPQASVGSDEATLSMTVENIPDIPKRTAKMIPTTTKNNYSPTAAGTERRKEDTPTSSRTLTYYTSTSSR
QIVKKYTPTPTGEMKSYSPTQVREKVKYTPSPRGRRVGTYASSTFMTTETSHAITPRTTVKDSDITTTYKILETNSLKRI
MEETTPTTLKGMVDSTPTFLTHEVETNVLTSPRSIVEKNNLSPPRRVESNSSAHPWGLVGKNNLKTPQGTVLTHTPATSE
GQVTISTMTGSNPSETKAFTAAWSVRNPSPRTSVSAIETAPTTVWRLAKKPYIAPSTSTTPTVRAKLTTQVHHCVVVKPT
PAMPTTPSPSLTTALLPEELSPSPSVLPPILPDLPPKGEYPPDLFSVEERRQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLIMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKQIEAWVKEQLSRRPAAKVMALGDLSKPGDGAIAVDE
LQDNKKLKLPSLLTRGSSSTSLHNSTIRSTIYQLMLHSLDPLREVCLAEEKEEESLNQEARAQPQAKSESKPEDEEPAKL
PAVTVTPAPAPDIKGDQKENPGGQEDVAEAESTGEMTGEEGETAGEGETEEKSGGETQPEGEGETGTQGKGEEREKENEA
EGKGDNEGEGEGEIHAEDGEMKGIEGETESQELSAENHGEAKSDEKGVEDGGGSDGGDNEEEEEEEEEEEEEEEEEEEE
EEEEEGNEEPLSLHWPETRQKQAIYLFLLPIVFPLWLTVPDVRRQVGETIGISEEIMGLTILAAGTSIPDLITSVIVARK
GLGDMAVSSSVGSNIFDITVGLPVPWLLFCLINGLQPVPVSSNGLFCAIVLLFLMLLFVISSIASCKWRMNKILGFTMFL
LYFVFLIISVMLEDRIISCPVSV
```

860 - 879:	EEEEEEEEEEEEEEEEEEEE
861 - 880:	EEEEEEEEEEEEEEEEEEEE
862 - 881:	EEEEEEEEEEEEEEEEEEEE
863 - 882:	EEEEEEEEEEEEEEEEEEEE
864 - 883:	EEEEEEEEEEEEEEEEEEEE
865 - 884:	EEEEEEEEEEEEEEEEEEEE
866 - 885:	EEEEEEEEEEEEEEEEEEEE

A0A2I3N4A7 **A0A2I3N4A7_PAPAN** (710 aa)
YTH domain containing 1. *Papio anubis (Olive baboon)*

```
MAADIREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSN
NKRIVSTKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEE
EEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSA
SESYADQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVILIFSVRESGKFQGFARLSS
ESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLLFPPDES
IDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQRPGYLKDPRYQEVDRRFS
GVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHHPVPHEARYRDKRVHDYD
MRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDRGERGRYRR
```

230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE

A0A2I3NG69 **A0A2I3NG69_PAPAN** (979 aa)
Solute carrier family 24 member 1. *Papio anubis (Olive baboon)*

```
MGKLIRMGPQDRRLLRTKRLPWSRLLFLLGMLIISSTYQHLRGPRGLSSLWAAVSSHQPVKLASRDLPSEEMMMVSSNPP
KPSSEMGGEMLVPQASVGSDEATLSMTVENIPDIPKRTAKMIPTTTKNNYSPTAAGTERRKEDTPTSSRTLTYYTSTSSR
QIVKKYTPTPTGEMKSYSPTQVREKVKYTPSPRGRRVGTYASSTFMTTETSHAITPRTTVKDSDITTTYKILETNSLKRI
MEETTPTTLKGMVDSTPTFLTHEVETNVLTSPRSIVEKNNLSPPRRVESNSSAHPWGLVGKNNLKTPQGTVLTHTPATSE
GQVTISTMTGSNPSETKAFTAAWSVRNPSPRTSVSAIETAPTTVWRLAKKPYIAPSTSTTPTVRAKLTTQVHHCVVVKPT
PAMPTTPSPSLTTALLPEELSPSPSVLPPILPDLPPKGEYPPDLFSVEERRQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
```

```
DVSFYILDLIMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKQIEAWVKEQLSRRPAAKVMALGDLSKEDVAEAESTG
EMTGEEGETAGEGETEEKSGGETQPEGEGETGTQGKGEEREKENEAEGKGDNEGEGEGEIHAEDGEMKGIEGETESQELS
AENHGEAKSDEKGVEDGGGSDGGDNEEEEEEEEEEEEEEEEEEEEEEEEEEEEGNEEPLSLHWPETRQKQAIYLFLLPIVFP
LWLTVPDVRRQESRKFFVFTFLGSIVWIAMFSYLMVWWAHQVGETIGISEEIMGLTILAAGTSIPDLITSVIVARKGLGD
MAVSSSVGSNIFDITVGLPVPWLLFCLINGLQPVPVSSNGLFCAIVLLFLMLLFVISSIASCKWRMNKILGFTMFLLYFV
FLIISVMLEDRIISCPVSV
```

746 - 765:	EEEEEEEEEEEEEEEEEEEE
747 - 766:	EEEEEEEEEEEEEEEEEEEE
748 - 767:	EEEEEEEEEEEEEEEEEEEE
749 - 768:	EEEEEEEEEEEEEEEEEEEE
750 - 769:	EEEEEEEEEEEEEEEEEEEE
751 - 770:	EEEEEEEEEEEEEEEEEEEE
752 - 771:	EEEEEEEEEEEEEEEEEEEE

A0A2I3RFU6 **A0A2I3RFU6_PANTR** (914 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Pan troglodytes (Chimpanzee)*

```
MELAVAVLRDLLRYAAQLPALFRDISMNHLPGLLTSLLGLRPECEQSALEGMKACMTYFPRACGSLKGKLASFFLSRVDA
LSPQLQQLACECYSRLPSLGAGFSQGLKHTESWEQELHSLLASLHTLLGALYEGAETAPVQNEGPGVEMLLSSEDGDAHV
LLQLRQRFSGLARCLGLMLSSEFGAPVSVPVQEILDFICRTLSVSSKNISLHGDGPLRLLLLPSIHLEALDLLSALILAC
GSRLLRFGILIGRLLPQVLNSWSIGRDSLSPGQERPYSTVRTKVYAILELWVQVCGASAGMLQGGASGEALLTHLLSDIS
PPADALKLRSPRGSPDGSLQTGKPSAPKKLKLDVGEAMAPPSHRKGDSNANSDVCAAALRGLSRTILMCGPLIKEETHRG
PLLCTHWGRLHDLVLPLVMGVQQGEVLGSSPYTSSRCRRELYCLLLALLLAPSPRCPPPLACALQAFSLGQREDSLEVSS
FCSEALVTCAALTHPRVPPLQPMGPTCPTPAPVPPPEAPSPFRAPPFHPPGPMPSVGSMPSAGPMPSAGPMPSAGPVSSA
RPGPPTTANHLGLSVPGLVSVPPRLLPGPENHRAGSNEDPILAPSGTPPPTIPPDETFGGRVPRPAFVHYDKEEASDVEI
SLESDSDDSVVIVPEGLPPLPPPPPSGATPPPIAPTGPPTASPPVPAKEEPEELPAAPGPLPPPPPPPPVPGPVTLPPP
QLVPEGTPGGGGPPALEEDLTVININSSDEEEEEEEEEEEEEEEEEEEDFEEEEEDEEEYFEEEEEEEEEFEEDFEEE
EGELEEEEEEEDDEEEELEDVEREGESPAAGPPPQELVEEEPSAPPTLLEEETEDGSDKVQPPPETPAEEEMETETEAEA
LQEKEQDDTAAMLADFIDCPPDDEKPPPPTEPDS
```

750 - 769:	EEEEEEEEEEEEEEEEEEEE
751 - 770:	EEEEEEEEEEEEEEEEEEEE

A0A2I3RPF7 **A0A2I3RPF7_PANTR** (205 aa)
Cysteine rich hydrophobic domain 1. *Pan troglodytes (Chimpanzee)*

```
MSILLPNMAEFDTISELEEEEEEEEAATSSSSPSSSSSVSGPDDDEEDEEEEEEEEEEEEEEEEEEEEEEEEAPPPPRVVSEE
HLRRYAPDPVLVRGAGHITVFGLSNKFDTEFPSVLTGKVAPEEFKTSIGRVNACLKKALPVNVKWLLCGCLCCCCTLGCS
LWPVICLNKRTRRSIQKLIEWENNRLYHKVILIEFLPKYPIFRPD
```

48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE

A0A2I3S2Q3 **A0A2I3S2Q3_PANTR** (536 aa)
YTH domain containing 1. *Pan troglodytes (Chimpanzee)*

```
KYGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESADTKRQKPSVHSRQLVSKPLSSSVSNNKRIVSTK
GKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVDRRASRSSQ
SSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEEEEEEEEEEEEEEEEEEEYEQDE
RDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSASESYAGSEKKHEKLS
SSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVILIFSVRESGKFQGFAR
LSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLLFPP
DESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRLETFFGLIIGTCIRIT
```

215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE

A0A2I3S8E4 **A0A2I3S8E4_PANTR** (1321 aa)
Tau tubulin kinase 1. *Pan troglodytes (Chimpanzee)*

```
MQCLAAALKDETNMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTRENVALKVESAQQPKQVLKMEVAV
LKKLQGKDHVCRFIGCGRNEKFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESIEAIHSVGFLHRDIKPSNF
AMGRLPSTYRKCYMLDFGLARQYTNTTGDVRPPRNVAGFRGTVRYASVNAHKNREMGRHDDLWSLFYMLVEFAVGQLPWR
KIKDKEQVGMIKEKYEHRMLLKHMPSEFHLFLDHIASLDYFTKPDYQLIMSVFENSMKERGIAENEAFDWEKAGTDALLS
TSTSTPPQQNTRQTAAMFGVVNVTPVPGDLLRENTEDVLQGEHLSDQENAPPILPGRPSEGLGPSPHLVPHPGGPEAEVW
EETDVNRNKLRINIGKSPCVEEEQSRGMGVPSSPVRAPPDSPTTPVRSLRYRRVNSPESERLSTADGRVELPERRSRMDL
PGSPSRQACSSQPAQMLSVDTGHADRQASGRMDVSASVEQEALSNAFRSVPLAEEEDFDSKEWVIIDKETELKDFPPGAE
PSTSGTTDEEPEELRPLPEEGEERRRLGAEPTVRPRGRSMQALAEEDLQHLPPQPLPPQLSQADGRSETSQPPTPGSPSH
SPLHSGPRPRRRESDPTGPQRQVFSVAPPFEVNGLPRAVPLSLPYQDFKRDLSDYRERARLLNRVRKVGFSHMLLTTPQV
PLAPVQPQANGKEEEEEEEEDEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEAAAAVALGEVLGPCSGSSSEGSERSTDRS
QEGAPSTLLADDQKESRGRASMADGDLEPEEGSKTLVLVSPGDMKKSPVTAELAPDPDLGTLAALTPQHERPQPTGSQLD
VSEPGTLSSVLKSEPKPPGPGAGLGAGTVATGVGGVAVTSSPFTKVERTFVHIAEKTHLNVMSSGGQALRSEEFSAGGEL
```

```
GLELASDGGAVEEGARAPLENGLALSGLNGAEIEGSALSGPPRETPSEMATNSLPNGPALADGPAPVSPLEPSPEKVATI
SPRRHAMPGSRPRSRIPVLLSEEDTGSEPSGSLSAKERWSKRARPQQDLARLVMEKRQGRLLLRLASGASSSSSEEQRRA
SETLSGTGSEEDTPASEPAAALPRKSGKAAATRSRIPRPIGLRMPMPVAAQQPASRSHGAAPASDTAITSRLQLQTPPGS
ATAADLRHKQPPGRGLGPGRAQAGARAPAPRSPRLPASTPAARNASASPRSQSLSRRESPSPSHQARSGVPPPRGVPPAR
AQPDGTPSPGGSKKGPRGKLQAQRATTKGRAGGAEGRAGAR
```

749 - 768:	EEEEEEEEEEEEEEEEEEEE
750 - 769:	EEEEEEEEEEEEEEEEEEEE
751 - 770:	EEEEEEEEEEEEEEEEEEEE
752 - 771:	EEEEEEEEEEEEEEEEEEEE

A0A2I3SBZ4 **A0A2I3SBZ4_PANTR** (1233 aa)
Euchromatic histone lysine methyltransferase 2. *Pan troglodytes (Chimpanzee)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGA
LLLEKETRGATERAHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDESENLEGDGDLR
GGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGSEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDLAKRRKLNSGGGLSEELGSARRSGEVTLTKGDPGSLEEWE
TVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAK
KKWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELS
GCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCG
EDASEAQEVTIPRGDGVTPPAGTAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGC
LSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGS
VEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVD
VNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHI
AARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPC
VNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFEC
NQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVY
CIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKH
SAEAIALEQSRLARLDPHPELLPELSSLPPVNT
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE

A0A2I3SKQ4 **A0A2I3SKQ4_PANTR** (727 aa)
YTH domain containing 1. *Pan troglodytes (Chimpanzee)*

```
KYGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESADTKRQKPSVHSRQLVSKPLSSSVSNNKRIVSTK
GKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVDRRASRSSQ
SSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEEEEEEEEEE
EYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSASESYAGSEK
KHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVILIFSVRESGK
FQGFARLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQL
CLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQRPGYLKDPR
YQEVDSFTNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHH
PVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDRG
ERGRYRR
```

222 - 241:	EEEEEEEEEEEEEEEEEEEE

A0A2I3T4L6 **A0A2I3T4L6_PANTR** (1249 aa)
Euchromatic histone lysine methyltransferase 2. *Pan troglodytes (Chimpanzee)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGA
LLLEKETRGATERAHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDESENLEGDGDLR
GGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGSEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDLAKRRKLNSGGGLSEELGSARRSGEVTLTKGDPGSLEEWE
TVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRRSGRLRGWRS
GPEGVRGAPGGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISER
AGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHK
ACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDPLAD
TIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSD
QQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKI
GNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNAR
CDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKI
ICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGR
LLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVRE
DDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDI
KSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELSSLPPVNT
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE

361 - 380:	EEEEEEEEEEEEEEEEEEEE

A0A2I3T6G1 **A0A2I3T6G1_PANTR** (1178 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Pan troglodytes (Chimpanzee)*

```
MLLPSLSPRVQPAFTQCARPQPPPQAPSPVGGRRGVFASSRHATTGTRGKMAAAVLSGPSAGSAAGVPGGTGGLSAVSSG
PRLRLLLLESVSGLLQPRTGSAVAPVHPPNRSAPHLPGLMCLLRLHGSVGGAQNLSALGALVSLSNARLSSIKTRFEGLC
LLSLLVGESPTELFQQHCVSWLRSIQQVLQTQDPPATMELAVAVLRDLLRYAAQLPALFRDISMNHLPGLLTSLLGLRPE
CEQSALEGMKACMTYFPRACGSLKGKLASFFLSRVDALSPQLQQLACECYSRLPSLGAGFSQGLKHTESWEQELHSLLAS
LHTLLGALYEGAETAPVQNEGPGVEMLLSSEDGDAHVLLQLRQRFSGLARCLGLMLSSEFGAPVSVPVQEILDFICRTLS
VSSKNISLHGDGPLRLLLLPSIHLEALDLLSALILACGSRLLRFGILIGRLLPQVLNSWSIGRDSLSPGQERPYSTVRTK
VYAILELWVQVCGASAGMLQGGASGEALLTHLLSDISPPADALKLRSPRGSPDGSLQTGKPSAPKKLKLDVGEAMAPPSH
RKGDSNANSDVCAAALRGLSRTILMCGPLIKEETHRGPLLCTHWGRLHDLVLPLVMGVQQGEVLGSSPYTSSRCRRELYC
LLLALLLAPSPRCPPPLACALQAFSLGQREDSLEVSSFCSEALVTCAALTHPRVPPLQPMGPTCPTPAPVPPPEAPSPFR
APPFHPPGPMPSVGSMPSAGPMPSAGPMPSAGPVSSARPGPPTTANHLGLSVPGLVSVPPRLLPGPENHRAGSNEDPILA
PSGTPPPTIPPDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDSVVIVPEGLPPLPPPPPSGATPPPIAPTGPPTASP
PVPAKEEPEELPAAPGPLPPPPPPPPPVPGPVTLPPPQLVPEGTPGGGGPPALEEDLTVININSSDEEEEEEEEEEEEEE
EEEEEEEDFEEEEEDEEEYFEEEEEEEEEFEEDFEEEEGELEEEEEEEDDEEEELEDVEDLEFGTAGGEVEEGAPPPPTL
PPALPPPESPPKVQPEPEPEPGLLLEVEEPGTEEERGADTAPTLAPEALPSQGEVEREGESPAAGPPPQELVEEEPSAPP
TLLEEETEDGSDKVQPPPETPAEEEMETETEAEALQEKVRGQAGKVPWARRWGWREKG
```

947 - 966:	EEEEEEEEEEEEEEEEEEEE
948 - 967:	EEEEEEEEEEEEEEEEEEEE

A0A2I3TW69 **A0A2I3TW69_PANTR** (1215 aa)
Euchromatic histone lysine methyltransferase 2. *Pan troglodytes (Chimpanzee)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGA
LLLEKETRGATERAHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDESENLEGDGDLR
GGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGSEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDLAKRRKLNSGGGLSEELGSARRSGEVTLTKGDPGSLEEWE
TVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRRSGRLRGWRS
GPEGVRGAPGGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRV
ALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVT
PPAGTAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKA
LVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVD
KQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEH
KHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGA
NPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISE
NCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSG
IKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLC
DPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPH
PELLPELSSLPPVNT
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE

A0A2I4AYB7 **A0A2I4AYB7_9TELE** (951 aa)
B-cell lymphoma/leukemia 11A-like. *Austrofundulus limnaeus*

```
MFLPTYPPLESDIVVNPVFDVDANLLLISSFLSSPNPLCPPPAAAAERLSTAVVSSEELSERCSEHSEESGSPNGHHPGP
AGVRLARLGHDAHHHHHHHHHHHAAEQDLLTCGQCQATFPLADILLFIEHKRKRCHGPPCFAGGRGLDKPPSPSPGLALT
PSPALSALRGRRPVEVGVQATLADEDDERFSSPRGICPKQEPLPGKEEPTTYTCTTCKQSYGSAWFLLQHAQNTHGFRIY
LESEHGSPLTPRMGGPSSLGGGADCPSQPPLHGLHLPPDASPFNLLRIPGSGSGGRDSVGAGGVIGASGPVAVGHHQRFP
PTPPLFSSPPRNHLDPHHLSPEELALAAHHPSAFDRVLRLNPPLPLDPPPTMDFSRRLRELAGNTSGSTPPLSPSRPSPM
QRLLQPFQTGGNGSTGGVGGSKPPYLATPPPLPGSMQSPVGSQTTPTTPLPSAGATPSSTTQLKSKCCEFCGKAFKFQSN
LIVHRRSHTGEKPYKCHLCDHACTQASKLKRHMKTHMHKSSSPNTGKSEDGLSIASSPEPGTSEHIGSASNALKSVVAKL
KSENNRMLRENGEEEEEEEEEEEEEEEEEEEEEEEEEEEEVEEEEVQNGERAVKRNNSYHFGLNLETARQHENSGGIGSRLG
GVADDASIPRSLPEVMQGMGLAASMQHFSEALNAHKRNAMAQENHLHHHLNRDHHHSREMCDGDSVLETDRGEESSVSVV
NGRGASPNESASVGLSKKLLLGSPSPLSPFSKRIKLEKEFDLPTPTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQS
PFASSSEHSSENGSLRFSTPPGELDGGMSGRSGTGSGGSTPHLGGPGRPSSKDGRRSDTCEYCGKVFKNCSNLTVHRRSH
TGERPYKCDLCNYACAQSSKLTRHMKTHGQVGKDVYKCEICKMPFSVYSTLEKHMKKWHSDRPLSTEIKSE
```

573 - 592:	EEEEEEEEEEEEEEEEEEEE
574 - 593:	EEEEEEEEEEEEEEEEEEEE
575 - 594:	EEEEEEEEEEEEEEEEEEEE
576 - 595:	EEEEEEEEEEEEEEEEEEEE
577 - 596:	EEEEEEEEEEEEEEEEEEEE
578 - 597:	EEEEEEEEEEEEEEEEEEEE
579 - 598:	EEEEEEEEEEEEEEEEEEEE

A0A2I4BQ74 **A0A2I4BQ74_9TELE** (1054 aa)
MORC family CW-type zinc finger protein 2. *Austrofundulus limnaeus*

```
MAYSSYSNLSRAQLTFEYLHTNSTTHEFLFGALAELVDNSRDADATRIDIYTEKRPELRGGFSLCFLDDGIGMDPLEATH
VIQFGKSSKRSPESTQIGQYGNGLKSGSMRIGKDFILFTKKENTLTCLFLSRTFHEEEGLDEVIVPLPSWDLKTKEPLTS
DPEKYAIETELIFKYSPFKNEQQLMEQFSKIESDSGTLVVIYNLKLMDNGEPELDVESDHQDILMAGTPVEGVKPERRSF
RAYTAVLYIDPRMRIFIQGHKVRTKRLSCCLYKPRMYKYTSTRFKTRAEQEVKKADHLSKIAEEKAREADSKRVAMEARL
GDDLSKESRAILRKVQDSAMMLRREADIRKRNLEAKQKALKEPKDLNFIFGLNIEQRDLDGMFVYNCSRLIKLYEKTGPQ
LEGGMACGGVVGVVDVPYLVLEPTHNKQDFADAKEYRHLLKAMGEYLAQYWKDINIAQKGIVKFWDEFGYLSASWSAPPS
SELRYKRRRAMEIPLTIQCDKCLKWRTLPFQLDAVDKRYPDSWVCLMNPDSSQDRCDAAEQRQNLPCGVLKKDKPTADDK
KKELAEKIKQQQEKLEALEKTSTIKSAEDIKKLPLEVSTRPTKTLQTTRSSERTTTRPRSPPLPAHLKNAPSVPPTRTAS
QRPSRTSAPPTPPAKVELSRTRAAAKPPPPAPKPVPKTPAKAPPLSRSPRASTKAASVKPAPAGQRKRIIEQENSEEEEE
EEEEEEEEEEEEEEEEEXSEEENEEEPQTKKLKMATATSNRGKVVEKAPPPKRGKLDEVKTQTQPEKKTISTPLRQPPTT
PASVAKSISTPQQDAKAKASEKEKEAENDIKNAQKDKGLLVEVRVNKEWFTGKVIAVETNKQSVRWKVKFDYVPRSTPKD
RWVFKGSDEVRLMRPPSPISQTPDTQQEVEKGPAPMEPDTTQPGTSREVTDSLVAMMRTMLRYFYPPAFRIPKDDVNSMT
AEELVAFPLKEYFQQYESGLQSLCNSYQSRADARAKAVEEKNNNAELKLKEADEKLQKLRTNIVALLQKVQEDIDINTDD
ELDAYIEDLLTKGD
```

716 - 735:	EEEEEEEEEEEEEEEEEEEE
717 - 736:	EEEEEEEEEEEEEEEEEEEE
718 - 737:	EEEEEEEEEEEEEEEEEEEE

A0A2I4C599 **A0A2I4C599_9TELE** (835 aa)
B-cell lymphoma/leukemia 11B-like isoform X1. *Austrofundulus limnaeus*

```
MSRRKQVNPQHFSLTHRETAQAEANHDSGARSPSPQPSSPSLRRPGHGEQDLLTCGQCQTNFPLGDILVFIEHKRRLCRG
PGGRPGSFTKPGETGGVMGVPVLPRARSLELGRGSVPVEVGVQVTPGGEEDEQRRLTPAKGICPKQEKGDKDEPSSYICT
TCKQTFSSAWFLLQHAQNTHGIRIYLDNHLANCSLTPRMALPPPPGVDALPRSPLPTFLGDTNNPFHLLRMAAPLLREHP
HPQAYIETRLPATPPFVSPPPPPRPPLERLGPEEMGLLSQHPSAFERVMRMTPMEPPPMDFSRRLRELAGNPTNNGGPTP
PLSPNRVPPMHRLLSPTLFQPGAKPPAFLTYAPQPPTSQGGHGSSSPPDVQGQNQALGKAKSCEFCGKVFKFQSNLIVHR
RSHTGERPYKCHLCDHACSQASKLKRHMKTHMHNKSGNMTDSPEQESRGEGGEGEDKGREGDVRAMELENEEEEEEEEEE
EEEEEEEEEELRDGSRPDSNLSEDSQEFNQNRENGPRQPHEDKPLSGDRVNDNAGVGIMHPYNHMDNHLRLNPKKRNMER
QPNGDGGERVEAERENERESDREREEQREARPLMNGRITVTEAESFPGLFQRRPTPITSPSPSNNKRIKIEKEPLELPPA
IPLISPENVYSQLLAGYAASRHFIREPFLGFTDSRQSPFATSSEHSSSETGSLRFSTPPGELMEGGSISGHSGSSTPHLL
RGPGPGRPPSSKDKRNDTCEYCGKVFKNCSNLTVHRRSHTGERPYKCDLCSYACAQSSKLTRHMKTHGQFGKEVYRCDIC
HMPFSVYSTLEKHMKKWHGEHLMASEVKLEQADRG
```

471 - 490:	EEEEEEEEEEEEEEEEEEEE

A0A2I4C5A8 **A0A2I4C5A8_9TELE** (834 aa)
B-cell lymphoma/leukemia 11B-like isoform X2. *Austrofundulus limnaeus*

```
MSRRKQVNPQHFSLTHRETAQEANHDSGARSPSPQPSSPSLRRPGHGEQDLLTCGQCQTNFPLGDILVFIEHKRRLCRGP
GGRPGSFTKPGETGGVMGVPVLPRARSLELGRGSVPVEVGVQVTPGGEEDEQRRLTPAKGICPKQEKGDKDEPSSYICTT
CKQTFSSAWFLLQHAQNTHGIRIYLDNHLANCSLTPRMALPPPPGVDALPRSPLPTFLGDTNNPFHLLRMAAPLLREHPH
PQAYIETRLPATPPFVSPPPPPRPPLERLGPEEMGLLSQHPSAFERVMRMTPMEPPPMDFSRRLRELAGNPTNNGGPTPP
LSPNRVPPMHRLLSPTLFQPGAKPPAFLTYAPQPPTSQGGHGSSSPPDVQGQNQALGKAKSCEFCGKVFKFQSNLIVHRR
SHTGERPYKCHLCDHACSQASKLKRHMKTHMHNKSGNMTDSPEQESRGEGGEGEDKGREGDVRAMELENEEEEEEEEEE
EEEEEEEEELRDGSRPDSNLSEDSQEFNQNRENGPRQPHEDKPLSGDRVNDNAGVGIMHPYNHMDNHLRLNPKKRNMERQ
PNGDGGERVEAERENERESDREREEQREARPLMNGRITVTEAESFPGLFQRRPTPITSPSPSNNKRIKIEKEPLELPPAI
PLISPENVYSQLLAGYAASRHFIREPFLGFTDSRQSPFATSSEHSSSETGSLRFSTPPGELMEGGSISGHSGSSTPHLLR
GPGPGRPPSSKDKRNDTCEYCGKVFKNCSNLTVHRRSHTGERPYKCDLCSYACAQSSKLTRHMKTHGQFGKEVYRCDICH
MPFSVYSTLEKHMKKWHGEHLMASEVKLEQADRG
```

470 - 489:	EEEEEEEEEEEEEEEEEEEE

A0A2I4DCQ7 **A0A2I4DCQ7_9TELE** (258 aa)
glutamic acid-rich protein-like. *Austrofundulus limnaeus*

```
MELKKKESFSRVAFRKKQRSLDIQEQEAQERRSKTPCCQTKSAEDENCVGVKIEQSRALGSSLIYKQPSASTVQDCLNRA
TAVTTNRTRGGVHGRGPGSRPRLPSKPEVPPKPAHLTSPVSQVSSPLITLRKAPFRSSMEDRGGKPGPVARERMRDKTNK
VSDLISRFEENSSTENKKDSSPAKHINITSNYSAAQRVFQKTEASRVQDKRLATPTAQDAKKPAANGVLVQMDQEKPKEE
EEEEEEEEEEEEEEEEEE
```

239 - 258:	EEEEEEEEEEEEEEEEEEEE

A0A2I4EEK3 **A0A2I4EEK3_JUGRE** (601 aa)
bromodomain-containing factor 2. *Juglans regia (English walnut)*

```
MKRKRGHKKGKPKGPPVVVKNEASLNAVSVNTEDNSGLDGYGNGTKYDSGMEVDTPSSTGTDQPHNVASIKPDGSIDKAV
GKSVGRVKVKLRTSKTLEAQHTSSDAPTQSDTDKSSQQLGLERQGMGMEKMEDSANSLPIGVLGNPAKRAGSIKIKSSKV
LDNSGGYHSSAVVVQGENPHQEEPKVLHQDTRYIKQELDTALMVIKKVMKMDAAEPFNVPVDPIALGIPDYFDVIDTPMD
FGTICSNLENGVKYKNSEDVYKDVQYIWENCNRYNNKGDYILDLMRRVKKNFMKYWTAAGLYGEQLRGTKGVESIQVEDV
VLSSLGKVPVKGGQSKQKTGKRHGRRHKSDCLCAICVLKRRRKEREENARLAKGHIGATDNNYAQETKQEKSLIVESPCT
EDSSSNAESLDTDANAEVEEKVEEVKLEVMEKKLNTSEEKHGKEEEEEEEEEEEEEEEEEEEEEEEEENEMEIQKKDGNET
PEQPQFGDRSGEDLDRQPKLRIVEKSGVGVLIDTQKEDSLMRHEAKSAAVQQQKHKESLEKHKKVEALKNFHLENPVLLD
LCGILFPDNQKSVWSGPHSLNQHHRSARTSSIRAAIQTFMK
```

444 - 463:	EEEEEEEEEEEEEEEEEEEE

445 - 464:	EEEEEEEEEEEEEEEEEEEE
446 - 465:	EEEEEEEEEEEEEEEEEEEE
447 - 466:	EEEEEEEEEEEEEEEEEEEE
448 - 467:	EEEEEEEEEEEEEEEEEEEE

A0A2J6LSU8 **A0A2J6LSU8_LACSA** (247 aa)
TPR_REGION domain-containing protein. *Lactuca sativa (Garden lettuce)*

```
MNKIERAHQMYRDGNYEEALEFYTEALSIAKTNPQKIALHSNRAACFLKLHHFKKAAEECTSVLELDHEHTGALMLRAQT
LVTLKEYHSALFDVNRLIELNPSSEVYQNLEARLKTQLSLAPIPELEEEEEEEEEEEEEEEEEEEEDNEEDEQSTSVEIA
ENDIDDTKGHEPDTAVSNLENVEITITPPQTQSLKEEIPKPKGHSRLDYSRWDKVEDDSSEEDEDDDEDSQPQYRFRVKN
IGVRSVK
```

127 - 146:	EEEEEEEEEEEEEEEEEEEE

A0A2J6M5Y9 **A0A2J6M5Y9_LACSA** (643 aa)
C3H1-type domain-containing protein. *Lactuca sativa (Garden lettuce)*

```
MPTTTSASAAAAGKSPIASDSDEYEYEYEYEEIEVEEEVEVEVEEEVSDEEVNEEEDEEEVEEKGEDILPTIIDGEDHKK
SAHHSVVKIDEEEEEEEEEEEEEEEEEEEEEEEEEEEEPEEQEEVEEKREDISPPIDDGDHEKGKTTTVDDGGMLYTDNDNK
PSQSDHGGITTSSVNTSNPVGVSVSAEVVKVSGESVIQVPNDDDDKFPPEKGSKESNEVIQSPLSEKETKETNEGNSNFP
PSSEKETKGTNDQDMDDKHQKQPVRLDVPLRRPRSSSPVTKTKEGNKRQVLVCEFFAKGWCIKGKSCRFLHIKESKEDKQ
CNSQNTPSISAQMTKIPPLNHSSVWTSNSLLFSSSSSSWNNPDSFPTMNDYKSGSETKHLYQNQNQNQDKVLSGDSHSTR
FYKYDWEPSKPFRSMFLLSQGLSPSTLYDPIRDSIDPPDYGVGVSKFSSSCQGPSTSTTHSPKNINPPVKGTPHDIDIDN
ASERHSVASHDKDTSSNKVNVEKGNEHMHTSHVYNGDMTEASEANDGPTKREIKETSEAKGDEVVMQRESKALRHFRGAL
IEFVKEIVKPAWREGNLSKDAHKVVVKKVVDKVLSTLSSENIPSTEDATDFYLSSCQQKLVKLVEVRVLYEVNYRMEDIF
YLI
```

91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE

A0A2J6PNA9 **A0A2J6PNA9_9HELO** (241 aa)
Uncharacterized protein. *Hyaloscypha hepaticicola*

```
MALLRPHRYIRATWSSAPPLARAGFIISSNLPEAGQPLPTRAKLADVLAPASASHGSSNEAMSTSNQQADQAKPHPKLIT
QADYIAADIMNRDNIEGILDEMEGPNAPDENATSSVMQMHQKTISIFREAHIHSSPVVSWNLECLAEGMMQVRWTIDDSN
TKPFSKDPDYKLVKDPEVDFEASKAAKLRLLKFMEDEARILGGIEAYEVGWWREEEEEEEEEEEEEEEEEEEEEEDEDE
D
```

214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE

A0A2J6PNJ1 **A0A2J6PNJ1_9HELO** (408 aa)
Uncharacterized protein. *Hyaloscypha hepaticicola*

```
MAGLGFQSDASATSDAHDSAEISTQDNPSVTFDPTRPLELRSNTGGDMSAMSSSNSLDEEDSDKERDGYFEGDSDMHSEG
HSEAYSDEDTDGEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
NFDLSRPRAILPSPEYVTRLYDDIEMEHFETAEDDPTLSVPVWDLTLRGDVGSLLHACHHSRVTAGQVFSLDLEESVEDW
NPKLWDPVNDTLYLKGLASSRRDNVFLWWLSDSRKRPYIGFISVEHIALKLDTLLATWLLPEADIPSEYEHFGGNNWLDN
LPSMQTINLCIDPLHFSKYKYGQADPYPPLDVPVRILNNFTPSQIQREVTNSLEEQIRDDRGSPSPRPARKAPTVEVSVL
CWRSTVLK
```

96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE

A0A2J6QUC9 **A0A2J6QUC9_9HELO** (77 aa)
Uncharacterized protein. *Hyaloscypha variabilis F*

```
MAAEMNHKALSFEVPNRFKGNKVEEGKEEGEEEGIEGIKEGREEEEKEEEEEEEEEEEEEEEEEEEEEEEWSSL
```

48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE

A0A2J7PGD5 **A0A2J7PGD5_9NEOP** (186 aa)
Uncharacterized protein. *Cryptotermes secundus*

```
MERNISIQSSWHFNVSFCITLSHSLYLYFISLFVLYMCIIGFTYLLCFRALTGKYPPKIQVASKYERRVDTRSYDDKKKL
FEGGLEAQTKEFIERQWTDKSSEFDSRQKSKLPKWFGERPGKKKGDPESPEEEEVKADVGVDEDLEEPTFEPEPEPEEEE
AAEEEVEEEEEEEEEEEEEEEEEEE
```

167 - 186:	EEEEEEEEEEEEEEEEEEEE

A0A2J7PGE3 **A0A2J7PGE3_9NEOP** (306 aa)
Troponin T. *Cryptotermes secundus*

```
MRADEEKRMAERKKQEEERRVREVEEKKQRDIEEKRRRLEEAEKKRQAMMQALKEQKQQKGPNFTIQKKDPSFNLSSAQI
ERNKTKEQLEEEKKISLSFRIKPLEIENLGVDKLRAKATELWEAIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHK
AQKRGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGLEAQTKEFIERQWTDKSSEFDSRQKSKLPKWFGERP
GKKKGDPESPEEEEVKADVGVDEDLEEPTFEPEPEPEEEEAAEEEVEEEEEEEEEEEEEEEEEEEE
```

287 - 306:	EEEEEEEEEEEEEEEEEEEE

A0A2J7PGF0 **A0A2J7PGF0_9NEOP** (306 aa)
Troponin T. *Cryptotermes secundus*

```
MRADEEKRMAERKKQEEERRVREVEEKKQRDIEEKRRRLEEAEKKRQAMMQALKEQKQQKGPNFTIQKKDPSFNLSSAQI
ERNKTKEQLEEEKKISLSFRIKPLEIENLGVDKLRAKATELWEAIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHK
AQKRGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWATISSESSEKNWKSKYDLFTNRSKSKLPKWFGERP
GKKKGDPESPEEEEVKADVGVDEDLEEPTFEPEPEPEEEEAAEEEVEEEEEEEEEEEEEEEEEEEE
```

287 - 306:	EEEEEEEEEEEEEEEEEEEE

A0A2J7PLE9 **A0A2J7PLE9_9NEOP** (167 aa)
Uncharacterized protein. *Cryptotermes secundus*

```
MESQQMMELLLKEIRTDQAKTEANRKTDKEEMLARMDANMKSCQENAELDRKTGQPINRKETMACQETEARLEEEEEEEE
EEEEEEEEEEEEDPTSGDMKPEAAERREVPVEDAAVIPVGPKKKLRRDRKLAAERRRQKPKYTTRKHFVSQKKLAVARRG
TSHRAKV
```

73 - 92:	EEEEEEEEEEEEEEEEEEEE

A0A2J8DN68 **A0A2J8DN68_VERDA** (2041 aa)
Histone transcription regulator 3 homolog. *Verticillium dahliae (Verticillium wilt)*

```
MPAFQAINVEPEENLDDEIDNTRQIHIDEALKRFQTALKLHAQGPRFFDEATDAYDDLFKSDIFQYPEAATEYERAELPA
SQLAVEASLAAGIDIQSGEVDGADSTLPQALFLAHKNHGQFLLDRIKHTARRTAVPPEAFFQQDDVKEQAQKALLDFNAA
LDRDPSDAELWRRIARVAGYLNSGRIRRYCLEAAIELDDDPTVEEVEPPSLAEGLAGEELKEHLQVLSDDMGLSHPILGP
WVKHDMPALIKRHLDPIPFLPNPTKSLEATRSILTVSESKISIRCPTAAWSELGMALVQLVAEVGFTGKGITIDLPNSEP
DEEAMDITDAIQKQLTEEVSSAAVDVGLPDVMDVSDSATKTEAADETAAADGLKPRGETASAPARKRSQSVAGLAEAGED
ENAGEKRSKRIRRRETAGAGEVVNSSALHATQLAQYQAVDQHLFQKTKDVLENIGVTDQSVLDRIGEVLELCTSEDRSDK
STSQATIDLKSTITSFSADNAKILINKKETDTLGMSAFLEHAKGGNQKVSASPAFRESHGLGSFAKRLNAGWTTVQDMAW
EWLKTIAPSYIEYRWSDMMKAAVVHVISRFDQDIYEMAKYEIEATAQSKHAEQELMRIHNLVEMLFELHLDIYERITNPN
SAVEYSIRVEAKGRLARWLAFASELFQACRDPRSDLAARFLWAAVFSTTLTDNVSREYILQCWTSLREFLTNEGVEALFL
QNNAVLTEISSAAADREISKLTTMDFFLGLFQDDISDPVAIIDNLEPVLNADSVYVPRSDSDGEATSGKNKRIPIRDCAS
QGLQDLWKFIKGTSTELRLFLWSRLSDAYGSIQYATKQFSCQLRAIEMVVADFEGDLYLKNPNDTRPVLLLRMMKSLDEL
LIRALSLALNEQSAYDIVDEDHLKATAAALAKLSCMLHVSASLEDEIRIGMTQAPSGGSVFQAFMNKLREIQVRTWCLQY
TVLKIGIIQHTDVFPKYESDLAEYLAAIHNVLGPRKSCKASNKIFLKMMRMELLKLKNIDNWEDYLGQVLYDLHGLKLGV
GIWEVQDHGCPPEKLERRNTIQLADKITVLARRMPMKDLLKSELKTTIEHMQGAIGPVRSTPQMVHNLRNYTEYFKRPVH
PLRLYQALRGGVELDTVSVNAPETVLANHGWFFLLGSIALSKYKLVDLSKRQTPGAMDDLRIGATFLRHQLQFTPNNWEG
WFRLAECFDYEVEDAVVWSADKMNKDRAELVKFQRNSIHCHTLALSKSVGADTDYEEGDPLHDLYHNFAMRLYASSREPF
AMEPFQHSNHERTFIENTGMGTFQRVLHNQMQDYKVWKNPFMISKCLWKMYQTPDENLSATDRATKPTVDRVIKALEHAI
DVASVVPKTRNSDPILEPHYKILSIAQKLVARGDLSSQQATIILARQPFGIRAETDDGDTSEDTEDWEEYVIRSLRHLRD
KDKSNWQHRMIVRHARLLFDDSAQSHADYVQAKAAFNVLRESMFTKTMVMNVWKCEAERPGRHHVFTEQYVRLMVKILVV
MSDRVSLEALLRRIRKKGTEFYHFADLWQTCCHSYLALLRQSHKVRPIEEDKFKLVATEDFEIMADRLAEWAGEFAGDLP
VLQCMKEAIELKKLNGGLMKAGAIDEVINDCYTYLYLEIGPTLPGPSPSEVLEARARARAREEAQNDVSNSLKPQSTLTN
ILNPPGSQEANGDGEKQTEALPRKKVGIRRPDILRRAEQVYTRAMEAPKSAGLASKSRLGSISSGKRGSNTPNGGEAGSP
ASDRSDMEEPVGDDTEMKDEPTIDEGDDPDATAQMTAASSPRGSIHDSADDESDLSDVPEGWDEEPPPSMLFHDMKAEDG
HHSSDEDADEADEEDDEEQEDEQEDEQEDETMGGVDADVEDETMEAHEEDETLAGPEDETLGDHEDETLEGHEEDETMED
HEEDETIGVHEEDDEEAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEEAEEGDEAEEAEEGDEAEEDEEAEEQGED
EAEEAEEDGEEEDEEEEEEEGDSREVADEDEEGSEAVETDG
```

1938 - 1957:	EEEEEEEEEEEEEEEEEEEE
1939 - 1958:	EEEEEEEEEEEEEEEEEEEE
1940 - 1959:	EEEEEEEEEEEEEEEEEEEE
1941 - 1960:	EEEEEEEEEEEEEEEEEEEE
1942 - 1961:	EEEEEEEEEEEEEEEEEEEE
1943 - 1962:	EEEEEEEEEEEEEEEEEEEE
1944 - 1963:	EEEEEEEEEEEEEEEEEEEE
1945 - 1964:	EEEEEEEEEEEEEEEEEEEE
1946 - 1965:	EEEEEEEEEEEEEEEEEEEE
1947 - 1966:	EEEEEEEEEEEEEEEEEEEE
1948 - 1967:	EEEEEEEEEEEEEEEEEEEE
1949 - 1968:	EEEEEEEEEEEEEEEEEEEE

A0A2J8DV06 **A0A2J8DV06_VERDA** (31 aa)
Uncharacterized protein. *Verticillium dahliae (Verticillium wilt)*

```
MPSSLLEEVLEEEEEEEEEEEEEEEEEEEEET
```

11 - 30:	EEEEEEEEEEEEEEEEEEEE

A0A2J8IVF8 **A0A2J8IVF8_PANTR** (382 aa)
FAM9A isoform 3. *Pan troglodytes (Chimpanzee)*

```
MEPVGRKRSRKAAKAQLEAQVRAAPAKKHTGSGVASNFPGQPTMEPVGRKRSRKAAKAQLEAQVRAAPAKKHTGKDPVSD
ECEERNPFTETREGDVTDEHGEREPFAETDEHTGIHTMKLEYIAADIKKGLAAIREMIKIDKAAYRETKNTIECALKKKQ
LKRQKRDYRHTRKLLNVLKEYIAEKQKDDEAEEAEAAAAAAEAAAAAEAAAAAAAAAAAEVIVVEDEEEEEKEEEEEKEEE
EEEGEEEGGGEEGEEEGGGGEGEETEEEEEEEEEGGGGEGEETEEEEEEEEEGGGGEGEETEEEEEEEEEEEEEEEEEEE
EEEEEQIKAFQEKQKRWQQPTGVRSWRLREMKPLLEQLLQAAKDTKDNYCIISSSEESLDN
```

302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE
306 - 325:	EEEEEEEEEEEEEEEEEEEE

A0A2J8IVG9 **A0A2J8IVG9_PANTR** (400 aa)
FAM9A isoform 1 (FAM9A isoform 2). *Pan troglodytes (Chimpanzee)*

```
MEPVGRKRSRKAAKAQLEAQVRAAPAKKHTGKHSPKGHERSCTPKEMVCSGVASNFPGQPTMEPVGRKRSRKAAKAQLEA
QVRAAPAKKHTGKDPVSDECEERNPFTETREGDVTDEHGEREPFAETDEHTGIHTMKLEYIAADIKKGLAAIREMIKIDK
AAYRETKNTIECALKKKQLKRQKRDYRHTRKLLNVLKEYIAEKQKDDEAEEAEAAAAAAEAAAAAEAAAAAAAAAAEVIV
VEDEEEEEKEEEEEKEEEEEEGEEEGGGEEGEEEGGGGEGEETEEEEEEEEEGGGGEGEETEEEEEEEEEGGGGEGEETE
EEEEEEEEEEEEEEEEEEEEEEQIKAFQEKQKRWQQPTGVRSWRLREMKPLLEQLLQAAKDTKDNYCIISSSEESELDN
```

320 - 339:	EEEEEEEEEEEEEEEEEEEE
321 - 340:	EEEEEEEEEEEEEEEEEEEE
322 - 341:	EEEEEEEEEEEEEEEEEEEE
323 - 342:	EEEEEEEEEEEEEEEEEEEE
324 - 343:	EEEEEEEEEEEEEEEEEEEE

A0A2J8KQT4 **A0A2J8KQT4_PANTR** (981 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Pan troglodytes (Chimpanzee)*

```
MELAVAVLRDLLRYAAQLPALFRDISMNHLPGLLTSLLGLRPECEQSALEGMKACMTYFPRACGSLKGKLASFFLSRVDA
LSPQLQQLACECYSRLPSLGAGFSQGLKHTESWEQELHSLLASLHTLLGALYEGAETAPVQNEGPGVEMLLSSEDGDAHV
LLQLRQRFSGLARCLGLMLSSEFGAPVSVPVQEILDFICRTLSVSSKNISLHGDGPLRLLLLPSIHLEALDLLSALILAC
GSRLLRFGILIGRLLPQVLNSWSIGRDSLSPGQERPYSTVRTKVYAILELWVQVCGASAGMLQGGASGEALLTHLLSDIS
PPADALKLRSPRGSPDGSLQTGKPSAPKKLKLDVGEAMAPPSHRKGDSNANSDVCAAALRGLSRTILMCGPLIKEETHRR
LHDLVLPLVMGVQQGEVLGSSPYTSSRCRRELYCLLLALLLAPSPRCPPPLACALQAFSLGQREDSLEVSSFCSEALVTC
AALTHPRVPPLQPMGPTCPTPAPVPPPEAPSPFRAPPFHPPGPMPSVGSMPSAGPMPSAGPMPSAGPVSSARPGPPTTAN
HLGLSVPGLVSVPPRLLPGPENHRAGSNEDPILAPSGTPPPTIPPDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDS
VVIVPEGLPPLPPPPPSGATPPPIAPTGPPTASPPVPAKEEPEELPAAPGPLPPPPPPPPPVPGPVTLPPPQLVPEGTPG
GGGPPALEEDLTVININSSDEEEEEEEEEEEEEEEEEEEEEDFEEEEEDEEEYFEEEEEEEEEFEEDFEEEEGELEEEEEE
EDDEEEELEDVEDLEFGTAGGEVEEGAPPPPTLPPALPPPESPPKVQPEPEPEPGLLLEVEEPGTEEERGADTAPTLAPE
ALPSQGEVEREGESPAAGPPPQELVEEEPSAPPTLLEEETEDGSDKVQPPPETPAEEEMETETEAEALQEKEQDDTAAML
ADFIDCPPDDEKPPPPTEPDS
```

741 - 760:	EEEEEEEEEEEEEEEEEEEE

A0A2J8KQT6 **A0A2J8KQT6_PANTR** (1178 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Pan troglodytes (Chimpanzee)*

```
MLLPSLSPRVQPAFTQCARPQPPPQAPSPVGGRRGVFASSRHATTGTRGKMAAAVLSGPSAGSAAGVPGGTGGLSAVSSG
PRLRLLLLESVSGLLQPRTGSAVAPVHPPNRSAPHLPGLMCLLRLHGSVGGAQNLSALGALVSLSNARLSSIKTRFEGLC
LLSLLVGESPTELFQQHCVSWLRSIQQVLQTQDPPATMELAVAVLRDLLRYAAQLPALFRDISMNHLPGLLTSLLGLRPE
CEQSALEGMKACMTYFPRACGSLKGKLASFFLSRVDALSPQLQQLACECYSRLPSLGAGFSQGLKHTESWEQELHSLLAS
LHTLLGALYEGAETAPVQNEGPGVEMLLSSEDGDAHVLLQLRQRFSGLARCLGLMLSSEFGAPVSVPVQEILDFICRTLS
VSSKNISLHGDGPLRLLLLPSIHLEALDLLSALILACGSRLLRFGILIGRLLPQVLNSWSIGRDSLSPGQERPYSTVRTK
VYAILELWVQVCGASAGMLQGGASGEALLTHLLSDISPPADALKLRSPRGSPDGSLQTGKPSAPKKLKLDVGEAMAPPSH
RKGDSNANSDVCAAALRGLSRTILMCGPLIKEETHRRLHDLVLPLVMGVQQGEVLGSSPYTSSRCRRELYCLLLALLLAP
SPRCPPPLACALQAFSLGQREDSLEVSSFCSEALVTCAALTHPRVPPLQPMGPTCPTPAPVPPPEAPSPFRAPPFHPPGP
MPSVGSMPSAGPMPSAGPMPSAGPVSSARPGPPTTANHLGLSVPGLVSVPPRLLPGPENHRAGSNEDPILAPSGTPPPTI
PPDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDSVVIVPEGLPPLPPPPPSGATPPPIAPTGPPTASPPVPAKEEPE
ELPAAPGPLPPPPPPPPPVPGPVTLPPPQLVPEGTPGGGGPPALEEDLTVININSSDEEEEEEEEEEEEEEEEEEEEDFE
EEEEDEEEYFEEEEEEEEEFEEDFEEEEGELEEEEEEEDDEEEELEDVEDLEFGTAGGEVEEGAPPPPTLPPALPPPESP
PKVQPEPEPEPGLLLEVEEPGTEEERGADTAPTLAPEALPSQGEVEREGESPAAGPPPQELVEEEPSAPPTLLEEETEDG
SDKVQPPPETPAEEEMETETEAEALQEKEQDDTAAMLADFIDCPPDDEKPPPPTEPDS
```

938 - 957:	EEEEEEEEEEEEEEEEEEEE

A0A2J8KQV5 **A0A2J8KQV5_PANTR** (904 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Pan troglodytes (Chimpanzee)*

```
MELAVAVLRDLLRYAAQLPALFRDISMNHLPGLLTSLLGLRPECEQSALEGMKACMTYFPRACGSLKGKLASFFLSRVDA
LSPQLQQLACECYSRLPSLGAGFSQGLKHTESWEQELHSLLASLHTLLGALYEGAETAPVQNEGPGVEMLLSSEDGDAHV
LLQLRQRFSGLARCLGLMLSSEFGAPVSVPVQEILDFICRTLSVSSKNISLHGDGPLRLLLLPSIHLEALDLLSALILAC
GSRLLRFGILIGRLLPQVLNSWSIGRDSLSPGQERPYSTVRTKVYAILELWVQVCGASAGMLQGGASGEALLTHLLSDIS
PPADALKLRSPRGSPDGSLQTGKPSAPKKLKLDVGEAMAPPSHRKGDSNANSDVCAAALRGLSRTILMCGPLIKEETHRR
LHDLVLPLVMGVQQGEVLGSSPYTSSRCRRELYCLLLALLLAPSPRCPPPLACALQAFSLGQREDSLEVSSFCSEALVTC
AALTHPRVPPLQPMGPTCPTPAPVPPPEAPSPFRAPPFHPPGPMPSVGSMPSAGPMPSAGPMPSAGPVSSARPGPPTTAN
HLGLSVPGLVSVPPRLLPGPENHRAGSNEDPILAPSGTPPPTIPPDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDS
VVIVPEGLPPLPPPPPSGATPPPIAPTGPPTASPPVPAKEEPEELPAAPGPLPPPPPPPPPVPGPVTLPPPQLVPEGTPG
GGGPPALEEDLTVININSSDEEEEEEEEEEEEEEEEEEEEEDFEEEEEDEEEYFEEEEEEEEEFEEDFEEEEGELEEEEEE
EDDEEEELEDVEREGESPAAGPPPQELVEEEPSAPPTLLEEETEDGSDKVQPPPETPAEEEMETETEAEALQEKEQDDTA
AMLADFIDCPPDDEKPPPPTEPDS
```

741 - 760:	EEEEEEEEEEEEEEEEEEEE

A0A2J8KQW1 **A0A2J8KQW1_PANTR** (1128 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Pan troglodytes*

(Chimpanzee)

```
MAAAVLSGPSAGSAAGVPGGTGGLSAVSSGPRLRLLLLESVSGLLQPRTGSAVAPVHPPNRSAPHLPGLMCLLRLHGSVG
GAQNLSALGALVSLSNARLSSIKTRFEGLCLLSLLVGESPTELFQQHCVSWLRSIQQVLQTQDPPATMELAVAVLRDLLR
YAAQLPALFRDISMNHLPGLLTSLLGLRPECEQSALEGMKACMTYFPRACGSLKGKLASFFLSRVDALSPQLQQLACECY
SRLPSLGAGFSQGLKHTESWEQELHSLLASLHTLLGALYEGAETAPVQNEGPGVEMLLSSEDGDAHVLLQLRQRFSGLAR
CLGLMLSSEFGAPVSVPVQEILDFICRTLSVSSKNISLHGDGPLRLLLLPSIHLEALDLLSALILACGSRLLRFGILIGR
LLPQVLNSWSIGRDSLSPGQERPYSTVRTKVYAILELWVQVCGASAGMLQGGASGEALLTHLLSDISPPADALKLRSPRG
SPDGSLQTGKPSAPKKLKLDVGEAMAPPSHRKGDSNANSDVCAAALRGLSRTILMCGPLIKEETHRRLHDLVLPLVMGVQ
QGEVLGSSPYTSSRCRRELYCLLLALLLAPSPRCPPPLACALQAFSLGQREDSLEVSSFCSEALVTCAALTHPRVPPLQP
MGPTCPTPAPVPPPEAPSPFRAPPFHPPGPMPSVGSMPSAGPMPSAGPMPSAGPVSSARPGPPTTANHLGLSVPGLVSVP
PRLLPGPENHRAGSNEDPILAPSGTPPPTIPPDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDSVVIVPEGLPPLPP
PPPSGATPPPIAPTGPPTASPPVPAKEEPEELPAAPGPLPPPPPPPPPVPGPVTLPPPQLVPEGTPGGGGPPALEEDLTV
ININSSDEEEEEEEEEEEEEEEEEEEEEDFEEEEEDEEEYFEEEEEEEEEFEEDFEEEEGELEEEEEEEDDEEEELEDVED
LEFGTAGGEVEEGAPPPPTLPPALPPPESPPKVQPEPEPEPGLLLEVEEPGTEEERGADTAPTLAPEALPSQGEVEREGE
SPAAGPPPQELVEEEPSAPPTLLEEETEDGSDKVQPPPETPAEEEMETETEAEALQEKEQDDTAAMLADFIDCPPDDEKP
PPPTEPDS
```

888 - 907:	EEEEEEEEEEEEEEEEEEEE

A0A2J8PF10 **A0A2J8PF10_PANTR** (727 aa)
YTHDC1 isoform 1. *Pan troglodytes (Chimpanzee)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESADTKRQKPSVHSRQLVSKPLSSSVSN
NKRIVSTKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEE
EEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSAS
ESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVILI
FSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEI
ELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQR
PGYLKDPRYQEVDRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHH
PVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDRG
ERGRYRR
```

230 - 249:	EEEEEEEEEEEEEEEEEEEE

A0A2J8PX12 **A0A2J8PX12_PANTR** (218 aa)
CHIC1 isoform 2. *Pan troglodytes (Chimpanzee)*

```
MAEFDTISELEEEEEEEEAATSSSSPSSSSSVSGPDDDEEDEEEEEEEEEEEEEEEEEEEEEEEAPPPPRVVSEEHLRRYAP
DPVLVRGAGHITVFGLSNKFDTEFPSVLTGKVAPEEFKTSIGRVNACLKKALPVNVKWLLCGCLCCCCTLGCSLWPVICL
NKRTRRSIQKLIEWENNRLYHKLALHWKLTKRKCETSNMMEYVILIEFLPKYPIFRPD
```

41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE

A0A2J8R2S9 **A0A2J8R2S9_PONAB** (1150 aa)
MYT1 isoform 1. *Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)*

```
MSLENEDKRARTRSKALRGPPETTAADLSCPTPGCTGSGHVRGKYSRHRSLQSCPLAKKRKLEGAEAEHLVSKRKSHPLK
LALDEGYGVDSDGSEDTEVKDASVSDESEGTLEGAEAETSGQDEIHRPETAEGRSPVKSHFGSNPIGSPTGSSKGSYSSY
QGIIATSLLNLGQIAEETLVEEDLGQAAKPGPGIVHLLQEATEGAASEEGEKSLFIQPEDAEEVVEVTTERSQDLCPQSL
EDAASEESSKQKGILSHEEEDEEDEEEEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAAPDVIFQEDTSHTS
AQKAPELRGPESPSLKPEYSVIVEVHSDDDKDEDTHSQKSTVTDESEMHDMMTRGNLGLLEQAIALKAEQVRTVCEPGCP
PAEQSQLGLGEPGKAAKPLDTVRKSYYSKDPSRAEKREIKCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRIPPEILAMHE
NVLKCPTPGCTGQGHVNSNRNTHRSLSGCPIAAAEKLAKSHEKQQPQTGDPSKSSSNSDRILRPMCFVKQLEVPPYGSYR
PSVAPATPRANLAKELEKFSKVTFDYASFDAQVFGKRMLAPKIQTSETSPKAFQCFDYSHDAEAAHMAATAILNLSTRCW
EMPENLSTKPQDLPSKSVDIEVDENGTLDLSMHKHRKRENAFPSSSSCSSSPGVKSPDASQRQSSTSAPSSSMTSPQSSQ
ASRQDEWDRPLDYTKPSLLREEEPEESEPAAHSFASSEADDQEVSEENFEERKYPGEVTLTNFKLKFLSKDIKKELLTCP
TPGCDGSGHITGNYASHRSLSGCPLADKSLRNLMAAHSADLKCPTPGCDGSGHITGNYASHRSLSGCPRAKKSGVKVAPT
KDDKEDPELMKCPVPGCVGLGHISGKYASHRSASGCPLAARRQKEGSLNGSSFSWKSLKNEGPTCPTPGCDGSGHANGSF
LTHRSLSGCPRATFAGKKGKLSGDEVLSPSSRLAMEVMPAVTCGFGDHWDQSPVEPMCLLENDEEIKQLNQEIRDLNESN
SEMEAAMVQLQSQISSMEKNLKNIEEENKLIEEQNEALFLELSGLSQALIQSLANIRLPHMEPICEHNFDAYVSTLTDHV
LQPGPREQGPPGEHQAGCEGHPGLGRVETR
```

276 - 295:	EEEEEEEEEEEEEEEEEEEE
277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE

286 - 305:	EEEEEEEEEEEEEEEEEEEE

A0A2J8R2T6 **A0A2J8R2T6_PONAB** (1177 aa)
MYT1 isoform 2. *Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)*

```
MSLENEDKRARTRSKALRGPPETTAADLSCPTPGCTGSGHVRGKYSRHRSLQSCPLAKKRKLEGAEAEHLVSKRKSHPLK
LALDEGYGVDSDGSEDTEVKDASVSDESEGTLEGAEAETSGQDEIHRPETAEGRSPVKSHFGSNPIGSPTGSSKGSYSSY
QGIIATSLLNLGQIAEETLVEEDLGQAAKPGPGIVHLLQEATEGAASEEGEKSLFIQPEDAEEVVEVTTERSQDLCPQSL
EDAASEESSKQKGILSHEEEDEEDEEEEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAAPDVIFQEDTSHTS
AQKAPELRGPESPSLKPEYSVIVEVHSDDDKDEDTHSQKSTVTDESEMHDMMTRGNLGLLEQAIALKAEQVRTVCEPGCP
PAEQSQLGLGEPGKAAKPLDTVRKSYYSKDPSRAEKREIKCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRIPPEILAMHE
NVLKCPTPGCTGQGHVNSNRNTHRSLSGCPIAAAEKLAKSHEKQQPQTGDPSKSSSNSDRILRPMCFVKQLEVPPYGSYR
PSVAPATPRANLAKELEKFSKVTFDYASFDAQVFGKRMLAPKIQTSETSPKAFQSKPFPKASSPRHSPSSSYVRSTSSSS
AGFDYSHDAEAAHMAATAILNLSTRCWEMPENLSTKPQDLPSKSVDIEVDENGTLDLSMHKHRKRENAFPSSSSCSSSPG
VKSPDASQRQSSTSAPSSSMTSPQSSQASRQDEWDRPLDYTKPSLLREEEPEESEPAAHSFASSEADDQEVSEENFEERK
YPGEVTLTNFKLKFLSKDIKKELLTCPTPGCDGSGHITGNYASHRSLSGCPLADKSLRNLMAAHSADLKCPTPGCDGSGH
ITGNYASHRSLSGCPRAKKSGVKVAPTKDDKEDPELMKCPVPGCVGLGHISGKYASHRSASGCPLAARRQKEGSLNGSSF
SWKSLKNEGPTCPTPGCDGSGHANGSFLTHRSLSGCPRATFAGKKGKLSGDEVLSPSSRLAMEVMPAVTCGFGDHWDQSP
VEPMCLLENDEEIKQLNQEIRDLNESNSEMEAAMVQLQSQISSMEKNLKNIEEENKLIEEQNEALFLELSGLSQALIQSL
ANIRLPHMEPICEHNFDAYVSTLTDHVLQPGPREQGPPGEHQAGCEGHPGLGRVETR
```

276 - 295:	EEEEEEEEEEEEEEEEEEEE
277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE

A0A2J8R4G8 **A0A2J8R4G8_PONAB** (1176 aa)
EHMT2 isoform 3. *Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)*

```
MAAAAGAAAAAAAEGEAPAEMGALLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGAD
TPVGATPLIEDESENLEGDGDLHGGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGA
AAAGPEPPPATASPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDMAKRRKLNSGGGLSEEL
GSARRSGEVTLTKGDPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEE
EEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAPK
IDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFR
VAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRP
PCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNL
DPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTC
LHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIA
EVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNR
AIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRC
WYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISD
AEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDY
GDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE

A0A2J8R4H5 **A0A2J8R4H5_PONAB** (1198 aa)
EHMT2 isoform 4. *Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)*

```
MRGLPRGRGLMRARGGVVRPLRAAEAAEGGGPIEEEGEAPAEMGALLLEKETRGATERVHGSLGDTPRSEETLPKATPDS
LEPAGPSSPASVTVTVGDEGADTPVGATPLIEDESENLEGDGDLHGGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAG
KSPPSVQSLAMRLLSMPGAQGAAAAGPEPPPATASPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLG
KVTSDMAKRRKLNSGGGLSEELGSARRSGEVTLTKGDPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQL
SEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTS
SLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHH
CCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLSQDA
PGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPR
QLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLE
VARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVT
LTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTP
ERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQ
HCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGV
RALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLR
FPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

322 - 341:	EEEEEEEEEEEEEEEEEEEE
323 - 342:	EEEEEEEEEEEEEEEEEEEE
324 - 343:	EEEEEEEEEEEEEEEEEEEE
325 - 344:	EEEEEEEEEEEEEEEEEEEE
326 - 345:	EEEEEEEEEEEEEEEEEEEE

A0A2J8R4H7 **A0A2J8R4H7_PONAB** (1210 aa)
EHMT2 isoform 2. *Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)*

```
MAAAAGAAAAAAAEGEAPAEMGALLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGAD
TPVGATPLIEDESENLEGDGDLHGGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGA
AAAGPEPPPATASPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDMAKRRKLNSGGGLSEEL
GSARRSGEVTLTKGDPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEE
EEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTL
SPNHAGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVL
CETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGT
AAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQE
SERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRT
PLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEV
IRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELR
NKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETS
TMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRL
QLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNII
PVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLP
ELGSLPPVNT
```

300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE

A0A2J8R4J5 **A0A2J8R4J5_PONAB** (1266 aa)
EHMT2 isoform 5. *Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)*

```
MRGLPRGRGLMRARRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGAL
LLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIEDESENLEGDGDLHG
GRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGPEPPPATASPEGQPKVHRAR
KTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDMAKRRKLNSGGGLSEELGSARRSGEVTLTKGDPGSLEEWET
VVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAKK
KWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEELP
LCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAG
TFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLSQDAPGRADTSQPSAR
MRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQ
KVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCV
YSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHW
ASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLN
RKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSN
CLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFI
CEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDI
RTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE

A0A2J8RVR8 **A0A2J8RVR8_PONAB** (736 aa)
YTHDC1 isoform 3. *Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSN
NKRIVSTKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEE
EEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSA
SESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVIL
IFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQE
IELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQ
RPGYLKDPRYQEVDSFTNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQ
AHPPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERER
LCDRDRDRGERGRYRR
```

230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE

A0A2J8RVW0 **A0A2J8RVW0_PONAB** (728 aa)
YTHDC1 isoform 1. *Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSN
NKRIVSTKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEE
EEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSA
SESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVIL
IFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQE
IELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQ
RPGYLKDPRYQEVDRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQAHPPYSGH
HPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDR
GERGRYRR
```

230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE

A0A2J8RVX0 **A0A2J8RVX0_PONAB** (710 aa)
YTHDC1 isoform 2. *Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSN
NKRIVSTKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEE
EEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSA
SESYADQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVILIFSVRESGKFQGFARLSS
ESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLLFPPDES
IDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQRPGYLKDPRYQEVDRRFS
GVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHHPVPHEARYRDKRVHDYD
MRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDRGERGRYRR
```

230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE

A0A2J8S2L3 **A0A2J8S2L3_PONAB** (1497 aa)
SHROOM4 isoform 1 (SHROOM4 isoform 2). *Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)*

```
MENRPGSFQYVPVQLQGGAPWGFTLKGGLEHCEPLTVSKIEDGGKAALSQKMRTGDELVNINGTPLYGSRQEALILIKGS
FRILKLIVRRRNAPVSRPHSWHVAKLLEGCPEAATTMHFPSEAFSLSWHSGCNTSDVCVQWCPLSRHCSTEKSSSIGSME
SLEQPGQATYESHLLPIDQNMYPNQRDSAYSSFSASSNASDCALSLRPEEPASTDCIMQGPGPTKAPSGRPNVAETSGGS
RRTSGGYLTPSSQMSSRPQEGYQSGPAKAVRGPPQPPVRRDSLQASRAQLLNGEQRRASEPVVPLAQKEKLSLETVLPAR
NPNRFCCLSGHDQVTSEGHQNCEFSQPPESSQQGSEHLLMHASTKAVGSPKACDKASSMDSNPLNEASAELAKASFGRPP
HLIGPTGHRHSAPEQLLLSHLQHVHLDTRGSKGMELPPGQDGHQWTLSPLHSSHKGKKSPCPPTGGTHDQSSKERKTRQV
DDRSLVLGHQSQSSPPHGEADGHPSEKGFLDPNRTSRAGSELANQQPSASGSLVQQARDCSSTTKVAGGTEAGEEGDSEP
KECSRMGGRRSGGTRGRSIQNRRKSERFATNLRNEIQRRKAQLQKSKGPLSQLCDTKEPVEETQEPPESPPLTASNTSLL
SSCKKPPSPRDKLFNKSMMLRARSSECLSQAPESHESRTGLEGRISPGQRPGQSSLGLNTWWKAPDPSSSDPEKAHAHCG
VRGGHWRWSPEHNSQPLVAVAMEGPSNPGDNKELKASTAQAGEDAILLPFADRRKFFEESSKSLSASHLPGLTTHSNKTF
TQRPKPIDQNFQPMSSSYRELRRHPMDQSYHSADQTYHATDQSYHSMSPLQSETPTYSECFASKGLENSMCCKPLHCGDF
DYHRTCSYSCSVQGALVHDPCIYCSGEICPALLKRNMMPNCYNCRCHHHQCIRCSVCYHNPQHSTLEDSSLAPGNTWKPR
KLTVQEFPGDKWNPITGNRKTSQSGREMAHSKTSFSWATPFHPCLENPALDLSSYRAISSLDLLGDFKHALKKSEETSVY
EEGSSLASMHHPLRSRAFSESHISLEPQSTRAWGQHRRELFSKGDETQSDVLGARKKAFPPPRPPPPNWEKYRLFRAAQQ
QKQQQQQQKQKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEELPPQYFSSETSGSCALNPEEVLEQPQPLSLGHLEGSRQ
GSQSVPAEQESFALHSSDFLPPIRGHLGSQPEQAQPPCYYGIGGLWRTSEQEATESAKQEFQHFSPPPGAPGIPTSYSAY
YNISVAKAELLNKLKDQPEMAEIGLGEEEVDHELAQKKIQLIESISRKLSVLREAQRGLLEDINANSALGEEVEANLKAV
CKPNEFEKYHLFVGDLDKVVNLLLSLSGRLARVENALNSIDSEANQEKLVLIEKKQQLTGQLADAKELKEHVDRREKLVF
GMVSRYLPQDQLQDYQHFVKMKSALIIEQRELEEKIKLGEEQLKCLRESLLLGPSNF
```

1132 - 1151:	EEEEEEEEEEEEEEEEEEEE
1133 - 1152:	EEEEEEEEEEEEEEEEEEEE
1134 - 1153:	EEEEEEEEEEEEEEEEEEEE
1135 - 1154:	EEEEEEEEEEEEEEEEEEEE
1136 - 1155:	EEEEEEEEEEEEEEEEEEEE

1137 - 1156:	EEEEEEEEEEEEEEEEEEEE
1138 - 1157:	EEEEEEEEEEEEEEEEEEEE
1139 - 1158:	EEEEEEEEEEEEEEEEEEEE
1140 - 1159:	EEEEEEEEEEEEEEEEEEEE
1141 - 1160:	EEEEEEEEEEEEEEEEEEEE
1142 - 1161:	EEEEEEEEEEEEEEEEEEEE
1143 - 1162:	EEEEEEEEEEEEEEEEEEEE

A0A2J8S2N3 **A0A2J8S2N3_PONAB** (1381 aa)
SHROOM4 isoform 4. *Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)*

```
MHFPSEAFSLSWHSGCNTSDVCVQWCPLSRHCSTEKSSSIGSMESLEQPGQATYESHLLPIDQNMYPNQRDSAYSSFSAS
SNASDCALSLRPEEPASTDCIMQGPGPTKAPSGRPNVAETSGGSRRTSGGYLTPSSQMSSRPQEGYQSGPAKAVRGPPQP
PVRRDSLQASRAQLLNGEQRRASEPVVPLAQKEKLSLETVLPARNPNRFCCLSGHDQVTSEGHQNCEFSQPPESSQQGSE
HLLMHASTKAVGSPKACDKASSMDSNPLNEASAELAKASFGRPPHLIGPTGHRHSAPEQLLLSHLQHVHLDTRGSKGMEL
PPGQDGHQWTLSPLHSSHKGKKSPCPPTGGTHDQSSKERKTRQVDDRSLVLGHQSQSSPPHGEADGHPSEKGFLDPNRTS
RAGSELANQQPSASGSLVQQARDCSSTTKVAGGTEAGEEGDSEPKECSRMGGRRSGGTRGRSIQNRRKSERFATNLRNEI
QRRKAQLQKSKGPLSQLCDTKEPVEETQEPPESPPLTASNTSLLSSCKKPPSPRDKLFNKSMMLRARSSECLSQAPESHE
SRTGLEGRISPGQRPGQSSLGLNTWWKAPDPSSSDPEKAHAHCGVRGGHWRWSPEHNSQPLVAVAMEGPSNPGDNKELKA
STAQAGEDAILLPFADRRKFFEESSKSLSASHLPGLTTHSNKTFTQRPKPIDQNFQPMSSSYRELRRHPMDQSYHSADQT
YHATDQSYHSMSPLQSETPTYSECFASKGLENSMCCKPLHCGDFDYHRTCSYSCSVQGALVHDPCIYCSGEICPALLKRN
MMPNCYNCRCHHHQCIRCSVCYHNPQHSTLEDSSLAPGNTWKPRKLTVQEFPGDKWNPITGNRKTSQSGREMAHSKTSFS
WATPFHPCLENPALDLSSYRAISSLDLLGDFKHALKKSEETSVYEEGSSLASMHHPLRSRAFSESHISLEPQSTRAWGQH
RRELFSKGDETQSDVLGARKKAFPPPRPPPPNWEKYRLFRAAQQQKQQQQQQKQKEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEELPPQYFSSETSGSCALNPEEVLEQPQPLSLGHLEGSRQGSQSVPAEQESFALHSSDFLPPIRGHLGSQPEQAQP
PCYYGIGGLWRTSEQEATESAKQEFQHFSPPPGAPGIPTSYSAYYNISVAKAELLNKLKDQPEMAEIGLGEEEVDHELAQ
KKIQLIESISRKLSVLREAQRGLLEDINANSALGEEVEANLKAVCKPNEFEKYHLFVGDLDKVVNLLLSLSGRLARVENA
LNSIDSEANQEKLVLIEKKQQLTGQLADAKELKEHVDRREKLVFGMVSRYLPQDQLQDYQHFVKMKSALIIEQRELEEKI
KLGEEQLKCLRESLLLGPSNF
```

1016 - 1035:	EEEEEEEEEEEEEEEEEEEE
1017 - 1036:	EEEEEEEEEEEEEEEEEEEE
1018 - 1037:	EEEEEEEEEEEEEEEEEEEE
1019 - 1038:	EEEEEEEEEEEEEEEEEEEE
1020 - 1039:	EEEEEEEEEEEEEEEEEEEE
1021 - 1040:	EEEEEEEEEEEEEEEEEEEE
1022 - 1041:	EEEEEEEEEEEEEEEEEEEE
1023 - 1042:	EEEEEEEEEEEEEEEEEEEE
1024 - 1043:	EEEEEEEEEEEEEEEEEEEE
1025 - 1044:	EEEEEEEEEEEEEEEEEEEE
1026 - 1045:	EEEEEEEEEEEEEEEEEEEE
1027 - 1046:	EEEEEEEEEEEEEEEEEEEE

A0A2J8SPL0 **A0A2J8SPL0_PONAB** (1124 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)*

```
MAAAVLSGPSAGSAAGVPGGTGGLSAVSSGPRLRLLLLESVSGLLQPRTGSAVAPVHPPNRSAPHLPGLMCLLRLHGSVG
GAQNLSALGALVSLSNARLSSIKTRFEGLCLLSLLVGESPTELFQQHCVSWLRSIQQVLQTQDPPATMELAVAVLRDLLR
YAAQLPALFRDISMNHLPGLLTSLLGLRPECEQSALEGMKACMTYFPRACGSLKGKLASFFLSRVDALSPQLQQLACECY
SRLPSLGAGFSQGLKHTESWEQELHSLLASLHTLLGALYEGAETAPVQNEGPGVEMLLSSEDGDAHVLLQLRQRFSGLAR
CLGLMLSSEFGAPVSVPVQEILDFICRTLSVSSKNISLHGDGPLRLLLLPSIHLEALDLLSALILACGSRLLRFGILISR
LLPQVLNSWSIGRDSLSPGQERPYSTVRTKVYAILELWVQVCGASAGMLQGGASGEALLTHLLSDISPPADALKLRSPRG
SPDGSLQTGKPSAPKKLKLDVGEAMAPPSHRKGDSNANSDVCAAALRGLSRTILMCGPLIKEETHRRLHDLVLPLVMGVQ
QGEVLGSSPYTSSRCRRELYCLLLALLLAPSPRCPPPLACALQAFSLGQREDSLEVSSFCSEALVTCAALTHPRVPPLQP
MGPTGPTPAPAPPPEAPSPFRAPPFHPPGPMPSAGPMPSAGPMPSAGPVPSARPGPPTTANHLGLSVPGLVSVPPRLLPG
PENHRAGSNEDPILAPSGTPPPTIPPDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDSVVIVPEGLPPLPPPPPSGA
TPPPIAPTGPPTASPPVPAKEEPEELPAAPGPLPPPPPPPPPVPGPVTLPPPQLVPEGTPGGGGPPALEEDLTVININSS
DEEEEEEEEEEEEEEEEEEEEEDFEEEEEDEEEYFEEEEEEEEEFEEEFEEEEGELEEEEEEEDEEEEEELEEVEDLEFG
TAGGEVEEGGPPPPTLPPTLPPPESPPKVQSEPEPEPGLLLEVEEPGTEEEHGADTAPTLAPEVLPSQGEVEREGESPAA
GPPPQELVEEEPSAPPTLLEEETEDGSDKVQPPPETPAEEEMETETEAEAHQEKEQDDTAAMLADFIDCPPDDEKPLPPT
EPDS
```

882 - 901:	EEEEEEEEEEEEEEEEEEEE
883 - 902:	EEEEEEEEEEEEEEEEEEEE

A0A2J8SPL2 **A0A2J8SPL2_PONAB** (977 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)*

```
MELAVAVLRDLLRYAAQLPALFRDISMNHLPGLLTSLLGLRPECEQSALEGMKACMTYFPRACGSLKGKLASFFLSRVDA
LSPQLQQLACECYSRLPSLGAGFSQGLKHTESWEQELHSLLASLHTLLGALYEGAETAPVQNEGPGVEMLLSSEDGDAHV
```

```
LLQLRQRFSGLARCLGLMLSSEFGAPVSVPVQEILDFICRTLSVSSKNISLHGDGPLRLLLLPSIHLEALDLLSALILAC
GSRLLRFGILISRLLPQVLNSWSIGRDSLSPGQERPYSTVRTKVYAILELWVQVCGASAGMLQGGASGEALLTHLLSDIS
PPADALKLRSPRGSPDGSLQTGKPSAPKKLKLDVGEAMAPPSHRKGDSNANSDVCAAALRGLSRTILMCGPLIKEETHRR
LHDLVLPLVMGVQQGEVLGSSPYTSSRCRRELYCLLLALLLAPSPRCPPPLACALQAFSLGQREDSLEVSSFCSEALVTC
AALTHPRVPPLQPMGPTGPTPAPAPPPEAPSPFRAPPFHPPGPMPSAGPMPSAGPMPSAGPVPSARPGPPTTANHLGLSV
PGLVSVPPRLLPGPENHRAGSNEDPILAPSGTPPPTIPPDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDSVVIVPE
GLPPLPPPPPSGATPPPIAPTGPPTASPPVPAKEEPEELPAAPGPLPPPPPPPPPVPGPVTLPPPQLVPEGTPGGGGPPA
LEEDLTVININSSDEEEEEEEEEEEEEEEEEEEEEDFEEEEEDEEEYFEEEEEEEEEFEEEFEEEEGELEEEEEEEDEEE
EEELEEVEDLEFGTAGGEVEEGGPPPPTLPPTLPPPESPPKVQSEPEPEPGLLLEVEEPGTEEEHGADTAPTLAPEVLPS
QGEVEREGESPAAGPPPQELVEEEPSAPPTLLEEETEDGSDKVQPPPETPAEEEMETETEAEAHQEKEQDDTAAMLADFI
DCPPDDEKPLPPTEPDS
```

735 - 754:	EEEEEEEEEEEEEEEEEEEE
736 - 755:	EEEEEEEEEEEEEEEEEEEE

A0A2J8SPM6 **A0A2J8SPM6_PONAB** (1174 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)*

```
MLLPSLSPRVQPAFIQCAGPQPPPHAPSPVGGRRGVFASSRHATTEAQGKMAAAVLSGPSAGSAAGVPGGTGGLSAVSSG
PRLRLLLLESVSGLLQPRTGSAVAPVHPPNRSAPHLPGLMCLLRLHGSVGGAQNLSALGALVSLSNARLSSIKTRFEGLC
LLSLLVGESPTELFQQHCVSWLRSIQQVLQTQDPPATMELAVAVLRDLLRYAAQLPALFRDISMNHLPGLLTSLLGLRPE
CEQSALEGMKACMTYFPRACGSLKGKLASFFLSRVDALSPQLQQLACECYSRLPSLGAGFSQGLKHTESWEQELHSLLAS
LHTLLGALYEGAETAPVQNEGPGVEMLLSSEDGDAHVLLQLRQRFSGLARCLGLMLSSEFGAPVSVPVQEILDFICRTLS
VSSKNISLHGDGPLRLLLLPSIHLEALDLLSALILACGSRLLRFGILISRLLPQVLNSWSIGRDSLSPGQERPYSTVRTK
VYAILELWVQVCGASAGMLQGGASGEALLTHLLSDISPPADALKLRSPRGSPDGSLQTGKPSAPKKLKLDVGEAMAPPSH
RKGDSNANSDVCAAALRGLSRTILMCGPLIKEETHRRLHDLVLPLVMGVQQGEVLGSSPYTSSRCRRELYCLLLALLLAP
SPRCPPPLACALQAFSLGQREDSLEVSSFCSEALVTCAALTHPRVPPLQPMGPTGPTPAPAPPPEAPSPFRAPPFHPPGP
MPSAGPMPSAGPMPSAGPVPSARPGPPTTANHLGLSVPGLVSVPPRLLPGPENHRAGSNEDPILAPSGTPPPTIPPDETF
GGRVPRPAFVHYDKEEASDVEISLESDSDDSVVIVPEGLPPLPPPPPSGATPPPIAPTGPPTASPPVPAKEEPEELPAAP
GPLPPPPPPPPPVPGPVTLPPPQLVPEGTPGGGGPPALEEDLTVININSSDEEEEEEEEEEEEEEEEEEEEEDFEEEEED
EEEYFEEEEEEEEEFEEEFEEEEGELEEEEEEEDEEEEEELEEVEDLEFGTAGGEVEEGGPPPPTLPPTLPPPESPPKVQ
SEPEPEPGLLLEVEEPGTEEEHGADTAPTLAPEVLPSQGEVEREGESPAAGPPPQELVEEEPSAPPTLLEEETEDGSDKV
QPPPETPAEEEMETETEAEAHQEKEQDDTAAMLADFIDCPPDDEKPLPPTEPDS
```

932 - 951:	EEEEEEEEEEEEEEEEEEEE
933 - 952:	EEEEEEEEEEEEEEEEEEEE

A0A2J8SPN5 **A0A2J8SPN5_PONAB** (900 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)*

```
MELAVAVLRDLLRYAAQLPALFRDISMNHLPGLLTSLLGLRPECEQSALEGMKACMTYFPRACGSLKGKLASFFLSRVDA
LSPQLQQLACECYSRLPSLGAGFSQGLKHTESWEQELHSLLASLHTLLGALYEGAETAPVQNEGPGVEMLLSSEDGDAHV
LLQLRQRFSGLARCLGLMLSSEFGAPVSVPVQEILDFICRTLSVSSKNISLHGDGPLRLLLLPSIHLEALDLLSALILAC
GSRLLRFGILISRLLPQVLNSWSIGRDSLSPGQERPYSTVRTKVYAILELWVQVCGASAGMLQGGASGEALLTHLLSDIS
PPADALKLRSPRGSPDGSLQTGKPSAPKKLKLDVGEAMAPPSHRKGDSNANSDVCAAALRGLSRTILMCGPLIKEETHRR
LHDLVLPLVMGVQQGEVLGSSPYTSSRCRRELYCLLLALLLAPSPRCPPPLACALQAFSLGQREDSLEVSSFCSEALVTC
AALTHPRVPPLQPMGPTGPTPAPAPPPEAPSPFRAPPFHPPGPMPSAGPMPSAGPMPSAGPVPSARPGPPTTANHLGLSV
PGLVSVPPRLLPGPENHRAGSNEDPILAPSGTPPPTIPPDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDSVVIVPE
GLPPLPPPPPSGATPPPIAPTGPPTASPPVPAKEEPEELPAAPGPLPPPPPPPPPVPGPVTLPPPQLVPEGTPGGGGPPA
LEEDLTVININSSDEEEEEEEEEEEEEEEEEEEEEDFEEEEEDEEEYFEEEEEEEEEFEEEFEEEEGELEEEEEEEDEEE
EEELEEVEREGESPAAGPPPQELVEEEPSAPPTLLEEETEDGSDKVQPPPETPAEEEMETETEAEAHQEKEQDDTAAMLA
DFIDCPPDDEKPLPPTEPDS
```

735 - 754:	EEEEEEEEEEEEEEEEEEEE
736 - 755:	EEEEEEEEEEEEEEEEEEEE

A0A2J8T816 **A0A2J8T816_PONAB** (1002 aa)
SLC24A1 isoform 1. *Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)*

```
MGKLIRMGPQERWLLRTKRLHWSRLLFLLGMLIIGSTYQHLRRPRGLSSLWAAVSSHQPIKLASRDLPSEEMMMVSSNPS
KPSSEMGGKMLVPQASVGSDEATLSMTVENIPSMPKRTAKMIPTTTKNNYSPTAAGTERRKEDTPTSSRTLTYYTSTSSR
QIVKKYTPTPRGEMKSYSPTQVREKVKYTPSPRGRRVGIYAPSTFMTMETSHAITPRTTVKDSDITATYKILETNSLKRI
TDETTPTTLKGMFDSTPTFLTHEVETNVLTSPRSVMEKNNLSPPRRVESNSSAHPWGLVGKNNLKTPQGTVLVHTPATSE
GQVTISTMTGSSPAETKAFTAAWSLRNPSPRTSVSAIKTAPATVWRLAKKPSTAPSTSTTPTVRAKLTTQVHHCVVVKPT
PAMPTTPSPSLTTALLLEELSPSPSVLPPSLPDLHPKGEYPPDLFSVEERRQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLIMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKHIEVWVKEQLSRRPVAKVMALGDLSKLPSLLTRGSS
STSLHNSTIRSTIYQLMIHSLDPLREVRLAKEKEEESLNQEARVQSQAKAESKPEEEEPAKLPAVTVTPAPAPDIKGDQK
ENPGGQEDVAEAESTGEMPGKEGKTAGEGETEEKSGGETQPEGEGETETQGKGEEREGENEAEGKGDNEGEGEGEIHAED
GEIKGNEGETESQELSAENDGEAKNDEKGVEDGGSDGGGSKEEEEEEEEEEEEEEEEEEEEEKGNEEPLSLDWPETRQKQ
AIYLFLLPIVFPLWLTVPDVRRQESRKFFVFTFLGSIVWIAMFSYLMVWWAHQVGETIGISEEIMGLTILAAGTSIPDLI
TSVIVARKGLGDMAVSSSVGSNIFDITVGVESCEMFQHGAIH
```

842 - 861:	EEEEEEEEEEEEEEEEEEEE
843 - 862:	EEEEEEEEEEEEEEEEEEEE

A0A2J8T817 **A0A2J8T817_PONAB** (1089 aa)

SLC24A1 isoform 3. *Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)*

```
MGKLIRMGPQERWLLRTKRLHWSRLLFLLGMLIIGSTYQHLRRPRGLSSLWAAVSSHQPIKLASRDLPSEEMMMVSSNPS
KPSSEMGGKMLVPQASVGSDEATLSMTVENIPSMPKRTAKMIPTTTKNNYSPTAAGTERRKEDTPTSSRTLTYYTSTSSR
QIVKKYTPTPRGEMKSYSPTQVREKVKYTPSPRGRRVGIYAPSTFMTMETSHAITPRTTVKDSDITATYKILETNSLKRI
TDETTPTTLKGMFDSTPTFLTHEVETNVLTSPRSVMEKNNLSPPRRVESNSSAHPWGLVGKNNLKTPQGTVLVHTPATSE
GQVTISTMTGSSPAETKAFTAAWSLRNPSPRTSVSAIKTAPATVWRLAKKPSTAPSTSTTPTVRAKLTTQVHHCVVVKPT
PAMPTTPSPSLTTALLLEELSPSPSVLPPSLPDLHPKGEYPPDLFSVEERRQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLIMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKHIEVWVKEQLSRRPVAKVMALGDLSKPGDGAIAVDE
LQDNKKLKLPSLLTRGSSSTSLHNSTIRSTIYQLMIHSLDPLREVRLAKEKEEESLNQEARVQSQAKAESKPEEEEPAKL
PAVTVTPAPAPDIKGDQKENPGGQEDVAEAESTGEMPGKEGKTAGEGETEEKSGGETQPEGEGETETQGKGEEREGENEA
EGKGDNEGEGEGEIHAEDGEIKGNEGETESQELSAENDGEAKNDEKGVEDGGSDGGGSKEEEEEEEEEEEEEEEEEEEEE
KGNEEPLSLDWPETRQKQAIYLFLLPIVFPLWLTVPDVRRQESRKFFVFTFLGSIVWIAMFSYLMVWWAHQVGETIGISE
EIMGLTILAAGTSIPDLITSVIVARKGLGDMAVSSSVGSNIFDITVGLPVPWLLFSLINGLQPVPVSSNGLFCAIVLLFL
MLLFVISSIASCKWRMNKILGFTMFLLYFVFLIISVMLEDRIISCPVSV
```

860 - 879:	EEEEEEEEEEEEEEEEEEEE
861 - 880:	EEEEEEEEEEEEEEEEEEEE

A0A2J8T825 **A0A2J8T825_PONAB** (975 aa)
SLC24A1 isoform 7. *Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)*

```
MGKLIRMGPQERWLLRTKRLHWSRLLFLLGMLIIGSTYQHLRRPRGLSSLWAAVSSHQPIKLASRDLPSEEMMMVSSNPS
KPSSEMGGKMLVPQASVGSDEATLSMTVENIPSMPKRTAKMIPTTTKNNYSPTAAGTERRKEDTPTSSRTLTYYTSTSSR
QIVKKYTPTPRGEMKSYSPTQVREKVKYTPSPRGRRVGIYAPSTFMTMETSHAITPRTTVKDSDITATYKILETNSLKRI
TDETTPTTLKGMFDSTPTFLTHEVETNVLTSPRSVMEKNNLSPPRRVESNSSAHPWGLVGKNNLKTPQGTVLVHTPATSE
GQVTISTMTGSSPAETKAFTAAWSLRNPSPRTSVSAIKTAPATVWRLAKKPSTAPSTSTTPTVRAKLTTQVHHCVVVKPT
PAMPTTPSPSLTTALLLEELSPSPSVLPPSLPDLHPKGEYPPDLFSVEERRQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLIMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKHIEVWVKEQLSRRPVAKVMALGDLSKEDVAEAESTG
EMPGKEGKTAGEGETEEKSGGETQPEGEGETETQGKGEEREGENEAEGKGDNEGEGEGEIHAEDGEIKGNEGETESQELS
AENDGEAKNDEKGVEDGGSDGGGSKEEEEEEEEEEEEEEEEEEEEEEKGNEEPLSLDWPETRQKQAIYLFLLPIVFPLWLT
VPDVRRQESRKFFVFTFLGSIVWIAMFSYLMVWWAHQVGETIGISEEIMGLTILAAGTSIPDLITSVIVARKGLGDMAVS
SSVGSNIFDITVGLPVPWLLFSLINGLQPVPVSSNGLFCAIVLLFLMLLFVISSIASCKWRMNKILGFTMFLLYFVFLII
SVMLEDRIISCPVSV
```

746 - 765:	EEEEEEEEEEEEEEEEEEEE
747 - 766:	EEEEEEEEEEEEEEEEEEEE

A0A2J8T831 **A0A2J8T831_PONAB** (1071 aa)
SLC24A1 isoform 8. *Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)*

```
MGKLIRMGPQERWLLRTKRLHWSRLLFLLGMLIIGSTYQHLRRPRGLSSLWAAVSSHQPIKLASRDLPSEEMMMVSSNPS
KPSSEMGGKMLVPQASVGSDEATLSMTVENIPSMPKRTAKMIPTTTKNNYSPTAAGTERRKEDTPTSSRTLTYYTSTSSR
QIVKKYTPTPRGEMKSYSPTQVREKVKYTPSPRGRRVGIYAPSTFMTMETSHAITPRTTVKDSDITATYKILETNSLKRI
TDETTPTTLKGMFDSTPTFLTHEVETNVLTSPRSVMEKNNLSPPRRVESNSSAHPWGLVGKNNLKTPQGTVLVHTPATSE
GQVTISTMTGSSPAETKAFTAAWSLRNPSPRTSVSAIKTAPATVWRLAKKPSTAPSTSTTPTVRAKLTTQVHHCVVVKPT
PAMPTTPSPSLTTALLLEELSPSPSVLPPSLPDLHPKGEYPPDLFSVEERRQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLIMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKHIEVWVKEQLSRRPVAKVMALGDLSKLPSLLTRGSS
STSLHNSTIRSTIYQLMIHSLDPLREVRLAKEKEEESLNQEARVQSQAKAESKPEEEEPAKLPAVTVTPAPAPDIKGDQK
ENPGGQEDVAEAESTGEMPGKEGKTAGEGETEEKSGGETQPEGEGETETQGKGEEREGENEAEGKGDNEGEGEGEIHAED
GEIKGNEGETESQELSAENDGEAKNDEKGVEDGGSDGGGSKEEEEEEEEEEEEEEEEEEEEEEKGNEEPLSLDWPETRQKQ
AIYLFLLPIVFPLWLTVPDVRRQESRKFFVFTFLGSIVWIAMFSYLMVWWAHQVGETIGISEEIMGLTILAAGTSIPDLI
TSVIVARKGLGDMAVSSSVGSNIFDITVGLPVPWLLFSLINGLQPVPVSSNGLFCAIVLLFLMLLFVISSIASCKWRMNK
ILGFTMFLLYFVFLIISVMLEDRIISCPVSV
```

842 - 861:	EEEEEEEEEEEEEEEEEEEE
843 - 862:	EEEEEEEEEEEEEEEEEEEE

A0A2J8T837 **A0A2J8T837_PONAB** (1059 aa)
SLC24A1 isoform 6. *Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)*

```
MGKLIRMGPQERWLLRTKRLHWSRLLFLLGMLIIGSTYQHLRRPRGLSSLWAAVSSHQPIKLASRDLPSEEMMMVSSNPS
KPSSEMGGKMLVPQASVGSDEATLSMTVENIPSMPKRTAKMIPTTTKNNYSPTAAGTERRKEDTPTSSRTLTYYTSTSSR
QIVKKYTPTPRGEMKSYSPTQVREKVKYTPSPRGRRVGIYAPSTFMTMETSHAITPRTTVKDSDITATYKILETNSLKRI
TDETTPTTLKGMFDSTPTFLTHEVETNVLTSPRSVMEKNNLSPPRRVESNSSAHPWGLVGKNNLKTPQGTVLVHTPATSE
GQVTISTMTGSSPAETKAFTAAWSLRNPSPRTSVSAIKTAPATVWRLAKKPSTAPSTSTTPTVRAKLTTQVHHCVVVKPT
PAMPTTPSPSLTTALLLEELSPSPSVLPPSLPDLHPKGEYPPDLFSVEERRQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLIMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKHIEVWVKEQLSRRPVAKVMALGDLSKPGDGAIAVDE
LQDNKKLKLPSLLTRGSSSTSLHNSTIRSTIYQLMIHSLDPLREVRLAKEKEEESLNQEARVQSQAKAESKPEEEEPAKL
PAVTVTPAPAPDIKGDQKENPGGQEDVAEAESTGEMPGKEGKTAGEGETEEKSGGETQPEGEGETETQGKGEEREGENEA
EGKGDNEGEGEGEIHAEDGEIKGNEGETESQELSAENDGEAKNDEKGVEDGGSDGGGSKEEEEEEEEEEEEEEEEEEEEE
KGNEEPLSLDWPETRQKQAIYLFLLPIVFPLWLTVPDVRRQVGETIGISEEIMGLTILAAGTSIPDLITSVIVARKGLGD
MAVSSSVGSNIFDITVGLPVPWLLFSLINGLQPVPVSSNGLFCAIVLLFLMLLFVISSIASCKWRMNKILGFTMFLLYFV
FLIISVMLEDRIISCPVSV
```

860 - 879:	EEEEEEEEEEEEEEEEEEEE
861 - 880:	EEEEEEEEEEEEEEEEEEEE

A0A2J8U5F1 **A0A2J8U5F1_PONAB** (1785 aa)
Histone acetyltransferase (EC 2.3.1.48). *Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)*

```
MVKLANPLYTEWILEAIQKIKKQKQRPSEERICHAVSTSHGLDKKTVSEQLELSVQDGSVLKVTNKGLASYKDPDNPGRF
SSVKPGTFPKSTKGSRGSCNDLRNVDWNKLLRRAIEGLEEPNGSSLKNIEKYLRSQSDLTSTTNNPAFQQRLRLGAKRAV
NNGRLLKDGPQYRVNYGSLDGKGAPQYPSAFPSSLPPVSLLPHEKDQPRADPIPICSFCLGTKESNREKKPEELLSCADC
GSSGHPSCLKFCPELTTNVKALRWQCIECKTCSACRVQGRNADNMLFCDSCDRGFHMECCDPPLSRMPKGMWICQVCRPK
KKGRKLLHEKAAQIKRRYAKPIGRPKNKLKQRLLSVTSDEGSMNAFTGRGSPDTEIKINIKQESADVNVIGNKDVVTEED
LDVFKQAQELSWEKIECESGVEDCGRYPSVIEFGKYEIQTWYSSPYPQEYARLPKLYLCEFCLKYMKSKNILLRHSKKCG
WFHPPANEIYRRKDLSVFEVDGNMSKIYCQNLCLLAKLFLDHKTLYYDVEPFLFYVLTKNDEKGCHLVGYFSKEKLCQQK
YNVSCIMIMPQHQRQGFGRFLIDFSYLLSRREGQAGSPEKPLSDLGRLSYLAYWKSVILEYLYHHHERHISIKAISRATG
MCPHDIATTLQHLHMIDKRDGRFVIIRREKLILSHMEKLKTCSRANELDPDSLRWTPILISNAAVSEEEREAEKEAERLM
EQASCWEKEEQEILSTRANSRQSPAKVQSKNKYLHSPESRPVTGERGQLLELSKESSEEEEEEDEEEEEEEEEEEEEDEE
EEEEEEEEEEEEEEEEEENIQSSPPRLTKPQSVAIKRKRPFVLKKKRGRKRRRINSSVTTETISETTEVLNEPFDNSDEE
RPMPQLEPTCEIEVEEDGRKPVLRKAFQHQPGKKRQTEEEEGKDNHCFKNADPCRNNMNDDSSNLKEGSKDNPEPLKCKQ
VWPKGTKRGLSKWRQNKERKTGFKLNLYTPPETPMEPDEQVTVEEQKETSEGKTSPSPIRIEEEVKETGEALLPQEENRR
EETCAPVSPNTSPGEKPEDDLIKPEEEEEEEEEEEEEEEGEEEEEEGGNVEKDPDGAKSQEKEEPEISTEKEDSARLDDH
EEEEEEDEEPSHNEDHDADDEDDSHMESAEVEKEELPRESFKEVLENQEAFLDLNVQPGHSNPEVLMDCGVDLTASCNSE
PKELAGDPEAVPESDEEPPPGEQAQKQDQKNSKEVDTEFKEGNPATMEIDSETVQAVQSLTQESSEQDDTFQDCAETQEA
CRSLQNYTRADQSPQIATTLDDCQQSDHSSPVSSVHSHPGQSVRSVNSPSVPALENSYAQISPDQSAISVPSLQNMETSP
MMDVPSVSDHSQQVVDSGFSDLGSIESTTENYENPSSYDSTMGGSICGNGSSQNSCSYSNLTSSSLTQSSCAVTQQMSNI
SGSCSMLQQTSISSPPTCSVKSPQGCVVERPPSSSQQLAQCSMAANFTPPMQLAEIPETGNANIGLYERMGQSDFGAGHY
PQPSATFSLAKLQQLTNTLIDHSLPYSHSAAVTSYANSASLSTPLSNTGLVQLSQSPHSVPGGPQAQATMTPPPNLTPPP
MNLPPPLLQRNMAASNIGISHSQRLQTQIASKGHVSMRTKSASLSPAAATHQSQIYGRSQTVAMQGPARTLTMQRGMNMS
VNLMPAPAYNVNSVNMNMNTLNAMNGYSMSQPMMNSGYHSNHGYMNQTPQYPMQMQMGMMGTQPYAQQPMQTPPHGNMMY
TAPGHHGYMNTGMSKQSLNGSYMRR
```

799 - 818:	EEEEEEEEEEEEEEEEEEEE

A0A2J8U5G0 **A0A2J8U5G0_PONAB** (1894 aa)
Histone acetyltransferase (EC 2.3.1.48). *Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)*

```
MVKLANPLYTEWILEAIQKIKKQKQRPSEERICHAVSTSHGLDKKTVSEQLELSVQDGSVLKVTNKGLASYKDPDNPGRF
SSVKPGTFPKSTKGSRGSCNDLRNVDWNKLLRRAIEGLEEPNGSSLKNIEKYLRSQSDLTSTTNNPAFQQRLRLGAKRAV
NNGRLLKDGPQYRVNYGSLDGKGAPQYPSAFPSSLPPVSLLPHEKDQPRADPIPICSFCLGTKESNREKKPEELLSCADC
GSSGHPSCLKFCPELTTNVKALRWQCIECKTCSACRVQGRNADNMLFCDSCDRGFHMECCDPPLSRMPKGMWICQVCRPK
KKGRKLLHEKAAQIKRRYAKPIGRPKNKLKQRLLSVTSDEGSMNAFTGRGSPGRGQKTKVCTTPSSGHAASGKDSSSRLA
VTDPTRPGATTKITTTSTYISASTLKVNKKTKGLIDGLTKFFTPSPDGRRSRGEIIDFSKHYRPRKKVSQKQSCTSHVLA
TDTEIKINIKQESADVNVIGNKDVVTEEDLDVFKQAQELSWEKIECESGVEDCGRYPSVIEFGKYEIQTWYSSPYPQEYA
RLPKLYLCEFCLKYMKSKNILLRHSKKCGWFHPPANEIYRRKDLSVFEVDGNMSKIYCQNLCLLAKLFLDHKTLYYDVEP
FLFYVLTKNDEKGCHLVGYFSKEKLCQQKYNVSCIMIMPQHQRQGFGRFLIDFSYLLSRREGQAGSPEKPLSDLGRLSYL
AYWKSVILEYLYHHHERHISIKAISRATGMCPHDIATTLQHLHMIDKRDGRFVIIRREKLILSHMEKLKTCSRANELDPD
SLRWTPILISNAAVSEEEREAEKEAERLMEQASCWEKEEQEILSTRANSRQSPAKVQSKNKYLHSPESRPVTGERGQLLE
LSKESSEEEEEEDEEEEEEEEEEEEEEDEEEEEEEEEEEEEEEEEEEEENIQSSPPRLTKPQSVAIKRKRPFVLKKKRGRKR
RRINSSVTTETISETTEVLNEPFDNSDEERPMPQLEPTCEIEVEEDGRKPVLRKAFQHQPGKKRQTEEEEGKDNHCFKNA
DPCRNNMNDDSSNLKEGSKDNPEPLKCKQVWPKGTKRGLSKWRQNKERKTGFKLNLYTPPETPMEPDEQVTVEEQKETSE
GKTSPSPIRIEEEVKETGEALLPQEENRREETCAPVSPNTSPGEKPEDDLIKPEEEEEEEEEEEEEEEGEEEEEEGGNVE
KDPDGAKSQEKEEPEISTEKEDSARLDDHEEEEEEDEEPSHNEDHDADDEDDSHMESAEVEKEELPRESFKEVLENQEAF
LDLNVQPGHSNPEVLMDCGVDLTASCNSEPKELAGDPEAVPESDEEPPPGEQAQKQDQKNSKEVDTEFKEGNPATMEIDS
ETVQAVQSLTQESSEQDDTFQDCAETQEACRSLQNYTRADQSPQIATTLDDCQQSDHSSPVSSVHSHPGQSVRSVNSPSV
PALENSYAQISPDQSAISVPSLQNMETSPMMDVPSVSDHSQQVVDSGFSDLGSIESTTENYENPSSYDSTMGGSICGNGS
SQNSCSYSNLTSSSLTQSSCAVTQQMSNISGSCSMLQQTSISSPPTCSVKSPQGCVVERPPSSSQQLAQCSMAANFTPPM
QLAEIPETGNANIGLYERMGQSDFGAGHYPQPSATFSLAKLQQLTNTLIDHSLPYSHSAAVTSYANSASLSTPLSNTGLV
QLSQSPHSVPGGPQAQATMTPPPNLTPPPMNLPPPLLQRNMAASNIGISHSQRLQTQIASKGHVSMRTKSASLSPAAATH
QSQIYGRSQTVAMQGPARTLTMQRGMNMSVNLMPAPAYNVNSVNMNMNTLNAMNGYSMSQPMMNSGYHSNHGYMNQTPQY
PMQMQMGMMGTQPYAQQPMQTPPHGNMMYTAPGHHGYMNTGMSKQSLNGSYMRR
```

908 - 927:	EEEEEEEEEEEEEEEEEEEE

A0A2J8U5H8 **A0A2J8U5H8_PONAB** (2077 aa)
Histone acetyltransferase (EC 2.3.1.48). *Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)*

```
MVKLANPLYTEWILEAIQKIKKQKQRPSEERICHAVSTSHGLDKKTVSEQLELSVQDGSVLKVTNKGLASYKDPDNPGRF
SSVKPGTFPKSTKGSRGSCNDLRNVDWNKLLRRAIEGLEEPNGSSLKNIEKYLRSQSDLTSTTNNPAFQQRLRLGAKRAV
NNGRLLKDGPQYRVNYGSLDGKGAPQYPSAFPSSLPPVSLLPHEKDQPRADPIPICSFCLGTKESNREKKPEELLSCADC
GSSGHPSCLKFCPELTTNVKALRWQCIECKTCSACRVQGRNADNMLFCDSCDRGFHMECCDPPLSRMPKGMWICQVCRPK
KKGRKLLHEKAAQIKRRYAKPIGRPKNKLKQRLLSVTSDEGSMNAFTGRGSPGRGQKTKVCTTPSSGHAASGKDSSSRLA
VTDPTRPGATTKITTTSTYISASTLKVNKKTKGLIDGLTKFFTPSPDGRRSRGEIIDFSKHYRPRKKVSQKQSCTSHVLA
TGTTQKLKPPPSSLPPPTPISGQSPSSQKSSTATSSPSPQSSSSQCSMPSLSSLTTNSQLKALFDGLSHIYTTQGQSRKK
GHPSYAPPKRMRRKTELSSTAKSKAHFFGKRDIRSRFISHSSSSSWGMARGSIFKAIAHFKRTTFLKKHRMLGRLKYKVT
PQMGTPSPGKGSLTDGRIKPDQDDDTEIKINIKQESADVNVIGNKDVVTEEDLDVFKQAQELSWEKIECESGVEDCGRYP
SVIEFGKYEIQTWYSSPYPQEYARLPKLYLCEFCLKYMKSKNILLRHSKKCGWFHPPANEIYRRKDLSVFEVDGNMSKIY
CQNLCLLAKLFLDHKTLYYDVEPFLFYVLTKNDEKGCHLVGYFSKEKLCQQKYNVSCIMIMPQHQRQGFGRFLIDFSYLL
SRREGQAGSPEKPLSDLGRLSYLAYWKSVILEYLYHHHERHISIKAISRATGMCPHDIATTLQHLHMIDKRDGRFVIIRR
EKLILSHMEKLKTCSRANELDPDSLRWTPILISNAAVSEEEREAEKEAERLMEQASCWEKEEQEILSTRANSRQSPAKVQ
SKNKYLHSPESRPVTGERGQLLELSKESSEEEEEEDEEEEEEEEEEEEEDEEEEEEEEEEEEEEEEEEEEENIQSSPPRLT
KPQSVAIKRKRPFVLKKKRGRKRRRINSSVTTETISETTEVLNEPFDNSDEERPMPQLEPTCEIEVEEDGRKPVLRKAFQ
HQPGKKRQTEEEEGKDNHCFKNADPCRNNMNDDSSNLKEGSKDNPEPLKCKQVWPKGTKRGLSKWRQNKERKTGFKLNLY
TPPETPMEPDEQVTVEEQKETSEGKTSPSPIRIEEEVKETGEALLPQEENRREETCAPVSPNTSPGEKPEDDLIKPEEEE
EEEEEEEEEEEGEEEEEEGGNVEKDPDGAKSQEKEEPEISTEKEDSARLDDHEEEEEEDEEPSHNEDHDADDEDDSHMES
AEVEKEELPRESFKEVLENQEAFLDLNVQPGHSNPEVLMDCGVDLTASCNSEPKELAGDPEAVPESDEEPPPGEQAQKQD
QKNSKEVDTEFKEGNPATMEIDSETVQAVQSLTQESSEQDDTFQDCAETQEACRSLQNYTRADQSPQIATTLDDCQQSDH
SSPVSSVHSHPGQSVRSVNSPSVPALENSYAQISPDQSAISVPSLQNMETSPMMDVPSVSDHSQQVVDSGFSDLGSIEST
TENYENPSSYDSTMGGSICGNGSSQNSCSYSNLTSSSLTQSSCAVTQQMSNISGSCSMLQQTSISSPPTCSVKSPQGCVV
ERPPSSSQQLAQCSMAANFTPPMQLAEIPETGNANIGLYERMGQSDFGAGHYPQPSATFSLAKLQQLTNTLIDHSLPYSH
SAAVTSYANSASLSTPLSNTGLVQLSQSPHSVPGGPQAQATMTPPPNLTPPPMNLPPPLLQRNMAASNIGISHSQRLQTQ
IASKGHVSMRTKSASLSPAAATHQSQIYGRSQTVAMQGPARTLTMQRGMNMSVNLMPAPAYNVNSVNMNMNTLNAMNGYS
MSQPMMNSGYHSNHGYMNQTPQYPMQMQMGMMGTQPYAQQPMQTPPHGNMMYTAPGHHGYMNTGMSKQSLNGSYMRR
```

1091 - 1110:	EEEEEEEEEEEEEEEEEEEE

A0A2J8UT42 **A0A2J8UT42_PONAB** (205 aa)
CHIC1 isoform 1. *Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)*

```
MSILLPNMAEFDTISELEEEEEEEAATSSSSPSSSSSVSGPDDDEEDEEEEEEEEEEEEEEEEEEEEEEAPPPPRVVSEE
HLRRYAPDPVLVRGAGHITVFGLSNKFDTEFPSVLTGKVAPEEFKTSIGRVNACLKKALPVNVKWLLCGCLCCCCTLGCS
LWPVICLNKRTRRSIQKLIEWENNRLYHKVILIEFLPKYPIFRPD
```

48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE

A0A2J8UT47 **A0A2J8UT47_PONAB** (218 aa)
CHIC1 isoform 2. *Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)*

```
MAEFDTISELEEEEEEEAATSSSSPSSSSSVSGPDDDEEDEEEEEEEEEEEEEEEEEEEEEEAPPPPRVVSEEHLRRYAP
DPVLVRGAGHITVFGLSNKFDTEFPSVLTGKVAPEEFKTSIGRVNACLKKALPVNVKWLLCGCLCCCCTLGCSLWPVICL
NKRTRRSIQKLIEWENNRLYHKLALHWKLTKRKCETSNMMEYVILIEFLPKYPIFRPD
```

41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE

A0A2K0TG70 **A0A2K0TG70_9HYPO** (1347 aa)
Uncharacterized protein. *Trichoderma gamsii*

```
MTGQPPQQLDGQQPQPELSDAHNVSSTPAKKTEDEHSAQTNAPGASEDGKSEDEPTGETGESVEGPTTKGDGGDEDGERS
SKVERKDGEVTDTDADNNKGAEGAEAEEEEEEEEEEEEEEEEEEEEEDDEEEEEEEEEEEDEEPLLKSVRLTQHLGAVYR
NGDATSACLVAGDKMIVGTHNGNIHVIQLPGFNTLRVYHAHSASVTAISISPFPPPLPDERAEVLQRTQTGSSGPPARPS
DISPSAASKRLREAPQVPRTPSNDIYIATASMDGNVCIQSLIDMKDVQLRNFARPVQAVALSPDYKSDRTYLSGGRAGQL
ILTVGGGPGRSTSNTVGTAAAVASDWLSTIGVKNSGGKDTVLHSGEGIINAIKWSLSGKYVAWINEHGTKIMRSKLHLDS
TEIEDAWKRIGHVDRPHTTQWETMAGVWKGRAEWIDEKSVESDESEVSPHDPTISSSASSTTKTFERLLVGWGGTMWIIH
VHPGGIGSGKHAGEKTIARAEIAKILHIDCIISGISLYAQNQLLVLAYCSPEDEDDAAEDDTSGPSHARDSPKKHKSKHS
TSSAENEQHHGQRPRLNALPPELRLIDLKSQAEVDRHTLTINRVDRLSAADYHMCLLPAQNAASVVASTKGALEALAGIG
SEMWNVAINPKSLFSSGASILSRESEDGASKAGSIAGTIRSSYIRARVPTVHPALSKPGVKIFIHSPYDSILATKRDLSD
HLTWLVEREQYQEAWELLDENPEILAESLDGVADPAAPATPSKYQGGADDFFDDESVADTVQRNMYSAVEKEKRRVGELW
IREVIDDGDWELAGQICGKVLTTPDRWEKWVWTFAGANKFDEITKHMPTKPMKPPIPTTIYEVLLGHYIQNNKPRFRELL
DIWSTDLFDIPAITTTLENQLKYRDVRENSVEDGEKGRDWKIVVEGLAKLYEAGGRHRDALKCYIRLQDADSAFRLIGDF
HLADAVVDDIPAFIGLRVSPERLKHMTEPDLVAATSEAITLLVDEAQHGLVRPEAVVEQLQARNLQLYLFFYMRGLWKGQ
GIAEHTGENLERLVMDSQSLVDNFADLAVRLFATFDRPLLMEFLKTSTSYGFEKAVQECEQCSYYDELVYLYSKTGQMKR
ALYLIIDRLNDVNKAIDFAKEQDDPDLWEDLLNYSMDKPSFIRALLEQVGTTINPITLVRRIPEGLEIQGLREGLIHMMK
EHELQHSISWGVATVLRSEVATAQNELRTGQRKGIKFEVVAEEDAAEKEKKKKEGEEDTAPKPGQCAKCLETFTEYEMEA
LIGFVCGHAFHVSHLLEMLHNGKRADVDLGPGPEEGGRYSVAMKVMKARLLRDRVRGGCPICHPAEA
```

107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE

A0A2K0TTC2 **A0A2K0TTC2_9HYPO** (798 aa)
Ysc84 domain-containing protein. *Trichoderma gamsii*

```
MQRVSAFLPSWEKRNSGSNKTGTFFGRRASQPPPPNGLAKINTETANLGAKRVQREAFWPATLDLECDKAARILKSFCVD
GYFAPTDNDAPASPSSTSTGIKTLDQIPKKIPRRIIQNAAGIAVFTCMRSGLWMTGSGGSGILIARKSDGTWSPPSGIML
HTPSLSFIIGVDVYDCVLIISSHTALESVTRPRLTLGEDVELRAGETVSLGSEEIDINWKELGNTVLTYMKARGQQQSVN
LYGCMLSERSNENERFYASDVTHMDILAGNVARDVEETTALNEVLKMAEGRTDYDSSVINKVAAEPAPSDALITSTPPKT
ASIPSSPHSSFGVPQVDDPDPFGILALEMAGLEIREAGSRIRPTSSLFDMNQNPMSPVASSKRSRQSMDTFVSRSNRGSY
VSMRTIRSQVTDAGTQTDTGNTPETSPSPGPSAGSGRASPAYIPVVKEEDEEEEEEEEEEEEEEEEEEEEKEEVVIPPRS
ANRLSKDVAVGPDSVDEDELSEGDTESLSESLRREEDAMSHGESSEEDELFEDEFEDDDESDEEFNDADDEDDIEEEPVV
FEVAAVQRTSTQMRSSGMIQARGNVVTIAKRVPPPLPTRSPARMSRIANKDATGEGIDLQSPLSQTFSSDGDLDSQDADA
KSIEAAITKEEQQPEIEQSESEKSDAAEKPEHQAVAQEDEASEASEGEKPGADETELETRKQDDVLLSEPHNEQTDNSDA
ASNKKKHTSSIYTGVTEDRWSCDGSSVTTPTSERRFSLTENQITDDATKKTVQERVEEIDDSRSAPTEAAHTPVAAAN
```

451 - 470:	EEEEEEEEEEEEEEEEEEEE

A0A2K0UN60 **A0A2K0UN60_GIBNY** (488 aa)
Uncharacterized protein. *Gibberella nygamai (Bean root rot disease fungus) (Fusarium nygamai)*

```
MIEQLDRLGLYLNQPEPAILCIQCKFALKADGDRVSRHLGERHGISKLARRGLGPFIRTLCLPDPKTLPMRSDGSSPYPH
LRIQQGAACRHCGLRSTSLEVLSRHLKEVHPQDIQHSRGRGFPESHWLQDHILDRLSFQAWTVSNIGRSWTVHLYRGQPQ
GPHTPVTIYQAPEAIQVFAKELFVREQQYLSQQARGSLPPPTGRTTSKRNRPSPHNELDAANWLGGDFPQYATRPNRRDG
SEDEHKLTRMMAALDRLFERSNDTIKHTDISLRRWLRGIYPDRPYKRPFELVVKPSTERRYRQLLKKCLCFWFRLWRLPP
TLTRRLCQRTLSKPQRMALETLWDDPAWEQYDSFENVSLLDEEEEEEYEEEEEEEEEEEEEEEEEEEEEEEEEEGNNSE
DEDPNAHFIQPPPPPPRQDPKADLVLQFCLFMATEDFADGNSKSTMLVYFSATCGLTSPMGADFLRPAQFTSILSSLIYC
LSMGNWIY
```

369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE

A0A2K0W243 **A0A2K0W243_GIBNY** (437 aa)
Uncharacterized protein. *Gibberella nygamai (Bean root rot disease fungus) (Fusarium nygamai)*

```
MQKHTKSKRSLSPTARVSPRKRLNYDADTRKMSSPTSYDDEDVQLSFLTIDEEEEEEEEEEEEEEEEEEEEDACSNSMEE
LMKLEKERYPGASTWAPAEERLFEILYMRQDLPMLPSTWDVDLRGVPISDIVFQTSDEFPPIIYAHSNNFRATTALIRLM
DLTAKTRTTIQSGHRMKVPQLIKQQLDKYLSWAAQDGDYLHLRIVPNILTEIVDTKMLEEEITEHIQKRMRTLAKLQREF
LREDRNPQFWDVIKPSVFASPKIKLEPDDGPTSFGGWLTPAQSRLGSHLQGGNVLSTTETHEVAVKIEPGFKSPSISAGV
LPKTTMLSRESYHSQSPSPSLPEEPQTPPRHTYRRHPPVVYGLFIINTWVLVLTVDSSKGPDAHVSFQVQVDFKDEHQGI
WNALTIAIAVCLARDELRTRATDFEELPCVEDSDPDA
```

52 - 71:	EEEEEEEEEEEEEEEEEEEE

A0A2K0W2H6 **A0A2K0W2H6_GIBNY** (499 aa)
Uncharacterized protein. *Gibberella nygamai (Bean root rot disease fungus) (Fusarium nygamai)*

```
MQIDAGLKRMLGEDAGWKTPQQRDGMYRIMGLENNGTRSEQLIVVLPTGGGKSIFFMLPAFMEDERGKGGPVSVVVVPFV
SLVQDLVSRAGELGIDCMEWKSDIDREERQRDARLVVVSADVAVSEGFTAYVESIRVRGLLERIFFDECHTVITDVGYRE
RLGQLTGLHRFGCPLVMLTATLPISMEAWFRERMLAQDAAIIRAPTMRVNIRYRVERVKPGRKAMEDGVMATIKAIEARM
SPAQRGVIYCRSIKQCEEMAGLVGCKAHHSKLTRDTRASVLQDWIDGRGGQRWIAATTGLGTGVDIRGIIGVIHVGPPFG
LVDFVQQTGRGGRQRGEVVDSVIVTDGKAGWGDEFGSDIDHINREGVGLFIEGKGCRRLVLGRFFDGAEAEVSSCREMQA
EYCDRCLKKGVNRVGDGEEEEEEEEEEEEEEEEEEEEEEEEDDDDKAERVPAVTTVNRLKENIQEESRRMIKLYGWLDQ
VRGTTSAAGSAVCRTAGAM
```

418 - 437:	EEEEEEEEEEEEEEEEEEEE
419 - 438:	EEEEEEEEEEEEEEEEEEEE
420 - 439:	EEEEEEEEEEEEEEEEEEEE
421 - 440:	EEEEEEEEEEEEEEEEEEEE
422 - 441:	EEEEEEEEEEEEEEEEEEEE
423 - 442:	EEEEEEEEEEEEEEEEEEEE

A0A2K1IYR9 **A0A2K1IYR9_PHYPA** (89 aa)
Uncharacterized protein. *Physcomitrium patens (Spreading-leaved earth moss) (Physcomitrella patens)*

```
MNVRTEILIRISIKKKKNKTKEEEEEEEEEEEEEEEEEEEEEEEEEESRPKFFIPNYPLWQTIADNTLARYCSRILLSKHP
GNRPCWTRT
```

22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE

A0A2K1WZ77 **A0A2K1WZ77_POPTR** (87 aa)
Uncharacterized protein (Fragment). *Populus trichocarpa (Western balsam poplar) (Populus balsamifera subsp. trichocarpa)*

```
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERKKERLVLIIKC
QSPSLIA
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE

6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE

A0A2K2CD87 **A0A2K2CD87_POPTR** (1404 aa)
NB-ARC domain-containing protein. *Populus trichocarpa (Western balsam poplar) (Populus balsamifera subsp. trichocarpa)*

```
MAIESVGGSILSKIAELLVEPTIRQFRYMFCFNNFVQEFNEQKKNLALTLDRLQNAVEVAERNAEEIEKDVNKWLEDAKN
EIEGVNRLENEKGKNSKCFNWCPNWIPQFKLSKALAKKIETLKKLEENSRKFPKVSHKAPLQDIEFLPSKGFTPSESSKE
AFEQIMKALKDDSVNMIGLYGMGGVGKTTLVKEVGRKAKELQLFNEVLIATVSQNPNVTDMQDQMADSLGLHFDEKSKEG
RAGRLWQRLQGKKMLIILDDVWKDIDLKEIGIPFGDAHRCCKIVITTRLENICSYMECQQKVFLRVLSEEEAWALFKINA
GLRDEDSDLNRVAKEVARECQGLPLALVAVGKALKDKSEHEWEVASEELKKSQSRHVETFDDRRNAYACLKLSYDYLKHE
ETKLCFLLCCLFSEDYNIPIEELTRYAVGYGLYQDVKFIEGARKRVYMEIENLKACCMLLGTETEEYVQMHDLVRDVAIQ
IASSEKYRFMVKAGFGLKEWPMSNRRFEGCTVISLMGNKLAELPQGLVCPQLKVLLLELDDGLNVPERFFEGMKEIEVLS
LKGGCLSLQSLEFSTNLQSLLLVECICKDLVSLRKLQRLKILVFMWCDSIKELPEEMGELKELRLLDVTGCMYVASIPVN
LIGRLKMLEELLIWDGSFTGWDSTGGMNARVTELNSLSHLAVLSLTIPKVECIPRDFVFPRLLKYDIVLGNGYSITAYPI
STRLYLGDISATSLNAKTFEQLFPTVSQIGFSNVEGLENIVLSSDQMTTHGHGSQKDFLQRLEHVEVAACGDIRTLFPAK
WRQALKNLRSVEINHCNSLEEIFELGEADEGSSEEKELPLLSSLTELQLSWLPELKWIWKGPSRHVSLQSLNHLELWYLS
```

```
KLTFIFTPSLAQSLIHLETLRIEYCRGLKHLIREKDDEREIIPESLRFPKLKTLSISDCDKLEHVFPVSVSPSLLNLEQI
KITFADNLKQIFYSGEVDALTRDGIINFPRLRELSLSCCSFFGPKNFTAQLPSLQELTIKGHEELSNLLTQLHGLTNLRG
IYITDCKGAQDLMQVGSFLTNRRTGHELSLLSLETLHLDSFPDIKCIWKGLLLSHLTTLVVRKCQRLAHVFTSSMIASLV
QLKVLDISTCEELEQIIAKDNDDEKLQILSRSDLQSSCFPNLCRLEIERCNKLKSLFPVAMASGFPKLQILKVSQCSQLL
GVFGQDDHASPFNVEKEVVLPDMLELLLENLPGIVCFSPGCYDFLFPRLKTLKVYECPKLTTKFSTTTNGSMSAQSEVSQ
VVEDSSTGCYVLTSTCRMWTRNNGWWEEEKEEEEWEEEEEEEEEEEEEEEKEEEEWEEEEEEEEEEEEEEEEEWEEEEEE
EEEEEEEEEEEEEEWEEEEEEEEEEGEEEEEKDEDGGGHEDQVK
```

1355 - 1374:	EEEEEEEEEEEEEEEEEEEE

A0A2K2CUC8 **A0A2K2CUC8_BRADI** (157 aa)
CCT domain-containing protein. *Brachypodium distachyon (Purple false brome) (Trachynia distachya)*

```
MAPYSRSRLAIGVEKEVRPYNATEKRDRIEKYRSKRSRRNFQKRILYTARKVNADNRVRINGRFAPRGYQPPAPAAGDDD
GDRPPQLKDEEEEEEEEEEEEEEEEEEEEEEEEEEEEGNGEPEWWPAMHESLNGAREADVITRILSGDYWDWEMCLL
```

90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE

A0A2K3CQM7 **A0A2K3CQM7_CHLRE** (398 aa)
Uncharacterized protein. *Chlamydomonas reinhardtii (Chlamydomonas smithii)*

```
MLSCVRALPEFTAVSEPLGLWKDLHKPLKGSEGLWRALEGSGGSEGSGGVWRALEGHTFGETANTNKKAKAEKAATSSAS
TPTKSGKESGKDTDGTKWYYCDFHGRNPSHPSKECRTLGNRRSAAAANSAANHQQPTYSGNDPLDKLVVAIQGLTRSAAA
TTRSASAGGAASGAPRTKYEADKAKRGNRPPHRGEGRRGEGDRPSEQCGFCFMFTHTRENCPIEDPDKASHSDWVPRSPA
MKLLFEQAKARKAQEKQQRQAAATAHRGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEYGTSCVTALLLRPHWCT
PTARQEDCYGQWRGAEAQAGQDAPCSGGSAASSPPAKPAGAKPCVIVRTPGVPYKPGVPGSEPTLHYDVHACAPPPCQ
```

269 - 288:	EEEEEEEEEEEEEEEEEEEE
270 - 289:	EEEEEEEEEEEEEEEEEEEE
271 - 290:	EEEEEEEEEEEEEEEEEEEE
272 - 291:	EEEEEEEEEEEEEEEEEEEE
273 - 292:	EEEEEEEEEEEEEEEEEEEE
274 - 293:	EEEEEEEEEEEEEEEEEEEE
275 - 294:	EEEEEEEEEEEEEEEEEEEE
276 - 295:	EEEEEEEEEEEEEEEEEEEE
277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE

A0A2K3CQX7 **A0A2K3CQX7_CHLRE** (1471 aa)
MYND-type domain-containing protein. *Chlamydomonas reinhardtii (Chlamydomonas smithii)*

```
MPTLALAILRGDTLNVYAQILAAVRTAVAAECSFADYAASSIADVSDVASSSSSSSSSRDNGRDGEQQMPYHAAVLDDAV
QLQLQTVVPVLLATTTLMQALSDDSPNGPLHTELLAELARSGVLEHAASALLWLELAIGIARVGPAEEEEEEEEEEEEEE
EEEEEEEEEEEWDEEEEAGQAEARAQCERQLAAASRKELRTLEQSLRVHITRLLHLHSWPPPQPPQRQQPQQPGPALTAS
ATATPTTQRATAPAASAAPATASASSVPAAATAAATAAATARQAGARRPELLRRILSGPALQWLSLSALQFSIDRFYDEE
EEEDEDEDEEVNEARARKQNQQVQGQGQQQAAGRGGGSGSSSRGGDGGGRGGSSASTAGGRAAQYSQAEVRAFTYMFAAI
ESAAHVFAFCPPGHSDLVTRAAAATATARIQSRRRRELASLAQQQPQQQPAEPLQPQPEPQPKPPQPQLLQPQQSQPLQP
LHQQQQAEQQQAAESLFCLALLRTLYSAEIAVPAVGLNGQELAAARRRWWVGFHLLLRVLGQQLQLQQPQQAAARLREVW
ALVATALPALPGAVTPSCNGHQLSAFHGLAAVLASPVVPAMVKMAGPPPAPQQAAAAAATATAATTTTAPAPAPAGAAAG
IALDTGSGCSYSLRCALDAGLLRALEQLLRRAMAGVASAVTAPSSAAASHGRGGGGAGVACHADACSACYAFGTLLCQSG
VWPAVLAHGAVEEVVPLVATLARAAATAVDAVVAEEAAGVAPSMATTVRRFLAGRLCLFLTAMLEQQQAVVAVIGRAAAS
RAAAAGVAAELAGVAQPEAAAVAAAEPEKAFELALSNWLCCNPSAPGACGTAPAARTHAPAAVWRPAGSSTCSIPPAAAG
PASTATAAGPTSAEAEAAVQTPPQAPSPQAPQTPQLLADWAALQWLPVLLSDNAIQLMAAELTREGNPAPMSAAVCEPLL
DSRLNRSLVWLGRHWVEATWRYRTCTLRSGECAGAVPEQQQGKTQQGQGQPGQGQTQQGQEQQQGHGQGKQQQAIPDMAI
AFRSVQARQAATYWSVFMGAAGLRMHVQEQLKRACSHFRTALALLALIGTQQQQPAKTAAAPPAGRRDGAGAGTGGGSGG
GGGAGMEGAADARRARDGRGGRGQRGGAAGSGDAHRLALATATAVMDLSELAVVDVWLDDAKYVDAELVHFNPLCAMEDG
ALLVQALQRFGLRQRPRLEAYLLLLCRQAQEHPPQSATTTAASTAARAGAAAAATAGAASGATTGAASGAGTKVQQRRGG
```

```
RQQQAAASAAAAAAEAQARVARREEWWAAASALWDELPERYGLADPSSVAMHQFVTMPANLGRRLLRSSMDVPTSAAATA
AAEGRSQIRSYSFMNTSELLLDSEGRAELCCNPACRSLDGPSALLLPGAGKVCARCKAVRYCCGACQLEHWRQGGHEREC
PSMRHAREAVQGLSPGREAVQQKAEAATEAV
```

147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE

A0A2K3CS95 **A0A2K3CS95_CHLRE** (1493 aa)
Uncharacterized protein. *Chlamydomonas reinhardtii (Chlamydomonas smithii)*

```
MELAFTGAFAWAAWQVLGRLQRHAAKIEKNIDDGLLLGMWEEECKNMAASKKRSSPAMGAGAAASGHQHIFEDWRNKKLR
PQQMIQLASDLADLAQWAGVGRHVPELRVDGPVKAWAEYGTAGKVHLLQAADALQFNFAEAARKQAEQLADNWLWQVTEA
LPSLSAEPLRTTAPNNAIASLKTRLTEAEAAVRAVFDAERTSQAAGLKGLVEPLSVARCARNLQVLKALAAEVGLNATMA
DPAVAAVRTTLSAPLSLEAAAPAVAAQKTAAADAVNSEADAAVAAERSARVAEIEAAAAKTYRRALVLQASSPTHWHMSS
ETPALHRLGLMSALLMQLACDSAAGTPEGDAAAAELADAVRKLMPQMRIKLSEDDAARRVMLLAALTPAPPAPPPAPKPE
PEEGEEDEEGKEGEEGAEEGEKAEKEEVPPPPARPSPAEAAQGLVSLMEGVIRAQLAEAVEARKAARAAAKEAKAAAAAA
AKAAQEEAQAGEGSEEAAEKAEEAEEVAADAEEQEEEEEEVDVPTAAETVDVAAVRKGVEQEARSRSDAEKEAAMLKLED
ALGALREATAAKAVTGLVDRLAVTAPPAAKGDEDGAVEEEEEEEEEEEEEEEEEEEEEDEAEEKEAAPAAPAAAPLDAGSR
LLALESLLRDAAKASDAGLAAATADAIAKLTDADLAALDGATSSALSALSAHLALVKLVADTGKLDLAPGACDTLRRVDT
WLAEHESQAAAAAAEAAEPQPATETVVEEGEKQEGEAEAEAETKEETPAPAPAKPKTADPARLAEGRRLVSELLGEGLVL
LELPPASYRKLQLLREAVDKLDPVAGDGAVQHSAIKTLGEVVSQLGPIGGSVDARLSQVSDEGERAKLGEVRSAAVAIYG
ALTTFLRLETETWTDAKSTLDKARTTVFGLKVERKAATLSEGVEACGGVHATCVKLGGMVSALGSQPAKAASGRAKTALQ
ETAEQAHSTAAALEEYLSYVRLREHALGGAVSAPAEVEDTFELQLPQLDEMTGKHNDEAVWLDLAGMGLPAVDEEDEASA
EAHEEALAGLQERLDGWHMTGLRLLARGQAALVTLGGATTEAGELRLTADIGLPSAKSLLQLCAEKIRRLQMMAAESVSG
PNSGVANPLHWYLLVPAAAEQPLKDFLAANEHFGLLPSQVHVAVNDVRPPLLTEEGLQVVLDSTGTRVARSQPGSGEVFL
ALRRSGALAHMRKVGVRCIEVETVEDNTIARPLDPAFLGACSATAIDAAAKVAVPGVQTEGTSALPELYSRYLELLGTSS
PLLERLGDYVPAIGTYYFSMDFVKRVDKLLRDRPMALYRLAPADKLPSRAAAAPGKAPAPGGGAAGYRLERRLSDFASPA
VCSLIDGVQLAMVAVDVAAEFAPVWGTAPFYKTASPTSAVDAMLLQQTRWVEEAGGALEDEEEGVVEVSPLVSYAGEGLA
PLVEGKVFAEAYVHELQGFDAASTGAGGNAGVWAVPAVVAFAGAAALQVVKGK
```

598 - 617:	EEEEEEEEEEEEEEEEEEEE

A0A2K3CVD8 **A0A2K3CVD8_CHLRE** (1202 aa)
PHD-type domain-containing protein. *Chlamydomonas reinhardtii (Chlamydomonas smithii)*

```
MAGKRFTPSAKLASRRVPEDWSKHQVFVLPHDLVKPHLSKEPSRKHPITLTVFYPSSDGKPPGAKSTPAKCKYALTEDVG
DDGQLQGRFDLAPAAKATHVLTDEGDEFELWCSGEPDHFVVKVVKETCPACGKETSDKKFGRTYFCEDCDRSWHPTCCGW
PDRRLTKDESFYCTECRPDFPPPPARAPPAKRARGRSGAAAAAPRSGGRAAARPTRRTVAAGVAGGGAAGGGAASAAARQ
AQHVTDNDTDGSDADSSSGTEEEEEEEEEEEEQVEEEEEEEEEEEEEEEEEEEEQVEQQQGGATNAAGSLLPASVNGAAA
AAAGAEQEEDGQERPGRAERLRPAKRARQTEAGRGSVRDAGGAMNGGAAGAAGPSGAAAAGAAAGGEQPGVPDGVFVTGR
EARRARHTNARQPLPAAASPGAAAAPAGAGSTAASPAQVPLPALPPGVRQQQHQQQQPAGRQRQLPPISQHPLVQALSPP
AQALAAPQPLPQLQPLPELPPLPADPNQELLQPQPGQQAGDADDGYEPEADAEFEAYDELDGDAGEADEAEEMEVEQQEE
EQEEQQEEEEQVEQQEEEQEEEEEQQQEEQQEEEQQEDGQAGEDEAAGLVPTPQRGSGAAAAAAASDGDDHPLLSTLVQS
AINEFPIPLGHVLQGRQLPGGFQPNDASGIHDAVLRVLGVNRSEAAGGAAAGPSGSTGRRRAGGRAAAAAVARQPLPRLR
DRLPGLPEGMRQALDEHQAELDEELKANHIHHSDTYRRASLAFLHLLEAAATAVADQQSEAAAGGASALRERAAAAAELR
AMRQQVEDARAAEGRKHVELLAALAAQRAAEDEAANLRAALAVLTGDATGGIPGAVLAQMGLAAADEEVRTLANQVAISD
TLRTSNEQLRIQLQNASAARDAALAASARDRAAALAAEQRAAAVPHPTVEVAQARAAVARAGASAEVAVAESARLRLVAR
QTAEENLRLRAELNDLQALLARVAAAHPDSAVTIEAAEPGRRAALQGAGLENYINGVEVTNARLREELSRLRDENNRLAA
ARYNCTTALERESAYWMSTAADAIRGPRVRPELWAQQAMLGGAAAAEGAAAGAGGGGGVGAAEGAAAGAPAGGGGGAGAG
VAAGAGVAAGAGVAAGPGAGVAAAAGGGGAVGGGAAPAGGAVDAPGGEAAGDGGDGGGGGGRGAGGRGRSRGRGRGRGR
GG
```

275 - 294:	EEEEEEEEEEEEEEEEEEEE

A0A2K3CVE3 **A0A2K3CVE3_CHLRE** (1206 aa)
PHD-type domain-containing protein. *Chlamydomonas reinhardtii (Chlamydomonas smithii)*

```
MAGKRFTPSAKLASRRVPEDWSKHQVFVLPHDLVKPHLSKEPSRKHPITLTVFYPSSDGKPPGAKSTPAKCKYALTEDVG
DDGQLQGRFDLAPAAKATHVLTDEGDEFELWCSGEPDHFVVKVVKETCPACGKETSDKKFGRTYFCEDCDRSWHPTCCGW
PDRRLTKDESFYCTECRPDFPPPPARAPPAKRARGRSGAAAAAPRSGGRAAARPTRRTVAAGVAGGGAAGGGAASAAARQ
AQHVTDNDTDGSDADSSSGTEEEEEEEEEEEEQVEEEEEEEEEEEEEEEEEEEEQVEQQQGGATNAAGSLLPASVNGAAA
AAAGAEQEEDGQERPGRAERLRPAKRARQTEAGRGSVRDAGGAMNGGAAGAAGPSGAAAAGAAAGGEQPGVPDGVFVTGR
EARRARHTNARQPLPAAASPGAAAAPAGAGSTAASPAQVPLPALPPGVRQQQHQQQQPAGRQRQLPPISQHPLVQALSPP
AQALAAPQPLPQLQPLPELPPLPADPNQELLQPQPGQQAGDADDGYEPEADAEFEAYDELDGDAGEADEAEEMEVEQQEE
EQEEQQEEEEQVEQQEEEQEEEEEQQQEEQQEEEQQEDGQAGEDEAAGLVPTPQRGSGAAAAAAASDGDDHPLLSTLVQS
AINEFPIPLGHVLQGRQLPGGFQPNDASGIHDAVLRVLGVNRSEAAGGAAAGPSGSTGRRRAGGRAAAAAVARQPLPRLR
DRLPGLPEGMRQALDEHQAELDEELKANHIHHSDTYRRASLAFLHLLEAAATAVADQQSEAAAGGASALRERAAAAAELR
AMRQQVEDARAAEGRKHVELLAALAAQRAAEDEAANLRAALAVLTGDATGGIPGAVLAQMGLAAADEEVRTVRVQLANQV
AISDTLRTSNEQLRIQLQNASAARDAALAASARDRAAALAAEQRAAAVPHPTVEVAQARAAVARAGASAEVAVAESARLR
LVARQTAEENLRLRAELNDLQALLARVAAAHPDSAVTIEAAEPGRRAALQGAGLENYINGVEVTNARLREELSRLRDENN
RLAAARYNCTTALERESAYWMSTAADAIRGPRVRPELWAQQAMLGGAAAAEGAAAGAGGGGGVGAAEGAAAGAPAGGGGG
AGAGVAAGAGVAAGAGVAAGPGAGVAAAAGGGGAVGGGAAPAGGAVDAPGGEAAGDGGDGGGGGGRGAGGRGRSRGRGR
GRGRGG
```

275 - 294:	EEEEEEEEEEEEEEEEEEEE

A0A2K3CVF1 **A0A2K3CVF1_CHLRE** (2789 aa)
SET domain-containing protein. *Chlamydomonas reinhardtii (Chlamydomonas smithii)*

```
MSSRGDRKPVFGSILNYMHRWRGTTADDQQTVAPDTVQSPDDAPATAAHDAPPDAAAPADRATVTAAVRVKTEPMPATPS
APGPGPGPGDAPPRHAHGPAGVDLAAGAAADVDMDADAGEHEAADELGPEPYPNSEQALNWYGSDVDDEPEEQKAGGLDA
PPPPLAGPVCGSADGAGAAGGASTAAQARRDAPAATAAKPQRSVVKPFQGVLVIAPRLAAAAFGDAAMEEALERQVRVRL
FGVRAGMSHPDADPSVDTASIEAAAAAATAATAAAGSPAAVGAGFWGADRAVLCTTAPMRVSGTSPVARFTSLTAFLREL
GVTGSDGSNGRVVVMLAPERPGTLLVVPLLAAAAGTDAGGLKEVAAQGAAAGAPAAAGGPGSVKGGAAAGALRRPRVSLA
GAEDAQRSVLTYGKLGRLSVSLRLARQLAGLPAVRGVRADAAMSFPVRLFGTRTRIACADAPLAVAPASIEAAATATAAF
EAAAASPTAAGSAPFAWGADGALLCGVVRVRLDQRAACGRISGLTNYMRALGVSPGDRAVLMPAPGRPDGLLLVPLLEPP
AAAAGAGAAAAAAAAAAAAAAAAAAAAAAAAAAGQGAPDEAAGAGEEGEGDEDEDVGEDEEQEREQEQEQEQERAQEQEQEQ
EQEGDGTEAGPAAGAGADALLRRSSIGRAVWGSGRSVVRCSNGTMVVGRRLVLAAVGEAAVQEAQDKQVRVRLFGVRAGM
ASLDADPGLSTASLEAAAAAATAAATAGAAGGVWGVDGPVLCVEAPMRLTRSPSGAVGQARFTSLTAFMRALGTGGGDRL
VVMPAPSQPGALLVVPLLAAAGGSEPCPAAGTTGAGAGAANCDGEQPPRPRQHELPAAALAAAPSPAQPEAPGASSGVHP
QRQEQQEQQEQQRAPRVSRRKPQQPMRLPMSLPPTPEPTAGAAAAAAGASGTVASHPPWGKVKSEPGDAAADAAGPGAVP
AAGGAGPAKAGDHNVCDAPSSPGARAGAGARPSTGGRALRATWRSNGCLDLSLGAARALFPQLTSSFGEYPCVLVQRLRP
VAGAAEVEYPEAVLVYAAKNTRIKKRSRLGRDLGLRNTDNATLELRRLPDGRVEVVSMQLHDTAPPQAQAQQAKQQQSQQ
AQRPQQLQQQQPAAADGYGDDAAGGMAVADAAAEAGSGPDSGRGGAMDVEGSAGAEGDASESMEDAEAGQEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEAEEETVAAASAEPSAPDPAAVQTGAPGTAGTGAAATTAAPANTAASAPLTPPAPLAG
AAVGDEVYLAYWRASGVLEIARGTARALLPHIKEDGQYPFVLVRRNPLATLLATRDASGGSSCGADGGALAEVEYKDMAL
TFTHRSYKVYIRNKAQLGRDLGLHNTDKATLGLRRLPDGRIELISVEQQQQAVAAAPQPGAAAAAPQVATPPAAGAAGLA
AAAGGLIRSGEQALEAAPVQDGQEGEEADDAGEQAGSKYGTPQGATPGSAAGNARADAVCSDADEPVDEAIEEQPQLQQD
EDRNQEQRQLRQEAAADSDEEFADACDGTEAGSEGESALGASDDDEETAAQRPAAGGGGGGSTGSGGSDGGPHAGPASQP
AARARCTNSMGVPGAPAAPSTSAGGATRSAFQQRRLTPLQGGTGSAERAAAAGTAAGAAAAPGLLKQQPVRWRKLRGADG
SQAMRRGLTAHMLQTGVLNVRELEKLPAMQAHFQRLLPDAAGQCVLEVLVSPPGAVAEAPTVGGAGAASTPAPALVPGAS
TGNSARAQPEAAMQPGAAMRVTLCRYVGKTRGGGAPVWSLHGLKLWLQSVAAAEGDLADLWFHPRDASLHLCVHVGSSES
RGPGAPGAGAATATAPAVGPATAGEAAAAGAGVSTGAAAVARRTEPRPGVHGRPPRAGAVGGEEGPLEVREKAPALLLPM
AVVRAQLEDVASGHGAGVDIPVRLRHEPSGETFDVTLRGYPYYKRRPAATAGPASDGGDGSGGGSTGAGAGATAAETGAG
AAVFLPLSHSQWYLKGMRHIYTRFDVQLGSQLYLTRVRDGDAAAGGAAGAATAATSGAVPVLTMRFERPGAGARSGSAML
AAVARAGLPPLPRRGSLAGAAAAAVAAPAAGDVEMADAEQAAGADADADEEAEADAEADADAEAELGTASGAFGSNICGD
TGADNHGHSGDTGGGDEVMQEAEGGAWAGVAAESGTPQEAPDAAGNDTGAAAAAAAAAAHAALPRGAKRRAEAADSAGAS
HVAGTMAESVQDGHADPDGFRCGRRPPPAKRARAETAAAPPTDTAALAECHSIGGSAGVATDAAVGAAAAAAAAAAEAAD
GPAAGLAFLHGCVPPAVGLPPLRPGELRLCGLTFHPDLAPAVLQLQASWLEKRSKRGEAGLLEMDPASVQIQIPEIEEAN
QVEQTTEIKPKEERKPEGAVRGVVGAHGLSPNVICSRLARVLGLSMRWGAPLPQAPPPLVDGVVVASDPERGGLGLAAAK
FIRKSTVLGVLGGYVLPAASAAAAAAAGGAGGTGWLPAPAGASAAEVFVARGFQELAAPVAAELAARAEPADVAQAWRFL
AGSFRAAYPGLQLTPAGDTAPVALELNMLGYGNATALVNDPRAHTRLWEEPPPPPAATAAATATAAGAGEAEANCVVVPV
AVRGVVLPVLVASRDVEAGEQLLLDYGGEGWWRALAPAWENVEFDGASPGQLLYGPDGPAALKAALSAAPRQRSEAGAGG
SGAERPPLAQLGWAGSGSGGGGGGMVSGGMGQARGVTEGNTGGRPGSRQPTPVASSVLESTVVAANSSS
```

1191 - 1210:	EEEEEEEEEEEEEEEEEEEE
1192 - 1211:	EEEEEEEEEEEEEEEEEEEE
1193 - 1212:	EEEEEEEEEEEEEEEEEEEE
1194 - 1213:	EEEEEEEEEEEEEEEEEEEE
1195 - 1214:	EEEEEEEEEEEEEEEEEEEE
1196 - 1215:	EEEEEEEEEEEEEEEEEEEE
1197 - 1216:	EEEEEEEEEEEEEEEEEEEE
1198 - 1217:	EEEEEEEEEEEEEEEEEEEE
1199 - 1218:	EEEEEEEEEEEEEEEEEEEE
1200 - 1219:	EEEEEEEEEEEEEEEEEEEE
1201 - 1220:	EEEEEEEEEEEEEEEEEEEE
1202 - 1221:	EEEEEEEEEEEEEEEEEEEE
1203 - 1222:	EEEEEEEEEEEEEEEEEEEE
1204 - 1223:	EEEEEEEEEEEEEEEEEEEE

A0A2K3CVL8 **A0A2K3CVL8_CHLRE** (57 aa)
Uncharacterized protein. *Chlamydomonas reinhardtii (Chlamydomonas smithii)*

```
MQGTNGNCDQEENQNQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEEE
```

17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE

29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE

A0A2K3CWH5 **A0A2K3CWH5_CHLRE** (1713 aa)
Uncharacterized protein. *Chlamydomonas reinhardtii (Chlamydomonas smithii)*

```
MAGLLGELGDAAGGDSESQTTWRDLPDHLMEAVGGHVFGHDFLAARLVSRAWRRALSPVTRTIKVHLHHPRPDPGAQLAA
VQTAFPRANRLMLYVDANSSRDQADVRANCLATLKAAADTNRTTNPQQPPQPPPQPPPPPQSQQQPQPQPQPQPQQQQQQ
QPQPQPQPQSQHQQQQQTATAGGGAARAAAAAEAPAGPPASPPRTASPPGPEVAAASAGAAAAAFASATTKWKPDSSTGT
GGPITTGGVATATGGGAGGVGGGGGVGGVGGSDGGSDGGGGGGSGSNGGGGGGGGALAWSHLGLTMSASVLPLNRDAPPW
DGVCGRLAASGAWVGRQLSAALCEAKPHLSRLRDLSSLELTTDVDTFNIAAGLLAASPLAAKLTEFKYTRAEGCGGRGGG
GGGGGGIAVALGLGLGLGMGLGLGGRAGAAAAAAAGVASVGRLTGLKSLSLHMGLHGGLAPTLALLTALTSLELTHQGEG
LAAVPAGGEWPLLALAGGPAGEGGGGGGGGGGGGGGGGGGGGGGDGGGAWRSGRVAAGLVSLKLKYVALADPGCLTALT
CLTHLEMTLPGYFFQPGEGEEEEEEAEEEEEEEEEEEEEEEEEEEEAEVEEEEEEEAEEEEEEEEEEEEEEDVLMADPAPG
QQQQPPQLQPPAPQLQPALQAQPPHRLAALQPPQPLQPDPWLLHVPHPAPPLHPWPDPLPQQHPLLPQQHPLLPQQHPLL
PQQHPLLPQQHPLLPQQHPLLPQQHPLLPQQHPLLPQQHLLLPQPRRPESMREDSAQWVASMVRAAQASLSGGLSAQGQA
LGAAAGATAGSAAGAASGAAVGKHGRGLTAAERAEADRHYEGLRAIMGSRMPLRVPHRREEEELEEEEAEEEEEEEEEEE
EEEEEEEEEEEAKDLDQQGRHWHVGPPAARPGPQFPRRQQPYKQQRQYKQQAQYKQRLLYTRQRQLYKQLRQYKQHAQYKQ
QAQYKQLRHYNQPRQPYKQRRQYKQQRQQQLLRQGPPLQPPPQAALQPPLQPQPSLQPQPPLQPQPLLQPPRLQQPPRLQ
PLQPPRLQQPAPGGLAVARTVAAAEQLVAAMMPPLPAEQMKPLAAALPAPLLLPACLEAPHPYPYTHRYPYPYPFLPAGA
AAAAAAAAAGAAGATAPTAATAAATAAAAATTATAAAAATAATAATAATATTAATAATAATAATAATAAGEGPAGRQLGI
VAAAVAAADADAAADADADDDDDASAAAAAFGGDAGRGARLDGGAAVAELEEVGEEEPEQLEGAVGDAGGREEQPEPEGA
SGGGGDEGGSGSGRAGGAGGSAGVGAEHPAAWQQGAQEALGRGEEGVEEEGAEEGAAEEEGAPFDQDPAHEGEDEGEEED
EEEEEEAEEDEDEEEEDEGPTEEELAAAAAHDAAASARLWAALARLPALKSLNVNAWQEAPLDDDRLGLLAKLVLQPSAG
ATAAAAAPGPLQPAPGAAAAAAVAAAWAGGGGAHPQQHPQPQQQPQQPGQLQQQQQQQQQQQQQQQQQQPLKDLVSLGL
LLHASSAASHLHCLAPMGPTLKELTLVVAPTKVCVKALSRLEELELWNVYGSDWAAEVDVAPLGGLTRLRSLKMEALRPH
MAYRVRRVMQAAVPYCKLRLVADNEMPEGPVGLHPLHLGAAGGGGGAGGGGAAGGGGAGGGGGAGGGGGGGGGGGGGGG
GGGGGGGGGVGGGGMGLLFPLPLHLIFGGGYPP
```

587 - 606:	EEEEEEEEEEEEEEEEEEEE
870 - 889:	EEEEEEEEEEEEEEEEEEEE
871 - 890:	EEEEEEEEEEEEEEEEEEEE

A0A2K3CY84 **A0A2K3CY84_CHLRE** (595 aa)
Uncharacterized protein. *Chlamydomonas reinhardtii (Chlamydomonas smithii)*

```
MVQGRGQQPSPRSPRAATGPGLLGRLRQVGQHVAQALGTKGKRLAFLLRESRARGTVGPAPRAVTCRRPPTPIHAMSTSR
LLHHVSNLREEQSLLTQMVREAAAAYEHQLLICTVSDYVPHPARVQMVLDAILRYMTDPDAPNPNDIAIDALLLCQAAVH
LKTLQDVRAQLGAVQSQLHAALDELYDRTAASAVAPHVHSGSSTGVAAAAAESEAQPEAPAAAQPSRNESCDLAARDVYH
PKSGRHLDLSPSRQSPAAAPPSTIASASSNMVRSGPSLHAVSVMLPGGGVLPANYPLTPEAKAWFEDLRKRAEEAEAQQL
AMEMASPAISDGSSRVDLVATADPFPPQQSVAAPSAAAGSFSYQHQPYRGGDYEPLAAPPPPPAYEESWQHPTHGSDAGA
WTGGDVDATASGSPGATSRGLDNGGVHTTASSGPWSIASGCGGSPGSAGADDVMACGAATGHLQLDSGGDSDMYRWEPQA
AAAPGARAAEFEGFNDIPLTSRSGASDASWAQQEQQEQQEQQDEEEEEEEEEEEEEEEEEEEEEEEEEEEEQAWPPRDQE
ALDALIAEGAGHAYACVVVEGVPFTWYTKAVFTPR
```

524 - 543:	EEEEEEEEEEEEEEEEEEEE
525 - 544:	EEEEEEEEEEEEEEEEEEEE
526 - 545:	EEEEEEEEEEEEEEEEEEEE
527 - 546:	EEEEEEEEEEEEEEEEEEEE
528 - 547:	EEEEEEEEEEEEEEEEEEEE
529 - 548:	EEEEEEEEEEEEEEEEEEEE
530 - 549:	EEEEEEEEEEEEEEEEEEEE
531 - 550:	EEEEEEEEEEEEEEEEEEEE
532 - 551:	EEEEEEEEEEEEEEEEEEEE

A0A2K3CY91 **A0A2K3CY91_CHLRE** (436 aa)
Uncharacterized protein. *Chlamydomonas reinhardtii (Chlamydomonas smithii)*

```
MVYKDRRDVGMCLLAVVAACSIVAVQARSLPHAPKDFVVADYKGIRQYLDDSGLSNIFLTWTTGPETLDALAVACITSVI
DVYSPLRQRTSGGVYILANHLDQRVAEAHGWVRPGVHLVRYEVGDVLQETPVESWYLDQRWQLEEGKFWFSHVTDLMRFA
LVYKHGGVYMDADVLLMRPISASHVNKVYRSLGDSKLFECAVVFFEAGSPYLFEVLKHIPRHYKTDDWCSAGPRPLTAVY
ERLTRPGGLHAAHEAPRQVLPSVYLGIRLKQARKFWNDGVLNVDDFIGCEAVHLWGSVARGYLSQATTYIKGKDKERAFR
DRVHALTRVSWCKPRAPRLDKCADAADCEEQLVALREEAALQEEAALQQEEEEAEEEAEEEEEEEEEEEEEEEEEEEEEE
EEEEEGGEGTGGEDGWGEGDGRDNDGANAYEAGGNE
```

379 - 398:	EEEEEEEEEEEEEEEEEEEE
380 - 399:	EEEEEEEEEEEEEEEEEEEE
381 - 400:	EEEEEEEEEEEEEEEEEEEE
382 - 401:	EEEEEEEEEEEEEEEEEEEE
383 - 402:	EEEEEEEEEEEEEEEEEEEE
384 - 403:	EEEEEEEEEEEEEEEEEEEE

385 - 404:	EEEEEEEEEEEEEEEEEEEE
386 - 405:	EEEEEEEEEEEEEEEEEEEE

A0A2K3D0B5 **A0A2K3D0B5_CHLRE** (1425 aa)
INCENP_ARK-bind domain-containing protein. *Chlamydomonas reinhardtii (Chlamydomonas smithii)*

```
MTSKIKSVLAGLEDWLQKDHVERKFLQDRSAKTNAEALGVVAQAQQRVYQLRSRNVPASSPKEGSRQRKAARTQEDTAAK
AHAAAPEVGEQANPQAVPAPEPLPAPVPVVDVDERPAAPVDEEQPEAGPSSAPAPVAGQKRGRQATRTTAAAAKRTRAKA
AEEPAPTAAAAPAAEPMAVDEGPAARKVEAAPAAAEAPAVEEPVEEAKPAAKRGRGRQRKQPAKTAAPAAADDELDDGSQ
EAAAGKSETDKHMAEQPAAAVVPTIEPRVTRARRGGAAAAVPAPAPAARATRGRAAQQKRTVQEAQLASPALQPKAKQAA
VEAAEALPAVPRSPIAPRASASPLKASNKPTPAAVLAPSPRPSANKPAHPTLQKAATRPSTAKSAPPSPKPAQQRSQQKQ
AQAQAQDGAGAPSGVFARMPSAVAATVAMLGGRPVTAMRSSAGAARGASAAANVASMTAVVDGGSAGTSTGAAAEAVDAT
GAAAVARASVPRSTAPTPSGQAAPQATAPAREVSLGTGFCFGVKADHESSPTIPHFGSATGADGEDGAAALAAADAAPGA
AAAAALAPQHVSRLPNAFAGPHTSASAPAPAPLAEVAALASDEATADTLAEEEEEEEEEEEEEEEEEEEEQEVEPIAAPA
TATAVAAASKTPVVVAQAEAERRPRSLSLAAMRLPSAAGLAADGSAGEAQMAAAGQEQGREAGAADASMQETAARSDTQE
HDNDNIDDVDMEAEPSSEADAEAAGDEAAAAVPAGEPEAAAPAAVALSKPEAVVAGTAQAPQPVKAAKGSNLVSAVRSFL
PQKLANSPPPAAGKKNVKVKALEAAAAAKAKEAAKAAERAARAAAIERNRQQQQADGAVAAAAAPSVITTAAPTVSTAAA
PLAAAPRPTPALTSTDAETLAPTTSVSTAAAARPAAAPAKSTAAGGAGGIGSGSDADAAISVAAVAAQPPPPSAIGSVKA
KAAFFQAKEEQAKRAGAGPPRPGAAGAGAGPAIPSYKAGALARVALAAGDEAKALAAAQGLASAQSVTAASGARPAGGAA
AAGTSAAAGPSTSAVTASAGTGAAPAETAADKHKRVEAKRKEEEERRRAELEARTQAKDDKLRKFEAAKQQQRTAGGGGG
GGGGGGGGGGGGGGATLRPPAPPSANPLAAHPAGKRPPINASGAAAGAATATIKAEPESNRSAPGPMNARTPGPKTGPVA
ANMSPAVQMQVKLLPAVHGPAVSTAATTTTGVDATAPKTAGKQAAGAPGLPKPAAPRPPTGVGAKQLAAVAAAAAAPKTA
SKPTAAEKTPGGVELTEEERRNVHAIQTSPYVVQVKPRTPAMMGTATKPAPTSYEISPYKSDSDEDDSPRRFKALPDWAL
GPRVQEALIAQQHVDADAIFGSCPKSIDVVRVFSDMPHPGKLDMRGRPRRDYARRGSSGIWDADA
```

611 - 630:	EEEEEEEEEEEEEEEEEEEE

A0A2K3D0C2 **A0A2K3D0C2_CHLRE** (1413 aa)
INCENP_ARK-bind domain-containing protein. *Chlamydomonas reinhardtii (Chlamydomonas smithii)*

```
MTSKIKSVLAGLEDWLQKDHVERKFLQDRSAKTNAEALGVVAQAQQRVYQLRSRNVPASSPKEGSRQRKAARTQEDTAAK
AHAAAPEVGEQANPQAVPAPEPLPAPVPVVDVDERPAAPVDEEQPEAGPSSAPAPVAGQKRGRQATRTTAAAAKRTRAKA
AEEPAPTAAAAPAAEPMAVDEGPAARKVEAAPAAAEAPAVEEPVEEAKPAAKRGRGRQRKQPAKTAAPAAADDELDDGSQ
EAAAGKSETDKHMAEQPAAAVVPTIEPRVTRARRGGAAAAVPAPAPAARATRGRAAQQKRTVQEAQLASPALQPKAKQAA
VEAAEALPAVPRSPIAPRASASPLKASNKPTPAAVLAPSPRPSANKPAHPTLQKAATRPSTAKSAPPSPKPAQQRSQQKQ
AQAQAQDGAGAPSGVFARMPSAVAATVAMLGGRPVTAMRSSAGAARGASAAANVASMTAVVDGGSAGTSTGAAAEAVDAT
GAAAVARASVPRSTAPTPSGQAAPQATAPAREVSLGTGFCFGVKADHESSPTIPHFGSATGADGEDGAAALAAADAAPGA
AAAAALAPQHVSRLPNAFAGPHTSASAPAPAPLAEVAALASDEATADTLAEEEEEEEEEEEEEEEEEEEEQEVEPIAAPA
TATAVAAASKTPVVVAQAEAERRPRSLSLAAMRLPSAAGLAADGSAGEAQMAAAGQEQGREAGAADASMQETAARSDTQE
HDNDNIDDVDMEAEPSSEADAEAAGDEAAAAVPAGEPEAAAPAAVALSKPEAVVAGTAQAPQPVKAAKGSNLVSAVRSFL
PQKLANSPPPAAGKKNVKVKALEAAAAAKAKEAAKAAERAARAAAIERNRQQQQADGAVAAAAAPSVITTAAPTVSTAAA
PLAAAPRPTPALTSTDAETLAPTTSVSTAAAARPAAAPAKSTAAGGAGGIGSGSAQPPPPSAIGSVKAKAAFFQAKEEQA
KRAGAGPPRPGAAGAGAGPAIPSYKAGALARVALAAGDEAKALAAAQGLASAQSVTAASGARPAGGAAAAGTSAAAGPST
SAVTASAGTGAAPAETAADKHKRVEAKRKEEEERRRAELEARTQAKDDKLRKFEAAKQQQRTAGGGGGGGGGGGGGGGGG
GGATLRPPAPPSANPLAAHPAGKRPPINASGAAAGAATATIKAEPESNRSAPGPMNARTPGPKTGPVAANMSPAVQMQVK
LLPAVHGPAVSTAATTTTGVDATAPKTAGKQAAGAPGLPKPAAPRPPTGVGAKQLAAVAAAAAAPKTASKPTAAEKTPGG
VELTEEERRNVHAIQTSPYVVQVKPRTPAMMGTATKPAPTSYEISPYKSDSDEDDSPRRFKALPDWALGPRVQEALIAQQ
HVDADAIFGSCPKSIDVVRVFSDMPHPGKLDMRGRPRRDYARRGSSGIWDADA
```

611 - 630:	EEEEEEEEEEEEEEEEEEEE

A0A2K3D128 **A0A2K3D128_CHLRE** (852 aa)
Uncharacterized protein. *Chlamydomonas reinhardtii (Chlamydomonas smithii)*

```
MHDHVVANRWAQLSPEIISCIASFIDPAEVAGAVKLINKATAAVLRESREIRLGGVATVYRSDASTSDPNLSLSVDLAAQ
PWPRAAFLAHWSSPSAWRTLNLLQRHRLVNLAASSGDAESLETALAHCGCSLTKGALTSAAAAGCVAACETLWAQGCDGD
LSEALTASASAGQLQALEWLLRHSLQAGRNRRRRRRAGRHRRWRRRSATPDYFGLGVTACRGGHAHVLSEVERQAAASRS
PFGLERTRFYDCCSYAAAAGGHTELISRLTPRLEARLVEWKWYRNAADEDDGRYVYDDITVAFRLREVVKAAAHGCSLEA
LRHYYHKWSRWVWYDEDPEEDGDREEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDSRW
GGREPSPVVGPEQRAREVLLPLVAAAAGSPTPDAFDKVDWLLAEMRRHAAAAAAAAPDGRAGAARAAAAAVGAHGGAAAA
TVPSPIAALPVSAAAKQPDFLQRLQQLESRGFADFVGAASSAAAEGRAEALAYLLQRAPAVAQVGPARDLLLEAAGRGGH
VAVLRVLCEHGVAEDPGELLADAPALLRHPGFLRAAPLDWVPDVKYAAMCQLEQELGSDDAGMDEGFRDEGLAQLFQDAV
VAGAGLPVLRALQEEGVPVDLAAVAAAGSEEALEWAAAVLREQEGGTLEPLSAEELWHCICGDYPGPGGLNSINGNFAAA
AWLQEHGLAPHLGLAFTMARLQQPQTVRLQPSPQPPRTSPRFQQLRWALSQQPGGWGALAVEDWRKVLACVEQLGKAGAA
WPHQLTWLQQRWLQEAQARLAEAEAAAGRLGRSWEEAVSKARAEVQAARAGK
```

345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE

356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE

A0A2K3D181 **A0A2K3D181_CHLRE** (2893 aa)
Uncharacterized protein. *Chlamydomonas reinhardtii (Chlamydomonas smithii)*

```
MLLGFAELQISSDASDSASESLTVRVHSKEDGSNARITFSWSERGQMELELPGAAAGTGLVRLLQLGILGASISTASGLA
GSGIAASPSHGPGPTASVLYLCAPGPSSQAMAASAAAAPQDCKPGDLNGQAWDGDEDGDGVVEGGSDWRPAVYRFSGGSS
SGGGTSSDLPGSGGGGGNSGIPPLETTGPRAATHAYGAGTSGAGPSGSADKSNANGLMWAGGQTGEQAQSGAGAGAGVRL
VLRLGVPAEAMEKVGVGQPEDTQQRAWQGQLLEVLTWLLPHHHLDGGGGGGGSSSPQPDRTLAAGASASGSGAAGAGPST
SGAGPSASVPGASPRGAAATASASASAAAAASAATAAATTAANAAATAANDAAAAAGFDAGWLYSAVKPSGAEPQWRGDP
PELRPRLRPYQRRAVAWMLAREQQQAGRQPGVEPGVEPGVEPGVEPGVERATQGEQGEGEQERRQGGRGGAPQEAEGGREAGMA
ADAAQAAGASGPLHPLWRRLHTLPGSAAPALYVNPYSGSLAAVGFAVPPPVRGGILADEMGLGKTVELLALITANRFSPP
AAPTTQPKVQRQHTEAEEEEEEPGDAAGRDGAGILEDEEQEDEEQEARPRRTRNRGGGARAGRGTAAHGGAGRDGARSRL
RRKPRAGDDSDADPDDSENDQNARMNETDEDLVLEDEDQEEEDQVEDDDDDDYVAPKRGGQAKGRRGAGGAASGAGRKRG
RGPAQRAGVAASRRQGRVERVDCPCGLRCEDPEDEAAAAYTGLWIQCDACAAWMHGACVGVRRTPRGAWVCTRCLRDTAA
ATVSEPCGATLIVVPSAILQQWYDELQRHVMPGALSVVVYGGQTQPGTGGGGGKGGGAAAGFSGGLILGGGGGGRAAGRG
GGGARGGGAAAAAAAAAGGGGPDKDGHYSIATSMVVSAPQLAAADVVLTSYDVLRRDVARQPDLEAPGHTRSLRRGKRYE
VVPTPLTRLTWWRVVLDEAQMVESGTAKAAEMALKLDTVHRWCVTGTPISRGLEDVFGLMAFLQAGPWAQRRWWSRCIAR
SVEAGQAAGRRLLLRLLRPRLRQGQQRGAVGEAQVQQRQGGMAGWKLEPGTGAATAAGADTDTAAATAAVAAAASAAAAA
AATARCYASLGLMWRSSKRDVEAELGLPPQSAHLTRLRLNAVELHFYNRQHQDCAAKARSVLPARVVAAMESGRLFSGEA
EAEEAAAAAAEAEARRAARAARRAQRAELGLGPRAGWSAGGLGGAAGAAGAAAAGAGPSGAGTSATPMDVDGAGAAGAVE
AAGGSDTGAAAVAAAAVAADGGGGSSAAADADGGSSTGGGGAGAGGAGAGAGALSELAALHRRRWEQQREAERRKQEEQE
EEARIEALRRARQEQEEHARRERGPPEEEEGDMGPMEGQEQQEEEEAEEAQGRGGGGRRRGRGGRGGRGRRGAAQEEEEE
EEEEEEEEEEEEEEEEEEEEEVESSETEEWEQWEGLLLQGPAAGSSDGAHGAAAANGDGGGGGAAGAANGVTEPSAVALA
AATGTGVGAQHQQHQQQQKRAAQQAKRPRRPPPLSSILDKPLAPHQARKLLEPLLKLRQACCHPQIGAGGLRSRRGGGGG
RGAGAAGAGGGPHPHGHHPHGHHLGSHQGRGEGPMSMNEILGVLVTRARLEAEEEQRKLVMALNGLAALFVIQGEPAQAV
STYRSALRAVEEHRQRDGIQADRLQRLHTLANLDLLLQAAAAAAEVLAGQAAAGSANPEAAAAAAAAGKRLRALLGSNGG
GGGRALGAAALTALAAVPRTLRDGGLAADAASIRERYLGQARSKVVAAESEYREVLVTATPFHGAAGWYLSAIDLLQVEG
QGEAAAEHIRTKLLEGDTYRQKTDVNASSFAHRFSSLLGLKMLLNEALDGIETHRAEALGSLEGLGRRAAQLPAPHPDFI
EQAGQCGRCRNGPVRALVCEHCRLDERFIQWEVRLFALYSRALTAGATVTAEEAARRAAAALVRWAGRGGLGEQEGGQEE
DELLAADGGRRGGGGSSQVAATATSWRQSEAEMVLRLLLSLLRQHVRGRSADERVERVLAEGKAHVGRLEAQRRLLVCGR
ALGLAQRMLLYAHDELGMAAARMRLAREGEPIPPHEANLKLQPAMVPVKSVELTNDRILAEADLRRALGTLRYLRKLQAI
QNRQQQNQRQQQQKQQQGGEGAAAAAAAAGPSTAAAAAAASDAAAGPSGSTAGAATAAAAAGATAAAAAAAAASGAAAAAP
GAGAANGGDDDDVQIVSGAGPQGAVPGPGQQQQRQQEGAEPEPAEEEIEMCPICHDPIDLPGTSTSTSTASTASVILPCG
HQMHPPCCEALVARTLGRATPYPMRRIHCPNCRTRVHIADIAYIDATGDMSSGGAAGGGAAGGGSGGDGGSGGGPWSGE
SGVVVRGSYGSKVEAVVRRIKFVLGEDAAAKVLVFSGWAELLELLAGALAANGVAAAVARGRGGMAAALAAFKDHPGEVE
EEALEEELLDAPGSTTATAGTSTATATATAAATATATATATATATATVGPEAESDGAKADPGLTPPPKTLAVTQEQQQQQQC
GGNPAPATAATTAAMVAAAAGAGPATAAARATATAAPLLNTGAYGSADDYHPAVAGSGAAAAGGGSSRAGRGRTPPPPLP
ALPGTPGGGGGGAGGGARGLLSPALGSPGGGGSALKRAKPQAHVKPRVLLLQLKQGGAGLNLTEAQHVVLVEPQLDPAAE
AQAVGRVHRIGQARPTHVHRFVVAHTVEEQVHRLADNRARGMDLSVAVPAARAGGGGGGGHGGRHGGHGGGGGGDGSEL
LTVRDVAMLLDNRWGAGGGGGGGGAPSVGIGLASLVPTAAAAAAAVSGAPPGGSGSAAAAGAVVATTTAEAAGDEGDGGG
EAERQQQQQQQQP
```

1436 - 1455:	EEEEEEEEEEEEEEEEEEEE
1437 - 1456:	EEEEEEEEEEEEEEEEEEEE
1438 - 1457:	EEEEEEEEEEEEEEEEEEEE
1439 - 1458:	EEEEEEEEEEEEEEEEEEEE
1440 - 1459:	EEEEEEEEEEEEEEEEEEEE
1441 - 1460:	EEEEEEEEEEEEEEEEEEEE
1442 - 1461:	EEEEEEEEEEEEEEEEEEEE

A0A2K3D4I6 **A0A2K3D4I6_CHLRE** (744 aa)
Na_H_Exchanger domain-containing protein. *Chlamydomonas reinhardtii (Chlamydomonas smithii)*

```
MRPSSEPGPRFPTSMDPAAAAALSQTAFLGILLLAVLSGYAIRRTRFQWATEGSVALLLGLVAGAGLFGYYYLTDPNHRI
PRRLVTFDEDVFFQTLLPPIIFSAGFSVKKKLFFRNFFTLMIFGVLGTMVSAGILASGSLGLMTAVGLPLHGLLRMSLAL
GSVLSCTDSVASLSVLDGERHPLLYSLLFGEGVVNDATAIVLLGSVSNLNAFDESQALGLSGLWALALQFLRLFVLSTAL
GLGVGMASAALVRRLFRRPGAPSPASAPAAGGAAAAAAGSDHGGSGSSNQEVLAVALLGLVAYFLAEALDLSAILSVFFC
GIAMSHYTWHSLSPAAKVITRHGFHVISSACEVTLFVYAGLDVWVTAVWWRPDVSRRYLLAAVLLAAGLLAMMAAARAAF
TFPVCWLANRLWRRADPIPAGGASVLWWGGLPRGAITLALAYHCFYKDANTKPEELVVISAVILVVVITTVGFGVITQPV
MQGFINQAANKPGPGGGLTPAPSLHAAPAGHRIPAFNLHVTAQAHGARAESDLRAPLLLPSAPLSAAKVTPAAPPSAAAA
AGGGGADALAAPPMVADMSAVEGMWQQANDMLWRGEVPGLATGVPVYTPPPPPAAAAALTPPPPPPVAQPRAEAYGGSSA
AGSGCAGAGVGAGAGAFAAAQLQAGGVGTPRGGEGAPHSAVLLPQGPRGVVGLGGVCAEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEVRMRERDSRA
```

699 - 718:	EEEEEEEEEEEEEEEEEEEE
700 - 719:	EEEEEEEEEEEEEEEEEEEE
701 - 720:	EEEEEEEEEEEEEEEEEEEE
702 - 721:	EEEEEEEEEEEEEEEEEEEE
703 - 722:	EEEEEEEEEEEEEEEEEEEE
704 - 723:	EEEEEEEEEEEEEEEEEEEE
705 - 724:	EEEEEEEEEEEEEEEEEEEE
706 - 725:	EEEEEEEEEEEEEEEEEEEE
707 - 726:	EEEEEEEEEEEEEEEEEEEE
708 - 727:	EEEEEEEEEEEEEEEEEEEE
709 - 728:	EEEEEEEEEEEEEEEEEEEE
710 - 729:	EEEEEEEEEEEEEEEEEEEE
711 - 730:	EEEEEEEEEEEEEEEEEEEE
712 - 731:	EEEEEEEEEEEEEEEEEEEE
713 - 732:	EEEEEEEEEEEEEEEEEEEE
714 - 733:	EEEEEEEEEEEEEEEEEEEE
715 - 734:	EEEEEEEEEEEEEEEEEEEE

A0A2K3DHH9 **A0A2K3DHH9_CHLRE** (184 aa)
Uncharacterized protein. *Chlamydomonas reinhardtii (Chlamydomonas smithii)*

```
MSALNTKAEPDWVDGTRRLSWSRYLPTKVVFLGSHHQWPSDAALGNIIMVNRESLMQSRVLMRDLVGSNGERKLGAMVWL
ARSFGWLAGRSLADFGVEASASTWAPATMPWRTWLIKRELEWVTEEEEEEEEEEEEEEEEEEEEEVEEEKEVAGEEEQGGV
GRGRGRGRGRGRGQGRGRKQARQC
```

125 - 144:	EEEEEEEEEEEEEEEEEEEE

A0A2K3DJ60 **A0A2K3DJ60_CHLRE** (826 aa)
Uncharacterized protein. *Chlamydomonas reinhardtii (Chlamydomonas smithii)*

```
MTRKSTRRSAATAGDGPTPEGATLLDVLRALDLDTLGNMLFRGYRKQYLGARLACKALRDAFDTTQRMVSVTATDNIARE
WQAGQRSYLARAPHCSHLVVKVATYPEIEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEGEEDSEDGCGQRAAGAAYPHDH
LARLALLGTTAEGRASVKNLRLTCNGSGLELSSVVSALLSQLPGLEALDAADCVSPAGMGIGDRTRPAVMHHALASYAPR
LDRLYLPSTSGMLHGLGALAACSGLTQLSIFGRCTFGGTSGDPAELDAQAVAGLSQLMHLKNLRLLCHDPSGGTHLAALL
GGRRPPSLQSLGLTCSVHVIAAAASARGSGRSAGGSGGRTQNLPAVSMGVEAGPGGPGRIVNVVTDPPGSHVPGPSGLDL
LCQVLVAATDRLPPHCRRLQMLYLQCFDMSCWAASEEHLHQSLGPEGPVPVLLERCDRVGLGLLELREARAQAACAVLRV
LGMPARLRLRHGCLDLEASAKPQPQPLQAGEPRSLSSLRLETATPDAVLREAVERLWRAATEQATDQHTDGESVVYSDID
SVDWRCYNASSSKFVLLRGVPQLPAVADSGGGDVHKALGRWLDGLAGLAPPADAQAPAARAGAEAGPSAEDAGLGLHVGR
PSIHVSALCANTFVCTCRSGDDAEELVAALAPAGAAAPTSWSCVGRSGGGEVGGMQGAEPRRPAPAVSAAARIAAHVPRR
LPGARAYNSTSLVKRAVLQVLSELWHRPPADDARGRRRSSAGGAMPAAAAGGPSAGQLGGAAVGRIRQVLDLDLALTRQW
RAVHTLSKALNLPDVDAETSDGDASE
```

109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE

A0A2K3DPD3 **A0A2K3DPD3_CHLRE** (147 aa)
Uncharacterized protein. *Chlamydomonas reinhardtii (Chlamydomonas smithii)*

```
MPGGSDSLVYEFDDPDFGLVPTQWEPLARGIAQSVTGSVHGKPWACDPQRPIVILTYVHVYALEGMVPRVPMPDQSWVAN
NTVVSWRSELCFQGLSDSEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVEEEEA
```

99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE

A0A2K3DPR6 **A0A2K3DPR6_CHLRE** (753 aa)
Uncharacterized protein. *Chlamydomonas reinhardtii (Chlamydomonas smithii)*

```
MATTLQHYAASVYGTEEAADCRLRFYVSQAHTEQEQSGQADPGAGSSGTATAAQLQQPSRTFVGEPLPAHSLILRGTSFR
LRALLSRWTGESAQPWSGGSLPELHVLLDAAEDLGPASEVVRFCYTGQLTELDFHALLLVQRQASYLQVPTCAAACDTAL
EAKAKSLLKQTKPEQILACLSDHSLFPDPGLEPGFRPVQQALTSALLAHFGCAFSIMSSWARLQQWMQLPEVAVAWALAS
EELQTDEESSVLLLVLWWLHWQQHEAGVLGWEEAGAAGRRLMQHVRLGCLSRPFLLVLLPQLEWLQLTPAQYAAVLALGT
ASGAERTCGMWGPGGGSAGTSSDAFSSLGSPQGAAAWYCGPRKRSMTAARQLTCVRHFSNAGMSSLISTGACPLVTKMCI
SHVAAAAGASRAPLWHHASGAALWCATQPHPVHTDPKSSPWAGGAVYQGGFFFGLELARRHDMDMAQPSAAGVGELRLCL
AAYEALPPGLRGRMRQHAFASVDALVSVKCAARDLGALTCRLTPGAPLPVRDWWSHDFSFAAKAVTAVVLPLAGSSPTRA
EAWKAYMTTTAHGSFLACELTLQPRPPPGAAAPQPVAPVSPEAYACMLLAGLELPDDDGPHQEWDLEELDTEEEEEEEEE
EEEEEEEEEEEELSDDSEEDEEAGEDVGMPQAAGSDADTDGRDPDWTPNKAPAWRSGGSGAEGMEVDGGEGQEVELGLEA
GPFRAVLLDLLRRDREAEIQGSDDDDEELVQEQ
```

632 - 651:	EEEEEEEEEEEEEEEEEEEE
633 - 652:	EEEEEEEEEEEEEEEEEEEE

A0A2K3DQN3 **A0A2K3DQN3_CHLRE** (703 aa)
Uncharacterized protein. *Chlamydomonas reinhardtii (Chlamydomonas smithii)*

```
MHSSVEQCKIILARPGSDRSGFSGNPFSHYNLCRIRLRLSGLTLDAHAMARAHLQEVEANATAAAGSAGASGGGGGGGAQ
ATGQGTAGQQAAEQAVIAASSPPPPPSPNPPPPSPPPPSPPPPSPPPPSPPPPSPAAAQDATQQQQAAAGAGGSTTTTTT
GAGAGTATGAGAARVEQAAWHEYDVSNLISTEISKTATDMHGDGVEDWSDFQLPRTQDDIRRLQGLPHVDECFYCKMCVP
TTAMNLDTSQHRRRQQQHRRRGLLSEEELASEAYRANPAEAEGLIYGLPPLEGPWPTAGSSSSGSSSCSGGGCGSSSSSG
SSSALYRRRLQASGEDPAAVEAELGRELLGLGGEDEEGDEEGEEQEWSEEDMTAAAAAAAEALVGVGRRGGIGAGGGGSS
SSSSSSSSSSSSRRLRRQQREERAEQRRRRLLEEEEEEEEEEEKYNALDTTESGPDYHIGGRVYNISDIAPGRRIFQAKQ
HLPNCTVCRGCDHTLEMMASGSVLLGSYFAHEPGGSPSWLFRVRTDRTQSGWAVVKVWCIPVLKAKQRGLGMCDPKKVYA
QVKLLLAQQKGEGEESAPGSEEEEEEEEEEEEEEEEEEEEEEEEEEEEVTSEDEEEEEEGEGEGGNSGSSRGQSPVPDP
RARSHAGAGGTGGPRQPVPRSAPHGRSVSVGGGGKAAASVAAARIAAKAAARRRGAGGAVTGV
```

581 - 600:	EEEEEEEEEEEEEEEEEEEE
582 - 601:	EEEEEEEEEEEEEEEEEEEE
583 - 602:	EEEEEEEEEEEEEEEEEEEE
584 - 603:	EEEEEEEEEEEEEEEEEEEE

585 - 604:	EEEEEEEEEEEEEEEEEEEE
586 - 605:	EEEEEEEEEEEEEEEEEEEE
587 - 606:	EEEEEEEEEEEEEEEEEEEE
588 - 607:	EEEEEEEEEEEEEEEEEEEE
589 - 608:	EEEEEEEEEEEEEEEEEEEE
590 - 609:	EEEEEEEEEEEEEEEEEEEE

A0A2K3DQW5 **A0A2K3DQW5_CHLRE** (915 aa)
AAA domain-containing protein. *Chlamydomonas reinhardtii (Chlamydomonas smithii)*

```
MHGQYSQQQQPPAALGGFGSARAAAARPPVAAAAGKGRTAAAPSAPRHHQQVTRCQAHQQQQALAPQLLVAAAPAAAYAA
EPAAIQHEALRVFGGGSQGYGGGAGGGGGGLQLSALLARPLRLRIGPDHRGRVSWDDGTEPSLHLEEAAAVYSRSSSRLA
GGRGGYGGGGAVAAGAAAEGLCGEGDLLKMLPASLRSHVRDAARRHGSSAAAGGASASSASPSSSASRSSSTCSWLVVDV
AVDEGRPVQVTFADGTKTRLPAGVQVSIEEALRVLHGYVARARGQRQQQQQQHLQWLEAPTGALANDGSTHGGGNGGGAG
DRKHGAPLREDTTEHLRKRARLSRRPPPAFGGGTGPTATNAAATVAPARHSHGIDRFTTGGYRGDGGAEATHWQQDAEEL
NEEEEEEEEEEEEEEEEEEEEEGEEEEDGDWVARDVEAYQHEPAAHRYGDEEVDASMRGEDEYGEDEYEQEEEDTETLR
PLAGGGGRRLAGGAAGGGAAGIGAVWRWQEAAGGQLAALAAVPVGPPPLFGSDGRCCPPGTLHRISAVREPGSGAVVGLT
YRLGRHVPGVAAALADVLSDLAGRGRGRDGEPNAASMAGSLLLLGRPGAGKTTLLRDIARFLADDLGLSVVVVDTSNEIA
GGDTVPHSCIGSARRLKVGRRDQLQAVMLEAVQNHGPQVVVVDELGSRQEAEAARSISQRGVMLVATAHGTDLRSIMGNP
DLNSLVGGMQTVILGDAAAGAAHGGAKTRTERRGEPTFRCLVEVQGRGLLRLRPDVAASVDALLGDDDARTGGGPGGGGG
RSSLPNAAVGSGGHRLLSPGSLLLCVNGGGSIGGRNGAAAVAAADAAGRQQEQRRVQEAERLLPPGGPPLEQLRWSRQKG
AGAHAAEPWTAGATDPGLCVRLLLPTADATWSAAH
```

402 - 421:	EEEEEEEEEEEEEEEEEEEE
403 - 422:	EEEEEEEEEEEEEEEEEEEE
404 - 423:	EEEEEEEEEEEEEEEEEEEE

A0A2K3DV43 **A0A2K3DV43_CHLRE** (1159 aa)
Uncharacterized protein. *Chlamydomonas reinhardtii (Chlamydomonas smithii)*

```
MADYAQYGSMPPSRVSVGRMGQVQGNSHGARAQVGGMLVGDDNKLYGATFPGSPLDAARVRPKSAMPAFRPLAGGPHHLT
HPAPQHQQHQQHPQQSPRPTSSPRNRPASAHVHGGGGAGGAAAAAAAAARSGSATRGAAAIAAGRAAAAAAASKRVTSAA
ARGLLDRSLPATRTAAALEDELTAARGQLAAARDEQRLAVAALRRNEAELQEERAARRRLEEQLRLAREEAAARTRAATW
AQTHSAVMPAPAAPHAADMDGDAAAGTGGGGQAGGAAGGGRRQRPDSASASHMEASLRREVRALTATRDALAAQLAEVKA
SARVQRLAELQAEVGRYKEEAARQRDMAAALAARLDAAEAEAADARAAARARAEAAEALAAAAPLALPAENDLSRRVVRA
ALVPLHRAHKMMTAEARLLKSSFPPLLSLPELRDVAAARPATAGALEALTFLSNHVSRLLEELRGLPGVPKARPAGPEAR
VAQEERLAAATSAAAGSGGGAARSPRGDASVGVSGGGGGVGAGGERALEAQSSLERDLEAQAAAVAAALERGQPPGAGTV
TAIKAARAAAAEKAAAERRRITGLAPLPASSAVPAKTSYERIGGRSPARRGSARASAPAGVPQRQALAEAIAALAAEERQ
RRGGGEDPLAEAMRDYLRASEDVAAGYTAGGGGGGGRSNAGSLRASREDAGASGGGAGDVSGGGHADSAKAYPEGGQQEL
EEQEGQAEQEEQVTAHRRHHPGSQHDHRHQPEHEERSHTDAHEGRHHHPDSDSQRLHDHQEGHPHEDHHDHRDRDHHDHG
THPDHSGPAEQVAEHVHVHVLELQLELGPDAYAATAEPEDSSRQGSGGGASHDRHSHQYEPLHHHDHDSHRGSQGVDEAG
AEAGAEQQWRPHEQAADGAEAEARDGTGAAPYGDGGDGDAPEPSRQDSGDGVRSRGRAGGSEVAEAAAAEAAEAEDERAG
STWGGAADGGDDVAGGGQTAAETEARGGGGDGDGGWGEARAALGDEAYPPAEDAATEVELEEAEEADSAGEAEEGEQQQQ
TQQEEREGGNFEEAEAEAQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERLGEAAAAAAAADPEYGGGEEEGFGARDLQPEPEPE
RQHEEAPRGVGRPQDEDEEEGVAVEEEVDFGVEDVAYEF
```

1060 - 1079:	EEEEEEEEEEEEEEEEEEEE
1061 - 1080:	EEEEEEEEEEEEEEEEEEEE
1062 - 1081:	EEEEEEEEEEEEEEEEEEEE
1063 - 1082:	EEEEEEEEEEEEEEEEEEEE
1064 - 1083:	EEEEEEEEEEEEEEEEEEEE
1065 - 1084:	EEEEEEEEEEEEEEEEEEEE
1066 - 1085:	EEEEEEEEEEEEEEEEEEEE

A0A2K3DVC1 **A0A2K3DVC1_CHLRE** (948 aa)
Uncharacterized protein. *Chlamydomonas reinhardtii (Chlamydomonas smithii)*

```
MHPNDVAGALQFINKETKASLGGIYKSIRVVSRQLELPHGLGEVTTADNSFPGYAFSTYWDRPEPWRALSRPRRLWLLRL
AASSHHAASLEVALAHAGVGLEGAVMESAAAAGDLAACRRLLEEGCDCGGALLVAAACDHLHILQWVWQDAYEQLPRLPG
VFRWCWSDLANAALTGSGDSGRVLSWLQTHWPTPPPPPRSCTAEQLPAAALPGGEEEELEEEEEEEEEEEEEEEEEEEEE
EQEVDEEREQEHWEQQQQSGDEVDMADAGAESSVAAMDGQAAAGAAADVDAQQHVAAGDCWADVVLVRPAAKDEVAMAAG
AEGAGAEQGPAVCPRGATMVLAAPAETTAQAAHLPAAPPLAAAPPAATITTTADADTAVATSLSPVLAPVPPPDAYVPRH
DKLPAVFQALARGGHSDALLRLLDRRTAAYLISVSEGHRWPPLTDTLCHVALGCCPLETLQAVHGQWVARCGAAPPLTRH
RVLAHAIGSTVEWQAKADFLLSHLLQQQQQQQQQQQWEPQAQPGPEPEETVRAEVRGVAAAVQVEPELQAVWAAAAGQA
DYLDRWRYLAAGGLQDGTWQARAAQAAAAAGNAAALGELLEEWDAMAAAAAAAAAGGNMGAGPHLAWTPPPPDTLTDTAAA
GGHVAVLQLLRQRHDPTLLRAQHLLLAASNKHIEAVRYLAAEAVAVAQEQAVAGVAGAPGIGNNGASEATDAHSSFAFRE
VAAAGADLPLLRLLHERCGADIDLDAVATGGSVEALQWAVETLPAQTVLAALNPSRVWSVAASGNLAAADWLIYQRGLII
TGSEDVGGTVAAAKAAGATGGSGAAAANKGGSRAVLMLMLPEEGELLQWFVGGGVFNRVLSRVRMWVARQARFIAVAGAA
GAATRVGSSSSSWGRLMLEDWARLLDLVQPPGAVVALPPQQLLWLRRQRQAAADRLLLPVGEEEGKTR
```

220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE

A0A2K3E049 **A0A2K3E049_CHLRE** (1654 aa)
Uncharacterized protein. *Chlamydomonas reinhardtii (Chlamydomonas smithii)*

```
MGPEERRQHALLLCVCGVSVVVSYAHFAKAYCAGLPHSLPDSSALLPRYPCTGSVWVRAVFLLRNAPATMLEQMQLKDTW
VSITMALMCGRLPLVLLLPPRVYDPLSAALTYGARAVTVTWHLARGPRSPLSPHGVWYFEHFHPWIDLFMFLTTPGAPSV
LGEALYGLLHLAALGVLAAEWDTRYPDLPIGTRVQLPRQLAILLTCLAVTHCTSQRRLLRRRGLSGGGGADPRQLQLGQG
QRRPRCQRLAALLGLQLGGVRAGSRPGAASGAGGSADGSISGDRAEPGHVGKAAADAVDGRSPGARGASERPEGDLKGHR
QQWRPEDLARSGAPSAAPATAALEVVAAEAHALQEPAAGEAPPAAATAAARWSAGRGGGRGGSGGGGGGGGGGSDSWCS
SLDGTPPGRAALTEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEKEEEEAVLVGGTHDGAPHAEGVGDSTEQQSHPPGPP
PYTGWTVRARPFHSLQLLSAMSQPAPVHDVGSRDVDLYREGLDTGPAAAGGGGGRAGADAAAGDQSVAATSAAAAASLSA
VLQLQPLARRAPDRALQPYTPFLNTRTYFAKLPGYDPAQITPGYQQRLALLLAALDGRAGSAVRGGGGPSGGVTGGSRDR
AGSRRLASVSVRAGCIELVLEEEQACWGSGVEESDFEAACVADEECDDEDGHGGAEGSWSASPVEVAAAGGGGTQAAAGG
GSGPKDGDDDAAEAEAEALLAGRTRREQQQHQQHQQHQQHQQHQQQQQQQHQQQQLVLFEGLGGLLLVDSGRRVADWSAA
AAGSRNTSGGPSMAPGGEHATDSQARAARGLGRRRRGGPTGLSPADIQHALQLVPAEQAAAAAQQMGGNQVSGGGGGGYA
ARVGRVGPGRDTQSSGGLASASALWRGPCPKVVSVHPRALVMPMLAAAAGGIASPLPAAATESVPPPPPQQQQRRQQEEQ
LASPMLRVVVSWTAPSHAPFDSDGGGAAAEEVDDVAAGLVAAAASAAVAPGSPLSHLEVLVRCRTGYLPVEVHCWKEEGA
AAEWCVTYCDISLLALPTEPGLLVVDVRWRGQPYAALPLVLMTDGAAAAELAAVASAWPRAQGELHAFIRDLGAFELEAA
AAAAGAGTAAAAAAAGTAAAAAAGGGGGGGGSPPVLLQDPAAACKPRPLLGELACHLEAYTRTCGWQRLAGYIRAAAARA
AAAAATAASSAAGAAAAAAAAGGGAAPCPGEPQPVPARGMPAAVARLQLGARVCTGGDSSAAGRDSGAAAAPLLAHTPCC
VVGGGRGRQVDGAGSVSHAAFATGGGDVGGFLCGPALQPQQVQQILVLGTEVTGTSGSGSRDSDSTPAAASPTCQPSGGE
EADAASAYTWTAGGCAGAAAAAAAAGVVPAQICAEAEAEAREWSSYQQRFMLTLGLPIRIVECAIMAATLLRCLVIADTS
CGPSLALDLVAFSGGLLSSALGLLLPRPAWAGLQPRLRLLQYGTYAAAKLVIAGGAVEVPRDNVFMYTASVAALLHEGVV
VPGSCLLPTRTALVLLPALHTLTAALLMAVRPEFGWLRAALVAARIALLGLLVNAACHAYMRNSFKRQWRQQQHGGQQQR
QQQQEQQQQQVVMGSGGRWLGLRGSPGASGGVPDQRAGMRGVAVSEAFRKEKDA
```

414 - 433:	EEEEEEEEEEEEEEEEEEEE
415 - 434:	EEEEEEEEEEEEEEEEEEEE
416 - 435:	EEEEEEEEEEEEEEEEEEEE
417 - 436:	EEEEEEEEEEEEEEEEEEEE
418 - 437:	EEEEEEEEEEEEEEEEEEEE
419 - 438:	EEEEEEEEEEEEEEEEEEEE
420 - 439:	EEEEEEEEEEEEEEEEEEEE
421 - 440:	EEEEEEEEEEEEEEEEEEEE
422 - 441:	EEEEEEEEEEEEEEEEEEEE
423 - 442:	EEEEEEEEEEEEEEEEEEEE

A0A2K3E0T5 **A0A2K3E0T5_CHLRE** (710 aa)
Uncharacterized protein. *Chlamydomonas reinhardtii (Chlamydomonas smithii)*

```
MPKVRDRTRIGQEFAVLPWQQRHDEKEIPEDALYSVQSVNLFAPSGTQFPREAALADAKPSDEDLTEEPDDEPDSGGWIK
KDTSAEPTPTRRRAATQAARPTGAPASVLTMVLHEPAATLQYTPGSGGDSDLASGSDAETQPPEQEEEDGVEADAADSLE
PQRPPELLGVCQLAITPSGRGMGHIVITGRHHLGVAGGAHACAGAASPAVLVLGVATQPVAATEELDPCFADESFDLLRL
RLTHMQPGARQAAADLNEAGPGPGSAAAAVAAPAAKRGCSSGGNGSGSSGGRSSSSRGGGRASSVEVLVSRTGGDMARLM
APPEEWLVRRTLGDHALALMRQRQQTRAQQQQRQRERERQRPGMGGETAEREDAEADDEEEGYRRHQAGAGGYCYSSDSEG
EPLLDPRLDPFIAQGLGLASGTRAAARRRRWPAGGAGGGAVGGGGGAKSPRQRGRGAANAEAKAEAGDADDGGPGMAPAG
EGSGGRAARVKRQRTGAGRPVQRERGQSEEGQQGEEEEEEEEEEEEEEEEEEEEEEEEEEGRQGEEEEEEGRQGEEEAGTTA
SEEDGTEAGDDADDDSDDDNDSEPEADIQLSFQPETLLSGGAALARMADFARPLLPRRLRLAAATAAAAAGPAGVDVKRE
GEAGAGAGTGAGAGDKGAEARGGAGGVPAAAGGQDGAGGWAEEDGEWEEAVVCVGPVRVRGLPRSWRRCL
```

515 - 534:	EEEEEEEEEEEEEEEEEEEE
516 - 535:	EEEEEEEEEEEEEEEEEEEE
517 - 536:	EEEEEEEEEEEEEEEEEEEE
518 - 537:	EEEEEEEEEEEEEEEEEEEE
519 - 538:	EEEEEEEEEEEEEEEEEEEE

A0A2K3E3N3 **A0A2K3E3N3_CHLRE** (1621 aa)
Protein kinase domain-containing protein. *Chlamydomonas reinhardtii (Chlamydomonas smithii)*

```
MASLQSAGAPGSVPPLLDPSKLSIGRVLGRGAFATVYLATYEGIGPAALKVAVPASKRLPPVFERLFMNEVSLLCRHRHR
RLVKCYGLLRLPPGWLPGIQAQAAPIPACLLELCEGETLRDVVLHAKAGRRPYSDATALSLLRDVTEALAALHAASPPAI
HRDVKAENILLKREGLTPAAAGAGGGCAASSLPAVASGGGEGQEQPYQQLTARVADLGLHVRVEQHRSVMLRRRGAASLD
GSAFVAISRHNSFGPHHRADTEHPGVLPTAHRFAADSAGGGGGSYHMPVMPAALGAPASGAPADDVTHPRAMYGGGAGTQ
AALPPPTSGALSHVACSCDDAGGRHLESISEAVRVVAASAAASGAPVARPEAGGSSGSGDGAGGGGGTGHALHLDSWLNS
GLYEETSADGRLPAAASPPMLEVAATSPVGGTPTVKITSVVEAALSLGGGGDSGSSAGGGCSMHTPGQHLPVGAPAAATG
RLVGGTSSRRSRFGSAQPVGFPPEPASALCCPLEPQHTDALLATAAATPHALLADSANCAAGTSVTAAGSSPAAAEAAAP
QVQRASGGGRSLHQRTSSFEVTGSPVMTSVQRESVESGRGGGIALGSLSRSMSIMIPAVDTAPEEAAAAATTDDRQSGEP
QAAGRAQNATSTQQHTLPADVLSPMPVTTPAGFAQPLQQPSAGLHRLYPVPAAELTASVQPPAAAITQRSSGGSSSGACR
ASFGLELDQREVAAGDVRGSSGGGGRGEQPGTAAAVAVAAAIDLDAVVARREVGAAPALVPASLAGPRSSSSGLNLQQQA
PSSKLLAPPWLNATAPGGSAATATSGNGRAAAGDVQSRAATGTGIASGGTGVCGPATSFVGGDSSLGASSREASSQHFGF
QAAFGPAAAAAAAPAASSPVVQHFAKTTAGAAAVAVVVGQGAAAVPVSANPATAHTAAESTSAVTRVGFPAGAPPPPQAQ
AGVSAPRRPQAGQPQTAPRTPLASPFATGLQKSGTTQPAPRTLPVGTNVHGQGALPSPHHTAGVDGNAGGGAVGQQDRAA
TAAAALGVSICAGNAGRAGVRALGGIVTSPPNPPSPHGRHANARAPYKGANGRPSSLGVVSLPSASAALGAAGSPAATAA
GGAAACGPDGAASRQYSRPGSAASVLSIGVLQEDSFVSLFSGSGNAAVRSSAAGLRRRSTATTALGLSGRLPGRFVTMSQ
GVAPFSRSSRGMSTAAGASVGSHHAPSIGAASGGGGGNRDRSLRPRQHTHDGGAHDSVMDRYGSEPLPPFGSAVPNPRVT
SNRAPLGVLVGVGPGASGGSRAVTGDCYADPDAQDSHPGAGGTLRRDMGLSGLTGEADFGKEEEEGEEEEEEEEEEEEEE
EEEEEEEEEEEEEEVEVEVEAEEGAVEVAAAEAMHQLEVSPGSVTKHMRRLQSITSLLGGGVAGGGDSGNGDGGGSPVLPQ
HEWLHFVFNLTGQAGSHMYMAPEVFLRLPYNDKVDVFSFGCLAYEVLGRQLLLVKYVGGTAAGRALGVKLPAEYAAKVAL
GFRPPRPAGHITDDQWDLICACWHPDPCERPPMAEVAARLGRMLAALPPPSPLRPHTAGRNLAQGSASQGAPSGAAAGLQ
GGSGDRQTQQQQGCGCGCVIC
```

1347 - 1366:	EEEEEEEEEEEEEEEEEEEE
1348 - 1367:	EEEEEEEEEEEEEEEEEEEE
1349 - 1368:	EEEEEEEEEEEEEEEEEEEE
1350 - 1369:	EEEEEEEEEEEEEEEEEEEE
1351 - 1370:	EEEEEEEEEEEEEEEEEEEE
1352 - 1371:	EEEEEEEEEEEEEEEEEEEE
1353 - 1372:	EEEEEEEEEEEEEEEEEEEE
1354 - 1373:	EEEEEEEEEEEEEEEEEEEE

A0A2K3JTR0 **A0A2K3JTR0_TRIPR** (114 aa)
Uncharacterized protein. *Trifolium pratense (Red clover)*

```
MWDLCDGDVSRKPRHVLTDEEAIYLIGLSSVVRARLDLGQLLTQSRTSGDLNWTLSCIDFTEKKYLKTQEEEEEEEEEEE
EEEEEEEEEDNLFTTYVEGESSHPFHQFKEFHYK
```

70 - 89:	EEEEEEEEEEEEEEEEEEEE

A0A2K3KF13 **A0A2K3KF13_TRIPR** (22 aa)
Uncharacterized protein (Fragment). *Trifolium pratense (Red clover)*

```
EEEEEEEEEEEEEEEEEEEEPE
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE

A0A2K3KH60 **A0A2K3KH60_TRIPR** (32 aa)
Uncharacterized protein (Fragment). *Trifolium pratense (Red clover)*

```
EEEEEEEEEEEEEEEEEEEEEEAMKNISVQNQN
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE

A0A2K3KHS7 **A0A2K3KHS7_TRIPR** (35 aa)
Uncharacterized protein (Fragment). *Trifolium pratense (Red clover)*

```
MPLIHLKSTLLIMSQEEEEEEEEEEEEEEEEEEEEE
```

16 - 35:	EEEEEEEEEEEEEEEEEEEE

A0A2K3KKC4 **A0A2K3KKC4_TRIPR** (31 aa)
Uncharacterized protein (Fragment). *Trifolium pratense (Red clover)*

```
EEEEEEEEEEEEEEEEEEEEREIEKNLDALS
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE

A0A2K3KLE0 **A0A2K3KLE0_TRIPR** (28 aa)
Uncharacterized protein (Fragment). *Trifolium pratense (Red clover)*

```
EEEEEEEEEEEEEEEEEEEEEELKEEAKQ
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE

A0A2K3KT34 **A0A2K3KT34_TRIPR** (140 aa)
Uncharacterized protein (Fragment). *Trifolium pratense (Red clover)*

```
REDEKITSEPDEQNAAAEEEVEENIENIILIDEEQGEEMNDVEEEVELFDANNNEEGDIGSENDYILIQEINIEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEESCISTEELNKKFEDFIRKMKEDLRIDARQHLVNGLI
```

74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE

A0A2K3KWN2 **A0A2K3KWN2_TRIPR** (36 aa)
Uncharacterized protein (Fragment). *Trifolium pratense (Red clover)*

```
MPITTTLFQMKNPTNFEEEEEEEEEEEEEEEEEEEE
```

17 - 36:	EEEEEEEEEEEEEEEEEEEE

A0A2K3L4V6 **A0A2K3L4V6_TRIPR** (49 aa)
Uncharacterized protein (Fragment). *Trifolium pratense (Red clover)*

```
ITAFTWTSVEDGGEEEEEEEEEEEEEEEEEEEEEEDSDIEDGGEEQDNDI
```

14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE

A0A2K3L5H5 **A0A2K3L5H5_TRIPR** (421 aa)
F-box protein. *Trifolium pratense (Red clover)*

```
MAATNEKVNSYIPDDISLSILSKLPVKSLKRFECVRKSWSLLFQNDHFMNMFRSNFLSYNDPSSLILNVNQSPDEDLFYS
FSGEMFENMVQLDWSNPFKGWRPLLTNIFGSGSINGTFCLYSSINVRIALWTPATQTGKLFHSSEAEWLHSHIPNSVTYN
IHGFGYEHATNDYKVIRHVHVSIGSSCDYFDEWVKILHNPIWEIYSLRSDSWRRLHINMPYSLECNGGTQVYMDGVCHWL
CEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERPKRPFLVSFYLNNEVFCITPIPSNVDNCYEVNSWINLAVFNG
FIALISYHNEASTFHISILGEFGIKESWTKFLIVGPLSCVERPMGVGMKGEIVFISKDGKLVWLDLNTQMIAELGYEGGL
VYYSQIVNYKENILPIQGISH
```

244 - 263:	EEEEEEEEEEEEEEEEEEEE
245 - 264:	EEEEEEEEEEEEEEEEEEEE
246 - 265:	EEEEEEEEEEEEEEEEEEEE
247 - 266:	EEEEEEEEEEEEEEEEEEEE
248 - 267:	EEEEEEEEEEEEEEEEEEEE
249 - 268:	EEEEEEEEEEEEEEEEEEEE
250 - 269:	EEEEEEEEEEEEEEEEEEEE
251 - 270:	EEEEEEEEEEEEEEEEEEEE
252 - 271:	EEEEEEEEEEEEEEEEEEEE

253 - 272:	EEEEEEEEEEEEEEEEEEEE
254 - 273:	EEEEEEEEEEEEEEEEEEEE
255 - 274:	EEEEEEEEEEEEEEEEEEEE
256 - 275:	EEEEEEEEEEEEEEEEEEEE
257 - 276:	EEEEEEEEEEEEEEEEEEEE
258 - 277:	EEEEEEEEEEEEEEEEEEEE

A0A2K3LG17 **A0A2K3LG17_TRIPR** (44 aa)
Uncharacterized protein. *Trifolium pratense (Red clover)*

```
MTMIMISEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEYIN
```

8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE

A0A2K3LSL4 **A0A2K3LSL4_TRIPR** (109 aa)
Uncharacterized protein. *Trifolium pratense (Red clover)*

```
MFRADDTRCNLNNPINDKFLQVSILGEEECIEEEEEEEEEEEEEEEEEEEEEXEEEEEEEEEEEEEEEEEEEEETRRAYV
ACGRCWDESGIVQPNVVERDIAQPNVVEN
```

32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE

A0A2K3LV03 **A0A2K3LV03_TRIPR** (45 aa)
Uncharacterized protein. *Trifolium pratense (Red clover)*

```
MLEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEELVLL
```

3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE

16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE

A0A2K3M0N4 **A0A2K3M0N4_TRIPR** (146 aa)
Uncharacterized protein. *Trifolium pratense (Red clover)*

```
MMSFLTGSPKSSWEPIMTVKTNTQSYWLNWRVLLCSIWVLFSIIFSSLLIWKYEKLLRNVSPRNGCERETQEEEEEEEEE
EEEEEEEEEEEDSAILYEDETWRPCLKGIHPAWLLAFRVFAFFVLLVLLTFNAVVDGGSIFYYYTQ
```

72 - 91:	EEEEEEEEEEEEEEEEEEEE

A0A2K3M199 **A0A2K3M199_TRIPR** (66 aa)
Uncharacterized protein. *Trifolium pratense (Red clover)*

```
MNQILIQTEMLQGSPAIPQSSGQNARFDLKNVEEEEEEEEEEEEEEEEEEEEELVLQLQTRCRLPH
```

33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE

A0A2K3MWV1 **A0A2K3MWV1_TRIPR** (359 aa)
Cullin-like protein. *Trifolium pratense (Red clover)*

```
MSTSRNPHGLPPFLRANMEYTGNEMEFHESLLTLLTEKMVDFESLKINGFDVEPYFISQGWKRYFDMLNGPVYPELLKHF
WMKAHVFTKYEAALEEKRAIAKDPSILGKTRAEMGLMDFTEPQIRSNICGLNIIFTKKHFIKLLDLEDRGKLLDSYEKEE
RLVKRLRKSFSILVDEEIRPEVLSAGFLTKMHIINTKLIHPQKSFVVNNKDPLYLGDYPIIFELDSEEVIQNYLAALREQ
IHNVTRDMVSPAPNCDPHGTRRRGKKRKTEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDVSKTKKNQPHISTPQPS
PTKPSPEPKQHDEAKTQLEQTFDNPEQMDIDKPESREFN
```

270 - 289:	EEEEEEEEEEEEEEEEEEEE
271 - 290:	EEEEEEEEEEEEEEEEEEEE
272 - 291:	EEEEEEEEEEEEEEEEEEEE
273 - 292:	EEEEEEEEEEEEEEEEEEEE
274 - 293:	EEEEEEEEEEEEEEEEEEEE
275 - 294:	EEEEEEEEEEEEEEEEEEEE
276 - 295:	EEEEEEEEEEEEEEEEEEEE
277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE

A0A2K3NH46 **A0A2K3NH46_TRIPR** (83 aa)
Uncharacterized protein. *Trifolium pratense (Red clover)*

```
MVGYGCIALLLKNPWKLEEEEEEEEEEEEEEEEEEEEEXXEEEEEEEEEEEEEEEEEEEEEISLSFTRLFVHSTNQPLDQ
SNG
```

18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE

A0A2K3PHC9 **A0A2K3PHC9_TRIPR** (77 aa)

Uncharacterized protein (Fragment). *Trifolium pratense (Red clover)*

```
EEEEEEEEEEEEEEEEEEEEDSVQVLIPNESELPIHLLDLQRKIMLTKACVRWVQLWRRSHPVSISSLPGVVTKLFP
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE

A0A2K5BV61 **A0A2K5BV61_AOTNA** (728 aa)
YTH domain containing 1. *Aotus nancymaae (Ma's night monkey)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDSKRQKPSVHSRQLVSKPLSSSVSN
NKRIVSTKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCLRKRDPERRAKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDRETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEGDEDGEEEEEEEEEEE
EEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSA
SESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNVAFRSARSVIL
IFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQE
IELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQ
RPGYLKDPRYQEVDRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQAHPPYSGH
HPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDR
GERGRYRR
```

230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE

A0A2K5BV62 **A0A2K5BV62_AOTNA** (710 aa)
YTH domain containing 1. *Aotus nancymaae (Ma's night monkey)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDSKRQKPSVHSRQLVSKPLSSSVSN
NKRIVSTKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCLRKRDPERRAKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDRETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEGDEDGEEEEEEEEEEE
EEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSA
SESYADQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNVAFRSARSVILIFSVRESGKFQGFARLSS
ESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLLFPPDES
IDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQRPGYLKDPRYQEVDRRFS
GVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHHPVPHEARYRDKRVHDYD
MRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDRGERGRYRR
```

230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE

A0A2K5BV64 **A0A2K5BV64_AOTNA** (731 aa)
YTH domain containing 1. *Aotus nancymaae (Ma's night monkey)*

```
VACDNGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDSKRQKPSVHSRQLVSKPLSSSVSNNKRIV
STKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCLRKRDPERRAKSPTPDGSERIGLEVDRRASR
SSQSSKEEVNSEEYGSDRETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEGDEDGEEEEEEEEEEEEEEE
EEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSASESYA
GSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNVAFRSARSVILIFSVR
ESGKFQGFARLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELEC
GTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQRPGYL
KDPRYQEVDSFTNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQAHPPY
SGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRD
RDRGERGRYRR
```

225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE

A0A2K5BZW2 **A0A2K5BZW2_AOTNA** (1311 aa)
SR-related CTD associated factor 1. *Aotus nancymaae (Ma's night monkey)*

```
MEEEDESRGKTEESGEDRGDGPPDRDPTLSPSAFILRAIQQAVGSSLQGDLPNDKDGSRCHGLRWRRCRSPRSEPRSQES
GGTDTATVLDMAADSFLAGLVSVLDPPDTWVPSRLDLRPGESEDMLELVAEVRIGDRDPIPLPVPSLLPRLRAWRTGKTV
SPQSNSSRPTCARHLTLGTGDGGPAPPPAPSSASSSPSPSPSSSSPSPPPPPPPPAPPAPPAPRFDIYDPFHPTDEAYSP
PPAPEQKYDPFEPTGSNPSSSAGTPSPEEEEEEEEEEEEEEEEEEEEEEEGLSQSISRISETLAGIYDDNSLSQDFPGDES
PRPDPQPAQPTPAPGTPPQADSTRADGATRRRVFVVGTEAEACREGKVSVEVVTAGGAALPPPLLPPGDSEIEEGEIVQP
EEEPRVALSLFRPSGRATRPPPAALATPAAQPLPQPPAPRAPEGDDFLSLHAESDGEGALQVDLGEPAPAPPAADSRWGG
LDLRRKILTQRRERYRQRSPSPAPAPAPAAAVGPPTRKKSRRERKRSGEAKEAASSSSGTQPAPPAPASPWDSKKHRSRD
RKPGSHTSSSARRRSRSRSRSTRRRSRSTDRRRGGSRRSRSREKRRRRRRSASPPPATSSSSSSRRERHRGKHRDGGGSK
KKKKRSRSRGEKRSGDGSEKAPAPAPPPSGSTSGGDRDSRRRGAVPPSIQDLTDHDLFAIKRTITVGRLDKSDPRGPSPV
PASSPKREVLYDSEGLSGEERGGKNSQKDRRRSGAASSSSSSREKGSRRKALDGGDRDRDRDRDRDRDRSSKKARPPKES
APSSGPPPKPPVSSGSGSSSSSSSCSSRKVKLQSKVAVLIREGVSSTTPAKDAASAGLGSIGVKFSRDRESRSPFLKPDE
RAPTEMAKAAPGSTKPKKTKVKAKAGAKKAKGTKGKTKPSKTRKKVRSGGGSGGSGGPVSLKKSKADSCSQAAGTKGAEE
TSWSGEERAAKVPSTPPPKVAPPPPALTPDSQTVDSSCKTPEVSFLPEEATEEAGVRGGAEEEEEEEEEEEEEEEEEQQ
PATTTATSTAAAAPSTAPSAGSTAGDSGAEDGPASRVSQLPTLPPPMPWNLPAGVDCTTSGVLALTALLFKMEEANLASR
AKAQELIQATNQILSHRKPPSSLGVTPAPVPTSLGLPPGPSSYLLPGSLPLGGCGSTPPTPTGLAATSDKREGSSSSEGR
GDTDKYLKKLHTQERAVEEVKLAIKPYYQKKDITKEEYKDILRKAVHKICHSKSGEINPVKVSNLVRAYVQRYRYFRKHG
RKPGDPPGPPRPPKEPGPPDKGGPGLPLPPL
```

268 - 287:	EEEEEEEEEEEEEEEEEEEE

269 - 288:	EEEEEEEEEEEEEEEEEEEE
270 - 289:	EEEEEEEEEEEEEEEEEEEE

A0A2K5D0D4 **A0A2K5D0D4_AOTNA** (1195 aa)
Euchromatic histone lysine methyltransferase 2. *Aotus nancymaae (Ma's night monkey)*

```
MAAAAGAAAAAAAAEGEAPAEMGALLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGAD
TPVGATPLIGDEPENLEGDGDLHGGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGT
AAAGPEPPPATTSPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEEL
GSARRSGEVTLAKGDPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEE
EEEEDEESGNQSDRRSGRLWGRMSGPKGGRGSPGGEGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLE
TERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCP
GCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLSQDAPGR
ADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLY
LSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVAR
YMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTD
NEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERS
DVWFALQLNRKLRLGVGNRAIRTERIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCT
CVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRAL
QTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPR
IAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELSSLPPVNT
```

300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE

A0A2K5D0D9 **A0A2K5D0D9_AOTNA** (1211 aa)
Euchromatic histone lysine methyltransferase 2. *Aotus nancymaae (Ma's night monkey)*

```
MAAAAGAAAAAAAAEGEAPAEMGALLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGAD
TPVGATPLIGDEPENLEGDGDLHGGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGT
AAAGPEPPPATTSPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEEL
GSARRSGEVTLAKGDPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEE
EEEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGT
LSPNHAGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMV
LCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAG
TAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQ
ESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQR
TPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIE
VIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPEL
RNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTERIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCET
STMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVR
LQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNI
IPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELL
PELSSLPPVNT
```

300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE

A0A2K5D0F4 **A0A2K5D0F4_AOTNA** (1191 aa)
Euchromatic histone lysine methyltransferase 2. *Aotus nancymaae (Ma's night monkey)*

```
MGALLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDEPENLEGDG
DLHGGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGTAAAGPEPPPATTSPEGQPKV
HRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEELGSARRSGEVTLAKGDPGSLE
EWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGR
RKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERG
FEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGY
FCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLSQDAPGRADTS
QPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVK
QGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQ
RGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEEN
ICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWF
ALQLNRKLRLGVGNRAIRTERIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDD
CSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIP
QGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFF
SSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELSSLPPVNT
```

280 - 299:	EEEEEEEEEEEEEEEEEEEE

281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE

A0A2K5D0G1 **A0A2K5D0G1_AOTNA** (1245 aa)
Euchromatic histone lysine methyltransferase 2. *Aotus nancymaae (Ma's night monkey)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGA
LLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDEPENLEGDGDLH
GGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGTAAAGPEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEELGSARRSGEVTLAKGDPGSLEEWE
TVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRVRDGARTLT
LSVSVSGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHK
CMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVS
QLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDS
SGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSK
RTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLE
MVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLH
AVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTERIICRD
VARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQE
FNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSY
LFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKY
FTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELSSLPPVNT
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE

A0A2K5D0G6 **A0A2K5D0G6_AOTNA** (1223 aa)
Euchromatic histone lysine methyltransferase 2. *Aotus nancymaae (Ma's night monkey)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGA
LLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDEPENLEGDGDLH
GGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGTAAAGPEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEELGSARRSGEVTLAKGDPGSLEEWE
TVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRVRDGEDPPG
VPVSEVQGLPQLLFSSIQGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRE
TMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVT
IPRGDGVTPPAGTAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGP
GREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQA
GANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWT
PIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCV
LLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTERIICRDVARGYENVPIPCVNGVDGEPCP
EDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNC
KNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNI
SRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQS
RLARLDPHPELLPELSSLPPVNT
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE

A0A2K5D0H4 **A0A2K5D0H4_AOTNA** (1157 aa)
Euchromatic histone lysine methyltransferase 2. *Aotus nancymaae (Ma's night monkey)*

```
MGALLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDEPENLEGDG
DLHGGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGTAAAGPEPPPATTSPEGQPKV
HRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEELGSARRSGEVTLAKGDPGSLE
EWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGR
RKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVD
GELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFC
PHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLP
NGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAA
QKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLST
GQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDT
PLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTERIICRDVARGYENV
PIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPL
IFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKD
```

```
GEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSE
KCKHSAEAIALEQSRLARLDPHPELLPELSSLPPVNT
```

280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE

A0A2K5EHP0 **A0A2K5EHP0_AOTNA** (1137 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Aotus nancymaae (Ma's night monkey)*

```
MAAAVLSGPTAGSAAGVPSGTGGLSAVSSGPRLRLLLLESVSGLLQPRTGSAVAPVHPPNRSAPHLPGLMCLLRLHGSVG
GAQNLSAVGALVSLSNARLSSIKTRFEGLCLLSLLVGESPTELFQQHCVSWLRSIQQVLQSQDPPPTMELAVAVLRDLLR
YAAQLPALFRDISMNHLPGLLTSLLGLRPECEQSALEGMKACMTYFPRACGSLKGKLASFFLSRVDALSPQLQQLACECY
SRLPSLGAGFSQGLKHTESWEQELHSLLASLHTLLGALYEGAETAPVQNEGPGVEMLLSSEDGDAHVLLRLRQRFSGLAR
CLGLMLSSEFGAPVSVPVQEILDFICRTLSVNSKNISLHGDGPLRLLLLPSIHLEALDLLSALILACGSRLLRFGILISR
LLPQVLNSWSIGRDSLSPGQERPYSTVRTKVYAVLELWVQVCGASAGVLQGGASGEALLTHLLSDISPPADALKLRSPRG
SPDGGLQTGKPSAPKKLKLDVGEAMAPPSHRKGDSNANSDVCAAALRGLSRTILMCGPLIKEETHRRLHDLVLPLVMGVQ
QGEVLGSSPYTSSRCRRELYCLLLALLLAPSPRCPPPLACALQAFSLGQREDSLEVSSFCSEALVTCAALTHPRVPPLQS
MGPTCPTPAPVPPPEAPSPFRAPPFHPPGPMPSVGPMPSAGPMPSAGPMPSAGPMPSAGPVPSARPGPPTTANHLGLSVP
GLVSVPPRLLPGPENHRASSNEDPVLAPSGTPPPTIPPDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDSVVIVPEG
LPTLPPPPPSGATPPPVAPSGPPTASPPVPAKEDPEELPAAPGPLPPPPPPPPPVPGPVTLPPPQLVPEGTPGGGGPPAL
EEDLTVININSSDEEEEEEEEEEEEEEEEEEEEEDFEEEEEDEEEYFEEEEEEEEEFEEEFEEEEGELEEEEEEEDEDEE
EEELEEVEELEFGTAGGDVEEGGPPPPTLPPALPPSESPPKVQPEPEPEPGLLLEVEEPGAEEEHEADTAPTLAPEVLPS
QGEVERDGGSPAAGLPPQELVEEEPSAPPTLLEEGTEDGGDKVQLPPETSAEEEMETETEAEALQEKEQDDTAAMLADFI
DCPPDDEKPPPATEPDS
```

894 - 913:	EEEEEEEEEEEEEEEEEEEE
895 - 914:	EEEEEEEEEEEEEEEEEEEE

A0A2K5EHP3 **A0A2K5EHP3_AOTNA** (901 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Aotus nancymaae (Ma's night monkey)*

```
MELAVAVLRDLLRYAAQLPALFRDISMNHLPGLLTSLLGLRPECEQSALEGMKACMTYFPRACGSLKGKLASFFLSRVDA
LSPQLQQLACECYSRLPSLGAGFSQGLKHTESWEQELHSLLASLHTLLGALYEGAETAPVQNEGPGVEMLLSSEDGDAHV
LLRLRQRFSGLARCLGLMLSSEFGAPVSVPVQEILDFICRTLSVNSKNISLHGDGPLRLLLLPSIHLEALDLLSALILAC
GSRLLRFGILISRLLPQVLNSWSIGRDSLSPGQERPYSTVRTKVYAVLELWVQVCGASAGVLQGGASGEALLTHLLSDIS
PPADALKLRSPRGSPDGGLQTGKPSAPKKLKLDVGEAMAPPSHRKGDSNANSDVCAAALRGLSRTILMCGPLIKEETHRR
LHDLVLPLVMGVQQGEVLGSSPYTSSRCRRELYCLLLALLLAPSPRCPPPLACALQAFSLGQREDSLEVSSFCSEALVTC
AALTHPRVPPLQSMGPTCPTPAPVPPPEAPSPFRAPPFHPPVGPMPSAGPMPSAGPMPSAGPMPSAGPVPSARPGPPTTA
NHLGLSVPGLVSVPPRLLPGPENHRASSNEDPVLAPSGTPPPTIPPDETFGGRVPRPAFVHYDKEEASDVEISLESDSDD
SVVIVPEGLPTLPPPPPSGATPPPVAPSGPPTASPPVPAKEDPEELPAAPGPLPPPPPPPPPVPGPVTLPPPQLVPEGTP
GGGGPPALEEDLTVININSSDEEEEEEEEEEEEEEEEEEEEEDFEEEEEDEEEYFEEEEEEEEEFEEEFEEEEAPTLAPE
VLPSQGEVERDGGSPAAGLPPQELVEEEPSAPPTLLEEGTEDGGDKVQLPPETSAEEEMETETEAEALQEKEQDDTAAML
ADFIDCPPDDEKPPPATEPDS
```

742 - 761:	EEEEEEEEEEEEEEEEEEEE
743 - 762:	EEEEEEEEEEEEEEEEEEEE

A0A2K5F1Q3 **A0A2K5F1Q3_AOTNA** (703 aa)
Phospholipid phosphatase related 3. *Aotus nancymaae (Ma's night monkey)*

```
MISTKEKNKTPKDSMTLLPCFYFVELPIVASSIVSLYFLELTDLFKPAKVGFQCYDRTLSMPYVETSEELIPLLMLLSLA
FAAPAASIMVAEGMLYCLQSRLWGHAGGPPGAEGSINAGGCNFNSFLRRTVRFVGVHVFGLCATALVTDVIQLATGYHTP
FFLTVCKPNYTLLGTSCEVNPYITQDICSGHDTHAILSARKTFPSQHATLSAFAAVYVSVSPARSALPRMYFNSVISDTT
KLLKPILVFAFAIAAGVCGLTQITQYRSHPVDVYAGFLIGAGIAAYLACHAVGNFQAPPTEKPAPPAPAKDALRALTQRG
HDSVYQQNKSVSTDELGPPGRLDGPPRPVVHEKTSLGSLKRASVDVDLLAPRSPMAKENMVTFSHTLPRASAPSLDDPAR
RHMTIHVPLDASRSKQLISEWKQKTLEGRGLGLPDDASPGHLRAPAEPMAEEEEEEEEEEEEEEEEEEEEEEGGPAPPSL
YPTVQARPGLGPRVILPPRAGPQALVHIPEEGAQAGPGLSPKSGAGVRAKWLMMAEKARVANPPRLLQVIAMSKAPGAPG
PKAAPETASSSSASSDSSQYRSPSDRDSASIVTIDAHAPHHPVVHLSAGGAPWEWKAAKAEADGGYELGDLARGFRGGPK
PPGVSPARRSANCDQEEPRFGAVATVNLSTLRRHAGGLGLAEREAEAEAEGYFRKMQARRFPD
```

451 - 470:	EEEEEEEEEEEEEEEEEEEE
452 - 471:	EEEEEEEEEEEEEEEEEEEE
453 - 472:	EEEEEEEEEEEEEEEEEEEE

A0A2K5H6P4 **A0A2K5H6P4_COLAP** (1266 aa)
Euchromatic histone lysine methyltransferase 2. *Colobus angolensis palliatus (Peters' Angolan colobus)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGA
LLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDESENLEGDGDLH
```

```
GGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGPEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVVKRRKLTSGGGLSEELGSARRSEVTLAKGDPGSLEEWET
VVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAKK
KWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEELP
LCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAG
TFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGAAAPAPPPLSQDAPGRADTSQPSAR
MRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQ
KVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCV
YSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHW
ASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLN
RKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGESCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSN
CLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFI
CEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDI
RTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELSSLPPVNT
```

356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE

A0A2K5H6U4 **A0A2K5H6U4_COLAP** (1232 aa)
Euchromatic histone lysine methyltransferase 2. *Colobus angolensis palliatus (Peters' Angolan colobus)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGA
LLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDESENLEGDGDLH
GGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGPEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVVKRRKLTSGGGLSEELGSARRSEVTLAKGDPGSLEEWET
VVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAKK
KWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSG
CNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGE
DASEAQEVTIPRGDGVTPPAGAAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCL
SAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSV
EICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDV
NAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIA
ARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCV
NGVDGESCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECN
QACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYC
IDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHS
AEAIALEQSRLARLDPHPELLPELSSLPPVNT
```

356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE

A0A2K5H7M8 **A0A2K5H7M8_COLAP** (1752 aa)
Histone acetyltransferase (EC 2.3.1.48). *Colobus angolensis palliatus (Peters' Angolan colobus)*

```
IPRADPIPICSFCLGTKESNREKKPEELLSCADCGSSGHPSCLKFCPELTTNVKALRWQCIECKTCSACRVQGRNADNML
FCDSCDRGFHMECCDPPLSRMPKGMWICQVCRPKKKGRKLLHEKAAQIKRRYAKPIGRPKNKLKQRLLSVTSDEGSMNAF
TGRGSPGRGQKTKVCTTPSSGHAASGKDSSSRLAVTDPTRPGATTKITTTSTYISASTLKVNKKTKGLIDGLTKFFTPSP
DGRRSRGEIIDFSKHYRPRKKVSQKQSCTSHVLATGTTQKLKPPPSSLPPPTPISGQSPSSQKSSTATSSPSPQSSSSQC
SVPSLSGLTTNSQLKALFDGLSHIYTTQGQSRKKGHPSYAPPKRMRRKTELSSTAKSKAHFFGKRDIRSRFISHSSSSSW
GMARGRIFKAIAHFKRTTFLKKHRMLGRLKYKVTPQMGTPSPGKGSLTDGRIKPDQDDDTEIKINIKQESADVNVIGNKD
VVTEEDLDVFKQAQELSWEKIECESGVEDYCGRYPSVIEFGKYEIQTWYSSPYPQEYARVPKLYLCEFCLKYMKSKNILL
RHSKKCGWFHPPANEIYRRKDLSVFEVDGNMSKIYCQNLCLLAKLFLDHKTLYYDVEPFLFYVLTKNDEKGCHLVGYFSK
EKLCQQKYNVSCIMIMPQHQRQGFGRFLIDFSYLLSRREGQAGSPEKPLSDLGRLSYLAYWKSVILEYLYHHHERHISIK
AISRATGMCPHDIATTLQHLHMIDKRDGRFVIIRREKLILSHMEKLKTCSRANELDPDKEEEEENIQSSPPRLTKPQSVA
IKRKRPFVLKKKRGRKRRRINSSVTTETISETTEVLNEPFDNSDEERPMPQLEPTCEIEVEEDGRKPVLRKAFQHQPGKK
RQTEEEEGKDNHCCKNADPCRNNMNDDSSNLKEGSKDNPEPLKCKQAWPKGTKRGLSKWRQNKERKTGFKLNLYTPPETP
MEPDEQVTVEEQKETSEGKTSPTPIRIEEEVKEAGEALLPQEENRRQETCAPVSPNTSPGEKPDDDLIKPEEEEEEEEEE
EEEEEEEEEEEGGNVEKDPDGAKSQEKEEPEISTEKEDSAPLDDHEEEEEEDEEPSHNEDHDADDEDDSHMESAEVEKEE
LPLPRESFKEVLENQEAFLDLNVQPSHSNPEVLMDCGVDLTASCNSEPKELAGDPEAVPESDEEPPPGEQAQKQDQKNSK
EVDTEFKEGNPATMEIDSETVQAVQSLTQESSEQDDTFQDCAETQEACRSLQNYTRADQSPQIATSLDDCQQSDHSSPVS
SVHSHPGQSVRSVNSPSVPALENSYAQISPDQSAISVPSLQNMETSPMMDVPSVSDHSQQVVDSGFSDLGSIESTTENYE
NPSSYDSTMGGSICGNGSSQNSCSYSSLTSSSLTQSSCAVTQQMSNISGSCSMLQQTSISSPPTCSVKSPQGCVVERPPS
SSQQLAQCSMAANFTPPMQLAEIPETGNANIGLYERMGQSDFGAAHYPQPSATFSLAKLQQLTNTLIDHSLPYSHSAAVT
SYANSASLSTPLSNTGLVQLSQSPHSVPGGPQAQATMTPPPNLTPPPMNLPPPLLQRNMAASNIGISHSQRLQTQIASKG
HVSMRTKSASLSPAAATHQSQIYGRSQTVAMQGPARTLTMQRGMNMSVNLMPAPAYNVNSVNMNMNTLNAMNGYSMSQPM
MNSGYHSNHGYMNQTPQYPMQMQMGMMGTQPYAQQPMQTPPHGNMMYTAPGHHGYMNTGMSKQSLNGSNMRR
```

1031 - 1050:	EEEEEEEEEEEEEEEEEEEE
1032 - 1051:	EEEEEEEEEEEEEEEEEEEE

A0A2K5HAR5 **A0A2K5HAR5_COLAP** (728 aa)
YTH domain containing 1. *Colobus angolensis palliatus (Peters' Angolan colobus)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSN
```

```
NKRIVSTKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEE
EEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSA
SESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVIL
IFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQE
IELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQ
RPGYLKDPRYQEVDRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQAHPPYSGH
HPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDR
GERGRYRR
```

230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE

A0A2K5HAS0 **A0A2K5HAS0_COLAP** (710 aa)
YTH domain containing 1. *Colobus angolensis palliatus (Peters' Angolan colobus)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSN
NKRIVSTKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEE
EEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSA
SESYADQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVILIFSVRESGKFQGFARLSS
ESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLLFPPDES
IDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQRPGYLKDPRYQEVDRRFS
GVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHHPVPHEARYRDKRVHDYD
MRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDRGERGRYRR
```

230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE

A0A2K5HAS6 **A0A2K5HAS6_COLAP** (540 aa)
YTH domain containing 1. *Colobus angolensis palliatus (Peters' Angolan colobus)*

```
LKSDNGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSNNKRIV
STKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVDRRASR
SSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEEEEEEEEEEEEEEEEEEEEY
EQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSASESYAGSEKKH
EKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVILIFSVRESGKFQ
GFARLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCL
LFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRLETFFGLIIGTCIRIT
```

218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE

A0A2K5HAT3 **A0A2K5HAT3_COLAP** (731 aa)
YTH domain containing 1. *Colobus angolensis palliatus (Peters' Angolan colobus)*

```
LKSDNGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSNNKRIV
STKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVDRRASR
SSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEEEEEE
EEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSASESYA
GSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVILIFSVR
ESGKFQGFARLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELEC
GTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQRPGYL
KDPRYQEVDSFTNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQAHPPY
SGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRD
RDRGERGRYRR
```

225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE

A0A2K5I7Y7 **A0A2K5I7Y7_COLAP** (1235 aa)
Tau tubulin kinase 1. *Colobus angolensis palliatus (Peters' Angolan colobus)*

```
MQCLAAALKDETNMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTRENVALKVESAQQPKQVLKMEVAV
LKKLQGKDHVCRFIGCGRNEKFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESIEAIHSVGFLHRDIKPSNF
AMGRLPSTYRKCYMLDFGLARQYTNTTGDVRPPRNVAGFRGTVRYASVNAHKNREMGRHDDLWSLFYMLVEFAVGQLPWR
KIKDKEQVGMIKEKYEHRMLLKHMPSEFHLFLDHIASLDYFTKPDYQLIMSVFENSMKERGIAENEAFDWEKAGTDALLS
TSTSTPPQQNTRQTAAMFGVVNVTPVPGDLLRENTEDVLQGEHLSDQENAPPILPGRPSEGLGPSPHLVPHPGGPEAEVW
EETDVNRNKLRINIGKSPCVEEEQSRGMGVPSSPVRAPPDSPTTPVRSLRYRRVNSPESERLSTADGRVELPERRSRMDL
PGSPSRQACSSQPAQMLSVDTGHADRQASGRMDVSASVEQEALSNAFRSVPLAEEEDFDSKEWVIIDKETELKDFPPGAE
PSTSGTTDEEPEELRPLVFSMAPPFEVNGLPRAVPLSLPYQDFKRDLSDYRERARLLNRVRRVGFSHMLLTAPQVPLSPV
QPQANGKEEEEEEEEDEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEAVAAVALGEVLGPRSGSSSEGSERSTDRSQE
GAPSTLLADDQKESRGRASMADGDLEPEEGSKTLVLVSPGDMKKSPVTAELAPDPDLGTLAALTPQHERPQPTGSQLDVS
EPGTLSSVLKSEPKPPGPGAGPGAGTVTTGAGGVAVTSSPFTKVERTFVHIAEKTHLNVMSSSGQALRPEEFSTGGELGL
ELASDGGTVEEGAPAPLENGLALSGLNGAEIEGCALSGPPGETPSEMATNLLLNGPALADGPAPVSPLEPSSEKVATISP
RHHAMPGSRPRSRIPVLLSEEDTGSEPSGSLSAKERWSKRARPQQDLARLVMEKRQGRLLLRLASGASSSSSEEQRRASE
TLSGTGSEEDTPASEPAASLPRKAGRAATTRSRIPRPIGLRMPMPAATQQLPGAAPASDTAITSRLQLQTPPGSATAADL
RPKQPPGRGLGPGRAQAGARPLVPRSPGLPTSTSAAHNASASPRSQSLSRRESPSPSHQARPGVPPPRGVPSARAQPDGT
```

PSPGGSKKGPRGKLQAQRATTKGRAGGAEGRAGAR

664 - 683:	EEEEEEEEEEEEEEEEEEEE
665 - 684:	EEEEEEEEEEEEEEEEEEEE
666 - 685:	EEEEEEEEEEEEEEEEEEEE
667 - 686:	EEEEEEEEEEEEEEEEEEEE
668 - 687:	EEEEEEEEEEEEEEEEEEEE
669 - 688:	EEEEEEEEEEEEEEEEEEEE
670 - 689:	EEEEEEEEEEEEEEEEEEEE

A0A2K5I925 **A0A2K5I925_COLAP** (1008 aa)
Solute carrier family 24 member 1. *Colobus angolensis palliatus (Peters' Angolan colobus)*

MGKLIRMGPQDRRLLRTKRLHWSRLLFLLGMLIIGSTYQHLRRPRGLSSLWAAVSSHQPVKLASRDLLSEEMMMVSSNPP
KPSSEMGGEMLVPQASVGSDEATLSMTVENIPNIPERTAKMIPTTTKNNYSPTAAGTERRKEDTPTSRRTLTYYTSTSSR
QIVKKYTPTPTGEMKSYSPTQVREKVKYTPSPRGRRVGTYASSTFMTMETSHATTPRTTVKDSDITTTYKILETNSLKRI
MEETTPTTLKGMVDSTPTFLTHEVETNVLTSPRSIVEKNNLSPPRRVESNSSAHPWGLVGKNNLKTPQGTVLTHTPATSE
GQVTISTMTGSSPSETKAFTAAWSVRNPSPRTSVSAIETAPATVWRLAKKPYTAPSTSTTHTVRAKLSTQVHHCVVVKPT
PAMPTTPSPSLTTALFPEELSPSPSVLPPILPDLPPKGEYPPDLFSVEERRQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLMMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKQIEAWVKEQLSRRPAAKVMALGDLSKLPSLLTRGSS
STSLHNSTIRSTIYQLMLHSLDPLREVRLAKEKEEESLNQEARAQPQAKSESKPEEEEPAKLPAVTVTPAPAPDIKEDQK
ENPGGQEDVAEAESTGEMTGKEGETAGEGETEEKSGGETQPEGEGETGTQGKGEEHEKENDAEGKGDNEGEGEGEIHAED
GEMKGIEGETESQELSAENHGEAKNDEKGVEDGGGSDGGDNEEEEEEEVEEEEEEEEEEEEEEEEEEEEGNEEPLSLDWP
ETRQKQAIYLFLLPIVFPLWLTVPDVRRQESRKFFVFTFLGSIVWIAMFSYLMVWWAHQVGETIGISEEIMGLTILAAGT
SIPDLITSVIVARKGLGDMAVSSSVGSNIFDITVGVESCEMFQLGAIH

850 - 869:	EEEEEEEEEEEEEEEEEEEE

A0A2K5I952 **A0A2K5I952_COLAP** (1065 aa)
Solute carrier family 24 member 1. *Colobus angolensis palliatus (Peters' Angolan colobus)*

MGKLIRMGPQDRRLLRTKRLHWSRLLFLLGMLIIGSTYQHLRRPRGLSSLWAAVSSHQPVKLASRDLLSEEMMMVSSNPP
KPSSEMGGEMLVPQASVGSDEATLSMTVENIPNIPERTAKMIPTTTKNNYSPTAAGTERRKEDTPTSRRTLTYYTSTSSR
QIVKKYTPTPTGEMKSYSPTQVREKVKYTPSPRGRRVGTYASSTFMTMETSHATTPRTTVKDSDITTTYKILETNSLKRI
MEETTPTTLKGMVDSTPTFLTHEVETNVLTSPRSIVEKNNLSPPRRVESNSSAHPWGLVGKNNLKTPQGTVLTHTPATSE
GQVTISTMTGSSPSETKAFTAAWSVRNPSPRTSVSAIETAPATVWRLAKKPYTAPSTSTTHTVRAKLSTQVHHCVVVKPT
PAMPTTPSPSLTTALFPEELSPSPSVLPPILPDLPPKGEYPPDLFSVEERRQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLMMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKQIEAWVKEQLSRRPAAKVMALGDLSKPGDGAIAVDE
LQDNKKLKLPSLLTRGSSSTSLHNSTIRSTIYQLMLHSLDPLREVRLAKEKEEESLNQEARAQPQAKSESKPEEEEPAKL
PAVTVTPAPAPDIKEDQKENPGGQEDVAEAESTGEMTGKEGETAGEGETEEKSGGETQPEGEGETGTQGKGEEHEKENDA
EGKGDNEGEGEGEIHAEDGEMKGIEGETESQELSAENHGEAKNDEKGVEDGGGSDGGDNEEEEEEEVEEEEEEEEEEEEE
EEEEEEEGNEEPLSLDWPETRQKQAIYLFLLPIVFPLWLTVPDVRRQVGETIGISEEIMGLTILAAGTSIPDLITSVIVA
RKGLGDMAVSSSVGSNIFDITVGLPVPWLLFCLINGLQPVPVSSNGLFCAIVLLFLMLLFVISSIASCKWRMNKILGFTM
FLLYFVFLIISVMLEDRIISCPVSV

868 - 887:	EEEEEEEEEEEEEEEEEEEE

A0A2K5I955 **A0A2K5I955_COLAP** (1077 aa)
Solute carrier family 24 member 1. *Colobus angolensis palliatus (Peters' Angolan colobus)*

MGKLIRMGPQDRRLLRTKRLHWSRLLFLLGMLIIGSTYQHLRRPRGLSSLWAAVSSHQPVKLASRDLLSEEMMMVSSNPP
KPSSEMGGEMLVPQASVGSDEATLSMTVENIPNIPERTAKMIPTTTKNNYSPTAAGTERRKEDTPTSRRTLTYYTSTSSR
QIVKKYTPTPTGEMKSYSPTQVREKVKYTPSPRGRRVGTYASSTFMTMETSHATTPRTTVKDSDITTTYKILETNSLKRI
MEETTPTTLKGMVDSTPTFLTHEVETNVLTSPRSIVEKNNLSPPRRVESNSSAHPWGLVGKNNLKTPQGTVLTHTPATSE
GQVTISTMTGSSPSETKAFTAAWSVRNPSPRTSVSAIETAPATVWRLAKKPYTAPSTSTTHTVRAKLSTQVHHCVVVKPT
PAMPTTPSPSLTTALFPEELSPSPSVLPPILPDLPPKGEYPPDLFSVEERRQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLMMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKQIEAWVKEQLSRRPAAKVMALGDLSKLPSLLTRGSS
STSLHNSTIRSTIYQLMLHSLDPLREVRLAKEKEEESLNQEARAQPQAKSESKPEEEEPAKLPAVTVTPAPAPDIKEDQK
ENPGGQEDVAEAESTGEMTGKEGETAGEGETEEKSGGETQPEGEGETGTQGKGEEHEKENDAEGKGDNEGEGEGEIHAED
GEMKGIEGETESQELSAENHGEAKNDEKGVEDGGGSDGGDNEEEEEEEVEEEEEEEEEEEEEEEEEEEEGNEEPLSLDWP
ETRQKQAIYLFLLPIVFPLWLTVPDVRRQESRKFFVFTFLGSIVWIAMFSYLMVWWAHQVGETIGISEEIMGLTILAAGT
SIPDLITSVIVARKGLGDMAVSSSVGSNIFDITVGLPVPWLLFCLINGLQPVPVSSNGLFCAIVLLFLMLLFVISSIASC
KWRMNKILGFTMFLLYFVFLIISVMLEDRIISCPVSV

850 - 869:	EEEEEEEEEEEEEEEEEEEE

A0A2K5I960 **A0A2K5I960_COLAP** (981 aa)
Solute carrier family 24 member 1. *Colobus angolensis palliatus (Peters' Angolan colobus)*

MGKLIRMGPQDRRLLRTKRLHWSRLLFLLGMLIIGSTYQHLRRPRGLSSLWAAVSSHQPVKLASRDLLSEEMMMVSSNPP
KPSSEMGGEMLVPQASVGSDEATLSMTVENIPNIPERTAKMIPTTTKNNYSPTAAGTERRKEDTPTSRRTLTYYTSTSSR
QIVKKYTPTPTGEMKSYSPTQVREKVKYTPSPRGRRVGTYASSTFMTMETSHATTPRTTVKDSDITTTYKILETNSLKRI
MEETTPTTLKGMVDSTPTFLTHEVETNVLTSPRSIVEKNNLSPPRRVESNSSAHPWGLVGKNNLKTPQGTVLTHTPATSE
GQVTISTMTGSSPSETKAFTAAWSVRNPSPRTSVSAIETAPATVWRLAKKPYTAPSTSTTHTVRAKLSTQVHHCVVVKPT
PAMPTTPSPSLTTALFPEELSPSPSVLPPILPDLPPKGEYPPDLFSVEERRQGWVVLHIFGMMYVFVALAIVCDEYFVPA

```
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLMMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKQIEAWVKEQLSRRPAAKVMALGDLSKEDVAEAESTG
EMTGKEGETAGEGETEEKSGGETQPEGEGETGTQGKGEEHEKENDAEGKGDNEGEGEGEIHAEDGEMKGIEGETESQELS
AENHGEAKNDEKGVEDGGGSDGGDNEEEEEEEVEEEEEEEEEEEEEEEEEEEEGNEEPLSLDWPETRQKQAIYLFLLPIV
FPLWLTVPDVRRQESRKFFVFTFLGSIVWIAMFSYLMVWWAHQVGETIGISEEIMGLTILAAGTSIPDLITSVIVARKGL
GDMAVSSSVGSNIFDITVGLPVPWLLFCLINGLQPVPVSSNGLFCAIVLLFLMLLFVISSIASCKWRMNKILGFTMFLLY
FVFLIISVMLEDRIISCPVSV
```

754 - 773:	EEEEEEEEEEEEEEEEEEEE

A0A2K5I9H9 **A0A2K5I9H9_COLAP** (1095 aa)
Solute carrier family 24 member 1. *Colobus angolensis palliatus (Peters' Angolan colobus)*

```
MGKLIRMGPQDRRLLRTKRLHWSRLLFLLGMLIIGSTYQHLRRPRGLSSLWAAVSSHQPVKLASRDLLSEEMMMVSSNPP
KPSSEMGGEMLVPQASVGSDEATLSMTVENIPNIPERTAKMIPTTTKNNYSPTAAGTERRKEDTPTSRRTLTYYTSTSSR
QIVKKYTPTPTGEMKSYSPTQVREKVKYTPSPRGRRVGTYASSTFMTMETSHATTPRTTVKDSDITTTYKILETNSLKRI
MEETTPTTLKGMVDSTPTFLTHEVETNVLTSPRSIVEKNNLSPPRRVESNSSAHPWGLVGKNNLKTPQGTVLTHTPATSE
GQVTISTMTGSSPSETKAFTAAWSVRNPSPRTSVSAIETAPATVWRLAKKPYTAPSTSTTHTVRAKLSTQVHHCVVVKPT
PAMPTTPSPSLTTALFPEELSPSPSVLPPILPDLPPKGEYPPDLFSVEERRQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLMMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKQIEAWVKEQLSRRPAAKVMALGDLSKPGDGAIAVDE
LQDNKKLKLPSLLTRGSSSTSLHNSTIRSTIYQLMLHSLDPLREVRLAKEKEEESLNQEARAQPQAKSESKPEEEEPAKL
PAVTVTPAPAPDIKEDQKENPGGQEDVAEAESTGEMTGKEGETAGEGETEEKSGGETQPEGEGETGTQGKGEEHEKENDA
EGKGDNEGEGEGEIHAEDGEMKGIEGETESQELSAENHGEAKNDEKGVEDGGGSDGGDNEEEEEEEVEEEEEEEEEEEE
EEEEEEEGNEEPLSLDWPETRQKQAIYLFLLPIVFPLWLTVPDVRRQESRKFFVFTFLGSIVWIAMFSYLMVWWAHQVGE
TIGISEEIMGLTILAAGTSIPDLITSVIVARKGLGDMAVSSSVGSNIFDITVGLPVPWLLFCLINGLQPVPVSSNGLFCA
IVLLFLMLLFVISSIASCKWRMNKILGFTMFLLYFVFLIISVMLEDRIISCPVSV
```

868 - 887:	EEEEEEEEEEEEEEEEEEEE

A0A2K5ICW2 **A0A2K5ICW2_COLAP** (1180 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Colobus angolensis palliatus (Peters' Angolan colobus)*

```
MLLPSLSPRVQPAFTQCAGPRPPPHAHSPVGGRRSVFASSRHATTGARGKMAAAVLSGPSAGSAAGVPGGTGGLSAVNSG
PRLRLLLLESVSGLLQPRTGSAVAPVHPPNRSAPHLPGLMCLLRLHGSVGGAQNLSALGALVSLSNARLSSIKTRFEGLC
LLSLLVGESPTELFQQHCVSWLRSIQQVLQTQDPPATMELAVAVLRDLLRYAAQLPALFRDISMNHLPGLLTSLLGLRPE
CEQSALEGMKACMTYFPRACGSLKGKLASFFLSRVDALSPQLQQLACECYSRLPSLGAGFSQGLKHTESWEQELHSLLAS
LHTLLGALYEGAETAPVQNEGPGVEMLLSSEDGDAHVLLRLLQRFSGLACCLGLMLSSEFGAPVSVPVQEILDFICRTLS
VSSKNISLHGDGPLRLLLLPSIHLEALDLLSALILACGSRLLRFGILISRLLPQVLNSWSIGRDSLSPGQERPYSTVRTK
VYAVLELWVQVCGASAGMLQGGASGEALLTHLLSDISPPADALKLRSPRGSPDGSLQTGKPSAPKKLKLDVGEAMAPPSH
RKGDSNANSDVCAAALRGLSRTILMCGPLIKEETHRRLHDLVLPLVMGVQQGEVLGSSPYTSSRCRRELYCLLLALLLAP
SPRCPPPLACALQAFSLGQREDSLEVSSFCSEALVTCAALTHPRVPPLQPMGPTCPTPAPVPPPEAPSPFRAPPFHPPGP
MPSVGPMPSAGPMPSAGPMPSAGPVPSARPGPPTTANHLGLSVSGLVSVPPRLLPGPENHRAGSNEDPILAPSGTPPPAI
PPDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDSVVIVPEGLPPLPPPPPSGATPPPIAPTGPPTASPPVPAKEEPE
ELPAAPGPLPPPPPPPPPVPGPVTLPPPQLVPEGTPGGGGPPALEEDLTVININSSDEEEEEEEEEEEEEEEEEEEEEDF
EEEEEDEEEYFEEEEEEEEEFEEEFEEEEGELEEEEEEEDEEEEEELEEVEELEFGTAGGEVEEGGPPPPTLPPALPPPE
SPPKVQPEPEPEPGLLLEVEEPGAEEEHGADTAPTLAPEVLPSQGEVEREEGSPAAGPPPQELVEEEPSAPPTLLEEGTE
DGGDRVQPPPETPAEEEMETETEAEALQEKEQDDTAAMLADFIDCPPDDEKPPPPTEPDS
```

938 - 957:	EEEEEEEEEEEEEEEEEEEE
939 - 958:	EEEEEEEEEEEEEEEEEEEE

A0A2K5ICZ2 **A0A2K5ICZ2_COLAP** (906 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Colobus angolensis palliatus (Peters' Angolan colobus)*

```
MELAVAVLRDLLRYAAQLPALFRDISMNHLPGLLTSLLGLRPECEQSALEGMKACMTYFPRACGSLKGKLASFFLSRVDA
LSPQLQQLACECYSRLPSLGAGFSQGLKHTESWEQELHSLLASLHTLLGALYEGAETAPVQNEGPGVEMLLSSEDGDAHV
LLRLLQRFSGLACCLGLMLSSEFGAPVSVPVQEILDFICRTLSVSSKNISLHGDGPLRLLLLPSIHLEALDLLSALILAC
GSRLLRFGILISRLLPQVLNSWSIGRDSLSPGQERPYSTVRTKVYAVLELWVQVCGASAGMLQGGASGEALLTHLLSDIS
PPADALKLRSPRGSPDGSLQTGKPSAPKKLKLDVGEAMAPPSHRKGDSNANSDVCAAALRGLSRTILMCGPLIKEETHRR
LHDLVLPLVMGVQQGEVLGSSPYTSSRCRRELYCLLLALLLAPSPRCPPPLACALQAFSLGQREDSLEVSSFCSEALVTC
AALTHPRVPPLQPMGPTCPTPAPVPPPEAPSPFRAPPFHPPGPMPSVGPMPSAGPMPSAGPMPSAGPVPSARPGPPTTAN
HLGLSVSGLVSVPPRLLPGPENHRAGSNEDPILAPSGTPPPAIPPDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDS
VVIVPEGLPPLPPPPPSGATPPPIAPTGPPTASPPVPAKEEPEELPAAPGPLPPPPPPPPPVPGPVTLPPPQLVPEGTPG
GGGPPALEEDLTVININSSDEEEEEEEEEEEEEEEEEEEEEEDFEEEEEDEEEYFEEEEEEEEEFEEEFEEEEGELEEEEE
EEDEEEEEELEEVEREEGSPAAGPPPQELVEEEPSAPPTLLEEGTEDGGDRVQPPPETPAEEEMETETEAEALQEKEQDD
TAAMLADFIDCPPDDEKPPPPTEPDS
```

741 - 760:	EEEEEEEEEEEEEEEEEEEE
742 - 761:	EEEEEEEEEEEEEEEEEEEE

A0A2K5IFP3 **A0A2K5IFP3_COLAP** (544 aa)
Ran GTPase activating protein 1. *Colobus angolensis palliatus (Peters' Angolan colobus)*

```
MASEDIAKLAETLAKTQVAGGQLSFKGKSLKLNTAEDRCHWSDMFTGRLRTEIPPALISLGEGLITAGAQLVELDLSDNA
FGPDGVQGFEALLKSSACFTLHELKLNNCGMGIGGGKILAAALTECHRKSSAQGKPLALKVFVAGRNRLENDGATALAEA
FRVIGTLEEVHMPQNGINHPGVTALAQAFAVNPLLRVINLNDNTFTEKGAVAMAETLKTLRQVEVINFGDCLVRSKGAVA
IADAIRGGLPKLKELNLSFCEIKRDAALAVAEAMADKTELEKLDLNGNTLGEEGCEQLQEVLEGFNMAKVLASLSDDEDE
EEEEEGEEEEEEAEEEEEEEEEEEEEEEEEEEEEPQQGGQGEKSATPSRKILDPNTGEPAPVLSSPPPADVSTFLAFPSP
```

```
EKLLRLGPKSSMLIAQQTDTSDPEKVVSAFLKVSSVFKDEAAVRTAVQDAVDALMKKAFSSSSFNSSAFLTRLLAHMGLL
KSEDKVKAIANLYGPLMALNHMVQQDYFPKALAPLLLAFITKPNSALESCSFARHSLLQTLYKV
```

334 - 353:	EEEEEEEEEEEEEEEEEEEE
335 - 354:	EEEEEEEEEEEEEEEEEEEE

A0A2K5K8Z8 **A0A2K5K8Z8_COLAP** (1497 aa)
Shroom family member 4. *Colobus angolensis palliatus (Peters' Angolan colobus)*

```
MENRPGSFQYVPVQLQGGAPWGFTLKGGLEHCEPLTVSKIEDGGKAALSQKMRTGDELVNINGTPLYGSRQEALILIKGS
FRILKLIVRRRNAPVSRPHSWHVAKLLEGCPEAATTMHFPSEAFSLSWHSGCNTSDVCVQWCPLSRHCSTEKSSSIGSME
SLEQPGQATYESHLLPIDQNMYPNQRDSAYSSFSASSNASDCALSLKPEEAASTDCIMQGPGPTKAPNGRPNVAETSGGS
RRTNGGHLTPSSQMSSRPQEGHQSGPAKAVRGPPQPPVRRDSLQASRAQLLNGEQRRASEPVVPLPQKEKLSLETVLPAR
NPNRFCCLSGHDQVTSESHQNCEFSQSPESSQQSSEHLLMQASTKAVGSPKACDKASSTDSNPLNEASAELAKASFGRPP
HLIGPTGHRHSAPEQLLASHLQHVHLDTRGSKGMELPSGQDGHQWTLSPLHSSHKGKKSPCPPAGGTHDQSSKERKTRQM
DDRSLVLGHQSQSSPPHGEADGHPSDKGLLDPNRTSRAGSELANQQPSASGSLVQKARDCSSTTKVAGGTEAGEEGDSEH
KECSRMGGRRSGGTRGRSIQNRRKSERFATNLRNEIQRRKAQLQKSKGPLSQLCDTKEPVEETQEPPESPPLTASNTSLL
SSCKKPPSPRDKLFNKSMMLRARSSECLSQAPESHESRTGLEGRISPGQRLGQSSLGLNTWWKAPDPSSSDPEKAHAHCG
VHGGHWRWSREHNSQPLVAVAMEGPSNPGDNKELKASSAQAGEDAILLPFADRRKFFEESSKSLSTSHLPGLTTHSSKTF
TQRPKPIDQNFQPVSSSYRELRRHPVDQSYHSADQPYHATDQSYHSMSPLQSETPTYSECFASRGLENSMCCKPLHCGDF
DYHRTCSYSCSVQGALVHDPCIYCSGEICPALLKRNMMPNCYNCRCHHHQCIRCSVCYHNPQHSTLEDSSLAPGNTWKPR
KPTVQEFPGDKWNPITGNRKTSQSGREMAHSKNSFSWATPFHPCLENPALDLSSYRAISSLDLLGDFKHALKKSEETSVY
EEGSSLASMPHPLRSRAFSESHISLDPQSTRAWGQHRRELFSKGNETQSDLLGARKKAFPPPRPPPPNWEKYRLFRAAQQ
QKQQQQQQQQQQQKQQEEEEEEEEEEEEEEEEEEEEAEEEEELPPQYFSSETSGSCALNSEEVLEQPQPLSLGHLEGSGQ
GSQSVPAEQESFALHSSDFLPPIRGHLGSQPEQAQPPCYYGIGGLWRTSEQEATESTKQEFQPFSPPPGAPGIPTSYSAY
YNISVAKAELLNKLKDQPEMAEIGLGEEEVDHELAQKKIQLIESISRKLSVLREAQRGLLEDINANSALGEEVEANLKAV
CKSNEFEKYRSFVGDLDKVVNLLLSLSGRLARVENALNSIDSEANQEKLVLIEKKQQLTGQLADAKELKEHVDRREKLVF
GMVSRYLPQDQLQDYQHFVKMKSALIIEQRELEEKIKLGEEQLKCLRESLLLGPSNF
```

1137 - 1156:	EEEEEEEEEEEEEEEEEEEE

A0A2K5KH86 **A0A2K5KH86_CERAT** (1497 aa)
Shroom family member 4. *Cercocebus atys (Sooty mangabey) (Cercocebus torquatus atys)*

```
MENRPGSFQYVPVQLQGGAPWGFTLKGGLEHCEPLTVSKIEDGGKAALSQKMRTGDELVNINGTPLYGSRQEALILIKGS
FRILKLIVRRRNAPVSRPHSWHVAKLLEGCPEAATTMHFPSEAFSLSWHSGCNTSDVCVQWCPLSRHCSTEKSSSIGSME
SLEQPGQATYESHLLPIDQNMYPNQRDSAYSSFSASSNASDCALSLRPEEAASTDCIMQGPGPTKAPNGRPNVAETSGGS
RRTNGGHLTPSSQMSSRPQEGHQSGPAKAVRGPPQPPVRRDSLQASRAQLLNGEQRRASEPVVPLPQKEKLSLETVLPTR
NPNRFCCLSGHDQVTSEGHQNCEFSQPPESSQQGSEHLLMQASTKAVGSPKACDKASSTDSNPLNEASAELAKASFGRPP
HLIGPTGHRHSAPEQLLASHLQHVHLDTRGSKGMELPPGQDGHQWTLSPLHSSHKGKKSPCPPAGGTHDQSSKERKTRQM
DDRSLVLGHQSQSSPPHVEADGHPSEKGLLDPNRTSRAGNELANQQPSASGSLVQKARDCSSTTKVAGGTEAGEEGDSEH
KECSRMGGRRSGGTRGRSIQNRRKSERFATNLRNEIQRRKAQLQKSKSPLSQLCDTKEPVEETQEPPESPPLTASNTSLL
SSCKKPPSPRDKLFNKSMMLRARSSECLSQAPESHESRTGLEGRISPGQRLGQSSLVLNTWWKAPDPSSSDPEKAHAHCG
VHGGHWKWSREHNSQPLVAVAMEGPSNPGDNKELKASTAQAGEDAILLPFADRRKFFEESSKSLSTSHLPGLTTHSNKTF
TQRPKPIDQNFQPVSSNYRELRRHPMDQSYHSADQPYHATDQSYHSMSPLQSETPTYSECFASRGLENSMCCKPLHCGDF
DYHRTCSYSCSVQGALVHDPCIYCSGEICPALLKRNMMPNCYNCRCHHHQCIRCSVCYHNPQHSTLEDSSLAPGNTWKPR
KPTVQEFPGDKWNPITGNRKTSQSGREMAHSKNSFSRATPFHPCLENPALDLSSYRAISSLDLLGDFKHALKKSEETSVY
EEGSSLASMPHPLRSRAFSESHISLDPQSTRAWGQHRRELFSKGDETQSDLLGARKKAFPPPRPPPPNWEKYRLFRAAQQ
QKQQQQQQQQQQKQQEEEEEEEEEEEEEEEEEEEEAEEEEELPPQYFSSETSGSCALNPEEVLEQPQPLSLGHLEGSGQ
GSQSVPAEQESFALHSSDFLPPIRGHLGSQPEQAQPPCYYGIGGLWRTSKQEAAESAKQEFQPFSPPPGAPGIPTSYSAY
YNISVAKAELLNKLKDQPEMAEIGLGEEEVDHELAQKKIQLIESISRKLSVLREAQRGLLEDINANSALGEEVEANLKAV
CKSNEFEKYRSFVGDLDKVVNLLLSLSGRLARVENALNSIDSEANQEKLVLIEKKQQLTGQLADAKELKEHVDRREKLVF
GMVSRYLPQDQLQDYQHFVKMKSALIIEQRELEEKIKLGEEQLKCLRESLLLGPSNF
```

1136 - 1155:	EEEEEEEEEEEEEEEEEEEE

A0A2K5KHA8 **A0A2K5KHA8_CERAT** (1476 aa)
Shroom family member 4. *Cercocebus atys (Sooty mangabey) (Cercocebus torquatus atys)*

```
LTGRILGRKSPHCLLSVLFSATQIEDGGKAALSQKMRTGDELVNINGTPLYGSRQEALILIKGSFRILKLIVRRRNAPVS
RPHSWHVAKLLEGCPEAATTMHFPSEAFSLSWHSGCNTSDVCVQWCPLSRHCSTEKSSSIGSMESLEQPGQATYESHLLP
IDQNMYPNQRDSAYSSFSASSNASDCALSLRPEEAASTDCIMQGPGPTKAPNGRPNVAETSGGSRRTNGGHLTPSSQMSS
RPQEGHQSGPAKAVRGPPQPPVRRDSLQASRAQLLNGEQRRASEPVVPLPQKEKLSLETVLPTRNPNRFCCLSGHDQVTS
EGHQNCEFSQPPESSQQGSEHLLMQASTKAVGSPKACDKASSTDSNPLNEASAELAKASFGRPPHLIGPTGHRHSAPEQL
LASHLQHVHLDTRGSKGMELPPGQDGHQWTLSPLHSSHKGKKSPCPPAGGTHDQSSKERKTRQMDDRSLVLGHQSQSSPP
HVEADGHPSEKGLLDPNRTSRAGNELANQQPSASGSLVQKARDCSSTTKVAGGTEAGEEGDSEHKECSRMGGRRSGGTRG
RSIQNRRKSERFATNLRNEIQRRKAQLQKSKSPLSQLCDTKEPVEETQEPPESPPLTASNTSLLSSCKKPPSPRDKLFNK
SMMLRARSSECLSQAPESHESRTGLEGRISPGQRLGQSSLVLNTWWKAPDPSSSDPEKAHAHCGVHGGHWKWSREHNSQP
LVAVAMEGPSNPGDNKELKASTAQAGEDAILLPFADRRKFFEESSKSLSTSHLPGLTTHSNKTFTQRPKPIDQNFQPVSS
NYRELRRHPMDQSYHSADQPYHATDQSYHSMSPLQSETPTYSECFASRGLENSMCCKPLHCGDFDYHRTCSYSCSVQGAL
VHDPCIYCSGEICPALLKRNMMPNCYNCRCHHHQCIRCSVCYHNPQHSTLEDSSLAPGNTWKPRKPTVQEFPGDKWNPIT
GNRKTSQSGREMAHSKNSFSRATPFHPCLENPALDLSSYRAISSLDLLGDFKHALKKSEETSVYEEGSSLASMPHPLRSR
AFSESHISLDPQSTRAWGQHRRELFSKGDETQSDLLGARKKAFPPPRPPPPNWEKYRLFRAQQQQQQQQQQKQQEEEEEE
EEEEEEEEEEEEEEAEEEEEELPPQYFSSETSGSCALNPEEVLEQPQPLSLGHLEGSGQGSQSVPAEQESFALHSSDFLP
PIRGHLGSQPEQAQPPCYYGIGGLWRTSKQEAAESAKQEFQPFSPPPGAPGIPTSYSAYYNISVAKAELLNKLKDQPEMA
EIGLGEEEVDHELAQKKIQLIESISRKLSVLREAQRGLLEDINANSALGEEVEANLKAVCKSNEFEKYRSFVGDLDKVVN
LLLSLSGRLARVENALNSIDSEANQEKLVLIEKKQQLTGQLADAKELKEHVDRREKLVFGMVSRYLPQDQLQDYQHFVKM
KSALIIEQRELEEKIKLGEEQLKCLRESLLLGPSNF
```

1115 - 1134:	EEEEEEEEEEEEEEEEEEEE

A0A2K5KHB6 **A0A2K5KHB6_CERAT** (1381 aa)
Shroom family member 4. *Cercocebus atys (Sooty mangabey) (Cercocebus torquatus atys)*

```
MHFPSEAFSLSWHSGCNTSDVCVQWCPLSRHCSTEKSSSIGSMESLEQPGQATYESHLLPIDQNMYPNQRDSAYSSFSAS
SNASDCALSLRPEEAASTDCIMQGPGPTKAPNGRPNVAETSGGSRRTNGGHLTPSSQMSSRPQEGHQSGPAKAVRGPPQP
PVRRDSLQASRAQLLNGEQRRASEPVVPLPQKEKLSLETVLPTRNPNRFCCLSGHDQVTSEGHQNCEFSQPPESSQQGSE
HLLMQASTKAVGSPKACDKASSTDSNPLNEASAELAKASFGRPPHLIGPTGHRHSAPEQLLASHLQHVHLDTRGSKGMEL
PPGQDGHQWTLSPLHSSHKGKKSPCPPAGGTHDQSSKERKTRQMDDRSLVLGHQSQSSPPHVEADGHPSEKGLLDPNRTS
RAGNELANQQPSASGSLVQKARDCSSTTKVAGGTEAGEEGDSEHKECSRMGGRRSGGTRGRSIQNRRKSERFATNLRNEI
QRRKAQLQKSKSPLSQLCDTKEPVEETQEPPESPPLTASNTSLLSSCKKPPSPRDKLFNKSMMLRARSSECLSQAPESHE
SRTGLEGRISPGQRLGQSSLVLNTWWKAPDPSSSDPEKAHAHCGVHGGHWKWSREHNSQPLVAVAMEGPSNPGDNKELKA
STAQAGEDAILLPFADRRKFFEESSKSLSTSHLPGLTTHSNKTFTQRPKPIDQNFQPVSSNYRELRRHPMDQSYHSADQP
YHATDQSYHSMSPLQSETPTYSECFASRGLENSMCCKPLHCGDFDYHRTCSYSCSVQGALVHDPCIYCSGEICPALLKRN
MMPNCYNCRCHHHQCIRCSVCYHNPQHSTLEDSSLAPGNTWKPRKPTVQEFPGDKWNPITGNRKTSQSGREMAHSKNSFS
RATPFHPCLENPALDLSSYRAISSLDLLGDFKHALKKSEETSVYEEGSSLASMPHPLRSRAFSESHISLDPQSTRAWGQH
RRELFSKGDETQSDLLGARKKAFPPPRPPPPNWEKYRLFRAAQQQKQQQQQQQQQQKQQEEEEEEEEEEEEEEEEEEEEA
EEEEEELPPQYFSSETSGSCALNPEEVLEQPQPLSLGHLEGSGQGSQSVPAEQESFALHSSDFLPPIRGHLGSQPEQAQP
PCYYGIGGLWRTSKQEAAESAKQEFQPFSPPPGAPGIPTSYSAYYNISVAKAELLNKLKDQPEMAEIGLGEEEVDHELAQ
KKIQLIESISRKLSVLREAQRGLLEDINANSALGEEVEANLKAVCKSNEFEKYRSFVGDLDKVVNLLLSLSGRLARVENA
LNSIDSEANQEKLVLIEKKQQLTGQLADAKELKEHVDRREKLVFGMVSRYLPQDQLQDYQHFVKMKSALIIEQRELEEKI
KLGEEQLKCLRESLLLGPSNF
```

1020 - 1039:	EEEEEEEEEEEEEEEEEEEE

A0A2K5KIA0 **A0A2K5KIA0_CERAT** (586 aa)
Ran GTPase activating protein 1. *Cercocebus atys (Sooty mangabey) (Cercocebus torquatus atys)*

```
MASEDIAKLAETLAKTQVAGGQLSFKGKSLKLNTAEDAKDVIKEIEDFDSLEALRLEGNTVGVEAARVIAKALEKKSELK
RCHWSDMFTGRLRTEIPPALISLGEGLITAGAQLVELDLSDNAFGPDGVQGFEALLKSSACFTLHELKLNNCGMGIGGGK
ILAAALTECHRKSSAQGKPLALKVFVAGRNRLENDGATALAEAFRVIGTLEEVHMPQNGINHPGVTALAQAFAANPLLRV
INLNDNTFTEKGAVAMAETLKTLRQVEVINFGDCLVRSRGAVAIADAICGGLPKLKELNLSFCEIKRDAALAVAEAMADK
TELEKLDLNGNTLGEEGCEQLQEVLEGFNMAKVLASLSDDEDEEEEEGEEEEEAEEEEEEEEEEEEEEEEEEEEEEPQQG
GQGEKSATPSQKILDPNTGEPAPVLSSPPPADVSTFLAFPSPEKLLRLGPKSSMLIAQQTDTSDPEKVVSAFLKVSSVFK
DEATVRTAVQDAVDALMKKAFSSSSFNSSAFLTRLLAHMGLLKSEDKVKAIANLYGPLMALNHMVQQDYFPKALAPLLLA
FITKPNSALESCSFARHSLLQTLYKV
```

375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE

A0A2K5KIA6 **A0A2K5KIA6_CERAT** (627 aa)
Ran GTPase activating protein 1. *Cercocebus atys (Sooty mangabey) (Cercocebus torquatus atys)*

```
MGLPRRPPVICGLYSRVAPAAPPPSRPTPTGGPGWRRCPWNRCESMHLTSEREPTSLVSMASEDIAKLAETLAKTQVAGG
QLSFKGKSLKLNTAEDGDVLNSYRLSGSFCYIVSIICPRSSRCHWSDMFTGRLRTEIPPALISLGEGLITAGAQLVELDL
SDNAFGPDGVQGFEALLKSSACFTLHELKLNNCGMGIGGGKILAAALTECHRKSSAQGKPLALKVFVAGRNRLENDGATA
LAEAFRVIGTLEEVHMPQNGINHPGVTALAQAFAANPLLRVINLNDNTFTEKGAVAMAETLKTLRQVEVINFGDCLVRSR
GAVAIADAICGGLPKLKELNLSFCEIKRDAALAVAEAMADKTELEKLDLNGNTLGEEGCEQLQEVLEGFNMAKVLASLSD
DEDEEEEEGEEEEEAEEEEEEEEEEEEEEEEEEEEEEPQQGGQGEKSATPSQKILDPNTGEPAPVLSSPPPADVSTFLAF
PSPEKLLRLGPKSSMLIAQQTDTSDPEKVVSAFLKVSSVFKDEATVRTAVQDAVDALMKKAFSSSSFNSSAFLTRLLAHM
GLLKSEDKVKAIANLYGPLMALNHMVQQDYFPKALAPLLLAFITKPNSALESCSFARHSLLQTLYKV
```

416 - 435:	EEEEEEEEEEEEEEEEEEEE
417 - 436:	EEEEEEEEEEEEEEEEEEEE
418 - 437:	EEEEEEEEEEEEEEEEEEEE

A0A2K5LPK3 **A0A2K5LPK3_CERAT** (1180 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Cercocebus atys (Sooty mangabey) (Cercocebus torquatus atys)*

```
MLLPSLSPRVQPAFIQCAGPQPPPHAHSPVGGRRGVFASSRHATTGAPGKMAAAVLSGPSAGSAAGVPGGTGGLSAVNSG
PRLRLLLLESVSGLLQPRTGSAVAPVHPPNRSAPHLPGLMCLLRLHGSVGGAQNLSALGALVSLSNARLSSIKTRFEGLC
LLSLLVGESPTELFQQHCVSWLRSIQQVLQTQDPPATMELAVAVLRDLLRYAAQLPALFRDISMNHLPGLLTSLLGLRPE
CEQSALEGMKACMTYFPRACGSLKGKLASFFLSRVDALSPQLQQLACECYSRLPSLGAGFSQGLKHTESWEQELHSLLAS
LHTLLGALYEGAETAPVQNEGPGVEMLLSSEDGDAHVLLRLRQRFSGLARCLGLMLSSEFGAPVSVPVQEILDFICRTLS
VSSKNISLHGDGPLRLLLLPSIHLEALDLLSALILACGSRLLRFGILISRLLPQVLNSWSIGRDSLSPGQERPYSTVRTK
VYAVLELWVQVCGASAGMLQGGASGEALLTHLLSDISPPADALKLRSPRGSPDGSLQTGKPSAPKKLKLDVGEAMAPPSH
RKGDSNANSDVCAAALKGLSRTILMCGPLIKEETHRRLHDLVLPLVMGVQQGEVLGSSPYTSSRCRRELYCLLLALLLAP
SPRCPPPLACALQAFSLGQREDSLEVSSFCSEALVTCAALTHPRVPPLQPMGPTCPTPAPVPPPEAPSPFRAPPFHPPGP
MPSVGPMPSAGPMPSAGPMPSAGPVPSARPGPPTTANHLGLSVSGLVSVPPRLLPGPENHRAGSNEDPILAPSGSPPPAI
PPDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDSVVIVPEGLPPLPPPPPSGATPPPIAPTGPPTASPPVPAKEEPE
ELPAAPGPLPPPPPPPPPVPGPVTLPPPQLVPEGTPGGGGPPALEEDLTVININSSDEEEEEEEEEEEEEEEEEEEEEDF
EEEEEDEEEYFEEEEEEEEEFEEEFEEEEGELEEEEEEEDEEEEEELEEVEELEFGTAGGEVEEGGPPPPTLPPALPPPE
SPPKVPPEPEPEPGLLLEVEEPGAEEEHGADTAPTLAPEVLPSQGEVEREEGSPSAGPPPQELVEEEPSAPPTLLEEGTE
DGGDRVQPPPETPAEEEMETETEAEALQEKEQDDTAAMLADFIDCPPDDEKPPPPTEPDS
```

938 - 957:	EEEEEEEEEEEEEEEEEEEE
939 - 958:	EEEEEEEEEEEEEEEEEEEE

A0A2K5LPK4 **A0A2K5LPK4_CERAT** (1168 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Cercocebus atys (Sooty mangabey) (Cercocebus torquatus atys)*

```
MLLPSLSPRVQPAFIQCAGPQPPPHAHSPVGGRRGVFASSRHATTGAPGKMAAAVLSGPSAGSAAGVPGGTGGLSAVNSG
PRLRLLLLESVSGLLQPRTGSAVAPVHPPNRSAPHLPGLMCLLRLHGSVGGAQNLSALGALVSLSNARLSSIKTRFEGLC
LLSLLVGESPTELFQQHCVSWLRSIQQVLQTQDPPATMELAVAVLRDLLRYAAQLPALFRDISMNHLPGLLTSLLGLRPE
CEQSALEGMKACMTYFPRACGSLKGKLASFFLSRVDALSPQLQQLACECYSRLPSLGAGFSQGLKHTESWEQELHSLLAS
LHTLLGALYEGAETAPVQNEGPGVEMLLSSEDGDAHVLLRLRQRFSGLARCLGLMLSSEFGAPVSVPVQEILDFICRTLS
VSSKNISLHGDGPLRLLLLPSIHLEALDLLSALILACGSRLLRFGILISRLLPQVLNSWSIGRDSLSPGQERPYSTVRTK
VYAVLELWVQVCGASAGMLQGGASGEALLTHLLSDISPPADALKLRSPRGSPDGSLQTGKPSAPKKLKLDVGEAMAPPSH
RKGDSNANSDVCAAALKGLSRTILMCGPLIKEETHRRLHDLVLPLVMGVQQGEVLGSSPYTSSRCRRELYCLLLALLLAP
SPRCPPPLACALQAFSLGQREDSLEVSSFCSEALVTCAALTHPRVPPLQPMGPTCPTPAPVPPPEAPSPFRAPPFHPPGP
MPSVGPMPSAGPMPSAGPMPSAGPVPSARPGPPTTANHLGLSVSGLVSVPPRLLPGPENHRAGSNEDPILAPSGSPPPAI
PPDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDSVVIVPEGLPPLPPPPPSGATPPPIAPTGPPTASPPVPAKEEPE
ELPAAPGPLPPPPPPPPPVPGPVTLPPPQLVPEGTPGGGGPPALEEDLTVININSSDEEEEEEEEEEEEEEEEEEEEEDF
EEEEEDEEEYFEEEEEEEEEFEEEFEEEEGELEEEEEEEDEEEEEELEEVEELEFGTAGGEVEEGGPPPPTLPPALPPPE
SPPKVPPEPEPEPGLLLEVEEPGAEEEHGADTAPTLAPEVLPSQGEVEREEGSPSAGPPPQELVEEEPSAPPTLLEEGTE
DGGDRVQPPPETPAEEEMETETEAEALQEKVRGLLISSWDYRRPPPPG
```

938 - 957:	EEEEEEEEEEEEEEEEEEEE
939 - 958:	EEEEEEEEEEEEEEEEEEEE

A0A2K5LPL1 **A0A2K5LPL1_CERAT** (1271 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Cercocebus atys (Sooty mangabey) (Cercocebus torquatus atys)*

```
MLLPSLSPRVQPAFIQCAGPQPPPHAHSPVGGRRGVFASSRHATTGAPGKMAAAVLSGPSAGSAAGVPGGTGGLSAVNSG
PRLRLLLLESVSGLLQPRTGSAVAPVHPPNRSAPHLPGLMCLLRLHGSVGGAQNLSALGALVSLSNARLSSIKTRFEGLC
LLSLLVGESPTELFQQHCVSWLRSIQQVLQTQDPPATMELAVAVLRDLLRYAAQLPALFRDISMNHLPGLLTSLLGLRPE
CEQSALEGMKACMTYFPRACGSLKGKLASFFLSRVDALSPQLQQLACECYSRLPSLGAGFSQGLKHTESWEQELHSLLAS
LHTLLGALYEGAETAPVQNEGPGVEMLLSSEDGDAHVLLRLRQRFSGLARCLGLMLSSEFGAPVSVPVQEILDFICRTLS
VSSKNISLHGDGPLRLLLLPSIHLEALDLLSALILACGSRLLRFGILISRLLPQVLNSWSIGRDSLSPGQERPYSTVRTK
VYAVLELWVQVCGASAGMLQGGASGEALLTHLLSDISPPADALKLRSPRGSPDGSLQTGKPSAPKKLKLDVGEAMAPPSH
RKGDSNANSDVCAAALKGLSRTILMCGPLIKEETHRRLHDLVLPLVMGVQQGEVLGSSPYTSSRCRRELYCLLLALLLAP
SPRCPPPLACALQAFSLGQREDSLEVAVMGQTLFGPWTLLFPGAHTCPFFFPQVSSFCSEALVTCAALTHPRVPPLQPMG
PTCPTPAPVPPPEAPSPFRAPPFHPPGPMPSVGPMPSAGPMPSAGPMPSAGPVPSARPGPPTTANHLGLSVSGLVSVPPR
LLPGPENHRAGSNEDPILAPSGSPPPAIPPDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDSVVIVPEGLPPLPPPP
PSGATPPPIAPTGPPTASPPVPAKEEPEELPAAPGPLPPPPPPPPPVPGPVTLPPPQLVPEGTPGGGGPPALEEDLTVIN
INSSDEEEEEEEEEEEEEEEEEEEEEEDFEEEEEDEEEYFEEEEEEEEEFEEEFEEEEGELEEEEEEEDEEEEEELEEVEE
LEFGTAGGEVEEGGPPPPTLPPALPPPESPPKVPPEPEPEPGLLLEVEEPGAEEEHGADTAPTLAPEVLPSQGEVEREEG
SPSAGPPPQELVEEEPSAPPTLLEEGTEDGGDRVQPPPETPAEEEMETETEAEALQEKVRGPGREGTLGEKVGLSGEWVA
AAYLRRRLPSLNHSVCVCDYSESCIFVPKRSRMTQLPCWPTSSIVPLMMRSHRLPQSLTPSHLLHPTLCFQ
```

966 - 985:	EEEEEEEEEEEEEEEEEEEE
967 - 986:	EEEEEEEEEEEEEEEEEEEE

A0A2K5LPL2 **A0A2K5LPL2_CERAT** (1243 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Cercocebus atys (Sooty mangabey) (Cercocebus torquatus atys)*

```
MLLPSLSPRVQPAFIQCAGPQPPPHAHSPVGGRRGVFASSRHATTGAPGKMAAAVLSGPSAGSAAGVPGGTGGLSAVNSG
PRLRLLLLESVSGLLQPRTGSAVAPVHPPNRSAPHLPGLMCLLRLHGSVGGAQNLSALGALVSLSNARLSSIKTRFEGLC
LLSLLVGESPTELFQQHCVSWLRSIQQVLQTQDPPATMELAVAVLRDLLRYAAQLPALFRDISMNHLPGLLTSLLGLRPE
CEQSALEGMKACMTYFPRACGSLKGKLASFFLSRVDALSPQLQQLACECYSRLPSLGAGFSQGLKHTESWEQELHSLLAS
LHTLLGALYEGAETAPVQNEGPGVEMLLSSEDGDAHVLLRLRQRFSGLARCLGLMLSSEFGAPVSVPVQEILDFICRTLS
VSSKNISLHGDGPLRLLLLPSIHLEALDLLSALILACGSRLLRFGILISRLLPQVLNSWSIGRDSLSPGQERPYSTVRTK
VYAVLELWVQVCGASAGMLQGGASGEALLTHLLSDISPPADALKLRSPRGSPDGSLQTGKPSAPKKLKLDVGEAMAPPSH
RKGDSNANSDVCAAALKGLSRTILMCGPLIKEETHRRLHDLVLPLVMGVQQGEVLGSSPYTSSRCRRELYCLLLALLLAP
SPRCPPPLACALQAFSLGQREDSLEVSSFCSEALVTCAALTHPRVPPLQPMGPTCPTPAPVPPPEAPSPFRAPPFHPPGP
MPSVGPMPSAGPMPSAGPMPSAGPVPSARPGPPTTANHLGLSVSGLVSVPPRLLPGPENHRAGSNEDPILAPSGSPPPAI
PPDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDSVVIVPEGLPPLPPPPPSGATPPPIAPTGPPTASPPVPAKEEPE
ELPAAPGPLPPPPPPPPPVPGPVTLPPPQLVPEGTPGGGGPPALEEDLTVININSSDEEEEEEEEEEEEEEEEEEEEEDF
EEEEEDEEEYFEEEEEEEEEFEEEFEEEEGELEEEEEEEDEEEEEELEEVEELEFGTAGGEVEEGGPPPPTLPPALPPPE
SPPKVPPEPEPEPGLLLEVEEPGAEEEHGADTAPTLAPEVLPSQGEVEREEGSPSAGPPPQELVEEEPSAPPTLLEEGTE
DGGDRVQPPPETPAEEEMETETEAEALQEKVRGPGREGTLGEKVGLSGEWVAAAYLRRRLPSLNHSVCVCDYSESCIFVP
KRSRMTQLPCWPTSSIVPLMMRSHRLPQSLTPSHLLHPTLCFQ
```

938 - 957:	EEEEEEEEEEEEEEEEEEEE
939 - 958:	EEEEEEEEEEEEEEEEEEEE

A0A2K5LPS0 **A0A2K5LPS0_CERAT** (906 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Cercocebus atys (Sooty mangabey) (Cercocebus torquatus atys)*

```
MELAVAVLRDLLRYAAQLPALFRDISMNHLPGLLTSLLGLRPECEQSALEGMKACMTYFPRACGSLKGKLASFFLSRVDA
LSPQLQQLACECYSRLPSLGAGFSQGLKHTESWEQELHSLLASLHTLLGALYEGAETAPVQNEGPGVEMLLSSEDGDAHV
LLRLRQRFSGLARCLGLMLSSEFGAPVSVPVQEILDFICRTLSVSSKNISLHGDGPLRLLLLPSIHLEALDLLSALILAC
GSRLLRFGILISRLLPQVLNSWSIGRDSLSPGQERPYSTVRTKVYAVLELWVQVCGASAGMLQGGASGEALLTHLLSDIS
PPADALKLRSPRGSPDGSLQTGKPSAPKKLKLDVGEAMAPPSHRKGDSNANSDVCAAALKGLSRTILMCGPLIKEETHRR
LHDLVLPLVMGVQQGEVLGSSPYTSSRCRRELYCLLLALLLAPSPRCPPPLACALQAFSLGQREDSLEVSSFCSEALVTC
AALTHPRVPPLQPMGPTCPTPAPVPPPEAPSPFRAPPFHPPGPMPSVGPMPSAGPMPSAGPMPSAGPVPSARPGPPTTAN
HLGLSVSGLVSVPPRLLPGPENHRAGSNEDPILAPSGSPPPAIPPDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDS
VVIVPEGLPPLPPPPPSGATPPPIAPTGPPTASPPVPAKEEPEELPAAPGPLPPPPPPPPPVPGPVTLPPPQLVPEGTPG
GGGPPALEEDLTVININSSDEEEEEEEEEEEEEEEEEEEEEEDFEEEEEDEEEYFEEEEEEEEEFEEEFEEEEGELEEEEE
EEDEEEEEEELEEVEREEGSPSAGPPPQELVEEEPSAPPTLLEEGTEDGGDRVQPPPETPAEEEMETETEAEALQEKEQDD
TAAMLADFIDCPPDDEKPPPPTEPDS
```

741 - 760:	EEEEEEEEEEEEEEEEEEEE
742 - 761:	EEEEEEEEEEEEEEEEEEEE

A0A2K5MA14 **A0A2K5MA14_CERAT** (1093 aa)
Solute carrier family 24 member 1. *Cercocebus atys (Sooty mangabey) (Cercocebus torquatus atys)*

```
MGKLIRMGPQDRRLLRTKRLPWSRLLFLLGMLIISSTYQHLRGPRGLSSLWAAVSSHQPVKLASRDLPSEEMMMVSSNPP
KPSSEMGGEMLVPQASVGSDEATLSMTVENIPDIPKRTAKMIPTTTKNNYSPTAAGTERRKEDTPTSSRTLTYYTSTSSR
QIVKKYTPTPTGEMKSYSPTQVREKVKYTPSPRGRRVGTYASSTFMTTETSHAITPRTAVKDSDITTTYKILETNSLKRI
MEETTPTTLKGMVDSTPTFLTHEVETNVLTSPRSIVEKNNLSPPRRVESNSSAHPWGLVGKNNLKTPQGTVLTHTPATSE
GQVTISTMTGSNPSETKAFTAAWSVRNPSPRTSVSAIETAPTTVWRLAKKPYTAPSTSTTPTVRAKPTTQVHHCVVVKPT
PAMPTTPSPSLTTALLPEELSPSPSVLPPILPDLPPKGEYPPDLFSVEERQQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLIMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKQIEAWVKEQLSRRPAAKVMALGDLSKPGDGAIAVDE
LQDNKKLKLPSLLTRGSSSTSLHNSTIRSTIYQLMLHSLDPLREVCLAEEKEEESLNQEARAQPQAKSESKPEDEEPAKL
PAVTVTPAPAPDIKGDQKENPGGQEDVAEAESTGEMTGEEGETAGEGETEEKSGGETQPEGEGETGTQGKGEEREKENEA
EGKGDNEGEGEGEIHAEDGEMKGIEGETESQELSAENHGEAKSDEKGVEDGGGSDGGDNEEEEEEEEEEEEEEEEEEEE
EEEEEGNEEPLSLHWPETRQKQAIYLFLLPIVFPLWLTVPDVRRQESRKFFVFTFLGSIVWIAMFSYLMVWWAHQVGETI
GISEEIMGLTILAAGTSIPDLITSVIVARKGLGDMAVSSSVGSNIFDITVGLPVPWLLFCLINGLQPVPVSSNGLFCAIV
LLFLMLLFVISSIASCKWRMNKILGFTMFLLYFVFLIISVMLEDRIISCPVSV
```

860 - 879:	EEEEEEEEEEEEEEEEEEEE
861 - 880:	EEEEEEEEEEEEEEEEEEEE
862 - 881:	EEEEEEEEEEEEEEEEEEEE
863 - 882:	EEEEEEEEEEEEEEEEEEEE
864 - 883:	EEEEEEEEEEEEEEEEEEEE
865 - 884:	EEEEEEEEEEEEEEEEEEEE
866 - 885:	EEEEEEEEEEEEEEEEEEEE

A0A2K5MA17 **A0A2K5MA17_CERAT** (1006 aa)
Solute carrier family 24 member 1. *Cercocebus atys (Sooty mangabey) (Cercocebus torquatus atys)*

```
MGKLIRMGPQDRRLLRTKRLPWSRLLFLLGMLIISSTYQHLRGPRGLSSLWAAVSSHQPVKLASRDLPSEEMMMVSSNPP
KPSSEMGGEMLVPQASVGSDEATLSMTVENIPDIPKRTAKMIPTTTKNNYSPTAAGTERRKEDTPTSSRTLTYYTSTSSR
QIVKKYTPTPTGEMKSYSPTQVREKVKYTPSPRGRRVGTYASSTFMTTETSHAITPRTAVKDSDITTTYKILETNSLKRI
MEETTPTTLKGMVDSTPTFLTHEVETNVLTSPRSIVEKNNLSPPRRVESNSSAHPWGLVGKNNLKTPQGTVLTHTPATSE
GQVTISTMTGSNPSETKAFTAAWSVRNPSPRTSVSAIETAPTTVWRLAKKPYTAPSTSTTPTVRAKPTTQVHHCVVVKPT
PAMPTTPSPSLTTALLPEELSPSPSVLPPILPDLPPKGEYPPDLFSVEERQQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLIMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKQIEAWVKEQLSRRPAAKVMALGDLSKLPSLLTRGSS
STSLHNSTIRSTIYQLMLHSLDPLREVCLAEEKEEESLNQEARAQPQAKSESKPEDEEPAKLPAVTVTPAPAPDIKGDQK
ENPGGQEDVAEAESTGEMTGEEGETAGEGETEEKSGGETQPEGEGETGTQGKGEEREKENEAEGKGDNEGEGEGEIHAED
GEMKGIEGETESQELSAENHGEAKSDEKGVEDGGGSDGGDNEEEEEEEEEEEEEEEEEEEEEEEEEEGNEEPLSLHWPET
RQKQAIYLFLLPIVFPLWLTVPDVRRQESRKFFVFTFLGSIVWIAMFSYLMVWWAHQVGETIGISEEIMGLTILAAGTSI
PDLITSVIVARKGLGDMAVSSSVGSNIFDITVGVESCEMFQLGAIH
```

842 - 861:	EEEEEEEEEEEEEEEEEEEE
843 - 862:	EEEEEEEEEEEEEEEEEEEE
844 - 863:	EEEEEEEEEEEEEEEEEEEE
845 - 864:	EEEEEEEEEEEEEEEEEEEE
846 - 865:	EEEEEEEEEEEEEEEEEEEE
847 - 866:	EEEEEEEEEEEEEEEEEEEE
848 - 867:	EEEEEEEEEEEEEEEEEEEE

A0A2K5MA22 **A0A2K5MA22_CERAT** (1063 aa)
Solute carrier family 24 member 1. *Cercocebus atys (Sooty mangabey) (Cercocebus torquatus atys)*

```
MGKLIRMGPQDRRLLRTKRLPWSRLLFLLGMLIISSTYQHLRGPRGLSSLWAAVSSHQPVKLASRDLPSEEMMMVSSNPP
KPSSEMGGEMLVPQASVGSDEATLSMTVENIPDIPKRTAKMIPTTTKNNYSPTAAGTERRKEDTPTSSRTLTYYTSTSSR
QIVKKYTPTPTGEMKSYSPTQVREKVKYTPSPRGRRVGTYASSTFMTTETSHAITPRTAVKDSDITTTYKILETNSLKRI
MEETTPTTLKGMVDSTPTFLTHEVETNVLTSPRSIVEKNNLSPPRRVESNSSAHPWGLVGKNNLKTPQGTVLTHTPATSE
GQVTISTMTGSNPSETKAFTAAWSVRNPSPRTSVSAIETAPTTVWRLAKKPYTAPSTSTTPTVRAKPTTQVHHCVVVKPT
PAMPTTPSPSLTTALLPEELSPSPSVLPPILPDLPPKGEYPPDLFSVEERQQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLIMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKQIEAWVKEQLSRRPAAKVMALGDLSKPGDGAIAVDE
LQDNKKLKLPSLLTRGSSSTSLHNSTIRSTIYQLMLHSLDPLREVCLAEEKEEESLNQEARAQPQAKSESKPEDEEPAKL
PAVTVTPAPAPDIKGDQKENPGGQEDVAEAESTGEMTGEEGETAGEGETEEKSGGETQPEGEGETGTQGKGEEREKENEA
EGKGDNEGEGEGEIHAEDGEMKGIEGETESQELSAENHGEAKSDEKGVEDGGGSDGGDNEEEEEEEEEEEEEEEEEEEE
EEEEEGNEEPLSLHWPETRQKQAIYLFLLPIVFPLWLTVPDVRRQVGETIGISEEIMGLTILAAGTSIPDLITSVIVARK
GLGDMAVSSSVGSNIFDITVGLPVPWLLFCLINGLQPVPVSSNGLFCAIVLLFLMLLFVISSIASCKWRMNKILGFTMFL
LYFVFLIISVMLEDRIISCPVSV
```

860 - 879:	EEEEEEEEEEEEEEEEEEEE
861 - 880:	EEEEEEEEEEEEEEEEEEEE

862 - 881:	EEEEEEEEEEEEEEEEEEEE
863 - 882:	EEEEEEEEEEEEEEEEEEEE
864 - 883:	EEEEEEEEEEEEEEEEEEEE
865 - 884:	EEEEEEEEEEEEEEEEEEEE
866 - 885:	EEEEEEEEEEEEEEEEEEEE

A0A2K5MA27 **A0A2K5MA27_CERAT** (979 aa)
Solute carrier family 24 member 1. *Cercocebus atys (Sooty mangabey) (Cercocebus torquatus atys)*

```
MGKLIRMGPQDRRLLRTKRLPWSRLLFLLGMLIISSTYQHLRGPRGLSSLWAAVSSHQPVKLASRDLPSEEMMMVSSNPP
KPSSEMGGEMLVPQASVGSDEATLSMTVENIPDIPKRTAKMIPTTTKNNYSPTAAGTERRKEDTPTSSRTLTYYTSTSSR
QIVKKYTPTPTGEMKSYSPTQVREKVKYTPSPRGRRVGTYASSTFMTTETSHAITPRTAVKDSDITTTYKILETNSLKRI
MEETTPTTLKGMVDSTPTFLTHEVETNVLTSPRSIVEKNNLSPPRRVESNSSAHPWGLVGKNNLKTPQGTVLTHTPATSE
GQVTISTMTGSNPSETKAFTAAWSVRNPSPRTSVSAIETAPTTVWRLAKKPYTAPSTSTTPTVRAKPTTQVHHCVVVKPT
PAMPTTPSPSLTTALLPEELSPSPSVLPPILPDLPPKGEYPPDLFSVEERQQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLIMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKQIEAWVKEQLSRRPAAKVMALGDLSKEDVAEAESTG
EMTGEEGETAGEGETEEKSGGETQPEGEGETGTQGKGEEREKENEAEGKGDNEGEGEGEIHAEDGEMKGIEGETESQELS
AENHGEAKSDEKGVEDGGGSDGGDNEEEEEEEEEEEEEEEEEEEEEEEEEEEGNEEPLSLHWPETRQKQAIYLFLLPIVFP
LWLTVPDVRRQESRKFFVFTFLGSIVWIAMFSYLMVWWAHQVGETIGISEEIMGLTILAAGTSIPDLITSVIVARKGLGD
MAVSSSVGSNIFDITVGLPVPWLLFCLINGLQPVPVSSNGLFCAIVLLFLMLLFVISSIASCKWRMNKILGFTMFLLYFV
FLIISVMLEDRIISCPVSV
```

746 - 765:	EEEEEEEEEEEEEEEEEEEE
747 - 766:	EEEEEEEEEEEEEEEEEEEE
748 - 767:	EEEEEEEEEEEEEEEEEEEE
749 - 768:	EEEEEEEEEEEEEEEEEEEE
750 - 769:	EEEEEEEEEEEEEEEEEEEE
751 - 770:	EEEEEEEEEEEEEEEEEEEE
752 - 771:	EEEEEEEEEEEEEEEEEEEE

A0A2K5MA36 **A0A2K5MA36_CERAT** (1075 aa)
Solute carrier family 24 member 1. *Cercocebus atys (Sooty mangabey) (Cercocebus torquatus atys)*

```
MGKLIRMGPQDRRLLRTKRLPWSRLLFLLGMLIISSTYQHLRGPRGLSSLWAAVSSHQPVKLASRDLPSEEMMMVSSNPP
KPSSEMGGEMLVPQASVGSDEATLSMTVENIPDIPKRTAKMIPTTTKNNYSPTAAGTERRKEDTPTSSRTLTYYTSTSSR
QIVKKYTPTPTGEMKSYSPTQVREKVKYTPSPRGRRVGTYASSTFMTTETSHAITPRTAVKDSDITTTYKILETNSLKRI
MEETTPTTLKGMVDSTPTFLTHEVETNVLTSPRSIVEKNNLSPPRRVESNSSAHPWGLVGKNNLKTPQGTVLTHTPATSE
GQVTISTMTGSNPSETKAFTAAWSVRNPSPRTSVSAIETAPTTVWRLAKKPYTAPSTSTTPTVRAKPTTQVHHCVVVKPT
PAMPTTPSPSLTTALLPEELSPSPSVLPPILPDLPPKGEYPPDLFSVEERQQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLIMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKQIEAWVKEQLSRRPAAKVMALGDLSKLPSLLTRGSS
STSLHNSTIRSTIYQLMLHSLDPLREVCLAEEKEEESLNQEARAQPQAKSESKPEDEEPAKLPAVTVTPAPAPDIKGDQK
ENPGGQEDVAEAESTGEMTGEEGETAGEGETEEKSGGETQPEGEGETGTQGKGEEREKENEAEGKGDNEGEGEGEIHAED
GEMKGIEGETESQELSAENHGEAKSDEKGVEDGGGSDGGDNEEEEEEEEEEEEEEEEEEEEEEEEEEEGNEEPLSLHWPET
RQKQAIYLFLLPIVFPLWLTVPDVRRQESRKFFVFTFLGSIVWIAMFSYLMVWWAHQVGETIGISEEIMGLTILAAGTSI
PDLITSVIVARKGLGDMAVSSSVGSNIFDITVGLPVPWLLFCLINGLQPVPVSSNGLFCAIVLLFLMLLFVISSIASCKW
RMNKILGFTMFLLYFVFLIISVMLEDRIISCPVSV
```

842 - 861:	EEEEEEEEEEEEEEEEEEEE
843 - 862:	EEEEEEEEEEEEEEEEEEEE
844 - 863:	EEEEEEEEEEEEEEEEEEEE
845 - 864:	EEEEEEEEEEEEEEEEEEEE
846 - 865:	EEEEEEEEEEEEEEEEEEEE
847 - 866:	EEEEEEEEEEEEEEEEEEEE
848 - 867:	EEEEEEEEEEEEEEEEEEEE

A0A2K5MKH9 **A0A2K5MKH9_CERAT** (736 aa)
YTH domain containing 1. *Cercocebus atys (Sooty mangabey) (Cercocebus torquatus atys)*

```
MAADIREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSN
NKRIVSTKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEE
EEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSA
SESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVIL
IFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQE
IELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQ
RPGYLKDPRYQEVDSFTNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQ
AHPPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERER
LCDRDRDRGERGRYRR
```

230 - 249:	EEEEEEEEEEEEEEEEEEEE

231 - 250:	EEEEEEEEEEEEEEEEEEEE

A0A2K5MKJ8 **A0A2K5MKJ8_CERAT** (710 aa)
YTH domain containing 1. *Cercocebus atys (Sooty mangabey) (Cercocebus torquatus atys)*

```
MAADIREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSN
NKRIVSTKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEE
EEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSA
SESYADQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVILIFSVRESGKFQGFARLSS
ESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLLFPPDES
IDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQRPGYLKDPRYQEVDRRFS
GVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHHPVPHEARYRDKRVHDYD
MRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDRGERGRYRR
```

230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE

A0A2K5MKK2 **A0A2K5MKK2_CERAT** (536 aa)
YTH domain containing 1. *Cercocebus atys (Sooty mangabey) (Cercocebus torquatus atys)*

```
DGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSNNKRIVSTKG
KSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVDRRASRSSQS
SKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEEEEEEEEEEEEEEEEEEEEEEEYEQDE
RDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSASESYAGSEKKHEKLS
SSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVILIFSVRESGKFQGFAR
LSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLLFPP
DESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRLETFFGLIIGTCIRIT
```

214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE

A0A2K5N0A6 **A0A2K5N0A6_CERAT** (1324 aa)
Tau tubulin kinase 1. *Cercocebus atys (Sooty mangabey) (Cercocebus torquatus atys)*

```
MQCLAAALKDETNMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTRENVALKVESAQQPKQVLKMEVAV
LKKLQGKDHVCRFIGCGRNEKFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESIEAIHSVGFLHRDIKPSNF
AMGRLPSTYRKCYMLDFGLARQYTNTTGDVRPPRNVAGFRGTVRYASVNAHKNREMGRHDDLWSLFYMLVEFAVGQLPWR
KIKDKEQVGMIKEKYEHRMLLKHMPSEFHLFLDHIASLDYFTKPDYQLIMSVFENSMKERGIAENEAFDWEKAGTDALLS
TSTSTPPQQNTRQTAAMFGVVNVTPVPGDLLRENTEDVLQGEHLSDQENAPPILPGRPSEGLGPSPHLVPHPGGPEAEVW
EETDVNRNKLRINIGKSPCVEEEQSRGMGVPSSPVRAPPDSPTTPVRSLRYRRVNSPESERLSTADGRVELPERRSRMDL
PGSPSRQACSSQPAQMLSVDTGHADRQASGRMDVSASVEQEALSNAFRSVPLAEEEDFDSKEWVIIDKETELKDFPPGAE
PSTSGTTDEEPEELRPLPEEGEERRRLGAEPTVRPRGRSMQVLAEEDLQHLPPQPLPPQLSQADGRSETSQPPTPGSPSH
SPLHSGPRPRRRESDPTGPQRQVFSVAPPFEVNGLPRAVPLSLPYQDFKRDLSDYRERARLLNRVRRVGFSHMLLTTPQV
PLSPVQPQANGKEEEEEEEEEEDEEEEEEDEEDEEEEEEEEEEEEEEEEEEEEEEAAAAVALGEVLGPRSGSSSEGSERST
DRSQEGAPSTLLADDQKESRGRASMADGDLEPEEGSKTLVLVSPGDMKKSPVTAELAPDPDLGTLAALTPQHERPQPTGS
QLDVSEPGTLSSVLKSEPKPPGPGAGPGAGTVTTGAGGVAVTSSPFTKVERTFVHIAEKTHLNVMSSSGQALRPEEFSTG
GELGLELASDGGTVEEGAPAPLENGLALSGLNGAEIEGCALSGPPGETPSAMATNSLPNGPALADSPAPVSPLEPSPEKV
ATISPRHHAMPGSRPRSRIPILLSEEDTGSEPSGSLSAKERWSKRARLQQDLARLVMEKRQGRLLLRLASGASSSSSEEQ
RRASETLSGTGSEEDTPASEPAVALPRKVGRAAATRSRIPRPIGLRMPMPAAAQQLPSKSHGAAPASDTAITSRLQLQTP
PGSATAADLRPKQPPGRGLGPGRAQAGARPSAPRSPGLPTSTSAARNASASPRSQSLSRRESPSPSHQARPGVPPPRGVP
SARAQPDGTPSPGGSKKGPRGKLQAQRATTKGRAGGAEGRAGAR
```

754 - 773:	EEEEEEEEEEEEEEEEEEEE
755 - 774:	EEEEEEEEEEEEEEEEEEEE

A0A2K5P1L2 **A0A2K5P1L2_CERAT** (1209 aa)
Euchromatic histone lysine methyltransferase 2. *Cercocebus atys (Sooty mangabey) (Cercocebus torquatus atys)*

```
MAAAAGAAKKKTAEGEKKKKMGALLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGAD
TPVGAKKKNGDESENLEGDGDLHGGRILLGHATKSFPKKKSKGGSCPSRAKMSMTGAKKKNPSVQSLAMRLLSMPGAQGA
AAAGPEPPPATTSPEGQPKKKRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEEL
GSARRSEVTLAKGDPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEE
EEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLS
PNHAGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLC
ETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGAA
APAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQES
ERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTP
LMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVI
RMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRN
KEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGESCPEDYKYISENCETST
MNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQ
LYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIP
VRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPE
LGSLPPVNT
```

299 - 318:	EEEEEEEEEEEEEEEEEEEE

300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE

A0A2K5P1M7 **A0A2K5P1M7_CERAT** (1266 aa)
Euchromatic histone lysine methyltransferase 2. *Cercocebus atys (Sooty mangabey) (Cercocebus torquatus atys)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPQKKKGRPRSLLSLPRAQASWTKKKTTGLTSPPVPCLPSQGEKKKKMGA
LLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGAKKKNGDESENLEGDGDLH
GGRILLGHATKSFPKKKSKGGSCPSRAKMSMTGAKKKNPSVQSLAMRLLSMPGAQGAAAAGPEPPPATTSPEGQPKKKRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEELGSARRSEVTLAKGDPGSLEEWET
VVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAKK
KWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEELP
LCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAG
TFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGAAAPAPPPLSQDAPGRADTSQPSAR
MRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQ
KVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCV
YSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHW
ASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLN
RKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGESCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSN
CLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFI
CEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDI
RTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE

A0A2K5P1P9 **A0A2K5P1P9_CERAT** (1199 aa)
Euchromatic histone lysine methyltransferase 2. *Cercocebus atys (Sooty mangabey) (Cercocebus torquatus atys)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPQKKKGRPRSLLSLPRAQASWTKKKTTGLTSPPVPCLPSQGEKKKKMGA
LLLEKETRGTLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGAKKKNGDESENLEGDGDLHGGRILLGHATKSFPKKK
SKGGSCPSRAKMSMTGAKKKNPSVQSLAMRLLSMPGAQGAAAAGPEPPPATTSPEGQPKKKRARKTMSKPGNGQPPVPEK
RPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEELGSARRSEVTLAKGDPGSLEEWETVVGDDFSLYYDSYSVDE
RVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRDPPGVPMGEVQGLPQLLFFSVQGVSNDT
SSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKH
HCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGAAAPAPPPLSQD
APGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHP
RQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHL
EVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADV
TLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLT
PERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGESCPEDYKYISENCETSTMNIDRNITHL
QHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWG
VRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDL
RFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

339 - 358:	EEEEEEEEEEEEEEEEEEEE
340 - 359:	EEEEEEEEEEEEEEEEEEEE
341 - 360:	EEEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEEE

A0A2K5P1S6 **A0A2K5P1S6_CERAT** (1226 aa)
Euchromatic histone lysine methyltransferase 2. *Cercocebus atys (Sooty mangabey) (Cercocebus torquatus atys)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPQKKKGRPRSLLSLPRAQASWTKKKTTGLTSPPVPCLPSQGEKKKKMGA
LLLEKETRGTLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGAKKKNGDESENLEGDGDLHGGRILLGHATKSFPKKK
SKGGSCPSRAKMSMTGAKKKNPSVQSLAMRLLSMPGAQGAAAAGPEPPPATTSPEGQPKKKRARKTMSKPGNGQPPVPEK
RPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEELGSARRSEVTLAKGDPGSLEEWETVVGDDFSLYYDSYSVDE
RVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRVRDGARTLTLSVSVSGVNGVGSSGPSEY
MEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAIL
KRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQ
EVTIPRGDGVTPPAGAAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLP
LGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVL
LQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSG
GWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYH
DCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGE
SCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCW
RNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYY
GNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIAL
EQSRLARLDPHPELLPELGSLPPVNT
```

339 - 358:	EEEEEEEEEEEEEEEEEEEE

340 - 359:	EEEEEEEEEEEEEEEEEEEE
341 - 360:	EEEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEEE

A0A2K5P1X5 **A0A2K5P1X5_CERAT** (1232 aa)
Euchromatic histone lysine methyltransferase 2. *Cercocebus atys (Sooty mangabey) (Cercocebus torquatus atys)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPQKKKGRPRSLLSLPRAQASWTKKKTTGLTSPPVPCLPSQGEKKKKMGA
LLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGAKKKNGDESENLEGDGDLH
GGRILLGHATKSFPKKKSKGGSCPSRAKMSMTGAKKKNPSVQSLAMRLLSMPGAQGAAAAGPEPPPATTSPEGQPKKKRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEELGSARRSEVTLAKGDPGSLEEWET
VVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAKK
KWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSG
CNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGE
DASEAQEVTIPRGDGVTPPAGAAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCL
SAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSV
EICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDV
NAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIA
ARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCV
NGVDGESCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECN
QACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYC
IDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHS
AEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE

A0A2K5QYV0 **A0A2K5QYV0_CEBIM** (1150 aa)
Myelin transcription factor 1. *Cebus imitator (Panamanian white-faced capuchin) (Cebus capucinus imitator)*

```
MSLENEDKRARTRSKALRGAPETTAADLSCPTPGCTGSGHVRGKYSRHRSLQSCPLAKKRKLEGAEAEHLVSKRKSHPLK
LALDEGYGVDSDGSEDTEVKDASVSDESEGTLEGAEAEASGQEEIHRPEPAEGRSPVKSHFGSNPISSPTGSSKGSYSSY
QGIIATSLLNLGQVAQETLVEEDLGQAAKPGPGIVHLLQETTEGAASTEGEKGLFIQPEDAEEVVEVTSERSQDLCPQSL
EDVASEESSKQKCILSHEEEEEEEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAAPDVIFQEDTSHISI
QKAPELRGPDSPSPKPEYSVIVEVRSDDDKDEDTHSQKSTVTDESEMHDMMTRGNLGLLEQAIALKAEQVHTACEPGCPP
AEQSQLGLGEPGKAAKPLDTVRKSYYSKDPSRAEKREIKCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRIPPEILAMHEN
VLKCPTPGCTGQGHVNSNRNTHRSLSGCPIAAAEKLAKSHEKQQPQTGDPSKNSSNSDRILRPMCFVKQLEVPPYGSYRP
NVAPATPRANLAKELEKFSKVTFDYASFDAQVFGKRMLAPKIQTSETSPKAFQSKPFPKASSPRHSPSSSYVRSTSSSSA
GFDYSHDAEAAHMAATAILNLSTRCWEMPENLSTKPQDLPSKSVDIEVDENGTLDLSMHKHRKRENAFPSSSSCSSSPGV
KSPDASQRQSSTSAPSSSMTSPQSSQASRQDEWDRPLDYTKPSRLREEEPEESEPAAHSFASSEADDQEVSEENFEERKY
PGEVTLTNFKLKFLSKDIKKELLTCPTPGCDGTGHITGNYASHRSLSGCPLADKSLRNLMAAHSADLKCPTPGCDGSGHI
TGNYASHRSLSGCPRAKKSGVKVAPTKDDKEDPELMKCPVPGCVGLGHISGKYASHRSASGCPLAARRQKEGSLNGSSFS
WKSLKNEGPTCPTPGCDGSGHANGSFLTHRSLSGCPRATFAGKKGKLSGDEVLTPKFKTSDVLENDEEIKQLNQEIRDLN
ESNSEMEAAMVQLQSQISSMEKNLKNIEEENKLIEEQNEALFLELSGLSQALIQSLANIRLPHMEPICEQNFDAYVSTLT
DMYSNQECYQNPENKDLLESIKQAVRGIQV
```

271 - 290:	EEEEEEEEEEEEEEEEEEEE
272 - 291:	EEEEEEEEEEEEEEEEEEEE
273 - 292:	EEEEEEEEEEEEEEEEEEEE
274 - 293:	EEEEEEEEEEEEEEEEEEEE
275 - 294:	EEEEEEEEEEEEEEEEEEEE
276 - 295:	EEEEEEEEEEEEEEEEEEEE
277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE

A0A2K5QZ01 **A0A2K5QZ01_CEBIM** (1126 aa)
Myelin transcription factor 1. *Cebus imitator (Panamanian white-faced capuchin) (Cebus capucinus imitator)*

```
GCNLEMRWRARGGSWVLQAPDLNPIALLFPLSCPTPGCTGSGHVRGKYSRHRSLQSCPLAKKRKLEGAEAEHLVSKRKSH
```

```
PLKLALDEGYGVDSDGSEDTEVKDASVSDESEGTLEGAEAEASGQEEIHRPEPAEGRSPVKSHFGSNPISSPTGSSKGSY
SSYQGIIATSLLNLGQVAQETLVEEDLGQAAKPGPGIVHLLQETTEGAASTEGEKGLFIQPEDAEEVVEVTSERSQDLCP
QSLEDVASEESSKQKCILSHEEEEEEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAAPDVIFQEDTSH
ISIQKAPELRGPDSPSPKPEYSVIVEVRSDDDKDEDTHSQKSTVTDESEMHDMMTRGNLGLLEQAIALKAEQVHTACEPG
CPPAEQSQLGLGEPGKAAKPLDTVRKSYYSKDPSRAEKREIKCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRIPPEILAM
HENVLKCPTPGCTGQGHVNSNRNTHRSLSGCPIAAAEKLAKSHEKQQPQTGDPSKNSSNSDRILRPMCFVKQLEVPPYGS
YRPNVAPATPRANLAKELEKFSKVTFDYASFDAQVFGKRMLAPKIQTSETSPKAFQCFDYSHDAEAAHMAATAILNLSTR
CWEMPENLSTKPQDLPSKSVDIEVDENGTLDLSMHKHRKRENAFPSSSSCSSSPGVKSPDASQRQSSTSAPSSSMTSPQS
SQASRQDEWDRPLDYTKPSRLREEEPEESEPAAHSFASSEADDQEVSEENFEERKYPGEVTLTNFKLKFLSKDIKKELLT
CPTPGCDGTGHITGNYASHRSLSGCPLADKSLRNLMAAHSADLKCPTPGCDGSGHITGNYASHRSLSGCPRAKKSGVKVA
PTKDDKEDPELMKCPVPGCVGLGHISGKYASHRSASGCPLAARRQKEGSLNGSSFSWKSLKNEGPTCPTPGCDGSGHANG
SFLTHRSLSGCPRATFAGKKGKLSGDEVLTPKFKTSDVLENDEEIKQLNQEIRDLNESNSEMEAAMVQLQSQISSMEKNL
KNIEEENKLIEEQNEALFLELSGLSQALIQSLANIRLPHMEPICEQNFDAYVSTLTDMYSNQECYQNPENKDLLESIKQA
VRGIQV
```

274 - 293:	EEEEEEEEEEEEEEEEEEEE
275 - 294:	EEEEEEEEEEEEEEEEEEEE
276 - 295:	EEEEEEEEEEEEEEEEEEEE
277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE
287 - 306:	EEEEEEEEEEEEEEEEEEEE
288 - 307:	EEEEEEEEEEEEEEEEEEEE

A0A2K5S1V1 **A0A2K5S1V1_CEBIM** (1597 aa)
Histone acetyltransferase (EC 2.3.1.48). *Cebus imitator (Panamanian white-faced capuchin) (Cebus capucinus imitator)*

```
MLFCDSCDRGFHMECCDPPLSRMPKGMWICQVCRPKKKGRKLLHEKAAQIKRRYAKPIGRPKNKLKQRLLSVTSDEGSMN
AFTGRGSPGRGQKTKVCTTPSSGHAASGKDSSSRLAVTDPTRPGATTKLTTTSTYISASTLKVNKKTKGLIDGLTKFFTP
SPDGRRSRGEIIDFSKHYRPRKKVSQKQSCTSHVLATDTEIKINIKQESADVNVIGNKDVVTEEDLDVFKQAQELSWEKI
ECESGVEDCGRYPSVIEFGKYEIQTWYSSPYPQEYARLPKLYLCEFCLKYMKSKNILLRHSKKCGWFHPPANEIYRRKDL
SVFEVDGNMSKIYCQNLCLLAKLFLDHKTLYYDVEPFLFYVLTKNDEKGCHLVGYFSKEKLCQQKYNVSCIMIMPQHQRQ
GFGRFLIDFSYLLSRREGQAGSPEKPLSDLGRLSYLAYWKSVILEYLYHHHERHISIKAISRATGMCPHDIATTLQHLHM
IDKRDGRFVIIRREKLILSHMEKLKTCSRANELDPDSLRWTPILISNAAVSEEEREAEKEAERLMEQASCWEKEEQEILS
SRANSRQSPAKVQSKNKYLHSPESRPVTGERGQLLELSKESSEEEEEEEEEEEEEEEEEEEEEEEEEEDEEEEDEEEENI
QSSPPRLTKPQSVAIKRKRPFVLKKKRGRKRRRINSSVTTETISETTEVLNEPFDNSDEERPMPQLEPTCEIEVEEDGRK
PVLRKAFQHQPGKKRQAEEDEGKDNHCFKNADPCRNNMNDDSSNLKEGSKDNPEPLKCKQVWPKGTKRGLSKWRQNKERK
TGFKLNLYTPPETPMEPDDQVTVEEPKETSEGKTSPTPIRIEEEVKETGEALLPPEENRREEACAPVSPNTSPGEKPEDL
IKPEEEEEEEEEEEEEEEEGNIEKDPDGDKSEEKEEPEISTEKEDPVRLDDHEEEEEEDEEPSHNEDHDADDEDDSHMES
AEVEKEELPRETFKEVLGNQEAFLDLNVQPSHSNPEVLMDCGVDLTASCNSEPKELAGDPEAAPESDEEPPPEEQAQKQD
QKNSKEVDSEFKEGNTATVEIDSETVQAVQSLTQESSEQDDTFQDCAETQEACRSLQNYTRADQSPQIAATLDDCQQSDH
SSPVSSVHSHPGQSVRSVNSPSVPALENSYAQISPDQSAISVPSLQNMETSPMMDVPSVSDHSQQVVDSGFSDLGSIEST
TENYENPSSYDSTMGGSICGNGSSQNSCSYSNLTSSSLTQSSCAVTQQMSNISGSCSMLQQTSISSPPTCSVKSPQGCVV
ERPPSSSQQLAQCSMAANFTPPMQLAEIPETGNTNIGLYERMGQSDFGAGHYPQPSATFSLAKLQQLTNTLIDHSLPYSH
SAAVTSYANSASLSTPLSNTGLVQLSQSPHSVPGGPQAQATMTPPPNLTPPPMNLPPPLLQRNMAASNIGISHSQRLQTQ
IASKGHVSMRTKSASLSPAAATHQSQIYGRSQTVAMQGPARTLTMQRGMNMSVNLMPAPAYNVNSVNMNMNTLNAMNGYS
MSQPMMNSGYHSNHGYMNQTPQYPMQMQMGMMGTQPYAQQPMQTPPHGNMMYTAPGHHGYMNTGMSKQSLNGSYMRR
```

603 - 622:	EEEEEEEEEEEEEEEEEEEE
604 - 623:	EEEEEEEEEEEEEEEEEEEE
605 - 624:	EEEEEEEEEEEEEEEEEEEE
606 - 625:	EEEEEEEEEEEEEEEEEEEE
607 - 626:	EEEEEEEEEEEEEEEEEEEE
608 - 627:	EEEEEEEEEEEEEEEEEEEE
609 - 628:	EEEEEEEEEEEEEEEEEEEE

A0A2K5S1V9 **A0A2K5S1V9_CEBIM** (2063 aa)
Histone acetyltransferase (EC 2.3.1.48). *Cebus imitator (Panamanian white-faced capuchin) (Cebus capucinus imitator)*

```
MVKLANPLYTEWILEAIQKIKKQKQRPSEERICHAVSTSHGLDKKTVSEQLELSVQDGSVLKVTNKGLASYKDPDNPGRF
SSVKPGTFPKSTKGSRASCNDLRNVDWNKLLRRAIEGLEEPNGSSLKNIEKYLRSQSDLTSTTNNPAFQQRLRLGAKRAV
NNGRLLKDGPQYRVNYGSLDGKGAPQYPSAFPSSLPPVSLLPHEKDQPRADPIPICSFCLGTKESNREKKPEELLSCADC
GSSGHPSCLKFCPELTTNVKALRWQCIECKTCSACRVQGRNADNMLFCDSCDRGFHMECCDPPLSRMPKGMWICQVCRPK
KKGRKLLHEKAAQIKRRYAKPIGRPKNKLKQRLLSVTSDEGSMNAFTGRGSPGRGQKTKVCTTPSSGHAASGKDSSSRLA
VTDPTRPGATTKLTTTSTYISASTLKVNKKTKGLIDGLTKFFTPSPDGRRSRGEIIDFSKHYRPRKKVSQKQSCTSHVLA
TGTTQKLKPPPSSLPPPTPISGQSPSSQKSSTATSPSPQSSSSQCSVPSLSSLTTNSQLKALFDGLSHIYTTQGQSRKKG
HPSYAPPKRMRRKTELSSTAKSKAHFFGKRDIRSRFISHSSSSSWGMARGRIFKAIAHFKRTTFLKKHRMLGRLKYKVTP
```

```
QMGTPSPGKGSLTDGRIKPDQDDDTEIKINIKQESADVNVIGNKDVVTEEDLDVFKQAQELSWEKIECESGVEDCGRYPS
VIEFGKYEIQTWYSSPYPQEYARLPKLYLCEFCLKYMKSKNILLRHSKKCGWFHPPANEIYRRKDLSVFEVDGNMSKIYC
QNLCLLAKLFLDHKTLYYDVEPFLFYVLTKNDEKGCHLVGYFSKEKLCQQKYNVSCIMIMPQHQRQGFGRFLIDFSYLLS
RREGQAGSPEKPLSDLGRLSYLAYWKSVILEYLYHHHERHISIKAISRATGMCPHDIATTLQHLHMIDKRDGRFVIIRRE
KLILSHMEKLKTCSRANELDPDSLRWTPILISNAAVSEEEREAEKEAERLMEQASCWEKEEQEILSSRANSRQSPAKVQS
KNKYLHSPESRPVTGERGQLLELSKESSEEEEEEEEEEEEEEEEEEEEEEEEEEDEEEEDEEEENIQSSPPRLTKPQSVA
IKRKRPFVLKKKRGRKRRRINSSVTTETISETTEVLNEPFDNSDEERPMPQLEPTCEIEVEEDGRKPVLRKAFQHQPGKK
RQAEEDEGKDNHCFKNADPCRNNMNDDSSNLKEGSKDNPEPLKCKQVWPKGTKRGLSKWRQNKERKTGFKLNLYTPPETP
MEPDDQVTVEEPKETSEGKTSPTPIRIEEEVKETGEALLPPEENRREEACAPVSPNTSPGEKPEDLIKPEEEEEEEEEEE
EEEEEGNIEKDPDGDKSEEKEEPEISTEKEDPVRLDDHEEEEEEDEEPSHNEDHDADDEDDSHMESAEVEKEELPRETFK
EVLGNQEAFLDLNVQPSHSNPEVLMDCGVDLTASCNSEPKELAGDPEAAPESDEEPPPEEQAQKQDQKNSKEVDSEFKEG
NTATVEIDSETVQAVQSLTQESSEQDDTFQDCAETQEACRSLQNYTRADQSPQIAATLDDCQQSDHSSPVSSVHSHPGQS
VRSVNSPSVPALENSYAQISPDQSAISVPSLQNMETSPMMDVPSVSDHSQQVVDSGFSDLGSIESTTENYENPSSYDSTM
GGSICGNGSSQNSCSYSNLTSSSLTQSSCAVTQQMSNISGSCSMLQQTSISSPPTCSVKSPQGCVVERPPSSSQQLAQCS
MAANFTPPMQLAEIPETGNTNIGLYERMGQSDFGAGHYPQPSATFSLAKLQQLTNTLIDHSLPYSHSAAVTSYANSASLS
TPLSNTGLVQLSQSPHSVPGGPQAQATMTPPPNLTPPPMNLPPPLLQRNMAASNIGISHSQRLQTQIASKGHVSMRTKSA
SLSPAAATHQSQIYGRSQTVAMQGPARTLTMQRGMNMSVNLMPAPAYNVNSVNMNMNTLNAMNGYSMSQPMMNSGYHSNH
GYMNQTPQYPMQMQMGMMGTQPYAQQPMQTPPHGNMMYTAPGHHGYMNTGMSKQSLNGSYMRR
```

1069 - 1088:	EEEEEEEEEEEEEEEEEEEE
1070 - 1089:	EEEEEEEEEEEEEEEEEEEE
1071 - 1090:	EEEEEEEEEEEEEEEEEEEE
1072 - 1091:	EEEEEEEEEEEEEEEEEEEE
1073 - 1092:	EEEEEEEEEEEEEEEEEEEE
1074 - 1093:	EEEEEEEEEEEEEEEEEEEE
1075 - 1094:	EEEEEEEEEEEEEEEEEEEE

A0A2K5S6W6 **A0A2K5S6W6_CEBIM** (1212 aa)
Euchromatic histone lysine methyltransferase 2. *Cebus imitator (Panamanian white-faced capuchin) (Cebus capucinus imitator)*

```
MAAAAGAAAAAAAEGEAPAEMGALLLEKETRGATERVHGSLGDTSRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGAD
TPVGTTPLIGDEPENLEGDGDLHGGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGT
AAAGPEPPPATTSPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGSLSEEL
GSARRSGEVTLAKGDPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEE
EEEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGT
LSPNHAGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMV
LCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAG
TAAPAPPPLSQDAPGRADTSQPRYWPSASLLSLLLPQRPNARPWGAPLRTLPDPAQWGLPGGPGKVREVSGKLVRAPVLS
CSLGRRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQ
RTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHI
EVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPE
LRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCE
TSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKV
RLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPN
IIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPEL
LPELSSLPPVNT
```

300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE

A0A2K5S6Z0 **A0A2K5S6Z0_CEBIM** (1223 aa)
Euchromatic histone lysine methyltransferase 2. *Cebus imitator (Panamanian white-faced capuchin) (Cebus capucinus imitator)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGA
LLLEKETRGATERVHGSLGDTSRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGTTPLIGDEPENLEGDGDLH
GGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGTAAAGPEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGSLSEELGSARRSGEVTLAKGDPGSLEEWE
TVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRVRDGEDPPG
VPVGEVQGLPQLLFSSVQGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRE
TMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVT
IPRGDGVTPPAGTAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGP
GREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQA
GANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWT
PIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCV
LLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCP
EDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNC
KNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNI
SRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQS
RLARLDPHPELLPELSSLPPVNT
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE

360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE

A0A2K5S6Z5 **A0A2K5S6Z5_CEBIM** (1268 aa)
Euchromatic histone lysine methyltransferase 2. *Cebus imitator (Panamanian white-faced capuchin) (Cebus capucinus imitator)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGA
LLLEKETRGATERVHGSLGDTSRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGTTPLIGDEPENLEGDGDLH
GGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGTAAAGPEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGSLSEELGSARRSGEVTLAKGDPGSLEEWE
TVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKA
KKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEE
LPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCT
AGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLSQDAPGRADTSQPS
ARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGE
LQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGG
CVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICL
HWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQ
LNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSS
SNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGT
FICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSR
DIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELSSLPPVNT
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE

A0A2K5S6Z7 **A0A2K5S6Z7_CEBIM** (1234 aa)
Euchromatic histone lysine methyltransferase 2. *Cebus imitator (Panamanian white-faced capuchin) (Cebus capucinus imitator)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGA
LLLEKETRGATERVHGSLGDTSRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGTTPLIGDEPENLEGDGDLH
GGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGTAAAGPEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGSLSEELGSARRSGEVTLAKGDPGSLEEWE
TVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKA
KKKWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGEL
SGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHC
GEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGG
CLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKG
SVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQV
DVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLH
IAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIP
CVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFE
CNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEV
YCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCK
HSAEAIALEQSRLARLDPHPELLPELSSLPPVNT
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE

A0A2K5SGG4 **A0A2K5SGG4_CEBIM** (1312 aa)
SR-related CTD associated factor 1. *Cebus imitator (Panamanian white-faced capuchin) (Cebus capucinus imitator)*

```
MEEEDESRGKTEESGEDRGDGPPDRDPTLSPSAFILRAIQQAVGSSLQGDLPNDKDGSRCHGLRWRHCRSPRSEPRSQES
GGTDTATVLDMAADSFLAGLVSVLDPPDTWVPSRLDLRPGESEDMLELVAEVRIGDRDPIPLPVPSLLPRLRAWRTGKTV
SPQSNSSRPTCARHLTLGTGDGGPAPPPAPSSASSSPSPSPSSSSPSPPPPPPPPAPPAPPAPRFDIYDPFHPTDEAYSP
PPAPEQKYDPFEPTGSNPSSSAGTPSPEEEEEEEEEEEEEEEEEEEEEGLSQSISRISETLAGIYDENSLSQDFPGDESP
RPDPQPTQPTTAPGTPPQADSTRADGATRRRVFVVGTEAEACREGKVSVEVVTAGGAAHPPPLLPPGDSEIEEGEIVQPE
EEPRVALSLFRSSGRATRPPPAASAAPAAQPLPQPPAPRAPEGDDFLSLHAESDGEGALQVDLGEPAPAPPAADSRWGGL
DLRRKILTQRRERYRQRSPSPAPAPAPAAAVGPPTRKKSRRERKRSGEAKEVASSSSATQSAPPAPASPWDSKKHRSRDR
KPGSHTSSSARRRSRSRSRSRSARRRSRSTDRRRGGSRRSRSREKRRRRRRSASPPPATSSSSSSRRERHRGKHREGGGS
KKKKKRSRSRGEKRSGDGNEKAPAPAPPPSGSTSGGDRDSRRRGAVPPSIQDLTDHDLFAIKRTITVGRLDKSDPRGPSP
APASSPKREVLYDSEGLSGEERGGKSSQKDRRRSGAASSSSSSREKGSRRKALDGGDRDRDRDRDRDRDRSSKKARPPKE
SAPSSGPPPKPPVSSGSGSSSSSSSCSSRKVKLQSKVAVLIREGVSSTTPAKDAASAGLGSIGVKFSRDRESRSPFLKPD
ERAPTEMAKAAPGSTKPKKTKVKAKAGAKKAKGTKGKTKPSKTRKKVRSGGGSGGSGGPVSLKKSKADSCSQAAGTKGAE
ETSWSGEERAAKVPSTPPPKVAPPPPALTPDSQTVDSSCKTPEVSFLPEEATEEAGVRGGAEEEEEEEEEEEEEEEEEEQ
QPATTTATSTAAAAPSTAPSAGSTAGDSGAEDGPASRVSQLPTLPPPMPWNLPAGVDCTTSGVLALTALLFKMEEANLAS
RAKAQELIQATNQILSHRKPPSSLGVTPAPVPTSLGLPPGPSSYLLPGSLPLGGCGSTPPTPTGLAATSDKREGSSSSEG
RGDTDKYLKKLHTQERAVEEVKLAIKPYYQKKDITKEEYKDILRKAVHKICHSKSGEINPVKVSNLVRAYVQRYRYFRKH
GRKPGDPPGPPRQPKEPGPPDKGGPGLPLPPL
```

268 - 287:	EEEEEEEEEEEEEEEEEEEE
269 - 288:	EEEEEEEEEEEEEEEEEEEE

A0A2K5SHN5 **A0A2K5SHN5_CEBIM** (1163 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Cebus imitator (Panamanian white-faced capuchin) (Cebus capucinus imitator)*

```
PPPSPLPLPTRRPSQCVCVIVPRHAITGARGKMAAAVLSGPTAGSAAGVPGGTGGLSAVSSGPRLRLLLLESVSGLLQPR
TGSAVAPVHPPNRSAPHLPGLMCLLRLHGSVGGAQNLSAVGALVNLSNARLSSIKTRFEGLCLLSLLVGESPTELFQQHC
VSWLRSIQQVLQSQDPPPTMELAVAVLRDLLRYAAQLPALFRDISMNHLPGLLTSLLGLRPECEQSALEGMKACMTYFPR
ACGSLKGKLASFFLSRVDALSPQLQQLACECYSRLPSLGAGFSQGLKHTESWEQELHSLLASLHTLLGALYEGAETAPVQ
NEGPGVEMLLSSEDGDAHVLLRLRQRFSGLARCLGLMLSSEFGAPVSVPVQEILDFICRTLSVSSKNISLHGDGPLRLLL
LPSIHLEALDLLSALILACGSRLLRFGILISRLLPQILNSWSIGRDSLSPGQERPYSTVRTKVYAVLELWVQVCGASAGV
LQGGASGEALLTHLLSDISPPADALKLRSPRGSPDGGLQTGKPSAPKKLKLDVGEAMAPPSHRKGDSNANSDVCAAALRG
LSRTILMCGPLIKEETHRRLHDLVLPLVMGVQQGEVLGSSPYTSSRCRRELYCLLLALLLAPSPRCPPPLACALQAFSLG
QREDSLEVSSFCSEALVTCAALTHPRVPPLQSMGPTCPTPAPVPPPETPSPFRAPPFHPPGPMPSVGPMPSAGPMPSAGP
MPSAGPVSSARPGPPTTANHLGLSVPGLVSVPPRLLPGPENHRASSNEDPILAPSGTPPPAIPPDETFGGRVPRPAFVHY
DKEEASDVEISLESDSDDSVVIVPEGLPPLPPPPPSGATPPPVAPSGPPTASPPVPAKEEPEELPAAPGPLPPPPPPPPP
VPGPVTLPPPQLVPEGTPGGGGPPALEEDLTVININSSDEEEEEEEEEEEEEEEEEEEEEEDFEEEEEDEEEYFEEEEEEE
EEFEEEFEEEEGELEEEEEEEDEDEEEEELEEVEELEFGTAGGEVEEGGPPPPTLPPALPPPESPPKVQPEPEPEPGLLL
EVEEPGAEEEHEADTAPTLAPEVLPSQGEVERDGGSPAAGLPPQELVEEEPSAPPTLLEEGTEDGGDKVQLPPETSAEEE
METETEAEALQEKEQDDTAAMLADFIDCPPDDEKPPPATEPDS
```

920 - 939:	EEEEEEEEEEEEEEEEEEEE
921 - 940:	EEEEEEEEEEEEEEEEEEEE

A0A2K5U1C5 **A0A2K5U1C5_MACFA** (906 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Macaca fascicularis (Crab-eating macaque) (Cynomolgus monkey)*

```
MELAVAVLRDLLRYAAQLPALFRDISMNHLPGLLTSLLGLRPECEQSALEGMKACMTYFPRACGSLKGKLASFFLSRVDA
LSPQLQQLACECYSRLPSLGAGFSQGLKHTESWEQELHSLLASLHTLLGALYEGAETAPVQNEGPGVEMLLSSEDGDAHV
LLRLRQRFSGLARCLGLMLSSEFGAPVSVPVQEILDFICRTLSVSSKNISLHGDGPLRLLLLPSIHLEALDLLSALILAC
GSRLLRFGILISRLLPQVLNSWSIGRDSLSPGQERPYSTVRTKVYAVLELWVQVCGASAGMLQGGASGEALLTHLLSDIS
PPADALKLRSPRGSPDGSLQTGKPSAPKKLKLDVGEAMAPPSHRKGDSNANSDVCAAALKGLSRTILMCGPLIKEETHRR
LHDLVLPLVMGVQQGEVLGSSPYTSSRCRRELYCLLLALLLAPSPRCPPPLACALQAFSLGQREDSLEVSSFCSEALVTC
AALTHPRVPPLQPMGPTCPTPAPVPPPEAPSPFRAPPFHPPGPMPSVGPMPSAGPMPSAGPMPSAGPVPSARPGPPTTAN
HLGLSVSGLVSVPPRLLPGPENHRAGSNEDPILAPSGTPPPTIPPDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDS
VVIVPEGLPPLPPPPPSGATPPPIAPTGPPTASPPVPAKEEPEELPAAPGPLPPPPPPPPVPGPVTLPPPQLVPEGTPG
GGGPPALEEDLTVININSSDEEEEEEEEEEEEEEEEEEEEEEDFEEEEEDEEEYFEEEEEEEEEFEEEFEEEEGELEEEEE
EEDEEEEEELEEVEREEGSPSAGPPPQELVEEEPSAPPTLLEEGTEDGGDRVQPPPETPAEEEMETETEAEALQEKEQDD
TAAMLADFIDCPPDDEKPPPPTEPDS
```

741 - 760:	EEEEEEEEEEEEEEEEEEEE
742 - 761:	EEEEEEEEEEEEEEEEEEEE

A0A2K5U1C9 **A0A2K5U1C9_MACFA** (1180 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Macaca fascicularis (Crab-eating macaque) (Cynomolgus monkey)*

```
MLLPSLSPRVQPAFIQCAGPQPPPHAHSPVGGRRGVFTSSRHATTGARGKMAAAVLSGSSAGSAAGVPGGTGGLSAVNSG
PRLRLLLLESVSGLLQPRTGSAVAPVHPPNRSAPHLPGLMCLLRLHGSVGGAQNLSALGALVSLSNARLSSIKTRFEGLC
LLSLLVGESPTELFQQHCVSWLRSIQQVLQTQDPPATMELAVAVLRDLLRYAAQLPALFRDISMNHLPGLLTSLLGLRPE
CEQSALEGMKACMTYFPRACGSLKGKLASFFLSRVDALSPQLQQLACECYSRLPSLGAGFSQGLKHTESWEQELHSLLAS
LHTLLGALYEGAETAPVQNEGPGVEMLLSSEDGDAHVLLRLRQRFSGLARCLGLMLSSEFGAPVSVPVQEILDFICRTLS
VSSKNISLHGDGPLRLLLLPSIHLEALDLLSALILACGSRLLRFGILISRLLPQVLNSWSIGRDSLSPGQERPYSTVRTK
VYAVLELWVQVCGASAGMLQGGASGEALLTHLLSDISPPADALKLRSPRGSPDGSLQTGKPSAPKKLKLDVGEAMAPPSH
RKGDSNANSDVCAAALKGLSRTILMCGPLIKEETHRRLHDLVLPLVMGVQQGEVLGSSPYTSSRCRRELYCLLLALLLAP
SPRCPPPLACALQAFSLGQREDSLEVSSFCSEALVTCAALTHPRVPPLQPMGPTCPTPAPVPPPEAPSPFRAPPFHPPGP
MPSVGPMPSAGPMPSAGPMPSAGPVPSARPGPPTTANHLGLSVSGLVSVPPRLLPGPENHRAGSNEDPILAPSGTPPPTI
PPDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDSVVIVPEGLPPLPPPPPSGATPPPIAPTGPPTASPPVPAKEEPE
ELPAAPGPLPPPPPPPPPVPGPVTLPPPQLVPEGTPGGGGPPALEEDLTVININSSDEEEEEEEEEEEEEEEEEEEEEDF
```

```
EEEEEDEEEYFEEEEEEEEEFEEEFEEEEGELEEEEEEEDEEEEEELEEVEELEFGTAGGEVEEGGPPPPTLPPALPPPE
SPPKVQPEPEPEPGLLLEVEEPGAEEEHGADTAPTLAPEVLPSQGEVEREEGSPSAGPPPQELVEEEPSAPPTLLEEGTE
DGGDRVQPPPETPAEEEMETETEAEALQEKEQDDTAAMLADFIDCPPDDEKPPPPTEPDS
```

938 - 957:	EEEEEEEEEEEEEEEEEEEE
939 - 958:	EEEEEEEEEEEEEEEEEEEE

A0A2K5UUM0 **A0A2K5UUM0_MACFA** (381 aa)
Stimulated by retinoic acid 8. *Macaca fascicularis (Crab-eating macaque) (Cynomolgus monkey)*

```
MATPEESSNAHDRATPQLPAQLQELEHRVARRRLSQARHRATLAALFNNLRRTVYSQSDLTASKWQVLNKAKSHIPELEQ
TLDNLLKLKASFNLEDGHASSLEEVKKEYASMYSGNDSLLSNSFSQNGSSPWCPIEAVRKDAEEGEDGEEEDQEEEEEEE
EEEEEEEEEEEEEEEEEEEEKKVLLYSPGTLSPDLMEFERYLNFYKQTMDLLTGSGIITPQEAALPIVSAAISHLWQNLS
EERKASLRQAWAQKHRGPASLAEACREPACAEGSVKDSGVDSQGASCSLVSTPEEILFEDAFDVASFLDKSEVPSTSSSS
SMLASCNPENPEDKFQLYMQIIDFFKGLSCANTQVKQEASFPVDEEMIMLQCTETFDDEDL
```

154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE

A0A2K5UZ42 **A0A2K5UZ42_MACFA** (736 aa)
YTH domain containing 1. *Macaca fascicularis (Crab-eating macaque) (Cynomolgus monkey)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSN
NKRIVSTKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEE
EEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSA
SESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVIL
IFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQE
IELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQ
RPGYLKDPRYQEVDSFTNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQ
AHPPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERER
LCDRDRDRGERGRYRR
```

230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE

A0A2K5UZA9 **A0A2K5UZA9_MACFA** (710 aa)
YTH domain containing 1. *Macaca fascicularis (Crab-eating macaque) (Cynomolgus monkey)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSN
NKRIVSTKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEE
EEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSA
SESYADQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVILIFSVRESGKFQGFARLSS
ESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLLFPPDES
IDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQRPGYLKDPRYQEVDRRFS
GVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHHPVPHEARYRDKRVHDYD
MRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDRGERGRYRR
```

230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE

A0A2K5V104 **A0A2K5V104_MACFA** (1189 aa)
Euchromatic histone lysine methyltransferase 2. *Macaca fascicularis (Crab-eating macaque) (Cynomolgus monkey)*

```
MGALLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDESENLEGDG
DLHGGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGPEPPPATTSPEGQPKV
HRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEELGSARRSEVTLAKGDSGSLEE
WETVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRK
AKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFE
ELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFC
TAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGAAAPAPPPLSQDAPGRADTSQP
SARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQG
ELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRG
GCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENIC
LHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFAL
QLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGESCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCS
SSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQG
TFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSS
```

RDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNT

279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE

A0A2K5V121 **A0A2K5V121_MACFA** (1222 aa)
Euchromatic histone lysine methyltransferase 2. *Macaca fascicularis (Crab-eating macaque) (Cynomolgus monkey)*

MRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGALLLEKETRGA
TERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDESENLEGDGDLHGGRILLGHAT
KSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGPEPPPATTSPEGQPKVHRARKTMSKPGNG
QPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEELGSARRSEVTLAKGDSGSLEEWETVVGDDFSLYY
DSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVK
PSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRET
MRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTI
PRGDGVTPPAGAAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPG
REALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAG
ANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTP
IIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVL
LFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGESCPE
DYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCK
NRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNIS
RFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSR
LARLDPHPELLPELGSLPPVNT

346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE

A0A2K5V133 **A0A2K5V133_MACFA** (1256 aa)
Euchromatic histone lysine methyltransferase 2. *Macaca fascicularis (Crab-eating macaque) (Cynomolgus monkey)*

MRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGALLLEKETRGA
TERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDESENLEGDGDLHGGRILLGHAT
KSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGPEPPPATTSPEGQPKVHRARKTMSKPGNG
QPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEELGSARRSEVTLAKGDSGSLEEWETVVGDDFSLYY
DSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVK
PSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEELPLCSCRMEAPK
IDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFR
VAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGAAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRP
PCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNL
DPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTC
LHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIA
EVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNR
AIRTEKIICRDVARGYENVPIPCVNGVDGESCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRC
WYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISD
AEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDY
GDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNT

346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE

A0A2K5V154 **A0A2K5V154_MACFA** (1155 aa)
Euchromatic histone lysine methyltransferase 2. *Macaca fascicularis (Crab-eating macaque) (Cynomolgus monkey)*

MGALLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDESENLEGDG
DLHGGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGPEPPPATTSPEGQPKV
HRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEELGSARRSEVTLAKGDSGSLEE
WETVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRK
AKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGE
LSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPH
CGEDASEAQEVTIPRGDGVTPPAGAAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNG
GCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQK
GSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQ
VDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPL
HIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPI
PCVNGVDGESCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIF
ECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGE
VYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKC

KHSAEAIALEQSRLARLDPHPELLPELGSLPPVNT

279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE

A0A2K5V169 **A0A2K5V169_MACFA** (1221 aa)
Euchromatic histone lysine methyltransferase 2. *Macaca fascicularis (Crab-eating macaque) (Cynomolgus monkey)*

MRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGALLLEKETRGA
TERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDESENLEGDGDLHGGRILLGHAT
KSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGPEPPPATTSPEGQPKVHRARKTMSKPGNG
QPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEELGSARRSEVTLAKGDSGSLEEWETVVGDDFSLYY
DSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVK
PSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEELPLCSCRMEAPK
IDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFR
VAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGAAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRP
PCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNL
DPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTC
LHHAAKIGNLEMVSLLLSTGQVDVNAQEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLL
FLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGESCPED
YKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKN
RVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISR
FINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRL
ARLDPHPELLPELGSLPPVNT

346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE

A0A2K5VYG0 **A0A2K5VYG0_MACFA** (1454 aa)
Shroom family member 4. *Macaca fascicularis (Crab-eating macaque) (Cynomolgus monkey)*

MENRPGSFQYVPVQLQGGAPWGFTLKGGLEHCEPLTVSKIEDGGKAALSQKMRTGDELVNINGTPLYGSRQEALILIKGS
FRILKLIVRSDVCVQWCPLSRHCSTEKSSSIGSMESLEQPGQATYESHLLPIDQNMYPNQRDSAYSSFSASSNASDCALS
LRPEEAASTDCIMQGPGPTKAPNGRPNVAETSGGSRRTNGGHLTPSSQMSSRPQEGHQSGPAKAVRGPPQPPVRRDSLQA
SRAQLLNGEQRRASEPVVPLPQKEKLSLETVLPARNPNRFCCLSGHDQVTSEGHQNCEFSQPPESSQQGSEHLLMQASTK
AVGSPKACDKASSTDSNPLNEASAELAKASFGRPPHLIGPTGHRHSAPEQLLASHLQHVHLDTRGSKGMELPPGQDGQQW
TLSPLHSSHKGKKSPCPPAGGTHDQSSKERKTRQMDDRSLVLGHQSQSSPPHGEADGHPSEKGLLDPNRTSRAGNELANQ
QPSASGSLVQKARDCSSTTKVAGGTEAGEEGDSEHKECSRMGGRRSGGTRGRSIQNRRKSERFATNLRNEIQRRKAQLQK
SKGPLSQLCDTKEPVEETQEPPESPPLTASNTSLLSSCKKPPSPRDKLFNKSMMLRARSSECLSQAPESHESRTGLEGRI
SPGQRLGQSSLVLNTWWKAPDPSSSDPEKAHAHCGVHGGHWRWSREHNSQPLVAVAMEGPSNPGDNKELKASTAQAGEDA
VLLPFADRRKFFEESSKSLSTSHLPGLTTHSNKTFTQRPKPIDQNFQPVSSNYRELRRHPMDQSYHSADQPYHATDQSYH
SMSPLQSETPTYSECFASRGLENSMCCKPLHCGDFDYHRTCSYSCSVQGALVHDPCIYCSGEICPALLKRNMIPNCYNCR
CHHHQCIRCSVCYHNPQHSTLEDSSLAPGNTWKPRKPTVQEFPGDKWNPITGNRKTSQSGREMAHSKNSFSWATPFHPCL
ENPALDLSSYRAISSLDLLGDFKHALKKSEETSVYEEGSSLASMPHPLRSRAFSESHISLDPQSTRAWGQHRRELFSKGD
ETQSDLLGARKKAFPPPRPPPPNWEKYRLFRAAQQQKQQQQQQQQQQKQQEEEEEEEEEEEEEEEEEEEEEEAEEEEEEL
PPQYFSSETSGSCALNPEEVLEQPQPLSLGHLEGSGQGSQSVPAEQESFALHSSDFLPPIRGHLGSQPEQAQPPCYYGIG
GLWRTSEQEAAESAKQEFQPFSPPPGAPAIPTSYSAYYNISVAKAELLNKLKDQPEMAEIGLGEEEVDHELAQKKIQLIE
SISRKLSVLREAQRGLLEDINANSALGEEVEANLKAVCKSNEFEKYRSFVGDLDKVVNLLLSLSGRLARVENALNSIDSE
ANQEKLVLIEKKQQLTGQLADAKELKEHVDRREKLVFGMVSRYLPQDQLQDYQHFVKMKSALIIEQRELEEKIKLGEEQL
KCLRESLLLGPSNF

1091 - 1110:	EEEEEEEEEEEEEEEEEEEE
1092 - 1111:	EEEEEEEEEEEEEEEEEEEE
1093 - 1112:	EEEEEEEEEEEEEEEEEEEE

A0A2K5VYH9 **A0A2K5VYH9_MACFA** (1499 aa)
Shroom family member 4. *Macaca fascicularis (Crab-eating macaque) (Cynomolgus monkey)*

MENRPGSFQYVPVQLQGGAPWGFTLKGGLEHCEPLTVSKIEDGGKAALSQKMRTGDELVNINGTPLYGSRQEALILIKGS
FRILKLIVRRRNAPVSRPHSWHVAKLLEGCPEAATTMHFPSEAFSLSWHSGCNTSDVCVQWCPLSRHCSTEKSSSIGSME
SLEQPGQATYESHLLPIDQNMYPNQRDSAYSSFSASSNASDCALSLRPEEAASTDCIMQGPGPTKAPNGRPNVAETSGGS
RRTNGGHLTPSSQMSSRPQEGHQSGPAKAVRGPPQPPVRRDSLQASRAQLLNGEQRRASEPVVPLPQKEKLSLETVLPAR
NPNRFCCLSGHDQVTSEGHQNCEFSQPPESSQQGSEHLLMQASTKAVGSPKACDKASSTDSNPLNEASAELAKASFGRPP
HLIGPTGHRHSAPEQLLASHLQHVHLDTRGSKGMELPPGQDGQQWTLSPLHSSHKGKKSPCPPAGGTHDQSSKERKTRQM
DDRSLVLGHQSQSSPPHGEADGHPSEKGLLDPNRTSRAGNELANQQPSASGSLVQKARDCSSTTKVAGGTEAGEEGDSEH
KECSRMGGRRSGGTRGRSIQNRRKSERFATNLRNEIQRRKAQLQKSKGPLSQLCDTKEPVEETQEPPESPPLTASNTSLL
SSCKKPPSPRDKLFNKSMMLRARSSECLSQAPESHESRTGLEGRISPGQRLGQSSLVLNTWWKAPDPSSSDPEKAHAHCG
VHGGHWRWSREHNSQPLVAVAMEGPSNPGDNKELKASTAQAGEDAVLLPFADRRKFFEESSKSLSTSHLPGLTTHSNKTF
TQRPKPIDQNFQPVSSNYRELRRHPMDQSYHSADQPYHATDQSYHSMSPLQSETPTYSECFASRGLENSMCCKPLHCGDF
DYHRTCSYSCSVQGALVHDPCIYCSGEICPALLKRNMIPNCYNCRCHHHQCIRCSVCYHNPQHSTLEDSSLAPGNTWKPR
KPTVQEFPGDKWNPITGNRKTSQSGREMAHSKNSFSWATPFHPCLENPALDLSSYRAISSLDLLGDFKHALKKSEETSVY
EEGSSLASMPHPLRSRAFSESHISLDPQSTRAWGQHRRELFSKGDETQSDLLGARKKAFPPPRPPPPNWEKYRLFRAAQQ
QKQQQQQQQQQQKQQEEEEEEEEEEEEEEEEEEEEEEEAEEEEEELPPQYFSSETSGSCALNPEEVLEQPQPLSLGHLEGS

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GQGSQSVPAEQESFALHSSDFLPPIRGHLGSQPEQAQPPCYYGIGGLWRTSEQEAAESAKQEFQPFSPPPGAPAIPTSYS
AYYNISVAKAELLNKLKDQPEMAEIGLGEEEVDHELAQKKIQLIESISRKLSVLREAQRGLLEDINANSALGEEVEANLK
AVCKSNEFEKYRSFVGDLDKVVNLLLSLSGRLARVENALNSIDSEANQEKLVLIEKKQQLTGQLADAKELKEHVDRREKL
VFGMVSRYLPQDQLQDYQHFVKMKSALIIEQRELEEKIKLGEEQLKCLRESLLLGPSNF
```

1136 - 1155:	EEEEEEEEEEEEEEEEEEEE
1137 - 1156:	EEEEEEEEEEEEEEEEEEEE
1138 - 1157:	EEEEEEEEEEEEEEEEEEEE

A0A2K5W265 **A0A2K5W265_MACFA** (641 aa)
Ran GTPase activating protein 1. *Macaca fascicularis (Crab-eating macaque) (Cynomolgus monkey)*

```
MGLPRRPPVICGLYSRVAPAAPPPSRPTPTGGPGWRRCPWNRFCRSPGEPTSLVSMASEDIAKLAETLAKTQVAGGQLSF
KGKSLKLNTAEDAKDVIKEIEDFDSLEALRLEGNTVGVEAARVIAKALEKKSELKRCHWSDMFTGRLRTEIPPALISLGE
GLITAGAQLVELDLSDNAFGPDGVQGFEALLKSSACFTLHELKLNNCGMGIGGGKILAAALTECHRKSSAQGKPLALKVF
VAGRNRLENDGATALAEAFRVIGTLEEVHMPQNGINHPGVTALAQAFAVNPLLRIINLNDNTFTEKGAVAMAETLKTLRQ
VEVINFGDCLVRSKGAVAIADAIRGGLPKLKELNLSFCEIKRDAALAVAEAMADKTELEKLDLNGNTLGEEGCEQLQEVL
EGFNMAKVLASLSDDEDEEEEEGEEEEEAEEEEEEEEEEEEEEEEEEEEEEEPQQGGQGEKSATPSQKILDPNTGEPAPVL
SSPPPADVSTFLAFPSPEKLLRLGPKSSMLIAQQTDTSDPEKVVSAFLKVSSVFKDEATVRTAVQDAVDALMKKAFSSSS
FNSSAFLTRLLAHMGLLKSEDKVKAIANLYGPLMALNHMVQQDYFPKALAPLLLAFITKPNSALESCSFARHSLLQTLYK
V
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430 - 449:	EEEEEEEEEEEEEEEEEEEE
431 - 450:	EEEEEEEEEEEEEEEEEEEE
432 - 451:	EEEEEEEEEEEEEEEEEEEE

A0A2K5YCH6 **A0A2K5YCH6_MANLE** (586 aa)
Ran GTPase activating protein 1. *Mandrillus leucophaeus (Drill) (Papio leucophaeus)*

```
MASEDIAKLAETLAKTQVAGGQLSFKGKSLKLNTAEDAKDVIKEIEDFDSLEALRLEGNTVGVEAARVIAKALEKKSELK
RCHWSDMFTGRLRTEIPPALISLGEGLITAGAQLVELDLSDNAFGPDGVQGFEALLKSSACFTLHELKLNNCGMGIGGGK
ILAAALTECHRKSSAQGKPLALKVFVAGRNRLENDGATALAEAFRVIGTLEEVHMPQNGINHPGVTALAQAFAVNPLLRV
INLNDNTFTEKGAVAMAETLKTLRQVEVINFGDCLVRSKGAVAIADAIRGGLPKLKELNLSFCEIKRDAALAVAEAMADK
TELEKLDLNGNTLGEEGCEQLQEVLEGFNMAKVLASLSDDEDEEEEEGEEEEEAEEEEEEEEEEEEEEEEEEEEEEPQQG
GQGEKSATPSQKILDPNTGEPAPVLSPPPPADASTFLAFPSPEKLLRLGPKSSMLIAQQTDTSDPEKVVSAFLKVSSVFK
DEATVRTAVQDAVDALMKKAFSSSSFNSSAFLTRLLAHMGLLKSEDKVKAIANLYGPLMALNHMVQQDYFPKALAPLLLA
FITKPNSALESCSFARHSLLQTLYKV
```

375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE

A0A2K5YCH9 **A0A2K5YCH9_MANLE** (639 aa)
Ran GTPase activating protein 1. *Mandrillus leucophaeus (Drill) (Papio leucophaeus)*

```
MGLPRRPPVICGLYSRVAPAAPPPSRPTPTGGPGWRRCPWNRCESMHLTSEISMASEDIAKLAETLAKTQVAGGQLSFKG
KSLKLNTAEDAKDVIKEIEDFDSLEALRLEGNTVGVEAARVIAKALEKKSELKRCHWSDMFTGRLRTEIPPALISLGEGL
ITAGAQLVELDLSDNAFGPDGVQGFEALLKSSACFTLHELKLNNCGMGIGGGKILAAALTECHRKSSAQGKPLALKVFVA
GRNRLENDGATALAEAFRVIGTLEEVHMPQNGINHPGVTALAQAFAVNPLLRVINLNDNTFTEKGAVAMAETLKTLRQVE
VINFGDCLVRSKGAVAIADAIRGGLPKLKELNLSFCEIKRDAALAVAEAMADKTELEKLDLNGNTLGEEGCEQLQEVLEG
FNMAKVLASLSDDEDEEEEEGEEEEEAEEEEEEEEEEEEEEEEEEEEEEEEPQQGGQGEKSATPSQKILDPNTGEPAPVLSP
PPPADASTFLAFPSPEKLLRLGPKSSMLIAQQTDTSDPEKVVSAFLKVSSVFKDEATVRTAVQDAVDALMKKAFSSSSFN
SSAFLTRLLAHMGLLKSEDKVKAIANLYGPLMALNHMVQQDYFPKALAPLLLAFITKPNSALESCSFARHSLLQTLYKV
```

428 - 447:	EEEEEEEEEEEEEEEEEEEE
429 - 448:	EEEEEEEEEEEEEEEEEEEE
430 - 449:	EEEEEEEEEEEEEEEEEEEE

A0A2K5ZPH3 **A0A2K5ZPH3_MANLE** (1098 aa)
Solute carrier family 24 member 1. *Mandrillus leucophaeus (Drill) (Papio leucophaeus)*

```
MGKLIRMGPQDRRLLRTKRLPWSRLLFLLGMLIISSTYQHLRGPRGLSSLWAAVSSHQPVKLASRDLPSEEMMMVSSNPP
KPNSEMGGEMLVPQASVGSDEATLSVTVENIPDIPKRTAKMIPTTTKNNYSPTAAGTERRKEDTPTSSRTLTYYTSTSSR
QIVKKYTPTPTGEMKSYSPTQVREKVKYTPSPRGRRVGTYASSTFMTTETSHAITPRTTVKDSDITTTYKILETNSLKRI
MEETTPTTLKGMVDSTPTFLTHEVETNVLTSPRSIVEKNNLSPPRRVESNSSAHPSGLVGKNNLKTPQGTVLTHTPATSE
GQVTISTMTGSNPSETKAFTAAWSVRNPSLRTSVSAIETAPTTVWRLAKKPYTAPSTSTTPTVRAKPTTQVHHCVVVKPT
PAMPTTPSPSLTTALLPEELSPSPSVLPPILPDLPPKGEYPPDLFSVEERRQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLIMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKQIEAWVKEQLSRRPAAKVMALGDLSKPGDGAIAVDE
LQDNKKLKLPSLLTRGSSSTSLHNSTIRSTIYQLMLHSLDPLREVCLAEEKEEESLNQEARAQPQAKSESKPEDEESAKL
PAVTVTPAPAPDIKGDQKENPGGQEDVAEAESTGEMTGEEGETAGERETEEKSGGETQPEGEGETGTQGKGEEREKENEA
EGKGDNEGEGEGEIHAEDGEMKGIEGETESQELSAENHGEAKSDEKGVEDGGGSDGGDNEEEEEEEEEEEEEEEEEEEEE
EEEEEEGEEEGNEEPLSLHWPETRQKQAIYLFLLPIVFPLWLTVPDVRRQESRKFFVFTFLGSIVWIAMFSYLMVWWAHQ
VGETIGISEEIMGLTILAAGTSIPDLITSVIVARKGLGDMAVSSSVGSNIFDITVGLPVPWLLFCLINGLQPVPVSSNGL
FCAIVLLFLMLLFVISSIASCKWRMNKILGFTMFLLYFVFLIISVMLEDRIISCPVSV
```

860 - 879:	EEEEEEEEEEEEEEEEEEEE
861 - 880:	EEEEEEEEEEEEEEEEEEEE
862 - 881:	EEEEEEEEEEEEEEEEEEEE
863 - 882:	EEEEEEEEEEEEEEEEEEEE
864 - 883:	EEEEEEEEEEEEEEEEEEEE
865 - 884:	EEEEEEEEEEEEEEEEEEEE
866 - 885:	EEEEEEEEEEEEEEEEEEEE
867 - 886:	EEEEEEEEEEEEEEEEEEEE

A0A2K5ZPJ1 **A0A2K5ZPJ1_MANLE** (1011 aa)
Solute carrier family 24 member 1. *Mandrillus leucophaeus (Drill) (Papio leucophaeus)*

```
MGKLIRMGPQDRRLLRTKRLPWSRLLFLLGMLIISSTYQHLRGPRGLSSLWAAVSSHQPVKLASRDLPSEEMMMVSSNPP
KPNSEMGGEMLVPQASVGSDEATLSVTVENIPDIPKRTAKMIPTTTKNNYSPTAAGTERRKEDTPTSSRTLTYYTSTSSR
QIVKKYTPTPTGEMKSYSPTQVREKVKYTPSPRGRRVGTYASSTFMTTETSHAITPRTTVKDSDITTTYKILETNSLKRI
MEETTPTTLKGMVDSTPTFLTHEVETNVLTSPRSIVEKNNLSPPRRVESNSSAHPSGLVGKNNLKTPQGTVLTHTPATSE
GQVTISTMTGSNPSETKAFTAAWSVRNPSLRTSVSAIETAPTTVWRLAKKPYTAPSTSTTPTVRAKPTTQVHHCVVVKPT
PAMPTTPSPSLTTALLPEELSPSPSVLPPILPDLPPKGEYPPDLFSVEERRQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLIMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKQIEAWVKEQLSRRPAAKVMALGDLSKLPSLLTRGSS
STSLHNSTIRSTIYQLMLHSLDPLREVCLAEEKEEESLNQEARAQPQAKSESKPEDEESAKLPAVTVTPAPAPDIKGDQK
ENPGGQEDVAEAESTGEMTGEEGETAGERETEEKSGGETQPEGEGETGTQGKGEEREKENEAEGKGDNEGEGEGEIHAED
GEMKGIEGETESQELSAENHGEAKSDEKGVEDGGGSDGGDNEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEGNEEPLSL
HWPETRQKQAIYLFLLPIVFPLWLTVPDVRRQESRKFFVFTFLGSIVWIAMFSYLMVWWAHQVGETIGISEEIMGLTILA
AGTSIPDLITSVIVARKGLGDMAVSSSVGSNIFDITVGVESCEMFQLGAIH
```

842 - 861:	EEEEEEEEEEEEEEEEEEEE
843 - 862:	EEEEEEEEEEEEEEEEEEEE
844 - 863:	EEEEEEEEEEEEEEEEEEEE
845 - 864:	EEEEEEEEEEEEEEEEEEEE
846 - 865:	EEEEEEEEEEEEEEEEEEEE
847 - 866:	EEEEEEEEEEEEEEEEEEEE
848 - 867:	EEEEEEEEEEEEEEEEEEEE
849 - 868:	EEEEEEEEEEEEEEEEEEEE

A0A2K5ZPK6 **A0A2K5ZPK6_MANLE** (1080 aa)
Solute carrier family 24 member 1. *Mandrillus leucophaeus (Drill) (Papio leucophaeus)*

```
MGKLIRMGPQDRRLLRTKRLPWSRLLFLLGMLIISSTYQHLRGPRGLSSLWAAVSSHQPVKLASRDLPSEEMMMVSSNPP
KPNSEMGGEMLVPQASVGSDEATLSVTVENIPDIPKRTAKMIPTTTKNNYSPTAAGTERRKEDTPTSSRTLTYYTSTSSR
QIVKKYTPTPTGEMKSYSPTQVREKVKYTPSPRGRRVGTYASSTFMTTETSHAITPRTTVKDSDITTTYKILETNSLKRI
MEETTPTTLKGMVDSTPTFLTHEVETNVLTSPRSIVEKNNLSPPRRVESNSSAHPSGLVGKNNLKTPQGTVLTHTPATSE
GQVTISTMTGSNPSETKAFTAAWSVRNPSLRTSVSAIETAPTTVWRLAKKPYTAPSTSTTPTVRAKPTTQVHHCVVVKPT
PAMPTTPSPSLTTALLPEELSPSPSVLPPILPDLPPKGEYPPDLFSVEERRQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLIMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKQIEAWVKEQLSRRPAAKVMALGDLSKLPSLLTRGSS
STSLHNSTIRSTIYQLMLHSLDPLREVCLAEEKEEESLNQEARAQPQAKSESKPEDEESAKLPAVTVTPAPAPDIKGDQK
ENPGGQEDVAEAESTGEMTGEEGETAGERETEEKSGGETQPEGEGETGTQGKGEEREKENEAEGKGDNEGEGEGEIHAED
GEMKGIEGETESQELSAENHGEAKSDEKGVEDGGGSDGGDNEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEGNEEPLSL
HWPETRQKQAIYLFLLPIVFPLWLTVPDVRRQESRKFFVFTFLGSIVWIAMFSYLMVWWAHQVGETIGISEEIMGLTILA
AGTSIPDLITSVIVARKGLGDMAVSSSVGSNIFDITVGLPVPWLLFCLINGLQPVPVSSNGLFCAIVLLFLMLLFVISSI
ASCKWRMNKILGFTMFLLYFVFLIISVMLEDRIISCPVSV
```

842 - 861:	EEEEEEEEEEEEEEEEEEEE
843 - 862:	EEEEEEEEEEEEEEEEEEEE
844 - 863:	EEEEEEEEEEEEEEEEEEEE
845 - 864:	EEEEEEEEEEEEEEEEEEEE
846 - 865:	EEEEEEEEEEEEEEEEEEEE
847 - 866:	EEEEEEEEEEEEEEEEEEEE
848 - 867:	EEEEEEEEEEEEEEEEEEEE
849 - 868:	EEEEEEEEEEEEEEEEEEEE

A0A2K5ZPK8 **A0A2K5ZPK8_MANLE** (984 aa)
Solute carrier family 24 member 1. *Mandrillus leucophaeus (Drill) (Papio leucophaeus)*

```
MGKLIRMGPQDRRLLRTKRLPWSRLLFLLGMLIISSTYQHLRGPRGLSSLWAAVSSHQPVKLASRDLPSEEMMMVSSNPP
KPNSEMGGEMLVPQASVGSDEATLSVTVENIPDIPKRTAKMIPTTTKNNYSPTAAGTERRKEDTPTSSRTLTYYTSTSSR
QIVKKYTPTPTGEMKSYSPTQVREKVKYTPSPRGRRVGTYASSTFMTTETSHAITPRTTVKDSDITTTYKILETNSLKRI
MEETTPTTLKGMVDSTPTFLTHEVETNVLTSPRSIVEKNNLSPPRRVESNSSAHPSGLVGKNNLKTPQGTVLTHTPATSE
GQVTISTMTGSNPSETKAFTAAWSVRNPSLRTSVSAIETAPTTVWRLAKKPYTAPSTSTTPTVRAKPTTQVHHCVVVKPT
```

```
PAMPTTPSPSLTTALLPEELSPSPSVLPPILPDLPPKGEYPPDLFSVEERRQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLIMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKQIEAWVKEQLSRRPAAKVMALGDLSKEDVAEAESTG
EMTGEEGETAGERETEEKSGGETQPEGEGETGTQGKGEEREKENEAEGKGDNEGEGEGEIHAEDGEMKGIEGETESQELS
AENHGEAKSDEKGVEDGGGSDGGDNEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEGNEEPLSLHWPETRQKQAIYLFLL
PIVFPLWLTVPDVRRQESRKFFVFTFLGSIVWIAMFSYLMVWWAHQVGETIGISEEIMGLTILAAGTSIPDLITSVIVAR
KGLGDMAVSSSVGSNIFDITVGLPVPWLLFCLINGLQPVPVSSNGLFCAIVLLFLMLLFVISSIASCKWRMNKILGFTMF
LLYFVFLIISVMLEDRIISCPVSV
```

746 - 765:	EEEEEEEEEEEEEEEEEEEE
747 - 766:	EEEEEEEEEEEEEEEEEEEE
748 - 767:	EEEEEEEEEEEEEEEEEEEE
749 - 768:	EEEEEEEEEEEEEEEEEEEE
750 - 769:	EEEEEEEEEEEEEEEEEEEE
751 - 770:	EEEEEEEEEEEEEEEEEEEE
752 - 771:	EEEEEEEEEEEEEEEEEEEE
753 - 772:	EEEEEEEEEEEEEEEEEEEE

A0A2K5ZPL1 **A0A2K5ZPL1_MANLE** (1068 aa)
Solute carrier family 24 member 1. *Mandrillus leucophaeus (Drill) (Papio leucophaeus)*

```
MGKLIRMGPQDRRLLRTKRLPWSRLLFLLGMLIISSTYQHLRGPRGLSSLWAAVSSHQPVKLASRDLPSEEMMMVSSNPP
KPNSEMGGEMLVPQASVGSDEATLSVTVENIPDIPKRTAKMIPTTTKNNYSPTAAGTERRKEDTPTSSRTLTYYTSTSSR
QIVKKYTPTPTGEMKSYSPTQVREKVKYTPSPRGRRVGTYASSTFMTTETSHAITPRTTVKDSDITTTYKILETNSLKRI
MEETTPTTLKGMVDSTPTFLTHEVETNVLTSPRSIVEKNNLSPPRRVESNSSAHPSGLVGKNNLKTPQGTVLTHTPATSE
GQVTISTMTGSNPSETKAFTAAWSVRNPSLRTSVSAIETAPTTVWRLAKKPYTAPSTSTTPTVRAKPTTQVHHCVVVKPT
PAMPTTPSPSLTTALLPEELSPSPSVLPPILPDLPPKGEYPPDLFSVEERRQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLIMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKQIEAWVKEQLSRRPAAKVMALGDLSKPGDGAIAVDE
LQDNKKLKLPSLLTRGSSSTSLHNSTIRSTIYQLMLHSLDPLREVCLAEEKEEESLNQEARAQPQAKSESKPEDEESAKL
PAVTVTPAPAPDIKGDQKENPGGQEDVAEAESTGEMTGEEGETAGERETEEKSGGETQPEGEGETGTQGKGEEREKENEA
EGKGDNEGEGEGEIHAEDGEMKGIEGETESQELSAENHGEAKSDEKGVEDGGGSDGGDNEEEEEEEEEEEEEEEEEEEE
EEEEEEGEEEGNEEPLSLHWPETRQKQAIYLFLLPIVFPLWLTVPDVRRQVGETIGISEEIMGLTILAAGTSIPDLITSV
IVARKGLGDMAVSSSVGSNIFDITVGLPVPWLLFCLINGLQPVPVSSNGLFCAIVLLFLMLLFVISSIASCKWRMNKILG
FTMFLLYFVFLIISVMLEDRIISCPVSV
```

860 - 879:	EEEEEEEEEEEEEEEEEEEE
861 - 880:	EEEEEEEEEEEEEEEEEEEE
862 - 881:	EEEEEEEEEEEEEEEEEEEE
863 - 882:	EEEEEEEEEEEEEEEEEEEE
864 - 883:	EEEEEEEEEEEEEEEEEEEE
865 - 884:	EEEEEEEEEEEEEEEEEEEE
866 - 885:	EEEEEEEEEEEEEEEEEEEE
867 - 886:	EEEEEEEEEEEEEEEEEEEE

A0A2K5ZZ41 **A0A2K5ZZ41_MANLE** (1174 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Mandrillus leucophaeus (Drill) (Papio leucophaeus)*

```
SDPPALAPQNPGITEPPPHAHSPVGGRRGVFASSRHATTGARGKMAAAVLSGPSAGSAAGVPGGTGGLSAVNSGPRLRLL
LLESVSGLLQPRTGSAVAPVHPPNRSAPHLPGLMCLLRLHGSVGGAQNLSALGALVSLSNARLSSIKTRFEGLCLLSLLV
GESPTELFQQHCVSWLRSIQQVLQTQDPPATMELAVAVLRDLLRYAAQLPALFRDISMNHLPGLLTSLLGLRPECEQSAL
EGMKACMTYFPRACGSLKGKLASFFLSRVDALSPQLQQLACECYSRLPSLGAGFSQGLKHTESWEQELHSLLASLHTLLG
ALYEGAETAPVQNEGPGVEMLLSSEDGDAHVLLRLRQRFSGLARCLGLMLSSEFGAPVSVPVQEILDFICRTLSVSSKNI
SLHGDGPLRLLLLPSIHLEALDLLSALILACGSRLLRFGILISRLLPQVLNSWSIGRDSLSPGQERPYSTVRTKVYAVLE
LWVQVCGASAGMLQGGASGEALLTHLLSDISPPADALKLRSPRGSPDGSLQTGKPSAPKKLKLDVGEAMAPPSHRKGDSN
ANSDVCAAALKGLSRTILMCGPLIKEETHRRLHDLVLPLVMGVQQGEVLGSSPYTSSRCRRELYCLLLALLLAPSPRCPP
PLACALQAFSLGQREDSLEVSSFCSEALVTCAALTHPRVPPLQPMGPTCPTPAPVPPPEAPSPFRAPPFHPPGPMPSVGP
MPSAGPMPSAGPMPSAGPVPSARPGPPTTANHLGLSVSGLVSVPPRLLPGPENHRAGSNEDPILAPSGTPPPAIPPDETF
GGRVPRPAFVHYDKEEASDVEISLESDSDDSVVIVPEGLPPLPPPPPSGATPPPIAPTGPPTASPPVPAKEEPEELPAAP
GPLPPPPPPPPPVPGPVTLPPPQLVPEGTPGGGGPPALEEDLTVININSSDEEEEEEEEEEEEEEEEEEEEEDFEEEEED
EEEYFEEEEEEEEEFEEEFEEEEGELEEEEEEEDEEEEEELEEVEELEFGTAGGEVEEGGPPPPTLPPALPPPESPPKVP
PEPEPEPGLLLEVEEPGAEEEHGADTAPTLAPEVLPSQGEVEREEGSPSAGPPPQELVEEEPSAPPTLLEEGTEDGGDRV
QPPPETSAEEEMETETEAEALQEKEQDDTAAMLADFIDCPPDDEKPPPPTEPDS
```

932 - 951:	EEEEEEEEEEEEEEEEEEEE
933 - 952:	EEEEEEEEEEEEEEEEEEEE

A0A2K5ZZ66 **A0A2K5ZZ66_MANLE** (1160 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Mandrillus leucophaeus (Drill) (Papio leucophaeus)*

```
QPPPHAHSPVGGRRGVFASSRHATTGARGKMAAAVLSGPSAGSAAGVPGGTGGLSAVNSGPRLRLLLLESVSGLLQPRTG
SAVAPVHPPNRSAPHLPGLMCLLRLHGSVGGAQNLSALGALVSLSNARLSSIKTRFEGLCLLSLLVGESPTELFQQHCVS
```

```
WLRSIQQVLQTQDPPATMELAVAVLRDLLRYAAQLPALFRDISMNHLPGLLTSLLGLRPECEQSALEGMKACMTYFPRAC
GSLKGKLASFFLSRVDALSPQLQQLACECYSRLPSLGAGFSQGLKHTESWEQELHSLLASLHTLLGALYEGAETAPVQNE
GPGVEMLLSSEDGDAHVLLRLRQRFSGLARCLGLMLSSEFGAPVSVPVQEILDFICRTLSVSSKNISLHGDGPLRLLLLP
SIHLEALDLLSALILACGSRLLRFGILISRLLPQVLNSWSIGRDSLSPGQERPYSTVRTKVYAVLELWVQVCGASAGMLQ
GGASGEALLTHLLSDISPPADALKLRSPRGSPDGSLQTGKPSAPKKLKLDVGEAMAPPSHRKGDSNANSDVCAAALKGLS
RTILMCGPLIKEETHRRLHDLVLPLVMGVQQGEVLGSSPYTSSRCRRELYCLLLALLLAPSPRCPPPLACALQAFSLGQR
EDSLEVSSFCSEALVTCAALTHPRVPPLQPMGPTCPTPAPVPPPEAPSPFRAPPFHPPGPMPSVGPMPSAGPMPSAGPMP
SAGPVPSARPGPPTTANHLGLSVSGLVSVPPRLLPGPENHRAGSNEDPILAPSGTPPPAIPPDETFGGRVPRPAFVHYDK
EEASDVEISLESDSDDSVVIVPEGLPPLPPPPPSGATPPPIAPTGPPTASPPVPAKEEPEELPAAPGPLPPPPPPPPVP
GPVTLPPPQLVPEGTPGGGGPPALEEDLTVININSSDEEEEEEEEEEEEEEEEEEEEEDFEEEEEDEEEYFEEEEEEEEE
FEEEFEEEEGELEEEEEEEDEEEEEELEEVEELEFGTAGGEVEEGGPPPPTLPPALPPPESPPKVPPEPEPEPGLLLEVE
EPGAEEEHGADTAPTLAPEVLPSQGEVEREEGSPSAGPPPQELVEEEPSAPPTLLEEGTEDGGDRVQPPPETSAEEEMET
ETEAEALQEKEQDDTAAMLADFIDCPPDDEKPPPPTEPDS
```

918 - 937:	EEEEEEEEEEEEEEEEEEEE
919 - 938:	EEEEEEEEEEEEEEEEEEEE

A0A2K6A613 **A0A2K6A613_MANLE** (1266 aa)
Euchromatic histone lysine methyltransferase 2. *Mandrillus leucophaeus (Drill) (Papio leucophaeus)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPNRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGA
LLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDESENLEGDGDLH
GGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGPEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEELGSARRSEVTLAKGDPGSLEEWET
VVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAKK
KWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEELP
LCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAG
TFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGAAAPAPPPLSQDAPGRADTSQPSAR
MRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQ
KVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCV
YSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHW
ASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLN
RKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGESCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSN
CLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFI
CEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDI
RTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE

A0A2K6A649 **A0A2K6A649_MANLE** (1216 aa)
Euchromatic histone lysine methyltransferase 2. *Mandrillus leucophaeus (Drill) (Papio leucophaeus)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPNRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGA
LLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDESENLEGDGDLH
GGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGPEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEELGSARRSEVTLAKGDPGSLEEWET
VVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRDPPGVPMGEVQ
GLPQLLFFSVQGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSR
VALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGV
TPPAGAAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEK
ALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAV
DKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAE
HKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRG
ANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGESCPEDYKYIS
ENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQS
GIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHL
CDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDP
HPELLPELGSLPPVNT
```

356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE

A0A2K6A654 **A0A2K6A654_MANLE** (1498 aa)
Shroom family member 4. *Mandrillus leucophaeus (Drill) (Papio leucophaeus)*

```
MENRPGSFQYVPVQLQGGAPWGFTLKGGLEHCEPLTVSKIEDGGKAALSQKMRTGDELVNINGTPLYGSRQEALILIKGS
FRILKLIVRRRNAPVSRPHSWHVAKLLEGCPEAATTMHFPSEAFSLSWHSGCNTSDVCVQWCPLSRHCSTEKSSSIGSME
SLEQPGQATYESHLLPIDQNMYPNQRDSAYSSFSASSNASDCALSLRPEEAASTDCIMQGPGPTKAPNGRPNVAETSGGS
RRTSGGHLTPSSQMSSRPQEGHQSGPAKAVRGPPQPPVRRDSLQASRAQLLNGEQRRASEPVVPLPQKEKLSLETVLPAG
NPNRFCCLSGHDQVTSEGHQNCEFSQPPESSQQGSEHLLMQASTKAVGSPKACDKASSTDSNPLNEASTELAKASFGRPP
HLIGPTGHRHSAPEQLLASHLQHVHLDTRGSKGMELPPGQDGHQWTLSPLHSSHKGKKSPCPPAGGTQDQSSKERKTRQM
DDRSLVLGHQSQSSPPHGEADGHPSEKGLLDPNRTSRAGNELANQQPSASGSLVQKARDCSSTTKVAGGTEAGEEGDSEH
KECSRMGGRRSGGTRGRSIQNRRKSERFATNLRNEIQRRKAQLQKSKGPLSQLCDTKEPVEETQEPPESPPLTASNTSLL
```

```
SSCKKPPSPRDKLFNKSMMLRARSSECLSQAPESHESRTGLEGRISPGQRLGQSSLVLNTWWKAPDPSSSDPEKAHAHCG
VHGGHWKWSREHNSQPLVAVAMEGPSNPGDNKELKASTAQAGEDAILLPFADRRKFFEESSKSLSTSHLPGLTTHSNKTF
TQRPKPIDQNFQPVSSNYRELRRHPMDQSYHSADQPYHATDQSYHSMSPLQSETPTYSECFASRGLENSMCCKPLHCGDF
DYHRTCSYSCSVQGALVHDPCIYCSGEICPALLKRNMMPNCYNCRCHHHQCIRCSVCYHNPQHSTLEDSSLAPGNTWKPR
KPTVQEFPGDKWNPITGNRKTSQSGREMAHSKNSFSWATPFHPCLENPALDLSSYRAISSLDLLGDFKHALKKSEETSVY
EEGSSLASMPHPLRSRAFSESHISLDPQSTRAWGQHRRELFSKGDETQSDLLGARKKAFPPPRPPPPNWEKYRLFRAAQQ
QKQQQQQQQQQQKQQEEEEEEEEEEEEEEEEEEEEEAEEEEEELPPQYFSSETSGSCALNPEEVLEQPQPLSLGHLEGSG
QGSQSVPAEQESFALHPSDFLPPIRGHLGSQPEQAQPPCYYGIGGLWRTSEQEAAESAKQEFQPFSPPPGAPGIPTSYSA
YYNISVAKAELLNKLKDKPEMAEIGLGEEEVDHELAQKKIQLIESISRKLSVLREAQRGLLEDINANSALGEEVEANLKA
VCKSNEFEKYRSFVGDLDKVVNLLLSLSGRLARVENALNSIDSEANQEKLVLIEKKQQLTGQLADAKELKEHVDRREKLV
FGMVSRYLPQDQLQDYQHFVKMKSALIIEQRELEEKIKLGEEQLKCLRESLLLGPSNF
```

1136 - 1155:	EEEEEEEEEEEEEEEEEEEE
1137 - 1156:	EEEEEEEEEEEEEEEEEEEE

A0A2K6A655 **A0A2K6A655_MANLE** (1477 aa)
Shroom family member 4. *Mandrillus leucophaeus (Drill) (Papio leucophaeus)*

```
LTGRILGRKSPHCLLSVLFSATQIEDGGKAALSQKMRTGDELVNINGTPLYGSRQEALILIKGSFRILKLIVRRRNAPVS
RPHSWHVAKLLEGCPEAATTMHFPSEAFSLSWHSGCNTSDVCVQWCPLSRHCSTEKSSSIGSMESLEQPGQATYESHLLP
IDQNMYPNQRDSAYSSFSASSNASDCALSLRPEEAASTDCIMQGPGPTKAPNGRPNVAETSGGSRRTSGGHLTPSSQMSS
RPQEGHQSGPAKAVRGPPQPPVRRDSLQASRAQLLNGEQRRASEPVVPLPQKEKLSLETVLPAGNPNRFCCLSGHDQVTS
EGHQNCEFSQPPESSQQGSEHLLMQASTKAVGSPKACDKASSTDSNPLNEASTELAKASFGRPPHLIGPTGHRHSAPEQL
LASHLQHVHLDTRGSKGMELPPGQDGHQWTLSPLHSSHKGKKSPCPPAGGTQDQSSKERKTRQMDDRSLVLGHQSQSSPP
HGEADGHPSEKGLLDPNRTSRAGNELANQQPSASGSLVQKARDCSSTTKVAGGTEAGEEGDSEHKECSRMGGRRSGGTRG
RSIQNRRKSERFATNLRNEIQRRKAQLQKSKGPLSQLCDTKEPVEETQEPPESPPLTASNTSLLSSCKKPPSPRDKLFNK
SMMLRARSSECLSQAPESHESRTGLEGRISPGQRLGQSSLVLNTWWKAPDPSSSDPEKAHAHCGVHGGHWKWSREHNSQP
LVAVAMEGPSNPGDNKELKASTAQAGEDAILLPFADRRKFFEESSKSLSTSHLPGLTTHSNKTFTQRPKPIDQNFQPVSS
NYRELRRHPMDQSYHSADQPYHATDQSYHSMSPLQSETPTYSECFASRGLENSMCCKPLHCGDFDYHRTCSYSCSVQGAL
VHDPCIYCSGEICPALLKRNMMPNCYNCRCHHHQCIRCSVCYHNPQHSTLEDSSLAPGNTWKPRKPTVQEFPGDKWNPIT
GNRKTSQSGREMAHSKNSFSWATPFHPCLENPALDLSSYRAISSLDLLGDFKHALKKSEETSVYEEGSSLASMPHPLRSR
AFSESHISLDPQSTRAWGQHRRELFSKGDETQSDLLGARKKAFPPPRPPPPNWEKYRLFRAQQQQQQQQQQKQQEEEEEE
EEEEEEEEEEEEEEEAEEEEEELPPQYFSSETSGSCALNPEEVLEQPQPLSLGHLEGSGQGSQSVPAEQESFALHPSDFL
PPIRGHLGSQPEQAQPPCYYGIGGLWRTSEQEAAESAKQEFQPFSPPPGAPGIPTSYSAYYNISVAKAELLNKLKDKPEM
AEIGLGEEEVDHELAQKKIQLIESISRKLSVLREAQRGLLEDINANSALGEEVEANLKAVCKSNEFEKYRSFVGDLDKVV
NLLLSLSGRLARVENALNSIDSEANQEKLVLIEKKQQLTGQLADAKELKEHVDRREKLVFGMVSRYLPQDQLQDYQHFVK
MKSALIIEQRELEEKIKLGEEQLKCLRESLLLGPSNF
```

1115 - 1134:	EEEEEEEEEEEEEEEEEEEE
1116 - 1135:	EEEEEEEEEEEEEEEEEEEE

A0A2K6A673 **A0A2K6A673_MANLE** (1382 aa)
Shroom family member 4. *Mandrillus leucophaeus (Drill) (Papio leucophaeus)*

```
MHFPSEAFSLSWHSGCNTSDVCVQWCPLSRHCSTEKSSSIGSMESLEQPGQATYESHLLPIDQNMYPNQRDSAYSSFSAS
SNASDCALSLRPEEAASTDCIMQGPGPTKAPNGRPNVAETSGGSRRTSGGHLTPSSQMSSRPQEGHQSGPAKAVRGPPQP
PVRRDSLQASRAQLLNGEQRRASEPVVPLPQKEKLSLETVLPAGNPNRFCCLSGHDQVTSEGHQNCEFSQPPESSQQGSE
HLLMQASTKAVGSPKACDKASSTDSNPLNEASTELAKASFGRPPHLIGPTGHRHSAPEQLLASHLQHVHLDTRGSKGMEL
PPGQDGHQWTLSPLHSSHKGKKSPCPPAGGTQDQSSKERKTRQMDDRSLVLGHQSQSSPPHGEADGHPSEKGLLDPNRTS
RAGNELANQQPSASGSLVQKARDCSSTTKVAGGTEAGEEGDSEHKECSRMGGRRSGGTRGRSIQNRRKSERFATNLRNEI
QRRKAQLQKSKGPLSQLCDTKEPVEETQEPPESPPLTASNTSLLSSCKKPPSPRDKLFNKSMMLRARSSECLSQAPESHE
SRTGLEGRISPGQRLGQSSLVLNTWWKAPDPSSSDPEKAHAHCGVHGGHWKWSREHNSQPLVAVAMEGPSNPGDNKELKA
STAQAGEDAILLPFADRRKFFEESSKSLSTSHLPGLTTHSNKTFTQRPKPIDQNFQPVSSNYRELRRHPMDQSYHSADQP
YHATDQSYHSMSPLQSETPTYSECFASRGLENSMCCKPLHCGDFDYHRTCSYSCSVQGALVHDPCIYCSGEICPALLKRN
MMPNCYNCRCHHHQCIRCSVCYHNPQHSTLEDSSLAPGNTWKPRKPTVQEFPGDKWNPITGNRKTSQSGREMAHSKNSFS
WATPFHPCLENPALDLSSYRAISSLDLLGDFKHALKKSEETSVYEEGSSLASMPHPLRSRAFSESHISLDPQSTRAWGQH
RRELFSKGDETQSDLLGARKKAFPPPRPPPPNWEKYRLFRAAQQQKQQQQQQQQQQKQQEEEEEEEEEEEEEEEEEEEE
AEEEEEELPPQYFSSETSGSCALNPEEVLEQPQPLSLGHLEGSGQGSQSVPAEQESFALHPSDFLPPIRGHLGSQPEQAQ
PPCYYGIGGLWRTSEQEAAESAKQEFQPFSPPPGAPGIPTSYSAYYNISVAKAELLNKLKDKPEMAEIGLGEEEVDHELA
QKKIQLIESISRKLSVLREAQRGLLEDINANSALGEEVEANLKAVCKSNEFEKYRSFVGDLDKVVNLLLSLSGRLARVEN
ALNSIDSEANQEKLVLIEKKQQLTGQLADAKELKEHVDRREKLVFGMVSRYLPQDQLQDYQHFVKMKSALIIEQRELEEK
IKLGEEQLKCLRESLLLGPSNF
```

1020 - 1039:	EEEEEEEEEEEEEEEEEEEE
1021 - 1040:	EEEEEEEEEEEEEEEEEEEE

A0A2K6A680 **A0A2K6A680_MANLE** (1232 aa)
Euchromatic histone lysine methyltransferase 2. *Mandrillus leucophaeus (Drill) (Papio leucophaeus)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPNRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGA
LLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDESENLEGDGDLH
GGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGPEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEELGSARRSEVTLAKGDPGSLEEWET
VVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAKK
KWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSG
CNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGE
DASEAQEVTIPRGDGVTPPAGAAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCL
SAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSV
EICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDV
NAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIA
ARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCV
NGVDGESCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECN
QACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYC
IDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHS
AEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE

A0A2K6A6A0 **A0A2K6A6A0_MANLE** (1192 aa)
Euchromatic histone lysine methyltransferase 2. *Mandrillus leucophaeus (Drill) (Papio leucophaeus)*

```
RAAGLGGVDAAGEAPAEMGALLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPV
GATPLIGDESENLEGDGDLHGGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAA
GPEPPPATTSPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEELGSA
RRSEVTLAKGDPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEED
EESGNQSDRVRDGATRGRPQGRREREGGEPRQSRGVHGVLGHGGEDPPGVPMGEVQGLPQLLFFSVQGVSNDTSSLETER
GFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCG
YFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGAAAPAPPPLSQDAPGRADT
SQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSV
KQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMV
QRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEE
NICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVW
FALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGESCPEDYKYISENCETSTMNIDRNITHLQHCTCVD
DCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTI
PQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAF
FSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

296 - 315:	EEEEEEEEEEEEEEEEEEEE
297 - 316:	EEEEEEEEEEEEEEEEEEEE
298 - 317:	EEEEEEEEEEEEEEEEEEEE
299 - 318:	EEEEEEEEEEEEEEEEEEEE
300 - 319:	EEEEEEEEEEEEEEEEEEEE

A0A2K6A6A2 **A0A2K6A6A2_MANLE** (1252 aa)
Euchromatic histone lysine methyltransferase 2. *Mandrillus leucophaeus (Drill) (Papio leucophaeus)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPNRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGA
LLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDESENLEGDGDLH
GGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGPEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEELGSARRSEVTLAKGDPGSLEEWET
VVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRVRDGATRGRPQ
GRREREGGEPRQSRGVHGVLGHGGEDPPGVPMGEVQGLPQLLFFSVQGVSNDTSSLETERGFEELPLCSCRMEAPKIDRI
SERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHR
FHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGAAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDP
LADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNF
QSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHA
AKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLL
NARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRT
EKIICRDVARGYENVPIPCVNGVDGESCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDK
DGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEAD
VREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRF
WDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE

A0A2K6A7S8 **A0A2K6A7S8_MANLE** (728 aa)
YTH domain containing 1. *Mandrillus leucophaeus (Drill) (Papio leucophaeus)*

```
MAADIREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSN
NKRIVSTKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEE
EEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSA
SESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVIL
IFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQE
IELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQ
RPGYLKDPRYQEVDRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQAHPPYSGH
HPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDR
GERGRYRR
```

230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE

A0A2K6A7T6 **A0A2K6A7T6_MANLE** (731 aa)
YTH domain containing 1. *Mandrillus leucophaeus (Drill) (Papio leucophaeus)*

```
LKSDNGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSNNKRIV
STKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVDRRASR
SSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEEEEEEE
EEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSASESYA
GSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVILIFSVR
ESGKFQGFARLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELEC
GTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQRPGYL
KDPRYQEVDSFTNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQAHPPY
SGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRD
RDRGERGRYRR
```

225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE

A0A2K6A7U3 **A0A2K6A7U3_MANLE** (540 aa)
YTH domain containing 1. *Mandrillus leucophaeus (Drill) (Papio leucophaeus)*

```
LKSDNGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSNNKRIV
STKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVDRRASR
SSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEEEEEEEEEEEEEEEEEEEEY
EQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSASESYAGSEKKH
EKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVILIFSVRESGKFQ
GFARLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCL
LFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRLETFFGLIIGTCIRIT
```

218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE

A0A2K6A7W1 **A0A2K6A7W1_MANLE** (1324 aa)
Tau tubulin kinase 1. *Mandrillus leucophaeus (Drill) (Papio leucophaeus)*

```
MQCLAAALKDETNMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTRENVALKVESAQQPKQVLKMEVAV
LKKLQGKDHVCRFIGCGRNEKFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESIEAIHSVGFLHRDIKPSNF
AMGRLPSTYRKCYMLDFGLARQYTNTTGDVRPPRNVAGFRGTVRYASVNAHKNREMGRHDDLWSLFYMLVEFAVGQLPWR
KIKDKEQVGMIKEKYEHRMLLKHMPSEFHLFLDHIASLDYFTKPDYQLIMSVFENSMKERGIAENEAFDWEKAGTDALLS
TSTSTPPQQNTRQTAAMFGVVNVTPVPGDLLRENTEDVLQGEHLSDQENAPPILPGRPSEGLGPSPHFVPHPGGPEAEVW
EETDVNRNKLRINIGKSPCVEEEQSRGMGVPSSPVRAPPDSPTTPVRSLRYRRVNSPESERLSTADGRVELPERRSRMDL
PGSPSRQACSSQPAQMLSVDTGHADRQASGRMDVSASVEQEALSNAFRSVPLAEEEDFDSKEWVIIDKETELKDFPPGAE
PSTSGTTDEEPEELRPLPEEGEERRRLGAEPTVRPRGRSMQVLAEEDLQHLPPQPLPPQLSQADGRSETSQPPTPGSPSH
SPLHSGPRPRRRESDPTGPQRQVFSVAPPFEVNGLPRAVPLSLPYQDFKRDLSDYRERARLLNRVRRVGFSHMLLTTPQV
PLSPVQPQANGKEEEEEEEEEEDEEEEEEDEEDEEEEEEEEEEEEEEEEEEEEEEAAAAVALGEVLGPRSGSSSEGSERST
DRSQEGAPSTLLADDQKESRGRASMADGDLEPEEGSKTLVLVSPGDMKKSPVTAELAPDPDLGTLAALTPQHERPQPTGS
QLDVSEPGTLSSVLKSEPKPPGPGAGPGAGTVTTGAGGVAVTSSPFTKVERTFVHIAEKTHLNVMSSSGQALRPEEFSTG
GELGLELASDGGTVEEGAPAPLENGLALSGLNGAEIEGCALSGPPGETPSAMATNSLPNGPALADSPAPVSLLEPSPEKV
ATISPRHHAMPGSRPRSRIPILLSEEDTGSEPSGSLSAKERWSKRARLQQDLARLVMEKRQGRLLLRLASGASSSSSEEQ
RRASETLSGTGSEEDTPASEPAVALPRKVGRAAATRSRIPRPIGLRMPMPAAAQQLPSKSHGAAPASDTAITSRLQLQTP
PGSATAADLRPKQPPGRGLGPGRAQAGARPSAPRSPGLPTSTSAARNASASPRSQSLSRRESPSPSHQARPGVPPPRGVP
SARAQPDGTPSPGGSKKGPRGKLQAQRATTKGRAGGAEGRAGAR
```

754 - 773:	EEEEEEEEEEEEEEEEEEEE
755 - 774:	EEEEEEEEEEEEEEEEEEEE

A0A2K6A7W5 **A0A2K6A7W5_MANLE** (710 aa)
YTH domain containing 1. *Mandrillus leucophaeus (Drill) (Papio leucophaeus)*

```
MAADIREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSN
NKRIVSTKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVD
```

```
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEE
EEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSA
SESYADQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVILIFSVRESGKFQGFARLSS
ESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLLFPPDES
IDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQRPGYLKDPRYQEVDRRFS
GVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHHPVPHEARYRDKRVHDYD
MRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDRGERGRYRR
```

230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE

A0A2K6BMK1 **A0A2K6BMK1_MACNE** (906 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Macaca nemestrina (Pig-tailed macaque)*

```
MELAVAVLRDLLRYAAQLPALFRDISMNHLPGLLTSLLGLRPECEQSALEGMKACMTYFPRACGSLKGKLASFFLSRVDA
LSPQLQQLACECYSRLPSLGAGFSQGLKHTESWEQELHSLLASLHTLLGALYEGAETAPVQNEGPGVEMLLSSEDGDAHV
LLRLRQRFSGLARCLGLMLSSEFGAPVSVPVQEILDFICRTLSVSSKNISLHGDGPLRLLLLPSIHLEALDLLSALILAC
GSRLLRFGILISRLLPQVLNSWSIGRDSLSPGQERPYSTVRTKVYAVLELWVQVCGASAGMLQGGASGEALLTHLLSDIS
PPADALKLRSPRGSPDGSLQTGKPSAPKKLKLDVGEAMAPPSHRKGDSNANSDVCAAALKGLSRTILMCGPLIKEETHRR
LHDLVLPLVMGVQQGEVLGSSPYTSSRCRRELYCLLLALLLAPSPRCPPPLACALQAFSLGQREDSLEVSSFCSEALVTC
AALTHPRVPPLQPMGPTCPTPAPVPPPEAPSPFRAPPFHPPGPMPSVGPMPSAGPMPSAGPMPSAGPVPSARPGPPTTAN
HLGLSVSGLVSVPPRLLPGPENHRAGSNEDPILAPSGTPPPTIPPDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDS
VVIVPEGLPPLPPPPPSGATPPPIAPTGPPTASPPVPAKEEPEELPAAPGPLPPPPPPPPPVPGPVTLPPPQLVPEGTPG
GGGPPALEEDLTVININSSDEEEEEEEEEEEEEEEEEEEEDFEEEEEDEEEYFEEEEEEEEEEFEEEFEEEEGELEEEEE
EEDEEEEEELEEVEREEGSPSAGPPPQELVEEEPSAPPTLLEEGTEDGGDRVQPPPETPAEEEMETETEAEALQEKEQDD
TAAMLADFIDCPPDDEKPPPPTEPDS
```

741 - 760:	EEEEEEEEEEEEEEEEEEEE
742 - 761:	EEEEEEEEEEEEEEEEEEEE

A0A2K6BMN5 **A0A2K6BMN5_MACNE** (1180 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Macaca nemestrina (Pig-tailed macaque)*

```
MLLPSLSPRVQPAFIQCAGPQPPPHAHSPVGGRRGVFTSSRHATTGARGKMAAAVLSGSSAGSAAGVPGGTGGLSAVNSG
PRLRLLLLESVSGLLQPRTGSAVAPVHPPNRSAPHLPGLMCLLRLHGSVGGAQNLSALGALVSLSNARLSSIKTRFEGLC
LLSLLVGESPTELFQQHCVSWLRSIQQVLQTQDPPATMELAVAVLRDLLRYAAQLPALFRDISMNHLPGLLTSLLGLRPE
CEQSALEGMKACMTYFPRACGSLKGKLASFFLSRVDALSPQLQQLACECYSRLPSLGAGFSQGLKHTESWEQELHSLLAS
LHTLLGALYEGAETAPVQNEGPGVEMLLSSEDGDAHVLLRLRQRFSGLARCLGLMLSSEFGAPVSVPVQEILDFICRTLS
VSSKNISLHGDGPLRLLLLPSIHLEALDLLSALILACGSRLLRFGILISRLLPQVLNSWSIGRDSLSPGQERPYSTVRTK
VYAVLELWVQVCGASAGMLQGGASGEALLTHLLSDISPPADALKLRSPRGSPDGSLQTGKPSAPKKLKLDVGEAMAPPSH
RKGDSNANSDVCAAALKGLSRTILMCGPLIKEETHRRLHDLVLPLVMGVQQGEVLGSSPYTSSRCRRELYCLLLALLLAP
SPRCPPPLACALQAFSLGQREDSLEVSSFCSEALVTCAALTHPRVPPLQPMGPTCPTPAPVPPPEAPSPFRAPPFHPPGP
MPSVGPMPSAGPMPSAGPMPSAGPVPSARPGPPTTANHLGLSVSGLVSVPPRLLPGPENHRAGSNEDPILAPSGTPPPTI
PPDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDSVVIVPEGLPPLPPPPPSGATPPPIAPTGPPTASPPVPAKEEPE
ELPAAPGPLPPPPPPPPPVPGPVTLPPPQLVPEGTPGGGGPPALEEDLTVININSSDEEEEEEEEEEEEEEEEEEEEEDF
EEEEEDEEEYFEEEEEEEEEFEEEFEEEEGELEEEEEEEDEEEEEELEEVEELEFGTAGGEVEEGGPPPPTLPPALPPPE
SPPKVQPEPEPEPGLLLEVEEPGAEEEHGADTAPTLAPEVLPSQGEVEREEGSPSAGPPPQELVEEEPSAPPTLLEEGTE
DGGDRVQPPPETPAEEEMETETEAEALQEKEQDDTAAMLADFIDCPPDDEKPPPPTEPDS
```

938 - 957:	EEEEEEEEEEEEEEEEEEEE
939 - 958:	EEEEEEEEEEEEEEEEEEEE

A0A2K6C8E7 **A0A2K6C8E7_MACNE** (728 aa)
YTH domain containing 1. *Macaca nemestrina (Pig-tailed macaque)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSN
NKRIVSTKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEE
EEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSA
SESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVIL
IFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQE
IELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQ
RPGYLKDPRYQEVDRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQAHPPYSGH
HPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDR
GERGRYRR
```

230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE

A0A2K6C8F6 **A0A2K6C8F6_MACNE** (710 aa)
YTH domain containing 1. *Macaca nemestrina (Pig-tailed macaque)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSN
NKRIVSTKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEE
EEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSA
SESYADQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVILIFSVRESGKFQGFARLSS
ESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLLFPPDES
```

```
IDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQRPGYLKDPRYQEVDRRFS
GVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHHPVPHEARYRDKRVHDYD
MRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDRGERGRYRR
```

230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE

A0A2K6C8G6 **A0A2K6C8G6_MACNE** (731 aa)
YTH domain containing 1. *Macaca nemestrina (Pig-tailed macaque)*

```
LKSDNGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSNNKRIV
STKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVDRRASR
SSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEEEEEEE
EEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSASESYA
GSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVILIFSVR
ESGKFQGFARLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELEC
GTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQRPGYL
KDPRYQEVDSFTNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQAHPPY
SGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRD
RDRGERGRYRR
```

225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE

A0A2K6C8H2 **A0A2K6C8H2_MACNE** (540 aa)
YTH domain containing 1. *Macaca nemestrina (Pig-tailed macaque)*

```
LKSDNGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSNNKRIV
STKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVDRRASR
SSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEEEEEEEEEEEEEEEEEEEEY
EQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSASESYAGSEKKH
EKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVILIFSVRESGKFQ
GFARLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCL
LFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRLETFFGLIIGTCVRIT
```

218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE

A0A2K6CFW1 **A0A2K6CFW1_MACNE** (1324 aa)
Tau tubulin kinase 1. *Macaca nemestrina (Pig-tailed macaque)*

```
MQCLAAALKDETNMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTRENVALKVESAQQPKQVLKMEVAV
LKKLQGKDHVCRFIGCGRNEKFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESIEAIHSVGFLHRDIKPSNF
AMGRLPSTYRKCYMLDFGLARQYTNTTGDVRPPRNVAGFRGTVRYASVNAHKNREMGRHDDLWSLFYMLVEFAVGQLPWR
KIKDKEQVGMIKEKYEHRMLLKHMPSEFHLFLDHIASLDYFTKPDYQLIMSVFENSMKERGIAENEAFDWEKAGTDALLS
TSTSTPPQQNTRQTAAMFGVVNVTPVPGDLLRENTEDVLQGEHLSDQENAPPILPGRPSEGLGPSPHLVPHPGGPEAEVW
EETDVNRNKLRINIGKSPCVEEEQSRGMGVPSSPVRAPPDSPTTPVRSLRYRRVNSPESERLSTADGRVELPERRSRMDL
PGSPSRQACSSQPAQMLSVDTGHADRQASGRMDVSASVEQEALSNAFRSVPLAEEEDFDSKEWVIIDKETELKDFPPGAE
PSTSGTTDEEPEELRPLPEEGEERRRLGAEPTVRPRGRSMQVLAEEDLQHLPPQPLPPQLSQADGRSETSQPPTPGSPSH
SPQHSGPRPRRRESDPTGPQRQVFSVAPPFEVNGLPRAVPLSLPYQDFKRDLSDYRERARLLNRVRRVGFSHMLLTTPQV
PLSPVQPQANGKEEEEEEEEEEDEEEEEEDEEDEEEEEEEEEEEEEEEEEEEEEEAAAAVALGEVLGPRSGSSSEGSERST
DRSQEGAPSTLLADDQKESRGRASMADGDLEPEEGSKTLVLVSPGDMKKSPVTAELAPDPDLGTLAALTPQHERPQPTGS
QLDVSEPGTLSSVLKSEPKPPGPGAGPGAGTVTTGAGGVAVTSSPFTKVERTFVHIAEKTHLNVMSSSGQALRPEEFSTG
GELGLELASDGGTVEEGAPAPLENGLALSGLNGAEIEGCALSGPPGETPSAMATNSLPNGPALADSPAPVSPLEPSPEKV
ATISPRHHAMPGSRPRSRIPILLSEEDTGSEPSGSLSAKERWSKRARLQQDLARLVMEKRQGRLLLRLASGASSSSSEEQ
RRASETLSGTGSEEDTPASEPAVALPRKAGRAAATRSRIPRPIGLRMPMPAAAQQLPSKSHGAAPASDTAITSRLQLQTP
PGSATAADLRPKQPPGRGLGPGRAQAGARPPAPRSPGLPTSTSAARNASASPRSQSLSRRESPSPSHQARPGVPPPRGVP
SARAQPDGTPSPGGSKKGPRGKLQAQRATTKGRPGGAEGRAGAR
```

754 - 773:	EEEEEEEEEEEEEEEEEEEE
755 - 774:	EEEEEEEEEEEEEEEEEEEE

A0A2K6CNJ8 **A0A2K6CNJ8_MACNE** (1209 aa)
Euchromatic histone lysine methyltransferase 2. *Macaca nemestrina (Pig-tailed macaque)*

```
MAAAAGAAAAAAAEGEAPAEMGALLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGAD
TPVGATPLIGDESENLEGDGDLHGGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGA
AAAGPEPPPATTSPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEEL
GSARRSEVTLAKGDSGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEE
EEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLS
PNHAGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLC
ETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGAA
APAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQES
ERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTP
LMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVI
RMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRN
KEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGESCPEDYKYISENCETST
MNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQ
```

```
LYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIP
VRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPE
LGSLPPVNT
```

299 - 318:	EEEEEEEEEEEEEEEEEEEE
300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE

A0A2K6CNV9 **A0A2K6CNV9_MACNE** (1266 aa)
Euchromatic histone lysine methyltransferase 2. *Macaca nemestrina (Pig-tailed macaque)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGA
LLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDESENLEGDGDLH
GGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGPEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEELGSARRSEVTLAKGDSGSLEEWET
VVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAKK
KWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEELP
LCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAG
TFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGAAAPAPPPLSQDAPGRADTSQPSAR
MRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQ
KVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCV
YSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHW
ASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLN
RKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGESCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSN
CLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFI
CEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDI
RTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE

A0A2K6CNZ7 **A0A2K6CNZ7_MACNE** (1232 aa)
Euchromatic histone lysine methyltransferase 2. *Macaca nemestrina (Pig-tailed macaque)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGA
LLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDESENLEGDGDLH
GGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGPEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEELGSARRSEVTLAKGDSGSLEEWET
VVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAKK
KWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSG
CNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGE
DASEAQEVTIPRGDGVTPPAGAAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCL
SAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSV
EICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDV
NAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIA
ARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCV
NGVDGESCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECN
QACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYC
IDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHS
AEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE

A0A2K6CP06 **A0A2K6CP06_MACNE** (1261 aa)
Euchromatic histone lysine methyltransferase 2. *Macaca nemestrina (Pig-tailed macaque)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGA
LLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDESENLEGDGDLH
GGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGPEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEELGSARRSEVTLAKGDSGSLEEWET
VVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRRSGRLWGWWSD
SPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEELPLCSCR
MEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLEC
HPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGAAAPAPPPLSQDAPGRADTSQPSARMRGHG
EPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILM
LLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEE
DGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTG
SAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRL
```

```
GVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGESCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQ
LSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVG
ELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEE
LGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE

A0A2K6CPY3 **A0A2K6CPY3_MACNE** (586 aa)
Ran GTPase activating protein 1. *Macaca nemestrina (Pig-tailed macaque)*

```
MASEDIAKLAETLAKTQVAGGQLSFKGKSLKLNTAEDAKDVIKEIEDFDSLEALRLEGNTVGVEAARVIAKALEKKSELK
RCHWSDMFTGRLRTEIPPALISLGEGLITAGAQLVELDLSDNAFGPDGVQGFEALLKSSACFTLHELKLNNCGMGIGGGK
ILAAALTECHRKSSAQGKPLALKVFVAGRNRLENDGATALAEAFRVIGTLEEVHMPQNGINHPGVTALAQAFAVNPLLRV
INLNDNTFTEKGAVAMAETLKTLRQVEVINFGDCLVRSKGAVAIADAIRGGLPKLKELNLSFCEIKRDAALAVAEAMADK
TELEKLDLNGNTLGEEGCEQLQEVLEGFNMAKVLASLSDDEDEEEEEGEEEEEAEEEEEEEEEEEEEEEEEEEEEPQQG
GQGEKSATPSQKILDPNTGEPAPVLSSPPPADVSTFLAFPSPEKLLRLGPKSSMLIAQQTDTSDPEKVVSAFLKVSSVFK
DEATVRTAVQDAVDALMKKAFSSSSFNSSAFLTRLLAHMGLLKSEDKVKAIANLYGPLMALNHMVQQDYFPKALAPLLLA
FITKPNSALESCSFARHSLLQTLYKV
```

375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE

A0A2K6CQ03 **A0A2K6CQ03_MACNE** (641 aa)
Ran GTPase activating protein 1. *Macaca nemestrina (Pig-tailed macaque)*

```
MGLPRRPPVICGLYSRVAPAAPPPSRPTPTGGPGWRRCPWNRFCRSPGEPTSLVSMASEDIAKLAETLAKTQVAGGQLSF
KGKSLKLNTAEDAKDVIKEIEDFDSLEALRLEGNTVGVEAARVIAKALEKKSELKRCHWSDMFTGRLRTEIPPALISLGE
GLITAGAQLVELDLSDNAFGPDGVQGFEALLKSSACFTLHELKLNNCGMGIGGGKILAAALTECHRKSSAQGKPLALKVF
VAGRNRLENDGATALAEAFRVIGTLEEVHMPQNGINHPGVTALAQAFAVNPLLRVINLNDNTFTEKGAVAMAETLKTLRQ
VEVINFGDCLVRSKGAVAIADAIRGGLPKLKELNLSFCEIKRDAALAVAEAMADKTELEKLDLNGNTLGEEGCEQLQEVL
EGFNMAKVLASLSDDEDEEEEEGEEEEEAEEEEEEEEEEEEEEEEEEEEEEEPQQGGQGEKSATPSQKILDPNTGEPAPVL
SSPPPADVSTFLAFPSPEKLLRLGPKSSMLIAQQTDTSDPEKVVSAFLKVSSVFKDEATVRTAVQDAVDALMKKAFSSSS
FNSSAFLTRLLAHMGLLKSEDKVKAIANLYGPLMALNHMVQQDYFPKALAPLLLAFITKPNSALESCSFARHSLLQTLYK
V
```

430 - 449:	EEEEEEEEEEEEEEEEEEEE
431 - 450:	EEEEEEEEEEEEEEEEEEEE
432 - 451:	EEEEEEEEEEEEEEEEEEEE

A0A2K6CX27 **A0A2K6CX27_MACNE** (603 aa)
Centromere protein B. *Macaca nemestrina (Pig-tailed macaque)*

```
MGPKRRQLTFREKSRIIQEVEENPDLRKGEIARRFNIPPSTLSTILKNKRAILASERKYGVASTCRKTNKLSPYDKLEGL
LIAWFQQIRAAGLPVKGIILKEKALRIAEELGMDDFTASNGWLDRFRRRHGVVSCSGVARARARNAAPRTPAAPASPAAV
PSEGSGGSTTGWRAREEQPPSVAEGYASQDVFSATETSLWYDFLPDQAAGLCGGDGRPRQATQRLSVLLCANADGSEKLP
PLVAGKSAKPRAGQAGLPCDYTANSKGGVTTQALAKYLKALDTRMAAESRRVLLLAGRLAAQSLDTSGLRHVQLAFFPPG
TVHPLERGVVQQVKGHYRQAMLLKAMAALEGQDRSGLQLGLTEALHFVAAAWQAVEPSDIAACFREAGFGGGPNATITTS
LKKEEEEEEEEEEEEEEEEEEEEGEGEEEEEEGEEEEEEAGEGEELGEEEEVEEEGDVDDSDEEEEEDEESSSEGLEAED
WAQGVVEAGGSFGGYGTQEEAQCPTLHFLEGGEDSDSDSEEEEDDEEEDDEDDDDDEEDGDEVPVPSFGEAMAYFAMVKR
YLTSFPIDDRVQSHILHLEHDLVHVTRKNHARQAGVRGLGHQS
```

404 - 423:	EEEEEEEEEEEEEEEEEEEE

A0A2K6DCX8 **A0A2K6DCX8_MACNE** (1498 aa)
Shroom family member 4. *Macaca nemestrina (Pig-tailed macaque)*

```
MENRPGSFQYVPVQLQGGAPWGFTLKGGLEHCEPLTVSKIEDGGKAALSQKMRTGDELVNINGTPLYGSRQEALILIKGS
FRILKLIVRRRNAPVSRPHSWHVAKLLEGCPEAATTMHFPSEAFSLSWHSGCNTSDVCVQWCPLSRHCSTEKSSSIGSME
SLEQPGQATYESHLLPIDQNMYPNQRDSAYSSFSASSNASDCALSLRPEEAASTDCIMQGPGPTKAPNCRPNVAETSGGS
RRTNGGHLTPSSQMSSRPQEGHQSGPAKAVRGPPQPPVRRDSLQASRAQLLNGEQRRASEPVVPLPQKEKLSLETVLPAR
NPNRFCCLSGHDQVTSEGHQNCEFSQPPESSQQGSEHLLMQASTKAVGSPKACDKASSTDSNPLNEASAELAKASFGRPP
HLIGPTGHRHSAPEQLLASHLQHVHLDTRGSKGMELPPGQDGQQWTLSPLHSSHKGKKSPCPPAGGTHDQSSKERKTRQM
DDRSLVLGHQSQSSPPHGEADGHPSEKGLLDPNRTSRAGNELANQQPSASGSLVQKARDCSSTTKVAGGTEAGEEGDSEH
KECSRMGGRRSGGTRGRSIQNRRKSERFATNLRNEIQRRKAQLQKSKGPLSQLCDTKEPVEETQEPPESPPLTASNTSLL
SSCKKPPSPRDKLFNKSMMLRARSSECLSQAPESHESRTGLEGQISPGQRLGQSSLVLNTWWKAPDPSSSDPEKAHAHCG
VHGGHWRWSREHNSQPLVAVAMEGPSNPGDNKELKASTAQAGEDAVLLPFADRRKFFEESSKSLSTSHLPGLTTHSNKTF
TQRPKPIDQNFQPVSSNYRELRRHPMDQSYHSADQPYHATDQSYHSMSPLQSETPTYSECFASRGLENSMCCKPLHCGDF
DYHRTCSYSCSVQGALVHDPCIYCSGEICPALLKRNMMPNCYNCRCHHHQCIRCSVCYHNPQHSTLEDSSLAPGNTWKPR
KPTVQEFPGDKWNPITGNRKTSQSGREMAHSKNSFSWATPFHPCLENPALDLSSYRAISSLDLLGDFKHALKKSEETSVY
EEGSSLASMPHPLRSRAFSESHISLDPQSTRAWGQHRRELFSKGDETQSDLLGARKKAFPPPRPPPPNWEKYRLFRAAQQ
QKQQQQQQQQQQKQQEEEEEEEEEEEEEEEEEEEEEEAEEEEEELPPQYFSSETSGSCALNPEEVLEQPQPLSLGHLEGSG
QGSQSVPAEQESFALHSSDFLPPIRGHLGSQPEQAQPPCYYGIGGLWRTSEQEAAEAAKQEFQPFSPPPGAPAIPTSYSA
```

```
YYNISVAKAELLNKLKDQPEMAEIGLGEEEVDHELAQKKIQLIESISRKLSVLREAQRGLLEDINANSALGEEVEANLKA
VCKSNEFEKYRSFVGDLDKVVNLLLSLSGRLARVENALNSIDSEANQEKLVLIEKKQQLTGQLADAKELKEHVDRREKLV
FGMVSRYLPQDQLQDYQHFVKMKSALIIEQRELEEKIKLGEEQLKCLRESLLLGPSNF
```

1136 - 1155:	EEEEEEEEEEEEEEEEEEEE
1137 - 1156:	EEEEEEEEEEEEEEEEEEEE

A0A2K6DCY6 **A0A2K6DCY6_MACNE** (1382 aa)
Shroom family member 4. *Macaca nemestrina (Pig-tailed macaque)*

```
MHFPSEAFSLSWHSGCNTSDVCVQWCPLSRHCSTEKSSSIGSMESLEQPGQATYESHLLPIDQNMYPNQRDSAYSSFSAS
SNASDCALSLRPEEAASTDCIMQGPGPTKAPNCRPNVAETSGGSRRTNGGHLTPSSQMSSRPQEGHQSGPAKAVRGPPQP
PVRRDSLQASRAQLLNGEQRRASEPVVPLPQKEKLSLETVLPARNPNRFCCLSGHDQVTSEGHQNCEFSQPPESSQQGSE
HLLMQASTKAVGSPKACDKASSTDSNPLNEASAELAKASFGRPPHLIGPTGHRHSAPEQLLASHLQHVHLDTRGSKGMEL
PPGQDGQQWTLSPLHSSHKGKKSPCPPAGGTHDQSSKERKTRQMDDRSLVLGHQSQSSPPHGEADGHPSEKGLLDPNRTS
RAGNELANQQPSASGSLVQKARDCSSTTKVAGGTEAGEEGDSEHKECSRMGGRRSGGTRGRSIQNRRKSERFATNLRNEI
QRRKAQLQKSKGPLSQLCDTKEPVEETQEPPESPPLTASNTSLLSSCKKPPSPRDKLFNKSMMLRARSSECLSQAPESHE
SRTGLEGQISPGQRLGQSSLVLNTWWKAPDPSSSDPEKAHAHCGVHGGHWRWSREHNSQPLVAVAMEGPSNPGDNKELKA
STAQAGEDAVLLPFADRRKFFEESSKSLSTSHLPGLTTHSNKTFTQRPKPIDQNFQPVSSNYRELRRHPMDQSYHSADQP
YHATDQSYHSMSPLQSETPTYSECFASRGLENSMCCKPLHCGDFDYHRTCSYSCSVQGALVHDPCIYCSGEICPALLKRN
MMPNCYNCRCHHHQCIRCSVCYHNPQHSTLEDSSLAPGNTWKPRKPTVQEFPGDKWNPITGNRKTSQSGREMAHSKNSFS
WATPFHPCLENPALDLSSYRAISSLDLLGDFKHALKKSEETSVYEEGSSLASMPHPLRSRAFSESHISLDPQSTRAWGQH
RRELFSKGDETQSDLLGARKKAFPPPRPPPPNWEKYRLFRAAQQQKQQQQQQQQQQKQQEEEEEEEEEEEEEEEEEEEE
AEEEEEELPPQYFSSETSGSCALNPEEVLEQPQPLSLGHLEGSGQGSQSVPAEQESFALHSSDFLPPIRGHLGSQPEQAQ
PPCYYGIGGLWRTSEQEAAEAAKQEFQPFSPPPGAPAIPTSYSAYYNISVAKAELLNKLKDQPEMAEIGLGEEEVDHELA
QKKIQLIESISRKLSVLREAQRGLLEDINANSALGEEVEANLKAVCKSNEFEKYRSFVGDLDKVVNLLLSLSGRLARVEN
ALNSIDSEANQEKLVLIEKKQQLTGQLADAKELKEHVDRREKLVFGMVSRYLPQDQLQDYQHFVKMKSALIIEQRELEEK
IKLGEEQLKCLRESLLLGPSNF
```

1020 - 1039:	EEEEEEEEEEEEEEEEEEEE
1021 - 1040:	EEEEEEEEEEEEEEEEEEEE

A0A2K6DCY9 **A0A2K6DCY9_MACNE** (1483 aa)
Shroom family member 4. *Macaca nemestrina (Pig-tailed macaque)*

```
ISLMFQPWWTTLKQKSPHCLLSVLFSATQIEDGGKAALSQKMRTGDELVNINGTPLYGSRQEALILIKGSFRILKLIVRR
RNAPVSRPHSWHVAKLLEGCPEAATTMHFPSEAFSLSWHSGCNTSDVCVQWCPLSRHCSTEKSSSIGSMESLEQPGQATY
ESHLLPIDQNMYPNQRDSAYSSFSASSNASDCALSLRPEEAASTDCIMQGPGPTKAPNCRPNVAETSGGSRRTNGGHLTP
SSQMSSRPQEGHQSGPAKAVRGPPQPPVRRDSLQASRAQLLNGEQRRASEPVVPLPQKEKLSLETVLPARNPNRFCCLSG
HDQVTSEGHQNCEFSQPPESSQQGSEHLLMQASTKAVGSPKACDKASSTDSNPLNEASAELAKASFGRPPHLIGPTGHRH
SAPEQLLASHLQHVHLDTRGSKGMELPPGQDGQQWTLSPLHSSHKGKKSPCPPAGGTHDQSSKERKTRQMDDRSLVLGHQ
SQSSPPHGEADGHPSEKGLLDPNRTSRAGNELANQQPSASGSLVQKARDCSSTTKVAGGTEAGEEGDSEHKECSRMGGRR
SGGTRGRSIQNRRKSERFATNLRNEIQRRKAQLQKSKGPLSQLCDTKEPVEETQEPPESPPLTASNTSLLSSCKKPPSPR
DKLFNKSMMLRARSSECLSQAPESHESRTGLEGQISPGQRLGQSSLVLNTWWKAPDPSSSDPEKAHAHCGVHGGHWRWSR
EHNSQPLVAVAMEGPSNPGDNKELKASTAQAGEDAVLLPFADRRKFFEESSKSLSTSHLPGLTTHSNKTFTQRPKPIDQN
FQPVSSNYRELRRHPMDQSYHSADQPYHATDQSYHSMSPLQSETPTYSECFASRGLENSMCCKPLHCGDFDYHRTCSYSC
SVQGALVHDPCIYCSGEICPALLKRNMMPNCYNCRCHHHQCIRCSVCYHNPQHSTLEDSSLAPGNTWKPRKPTVQEFPGD
KWNPITGNRKTSQSGREMAHSKNSFSWATPFHPCLENPALDLSSYRAISSLDLLGDFKHALKKSEETSVYEEGSSLASMP
HPLRSRAFSESHISLDPQSTRAWGQHRRELFSKGDETQSDLLGARKKAFPPPRPPPPNWEKYRLFRAQQQQQQQQQQKQQ
EEEEEEEEEEEEEEEEEEEEEAEEEEEELPPQYFSSETSGSCALNPEEVLEQPQPLSLGHLEGSGQGSQSVPAEQESFAL
HSSDFLPPIRGHLGSQPEQAQPPCYYGIGGLWRTSEQEAAEAAKQEFQPFSPPPGAPAIPTSYSAYYNISVAKAELLNKL
KDQPEMAEIGLGEEEVDHELAQKKIQLIESISRKLSVLREAQRGLLEDINANSALGEEVEANLKAVCKSNEFEKYRSFVG
DLDKVVNLLLSLSGRLARVENALNSIDSEANQEKLVLIEKKQQLTGQLADAKELKEHVDRREKLVFGMVSRYLPQDQLQD
YQHFVKMKSALIIEQRELEEKIKLGEEQLKCLRESLLLGPSNF
```

1121 - 1140:	EEEEEEEEEEEEEEEEEEEE
1122 - 1141:	EEEEEEEEEEEEEEEEEEEE

A0A2K6DJM6 **A0A2K6DJM6_MACNE** (979 aa)
Solute carrier family 24 member 1. *Macaca nemestrina (Pig-tailed macaque)*

```
MGKLIRMGPQDRRLLRTKRLPWSRLLFLLGMLIISSTYQHLRGPRGLSSLWAAVSSHQPVKLASRDLPSEEMMMVSSNPP
KPSSEMGGKMLVPQASVGSDEATLSMTVENIPDIPKRTAKMIPTTIKNNYSPTAAGTERRKEDTPTSSRTLTYYTSTSSR
QIVKKYTPTPTGEMKSYSPTQVREKVKYTPSPRGRRVGTYASSTFMTTETSHAITPRTTVKDSDITTTYKILETNSLKRI
MEETTPTTLKGMVDSTPTFLTHEVETNILTSPRSIVEKNNLSPPRRVESNSSAHPWGLVGKNNLKTPQGTVLTHTPATSE
GQVTISTMTGSNPSETKAFTAAWSVRNPSPRTSVSAIETAPTTVWRLAKKPYTAPSTSTTPTVRAKPTTQVHHCVVVKPT
PAMPTTPSPSLTTALLPEELSPSPSVLPPILPDLPPKGEYPPDLFSVEERRQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLIMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKQIEAWVKEQLSRRPAAKVMALGDLSKEDVAEAESTG
EMTGEEGETAGEGETEEKSGGETQPEGEGETGTQGKGEEREKENEAEGKGDNEGEGEGEIHAEDGEMEGIEGETESQELS
AENHGEAKSDEKGVEDGGGSDGGDNEEEEEEEEEEEEEEEEEEEEEEEEEEEEGNEEPLSLHWPETRQKQAIYLFLLPIVFP
LWLTVPDVRRQESRKFFVFTFLGSIVWIAMFSYLMVWWAHQVGETIGISEEIMGLTILAAGTSIPDLITSVIVARKGLGD
MAVSSSVGSNIFDITVGLPVPWLLFCLINGLQPVPVSSNGLFCAIVLLFLMLLFVISSIASCKWRMNKILGFTMFLLYFV
FLIISVMLEDRIISCPVSV
```

746 - 765:	EEEEEEEEEEEEEEEEEEEE
747 - 766:	EEEEEEEEEEEEEEEEEEEE
748 - 767:	EEEEEEEEEEEEEEEEEEEE
749 - 768:	EEEEEEEEEEEEEEEEEEEE

750 - 769:	EEEEEEEEEEEEEEEEEEEE
751 - 770:	EEEEEEEEEEEEEEEEEEEE
752 - 771:	EEEEEEEEEEEEEEEEEEEE

A0A2K6DJN8 **A0A2K6DJN8_MACNE** (1063 aa)
Solute carrier family 24 member 1. *Macaca nemestrina (Pig-tailed macaque)*

```
MGKLIRMGPQDRRLLRTKRLPWSRLLFLLGMLIISSTYQHLRGPRGLSSLWAAVSSHQPVKLASRDLPSEEMMMVSSNPP
KPSSEMGGKMLVPQASVGSDEATLSMTVENIPDIPKRTAKMIPTTIKNNYSPTAAGTERRKEDTPTSSRTLTYYTSTSSR
QIVKKYTPTPTGEMKSYSPTQVREKVKYTPSPRGRRVGTYASSTFMTTETSHAITPRTTVKDSDITTTYKILETNSLKRI
MEETTPTTLKGMVDSTPTFLTHEVETNILTSPRSIVEKNNLSPPRRVESNSSAHPWGLVGKNNLKTPQGTVLTHTPATSE
GQVTISTMTGSNPSETKAFTAAWSVRNPSPRTSVSAIETAPTTVWRLAKKPYTAPSTSTTPTVRAKPTTQVHHCVVVKPT
PAMPTTPSPSLTTALLPEELSPSPSVLPPILPDLPPKGEYPPDLFSVEERRQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLIMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKQIEAWVKEQLSRRPAAKVMALGDLSKPGDGAIAVDE
LQDNKKLKLPSLLTRGSSSTSLHNSTIRSTIYQLMLHSLDPLREVCLAEEKEEESLNQEARAQPQAKSESKPEDEEPAKL
PAVTVTPAPAPDIKGDQKENPGGQEDVAEAESTGEMTGEEGETAGEGETEEKSGGETQPEGEGETGTQGKGEEREKENEA
EGKGDNEGEGEGEIHAEDGEMEGIEGETESQELSAENHGEAKSDEKGVEDGGGSDGGDNEEEEEEEEEEEEEEEEEEEE
EEEEEGNEEPLSLHWPETRQKQAIYLFLLPIVFPLWLTVPDVRRQVGETIGISEEIMGLTILAAGTSIPDLITSVIVARK
GLGDMAVSSSVGSNIFDITVGLPVPWLLFCLINGLQPVPVSSNGLFCAIVLLFLMLLFVISSIASCKWRMNKILGFTMFL
LYFVFLIISVMLEDRIISCPVSV
```

860 - 879:	EEEEEEEEEEEEEEEEEEEE
861 - 880:	EEEEEEEEEEEEEEEEEEEE
862 - 881:	EEEEEEEEEEEEEEEEEEEE
863 - 882:	EEEEEEEEEEEEEEEEEEEE
864 - 883:	EEEEEEEEEEEEEEEEEEEE
865 - 884:	EEEEEEEEEEEEEEEEEEEE
866 - 885:	EEEEEEEEEEEEEEEEEEEE

A0A2K6DJN9 **A0A2K6DJN9_MACNE** (1006 aa)
Solute carrier family 24 member 1. *Macaca nemestrina (Pig-tailed macaque)*

```
MGKLIRMGPQDRRLLRTKRLPWSRLLFLLGMLIISSTYQHLRGPRGLSSLWAAVSSHQPVKLASRDLPSEEMMMVSSNPP
KPSSEMGGKMLVPQASVGSDEATLSMTVENIPDIPKRTAKMIPTTIKNNYSPTAAGTERRKEDTPTSSRTLTYYTSTSSR
QIVKKYTPTPTGEMKSYSPTQVREKVKYTPSPRGRRVGTYASSTFMTTETSHAITPRTTVKDSDITTTYKILETNSLKRI
MEETTPTTLKGMVDSTPTFLTHEVETNILTSPRSIVEKNNLSPPRRVESNSSAHPWGLVGKNNLKTPQGTVLTHTPATSE
GQVTISTMTGSNPSETKAFTAAWSVRNPSPRTSVSAIETAPTTVWRLAKKPYTAPSTSTTPTVRAKPTTQVHHCVVVKPT
PAMPTTPSPSLTTALLPEELSPSPSVLPPILPDLPPKGEYPPDLFSVEERRQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLIMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKQIEAWVKEQLSRRPAAKVMALGDLSKLPSLLTRGSS
STSLHNSTIRSTIYQLMLHSLDPLREVCLAEEKEEESLNQEARAQPQAKSESKPEDEEPAKLPAVTVTPAPAPDIKGDQK
ENPGGQEDVAEAESTGEMTGEEGETAGEGETEEKSGGETQPEGEGETGTQGKGEEREKENEAEGKGDNEGEGEGEIHAED
GEMEGIEGETESQELSAENHGEAKSDEKGVEDGGGSDGGDNEEEEEEEEEEEEEEEEEEEEEEEEEGNEEPLSLHWPET
RQKQAIYLFLLPIVFPLWLTVPDVRRQESRKFFVFTFLGSIVWIAMFSYLMVWWAHQVGETIGISEEIMGLTILAAGTSI
PDLITSVIVARKGLGDMAVSSSVGSNIFDITVGVESCEMFQLGAIH
```

842 - 861:	EEEEEEEEEEEEEEEEEEEE
843 - 862:	EEEEEEEEEEEEEEEEEEEE
844 - 863:	EEEEEEEEEEEEEEEEEEEE
845 - 864:	EEEEEEEEEEEEEEEEEEEE
846 - 865:	EEEEEEEEEEEEEEEEEEEE
847 - 866:	EEEEEEEEEEEEEEEEEEEE
848 - 867:	EEEEEEEEEEEEEEEEEEEE

A0A2K6DJQ5 **A0A2K6DJQ5_MACNE** (1075 aa)
Solute carrier family 24 member 1. *Macaca nemestrina (Pig-tailed macaque)*

```
MGKLIRMGPQDRRLLRTKRLPWSRLLFLLGMLIISSTYQHLRGPRGLSSLWAAVSSHQPVKLASRDLPSEEMMMVSSNPP
KPSSEMGGKMLVPQASVGSDEATLSMTVENIPDIPKRTAKMIPTTIKNNYSPTAAGTERRKEDTPTSSRTLTYYTSTSSR
QIVKKYTPTPTGEMKSYSPTQVREKVKYTPSPRGRRVGTYASSTFMTTETSHAITPRTTVKDSDITTTYKILETNSLKRI
MEETTPTTLKGMVDSTPTFLTHEVETNILTSPRSIVEKNNLSPPRRVESNSSAHPWGLVGKNNLKTPQGTVLTHTPATSE
GQVTISTMTGSNPSETKAFTAAWSVRNPSPRTSVSAIETAPTTVWRLAKKPYTAPSTSTTPTVRAKPTTQVHHCVVVKPT
PAMPTTPSPSLTTALLPEELSPSPSVLPPILPDLPPKGEYPPDLFSVEERRQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLIMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKQIEAWVKEQLSRRPAAKVMALGDLSKLPSLLTRGSS
STSLHNSTIRSTIYQLMLHSLDPLREVCLAEEKEEESLNQEARAQPQAKSESKPEDEEPAKLPAVTVTPAPAPDIKGDQK
ENPGGQEDVAEAESTGEMTGEEGETAGEGETEEKSGGETQPEGEGETGTQGKGEEREKENEAEGKGDNEGEGEGEIHAED
GEMEGIEGETESQELSAENHGEAKSDEKGVEDGGGSDGGDNEEEEEEEEEEEEEEEEEEEEEEEEEGNEEPLSLHWPET
RQKQAIYLFLLPIVFPLWLTVPDVRRQESRKFFVFTFLGSIVWIAMFSYLMVWWAHQVGETIGISEEIMGLTILAAGTSI
PDLITSVIVARKGLGDMAVSSSVGSNIFDITVGLPVPWLLFCLINGLQPVPVSSNGLFCAIVLLFLMLLFVISSIASCKW
RMNKILGFTMFLLYFVFLIISVMLEDRIISCPVSV
```

842 - 861:	EEEEEEEEEEEEEEEEEEEE

843 - 862:	EEEEEEEEEEEEEEEEEEEE
844 - 863:	EEEEEEEEEEEEEEEEEEEE
845 - 864:	EEEEEEEEEEEEEEEEEEEE
846 - 865:	EEEEEEEEEEEEEEEEEEEE
847 - 866:	EEEEEEEEEEEEEEEEEEEE
848 - 867:	EEEEEEEEEEEEEEEEEEEE

A0A2K6ER50 **A0A2K6ER50_PROCO** (1210 aa)
Euchromatic histone lysine methyltransferase 2. *Propithecus coquereli (Coquerel's sifaka) (Propithecus verreauxi coquereli)*

```
MAAAAGAAAAAAAEGEAPAEMGALLLEKETRGAPERVHGSLGDNPHSEETLPKANPDSLEPTGPSSPASVTVTVGDEGAD
TPVGAIPLIGDEPGTLEGDGDLHGGRILLGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGT
ASAGPEPPPATSSPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTADVAKRRKLNSGAGLSEEL
GSARGSEVTVQKGNPGPLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEE
EEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTL
SPNHAGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELLGCNAAILKRETMRPSSRVALMVL
CETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGT
AAPAPPPLAQDAPGRADTSQPSARMRGHGEPRRPPCDPLTDTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQE
SERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRT
PLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLGTGQVDVNAQDSGGWTPIIWAAEHKHIEV
IRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELR
NKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETS
TMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRL
QLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNII
PVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLP
ELGSLPPVNT
```

299 - 318:	EEEEEEEEEEEEEEEEEEEE
300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE

A0A2K6ER56 **A0A2K6ER56_PROCO** (1226 aa)
Euchromatic histone lysine methyltransferase 2. *Propithecus coquereli (Coquerel's sifaka) (Propithecus verreauxi coquereli)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWAPQLPTGLTSPPVPCRPSQGEAPAEMGA
LLLEKETRGAPERVHGSLGDNPHSEETLPKANPDSLEPTGPSSPASVTVTVGDEGADTPVGAIPLIGDEPGTLEGDGDLH
GGRILLGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGTASAGPEPPPATSSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTADVAKRRKLNSGAGLSEELGSARGSEVTVQKGNPGPLEEWET
VVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRVRVGRAGARG
PARDPAGEGQSPLQLPFSSVQGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELLGCNAAIL
KRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQ
EVTIPRGDGVTPPAGTAAPAPPPLAQDAPGRADTSQPSARMRGHGEPRRPPCDPLTDTIDSSGPSLTLPNGGCLSAVGLP
LGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVL
LQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLGTGQVDVNAQDSG
GWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYH
DCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGE
PCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCW
RNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYY
GNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIAL
EQSRLARLDPHPELLPELGSLPPVNT
```

356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE

A0A2K6ER59 **A0A2K6ER59_PROCO** (1233 aa)
Euchromatic histone lysine methyltransferase 2. *Propithecus coquereli (Coquerel's sifaka) (Propithecus verreauxi coquereli)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWAPQLPTGLTSPPVPCRPSQGEAPAEMGA
LLLEKETRGAPERVHGSLGDNPHSEETLPKANPDSLEPTGPSSPASVTVTVGDEGADTPVGAIPLIGDEPGTLEGDGDLH
GGRILLGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGTASAGPEPPPATSSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTADVAKRRKLNSGAGLSEELGSARGSEVTVQKGNPGPLEEWET
VVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAK
KKWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELL
GCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCG
EDASEAQEVTIPRGDGVTPPAGTAAPAPPPLAQDAPGRADTSQPSARMRGHGEPRRPPCDPLTDTIDSSGPSLTLPNGGC
LSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGS
VEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLGTGQVD
VNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHI
AARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPC
```

```
VNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFEC
NQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVY
CIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKH
SAEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE

A0A2K6ER60 **A0A2K6ER60_PROCO** (1267 aa)
Euchromatic histone lysine methyltransferase 2. *Propithecus coquereli (Coquerel's sifaka) (Propithecus verreauxi coquereli)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWAPQLPTGLTSPPVPCRPSQGEAPAEMGA
LLLEKETRGAPERVHGSLGDNPHSEETLPKANPDSLEPTGPSSPASVTVTVGDEGADTPVGAIPLIGDEPGTLEGDGDLH
GGRILLGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGTASAGPEPPPATSSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTADVAKRRKLNSGAGLSEELGSARGSEVTVQKGNPGPLEEWET
VVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAK
KKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEEL
PLCSCRMEAPKIDRISERAGHKCMATESVDGELLGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTA
GTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLAQDAPGRADTSQPSA
RMRGHGEPRRPPCDPLTDTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGEL
QKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGC
VYSKEEDGSTCLHHAAKIGNLEMVSLLLGTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLH
WASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQL
NRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSS
NCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTF
ICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRD
IRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE

A0A2K6ER64 **A0A2K6ER64_PROCO** (1243 aa)
Euchromatic histone lysine methyltransferase 2. *Propithecus coquereli (Coquerel's sifaka) (Propithecus verreauxi coquereli)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWAPQLPTGLTSPPVPCRPSQGEAPAEMGA
LLLEKETRGAPERVHGSLGDNPHSEETLPKANPDSLEPTGPSSPASVTVTVGDEGADTPVGAIPLIGDEPGTLEGDGDLH
GGRILLGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGTASAGPEPPPATSSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTADVAKRRKLNSGAGLSEELGSARGSEVTVQKGNPGPLEEWET
VVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRVRVARTLTLS
VSVSGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCM
ATESVDGELLGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQL
NGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLAQDAPGRADTSQPSARMRGHGEPRRPPCDPLTDTIDSSG
PSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRT
PLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMV
SLLLGTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAV
NYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVA
RGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFN
KIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLF
DLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFT
CQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE

A0A2K6EUZ8 **A0A2K6EUZ8_PROCO** (203 aa)
Cysteine rich hydrophobic domain 1. *Propithecus coquereli (Coquerel's sifaka) (Propithecus verreauxi coquereli)*

```
MSILLPNMAEFDTISELEEEEEEEAATSSSSPSSSSVSGPDDDEDDDEEEEEEEEEEEEEEEEEEEEEAPPPPRVVSEEHL
RRYAPDPVLVRGAGHITVFGLTNKFDTEFPSVLTGKVAPEEFKTSIGRVNACLKKSLPVNVKWLLCGCLCCCCTLGCSLW
PVICLNKRTRRSIQKLLEWENNRLYHKVILIEFLPKYPIFRPD
```

48 - 67:	EEEEEEEEEEEEEEEEEEEE

A0A2K6EV06 **A0A2K6EV06_PROCO** (223 aa)
Cysteine rich hydrophobic domain 1. *Propithecus coquereli (Coquerel's sifaka) (Propithecus verreauxi coquereli)*

```
MSILLPNMAEFDTISELEEEEEEEAATSSSSPSSSSVSGPDDDEDDDEEEEEEEEEEEEEEEEEEEEAPPPPRVVSEEHL
RRYAPDPVLVRGAGHITVFGLTNKFDTEFPSVLTGKVAPEEFKTSIGRVNACLKKSLPVNVKWLLCGCLCCCCTLGCSLW
PVICLNKRTRRSIQKLLEWENNRLYHKLALHWKLTKRKCETSNMMEYVILIEFLPKYPIFRPD
```

48 - 67:	EEEEEEEEEEEEEEEEEEEE

A0A2K6EZU4 **A0A2K6EZU4_PROCO** (741 aa)
Phospholipid phosphatase related 3. *Propithecus coquereli (Coquerel's sifaka) (Propithecus verreauxi coquereli)*

```
MISTKEKNKTPKDSMTLLPCFYFVELPIVASSIVSLYFLELTDLFKPAKVGFQCYDRTLSMPYVETNEELIPLLMLLSLA
FAAPAASIMVGEGMLYCLQSRLWGRGGGLGGTEGSINAGGCNFNSFLRRTVRFVGVHVFGLCATALVTDVIQLATGYHAP
FFLTVCKPNYTMLGTSCEVNPYITQDICSGHDTHAILSARKTFPSQHATLSAFAAVYVSVSVAPTAPAHMYFNSVISDTT
KLLNHPVDVYAGFLIGAGIAAYLVRHSEVPSPMSVSAPGRQVGQGWPHACHAVGNFQAPPAEKPAAPAPAKDALRALTQR
GHDSVYQQNKSVSTDELGPPGRLEGVPRPVAREKTSLGSLKRASVDVDLLAPRSPMGKENMVTFSNTLPRVSTPSLDDPA
RRHMTIHVPLDASRSKQLISEWKQKSLEGRGLGLPDEASPGHLRAPAEPMAEEEEEEEEEEEEEEEEEEEEEDGPTPPSL
YPTVQARPGLGPRVILPPRAGPQPLVHIPEEGVQAGASLSPKSSATVRAKWLMMAEKGGAAVASGTTPPRVANPPRLLQV
IAMSKASGAPSPKAAETASSSSASSDSSQYRSPSDRDSASIVTIDAHAPHHPVVHLSAGNAPWEWKAAGGGAKGVEGEGG
YELGDLARGFRGGSRPPGVSPGSSISDVDQEEPRFGAVATVNLATGEGLPPLGTADGALGPASRESTLRRHTGGLVLAER
EAGEAEVESYYRKMQARRFQD
```

452 - 471:	EEEEEEEEEEEEEEEEEEEE
453 - 472:	EEEEEEEEEEEEEEEEEEEE

A0A2K6FLD7 **A0A2K6FLD7_PROCO** (675 aa)
YTH domain containing 1. *Propithecus coquereli (Coquerel's sifaka) (Propithecus verreauxi coquereli)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLISKPLSSSVSN
NKRIVSTKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKSQPEKTCLRKRDPERRTKSPTPDGSERVGLEVD
RRASRSSQSSKEEVNSEEYGSDRETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDEEVDEDGEEEEEEEEEEEEEEE
EEEEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSASES
YAGVWSTLPVNEKKLNAAFRSARSVILIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRE
LPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDV
GRRRPEDYDIHNSRKKPRIDYPPEFHQRPGYLKDPRYQEVDRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYP
GMEQPPHHPYYQHHAPPPQAHPPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRD
NRRDRERDRGRDRERERERLCDRDRDRGERGRYRR
```

226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE

A0A2K6FLD9 **A0A2K6FLD9_PROCO** (701 aa)
YTH domain containing 1. *Propithecus coquereli (Coquerel's sifaka) (Propithecus verreauxi coquereli)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLISKPLSSSVSN
NKRIVSTKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKSQPEKTCLRKRDPERRTKSPTPDGSERVGLEVD
RRASRSSQSSKEEVNSEEYGSDRETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDEEVDEDGEEEEEEEEEEEEEEE
EEEEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSASES
YAGSEKKHEKLSSSVRAVRKGVWSTLPVNEKKLNAAFRSARSVILIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGM
NAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMH
SQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQRPGYLKDPRYQEVDSFTNLIPNRRFSGVRRDVFLN
GSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRR
TQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDRGERGRYRR
```

226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE

A0A2K6G9E4 **A0A2K6G9E4_PROCO** (1178 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Propithecus coquereli (Coquerel's sifaka) (Propithecus verreauxi coquereli)*

```
MLLPGLSPRVQPPFPQCAGPQPPPQTPSPPSVRRGVFASSRHATTRARGKMAAAVLSGPSTGSAAGVPGGTGGLSAVNSG
PRLRLLLLESVSGLLQPRAGPAVAPVHPPVRSAPHLPGLMCLLRLHGTVGGAQNLSAVAALVSLSNARLGSIKTRFEGLC
LLSLLVGESPTEIFQQHCVSWLRSIQQVLQSQDPPPTMELAVAVLRDLLRYAAQLPALFRDISMNHLPGLLTSLLGLRPE
CEQSALEGMKACMTYFPRACGSLKGKLASFFLSRVDSLIPQLQQLACECYSRLPSLGAGFSQGLKHTESWEQELHSLLTS
LHSLLGTLYEGAETAPVQNEGPGVETLLSSSEDGDAHVLLRLRQRFSGLARCLVLMLSSEFGAPVSVPVQEILDLICRTL
SISGKNINLLGDGPLRLLLLPSIHLEALDLLCALILACGGRLLRFGVLISRLLPQVLNAWSIGRDSLSPGQERPYSTIRT
KVYAILELWVKVCGASAGVLQGGASGEALLTHLLSDISPPADALKLRSPRGSPDGGLQTGKPSAPKKLKLDVGEAMAPPS
HRKGDSNANSDVCAAALRGLSRTILMCGWHSNLGVLHDLVLPLVMGVQQGEVLGSSPYTSSCCRRELYRLLLALLLAPSP
RCPPPLACALQAFSLGQQEDSLEVSSFCSEALVTCAALTHPRVPPLQSMGPTCPAPAQVPPPEAPSPFRAPPFHPPGPMP
SAGSMASAGPMPSAGPMPSTGSMPSAGPVPPAPTANHLGLPVPGLVSVPPRLLPGPENHRAGSNEDPVLAPSGTPPPTIP
```

```
PDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDSVVIVPEGLPPLPPPPPSGTTPPPIAPAGPPTASPPVPAKEEPEE
LPAAPGPLPPPPPPPPPVPGPVTLPPPQLVPEGTPGWGGPPALEEDLTVININSSDEEEEEEEEEEEEEEEEEEEEEDFE
EEEEDEEEYFEEEEEEEEEFEEEFEEEEGELEEEEEEEDEEEEEELEEVEELEFGSAGGEVEEGGPPPPTLPPALPPPES
PKVQPEPEPEPGLLLEVEEPGAEEEHGAETAPTLAPEVLPSQGEVEREGGSPAAGPPPQELVEEEPSAPPTLLEEGTEGG
GDKVPPPPETPAEEEMETEAEATALQEKEQDDTAAMLADFIDCPPDDEKPPPTTEPDS
```

937 - 956:	EEEEEEEEEEEEEEEEEEEE
938 - 957:	EEEEEEEEEEEEEEEEEEEE

A0A2K6G9H7 **A0A2K6G9H7_PROCO** (905 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Propithecus coquereli (Coquerel's sifaka) (Propithecus verreauxi coquereli)*

```
MELAVAVLRDLLRYAAQLPALFRDISMNHLPGLLTSLLGLRPECEQSALEGMKACMTYFPRACGSLKGKLASFFLSRVDS
LIPQLQQLACECYSRLPSLGAGFSQGLKHTESWEQELHSLLTSLHSLLGTLYEGAETAPVQNEGPGVETLLSSSEDGDAH
VLLRLRQRFSGLARCLVLMLSSEFGAPVSVPVQEILDLICRTLSISGKNINLLGDGPLRLLLLPSIHLEALDLLCALILA
CGGRLLRFGVLISRLLPQVLNAWSIGRDSLSPGQERPYSTIRTKVYAILELWVKVCGASAGVLQGGASGEALLTHLLSDI
SPPADALKLRSPRGSPDGGLQTGKPSAPKKLKLDVGEAMAPPSHRKGDSNANSDVCAAALRGLSRTILMCGWHSNLGVLH
DLVLPLVMGVQQGEVLGSSPYTSSCCRRELYRLLLALLLAPSPRCPPPLACALQAFSLGQQEDSLEVSSFCSEALVTCAA
LTHPRVPPLQSMGPTCPAPAQVPPPEAPSPFRAPPFHPPGPMPSAGSMASAGPMPSAGPMPSTGSMPSAGPVPPAPTANH
LGLPVPGLVSVPPRLLPGPENHRAGSNEDPVLAPSGTPPPTIPPDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDSV
VIVPEGLPPLPPPPPSGTTPPPIAPAGPPTASPPVPAKEEPEELPAAPGPLPPPPPPPPPVPGPVTLPPPQLVPEGTPGW
GGPPALEEDLTVININSSDEEEEEEEEEEEEEEEEEEEEEEDFEEEEEDEEEYFEEEEEEEEEFEEEFEEEEEHGAETAPT
LAPEVLPSQGEVEREGGSPAAGPPPQELVEEEPSAPPTLLEEGTEGGGDKVPPPPETPAEEEMETEAEATALQEKEQDDT
AAMLADFIDCPPDDEKPPPTTEPDS
```

740 - 759:	EEEEEEEEEEEEEEEEEEEE
741 - 760:	EEEEEEEEEEEEEEEEEEEE

A0A2K6GXE5 **A0A2K6GXE5_PROCO** (968 aa)
Solute carrier family 24 member 1. *Propithecus coquereli (Coquerel's sifaka) (Propithecus verreauxi coquereli)*

```
MGKLIRMGSQERRLLRPKRLHWSRLLFLLAILIIGSTYQHLRKPWGFPSLWAEVPSRQPVKLASRDLPSDEMMMVSSDLP
KASSEMESEMVVPQGTAGRDAATPSTTMENTPNMPRGTAETIPTTTKNTYSPTAAGTERVKENAPTTSSRVLNHYTPTSS
RQTVKYYTPIPRGERQSHGPTKAREKVEKYTASPPVRTVDSYAPSTFLAKETSHATTPRTTAKDGETMATYNILKTNSPK
RIVEETTPATLKGMAGNTPTSLTHEIETNILTSPRSIVEKTTLTTPRRVENDSSTSPWGLVGKNNLMTPQRTVLEHTPAI
SEGQVTISTMTGSSPAETKASTAPWSVKNPPPRTSASAVRTAPATVWRLTKKSSAPPSTSATLKVRADPTTQVRQCVVVD
PAPAMPIAPSLSLTTALPPEVPSPSPSELPPGWSDHHPKAEYPPDLFTVEERRQGWVVLHIFGMMYVFVALAIVCDEYFV
PALGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCALFSREILNLTWWPL
FRDVSFYILDLMMLILFFLDSLIAWWESLLLLMAYALYVFAMKWNRWIELWVKEQLSRRPAVKVTALGDLSKGDVAGAEN
TGEMTGEEGETLNEHEGETEAEAEEKGEDEQEAEGKGDNESEGEDEHEGEIQAEDGEMKGDEGETEGQKLNAENQDEAKN
DEKDVGGEGGSDGGDSEEEEEEEEEEEEEEEEEEEEEEEEGENEEPLSLDWPETRQKQAIYLFLLPIVFPLWLTVPDVRRQ
ESKKFFVITFLGSIIWIAMFSYLMVWWAHQVGETIGISEEIMGLTILAAGTSIPDLITSVIVARKGLGDMAVSSSVGSNI
FDITVGLPVPWLLFSLINGLQPVPVSSNGLFCAIVLLFLMLLFVISSIALCKWRMNKILGFTMFLLYFVFLIISVMLEDR
IISCPVSV
```

737 - 756:	EEEEEEEEEEEEEEEEEEEE
738 - 757:	EEEEEEEEEEEEEEEEEEEE
739 - 758:	EEEEEEEEEEEEEEEEEEEE
740 - 759:	EEEEEEEEEEEEEEEEEEEE

A0A2K6GXH4 **A0A2K6GXH4_PROCO** (1109 aa)
Solute carrier family 24 member 1. *Propithecus coquereli (Coquerel's sifaka) (Propithecus verreauxi coquereli)*

```
MGKLIRMGSQERRLLRPKRLHWSRLLFLLAILIIGSTYQHLRKPWGFPSLWAEVPSRQPVKLASRDLPSDEMMMVSSDLP
KASSEMESEMVVPQGTAGRDAATPSTTMENTPNMPRGTAETIPTTTKNTYSPTAAGTERVKENAPTTSSRVLNHYTPTSS
RQTVKYYTPIPRGERQSHGPTKAREKVEKYTASPPVRTVDSYAPSTFLAKETSHATTPRTTAKDGETMATYNILKTNSPK
RIVEETTPATLKGMAGNTPTSLTHEIETNILTSPRSIVEKTTLTTPRRVENDSSTSPWGLVGKNNLMTPQRTVLEHTPAI
SEGQVTISTMTGSSPAETKASTAPWSVKNPPPRTSASAVRTAPATVWRLTKKSSAPPSTSATLKVRADPTTQVRQCVVVD
PAPAMPIAPSLSLTTALPPEVPSPSPSELPPGWSDHHPKAEYPPDLFTVEERRQGWVVLHIFGMMYVFVALAIVCDEYFV
PALGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCALFSREILNLTWWPL
FRDVSFYILDLMMLILFFLDSLIAWWESLLLLMAYALYVFAMKWNRWIELWVKEQLSRRPAVKVTALGDLSKPGDGAIAV
DEPQDNKKLKLPSLLTRGSSSASLHNSTIRSTIYQLMLHSLDPLGEAHPAKDKEEESLNQEARAQPQAEAESRAEEEPAE
LPAVTVTPAPAPDVQGDQEEDLAGQGDVAGAENTGEMTGEEGETLSEGEIGEKDEGETQLDGDGEIKTEGKGDNESEGEI
EAQGKGKGEDEHEAEGKGDNERKGEDEHEGEIQAEDGEMKGDEGETEGQKLNAENQDEAKNDEKDVGGEGGSDGGDSEEE
EEEEEEEEEEEEEEEEEEEEGENEEPLSLDWPETRQKQAIYLFLLPIVFPLWLTVPDVRRQESKKFFVITFLGSIIWIAM
FSYLMVWWAHQVGETIGISEEIMGLTILAAGTSIPDLITSVIVARKGLGDMAVSSSVGSNIFDITVGLPVPWLLFSLING
LQPVPVSSNGLFCAIVLLFLMLLFVISSIALCKWRMNKILGFTMFLLYFVFLIISVMLEDRIISCPVSV
```

878 - 897:	EEEEEEEEEEEEEEEEEEEE
879 - 898:	EEEEEEEEEEEEEEEEEEEE
880 - 899:	EEEEEEEEEEEEEEEEEEEE
881 - 900:	EEEEEEEEEEEEEEEEEEEE

A0A2K6GXM9 **A0A2K6GXM9_PROCO** (1091 aa)
Solute carrier family 24 member 1. *Propithecus coquereli (Coquerel's sifaka) (Propithecus verreauxi coquereli)*

```
MGKLIRMGSQERRLLRPKRLHWSRLLFLLAILIIGSTYQHLRKPWGFPSLWAEVPSRQPVKLASRDLPSDEMMMVSSDLP
KASSEMESEMVVPQGTAGRDAATPSTTMENTPNMPRGTAETIPTTTKNTYSPTAAGTERVKENAPTTSSRVLNHYTPTSS
RQTVKYYTPIPRGERQSHGPTKAREKVEKYTASPPVRTVDSYAPSTFLAKETSHATTPRTTAKDGETMATYNILKTNSPK
RIVEETTPATLKGMAGNTPTSLTHEIETNILTSPRSIVEKTTLTTPRRVENDSSTSPWGLVGKNNLMTPQRTVLEHTPAI
SEGQVTISTMTGSSPAETKASTAPWSVKNPPPRTSASAVRTAPATVWRLTKKSSAPPSTSATLKVRADPTTQVRQCVVVD
PAPAMPIAPSLSLTTALPPEVPSPSPSELPPGWSDHHPKAEYPPDLFTVEERRQGWVVLHIFGMMYVFVALAIVCDEYFV
PALGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCALFSREILNLTWWPL
FRDVSFYILDLMMLILFFLDSLIAWWESLLLLMAYALYVFAMKWNRWIELWVKEQLSRRPAVKVTALGDLSKLPSLLTRG
SSSASLHNSTIRSTIYQLMLHSLDPLGEAHPAKDKEEESLNQEARAQPQAEAESRAEEEPAELPAVTVTPAPAPDVQGDQ
EEDLAGQGDVAGAENTGEMTGEEGETLSEGEIGEKDEGETQLDGDGEIKTEGKGDNESEGEIEAQGKGKGEDEHEAEGKG
DNERKGEDEHEGEIQAEDGEMKGDEGETEGQKLNAENQDEAKNDEKDVGGEGGSDGGDSEEEEEEEEEEEEEEEEEEEE
EEGENEEPLSLDWPETRQKQAIYLFLLPIVFPLWLTVPDVRRQESKKFFVITFLGSIIWIAMFSYLMVWWAHQVGETIGI
SEEIMGLTILAAGTSIPDLITSVIVARKGLGDMAVSSSVGSNIFDITVGLPVPWLLFSLINGLQPVPVSSNGLFCAIVLL
FLMLLFVISSIALCKWRMNKILGFTMFLLYFVFLIISVMLEDRIISCPVSV
```

860 - 879:	EEEEEEEEEEEEEEEEEEEE
861 - 880:	EEEEEEEEEEEEEEEEEEEE
862 - 881:	EEEEEEEEEEEEEEEEEEEE
863 - 882:	EEEEEEEEEEEEEEEEEEEE

A0A2K6H080 **A0A2K6H080_PROCO** (590 aa)
Ran GTPase activating protein 1. *Propithecus coquereli (Coquerel's sifaka) (Propithecus verreauxi coquereli)*

```
MASEDIAKLAETLAKTQVAGGQLSFKGKSLKLNTAEDAKDVIKEIEDFDGLEALRLEGNTVGVEAARVIAKALEKKSELK
RCHWSDMFTGRLRSEIPPALISLGEGLITAGAQLVELDLSDNAFGPDGVQGFEALLKSSACFTLHELKLNNCGMGIGGGK
ILAEALTECHRKSSAQGKPLALKVFVAGRNRLENDGATALAEAFGVIGTLEEVHMPQNGINHPGVTALAQAFAINPLLRV
INLNDNTFTEKGAVAMAETLKTLRQVEVINFGDCLVRSKGAVAIADAIRGGLPKLKELNLSFCEIKRDAALAVAEAMADK
AELEKLDLNGNALGEEGCEQLQEVLDSFNMAKVLASLSDDEDEEEEEEGDEEEEGDEEEEEEEEEEEEEEEEEEEEEEE
PQQRGQGEESATPSRKILDPNGGEPAPVLSSPPPADVSTFLAFPSPEKLLRLGPKSSMLIAQQTDTSDPEKVVSAFLKVS
SVFKDEATVRTAVQDAVDALMKKAFSSSAFNANAFLTRLLVHMGLLKSEDKIKAIANLYGPLMALNHMVQQDYFPKALAP
LLLAFMTKPNGALESCSFARHSLLQTLYKV
```

377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE
379 - 398:	EEEEEEEEEEEEEEEEEEEE
380 - 399:	EEEEEEEEEEEEEEEEEEEE
381 - 400:	EEEEEEEEEEEEEEEEEEEE

A0A2K6KCS3 **A0A2K6KCS3_RHIBE** (676 aa)
YTH domain-containing protein. *Rhinopithecus bieti (Black snub-nosed monkey) (Pygathrix bieti)*

```
LKSDNGELNVLDDILTEVPEQDDELYNPESEQDKTRKGYVRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSNNKRIVS
TKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVDRRASRS
SQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEEEEEEEE
EEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSEKKERKRARGISPIVFDRSGSSASESYAGIL
IFLGVWSTLPVNEKKLNLAFRSARSVILIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRR
ELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRD
VGRRRPEDYDIHNSRKKPRIDYPPEFHQRPGYLKDPRYQEVDRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPY
PGMEQPPHHPYYQHHAPPPQAHPPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPR
DNRRDRERDRGRDRERERERLCDRDRDRGERGRYRR
```

224 - 243:	EEEEEEEEEEEEEEEEEEEE
225 - 244:	EEEEEEEEEEEEEEEEEEEE

A0A2K6KCS5 **A0A2K6KCS5_RHIBE** (728 aa)
YTH domain-containing protein. *Rhinopithecus bieti (Black snub-nosed monkey) (Pygathrix bieti)*

```
LKSDNGELNVLDDILTEVPEQDDELYNPESEQDKTRKGYVRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSNNKRIVS
TKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVDRRASRS
SQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEEEEEEEE
EEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSEKKERKRARGISPIVFDRSGSSASESYAGSE
KKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVILIFSVRESG
KFQGFARLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQ
LCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQRPGYLKDP
RYQEVDSFTNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQAHPPYSGH
HPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDR
GERGRYRR
```

224 - 243:	EEEEEEEEEEEEEEEEEEEE
225 - 244:	EEEEEEEEEEEEEEEEEEEE

A0A2K6KD03 **A0A2K6KD03_RHIBE** (537 aa)
YTH domain-containing protein. *Rhinopithecus bieti (Black snub-nosed monkey) (Pygathrix bieti)*

```
LKSDNGELNVLDDILTEVPEQDDELYNPESEQDKTRKGYVRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSNNKRIVS
TKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVDRRASRS
```

```
SQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEEEEEEEEEEEEEEEEEEEEYE
QDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSEKKERKRARGISPIVFDRSGSSASESYAGSEKKHEKL
SSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVILIFSVRESGKFQGFA
RLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLLFP
PDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRLETFFGLIIGTCIRIT
```

217 - 236:	EEEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE

A0A2K6KL84 **A0A2K6KL84_RHIBE** (1012 aa)
Uncharacterized protein. *Rhinopithecus bieti (Black snub-nosed monkey) (Pygathrix bieti)*

```
MGKLIRMGPQDRRLLRTKRLHWSRLLFLLGMLIIGSTYQHLRRPRGLSSLWAAVSSHQPVKLASRDLPSEEMMMVSSNPP
KPSSEMGGEMLVPQASVGSDEATLSMTVENIPDIPKRTAKMIPTTTKNNYSPTAAGTERRKEDTPTSRRTLTYYTSTSSR
QIVKKYTPTPTGEMKSYSPTQVREKVKYTPSPRGRRVGTYASSTFMTMETSHATTPRTTVKDSDITTTYKILETNSLKRI
MEETTPTTLKGMVDSTPTFLTHEVETNVLTSPRSIVEKNNLSPPRRVESNSSAHPWGLVGKNNLKTPQGTVLTHTPATSE
GQVTISTMTGSNPSETKAFTAAWSVRNPSPRTSVSAIETAPATVWRLAKKPYTAPSTSTTPTVRAKPTTQVHHCVVVKPT
PAMPTTPSPSLTTALLPEELSPSPSVLPPILPDLPPKGEYPPDLFSVEERRQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLIMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKQIEAWVKEQLSRRPAAKVMALGDLSKLPSLLTRGSS
STSLHNSTIRSTIYQLMLHSLDPLREVRLAKEKEEESLNQEARAQPLAKSESKPEEEEPAKLPAVTVTPAPAPDIKGDQK
ENPGGQEDVAEAESTGEMTGEEGETAGEGETEEKSGGETQPEGEGETGTQGKGEEHEKENEAEGKGDNEGEGEGEIHAED
GEMKGIEGETESQELSAENHGEAKIDEKGVEDGGGSDGGDNEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGNEEPLS
LDWPETRQKQAIYLFLLPIVFPLWLTVPDVRRQESRKFFVFTFLGSIVWIAMFSYLMVWWAHQVGETIGISEEIMGLTIL
AAGTSIPDLITSVIVARKGLGDMAVSSSVGSNIFDITVGVESCEMFQLGAIH
```

842 - 861:	EEEEEEEEEEEEEEEEEEEE
843 - 862:	EEEEEEEEEEEEEEEEEEEE
844 - 863:	EEEEEEEEEEEEEEEEEEEE
845 - 864:	EEEEEEEEEEEEEEEEEEEE
846 - 865:	EEEEEEEEEEEEEEEEEEEE
847 - 866:	EEEEEEEEEEEEEEEEEEEE
848 - 867:	EEEEEEEEEEEEEEEEEEEE
849 - 868:	EEEEEEEEEEEEEEEEEEEE
850 - 869:	EEEEEEEEEEEEEEEEEEEE
851 - 870:	EEEEEEEEEEEEEEEEEEEE
852 - 871:	EEEEEEEEEEEEEEEEEEEE
853 - 872:	EEEEEEEEEEEEEEEEEEEE
854 - 873:	EEEEEEEEEEEEEEEEEEEE

A0A2K6KL97 **A0A2K6KL97_RHIBE** (1099 aa)
Uncharacterized protein. *Rhinopithecus bieti (Black snub-nosed monkey) (Pygathrix bieti)*

```
MGKLIRMGPQDRRLLRTKRLHWSRLLFLLGMLIIGSTYQHLRRPRGLSSLWAAVSSHQPVKLASRDLPSEEMMMVSSNPP
KPSSEMGGEMLVPQASVGSDEATLSMTVENIPDIPKRTAKMIPTTTKNNYSPTAAGTERRKEDTPTSRRTLTYYTSTSSR
QIVKKYTPTPTGEMKSYSPTQVREKVKYTPSPRGRRVGTYASSTFMTMETSHATTPRTTVKDSDITTTYKILETNSLKRI
MEETTPTTLKGMVDSTPTFLTHEVETNVLTSPRSIVEKNNLSPPRRVESNSSAHPWGLVGKNNLKTPQGTVLTHTPATSE
GQVTISTMTGSNPSETKAFTAAWSVRNPSPRTSVSAIETAPATVWRLAKKPYTAPSTSTTPTVRAKPTTQVHHCVVVKPT
PAMPTTPSPSLTTALLPEELSPSPSVLPPILPDLPPKGEYPPDLFSVEERRQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLIMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKQIEAWVKEQLSRRPAAKVMALGDLSKPGDGAIAVDE
LQDNKKLKLPSLLTRGSSSTSLHNSTIRSTIYQLMLHSLDPLREVRLAKEKEEESLNQEARAQPLAKSESKPEEEEPAKL
PAVTVTPAPAPDIKGDQKENPGGQEDVAEAESTGEMTGEEGETAGEGETEEKSGGETQPEGEGETGTQGKGEEHEKENEA
EGKGDNEGEGEGEIHAEDGEMKGIEGETESQELSAENHGEAKIDEKGVEDGGGSDGGDNEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEGNEEPLSLDWPETRQKQAIYLFLLPIVFPLWLTVPDVRRQESRKFFVFTFLGSIVWIAMFSYLMVWWAH
QVGETIGISEEIMGLTILAAGTSIPDLITSVIVARKGLGDMAVSSSVGSNIFDITVGLPVPWLLFCLINGLQPVPVSSNG
LFCAIVLLFLMLLFVISSIASCKWRMNKILGFTMFLLYFVFLIISVMLEDRIISCPVSV
```

860 - 879:	EEEEEEEEEEEEEEEEEEEE
861 - 880:	EEEEEEEEEEEEEEEEEEEE
862 - 881:	EEEEEEEEEEEEEEEEEEEE
863 - 882:	EEEEEEEEEEEEEEEEEEEE
864 - 883:	EEEEEEEEEEEEEEEEEEEE
865 - 884:	EEEEEEEEEEEEEEEEEEEE
866 - 885:	EEEEEEEEEEEEEEEEEEEE
867 - 886:	EEEEEEEEEEEEEEEEEEEE
868 - 887:	EEEEEEEEEEEEEEEEEEEE
869 - 888:	EEEEEEEEEEEEEEEEEEEE

870 - 889:	EEEEEEEEEEEEEEEEEEEE
871 - 890:	EEEEEEEEEEEEEEEEEEEE
872 - 891:	EEEEEEEEEEEEEEEEEEEE

A0A2K6KLB1 **A0A2K6KLB1_RHIBE** (1069 aa)
Uncharacterized protein. *Rhinopithecus bieti (Black snub-nosed monkey) (Pygathrix bieti)*

```
MGKLIRMGPQDRRLLRTKRLHWSRLLFLLGMLIIGSTYQHLRRPRGLSSLWAAVSSHQPVKLASRDLPSEEMMMVSSNPP
KPSSEMGGEMLVPQASVGSDEATLSMTVENIPDIPKRTAKMIPTTTKNNYSPTAAGTERRKEDTPTSRRTLTYYTSTSSR
QIVKKYTPTPTGEMKSYSPTQVREKVKYTPSPRGRRVGTYASSTFMTMETSHATTPRTTVKDSDITTTYKILETNSLKRI
MEETTPTTLKGMVDSTPTFLTHEVETNVLTSPRSIVEKNNLSPPRRVESNSSAHPWGLVGKNNLKTPQGTVLTHTPATSE
GQVTISTMTGSNPSETKAFTAAWSVRNPSPRTSVSAIETAPATVWRLAKKPYTAPSTSTTPTVRAKPTTQVHHCVVVKPT
PAMPTTPSPSLTTALLPEELSPSPSVLPPILPDLPPKGEYPPDLFSVEERRQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLIMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKQIEAWVKEQLSRRPAAKVMALGDLSKPGDGAIAVDE
LQDNKKLKLPSLLTRGSSSTSLHNSTIRSTIYQLMLHSLDPLREVRLAKEKEEESLNQEARAQPLAKSESKPEEEEPAKL
PAVTVTPAPAPDIKGDQKENPGGQEDVAEAESTGEMTGEEGETAGEGETEEKSGGETQPEGEGETGTQGKGEEHEKENEA
EGKGDNEGEGEGEIHAEDGEMKGIEGETESQELSAENHGEAKIDEKGVEDGGGSDGGDNEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEGNEEPLSLDWPETRQKQAIYLFLLPIVFPLWLTVPDVRRQVGETIGISEEIMGLTILAAGTSIPDLITS
VIVARKGLGDMAVSSSVGSNIFDITVGLPVPWLLFCLINGLQPVPVSSNGLFCAIVLLFLMLLFVISSIASCKWRMNKIL
GFTMFLLYFVFLIISVMLEDRIISCPVSV
```

860 - 879:	EEEEEEEEEEEEEEEEEEEE
861 - 880:	EEEEEEEEEEEEEEEEEEEE
862 - 881:	EEEEEEEEEEEEEEEEEEEE
863 - 882:	EEEEEEEEEEEEEEEEEEEE
864 - 883:	EEEEEEEEEEEEEEEEEEEE
865 - 884:	EEEEEEEEEEEEEEEEEEEE
866 - 885:	EEEEEEEEEEEEEEEEEEEE
867 - 886:	EEEEEEEEEEEEEEEEEEEE
868 - 887:	EEEEEEEEEEEEEEEEEEEE
869 - 888:	EEEEEEEEEEEEEEEEEEEE
870 - 889:	EEEEEEEEEEEEEEEEEEEE
871 - 890:	EEEEEEEEEEEEEEEEEEEE
872 - 891:	EEEEEEEEEEEEEEEEEEEE

A0A2K6KLB2 **A0A2K6KLB2_RHIBE** (1081 aa)
Uncharacterized protein. *Rhinopithecus bieti (Black snub-nosed monkey) (Pygathrix bieti)*

```
MGKLIRMGPQDRRLLRTKRLHWSRLLFLLGMLIIGSTYQHLRRPRGLSSLWAAVSSHQPVKLASRDLPSEEMMMVSSNPP
KPSSEMGGEMLVPQASVGSDEATLSMTVENIPDIPKRTAKMIPTTTKNNYSPTAAGTERRKEDTPTSRRTLTYYTSTSSR
QIVKKYTPTPTGEMKSYSPTQVREKVKYTPSPRGRRVGTYASSTFMTMETSHATTPRTTVKDSDITTTYKILETNSLKRI
MEETTPTTLKGMVDSTPTFLTHEVETNVLTSPRSIVEKNNLSPPRRVESNSSAHPWGLVGKNNLKTPQGTVLTHTPATSE
GQVTISTMTGSNPSETKAFTAAWSVRNPSPRTSVSAIETAPATVWRLAKKPYTAPSTSTTPTVRAKPTTQVHHCVVVKPT
PAMPTTPSPSLTTALLPEELSPSPSVLPPILPDLPPKGEYPPDLFSVEERRQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLIMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKQIEAWVKEQLSRRPAAKVMALGDLSKLPSLLTRGSS
STSLHNSTIRSTIYQLMLHSLDPLREVRLAKEKEEESLNQEARAQPLAKSESKPEEEEPAKLPAVTVTPAPAPDIKGDQK
ENPGGQEDVAEAESTGEMTGEEGETAGEGETEEKSGGETQPEGEGETGTQGKGEEHEKENEAEGKGDNEGEGEGEIHAED
GEMKGIEGETESQELSAENHGEAKIDEKGVEDGGGSDGGDNEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGNEEPLS
LDWPETRQKQAIYLFLLPIVFPLWLTVPDVRRQESRKFFVFTFLGSIVWIAMFSYLMVWWAHQVGETIGISEEIMGLTIL
AAGTSIPDLITSVIVARKGLGDMAVSSSVGSNIFDITVGLPVPWLLFCLINGLQPVPVSSNGLFCAIVLLFLMLLFVISS
IASCKWRMNKILGFTMFLLYFVFLIISVMLEDRIISCPVSV
```

842 - 861:	EEEEEEEEEEEEEEEEEEEE
843 - 862:	EEEEEEEEEEEEEEEEEEEE
844 - 863:	EEEEEEEEEEEEEEEEEEEE
845 - 864:	EEEEEEEEEEEEEEEEEEEE
846 - 865:	EEEEEEEEEEEEEEEEEEEE
847 - 866:	EEEEEEEEEEEEEEEEEEEE
848 - 867:	EEEEEEEEEEEEEEEEEEEE
849 - 868:	EEEEEEEEEEEEEEEEEEEE
850 - 869:	EEEEEEEEEEEEEEEEEEEE
851 - 870:	EEEEEEEEEEEEEEEEEEEE
852 - 871:	EEEEEEEEEEEEEEEEEEEE
853 - 872:	EEEEEEEEEEEEEEEEEEEE
854 - 873:	EEEEEEEEEEEEEEEEEEEE

A0A2K6KLB5 **A0A2K6KLB5_RHIBE** (985 aa)
Uncharacterized protein. *Rhinopithecus bieti (Black snub-nosed monkey) (Pygathrix bieti)*

```
MGKLIRMGPQDRRLLRTKRLHWSRLLFLLGMLIIGSTYQHLRRPRGLSSLWAAVSSHQPVKLASRDLPSEEMMMVSSNPP
KPSSEMGGEMLVPQASVGSDEATLSMTVENIPDIPKRTAKMIPTTTKNNYSPTAAGTERRKEDTPTSRRTLTYYTSTSSR
QIVKKYTPTPTGEMKSYSPTQVREKVKYTPSPRGRRVGTYASSTFMTMETSHATTPRTTVKDSDITTTYKILETNSLKRI
MEETTPTTLKGMVDSTPTFLTHEVETNVLTSPRSIVEKNNLSPPRRVESNSSAHPWGLVGKNNLKTPQGTVLTHTPATSE
GQVTISTMTGSNPSETKAFTAAWSVRNPSPRTSVSAIETAPATVWRLAKKPYTAPSTSTTPTVRAKPTTQVHHCVVVKPT
PAMPTTPSPSLTTALLPEELSPSPSVLPPILPDLPPKGEYPPDLFSVEERRQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLIMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKQIEAWVKEQLSRRPAAKVMALGDLSKEDVAEAESTG
EMTGEEGETAGEGETEEKSGGETQPEGEGETGTQGKGEEHEKENEAEGKGDNEGEGEGEIHAEDGEMKGIEGETESQELS
AENHGEAKIDEKGVEDGGGSDGGDNEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGNEEPLSLDWPETRQKQAIYLFL
LPIVFPLWLTVPDVRRQESRKFFVFTFLGSIVWIAMFSYLMVWWAHQVGETIGISEEIMGLTILAAGTSIPDLITSVIVA
RKGLGDMAVSSSVGSNIFDITVGLPVPWLLFCLINGLQPVPVSSNGLFCAIVLLFLMLLFVISSIASCKWRMNKILGFTM
FLLYFVFLIISVMLEDRIISCPVSV
```

746 - 765:	EEEEEEEEEEEEEEEEEEEE
747 - 766:	EEEEEEEEEEEEEEEEEEEE
748 - 767:	EEEEEEEEEEEEEEEEEEEE
749 - 768:	EEEEEEEEEEEEEEEEEEEE
750 - 769:	EEEEEEEEEEEEEEEEEEEE
751 - 770:	EEEEEEEEEEEEEEEEEEEE
752 - 771:	EEEEEEEEEEEEEEEEEEEE
753 - 772:	EEEEEEEEEEEEEEEEEEEE
754 - 773:	EEEEEEEEEEEEEEEEEEEE
755 - 774:	EEEEEEEEEEEEEEEEEEEE
756 - 775:	EEEEEEEEEEEEEEEEEEEE
757 - 776:	EEEEEEEEEEEEEEEEEEEE
758 - 777:	EEEEEEEEEEEEEEEEEEEE

A0A2K6L6G4 **A0A2K6L6G4_RHIBE** (1213 aa)
Uncharacterized protein. *Rhinopithecus bieti (Black snub-nosed monkey) (Pygathrix bieti)*

```
MHFPSEAFSLSWHSGCNTSDVCVQWCPLSRHCSTEKSSSIGSMESLEQPGQATYESHLLPIDQNMYPNQRDSAYSSFSAS
SNASDCALSLRPEEAASTDCIMQGPGPTKAPNGRPNVAETSGGSRRTNGGHLTPSSQMSSRPQEGHQSGPAKVVRGPPQP
PVRRDSLQASRAQLLNGEQRRASEPVVPLPQKEKLSLETVLPARNPNRFCCLSGHDQVTSEGHQNCEFSQSPESSQQGSE
HLLMQASTKAVGSPKACDKASSTYSNPLNEASAELAKASFGRPPHLIGPTGHRHSAPEQLLASHLQHVHLDTRGSKGMEL
PPGQDGHQWTLSPLHSSHKGKKSPCPPAGGTHDQYSKERKTRQMDDRSLVLGHQSQSSPPHGEADGHPSEKGLLDPNRTS
RAGSELANQQPSASGSLVQKARDCSSTTKVAGGTEAGEEGDSEHKECSRMGGRRSGGTRGRSIQNRRKSERFATNLRNEI
QRRKAQLQKSKGPLSQLCDTKEPVEETQEPPETPPLTASNTSLLSSCKKPPSPRDKLFNKSMMLRARSSECLSQAPESHE
SRTGLEGRISPGQRLGQSSLGLNTWWKAPDPSSSDPEKAHAHCGVHGGHWRWSREHNSQPLVAVAMEGPSNPGDNKELKA
STAQAGEDAILLPFADRRKFFEESSKSLSTSHLPGLTTHSNKTFTQRPKPIDQNFQPVSSSYRELRRHPVDQSYHSAEQP
YHATDQSYHSMSPLQSETPAYSECFASRGLENSMCCKPLHCGDFDYHRTCSYSCSVQGALVHDPCIYCSGEICPALLKRN
MMPNCYNCRCHHHQCIRCSVCYHNPQHSTLEDNSLAPGNTWKPRKPTVQEFPGDKWNPITGNRKTSQSGREMAHSKNSFS
WATPFRPCLENPALDLSSYRAISSLDLLGDFKHALKKSEETSVYEEGSSLASMPHPLRSRAFSESHISLDPQSTRAWGQH
RRELFSKGDETQSDLLGARKKAFPPPRPPPPNWEKYRLFRAAQQQKQQKQQQQQQQQQQKQQEEEEEEEEEEEEEEEEEE
EEEAEEEEEELPPQYFSSETSGSCALNPEEVLEQPQPLSLGHLEGSGQGSQSVPAEQESFALHSSDFLPPIRGHLGSQPE
QAQPPCYYGIGGLWRTSEQEATESTKQEFQPFSPPPGAPGIPTSYSAYYNISVAKAELLNKLKDQPEMAEIGLGEEEVDH
ELAQKKVKCFDVP
```

1023 - 1042:	EEEEEEEEEEEEEEEEEEEE
1024 - 1043:	EEEEEEEEEEEEEEEEEEEE

A0A2K6L6I1 **A0A2K6L6I1_RHIBE** (1329 aa)
PDZ domain-containing protein. *Rhinopithecus bieti (Black snub-nosed monkey) (Pygathrix bieti)*

```
MENRPGSFQYVPVQLQGGAPWGFTLKGGLEHCEPLTVSKIEDGGKAALSQKMRTGDELVNINGTPLYGSRQEALILIKGS
FRILKLIVRRRNAPVSRPHSWHVAKLLEGCPEAATTMHFPSEAFSLSWHSGCNTSDVCVQWCPLSRHCSTEKSSSIGSME
SLEQPGQATYESHLLPIDQNMYPNQRDSAYSSFSASSNASDCALSLRPEEAASTDCIMQGPGPTKAPNGRPNVAETSGGS
RRTNGGHLTPSSQMSSRPQEGHQSGPAKVVRGPPQPPVRRDSLQASRAQLLNGEQRRASEPVVPLPQKEKLSLETVLPAR
NPNRFCCLSGHDQVTSEGHQNCEFSQSPESSQQGSEHLLMQASTKAVGSPKACDKASSTYSNPLNEASAELAKASFGRPP
HLIGPTGHRHSAPEQLLASHLQHVHLDTRGSKGMELPPGQDGHQWTLSPLHSSHKGKKSPCPPAGGTHDQYSKERKTRQM
DDRSLVLGHQSQSSPPHGEADGHPSEKGLLDPNRTSRAGSELANQQPSASGSLVQKARDCSSTTKVAGGTEAGEEGDSEH
KECSRMGGRRSGGTRGRSIQNRRKSERFATNLRNEIQRRKAQLQKSKGPLSQLCDTKEPVEETQEPPETPPLTASNTSLL
SSCKKPPSPRDKLFNKSMMLRARSSECLSQAPESHESRTGLEGRISPGQRLGQSSLGLNTWWKAPDPSSSDPEKAHAHCG
VHGGHWRWSREHNSQPLVAVAMEGPSNPGDNKELKASTAQAGEDAILLPFADRRKFFEESSKSLSTSHLPGLTTHSNKTF
TQRPKPIDQNFQPVSSSYRELRRHPVDQSYHSAEQPYHATDQSYHSMSPLQSETPAYSECFASRGLENSMCCKPLHCGDF
DYHRTCSYSCSVQGALVHDPCIYCSGEICPALLKRNMMPNCYNCRCHHHQCIRCSVCYHNPQHSTLEDNSLAPGNTWKPR
KPTVQEFPGDKWNPITGNRKTSQSGREMAHSKNSFSWATPFRPCLENPALDLSSYRAISSLDLLGDFKHALKKSEETSVY
EEGSSLASMPHPLRSRAFSESHISLDPQSTRAWGQHRRELFSKGDETQSDLLGARKKAFPPPRPPPPNWEKYRLFRAAQQ
QKQQKQQQQQQQQQQKQQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
GSGQGSQSVPAEQESFALHSSDFLPPIRGHLGSQPEQAQPPCYYGIGGLWRTSEQEATESTKQEFQPFSPPPGAPGIPTS
YSAYYNISVAKAELLNKLKDQPEMAEIGLGEEEVDHELAQKKVKCFDVP
```

1139 - 1158:	EEEEEEEEEEEEEEEEEEEE

1140 - 1159:	EEEEEEEEEEEEEEEEEEEE

A0A2K6L6K7 **A0A2K6L6K7_RHIBE** (1461 aa)
Uncharacterized protein. *Rhinopithecus bieti (Black snub-nosed monkey) (Pygathrix bieti)*

```
NDTALSFSLSLSFFLAAGSSDCEIEDGGKAALSQKMRTGDELVNINGTPLYGSRQEALILIKGSFRILKLIVRRRNAPVS
RPHSWHVAKLLEGCPEAATTMHFPSEAFSLSWHSGCNTSDVCVQWCPLSRHCSTEKSSSIGSMESLEQPGQATYESHLLP
IDQNMYPNQRDSAYSSFSASSNASDCALSLRPEEAASTDCIMQGPGPTKAPNGRPNVAETSGGSRRTNGGHLTPSSQMSS
RPQEGHQSGPAKVVRGPPQPPVRRDSLQASRAQLLNGEQRRASEPVVPLPQKEKLSLETVLPARNPNRFCCLSGHDQVTS
EGHQNCEFSQSPESSQQGSEHLLMQASTKAVGSPKACDKASSTYSNPLNEASAELAKASFGRPPHLIGPTGHRHSAPEQL
LASHLQHVHLDTRGSKGMELPPGQDGHQWTLSPLHSSHKGKKSPCPPAGGTHDQYSKERKTRQMDDRSLVLGHQSQSSPP
HGEADGHPSEKGLLDPNRTSRAGSELANQQPSASGSLVQKARDCSSTTKVAGGTEAGEEGDSEHKECSRMGGRRSGGTRG
RSIQNRRKSERFATNLRNEIQRRKAQLQKSKGPLSQLCDTKEPVEETQEPPETPPLTASNTSLLSSCKKPPSPRDKLFNK
SMMLRARSSECLSQAPESHESRTGLEGRISPGQRLGQSSLGLNTWWKAPDPSSSDPEKAHAHCGVHGGHWRWSREHNSQP
LVAVAMEGPSNPGDNKELKASTAQAGEDAILLPFADRRKFFEESSKSLSTSHLPGLTTHSNKTFTQRPKPIDQNFQPVSS
SYRELRRHPVDQSYHSAEQPYHATDQSYHSMSPLQSETPAYSECFASRGLENSMCCKPLHCGDFDYHRTCSYSCSVQGAL
VHDPCIYCSGEICPALLKRNMMPNCYNCRCHHHQCIRCSVCYHNPQHSTLEDNSLAPGNTWKPRKPTVQEFPGDKWNPIT
GNRKTSQSGREMAHSKNSFSWATPFRPCLENPALDLSSYRAISSLDLLGDFKHALKKSEETSVYEEGSSLASMPHPLRSR
AFSESHISLDPQSTRAWGQHRRELFSKGDETQSDLLGARKKAFPPPRPPPPNWEKYRLFRAQQQQQQQQQQKQQEEEEEE
EEEEEEEEEEEEEEEAEEEEEELPPQYFSSETSGSCALNPEEVLEQPQPLSLGHLEGSGQGSQSVPAEQESFALHSSDFL
PPIRGHLGSQPEQAQPPCYYGIGGLWRTSEQEATESTKQEFQPFSPPPGAPGIPTSYSAYYNISVAKAELLNKLKDQPEM
AEIGLGEEEVDHELAQKKVKYGLFEGISQKLSVLREAQRGTARGPLNAILPLGRGGGQLKSVLPLVFGDLSKWSNLLNAL
KRSSNSEATKEKLVLIEKKQQLTGQLADAKELKEHVDRREKLVFGMVSRYLPQDQLQDYQHFVKMKSALIIEQRELEEKI
KLGEEQLKCLRESLLLGPSNF
```

1115 - 1134:	EEEEEEEEEEEEEEEEEEEE
1116 - 1135:	EEEEEEEEEEEEEEEEEEEE

A0A2K6LC99 **A0A2K6LC99_RHIBE** (1323 aa)
Protein kinase domain-containing protein. *Rhinopithecus bieti (Black snub-nosed monkey) (Pygathrix bieti)*

```
MQCLAAALKDETNMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTRENVALKVESAQQPKQVLKMEVAV
LKKLQGKDHVCRFIGCGRNEKFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESIEAIHSVGFLHRDIKPSNF
AMGRLPSTYRKCYMLDFGLARQYTNTTGDVRPPRNVAGFRGTVRYASVNAHKNREMGRHDDLWSLFYMLVEFAVGQLPWR
KIKDKEQVGMIKEKYEHRMLLKHMPSEFHLFLDHIASLDYFTKPDYQLIMSVFENSMKERGIAENEAFDWEKAGTDALLS
TSTSTPPQQNTRQTAAMFGVVNVTPVPGDLLRENTEDVLQGEHLSDQENAPPILPGRPSEGLGPSPHLVPHPGGPEAEVW
EETDVNRNKLRINIGKSPCVEEEQSRGMGVPSSPVRAAPDSPTTPVRSLRYRRVNSPESERLSTADGRVELPERRSRMDL
PGSPSRQACSSQPAQMLSVDTGHPDRQASGRMDVSASVEQEALSNAFRSVPLAEEEDFDSKEWVIIDKETELKDFPPGAE
PSTSGTTDEEPEELRPLPEEGEERRRLGAEPTVRPRGCSMQVLAEEDLQHLPPQPLPPQLSQADGRSETSQPPTPGSPSH
SPLHSGPRPRRRESDPTGPQRQVFSMAPPFEVNGLPRAVPLSLPYQDFKRDLSDYRERARLLNRVRRVGFSHMLLTTPQV
PLSPVQPQANGKEEEEEEEEDEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEAVAAVALGEVLGPRSGSSSEGSERSTD
RSQEGAPSTLLADDQKESRGRASMADGDLEPEEGSKTLVLVSPGDMKKSPVTAELAPDPDLGTLAALTPQHERPQPTGSQ
LDVSEPGTLSSVLKSEPKPPGPGAGPGAGTVTTGAGGVAVTSSPFTKVERTFVHIAEKTHLNVMSSSGQALRPEEFSTGG
ELGLELASDGGTVEEGAPAPLENGLALSGLNGAEIEGCALSGPPGETPSEMAINSLLNGPALADGPAPVSPLEPSPEKVA
TISPRHHAMPGSRPRSRIPVLLSEEDTGSEPSGSLSAKERWSKRARPQQDLARLVMEKRQGRLLFRLASGASSSSSEEQR
RASETLSGTGSEEDTPASEPAAYLPRKAGRAATTRSRIPRPIGLRMPMPAAAQQLPSRSHGAAPASDTAITSRLQLQTPP
GSATAADLRPKQPPGRGLGPGRAQAGARPPVPRSPGLPTSTSAARNASASPRSQSLSRRESPSPSHQARPGVPPPRGVPS
ARAQPDCTPSPGGSKKGPRGKLQAQRATTKGRAGGAEGRAGAR
```

749 - 768:	EEEEEEEEEEEEEEEEEEEE
750 - 769:	EEEEEEEEEEEEEEEEEEEE
751 - 770:	EEEEEEEEEEEEEEEEEEEE
752 - 771:	EEEEEEEEEEEEEEEEEEEE
753 - 772:	EEEEEEEEEEEEEEEEEEEE
754 - 773:	EEEEEEEEEEEEEEEEEEEE

A0A2K6M8K2 **A0A2K6M8K2_RHIBE** (1232 aa)
Uncharacterized protein. *Rhinopithecus bieti (Black snub-nosed monkey) (Pygathrix bieti)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGAHRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGA
LLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDESENLEGDGDLH
GGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGPEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVVKRRKLTSGGGLSEELGSARRSEVTLAKGDPGSLEEWET
VVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAKK
KWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSG
CNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGE
DASEAQEVTIPRGDGVTPPAGAAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCL
SAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSV
EICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDV
NAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIA
ARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCV
NGVDGESCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECN
QACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYC
IDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHS
AEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE

359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE

A0A2K6M8K7 **A0A2K6M8K7_RHIBE** (1266 aa)
Uncharacterized protein. *Rhinopithecus bieti (Black snub-nosed monkey) (Pygathrix bieti)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGAHRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGA
LLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDESENLEGDGDLH
GGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGPEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVVKRRKLTSGGGLSEELGSARRSEVTLAKGDPGSLEEWET
VVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAKK
KWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEELP
LCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAG
TFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGAAAPAPPPLSQDAPGRADTSQPSAR
MRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQ
KVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCV
YSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHW
ASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLN
RKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGESCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSN
CLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFI
CEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDI
RTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE

A0A2K6M8L7 **A0A2K6M8L7_RHIBE** (1237 aa)
Uncharacterized protein. *Rhinopithecus bieti (Black snub-nosed monkey) (Pygathrix bieti)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGAHRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGA
LLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDESENLEGDGDLH
GGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGPEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSGQSYPPPPSEELGSARRSEVTLAKGDPGSLEEWETVVGDDF
SLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRVRDGATRGRPQGRRERE
GGEPRQSRGVHGVLGHGGEVQGFPQLLFSSVQGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVD
GELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFC
PHCGEDASEAQEVTIPRGDGVTPPAGAAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLP
NGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAA
QKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLST
GQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDT
PLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENV
PIPCVNGVDGESCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPL
IFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKD
GEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSE
KCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE

A0A2K6M8M1 **A0A2K6M8M1_RHIBE** (1215 aa)
Uncharacterized protein. *Rhinopithecus bieti (Black snub-nosed monkey) (Pygathrix bieti)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGAHRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGA
LLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDESENLEGDGDLH
GGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGPEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSGQSYPPPPSEELGSARRSEVTLAKGDPGSLEEWETVVGDDF
SLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRVRDGEDPPGVPMGEVQG
FPQLLFSSVQGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRV
ALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVT
PPAGAAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKA
LVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVD
KQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEH
KHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGA
NPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGESCPEDYKYISE
NCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSG
IKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLC
DPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPH
PELLPELGSLPPVNT
```

350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE

352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE

A0A2K6MRA3 **A0A2K6MRA3_RHIBE** (1001 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Rhinopithecus bieti (Black snub-nosed monkey) (Pygathrix bieti)*

```
MLLPSLSPRVQPAFTQCAGPQPPPHAHSPVGGRRGVFASSRHATTGARGKMAAAVLSGPSAGSAAGVPGGTGGLSAVNSG
PRLRLLLLESVSGLLQPRTGSAVAPVHPPNRSAPHLPGLMCLLRLHGSVGGAQNLSALGALVSLSNARLSSIKTRFEGLC
LLSLLVGESPTELFQQHCVSWLRSIQQVLQTQDPPATMELAVAVLRDLLRYAAQLPALFRDISMNHLPGLLTSLLGLRPE
CEQSALEGMKACMTYFPRACGSLKGKLASFFLSRVDALSPQLQQLACECYSRLPSLGAGFSQGLKHTESWEQELHSLLAS
LHTLLGALYEGAETAPVQNEGPGVEMLLSSEDGDAHVLLRLRQRFSGLARCLGLMLSSEFGAPVSVPVQEILDFICRTLS
VSSKNISLHGDGPLRLLLLPSIHLEALDLLSALILACGSRLLRFGILISRLLPQVLNSWSIGRDSLSPGQERPYSTVRTK
VYALLELWVQVCGASAGVLQGGASGEALLTHLLSDISPPADALKLRSPRGSPDGSLQTGKPSAPKKLKLDVGEAMAPPSH
RKGDSNANSDVCAAALRGLSRTILMCGPLIKEETHRRLHDLVLPLVMGVQQGEVLGSSPYTSSRCRRELYCLLLALLLAP
SPRCPPPLACALQAFSLGQREDSLEVSSFCSEALVTCAALTHPRVPPLQPMGPTCPTPAPVPPPEAPSPFRAPPFHPPGP
MPSVGPMPSAGPMPSAGPMPSAGPVPSARPGPPTTANHLGLSVSGLVSVPPRLLPGPENHRAGSNEDPILAPSGTPPPAI
PPDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDSVVIVPEGLPPLPPPPPSGWGTPVPAKEEPEELPAAPGPVPPPP
PPPPPVPGPVTLPPPQLVPEGTPGGGGPPALEEDLTVININSSDEEEEEEEEEEEEEEEEEEEEEDFEEEEEDEEEYFEE
EEEEEEEFEEEFEEEEAAMLADFIDCPPDDEKPPPPTEPDS
```

925 - 944:	EEEEEEEEEEEEEEEEEEEE
926 - 945:	EEEEEEEEEEEEEEEEEEEE

A0A2K6N291 **A0A2K6N291_RHIBE** (2079 aa)
Histone acetyltransferase (EC 2.3.1.48). *Rhinopithecus bieti (Black snub-nosed monkey) (Pygathrix bieti)*

```
MVKLANPLYTEWILEAIQKIKKQKQRPSEERICHAVSTSHGLDKKTVSEQLELSVQDGSVLKVTNKGLASYKDPDNPGRF
SSVKPGTFPKSTKGSRGSCNDLRNVDWNKLLRRAIEGLEEPNGSSLKNIEKYLRSQSDLTSTTNNPAFQQRLRLGAKRAV
NNGRLLKDGPQYRVNYGSLDGKGAPQYPSAFPSSLPPVSLLPHEKDQPRADPIPICSFCLGTKESNREKKPEELLSCADC
GSSGHPSCLKFCPELTTNVKALRWQCIECKTCSACRVQGRNADNMLFCDSCDRGFHMECCDPPLSRMPKGMWICQVCRPK
KKGRKLLHEKAAQIKRRYAKPIGRPKNKLKQRLLSVTSDEGSMNAFTGRGSPGRGQKTKVCTTPSSGHAASGKDSSSRLA
VTDPTRPGATTKITTTSTYISASTLKVNKKTKGLIDGLTKFFTPSPDGRRSRGEIIDFSKHYRPRKKVSQKQSCTSHVLA
TGTTQKLKPPPSSLPPPTPISGQSPSSQKSSTATSSPSPQSSSSQCSVPSLSGLTTNSQLKALFDGLSHIYTTQGQSRKK
GHPSYAPPKRMRRKTELSSTAKSKAHFFGKRDIRSRFISHSSSSSWGMARGRIFKAIAHFKRTTFLKKHRMLGRLKYKVT
PQMGTPSPGKGSLTDGRIKPDQDDDTEIKINIKQESADVNVIGNKDVVTEEDLDVFKQAQELSWEKIECESGVEDCGRYP
SVIEFGKYEIQTWYSSPYPQEYARLPKLYLCEFCLKYMKSKNILLRHSKKCGWFHPPANEIYRRKDLSVFEVDGNMSKIY
CQNLCLLAKLFLDHKTLYYDVEPFLFYVLTKNDEKGCHLVGYFSKEKLCQQKYNVSCIMIMPQHQRQGFGRFLIDFSYLL
SRREGQAGSPEKPLSDLGRLSYLAYWKSVILEYLYHHHERHISIKAISRATGMCPHDIATTLQHLHMIDKRDGRFVIIRR
EKLILSHMEKLKTCSRANELDPDSLRWTPILISNAAVSEEEREAEKEAERLMEQASCWEKEEQEVLSTRANSRQSPAKVQ
SKNKYLHSPESRPVTGERGQLLELSKESSEEEEEEEEEEEDEEEEEEEEEEEEEDEEEEEEEEEEEEENIQSSPPRLTKP
QSVAIKRKRPFVLKKKRGRKRRRINSSVTTETISETTEVLNEPFDNSDEERPMPQLEPTCEIEVEEDGRKPVLRKAFQHQ
PGKKRQTEEEEGKDNHCFKNGDPCRNNMNDDSSNLKEGSKDNPEPLKCKQAWPKGTKRGLSKWRQNKERKTGFKLNLYTP
PETPMEPDEQVTVEEQKETSEGKTSPTPIRIEEEVKEAGEALLPQEENRRQETCAPVSPNTSPGEKPEDDLIKPEEEEEE
EEEEEEEEEEEEEEEEGGGGNVEKDPDGAKSQEKEEPEISTEKEDSARLDDHEEEEEEDEEPSHNEDHDADDEDDSHMES
AEVEKEELPLPRESFKEVLENQEAFLDLNVQPSHSNPEVLMDCGVDLTASCNSEAKELAGDPEAVPESDEEPPPGEQAQK
QDQKNSKEVDTEFKEGNPATMEIDSETVQAVQSLTQESSEQDDTFQDCAETQEACRSLQNYTHADQSPQIATTLDDCQQS
DHSSPVSSVHSHPGQSVRSVNSPSVPALENSYAQISPDQSAISVPSLQNMETSPMMDVPSVSDHSQQVVDSGFSDLGSIE
STTENYENPSSYDSTMGGSICGNGSSQNSCSYSNLTSSSLTQSSCAVTQQMSNISGSCSMLQQTSISSPPTCSVKSPQGC
VVERPPSSSQQLAQCSMAANFTPPMQLAEIPETGNANIGLYERMGQSDFGAGHYPQPSATFSLAKLQQLTNTLIDHSLPY
SHSAAVTSYANSASLSTPLSNTGLVQLSQSPHSVPGGPQAQATMTPPPNLTPPPMNLPPPLLQRNMAASNIGISHSQRLQ
TQIASKGHVSMRTKSASLSPAAATHQSQIYGRAQTVAMQGPARTLTMQRGMNMSVNLMPAPAYNVNSVNMNMNTLNAMNG
YSMSQPMMNSGYHSNHGYMNQTPQYPMQMQMGMMGTQPYAQQPMQTPPHGNMMYTAPGHHGYMNTGMSKQSLNGSYMRR
```

1355 - 1374:	EEEEEEEEEEEEEEEEEEEE
1356 - 1375:	EEEEEEEEEEEEEEEEEEEE
1357 - 1376:	EEEEEEEEEEEEEEEEEEEE

A0A2K6NXP5 **A0A2K6NXP5_RHIRO** (1209 aa)
Uncharacterized protein. *Rhinopithecus roxellana (Golden snub-nosed monkey) (Pygathrix roxellana)*

```
MAAAAGAAAAAAAEGEAPAEMGALLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGAD
TPVGATPLIGDESESLEGDGDLHGGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGA
AAAGPEPPPATTSPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVVKRRKLTSGGGLSEEL
GSARRSEVTLAKGDPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEE
EEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLS
PNHAGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLC
ETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGAA
APAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQES
ERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTP
LMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVI
RMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRN
KEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGESCPEDYKYISENCETST
MNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQ
LYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIP
VRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPE
LGSLPPVNT
```

299 - 318:	EEEEEEEEEEEEEEEEEEEE
300 - 319:	EEEEEEEEEEEEEEEEEEEE

301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE

A0A2K6NXQ5 **A0A2K6NXQ5_RHIRO** (1187 aa)
Uncharacterized protein. *Rhinopithecus roxellana (Golden snub-nosed monkey) (Pygathrix roxellana)*

```
MAAAAGAAAAAAAAEGEAPAEMGALLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGAD
TPVGATPLIGDESESLEGDGDLHGGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGA
AAAGPEPPPATTSPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSGQSCPPPPSEELGSARRS
EVTLAKGDPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEDEES
GNQSDRRSGRLWGWRSGPEGVGGPPWGEGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEEL
PLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTA
GTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGAAAPAPPPLSQDAPGRADTSQPSA
RMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGEL
QKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGC
VYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLH
WASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQL
NRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGESCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSS
NCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTF
ICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRD
IRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

293 - 312:	EEEEEEEEEEEEEEEEEEEE
294 - 313:	EEEEEEEEEEEEEEEEEEEE
295 - 314:	EEEEEEEEEEEEEEEEEEEE
296 - 315:	EEEEEEEEEEEEEEEEEEEE
297 - 316:	EEEEEEEEEEEEEEEEEEEE

A0A2K6NXQ8 **A0A2K6NXQ8_RHIRO** (1189 aa)
Uncharacterized protein. *Rhinopithecus roxellana (Golden snub-nosed monkey) (Pygathrix roxellana)*

```
MGALLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDESESLEGDG
DLHGGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGPEPPPATTSPEGQPKV
HRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVVKRRKLTSGGGLSEELGSARRSEVTLAKGDPGSLEE
WETVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRK
AKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFE
ELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFC
TAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGAAAPAPPPLSQDAPGRADTSQP
SARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQG
ELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRG
GCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENIC
LHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFAL
QLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGESCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCS
SSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQG
TFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSS
RDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE

A0A2K6NXR8 **A0A2K6NXR8_RHIRO** (1155 aa)
Uncharacterized protein. *Rhinopithecus roxellana (Golden snub-nosed monkey) (Pygathrix roxellana)*

```
MGALLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDESESLEGDG
DLHGGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGPEPPPATTSPEGQPKV
HRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVVKRRKLTSGGGLSEELGSARRSEVTLAKGDPGSLEE
WETVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRK
AKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGE
LSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPH
CGEDASEAQEVTIPRGDGVTPPAGAAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNG
GCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQK
GSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQ
VDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPL
HIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPI
PCVNGVDGESCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIF
ECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGE
VYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKC
KHSAEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE

282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE

A0A2K6NXS2 **A0A2K6NXS2_RHIRO** (1237 aa)
Uncharacterized protein. *Rhinopithecus roxellana (Golden snub-nosed monkey) (Pygathrix roxellana)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGAHRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGA
LLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDESESLEGDGDLH
GGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGPEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSGQSCPPPPSEELGSARRSEVTLAKGDPGSLEEWETVVGDDF
SLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRVRDGARTLTLSVSVSGV
NGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVD
GELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFC
PHCGEDASEAQEVTIPRGDGVTPPAGAAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLP
NGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAA
QKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLST
GQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDT
PLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENV
PIPCVNGVDGESCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPL
IFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKD
GEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSE
KCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE

A0A2K6NXT4 **A0A2K6NXT4_RHIRO** (1215 aa)
Uncharacterized protein. *Rhinopithecus roxellana (Golden snub-nosed monkey) (Pygathrix roxellana)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGAHRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGA
LLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDESESLEGDGDLH
GGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGPEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSGQSCPPPPSEELGSARRSEVTLAKGDPGSLEEWETVVGDDF
SLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRVRDGEDPPGVPMGEVQG
FPQLLFSSVQGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRV
ALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVT
PPAGAAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKA
LVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVD
KQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEH
KHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGA
NPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGESCPEDYKYISE
NCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSG
IKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLC
DPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPH
PELLPELGSLPPVNT
```

350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE

A0A2K6P9Q7 **A0A2K6P9Q7_RHIRO** (852 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Rhinopithecus roxellana (Golden snub-nosed monkey) (Pygathrix roxellana)*

```
MELAVAVLRDLLRYAAQLPALFRDISMNHLPGLLTSLLGLRPECEQSALEGMKACMTYFPRACGSLKGKLASFFLSRVDA
LSPQLQQLACECYSRLPSLGAGFSQGLKHTESWEQELHSLLASLHTLLGALYEGAETAPVQNEGPGVEMLLSSEDGDAHV
LLRLRQRFSGLARCLGLMLSSEFGAPVSVPVQEILDFICRTLSVSSKNISLHGDGPLRLLLLPSIHLEALDLLSALILAC
GSRLLRFGILISRLLPQVLNSWSIGRDSLSPGQERPYSTVRTKVYALLELWVQVCGASAGVLQGGASGEALLTHLLSDIS
PPADALKLRSPRGSPDGSLQTGKPSAPKKLKLDVGEAMAPPSHRKGDSNANSDVCAAALRGLSRTILMCGPLIKEETHRR
LHDLVLPLVMGVQQGEVLGSSPYTSSRCRRELYCLLLALLLAPSPRCPPPLACALQAFSLGQREDSLEVSSFCSEALVTC
AALTHPRVPPLQPMGPTCPTPAPVPPPEAPSPFRAPPFHPPGPMPSVGPMPSAGSMPSAGPMPSAGPVPSARPGPPTTAN
HLGLSVSGLVSVPPRLLPGPENHRAGSNEDPILAPSGTPPPAIPPDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDS
VVIVPEGLPPLKKSHPAGVSGWGTPVPAKEEPEELPAAPGPLPPPQLVPEGTPGGGGPPALEEDLTVININSNDEEEEEE
EEEEEEEEEEEEEEEEEEHGADTAPTLAPEVLPSQGEVEREEGSPLAGPPPQELVEEEPSAPPTLLEEGTEDGGDRVQPP
PETPAEEEMETETEEAEALQEKEQDDTAAMLADFIDCPPDDEKPPPPTEPDS
```

715 - 734:	EEEEEEEEEEEEEEEEEEEE
716 - 735:	EEEEEEEEEEEEEEEEEEEE
717 - 736:	EEEEEEEEEEEEEEEEEEEE
718 - 737:	EEEEEEEEEEEEEEEEEEEE

719 - 738:	EEEEEEEEEEEEEEEEEEEE

A0A2K6PGT5 **A0A2K6PGT5_RHIRO** (2078 aa)
Histone acetyltransferase (EC 2.3.1.48). *Rhinopithecus roxellana (Golden snub-nosed monkey) (Pygathrix roxellana)*

```
MVKLANPLYTEWILEAIQKIKKQKQRPSEERICHAVSTSHGLDKKTVSEQLELSVQDGSVLKVTNKGLASYKDPDNPGRF
SSVKPGTFPKSTKGSRGSCNDLRNVDWNKLLRRAIEGLEEPNGSSLKNIEKYLRSQSDLTSTTNNPAFQQRLRLGAKRAV
NNGRLLKDGPQYRVNYGSLDGKGAPQYPSAFPSSLPPVSLLPHEKDQPRADPIPICSFCLGTKESNREKKPEELLSCADC
GSSGHPSCLKFCPELTTNVKALRWQCIECKTCSACRVQGRNADNMLFCDSCDRGFHMECCDPPLSRMPKGMWICQVCRPK
KKGRKLLHEKAAQIKRRYAKPIGRPKNKLKQRLLSVTSDEGSMNAFTGRGSPGRGQKTKVCTTPSSGHAASGKDSSSRLA
VTDPTRPGATTKITTTSTYISASTLKVNKKTKGLIDGLTKFFTPSPDGRRSRGEIIDFSKHYRPRKKVSQKQSCTSHVLA
TGTTQKLKPPPSSLPPPTPISGQSPSSQKSSTATSSPSPQSSSSQCSVPSLSGLTTNSQLKALFDGLSHIYTTQGQSRKK
GHPSYAPPKRMRRKTELSSTAKSKAHFFGKRDIRSRFISHSSSSSWGMARGRIFKAIAHFKRTTFLKKHRMLGRLKYKVT
PQMGTPSPGKGSLTDGRIKPDQDDDTEIKINIKQESADVNVIGNKDVVTEEDLDVFKQAQELSWEKIECESGVEDCGRYP
SVIEFGKYEIQTWYSSPYPQEYARLPKLYLCEFCLKYMKSKNILLRHSKKCGWFHPPANEIYRRKDLSVFEVDGNMSKIY
CQNLCLLAKLFLDHKTLYYDVEPFLFYVLTKNDEKGCHLVGYFSKEKLCQQKYNVSCIMIMPQHQRQGFGRFLIDFSYLL
SRREGQAGSPEKPLSDLGRLSYLAYWKSVILEYLYHHHERHISIKAISRATGMCPHDIATTLQHLHMIDKRDGRFVIIRR
EKLILSHMEKLKTCSRANELDPDSLRWTPILISNAAVSEEEREAEKEAERLMEQASCWEKEEQEVLSTRANSRQSPAKVQ
SKNKYLHSPESRPVTGERGQLLELSKESSEEEEEEEEEEEDEEEEEEEEEEEEEDEEEEEEEEEEEENIQSSPPRLTKPQ
SVAIKRKRPFVLKKKRGRKRRRINSSVTTETISETTEVLNEPFDNSDEERPMPQLEPTCEIEVEEDGRKPVLRKAFQHQP
GKKRQTEEEEGKDNHCFKNGDPCRNNMNDDSSNLKEGSKDNPEPLKCKQAWPKGTKRGLSKWRQNKERKTGFKLNLYTPP
ETPMEPDEQVTVEEQKETSEGKTSPTPIRIEEEVKEAGEALLPQEENRRQETCAPVSPNTSPGEKPEDDLIKPEEEEEEE
EEEEEEEEEEEEEEEGGGGNVEKDPDGAKSQEKEEPEISTEKEDSARLDDHEEEEEEDEEPSHNEDHDADDEDDSHMESA
EVEKEELPLPRESFKEVLENQEAFLDLNVQPSHSNPEVLMDCGVDLTASCNSEAKELAGDPEAVPESDEEPPPGEQAQKQ
DQKNSKEVDTEFKEGNPATMEIDSETVQAVQSLTQESSEQDDTFQDCAETQEACRSLQNYTHADQSPQIATTLDDCQQSD
HSSPVSSVHSHPGQSVRSVNSPSVPALENSYAQISPDQSAISVPSLQNMETSPMMDVPSVSDHSQQVVDSGFSDLGSIES
TTENYENPSSYDSTMGGSICGNGSSQNSCSYSNLTSSSLTQSSCAVTQQMSNISGSCSMLQQTSISSPPTCSVKSPQGCV
VERPPSSSQQLAQCSMAANFTPPMQLAEIPETGNANIGLYERMGQSDFGAGHYPQPSATFSLAKLQQLTNTLIDHSLPYS
HSAAVTSYANSASLSTPLSNTGLVQLSQPPHSVPGGPQAQATMTPPPNLTPPPMNLPPPLLQRNMAASNIGISHSQRLQT
QIASKGHVSMRTKSASLSPAAATHQSQIYGRAQTVAMQGPARTLTMQRGMNMSVNLMPAPAYNVNSVNMNMNTLNAMNGY
SMSQPMMNSGYHSNHGYMNQTPQYPMQMQMGMMGTQPYAQQPMQTPPHGNMMYTAPGHHGYMNTGMSKQSLNGSYMRR
```

1354 - 1373:	EEEEEEEEEEEEEEEEEEEE
1355 - 1374:	EEEEEEEEEEEEEEEEEEEE
1356 - 1375:	EEEEEEEEEEEEEEEEEEEE

A0A2K6Q0P7 **A0A2K6Q0P7_RHIRO** (728 aa)
YTH domain-containing protein. *Rhinopithecus roxellana (Golden snub-nosed monkey) (Pygathrix roxellana)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSN
NKRIVSTKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEE
EEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSA
SESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVIL
IFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQE
IELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQ
RPGYLKDPRYQEVDRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQAHPPYSGH
HPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDR
GERGRYRR
```

230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE

A0A2K6Q0R3 **A0A2K6Q0R3_RHIRO** (710 aa)
YTH domain-containing protein. *Rhinopithecus roxellana (Golden snub-nosed monkey) (Pygathrix roxellana)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSN
NKRIVSTKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEE
EEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSA
SESYADQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVILIFSVRESGKFQGFARLSS
ESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLLFPPDES
IDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQRPGYLKDPRYQEVDRRFS
GVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHHPVPHEARYRDKRVHDYD
MRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDRGERGRYRR
```

230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE

A0A2K6Q0R8 **A0A2K6Q0R8_RHIRO** (731 aa)
YTH domain-containing protein. *Rhinopithecus roxellana (Golden snub-nosed monkey) (Pygathrix roxellana)*

```
LKSDNGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSNNKRIV
STKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVDRRASR
SSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEEEEEE
EEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSASESYA
GSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVILIFSVR
ESGKFQGFARLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELEC
GTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQRPGYL
KDPRYQEVDSFTNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQAHPPY
SGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRD
```

RDRGERGRYRR

225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE

A0A2K6Q0S4 **A0A2K6Q0S4_RHIRO** (540 aa)
YTH domain-containing protein. *Rhinopithecus roxellana (Golden snub-nosed monkey) (Pygathrix roxellana)*

LKSDNGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSNNKRIV
STKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVDRRASR
SSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEEEEEEEEEEEEEEEEEEEEY
EQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSASESYAGSEKKH
EKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVILIFSVRESGKFQ
GFARLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCL
LFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRLETFFGLIIGTCIRIT

218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE

A0A2K6QDX4 **A0A2K6QDX4_RHIRO** (1094 aa)
Uncharacterized protein. *Rhinopithecus roxellana (Golden snub-nosed monkey) (Pygathrix roxellana)*

MGKLIRMGPQDRRLLRTKRLHWSRLLFLLGMLIIGSTYQHLRRPRGLSSLWAAVSSHQPVKLASRDLASEEMMMVSSNPP
KPSSEMGGEMLVPQASVGSDEATLSMTVENIPDIPKRTAKMIPTTTKNNYSPTAAGTERRKEDTPTSRRTLTYYTSTSSR
QIVKKYTPTPTGEMKSYSPTQVREKVKYTPSPRGRRVGTYASSTFMTMETSHATTPRTTVKDSDITTTYKILETNSLKRI
MEETTPTTLKGMVDSTPTFLTHEVETNVLTSPRSIVEKNNLSPPRRVESNSSAHPWGLVGKNNLKTPQGTVLTHTPATSE
GQVTISTMTGSNPSETKAFTAAWSVRNPSPRTSVSAIETAPATVWRLAKKPYTAPSTSTTPTVRAKPTTQVHHCVVVKPT
PAMPTTPSPSLTTALLPEELSPSPSVLPPILPDLPPKGEYPPDLFSVEERRQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLIMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKQIEAWVKEQLSRRPAAKVMALGDLSKPGDGAIAVDE
LQDNKKLKLPSLLTRGSSSTSLHNSTIRSTIYQLMLHSLDPLREVRLAKEKEEESLNQEARAQPLAKSESKPEEEEPAKL
PAVTVTPAPAPDIKGDQKENPGGQEDVAEAESTGEMTGEEGETAGEGETEEKSGGETQPEGEGETGTQGKGEEHEKENEA
EGKGDNEGEGEGEIHAEDGEMKGIEGETESQELSAENHGEAKIDEKGVEDGGGSDGGDNEEEEEEEEEEEEEEEEEEEEE
EEEEEEGNEEPLSLDWPETRQKQAIYLFLLPIVFPLWLTVPDVRRQESRKFFVFTFLGSIVWIAMFSYLMVWWAHQVGET
IGISEEIMGLTILAAGTSIPDLITSVIVARKGLGDMAVSSSVGSNIFDITVGLPVPWLLFCLINGLQPVPVSSNGLFCAI
VLLFLMLLFVISSIASCKWRMNKILGFTMFLLYFVFLIISVMLEDRIISCPVSV

860 - 879:	EEEEEEEEEEEEEEEEEEEE
861 - 880:	EEEEEEEEEEEEEEEEEEEE
862 - 881:	EEEEEEEEEEEEEEEEEEEE
863 - 882:	EEEEEEEEEEEEEEEEEEEE
864 - 883:	EEEEEEEEEEEEEEEEEEEE
865 - 884:	EEEEEEEEEEEEEEEEEEEE
866 - 885:	EEEEEEEEEEEEEEEEEEEE
867 - 886:	EEEEEEEEEEEEEEEEEEEE

A0A2K6QDY0 **A0A2K6QDY0_RHIRO** (1064 aa)
Uncharacterized protein. *Rhinopithecus roxellana (Golden snub-nosed monkey) (Pygathrix roxellana)*

MGKLIRMGPQDRRLLRTKRLHWSRLLFLLGMLIIGSTYQHLRRPRGLSSLWAAVSSHQPVKLASRDLASEEMMMVSSNPP
KPSSEMGGEMLVPQASVGSDEATLSMTVENIPDIPKRTAKMIPTTTKNNYSPTAAGTERRKEDTPTSRRTLTYYTSTSSR
QIVKKYTPTPTGEMKSYSPTQVREKVKYTPSPRGRRVGTYASSTFMTMETSHATTPRTTVKDSDITTTYKILETNSLKRI
MEETTPTTLKGMVDSTPTFLTHEVETNVLTSPRSIVEKNNLSPPRRVESNSSAHPWGLVGKNNLKTPQGTVLTHTPATSE
GQVTISTMTGSNPSETKAFTAAWSVRNPSPRTSVSAIETAPATVWRLAKKPYTAPSTSTTPTVRAKPTTQVHHCVVVKPT
PAMPTTPSPSLTTALLPEELSPSPSVLPPILPDLPPKGEYPPDLFSVEERRQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLIMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKQIEAWVKEQLSRRPAAKVMALGDLSKPGDGAIAVDE
LQDNKKLKLPSLLTRGSSSTSLHNSTIRSTIYQLMLHSLDPLREVRLAKEKEEESLNQEARAQPLAKSESKPEEEEPAKL
PAVTVTPAPAPDIKGDQKENPGGQEDVAEAESTGEMTGEEGETAGEGETEEKSGGETQPEGEGETGTQGKGEEHEKENEA
EGKGDNEGEGEGEIHAEDGEMKGIEGETESQELSAENHGEAKIDEKGVEDGGGSDGGDNEEEEEEEEEEEEEEEEEEEEE
EEEEEEGNEEPLSLDWPETRQKQAIYLFLLPIVFPLWLTVPDVRRQVGETIGISEEIMGLTILAAGTSIPDLITSVIVAR
KGLGDMAVSSSVGSNIFDITVGLPVPWLLFCLINGLQPVPVSSNGLFCAIVLLFLMLLFVISSIASCKWRMNKILGFTMF
LLYFVFLIISVMLEDRIISCPVSV

860 - 879:	EEEEEEEEEEEEEEEEEEEE
861 - 880:	EEEEEEEEEEEEEEEEEEEE
862 - 881:	EEEEEEEEEEEEEEEEEEEE
863 - 882:	EEEEEEEEEEEEEEEEEEEE
864 - 883:	EEEEEEEEEEEEEEEEEEEE
865 - 884:	EEEEEEEEEEEEEEEEEEEE

866 - 885:	EEEEEEEEEEEEEEEEEEEE
867 - 886:	EEEEEEEEEEEEEEEEEEEE

A0A2K6QDY1 **A0A2K6QDY1_RHIRO** (1076 aa)
Uncharacterized protein. *Rhinopithecus roxellana (Golden snub-nosed monkey) (Pygathrix roxellana)*

```
MGKLIRMGPQDRRLLRTKRLHWSRLLFLLGMLIIGSTYQHLRRPRGLSSLWAAVSSHQPVKLASRDLASEEMMMVSSNPP
KPSSEMGGEMLVPQASVGSDEATLSMTVENIPDIPKRTAKMIPTTTKNNYSPTAAGTERRKEDTPTSRRTLTYYTSTSSR
QIVKKYTPTPTGEMKSYSPTQVREKVKYTPSPRGRRVGTYASSTFMTMETSHATTPRTTVKDSDITTTYKILETNSLKRI
MEETTPTTLKGMVDSTPTFLTHEVETNVLTSPRSIVEKNNLSPPRRVESNSSAHPWGLVGKNNLKTPQGTVLTHTPATSE
GQVTISTMTGSNPSETKAFTAAWSVRNPSPRTSVSAIETAPATVWRLAKKPYTAPSTSTTPTVRAKPTTQVHHCVVVKPT
PAMPTTPSPSLTTALLPEELSPSPSVLPPILPDLPPKGEYPPDLFSVEERRQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLIMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKQIEAWVKEQLSRRPAAKVMALGDLSKLPSLLTRGSS
STSLHNSTIRSTIYQLMLHSLDPLREVRLAKEKEEESLNQEARAQPLAKSESKPEEEEPAKLPAVTVTPAPAPDIKGDQK
ENPGGQEDVAEAESTGEMTGEEGETAGEGETEEKSGGETQPEGEGETGTQGKGEEHEKENEAEGKGDNEGEGEGEIHAED
GEMKGIEGETESQELSAENHGEAKIDEKGVEDGGGSDGGDNEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGNEEPLSLDWPE
TRQKQAIYLFLLPIVFPLWLTVPDVRRQESRKFFVFTFLGSIVWIAMFSYLMVWWAHQVGETIGISEEIMGLTILAAGTS
IPDLITSVIVARKGLGDMAVSSSVGSNIFDITVGLPVPWLLFCLINGLQPVPVSSNGLFCAIVLLFLMLLFVISSIASCK
WRMNKILGFTMFLLYFVFLIISVMLEDRIISCPVSV
```

842 - 861:	EEEEEEEEEEEEEEEEEEEE
843 - 862:	EEEEEEEEEEEEEEEEEEEE
844 - 863:	EEEEEEEEEEEEEEEEEEEE
845 - 864:	EEEEEEEEEEEEEEEEEEEE
846 - 865:	EEEEEEEEEEEEEEEEEEEE
847 - 866:	EEEEEEEEEEEEEEEEEEEE
848 - 867:	EEEEEEEEEEEEEEEEEEEE
849 - 868:	EEEEEEEEEEEEEEEEEEEE

A0A2K6QDY4 **A0A2K6QDY4_RHIRO** (1007 aa)
Uncharacterized protein. *Rhinopithecus roxellana (Golden snub-nosed monkey) (Pygathrix roxellana)*

```
MGKLIRMGPQDRRLLRTKRLHWSRLLFLLGMLIIGSTYQHLRRPRGLSSLWAAVSSHQPVKLASRDLASEEMMMVSSNPP
KPSSEMGGEMLVPQASVGSDEATLSMTVENIPDIPKRTAKMIPTTTKNNYSPTAAGTERRKEDTPTSRRTLTYYTSTSSR
QIVKKYTPTPTGEMKSYSPTQVREKVKYTPSPRGRRVGTYASSTFMTMETSHATTPRTTVKDSDITTTYKILETNSLKRI
MEETTPTTLKGMVDSTPTFLTHEVETNVLTSPRSIVEKNNLSPPRRVESNSSAHPWGLVGKNNLKTPQGTVLTHTPATSE
GQVTISTMTGSNPSETKAFTAAWSVRNPSPRTSVSAIETAPATVWRLAKKPYTAPSTSTTPTVRAKPTTQVHHCVVVKPT
PAMPTTPSPSLTTALLPEELSPSPSVLPPILPDLPPKGEYPPDLFSVEERRQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLIMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKQIEAWVKEQLSRRPAAKVMALGDLSKLPSLLTRGSS
STSLHNSTIRSTIYQLMLHSLDPLREVRLAKEKEEESLNQEARAQPLAKSESKPEEEEPAKLPAVTVTPAPAPDIKGDQK
ENPGGQEDVAEAESTGEMTGEEGETAGEGETEEKSGGETQPEGEGETGTQGKGEEHEKENEAEGKGDNEGEGEGEIHAED
GEMKGIEGETESQELSAENHGEAKIDEKGVEDGGGSDGGDNEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGNEEPLSLDWPE
TRQKQAIYLFLLPIVFPLWLTVPDVRRQESRKFFVFTFLGSIVWIAMFSYLMVWWAHQVGETIGISEEIMGLTILAAGTS
IPDLITSVIVARKGLGDMAVSSSVGSNIFDITVGVESCEMFQLGAIH
```

842 - 861:	EEEEEEEEEEEEEEEEEEEE
843 - 862:	EEEEEEEEEEEEEEEEEEEE
844 - 863:	EEEEEEEEEEEEEEEEEEEE
845 - 864:	EEEEEEEEEEEEEEEEEEEE
846 - 865:	EEEEEEEEEEEEEEEEEEEE
847 - 866:	EEEEEEEEEEEEEEEEEEEE
848 - 867:	EEEEEEEEEEEEEEEEEEEE
849 - 868:	EEEEEEEEEEEEEEEEEEEE

A0A2K6QDZ1 **A0A2K6QDZ1_RHIRO** (980 aa)
Uncharacterized protein. *Rhinopithecus roxellana (Golden snub-nosed monkey) (Pygathrix roxellana)*

```
MGKLIRMGPQDRRLLRTKRLHWSRLLFLLGMLIIGSTYQHLRRPRGLSSLWAAVSSHQPVKLASRDLASEEMMMVSSNPP
KPSSEMGGEMLVPQASVGSDEATLSMTVENIPDIPKRTAKMIPTTTKNNYSPTAAGTERRKEDTPTSRRTLTYYTSTSSR
QIVKKYTPTPTGEMKSYSPTQVREKVKYTPSPRGRRVGTYASSTFMTMETSHATTPRTTVKDSDITTTYKILETNSLKRI
MEETTPTTLKGMVDSTPTFLTHEVETNVLTSPRSIVEKNNLSPPRRVESNSSAHPWGLVGKNNLKTPQGTVLTHTPATSE
GQVTISTMTGSNPSETKAFTAAWSVRNPSPRTSVSAIETAPATVWRLAKKPYTAPSTSTTPTVRAKPTTQVHHCVVVKPT
PAMPTTPSPSLTTALLPEELSPSPSVLPPILPDLPPKGEYPPDLFSVEERRQGWVVLHIFGMMYVFVALAIVCDEYFVPA
LGVITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILNLTWWPLFR
DVSFYILDLIMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKQIEAWVKEQLSRRPAAKVMALGDLSKEDVAEAESTG
EMTGEEGETAGEGETEEKSGGETQPEGEGETGTQGKGEEHEKENEAEGKGDNEGEGEGEIHAEDGEMKGIEGETESQELS
AENHGEAKIDEKGVEDGGGSDGGDNEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGNEEPLSLDWPETRQKQAIYLFLLPIVF
PLWLTVPDVRRQESRKFFVFTFLGSIVWIAMFSYLMVWWAHQVGETIGISEEIMGLTILAAGTSIPDLITSVIVARKGLG
DMAVSSSVGSNIFDITVGLPVPWLLFCLINGLQPVPVSSNGLFCAIVLLFLMLLFVISSIASCKWRMNKILGFTMFLLYF
VFLIISVMLEDRIISCPVSV
```

746 - 765:	EEEEEEEEEEEEEEEEEEEE
747 - 766:	EEEEEEEEEEEEEEEEEEEE
748 - 767:	EEEEEEEEEEEEEEEEEEEE
749 - 768:	EEEEEEEEEEEEEEEEEEEE
750 - 769:	EEEEEEEEEEEEEEEEEEEE
751 - 770:	EEEEEEEEEEEEEEEEEEEE
752 - 771:	EEEEEEEEEEEEEEEEEEEE
753 - 772:	EEEEEEEEEEEEEEEEEEEE

A0A2K6QJM3 **A0A2K6QJM3_RHIRO** (1201 aa)
SR-related CTD associated factor 1. *Rhinopithecus roxellana (Golden snub-nosed monkey) (Pygathrix roxellana)*

```
MEEEDESRGKTEESGEDRGDGPPDRDPTLSPSAFILRAIQQAVGSSLQGDLPNDKDGSRCHGLRWRRCRSPRSEPRSQES
GGTDTATVLDMAADSFLAGLVSVLDPPDTWVPSRLDLRPGESEDMLELVAEVRIGDRDPIPLPVPSLLPRLRAWRTGKTV
SPQSDSSRPACARHLTLGTGDGGPAPPPAPSSASSSPSPSPTYSPPPAPEQKYDPFEPTGSNPSSSAGTPSPEEEEEEEE
EEEEEEEEEEEEEEGLSQSISRISETLAGIYDDNSLSQDFPGDESPRPDPQPTQPPPAPGTPPQADSTRADGATRRRVFV
VGTEAEACREGKVSVEVVTAGGTTLPPPLMPPGDSEIEEGEIVQPEEEPRVALSLFRPGGRAARPPPAASATPTAQPLPQ
PPAPRAPEGDDFLSLHAESDGEGALQVDLGEPAPAPPAADSRWGGLDLRRKXXXXXXXXXXXXXXXXXXXXXXXXXXXX
RRRGGSRRSRSREKRRRRRRSASPPPATSSSSSSRRERHRGKHRDGGGSKKKKKRSRSRGEKRSGDGSEKAPAPAPPPSG
STSGGDRDSRRRGAVPPSIQDLTDHDLFAIKRTITVGRLDKSDPRGPSPAPASSPKREVLYDSEGLSGEERGGKSSQKDR
RRSGAASSSSSSREKGSRRKALDGGDRDRDRDRDRDRDRSSKKARPPKESAPSSGPPPKPPVSSGSGSSSSSSSCSSRKV
KLQSKVAVLIREGVSSTTPAKDAASAGLGSIGVKFSRDRESRSPFLKPEERAPTEMAKAAPGSTKPKKTKVKAKAGAKKA
KGTKGKTKPSKTRKKVRSGGGSGGSGGPVSLKKSKADSCSQAAGTKGAEETSWSGEERAAKVPSTPPPKVAPPPPALTPD
SQTVDSSCKTPEVSFLPEEATEEAGVRGGAEEEEEEEEEEEEEEEEEEQQPATTTATSTAAAAPSTAPSAGSTAGDSGAE
DGPASRVSQLPTLPPPMPWNLPAGVDCTTSGVLALTALLFKMEEANLASRAKAQELIQATNQILSHRKPPSSLGVTPAPV
PTSLGLPPGPSSYLLPGSLPLGGCGSTPPTPTGLAATSDKREGSSSSEGRGDTDKYLKKLHTQERAVEEVKLAIKPYYQK
KDITKEEYKDILRKAVHKICHSKSGEINPVKVSNLVRAYVQRYRYFRKHGRKPGDPPGPPRPPKEPGPPDKGGPGLPLPP
L
```

233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE

A0A2K6R034 **A0A2K6R034_RHIRO** (1386 aa)
ASD2 domain-containing protein. *Rhinopithecus roxellana (Golden snub-nosed monkey) (Pygathrix roxellana)*

```
MHFPSEAFSLSWHSGCNTSDVCVQWCPLSRHCSTEKSSSIGSMESLEQPGQATYESHLLPIDQNMYPNQRDSAYSSFSAS
SNASDCALSLRPEEAASTDCIMQGPGPTKAPNGRPNVAETSGGSRRTNGGHLTPSSQMSSRPQEGHQSGPAKVVRGPPQP
PVRRDSLQASRAQLLNGEQRRASEPVVPLPQKEKLSLETVLPARNPNRFCCLSGHDQVTSEGHQNCEFSQSPESSQQGSE
HLLMQASTKAVGSPKACDKASSTYSNPLNEASAELAKASFGRPPHLIGPTGHRHSAPEQLLASHLQHVHLDTRGSKGMEL
PPGQDGHQWTLSPLHSSHKGKKSPCPPAGGTHDQYSKERKTRQMDDRSLVLGHQSQSSPPHGEADGHPSEKGLLDPNRTS
RAGSELANQQPSASGSLVQKARDCSSTTKVAGGTEAGEEGDSEHKECSRMGGRRSGGTRGRSIQNRRKSERFATNLRNEI
QRRKAQLQKSKGPLSQLCDTKEPVEETQEPPETPPLTASNTSLLSSCKKPPSPRDKLFNKSMMLRARSSECLSQAPESHE
SRTGLEGRISPGQRLGQSSLGLNTWWKAPDPSSSDPEKAHAHCGVHGGHWRWSREHNSQPLVAVAMEGPSNPGDNKELKA
STAQAGEDAILLPFADRRKFFEESSKSLSTSHLPGLTTHSNKTFTQRPKPIDQNFQPVSSSYRELRRHPVDQSYHSAEQP
YHATDQSYHSMSPLQSETPAYSECFASRGLENSMCCKPLHCGDFDYHRTCSYSCSVQGALVHDPCIYCSGEICPALLKRN
MMPNCYNCRCHHHQCIRCSVCYHNPQHSTLEDSSLAPGNTWKPRKPTVQEFPGDKWNPITGNRKTSQSGREMAHSKNSFS
WATPFRPCLENPALDLSSYRAISSLDLLGDFKHALKKSEETSVYEEGSSLASMPHPLRSRAFSESHISLDPQSTRAWGQH
RRELFSKGDETQSDLLGARKKAFPPPRPPPPNWEKYRLFRAAQQQKQQKQQQQQQQQQQKQQEEEEEEEEEEEEEEEEEE
EEEEAEEEEEELPPQYFSSETSGSCALNPEEVLEQPQPLSLGHLEGSGQGSQSVPAEQESFALHSSDFLPPIRGHLGSQP
EQAQPPCYYGIGGLWRTSEQEATESTKQEFQPFSPPPGAPGIPTSYSAYYNISVAKAELLNKLKDQPEMAEIGLGEEEVD
HELAQKKIQLIESISRKLSVLREAQRGLLEDINANSALGEEVEANLKAVCKSNEFEKYRSFVGDLDKVVNLLLSLSGRLA
RVENALNSIDSEANQEKLVLIEKKQQLTGQLADAKELKEHVDRREKLVFGMVSRYLPQDQLQDYQHFVKMKSALIIEQRE
LEEKIKLGEEQLKCLRESLLLGPSNF
```

1023 - 1042:	EEEEEEEEEEEEEEEEEEEE
1024 - 1043:	EEEEEEEEEEEEEEEEEEEE
1025 - 1044:	EEEEEEEEEEEEEEEEEEEE

A0A2K6R051 **A0A2K6R051_RHIRO** (1485 aa)
Uncharacterized protein. *Rhinopithecus roxellana (Golden snub-nosed monkey) (Pygathrix roxellana)*

```
LGLIKCFQPWWTTLKQELPHYLLSVLFSATQIEDGGKAALSQKMRTGDELVNINGTPLYGSRQEALILIKGSFRILKLIV
RRRNAPVSRPHSWHVAKLLEGCPEAATTMHFPSEAFSLSWHSGCNTSDVCVQWCPLSRHCSTEKSSSIGSMESLEQPGQA
TYESHLLPIDQNMYPNQRDSAYSSFSASSNASDCALSLRPEEAASTDCIMQGPGPTKAPNGRPNVAETSGGSRRTNGGHL
TPSSQMSSRPQEGHQSGPAKVVRGPPQPPVRRDSLQASRAQLLNGEQRRASEPVVPLPQKEKLSLETVLPARNPNRFCCL
SGHDQVTSEGHQNCEFSQSPESSQQGSEHLLMQASTKAVGSPKACDKASSTYSNPLNEASAELAKASFGRPPHLIGPTGH
RHSAPEQLLASHLQHVHLDTRGSKGMELPPGQDGHQWTLSPLHSSHKGKKSPCPPAGGTHDQYSKERKTRQMDDRSLVLG
HQSQSSPPHGEADGHPSEKGLLDPNRTSRAGSELANQQPSASGSLVQKARDCSSTTKVAGGTEAGEEGDSEHKECSRMGG
RRSGGTRGRSIQNRRKSERFATNLRNEIQRRKAQLQKSKGPLSQLCDTKEPVEETQEPPETPPLTASNTSLLSSCKKPPS
PRDKLFNKSMMLRARSSECLSQAPESHESRTGLEGRISPGQRLGQSSLGLNTWWKAPDPSSSDPEKAHAHCGVHGGHWRW
SREHNSQPLVAVAMEGPSNPGDNKELKASTAQAGEDAILLPFADRRKFFEESSKSLSTSHLPGLTTHSNKTFTQRPKPID
QNFQPVSSSYRELRRHPVDQSYHSAEQPYHATDQSYHSMSPLQSETPAYSECFASRGLENSMCCKPLHCGDFDYHRTCSY
SCSVQGALVHDPCIYCSGEICPALLKRNMMPNCYNCRCHHHQCIRCSVCYHNPQHSTLEDSSLAPGNTWKPRKPTVQEFP
GDKWNPITGNRKTSQSGREMAHSKNSFSWATPFRPCLENPALDLSSYRAISSLDLLGDFKHALKKSEETSVYEEGSSLAS
MPHPLRSRAFSESHISLDPQSTRAWGQHRRELFSKGDETQSDLLGARKKAFPPPRPPPPNWEKYRLFRAQQQQQQQQQKQ
QEEEEEEEEEEEEEEEEEEEEEEAEEEEEELPPQYFSSETSGSCALNPEEVLEQPQPLSLGHLEGSGQGSQSVPAEQESF
ALHSSDFLPPIRGHLGSQPEQAQPPCYYGIGGLWRTSEQEATESTKQEFQPFSPPPGAPGIPTSYSAYYNISVAKAELLN
KLKDQPEMAEIGLGEEEVDHELAQKKIQLIESISRKLSVLREAQRGLLEDINANSALGEEVEANLKAVCKSNEFEKYRSF
```

VGDLDKVVNLLLSLSGRLARVENALNSIDSEANQEKLVLIEKKQQLTGQLADAKELKEHVDRREKLVFGMVSRYLPQDQL
QDYQHFVKMKSALIIEQRELEEKIKLGEEQLKCLRESLLLGPSNF

1122 - 1141:	EEEEEEEEEEEEEEEEEEEE
1123 - 1142:	EEEEEEEEEEEEEEEEEEEE
1124 - 1143:	EEEEEEEEEEEEEEEEEEEE

A0A2K6RQ74 **A0A2K6RQ74_RHIRO** (1323 aa)
Protein kinase domain-containing protein. *Rhinopithecus roxellana (Golden snub-nosed monkey) (Pygathrix roxellana)*

MQCLAAALKDETNMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTRENVALKVESAQQPKQVLKMEVAV
LKKLQGKDHVCRFIGCGRNEKFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESIEAIHSVGFLHRDIKPSNF
AMGRLPSTYRKCYMLDFGLARQYTNTTGDVRPPRNVAGFRGTVRYASVNAHKNREMGRHDDLWSLFYMLVEFAVGQLPWR
KIKDKEQVGMIKEKYEHRMLLKHMPSEFHLFLDHIASLDYFTKPDYQLIMSVFENSMKERGIAENEAFDWEKAGTDALLS
TSTSTPPQQNTRQTAAMFGVVNVTPVPGDLLRENTEDVLQGEHLSDQENAPPILPGRPSEGLGPSPHLVPHPGGPEAEVW
EETDVNRNKLRINIGKSPCVEEEQSRGMGVPSSPVRAAPDSPTTPVRSLRYRRVNSPESERLSTADGRVELPERRSRMDL
PGSPSRQACSSQPAQMLSVDTGHPDRQASGRMDVSASVEQEALSNAFRSVPLAEEEDFDSKEWVIIDKETELKDFPPGAE
PSTSGTTDEEPEELRPLPEEGEERRRLGAEPTVRPRGCSMQVLAEEDLQHLPPQPLPPQLSQADGRSETSQPPTPGSPSH
SPLHSGPRPRRRESDPTGPQRQVFSMAPPFEVNGLPRAVPLSLPYQDFKRDLSDYRERARLLNRVRRVGFSHMLLTTPQV
PLSPVQPQANGKEEEEEEEEDEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEAVAAVALGEVLGPRSGSSSEGSERSTD
RSQEGAPSTLLADDQKESRGRASMADGDLEPEEGSKTLVLVSPGDMKKSPVTAELAPDPDLGTLAALTPQHERPQPTGSQ
LDVSEPGTLSSVLKSEPKPPGPGAGPGAGTVTTGAGGVAVTSSPFTKVERTFVHIAEKTHLNVMSSSGQALRPEEFSTGG
ELGLELASDGGTVEEGAPAPLENGLALSGLNGAEIEGCALSGPPGETPSEMAINSLLNGPALADGPAPVSPLEPSPEKVA
TISPRHHAMPGSRPRSRIPVLLSEEDTGSEPSGSLSAKERWSKRARPQQDLARLVMEKRQGRLLFRLASGASSSSSEEQR
RASETLSGTGSEEDTPASEPAAYLPRKAGRAATTRSRIPRPIGLRMPMPAAAQQLPSRSHGAAPASDTAITSRLQLQTPP
GSATAADLRPKQPPGRGLGPGRAQAGARPPVPRSPGLPTSTSAARNASASPRSQSLSRRESPSPSHQARPGVPPPRGVPS
ARAQPDCTPSPGGSKKGPRGKLQAQRATTKGRAGGAEGRAGAR

749 - 768:	EEEEEEEEEEEEEEEEEEEE
750 - 769:	EEEEEEEEEEEEEEEEEEEE
751 - 770:	EEEEEEEEEEEEEEEEEEEE
752 - 771:	EEEEEEEEEEEEEEEEEEEE
753 - 772:	EEEEEEEEEEEEEEEEEEEE
754 - 773:	EEEEEEEEEEEEEEEEEEEE

A0A2K6SCG9 **A0A2K6SCG9_SAIBB** (1906 aa)
Uncharacterized protein. *Saimiri boliviensis boliviensis (Bolivian squirrel monkey)*

MEGSLAGSLAAPDRPRGPERLPGPATRDNIEGGAEAAEGEGGIFRSARYLPVTKEGPRDILDGRGGISDGQPHPDLSEAL
PCATSATHRISSCCWDGGSLDFRPGSPPPHLLGHFPGTPDVRGPWENPLVQEAGEGILSEQRFEDSVIVRTMKPHAELES
SRRFLHLRGDPRILEKRPRGGPRFDWLQDEDEPGSPQDAGLPLDLPAQPPPLAPFRRVFVPVEDTPKTLDMAVVGGREDL
EDLQELAQPSEWGLPTSASEVATQTWTVNSEASVERLQPLLPPIQTGAYLCELLEEVAEGVASLDEDEDEEPAVFPCIEC
SIYFKQKEHLLEHMSQHRRAPGQEPPADLAPLACGECGWAFADPAALEKHRQLHQASREKIIEEIQKLKQVPGDEGREAR
LQCPKCVFGTNSSRAYVQHAKLHVRERPSQTAKEPFGGSSGAGSPSPEAGTLLYQPYSAAAAGLSACVFCGFPAPSESLL
REHVKLVHARPHWEEDSEAYEEDPASQPGTSQDAHACFPDTAVDYFGKAEPPLAPMWRENTTGYDPSLAFGPGCQQLGMR
DFPLSKPLPHGMGQRPLGRLAFPSALASTPYALQLGRNKSTVHPQGLGERRRPWSEEEEEEEEEEEEEEEEEEEEEEEDED
EEEEEDVMLTSEMDFSPLATPSLIPQPALELKRTFREALQAAEATQEQQQQLRGMVPIVLVAKLGPQVMAAARVPPRLQP
EELGLAGAHPLDLLLLDAPLGSPLGLDTLLDGDPAMVLKHEERKCPYCPDRFHNGIGLANHVRGHLNRVGVSYNVRHFIS
AEEVKAIERRFSFQKKKKKVANFDPGTFSLMRCDFCGAGFDTRAGLSSHARAHLRDFGITNWELTVSPINILQELLATSA
AEQPPSPLGREPGGLPGSFLTSRRPRLPLTVPFPPTWAEDPGPAYGDGLGSEENAMVAMDLGSPSLPKKSLPVPGALEQV
ASRLSSKVAAEVPHGSKQELQDLKAQSLTTCEVCGACFETRKGLSSHARSHLRQLGVAESESSGAPIDLLYELVKQKGLP
DAHLGLPPGLAKKSSSLKEVVAGAPRPGLLTLAKPLDAPAVNKAIKSPPGFSAKGLGHPPSSPLLKKTPLALAGSPTPKN
PEDKTPQLSLSPRPASPKAQWPQSEDEGPLNLTLDSDGGRELDCQLCGAWFETRKGLSSHARAHLRHLGVSDPDAKGSPI
DVLHGLIRRDGVQIRLPPRRGALAHLGRPPPTSAALSLLPPPPPAKKAKLKAAGMASPWGKQDLSAAAAAGIFWASDVEP
SPLNLSSGPEPARDIRCEFCGEFFENRKGLSSHARSHLRQMGVTEWYVNGSPIDTLREILKRRTQSRPGGPPNPPGPSPK
ALAKMMGGAGPGSSLEARSPSDLHISPLAKKLPPPPGSPLGHSPTASPPPTARKMFPGLAAPSLPKKLKPEQIRVEIKRE
MLPGALHGELHPSEGPWGAPREDMTPLNLSSRAEPVRDIRCEFCGEFFENRKGLSSHARSHLRQMGVTEWSVNGSPIDTL
REILKKKSKPCLIKKEPPAGDLAPALAEDGPPTVAPGPVQSPLPLSPLAGRPGKPGAGPAQVPRELSLTPITGAKPSATG
YLGSVAAKRPLQEDRLLPAEVKAKTYIQTELPFKAKTLHEKTSHSSTEACCELCGLYFENRKALASHARAHLRQFGVTEW
CVNGSPIETLSEWIKHRPQKVGAYRSYIQGGRPFTKKFRSAGHGRDSDKRPSLGLAPGGLAGVVRSEGSAGGEPGPEAGR
AADSGERPLAASPPGAVKAEEHQRQNINKFERRQARPPDASAARGGEETNDLQQKLEEVRQPPPRVRPVPSLVPRPPQTS
LVKFVGNIYTLKCRFCEVEFQGPLSIQEEWVRHLQRHILEMNFSKADPPPEESQAPQAQTAAAEAP

616 - 635:	EEEEEEEEEEEEEEEEEEEE
617 - 636:	EEEEEEEEEEEEEEEEEEEE
618 - 637:	EEEEEEEEEEEEEEEEEEEE

A0A2K6SCH8 **A0A2K6SCH8_SAIBB** (1773 aa)
Uncharacterized protein. *Saimiri boliviensis boliviensis (Bolivian squirrel monkey)*

MEGSLAGSLAAPDRPRGPERLPGPATRDNIEGGAEAAEGEGGIFRSARYLPVTKEGPRDILDGRGGISDGQPHPDLSEAL
PCATSATHRISSCCWDGGSLDFRPGSPPPHLLGHFPGTPDVRGPWENPLVQEAGEGILSEQRFEDSVIVRTMKPHAELES
SRRFLHLRGDPRILEKRPRGGPRFDWLQDEDEPGSPQDAGLPLDLPAQPPPLAPFRRVFVPVEDTPKTLDMAVVGGREDL
EDLQELAQPSEWGLPTSASEVATQTWTVNSEASVERLQPLLPPIQTGAYLCELLEEVAEGVASLDEDEDEEPAVFPCIEC
SIYFKQKEHLLEHMSQHRRAPGQEPPADLAPLACGECGWAFADPAALEKHRQLHQASREKIIEEIQKLKQVPGDEGREAR
LQCPKCVFGTNSSRAYVQHAKLHVRERPSQTAKEPFGGSSGAGSPSPEAGTLLYQPYSAAAAGLSACVFCGFPAPSESLL
REHVKLVHARPHWEEDSEAYEEDPASQPGTSQDAHACFPDTAVDYFGKAEPPLAPMWRENTTGYDPSLAFGPGCQQLGMR
DFPLSKPLPHGMGQRPLGRLAFPSALASTPYALQLGRNKSTVHPQGLGERRRPWSEEEEEEEEEEEEEEEEEEEEEEEDED
EEEEEDVMLTSEMDFSPLATPSLIPQPALELKRTFREALQAAEATQEQQQQLRGMVPIVLVAKLGPQVMAAARVPPRLQP
EELGLAGAHPLDLLLLDAPLGSPLGLDTLLDGDPAMVLKHEERKCPYCPDRFHNGIGLANHVRGHLNRVGVSYNVRHFIS

```
AEEVKAIERRFSFQKKKKKVANFDPGTFSLMRCDFCGAGFDTRAGLSSHARAHLRDFGITNWELTVSPINILQELLATSA
AEQPPSPLGREPGGLPGSFLTSRRPRLPLTVPFPPTWAEDPGPAYGDGLGSEENAMVAMDLGSPSLPKKSLPVPGALEQV
ASRLSSKVAAEVPHGSKQELQDLKAQSLTTCEVCGACFETRKGLSSHARSHLRQLGVAESESSGAPIDLLYELVKQKGLP
DAHLGLPPGLAKKSSSLKEVVAGAPRPGLLTLAKPLDAPAVNKAIKSPPGFSAKGLGHPPSSPLLKKTPLALAGSPTPKN
PEDKTPQLSLSPRPASPKAQWPQSEDEGPLNLTSGPEPARDIRCEFCGEFFENRKGLSSHARSHLRQMGVTEWYVNGSPI
DTLREILKRRTQSRPGGPPNPPGPSPKALAKMMGGAGPGSSLEARSPSDLHISPLAKKLPPPPGSPLGHSPTASPPPTAR
KMFPGLAAPSLPKKLKPEQIRVEIKREMLPGALHGELHPSEGPWGAPREDMTPLNLSSRAEPVRDIRCEFCGEFFENRKG
LSSHARSHLRQMGVTEWSVNGSPIDTLREILKKKSKPCLIKKEPPAGDLAPALAEDGPPTVAPGPVQSPLPLSPLAGRPG
KPGAGPAQVPRELSLTPITGAKPSATGYLGSVAAKRPLQEDRLLPAEVKAKTYIQTELPFKAKTLHEKTSHSSTEACCEL
CGLYFENRKALASHARAHLRQFGVTEWCVNGSPIETLSEWIKHRPQKVGAYRSYIQGGRPFTKKFRSAGHGRDSDKRPSL
GLAPGGLAGVVRSEGSAGGEPGPEAGRAADSGERPLAASPPGAVKAEEHQRQNINKFERRQARPPDASAARGGEETNDLQ
QKLEEVRQPPPRVRPVPSLVPRPPQTSLVKFVGNIYTLKCRFCEVEFQGPLSIQEEWVRHLQRHILEMNFSKADPPPEES
QAPQAQTAAAEAP
```

616 - 635:	EEEEEEEEEEEEEEEEEEEE
617 - 636:	EEEEEEEEEEEEEEEEEEEE
618 - 637:	EEEEEEEEEEEEEEEEEEEE

A0A2K6SJL7 **A0A2K6SJL7_SAIBB** (1189 aa)
Euchromatic histone lysine methyltransferase 2. *Saimiri boliviensis boliviensis (Bolivian squirrel monkey)*

```
RAAGLGGVDAAGEAPAEMGALLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPV
GATPLIGDEPENLEGDGDLHGGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGTAAA
GPEPPPATTSPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGSLSEELGSA
RRSEVTLAKGDPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEE
DEESGNQSDRVRDGGSAGRARTLTLSVSVSGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFE
ELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFC
TAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLSQDAPGRADTSQP
SARMRGHGEPRRPPSDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQG
ELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRG
GCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENIC
LHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFAL
QLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCS
SSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQG
TFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSS
RDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

296 - 315:	EEEEEEEEEEEEEEEEEEEE
297 - 316:	EEEEEEEEEEEEEEEEEEEE
298 - 317:	EEEEEEEEEEEEEEEEEEEE
299 - 318:	EEEEEEEEEEEEEEEEEEEE
300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE

A0A2K6SJN1 **A0A2K6SJN1_SAIBB** (1233 aa)
Euchromatic histone lysine methyltransferase 2. *Saimiri boliviensis boliviensis (Bolivian squirrel monkey)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGA
LLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDEPENLEGDGDLH
GGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGTAAAGPEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGSLSEELGSARRSEVTLAKGDPGSLEEWET
VVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAK
KKWRKDSPWVKPSRKRRKREPPRTKEPRGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELS
GCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCG
EDASEAQEVTIPRGDGVTPPAGTAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPSDPLADTIDSSGPSLTLPNGGC
LSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGS
VEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVD
VNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHI
AARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPC
VNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFEC
NQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVY
CIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKH
SAEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE

A0A2K6SJQ1 **A0A2K6SJQ1_SAIBB** (1267 aa)
Euchromatic histone lysine methyltransferase 2. *Saimiri boliviensis boliviensis (Bolivian squirrel monkey)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGA
LLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDEPENLEGDGDLH
GGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGTAAAGPEPPPATTSPEGQPKVHRA
```

```
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGSLSEELGSARRSEVTLAKGDPGSLEEWET
VVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAK
KKWRKDSPWVKPSRKRRKREPPRTKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEEL
PLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTA
GTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLSQDAPGRADTSQPSA
RMRGHGEPRRPPSDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGEL
QKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGC
VYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLH
WASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQL
NRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSS
NCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTF
ICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRD
IRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE

A0A2K6SJV4 **A0A2K6SJV4_SAIBB** (1242 aa)
Euchromatic histone lysine methyltransferase 2. *Saimiri boliviensis boliviensis (Bolivian squirrel monkey)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGA
LLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDEPENLEGDGDLH
GGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGTAAAGPEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGSLSEELGSARRSEVTLAKGDPGSLEEWET
VVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRVRDGGSAGRG
GSRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMA
TESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLN
GMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPSDPLADTIDSSGP
SLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTP
LHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVS
LLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVN
YHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVAR
GYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNK
IEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFD
LDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTC
QCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNT
```

356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE

A0A2K6SJV7 **A0A2K6SJV7_SAIBB** (1208 aa)
Euchromatic histone lysine methyltransferase 2. *Saimiri boliviensis boliviensis (Bolivian squirrel monkey)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWTPQLSTGLTSPPVPCLPSQGEAPAEMGA
LLLEKETRGATERVHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDEPENLEGDGDLH
GGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGTAAAGPEPPPATTSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGSLSEELGSARRSEVTLAKGDPGSLEEWET
VVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRVRDGGSAGRG
GSRGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCE
THRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAA
PAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPSDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESE
RRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPL
MEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIR
MLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNK
EGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTM
NIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQL
YRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPV
RVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPEL
GSLPPVNT
```

356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE

A0A2K6SUL5 **A0A2K6SUL5_SAIBB** (710 aa)
YTH domain containing 1. *Saimiri boliviensis boliviensis (Bolivian squirrel monkey)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSN
NKRIVSTKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCLRKRDPERRAKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEE
EEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSA
SESYADQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNVAFRSARSVILIFSVRESGKFQGFARLSS
ESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLLFPPDES
IDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQRPGYLKDPRYQEVDRRFS
GVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHHPVPHEARYRDKRVHDYD
MRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDRGERGRYRR
```

230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE

A0A2K6SUP6 **A0A2K6SUP6_SAIBB** (736 aa)
YTH domain containing 1. *Saimiri boliviensis boliviensis (Bolivian squirrel monkey)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSN
NKRIVSTKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCLRKRDPERRAKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEE
EEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSA
SESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNVAFRSARSVIL
IFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQE
IELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQ
RPGYLKDPRYQEVDSFTNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQ
AHPPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERER
LCDRDRDRGERGRYRR
```

230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE

A0A2K6SUQ6 **A0A2K6SUQ6_SAIBB** (731 aa)
YTH domain containing 1. *Saimiri boliviensis boliviensis (Bolivian squirrel monkey)*

```
FKSDNGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSNNKRIV
STKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCLRKRDPERRAKSPTPDGSERIGLEVDRRASR
SSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEEEEEE
EEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSASESYA
GSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNVAFRSARSVILIFSVR
ESGKFQGFARLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELEC
GTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQRPGYL
KDPRYQEVDSFTNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQAHPPY
SGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRD
RDRGERGRYRR
```

225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE

A0A2K6SUR8 **A0A2K6SUR8_SAIBB** (540 aa)
YTH domain containing 1. *Saimiri boliviensis boliviensis (Bolivian squirrel monkey)*

```
FKSDNGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSNNKRIV
STKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCLRKRDPERRAKSPTPDGSERIGLEVDRRASR
SSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEEEEEEEEEEEEEEEEEEEEY
EQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSASESYAGSEKKH
EKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNVAFRSARSVILIFSVRESGKFQ
GFARLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCL
LFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRLETFFGLIIGTCIRIT
```

218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE

A0A2K6SZB7 **A0A2K6SZB7_SAIBB** (1192 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Saimiri boliviensis boliviensis (Bolivian squirrel monkey)*

```
MLLPSLSPRVQLAFTQCAGPQPPPHTPSPLGGRRSVFASSRHATTGAPGKMAAAVLSGPTAGSAAGVPGGTGGLSAVSSG
PRLRLLLLESVSGLLQPRTGSAVAPVHPPNRSAPHLPGLMCLLRLHGSVGGAQNLSAVGALVSLSNARLSSIKTRFEGLC
LLSLLVGESPTELFQQHCVSWLRSIQQVLQSQDPPPTMELAVAVLRDLLRYAAQLPALFRDISMNHLPGLLTSLLGLRPE
CEQSALEGMKACMTYFPRACGSLKGKLASFFLSRVDALSPQLQQLACECYSRLPSLGAGFSQGLKHTESWEQELHSLLAS
LHTLLGALYEGAETAPVQNEGPGVEMLLSSEDGDAHVLLQLRQRFSGLARCLGLMLSSEFGAPVSVPVQEILDFICRTLS
VSSKNISLHGDGPLRLLLLPSIHLEALDLLSALILACGSRLLRFGILISRLLPQVLNSWSIGRDSLSPGQERPYSTVRTK
VYAVLELWVQVCGASAGVLQGGASGEALLTHLLSDISPPADALKLRSPRGSPDGGLQTGKPSAPKKLKLDVGEAMAPPSH
RKGDSNANSDVCAAALRGLSRTILMCGPLIKEETHRRLHDLVLPLVMGVQQGEVLGSSPYTSSRCRRELYCLLLALLLAP
SPRCPPPLACALQAFSLGQREDSLEVSSFCSEALVTCAALTHPRVPPLQSMGPTCPTPAPVPPPEAPSPFRAPPFHPPGP
```

```
MPSVGPMPSAGPMPSAGPMPSAGPMPSAGPMPSAGPVPSVRPGPPTTANHLGLSVPGLVSVPPRLLPGPENHRASSNEDP
ILAPSGTPPPTIPPDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDSVVIVPEGLPPLPPPPPSGATPPPVAPSGPPT
ASPPVPAKEEPEELPAAPGPLPPPPPPPPPVPGPVTLPPPQLVPEGTPGGGGPPALEEDLTVININSSDEEEEEEEEEE
EEEEEEEEEEDFEEEEEDEEEYFEEEEEEEEEFEEEFEEEGELEEEEEEEDEDEEEEELEEVEELEFGTAGGEAEEGGPP
PPTLPPALPPPESPPKVQPEPEPEPGLLLEVEEPGAEEEHEADTAPTLAPEVLPSQGEVERAGGSPEAGLPPQELVEEEP
SAPPTLLEEGTEDGGDKVQLPPETSAEEEMETETEAEALQEKEQDDTAAMLADFIDCPPDDEKPPPATEPDS
```

950 - 969:	EEEEEEEEEEEEEEEEEEEE
951 - 970:	EEEEEEEEEEEEEEEEEEEE

A0A2K6U8X8 **A0A2K6U8X8_SAIBB** (1124 aa)
Myelin transcription factor 1. *Saimiri boliviensis boliviensis (Bolivian squirrel monkey)*

```
MSLENEDKRARTRSKALRGAPETTAADLSCPTPGCTGSGHVRGKYSRHRSLQSCPLAKKRKLEGAEAEHLVSKRKSHPLK
LALDEGYGVDSDGSEDAEVKDASVSDESEGTLEGAEAEASGQEEIHRPEPAEGRSPVKSHFGSNPISSPTGSSKGSYSSY
QGIIATSLLNLGQVAQETLVEEDLGQAAKPGPGIAHLLQEATEGAASMEGEKGLFIQPEDAEEVVEVTSERSQDLCPQSL
EGVASAESSKQKGILSHEEEEEEEEEDEEEEEDEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEAAPDVIFQEDASRVS
AQKAPELRGSESPSPKPEYSVIVEVRSDDDKDEDTRSQKSAVTDESEMHDMMTRGNLGLLEQAIALKAEQVLTVCEPGCP
PAEQSQLGLGEPGKAAKPLDTVRKSYYSKDPSRAEKREIKCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRIPPEILAMHE
NVLKCPTPGCTGQGHVNSNRNTHRSLSGCPIAAAEKLAKSHEKQQPQTGDPSKNSSNSDRILRPMCFVKQLEVPPYGSYR
PNVAPATPRANLAKELEKFSKVTFDYASFDAQVFGKRMLAPKIQTSETSPKAFQCFDYSHDAEAAHMAATAILNLSTRCW
EMPENLSTKPQDLPSKSVDIEVDENGTLDLSMHKHRKRENTFPSSSSCSSSPGVKSPDASQRQSSSSAPSSSMTSPQSSQ
ASRQDEWDRPLDYTKPSRLREEEPEESEPAAHSFASSEADDQEVPEENFEERKYPGEVTLTNFKLKFLSKDIKKELLTCP
TPGCDGTGHITGNYASHRSLSGCPLADKSLRNLMAAHSADLKCPTPGCDGSGHITGNYASHRSLSGCPRAKKSGVKVAPT
KDDKEDPELMKCPVPGCVGLGHISGKYASHRSASGCPLAARRQKEGSLNGSSFSWKSLKNEGPTCPTPGCDGSGHANGSF
LTHRSLSGCPRATFAGKKGKLSGDEVLTPKFKTSDVLENDEEIKQLNQEIRDLNESNSEMEAAMVQLQSQISSMEKNLKN
IEEENKLIEEQNEALFLELSGLSQALIQSLANIRLPHMEPICEQNFDAYVSTLTDMYSNQECYQNPENKDLLESIRQAVR
GIQV
```

282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE

A0A2K6UEI6 **A0A2K6UEI6_SAIBB** (203 aa)
Cysteine rich hydrophobic domain 1. *Saimiri boliviensis boliviensis (Bolivian squirrel monkey)*

```
MSILLPNMAEFDTISELEEEEEAATSSSSPSSSSSVSGPDDDEDDEEEEEEEEEEEEEEEEEEEEEEEAPPPPRVVSEEHL
RRYAPDPVLVRGAGHITVFGLSNKFDTEFPSVLTGKVAPEEFKTSIGRVNACLKKALPVNVKWLLCGCLCCCCTLGCSLW
PVICLNKRTRRSIQKLIEWENNRLYHKVILIEFLPKYPIFRPD
```

46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE

A0A2K6UEJ9 **A0A2K6UEJ9_SAIBB** (223 aa)
Cysteine rich hydrophobic domain 1. *Saimiri boliviensis boliviensis (Bolivian squirrel monkey)*

```
MSILLPNMAEFDTISELEEEEEAATSSSSPSSSSSVSGPDDDEDDEEEEEEEEEEEEEEEEEEEEEEEAPPPPRVVSEEHL
RRYAPDPVLVRGAGHITVFGLSNKFDTEFPSVLTGKVAPEEFKTSIGRVNACLKKALPVNVKWLLCGCLCCCCTLGCSLW
PVICLNKRTRRSIQKLIEWENNRLYHKLALHWKLTKRKCETSNMMEYVILIEFLPKYPIFRPD
```

46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE

A0A2L2SQC2 **A0A2L2SQC2_9HYPO** (1181 aa)
Uncharacterized protein. *Fusarium venenatum*

```
MFPSLLRRPRAGPRRIDRRQNTSASPSPGPARRRYTLERHATADFTEADDDDADFTHDEGLRRFRNNERRTNNDGDEEEE
EEEEEEEEEEEEEEEEEEDEDDNDGNEEYGMNEDGRQSGLPVLPLFSASHLDSLPVYSITHAIRIIISTRTETTLSWDQL
RSPQVSQFLVKPMQQQIRAQHFNRATLYALMINCLQFSKEGARYPGNAGISSTRAKVCELLTLKLLKEYNTRELIDALAY
DFYPLQGLPGSQLPTSPRKSPPANTLPLIASRTSTLEVAIRASAKHLLAHPLVVQQLEAIWSGAITFHSSADSLHREPPP
INNRNSNGFIGKADDRTPLLGSSARKDAYFTPPGRRTASLYDPRQASLLKLSRLRVPRYRSFLSTISLAVLIGLFLAVLA
ERSVQITGLELIFWFWSAGFMLDELVGFNEQGFELYIMSVWRVFDLGILLLLIVYYCMRAYGVFLVDPHHWNDLAYDVLA
ANAILLLPRIFSILDHYQYFSQLLIAFRLMAVDLVAVFILIGILCSGFFFFFTLTKNSFGASDVAYKIFQILMGFTPAAW
EVWDAYNWLGRALLVLFLSICHFLVVTILITVLTNSFMAIASNANEEHQYLFAINTISMVKNDALFSYIAPSNIFAWLLM
PLRYFMPLRHFVWLNRTVIKVTHFPVLFCIYLYERYWLAPSMYEPTDLVEHPNRERTRHISFMDPASRAAIFSPSVRMRE
ESVAGFQQDRALEEVFRRMPDPLTLRTQRRQERRKTQTAIRNWMDQHDDNEASPEPTMPHWQRRSSVGLVRTSNLRRVSD
VRSIASDPADLISNVGQPLRPSHFSRTRLAGETEYKDQTDADGDDELVTNDEDEDDHNTNAAQSQVARSHRISEEADSYF
APNANSFGKLASSVSSSGKSKNLAPTPRPKRGAHNRTLSTNTILFNPQDFKQVSKASSLSPPPGQQRPRTSGRPATGEKT
PRRSSPRRTIYVTNTKPRPVMPPRGMTEAGAVSRSALLSIEPRNRPKDVRRLSSVDLSAISDHVGGDPIGAMPGSFQTQM
AMAMMKDNHLRGVGGNDSGDRDRMGRLVLARMKTLEESFADVIKEMRDLKKSSTVPTTRRNSSGDEGNSAQMIEVAGRDR
LRKYTMENNQRKVASKRPVSRRSFKEAKPGWDTKGKGKEVAYESDDEAETDGSLFQKGGSL
```

77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE

A0A2L2T635 **A0A2L2T635_9HYPO** (3267 aa)
Uncharacterized protein. *Fusarium venenatum*

```
MPINGTGRNANRRLPSWLTSSPLPPSDAQKERHQPNDKIISDPASDILIDFNSSKGFYEAAKKSKKAKPPTAPPPPPPPP
AAPPADDGQKDDMNGSGGGASGGSAAGGAGDGDGSNGGSAPPKPPTTFDNISLGASKLDLGLSPPENKSISSWGAKLGFG
GGGWGWGGGSKNEPQPAPTPPPPESKAEDNPWDKPKGSTGDLGMKDDDDAWGFGTKKDKKPSALWGAEPEEEPKEAGDPW
GWGNQKKKGKPGGILEELALDTEPEGPPGGKKDIWDTWGISKKDRAKKKGIMEEVALAAAPDPPSMDDQWGGGWSGKKDQ
SPQDSLWGPQDPIPAVPDPPSFEDKDGDDFWSTFGSGKTKPVEDNPGGWGSWGISKTGEDETSESNFYNAHRIPEPPKIE
DDGRDLWGTGKKKKKAGDLIQLEDEIPPPAPDPVEAVDTGDFLDSWGFGKKTKKPAADPFDFKTSDANDPNHAFWGSIDT
KPGAHDFLIDTTDPEQAAREAEERAAREAEDAEAAREDEEIASLVEKKAKRGGRLLKSDRERLAVLEGNAVRRSEARAAR
EAEAAAAAAEAAQAEAQAVVDAQAAAEAEAAALQAAEDAEVAKENEEIALLLAKKQKRGGKLLKKDQERLTLLEGNVSRRA
EAQAAREAEAEAAAAAADAAAFEVINDIPLDEAPPPESSEQDAAAQAAAETEAALASEIAHEEAEMESLKLKKAKKGKLI
KKDQERLNILIDNAAKRVEQAAAKEAEEQAAKDAEDAAAAAAIEAAEAESAAQAAAEVEAAAQAALDAEAEEAAKEEEEM
AALKAKKAKKAKLTKVETARLMALVGSSVKRAQAKSAKEAEEAAAAQAVREAEESAIREAEEKAAREAEEAAAREAEAAI
AAEEEKELAALDALKTKRGGNLIKKKDVDRYNVLTQRVAERAAKNAEAAAAEVVQAEATPEISDEPTGPTPEPVPEDPPA
DADAAPVEPEPLPGPDATVIAAEDAELASLDAKKAKKGKLGKKDTDRYNLLNENAVQRQAAKEAEENAAREAAEAEAAAA
DEAAAQITEAEALTASEAEAILIADEEAELATLVAKKAKKGKLIKKDLERFNILTENAAQRQASREAEEAAVAAAAEAEA
QAAKDAEEAAAAEAAEAEVSAAREAEAIAIAEEEAELAALTTKKAKKGKLIKRDAERFAILTENAERRAQEAAIVTEQPE
DSTTIPEVEAEETPPEPPVDELPVEGDNPDANATAIAEEEAELAALVAKKEKKGKLGKKDTDRFNLLTANATTRAEKAAE
EEATAAAAAAEAEEAAAAEAAAIEETAAREAAEAEAAVIAEEEAELAALVAKKNKKGKLGKKDSDRFAVLTENATQRAEK
AAEAVEVEPEAEPEPEPEPEPEPEPEPEEEALPEVEDPLVDEFDDAAASEADDEEAAIAAEAAAIAATIAAEEEEEMQALIA
KKNKKGKLGKKDSDRLAVLADNAAQRAEKAAQEEAAALAESEVIEDPPAYIEEPAPEDAPEAPPEEEAPPEEHDAAAAAE
EQELADLDAKKARKGKLGRKDTDRYNVLTENATKRAEEQAAKEADKAAAAEAAAAAEAEEIAAREAAEADAAIAAAEAEK
EAAKVEAEAVIAQEEEELAALEAKMERKGKLGRKDTDRLNVLMDSKAARDAQATEEQAAQEVEEAAAREAAEAEAAAVAA
EEEAELAALTAKKTRKGKLGRKDTERFDQLASNAAQRAEEQAARQAEAVTEVDPAEEEIAPVEFEEPEEPTPDVEELVEE
VPEDPAPDVDDEAAAMAAEEEAELASLEAKKARKGRLGNKDTQRFNFLTENLAKRAEEKAAKEAEVQAAAAEAAAEAAAE
AAAEAAAEAEAEAEEAVVEDALEDAAEDNDEDTAAREAAEAEAAAEAEAAAVAAEEEAELAALVAKKTRKGKLGRKDTER
FDVLNENVARRAEEQAAKEAEVELEEPAFEQTEDAAEPEPEENPGDEDAAAKEAAEAEAQAIAAEAQAIAAEAQAIAAEE
EAELAALNKKKAKKGRLGRSDTERFNILMDNAAKRAETQAAKEAAEAAEEAPPAEEEEDDEFVDAEDELAEEHEPEAEEA
AEPDGEDAAVAAAAAEAEAEAQAAAIAEEEAELASLTKKKIKKGKLGRKDTERFQVLTDNAARRNEEAAAREAEEAAAAE
VEPEAEPEPGPEAELEAEPEVEPEPEADQEPEDDSNEIDEAEQAAIAEEEAAELAALIKKKAKKGRLGRKDTERFEILTE
NAARREDERAAKEAAAAAAIAEAEFEAAEEDPEAEVIEEAEEPANEEEGEDLAEAEDEEAADREAEETAIADAEEEELES
LKAKRARKGRLGRKDTERFAVLEENAARRAEERAAKEAAAVEDEPDEPVEDDEPNEDEEEEEEEEEEEEEEEKEEEEDEDD
AAVEEEAAREAEETAAREAEEAATAEAEEDELESLKAKRARKGRLGRKDTERFAVLEENAARRVEERATREAAAAAEAEV
DEVEEEEEEEEEEEEEEEEEEEEEDDDDDGEEEDDEDGAADDDEVAVREAEEAAAREAIEAAARDAEAAAIAEAEEAELD
SLRFKKSRKGRLGRKDTDRLKFLEDSAAKRAEELAAKEAAATAEAEVDKAPEEEEDEEEDEEEDDEDAAEEPTEVANNDV
AEESDQEEVEAAPEEAPEEVEAEAPMDDEIVEVIDLSPKKDRRSRKSRSRRDAPPPPAVPDPPLTPPPEPKQSRRPKLTR
EGAPWGKWGATPREEPDEYYQEKSSRHRRREEKTSSKGSSSDKVEKNSRTAAPFGKPSLSRSASTRERRDGVSSKRRHSE
AARGIVSPPPEEMLVHEEPGSRRKSRKPRSREDDDAMMSGAAPVPERYERRHSQKTRSREDDDVIMVDPDLANDRRERRR
SHKTRSREDEDMAMADDIITPGLRDRRRRDRKSRDEEPVMVEPDVPTDHALPRGSKKGFAGLFSGLRTPKNERPDPLRRR
STYATTDDEALRTARMDGDAVIVDADREARRAARKAKRVDPEEEARRAKDEARRERRRQREKGADTQRQDQDTRRAERRA
ARQRGEEERRAQEEQQAEEELQRAQEAKEAQRSERRRLRREQEAAAAAEQEEQEARRAARRERRRPRPVDPSEDEHERRR
RREAKRAARATDEAEGHQRRPRRHEEMQQPAWPHLGTSSWVQEHVDAPPPPDLPQAGDASGEQDEDDEMARREARRAQHR
SKYSDETPDEAEERRKRRARREERERGGRHRDRRSEGSDERHHTRRPSNVVDTAAAPRTSWWKKIKR
```

2484 - 2503:	EEEEEEEEEEEEEEEEEEEE
2485 - 2504:	EEEEEEEEEEEEEEEEEEEE

A0A2L2T7H4 **A0A2L2T7H4_9HYPO** (69 aa)
Uncharacterized protein. *Fusarium venenatum*

```
MYLILAYYYACAEPLSKPSFWPSFIKEEEEEEEEEEEEEEEEEEEEEEEEEERTGFDFKAIGGTTREHKYK
```

27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE

A0A2L2TEC8 **A0A2L2TEC8_9HYPO** (461 aa)
Uncharacterized protein. *Fusarium venenatum*

```
MLLWLAGLGLVTASITIPLSPVAPLPLSHQGAATSVDDLFRRSCPEEVASSNPYKPSLLASSFSNDVFSTGRVFPSSGGF
IRGAVEAWAQHQHLVLRPEEVWFEVLVQMNLYMSVHSEKVRSLFVEHEGGKKKIVVEGNSWDDMVVGFSDEIDKRVKPKW
LKDWIMPGFSTSTPKDDVTAAVLMMGLMKQFFDFEGWLVCGIPSVTLLGTKEDWVKLEAKLDYLKEFGPDPELFAEMLRP
IMKRFVSSWDDAHAEETKLFWEQIVRVKKQWSCGEGANEWGVSGWITGFDFFERNGWRRGYDAWEDYDDDEEEKETVKEE
PRMGIYPNDWTLIMDGQQYLPLSLSDVSTGYAKAPVTMKGYPHPGVDMEAYILAGNVGVERMEEGGKVTAQPVSGWFAYG
PVNSNDTVGPFIGNGNELESIAVGIEDCKATKKEEEEEEEEEEEEEEEEEEEEEEEEVKDL
```

434 - 453:	EEEEEEEEEEEEEEEEEEEE
435 - 454:	EEEEEEEEEEEEEEEEEEEE
436 - 455:	EEEEEEEEEEEEEEEEEEEE
437 - 456:	EEEEEEEEEEEEEEEEEEEE
438 - 457:	EEEEEEEEEEEEEEEEEEEE

A0A2L2TIP5 **A0A2L2TIP5_9HYPO** (77 aa)
Uncharacterized protein. *Fusarium venenatum*

```
MALEDLDDWKELGQAQAGRFLASGGCIIDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERKIKSLTWKRGAGAF
```

30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE

A0A2L2Y779 **A0A2L2Y779_PARTP** (226 aa)
Uncharacterized protein (Fragment). *Parasteatoda tepidariorum (House spider) (Achaearanea tepidariorum)*

```
EEYSPVESPTLVPIRRRDDVWPPRTSSVRYLPKTGFSPTIVREGGPGKRFVWPPPKQGQDQMQNDVGLLGHGKVGEAWNP
DANALGNRPPAFAPRTMPTKRCNDDIWPPKDSEYQANRKPSPRPVQTVGRFEDYIRCRAGPNVPPTYRTPPGTQHILVQQ
LEGEYIHESKTTTTVMSNSTSVQQQRVVTQPQPVARRPVEEEEEEEEEEEEEEEEEEEEEEEESEEE
```

200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE

A0A2M4CJ64 **A0A2M4CJ64_ANODA** (359 aa)
Putative troponin t skeletal muscle (Fragment). *Anopheles darlingi (Mosquito)*

```
KPAAKSEGDDPEFIKRQDQKRSDLDEQLKEYINEWRKQRAKEEDELKKLKDKQAKRKVSRAEEEQRMAQRKKEEEERRVR
EIEEKKQREIDEKRKRLEEAEKKRQAMLQAMKDKDKKGPNFTITKKDSSFGMSNAQMERNKTKEQLEEEKKISLSFRIKP
LEVDGLSADSLRARATELWETIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQVAS
KYERRVDTRSYDDKKKLFEGGFDTLNKEVLEKNWAERKEQFGGRQKSKLPKWFGERPGKKSGDPETPEGEDEVKPEDEEV
EEVEEEVVEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

333 - 352:	EEEEEEEEEEEEEEEEEEEE
334 - 353:	EEEEEEEEEEEEEEEEEEEE
335 - 354:	EEEEEEEEEEEEEEEEEEEE
336 - 355:	EEEEEEEEEEEEEEEEEEEE
337 - 356:	EEEEEEEEEEEEEEEEEEEE
338 - 357:	EEEEEEEEEEEEEEEEEEEE

339 - 358:	EEEEEEEEEEEEEEEEEEEE
340 - 359:	EEEEEEEEEEEEEEEEEEEE

A0A2M4CNE1 **A0A2M4CNE1_ANODA** (146 aa)
Putative dna repair protein rhp54 (Fragment). *Anopheles darlingi (Mosquito)*

```
VTEDEEVKEEEEEEEEEEEEEEEEEEEEEVEEEEEKEEEKEEEEEEEEKEEEEEEEEEEGLILLGFISTGQVFDWTPMAVP
SPAADAAQTAHGVRTDPGTATSSVHKYLRGLGHDQLNRSLQLYRYERRSPLGEAKKEKEKKKELEG
```

9 - 28:	EEEEEEEEEEEEEEEEEEEE

A0A2M4CVE6 **A0A2M4CVE6_ANODA** (383 aa)
Putative troponin t skeletal muscle (Fragment). *Anopheles darlingi (Mosquito)*

```
NNKPTTLPYPSNSPNLHFQTINTTRPAAKSEGDDPEFIKRQDQKRSDLDEQLKEYINEWRKQRAKEEDELKKLKDKQAKR
KVSRAEEEQRMAQRKKEEEERRVREIEEKKQREIDEKRKRLEEAEKKRQAMLQAMKDKDKKGPNFTITKKDSSFGMSNAQ
MERNKTKEQLEEEKKISLSFRIKPLEVDGLSADSLRARATELWETIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRH
KALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGFDTLNKEVLEKNWAERKEQFGGRQKSKLPKWFGER
PGKKSGDPETPEGEDEVKPEDEEVEEVEEEVVEEVVEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE

A0A2N0RCX6 **A0A2N0RCX6_9GLOM** (275 aa)
Uncharacterized protein (Fragment). *Rhizophagus irregularis*

```
METTKTADAGSKNWLKERAAISAAHRRQKTDPAAARLIEKADQLHKERTQKNLRETVDEDDEAVDEVPETTVKKNEGRDR
RTNVKSSFRRSVVFSSPLNYSSTPAEDEDLEDIDAIVSVPPPEEIVVKIAQKPAEEDTIASNHGKETSEDVYRSFAESVL
EQGLTTKSELELSFDLKPEDIKIKEEEEEEEEEEEEEEEEEEEEEEEKGEEETQEDLNEADITEEKVQEKLKDADVEIN
HNEENKGDVKDQEDDKSEESTLTKEVDVDTVPKNN
```

185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE

A0A2N1J8E8 **A0A2N1J8E8_9BASI** (808 aa)
Uncharacterized protein. *Malassezia vespertilionis*

```
MIASGASEQELKDTMASAKQTAVGERVDTTTQQAEQTEEAKDTEQYPPSFNTIVELIATGQGDKIKGVREIPLKINQTAT
KTLFDHVKYESASLPYISSLLESVAPHISSSISKRTHPLFPATDLNELILDGMDNDQLWQQLELRSGKLGRVLDTVMSSG
MEMDSEDEEGTCDTNSMSTNDADNDADDDEGWEDASEDAEEGFAGASDLSDVDPDELIYEPLHSEEQQQHVKQVKEREEL
MRMYGIRGPVPGDQDLIDLLDDEQGSSRGRKPKHPSLDDDFFSIDEFNRLTEQDERGENAAEPGLDLFTPVNVEAEEEDE
EEDSGDPAHMSGTDIHYSDFFEPPKEAKRRTGKSRPPVAHPEVPVCKHRVRFNEQVRVRPIKKCSQRQTAGLLMSPPDGG
WEKDASHKDEIEVEDAVSGMPEENSESWDEEEEEEVEEEEEEEEEEEEEEEEEEEEEEGDGMDVDESDTFETEEEKEAHM
LQRVSNDLFDDGQDAELDDRSTHERRLAALNEEIAQYEQENVQKKSWALMGEASTRERPVNSLLEEDLDFEHTAKVKPVA
TEERIDSIEEMIKQRILAKQYDDVIRQQDMDTLPFAPSKLLELSDAKNAKSLAELYEDEYRTAHGESDAPLAGADAKLAN
EHTQIGNDLDRLLNSLDALSNAHYTPKAPKAAITTISNTPSIAMESALPSTMSTGTMLAPEEVYAASTHAPAMTGAKSEM
APGEKRKMHNQLRQVKRKRNDRIRRAEDEIARSRGAPLTKGTKTEKDKALKSLMGNKGVSVVGKDSKRTGFQDRQAKQSI
PAGSQWKL
```

437 - 456:	EEEEEEEEEEEEEEEEEEEE
438 - 457:	EEEEEEEEEEEEEEEEEEEE
439 - 458:	EEEEEEEEEEEEEEEEEEEE

A0A2N1J8S0 **A0A2N1J8S0_9BASI** (561 aa)
WD_REPEATS_REGION domain-containing protein. *Malassezia vespertilionis*

```
MAKQANGKRGAARPTSKGTAFRKSAKRARVDEPAPQHAHAARARAPAPRAGLNDAKGVHTKRHVQPKNGAAATKAPSSQA
SSKTGKAVHDVQPRKARPKKSTAPSSPQHALRIIAGSYERFLYGLTGRMCVTDDGSYTMTIEPDFVFPAHASSIRTVACA
NETKWLVTGGTDETIKVWDLRRRKEVGALTGHQGTITSLSFPSRTFMLSTGDDGVLNLYRTRDWALLRTMRGHTGRINGA
STHPSGRLALSIGKDRTIRMWDFLRGVGSSSVKIGAEADKIAWDTLGKRFAVLVDRQAMVFGTDMTKLAEIEQSRRLHDV
```

```
SFFRAAIGGKEHELLLVASESGLVYVYDLDASASADAASPREIARLVGHANRVRAAAAVYIAADDGLIVPLVSTISSDGF
IRVFNLMPALVDDALVELEAIAEYDTHKTRLTCLSVATYDPAGADDADEEVLDAADDDAGAEAFDTTDDDELDAMSSDEG
DLDDAELEELARLEEEVRRAQEAGIVITEDGGVVVEGDDDEEESEDEEGDEDGDGDGEEEEEEEEEEEEEEEEEEEEEE
E
```

538 - 557:	EEEEEEEEEEEEEEEEEEEE
539 - 558:	EEEEEEEEEEEEEEEEEEEE
540 - 559:	EEEEEEEEEEEEEEEEEEEE
541 - 560:	EEEEEEEEEEEEEEEEEEEE
542 - 561:	EEEEEEEEEEEEEEEEEEEE

A0A2N1JH74 **A0A2N1JH74_9BASI** (1518 aa)
Swr1p. *Malassezia vespertilionis*

```
MEKNALPPETHASTGAHVSIPSELAASIAPYVEHANEARKEPTTPVNTGRPIEKPVGKRRRLDSELSFSSPGPAFQLEGV
TPTEDSVSTRRHSSRAIRPRRLSLDGGVATVARPKQAQQTDINFTERLAECRALEAQLRRAPADEHDALLHAMLKLTQVT
TKKDVSQDLHTELAPYNELATRRLEERHGPGAAARSARRAATEMKQAPSQSPLWAKPKRPRPESRPRPELRTRPEPRPRR
SVPVQPTDTNIALVSLSSAKLPKRTPPLYITSPHQRPSVSIHGSFANFLQSYTMWDDDVVTPAVRAQRLARDTYLYRRMD
QLRREGKSLEPEHPVPMQKLKLQEAPRAKAHRDHLLDAVPWRAQRMRQFSKGRIQLAKKVSRMVTTYWDRFQNSDEREKK
LELRHQRALAKWTMREVARQWKFAITIVRAQRQAIEKAEREKLGKKQLQAIIEHSTQMLKTQHADLSNVYNGEEEEEEEE
DEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEMDENKRVDEKVDKMEQDITQDVELAIVKRSSSHK
GTDAASNIEPSIASNTATNETESATHSASESSSSDRDDEDNDLEQEMLEGDEEDASEEDDLKADADMSIEELMRKYGYGG
RDNEDDASSGKPTHASDADTSAAPDSDSDTSDHDQDATLHALLGDENKAEPTPFIRPPFLLRGTLRGYQQNGLEWLVSLY
NNDMNGILADEMGLGKTIQTISLLAHLACDRGIWGPHLVIAPTSVMLNWEVEFKKFLPGFKVLSYYGNQKQRKAKRVGWN
TENSFNVCITSYQLVLADQHIFRRKPWMYLVLDEAHHIKNFRSQRWQTLLGFNSRRRLLLTGTPLQNNLMDLWSLMYFLM
PQGIEKVAAAAGAFSNMKDFQDWFSNPLGRAAENAEGVDEETRATVAKLHTVLRPYVLRRLKSDVEREMPKKFEHVIPCR
LSKRQRFLYNDFMSRAKTRESFASGNYMSIINCLMQLRKVCNHPDLFEQRPIVTAFVQSRSVAADYEIKDLLVRRHLLKE
GNDNVNLDFLNLQFTQREELLTPLATRRYDALQVSDALSNVPPPVEEAPLTTHSIAGLRAAIETRRRNAAYEKAQHAAYV
NRMRCNAQPLYGRSLLAMLRRFGSPKLRSYEIVERERGAYWQRCDALCEAVQSYAQRGESCADLVSRFAFATPPAVAANM
PQYALPGVPLETQFAIGAPELDPLHKAAVALNIAFPDASLLQYDCGKLQQLDVLMRRLVAGGHRILIFTQMTKVLDILEK
FLNYQGYRYLRLDGATKIEQRQVLTERFNRDSRISAFILSTRSGGLGINLIGADTVLFYDLDWNAAIEAQCMDRAHRIGQ
TRDVHIYRFVSEHTIEENMLRKANQKRRLDSMVIQQGEFTTEHLMRNDWRDMLDEGGATLGGVSIGEDNEAQSTRDVDRA
FAAAEDVEDAAAAHVATEELQLDAADFAAESVPIPDVAVQGPDSPPPEHDQGAEEDLTGSIDDYMLRMVQADWDFFGA
```

484 - 503:	EEEEEEEEEEEEEEEEEEEE
485 - 504:	EEEEEEEEEEEEEEEEEEEE
486 - 505:	EEEEEEEEEEEEEEEEEEEE
487 - 506:	EEEEEEEEEEEEEEEEEEEE
488 - 507:	EEEEEEEEEEEEEEEEEEEE
489 - 508:	EEEEEEEEEEEEEEEEEEEE
490 - 509:	EEEEEEEEEEEEEEEEEEEE
491 - 510:	EEEEEEEEEEEEEEEEEEEE
492 - 511:	EEEEEEEEEEEEEEEEEEEE
493 - 512:	EEEEEEEEEEEEEEEEEEEE
494 - 513:	EEEEEEEEEEEEEEEEEEEE
495 - 514:	EEEEEEEEEEEEEEEEEEEE
496 - 515:	EEEEEEEEEEEEEEEEEEEE
497 - 516:	EEEEEEEEEEEEEEEEEEEE
498 - 517:	EEEEEEEEEEEEEEEEEEEE
499 - 518:	EEEEEEEEEEEEEEEEEEEE
500 - 519:	EEEEEEEEEEEEEEEEEEEE
501 - 520:	EEEEEEEEEEEEEEEEEEEE
502 - 521:	EEEEEEEEEEEEEEEEEEEE
503 - 522:	EEEEEEEEEEEEEEEEEEEE
504 - 523:	EEEEEEEEEEEEEEEEEEEE
505 - 524:	EEEEEEEEEEEEEEEEEEEE
506 - 525:	EEEEEEEEEEEEEEEEEEEE
507 - 526:	EEEEEEEEEEEEEEEEEEEE

A0A2N1N335 **A0A2N1N335_9GLOM** (222 aa)
Uncharacterized protein. *Rhizophagus irregularis*

```
METTKTADAGSKNWLKERAAISAAHRRQKTDPAAARLIEKADQLHKERTQKNLRETVDEDDEAVDEVPETTVKKNEGRDR
RTNVKSSFRRSVVFSSPLNYSSTPAEDEDLEDIDAIVSVPPPEEIVVKIAQKPAEEDTIASNHGKETSEDVYRSFAESVL
EQGLTTKSELELSFDLKPEDIKIKEEEEEEEEEEEEEEEEEEEEEKGEEETQEGMIKTEHA
```

185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE

A0A2N5S7M3 **A0A2N5S7M3_9BASI** (529 aa)
Uncharacterized protein. *Puccinia coronata f. sp. avenae*

```
MTNNQQPSGFKLKLKLNGPPPPPPPQKPTNYHVERYQEEEDQLASSDMEEEEEEEEEEEEEEEEEEEEQINNNRTNNNRT
NTIQEAHLIPSKLAQPSNKRPSKSLSATPRAVAAAAPAPSKPPPKKRKTTSQSIAIHPHRAQQLTTDQEHADSEHSSYAS
DQQQQQQQQQQQQQQQQPHSAPPKPRTIKISHPKPTKPKSKAHLVPLTDAELLSLAAGGSPHYPQQVQDAPITVPTLPAK
SKATQQPSAIAPKTTTATTKKKTPATSQGAKKGKTIPAQTIAAATAAAATAPDPRQSTQQAATPTHPHGVKATGTGSSIA
KPKTKKGVKPKPQDPLQPASVAAPAVVPRPPPGPRPQHDYALGPPPPPPVPALKILPVGPPPRTQGQFLPAQILEKRTPP
TRSWRKVKRQVVGISGIPFWIWTYAGDEHSEYAAFKVQKPPPLPGTVHLNPEAQYYPPAQPSRPASVAPTQHAKPSPMRH
PSGTSKAKYVPSDPSASLNLGGPVLPASFRRPPMSIGSPLSGKGATPYP
```

49 - 68:	EEEEEEEEEEEEEEEEEEEE

A0A2N5SUI3 **A0A2N5SUI3_9BASI** (995 aa)
HTH CENPB-type domain-containing protein. *Puccinia coronata f. sp. avenae*

```
MLSRSSSSTLLAQQPFLPSISTLTPEHPSYHHSNNNNNNNNPSQQQQQQQQQQQQQQQQQRQHRQQQQQQQHQFQQLQKQ
ELYHLHQQQQQHHHLHHHPHHHHQIPHQPMLSSPPLHPSYHHHHHLHHPNPHILHSRSLSTSTVSGRPPPKTSRRQSKLN
NLDRRRICEYAAAHPKSTQEDIAVQWGIDRSSVSKILKYRDKWLSISPTARAAKVIKHRGGRFPQLESEVVRRCKEKSIS
GGFLGDRTIKDVALDVSQEMGLGEGAFKASNGWLDAFKERAQIKGGRFLDSQQQQQPTAPSSITFNTPAQPLDQLPHSNI
KELIHPSSTLASIDRSSTANHRMEEEHHHISSVEEVDDLEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVEE
EEEEEDQEEEQDKAQQQPSAHPTGTKQGTNIPNSEAHHQQSPSQSSPATDSHHHPTSAPTPSLSSSNSSASQEDGSNGVK
MQDLADSLKSPVDQVMDTGTQSISEATPVNTHDRASEGEPEEPDAMDGIEHISSAIGSGSADQTIVFKCPPSYPAGNFHP
GTGGYTRPIHTSQTDYTSQQQQQQQAQQQQQHSLARRQASSSHSRSSSLSIGSLSQPSSVYGDEYHHTNSPARGGLKIHA
GSPALTSYGSYPNFHPPPLRTTPVRRTFPSLRHAMSHPAFNSPGSGGGGSSQTSSQAPSSSLLPPPMSACSSSNTTASSS
HPSGGGHQYASFPSPAAAAHHPYAFSPFSAPPNHHSHQASSNSNNQPAPLASSRSSSHRLELAPVCSSRIGHPHHPHHLL
NHHHLPRHHHHASHREDAIEWPSSADDFGVGFDEALGALETVMRFLQDQPTSFATPRDYMVVGELFGRMKEKKQEMMTMN
GGNKTGGAGGGNAASTGPPSAGVPRRLISSSGSSSNSSAPLRSSKSSAQSAGHSQQQQQQQQQQQQQQQLQHQQQQLQQ
QQQQQHQAGGASPAAASSAALEFVKEDCSSDRMEH
```

363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE

A0A2N5T5S8 **A0A2N5T5S8_9BASI** (807 aa)
Uncharacterized protein. *Puccinia coronata f. sp. avenae*

```
MNPHQAYNRQDVQQYSYPFPQGQGQGEYEEEDGAEEGSQEDEEGEEEGEGEEDEGEEDNAEVEDGINEGEEEEEDEEDEE
EEEEEEEEEEEEEEEEEEVEERAPSTLPDSTAPQMTFPLVQKPMTVRQRKEQEKIARQRERQIKKELKEREKAERLAKRE
QERLARIAKKEQLLLQSKAAKKAKATMDGDQRAWSIGRPMKGASSSSQLVARKIKVDSRIETVRKLVTYTETGELHIHPN
GTAAEASGNARWCDTKVHQGVTYLVEEDELILPSDPKGDTKVTPEGILLGGRQYKIPTFTSKDRANPNKHFMLSIDAARA
AGYRDSLYFFRRNPLIQKLPCTQTEKDELITAGFLSGNLKSRAVTMCSARNAFKVMGARFLKDGRHVIDDYYEDAALASG
ASSGEIAVADGMEPQDRAAAAAQPGDPSAGPAVPDIPESATRLPCQSAFRLALNRVNPSATGSAVLGTKTIFGGDGKAPS
IAIPNDSKERRRRMASHLTAKNWMIQYCRAISEMNRHLRSIRNERMVPFPKYPSIACLATDPSTNGTSGTTTDAITDEDQ
EWREVEVEMRLNNDGKIIEPGEELDNNVEPNDDDDNNSNSGAPSAAPEPSQVFSRVTHALPPESIITIYGVKNSSASQEQ
HNSGDGFSGQGVGGADSSRSRARSPHKRFFKSRGKKSQNDWWTTTIRVVEQRPKRPVMGLLDVHTGQPHVRRDTQSTMAV
WETADDLADWPGSNKRQKLNGSHADHEVDTDLSCQQSRTIMTGPGLCRPGTGSVNDTILIETIFKDGLSQPSHELLPGMW
DFRSIDP
```

79 - 98:	EEEEEEEEEEEEEEEEEEEE

A0A2N5TBH8 **A0A2N5TBH8_9BASI** (383 aa)
Casein kinase II subunit beta (CK II beta). *Puccinia coronata f. sp. avenae*

```
MDQEPRKDMAETHSQSGSRVQPQAQQRKDASNEPGRGSPTGAGKHGEEEEEEEEEEEEEEEEEEEEEEEDEIGQDEQENL
GDPVEPDENLVIDDSAHEQLSPGAVAPREDLNYDTDTSASVTDSLTWISWFCSLAGHEYFAEVAEDFIEDDFNLTGLTTY
VPFYKEALEMILDVEPDDSVKVPEVSLVESSAEILYGMIHQRYIITRQGLSQMNAKYESAHFGYCPRVYCQPSKVVPCGR
SDVPGDGEVVLFCPNCMDIYHPPSSRYHCIDGAYFGTSFPHLLFQTYRDSPSILAPSPTASLSSPEPPCDLQSKSGFMTD
SLTPYNSSRAKIYGPRIYGFRVSERARSGPRMQWLRIRPRTEEQLRLGLEYRERDQTEEAEAS
```

47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE

A0A2N5TKK1 **A0A2N5TKK1_9BASI** (171 aa)
Uncharacterized protein. *Puccinia coronata f. sp. avenae*

```
MSVVIVIYTGGCVAQGLPALRTPLRSCGARRPLNDGIEHHPVFSNQSSQCVEVHHCIRMLKTRWPSLKRLRTHISGAPSA
RRVNRWIHVCIILHNFLLEEESHWELLMTASDQSIQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAGTEESFHDSPSP
SDPAEDSQFRS
```

117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE

A0A2N5TX34 **A0A2N5TX34_9BASI** (807 aa)
Uncharacterized protein. *Puccinia coronata f. sp. avenae*

```
MNPHQAYNRQDVQQYSYPFPQGQGQGEYEEEDGAEEGSQEDEEGEEEGEGEEDEGEEDNAEVEDGINEGEEEEEDEEDEE
EEEEEEEEEEEEEEEEEEVEERAPSTLPDSTAPQMTFPLVQKPMTVRQRKEQEKIARQRERQIKKELKEREKAERLAKRE
QERLARIAKKEQLLLQSKAAKKAKATMDGDQRAWSIGRPMKGASSSSQLVARKIKVDSRIETVRKLVTYTETGELHIHPN
GTAAEASGNARWCDTKVHQGVTYLVEEDELILPSDPKGDTKVTPEGILLGGRQYKIPTFTSKDRANPKKHFMLSIDAARA
AGYRDSLYFFRRNPLIQKLPCTQTEKDELITAGFLSGNLKSRAVTMCSARNAFKVMGARFLKDGRHVIDDYYEDAALASG
ASSGEIAVADGMEPQDRAAAAAQPGDPSAGPAVPDIPESATRLPCQSAFRLALNRVNPSATGSAVLGTKTIFGGDGKAPS
IAIPNDSKERRRRMASHLTAKNWMIQYCRAISEMNRHLRSIRNERMVPFPKYPSIACLATDPSTNGTSGTTTDAITDEDQ
EWREVEVEMRLNNDGKIIEPGEELDNNVEPNDDDDNNSNSGAPSAAPEPSQVFSRVTHALPPESIITIYGVKNSSASQEQ
HNSGDGFSGQGVGGADSSRSRARSPHKRFFKSRGKKSQNDWWTTTIRVVEQRPKRPVMGLLDVHTGQPHVRRDTQSTMAV
WETADDLADWPGSNKRQKLNGSHADHEVDTDLSCQQSRTIMTGPGLCRPGTGSVNDTILIETIFKDGLSQPSHELLPGMW
DFRSIDP
```

79 - 98:	EEEEEEEEEEEEEEEEEEEE

A0A2N5U3P0 **A0A2N5U3P0_9BASI** (384 aa)
Casein kinase II subunit beta (CK II beta). *Puccinia coronata f. sp. avenae*

```
MDQEPRKDMAETHSQSGSRVQPQAQQRKDASNEPGRGSPTGAGKHGEEEEEEEEEEEEEEEEEEEEEEEDEIGQDEQENL
GDPVEPDENLVIDDSAHEQLSPGAVAPREDLNYDTDTSASVTDSLTWISWFCSLAGHEYFAEVAEDFIEDDFNLTGLTTY
VPFYKEALEMILDVEPEDDSVKVPEVSLVESSAEILYGMIHQRYIITRQGLSQMNAKYESAHFGYCPRVYCQPSKVVPCG
RSDVPGDGEVVLFCPNCMDIYHPPSSRYHCIDGAYFGTSFPHLLFQTYRDSPSILAPSPTASLSSPEPPCDLQSKSGFMT
DSLTPYNSSRAKIYGPRIYGFRVSERARSGPRMQWLRIRPRTEEQLRLGLEYRERDQTEEAEAS
```

47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE

A0A2N5U5S7 **A0A2N5U5S7_9BASI** (523 aa)
Uncharacterized protein. *Puccinia coronata f. sp. avenae*

```
MTNNQQPSGFKLKLKLNGPPPPPPPQKPTNYHVERYQEEEDQLASSDMEEEEEEEEEEEEEEEEEEEEEQINNNRTNTIQE
AHLIPSKLAQPSNKRPSKSLSATPRAVAAAAPAPSKPPPKKRKTTSQSIAIHPHRAQQLTTDQEHADSEHSSYASDQQQQ
QQQQQQQQQQQPHSAPPKPRTIKISHPKPTKPKSKAHLVPLTDAELLSLAAGGSPHYPQQVQDAPITVPTLPAKSKATQQ
PSAIAPKTTTATTKKKTPVTSQGAKKGKTIPAQTIAAATAAAATAPDPRQSTQQAATPTHPHGVKATGTGSSIAKPKTKK
```

```
GAKPKPQDPLQPASVAAPAVVPRPPPGPRPQHDYALGPPPPPPVPALKILPVGPPPRTQGQFLPAQILEKRTPPTRSWRK
VKRQVVGISGIPFWIWTYAGDEHSEYAAFKVQKPPPLPGTVHLNPEAQYYPPAQPSRPASVAPTQHAKPSPMRHPSGTSK
AKYVPSDPSASLNLGGPVLPASFRRPPMSIGSPLSGKGATPYP
```

49 - 68:	EEEEEEEEEEEEEEEEEEEE

A0A2N5UDK0 **A0A2N5UDK0_9BASI** (246 aa)
Uncharacterized protein. *Puccinia coronata f. sp. avenae*

```
MPQTDAQPKGIAVRLGIVLLRHRHRTRCEISKFQRRILEQHLAYEQAHGIVALIDHVCSHCYLHRRVRRPRIASLADTFE
VLWSTSAFERWARITLPSFLKLHTAQNRTPSRLLELVEPRLRTHISGAPSARRVNRWIHVCIILHNFLLEEESHWELLMT
ASDQSIQEEEEEEEEEEEEEEEEEEEEEEEEEAGTEESFHDSPSPDPAEDSQFRSELFKQFCVSSERYLISVIVCFILHFH
PIILAS
```

168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE

A0A2N5ULS2 **A0A2N5ULS2_9BASI** (219 aa)
Uncharacterized protein. *Puccinia coronata f. sp. avenae*

```
MVTDAQPKGIAVRLGIVLLRHRHRTRCEISKFQRRILEQHLAYEQAHGIVALIDHVCSHCYLHRRVRRPRIASLADTFEV
LWSTSAFERWSSQCVEVHHCIRMLKTRWPSLKRLRTHISGAPSARRVNRWIHVCIILHNFLLEEESHWELLMTASDQSIQ
EEEEEEEEEEEEEEEEEEEEEEEEAGTEESFHDSPSPDPAEDSQFRSELFKQFCVSSES
```

161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE

A0A2N5VGD9 **A0A2N5VGD9_9BASI** (992 aa)
HTH CENPB-type domain-containing protein. *Puccinia coronata f. sp. avenae*

```
MLSRSSSSTLLAQQPFLPSISTLTPEHPSYHHSNNNNNNNNPSQQQQQQQQQQQQQQQQQQQQQQQQQQQQQHRQQQQQH
QFQQLQKQELYHLHQQQQQHHHLHHHPHHHHQIPHQPMLSSPPLHPSYHHHHHLHHPNPHILHSRSLSTSTVSGRPPPKT
SRRQSKLNNLDRRRICEYAAAHPKSTQEDIAVQWGIDRSSVSKILKYRDKWLSISPTARAAKVIKHRGGRFPQLESEVVR
RCKEKSISGGFLGDRTIKDVALDVSQEMGLGEGAFKASNGWLDAFKERAQIKGGRFLDSQQQQQPTAPSSITFNTPAQPL
DQLPHSNIKELIHPSSTLASIDRSSTANHRMEEEHHHISSVEEVDDLEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEVEEEEEEEDQEEEQDKAQQQPSAHPTGTKQGTNIPNSEAHHQQSPSQSSPATDSHHHPTSAPTPSLSSSNSSASQE
DGSNGVKMQDLADSLKSPVDQVMDTGTQSISEATPVNTHDRASEGEPEEPDAMDGIEHISSAIGSGSADQTIVFKCPPSY
PAGNFHPGTGGYTRPIHTSQTDYTSQQQQQQQAQQQQQHSLARRQASSSHSRSSSLSIGSLSQPSSVYGDEYHHTNSPAR
GGLKIHAGSPALTSYGSYPNFHPPPLRTTPVRRTFPSLRHAMSHPAFNSPGSGGGGSSQTSSQAPSSSLLPPPMSACSSS
NTTASSSHPSGGGHQYASFPSPAAAAHHPYAFSPFSAPPNHHSHQASSNSNNQPAPLASSRSSSHRLELAPVCSSRIGHP
HHPHHLLNHHHLPRHHHHASHREDAIEWPSSADDFGVGFDEALGALETVMRFLQDQPTSFATPRDYMVVGELFGRMKEKK
QEMMTMNGGNKTGGAGGGNAASTGPPSAGVPRRLISSSGSSSNSSAPLRSSKSSAQSAGHSQQQQQQQQQQQLQHQQQQ
QQHQAGGASPAAASSAALEFVKEDCSSDRMEH
```

371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE
379 - 398:	EEEEEEEEEEEEEEEEEEEE
380 - 399:	EEEEEEEEEEEEEEEEEEEE
381 - 400:	EEEEEEEEEEEEEEEEEEEE
382 - 401:	EEEEEEEEEEEEEEEEEEEE
383 - 402:	EEEEEEEEEEEEEEEEEEEE
384 - 403:	EEEEEEEEEEEEEEEEEEEE
385 - 404:	EEEEEEEEEEEEEEEEEEEE

A0A2N5W7D2 **A0A2N5W7D2_9BASI** (995 aa)
HTH CENPB-type domain-containing protein. *Puccinia coronata f. sp. avenae*

```
MLSRSSSSTLLAQQPFLPSISTLTPEHPSYHHSNNNNNNNNPSQQQQQQQQQQQQQQQQQQQHRQQQQQQQHQFQQLQK
QELYHLHQQQQQHHHLHHHPHHHHQIPHQPMLSSPPLHPSYHHHHHLHHPNPHILHSRSLSTSTVSGRPPPKTSRRQSKL
NNLDRRRICEYAAAHPKSTQEDIAVQWGIDRSSVSKILKYRDKWLSISPTARAAKVIKHRGGRFPQLESEVVRRCKEKSI
SGGFLGDRTIKDVALDVSQEMGLGEGAFKASNGWLDAFKERAQIKGGRFLDSQQQQQPTAPSSITFNTPAQPLDQLPHSN
IKELIHPSSTLASIDRSSTANHRMEEEHHHISSVEEVDDLEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVEE
DEEEEDQEEEQDKAQQQPSAHPTGTKQGTNIPNSEAHHQQSPSQSSPATDSHHHPTSAPTPSLSSSNSSASQEDGSNGVK
MQDLADSLKSPVDQVMDTGTQSISEATPVNTHDRASEGEPEEPDAMDGIEHISSAIGSGSADQTIVFKCPPSYPAGNFHP
GTGGYTRPIHTSQTDYTSQQQQQQQAQQQQQHSLARRQASSSHSRSSSLSIGSLSQPSSVYGDEYHHTNSPARGGLKIHA
GSPALTSYGSYPNFHPPPLRTTPVRRTFPSLRHAMSHPAFNSPGSGGGGGGGSSQTSSQAPSSSLLPPPMSACSSSNTTA
SSSHPSGGGHQYASFPSPAAAAHHPYAFSPFSAPPNHHSHQASSNCNNQPAPLASSRSSSHRLELAPVCSSRIGHPHHPH
HLLNHHHLPRHHHHASHREDAIEWPSSADDFGVGFDEALGALETVMRFLQDQPTSFATPRDYMVVGELFGRMKEKKQEMM
TMNGGNKTGGAGGGNAASTGPPSAGVPRRLISSSGSSSNSSAPLRSSKSSAQSAGHSQQQQQQQQQQQQLQHQQQQLQQ
QQQQQHQAGGASPAAASSAALEFVKEDCSSDRMEH
```

364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE

A0A2N6NC57 **A0A2N6NC57_BEABA** (598 aa)
F-box domain-containing protein. *Beauveria bassiana (White muscardine disease fungus) (Tritirachium shiotae)*

```
MPSGDAKTEPWSPSHEDMERTLGDVVLHRPPGSPPPPYSPEDTPHTSLSNPAWTRIHSAPRENFKNSPLLRLPDSLLTKI
MSFTDVDSLLRLRHTSRTFMRLFSSSEQFSDLRFANCTGGAQARTNVWRTPNCKYPEQRESTLCSSCENRRGYNEQTIVK
NMAQIWCSRCRRLHSAMHFSRHERQNKRDRDRSCIGWAEHVRLCSDVFLDWDLVLALSSSTGDESNSLVCNQHDDNGWNC
SRTKCTFENGVRVLVGTREDGRYELEFTSSSHIPFNRGPSGEKPGWYGVFNAIHEVTNPNDPYCFLASRRFEGCDPMRMF
DPSLCSCLDWNLLPSETNASTQNCFKWHLGGNVCRRWRCKADFGEYAGSEFTECDPETDRCHGARHGFDADLGPGRLVSI
DFVNCPDDGNMLVLVQRTHLIVEGPTDPNWVQLICPQSILQTRDTDMLGKTWCYSKNCAVSKRPGCITRRSLLDLEWRLS
HPNWGADYYDNDDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEENMGDYDGDGSNEAIDSVEEEGSEARNGFDGAIDDDRVF
VTAGEDDTDAKWARTAPVLNSNPNLYSDQLLEYHHLLF
```

494 - 513:	EEEEEEEEEEEEEEEEEEEE
495 - 514:	EEEEEEEEEEEEEEEEEEEE
496 - 515:	EEEEEEEEEEEEEEEEEEEE
497 - 516:	EEEEEEEEEEEEEEEEEEEE
498 - 517:	EEEEEEEEEEEEEEEEEEEE
499 - 518:	EEEEEEEEEEEEEEEEEEEE
500 - 519:	EEEEEEEEEEEEEEEEEEEE
501 - 520:	EEEEEEEEEEEEEEEEEEEE
502 - 521:	EEEEEEEEEEEEEEEEEEEE
503 - 522:	EEEEEEEEEEEEEEEEEEEE

A0A2N6NXF8 **A0A2N6NXF8_BEABA** (964 aa)
ANK_REP_REGION domain-containing protein. *Beauveria bassiana (White muscardine disease fungus) (Tritirachium shiotae)*

```
MSSFKFSAFEYDPLPTPTSVRLLTVRNPLAKASPTVSGVTLLSCKLFTVDLKDKPDFNCLSYTWGNPNPLDQSKDGSEDP
YAPHNQWPISVNGRLFFITKNLYDALSQLRVDEWSDDAKVDSRFEPYDKTRLIQAAEDGRYDDVEDCLRRGANVHNVDCF
GETALHYAAENGHLDIVELLLSQGADRTVIDSTDRTPLDCCLQRKRRRYLDIARILENTSDTSVTVSGPGVQHHRSKPIW
IDAICVNQHDLLERNIQVSMMTQIYGQAQSVIIWLGGFDSEASTELYHSLPTILSSSVECFKRSWEAWHRRRRRGESDED
DQEVQNGTILSSDSISIVLEFVRRSYFHRIWVLQEVALARDVRIMFGGDDLPWAALFQVFQSAIDFEYVAMNYNTTLVKY
RYGDMGTLAWSLADVRLHSRRTKLEDTIVTTQLEALRESNPDFVAMEHDWWCSKLPLATLIALTWNFAATDPRDKIFALL
GIAQPIPGDEPIVPDYHKTITEVFTQVGKAYIQAKGDNRYQDWRSGEIEDFEPLEALSFVQDISEHHEGWCWVRPFADTH
NLLPRPDDLPSWVPSFHWPLATRRLFSTKFRAAGSTVARIHPFESDTLQLNGLMVDTVAHVEKQRHDQARCYCGTANVLE
WLRTMATVDSIYPTGCDRVEALWQVLSANCYLKRSFPLTAYSYAEDPVGEDFADYIKSTLPAELVHLGLCDEHGIPNPDT
AAWLRDVFGKDTSGSFPDVEDVLAAVKVAKEEDDKEDEDDNAGGEEEDEGEGNDGEQAEVKAASGDGHDEAQHEDADEQV
PNQDESAGKVAAVDGEEGNPASAEQGKEEDDKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDGVNSFE
```

```
YFMWCVWPLRRVVSTVNGYLGLVPRAAQQGDQVWLFSGGRTPYILRPTDRSGQFIFVGEAYIHGIMDGEAAEGNENNFRP
VQLI
```

833 - 852:	EEEEEEEEEEEEEEEEEEEE
834 - 853:	EEEEEEEEEEEEEEEEEEEE
835 - 854:	EEEEEEEEEEEEEEEEEEEE
836 - 855:	EEEEEEEEEEEEEEEEEEEE
837 - 856:	EEEEEEEEEEEEEEEEEEEE
838 - 857:	EEEEEEEEEEEEEEEEEEEE
839 - 858:	EEEEEEEEEEEEEEEEEEEE
840 - 859:	EEEEEEEEEEEEEEEEEEEE
841 - 860:	EEEEEEEEEEEEEEEEEEEE
842 - 861:	EEEEEEEEEEEEEEEEEEEE
843 - 862:	EEEEEEEEEEEEEEEEEEEE
844 - 863:	EEEEEEEEEEEEEEEEEEEE
845 - 864:	EEEEEEEEEEEEEEEEEEEE
846 - 865:	EEEEEEEEEEEEEEEEEEEE
847 - 866:	EEEEEEEEEEEEEEEEEEEE
848 - 867:	EEEEEEEEEEEEEEEEEEEE
849 - 868:	EEEEEEEEEEEEEEEEEEEE
850 - 869:	EEEEEEEEEEEEEEEEEEEE
851 - 870:	EEEEEEEEEEEEEEEEEEEE
852 - 871:	EEEEEEEEEEEEEEEEEEEE
853 - 872:	EEEEEEEEEEEEEEEEEEEE

A0A2N8UM39 **A0A2N8UM39_9BASI** (470 aa)
Related to RRP1-involved in processing rRNA species to mature rRNAs. *Sporisorium reilianum f. sp. reilianum*

```
MAAASSSKASSSTKRKASAPSATTSSSGGKSKKAKSSAAPTDEASIPLGRALASTEKRVRDGAVRSLTAYLSANGAHTIG
ALELQKLWKGLFYCFWMSDKPLVQQRLANDLAQLVLVHPSTTTVVDEGEMTERAQAGLKFLEAFWDTLVAEWAGLDKHRI
DKFYLLVRRFTASGFQLLAEEKWPRAAVHDFKRILGKFDAGVLSTNNPTVPDSLTYHLSDIYLDELEKVIEALHDADDGE
EDDELALVPTLELLMPFVDALATAKSKAMYDRIWSNVFEPLLADTLVASARDEDDVDFDDADEHDEEDDEDAAEQEADET
ANGTEFHSFADESALAPNDDESEPSLPPSSSDSEDDSDDVRYPLLLALSSVPTPSPSKDVEEEDDLDEANIDVALLLRKA
IFQALFAAASRKDATEARRRLLYQLWRDEQDRLNDLQGSDDEDEEEEDEEEEEEEEEEEEEEEEEEEEEE
```

449 - 468:	EEEEEEEEEEEEEEEEEEEE
450 - 469:	EEEEEEEEEEEEEEEEEEEE
451 - 470:	EEEEEEEEEEEEEEEEEEEE

A0A2N9EY07 **A0A2N9EY07_FAGSY** (391 aa)
Uncharacterized protein. *Fagus sylvatica (Beechnut)*

```
MIEMKEKKEEEKEGGENEELEQARRQMGAQEEEEQIMEREEEEDPNMEVEQEAESPGSPPEEVEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVEQEAESLDSPLEEVPHQTEIEEEDEPNIEDQQHQPQQEEPESEHQEKT
GDFKGKTTFTVVICWILTLFGGLVLGYNIGMLVMKRFARETNFCKFDSLIIHLIISTPYFIAVPFPFVCMWLSSKWGRRP
VFLVATVSFIMGVFLNVLALNSYYPFVGLAILGVGIGLYNQLSIGGIIHRLKPLAFLEEKEAIAVLVLSLIYSICFTLIS
GPSGWLSETFPPETKMEGMVLSNTLTIAVNVLLANASETTDVPSNEMIERVWKKHPFWRICFSSESRTIIV
```

64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE

76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE

A0A2N9FWE9 **A0A2N9FWE9_FAGSY** (630 aa)
Uncharacterized protein. *Fagus sylvatica (Beechnut)*

```
MAIVEGGVRFPLHSFLIDFLQTVNATPSQISVNTFRIIMGVIAINRLLDVNLTTREILAVYQYRCPGEKSSTLCHLTARK
VHEKLVNGLPSSNKGYEKDYLRVRGEWFSGNSVCRSEYEYPDFKRLELERRQGDAELVRRILSTNICVDDRGEPRSAPLL
LGYEPQVRSFLEGPTVRRAEALEIPPRAPYTAQPATVEQPQDLPDHIPTGQVYTMAPPINPFKLMGKTADASSSKKVKGK
GRGKSRGTEAPKIPKKLPEEASTTESVSQPIPEQEPTSEPAKVHILEDSEQEEELQPRKKRGRTEPSIIPVEGPSSHALA
WDRALLFGQHPISVRNSIMDNSDIDVSAQVARGLAFAACLPEDMKKWAGTQPGPAFRQITKNLMMATQGVMSIEAKFYRL
TEKHQKSEAEHEKAMSETLRAASKNHKKLEDELSRNVNLMKEAEERAWTEETKRAQAEAEIAKIQEKMKELEAECISRLG
NAHKEGMEEGLKKRKELGKEGAMGEVATQFKLVYNSGFRHGWKSALSKTEQPETSDLFLRTNTPLPYSDAGLKNSDNEGE
EEEEEEEEEEEEEEEEEEEEEEEEEERKEKEEEEEEKEEKKKKKKRKREKWCKKKTNVKEMVKPNQPRVC
```

560 - 579:	EEEEEEEEEEEEEEEEEEEE
561 - 580:	EEEEEEEEEEEEEEEEEEEE
562 - 581:	EEEEEEEEEEEEEEEEEEEE
563 - 582:	EEEEEEEEEEEEEEEEEEEE
564 - 583:	EEEEEEEEEEEEEEEEEEEE
565 - 584:	EEEEEEEEEEEEEEEEEEEE
566 - 585:	EEEEEEEEEEEEEEEEEEEE
567 - 586:	EEEEEEEEEEEEEEEEEEEE

A0A2N9FXZ1 **A0A2N9FXZ1_FAGSY** (333 aa)
Uncharacterized protein. *Fagus sylvatica (Beechnut)*

```
MAPKKWDEGKQRKRRRSTESTEEEEARCLKKRRNGVMIEMKEKKEEEKEGGENEELEQAWRQMGAQEEEEQIMEREEEED
PNMEVEQEAESPGSPPKEVEEEEEEEEEEEEEVEEEEEEEEEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVEQEAESL
DSSLEEGDFKGKTTFTVVICWILTLFGGLVLGYNIGMLGVMTTSRYLKDLFHDLAIMKRLAQETNFCKYDSLIIHLIIST
PYLIAVPFPFVCMWLSSKWGRRPVFLVATIIPLFMTEIPHPKLEELADNPTWPGRTFVHPAYLLLLSWRDTEKLDLEGKI
KGGRTSIKEDKRN
```

125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE

A0A2N9GN15 **A0A2N9GN15_FAGSY** (682 aa)
Phorbol-ester/DAG-type domain-containing protein. *Fagus sylvatica (Beechnut)*

```
MASSVINEAESPRYRLQRSSSAPSLAKLNLSDQTRVFVSSHQSETMASSGINEAESPWYRLQPSSSAPSLAKSNKLYLFF
WHAYSPVMYALYEIDLPKPPLSPPSKDAQDAEIRDPKPLFPILEFRTGEYPDQMSCVQLGSKLYFFGGEFNIDDPYIDED
VKNKLKNEKRDVFPREVYIFNLDTQDELLDKLLVRGTPMNSGKASPQAFVADEKIYVVGSTIEMNISDRSKMKDLDPKSF
AYFEVYDPVFDKWTVLPNPPIRNVETRWVGQAVVERKALLVAWQRGKERLYCFDLDSCEWTKHASLPYYPGDFSGRTQFV
ENTLYGCCLNTIAAIAPLDEEEEEEEEEEEEEEEEEEEEEAEEVQQAGSLFKRARLLKGHNLHLVSREMGMDAIFNVPPQL
QSSMSLLHLGKRCFCYVRTGMPPHPNGSDHALLNDKERFISIVIFEALGETYKVDATRFFRAKFLHSAHYVVKTSFPIEG
FIEGCFSPNLKATKKGKTCTSHPEYELKLKNYDKPYICSGCKEHGFGKRYRCEECDYELHKDCMFTTPTTSHQFFRNSTF
KFYEQPPIKRNHLYCDDCKRYCDACGKHVKGFVYHCPKTLKDLHPCCCNLKNELEIDGVKFRLRETVSKCSWCNQTKIKD
VWSKIKGWSYVSECDMYNFHVYCTMEMVFGESGATIYSRSLE
```

340 - 359:	EEEEEEEEEEEEEEEEEEEE

A0A2N9GPH7 **A0A2N9GPH7_FAGSY** (531 aa)
Uncharacterized protein. *Fagus sylvatica (Beechnut)*

```
MAFLVPTKDQRRIDAERKQGNAELIRRVLSTNICVDERGEPRSAPLLLGYEPQVKSFLEGPTVPRSEAFEIPPRAPYTAQ
PAEVEQPQDFPDRIPTGQVYAMAPPINPFKLMGKTADAGSSKKAKDKGKGKRKGPEVPKIPKKLPEETSTTESVSHPTPK
QGPVSEPPKVHILEDSEQEEELQPRKKRGRTEQPAIPVEGPSLHAVAWDPALLFGQHPISVRDIILDNSNADVSAQVARG
LAFAACLPEDMKQWAGTQPSPAFRQITRGLMMATQGVMSMEARHFKLTEKFQKSEEEHEKAMSDMLRAAGENHKKLEDEL
SRSMNMLKEAEERVRTKESKRAKAEADGMEEGLKKGKELGREGAMGEVTAQFKMVYNSRFRHGWKSALSKIEQPKTSDLF
LRANTPLPYPDAGLKNSDDEGGEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVTGEHGQKEEERKEEEKEKKRK
DEMQEKGQHSGSDQTIQTTEVEDVVGTTEQLSDIPDKTGQAEDVTEQPPSS
```

426 - 445:	EEEEEEEEEEEEEEEEEEEE
427 - 446:	EEEEEEEEEEEEEEEEEEEE
428 - 447:	EEEEEEEEEEEEEEEEEEEE
429 - 448:	EEEEEEEEEEEEEEEEEEEE
430 - 449:	EEEEEEEEEEEEEEEEEEEE
431 - 450:	EEEEEEEEEEEEEEEEEEEE
432 - 451:	EEEEEEEEEEEEEEEEEEEE
433 - 452:	EEEEEEEEEEEEEEEEEEEE
434 - 453:	EEEEEEEEEEEEEEEEEEEE
435 - 454:	EEEEEEEEEEEEEEEEEEEE
436 - 455:	EEEEEEEEEEEEEEEEEEEE
437 - 456:	EEEEEEEEEEEEEEEEEEEE
438 - 457:	EEEEEEEEEEEEEEEEEEEE
439 - 458:	EEEEEEEEEEEEEEEEEEEE

A0A2P0NDU9 **A0A2P0NDU9_PALCI** (385 aa)
Troponin T. *Palaemon carinicauda (Ridgetail white prawn) (Exopalaemon carinicauda)*

```
MSDDESAYSGEEGGSDYEEGAQPRQEVKEKVKEVDTDEEERRKKGDEGANFLKNRQQMKMSELDEQLAEYIAEWRKQRSK
EEDELKKLKEKQAKRKILRAEEEKKLTEKKRAEEDRKLREESERKQKEQEEKRRRLEEAEKKRQSMMKGSSKEDAKKFSK
TGGDKFSNIQAAKGELGKTREQLAEEKKIALSIRVKPLNVDAISANSLRDKANEMWNLIIKLETEKYDMEERMKRQDYDL
KELKERQKQQLRQKALKRGLDAEALTGKHPPKIQTASKFERRTDRRTYEDKKKLFEGGWDVVIKAELEKIWKEKYEEFMS
RTKTKLPKWFGERPGKKAGEPETPEGEEVEEEFEPPPPEPEPEEEEEEEEEEEEEEEEEEEEEE
```

363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE

A0A2P1ANK7 **A0A2P1ANK7_9ORTH** (389 aa)
Troponin T. *Teleogryllus emma (emma field cricket)*

```
MSDDEDVYSEEEEEVEVKKQPETKKEPRKSIVGDQPQGDPEFIKRQEQKSSALDEQLKEYIAEWRKQRSKEEDELKRLKE
KQAKRKVMRADEEKRLAERKKQEEERRQREIEEKKQRDIEEKRRRLEEAERKRQAMMQAMKEQNKKGPNFTITKKDQSFN
LSSAQIERNKTKEQLEEEKKISLSFRIKPLEIEGLSVDKLRNKATELWEAIVKLETEKYDLEERQKRQDYDLKELKERQK
QQLRHKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWATLSSEVNEKVWKSKYEVFTNRTKSKLPK
WFGERPGKKKGDPESPEEEEVKVPGAEDDLDEPTFEPEPEPEPEEEEVEEEEEEEEEEEEEEEEEEEEE
```

369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE

A0A2P1EL02 **A0A2P1EL02_9VIRU** (187 aa)
Uncharacterized protein. *Moumouvirus australiensis*

```
MSNTNSIEDDCSSDSEYESNSVNELSSSESEEEEEEEEEEEEEEEEEEEEEYGLDKYKKKNKPNIQLNSAGKILSKTSVEK
ITIDLAVTRYYKVLNYWENKYFEKNTKLGDIVSYYDGTKPEVLIGYSKDDYITLPTFVRYLSEGETIYANDYYPDESIYF
```

SGHVDIKPVLKTIGESIKRQYEDLGNK

31 - 50:	EEEEEEEEEEEEEEEEEEEE

A0A2P2SXA4 **A0A2P2SXA4_9PEZI** (410 aa)
NADAR domain-containing protein. *Pseudogymnoascus verrucosus*

MPPIFFWRDTNPSFAFLSQDSHAPFHDNETETVWPTTEHYMLSEMAMLFAAPDIAARIAHEPHVEDIRALARGVDNFDEK
IWEEDRYGIVEEATYHKFAHSLVRERDLKAALLATGEDELVLASPLDGIWGIGYEAGEAVGQRETWGTNLLGKALMMVRA
WIRMEETGSASWEKGGAFDVTAEQRRVDMPLEVQTYEASKGYISPSDHMYWDTERGEGLAAEYYDKTREFGPPGGYPDHG
VPEEQTEGSRAIEGAPDASGSDNALAVLGALGAGGLVLHEARGGSYGVEEEEEENSDDELRKEVIENLFRKKPEEEEEEL
HDSEDEKTPEPESEEEPEEEEEEEPEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEPESESESEEEEEVAEEEAEEED
AGSDSDGDSD

346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE

A0A2P4P6P7 **A0A2P4P6P7_RHIID** (276 aa)
Uncharacterized protein. *Rhizophagus irregularis (strain DAOM 181602 / DAOM 197198 / MUCL 43194) (Arbuscular mycorrhizal fungus) (Glomus intraradices)*

METTKTADAGSKNWLKERAAISAAHRRQKTDPAAARLIEKADQLHKERTQKNLRETVDEDDEAVDEVPETTVKKNEGRDR
RTNVKSSFRRSVVFSSPLNYSSTPAEDEDLEDIDAIVSVPPPEEIVVKIAQKPAEEDTIASNHGKETSEDVYRSFAESVL
EQGLTTKSELELSFDLKPEDIKIKEEEEEEEEEEEEEEEEEEEEEEEEKGEEETQEDLNEADITEEKVQEKLKDADVEIN
HNEENKGDVKDQEDDKSEESTLTKEVDVDTVPKNND

185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE

A0A2P4SSW5 **A0A2P4SSW5_BAMTH** (174 aa)
Uncharacterized protein (Fragment). *Bambusicola thoracicus (Chinese bamboo-partridge) (Perdix thoracica)*

MAALAAMRAAAAGLSHSSSPGLSEESQEEEERGEEEEEEEDGGGGYQQEMGSEEEEDLKGKWDEEEFEEDLGEEEEEEEE
EEEEEEEEEEEEEDYEEEEDMGEEGLGSAEAVRTGTGSLLLRKPPAPQHCRGEAQRLPGTQERLPAGLGPQGHAQLPQPA
PDHGDWTYEEQFKQ

73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE

A0A2P4TIG4 **A0A2P4TIG4_BAMTH** (538 aa)
RanGAP1_C domain-containing protein (Fragment). *Bambusicola thoracicus (Chinese bamboo-partridge) (Perdix thoracica)*

KMASEDIAKLAESLAKTKVGGGQLSFKGQSLKLNTAEDAEEVIKQIEEFDGLEALRLEGNTVGVEAAKVIAKALEKKSEL
RISLGDALITAGAQLVELDLSDNAFGPDGVRGFEALLKSPACYTLQELKLNNCGMGIGGGKILAAALKECHRKSSAQGKP
LALKIFMAGRNRLENDGATALAEAFGIIGTLEEVHMPQNGINHPGITALAQAFAINSLLKVINLNDNTFTEKGAVAMAET
LKALRQVEVINFGDCLVRSKGALAIADALKEGLHKLKELNLSFCEIKRDAALSVAEAIEDKVELEKLDLNGNSLGEEGCE
QLQEILEGFNMATVLGSLSDDEGEEEDEEEEEEEEEEEEEEEEEEEEEEEQQQLKERGQGEQDTMTPKKIIGSQDSTSV
PSPPVDVATFLAFPSPEKLLRLGPKCSVLIAQQTDTSDVEKVVTALLRISSVFKDEAQVKTAVHETTDALMKKAFSSATF
NSDAFITRLLIHMGLLKSEEKIKAVPSLYGILMTLNHMVQQDYFPKSLAPVLSAFVTK

348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE

A0A2P4VTB0 **A0A2P4VTB0_CAERE** (143 aa)
Uncharacterized protein. *Caenorhabditis remanei (Caenorhabditis vulgaris)*

```
MWLRVGEEEEEEEEEEEEEEEEEEEEEEEEEEEXEEEEEEEEEEEEEEEEEEEEEEEKEGETKTVITWLKCATASEVPHEA
LVVTYRTVTLVQNGGDDGSIIVTSSLPRLIQRLTNNEKQRKTTTDQPICVIKNFEPSEIITCD
```

7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE

A0A2P4YWT7 **A0A2P4YWT7_9CRYT** (1160 aa)
Uncharacterized protein. *Cryptosporidium meleagridis*

```
MGKRLLKPVESGEELDEELPHSVGEESSHGFGTKKKLIKNKSRVFNESLDRISQNRENRRGATGVLGALIDSIREKDTQK
IDDSELESVSETDEQFKASKAKRLSKKRKKKGTDSIDVSNLLCSLNNTTKQKSKKNQSNRDLDTMFELFSMPSSDSESNF
GSRIDDFENVVNRKVDQEVHDSTSEEDYECLNLTEIEMALRKCVKNDYNPSLELNEWLPTQCIDVRSEIARQMDDDVKIS
EITEKHEFFYSQWIEQIGYLSSLTKGFTRSIQECFVREGQILSISNIKESNPELLLDPEDKILITVQNSDACVILNRLVN
IANSQEKLIIEMIKKTGISNIDEEDSTTRLKYGIISLKARSKLWWFCRMAEHCGLVGREGNNMIKYYVLDKSRKKTSNSI
FSTNADIISSIDPSMELFNKNDSESNMDDDNDLTGDECGENHAETEQISEMDSKWLDISSIKVSNKPRPWEGRAKQVKTK
SQNVEESTANCSKKELFKFMLKNIGPRPVWTNSGVIGDLYNHDKFKIEIEPPTNLSLREQGQMKINWLQMKNQAEKLATH
HFKIMDPETKDLDHDSLKYWCKLFKVNLLFPPCKSDKIRVRNNNTINSSIPLEEIPEMAEIMEDGKNGQYLNDQKICPTN
HFDNITGTKRNSLPLDVEYIDDLDGEAVEEVGQGYYHDSEKLEEEKVEEEEEEEEEEEEEEEEEEEEEEEEEENNRETDY
MDEVNASNCNEGENKLIDDVNEYHSAEEIFDQEMDEKIESDKEGSIKEKEANENSEEETNLKMRIEAHKRLKAIRKKRIM
LKRKMMEKYGHLFENEAEESDEDGIKILRREIGGDYSDDDDDDDIDWDELSGFSDFIDDNNYENGELDGDAIQAHLKHMK
EIEEKQYRQLFTLEGIKERKNKVYGFAAGEDDGIEGETRLEKKKNELIFNSAFFDDDVISELWTDEEELEDYEEEIDERN
LTEMLGLNYEEWENSLPKKANSSDESLNEQRKLKYNILKESLIKEASGSINVLKQRLKSIQTKLSLQEDISLNEKNQLQT
KYIECMEKLKKLLQLIHSACNRCIYENSQFFDHIDIYEYIQKREESRSKKKPKAKNTIEDKIKQRCKYQNKYLRENVNPL
NKIGKTGSDSEDDVIIQKRVQKKEKNTVNVKGGRFKISKK
```

688 - 707:	EEEEEEEEEEEEEEEEEEEE
689 - 708:	EEEEEEEEEEEEEEEEEEEE
690 - 709:	EEEEEEEEEEEEEEEEEEEE
691 - 710:	EEEEEEEEEEEEEEEEEEEE
692 - 711:	EEEEEEEEEEEEEEEEEEEE
693 - 712:	EEEEEEEEEEEEEEEEEEEE
694 - 713:	EEEEEEEEEEEEEEEEEEEE

A0A2P4YZG8 **A0A2P4YZG8_9CRYT** (1100 aa)
Uncharacterized protein. *Cryptosporidium meleagridis*

```
MAELIMGVDFENKKEYIKEYNLGRNEDIVELIRILRIQEESRKSLEEEIQVIVSNNESLKQELISSNEMVNYWKDQYEIC
NSSLKIINKEFEQLKAYDENMNTFNKTFKSMECKKCGYEWKKISVENDYRDLNSKIAENDLENFLDITNILVSSLYINEM
EGLTTEENNDIILNEDNIIKDQELEKLKIENEELKILLKKKEGIIMGLQDELGQIKSRLMIEKSLPNIFKIVNKDLFDDK
TSEDDDNPESSHFKDKSNDIELKNDKNKKNYLDQLKSINKKRKIAFCLDNDLDTKELKLSESLQDLNVTNNNNNELLEQV
NVMNKISDFENIETNLDVNEKSGKHEEASNNEISKLKVESELVEGLSWEDDIWEEEEEEEEEEEEEEEEEEEEEEEEEE
EELVANITNEDDLNEPIKEDELKSNEIMINGLEGSKKNIIGLKSFLDDFVSHISGSIDDDINEKEENKDESSFKDIFDSY
NNNNNSNNSNNNSNNIPSFTGFVSNIKSFFNDERINPVVDWNLKKIQDNLIDSMSSSNKSMISEQINMNSEGNGIINSNW
DCDNWGFDEEDEEEEAEKEEGQEKTMRREEERKEDEKVVQDNLGDDFFSDESDGNNNKGYKEDEFDLRKNDDLDIINSLN
FNELSSEEKVQDQTKKVESSKNEFNNWDNIDDWSDEFGSFEKEEEEEERLRKEEEEERLRKEEEEERLRKEEEEERLRKE
EEEERLRKEEEERIRKEEEEERLRKEEEERIIKEEEERLRKEEEERLRKEEEEERLRKEEEERIRKEEEERLRKEEEE
RLRKEEEEERLRKEEEERIRKEEEERIIKEEEEERLRKEEEEERLRKEEEEKIKNNNFEIEKKIDSSWEDEWDFDDDLDN
CNNNTISNSNIEIENNESEDEWGHNHKDKFTDNLINETKEKTITDDKELKEINDNSWENEWDFEDDLDNYNNNTISNSNS
NNNNNSAFIQNFSWDDKWSSNDEININENNNNNQIISSNFNINSEKIDQNNQKLNEQLISLSSTNNANSNNSNAISNNIN
NNNPPSFVEWKNEDDFWSESEINSDKLSNKDSFKFKDNNNDEKSNSNSNWSDLNWSDDEF
```

374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE
379 - 398:	EEEEEEEEEEEEEEEEEEEE
380 - 399:	EEEEEEEEEEEEEEEEEEEE
381 - 400:	EEEEEEEEEEEEEEEEEEEE
382 - 401:	EEEEEEEEEEEEEEEEEEEE
383 - 402:	EEEEEEEEEEEEEEEEEEEE

A0A2P4Z1D5 **A0A2P4Z1D5_9CRYT** (315 aa)
Nucleoplasmin family protein. *Cryptosporidium meleagridis*

```
MFCGLIIKPGQKVKLDSTQGEILHLSQACLSEPKDNGRVYVQAIDNGNAYTICSLQKGTVEHANLDLFLSTSAEIELSVI
GKNEVHISGFYEPEMEEDFEDDDALMGMSEEEEEEEEEEEEEEEEEEEEEELGLENSKADNKKNLKRKLPSKSDESTDEE
IDDEEIDSDEADDLDLDELIQDNDEDDDEEDDLDDLDDNDEDDEEEEEEEEEEEPVKAPTTKNKNKQSSASQKSKSSDSQ
PPSKKSRLESKSQSKPDQLYEESIIDFLKKNGRTNMAMIGNKIRRPEGVTKKLGSFIAERTDLFKVENNMISLVK
```

110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE

A0A2P4Z1M5 **A0A2P4Z1M5_9CRYT** (472 aa)
Divergent CRAL/TRIO domain protein. *Cryptosporidium meleagridis*

```
MLLRNTGYYMDSDAEVDPSYYEAIIEATQDKVFNSYEETRFIFYLGDDVLQRPVIMLVSCFLPPTVDELDKAMRYAVHYT
KEFVRTEFIIVQCLTRTNILSDGSSNFLQQFYSLLPTEYKKNLKKVIMFHYGVSNRALLTITSSYMSPRFMRKLEYADSI
KELYRFIPDISEEELLNRLPFIVKHDDAELLGLEAPALLSMSLLEQCICNGYYVPGYGKIPAIIVDFVQKLSKPDIVIIP
NLFSLQTSADKLTSIIGEVDSGVPFRSGDSDPSALVSAFKLILNSLDEPLLGSEIFHSIVRQCKNSGTHELAHSFYINLL
KETISKLPDSSKLVIKFLVDFLQYVSTKSSINNMTAHKIAEILSPAFCRPNSMKNITMYQSIPPCVECITVLISDCQSIF
NNILPDISSFDHLREVKENLRKKQLEEAEEEEEEEEEEEEEEEEEEEEEEEGQPELLRTGDNDEVESEENN
```

429 - 448:	EEEEEEEEEEEEEEEEEEEE
430 - 449:	EEEEEEEEEEEEEEEEEEEE
431 - 450:	EEEEEEEEEEEEEEEEEEEE
432 - 451:	EEEEEEEEEEEEEEEEEEEE
433 - 452:	EEEEEEEEEEEEEEEEEEEE

A0A2P4Z1V7 **A0A2P4Z1V7_9CRYT** (367 aa)
Thioredoxin family protein. *Cryptosporidium meleagridis*

```
MELKLAVLNLILLLVIGIRGDEINASVYGHNRAQKHAESTASASSYSPQKHPTVSVNSEKKIQSFVKELNDNNFEHLTQS
ATGSTTGDWFVLFYLPNCQQSQLSLVELDKLSVIARESLNVAKIDVSKNQQLINRFGIVAVPSFRFFKNGKMYTYTGMRN
AEVIKAFIWNKDYKKLTPQPVPDPLSTLDIIISEIKHTINDINKLIKLAPLVTIIILLIGFFTGIGVTNIFSRSSNRSKT
TTSNNRVKRDKYSDDECEDHEEGEEEEEEEEEEEEEEEEEEEEEEEEEDEEEEEEEEDEEEEDEEEEEEDEEEEEEEEEEEEEE
EEEEEVVRQLKTPQKGRRAAENTAKEDDRLNNTYNTSVRRSNRLKKL
```

264 - 283:	EEEEEEEEEEEEEEEEEEEE
306 - 325:	EEEEEEEEEEEEEEEEEEEE

A0A2P4Z4R4 **A0A2P4Z4R4_9CRYT** (302 aa)
18S rRNA aminocarboxypropyltransferase (EC 2.5.1.-). *Cryptosporidium meleagridis*

```
MKSRNSTKTQVETNFVSEFTSETDSSEIESKLESGKNVESDMDEEKAGKKTDTDEVIKVNKEEKVEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEPTIKIGLWDFCQCDVARCSGRKLLRFNLAKKLQFSSNYARKWPGIILSPRAKRKISMEDL
PLILKGGVGVIDCSWNKIDQVPFHKIHNGNERLLPFLVAANSTHYGRPYELSCAEAISACLYFFGFPKQAEKLLGIFKGG
YHFLELNKEAFDLYKSKGINSQSIINAEQDFINKYMNKHQQRESRDYDSLFSSSYDDDDDDG
```

66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE

71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE

A0A2P4Z544 **A0A2P4Z544_9CRYT** (1262 aa)
Helicase conserved C-terminal domain protein. *Cryptosporidium meleagridis*

```
MIPDKILEENLLEYDLQGSNALVLPNSKIERKRIHQENNYSESDQNTRKPCKEKKMSNRKKRKLKQLEEKKRLNKIHEDL
TNDLKKYTLSDQELQLMMGITNTRMNNRQKQILRSRYLAAKLELPDFLKLKNYSSKSKNYISESESESESESESESKPEH
EAEREPESSKVDDLVHPIDRDKKLKSENKNFDSESKLELKKNEQLKKESQKKESKGRYIRKFTSLVIKNDSDRPIISRTP
EIEFQRSELPVRVYEFEILDAIENNDVVIVTGATGSGKSTQVPQLLYESGYCQLKKSQNNNNANEGEKRYMIGLTQPRRI
AATSLSNRIGEELNDSKVVGYQIRYDKKNCTNETVIKVMTDGVLLQEIQKDLLCSKYSVILIDEAHERTVNTDILIGLLS
RIVIFRREEYIRKTKQGLEDILPPLKLVIMSATLRVTDFSENPKLFSKPPPVINIETPNFPVSLHFSKNTPKDYISAAYK
KIQQIHNRLPPGSILVFVTGKKEVNLLVNLINNKGRNKAKRNCLLNNKTNSKTNMLLDFTENNLEEEELEELEEEEEEEE
EEEEEEEEEEEEEGDDDDDDELEEEELGELEQEELEKEEKGQQKEQEYEGSEESKNVWESFGKKDIRKRKIRLHKDVDSS
VWKGGGVIEEDDSEEEKDSVKKEEGIKDRKSESIKVQLIAFPLYASMSFDEQKKAFKLPESNNIRHVIISTNVSETSITI
PNVRYVIDTGKEKRREYTKGSDSSHFTVEWISKASASQRSGRAGRVGPGHCYRLYSSPIYENIFPKFAPIDILSIPLDSV
LLYMHSLGIPDIVDFPFPTPPEKSQIDQAYQLLTILGLVESRKSKYMLTNQGISMSSFPLPPRYAKILLLTTAYIRKNLI
NDDLKSSTELLQQACILVSYLSIGNLRDESFSSAIQEEQNQGIMNVDNQNLKDDFESFPSNLGNDIEINLWFCIKYLEYY
GSGKKHERLLSDKFSKKFELNSRGLSEIRLMSIQLFHITKKKYLDRLINSEANLHIKWPPSLPNFTQKNLLRTFFISSFI
DHVAVRNDGNLVSKTSYQIPNESPNSYSAFIHPRSVLKSSKPKLLIYSQVISSNDKSRHNLCDCLLITADDISKATSLKH
SLVDCSKILSFPAPYYNIESDSIIGYCTPKYRNNSVVIDLPSSEIQLEINNNIVFEIFARAILNGQVFKEFTNQRILKGL
KSKNNSNQFKLLVNTLEKNLIFNKSSLISKFKTKRDFLIKNILQLYEISVHNDIRSFWPPMK
```

553 - 572:	EEEEEEEEEEEEEEEEEEEE
554 - 573:	EEEEEEEEEEEEEEEEEEEE

A0A2P5DPB0 **A0A2P5DPB0_PARAD** (107 aa)
Uncharacterized protein. *Parasponia andersonii (Sponia andersonii)*

```
MASPPALHDRPRSLYRPSRTIFRSIARLQALLDPTAEAMEASAAYLTLRYRLEVSLEEEEDEEEEEEEEEEEEEEEEEEE
EDEEETKGFWPFILLRARRNPRMNLYL
```

62 - 81:	EEEEEEEEEEEEEEEEEEEE

A0A2P5I774 **A0A2P5I774_9PEZI** (203 aa)
Uncharacterized protein. *Diaporthe helianthi*

```
MKSTTFFLAAGVATIIYAQNGPRERLSRRSVESNNRRVDFITGNAKTLKRQDAVPSAVPVTSNGTTDLEQKPEEEEDEKE
EEESESESESESESESEEEEEEEEEEEEEEEEEEEEEEEPEADQGEPSEAGEEQEESEETEAVGIIAEESGGQDQAEVQPPVGN
GGTAPAAVIEGPDGGQIAMGMGITNADGSCTCNAVCPAGGMQG
```

95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE

A0A2P6MP99 **A0A2P6MP99_9EUKA** (690 aa)
Photolyase/cryptochrome alpha/beta domain-containing protein. *Planoprotostelium fungivorum*

```
MKHVTHNGNSNIMPPRVIYWFRTDLRLHDSPALSKALELEPECLYPVWTWDDHYVFHARVGVNRWQFLLDSQSQLSENIT
KINPKSKLHVLRGPPLQILPIVVKQWKITHLVFEKDTDTYGRSRDDQVMEMMRKLKVEVISVSGRTLWDVDEVLKRNKGK
PPNTINALSKITEKMGPPEHPLPTPTSLPDPGDLDLDIESQSVDDAEDLNAEQREKPAVCYDSIRGPKGDFSVPTFEELG
LKPATSPWRGGESVALKMLTEYTDDIEKTAKFSKPDTPPTQFLPPATTNLSAHLHFGTLSVRTFWYKVEESVAKFKGKKS
SFPTNLPGQLMFRDMYFCCQAGWENFERMEGNKECRFIPWALRNSYVLSHTYRTSHVISYDEEGRVNGQERDGEAEEWFT
RWKEGRTGFPWIDALMRQLKHEGFIHHLGRHSVACFLTRGHCYISWERGQEVFEEWLIDHEAACNSGNWQWLSASAFFHQ
YHRVYSPIAFPKKYDKTGRLVRHYCPELSKFPDKYIYEPWRAPKAEQKAAGCIIGEDYPLPMFDEGERRKRCLDAMGHAY
KGVGDERLRDGSWRELFPEVKVKKEKVKEEKGGKVKEEKVKEEKGGKVKEEKEERGKKRKGTLDEYVSKKEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEERGGKRGKDKKEKEKLASMGPSKPKRRKR
```

631 - 650:	EEEEEEEEEEEEEEEEEEEE
632 - 651:	EEEEEEEEEEEEEEEEEEEE
633 - 652:	EEEEEEEEEEEEEEEEEEEE
634 - 653:	EEEEEEEEEEEEEEEEEEEE

635 - 654:	EEEEEEEEEEEEEEEEEEEE
636 - 655:	EEEEEEEEEEEEEEEEEEEE
637 - 656:	EEEEEEEEEEEEEEEEEEEE
638 - 657:	EEEEEEEEEEEEEEEEEEEE
639 - 658:	EEEEEEEEEEEEEEEEEEEE
640 - 659:	EEEEEEEEEEEEEEEEEEEE
641 - 660:	EEEEEEEEEEEEEEEEEEEE
642 - 661:	EEEEEEEEEEEEEEEEEEEE
643 - 662:	EEEEEEEEEEEEEEEEEEEE

A0A2P6MPR4 **A0A2P6MPR4_9EUKA** (689 aa)
Uncharacterized protein (Fragment). *Planoprotostelium fungivorum*

```
VRYLKIIEKSGYQALPWVRYITQSGTYEIVPLTDQMTTEASFRCPYSVQVEWSRCCPARDTRNNRTIADPDTMNLSQDVD
PIANVLVDDDYERGLSQRYEAEGGSLMMHPFEGDPFDAKCILEIEMNRLSRSIRIEAKWLKEAGRVRKAIVSVFDRVWQK
MKEEAVQHVLDEVKWLSSFPDGSISPSVVEDVWECDGLISEETRQELLKGAKELEDVPEEEKDWHPGSNHQVLDLVHPSL
YCYVYGVTKEVKQQIKPTLPSQGLFVRDRINKESASYPSENRYGSNIVKRSTQFQWLPAEFLVGHDGKVEIDSYINNLHP
IKHRQLYNTIGKIFERFVPLLEKVLYRGNISKNKIKVDMYSIVWEKEDKKGDDEEEEGEDDDPDEGEEEEKEDKKGDDEE
EEEEEEEEEEEEEEEEEEEEEEGELDQPAYKSNIGHTRGYGGYYSDNMGDFEPKIPQFVPPVPNYISLRGRRLQVIVKMA
NIELTPEKPEYAGGSWHVEGMLNEQIAASGIYYYGSENISTSKLAFRKRVEQPFDQGRQDQGQTECRDVYRLYNGGKLNE
YMGSVDTKENRCIAFPNRHQHLVLPFKLDDPTKPGSRKILVFFLVDPFVRIISTARVPPQRRDWMWDYIREEADLSVLPV
DMLKLIESHSDLMTREEACKYREELMKERGRTAEGLSDLFEEDFDLCEH
```

399 - 418:	EEEEEEEEEEEEEEEEEEEE
400 - 419:	EEEEEEEEEEEEEEEEEEEE
401 - 420:	EEEEEEEEEEEEEEEEEEEE
402 - 421:	EEEEEEEEEEEEEEEEEEEE
403 - 422:	EEEEEEEEEEEEEEEEEEEE

A0A2P6MX15 **A0A2P6MX15_9EUKA** (1184 aa)
Uncharacterized protein. *Planoprotostelium fungivorum*

```
MSTSWGGQYARVLIENILPNVDATDIFSIALVCRSWKDALYQSVTVWQAIELGIPKPRQWSDELLFVRLLDSFSNCPYIR
ENIRVLRISHAQEYGSTFEEVLSHLQFVVRFPQLRSLILSNEIKITITQVKWVITALPELQTFKANIRHSQQYTDGLEEL
VLYKDELKCLAIGRLRGVACTQIFGSTTQLMEPWKGKRVRKLKLSGRLFSLDGKEKVFDLRPIFSRGGLLQNHRFNDSDQ
VIQDLNVLTERLKECKPLDGWSTQQLSFKSELPPILILPEGQSIDNPQEQQVLDAWKTFTSTLCRAIPVLLPLRLSPRRH
RILFSSRWFKGASFQPGTNLDRCCSPEEAVRLVRSGLIVAHGPDARERWMLDKIFSDIVCREDDLIHRKEILKKVLSLAP
HYRLCTKKTTDIHLKGVPFVPLLEEDHLNLLALHMSKYGQQGKFTHAAVQETNRFIHSLFHAYDRVDEHVPRVRAYRTLA
PLPTFLTNKRTIGLFRGMDLSDDRDLHAISMESPRQERVESMTRDQREMIELEDSMRRLFVSDRQNHKLDDLYLDLIDVY
RHPSEFKRSPLNLEERKCVLLFRHFMRDDRGISQVPSSNVPSIVEPLVFTERVKSMLGDTFRGLDWKNIFIAGGSILGAL
SSDNMAMNPGSDIDLFVYGLEVEEAKEKARKIAEVVCENFGPDYENKLLIFRSKYSITITRPWPLPHIQIILRLYKSPAE
ILLGFDVDCCCVGYDGRALNKGYNLINWTRRSTTYESRLYKYALRGFGVMTSGFTRDQINPEVYTKRVKNGLGYLLSLDW
GKSSQLPHNLRTRRGLRKSNESFRREDFPPYGDYGWSPPNRPDWNPDRIRIHMNQTSSIMDELSLKKREDWSDIVWRQDD
PGGQEGHLLTGSFQPLPPHQEDYVFLVDRLPCAEEKAVDVESEEDTVASTPSVQFKEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEYEFSYIKVPFKVLFTNSESMSQLKLPGYGSSWCISGASQENDDEGDTSPFLSNKRQLMSNGILSGHDVTKVI
LHMAMEDESPDARRRQFSILRLTCKLRKDIEYESTEIVRLLLDDARMDPSAADNDAIINAAEQGLINNVQLLLSNPRVDP
SAQDNLAIGCAAYEGYTETVRLLLSDPRVDPSADYNYAFTMAVGGGHTETVRLLLSDSRVDPSI
```

937 - 956:	EEEEEEEEEEEEEEEEEEEE
938 - 957:	EEEEEEEEEEEEEEEEEEEE
939 - 958:	EEEEEEEEEEEEEEEEEEEE
940 - 959:	EEEEEEEEEEEEEEEEEEEE
941 - 960:	EEEEEEEEEEEEEEEEEEEE
942 - 961:	EEEEEEEEEEEEEEEEEEEE
943 - 962:	EEEEEEEEEEEEEEEEEEEE
944 - 963:	EEEEEEEEEEEEEEEEEEEE
945 - 964:	EEEEEEEEEEEEEEEEEEEE
946 - 965:	EEEEEEEEEEEEEEEEEEEE
947 - 966:	EEEEEEEEEEEEEEEEEEEE
948 - 967:	EEEEEEEEEEEEEEEEEEEE
949 - 968:	EEEEEEEEEEEEEEEEEEEE

A0A2P6MXE5 **A0A2P6MXE5_9EUKA** (666 aa)
Uncharacterized protein. *Planoprotostelium fungivorum*

```
MAETKEQRKGIFIQNLPPTVTKEEIDAIFGDIGPLRRTTVLTKKGSSQCNGQAIVHYSLESDAAEAIKKLDKTKFPGAEK
LLRVSKAKPKIQKEKETEGEEKVEEKKIPRADSDELAKSQQGRLIIRNLSWKVTEEALKKEMEKIGPLAKIDIPKLADGK
MRGFGFIRFKDKNHAKKAIETKNGLQLMGRPIAVDWAIPKNQYEQIQNPQNQEVEEEDEEEEEEEDEDEEEEEEEEEEE
```

```
EEEEEEEEEEEETKKGKERNEEEDGRCAFLSNLSIDTERRNIIQRFKEYGEIDKVYIVKDKVTNTNKGSAFLYYKSKESVD
NLMMEIERYHLGQVVDQTVLLDSPIIIDGKNVKISRYSNVDEKKKTANQGDKRNRYLADEGFIAQNSKSAVGVSAADLAK
RKAILKETKEKLKSSTFYYISQTRLMISNIPLELTDKELKALMKEHSSSHFKQVKIVRDEYRNSRGFGYIEHNTHEEAMS
TLKALNNHPKVFLKNRRPIVSFAVENAKKVLQSQQRKEGQKRKLEEKKEETKEEKSIKIKTKKGLNAQSKDMLQQNKDLL
EKGSKLKVEGNNKKRKREQGGEKEEKEGKEKREKEGKEKREKEGKEKREKREEKKRQGKEKRGEKRKEKEEGREKKKQKR
QANGGKVEESIVKQMKRGTQSLDEWA
```

229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE

A0A2P6N2B5 **A0A2P6N2B5_9EUKA** (806 aa)
Uncharacterized protein. *Planoprotostelium fungivorum*

```
MPQSRKGPKITSEESYPFPEANVGTEEMYRQILKDGFDRAPPSKESSLGILFEQGNMVPGLEVKDFGLIGLPLHPLLLTM
LKSTGTRVNDHIYQWKAGSKRNEWMRLLKSKMQGITSVFGRSMSSDDVELVLRGMILEEASASAHTWPSNDSDDKGFFGY
LIVTLPTHHEGGIIKISNDQEEKIYLSSPRSSYHYQILSFFRQCNYTSSPITKGQRFQLLFRMVARGKEQYVRQMVKAMR
VWKTDPDRTEALCYQYSSNGEAMEDITRKKIAEVLKKELGVGCYHGTMTPQNETQVTLSDHLGRCSFLPACWLNGANMGR
AAVDQLLFRLGTSSDYFQSLMSRVNYTTKKRKKIDMGILKNVPNDILDYILSSYMSGKDLVQLDGVSRGMIARVDHSVRT
IMNRFAQEAIRMGKHEILSDWRGLLKYHKQYKKTAPYEAIICIMPDLVFTDNPVITDLVATYGGVIMMPKMMGYLSVLID
PFFIVEEDCQEIIGRLMDQVRRSYLSLGIEFDSTTPYCTYIESWIAAVLRDNLSKGIPLLKHLFLAERYTDMERVVLAHY
VNFYDSLDHYKTMSPLITYMLDFDKGEEKRDLKGIKIFVDLSRNLMDSIAELMRVPVPSDDWTMRVSEALTDHCAHCKAM
GNFLRHPTERRLVLRYPKLQRIHVVCCLVMNLTPLWIKKMERAEKTFAALKSITKYEPMDLLEEKEGEDDEHEEEEREEE
EEEEEKEEEKEEEKEEEEEEEGEEEEEEEEEKEEEEEEEEEEEEEEEEEEEEEEKEEKEEEKREEKSKKRVARGKKGPAR
KQQRRK
```

753 - 772:	EEEEEEEEEEEEEEEEEEEE
754 - 773:	EEEEEEEEEEEEEEEEEEEE
755 - 774:	EEEEEEEEEEEEEEEEEEEE

A0A2P6N5L8 **A0A2P6N5L8_9EUKA** (1314 aa)
Bromodomain and PHD finger-containing protein 3. *Planoprotostelium fungivorum*

```
MEKRLNACTNCRASHTGCSRSGPPCERCSRSNLETPCSFEAGSSSSTPPRKPKTPKKSVTPRAKSPRVSTPRVPALFIDE
FDFEEEEQVVKEKPKPITIDPDRLKSPNQLGPIKLTPKKKKVGRPRKIPITPQPQMRGADISQEHSDHQEDPKHAHAVSD
TLFLMGGEYKDTKKRDVPPFPLGISSELPIYGPDPEESSELPGDDAQDCAPSQDTLENHYMNFYQKGHKIHEPLQKAIVR
PADLTDAPKQRLWNRPASYIVHLEKNLDDQDVYIEYDIDSEDEIWLSEINKQREEKKLPPISEDDFEMMIDRLEKESFAL
ETLREPLPEEEVDTDNTNCCVCDDGSSDDTNQIVFCDGCDIAVHQGELHRDIQKYHGELTDAECYGIRYIPEGRWFCQKC
QAKESSVRCILCPNFGGAYKKTAEGRWAHVICALWIPEVKFSTTTEEMRGHVTGVENIPKARYKLPCALCKKKGACIQCR
DRLCKVSFHVTCAQAASYYMNFVETDDKLDMIALCPKHSPEPYSLNPSRWEKFLERNENKGRKKPRQTRKKKVEERWAGR
TFQEIDGSSEGEGVVREEGKKKKRKGSALEGNSKKKTKFLDLISHQTITLPKAKEVIKGVPKGCIPQLFKYWTRKRQSRS
GNPLVKKFNKSILFSPHFTPKKLEKDEYSNYLKAMKDIRRDLERCRLLLELVHKREVAKKNVVVARRDVILYEMNPDLST
MDLLLTYLINEDIEGHFQSMLHGMMDDIWSDGYQSYEQLWNRLKGHFEENSSRPESNRMLHVLQNIERTVQFKRDKDQAR
KLSVKMIEVDESVSPAEETMKRKEETMKRKEETARKRQESHRKREELKKLKEKETIQSATKAQKEEGREERDEEKGEKEK
IEKEEPPKKKKGRPRKDKKEETVTPVTPERQQLNEKCSKLLDILSGLDADHYFSFPVDTKSFPQYKRIIKRPICLLDMKK
KAEKNGYSTMEELRGEIHLMSQNATTFNEHLSDVFWSANRLKWKSDRIISKERSTEPKTKRPCHICKSSTDEDMEACSGC
YNLFHLACAPSHTKGSLFFCDECDPSKHCDLCGVRFEGEKPATCPGCQKSWHYRCLEKDSRRQAEGKSAYCTECDECGLL
KPADLAEPSDREEVIEDSEGEGVDMDVDLEEREKEDKKEETEEKKETEETEEPMEVEEPMEVEDVEEGGEMKEKEEEIEE
KIEEEEEEKIEEEEEEKIEEEEEEEIEEEEEESEEEKIVKEKNKHAKRNKEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEIEEEAITDEIEEKEEKTPQKKKQKARR
```

1251 - 1270:	EEEEEEEEEEEEEEEEEEEE
1252 - 1271:	EEEEEEEEEEEEEEEEEEEE
1253 - 1272:	EEEEEEEEEEEEEEEEEEEE
1254 - 1273:	EEEEEEEEEEEEEEEEEEEE
1255 - 1274:	EEEEEEEEEEEEEEEEEEEE
1256 - 1275:	EEEEEEEEEEEEEEEEEEEE
1257 - 1276:	EEEEEEEEEEEEEEEEEEEE
1258 - 1277:	EEEEEEEEEEEEEEEEEEEE
1259 - 1278:	EEEEEEEEEEEEEEEEEEEE
1260 - 1279:	EEEEEEEEEEEEEEEEEEEE
1261 - 1280:	EEEEEEEEEEEEEEEEEEEE
1262 - 1281:	EEEEEEEEEEEEEEEEEEEE
1263 - 1282:	EEEEEEEEEEEEEEEEEEEE
1264 - 1283:	EEEEEEEEEEEEEEEEEEEE
1265 - 1284:	EEEEEEEEEEEEEEEEEEEE
1266 - 1285:	EEEEEEEEEEEEEEEEEEEE
1267 - 1286:	EEEEEEEEEEEEEEEEEEEE
1268 - 1287:	EEEEEEEEEEEEEEEEEEEE

A0A2P6NBV9 **A0A2P6NBV9_9EUKA** (1372 aa)
Uncharacterized protein. *Planoprotostelium fungivorum*

```
MQQQPLTTGKNYRHLLKDCLDNVAETDRVSDSGILMIEGSAGIYIHGFGEIGLPLHPLVVAELKKTGRRESEHFYRWEAG
EMPHQVSIKNKEWILKVTNQLGEVTRRLGKEMRKGDQMIELKCLMLEEASVDPARWSVEAGVGAFAILNVILPTSHKGGN
TTIWNNPDREYQNTSEQSPYELQYLSYLKDCKITSEPITEGYRLQLSFAISTREGVAPPVMFREEDYIDDLTEIVRQWKA
EQEKTDCLCYTLYSDGIVASTRRNQTRCRIAETFKGRFGIHFKAVRITRTTSSHPHIWAIFALKVTGTLCISSSHTYRFL
LGQRNYQSSSEELVLRYGSSNDYFHFLFRRAECPSSGVEGDRDNLGVMQRVPDDIFDHILTYYVPPLEMKGMYLASRSYM
VRARSVIETAVDRLIKEYILSHMPPMSLADLHLEQWRELMTFFRGHVVAPHMINAVRDLMAGPDDVNWQEAFFEIMNDVY
CTSPPDKPNLAHDEMVQMWINKSRTVHMWLSYLLAEHLFKARRWEDLQERSEANWKLLYRIGEYIVNRFTLLDKEVTSQN
PVVQSIVIDVIAFGERLLEETARIRREEEERRERKREKEMNVRIQMTELQKVNKMEPERRKKRKKRKKKRKKRKSNGRRK
KKEAKERRGKKRREVEQSLNSLPQSIKRDQIESKNFKNQRLKLERNKSFLIGVFISGKGYRDLLKDCLDNVAESDQVSDS
EILSLDESTPGIHLFDFGDIGLPLHPLMVAELKKTGHRVTKHLYRWDAGEMSHQVSIENEGWISKVADQLGELTKRLGKE
LEPQDLAMEFKYMTLEEASGCEIEYPTETEENTFGVLKVTLPTLHKGGNITIFNGRCKETHDTSEESGYEYQYLSYFKEC
KMKSKPITEGYRLQLSFAISTREGVAPPVMFREEDYIDELTEIVRQWKAEQEEAKCLCYTLSFNRELSVRDQTRSKISTL
IRERFGICVHVGGRNIRAMIPGLGKIRFDDRYWINTVNQHNSCLIFSFCDDEELILRYGMTNDYFDSLFRRAEYPSFGVK
GDRDNLGVMQRVPDDIFDHILTYYVPPSEMWGIWFSSRSYMERALNVVHTTIDRLIKRACQMGNTSILFTWPLLVQSSDD
IFAYPSYRLHEEYILSHMPPLSLQDLRSTYWNDLIVLFGGHVVAPHMIDAVRKLLNEFDDSESQDALYKLMNDVNCNTHG
KQPNLAYNEMIRMWINMSRDDELWLGYSLTQHLFKARRWEDLREVWQIFVANYEHNPKELYNHAECIVDFVFGEAVLEEK
LRSILNLPKEQQDGTGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEEERSKGEERKEKKRSGAEP
EQPSTKHQKRSN
```

1297 - 1316:	EEEEEEEEEEEEEEEEEEEE
1298 - 1317:	EEEEEEEEEEEEEEEEEEEE
1299 - 1318:	EEEEEEEEEEEEEEEEEEEE
1300 - 1319:	EEEEEEEEEEEEEEEEEEEE
1301 - 1320:	EEEEEEEEEEEEEEEEEEEE
1302 - 1321:	EEEEEEEEEEEEEEEEEEEE
1303 - 1322:	EEEEEEEEEEEEEEEEEEEE
1304 - 1323:	EEEEEEEEEEEEEEEEEEEE
1305 - 1324:	EEEEEEEEEEEEEEEEEEEE
1306 - 1325:	EEEEEEEEEEEEEEEEEEEE
1307 - 1326:	EEEEEEEEEEEEEEEEEEEE
1308 - 1327:	EEEEEEEEEEEEEEEEEEEE
1309 - 1328:	EEEEEEEEEEEEEEEEEEEE
1310 - 1329:	EEEEEEEEEEEEEEEEEEEE
1311 - 1330:	EEEEEEEEEEEEEEEEEEEE
1312 - 1331:	EEEEEEEEEEEEEEEEEEEE
1313 - 1332:	EEEEEEEEEEEEEEEEEEEE
1314 - 1333:	EEEEEEEEEEEEEEEEEEEE
1315 - 1334:	EEEEEEEEEEEEEEEEEEEE
1316 - 1335:	EEEEEEEEEEEEEEEEEEEE
1317 - 1336:	EEEEEEEEEEEEEEEEEEEE
1318 - 1337:	EEEEEEEEEEEEEEEEEEEE
1319 - 1338:	EEEEEEEEEEEEEEEEEEEE
1320 - 1339:	EEEEEEEEEEEEEEEEEEEE

A0A2P6ND56 **A0A2P6ND56_9EUKA** (1504 aa)
Peptidylprolyl isomerase (EC 5.2.1.8). *Planoprotostelium fungivorum*

```
MSGYSRYEGSLFDAPSNAPGQRGNANSLGNLFSDSALDEKTMNTSLSYQAKKQPKAEPAPAPVKEESQIVLSLTGNLHAF
NAATQSYNEAERVGIAFVRVKPSNRTDLIVYREKDKKQDTIFTVTITAEFSFTVTNKIYTYLKDKNENQYTISFKKEEEC
ILMSVAVTAAKVAASGYQQVKFVDVVEGEKGRRVANGCNVSLKYTGYVTDGLRVGPSFYSNKDSGSDHQFKVGTGVVVRG
LSEGIIGMRPGSRRILVVPSELGYGKSSPMDAVPANSHLVYDIVCNKVRKEDAAPAPTPTPTPTPAATIPTTAFNLRQSS
EREEGRSRAGSREDLVARMARLGQPAMMPGTSPKDAPQTQQPQQQPSQSAPTQQHQAPVQQHQIPVQQPVQHQAVQQHQT
PVQQPTYNTYGSSTPTSPGHYAPSQTFSQNNPNYDPRIQGNFPGSSVPPQFASSGSHSHYPNYLGPQSFYNQPTGNFPSS
LTGAHRPGEFGESFQQQLDQRGFQLELKSNLNHMTTKVDEIHSRLENSSFFKDRERGKGEEFLHGVHLIQSIQRLVDDND
KLRTDLGQKVEHIDSLRDKIARLHEKNEKFIEENNRIMEQRNEAMKESGEITRRQLKELIDEKARLEKEMTEAHATITDN
DRKVAALNRQLLTANAESASLKDELEKKANEIAAGQQREHELHQRLRHQMQRTEEEIANKKGVESAYESLKEELMEAKDI
CTKMASKLDKERQKRSETEKAFETEKTAFESQIAELHENLRKQRAANGIVAQEEIARIEKEAEDRYKTILETRKVSENSP
KSPTHLVQAEAARNTRDDIEAKEKPQWEKKAYDNGHRAGREEVSIRDKPIWEQAAYQEGKRAGVTEAAEAARSAAEAARS
AEKPNAEAEAVEKQLLQRKVVELEGSLMEKEMSLKEKEEALKVKEEQLEEEKKRPTAVAVSSGGVSQEQVAEIREKMKEQ
GVERVKKEEIEEEEKYEGNQVLKMLVTTIKTTTLNMVYKEEEEEEEEEEEEEEEEEEEEEEEEEEKAAELPQITEEEEG
ESTPVPLPVPMQKKGEEEEEEEEEEEDDDEEEETVVEVTSTLVEEKVEIEEKSEAVDPLSTTSHEDTPVDPLSTTSHEVA
SVDPLSTTSHEVAPVDPLSETIQETITEDPLSTTSQDTTSVDPLSTTNQQEQVEEAPVTEVEEKSVDPLSTTSQEESSAP
APVDPLSTTSQEKSTPKKANPLFGDSDDEEPVLPAKSSPKVEPAKSSPKVEPIKVESPRVEAKSAVPTPTKQSNPLFGDD
EEDSEDPLAAHTPIKTSAPIQEEKQEEKEEEKQEEKEEEKQEEKEEEKEEKEEEKKEAEVEQEEKTTKEEPTTFSFNIPS
FEDAGEKKERAKSTLFGDEEENPGTPQLSSPFGSTSSATKNKDNSKPLDPRKSEVFSSDFNYFGEEQKKPAPAAVSSLFA
EPTGAFADFDSSSDFVIPASVAPITEKKKGANSATKAKAKKMLFDDSDKDPLGGAGGADDFFSF
```

1000 - 1019:	EEEEEEEEEEEEEEEEEEEE

1001 - 1020:	EEEEEEEEEEEEEEEEEEEE
1002 - 1021:	EEEEEEEEEEEEEEEEEEEE
1003 - 1022:	EEEEEEEEEEEEEEEEEEEE
1004 - 1023:	EEEEEEEEEEEEEEEEEEEE
1005 - 1024:	EEEEEEEEEEEEEEEEEEEE
1006 - 1025:	EEEEEEEEEEEEEEEEEEEE
1007 - 1026:	EEEEEEEEEEEEEEEEEEEE

A0A2P6NEC8 **A0A2P6NEC8_9EUKA** (1745 aa)
Uncharacterized protein. *Planoprotostelium fungivorum*

```
MFHQHASKTILKRGGDIFAAIPPTPLIVSVATIVGVPWLLSFFQESYKFYKSLGPGGIPYNTFGWTLHQLMRPFAIKRER
LQQLNYWFGDKNISSDLQDLPYRVGHRPKVAGFSPHKQLDQLAPWMADDVSAMLDEIVSQVKGLFISTARHINCKAIFVE
QEILKRSHPGRRMAHKSYGEVAHVHDDGTIHVTLSRADARHVLKMGWGERHPMARGWPFPRWSGFLAESYVLLYVPRNEM
ELDIVKDIVKAAAEYLVGVHEFDGEETAGESEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERDEKEEGVEEEERRERDRA
AMDLLLEMMKADQNGGETDEEEEEGEGEMMEETRNTRDEATMELKELFTLRSVKLQVDMGFPRDRTEGRQMKKVLLFLFF
LLVENQAVSTEDAVLTSIYNSLGGDSSEHTVCLKNAGDSWSQRRWTLPINNACTSSLPGVSCRNGLVDTLNLTNNNLVGS
LSRDVFLNLTQISTVDLSNNRYLTGEAPNLPPALSYIFDISLCNFTGSAAKYFTQKPIQHLFAFSNRFEGPLPSVVDWTD
CSYAGDYDFRFNQISGSIPTFIFTNCYVDRLKFQYNKFSGSIPNGLPFTASTIDFGSNQLSGPLPQYLLDRTGRQANNAS
SIRYFNVSSNQLTGSIPSMWYSTSTAGAVLDFSYNQLTGNISSFAYSEKLYLRNNNFTGPLPSISSTNLYEYDVSGNNFI
SLPPDLCTVLPQMNRLNLGNNPYVNTVIPACAGVTINPSQLAFLIMANGQLQGGIPQWIKNLVLSRKEYFDDSSVYWNRN
STGVLDLSGNFLAGRASDFASVHAAVLNISNNQFHGIVDTSFTVDTFSASNNLFTGVSVKPSNITCQLPGNPMICEPPVN
GTTSFMNQCNATCNITWYCSDVVQYENCTQMSTPQVLLDRLSQLSNASQPYIDWSHRLEEILDASLSQSVTWGGAVINAT
DYCNTSAYTIAQSSSGTFYNYCTSYIQSLAVTTQTSTITSSSTIAPTSSVSPTTSSTVSPTTSSSSSSTTSDTTSSSTSS
TTTSSTSLTTSSTTSSTTSSTTSEPTSSTTSESTSSTSSTTSSTTSEPTSSTTSSTTSSTTSSTTSSTTSELTSSTTSST
TLSSSSSSTTTDSTSSTTSSTTSSTTSESTSSSSSSTTTDSTSSTSSTSLSPTNTTSSTTSQSTSGTSAPTTTNSTLFTA
DILNRITTNISSNDSSAAWTQLYEFADGYNGTLYAEQVAISTTSIRNESVSLELHLGGNSTVKISRDVADEIMRRNGTKL
FLAQFEFHFLEPRNESLWEILTNVTGLSVLGENGREIQISNLEGRISLTLSVSNTTDVVCLWWNETDRNWDKEGCTSIPL
YNSVECQCNHLTNFTLGRASSLPLPADSNGDSSQISGNQISRKNTGVIVGVTLGVSALLLAAIVLIVIVYKRRERRTRAS
SVDMSVVVDQILAENLVDFVLVNKGERADVYKAKYNEMTDVVAKVYASEYVGRFEDESELMMKLHHPNIVQLLGISETPA
GKAIITEYAPCGTLNTFYKDEAQTITDPQDVYNIVVQLCSVMNYLKDQGVVHGNLTCDNVMMTSRERPFSVKLCGFGLSG
MNRSTIPNGISPDPRRTAPEVLKSNRMTHSSDVYSLTVLLWEIFSNGIKPFAEMSDVQVRNHVISGSVNVKQDFQTDVLV
PEGARNIVERCLKADYRLRPDIRSVSTQMVSLWRETQPRASAIGLARSWVERNEYVFSPEGSAEQ
```

272 - 291:	EEEEEEEEEEEEEEEEEEEE
273 - 292:	EEEEEEEEEEEEEEEEEEEE
274 - 293:	EEEEEEEEEEEEEEEEEEEE
275 - 294:	EEEEEEEEEEEEEEEEEEEE
276 - 295:	EEEEEEEEEEEEEEEEEEEE
277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE

A0A2P6NF88 **A0A2P6NF88_9EUKA** (236 aa)
Uncharacterized protein. *Planoprotostelium fungivorum*

```
MARKPSAKSLEKKTKERLEKYVEHSESDEELEEERKEVKKAIAKEEEEAAEEAKSEEDDEEDKEDEKPVKRGRGRPPKAK
TIKPTDKEEAVTQKRGRGRPRKAKKEEDDDAPATPKRGRGRPPKAKKEEEEEEEEEEEEEEEEEEEEEEEEEIATPKKRTS
KAKKEDDDEDASARPKRGRGRPPKKKSKTSEDEEEDDEEETPKKGRHSSKKDEEEEEFDGEEEEKPAKKGRGRSKK
```

128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE

A0A2P6NNF3 **A0A2P6NNF3_9EUKA** (307 aa)
Uncharacterized protein. *Planoprotostelium fungivorum*

```
MKYTIEPPKPNLAYLRPRLMQDPDFWMRWYPYNDEPFDWRRILLPSISIGIIGVIISILVNQRRPILSATAIEEEEELDF
QEHYLARIQRKEEEILVAKKDKIISQFEQSIENAQDRFEQVVAESKNKPLHTLTRSVDLISEDLEQLQLQVDGLRERRED
RKRLTHLIEQLQRKLDFFLVKVREASQQRAKMIEAQEAAARAQQRPPTMRVAPVAAIKEEKASRVVELIDDEEEEEEEEE
EEEEEEEEEEEEEKRHEETVEAIEEKTVEEIEEKTVGKIEETVEREEEEEEEPGEYVDEYEDDDEL
```

232 - 251:	EEEEEEEEEEEEEEEEEEEE

233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE

A0A2P6P962 **A0A2P6P962_ROSCH** (362 aa)
DUF2052 domain-containing protein. *Rosa chinensis (China rose)*

```
METKVVRSEAIESISDRLSASEDLYFPRALQSTTITPSQRKAILLDLLSRDAAVFLERYGSKLTSEELLEFDALTDDYEV
SWHVKHLRSLLSPTSDELKSRAVQVKNRRRAYLNKLIFGGQYFSEDSMRREPYLHHEYVGKFQDPSGRSMARPGERWSD
TLLRRSEEAILVAKIRGEQQRLGVAESDWVGGERIQEVEEQEEEEEEEEEEEEEEEEEEEEEEEEEESNKANGGTQSSEML
VDPPNVASGAETADHTDAANVAQATTAGQSEQATVSAEELQDLMDQFTYIMHEKFLLGEDHEYLDYSKIDNDETLDDHWQ
REANHDAEEKYFDDIIDEDETLDDHRQREVNHDAEQKYFDED
```

202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE

A0A2P6QC37 **A0A2P6QC37_ROSCH** (212 aa)
Putative transcription factor interactor and regulator CCHC(Zn) family. *Rosa chinensis (China rose)*

```
MSIKNRIPNTLSPTGETMSLAIPAQPPSLNLTDQDDKIRNHGTGSKDSKLAGKSLTQQFDYLSLALPLPLPHEQEEESAK
GEEEEEEEEEEEEEEEEEEEEGEDEEEVFDVCRVCLKDKEHWTFDCPYLDRIPNPKTTTVGSGYAIVCRGCHVLGGHGD
RAWVGRAIMKSCSICEVPASHWNYECPKNPDPRKYDYSKNRKVLKQEVYSVA
```

82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE

A0A2P6QSI3 **A0A2P6QSI3_ROSCH** (959 aa)
Putative P-loop containing nucleoside triphosphate hydrolase, leucine-rich repeat domain, L. *Rosa chinensis (China rose)*

```
MADLAVSVAILLVEKVISSLDQKITSNVHGDVEKAWKCLRRMQAYLRDSEEIDVGSQMFQNRVKEVQSLAYEIEDAIDKF
MVQIPHHFHSNMFSEAIHDIAYFFTERRAISEFSSKIKDIETRVGSFSALDSLLLEPTSSSTRTEENLTHQVLEEDEVVG
FEERKGTLLKQLTEANSKLLTILIVGPGGSGKTTIVKNVYDSKLVQGFFDCHSWIDVSRPPKLGKLLRNMLIDFRLKKNN
SAWSKYEAVRQIVPRAGMRLFPQQKLKRQKPVHDEEEEEEEEEEEEEEEEEEEEEAAENPKAELNNFLKAKRFLLVLDNV
WRVQDLESIVNALPKGLPGSKIIITTRKSDVAPVATYIHDLSCGLSWKYAWYLFCKKAFQSSDENCPRELEHWAKKILKK
CEGLPLAISAVGTLLWKKPQTPVEWKKLHESLGSEIRPDSSLSVISRILQPSYMDLPSHLKTCFLYFGMFPEDYLISREK
LTRLWLAEGFVMPGRGKTMEEVAESYLNELIARNLVNATRREIDGRVRSCRVLSLVREFIITKAENFITVLEPNCSTTTS
GEKIRRLSVQNVEINLLLRDRDLSHIRTLLVFGQACSPSDLEMVLKTSKFLRVFDLQGVPLKIFPKSIIGLRLLRYLCLR
QTKIRSVPKSIKNLAFLQTLDLRSTKVTKLPKTIYKFQNMRHLLAYSCDMKSGVARGVDVSAGNIGSLSSIQKLLLVKVQ
KNRKAIKALRELIGLRKLGLVDLGREHGRELCCSIQKMSELSTLEVRSTSEEEYLDLDHMNSPPGPPLYLQRLSLTGRLK
ILPQWIAQLHSLIRIALKGSKLNAGANIVEVLQDLPNLMELELVDSFTGVSLIFKAEKFKKLKALRIEKFDQLDLMVVEG
GAMPQLKKLTMSKCQNLKLLPFGIDHLIFLQELLLIDMHHEFLARLQKDSEDRYLVENIRVIHSFSGSYQSYTGFQNLS
```

275 - 294:	EEEEEEEEEEEEEEEEEEEE
276 - 295:	EEEEEEEEEEEEEEEEEEEE

A0A2P6TEM1 **A0A2P6TEM1_CHLSO** (2710 aa)
Putative polyamine oxidase 4. *Chlorella sorokiniana (Freshwater green alga)*

```
MQEQPAFSKGLTSSYLSGAALGLPAKLFSAVFPETRPVRLRNAAGQETSGKVSVRDDEHRTPGRIEVTSGWGVFAKANGM
RAGDEVRVQYKPKDLLLVTVADPAATASGTTARAATPAASQRGAQHSSSDGLAALAAAAAAGQAAEQPPSGLPQQKRFTK
DLTRSYLSGAALMLPTAIFADCFPKTTECVLRNADGEEWAGKVTRRIHGTCGNVRLDLTGGWGKFVKANELRLGDEVKLE
FLPPNVLLVTLLQRGVGPTATQCCRDKAQQDAERYHAAKGSGRRQQKQPKQPKQQQQKGQQQGQKRKRQQQGSKAATAAQ
HPQQCSPAAGRLIGAALAEEVAQQAAAEQAAAEALQPLVAAEGGPMLVDGEEPYIRHSQQPTQPLTQQQQQQQRGAGQRQ
QQQQGAGQRQQEDEAEDEQQWYDCENDQDGGTPYSGQYALHSSGEEEEEEEAAEGAAAAAAAAAAGQVERADSEGEAAAAA
ASATESEGEESPVRRPTKRPRQQQGGGRGRLGALAAAAGGLELGSRSGSEEAAEGGEHPAWSVGQLVVARDKQGRHMAGR
VMAILPGLDGSVALGDSVLLDQLGAAHGFPVAVPANKVLAEVPHGLVGWQVEKQFKRGWFPGEVDDVWWDAEQGEQVYHV
TYSDGDGEDMNLQELLPLLMGRGPAGAAGAAARAAAKRRGRPPKQQRQQRQQRRAEQEAAAAAAEEEEEEEEEEEEEEE
EEEEEPGRRPGRQPKQQAQGEQRAQQATLTGGRQRRPASAAAAVLGDASSVGVWVPPEPSADALEASREQGGLYEASGAG
HERGVYAWDSKAGTMRPVGPWLAHKDSKVGTVLGRVSKSDKRYLPDQEAPEGYRSPYVPGWIGVRTTGDNWTPDYTGQYC
VALYDSHAATSYLVACSGARFDSVEEAAELYDRIALCYHGQTADTNYPTTQALWQELGQQDEFPGSKNCISLAARLAGME
QSVPYAAVNDDVEQKEWDDWEEDLVATYLCKRPTLGTAAGLAGKLKWLLQTLHEGALFPGYRGAPLQRLLAACDACAAPG
TVKDHYAASSSACYVCASNRKGADQRNCYHHGSTNLAALIKETETAVMSQDALKSFESNPSKAAADAAATEEQQELDEQL
AAWAGGCPASPAAGSAGGRPAGRRPRGGAAAPPAVATAGVRALRAAAKYRHIPVEPGLKVIVIGGGVAGLKAAGDLQRGG
AEVTLLEARDRLGGRIHTHTLRADGVECNVDLGATFVCGTDRTPPINPIFEYAVDVLGLRLQPKHRDGPGATALYDRDGG
RIPDDALVGAEEKYHELIDQLHERTEPGSKAPRGETIQQAVDDILSGMELSEQERDIIRAFTVDLYVAEMHQLSLRGMTS
QGFAGKHELVVGGFKQVVQALREGRVAPDVPAEPLRDVRTGTVVSAVRLLPGGVGVEVGVEGEEEPLWAHAVVCTLPLGV
LQRGGVAFDPPLPEYKQTAISGLGMGTENRVAMLFSEVFWPAEQHFLRPVTGHYTFANMHALGVPNVLSAWVRPEAVDEL
EAMSDEEILADVLASLKQVCPEGFHAPLDHTITRWKQDPFSYGAYSYVPPGGKKSYYDCLGHPVSGVPELDGKQEAASGR
VVELQTRLWFAGEATSKEDAYTVHGAYKTGEVQAVRIKKWWKAHHEQIERLRSKQQQQQQQQQQQQQHTMAGELSPFAGL
SAFASASPPASDEPSPGSAQGSSSLSRVGSRTVGFHEPPPAALEPSPKPAACPLAARQHSMGSLGQLLRAAQAEQARPRL
TISTARSLKAQAATRGRRVLRIAEHEEGPAGGSTSDLMGTTAPSHAAPAALSMHRSSSIDIGASRLSKAKTAPEALPDSL
VLAAINAGYLEGRGPGASPADDSPAAASLAMSATGTLPSRQGPLVAAANEGGGGGGGATLPIRQGQLHLPPDMRPQQTQP
PQQQQTRQQQHSPGAYHRTGSSSSTGAGSDSSSTAAGRPPMPVTPAALASSRSGSLAQRGGSGRSLLAPQQQQQPGRQQQ
QQQGGPRSPLGVSRQGSFRELFDAQTEAAMAQATMAGLHEALRRRSCPRTPTTQPDNTRRSAPDSGIHDQHAGGLPPPPR
ACGPLVTPCGGAEALDADCRPRKLEPDGSPFAVVPAADAASVSSSGSTAKMAAAADFVSPFASSFAQHASSGSPVQPESP
```

```
LPQPSQTSRSGSPVRVVGFQSSPNSVVAPRRWQSAALPGSTEAREAAAAMDAAIAAAAGGSSSGTSGASFPPQGRPSLAS
LERKGSLGTLLRQQDQLNSVQRRLTAINTARPLNLRRSPPRGPLPAPQPSPCQQAPLHAAPAQAAIVQDLESDWMAALTP
GSSELEAAARAAQAQAAAAAAPAAAVPAGPFAAAAAVGFEGAAGTLPAGGGMGGALQRQVPLPPGRPVPSRQHSSRLARA
GSASINIPYQNMRRAETAPALTDDLIAAAMAASGASSASGLAKAAAAAAAAGSGSSAGSSYRGSPPKAPLATLPERQASA
TREVFEAQAEAVAALTQAKVLQQALSQEQERVERLEQQLRSLMRERAEERARHQAEQQRWMVMQEQQAMFLQQMQQLQQQ
QQQMQQMQFRPHMQAPAPQPRLAQAPPRFHPAPPLPLPPAAVGAGWQAGAARPHQPMETWLEETYSQMAVQQMSIGIEAP
APMPTVLEQAADEEPSPRQLQPPAPVRAPPPPVHRPAAPPPPAAAAATALERQQPTTLDELALALAAVQP
```

705 - 724:	EEEEEEEEEEEEEEEEEEEE
706 - 725:	EEEEEEEEEEEEEEEEEEEE

A0A2P6TPJ7 **A0A2P6TPJ7_CHLSO** (1549 aa)
Methyltransf_25 domain-containing protein. *Chlorella sorokiniana (Freshwater green alga)*

```
MARAAGLQQQGAEGWESGGEDGSEAGAAAQPGGQAAAAAAEGEEEQQIDLVDLISSDDEEQDSEGSADEAAAAAAAAAAA
EAAVAAAGGQRNAAGEESDGAAAANAGGEQSLGGSDSLPPTEVYGGGAGGCSGDEAEGPAERTGGGSGGGDGGSGGSWED
GPALAARRRRGSRGPTRSEPEEGQEVEGAEGAAAPAAQRGTSAKRKVRRSKAAAAAEAAAGRAEAVGRQRGVWEMECSDE
DGSDQARAIGLLMRANGYRGFKLWRSVRMAAQDGDVAEGPAAAAEQQLFRAGEWVLFRYTRPFDPERTLAPARILTFAEL
ADGLVLPCLQWGELWEDIVGRPNEHIPGDEALRGQNRLWLRSLDLTNPDHLRFMLYEGTKAEDILCHCTVRHEREILEQY
GGLYASIAEYEAAEGPHAYWYNCLRVPELLRFADAPVPGAPPPKPKRLEGGAPRAADLFAGIGNVSVGLSWAGFEPALAV
EQNGPAFTALSNNVPSAIAKLEPQSLAEALAAAKAGEKGYPNPGELDHLHFSPPCQSLSAMNGSTTAAEARATLTDLCNQ
ILEWIEYYSPASISLEEVVQFMYAKVRRDPPPRMGRKPKAAAAAAAVAAAAASNGDADLEADEDFYDNGASAADEEEEAA
GAASGGGKGGKRKRGPVVPKEELRPWLYLMPGLIRLGYQVDWRLLPAGAYGAANPRFRCWMLAIKCGFELPQPPQPKYYV
EIKQAGVLCSDDRLIDSLGEGGNGRGANLQRLVVQPSHDLPWSPNMREAIGGLPPLPLGHKTNKYGWEEMEMPRDEPGRP
ISRYQQYARSAKVPENGGYRWSDSRLYGHHRRKSDSTQGRHMMWDRPAGTVCRGDDVNRGAILHPEQRRPLTVLEKKLAQ
AIPHQLMLSGSIEEQYRQVGNAVPPPMAYAIGAVIYSSLTGRQPAYQLPLLVGYEGEGRPETAREWELRQDIPDHRGERR
RAADELPAGLGVAQQAQQAQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGSAGQLGGSGSLRASE
GDEEEEGEEGEDEPPPLQRRRSPRQPPKSAAGQQQRQQQQPKQKAPQMQQQEPSPGRQLRLQDVVRRAAPAEPPADVILP
AWPAAGEDPQQAEEQEEEAQEQAQQAQQAQQQAQQQQPPVPSQGSEGSGVAEAAAAATQTAREQAAVAVAALEAAKQAAA
AAAAAYRKRGAGQPLLGESPTKRQAGAAERQVEPIGQQQQQQQPQQQLQQQQQQQQQQQQQQQQAAGLPAVQVKEEQPEG
QTHSARAQQAQQAQQEQQAVEPGTPRRRANMPGDAEQRKEASKATFDAKAKEFDTNPVILACVGAAREALEQGGLLQPGA
AVLDFGCGTGLLAMAVADSVGSVLGVDSSQGMVQFVRQKAEARGPGCNVRAACCEVTSPSSLHEVNDPADPFPEQFDLIV
SSLTFHHVEHIPDLLRLLVGHLKPGGRLAVFDYQKSAVSDQFHPPEMLHTVFHPAGFAQQELCGYFEGAGLVDVSCREVG
AFDKPSGMKPGERMPYELLMVLGTKPAAQ
```

981 - 1000:	EEEEEEEEEEEEEEEEEEEE
982 - 1001:	EEEEEEEEEEEEEEEEEEEE
983 - 1002:	EEEEEEEEEEEEEEEEEEEE
984 - 1003:	EEEEEEEEEEEEEEEEEEEE
985 - 1004:	EEEEEEEEEEEEEEEEEEEE
986 - 1005:	EEEEEEEEEEEEEEEEEEEE
987 - 1006:	EEEEEEEEEEEEEEEEEEEE
988 - 1007:	EEEEEEEEEEEEEEEEEEEE
989 - 1008:	EEEEEEEEEEEEEEEEEEEE
990 - 1009:	EEEEEEEEEEEEEEEEEEEE
991 - 1010:	EEEEEEEEEEEEEEEEEEEE
992 - 1011:	EEEEEEEEEEEEEEEEEEEE
993 - 1012:	EEEEEEEEEEEEEEEEEEEE
994 - 1013:	EEEEEEEEEEEEEEEEEEEE
995 - 1014:	EEEEEEEEEEEEEEEEEEEE
996 - 1015:	EEEEEEEEEEEEEEEEEEEE
997 - 1016:	EEEEEEEEEEEEEEEEEEEE
998 - 1017:	EEEEEEEEEEEEEEEEEEEE
999 - 1018:	EEEEEEEEEEEEEEEEEEEE
1000 - 1019:	EEEEEEEEEEEEEEEEEEEE
1001 - 1020:	EEEEEEEEEEEEEEEEEEEE
1002 - 1021:	EEEEEEEEEEEEEEEEEEEE
1003 - 1022:	EEEEEEEEEEEEEEEEEEEE
1004 - 1023:	EEEEEEEEEEEEEEEEEEEE
1005 - 1024:	EEEEEEEEEEEEEEEEEEEE

A0A2P6TR47 **A0A2P6TR47_CHLSO** (1417 aa)
Protein translocase subunit SecA. *Chlorella sorokiniana (Freshwater green alga)*

```
MATAGLCCTAARATEALAAPVAARQHAALRPVPFTAVHQRGAAGRRQGSGGAAAPSASRRRGAARVHALLGGLGSMFKND
PSERTRKQYQSRVDAINALEPDMQKLSDAQLRELTQALKQRAAAGEPLDSLLVESFALVREASKRVLGLRPFDVQLIGGM
ILHEGQIAEMRTGEGKTLVAVLPSFLNALSGQGVHVVTVNDYLARRDSEWVGQVHKFLGLEVGLVQQGLNEKQRRAAYNA
DVTYVTNSELGFDYLRDNLAQDKEELVLRPFNFCVIDEVDSILIDEARTPLIISGTADKPSDKYYKAAKLAGALAKATHY
TVDEKQRNVLLTEEGYEAAEDVLQVSDLYDPREQWASYILNAIKAKELFIRDVSYIVRANEAKELFIRDVSYIVRANEII
```

```
IVDEFTGRTMPGRRWSDGLHQAIEAKEGLEIQNESVTLASISYQNFFRAYPKLAGMTGTAATESAEFSQIYNLPVTVVPP
NRTVSRTDNPDVVFRNESGKWKAVVQEIRRMHKTGRPVLVGTTSVEKSEILAGMLEQEGIPYQLLNAKPENVERESEIVA
QSGRRGAVTIATNMAGRGTDILLGGNPEFMARLKLRELLMPEVVSQVDMEGGDKKSVRVRKIKSWAVSPALFPCDLSAEA
KALCQDAVKAAVSGWGERQLEELEAEERLAFACEKAPTSDPVIEKIRAAFLKVEAEYKQVTDVEKVEVQKLGGLHVVGTE
RHESRRIDNQLRGRSGRQGDQGSTRYFLSLEDNLFRIFGGDRIKGLMSAFRIEDLPIESQMLTNALDEAQRKVESYFYDI
RKQLFDYDQVLNTQRDKVYAERRRALEASDLTPLMVEYAERTIDDILEANIPPTTPPEEWPLEPLVAKLRQYCYLLEDLT
PQALAAEAGGDYERMRDYLRKRGVEAYYRKREEMEGAEAGLSSKAERFFVLVQTDNLWKEHLQAIKFLQQAVSLRGYAQR
DPLVEYKLEGYNLFVEMMAQIRRNVIYNVYMFKPAEAEAKQRAFEEEQRQKAAAAQNGGSRGKGKKAAPAAAPCQGCAVH
GTNAPLACPIVVLTVTQPIWTAHKTQMSQERDAPKAASARVVRHPAAEPSPAWAAIPNEDNLPNDVHALAAALALRLGVG
VLDCGWFRSVSNPGRFLCLHLVALNRSTGAYTLAQLESREGLLTALHNALGRPVWNVLPAAEGVEEEEEEEEEEEEEEEE
EEEEEEEAGEPGAPLLRKARHFTAQWAVVVLLLAVLALRAAPTVPITSLATALVQPLSAAMPAMFQRNGAGGADVTADWP
PALRWLDAQPSQDDVIALLSRNDTKERLSMGNTVLHAARAGKEELARNCSSREIAIRKELAAELTAIAAGVEAGQPLLPD
LLAAPVRRGNSTLEALSASCAAAKAGKDEEIKRITRLVHKLARQLELLGPGATAAAE
```

1185 - 1204:	EEEEEEEEEEEEEEEEEEEE
1186 - 1205:	EEEEEEEEEEEEEEEEEEEE
1187 - 1206:	EEEEEEEEEEEEEEEEEEEE
1188 - 1207:	EEEEEEEEEEEEEEEEEEEE

A0A2P6TR48 **A0A2P6TR48_CHLSO** (1408 aa)
Protein translocase subunit SecA. *Chlorella sorokiniana (Freshwater green alga)*

```
MATAGLCCTAARATEALAAPVAARQHAALRPVPFTAVHQRGAAGRRQGSGGAAAPSASRRRGAARVHALLGGLGSMFKND
PSERTRKQYQSRVDAINALEPDMQKLSDAQLRELTQALKQRAAAGEPLDSLLVESFALVREASKRVLGLRPFDVQLIGGM
ILHEGQIAEMRTGEGKTLVAVLPSFLNALSGQGVHVVTVNDYLARRDSEWVGQVHKFLGLELHKFLGLEVGLVQQGLNEK
QRRAAYNADVTYVTNSELGFDYLRDNLAQDKEELVLRPFNFCVIDEVDSILIDEARTPLIISGTADKPSDKYYKAAKLAG
ALAKATHYTVDEKQRNVLLTEEGYEAAEDVLQVSDLYDPREQWASYILNAIKAKELFIRDVSYIVRANEIIIVDEFTGRT
MPGRRWSDGLHQAIEAKEGLEIQNESVTLASISYQNFFRAYPKLAGMTGTAATESAEFSQIYNLPVTVVPPNRTVSRTDN
PDVVFRNESGKWKAVVQEIRRMHKTGRPVLVGTTSVEKSEILAGMLEQEGIPYQLLNAKPENVERESEIVAQSGRRGAVT
IATNMAGRGTDILLGGNPEFMARLKLRELLMPEVVSQVDMEGGDKKSVRVRKIKSWAVSPALFPCDLSAEAKALCQDAVK
AAVSGWGERQLEELEAEERLAFACEKAPTSDPVIEKIRAAFLKVEAEYKQVTDVEKVEVQKLGGLHVVGTERHESRRIDN
QLRGRSGRQGDQGSTRYFLSLEDNLFRIFGGDRIKGLMSAFRIEDLPIESQMLTNALDEAQRKVESYFYDIRKQLFDYDQ
VLNTQRDKVYAERRRALEASDLTPLMVEYAERTIDDILEANIPPTTPPEEWPLEPLVAKLRQYCYLLEDLTPQALAAEAG
GDYERMRDYLRKRGVEAYYRKREEMEGAEAGLSSKAERFFVLVQTDNLWKEHLQAIKFLQQAVSLRGYAQRDPLVEYKLE
GYNLFVEMMAQIRRNVIYNVYMFKPAEAEAKQRAFEEEQRQKAAAAQNGGSRGKGKKAAPAAAPCQGCAVHGTNAPLACP
IVVLTVTQPIWTAHKTQMSQERDAPKAASARVVRHPAAEPSPAWAAIPNEDNLPNDVHALAAALALRLGVGVLDCGWFRS
VSNPGRFLCLHLVALNRSTGAYTLAQLESREGLLTALHNALGRPVWNVLPAAEGVEEEEEEEEEEEEEEEEEEEEEEAG
EPGAPLLRKARHFTAQWAVVVLLLAVLALRAAPTVPITSLATALVQPLSAAMPAMFQRNGAGGADVTADWPPALRWLDAQ
PSQDDVIALLSRNDTKERLSMGNTVLHAARAGKEELARNCSSREIAIRKELAAELTAIAAGVEAGQPLLPDLLAAPVRRG
NSTLEALSASCAAAKAGKDEEIKRITRLVHKLARQLELLGPGATAAAE
```

1176 - 1195:	EEEEEEEEEEEEEEEEEEEE
1177 - 1196:	EEEEEEEEEEEEEEEEEEEE
1178 - 1197:	EEEEEEEEEEEEEEEEEEEE
1179 - 1198:	EEEEEEEEEEEEEEEEEEEE

A0A2P6TR53 **A0A2P6TR53_CHLSO** (1400 aa)
Protein translocase subunit SecA. *Chlorella sorokiniana (Freshwater green alga)*

```
MATAGLCCTAARATEALAAPVAARQHAALRPVPFTAVHQRGAAGRRQGSGGAAAPSASRRRGAARVHALLGGLGSMFKND
PSERTRKQYQSRVDAINALEPDMQKLSDAQLRELTQALKQRAAAGEPLDSLLVESFALVREASKRVLGLRPFDVQLIGGM
ILHEGQIAEMRTGEGKTLVAVLPSFLNALSGQGVHVVTVNDYLARRDSEWVGQVHKFLGLEVGLVQQGLNEKQRRAAYNA
DVTYVTNSELGFDYLRDNLAQDKEELVLRPFNFCVIDEVDSILIDEARTPLIISGTADKPSDKYYKAAKLAGALAKATHY
TVDEKQRNVLLTEEGYEAAEDVLQVSDLYDPREQWASYILNAIKAKELFIRDVSYIVRANEIIIVDEFTGRTMPGRRWSD
GLHQAIEAKEGLEIQNESVTLASISYQNFFRAYPKLAGMTGTAATESAEFSQIYNLPVTVVPPNRTVSRTDNPDVVFRNE
SGKWKAVVQEIRRMHKTGRPVLVGTTSVEKSEILAGMLEQEGIPYQLLNAKPENVERESEIVAQSGRRGAVTIATNMAGR
GTDILLGGNPEFMARLKLRELLMPEVVSQVDMEGGDKKSVRVRKIKSWAVSPALFPCDLSAEAKALCQDAVKAAVSGWGE
RQLEELEAEERLAFACEKAPTSDPVIEKIRAAFLKVEAEYKQVTDVEKVEVQKLGGLHVVGTERHESRRIDNQLRGRSGR
QGDQGSTRYFLSLEDNLFRIFGGDRIKGLMSAFRIEDLPIESQMLTNALDEAQRKVESYFYDIRKQLFDYDQVLNTQRDK
VYAERRRALEASDLTPLMVEYAERTIDDILEANIPPTTPPEEWPLEPLVAKLRQYCYLLEDLTPQALAAEAGGDYERMRD
YLRKRGVEAYYRKREEMEGAEAGLSSKAERFFVLVQTDNLWKEHLQAIKFLQQAVSLRGYAQRDPLVEYKLEGYNLFVEM
MAQIRRNVIYNVYMFKPAEAEAKQRAFEEEQRQKAAAAQNGGSRGKGKKAAPAAAPCQGCAVHGTNAPLACPIVVLTVTQ
PIWTAHKTQMSQERDAPKAASARVVRHPAAEPSPAWAAIPNEDNLPNDVHALAAALALRLGVGVLDCGWFRSVSNPGRFL
CLHLVALNRSTGAYTLAQLESREGLLTALHNALGRPVWNVLPAAEGVEEEEEEEEEEEEEEEEEEEEEEEEAGEPGAPLLR
KARHFTAQWAVVVLLLAVLALRAAPTVPITSLATALVQPLSAAMPAMFQRNGAGGADVTADWPPALRWLDAQPSQDDVIA
LLSRNDTKERLSMGNTVLHAARAGKEELARNCSSREIAIRKELAAELTAIAAGVEAGQPLLPDLLAAPVRRGNSTLEALS
ASCAAAKAGKDEEIKRITRLVHKLARQLELLGPGATAAAE
```

1168 - 1187:	EEEEEEEEEEEEEEEEEEEE
1169 - 1188:	EEEEEEEEEEEEEEEEEEEE
1170 - 1189:	EEEEEEEEEEEEEEEEEEEE
1171 - 1190:	EEEEEEEEEEEEEEEEEEEE

A0A2P6TR56 **A0A2P6TR56_CHLSO** (1405 aa)
Protein translocase subunit SecA. *Chlorella sorokiniana (Freshwater green alga)*

```
MATAGLCCTAARATEALAAPVAARQHAALRPVPFTAVHQRGAAGRRQGSGGAAAPSASRRRGAARVHALLGGLGSMFKND
PSERTRKQYQSRVDAINALEPDMQKLSDAQLRELTQALKQRAAAGEPLDSLLVESFALVREASKRVLGLRPFDVQLIGGM
ILHEGQIAEMRTGEGKTLVAVLPSFLNALSGQGVHVVTVNDYLARRDSEWVGQVHKFLGLEVGLVQQGLNEKQRRAAYNA
DVTYVTNSELGFDYLRDNLAQDKEELDKEELVLRPFNFCVIDEVDSILIDEARTPLIISGTADKPSDKYYKAAKLAGALA
```

```
KATHYTVDEKQRNVLLTEEGYEAAEDVLQVSDLYDPREQWASYILNAIKAKELFIRDVSYIVRANEIIIVDEFTGRTMPG
RRWSDGLHQAIEAKEGLEIQNESVTLASISYQNFFRAYPKLAGMTGTAATESAEFSQIYNLPVTVVPPNRTVSRTDNPDV
VFRNESGKWKAVVQEIRRMHKTGRPVLVGTTSVEKSEILAGMLEQEGIPYQLLNAKPENVERESEIVAQSGRRGAVTIAT
NMAGRGTDILLGGNPEFMARLKLRELLMPEVVSQVDMEGGDKKSVRVRKIKSWAVSPALFPCDLSAEAKALCQDAVKAAV
SGWGERQLEELEAEERLAFACEKAPTSDPVIEKIRAAFLKVEAEYKQVTDVEKVEVQKLGGLHVVGTERHESRRIDNQLR
GRSGRQGDQGSTRYFLSLEDNLFRIFGGDRIKGLMSAFRIEDLPIESQMLTNALDEAQRKVESYFYDIRKQLFDYDQVLN
TQRDKVYAERRRALEASDLTPLMVEYAERTIDDILEANIPPTTPPEEWPLEPLVAKLRQYCYLLEDLTPQALAAEAGGDY
ERMRDYLRKRGVEAYYRKREEMEGAEAGLSSKAERFFVLVQTDNLWKEHLQAIKFLQQAVSLRGYAQRDPLVEYKLEGYN
LFVEMMAQIRRNVIYNVYMFKPAEAEAKQRAFEEEQRQKAAAAQNGGSRGKGKKAAPAAAPCQGCAVHGTNAPLACPIVV
LTVTQPIWTAHKTQMSQERDAPKAASARVVRHPAAEPSPAWAAIPNEDNLPNDVHALAAALALRLGVGVLDCGWFRSVSN
PGRFLCLHLVALNRSTGAYTLAQLESREGLLTALHNALGRPVWNVLPAAEGVEEEEEEEEEEEEEEEEEEEEEEEAGEPG
APLLRKARHFTAQWAVVVLLLAVLALRAAPTVPITSLATALVQPLSAAMPAMFQRNGAGGADVTADWPPALRWLDAQPSQ
DDVIALLSRNDTKERLSMGNTVLHAARAGKEELARNCSSREIAIRKELAAELTAIAAGVEAGQPLLPDLLAAPVRRGNST
LEALSASCAAAKAGKDEEIKRITRLVHKLARQLELLGPGATAAAE
```

1173 - 1192:	EEEEEEEEEEEEEEEEEEEE
1174 - 1193:	EEEEEEEEEEEEEEEEEEEE
1175 - 1194:	EEEEEEEEEEEEEEEEEEEE
1176 - 1195:	EEEEEEEEEEEEEEEEEEEE

A0A2P6U0V9 **A0A2P6U0V9_CHLSO** (1372 aa)
RNA-splicing ligase RtcB homolog (EC 6.5.1.8) (3'-phosphate/5'-hydroxy nucleic acid ligase). *Chlorella sorokiniana (Freshwater green alga)*

```
MKARAAVGLLLLCLGTAWAAHFNVAQGGLDGWTHSEDAKYSGKFKTTGEGLTVPEKAKHYGIARLLDTPVDPAQDLVLQY
ELKLGNGLSCGGAYLKFVTADDTFTPGGLKDDTPYTVMFGPDKCGATNKVHLILRHKSPKTGKIEEKHLKSPPFVETDTK
THVYTAILRASNNSYAVLVDGEEKKAGSLFEDFEPSINPPETIPDPEDKKPDDWVDEARIADPDAKKPEDWDEDAPREIP
DEDAKKPEGWLDEEPAEVDDPDATKPEDWDEEEDGDWEPPKIVNPKCKDAPGCGEWKRPNKPNPAYKGKWSAPMIDNPAY
KGVWKPRDIPNPDYHKDDAPLTNIGKVGAAAIEIWTMDDGYSFDNVVVSNSAQEAAEVREKTWVAKRAAEDAKEAEEKKA
AEEKRKAEEKAAAEKKAAAGEDKLAALVATIFDAPLLAPYASQLAPVRAYFEANPIYLLAALVGLLCLPVSALILRSSGK
AAQPTVSEAKKRDITGQDDKPAKKAGGRKAAAAEKEEIEEEEEEEEEEEEEEEEEEEEKQPRTAVGSPFLPSAIKQWGDA
RSAMAGLEGSLLTAGNPLLDLSAVVEDSLLQKYGLKLGDQILAEEKHLPLYKELEEKFQVEYIAGGATQNSARVAQWMLQ
VPGATTYFGCVGADHYAEELKKVASKDGVNVHYMVDASTPTGTCAACIVGGERSLVANLAAANNYKVEHLMQPENFACLE
KARVIYSAGFFITVSPESMLTMAKHACENDKTYCLNLSAPFICEVPPFKKTLMDLMPYVDYLFGNENEARAFAKSEGWET
EDVEEIALRIARFGKASGVRPRTVVITQGADPTVVALGGRILKFPVTRVPADKLVDTNGAGDAFVGGFLSQLVCGKDVAE
CVRAGSYAAGVAPDVWQIAPGYVPGMNVPVRLYASPQLLRLLLGEVEKAQPGGFLPALQQLANVATLPGIVGASTGMPDL
HSGYAFPIGHVAAFDMEHGIVSPGGVGFDISCGVRLLRTDLRDKDLTAAKREQLADALARIIPVGVGEGGANTISKADLD
SVLRHGMRWTEERGLSWPEDREVVEEGGCYPGADPGEVSDKAKKRGLKELGSLGSGNHYCEVQVVDEIYDKEAAAAMGID
SVDQVCVMVHTGSRGLGHQVCQDTLEACQRRMAAARERPIDPQLSYVPIRSPEGQAYLKAMAAAANFALCNRTVVMDCVR
RAFEAVFGRSARQLGMRTVYDVSHNLAKVERHHGKEVLVHRKGATRAFPPHHPALPARYAAVGQPVLIGGSMGTYSYVLA
GTQRAMEEAFGSTSHGAGRALSRSQALKQIDSEEVLRSLQARGIAVRVASPHLAAEEAPQSYKDVEAVVETCQTAGLSRK
VARLRPVAVVKG
```

519 - 538:	EEEEEEEEEEEEEEEEEEEE

A0A2P6V336 **A0A2P6V336_9CHLO** (427 aa)
Golgi SNAP receptor complex member 1-2. *Micractinium conductrix*

```
MSLPSTLDTSLQPPVGHRVATAYAQPMTPPKRPMATESAQKAWDELRREARKLESELDIKVAAYGKLCSGFEYGYGRGSE
SGLATDQLLHTKAGDIEKLLARLSDINDSMRSALSGGADSRSHMLARHRDIMHDFQQEFRRLQSAVGAARDRLDLLGGAG
GSGQHAPLLQQGSNAGLLLRERGMLASTNAALDEVMGTAQSVSSGLGQQRSVFEGIGGKMAGLGAKFPVVNTLLNAVRRR
KNRASGDLRLGVESENPEGRRSTRWRHWTCLGGRVLTNIGGAGNLEGYDDLPAKEQDMVTKAFEDKQAGVKGGPGGGKKS
GGGAKGGGAAKKPAKKKAKQEESEEEEEEEEEALEESELEGEEEGEEEAALPAKGAAGPEEEAQEEEGEGEEEEEEEEEE
EEEEEEEEEEEEEEEEEAAAVPKRKGRN
```

391 - 410:	EEEEEEEEEEEEEEEEEEEE
392 - 411:	EEEEEEEEEEEEEEEEEEEE
393 - 412:	EEEEEEEEEEEEEEEEEEEE
394 - 413:	EEEEEEEEEEEEEEEEEEEE
395 - 414:	EEEEEEEEEEEEEEEEEEEE
396 - 415:	EEEEEEEEEEEEEEEEEEEE
397 - 416:	EEEEEEEEEEEEEEEEEEEE

A0A2P6V349 **A0A2P6V349_9CHLO** (606 aa)
Charged multivesicular body 1. *Micractinium conductrix*

```
MDQIFNLKFTSKQLVRAAKKCEKEEKDEKLKIKKAIEKGNMDGAKIYAQNAIRKKNEALNYLRLGSRLDAVVSRLDQQAK
MQIINKSMAGIVKNLDSALKANNLEKFERQFENLDVQSEFVEQAMQNQAVLSTPEEDVTTLVQQVADEHGLETGLSLPQA
SGAKMPAAKAPAQSDDLTARLAELRGKPMTPPKRPMATESAQKAWDELRREARKLESELDIKVAAYGKLCSGFEYGYGRG
SESGLATDQAGGAARRSSSEARRGCWLLHTKAGDIEKLLARLSDINDSMRSALSGGADSRSHMLARHRDIMHDFQQEFRR
LQSAVGAARDRLDLLGGAGGSGQHAPLLQQGSNAGLLLRERGMLASTNAALDEVMGTAQSVSSGLGQQRSVFEGIGGKMA
GLGAKFPVVNTLLNAVRRRKNRASGDLRLGVESENPEGRRSTRWRHWTCLGGRVLTNIGGAGNLEGYDDLPAKEQDMVTK
AFEDKQAGVKGGPGGGKKSGGGAKGGGAAKKPAKKKAKQEESEEEEEEEEEALEESELEGEEEGEEEAALPAKGAAGPEE
EAQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAAAVPKRKGRN
```

564 - 583:	EEEEEEEEEEEEEEEEEEEE

565 - 584:	EEEEEEEEEEEEEEEEEEEE
566 - 585:	EEEEEEEEEEEEEEEEEEEE
567 - 586:	EEEEEEEEEEEEEEEEEEEE
568 - 587:	EEEEEEEEEEEEEEEEEEEE
569 - 588:	EEEEEEEEEEEEEEEEEEEE
570 - 589:	EEEEEEEEEEEEEEEEEEEE
571 - 590:	EEEEEEEEEEEEEEEEEEEE
572 - 591:	EEEEEEEEEEEEEEEEEEEE
573 - 592:	EEEEEEEEEEEEEEEEEEEE
574 - 593:	EEEEEEEEEEEEEEEEEEEE
575 - 594:	EEEEEEEEEEEEEEEEEEEE
576 - 595:	EEEEEEEEEEEEEEEEEEEE

A0A2P6VKP5 **A0A2P6VKP5_9CHLO** (846 aa)
Nucleosome assembly. *Micractinium conductrix*

```
MLRRPPSATQRLPAMPPKPNAEEGDEAFEVSPEVLRQLMSSGNQQLVEALQVRLRSPTASCRTPPLRGYVEALPAPVRTR
ISFLKELDGERAELHERYREERRALEEKYEKLYAPLYDKRRDVVNGAAEAPENETEEGKQAAAAAEEEVPKGVPDFWMIA
LRNAMEEETINDKDAEVLSYCTDVRCERFQNEEEEEEGFKLIFAFRENPFFTNKELVKTYHLSEEDDMMLRKVETSGVSW
KAGKDVTVKLLKKKPKPGSKGGKPQTKTEPVESFFRWFTEVPEIPEDDEEDALTQEEMEALEEDMQGDFEIAEMIKEKVI
PEATAWFTGEALLEFEGDDEEDEEEEDESDGEGDEDDDEDEEEEDEDSEEGGAAQSKRVPAAADAKEQPQECKQHAEPPR
AGVLTSRSSFDQQPRMGNALGVEDGYATASEGGASESGTPRAAAAAAAEPAIAAREDSGHLTAGVLNLAGSASARRRTGS
TGAEATWLSATNSPAAPQLVPPPAGAVQRHGPAPPGGAVRQRPSGSGDGGTAAAAEAAEAGSEEEEEEEDDEEEEEVGGQ
RRRGWNILGGVPFLPRIVELLSPKAGEYDEEEEEEEEEEEEEEEEEEEEEEEGSERGKAHGGQLQQPMSPGGTSRYPTL
AADAPHAAPRADDADLQGTTTDPAPLAPGQQPLPPLSEPSGLMSEDHIRALSAAVPARYRQASWTLLYATARDGISLQTM
LRNAARRSPTVLVVRDFDRNVFGAYCSEPWKVDKRFFGTGESFVFQLQPRAAAWYWWWRRMAKEHNDYFQWCTPEAIAVG
GSGGYALWLDADLASGISRNSTTFGNECLAGSPEFKVGAVEMWGLS
```

590 - 609:	EEEEEEEEEEEEEEEEEEEE
591 - 610:	EEEEEEEEEEEEEEEEEEEE
592 - 611:	EEEEEEEEEEEEEEEEEEEE
593 - 612:	EEEEEEEEEEEEEEEEEEEE
594 - 613:	EEEEEEEEEEEEEEEEEEEE

A0A2P6VN51 **A0A2P6VN51_9CHLO** (654 aa)
Dynein heavy chain. *Micractinium conductrix*

```
MALLVEEIPSAASVGDLNELVSQFTPVRRVLLAYPQGSALGSALVLLGGHPDLPGLAELLDCHPCPGGLLTVSVCEDPQR
WLASSSTGQLLQQLAATSGGGGVPARPLPSSMQRAPAAPPPAPAAGGRGGGAAALEEEMRQPQLQMQQQASAAAAARSPR
GGARGLVHSTPWDVLAGSSSGEAGSGEEEEEGGEEESYVQQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGWQEEEGWQEEEEEEEEEGWQEEEGWQEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEGWQEEEGWQEEEEEEEEEEEEEEEEEEEEEEEEEEGWQEEEEEEEEEEEEEEEEEEGWQEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEGWQEEAGGHLPPFGAGPSGRGAAAPGGGGGGTVAAAPGGGTRIIVRNLDQTVPYQQMKACFR
RFGWVEEVIKFPEACHAFVHFSGAAAAAAAVRELDGQLVPELNPREPVIVQHRSGGGDCGTSASSVGGSGVGGSGGGGRR
GGAGEGSQPPSKTLFVGCIVAQATKDTLLRVFGRFGPVFVLALQPSNNRVGEQWAIVRFRRVEDAERAVVALQGTVLPEL
TGREPVKTQFRPDT
```

202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE
208 - 227:	EEEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE

218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEEE
225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE
239 - 258:	EEEEEEEEEEEEEEEEEEEE
240 - 259:	EEEEEEEEEEEEEEEEEEEE
241 - 260:	EEEEEEEEEEEEEEEEEEEE
242 - 261:	EEEEEEEEEEEEEEEEEEEE
243 - 262:	EEEEEEEEEEEEEEEEEEEE
244 - 263:	EEEEEEEEEEEEEEEEEEEE
245 - 264:	EEEEEEEEEEEEEEEEEEEE
246 - 265:	EEEEEEEEEEEEEEEEEEEE
247 - 266:	EEEEEEEEEEEEEEEEEEEE
248 - 267:	EEEEEEEEEEEEEEEEEEEE
249 - 268:	EEEEEEEEEEEEEEEEEEEE
250 - 269:	EEEEEEEEEEEEEEEEEEEE
251 - 270:	EEEEEEEEEEEEEEEEEEEE
252 - 271:	EEEEEEEEEEEEEEEEEEEE
253 - 272:	EEEEEEEEEEEEEEEEEEEE
254 - 273:	EEEEEEEEEEEEEEEEEEEE
255 - 274:	EEEEEEEEEEEEEEEEEEEE
256 - 275:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE
306 - 325:	EEEEEEEEEEEEEEEEEEEE
307 - 326:	EEEEEEEEEEEEEEEEEEEE
308 - 327:	EEEEEEEEEEEEEEEEEEEE
309 - 328:	EEEEEEEEEEEEEEEEEEEE
310 - 329:	EEEEEEEEEEEEEEEEEEEE
311 - 330:	EEEEEEEEEEEEEEEEEEEE
312 - 331:	EEEEEEEEEEEEEEEEEEEE
341 - 360:	EEEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEEE

343 - 362:	EEEEEEEEEEEEEEEEEEEE
344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
391 - 410:	EEEEEEEEEEEEEEEEEEEE
392 - 411:	EEEEEEEEEEEEEEEEEEEE
393 - 412:	EEEEEEEEEEEEEEEEEEEE
394 - 413:	EEEEEEEEEEEEEEEEEEEE
395 - 414:	EEEEEEEEEEEEEEEEEEEE
396 - 415:	EEEEEEEEEEEEEEEEEEEE
397 - 416:	EEEEEEEEEEEEEEEEEEEE
398 - 417:	EEEEEEEEEEEEEEEEEEEE
399 - 418:	EEEEEEEEEEEEEEEEEEEE

A0A2P6VS89 **A0A2P6VS89_9CHLO** (209 aa)
Uncharacterized protein. *Micractinium conductrix*

```
MRRAKPATAGGRDLREGGAGAAAGEAGPERCGGADGLGGDQAGQAAAEGEEEEDEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
WRTLGLIALCAAALPAGRCNGAPAAPRVAGRNGKWLPPPGLTFAESLLP
```

55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE

88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE

A0A2P8A0D0 **A0A2P8A0D0_9PEZI** (605 aa)
Uncharacterized protein. *Elsinoe australis*

```
MANLMTTAERATMDFVVANGGSIPSGFTIANSRPTKSDWKPNQFDTAPNLRRYLPDQAWGKDTLKVLDVDTNSRIYVRMM
DGTGEGWVLWDHVPLSNRRSAAATKQRFLKTWMGVNGLVQEPQATAGARRSPPSASRTTAQRQGPLQTSSTPSSAPNSYQ
RALRSSARGATSNPNGSPSTALGNAAYDGYCNEPLNPGCTHGGKSAICQGDNKGRNFHGIEAHFHSTSASESVMCEDDGC
LVYVYREYGVCEACELNVFDHVYTEEERMWVKQSLADGLPIAHRQLCDQCIINSDLFTDFGELVNPCGCKHYRVTEHARC
AASRKEEVSSGVAKLLAPGYAESMPFCANSHCGKRLTGHEKIYECGSCYGLVNKGFVLNQYDPVKFPIFSHDELFGPDAP
NVWDANGNVMLDTDLSMADLAATRPRIRLSRARPQSPSKPQTTIVEKGKGRVVKISASPLYRYPATRARIPTARAEQDTV
AGAESTAGGSQTNPFPVPDDVAEHQANPVRISEDDEVSLEDGTAEEEEEEGEESEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEETEDEDEEMEDGDADGNENEDVMKVD
```

535 - 554:	EEEEEEEEEEEEEEEEEEEE
536 - 555:	EEEEEEEEEEEEEEEEEEEE
537 - 556:	EEEEEEEEEEEEEEEEEEEE
538 - 557:	EEEEEEEEEEEEEEEEEEEE
539 - 558:	EEEEEEEEEEEEEEEEEEEE
540 - 559:	EEEEEEEEEEEEEEEEEEEE
541 - 560:	EEEEEEEEEEEEEEEEEEEE
542 - 561:	EEEEEEEEEEEEEEEEEEEE
543 - 562:	EEEEEEEEEEEEEEEEEEEE
544 - 563:	EEEEEEEEEEEEEEEEEEEE
545 - 564:	EEEEEEEEEEEEEEEEEEEE
546 - 565:	EEEEEEEEEEEEEEEEEEEE
547 - 566:	EEEEEEEEEEEEEEEEEEEE
548 - 567:	EEEEEEEEEEEEEEEEEEEE
549 - 568:	EEEEEEEEEEEEEEEEEEEE
550 - 569:	EEEEEEEEEEEEEEEEEEEE

551 - 570:	EEEEEEEEEEEEEEEEEEEE
552 - 571:	EEEEEEEEEEEEEEEEEEEE
553 - 572:	EEEEEEEEEEEEEEEEEEEE
554 - 573:	EEEEEEEEEEEEEEEEEEEE
555 - 574:	EEEEEEEEEEEEEEEEEEEE
556 - 575:	EEEEEEEEEEEEEEEEEEEE
557 - 576:	EEEEEEEEEEEEEEEEEEEE
558 - 577:	EEEEEEEEEEEEEEEEEEEE
559 - 578:	EEEEEEEEEEEEEEEEEEEE
560 - 579:	EEEEEEEEEEEEEEEEEEEE
561 - 580:	EEEEEEEEEEEEEEEEEEEE

A0A2P8A5N5 **A0A2P8A5N5_9PEZI** (716 aa)
Fe2OG dioxygenase domain-containing protein. *Elsinoe australis*

```
MKRKYQAGDSGQNGAAPKSLKTSSSISEEFAPQLLSDSIVETYRESYASSGPYKHAVVQPLISDSLLRSVRQEIIDNIHF
TPKETDIYRIFQSGDLANLDGLPESALKRLPSLLRLRDALYSPDFRSWISTVSGAGPVSGKKTDMAINVYKPGCHLLCHD
DVIGSRRVSYILYLTDPDRPWKAQWGGALRLYPTEQKVTDDGRKVRVPDPEWSKVIPPAWNQLSFFAVQPGESFHDVEEV
YHKKEGEDEDDGGRVRMAISGWFHIPQEGEDGYEEGLEEKLAEQSSLQQLQAKNDALDLPQLRFVEPKSVAEEKDDQDED
EGDLLKADLDFLLKYMTPQYLTPDTVEELNELFTEESSLQLANILSPKIISKLETQILELEHLEKTDSRWQIASPPHKHR
YLFRQPATNDKPPTEANPDDILSDILDNFLPSAPFHKWLSLATGLTIGAAAHLGRRFRKGLDYTLATAHEDDSMQLEWCL
NLTPSKGWVSASDNDEEDNAEAADGAASSSNAPAPATNGYSNGKPTVSEPATDDEEDANAGGYELYMAGDDADDGDDAAS
DDGGSDHGVSLPSNAGQTQGSSSTGGGHRRVLKAKTAGGAKNKAADPAIYKASGEDEDDGILFTNPAAWNSLSVVLRDKG
TLRFVKYVSGNAPGDRWDVVGCAEVEGGSDDEEDGEDGEDGDGDEEGVEEDEEEEEEEEEEEEEEEEEEEEEREEE
```

692 - 711:	EEEEEEEEEEEEEEEEEEEE
693 - 712:	EEEEEEEEEEEEEEEEEEEE

A0A2P8A915 **A0A2P8A915_9PEZI** (200 aa)
Uncharacterized protein. *Elsinoe australis*

```
MAAAEYYDPKFTLPACYQHYLDQRNGGEGEAPPQPSPMHQAATAQYQQHFASGAHLSQTSSNPAGGKSSGGLGVMALSAG
MAMLGGKKNKPAITTGGSGKVGMGALVGGLGGMGLGDMMGKRKGEKGQHEVEVHEVGSDSEEEDDEDEGSGSGSEEEDEE
QEEDEEKQDEEEEEEEEEEEEEEEEEEEEGSESGSGRDSD
```

170 - 189:	EEEEEEEEEEEEEEEEEEEE

A0A2P8XFR2 **A0A2P8XFR2_BLAGE** (527 aa)
Uncharacterized protein. *Blattella germanica (German cockroach) (Blatta germanica)*

```
MGVALDIVRNSHVLVIRKFHFTKNVSYPIGLEEEEEEEEEEEEEEEEEEEEEEEDLLNKMKIIRTQCRYSGPLLEEGCLEK
ALDGGPKSVDYTSLVEWLSKELKALCNLDEQVNAISSADDSSSFLLEVSSFLKELGCAYSCLMEGHMSERLHTRENRILL
LDFLLTELEAARMIKVNKPDLSKVMEVQLTESSTASDLKTMLIALKFPKPPANITPALLFGKVEQKMKEVLSKASPELVG
SPLFVGVLSDKQWHQLSELQEELKEEYRMRREMLIKRLDVTIQSFQWSERVKNQEDQIAALFMAKRKGLTIQPDVHLSDL
LAAREDLAIIEKTSNATVRKNTQSSINKVIIGRVPDRGGRPSEQQPPPPEMPSWQQQRPGGGGPGGGGRGGFQGGGRGGF
QGGGRGGGGGDNRGGRVQGGWNQGGGGGGYQGGGGYQDRGGGGGGGYQDRGSSGYQDRGGGGGGGGYGGGYQDRGGGYQD
RGGYHQDRGGGGGGGYGGNYQDRNSGYQDRGNRGRGGRGGRGRDNYY
```

32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE

A0A2P8XJZ1 **A0A2P8XJZ1_BLAGE** (94 aa)
Uncharacterized protein. *Blattella germanica (German cockroach) (Blatta germanica)*

```
MFVTIALMKRSSNGWPLDEEEEEEEEEEEEEEEEEEEEEDFLTLSIFAAAENVFASGPVPLKETGRVLNVADDESKNGEAK
NDESKGDSINDSQE
```

19 - 38:	EEEEEEEEEEEEEEEEEEEE

A0A2P8XKB1 **A0A2P8XKB1_BLAGE** (174 aa)
Uncharacterized protein. *Blattella germanica (German cockroach) (Blatta germanica)*

```
MTPSPVLFKEEYNNTLVQGICHRDPERMRYGILKLKTKPCGKAAHGGLRPTSRLLASHVLGHEGEAVKRRCVIPGGHNTL
PDDRRNPRPITHDTGIVFVDDDVLKNILEGRISGSKKRGRPKLTWRGDGKFFSLLNSCDAFLSEEEEEEEEEEEEEEEE
EEEEEEEKEEEDIK
```

144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE

A0A2P8XSC2 **A0A2P8XSC2_BLAGE** (178 aa)
DUF4817 domain-containing protein (Fragment). *Blattella germanica (German cockroach) (Blatta germanica)*

```
VATQRAYQKEFGVHNPPQRNKVLVLVNKLEITGSLNFSMTVRTLFGLVVLLGKEEEEEEEEEEEEEEEEEEEEEEEEE
GTHSGIAGGCPIIGQVPMPHKHLLPMVSNGFEREVLGNPEPEGRRDVLPGFGRKAGGTDGPLTLIESCQDDVWYLLIPLD
DVDSLQKKNSDVKSSSIY
```

54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE

A0A2P8XX03 **A0A2P8XX03_BLAGE** (339 aa)
Radial spoke head protein 3. *Blattella germanica (German cockroach) (Blatta germanica)*

```
MQYSLDDGPVPYGNIMYDRRVVRGSTYAQHPMPVINMQELKEEEEKDQEEEKEGGGEGRPRKHWIDDALQDIASLRTKEE
EEEEEEEEEEEEEEEEEEARPRRSTDGETQAQRQQEARRRAMARRRAQGQQTRNARFRLRTPPPVPGRKHENVQTEKYLE
EISDRPPETDASCQTDLFLDRPETPVYVPAKVGLDAETQIYPGDLFDFDLEVQPILEVLVGKTIEQALVEVLEEEELEAL
RAQQRRFLELRAGEKAEQQRLEEQERRLREEKDNRLQQFKEATEKQKETEERIAAAVLSHGYLADLLPSVLEGLKEAGYL
IDDIKLGTLYFNTNLTSIP
```

79 - 98:	EEEEEEEEEEEEEEEEEEEE

A0A2P8Y0A3 **A0A2P8Y0A3_BLAGE** (432 aa)
Uncharacterized protein (Fragment). *Blattella germanica (German cockroach) (Blatta germanica)*

```
IVCIVTDIILQTYIKRNNCLSTYLFLCTNGIYLLINVSHPMRKLCVLAERAKREAEATASSQSAKEGSGPRLKELKERQK
QQLRHKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGWATLSSEVSEKVWKSKYEMFSNRSKSNTFK
ENSLLGNLACKEFVGEGFHGQNLLNYVFRGCVMSSSVQNLTFQLSGCGSLERCSDLLYINSYLRKVYCKAKLPKWFGERP
GKKKGDPESPEEEEVKADVLVDDDLEEPSFEPEPEPEEEEAAEEEAEEEEEEEEEEEEEEEEEEEELNEDILSLNLVDQM
RHSAQSVLHRVFHEENKPTPQSCYHSQALPSDSPEQGIESSNLHKYLQGPFLNQYEGEQTQLLPARWKYAAFIGGIVGFI
GAAIYPIVIYPMMNIDQYNMKVWTDPFDRKKS
```

287 - 306:	EEEEEEEEEEEEEEEEEEEE

A0A2P8Y1V9 **A0A2P8Y1V9_BLAGE** (586 aa)
Uncharacterized protein. *Blattella germanica (German cockroach) (Blatta germanica)*

```
MKMEKFYKFKAKYKDYMNCEPPSKLKSFISQNACNLLEDFSHDGRRVLVFNIGNIDTTKNDIRDIGQVMDLYTEMILDEE
ETQKNGVHYISDMAGFPLRLFKFFSNKTTILYAIREELSMSSLKQQSDEQGSQKEIDEERIQKVIEELRALVSEEKKLKV
RMDDNFMLRYLRSCDYNPKEAFSKMRPWKKIDIHLVNTSKFVNILMSIIFPFLSEKFKEQIHIHGKNWESLHQFIRPDIL
SKEHGGVKDKYDVKEANNYLYKNEDKLKGSSITSAIEQIEEEEEEEEEEEEEEEEEEEEEEDDNNNNNNNNNNNNNNSH
WNTMAKAEADSNDVHNEDENSDIENDMTKKLEYVNELRALVTEEKNLRVRMDDGFMLRYLRAHNFDVKESFEKMIKVYKY
KSKHKEYFCSGSISEYRDLLSKSHVTLLEDRDQSDIDTEHEDIVENIRLNDLWLELAMDEEETQKSGIHFIMDMGGFPMR
LLKFFLSKHTIMSAMKEEMRPWKTFNIHVVNTSNMIDKMVAFVYPVLGSKIKKHIHFHGQDWASLHKFIDPKVLPTEYGG
QKSVVDYDKMRQYVLDNEEKLMGKYV
```

280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE

A0A2P8Y413 **A0A2P8Y413_BLAGE** (856 aa)
Uncharacterized protein. *Blattella germanica (German cockroach) (Blatta germanica)*

```
MVEEEEEEEEEEEEEEEEEEEEEEEKRRRRRKYVDRKYRNQTPVAPCNFYLKLKKYLRGSLFQSSKTVLKAAEAVLIDMSK
MVSSIISHYHNNTKHRKMSPGVKIKPLNYEEPVHYKPTPVGEERSSDFEDDEGLRTGIGIIQWKRNDGLYKNNKRFGPGL
RTYPDGSQDIGLWVNNKLIALARHLDFVPHLSTSQEGKEILSTYLKVVEIKQLTSSTQEEKNINNYSEFHNSVQYCPLVR
DQRSCFFNTSLFEEEYFKDQLSLKESSTTLIRDATHSTVISNISEIQTQSLQGSGMQMIKEQSPGNSLIISISQRNKFRK
```

```
PGEHENDCVEMLESCRDGNDSKVRTLLMNNGVHPNVMEFNGNTGVMIAAIYNRPEIINILLDFGANVNHWNDECLTALNL
CILQYIADNHDILNWEQAFLYHKTLPIKQGDDDEYVRGKRRNLLQALIELNKKSSTSTRSDNLCPPDRVTQFYPQALSVH
LFTSYESYELMVGLRYYNVSNGLSNTVESAVSFSFRIQEFKTSTASLYEERKSVDILKAKKEFLILLPSHDKLLAQTGSR
TYLIEIIKLLLDRGADPNLCKVPFPSLMLAVYSRSLSIVDTLLSHGAEVNAITDPADGGLTALHAITMLPACDLLTAICK
ILLLHGADPNIETQGLDDVTTVQRDTNEKEADVNENEEDKDIENKNAIQKIESLSFDNVSEDHTPSCIEVIKGRTALHTL
CIRPNMEENKKSLRVMCMMLLQDSEANPNALYRGHSPLSLAIKQGDLILVKDLLSSGKVDPNQQLEPMFGVPLTMLLSDE
CQLSSDVKINMINLLLEYGADPLKKVEIGDSFTGSVIEYGHFIVEQKDVIYNTGQH
```

3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE

A0A2P8Y4F0 **A0A2P8Y4F0_BLAGE** (100 aa)
Uncharacterized protein. *Blattella germanica (German cockroach) (Blatta germanica)*

```
MSQEEEEEEEEEEEEEEEEEEEEEEKEKANIDIIRKIKSHRLRWAGHVKLGRPRMKWEKYINNDLREVVYTWNDWKTLAHD
RDVWRAYVRTAMNLRVRECQ
```

4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE

A0A2P8Y7V4 **A0A2P8Y7V4_BLAGE** (196 aa)
Uncharacterized protein. *Blattella germanica (German cockroach) (Blatta germanica)*

```
MCIWTLGEDEEEWTSEAEGEVASSSGGGGSGEGGESGEGGTPGDIAGGGSGEGGESGEGGTPGDIANSESKASSPPPPPT
PTSPVNSGQEEGSSPPPPPPRLRLKAGLATDPALRAAAPSPVVTTAPPPGLPPTAPGLEYLAALNPAFHSEEEEEEEEEE
EEEEEEEEEEEEEEEEEENDDESHTMFVCSFLERGK
```

151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE

A0A2P8Y956 **A0A2P8Y956_BLAGE** (367 aa)
Phosphatidylserine decarboxylase (EC 4.1.1.65). *Blattella germanica (German cockroach) (Blatta germanica)*

```
MVFWFIPNLFGFLPQRKAFRCIATFHCIPRTSTLVHHNLKHHASISTDPTVNTTQKRWHGLRHHLLRFWKPLPISVGLIL
LAVLQWRHIRRREANNDDKTVVVAKNWEIVCYRAVPLRALSRVWGWLTNKELPASVSPADGKIISFGPVDTCKVEQVKGV
TYSLQAFLGEPLWTNKLSETKTSEKVNKSTAQLTPEEYRQSLLMNKDTTLYQCVVYLAPGDYHRFHSPVQWDVIFRRHFQ
GELLSVNPKVAQWIPDLFTLNERAVYVGQWKYGFFSLTAVGATNVGSIREKVHMCKGEPFGEFRLGSTIVLLFEAPRNYK
FRLQPGQRIQVGSGPTRIVTPWEEEEEEEEEEEEEEEEEEEEGFKKN
```

343 - 362:	EEEEEEEEEEEEEEEEEEEE

A0A2P8Y9P0 **A0A2P8Y9P0_BLAGE** (51 aa)
Uncharacterized protein. *Blattella germanica (German cockroach) (Blatta germanica)*

```
MRSNEEEEEEEEEEEEEEEEEEEEEEECKSIICNYQHFIHGWCWKGSICKCI
```

5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE

A0A2P8YAR7 **A0A2P8YAR7_BLAGE** (249 aa)
Uncharacterized protein. *Blattella germanica (German cockroach) (Blatta germanica)*

```
MPTMEEEEEEEEEEEEEEEEEEEEEEEEEEEEEWMATVNESQNIARTYLDYYRAVGVITASLPPPVSTSPELKRRPRSNHS
PSSRPRSRPRTSRGQAVLHLHELTASTDRCGGSSSSECGDGSPQRLVPSSPPRQHSTRRRSAALIHYRQLPAPGSEPPIS
AGIKSLAGRKVGGGGMVCRSASNVFSKPQPALPSPPRLAIIDFNKLTRGGLDQATGRGRGGPHRSRGKLKKRSSRKPRTA
SSSPSDGHP
```

5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE

A0A2P8YBL5 **A0A2P8YBL5_BLAGE** (236 aa)
Uncharacterized protein. *Blattella germanica (German cockroach) (Blatta germanica)*

```
MIKLFQRSNGNEEEEEEEEEEEEEEEEEEEEEEEEEEEDTCNDRRTLFIFAAVVAVARAGLLGAPAVVAPGAPLARAYAAPV
AAVAHAPLAYAAPAVAKVAVDTDYDPNPQYSYAYDIQDALTGDSKGQQETRNGDVVQGSYSLVEPDGTRRTVEYTADPVN
GFNAVVHREPAVAAVAKVAAPVAAYAAPVARYAAPVAAVAHAPVHAAVAAPALAYGRGLAYGAGLGYGYGARPYYG
```

12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE

A0A2P8YC50 **A0A2P8YC50_BLAGE** (754 aa)
Ionotropic receptor 595. *Blattella germanica (German cockroach) (Blatta germanica)*

```
MEYHIRLIVIFIIYTEFLHKKLFSTHIGTKDAVHEEFLLCFETILTQQLTGDDSLLILIPSTGTIVRNQHDKFKALININ
GNSFIDKFLRTVHSRVILKIQTIGTDYKESNLYLIPPDVYVMILAEEDEDDVDEFNIEEEAGIGRTLEDEEREEEEEEEE
EEEEEEEEEEEEEDTIAELEMLLEDQLLALKDMVIWNARAKFIIIVDVKRGPKYSPDFVALQICRFLGIWNIINIVIVVP
NFNNGFVVDLFTWFPYNNGTCGEVQNVVMLDQWINQTFREGSIFFHKKIPKKFNKCPIRIAAIGLEPFIVYVDNYTHNKD
IGNTYNFRGLSAESPLIALDMLNVTVHTKYLSNDASMGNALDVSAGILGGSYDVLICPVPWIPSTMILDVSFPTIYFNLR
FQVPCSLPVPHLQRILKTYQVAVWLSTLLTLVISGFVFYLSAKVHNLEEAFTFKSVVNCLCHSWAILMGVSVPEQPKTRV
LRIFFYIYVCYCFSISTVFQAFFTTYLVEPGYGKPLRTFQDLLDAGFTFGVLPSLGILMSTVDFSEVSLFKKEETFNDFE
NATIRIMKKRDLCMISATLYSNYIANKLGVDDISKAICFLDDDLLGAKLGTGVPKGSPFLASLNYYTMLGFEAGFLERYS
SLFTQSLILSNNGGYQTVNSEYLVLNLSHLSPAFMVLLMGFSVSFIVFCFEICFYSFEIWKAHPVPRTKDVMFIPSTPSP
RKLQKRRKYWIKIRPTPSQIMTARLNNTISYDFS
```

153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE

A0A2P8YCD1 **A0A2P8YCD1_BLAGE** (145 aa)
Uncharacterized protein. *Blattella germanica (German cockroach) (Blatta germanica)*

```
MPRISLQWKSPYLLGSDVQRQRRLCRDLIAESQLDAIRILAALKLKVEPDDRPVRTKVDFIINAGIETELQKYGRLFHVP
IIFVLYPWPLYSETKEYLHGINTNCKTIDIPGKEEEEEEEEEEEEEEEEEEEEEEEEEEQEEEEEE
```

114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE

A0A2P8YEK6 **A0A2P8YEK6_BLAGE** (238 aa)
Uncharacterized protein. *Blattella germanica (German cockroach) (Blatta germanica)*

```
MKRRKNKNDCASLTFKQHQQRPEFATEICLTNALLTIALVPGCSIALAFDCSIVLVPGYSIALAFDCSIALVPGCSIMLV
PGCSIALVPGCTIVLVPGCSIALVSGFPLASVLRSAFSDCFFFEFCTNSILSFFTASQPFPTDANVTVKHNFETGRIAPI
IKILYCKYLRTHMCVSIFEDRLHQANPNHNNRILKEEEEEEEEEEEEEEEEEEEEEGRHLMRKEGNCWKELKIYCWNS
```

196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE

A0A2P8YG00 **A0A2P8YG00_BLAGE** (130 aa)
Uncharacterized protein. *Blattella germanica (German cockroach) (Blatta germanica)*

```
MIRKSPAQKGLGEAGYTTVPPGPTPPPTAAAVTVVGLDGMIQKIGGLDLLWAVIPLKKEEEGEGGEEGGGGEEGGGGEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKKKIHKQFCVLLFINSK
```

78 - 97:	EEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEE

A0A2P8YH82 **A0A2P8YH82_BLAGE** (689 aa)
Uncharacterized protein. *Blattella germanica (German cockroach) (Blatta germanica)*

```
MMCDLECLVLDRDFHTEVHKITTEKLREIFSEKGHVTDVQLKYTKDGKFRHFGFVGFKTDEEAQNAMEYFDNTCIKATRI
KVEVCSGLGDPNKPKAWSKYAPDSSAYKKEHKESKEEKIDKNEGKSKKEKKKEKKRNSIEDKVSSSKDANEEEDEEEEDE
EEEEEEEEEEEEEEEEEEEEEKKVVKEKNRKKEKAPKEFVDYFTVKLKGLAYKFKKKDIKQFFHPLKPKSIRLPPKNRAG
KRIWVSRYENKKPESLNVESKEPSKWKDQEESLKNEETIAESGRVFVRNLAYTVTEDEVEKLFNKYGEVTEVVMPVDRHT
RKIKGYAVITFLIPENAAKAYMELDGSVFHGRMLHLLPGKAKLSLEELMAKEGLTYKEKQMLKKKAEAASSHNWNTLFLG
QNAVADLIAETYQTTKDKAPKERSKTIILAKNLPAKTSSTEITQMFMKFGELGRVVLPPSGVTEVEDQTDEVEVEEGTEN
TKDVSDDDDDDDDEEEEEAPEPDTTLFIKNLNFDTDKEQIEKHFKNCGPIHEIIVAKKKDPKNPGKLLSMGYGFIQFKRN
ASVEKALKTLQHSQIDGHAIELKRSNKTSKTFGEIKALRLPKKMVGTGSHRGFAFVDFYTKHDAKRAFKALCQSTHLYGR
RLVLEWATTEDSLNDIRKRTTEEYGEGPLHKTLKKSTFKDDGIEDNDSD
```

160 - 179:	EEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEE

A0A2P8YIK3 **A0A2P8YIK3_BLAGE** (1032 aa)
Uncharacterized protein. *Blattella germanica (German cockroach) (Blatta germanica)*

```
MGLLLSVLVVCVGVLEVIACVRHFQDGYLPLWTPHCAVTSGYARTHERWRKKPSDSFEFRSSIDVSGTLDHSQDQSSESY
LQPSHTVENGYTAKHELQETTELIKSTGDFPESKTYDAILPSLIGDGNIEDLSRTDILPPSLDTSGHNLEAISANDGELF
IPSEEYIERKDCTNYSDSSFVEKPPNDKNEGFLKSAESDAPSYAEDVTAIAYSENFETQICPKETQQLSHIIESNTPSSR
DNIGAFDGPSETQENIPLKHEYNIPTVEESSSDDLYKAEKEKHALTLDYEITSTEVTGEYNNENPSREILLELETDDNIG
SSQFTQNKEFSNLQAFENQYEANEYNTGSEYSSPDANASSRLKDRHTGEQEVNDSFQTVPLLSNQVELPSQGLSEENLQE
TIVPDIINHELQSTCVELEAVTSPTSPITQIQTEVSGYDSVAETVKYQEVFDAPPGIESREKAFSQIQEEAKEEIKTETT
LNLPEEEEEEEEEEEEEEEEEEEEEAEIQLNTSQQVQKHTDVTSSLVLKEEAKDEIRKETSLIPPEQDEEEEEEEEEEEE
EEEEEVGEKEVLTKHVPKEIQQLEDTRQIQKKGLEEEMINLPEEEEEEEEEEEEEEEVEIEQEVFRQLPKPKTEPIPELQ
IQSSSVNENEQPIKFDQKDIAEGRLENQTISSEFTFKNDEEQQPDVQVSGPHAETPKVIPKVHSPLTIDPSGSPPLTRHA
SHQSSMSPPQLPSTPTRKSKADISWPTFFPGAPVIKRPSVSFATPEAVFTNEDQELLRKYAEEATDIAPCIKKSEDNSSA
ADTEAITSSTSEGKSTESTEASERSDSFEEEVIPITFKERSPSNIVSGNDFSRKELALQRRKSYKHKRYSSATELASREE
ETEDKSFSENKPGLTRASSLREPKRRYKKPAKASSFEDAILRREEDSSITVPEEKETDIQEEKAVTEEETKESDDHQELS
SERNDSKTRGSTVRFEEKKEDKKSVERNIDTNTKKEGEEEEEEYSVSEEQSSSQQKSPANEAFWVSSEEESD
```

485 - 504:	EEEEEEEEEEEEEEEEEEE
486 - 505:	EEEEEEEEEEEEEEEEEEE

A0A2P8YIX6 **A0A2P8YIX6_BLAGE** (199 aa)
Uncharacterized protein. *Blattella germanica (German cockroach) (Blatta germanica)*

```
MIVPVRDTNKRTGGKQGGGGGGGEEEEEEEEEEEEEEEEEEEEEEEEGHLHFVECLISTAQRKAEPLWEKLNVRKFRT
VILFSNTRDRFGYASTLFRGTTSSGEGLVIKLAALQQFNNSLRNAMELASGKDNELSLFYKFLNIFRHHKMSESSDEDCL
TPPEILQEAMAITSNLLPQKSKKKYEKLYEQFMDWKLHD
```

24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE

A0A2P8YK07 **A0A2P8YK07_BLAGE** (161 aa)
Uncharacterized protein. *Blattella germanica (German cockroach) (Blatta germanica)*

```
MPAGYDRNMIRHGTKICYDHIIILMTPCSAKRRYSFDFRATYRGSTLNCTAIEEEEEEEEEEEEEEEEEEEEEEEEHYEL
HKTALKHYVTDCFLWSGRRGAHYRMNKICSDKDGTLEDAAASNTDEISTPTPRTDKNGQTKKHTVDIRNKLKAQNYPDEK
W
```

53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE

A0A2P8YSP4 **A0A2P8YSP4_BLAGE** (96 aa)
Uncharacterized protein. *Blattella germanica (German cockroach) (Blatta germanica)*

```
MAGGRSIKKIFEGKFEGRRDRGRPRLRWTDFVERDLCSLGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERRKHLVESY
VIKYNMRSRAPHPICI
```

41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE

A0A2P8YTF6 **A0A2P8YTF6_BLAGE** (1192 aa)
Uncharacterized protein. *Blattella germanica (German cockroach) (Blatta germanica)*

```
MHVLNRAQLIDDSLKMAHAGILSYDIALDLTKYLTTETDYIPWVSFFNGITYLNNRLIGKAIYDNFKEYMRSLLINLYNY
IGFEESADDTDVTRLHRVNALTWTCNFEHQPCIEKASALFSEFMNNGVTVTPDLKSLAYCYGISNGGRAEWDFLWERYES
TQLSSEQVLILNALGCSKDSTMLQEFLKMAINSTSGVRRQDSNTVFTSVYSRPFGIDVALDFLINNFDDMQNYFSSKNIL
SIIYGIASRINTEEQISKIKKFIEDHLAEIPGDFKMIIINILLCFLLITYTKALMPHDAVVVSEKQEENTNYRLPKDVKP
ESYDIDLKADVNVNFEFEGSVSIVVLIETATNTIVLHSNGLTNSDPEVVDIATDQEVTTTHDTVEQTHLLRITSESGFEQ
GKKYRITINFKGKMADDMYGFYKSSYFAADNSERWIGATQFQPTHARRVFPCFDEPEFKATFKINIRTPVGYHALSNMPL
ERESRQMSSSSYYRVNYDADNWHLIIQGLHNNPSEIHVLNRAQLVDDSLNLARAGQLDYTVALELADYLTNEEDYIPWVS
AFNALSFLDRRLTSEEGHADFKTYLLGLIEKTYNTLGFEEDAADKQDTKLHRISLLNWACRFDLEDCINNANQKFQAYLN
DGTALVPANLRSVVYCTALRKGGNREWEYLWAKYKESNIATEKVVILSALGCTEDQDILENYGGMNAISNILTGIAGQLT
TAEQVTKLEEFIANNENELGSAAEAGRIAAESSKANMAWTNEHKDVILNWYKQKVNSETTPGTQTSPGTQTSTGTQTSTG
PQTSTGPQTSTGPQTSTGPQTSTETQSSTEIETTTQPQETTTDAGSKQELAGLTFTFFILTYIIQFLIHIPLFNRWIAAT
QFEPTHARKAFPCFDEPEYKATFKITIITPYGYHALSNMPFQTIMETSQWSNTTRADLYDALEIQRLEDNIGMHSVSTIF
EQWITQPGYPERFLVLEHEKAVEALKWWVPLTWTVKGNAPNGFNDTEPQEWITPFEEIKSINIEVKDNEWIIFNNQATDD
ALNLARAGKLKYSTALEVSFYLQEETDYIPWASGFAALSYLNSRFLSFPEYDLFKNYTLFLLESIYQKLGFEENYRDNHL
TKLHRIDVLTWICKLGHKDAIKKAQELFNKFCSKPSHYPLFPEEEEEEEEEEEEEEEEEEEEEEEKEKMQKL
```

1163 - 1182:	EEEEEEEEEEEEEEEEEEEE
1164 - 1183:	EEEEEEEEEEEEEEEEEEEE
1165 - 1184:	EEEEEEEEEEEEEEEEEEEE
1166 - 1185:	EEEEEEEEEEEEEEEEEEEE

A0A2P8YXG3 **A0A2P8YXG3_BLAGE** (106 aa)
Uncharacterized protein. *Blattella germanica (German cockroach) (Blatta germanica)*

```
MKAPVTYFKNDHCLCSEQERLREEMSGGRRNRGKGFEMTVFAVMGDLDWQNVTFSFEQGSLERGTSANAKLDWIAYLMEE
EEEEEEEEEEEEEEEEEEEEEEEEE
```

79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE

A0A2P8YY75 **A0A2P8YY75_BLAGE** (168 aa)
Uncharacterized protein. *Blattella germanica (German cockroach) (Blatta germanica)*

```
MESTVEKYKDLRRKEKSIHKKKKKAHYEAMLQEIQEQNCGNNSRKFYHCVNNMRKGYTPKIVTYRKANGELTADRREALG
RWKEYFKDLLDGTEEDTSNMEILDTVVQISEEELPTIEEVDMAIDKLKNNKAPGGNVLEEEEEEEEEEEEEEEEEEEED
GVGLITIG
```

139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE

A0A2P8Z1G7 **A0A2P8Z1G7_BLAGE** (208 aa)
Uncharacterized protein. *Blattella germanica (German cockroach) (Blatta germanica)*

```
MTIVDESKHNFYESKFWKRHYFSETGKSQSLILEEEEEEEEEEEEEEEEEEEEEEEEEEEEEHYFCNKMLTWDAGNLECSS
KVFASSSFWCTYSKLKTILRVREKVDVSSFTNVVSFLKKMSVRHVPRKSNVLSRSHIDEFLLNAPDDVFLLIKVVTAFGV
FGAYRRQELHDLCFNDVKVEGSVFVLGADDRDAKERDALKVTVLRLEN
```

34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE

A0A2P8Z4G2 **A0A2P8Z4G2_BLAGE** (76 aa)
Uncharacterized protein. *Blattella germanica (German cockroach) (Blatta germanica)*

```
MVMKMEHRPKKVLNTRNYIGGKRRISEPRRIGKLEKKKPDNIEEEEEEEEEEEEEEEEEEEEQQQQQETEDCINRW
```

43 - 62:	EEEEEEEEEEEEEEEEEEEE

A0A2P8Z8I3 **A0A2P8Z8I3_BLAGE** (2097 aa)
Uncharacterized protein. *Blattella germanica (German cockroach) (Blatta germanica)*

```
MANAIGEYDHTFPWKGETNQLHIILYAVEQLFRWYRYDNKNETFMKAEISVTPDLLDEDEVETLLTMRFGKVVKFFLYIS
NWFAEKSGEALRKRSLIILHVIIKKLQSQDFFPKLYHLLTLSECITKMFKYEKTDPVRNGFLTLVKYLDSRLYAIHTLTQ
LAGLTKRLTKYYQIWGPDDYIRKIILELADVFLVKANKFMSRPFDFSSLSDFLQAFCYWCHRDNDSNLIRRAVEQIASVF
VFKYRDSRECSSKNIYNFQETAHAVDPEGDGSNIENDTYTNEKEFIIHVPVNAVPDQNVELVERDQTNVGDATNVASMDK
HEVENVAEKNNRSSESSGSDSKFHLHFNAFSDNSGKNEHFTPKNIAGFACRLSTWSGSDFGDTLLTAMNLLAKIVVHNSG
NNGIDLKSCDEQDLNLLMYSFTKWKKDDGIIKTAVVAIAEVLGDLDSCGKLKDFSIRILARLAKYFSQWQRYHNDDIFSC
IIVNIAKTVETLYSEEEEEEEEEEEEEEEEEEEEEKPLNHKPSDLVELADAFSLVSGTGIAINPFNGAIDVIAKIFYKGF
SIQSQLISYLPRYLRKLAVVFRKFYEFNKHDCIYEAIKVISLHIRYEHYGNKLEHFGIKDLAVLSDTFINWLGENHMLLS
TVHIAETVIDRHEKGNLDFHIESLSLLTKAFAVWRANDEKGMLQKATIAIADIILNDLKSRFTPYNLQALTLLSLSFNEW
LINGAPTEIPPAIQAIASNITLQFVVKVVRGGTLEEFGKVATELSDFKEYTECICCISTAIVHNTVDSLREVSNETLSNL
IIAIAKCYNNGNESRDILVHATSTLLERAIGNVNTLNYAFCYWRHRDNDSNLIRRAVEQIASVFVFKYKDSRECSSENIY
NFQETAHAVDPEGDGSNFENDTSTSEEEFTMHVPVNAVPDQNVEQVVRDQTNVGNATNVGSMDKREVENVAEKKNRSSES
SGSDSKLNLPFNAFSDNSGKNEHFTPKNIAAFACRLSTWYGSDFGDVLFTAMNLVAKIVAHNSGNNGIDLKSCDEQDLNL
LMYAFTKWKKDDGIIKTAVVAIAEVLGNLDSSGKLKDFSIRILARLAKYLSQWQRYHNDDIFSCIIVKIAKTVETIYSEA
EKPLNHKLSDLVDLADAFSLVSGTEIAINPFNGAIDIIAKLFYEGFSIQSQLISFLPRYLRKLAVVFRKFYEVNKHDSIN
```

```
EALKAISLYISYEHYQNKLEDFSIKDLAVLSDAFINWLGVNQMLLSTIHIADTVIHRHKKGILDFHIESLSLLTKAFAVW
RDLDVDRKLQEATIAIADIILNDLKSRFTPYNLQALTLLSLSFNEWLINGAPTEIPPAIQAIAFNITLQFVVKVVRGSTL
EEFGKVATELSDFKEYTECICCISTAIVNNTVDSLREVSNETLSNFIIAIAKCYNNGNESRDILVHATSTLLERAIGNVN
TLNYAFCYFRNRENGSNLIRRAVEQIASVFVFKYKDSRECSSENIYNFQERAHAVDPEGDGSNFENDTSTSEEEFTMHVP
VNAVPDQNVEHVLRDQTNVGNATNVGSMDKREVENVAEKKNRSSESSGSDSKLNLPFNAFSDSCGKNEHFTPKNIAAFAC
RLSTWSGSDFGDVLFTAMNLLAKIVLHNSGNNGMDLKSFDEQDLNLLMYAFTKWNKDDGIIKTAVVAIAEVLGDLDSCGK
LKDFSIRILARLAKYFSQWQRYHNDDIFSCIIVKIAKTVETIYSEAEKPLNHKLSDLVDLADAFSLVSGTGIAINPFNGA
IDIIAKIFYEGFSIPSQLISYFPRYLRKLAVVFRKCYEVYKHNSINEAVKAISLYIPYEHYQNKLEDFSIKDLAVLSDAF
INWLGENHMLLSTIHIADTVIDRHKKGILDLHIESLSLLTKAFAVWRDLDVDRKLQEATIAIADIILNDFKSRFTPYNLE
ALNLLSLSFKKWLMNGAPTEIPPAIQAIASNITLQFRDKVVRGSTLEEFGKVATELSDFKEYTDCICCISTDIVYYTEDS
LREVSNETLSNLIIAIAKCYNNGNQSRDILVHATSTLLVRAIGNINTRIYVIDKIMPYKEELYNMVDLYNMINLYINGTN
LRSFSIINLVVLYLYLK
```

495 - 514:	EEEEEEEEEEEEEEEEEEEE
496 - 515:	EEEEEEEEEEEEEEEEEEEE

A0A2P8Z9V0 **A0A2P8Z9V0_BLAGE** (275 aa)
Transcription factor LBX1. *Blattella germanica (German cockroach) (Blatta germanica)*

```
MPYVGVYIASGAYQKVIIVATKSDDVLGVSLRSKAPMSVVQRCQGNDGRPEVGRSLLVTCLSAVTNSSRRLPLHTENYWE
EEEEEEEEEEEEEEEEEEEEEEALLNSQADVVIAFFRHGQANHLNLFNNRQQAKKKRKSRTAFTNHQIFELEKRFLYQKY
LSPADRDEIAGQLGLSNAQVITWFQNRRAKLKRDMEELKKDVESTKILTAHKSFLENVQDLGILKKKSSGTALYQIDKAD
FYSTDVNVWFPLSPSAVFETKRVTVDCEIALSKVL
```

80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE

A0A2P8ZCZ1 **A0A2P8ZCZ1_BLAGE** (106 aa)
Uncharacterized protein. *Blattella germanica (German cockroach) (Blatta germanica)*

```
MDEEEEEEEEEEEEEEEEEEEEEGLEVHVNKTKYMVTRRNASGNANGQLMKNEGNFEEVAEFKYLGALITNRNEIQKEMK
HRLNPGNACYYALQRLLSSQLLSKKH
```

3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE

A0A2P8ZG28 **A0A2P8ZG28_BLAGE** (414 aa)
Uncharacterized protein. *Blattella germanica (German cockroach) (Blatta germanica)*

```
MGIHSVQLLYRPPQLQKSIMNIPFQELVLRLPSVKREHIGKQLKQSSKLQPTLKTRPNDFAEGGKRNRLPLSAATGKAHP
SDDDVVNVSIPETSFPQPSQEQSPFIYHQIYPLHYILTSLRPQEGKAFMEGIKDIDDDLKSCRPYDVKTEENVKKFDKIV
RGNPRLSIREIPGLTNINMESGGKNSYGISDQKKYQVNCFADVLENIQNDPGLLLKRHSSSSSDDDDDDDDDDDIPNTNL
MKPQSRCPCHEFGPLPLDLLQVNPNDDRDCSQMPFDVAMSGSDDEADEHEEEDGDNVVLKAGPVVDMEGRYKSSHQHKEY
SAGSKDGAAHQHNLQHNHTRELSFLLFEEEEEEEEEEEEEEEEEEEEEEEERANSNLCQQKEHMDRRHLGRCPALLRTEQ
HEIYWEARSLLRNI
```

348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE

A0A2P8ZH61 **A0A2P8ZH61_BLAGE** (117 aa)
Uncharacterized protein. *Blattella germanica (German cockroach) (Blatta germanica)*

```
MGVDISAYRSRIGRRRRFSSSERGKQEEEIEQLNYRKPGSPTTRTSTYEGIENLRESRSEKRRSRDIRKPNYSNEHDQKN
SCHIQEEEEEEEEEEEEEEEEEEEEEEEEEEANLQKC
```

86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE

A0A2P8ZJA5 **A0A2P8ZJA5_BLAGE** (493 aa)
Uncharacterized protein (Fragment). *Blattella germanica (German cockroach) (Blatta germanica)*

```
NFGRFNQAGGCGSKFLLSLPTTGSLNPPQYLVTNMQLKHEQIEERRLKKSQGTRLNEHELGLELASVQWPGTKAYCLSPL
SHGAGWKVWTTILIFNNLLDRKAMLVSLVRPFPNTSKSESSGPILEGTFSHAVNKKGFKEINAIEMKFLTASSIKGSSLQ
DSFPNKNTLCYNITNFLNLETLLITEIGYWSDMNMNPQFVKEESSEEDCILIHIVNFQGFLKLDQYLEEEEEEEEEEEEE
EEEEEEEEEGAGGGGRKLNNFYGYVRNEGLRTYCPKAGYTKWDHKHNNDIMDELQLEPIINYIQQYQNQWTKHVHRMSNT
RIPKAMLYYQPRGKRYLVRPMKRWSENPQRVTAADEKNPGKCCKHPAGLVGNVYPSACLECLHSCDLSAASDLGLKGGGE
TDGTPLVSFSVVGGKHSGMQRTSSMKPYKCHSGSESMFTRSVCISNKQKKKKKKKKKKKKKKKKNKKKKKKKTPFVIENE
AAFFINSTTNKDK
```

228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE

A0A2P8ZMW3 **A0A2P8ZMW3_BLAGE** (109 aa)
Uncharacterized protein. *Blattella germanica (German cockroach) (Blatta germanica)*

```
MGKWKIKYMLNVLMLNSILKDPDIGREMKARRVRWFGHLYRTEERHRTTKRRRRVVGALTAVEPEVEEEEEEEEEEEEEE
EEEEEEEEEEEEEEKEHHIPSLPNKQRKR
```

67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE

A0A2P9B7B3 **A0A2P9B7B3_9APIC** (3110 aa)
Transmission-blocking target antigen s230. *Plasmodium sp. gorilla clade G1*

```
MKKIITLKNLFLIILVYIFSEKKDLRCNVIKGNNIKDDEDKRFHLFYYSHNLFKTPETKEKKNKKECFYKNDGIYNLSKE
IRMRKDTSVKIKQRTCLFHKEGSLFEMGSKNITCFYPIVGKKERKTLDTIIIKKNVTNDHVVSSDMHSNVQEKNMILIRN
IDKENKNDIQNVEEKIQRDTYENKDYESDDKLIEWFDDNTNEENFLLTFLKRCLMKIFSSPKRKKTVVQKKHKSNFFINS
SLKYIYMYLTPSDSFNLVRRNRNLDEEDMSPRDNFVIDDEEEEEEEEEEEEEEEEEEEEEEEEEYDDYVYEESGDETEEQ
LQEEHQEEVGAESSEESFNDEDEDYVEAQDGDMIRVDEYYEDQDGDTYDSTIKNEDADEEVGEEVGEEVGEEEGEEVGEG
VGEEVGEEEGEEVGEEEGEYVYEKERQGEIYPFGDEEEKDEGGESFTYEKSEIDKTDLFKFIEGGEGDDVYKVDSSKVLL
DDDTISRVSKKHTARDGEYGEYGEAVEDGENVIKIIKSVLQSGALPSVGVDELDKIDLSYETTESGDTAVSEDSYDKYAS
NNTNKEYVCDFTDQLKPTESSPKVKKCEVKVNEPLIKVKIICPLKGSVEKLYDNIEYVPKKSPYVVLTKEETKLKENLLS
KLIYGLLISPTVNEKENNFKEGVIEFTLPPVVHKATVFYFICDNSKTEDDNKKGNRGIVEVYVEPYGNKINGCAFLDEDE
EEEKYGDQIEEDEHNEKIKMKTFFTQNIYKKNNIYPCYMKLYSGDIGGILFPKNIKSTTCFEEMIPYNKEIKWNKEKKSL
GNLVNNSVVYNKEMNAKYFNVQYVHIPTSYKDTLNLFCSIILKEEESNLISTSYLVYVSINEELNFSLFDFYESFVPIKK
TIQVAQKNVNNKEHDYTCDFTDKLDKTVPSTANGKKLFICRKHLKEFDTFTLKCNVNKTQYPNIEIFPKTLKDKKEVLKL
DLDIQYQMFSKFFKFNTQNAKYLNLYPYYLIFPFNHIGKKELKNNPTYKNHKDVKYFEQSSVLSPLSSADSLGKLLNFLD
TQETVCLTEKIRYLNLSMNELGSDNNTFSVTFQVPPYIDIKEPFYFMFGCNNNKGEGNIGIVELLISKQEEKIKGCNFHE
SKLDYFNKNISSDTDECTLHAYENDIIGFNCLETTHPNEVEVEVEDAEISLQPENCFNNVYKGLNSVDITTILKNAQTYN
INNKKTPTFLKIPPYNLLEDVEISCKCTIEQVVKKIKVIITKNDTVLLKREVQSESTLDEKIYKCEHENFINPRVNKTFD
ENVEYTCNIKIENFFNYIQIFCPAKDLGIYKNIQMYYDIVKPTRVPQFKKFNNEELHKLIPNSEMLHKTKEMLILYNEEK
VDLLHFYVFLPIYIKDIYEFNIVCDNSKTMWKNQLGGKVIYHITVSKREQKVKGCSFDNEHAHMFSDNKTNVKNCIIDAK
PKDLIGFVCPSGTLKLTNCFKDAIVHTNLTNINRILYLKNNLANFTYKHQFNYMEIPALMDNDISFKCICVDLKKKKYNV
KSPLGPKVLRALYKKLNIKFDKYVTGTDQNKYLMTYMDLHLSHKRNYLKELFHDLDKKKPADTDANPESIIESLSINESN
ESGPFPTGDVDAEHLILEGYDTWESLYDEQLEEVIYNDIESLELKDIEQYVLQVNLKAPKLMMSAQIHNNRHVCDFSKNN
LIVPESLKKKEEVGGNPVNIHCYALLKPLDTLYVKCPTSKDNYEAAKANISEDDNEYELQVISLIEKRFHNFETLESKKP
GNGDVVVHNGVVDTGPVLDNSTFEKYFKNIKIKPDKFFEKVINEIDDTEEEKDLESILPGAIVSPMKVLKKKDPFTSYAA
FVVPPTVPKDLHFKVECNNTEYKDENQYISGYNGIIHIDISNSNTKINGCDFSTKNSSILTSSVELVNGETKNCEININN
NEVFGIICDNETNLDPEKCFHEIYSKDNKTVKKFREVIPNIDIFSLHNSNKKKVAYAKVPLDYINKLSFSCSCKTSHTNT
IGTMKVTLNKDEKEEEDFKTAQGIKHNNVHLCNFFDNPELTFDNNKIVLCKIDAELFSEVIIQLPIFGTKNVEEGVQNEE
YKKFSLKPSLVFDDNNNDIKVIGKEKNEVSISLALKGVYGNRIFTFDKNGKKGEGISFFIPPIKQDTDLKFIINETIDNS
NIKQRGLIYIFVRKNVSENSFKLCDFTTGSTSLMELNSHVKEKKCTVKIKKGDIFGLKCPKGFAIFPQACFSNVLLEYYK
SDYEDSEHINYYIHKDKKYNLKPKDVIELMDENFRELQNIQQYTGISNITDMLHFKNFNLGNLPLNFKNHYSTAYAKVPD
TFNSIINFSCNCYNPEKHVYGTMQVESDNRNFDNIKKNENVIKNFLLPNIEKYALLLDDEERQKKKNNNNNKKKNKNDKN
DDRLSRHDDYNKNHTYILYDSNEHICDYEKNESLISTLPNDTKKIQKSICKINAKALDVVTIKCPHTKNFTPKDYFPNSS
LITNDKKIVITFDKKHFVTYIDPTKKTFSLKDIYIQSFYGVSLDHLNQIKKIHEEWDDVHLFYPPHNVLHNVVLNNHIVN
LSSALEGVLFMKSKVTGDETATKKNTTLPTDGVSSILIPPYVKEDITFHLFCGKSTTKKPNKKNTSLALIHIHISSNRNI
IHGCDFLYLENQTNHAISNNNNNNSYSIFTHNKNTENNLICDISLIPKTVIGIKCPNKKLNPQTCFDEVYYVKQEDVPSK
TITADKYNTFSKDKIGNILKNAISINNPDEKDNTYSYLILPEKFEEELIDTKKVLACTCDNKYIIHMKIEKSTMDKIKID
EKKTIGKDICKYDVTTKVATCEIIDTIDSSVLKEHHTVHYSITLLRWDKLIIKYPTNEKTHFENFFVNPFNLKDKVLYNY
NKPINIEHILPGAITTDIYDTRTKIKQYILRIPPYVHKDIHFSLEFNNSLSLTKQNQNIIYGNVAKIFIHINQGYKEIHG
CDFTGKYSHLFTYSKKPLPNDDDICNVTIGNNTFSGFACLSHFELKPNNCFSSVYDHNEANKVKKLFDLSTKVELDHIKQ
NTSGYTLSYIIFNKESTKLKFSCTCSSNYSNYTIRITFDPNYITPEPQSRAIIKYVDLQDKNFAKYLRKL
```

280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE

283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE

A0A2P9BG11 **A0A2P9BG11_9APIC** (779 aa)
Serpentine receptor, putative. *Plasmodium sp. gorilla clade G1*

```
MIKIIIGVIGYYILYSSYHIYENIKSPIFNDGNVIKNNEGDKNEQLVIPKEGKKRNSINEEEEEYINKPFKNVLKKDDII
DYHLYFSCEEDIDINKHMQDKYLEKDERFISVYKILNGKYSWNNNVDLLDEKRKKNSFFFLFEKVHPSFDISIPKELIDQ
RKDIYLHILTYVNKELYRYGSRTVVITKRKEKTTTRGKKKFLWKSLIDEEEEEEEEEEEVIEDEEEIEDEEEEEEEEEE
EEEEEEEEEEEEKKKYQHGNYEKGGSYKVHKNISNNKPNNKNPNDKRDIKHNNNNNNNKMKKDNFIKSNQNSLNIHKKKK
KRKHKDFLFYIPKKIRFGPVIEYNDFHISKLGFFSNMHVDKDTNTYLLPIYINNDLTPDDEYRMIKMKNSDDMMKKKLKK
KRLSEKNDPYYKENVRNDDNNNNNNNNIKNNYLEIYDLSKRTYEMRNERNKKIYEKNSSINNNVHKLEHELMDYIINIEY
VPINYNYYNLLNMLKLNVSYVKKKYNFISFDMDSITTFLCCHITCSMIIYILCIIYIIMEITYLLFDIKMWKRWNNLYTF
TYNNDIVMNITLLFFILLYLRNIDYGRVIMIYYIMKMMVLIFKIIYNYDICILNDYPYICINKKSLKEMNKEMIMDEEFE
KKIKKKVNIFMIFSIILIFIYNYFYTKYDSYYSYVIHTLGFSSYLYKFILMLPQIITNIYTRTVQRMSFPFFLFLLVNVL
INDLFIIFLRMPKVHKYYLFADDFILFLFIIQYCIYKKENKIFGAREKLVLLKNAKKNK
```

230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE

A0A2P9BI48 **A0A2P9BI48_9APIC** (2002 aa)
Uncharacterized protein. *Plasmodium sp. gorilla clade G1*

```
MNVCKMKVQQKKNLKDCNLKSKNTILTSFEKKKNEKDENNLLKFSKLIDNKNKVVNSKLLKNDNYKFNERKESLTRCSTN
ESLKMKNIKTLTKDFDYNNNNNNNNNNNNNNNNINNNNNDYNNNNNNNNNNNNNNNNNNKNNNKNNNNNNNNNGHSKLVFK
KNDKDIESKVREEDGKKSEKKNNDLINNKNEFKVNNKLILKSKEFKSNNNNNNNNNICKLNNIDDKNKKQQMDTYSPKEN
EEDNSNNMKKNSSLKNIKKNHINEMEIISNSVEENHDTHSKGDKENNGVSTKNVKRMNTMSKEINHKNNNLKKHVSKSNS
LELKKGKKGEKSKDKLSNNLSGKKGMNKEKEVVQSSSVRRNSSRYSIEYGRRDSSRRGSVKQEKGKERRGSKNVSKKVSN
SKYTRKKSKRIKEESDESDDDDDEEEEEDDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDNDNSDNNDES
DEVYTNRSRRSTRCSIVKRKSSLCIGKKNSKIIKKSTSKTKNNKKKKGSVIKLVKKKEKLSKKGILKKTNKKTKGKLRKN
SKLYHRKKNIKNEKDGIDEEDIDEEDIEEDIEEEEEPSYFDEYNLSYEERKKDLEEKEKKKEIKEKYIKQIKLPKYADDE
SIIFINNPNYVMVLLFLTVYKDVLKMNWNFKDIEEMFQNKETTEFGRNFILKLFFFLGRYFNSKSIFMYKYISRIFEDKE
ESLSRVVNFHELFPVLETKKEIKNSGVGSKRKKDKRGKKMKIHQKEDELLYDEEVIGNEDVHIFEEEEDNEHSNDDEDEE
EEDNEHSNDDEDEEEEDNEHSNDDEEKEDVHYNDEEEKKSDLNNDSTKNTVIKEEKDGLHISEGSHNLVNIVNDSMKREE
SCKNGHIGDNERSADINTNDDKNNADNNDDVDGEKMVDSKNNIENKLDNTVEGKHDINSTEGIIKSENVDDEKGLLTNKL
FLEWDDLSVISKLRIIRMLLNLVLCESNNLKKMLGDEKLNYNNGYLGKINNEKYWFIFNDTINIEYKLYLEREEEGSFIF
ICDDDDMLYTIGYNFLRNSDTKFMGEALIERYNKVCRERRNRSRMLKQQKKLLCADINLNDPLLGTKKRQHKQVEYFNFD
NNEKMRRKKSDMNNNNPYSVPPTKSYQKNDRSFRLAARNAQKGSVDDLEAWKLNEGSLGIENQGATSGNYNIANDGTNMT
ETNNINDNHNNDNNNNNDGVVNADGNNIYGPNNNNVIGSDGNVNNANNTTTNNNNNNNNNNLGTVKIPLKRGRKKKSEK
KKRGRKKKILSVDGIGEIANNLSTLNVDENRRKSMPNIGRGRRGTYTKRNTKPSVSIKYGTRSHSINKYENDVMSFNEYS
LNPGLSMDDFYKNMVMDPKFFHANMNMNNYMNGGFNMPNNNNSMMNMRNGSKMGNMNNIGGYNFPYMCTPPPMYNQYYMY
NGNNMYLPNGGPNNNMNMSNANNGASVVMGGNVVSNQNTVKDVKAENMHMAKNSIMENRNSIIVNNMNNMNNMNNINMNS
MPHKNSFMGNDGINNMNSMNNNNNNNNNVNNNNNNNNNVSNNNNNNVSNNNNNNVNFMDNMGNNNNNNNNNNPMNKYNNY
MMNRNVLNNMGGTNPLYNNMYNMKFPYMNNDMMNYNYNINSFQNMNYDKMNKSMFKRYPNFMGGYPYNNMNPYNNFNAFN
MNYQQNDQMNQLPNMQGGYKSKLMNDNLSNYQSFNNNNVKQNHHDNNDNNNNNNINKNNSEGGNKNMDDSNKNNDINKND
ILDSTKLTEQPVGGLVPNNDCITRGEDNHRIDLKGDIAEALVGNNNEKMNSSDHNLNSLKNLPNINNAYNMDHMSHMRNS
VSASSIGMINPGHMNSSHSGSIMNKDKFRDLQLNSSNNNNNNNNNNNNNYVKVNPFDHPMKNMNPNLMDDKYPKDNNNMM
MMMMNSVYNMMGSDHFHMNNSHMMDPMGSPKMNDNMYNHNNMNFENTNTNHNNHNNHNNHNNINNLNNLNNHNNRIQDKL
PE
```

431 - 450:	EEEEEEEEEEEEEEEEEEEE
432 - 451:	EEEEEEEEEEEEEEEEEEEE
433 - 452:	EEEEEEEEEEEEEEEEEEEE
434 - 453:	EEEEEEEEEEEEEEEEEEEE
435 - 454:	EEEEEEEEEEEEEEEEEEEE
436 - 455:	EEEEEEEEEEEEEEEEEEEE
437 - 456:	EEEEEEEEEEEEEEEEEEEE
438 - 457:	EEEEEEEEEEEEEEEEEEEE
439 - 458:	EEEEEEEEEEEEEEEEEEEE
440 - 459:	EEEEEEEEEEEEEEEEEEEE
441 - 460:	EEEEEEEEEEEEEEEEEEEE
442 - 461:	EEEEEEEEEEEEEEEEEEEE
443 - 462:	EEEEEEEEEEEEEEEEEEEE
444 - 463:	EEEEEEEEEEEEEEEEEEEE
445 - 464:	EEEEEEEEEEEEEEEEEEEE
446 - 465:	EEEEEEEEEEEEEEEEEEEE
447 - 466:	EEEEEEEEEEEEEEEEEEEE
448 - 467:	EEEEEEEEEEEEEEEEEEEE

449 - 468:	EEEEEEEEEEEEEEEEEEEE
450 - 469:	EEEEEEEEEEEEEEEEEEEE

A0A2P9BJC2 **A0A2P9BJC2_9APIC** (383 aa)
Casein kinase II subunit beta (CK II beta). *Plasmodium sp. gorilla clade G1*

```
MEFVSNDESADDIIQDESNEGEVELTDADFYDLTVINDKIDEEIIEDDEEEADNDDQENDNVQEVYNIDDEDNDIHNDKL
LLDQQRDNDVNEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEDDDDDDDDDDDDDDDDDDDDYDDEYDEDDFNEATVSWI
EWFCQLKQNLFLVEVDEDFIRDEFNLIGLQTKVPHFKKLLKIILDEDDDDDDDDDDDYDDEDDEINRDSEEMYKNKDMHE
QNAACLYGLIHSRFILTSKGLALMREKYKSGIYGTCPSIYCENAKLLPTAISEIPKFLSPLLYCPRCCETYYPSKNSLLN
QLDGCYFGTSFASFFALSFNIASDKKKVYYTPQICGFTINRNIRETLYMDVNKDNTESSEECQ
```

92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE

A0A2P9BMC5 **A0A2P9BMC5_9APIC** (5960 aa)
Cysteine repeat modular protein 4. *Plasmodium sp. gorilla clade G1*

```
MKNITFLVSFLIFLRSINANISITNFTYTNQKGDIKVEFFQTDYIAIFKLPFGGSHEQIFEISDDYIITNDKETNNCNIP
NNNFGFVYSKSNSQNKFLIVQREYTTIYIKDKNNNCSLISKVEPSLYSFQTIEYKKEKIKLGTTTKCDEKMVEKLKTYID
LLNDMNLSEDKVCNQIISSSFIQNIEIIDCTVYIGSIFLRNNLNREEYYICIKKEDNNNKMKNNISLLINTIDLNNTLIM
NTFYCNMERDICSIIINSIYFNNIPNITDDTLVLKAQCNIDSNPLINIDHVLREGYYTFHFRNPKIYFLQICIIDNLKKY
RMLGKIYFLKAYEPIICFIGTPCVIKSFTVKENVQYVQNNIDNETFIFTNKKCDNENVNENMMMIETDYDMKELENHQHF
YLFSKNPLTDEKYLCTSNNKKFLLLFNIFLIKLPEYNIHYSIINNVVINYSTLFFEYNNYLGPYVKYECSDKSIVPDEYN
NFNNNKDNNFLLKNEELNFTIKFKAIIMRLCLKQNNYYYDIGKIYIENFINYKKISSLKDFIFNADVSLHADDINTKLLK
FAIKEDHNCHSDQGFFVQSKDNFLADKKPFYKNIFINHTTVYESINQIILDKDIYYICMCSLHQKCYDNNNLIDYNVYTN
ISIQNEIQPLQNKKKFICKIFADCSFTINFENEYNNTSDIWVAKKGQSCNSKDIQVGIHVSHQNVKEINKEKLNVTKVNF
KIYYLISHIHYSYLFNKDIFICGNYRNQHFIVHIKSDFFLLYYALPFEEEINIKNVTQTNVATNTYEAQEKNINIQSFEN
VKQKFKRLFIYSYRDDAKSNLYKTMNINQDENQISNTIKFEIPNDHPTKYNEIYFINECHYDQGVIIYDHKRESNNIAIN
NDNDNNNNNNHIIKSKELYWARKKRIYNKKLKKKENKNEIINIYNCSNEIMNNHTLTSILIFDGPLKPLDIYCYMELDCI
HKENFSILNFDYSLFVEISDTQRIIIHIKESEGNNKEKLNKAEKIYFNDSKRTTELILSIPKHISKGLEPGPYKIIYTRK
FKQFIHELYVGTFHFIGAPSQKYHLIRENEENIIIHGYFKNIENERIHILKHQNTCVLTNKDKNKKLLKSSEIEYILNEI
KTNIQNCTYLDDTKLLCKNDLPVEGKFILCWCYNILNDQNNLCHNLNIYRPKITEVSSLLYSIDPILEISKSSLTNFLNY
NIGDFFFIIDDDCKNIKNLKLKSKLNDEQNILDIYKHLQYPKKYDLCICIVQHNIPCDKEENFKNFYIKLNEQIYFTMEM
GSIDEFNNKDKFIKDFTFSTDYLDQLKLNIVPVFVFLPGPVEYKEYVCFAGIPCNATIKIKRSAQTRLSTGNKQIIGEKK
DVANPYTGSYGNRNKANIKKGEEKKEQKRNDKKEGEIRHKKEDELGDKKEGEIGHKKEGELGDKKEGELGDKKEDELGDK
KEDNNEDQNQDNKQDKIENMNKDINKDKEIKTKETNIEEEEEVEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEEEEEE
EEEKQEEEKEEKQEEEQEEQFDHNEHEVKGADKNKDKNFNQNKGESQNVNPNTQQNQYDEQIISEEEQDNIENSLLGKHQ
YIYYTLNDTKECKNEYETVYKSNASSIYVSQEINYLHHEFIDGVYNLKIDIVPTDITKRYEICASFYEDDKYFYNIGNVI
FYGIFNESNTLDIISGVPFSFEINQFYSKYDLFVRLIYEKHGDSKTCRLYNNNFENVFLQGTIERTIVQHDKKVLDNYIT
NYKWKDVTIILDTDNNNYMTSYQNVDGSYNLYVCSCYELTEGHCQSGNYFSTQVMKFYVHTVELKEPKMNSLMHFLKPFT
LKLETTKILNGSIKVIPIDIISDLSKLCLELNLKNIYLKYQAEINEYEQTYNITINFLSQGFIICWCGKDNCKDHEYLTK
VAFFRLNSPNFIDVHTDLNGNFSFHFLNQFVNINDRVRFVGQASSCLDDENVDLFNNHIVIRNVQNKKGKTSNGGNTKKE
QEKNNNKINSNNNEEDENDNENKNTNKNKNESKDEDDNYESYSIDWEQIIEIYGKPRNIFKGINQNWTWVSENYKMKTSN
EKYIKICYCFHFFYKNCKDTKNFLYIGLVHNHIWNSKTTIMQNELDTNYEISNMIYFNKDSIKFVAINSFNDLNRNVCDN
INYEKNIIMPFFSGYNKFHNTTINQKNILNILKTYYHNEFIFILCYNTEYYKKKTNFLLTTKDMTEFNDFTTYYNEEINT
YNIIQSSFSYHSDIKDISTTNENIEKYEHMQLLLQNRGNTPNIFENYFYLKDVYKKNNMSIYNMNLYNMSPYVIYNNNKK
KITNIQVKNRLKIILTKMYHMTSVDINEVIYYKGKGELLTDLNLQNIFILPKQKKVILCCYNDDYIEVIINDDNKIGMKK
SNKIQELIDILKKYHPNFERNKKKQNDILEQFNNINDILFKYDYIRDVNKNQIYYDTGFFRNNIYIQLINQPFDLKIYGS
NIQKKKNKDYILYIIEFHNICYNNMNKNGFFLEHKRYNEMENYIHFLQISMNKINNYKLCLYDKERDIYSNVGILNITDY
FVIKESSFFDNEDIGNIKKKNMETDSYNYNNDNNYDRNYDNNYDSNYDNNYDNNYDNNYDNNYNQDVIKNVCLIMDNNTN
QIIVIKGKGSFYFNLQIEKGIFIEKKDQKLNELFPDIKNHELISCKNKKKNTIILTKTHIFFYTNNNDISFSTKHNLPFP
YDIDFDDQYIYVNDLYLNKIARIQILSNKDNKTPIPIINNKQRSKRSIINHGHESQQNIQKTHQTYNHFTPLHKVEKKEI
LQNNNIVQLKENEFPITNLKNIEYSKNNIPNQKISSNDDIYKMSDFQAFINKYANLITTNLFRLYNYFEKKKYYGTLNYF
IKRLWFNKVGPSREENYSTESKIEQNDKNNNNNNNNNINNNYNDHHNNNHNIILNSNNYNNNNQSSRHQNFIYSYHVSLD
GKKKQSENLLTHSLNNFIQFFQNKKNSILKKEKEKRKNIPSYNIMYKNINHITNTLNKRKQQELTSSIIKKRAKRNVQEK
RMSQSAYNELVLASIKKYTNKVEPAHFVNNKLDYLNYITNLKSPLNISVQNNILYILDSIKNTFFSYNLINKEIKELEKY
DFNDHPLILKNPLHFSIYNGIITEYTEHKNNLAFVTQIDSNEIKVIDLNSSKKYKIIKAIKLRKGYKHNHINYVIGIKQK
LLIITSQSQNIDHYKNIIYHYHFNSFDQYFSISFNYTFAKNYNANDNLYITPDIDKYSDNIIYFCFLNSNNKCTNIDELT
KLSISHETGIITGKLNYFGTFSLKIFAKTYFQYKINTYSNLYSYCGISQEYNKTKSTCESCPIGTFWNSEKLLCENCQKY
IENTSTLKNGSKLKTDCLCSPGYEYSDKSSKCEKCKPGYYKRSVGNFICIKGCPINEKSITYGAKSYGEMDCKCIEGYYR
KEDKCVLCLSNYYCPGNELIKPCDKNKISKEGVIHKNDCICKENYIKDNKNNNCVYCASIAKILGKPIYCSLCDPIYFHE
DIYKNIFLLPNNIHNYGLINNIYNYDEDLSLQGNIMKYAYFHKTTNTERNFTHYINIKNIYHTFNNNINNYDYLTNSKFA
IEIDIPEPKKCIFCDSGYYIKKKKCISCTTKYCEGFNHNPKACPKNSVVNKMKASSIFDCSCKRGYGILNERRNAYSNTI
TCQICPQNFFKHIISDDSCFPCPLYTYTLNQGATSILQCLPKKGYFIYMFKSINIDYLRYKFDINTENRIYNYFENNNKI
FDEDVYNFFLNKQYSKFFYNTENKTNTNNNHNNNHNNHNNNNNNNNNNNNNNNNNNNKNNNKYTKDNHFDNQVGNINKHTNN
LQIKITENIYNIQYLEHLGFIKKTSLFYIYMILLRNIEERYNFNMDKMLKITCHINLHLKKNPHFTITYKKNLQECIDSC
KTNIYCTGIEFSRKRVEYTQIILKNNKKIILGYFKCKQFYFQNIYDYSSYNLDSYLNEHIENQINIKSTLTYTNFIMRNK
PDIIYTCSIDRDPKYLLYKNYKLVECVIGKFCPGNNTPYMISCPINSTTIIPASEDVNKCLCLKGYSYVGVTSYRCSLCD
RGSYKNSVGNNKCDNCPLTFSTTHRGSTNIKDCSCTSGNYLTFDTLGNFIRTENMQHKNISDQYFVIPIKQESQPENEIK
DDNKNINIYNANNINNHDIVYKTKMIKINLHKENDNHNDYMNNILKQTIGLCKPCTLENHYCEGGLESDITFNNKLIKGK
FHTLPKKCPRGLGIPNIIKERNSINNCLCIHGKVQRTTENKNVECFPCPPNTFKENEYDNSCSGACPPFSTTFVGSSYEN
QCFCKNNYYLVSTDDENDTNGNSLNNNKNIYNNNNIYNNNNNNNNNNNNNFNNKSDVKKKSCKICPIGAICNRGFNIYIYL
KLLNDRSYNNINVIDHETPFPKYGYYAVYREKTNPTKLWDPLDDSAILNYVYPYHKLLLFIQKNIQKGNYFFLEKGNKFF
LNDDFVEKMNEKSKYEEENANKFVTKSEIIHNVNTNNLKGKHNTLNNNNNNNINKSSSFLNQNNYNNDIIQLSSYENIPF
KKLSSTSEVSSNNNVISFIQNNDKTNNSTNDNNIENLVDIFNKYVQEAKELQIQNRKFERIPDIHPCTIPNRCLGTLINL
```

CSDGSTGYQCNNCSKNYDMSYFKSKCKKCQNLFYEILHFILLKLLYYIIVIFICSLNGNILNKLHVSGILMRIWLNCSFT
FIAYGFFIPNMNSFISKYWYLYKTAFSYHMKIFAYYLRVQCLLNSLNINLSYNQMWYIQKYMNICTPIFDSIFITILLFA
VIHIYKFFFYKKNIDIFEQLLCTIPELNTLYKKNCIDSNHKVKNKKFANKVESFEENENQNKEKKNKKNIKRNKKAKNKD
NNDNNDNNDNNNDNNDNNNDNNNDNNKININSKDEQINHFEKCSSITTILNNLELNNQEKNKESKKKKIFDIKKKTSIEN
IKENETNHLWNDTHNNVKNKESNINTTNISNNINYELKYIKNKEWYNIFLNKTIQYIYKEKKIFGLWHFIFTKNDNWFKN
MGTFLSDTLPCYVLIMILSIPYILLELVQLTYCTPMKYKTQKTYFYLTYLITQKCSLSSKLFITGLIVTITMFALYIFLW
ILLLYLYSKRKRLNLFDLLTTNLLSGFRKGKGIFELIFLLKHILIVLLICFNIYYGFYYIVFLTLILITFAILEILSNPY
DKRSFNILNKSLNIGNVLNIFFPLIIWGSFYWTYEKFFIFPIFVIYAYHIYMFYHIVKEFTLSIHFIKTENIVNIQTIGY
DPENIKNKNYKIYYKVMNKIKYFLNKNQKKNISNINENKDKHLNKNNNSKDHVKFEPIENIIKRYNLKLNKGILKDANNN
NNNINNMSDQVEDNKKDILFIKKNVLPVNVHNVASIWYDEQNEDLLFQMPYQNKFCLNMNNEANENNDQINDLTKDKTSE
EENNNDHVNDPTKNQTNDEKNKNKNNNNNNNNNNNNNNNENNGHSNDNSNSNNNKEVHENDDNINHNNINNHNKSSNIST
TNKKNYFNKFSDYIIDKRNKKSIKYFITSLMEVIEKFLDSSTHGFIYENWFDFTIRFAFVYISWIKKCNKKNNIMLPMNI
QQLHIHMDLFIFTPIFSKNNSTCINEQNIQNYSKKKKIYNKINMYDENIETGELLEKHNSFENTEIKISRSFGSHNYMPN
IKNRKNNYDKKEDITSINDINVDIIKQDDQKEDSNINHLINEHNQKEPSQHIYNINDQNIMDYNIHENISKNNEKEKHIK
IPPKNISLTQKEYYNNNDIFNYSLDIFSSEMFNEKMFHSIISLFELYMAIKTLKLMNPHIFNKLYQMYNKKIITFDTSVM
FYINKLRDDIKSEIEQIDKEINTGDTTEKERIQNYYYYKEELFKRKKLEEELLSKIKSLEECIEVNKRSQSLRNMLLTKK
KENNNLNNENLEEHINYIFSHLHNEGTYKLNHSQNMDKKN

1484 - 1503:	EEEEEEEEEEEEEEEEEEEE
1485 - 1504:	EEEEEEEEEEEEEEEEEEEE
1486 - 1505:	EEEEEEEEEEEEEEEEEEEE
1487 - 1506:	EEEEEEEEEEEEEEEEEEEE
1488 - 1507:	EEEEEEEEEEEEEEEEEEEE
1489 - 1508:	EEEEEEEEEEEEEEEEEEEE
1490 - 1509:	EEEEEEEEEEEEEEEEEEEE
1491 - 1510:	EEEEEEEEEEEEEEEEEEEE

A0A2P9BP54 **A0A2P9BP54_9APIC** (3059 aa)
Transmission-blocking target antigen s230. *Plasmodium gaboni*

MKKLLTLKNLFLIILLFILTKKKDVRCNIIKENNIKDDEDKRFHLFYYSHNFFKTPETKQKKKKKKKQLYKNVGINNLSK
EISIRKDTYVKTKQRTCPFDKEESSFEIGSRIITCYDPIIWKKERKYMNKTVIKKNVTNHQFVYSDINKEYKNDIKNVEE
KIQRDTYEKKDYENNDNLVVGYDDNFLLSFLKKCLMKIFSSPKKKKTVVQKKHKSNFFINSSLKYIYMYLTPSDSFNLVR
RNRNLDEEDMPPKDNFVIDDDEEEEEEEEEEEEEEEEEEEEEEEEEEEEYDDYVYEQSVDETEEPLQQLQEEQQDEVTV
EGSEESSNDVGEDYVEGEDEDMIRVDGYYEDQFADTYDSKIKDEREDDAVDEYIDEYLDEYSDEYSDEYSDEYEKERESQ
GETYSVDDEGEESFTYEKSDISKTDLFKFIEDSEGDDIYKVDSSKVLLEDDTTISKVSKKSVDVEGEEDEESVIKMIRNV
LQSSVLPSEGADEFDKIDLSFETTESGDTSVSEDSFDKYASNNTNKEYVCDFTDQLKPTESTPKVKKCEVKVDEPLIKVK
IICPLKGSVEKIYDNIEYIPKKSPYVVLTKEETKLKEHILSKLIYGLIISPTVNEKENNFKEGVIEFTLPPMVKKPTVFY
FICDNSKTEDENKKGNRGIVEVSIEPYGNKINGCAFLDDDEEEEKYGDQGEVDENNDKIKLQRFFTQNIYKKNNIYPCYM
KLYSGDIGGIMFPKNIKSTTCFEEMIPYNKEIKWNKEKKSLTNLINNSVVYNKDMNAKYYNVQYVHIPTSYKDTLNLFCS
IILKEDESNLNLNSYLVYVSINEELNFSLLDFYESFVPIKKTIQAAQKNVNNKEHDYICDFTDKLDKSLAPLIEEKKLFI
CRKYLKEFDTFTLKCNVNKTQYPNIEIFPKNLKDKKEVLKLDLDIQYQMFSKFFKFNIQNSKYLNLYPSYLMFPFNHIGK
KELKNNPIYKSHKDIKYFEQSSLLSPLSSSDSLGKLLNFIDTQETVSLTEKIRYLNISINELESDNNTFSLTLQVPPYID
IKEPFYFMFGCNNNKGDGNIGVVELLISKHEEIIKGCNFHETKLDYFNNNVSSSKDECTLYGYENDIIGFNCSETNNASD
EEEDGVEISLQPENCFNKVYKGLEIIDINTILNNAQVYNINNKKTPVFIKIPPHNLLEDTKLSCKCTIDHVVKNINVILT
KNDKVLLKREIQNEFKLDDKIYTCEHENFINPRVNKIFDEKVEHTCNVKIEKFFNYIQILCPAKDLGIYKDIQIYYDIIK
PTKVPEFKKFNNEELHKLIPNSEMLHKTKEMLILYNEEKVDLLHFYVFLPIYIKDNYEFNIVCDNSKTTWNNQIGGKVIY
HITVSKREQKVKGCSFNEEYTYMFIDNKSNVKNCVIDANPKDIIGFVCPSGTLKITSCFKDAIVNTNLTNINHILHLKNN
LANFTYKHYFNYMEVPALIDYDISFKCICVDLKKKKYNIKSPLGPKVLNAIYKKLNIKYDKYVTGTLQNKYLMTYMDLHL
SHKRNYIKELFNDLNKKKPADTDANPEAIIESLTINESNESTPFPTGDVDAEHLLLEGYDVWENLYDETLEDVIYKDIES
LELKDIEQYVLQVNLKAPKLMMSSQINNNRHVCDFSMKNLIVPDSLKKKKEEGGNNPIDIHCYALLKPLDTLYVKCPTSK
DNYEAAKVNISESDNEYELKVISLIEKRLQNFELLDSKRNGNGHAILTNGVVDPTSVILDSSIFEKYFKNIKIEPDKFFE
KVIKEVDDTEEEKELESILPGVIVSPMKVLKKKDPFTSYAGLVVPPVVSKDLHLKVKCNNTEYKDEDENILGYNGIVHIE
ISSSDQKIKGCDFSTDDSSILTTSIKLVNGETKNCEININNNEFFGIICDNDTNLDPEECFNEIYDKDKSNVKKFHELIP
NIDIYTLPNSNKKKVAYAKIPLDYINKLSFSCSCKSSHNNTIGNMKVILNKDEKEEDEFKTSLSIKHNNINLCNFFDNTE
LTFDNNKIILCKIDAELFSEVIIQLPLFGNNKTLEGDQNEEYKKFSLKPLLPINEDDNDIKVIGKEKNEISINLALKGVY
GNRTFKFEKDGKKGEGISFFIPPTKIDTDLKFIINETIDNSNIKQRGLIYIFVRKNVKENTLKLCDFTTGSTSLMELNSQ
MKEKKCNIKIKKGDIFGIKCPKGFAIFPQACFSNVLLEYYKSNHTDNEDINYYIHKDIKYNLKPKYVIELMDENFRELKN
IQQYTGISNITDMLHFTNYNLGNLPLNYKNNYSTAYAKVSDNFNSIINFSCNCYNPEKHVYGTMQVESDNTNFDNIKKNE
NIKKNVLLPTIDKFPLLLDEEQRQKFKLKLKLRDADDIFNTDDINHIYMLYNSNEHICDYQKNETLISNIPSDNKKIQKS
TCRINAKALDVVTIKCPHTKNFTPKDFLDNSTLQSNDKKIVITFDKKNFVTYIDPTKKTFSLKDIYIQSFYGVTLDHLNK
IKKIQQDWDDEHLFYPPHNVLHNVVVNNHIVKLSSALEGVLFIKSKVTGDETNTKKNTTLPTDGVSSILIPPYVKEDITF
HIFCGKSTTKKPNKNNTSLALIHIHIASNTNIIHGCDFIYLEKNTSVTSTVNNTSTIFTHNKNKENNLICDISLVPQTVI
GINCPNKKINPPTCFDEIYYVKEEDVPPKTITADKYNTFTKDKITNILKNAISITNPDEKDNTYSYLILPDKFEEELIDT
KKVLACTCDNKYMIHMKIEKNTIEKIKNDEKKTIGKDICKYDVTTKVATCDIIDVIDSSSIKEHHTVNYSVTLSRWDKLI
IKYPTNEKTHFEKLFVNPSNLKDKVLYNYTNPINIEHILPGAITTDLYDTRTKLKQYILRIPPYVHKDIHFSLQFNNSLT
STKQNQNVIYGNVANIFIHINQGYKEIHGCDFTGKYSHLFTYSKKPLPNHNDTCNVTITNNTFSGFACLSHFELKPDNCF
SSVYDNNEANKVKKLFDLSTNVELDHIKQNTSGYTLSYIIFKKESNKLKFSCTCSSHYSNYTIQITFDPNYITPEPQSRA
IIKYVDLQDKNFGKYLRKH

262 - 281:	EEEEEEEEEEEEEEEEEEEE
263 - 282:	EEEEEEEEEEEEEEEEEEEE
264 - 283:	EEEEEEEEEEEEEEEEEEEE
265 - 284:	EEEEEEEEEEEEEEEEEEEE
266 - 285:	EEEEEEEEEEEEEEEEEEEE
267 - 286:	EEEEEEEEEEEEEEEEEEEE
268 - 287:	EEEEEEEEEEEEEEEEEEEE
269 - 288:	EEEEEEEEEEEEEEEEEEEE
270 - 289:	EEEEEEEEEEEEEEEEEEEE

271 - 290:	EEEEEEEEEEEEEEEEEEEE

A0A2P9C8G5 **A0A2P9C8G5_9APIC** (1961 aa)
Uncharacterized protein. *Plasmodium sp. gorilla clade G2*

```
MNVCKMKVQQKKNLKDCNLKSKNTILTNYEKKKVENDEKDSLKFFKLSDNKNKVVNSKFLKNDNYKLNERKESLTRCSTN
ESLKLKNIKTTTKDNNNNNNNNNNNNNNDNIDNIGKCKLIFKKNDKDIESTVREEDGKKIEKKTNDFINNKNEYRVNNKSV
LKSKENKSNDNNNININNNNNNINNNNNINNNNNINICKLKSIDDKNKKQQTDSYSQKENVEDTSNNMKKNSSLKNIKKN
QLNEKDIVSNTVEEKKNNSHSKGDKENNTVVTKNVKKMNSVSKDINNKNNNSKKDVLKSKKSEKLKDKLINNVSGKKSVN
KENEIIQSSSGRRSSSRYSIDYGRRESSRRGSIKEEKGKERRGSKNVSKKVSKSKYTRKKSKRINDESDESDDDDDEEED
DDEEEEEEEEEEEEEEEEEEEEEDDEEDDEEDDEEDDEEDNEEDNDDNDDDDDNENNDNSDNNDEESDDVYTNRSRRSTRC
SIVKRKSVRSIGKRGSKIIKKSESKTKNNKKKKGSVIKLVKKKGKLSKKEILKKKKKKTKGKLKKNSKVYQKKKNIKNEK
NDMDEEELEEELEEEEEVEPSYFDEYNLSVEERKKDLEEKEKKREIKENYIKQIKLPKYADDESIIFINNPNYVMVLLFL
TVYKDVLKMNWNFKDIEEMFQNKETTEFGRNFILKLFFFLGRYFNSKSIFMYKYISRIFEDKEESLSRVVNFHELFPILE
MKKEMKNSGVGSKRKKDKRGKKMKMHQKEDELLYDEEAIGNEDVNIFEEEEEEDGDEEENEHFNDEEEDEEEENDGNYND
DDEEEKKSVSNNDSTKNTVIKEEKDGLNILESSHNKININNDNMKREESCPNGLNGSNEKVKDFHTNDNINDEHNNNNNN
SQVVDTENNIENEVNNTVETSKDINNNEGIIKSENVDDEKGLSTKLFLEWDDLSVTSKLRIIRMLLNLVLCESTNLKKML
GDEKLNYNNGYLGKVKNEKYWFIFNDTINIEYKLYLEREEEGSFIFICDDDDMLYTIGYNFLRNSDTKFMGEALIERYNK
VCRERRNRSRMLKQQKKLLCADINMNDPLFGTKKRQTKQVEYFNFDNNEKMRRKKSDISNNPYSVPPTKSYQKNDRSFRL
AARNAQKGSVDDLEAWKLNEGLMGVDNQGSISGNYNIGYDGNNMVDTSNTNDNMNNHNNNTNVVVGADGNNIYGVNNNNV
VGSDGNIIMNNNNINNNNNNNINNNNLGTVKIPLKRGRKKKSEKKKRGRKKKILSLDGIGDLTNNLSGVGVDENRRKTIA
APGRVKRGTYTKRNTKPSISIKYGTRSNSINKFENDVMSFNDYTLNPGLSMDEFYKNMVMDPKFFHANMSMNNYMNGGFN
MPNNNTTTTNNNNISLMNMRNGSKMGGAINNLGGYNFPYMCTPPPPMFNQYYMYNGSNMYIPPNGTNNNMNIGNTNNGSA
AVVGNVLSNQNSVKDMKGENILMSKNNMMENRNSVILNGMNNINMNNMVNKNSLIGNDGINMMNNNNNNNVNNVNNVNFM
DNIGSNNNNNSNNNNSNSNNNSSSNNNNSNNPMNKFNNYMMNRNVLNNMGGTNAMYNHMYNMKFPYMNNEMMNYNYNINS
FQNMNYDKINKSMFKRYPNFMSGYPYNNMNPYNNFNAFNMNYQQNEQLNQLSNMQGAYKGKLMNDNLSTFQLYNNNNNNN
NNNNTKQNNNDNNNNNNIEGGNKNIDDGNKNNDINKNDIIDNSKHNEQPVGGIAPNNDCINRGEDNQKMDLKGDTVEALV
GNNNDKMNNSDNNLNSLKNLGNINSSYNMDHISHMRNSVGGSSMGMINPGHMNSSYGGSIMNKDKLRDLQMNNNNNNNNN
NNSNSNNSNNSNNNNSSNYLKANPFDHPMKNMNNNSMDDKYTKDNNNNNNNNMMMMMMNGVYNIMGTDNFHMNNSHMMDP
MGAPKMNENIYNHNNNINFESNTNNINNNNNNNRIQDKLPE
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403 - 422:	EEEEEEEEEEEEEEEEEEEE

A0A2P9CAH9 **A0A2P9CAH9_9APIC** (388 aa)
Casein kinase II subunit beta (CK II beta). *Plasmodium gaboni*

```
MEYVSNDESANDIIQDESNEGEIELTEAEFYDLTNINDKIDEEIIDDDEEEVNKDDQENDNVQEVYNIDDDDNGVNNDVN
DDVNNDVLLLEQQRDNDVNEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDDDDDDDDDDDDDDDDDDDYDDEYDEDDFNEA
TVSWIEWFCQLKQNLFLVEVDEDFIRDEFNLIGLQTKVPHFKKLLKIILDEDDDDDDDDDDDYDDDDDEINRDSEEMYKN
KDMHEQNAACLYGLIHSRFILTSKGLALMREKYKSGIYGTCPSIYCENAKLLPTAISEIPKFLSPLLYCPRCCETYYPSK
NSLLNQLDGCYFGTSFASFFALSFNIASDKKKVYYTPQICGFTINRNIRETLYMDVNKDNTESSEECQ
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100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE

A0A2P9CB90 **A0A2P9CB90_9APIC** (387 aa)
Casein kinase II subunit beta (CK II beta). *Plasmodium sp. gorilla clade G2*

```
MEYVSNDESANDIIQDESNEGEIELTEAEFYDLTNINDKIDEEIIDDDEEEVNKDDQENDNVQVYNIDDDDNDVNNDVNN
DVLLLEKQRDNDVNEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDDDDDDDDDDDDDDDDDDDYDDEYDEDDFNEAT
VSWIEWFCQLKQNLFLVEVDEDFIRDEFNLIGLQTKVPHFKKLLKIILDEDDDDDDDDDDDYDDDDDEINRDSEEMYKNK
DMHEQNAACLYGLIHSRFILTSKGLALMREKYKSGIYGTCPSIYCENAKLLPTAISEIPKFLSPLLYCPRCCETYYPSKN
SLLNQLDGCYFGTSFASFFALSFNIASDKKKVYYTPQICGFTINRNIRETLYMDVNKDNTESSEECQ
```

95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE

105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE

A0A2P9CIJ1 **A0A2P9CIJ1_9APIC** (3060 aa)
Transmission-blocking target antigen s230. *Plasmodium sp. DRC-Itaito*

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MKKLLTLKNLFLIILLFILTKKKDVRCNIIKENNIKDDEDKRFHLFYYSHNFFKTPETKQKKKKKKKQLYKNVGISNLSK
EISIRKDTYVKTKQRTCPFDKEESSFEMGSRIITCYDPIIWKKERKYIYKTVIKKNVTNHQFVYSDINKEYKNDIKNVEE
KIQRDTYEKKDYENNDNLVVGYDDNFLLSFLKKCLMKIFSSPKKKKTVVQKKHKSNFFINSSLKYIYMYLTPSDSFNLVR
RNRNLDEEDMPPKDNFVIDDDEEEEEEEEEDEEEEEEEEEEEEEEEEEEEYDDYVYEQSVDETEEPLQQLQEEQQDEVA
VEGSEESSNDVGEDYVEGEDEDMIRVDGYYEDQFADTYDSKIKDEREDDAVDEYLDEYLDEYLDEYSDEYSDEYEKERES
QGETYSVDDEGEESFTYEKSDISKTDLFKFIEDSEGDDIYKVDSSKVLLEDDTTVSKVSKKSADVEGEEDEESVIKMIRN
VLQSSVLPSEGADEFDKIDLSFETTESGDTSVSEDSFDKYASNNTNKEYVCDFTDQLKPTESTPKVKKCEVKVDEPLIKV
KIICPLKGSVEKIYDNIEYIPKKSPYVVLTKEETKLKEHVLSKLIYGLIISPTVNEKENNFKEGVIEFTLPPMVKKPTVF
YFICDNSKTEDENKKGNRGIVEVSIEPYGNKINGCAFLDDDEEEEKYGDQGEVDENNDKIKLQRFFTQNIYKKNNIYPCY
MKLYSGDIGGIMFPKNIKSTTCFEEMIPYNKEIKWNKEKKSLTNLINNSVVYNKDMNAKYYNVQYVHIPTSYKDTLNLFC
SIILKEDESNLNLNSYLVYVSINEELNFSLLDFYESFVPIKKTIQAAQKNVNNKEHDYICDFTDKLDKSLAPLIEEKKLF
ICRKYLKEFDTFTLKCNVNKTQYPNIEIFPKNLKDKKEVLKLDLDIQYQMFSKFFKFNTENSKYLNLYPSYLMFPFNHIG
KKELKNNPIYKSHKDIKYFEQSSLLSPLSSSDSLGKLLNFIDTQETVSLTEKIRYLNISINELESDNNTFSLTLQVPPYI
DIKEPFYFMFGCNNNKGDGNIGVVELLISKHEEIIKGCNFHETKLDYFNNNVSSSKDECTLYGYENDIIGFNCSETNNAS
DEEEDGVEISLQPENCFNKVYKGLEIIDINTILNNAQVYNINNKKTPVFIKIPPHNLLEDTKLSCKCTIDHVVKNINVIL
TKNDKVLLKREIQNEFKLDDKIYTCEHENFINPRVNKIFDEKVEHTCNVKIEKFFNYIQILCPAKDLGIYKDIQIYYDII
KPTKVPEFKKFNNEELHKLIPNSEMLHKTKEMLILYNEEKVDLLHFYVFLPIYIKDNYEFNIVCDNSKTTWNNQIGGKVI
YHITVSKREQKVKGCSFNEEYTYMFIDNKSNVKNCVIDANPKDIIGFVCPSGTLKITSCFKDAIVNTNLTNINHILHLKN
NLANFTYKHYFNYMEVPALIDYDISFKCICVDLKKKKYNIKSPLGPKVLNAIYKKLNIKYDKYVTGTLQNKYLMTYMDLH
LSHKRNYIKELFNDLDKKKPADTDANPEAIIESLTINESNETTPFPTGDVDAEHLLLEGYDVWENLYDETLEDVIYKDIE
SLELKDIEQYILQVNLKAPKLMMSSQINNNRHVCDFSMKNLIVPDSLKKKKEEGGNNPIDIHCYALLKPLDTLYVKCPTS
KDNYEAAKVNISESDNEYELKVISLIEKRLQNFELLDSKRNGNGHAILTNGVVDPTSVILDSSIFEKYFKNIKIEPDKFF
EKVIKEVDDTEEEKELESILPGVIVSPMKVLKKKDPFTSYAGLVVPPVVSKDLHLKVKCNNTEYKDEDENILGYNGIVHI
EISSSDQKIKGCDFSTDDSSILTTSIKLVNGETKNCEININNNEFFGIICDNDTNLDPEECFNEIYDKDKSNVKKFHELI
PNIDIYTLPNSNKKKVAYAKIPLDYINKLSFSCSCKSSHNNTIGNMKVILNKDEKEEDEFKTSLSIKHNNINLCNFFDNT
ELTFDNNKIILCKIDAELFSEVIIQLPLFGNNKTLEGDQNEEYKKFSLKPLLPINEDDNDIKVIGKEKNEISINLALKGV
YGNRTFKFEKDGKKGEGISFFIPPTKIDTDLKFIINETIDNSNIKQRGLIYIFVRKNVKENTLKLCDFTTGSTSLMELNS
QMKEKKCNIKIKKGDIFGIKCPKGFAIFPQACFSNVLLEYYKSNHTDNEDINYYIHKDIKYNLKPKYVIELMDENFRELK
NIQQYTGISNITDMLHFTNYNLGNLPLNYKNNYSTAYAKVPDNFNSIINFSCNCYNPEKHVYGTMQVESDNTNFDNIKKN
ENIKKNVLLPTIDKFPLLLDDEQRQKFKLKLKLRDADDIFNTDDINHIYMLYNSNEHICDYQKNETLISNIPSDNKKIQK
STCKINAKSLDVVTIKCPHTKNFTPKDLLDNSTLQSNDKKIVITFDKKTFVTYIDPTKKTFSLKDIYIQSFYGVTLDHLN
KIKKIQQDWDDEHLFYPPHNVLHNVVVNNHIVKLSSALEGVLFIKSKVTGDETNTKKNTTLPTDGVSSILIPPYVKEDIT
FHIFCGKSTTKKPNKNNTSLALIHIHIASNTNIIHGCDFIYLEKNTSVTSTVNNTSTIFTHNKNKENNLICDISLVPQTV
IGINCPNKKINPPTCFDEIYYVKEEDVPPKTITADKYNTFTKDKITNILKNAISITNPDEKDNTYSYLILPDKFEEQLID
TKKVLACTCDNKYMIHMKIEKNTIEKIKNDEKKTIGKDICKYDVTTKVATCDIIDVIDSSSIKEHHTVNYSVTLSRWDKL
IIKYPTNEKTHFEKLFVNPSNLKDKVLYNYTNPINIEHILPGAITTDLYDTRTKLKQYILRIPPYVHKDIHFSLQFNNTL
SSTKQNQNVIYGNVANIFIHINQGYKEIHGCDFTGKYSHLFTYSKKPLPNDNDTCNVTITNNTFSGFACLSHFELKPDNC
FSSVYDNNEANKVKKLFDLSTNVELDHIKQNTSGYTLSYIIFKKESNKLKFSCTCSSHYSNYTIQITFDPNYITPEPQSR
AIIKYVDLQDKNFGKYLRKH
```

272 - 291:	EEEEEEEEEEEEEEEEEEEE

A0A2P9CT37 **A0A2P9CT37_9APIC** (1962 aa)
Uncharacterized protein. *Plasmodium sp. DRC-Itaito*

```
MNVCKMKVQQKKNLKDCNLKSKNTILTNYEKKKIENDEKDSLKFSKLSDNKNKVVNSKFLKNDNYKLNERKESLTRCSTN
ESLKLKNIKTTTKDNNNDNIDNIGNCKLIFKKNDRDIESTVIEEDGKKIEKKTNDFINNKNEYRVNNKSILKSKDSKSNN
NNNDNNGNNNNNIYNNINICKLKSIDDKNKKQQTDTYSQKENVEDTSNNMKKNSSLKNIKKNQLNEKEIISNTVEEKKNN
THSKGDKENNMVVTKNVKKMNSVSKDINNKNNNSKKDVLKSKKSEKLKDKLINNVSGKKSVNKENEIIQSSSGRRSSSRY
SIDYGRRESSRRGSIKEEKGKERRGSKNVSKKVSKSKYTRKKSKRINDESDESDDDDDDEEEDDEEEEEEEEEEEEEEE
EEEEEEDEEDDEEDNEDNDDDDNNDNNDNSDNSDNSDNNDEESDDVYTNRSRRSTRCSIVKRKSVRSIGKRESKIIKKST
SKTKNNKKKKGSVIKLVKKKGKVSKKEILKKKNKKKTKSKLKKNSKVYQKKKNIKNEKNDMDEEELEEELEEEEVEPSYF
DEYNLSIEERKKDLEEKEKKREIKENYIKQIKLPKYADDESIIFINNPNYVMVLLFLTVYKDVLKMNWNFKDIEEMFQNK
ETTEFGRNFILKLFFFLGRYFNSKSIFMYKYISRIFEDKEESLSRVVNFHELFPILEMKKEMKNSGVGSKRKKDKRGKKM
KMHQKEDELLYDEEAIGNEDVNIFEEEEEEDDDEEENEHFNDDEEEEEEENDGNYNDDEKEHGSYNDEDEEEKKSACNND
STKNTVIKEEKDGLNISESSHNKVNIKNDNMKREESCPNGSNGPNEKVKDFHINDNINDEHNNNNNNNQVVDIKNNIENE
VNNTVETSKDINNNEGIIKSENVDDEKGLSNKLFLEWDDLSVTSKLRIIRMLLNLVLCESTNLKKMLGDEKLNYNNGYLG
KVKNEKYWFIFNDTINIEYKLYLEREEEGSFIFICDDDDMLYTIGYNFLRNSDTKFMGEALIERYNKVCRERRNRSRMLK
QQKKLLCADVNMNDPLFGTKKRQTKQVEYFNFDNNEKMRRKKSDISNNPYSVPPTKSYQKNDRSFRLAARNAQKGSVDDL
EAWKLNEGLMGVENQGSISGNYNIGYDGNNMVDTSNRNDNINNNNNNTNVLVGADGNNIYGVNNNNVVGSDGNIIMNNNN
INNNNNNNNNNNLGTVKIPLKRGRKKKSEKKKRGRKKKILSLDGIGDLTNNLSGVGVDENRRKTIGAPGRVKRGTYTKRN
TKPSISIKYGTRSNSINKYENDVMSFNDYTLNPGLSMDEFYKNMIMDPKFFHANMSMNNYMNGGFNIPNNNNNTSNTNNN
NNNNNNISMMNMRNGSKMGGAMNNLGGYNFPYMCTPPPMFNQYYMYNGSNMYLPTSATNNNMNISNTNNGSAAVVGNVLS
NQNSVKDMKGENILMSKNNIMENRNSVLLNSMNNINMNNMAHKNSLIGNDGINMMNNNNNSNNNNVNNVNFMDNIGTNNN
NNNSNNNSNNNNNNSSNNNSSNNPMNKFNNYMMNRNVLNNMGGTNPIYNHMYNMKFPYMNNEMMNYNYNINSFQNMNYDK
INKSMFKRYPNFMSGYPYNNMNPYNNFNAFNMNYQQNEQLNQLSNMQGAYKGKLMNDNLSSFQLYNNNNNNNNTKQNNND
NNNNNNNIEGGNNNIDDGNKNNDINKNDIIDNSKHNEQPVGGIAPNNDCINRGEDNQKMDLKGDTVEALVGNNNDKMNNS
DTNLNSLKNLGNINSPYNMDNISQMRNSVGGSSMGMINPGHMNSSHGGSIMNKDKLRDLQMNNNNNNNNNNNSNNNNNN
NNNNNNNNNNNNNNSNYLKANPLDHPMKNMNNNSMDDKYTKDNNNNNNNNNNNNNMMMMMMNSVYNIMGTDNFHMNNSHM
MDPMGTSKMNENIYNHNNNINFENNTNHNNNNNNRIQDKLPE
```

386 - 405:	EEEEEEEEEEEEEEEEEEEE
387 - 406:	EEEEEEEEEEEEEEEEEEEE

A0A2P9CUG0 **A0A2P9CUG0_9APIC** (393 aa)
Casein kinase II subunit beta (CK II beta). *Plasmodium sp. DRC-Itaito*

```
MEYVSNDESANDIIQDESNEGEIELTEAEFYDLTNINDKIDEEIIDDDEEEVNKDDQENDNVQEVYNIDDDDNGVNNDVN
DDVNNDVNNDVLLLEQQRDNDVNEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDDDDDDDDDDDDDDDDDDYDDEYDED
```

```
DFNEATVSWIEWFCQLKQNLFLVEVDEDFIRDEFNLIGLQTKVPHFKKLLKIILDEDDDDDDDDDDDYDDDDDEINRDSE
EMYKNKDMHEQNAACLYGLIHSRFILTSKGLALMREKYKSGIYGTCPSIYCENAKLLPTAISEIPKFLSPLLYCPRCCET
YYPSKNSLLNQLDGCYFGTSFASFFALSFNIASDKKKVYYTPQICGFTINRNIRETLYMDVNKDNTESSEECQ
```

104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE

A0A2P9CY58 **A0A2P9CY58_9APIC** (3096 aa)
Transmission-blocking target antigen s230. *Plasmodium sp. gorilla clade G3*

```
MKKVITLKNLFIIILAYILTEKKDLRCNVIKENNIKDDEDKRFHLFYYSYNFLKTPETIQKKKKYFYKNVGIYNFSKEIT
IRNDTYVNKKQRTCPFDKEKSSFEMSSKNIISFEPIIREKERITMDKTVIKKNVSIDNFVSSDMHSSVQEKNMILIRNIY
KENKNYIKNIEEKIQRDTHENVDYESNDKLIVWFNENTNEENFLLTFLKKCLMKIFSSHKKKKTVVQKKHKSNFFINSSL
KYIYMYLTPSDSFNLVRRHRNLDEEDMSPRDDFVIDDDEEEEEEEEEEEEEEEEEEEEEEEYDDYVYEQSEDETEEQL
QEQQQEEVAVEPSEEISNDVDEEYVEAEDGDMIKIDEYYEDQEGDTYDSTIKDENEDEDEEGGEAEYEDSYEDEKEKEIQ
AEIYSVDDEEVRDEGAESFTYEKSEIDKTDLFKFIEGNEGDDVYKVDSSKVLLDDDTVSRVYKKHAEEEGGDEEEGGDEE
GGRDAEEGRDAEEGRDAEEGGDEGKGGDGEDEKSVTKMIRSVLQSSVLPSEGADELDKIDLSYETTESGDTNVAEDSYDK
YASNNTNKEYVCDFTDQLKPTESTPKIKKCELKVNEPLIKVKIICPLKGSVEKIYDNIEYIPKKSPYVVLIKEETKLKEN
LLSKLIYGLLISPTVNEKENNFKEGIIEFTLPPMVKKPAVFYFICDNSKTEDENKKGNRGIVEVSVEPYGNKINGCAFLD
DDEEEEKYGDQDEEDEQNEKIKMKKFFTQNIYKKNNIYPCYIKLYSGDIGGIMFPKNIKSTTCFEEMIPYNKEIKWNKEK
KSLTNLVNNSVVYNKDMNAKYFNIQYVHIPTSYKDTLNLFCTIILKEDESNLSSKSYLIYVSINEELNFSILDFYESFAP
IKKTIQVAQKNVNNKENDYTCDFTDKLDKSVPSIADGKKLFICRKHLKEFDTFTLKCNVNKTQYPNIEIFPKTLKDKKEV
LKLDLDIQYQMFSKFFKFNTENSKYLNLYPSYLIFPFNHIGKKELKNNPIYKNHRDVKYFEQSSLLSPLSSSDSLGKLLN
FLDTQETVSITEKIKSLNITINELESDNNTFSVTFQVPPYIEINEPFYFMFGCNNNKGEGNIGIVELLISKHEEKIKGCN
FHESKLDYFHMNVDDNTNECTLHAYENDIIGFNCLETTHSDEEEDRTEISLQPENCFNNVYKGLNSVDISTILKNAETYN
IKNKKTPVFLKIPHYNLLEDVEISCKCTIEQVVKKIKVVIMKSDIVLLKREVQSEFIQDEKIYKCEHENFINPRVNKTFD
ENVEYTCDVKVENFFNYIQILCPAKDLGIYKNIQMYYDIIKPTRVPQYKKFNDQELHKLIPNSEMLHKTKEMLILYNEEK
VDLLHFYLFLPVYIKDIYEFNIVCDNSKTVWKNQLGGKVIYHITASKREQKVKGCSFNDEHTNMFIDNKSNVKNCVIDAK
PKDIIGFVCPSGTLKITNCFKDAIVHTNLTNINRILYLKNNLANFTYKHHFNYMEIPALMDNDISFKCICVDLKKKKYNI
KSPLGPKILNALYKKLNIRYDKYVTGINENKYLMTYMDLHLSHKRDYLNELFNDLNKKKPGDTDANPESIIESLSINESN
ESGPFPTGDVDGEHLLLEGYDTWESLYDEKLEDDIYKDIESLELKDIEQYVLQVNLKAPKLMMSAQINDNRHVCDLSNNN
LIVPESLKKKEVSGNPIDIHCYALLKPLDTLYVKCPTSKDNYEAAKVNISESDNEYELQVISLIEKRFHNFETLDSNRLV
NGDTVHNGVVDTASALDNSTFEKYFKNIKIKPDKFFEKVINEIDDKEEEKDLESILPGVIVSPMKILKKKDPFTSYAALV
VPPVVSKDLHLKVECNNTEYKDENQYIGGYNGIIHIDISNSDKKINGCDFSTDNSSILTSSVELVNGETKNCEININNNE
VFGIICDNETNLDPEKCFYEIYDKDKSNVKKFHELIPNIDIFALHNSNKKKVAYAKIPLDYINKLVFSCSCKASHNNTIG
NMKVILNKDEKEEEEFKKSIGIKHNNVHLCNFFDNPELTFDNNKIILCKIDAELFSEVIIQLPLFGTKNVEGVQDEQYKK
FSLKPSLDINENDIKVIGKEKNEISISLALKGVYGNRTFTFDKNGKKGEGISFFIPPTKQDTDLKFIINETIDNSNIKQR
GLIYIFVRKNVPENAFKLCDFTTGSTSLMELNSQMKEKKCTVKIKKGDIFGIKCPKGFAIFPQACFSNVLLEYYKSDYTD
SEHINYYIHKDKKYNLKPKDVIELMDENFRELQNIQQYTGISNITDMLHFKNFNLGNLPLNYKNHYSTAYAKVPDTFNSI
INFSCNCYNPEKHVYGTMQVESDNRNFDNIKKNENLIKNFLLPNIEKYPLLDDDQKAKQILKDQNDTLNTNHDNNNNNNN
NNYIYMLYDSNEHICDYEKNESLISTLPNDTKKIQKSICKINAKALDVVTIKCPHTKNFTPKDYFANSSLTTNDKKIVIT
FDKKNYVTYIDPTKKTFSLKDIYIQSFYGVTLDHISQLKKIQEEWDDVHVFYPPHNVLHNVVLNNHIVKLSSALEGVLFI
KSKVTGDDTGTKKNTTLPTDGVSSILIPPYVKEDITFHIFCGKSTTKKPNKNNTSLAVIHIHISSNRNIIHGCDFIYLQN
HTSDGIQNNAFSTIFTHNKNTENNLICDISLVPQTVIGINCPNKKISPQTCFDEVYYVKEDDVPPKTITADKYNTFTKDK
IGNILKNAVSITNPDEKDNTYSYLILPEKFEEELIDTKKVLACTCDNKYIIHMKIEKSTMDKIKSDEKKTFGKDICKYDV
ATKVATCEIIDAIDSSSLKEHHTVHYAVTLSRWDKLIIKYPTNEKTHFEKFFVNPFNLKDKVLYNYNKPINIEHILPGAI
TTDIYDTRTKIKQYILRIPPYVHKDIHFSLEFNNSLSSSKQNQNIIYGNIAKIFIHINQGYKEIHGCDFTGKYSHLFTYS
KKPVPNDSDICNVTIGNNTFSGFACLSHFELKPDNCFSSIYDNNEANKVKKLFDLSTKVELDHIKQNTSGYTLSYIIFNN
ESTKLKFSCTCSSHYSNYTIRITFDPNYITSEPQSRAIIKYVDLQDKHFGKYLRKH
```

279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE

A0A2P9CZY3 **A0A2P9CZY3_9APIC** (1722 aa)
Structural maintenance of chromosomes protein 4. *Plasmodium sp. gorilla clade G3*

```
MTDDMNMNEKIIINEEENGENMNMLSIISNDKIDDKENNIHNDDSGKNNILCLKDVKVNRKRIIIEKLVLENFKSYSGVK
VIGPFYKKFSCIVGPNGSGKSNIIDAMLFVFGRRAKKIRQNKLSDLIHNSKFSVKNNFTKVSIHFKTITDEEEPIVEEEF
YYDEYDDEDDYDDDGDDDDDDDDDGGDDDGGDNEEEDYEEDYDENYDDDNSNDNNHYDVNKSEKENNNNEEEEKYYSGGE
EDNKLHNRRNNIEKTNKISNNVSNKKKKKRRKRKKRKRKRFLFRNTENPLYQHYYHDGDDIEDFVISREATIDNQSKYRI
NEKVVTQKDVSDLLYKKGIDLNNNRFLILQGEVEQIAQMNPKGNKNEDGLLEYLEEIIGTNKYIESINEHLEKLERCEEI
HHEKVHRLKHVYNELKELAGPKKEAKYYMTLQKYTYKLHIIINKKDQYELSKMINDKEKELNMFLNKRNNHDMEYKQLLE
TRKEMNISLSNLEKEEEEVMKKKNFKNNEFKKLNIEDENIKKELLIIIQKMQNLYVKREELKEKDIPSYKKIIEEKQKII
NEIKKEKMHLLEDELEKCEEELENYNEEIKQDIDKMNTIYSNEEKKLAPLQNSYDNIIKNISEYTNQCHIIEKKKKEYLT
HIENLKYLQAKIINELKEKDIHTKYLTKTEEEKRKNLKNKQNDLDDIENKIQKLNTNLIDETIKYENIKKEVVTDRNMNK
LHQFIYNLKRSKIKGIHGMLIDLGYIEKKYEKAFTIASNNCSDFVVVENPNDAVQLFEEVRKANIGRVNVLSLSILNKNL
MTIMLKNEEMYTQLLPNVYRLIDLIKFKNDKYKICFYYIIKETLLTNSLEQAHVIAYSHKKRVVTINGELIENDGRICGG
```

```
GMENKNVKANDGNSGRTINSSRTSTNNKNSNNNNNYNSGSSIKTSEYDESHLLNSEKIIKELNKNIQDKKKQKDILINDI
KDINTFLEDNECKIVIAKKKMDNLKKQLEDIDDQLQNSKIPELTKEEENELNTLKNLIEEKNNEKSKVEIVLKAQETKVK
KYYEQLQDVGGEKKKKLKNKFINAERQLNIMKDQLQEHTNDEANALASLEKSEKDIRMFSENILEYEANEKELENELKII
ENKGCAVYEEVETLTKLLNDIQSNIEEKQKKKQQVDENISKKDLENVDLVYKIEHLQKELNQYKNKNENYQNKIDEYMDL
IKQSDKVIHENMLSEMRCRRLLGKKKKINKDQEDQSTREDIKMDEHDGKDQQMDDDYDGLGEEEEEEEEEEEEEEEEEE
EEEEEEEEEVEEEEQQEEQQQQEEQEEEQQEEQQQQEEQEEEQEEEEQDMQEEATRKKNIHGHYQPYDDIKGYDQNDQYH
KLEKQIILPNGRNNHVNVTRNNHMNQDKSTLYLLHMDKNKKRKLNENDTTTKCPEKKKVKKKKKLFDDLKDLEELFGDSD
ELKELEHEYDHININDTDLDMLNKKDIETKLENKLSILEKKTPNLKIFQDYNLKLYDYKVRRKDVKKSKKEKDKIKAAYD
SLCNKRKEEFVVAFNVISSKLKEMYQMIAIGGDAELEIIDSSEIFNEGILFSVRPPKKSWKHIQNLSGGEKTLSSLALVF
ALHYFKPNPIYFMDEIDAALDFKNVSIISHYIQTKTRNAQFIVISLRNQMFELCDRMIGIYKTNDITKCITLNPHQCTML
KIPNIKLKRKSKLEKNIKYENTDENEKHLAITNEMGNVKKLL
```

1262 - 1281:	EEEEEEEEEEEEEEEEEEEE
1263 - 1282:	EEEEEEEEEEEEEEEEEEEE
1264 - 1283:	EEEEEEEEEEEEEEEEEEEE
1265 - 1284:	EEEEEEEEEEEEEEEEEEEE
1266 - 1285:	EEEEEEEEEEEEEEEEEEEE
1267 - 1286:	EEEEEEEEEEEEEEEEEEEE
1268 - 1287:	EEEEEEEEEEEEEEEEEEEE
1269 - 1288:	EEEEEEEEEEEEEEEEEEEE
1270 - 1289:	EEEEEEEEEEEEEEEEEEEE

A0A2P9D316 **A0A2P9D316_PLARE** (3081 aa)
Transmission-blocking target antigen s230. *Plasmodium reichenowi*

```
MKKIITLKNLFLIILVYIFIEKKDLRCNVIKGNNIKDDEDKRLHLFYYSHNLFKTPERKEKKNKKEYVSKNGDIYNLSKE
ITMRKDTSVKIKQRTCPFHKEGSSFEMGSKNITCFYPIVGKKERKTLDTIIIKKNVTNDHFVSSNMHSNVQEKNMILIRN
IDKENKNDIQNVEEKIQRDTYENEDYESDDKLIEWFDDNTNEENFLLTFLKRCLMKIFPSPKKKKTVVQKKHKSNFFINS
SLKYIYMYLTPSDSFNLVRRNRNLDEEDMSPRDNFVIDDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEYDDYVYEESR
DETEEPLQEEQHEEVAAESSEESFNDEEEDYVETQDGDMIRVDEYYEDQDSDTYDSTIKNEDADEEVGEEEGEYVDTYED
EKESQGEIYRVGDEEEKDEGGESVTYEKSDIDKTDLFKFIEGGEGDDVYKVDSSKLLLDDDTISRVSKKHAVRDGEEGED
VEEGEDVEEGEDEESVIKIIRSVLQSGALPSVGVDEVDKIDLSYETTESGDTAVSEDSYDKYASNNTNKEYVCDFTDQLK
PTESSPKVKKCELKVNEPLIKVKIICPLKGSVEKLYDNIEYAPKKSPYVVLTKEETKLKENLLSKLIYGLLISPTVNEKE
NNFKEGVIEFTLPPVVQKTTVFYFICDNSKTEDDSKKGNRGIVEVHVEPYGNKINGCAFLDEDEEEEEKYGDQVVEDEHN
EKIKMKTFFTQNIYKKNIIYPCYMKLYSGDVGGIMFPKNIKSTTCFEEMIPYNKEIKWNKEKKSLTNLVNNSVIYNKEMN
AKYFNVQYVHIPTSYKDTLNLFCTIILKDEESNLNSNSYLVYVSINEELNFSLLDFYESFVPIKKTIQVAQKNGNNKEHD
YTCDFTDKLDKTIPSTVDGKKLFICRKHLKEFDTFTLKCNVNKIQYPNMEIFPKTLKDKKEVLKLDLDIQYNMFSKFYKF
NTENSKYLNLYPYYLIFPFNHIGKKELKNNPTYKNHKDVKYFEQSSILSPLSSSDSLGKLLNFLDTQETVCLTEKIRYLN
LTINELESDNNTFSVTFQVPPYIDIKEPFYFMFGCNNNKGEGNIGIVELLISKQEEKIKGCNFHKSKLDYFSKNISSDTD
ECTLHAYENDIIGFNCLETTHSNEAESDDGTEISLQPENCFNNVYKGLNSVDITTILKNAQTYNINNKKTPTFLKIPQYN
LLEDVEISCKCTIDHVVKKIKVIITKSDTVLLKREVQSESTLDDKIYKCEHENFINPRVNKTFDQNVEYTCNIKIENFFN
YIQIFCPAKDLGIYKNIQMYYDTIKPTRVPQFKKFNNEELHKLIPNSEMLHKTKEMLILYNEEKVDLLHFYVFLPIYIKD
IYEFNIVCDNSKSTWKNQLGGKVIYHITVSRREQKVKGCSFNDEHAHMFSDNKTNVKNCIIDAKPKDIIGFVCPSGTLKL
TNCFKDAIIHSNLTNINHILYLKNNLANFTYKHQFNYMEIPTLMDNDISFKCICVDLKKKKYNIKSPLGPKVLRALYKKL
NIKFDKYVTGTDQNTYLMTYMDLYLSHKRNYLNELFNDLDKKKPAETDSNPESIIESLSINESNESGPFPTGDVDAEHLI
LEGYDTWESLYDEQLEEIIYNDIESLELKDIEQYVLQVNLKAPKLMMSAKINKNKHVCDFSRNNLIVPESLKKKEELGSN
PVSIHCYALLKPLDILYVKCPTSKDNYEAAKANISESDNEYELQVISLIEKKFHNFEVLDSKNPGNGDVAHNGVVDTGPV
LDNSTFEKYFKNIKIKPDKFFEKIIIKTDDTEEEKDFESILPGVIVSPMKILKKKDPFTSYAALVVPPIVPKDLHLKVEC
NNTEYKDENQYISGYNGIIHIDISNSDKKINGCDFSTNNSSILTSSVELVNGETKNCEININNNEIFGIICDNETNLDPE
KCFHEIYDKDNINVKKFREVIPNIDIFSLHNSNKKKVAYAKIPLDYINKLSFSCSCKTSHTNTIGTMKVTLNKDEKEEED
FKTAQGIKHNNVHLCNFFDNPELTFDNNKIVLCKIDAELFSEVIIQLPIFGTKKVEGVQDEQYKKFSLKPSLVFDDNDND
IRVIGKEKNEVSISSALKGVYGNRIFTFDKNGKKGEGISFFIPPTKVDTDLKIIINETIDNSNIKQRGLIYIFVRKNVSE
NSFKLCDFTTGSTSLMELNSQVKEKKCSVKIKKGDIFGLKCPKGFAIFPQACFSNVLLEYYKSDYADSQHINYYIHKDKK
YNLKPKDVIELMDENFRELQNIQQYTGISNITDMLHFKNFNLGNLPLNFKNHYSTAYAKVPDTFNSIITFSCHCYNPEKH
VYGTMQVESDNRNIDNINKNENIIKNFLLPNIEKYALLLDDEEREKKQKNLKDQDETLTTHDDDFNKNHIYMLYDSNEHI
CDYEKNESLISTLPNDTKKIQKSICKINAKALDVVTIKCPHTKNFTPKDYFSNSSLTTNDKKIVITFDKKNFVTYFDPTK
KTFSLKDIYVQSFYGVTLDHLNQIKKIQEEWDDVHLFYPPHNVLHNVVLNNHIVKLSSALEGVLYMKSKVTTDETSTKKN
TTLPSDGVSSILIPPYVKEDMTFHIFCGKSTTKKPNKNNTSLALIHIHISANRNIIHGCDFLYLEKHTNDSINNNSYSIF
THNKNTENNLICDISLIPKTVIGIKCPNKKLSPQTCFDEVYYVKEDDVPSKTITADKYNTFSKDKIENILKNAISINNPD
QNDNTYTYLILPEIFEEELIDIKKVLACTCDNKYIIHMKIEKSTMDKIKIDEKKTIGKDICKYDVATKVATCEIIDTIDS
STLKEHHTVHYSITLSRWDKLIIKYPTNEKTHFEKFFVNPFNLKDKVLYNYNKPINIEHILPGAITTDIYDTRTKIKQYI
LRIPPYVHKDIHFSLEFNNSLSLTKQNQNIIYGNVAKIFIHINQGYKEIHGCDFTGKYSHLFTYSKKPLPNDQDICNVTI
GNNTFSGFACLSHFELKPNNCFSSIYDHNEANKVKKLFDLSTNVELDHIKQNTSGYTLSYIIFNKESTKLKFSCTCSSNY
SNYTIQITFDPNYITPEPQSRAIIKYVDLKDKNFAKYLRKP
```

280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE
287 - 306:	EEEEEEEEEEEEEEEEEEEE
288 - 307:	EEEEEEEEEEEEEEEEEEEE
289 - 308:	EEEEEEEEEEEEEEEEEEEE
290 - 309:	EEEEEEEEEEEEEEEEEEEE
291 - 310:	EEEEEEEEEEEEEEEEEEEE

A0A2P9DFK4 **A0A2P9DFK4_9APIC** (403 aa)
Uncharacterized protein. *Plasmodium sp. gorilla clade G3*

```
MSDYFTILSNILTSTSLKKKYSSKLNTKSRKNQKRVKLIRLRNGHFRRIVDISNIEEKSIFPRSCTFASISSASNEHERK
NSTEDTKEPEEYLYGKSNTSSSITIKINFDESDENKSVQDNHSIDTISDISFTQTSRKSMDIESNTYESYREVEKEEIEE
EDEEEEEEEEEEEEEEEEEEEEEKEVEEEEEEEEEEEEKEEEDEEDEEDEGLKTEEEKEDEDKEAQPEEELKEEEKEIEE
KKEDEEEKILEAPSKTLMKGVKTNIYFLSTKERIEALMCYNYISNAIIFEKGKFLRYIFMNNVNNIIVNEHMINMLCKKE
KIKYVLSSNSIIIESNDFIKPLIIEFDSNISKKIFVKHLKMVDSFKLDDKLYRKYLNDLSEHERDRLKHVESFYSNAIKV
HNT
```

163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE

A0A2P9DIT9 **A0A2P9DIT9_PLARE** (2012 aa)
Uncharacterized protein. *Plasmodium reichenowi*

```
MNVCKMKVQQKKNLKDCNLKSKNTILTSFEKKKNEKDENNLLKFAKLIDNKNKVVNSKFLKNDNYKCNERKESLTRCSTN
ESLKLKNMKTLTKDFDYNNNNDDYNNNNDDYNNNNDDYNNNNDDYNNNNDDYNNNINNNNNNNNNNNNNNGHSKLVFKKK
SKDIESTVIEENEKKSEKKTNDLINNKNEFKVNNKLILKSKEFKSNNNNNNNNNNNNNNNICKLKNVDDKNKKQQMDTYS
PKENEEDNSNNMKKNSCLKNIKKNQINEKEIIPNTVEEKHDTHSKGDKEHNGVSTKNVKRMNTMSKEINHKNNNILKKNL
SKSNSLELKKGKKGDKLKDKLINNLSGKKGMNKEKEVVQSSSAKRSSSRYSIDYGRRDSSRRGSAKQEKGKERRASKNVS
KKVSKSKYTRKKSKRIKEESDESDDDDEEEEEDDDDDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
DNENNNSDNNDESDEVYTNRSRRSTRCSIVKRKSSLCIGKKNSKIIKKSTSKTKNNKKKKGSVIKLEKKKEKLSKKGILK
KKNKKTKGKLRKNSKVYHRKKNIKNEKVGIDEEDIEEEIEEEEEPSYFDEYNLSIEERKKDLEEKEKKKEIKEKYIKQIK
LPKYADDESIIFINNPNYVMVLLFLTVYKDVLKMNWNFKDIEDMFQNKETTEFGRNFILKLFFFLGRYFNSKSIFMYKYI
SRIFEDKEESLSRVVNFHELFPVLETKKEIKNSGVGSKRKKDKRGKKMKIHQKEDELLYDEEVIGNEDVNIFEEEEEDDE
EEDDDEEDNEHSNDDEDEEEEDNEHYNDDEEKENVNYKDEEEKKSDMNNDSTKNTVIKEEKDGLHISESNHNLVNIVNDS
MKREESCKNGHVVDNERSADFKINDDKNNEDNNDDGDKIVDSKNNIENKLDKSVDGMKDINSTEGIIKNENVDDEKGLTN
KLFLEWDDLSVISKLRIIRMLLNLVLCESNNLKKMLGDEKLNYNNGYLGKINNEKYWFIFNDTINIEYKLYLEREEEGSF
IFICDDDDMLYTIGYNFLRNSDTKFMGEALIERYNKVCRERRNRSRMLKQQKKLLCSDINLNDPLLGTKKRQPKQVEYFN
FNNNEKIRRKKSDINNNNNNPYSVPLTKSYQKNDRSFRLAARNAQKGSVDDLEAWKLNEGLLGIENEGGISGNYNIENDG
NNMVETNNINDNNNDNNKKNNNNNNNNNNNNNVVVKADGNNIYGPNNNNVIGSDGNMNNGNNTTTTNNNNNNNNLGTVKVP
LKRGRKKKSEKKKRGRKKKILSVDGIGDVGNNLSSLNVDENRRKSMPNIGRGRRGTYTKRNTKPSVSIKYGTRSNSINKY
ENDVMSFNEYSLNPGLSMDDFYKNMVMDAKFFHGNMSMNNYMNGGFNMPNNNNSMMNMRNGSKMGNINNLGGYNFPYMCT
PPPPMYNQYYMYNGNNMYLPNGGAINNMNMSNTNNSASVGIGGNVVSNQNTVKDVKTENMNMAKNSIMENRNSISVNSMN
NINMNNMPHKNSFLGNDGINNMNSMMNNNNNNNVSNNNNNNNNNNNNVNFMDNMGNNNNSNNNSNNSNNPMNKYNNYMMN
RNALNNMGGTNPMYNNMYNMKFPYMNNDMMNYNYNINTFQNMNYDKMNKSMFKRYPNFMGGYPYNNMNPYNNFNAFNMNY
QQNDQMNQLPNMQGAYKSKLMNDNLSNYQSFNNNNIKQNHHDNNNNNNNDNNNNINKNNSECGNKNVDDSNKNNDINKND
ILDSTKFTEQAVGGVALNNDCTTRGEDNHRIDLKGDVVEALVGNNNEKMNSSDHNLNSLKNLQNINSTYNMDHMSHMRNS
VSGSSIGMINPGHMNSSHSGSIMNKDKFRDLQLNNNNNNNNNNNNNNNNNNYVKVNPFDHPMKNMNQNLMDDKYPKDNNM
MMMMMNSVYNIMGSDHFHMNNSHMMDPMGSPKMNDNMYNHNNMNFENTNTNHNNHNNHNNHNNHNNHNNHNNHNNHNHN
NHNNRIQDKLPE
```

438 - 457:	EEEEEEEEEEEEEEEEEEEE
439 - 458:	EEEEEEEEEEEEEEEEEEEE
440 - 459:	EEEEEEEEEEEEEEEEEEEE
441 - 460:	EEEEEEEEEEEEEEEEEEEE
442 - 461:	EEEEEEEEEEEEEEEEEEEE
443 - 462:	EEEEEEEEEEEEEEEEEEEE
444 - 463:	EEEEEEEEEEEEEEEEEEEE
445 - 464:	EEEEEEEEEEEEEEEEEEEE
446 - 465:	EEEEEEEEEEEEEEEEEEEE
447 - 466:	EEEEEEEEEEEEEEEEEEEE
448 - 467:	EEEEEEEEEEEEEEEEEEEE
449 - 468:	EEEEEEEEEEEEEEEEEEEE
450 - 469:	EEEEEEEEEEEEEEEEEEEE
451 - 470:	EEEEEEEEEEEEEEEEEEEE
452 - 471:	EEEEEEEEEEEEEEEEEEEE
453 - 472:	EEEEEEEEEEEEEEEEEEEE
454 - 473:	EEEEEEEEEEEEEEEEEEEE
455 - 474:	EEEEEEEEEEEEEEEEEEEE
456 - 475:	EEEEEEEEEEEEEEEEEEEE
457 - 476:	EEEEEEEEEEEEEEEEEEEE
458 - 477:	EEEEEEEEEEEEEEEEEEEE
459 - 478:	EEEEEEEEEEEEEEEEEEEE
460 - 479:	EEEEEEEEEEEEEEEEEEEE
461 - 480:	EEEEEEEEEEEEEEEEEEEE

A0A2P9DLG7 **A0A2P9DLG7_9APIC** (388 aa)

Casein kinase II subunit beta (CK II beta). *Plasmodium sp. gorilla clade G3*

```
MEFVSNDESANDIIQDESNEGEVELTEADFYDLTIINDKINEEIDEEIIDDEEEEANKDDQENDNVQEVYNIDDEDNDVH
NDKLLLDQQRDNDVNEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDDDDDDDDDDDDDDDDDYDDEYDEDDFNE
ATVSWIEWFCQLKQNLFLVEVDEDFIRDEFNLIGLQTKVPHFKKLLRIILDEDDDDDDDDDDDYDDDDDEINRDSEEMYK
NKDMHEQNAACLYGLIHSRFILTSKGLALMREKYKSGIYGTCPSIYCENAKLLPTAISEIPKFLSPLLYCPRCCETYYPS
KNSLLNQLDGCYFGTSFASFFALSFNIASDKKKVYYTPQICGFTINRNIRETLYMDVNKDNTESSEEF
```

96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE

A0A2P9DM10 **A0A2P9DM10_PLARE** (381 aa)
Casein kinase II subunit beta (CK II beta). *Plasmodium reichenowi*

```
MEFVSNDESADDIIQDESNEGEVELTDADFYDLTVINDKIDEEIIEDDEEEADMDDQENDNVQEVYNIDDDDNDIHNDKL
LLDQQRDNDVNEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEDDDDDDDDDDDDDDDDDYDDEYDEDDFNEATVSWIEW
FCQLKQNLFLVEVDEDFIRDEFNLIGLQTKVPHFKKLLKIILDEDDDDDDDDDDDYDDDDDEINRDSEEMYKNKDMHEQN
AACLYGLIHSRFILTSKGLALMREKYKSGIYGTCPSIYCENAKLLPTAISEIPKFLSPLLYCPRCCETYYPSKNSLLNQL
DGSYFGTSFASFFALSFNIASDKKKVYYTPQICGFTINRNIRETLYMDVNKDHTESSEEYQ
```

92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE

A0A2P9DRH2 **A0A2P9DRH2_PLARE** (6062 aa)
Cysteine repeat modular protein 4. *Plasmodium reichenowi*

```
MKNITFLVSFLIFLRSINANISITNFTYTNQKGDIKVEFFQTDYIAIFKLPFGGNDEQIFEISDDYIITNDKETNNCNIP
NNNFGFVYSKSNSQNKFLIVQREYTTIYIKDKNNNCSLISKVEPSLYSFQTIEYKKEKIKLGNTTKCDEKIVEKLKTYID
LLNDMNLSEDKMCNQIISSSFIQNIEIIDCTVYIGSIFLRNNLNREEYYICIKKEDNNNKMKNNISLLINTIDLNNTLIM
NTFYCNMESDICSIIINSIYFNNIPNITDDTLVLKAQCNIDSYPIINIDHVLREGYYTFHFRNPKIYFLQICIIDNLKKY
RMLGKIYFLKAYEPIICFIGTPCVIKSFTDKENVQYVQNNIDNETFIFTNKKCDNENINENMNIIETDFDMKELENHQHL
YLFSKNPLTDEKYLCTSNNKKFLLLFTIVLIKLPEYNIHYSIINNVVINYSTLFFEYNNYLGPYVKYECSDKSIVPDEYN
NFNNNKDNHFLLKNEELNFTIKFKAIIMRLCLKQNNFYYDIGKIYIENFINYKQISSLKDFTFNADVSLHADDINTKLLK
FAIKEDHNCHSDHGFFVQSNKDNFRADKKPFYKNIFFNHTTLYESINQIILDKDIYYICMCSLHEKCYDNNNLIDYNVYT
NISIQNEIQPLQNKKKFICEIFADCSFTINFENEHNNISDIWVAKKGQSCNSKDIQVGIHISHQNVKEINKENLHVTKVN
FKIYYLISHIHYSYLFNKDIIICGNYRNQHFIIHIKSDFFLLYYALPFEEEIKIKNVTQTNVATNTYEAQEKNINIQSFE
NVKQKYKRLFIYSYRDDTKSNLYKTMNFNQDENQISNTIKFEIPNDHPTKYKEIYFINECHYDQGVIIYKHKRESNNIVI
NNNNDNHIIKSKELYWARKKRIYNKKLKRKEKKNEIIHIYNCSNEIMNNHTLTSIIIFDGPLKPLDIYCYMELDCIHKEK
FSILNFDYSLFVEISDTQRIIIHTKESEGNNKEKLNKAEKIDFNDSKRITELILSIPKHISKGLEPGPYKIIYTRKFKQF
IHELYVGTFHFIGAPSQKYHLIRENEENIIIHGYFKNIENERIHILKHQNTCVLTNKDKNKKLLKSSEIESILNEIKTNI
QNCTYLDDTKLLCKNDLPVEGKFILCWCYNILNDQNNLCHNLNIYRPKITEVSSLLYSIDPILEISKSSLTNFLNYNIGD
FFFIIDDDCKNIKNIKLKSKLNDEQNILDIYKHLQYPKKYDLCICIVQHNILCDKQENYKNFYIKLNEQIYFTMEMGNLD
EFNNKDKIVKDFTFSTDYLDQLKLNIVPVFVFLPGPVEYKEYVCFAGIPCNATIKIKRSAQTRLKTGSTQIVGEKKDVAN
TYRGSYGNRNKANVKGANIKKVEDKKEQKRNDKKEGEIRDKKEDELGDKKDDELGDKKDDELGDKKEGELGDKKEDELGD
KKEDNNEDQNQDNKQDKIENMNKDINKDKEIKTKETNIEEEEVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKQEEE
QEEQEEKKEKEDKEDKEEKEEKEEKEDKEEQFDHNEHEVKGANKNKDKHFNQNKGESHNVNPNAQQNQYAEQIISEEEQD
```

```
NMENEPLGKHHYIYYTLNDTKECKNEYETVYKSNASSIYVSQEINYLHHEFIDGVYNLKIDIVPTDITKRYEICASFYQD
DKYFYNIGNVIFYGIFNESNTLDIISGVPFSFEINQFYSKYDLFIRLIYEKHGDSKTCRIYNNNFENVFLEGTIERTIVQ
HDKKVLDNYITNYKWKDLTIILDTDNNNYMTSYQNLDGSYNLYVCSCYELTEGHCQSDNYFSTQVMKFYVHTVELKEPKM
NSLIHFLKPFTLKLETTKILNGSIKVIPIDIISDLSKLCLELNLKNIYLKYQAEINEYEQTYNININFLSQGFIICWCGK
DNCKDHEYLTKVAFFRLNSPNFIDVHTDLNGNFSFHFLNQFVNINDRVRFVGQASSCLDDENMDLFNNHIVIRNIQNKKG
KTSNGGNTTKEQQKNNNKINSNNKINSNNKINSNNKINSNNKINSNNKINSNNNNNEENENERKDEDNNYESYSIDWEQI
IEIYGKPRNIFKGINQNWTWVSENYKMKTSNEEYIKICYCFHFYYKNCKDTKNFLYIGLVHNHIWNSKTTIMQNELDTNY
EISNMIYFNKDSIKFVAINSFNDLNRNVCDNINYEKNIIMPFFSGYNTFHNTTFNQKNIINILKTYYHNEFIFILCYNTE
YYKKKTFFLLTTKDMNELNDFTTYYNEKINTYNIIQSSFSYHSDIKDISTKNENIEKYEHIQLLLQNRGNTPNIFENYFY
LKDVYKKNNMSIYNMNPYVIYNNNKKKITNIQVKNKLKIILTKMYHMTSVDINEVIFYKGKGELLTDLNLQNIFILPKQK
KVILCCYNDDYIEVVINDDNKIGMKKSNKIQELIDILKKYHPNFERNKKKQNDILEQFNNINDILFKYDYIRDVNKNLIY
YDTGFFRNNIYIQLINQPFDLKIYGSNIQKKKNKDYILYIIDFHNICYNNMNKNGFFLEHKRYNEMENYIHFLQISMNKI
NNYKLCLYDKARDIYSNVGILNITDYYVIKESSFFDNEDIGNIKKKNMEIDSYNYNNDSNYDNNYDSNYENNYDSNYDSN
YDQNNNTYYIKNYNQNVIKNVCLIMDNNTNLIIVIKGKGSFYFNLQMEKGIFIENKGKKLNELFPDIKNHEPISCKNKKK
NTIILTKTHIFFYTNNYDISFSTKHNLPFPYDIDFDDKYIYVNDLYLNKIARIQILSTQDNKTPIPIINNKQRSKRSIIN
HDHESQQNIQKTHQIYNHFTPLHKLEKKEILQNNNRVQLKKNEFPITNLKNIEYSKNNIPNQKISSKDDIYKMSDFQAFI
NKHANLITTNLFRLYNYFEKKKYYGTLNYFIKRLWSNKVGPSGEEKYSTKSKIEQNDKNKNNNNNNNNNNNINDNYNYNY
NNHNNNDNIILNSNNYNNNNQSSGHQNFITSYHVGVDGKKKQTENLPTHSLNNFIQFFQNKKNSILKKEKEKRKNIPSYN
IMYQNINHISNTLNKRKQQELTSSIIKKRTKRNVQEKRMSQSAYNELILASIKKYTNKVEPAHFVNNKLDYLNYITNLKS
PLNISVQNNILYILDSIKNTFFSYNLINKEIKELEKYDFNDHPLILKNPLHFSIYNGIITEYTEHKNNLAFVTQIDSNEI
KVIDLNNSKKYKIIKAIKLRKGYKHNHINYVIGIKQKLLIITSQSQNINHYKNIIYHYHFNSFDQYFSISFNYTFAKNYN
ANDNLYITPDIDKYSDHIIYFCFLNSNNKCTNIDELTKLSISHETGIITGKLNYFGTFSLKIFAKTYFQYKINTYTNLYS
YCGISQEYNKTKSTCESCPIGTFWNSEKLLCENCQKYIENTSTLKNGSKLKTDCLCSPGYEYSDKSSKCEKCKPGYYKRS
VGNFICIKGCPINEKSITYGAKSYGEMDCKCIEGYYRKEDKCVLCLSNYYCPGNELIKACDKNKISKEGVIHKNDCICKE
NYIKDNTNNNCVYCASIAKILRKPIYCSLCDPIYFHEDIYKNIFLLPNNIHNYGLINNIYNYDEDLSLQGNIMKYAYFHK
TTNIERNFTHYINIKNIYHTFNNNINNYDYLKNSKFAIEIDIPQPKKCIFCDSGYYIKKKKCISCTTKYCEGFNHHPKAC
PKNSVVNKMKASSIFDCSCKRGYGILNERRNAYSNTITCQICPQNFFKHIISDDSCFPCPLYTYTLNQGATSILECLPKK
GYFIYMFQNINIDYLRYKFDINTENRIYNYFENNNRIFHEDVYNFFLNKQYSKFFYNTEHKTNTNTNNNNDNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNKYIKDNHFDNQVGNINKHNNNLQIKNTENIY
NIQYLEHLGFIKKTSLFYIYMILLRNIEERYNFNMDKMLKITCHINLHLKKNPHFTITYKKNLQECIDSCKTNIYCTGIE
FSRKRVEYTQIILKNNKKIILGYFKCKQFYFQNIYDYSSYNLDSYLNEHIENQINIKSTLTYTNFIMRNKSDIIYTCSID
RDPKYLLYKNYKLVECVIGKFCPGNNTPYMISCPINSTTIIPASADVNKCLCLKGYSYVGVTSYRCSLCDRGSYKNSVGN
NKCDNCPLTFSTTHRGSTNIKDCSCTSGNYLTFDTLGNFIRTENIQHKNISDQYFVIPIKQESQPENEKKDDDKNINIYN
ANNIYNHNIVYKTKMIKINLHKENDNNNDYMNNILKQTIGLCKPCTLENHYCEGGLESDITFNNKLIKGKFHTLPKKCPR
GLGIPNIIKERNSINNCLCIHGKVQRTTQNKNVECFPCPPNTFKENEYDNSCSGACPPFSTTFVGSSYENQCFCKNNYYL
VSTDDENDTNPNSINNNKNIYNNNNIYNNNNNNNNSNNSNNSNNSNNNNNNNNNKSDVKKKSCKMCPIGAICNRGFNIYI
YLKLLNDRSYNNINVIDHETPFPKYGYYAVYREKRNPTKLWGPLDDSPNLNYVYPYHKLLLFIQKNIQKGNYFFLEKGTK
FFLNDDFVEKMNEKSKYEEENANKFVTKSEIKHNVNTNNLKGKHNTLNNHNNINKSTSFLNQNNIHQNNYNDDIIQLSSY
ENNPFKKLSSTSKVSSNNNVISFIQNNDKTNNSTNDNNIENLDNIFNKYVQEAKELQIQNRKFERIPDIHPCTIPNRCLG
TLINLCSEGSTGYQCNNCSKNYDISYFKSKCKKCQNFFYEILHFILLKLLYYIIVIFICSLNGNILNKLHVSGILMRIWL
NCSFTFIAYGFFIPNMNSFISKYWYLYRTAFSYHMKIFAYYLRVQCLFNSLNINLSYNQMWYIQKYMNICTPIFDSIFIT
ILLFAVIHIYKFLFYKKNIDIFEQLLCTIPELNTLYKKNCIDNIHKVENKKRANKVESFEENKNQNKEKKNKKNIKRMNK
AKNKDNNNDNKNNNYDNDNNYDNDNNNDNKNNNYDNNNNINNNNNKKININSKDEQINHFKKCSSITTILNNLELNDEEK
NKESKKKIFDIKKKASIENIQENETNHLWNHTHNNVKNKESNINITNISNNINYELKYIKNKEWYNIFLNKTIQYIYKEK
KIFGLWHFLFTKNDNWFKNMGTFLNDTLPCYVLIMILSIPYILLELVQLTYCTPIKYKSQKTYFYLTYLITQKCSLSSKL
FITGLIVTIASFASYIFLWILLLYLYSKRKRLNLFDLLTTNLLSGYRKGKGIFEFIFLLKHILIVLLISFNIYHEFYYIV
FLTLILITFAILEILSNPYDKRSFNILNKSLNIGNVLNIFFPLIIWGSFYWTYEKFFIIPIFVIYAYHIYMFHHIVKEFT
LSIHFIKKENIVNIQTIGYDPENIKNKNYKIYYKVMNKIKYFLNKNQKKNISNINENKDKHLNKNNNSKDHVKFEPIENI
IKRYNLKLNKGILKDANNNNNNNNNMRDQVEDNKKDILFIKKNVLPVNVHNVASIWYDEQNEDLLFQMPYQNKFCLNMNNE
GNENNDQINDLTKDKTSEEENNNDHVNVPTKDKTNDKKKKIKKKNNNNNNNNNNNNNKEVHENDDNINHNNNNNNNNNKEVH
ENDDNINHNNINNHNKSSNISTTNKKNYFNKFSDYIIDKRNKKSIKYFVTSLMEVIEKFLDSSTHGFIYENWFDFTIRFA
FVYISWIKKCNKKNNIMLPMNIQQLHIHMDLFIFTPIFSKNNSTCINEQNIQNYSKKKKIYNKINMYDEKIETGELLEKH
NSFENTEIKISRSFGSHNYIPNIKNRKNNYDKKEDITSINNINVDIVKQDDQKEDSNINHLTNVHNQKEPSKHIYNINEQ
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HIFNKLYQMYNKKIITFDTSVMFYINKLRDDIKSEIEQIDKEINTGDTTEKERIQNYYYYKEELIKRKKLEEELLSKIKS
LEECIEVNKRSQSLRNMLLTKKKKNNNLNNENLEQHINYIFSHLHNEGTYKLNHSQNMDKKT
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1484 - 1503:	EEEEEEEEEEEEEEEEEEEE
1485 - 1504:	EEEEEEEEEEEEEEEEEEEE
1486 - 1505:	EEEEEEEEEEEEEEEEEEEE
1487 - 1506:	EEEEEEEEEEEEEEEEEEEE
1488 - 1507:	EEEEEEEEEEEEEEEEEEEE
1489 - 1508:	EEEEEEEEEEEEEEEEEEEE
1490 - 1509:	EEEEEEEEEEEEEEEEEEEE
1491 - 1510:	EEEEEEEEEEEEEEEEEEEE
1492 - 1511:	EEEEEEEEEEEEEEEEEEEE
1493 - 1512:	EEEEEEEEEEEEEEEEEEEE
1494 - 1513:	EEEEEEEEEEEEEEEEEEEE
1495 - 1514:	EEEEEEEEEEEEEEEEEEEE
1496 - 1515:	EEEEEEEEEEEEEEEEEEEE

A0A2P9GEA3 **A0A2P9GEA3_9APIC** (3071 aa)
Transmission-blocking target antigen s230. *Plasmodium sp. DRC-Itaito*

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MKKIISLKNIFLIILVYILSEKKDLRCNVIKENNIKDDEDKRFHLFDYSHKFLKSRETKQKKNKKEYVHKNVDIYNLSKE
ITMRKDTFVKMKQRTCPFNKERSSFEIGSNNITCFNPIVRKKEREIIDTIVLKKNVTNDHFVSSDMHSNVQEKNIILIRN
IDKENKNDIKNVDEKIQRDTYENVDYESNDKLIVWFDDNTNEENFLLTFLKKCLMKIFSSPKKKKTVVQKKHKTNFFINS
SLKYIYMYLTPSDSFNLVRRNRNLDEEDMSPRDNFVIDDDEEEEEEEEEEEEEEEEEEEEEEEEEEEEYDDYVYEESEDH
TEENLQEEQQEEIAVESSEESFNDVDEDYVEAEDGDMIRVDEYYDNQDGDTYDSTIKDEKEGEGAYEGAYEGAYEGAYED
AYEEAYEYEKESQDEIYPGGDKKERDEGEESFTYEKSDIDKTDLFKFIEGSEGDDVYKVDSSKILLDGDTFSRVSKKHSL
GDGGDEGDDESVVKMIRSVLQSGVLPSEGVDELDKIDLSYETTESGDTAVSEDSYDKYASNNTNKEYVCDFTDQLKPTES
TPKVKKCEVKVNEPLIKVKIICPLKGSVEKIYDNIEYIPKKSPYVVLTKDETKLKEMLLSKLIYGLLISPTVNEKENNFK
EGIIEFTLPPVVKKYTVFYFICDNSKTEDENKKGNRGIVEVSVEPYGNKINGCAFLDDDEEEEKYGDKGEEDEHNEKIKM
KTLFIQNIYKKNNIYPCYIKLYSGDIGGIMFPKNIKSTTCFEEMIPYNKEIKWNKEKKSLTNLVNNSVVYNKDMNAKYFN
VQYIHIPTSYKDTLNLFCTIILKEDESNLISNSYLVYISINEELNFSFLDFYESFVPIKKTIQVPQKNVNNKEHDYTCDF
```

TDKLDKTVPSIVDGKKLFICRKHLKEFDTFTLKCNVNKTQYPNIEIFPKTLKDKKDVLKLDLDIPYHMFSKFFKFNTQNS
KYLNLYPYYLMFPFNHIGKKELKNNSLYKNHKDVKYFEQSSLLSPLSSSDSLGKLLNFLDTQETVCLTEKIKYLNITINE
LESDNNTFSVTFQVPPYIDINEPFYFMFGCNNNKGEGNIGIVELLISKHEEKIKGCNFHESKIDYFNTNISNDTNECTLH
AYENDVIGFNCLETTHSDEGEEGTEISLQPENCFNNVYKGLDTIDITTILKNAQTYNINNKKTPTFLKIPKYNLLEDVEI
SCRCTIDHIVKKIKVILTKSDTVLLKREVESQFTLDEKIYKCEHENFINPRVNKKFDENVEYTCNVTIENFFNYIQILCP
AKDLGIYKNIQMYYDTIKPTRVPEFKKFNDEELQKLIPNTEMLHKTKEMLILYNEEKVDLLHFYLFLPIYIKDIYEFNIV
CDNSQTLWENQLGGKVIYHITVSKREQKVKGCSFNDEHTHMFIDNKSNVKNCIIDAKPKDIIGFVCPSGTLKITNCFKDA
IVHTNLTNIHHIFHLKNNLANFTYKHHFNYMEIPALMDNDISFKCICVDLKKKKYNIKSPLGPKILHALYKKLNIKYDKY
VTGTIQNKYLMTHMDLHLSHKRNYLNELFNDLDKKKPADTDANPESIIESLSIKDSNESGPFPTGDVDGEHLILEDYDTW
ESLYDDKLEEVIYNDIESLELKDIEQYVLQVNLKAPKLIMSAQINNNRHVCDFSKTNLIIPESLKKKEQVDINPIDVHCY
ALLKPLDTLYVKCPTSKDNYEAAKVNISESDNEYELQVISLIEKKFHHFDMLDSKNPGNGDELHSGIVDTSSDLDNSTFE
KYFKNIKIKPDKFFEKVINEIDNNEEEKDLESILPGVIVSTMNILKKKDPFTSYAALIIPPVVSKDFHLKVECNNTEYKD
ENQHIGGYNGIIHIDISNNDKKINGCDFSTSNSSILTSSVELVNGETKNCEININNNDVFGIICDNETNLDPEKCFHEIY
DKENTNVKKFRELIPNIDIFSLHNSNKKKVAYAKIPLDYINKLSFSCSCKTSHNNTIGNMKVILNKDEKEEEEFKIIQGI
KHNNVHLCNFFDNPELTFDNNKIILCKIDAELFSEVIIQLPIFGTKNIEGVQDEQYKKFSLKPLLDINENDNDIKVIGKE
KNEISISLALKGVYGNRTFTFDKDGKKGEGISFFIPPTKEDTDLKFIINETIDNSNIKQRGLIYIFVRKNVSDNSFKLCD
FTTGSTSLMELNSEMKEKKCTIKIKKGDIFGMKCPKGFAIFPQACFSNVLLEYYKSDYTDSEHINYYIHKDKKYNLKPKD
VIELMDENFRELQNIQQYTGISNITDMLHFKNYNLGNLPLNYKNHYSTTYAKVPDTFNSIINFSCNCYNPEKHVYGTMQV
ESDNRNFDNIKKNENIIKNFLLPNIEKYPLLLDDEERNKQKLKDHNDNLTIYNNHEQNDIYMLYDSNEHICDYEKNESLI
SILPNDTKKIQKSICKIYAKALDVVTIKCPHTKNFTPKDYFDTLSLTTNDKQILITFDKKNFVTYIDPTKKTFSLKDIYI
QSFYGVTLDHLNKIKKIQEEWDDVHVFYPPHNVLHNVLLNNHIVKLSSVLEGVLFIKSKVTTDDTGTKKNTTLPTDGISS
ILIPPYVKEDITFQIFCGKSTTKKPNKNNTSLAIIHIHISSNRNIIHGCDFIYLEKQTSDPIHNNGYSIFTHNKNTENNL
ICDISLIPKTVIGIKCPNKKINPETCFDEIYYVKEDDISPKTITADKYNVFTKEKLGNILKNAVSITNPDEKDNTYTYLI
LPEKFEEELIDTKKVLACTCDNKYIIHMKIEKNTMDKIKTDEKKTIGKDICKYDVNTKVATCEIINTIDSSSLKEHHTVH
YSITLSRWDKLIIKYPTNEKTHFENFFVNPFNLKDKVLYNHNKPINIEDILPGAITTDIYDTRTKIKQYILRIPPYVHKD
IYFSLEFNNSLSLTKQNQNIIYGNVAKIFIHINQGYKEIHGCDFTGKYSHLFTYSKKPLPNDNDICNVTIGNNTFSGFAC
LSHFELKPNNCFSSVYDHNETNKVKKLFDLSTNVELDHIKQNTSGYTLSYIIFNKESAKLNFSCTCSSHYSNYTIQITFD
PNYITPEPQSRAIIKYVDLQDKNFAKYLRKH

281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE
287 - 306:	EEEEEEEEEEEEEEEEEEEE
288 - 307:	EEEEEEEEEEEEEEEEEEEE
289 - 308:	EEEEEEEEEEEEEEEEEEEE

A0A2P9GMJ1 **A0A2P9GMJ1_9APIC** (2087 aa)
Serine/threonine protein kinase, putative. *Plasmodium sp. DRC-Itaito*

MDYSNNKKNIKAMNQHQNKDSSEYNENYYKKQYNIKNRKNEEIKVGSNLSTNNDVLQLPSVLHNHIRIVRTNDSCFKDYI
VLSNLGKGTYAQVWKVKHKITNEIYAAKLLQPNQFPKESFNRIVEMFTKEIINLSICQCPGVIKLHKVIGGKEGWILIQD
FANDGTLWKENLSSNMNEAFLYFIQLLQGMWYIQEMNIVHRDLKPTNILRYDNKRIVIADFGWSEHIDSCNLHPTEWPGT
LEINPPEVLRNTGPMTEKIDNYALGMNMILFISGRFVCRQKGIECSKVAQTILKTVHNLRHSKPPSRFRENLKAWDLFVK
LTSSNPIERLSLQNVLDHPWVTEMLNNFSLQNSKFLWHEKVKSRWIYLLSNNWDFFKNISSISCSKKNNNNDDNNNNDNN
NNDNNNNDNNINNNNNNNNNNNNNNNNNNNNNNNNYSSRNIISTTHNNNININNNNNSSSNTKIIGKYNDIENEHNLSSTSTK
ANKNTLIIDNEKNNKEKINMYSRSCLKNDYELLFYMMKNNFKGKINCCSVKKNEITKIENIQEIKNGDGINQNEVMQNKQ
ELENIPNMEHSGNIEKLEIMKKNENIRMCDQMNVDGNKYSNDVDKYKYKNDVDKYKYKNDVDKYKYKNDVDKDKYKNDVD
KDKYKNDVDKDKYNTDVDKEKYNTDVDKEKYNTDVDDDDINNHKNNKSNNFDDIQINRNNNGGDQYVPYNNDKEIQHICTK
NKEYNSKNYIANIQKKKYITVPKNHMINIPSTTSHETNKEYKMSRPIGVVPKGYYDHNNHNINNNVVNNNNNNNNFNHNN
HILYYNRRHVHKDHIVVNSNNCSRKCKNNHAEEQKEIFIISDSFEENTKGTYDKKKNNKNKKNSKKYDPINKKNTDHRKD
INMKFNNKEEKNKYYNKFKTMNEKIFYNKNQLLIHNNNIYKVNENVDVYNKNADSSESMKRTKGHIFDKQASRSTYNQIY
DDNIYDDNRYFEEGKGNLDTYKNDKYNMSDIKNVERDTNVDNEEYVDNDGHVYKEKEEEEKEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEKEEEEKEEEEEEEEEEEEEEDEHQLNHNKENIGNEEEEEEEEEEEEEDEEDNDDNSDDNSDDNSNDDDDHNN
DNNDNNDDNNSGKKNSDRHIYNYHNYITYLKKNKQMNDKTNGDMKNVQDKFSNIRDTEDFMHYNQKECNSIFLSDIDNMK
KILKNYKKEIHDTKGVLTKTTFKMSDLRRKNDKEQKYINKKDTSTNDIIIYPMLSNNRNDIDKYEKNKNDSTYIKEKKYR
DIKKNAHIYKYDCDKMNNENHYQYDTNYKKDMINVLSGKNIKVEDINFRWHHDKETILSRQKGNNISREGKDSKMIDTVH
KKDNVDITIRYMNLHDNNNNNDNNNNNNNNDNNNIGKDPFIKQHDKNSNEYINKYEEEYNIFLDRLNNKEKKKRDNTINS
TNCRNNINDKEINMKKDDKNNMLPRLLLKINKILDENDVDYKKEKNEKNMRNKYYDGINKTNECHDRNITHDKVELEKES
NYNKYEKYNKYNEYEKYNKYKKYEKYNKYKKYEKYNKYEKYDSCYNSSCCSTYKKDDHKIDSKNNIDSTTQRDSLTSDKE
FIFKKKSTYDNLKENNLNISIGKRRNTYKNDFVNILNEKEERLADVFKEENSYKETDKKVDAEIYRNEKKNSLDISNNII
INKFMNNTYHHKNNNIEKRTDSPMKYYMDTLNYFDNKNMLEMCKEKEKVLMMNNDKKQSGFYNYDIMINNDDKEDMCTNV
FVNKYERVEKYNYQSDGDIEVEMVKKENIKKKINNIVINIEDKNVNYDEKNMIEKVNTGYNNIFIGKKKNDDSKKNMPSY
NIHTYDNNNKSRKYDIKEDKKKNNVHNFNNYDNDMSDNLYVYRKNSLSCINEQEAKIYHSTKCGHNTSLCSYKKDQEDKI
LEELIKGESIDTTTTTSTTESETFIDKKYNNDNKPCSYFSVHNNIKIYNKPLSITLDDSIKESSVKNSSCSTFDYSDLEF
QYFSNKENIVDSYNTEYKYGPRELGDVSRYDNKSMLGEKKKNHTKQNQVHDNNIIGKKKSVDHISNFTLHNNDIFLKMHD
IQNLTKV

1022 - 1041:	EEEEEEEEEEEEEEEEEEEE
1023 - 1042:	EEEEEEEEEEEEEEEEEEEE
1024 - 1043:	EEEEEEEEEEEEEEEEEEEE
1025 - 1044:	EEEEEEEEEEEEEEEEEEEE
1026 - 1045:	EEEEEEEEEEEEEEEEEEEE
1027 - 1046:	EEEEEEEEEEEEEEEEEEEE
1028 - 1047:	EEEEEEEEEEEEEEEEEEEE
1029 - 1048:	EEEEEEEEEEEEEEEEEEEE
1030 - 1049:	EEEEEEEEEEEEEEEEEEEE

1031 - 1050:	EEEEEEEEEEEEEEEEEEEE
1032 - 1051:	EEEEEEEEEEEEEEEEEEEE

A0A2P9GNT9 **A0A2P9GNT9_9APIC** (1997 aa)
Uncharacterized protein. *Plasmodium sp. DRC-Itaito*

```
MNVCKMKVQQKKNLKDCNLKSKNTILTSFEKKKNEKDENNLLKFSKLSDNKNKVVNSKFLKNDNYKFNERKESLTRCSTN
ESLKLKNINTLTKDSNYNNNNDDGSNNNNNNNGNIKLIFKPNDKDIESTVREEDGKKSEKKTNDLINNKNEFKVNNKLIL
KSKEYKNNINNNNNICKLKSIDDQNKKQQLDTYSPKENEEDTSNNVKKNSCLKNIKKSQINEKEVISNTVDENHNTHSKG
DKENNVVATKNVKRMNTISKELNNRNNNLKKHVSKSNSLDLKKGKKGEKLKDKLINNLSGKKCMNKEKEIVESSSVRRSS
SRYSIDYGRRDSSRGGSVKQEKGKERRGSKNVSKKVSKSKYTRKKSKRIKEESDESDDDDEEEDDDDEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEKGEEEEDEEGEEEEEEKGEEEEEEEEDKDHNENSDDAYTNRSRRSTRCSIVKRKTSRC
IGKKKSKIIKKSTSKMKNNKKKKASVIKLEKKKEKLSKKGILKKKNKKTKGKLKKNSKVYHRKKKIKNEKNLIDEEEIEE
EIEEEEEVIEPSYFDEYNLSIEERKKDLEEKEKKKEIKENYIKQIKLPKYADDESIIFINNPNYVMVLLFLTVYKDVLKM
NWNFKDIEEMFQNKETTEFGRNFILKLFFFLGRYFNSKSIFMYKYISRIFEDKEESLSRVVNFHELFPVFETKKEIKNTG
VGSKRKKDKRGKKMKMHQKEDELLYDEEIIGNDDVNIFEEEEEEEEEEEEDEEDNEHYNDDEEEEEEDHEHYNDDEEKVH
GIYNDEEEEEKEENNGNYNEEEEKKSDSNNGSTKNTIIKEEKDGLNISESSHNEVNVNNDNMNREESCKNGNNGENEKSG
DFNINDDIINDDINNTENNNNNNNNNNNNNNSNNEIVNSKNNVEIKLDKIAEKNKDMNNTEGIIKSENVDDEKGLTNKLFL
EWDDLSVTSKLRIIRMLLNLVLCESNNLKKMLGDEKLNYNNGYLGKINNEKYWFIFNDTINIEYKLYLEREEEGSFIFIC
DDDDMLYTIGYNFLRNSETKFMGEALIERYNKVCRERRNRSRMLKQQKKLLCADINLNDPLLGTKKRQPKQVEYFNFDNN
EKMRRKKSDINNNPYSVPPTKSYQKNDRSFRLAARNAQKGSVYDLEAWKLNEGLLGIENQGTISGNYNIANDGNNMIEAN
NIIDSNNNNNNNNIAVDGDGNNIYGLNNNKLVGSEGNTINGNNNNNNNINNNNNNNNNNSNNNNNSNSNNNLGTVKIPLK
RGRKKKSEKKKRGRKKKVLSVDGVGDIANNLTGLGVDENKKKSTQSTGRGKRGTYTKRNTRPSVSIKYGTRSHSLNKYEN
DVMSFNEYSLNPGLSMDEFYKNMVMDPKFFHANMSMNNYMNGAFNMPNNNNNNSMMNMRNGSKMGSMNNLGGYNFPYMCT
PPHMYNQYYMYNGNSMYLPNGGANSNMNMSNTNNGASVGIGGNVVSNQNAVKDVKGENMLMTKNSIMENRNSILMNSMNN
MNMNNMPHKNSFLGNDGINNMNSMMNNMNNNNNNVNNNNNNNNNNVNNNNNNSVNNNNNVNFMDNVGNNNNSNNSMNKYN
NYMMNRNALNNMGGTNALYNNMYNMKFPYMNNDMMNYNYNINSFQNINYDKINKSMFKRYPNFMGGYPYNNMNPYNNFNA
FNMNYQQNEQLNQLPNIQGAYKNKLMNDNLSSYQLYNNNNNNNNNNNTKQNHHDNDNNNNINKNNSEGGNKNIDDSNKNND
LNKNNDIIDSTKLNEQPVGGLAVNNDCSTRGEDNQRIDLKGDVVEALVGNNNDKMNSSDHNLNSLKNLGNINNTYNMDHM
SHMRNSVSGSSIGMINPGHMNSSHSGSIMNKDKLRDLQLNNNMNSNNNNNNNNNNYVKLNPFDHPMKNINNNLMDDKYPK
DNNNNNNNNNMMMMMMNSVYNMMGSDHFHMNNSHMMDPMGAPKMNENIYNHNNMSFENNTNHNNHNNHNNRIHDKLPE
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388 - 407:	EEEEEEEEEEEEEEEEEEEE
389 - 408:	EEEEEEEEEEEEEEEEEEEE
390 - 409:	EEEEEEEEEEEEEEEEEEEE
391 - 410:	EEEEEEEEEEEEEEEEEEEE
392 - 411:	EEEEEEEEEEEEEEEEEEEE
393 - 412:	EEEEEEEEEEEEEEEEEEEE
394 - 413:	EEEEEEEEEEEEEEEEEEEE
395 - 414:	EEEEEEEEEEEEEEEEEEEE
396 - 415:	EEEEEEEEEEEEEEEEEEEE
397 - 416:	EEEEEEEEEEEEEEEEEEEE
398 - 417:	EEEEEEEEEEEEEEEEEEEE
399 - 418:	EEEEEEEEEEEEEEEEEEEE
400 - 419:	EEEEEEEEEEEEEEEEEEEE
401 - 420:	EEEEEEEEEEEEEEEEEEEE
402 - 421:	EEEEEEEEEEEEEEEEEEEE
403 - 422:	EEEEEEEEEEEEEEEEEEEE

A0A2P9GU27 **A0A2P9GU27_9APIC** (6101 aa)
Cysteine repeat modular protein 4. *Plasmodium sp. DRC-Itaito*

```
MKNITFLVSFLIFLTSINANISITNFTYTNQKGDINVEFFQTDYIAIFKLPFGGNDEQIFEISDDYIITNDKETNNCNIP
NNNFGFVYSKSNSKNKFLFVQREYTTIYIKDKNNACSLISKVDPSLYSFQTIEYKKEKIKLGNTTKCDEKIVEKLKQYVD
LLNDMNLSEDKECNQMIPSSFLQNIEIIDCTVYIGNIFLRNNLNREEYYICIRKEDKNNKIKKNISLLINTIDLNNTLIM
NTFYCNMESDICSIIINSIYFNNIPNITDDTLVLKPQCNIDSNPLINIDHVLREGYYTFHFRNPKIYFLQICIIDNLKKY
RMLGKIYFLKAYEPIICFIGTPCVIKTFTVKENVQYVQNNIDNETFIFSNKKCDNENVNENINMIETNCDTKELENYQHL
YLFSNNPLTDEKYLCTSNNRKFLLLFTIILIKLPEYNIHYSIINNVVINYSTPFFEYNNYLGPYVKYECSDKSIVLDEYN
NFNSNEDNNFLLKNEELNFTIKFKAIIMRLCLKQYNYYYDIGKIYIENFINYKKISSLNDFTFNADVSLHADDINTKLLK
FAIKEDHNCHSDKGFFVQSKENFRVEKKSFYKNIFINHTTLYESINQIILDKDIYYICMCSLHEKCYDNNNLIDYNTYTN
ISIPNEIQSLQNKKFVCTIFEDCSFSINFENEHNNISDIWVAKKGISCNSKDIQVGIHIIHQNDKEINKENIHVTKVNFK
IYYLISHIHDSYLFNKDIIICGNYRNQHFIIHIKSDFFLLYYALPFEEEIKIKNVTQTNVSTTTYKAQEKYINIQSFENI
KKKYKRLFIYSYHDDGKKNLYKTINFNEHENQISNNIKFEIPNDHPTKYNEIYFINECHYNQGVIIYDHKRESNNIAINN
NDNHIIKSKEVYWARKKRIFNKKVKKKDIKNEIINIYNCSNEIMNNHSLTSILIFDGPLKPLDIYCYMELDCIHKEKFSI
LNYDYSLFVEISNTQRIIIHSKESEENNKEKLNKAENINLNDSKRITELILNIPKHISKGLEPGPYKIIYTRKFKQFIHE
LYVGTFHFIGAPSQKYHIIRENEENIIIHGYFKNIENERIHILKHQNTCVLTNKDKNKKLLKSSELEFILNEIKTNVQNC
TYLDDTKLICKNDLPVEGKFILCWCYNILNNQNNLCHNLNIYRPKITEVSSLLYSIDPILEISKSSLTNFLNYNIGDFFF
IIDDDCKNIKNIKLKSKLNDEQNIIDIYKHLQYPKKYDLCVCIVQHNISCDKEENYKNFYIKLNEQIYFTMERGSVDEFN
NKDKIIKDFTFTIDYLEQLKSNIVPVFVFLPGPVEYKEYVCFSGIPCSAPIKIKRSAQTRLRTDKTQIIGEKKDIANPHL
GFYGNRNKENIKGANIKKVEEKREQKRNDNKKEDNKKDENQDNKKDENQDNKKDENQDNKQDENQDNKQDENQDNKQDKN
KNNEQDKNQDNKQDENQDNKQDKVENINKDMNKDKKIKVKETNIEKDEYKEDDDEEEVEEEEEEEEEEEEEEEEEEEVE
EEEEEEEQPKQQQFDHNEHEVKGADENKDKNFNQNQEETQNVNTNTQQNEYAEEITSEEEQVSIENEPLGKHHYIYYTLN
DTKECNNEYETVYKSDASSIYVSQEINYLHHEFIDGVYNLKIDIVPIDVTKRYEICASFYEDDKYFYNIGNVIFYGIFNE
SNTLDIISGVPFSFEINQFYSKYDLFIRLIYEKHGDSKTCRIYNNNFESVFLESSVEHTIVQHEKKVLDNYISNYKWKDV
TIILDTDNNNYMTSYQNVDGSYNLYVCSCYELTEGHCQSDNYFSTQVMKFYVHTVELKEPKMNSLMHFLKPFTLKLETTK
ILNGSIKVIPIDIISDLSKLCLELNLKKIYLKYQAEINEYEQTYNITINFLSQGFIICWCGKDNCKDHEYLTKVAFFRLK
SPNFIDVHTDLKGNFSFQFLNQFVNINDRVRFVGQASSCLDDENVDLFNNHIEIRNIENKKGKTSNDGNRKITQQENSNK
INSNNNNNNEEDDNYERYTIDWEQIIEIYGKPRNIFKGINQNWTWVSENYKMKTSNEKYIKICYCFHFYYKNCKDTKNFL
YIGLVHNHIWNSKTTIMQNELETNYEISNLIYFNKDSIKFVAINSFNDLNRNVCDNINYEKNIIMPFFSGYNNFHNSTFN
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QKNTLNILKTYYHNEFIFILCYNTEYYKKKTFFLLTTNDMTELNDLTTYYNEKINTYNLIQSGFSYHSDIKDISTKNENI
EKYENIQLLLQNKENVPNIFDNYFYLKDVYKKNNINIYNMNLYNMSPYIIYNNNKKITNMQVKKRLKILLTKMYHMASVD
INEVIFYKGKGELLTDLNLQNIFILPKQKKVILCCYNDDYIEVVINDDNKIGMKKSNKIQDLIDILKKYHPNFERNKKKQ
NDILEQFNHINDVLFKYDYIRDVNKKEIYYDIGFFRNNIYIQLINQPFDLKIYGSNIQKKKKKDYILYIIDFHNICYNNM
NKNGFILEHERYNEMENYIHFLQISMNKINNYKLCLYDKERDIYSNVGILNITDYYVIKESSFFDNEDLGNINKKNMEID
SYDYNNNNDSNYDNNNDSNYDNNNDSNYDNNYDNNYDHNINKYYIKNYNQNVIKNVCLIIDNNTNQIIVIKGKGSFYFNL
QIEKGIFIENKAQKLNELFPDIKNHELISCKNKKQNTIILTKTHIFFYTNNNNDISFSTKHNLPFPYDIDFDDKYIYVND
LYLNKIARLQILSTKDNKTPIPIINNKQRSKRSIINHDNKSQQNILSYTTHRTNRINEKTNQFKHENIPKTHQTYHQFTP
LHKVKKKNILQNNNIVQLEENEFPIINLKNIEYSKNNIPPNQKISSNDDIYKMSDFQAFINKHTNLITTNLFRLYNYFEK
KKYYNTLNYFIKKVWSNKVGPSQEEKCSPKSKIEQNNSNDDNDNDNYDNDNNDNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
KKNCIHKKEKEKSKNTPSYNIMYKNINHISNKLNKRKQQELTSTIIKKRTKRNVQEKRIDQSGYNELILSNIKKHTNKVE
SPHFVNNKLDYLNYITNLKSPLNISVQNNILYVLDSIKNTFFSYNLINKEIKELEKYDFNDHPLILKNPLHFSIYNGIIT
EYTEHKNNLAFVTQIDSNEIKVIDLNNSKKYKIIKAIKLRKGYKHNHINYVIGIKQKLLIITSQSENMNHYENIIYHYHF
NSFDQYFSISFNYTFAKNYNASDNLYITPDIDKYSDHIIYFCFLNSNNKCTNIDELTNLSISHEKGIITGKLNYFGTFSL
KIFAKTYFQYKINTYTNLYSYCGISQEYNKIKSICESCPIGTFWNSEKLLCDNCNKYIENTSTLKNGSKLKTDCLCSPGY
EYSDKSSKCEKCKPGYYKRTVGNFICIKGCPINEKSITYGAKSYEEMDCKCIEGYYRKGDKCVLCLSNYYCPGNELIKAC
DKNKISKEGIIHQNDCKCKENYIKDNENNNCVYCASIAKILGKPIYCSLCDPIYFHDDIYKNIFLLPNNIHNYGLINNIY
NYDEDLSLQGNIMKYAYFHKTTNIERNFTNYINIKNIYHTFNNNINNYDYLNTSKFAIEIDIPKTKKCIFCDSGYYIKKN
KCISCTKKYCEGFNQNPKDCPKNAVVNKMNASSIFDCSCKRGYGILNERRNAYGNTITCQLCPQNFFKHIISDDSCFPCP
LYTYTLNQGATSILQCLPKKGYFIYMFKNINIDYLRYKFDINTENRIYNYFENHNEIFDEDVYNFFLNKQYSKFFYNTEH
KTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
LGFIKKTSLYYIYMILLRNIEERYNFNIDKMLKITCHINLHLKKNPHFTITYKTNLQECIDSCKTNIYCTGIEFSRKRVE
YTQIILKNNKKIILGYFKCKQFYFQNMYDYSSYNLDSYLNEHIENQINIKSTLTYTNFIMRNKSDIIYTCSIDRDPKYLL
YKNYKLVECVIGKFCPGNNTPYMISCPIHSTTIIQASTDVNKCLCLKGYSYVGVTSYRCSLCDRGSYKNSTGNNKCENCP
LSFSTTHRGSTSIKDCSCTSGNYLTFDTLGNFMRTENIQHKNINDQYFVIPIKEESPYENENKDDNKNINIFNTNNTYDH
NLVYKTKMIKISFHKENDNNNAYMNNLLKQTIGLCKPCTLENHYCEGGLESDITFNNKIIKGKFHTLPKKCPRGLGIPNI
IKERNSINNCLCIHGKVQRTTQNKNVECFPCPPNTFKENEYDNSCSGACPPFSTTFVGSSYENQCFCKNNYYLISTDDEN
DNNNNMNNENSMNSENSMNNENSMNNENSMNNERNTNNRNNNNHNNNKSDVKKNSCKICPIGAICNRGFNIYIYLKLLNDR
SYNKINVIDHETPFPKYGYYAVYREKTNPTKLWDPLDDNAILTYVYPYHKLLLFIQKNIQKGNYFFLEKGNKFFLNDDFV
EKMNEKSKYEEKNANKFVTENKIIHNINTNNLKGKRKTLNNNNNNNNNINKSSSSLYQDNINENNYNHDIIELSSYEDNP
FKKLSSVSVVSSNNNIISFIQKNDKINDSSNDNNIENLVDIFNKYVQEAKELQIQNRKFERIPDIHPCTIPNRCLGTLIN
LCSDGSTGYQCNNCSKNYDMSYFKSKCKKCQNLFYEILHIILLKLLYYIIVIFICSLNGNILNKLHVSGILMRIWLNCSF
TFIAYGFFIPNMNSFISKYWYLYKTAFSYHMKVFAYYLRVQCLLNSLNINLSYNEMWYIQKYINIFTPIFDSIFITVLLF
AVIHIYKFFFYKKNIDIFEQLLCTIPELNTLYKKNYIDNIHKVENKNRANKVEGFEENENQNKEKKNKKNIKRKNNTKNK
DNNNDNNNDNNNDNNNDNNNDYNNDNNNDNDNNNDYNNDYNNDYNNDYNNDYNNDFDCNNNKVNIKSKDEQINHFE
KCSSITTILNNLELNSEEKNKESKKKIFGIKKKASIEYIKKNEANHLWNDTHNNVKNKQSNINTTNISNNINYELNYIKN
KEWYNIFLNKTIQYIYKEKKIFGLWHFIFKKNDNWLKNIGTFLNDTLPCYILIMILSIPYILLELIQLTYCTPIKYKSQK
TYFYLTYLITQKCSLSSKLFITGLIVTIAIFAFYVFLWILLLYLYSKRKRLNLFDLLTTNLLSGYREGKSIFELIFLLKH
ILIVFLICFNIYYEFYYIVFLTLILITFAILEILSNPYDKRSFNILNKSLNIGNVLNIFFPLIIWGSFYWTYEKFFIFPI
FVIYAYHIYMFHHIVKEFTLSIHFIKKENIVNIQTIGYDPENIKNKNYKIYYKVMNKIKYFLNKNQKKNISNANENKDKH
LNKNNNSKNHLKFEPIENIIKRYNLKLNKGILKDTNKNNNNGNNNNNNINNMQAQVEDNGNDILFIKKNVLPVNVHNVAS
IWYDEQNEDLLFQMPYQNKFCLNINNEENEESENNDNVNDPTKDKTNEEKNNNNENNDEVNDPSKDKTSEEKNSNNENKD
HSNDNTNKKKNNNKNNNKNKNSNNNNNKELHENNDNINHNNIGNQNNSSNTSNSSNKKKKKKNYFNKISDYIIDKRNKKN
IKYFITSLMEVIEKFLDSSTHGFIYENWFDFTIRFAFVYISWIKKCNKKNNIMLPMNIQQLHIHMDLFIFTPLFSKNNST
CISEQNIQNYSKKKIYNKINMYDEKKESGELLEKHNSFENTEIKISRSFGSHNYMPNIKNRKNNYDKKENITSINDINID
NIKQDNNNQDSNINHLINEHNQKETSKNIYNINNLNIMEYNIDENISKNNEKEKHIKIPPKNISLTQKEYNNNFSNNNDI
FNYSLDIFSSEMFNEKIFHSIISLFELYMAIKTLKLMNPHIFNKLYQIYNKKIITFDTSVMFYINKLRDDIKSEIEQIDK
EINTGDTTEKERIQNYYYYKEELIKRKKLEEELLSKIKSLEECIEVNKRSQSLRNMLLTKKKNINKVNNENLEEHINYIF
SHLHNEGTYKLNHSQNMDKKN

1499 - 1518:	EEEEEEEEEEEEEEEEEEE

A0A2R5GQA1 **A0A2R5GQA1_9STRA** (508 aa)
Adenylate kinase. *Hondaea fermentalgiana*

MGCVASKAADGKNLDDVEVVFFDMDDTLYQNNWATAIRLKKSIERYTVEELGLGEDEAYELYLEHGTALRGLLKTKKLPE
DRIEHFLADVHNVSLEEILPNPALAEMLERLSQHKKIWIFTASIKEHAQRCLERLGIDESIFEGIIDSRAVGLVTKHSPV
AFTQAMTIANVSEGNKCMFFDDSVKNIKTAKEMGWHTCTVGLERGTDLPLKCPYADFAVVTVLEVPEMMPALFDGDTDGI
LALAPAKIPEFDEEDPLADDDDEEEEEDEEEEEEEEEEEEEEEEEEEEEDIEDILEEGEVEDEVSEAKPRFAIFILGGPG
CGKGTQSQKLAKKRNFVHLSAGDLLREERSNPDSEYGALIEKTINEGAIVPSEITMKLIVKAFDKYPDTTTFLIDGCPRD
MANLEGWREFVEEPGHATAVGVLFYDTTEDVMLERILARADASTEKRSDDNEATARKRFQTFRDLTMPVMDELRKDGIVR
DIDASRPVDEVFQDTVREVDDLLLQAKA

269 - 288:	EEEEEEEEEEEEEEEEEEE
270 - 289:	EEEEEEEEEEEEEEEEEEE

A0A2R5LNL6 **A0A2R5LNL6_9ACAR** (377 aa)
Putative troponin t skeletal muscle. *Ornithodoros turicata*

MTEAEMLMEEKLRKKKEEEEEMWAEYLEQRRKQRAKEEEELRRLKERQAKRKMQRAEQEAKLMELKKKQEEQRIREMEEK
KAREAEAKRKRLEEAERKRQAMQAAKEKREAEPVKPNFVITKKEGDDMGSALGGSGFDKFANIMYARGEMGKTKEQLDDD
KKAIMSFRVKPLEMEGLTVEQLREKAKELWERIVGLESDKYDLEERQKRQDYDLKELAERQRQINRNRALKKGLDPEALQ
GKHPPKIQVASKYERRTDRRTFTDKKDLFAGGLEAMTDAEMEKQWEERMLNFKEAARGGLPKWDPENPKNKQSVVHRHVD
DEEEEEELAPPVFEPPPAPKPAPKPVQQQEEEEEEEEEEEEEEEEEEEEEEEEE

350 - 369:	EEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEE

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE

A0A2R6XI97 **A0A2R6XI97_MARPO** (477 aa)
Uncharacterized protein. *Marchantia polymorpha (Liverwort) (Marchantia aquatica)*

```
MKIDEKDVEEKEVQAKVGERKDGAKKERVLKEEDKHEEELEEEEEEEEEEEEEEEEEEEEPLQARMVSSKDEKMEEEEEE
EEEEEEEEEEEEEVEEEEVEEEEVEEDEVDDKDGSIEEQIAFTRVLENFFRDRNLEYKAPKFYGEELNVLKLWKAVTSLG
GYEQVTSGKLWRQVGEQFKPPKTCTTISWSFRGFYEKALLDYERFQTGGCLPSSFGGKDLNQGDALLSGFENQAAMSPTT
PSSQPNAAAASGSGRARRDAAARAMQGWHSQRAGNGEVGDPIIKEKSGVLKKEKQLKSLGGTKRKETASLVERAVKVARA
KGVRSRSLDDVPSENALSAGANISKAGPLLKKSAKQDRSKHGTKSTSMEPMKGLKLVITDDGPPADWVKINAYRNTDGYE
IYALVPGLAREEVRIQCEEGGRVVICGSPEQPSNPWGVTAFRKVINLPSKIDAHHTSAVVTLYGQLFVRVPFAHSFQ
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41 - 60:	EEEEEEEEEEEEEEEEEEEE

A0A2R6XIB9 **A0A2R6XIB9_MARPO** (560 aa)
Uncharacterized protein. *Marchantia polymorpha (Liverwort) (Marchantia aquatica)*

```
MTEPETEIGNGASATIDSQPTVTDAPQEPVEAEVVKTSSGEHTESLRPRDVKQAPNVSTEGLFAKKAESEEVVNKEDDKK
VAEMKIDEKDVEEKEVQAKVGERKDGAKKERVLKEEDKHEEELEEEEEEEEEEEEEEEEEEEEPLQARMVSSKDEKMEEE
EEEEEEEEEEEEEEEEVEEEEVEEEEVEEDEVDDKDGSIEEQIAFTRVLENFFRDRNLEYKAPKFYGEELNVLKLWKAVT
SLGGYEQVTSGKLWRQVGEQFKPPKTCTTISWSFRGFYEKALLDYERFQTGGCLPSSFGGKDLNQGDALLSGFENQAAMS
PTTPSSQPNAAAASGSGRARRDAAARAMQGWHSQRAGNGEVGDPIIKEKSGVLKKEKQLKSLGGTKRKETASLVERAVKV
ARAKGVRSRSLDDVPSENALSAGANISKAGPLLKKSAKQDRSKHGTKSTSMEPMKGLKLVITDDGPPADWVKINAYRNTD
GYEIYALVPGLAREEVRIQCEEGGRVVICGSPEQPSNPWGVTAFRKVINLPSKIDAHHTSAVVTLYGQLFVRVPFAHSFQ
```

124 - 143:	EEEEEEEEEEEEEEEEEEEE

A0A2R6XTI0 **A0A2R6XTI0_MARPO** (576 aa)
RING-type domain-containing protein. *Marchantia polymorpha (Liverwort) (Marchantia aquatica)*

```
MPLSAKKVAASYGSGGVRVPRAPLILCLTCPLCGDLFREATTVSECLHTFCRDCIQGRLSDGETNSCPICNVSLGTLPLE
KLRADHQLDDVKAKLFPDASRKRKNGPGSSPAVSAAPIRRKERSLYSLGIGAQPQSANPGFATRATRGSPGKSLAVRDTS
SSEEEEEEEEEEEEEEEEEEEEEEEEEDADEVDEQDEEEDEPTDAEDYVGKEGTNGMVESAPFSTTGAKRMEVEHEINDL
DFIPFRPSRPKEEPRRAPIREPPAPSSDVGIYHARRSVLTANGVARTRSGSGMEPMVSADETGAGSAKGPANSQDGRGLG
SDNLLATLAEVAEASGIGKASRGEQPQTGASGLANNGPDISRGRDIVSHDAKSIETRPSSAITQALDSSTLHASPPRARR
SSPQLQRNPSLKLFVNGGVERPAILMHPTPPANGSLLASTSFAPNSCGIWFALQAARNQSADNPLPQLSSPYLRIKDGKL
PVSHVKKYLVKKLGLSNETEVEITCRGQPVVSSLPLESVRNIWFATAAAPNTKDQENQGLAANETTTGLMHLDASSAKEL
IMVLTYQRHRRNTRIC
```

163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE

A0A2R7VY08 **A0A2R7VY08_ONCFA** (68 aa)
Uncharacterized protein. *Oncopeltus fasciatus (Large milkweed bug)*

```
MSLNDFSTTTRLRSLTQGPRVMGRVTFRFTMNIEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEFSY
```

34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE

A0A2R7X5R5 **A0A2R7X5R5_ONCFA** (362 aa)
Uncharacterized protein. *Oncopeltus fasciatus (Large milkweed bug)*

```
MSSSTSLSNNKGISCKEQIEYLTRIISVTSLESALAPTTILKQVQRIQKIVTWFRRGTKCRFRITLSPQKSLRNEHCGFI
TVGLQRDFHGKEFCSSGAGLSGAFATRECITAVLPLACTLLCEESRLCKSQLFNWICLQGLTVECCFKVSWRFACGRRSG
YGGSTSYIRLNAPLIVFFYQIISWFRNEWICLFPVACLISKSPILMFAHVVFLEVIRFQKLVFLTTRNVNITMCLTILEG
LYSLKSINFVNLSLPKGDSLRFPDIHSISNRILPHFQSDNLSCSFSWRSWSSVEVACIAFTLESLDSLQARGRQASRAIE
EEEEEEEEEEEEEEEEEEEEKEEEEEEEEEEEEEEEEEEE
```

320 - 339:	EEEEEEEEEEEEEEEEEEEE
321 - 340:	EEEEEEEEEEEEEEEEEEEE
322 - 341:	EEEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEEE

A0A2R7X7C4 **A0A2R7X7C4_ONCFA** (137 aa)
Uncharacterized protein. *Oncopeltus fasciatus (Large milkweed bug)*

```
MKRTTPTYNSSGNNPCHSGGTGGELDKRAMGHRARRINGCERSWEISPSQVKLVVVADGEILEFYPDTKAGEGWEKSAGG
RVTLALGGRQEEENEFMRRTYEEEEEEEEEEEEEEEEEEEEEEFIIYEEEFMRKNL
```

102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE

A0A2R8M6T4 **A0A2R8M6T4_CALJA** (1012 aa)
Solute carrier family 24 member 1. *Callithrix jacchus (White-tufted-ear marmoset)*

```
MRKLIRMGPQERRLFRTKRLHWSRLLFLLGMLIIGSTYQHLRRPRGLSSLWGAVSSHQPVKLASRDLPSEEMMMASSDPP
KPSSEMRGEMLVPQASVDSDEATLSITVGNIPNIPKRTAKMISTTTKNNYSPTAAGTERRKENTPTFSRTLTYYTPTSSR
QIVKKYTPTSRGEVKSYSPTQASEKVKYTPSPRGRRVGTYAPSTFMTMETSMITPRTTVKDSDIMATYKILETNSLKRME
ETALTTLKGMVDSTPPYLTYEVETNVLTSPRNIVEKNNLTPPRRMENNSSTHPWGLVGKNNLMTQGTVLTHTPATSEGQV
TISTMTGSSPAETKASTAARSVRNPSPGTSVSAIETTPATVWRLAKKPSTAPSTSATPMVRAKLTTQVHHCVVVKPTPAM
PTTLSPSLSTALLPEELSPSPSVLPSSLPDLHPKGEYPPDLFSVEERRQGWVVLHIFGMMYVFVALAIVCDEYFVPALGV
ITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILHLTWWPLFRDVS
FYILDLIMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKQIEVWVKEQLSRRSAAKVMALGNLSKLPSLLTRGSSSTS
LHNSTIRSTIYQLMLHSLDPLREVRLAKEKEEESLNQEARAQPQAKAESKPEEEEPAKLPVVTVTSAPALDIKGDQKKNP
GGQEDEAEAESTGEEGETVGEGETKEKSGGETQPGSEGETETKEKRGGGEGETETQVKGEGKGDNEGEGEGEICTEDSEM
KGNEGKTESQKLRGENHGEAKNDEKDIEAEGGSDGGDSEEEEKEEEEEEEEEEEEEEEEEEEEQEQEEEEEEENEEPLS
LDWPETRQKQAIYLFLLPIVFPLWLTVPDVRRPESRKFFVLTFLGSIVWIAMFSYLMVWWAHQVGETIGISEEIMGLTIL
AAGTSIPDLITSVIVARKGLGDMAVSSSVGSNIFDITVGVESCEMFQLGAIH
```

844 - 863:	EEEEEEEEEEEEEEEEEEEE
845 - 864:	EEEEEEEEEEEEEEEEEEEE

A0A2R8M9U5 **A0A2R8M9U5_CALJA** (1213 aa)
Myelin transcription factor 1. *Callithrix jacchus (White-tufted-ear marmoset)*

```
MTHTDKCVQLYFIFSDGVLLCHPGGVQWGDLSSLQPLPVGSGDSPASASGVSGIAENEFQGELLNQRWTHGGKASSCKTS
RPLLGRPCKMSLENEDKRARTRSKALRGAPETTAADLSCPTPGCTGSGHVRGKYSRHRSLQSCPLAKKRKLEGTEAEHLV
SKRKSHPLKLALDEGYGVDSDGSEDTEVKDASVSDESEGTLEGAEAETSGQEEIHRPKPAEGRSPVKSHFGSNPISSPTG
SSKGSYSSYQGIIATSLLNLGQLAEETLVEENLGQAAKPGPGIVHLLQEATEGAASVEGKKGLFIQPEDAEEVIEVTSER
SQDLCPQSLEDVASEESSKQKGILSHEEEDEEEEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAASDVI
FQEDASHISAQKAPELRGPESPSPKSEYSVIVEVRSDDDKDEDTHSQKSTVTDESEMHDMMTRGNLGLLEQAIALKAEQV
RTVCEPGCLPAEQSKLGLAEPGKAAKPLDTVRKSYYSKDPSRAEKREIKCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRI
PPEILAMHENVLKCPTPGCTGQGHVNSNRNTHRSLSGCPIAAAEKLAKSHEKQQPQTADPSKNSSNSDRILRPMCFVKQL
EVPPYGSYRPNVAPTTPRANLAKELEKFSKVTFDYASFDAQVFGKRMLAPKIQTSETSPKAFQCFDYSHDAEAAHMAATA
ILNLSTRCWERPENLSMKPQDLPSKSVDIEVDENGTLDLSMHKHRRRENAFPSSSSCSSSPGVKSPDPSQRQSSTSAPNS
SMTSPQSSQASRQDEWDRPLDYTKPSRLREEEPEESEPAAHSFASSEADDQEVSEENFEERKYPGEVTLTNFKLKFLSKD
IKKELLTCPTPGCDGSGHITGNYASHRSLSGCPLADKSLRNLMAAHSADLKCPTPGCDGSGHITGNYASHRSLSGCPRAK
KSGVKVAPTKDDKEDPELMKCPVPGCVGLGHISGKYASHRSASGCPLAARRQKEGSLNGSSFSWKSLKNEGPTCPTPGCD
GSGHANGSFLTHRSLSGCPRATFAGKKGKLSGDEVLTPKFKTSDVLENDEEIKQLNQEIRDLNESNSEMEAAMVQLQSQI
SSMEKNLKNIEEENKLIEEQNEALFLELSGLSQALIQSLANIRLPHMEPICEQNFDAYVSTLTDMYSNQECYQNPENKDL
LESIKQAVRGIQV
```

362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE

369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE

A0A2R8MDE0 **A0A2R8MDE0_CALJA** (1069 aa)
Solute carrier family 24 member 1. *Callithrix jacchus (White-tufted-ear marmoset)*

```
MRKLIRMGPQERRLFRTKRLHWSRLLFLLGMLIIGSTYQHLRRPRGLSSLWGAVSSHQPVKLASRDLPSEEMMMASSDPP
KPSSEMRGEMLVPQASVDSDEATLSITVGNIPNIPKRTAKMISTTTKNNYSPTAAGTERRKENTPTFSRTLTYYTPTSSR
QIVKKYTPTSRGEVKSYSPTQASEKVKYTPSPRGRRVGTYAPSTFMTMETSMITPRTTVKDSDIMATYKILETNSLKRME
ETALTTLKGMVDSTPPYLTYEVETNVLTSPRNIVEKNNLTPPRRMENNSSTHPWGLVGKNNLMTQGTVLTHTPATSEGQV
TISTMTGSSPAETKASTAARSVRNPSPGTSVSAIETTPATVWRLAKKPSTAPSTSATPMVRAKLTTQVHHCVVVKPTPAM
PTTLSPSLSTALLPEELSPSPSVLPSSLPDLHPKGEYPPDLFSVEERRQGWVVLHIFGMMYVFVALAIVCDEYFVPALGV
ITDKLQISEDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCSLFSREILHLTWWPLFRDVS
FYILDLIMLILFFLDSLIAWWESLLLLLAYAFYVFTMKWNKQIEVWVKEQLSRRSAAKVMALGNLSKPGDGAVAVDELQD
NNKLKLPSLLTRGSSSTSLHNSTIRSTIYQLMLHSLDPLREVRLAKEKEEESLNQEARAQPQAKAESKPEEEEPAKLPVV
TVTSAPALDIKGDQKKNPGGQEDEAEAESTGEEGETVGEGETKEKSGGETQPGSEGETETKEKRGGGEGETETQVKGEGK
GDNEGEGEGEICTEDSEMKGNEGKTESQKLRGENHGEAKNDEKDIEAEGGSDGGDSEEEEKEEEEEEEEEEEEEEEEEE
EEQEQEEEEEEENEEPLSLDWPETRQKQAIYLFLLPIVFPLWLTVPDVRRPVGETIGISEEIMGLTILAAGTSIPDLITS
VIVARKGLGDMAVSSSVGSNIFDITVGLPVPWLLFSLINGLQPVPVSSNGLFCAIVLLFLMLLFVISSIASCKWRMNKIL
GFTMFLLYFVFLIISVMLEDRIISCPVSV
```

862 - 881:	EEEEEEEEEEEEEEEEEEEE
863 - 882:	EEEEEEEEEEEEEEEEEEEE

A0A2R8MY35 **A0A2R8MY35_CALJA** (1141 aa)
Myelin transcription factor 1. *Callithrix jacchus (White-tufted-ear marmoset)*

```
MSLENEDKRARTRSKALRGAPETTAADLSCPTPGCTGSGHVRGKYSRHRSLQSCPLAKKRKLEGTEAEHLVSKRKSHPLK
LALDEGYGVDSDGSEDTEVKDASVSDESEGTLEGAEAETSGQEEIHRPKPAEGRSPVKSHFGSNPISSPTGSSKGSYSSY
QGIIATSLLNLGQLAEETLVEENLGQAAKPGPGIVHLLQEATEGAASVEGKKGLFIQPEDAEEVIEVTSERSQDLCPQSL
EDVASEESSKQKGILSHEEEDEEEEEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAASDVIFQEDASHIS
AQKAPELRGPESPSPKSEYSVIVEVRSDDDKDEDTHSQKSTVTDESEMHDMMTRGNLGLLEQAIALKAEQVRTVCEPGCL
PAEQSKLGLAEPGKAAKPLDTVRKSYYSKDPSRAEKREIKCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRIPPEILAMHE
NVLKCPTPGCTGQGHVNSNRNTHRSLSGCPIAAAEKLAKSHEKQQPQTADPSKNSSNSDRILRPMCFVKQLEVPPYGSYR
PNVAPTTPRANLAKELEKFSKVTFDYASFDAQVFGKRMLAPKIQTSETSPKAFQCFDYSHDAEAAHMAATAILNLSTRCW
ERPENLSMKPQDLPSKSVDIEVDENGTLDLSMHKHRRRENAFPSSSSCSSSPGVKSPDPSQRQSSTSAPNSSMTSPQSSQ
ASRQDEWDRPLDYTKPSRLREEEPEESEPAAHSFASSEADDQEVSEENFEERKYPGEVTLTNFKLKFLSKDIKKELLTCP
TPGCDGSGHITGNYASHRSLSGCPLADKSLRNLMAAHSADLKCPTPGCDGSGHITGNYASHRSLSGCPRAKKSGVKVAPT
KDDKEDPELMKCPVPGCVGLGHISGKYASHRSASGCPLAARRQKEGSLNGSSFSWKSLKNEGPTCPTPGCDGSGHANGSF
LTHRSLSGCPRATFAGKKGKLSGDEVLTPKFKTSDVLENDEEIKQLNQEIRDLNESNSEMEAAMVQLQSQISSMEKNLKN
IEEENKLIEEQNEALFLELSGLSQALIQSLANIRLPHMVGSTRPCGHHGYPPGFLQKAVGQVSPTPLPLGPTLGVLCPCG
DSLDPEWPGQDVGCGGFSSPE
```

273 - 292:	EEEEEEEEEEEEEEEEEEEE
274 - 293:	EEEEEEEEEEEEEEEEEEEE
275 - 294:	EEEEEEEEEEEEEEEEEEEE
276 - 295:	EEEEEEEEEEEEEEEEEEEE
277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE

A0A2R8PI86 **A0A2R8PI86_CALJA** (736 aa)
YTH domain containing 1. *Callithrix jacchus (White-tufted-ear marmoset)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLVSKPLSSSVSN
NKRIVSTKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCLRKRDPERRAKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEE
EEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSA
SESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNVAFRSARSVIL
```

```
IFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQE
IELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQ
RPGYLKDPRYQEVDSFTNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQ
AHPPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERER
LCDRDRDRGERGRYRR
```

230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE

A0A2R9AEN7 **A0A2R9AEN7_PANPA** (1195 aa)
Euchromatic histone lysine methyltransferase 2. *Pan paniscus (Pygmy chimpanzee) (Bonobo)*

```
GEAPAEMGALLLEKETRGATERAHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDESE
NLEGDGDLRGGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGSEPPPATTSP
EGQPKVHRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDLAKRRKLNSGGGLSEELGSARRSEVTLTKGD
PGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSG
SSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLE
TERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCP
GCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLSQDAPGR
ADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLY
LSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVAR
YMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTD
NEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERS
DVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCT
CVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRAL
QTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPR
IAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELSSLPPVNT
```

285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE
287 - 306:	EEEEEEEEEEEEEEEEEEEE
288 - 307:	EEEEEEEEEEEEEEEEEEEE
289 - 308:	EEEEEEEEEEEEEEEEEEEE

A0A2R9AFS5 **A0A2R9AFS5_PANPA** (1278 aa)
Euchromatic histone lysine methyltransferase 2. *Pan paniscus (Pygmy chimpanzee) (Bonobo)*

```
MDAPRAALGTAGPETHHPWEQVAAPAAERTGARARCGIRRGRGARGRGASSAMGSRDWGGGPHRGRGRPRSLLSLPRAQA
SWTPQLSTGLTSPPVPCLPSQGEAPAEMGALLLEKETRGATERAHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVT
VGDEGADTPVGATPLIGDESENLEGDGDLRGGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLS
MPGAQGAAAAGSEPPPATTSPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDLAKRRKLNSG
GGLSEELGSARRSEVTLTKGDPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEE
EEEEEEEEEDEESGNQSDRRSGRLRGWRSGPEGVRGAPGGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTS
SLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHH
CCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLSQDA
PGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPR
QLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLE
VARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVT
LTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTP
ERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQ
HCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGV
RALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLR
FPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELSSLPPVNT
```

386 - 405:	EEEEEEEEEEEEEEEEEEEE
387 - 406:	EEEEEEEEEEEEEEEEEEEE
388 - 407:	EEEEEEEEEEEEEEEEEEEE
389 - 408:	EEEEEEEEEEEEEEEEEEEE
390 - 409:	EEEEEEEEEEEEEEEEEEEE

A0A2R9AJI6 **A0A2R9AJI6_PANPA** (1161 aa)
Euchromatic histone lysine methyltransferase 2. *Pan paniscus (Pygmy chimpanzee) (Bonobo)*

```
GEAPAEMGALLLEKETRGATERAHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDESE
NLEGDGDLRGGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAAGSEPPPATTSP
EGQPKVHRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDLAKRRKLNSGGGLSEELGSARRSEVTLTKGD
PGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSG
SSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMAT
ESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNG
MVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPS
LTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPL
HAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSL
LLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNY
HGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARG
YENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKI
EPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDL
DNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQ
CGSEKCKHSAEAIALEQSRLARLDPHPELLPELSSLPPVNT
```

285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE
287 - 306:	EEEEEEEEEEEEEEEEEEEE
288 - 307:	EEEEEEEEEEEEEEEEEEEE
289 - 308:	EEEEEEEEEEEEEEEEEEEE

A0A2R9AJL8 **A0A2R9AJL8_PANPA** (1244 aa)
Euchromatic histone lysine methyltransferase 2. *Pan paniscus (Pygmy chimpanzee) (Bonobo)*

```
MDAPRAALGTAGPETHHPWEQVAAPAAERTGARARCGIRRGRGARGRGASSAMGSRDWGGGPHRGRGRPRSLLSLPRAQA
SWTPQLSTGLTSPPVPCLPSQGEAPAEMGALLLEKETRGATERAHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVT
VGDEGADTPVGATPLIGDESENLEGDGDLRGGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLS
MPGAQGAAAAGSEPPPATTSPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDLAKRRKLNSG
GGLSEELGSARRSEVTLTKGDPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEE
EEEEEEEEEDEESGNQSDRRSGRLRGWRSGPEGVRGAPGGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKC
MATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQ
LNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLSQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSS
GPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKR
TPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEM
VSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHA
VNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDV
ARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEF
NKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYL
FDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYF
TCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELSSLPPVNT
```

386 - 405:	EEEEEEEEEEEEEEEEEEEE
387 - 406:	EEEEEEEEEEEEEEEEEEEE
388 - 407:	EEEEEEEEEEEEEEEEEEEE
389 - 408:	EEEEEEEEEEEEEEEEEEEE
390 - 409:	EEEEEEEEEEEEEEEEEEEE

A0A2R9ALG4 **A0A2R9ALG4_PANPA** (1188 aa)
Euchromatic histone lysine methyltransferase 2. *Pan paniscus (Pygmy chimpanzee) (Bonobo)*

```
RAAGLGGVDAAGEAPAEMGALLLEKETRGATERAHGSLGDTPRSEETLPKATPDSLEPAGPSSPASVTVTVGDEGADTPV
GATPLIGDESENLEGDGDLRGGRILLGHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAA
GSEPPPATTSPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDLAKRRKLNSGGGLSEELGSA
RRSEVTLTKGDPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEED
EESGNQSDRRSGRLRGWRSGPEGVRGAPGGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEE
LPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCT
AGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLSQDAPGRADTSQPS
ARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGE
LQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGG
CVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICL
HWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQ
LNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSS
SNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGT
FICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSR
DIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELSSLPPVNT
```

296 - 315:	EEEEEEEEEEEEEEEEEEEE
297 - 316:	EEEEEEEEEEEEEEEEEEEE
298 - 317:	EEEEEEEEEEEEEEEEEEEE
299 - 318:	EEEEEEEEEEEEEEEEEEEE
300 - 319:	EEEEEEEEEEEEEEEEEEEE

A0A2R9AT67 **A0A2R9AT67_PANPA** (1315 aa)
Tau tubulin kinase 1. *Pan paniscus (Pygmy chimpanzee) (Bonobo)*

```
MQCLAAALKDETNMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTRENVALKVESAQQPKQVLKMEVAV
LKKLQGKDHVCRFIGCGRNEKFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESIEAIHSVGFLHRDIKPSNF
AMGRLPSTYRKCYMLDFGLARQYTNTTGDVRPPRNVAGFRGTVRYASVNAHKNREMGRHDDLWSLFYMLVEFAVGQLPWR
KIKDKEQVGMIKEKYEHRMLLKHMPSEFHLFLDHIASLDYFTKPDYQLIMSVFENSMKERGIAENEAFDWEKAGTDALLS
TSTSTPPQQNTRQTAAMFGVVNVTPVPGDLLRENTEDVLQGEHLSDQENAPPILPGRPSEGLGPSPHLVPHPGGPEAEVW
EETDVNRNKLRINIGKSPCVEEEQSRGMGVPSSPVRAPPDSPTTPVRSLRYRRVNSPESERLSTADGRVELPERRSRMDL
PGSPSRQACSSQPAQMLSVDTGHADRQASGRMDVSASVEQEALSNAFRSVPLAEEEDFDSKEWVIIDKETELKDFPPGAE
PSTSGTTDEEPEELRPLPEEGEERRRLGAEPTVRPRGRSMQALAEEDLQHLPPQPLPPQLSQADGRSETSQPPTPGSPSH
SPLHSGPRPRRRESDPTGPQRQVFSVAPPFEVNGLPRAVPLSLPYQDFKRDLSDYRERARLLNRVRRVGFSHMLLTTPQV
PLAPVQPQANGKEEEEEEEEDEEEEEDEEEEEEEEEEEEEEEEEEEEEEEAAAAVALGEVLGPCSGSSSEGSERSTDRS
QEGAPSTLLADDQKESRGRASMADGDLEPEEGSKTLVLVSPGDMKKSPVTAELAPDPDLGTLAALTPQHERPQPTGSQLD
VSEPGTLSSVLKSEPKPPGPGAGLGAGTVATGVGGVAVTSSPFTKVERTFVHIAEKTHLNVMSSGGQALRSEEFSAGGEL
GLELASDGGAVEEGARAPLENGLALSGLNGAEIEGSALSGPPRETPSEMATNSLPNGPALADGPAPVSPLEPSPEKVATI
SPRRHAMPGSRPRSRIPVLLSEEDTGSEPSGSLSAKERWSKRARPQQDLARLVMEKRQGRLLLRLASGASSSSSEEQRRA
SETLSGTGSEEDTPASEPAAALPRKSGKAAATRSRIPRPIGLRMPMPVAAQQPASRSHGAAPASDTAITSSRLQLQTPPG
SATAADLRPKQPPGRGLGPGRDQAGARAPAPRSPHLPASTSAARNASASPRSQSLSRRESPSPSHLAPVRGPPAPGLMAP
PPPGGSKKGPRGKLQAQRATTKGRAGGAEGRAGAR
```

749 - 768:	EEEEEEEEEEEEEEEEEEEE
750 - 769:	EEEEEEEEEEEEEEEEEEEE
751 - 770:	EEEEEEEEEEEEEEEEEEEE
752 - 771:	EEEEEEEEEEEEEEEEEEEE

A0A2R9BG80 **A0A2R9BG80_PANPA** (1231 aa)
Cyclic nucleotide gated channel subunit beta 1. *Pan paniscus (Pygmy chimpanzee) (Bonobo)*

```
MLGWVQRVLPQPPGTPRKTKMQEEEKVEPEPETEAEVESELNPEEAETESESMPPEESFKEEEVAVADPSPQETKEAALT
STISLRAQGAEISEMNSPSRRVLTWLMKGVEKVIPQPVHSITEDPAQVLLGGCTDEPNEAQDTRPGLRLLLWLEQNLDRV
LPQPPKSSEVWRDEPAVATGAASDPAPPGRPQEMGPKLQARETPSLPTPIPLQPKEEPKEAPAPEPQPGSQVQTSSLPPP
RDPARLVAWVLHRLEMALPQPVLHGKMGEQVSAGLSILPGGQVEPDLVLEEVEPPWEDAHQDISTSPQGTEVVPAYEEEN
KAVEKMPRELSRIEEEKEDEEEEEEEEEEEEEEEEEEEEEEEVTEVLLDSCAVSQVGVGQSEEDGTRPQSASDQKLWEEV
GEEAKEEAEEKAKEEAEEAAEEEAEKEPQDWAETKEEPEAEAEAASSGVPATKQHPEVQVEDTDADSCPLMAEENPPSTV
LPPPSPAKSDTLIVPSSASGTHRKKLPSEDDEAEELKALSPAESPVVAWSDPTTPKDTDGQDRAASTASTNSAIINDRLQ
ELVKLFKERTEKVKEKLIDPDVTSDEESPKPSPAKKAPEPAPDTKPAEAKPVEEEHYCDMLCCKFKRRPWKKYQFPQSID
PLTNLMYVLWLFFVVMAWNWNCWLIPVRWAFPYQTPDNIHLWLLMDYLCDLIYFLDITVFQTRLQFVRGGDIIVSHRQVM
DLLSLLPLDFLYLKVGVNPLLRLPRCLKYMAFFEFNSRLESILSKAYVYRVIRTTAYLLYSLHLNSCLYYWASAYQGLGS
THWVYDGVGNSYIRCYYFAVKTLITIGGLPDPKTLFEIVFQLLNYFTGVFAFSVMIGQMRDVVGAATAGQTYYRSCMDST
VKYMNFYKIPKSVQNRVKTWYEYTWHSQGMLDESELMVQLPDKMRLDLAIDVNYNIVSKVALFQGCDRQMIFDMLKRLRS
VVYLPNDYVCKKGEIGREMYIIQAGQVQVLGGPDGKSVLVTLKAGSVFGEISLLAVGGGNRRTANVVAHGFTNLFILDKK
DLNEILVHYPESQKLLRKKARRMLRNNNKPKEEKSVLILPPRAGTPKLFNAALAMTGKMGGKGAKGGKLAHLRARLKELA
VLEAAAKQQELVEQAKSSQDVKGEEGSAAPDQHTPPKEAATDPPAPRTPPEPPGSPPSSPPPASLGRPEGEEEGPAEPEE
HSVRICMSPGPEPGEQILSVEMPEEREEKAE
```

340 - 359:	EEEEEEEEEEEEEEEEEEEE
341 - 360:	EEEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEEE

A0A2R9BP91 **A0A2R9BP91_PANPA** (225 aa)
Cysteine rich hydrophobic domain 1. *Pan paniscus (Pygmy chimpanzee) (Bonobo)*

```
MSILLPNMAEFDTISELEEEEEEEAATSSSSPSSSSSVSGPDDDEEDEEEEEEEEEEEEEEEEEEEEEEEEAPPPPRVVSEE
HLRRYAPDPVLVRGAGHITVFGLSNKFDTEFPSVLTGKVAPEEFKTSIGRVNACLKKALPVNVKWLLCGCLCCCCTLGCS
LWPVICLNKRTRRSIQKLIEWENNRLYHKLALHWKLTKRKCETSNMMEYVILIEFLPKYPIFRPD
```

48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE

A0A2R9BQ99 **A0A2R9BQ99_PANPA** (913 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Pan paniscus (Pygmy chimpanzee) (Bonobo)*

```
MELAVAVLRDLLRYAAQLPALFRDISMNHLPGLLTSLLGLRPECEQSALEGMKACMTYFPRACGSLKGKLASFFLSRVDA
LSPQLQQLACECYSRLPSLGAGFSQGLKHTESWEQELHSLLASLHTLLGALYEGAETAPVQNEGPGVEMLLSSEDGDAHV
LLQLRQRFSGLARCLGLMLSSEFGAPVSVPVQEILDFICRTLSVSSKNISLHGDGPLRLLLLPSIHLEALDLLSALILAC
GSRLLRFGILIGRLLPQVLNSWSIGRDSLSPGQERPYSTVRTKVYAILELWVQVCGASAGMLQGGASGEALLTHLLSDIS
PPADALKLRSPRGSPDGSLQTGKPSAPKKLKLDVGEAMAPPSHRKGDSNANSDVCAAALRGLSRTILMCGPLIKEETHRG
PLLCTHWGRLHDLVLPLVMGVQQGEVLGSSPYTSSRCRRELYCLLLALLLAPSPRCPPPLACALQAFSLGQREDSLEVSS
FCSEALVTCAALTHPRVPPLQPMGPTCPTPAPVPPPEAPSPFRAPPFHPPGPMPSVGSMPSAGPMPSAGPMPSAGPVSSA
RPGPPTTANHLGLSVPGLVSVPPRLLPGPENHRAGSNEDPILAPSGTPPPTIPPDETFGGRVPRPAFVHYDKEEASDVEI
SLESDSDDSVVIVPEGLPPLPPPPPSGATPPPIAPTGPPTASPPVPAKEEPEELPAAPGPLPPPPPPPPVPGPVTLPPP
QLVPEGTPGGGGPPALEEDLTVININSSDEEEEEEEEEEEEEEEEEEEEEDFEEEEEDEEEYFEEEEEEEEFEEDFEEEE
GELEEEEEEEDDEEEELEDVEREGESPAAGPPPQELVEEEPSAPPTLLEEETEDGSDKVQPPPETPAEEEMETETEAEAL
QEKEQDDTAAMLADFIDCPPDDEKPPPPTEPDS
```

750 - 769:	EEEEEEEEEEEEEEEEEEEE
751 - 770:	EEEEEEEEEEEEEEEEEEEE

A0A2R9BTR3 **A0A2R9BTR3_PANPA** (1178 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Pan paniscus (Pygmy chimpanzee) (Bonobo)*

```
MLLPSLSPRVQPAFTQCARPQPPPQAPSPVGGRRGVFASSRHATTGTRGKMAAAVLSGPSAGSAAGVPGGTGGLSAVSSG
PRLRLLLLESVSGLLQPRTGSAVAPVHPPNRSAPHLPALMCLLRLHGSVGGAQNLSALGALVSLSNARLSSIKTRFEGLC
LLSLLVGESPTELFQQHCVSWLRSIQQVLQTQDPPATMELAVAVLRDLLRYAAQLPALFRDISMNHLPGLLTSLLGLRPE
CEQSALEGMKACMTYFPRACGSLKGKLASFFLSRVDALSPQLQQLACECYSRLPSLGAGFSQGLKHTESWEQELHSLLAS
LHTLLGALYEGAETAPVQNEGPGVEMLLSSEDGDAHVLLQLRQRFSGLARCLGLMLSSEFGAPVSVPVQEILDFICRTLS
VSSKNISLHGDGPLRLLLLPSIHLEALDLLSALILACGSRLLRFGILIGRLLPQVLNSWSIGRDSLSPGQERPYSTVRTK
VYAILELWVQVCGASAGMLQGGASGEALLTHLLSDISPPADALKLRSPRGSPDGSLQTGKPSAPKKLKLDVGEAMAPPSH
RKGDSNANSDVCAAALRGLSRTILMCGPLIKEETHRRLHDLVLPLVMGVQQGEVLGSSPYTSSRCRRELYCLLLALLLAP
SPRCPPPLACALQAFSLGQREDSLEVSSFCSEALVTCAALTHPRVPPLQPMGPTCPTPAPVPPPEAPSPFRAPPFHPPGP
MPSVGSMPSAGPMPSAGPMPSAGPVSSARPGPPTTANHLGLSVPGLVSVPPRLLPGPENHRAGSNEDPILAPSGTPPPTI
PPDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDSVVIVPEGLPPLPPPPPSGATPPPIAPTGPPTASPPVPAKEEPE
```

```
ELPAAPGPLPPPPPPPPPVPGPVTLPPPQLVPEGTPGGGGPPALEEDLTVININSSDEEEEEEEEEEEEEEEEEEEEDF
EEEEEDEEEYFEEEEEEEEFEEDFEEEEGELEEEEEEEDDEEEELEDVEDLEFGTAGGEVEEGAPPPPTLPPALPPPESP
PKVQPEPEPEPGLLLEVEEPGTEEERGADTAPTLAPEALPSQGEVEREGESPAAGPPPQELVEEEPSAPPTLLEEETEDG
SDKVQPPPETPAEEEMETETEAEALQEKEQDDTAAMLADFIDCPPDDEKPPPPTEPDS
```

938 - 957:	EEEEEEEEEEEEEEEEEEEE
939 - 958:	EEEEEEEEEEEEEEEEEEEE

A0A2R9BXI7 **A0A2R9BXI7_PANPA** (205 aa)
Cysteine rich hydrophobic domain 1. *Pan paniscus (Pygmy chimpanzee) (Bonobo)*

```
MSILLPNMAEFDTISELEEEEEEEAATSSSSPSSSSSVSGPDDDEEDEEEEEEEEEEEEEEEEEEEEEAPPPPRVVSEE
HLRRYAPDPVLVRGAGHITVFGLSNKFDTEFPSVLTGKVAPEEFKTSIGRVNACLKKALPVNVKWLLCGCLCCCCTLGCS
LWPVICLNKRTRRSIQKLIEWENNRLYHKVILIEFLPKYPIFRPD
```

48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE

A0A2R9BZC1 **A0A2R9BZC1_PANPA** (1177 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Pan paniscus (Pygmy chimpanzee) (Bonobo)*

```
MLLPSLSPRVQPAFTQCARPQPPPQAPSPVGGRRGVFASSRHATTGTRGKMAAAVLSGPSAGSAAGVPGGTGGLSAVSSG
PRLRLLLLESVSGLLQPRTGSAVAPVHPPNRSAPHLPALMCLLRLHGSVGGAQNLSALGALVSLSNARLSSIKTRFEGLC
LLSLLVGESPTELFQQHCVSWLRSIQQVLQTQDPPATMELAVAVLRDLLRYAAQLPALFRDISMNHLPGLLTSLLGLRPE
CEQSALEGMKACMTYFPRACGSLKGKLASFFLSRVDALSPQLQQLACECYSRLPSLGAGFSQGLKHTESWEQELHSLLAS
LHTLLGALYEGAETAPVQNEGPGVEMLLSSEDGDAHVLLQLRQRFSGLARCLGLMLSSEFGAPVSVPVQEILDFICRTLS
VSSKNISLHGDGPLRLLLLPSIHLEALDLLSALILACGSRLLRFGILIGRLLPQVLNSWSIGRDSLSPGQERPYSTVRTK
VYAILELWVQVCGASAGMLQGGASGEALLTHLLSDISPPADALKLRSPRGSPDGSLQTGKPSAPKKLKLDVGEAMAPPSH
RKGDSNANSDVCAAALRGLSRTILMCGPLIKEETHRGPLLCTHWGRLHDLVLPLVMGVQQGEVLGSSPYTSSRCRRELYC
LLLALLLAPSPRCPPPLACALQAFSLGQREDSLEVSSFCSEALVTCAALTHPRVPPLQPMGPTCPTPAPVPPPEAPSPFR
APPFHPPGPMPSVGSMPSAGPMPSAGPMPSAGPVSSARPGPPTTANHLGLSVPGLVSVPPRLLPGPENHRAGSNEDPILA
PSGTPPPTIPPDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDSVVIVPEGLPPLPPPPPSGATPPPIAPTGPPTASP
PVPAKEEPEELPAAPGPLPPPPPPPPPVPGPVTLPPPQLVPEGTPGGGGPPALEEDLTVININSSDEEEEEEEEEEEEEE
EEEEEEEDFEEEEEDEEEYFEEEEEEEEFEEDFEEEEGELEEEEEEEDDEEEELEDVEDLEFGTAGGEVEEGAPPPPTLP
PALPPPESPPKVQPEPEPEPGLLLEVEEPGTEEERGADTAPTLAPEALPSQGEVEREGESPAAGPPPQELVEEEPSAPPT
LLEEETEDGSDKVQPPPETPAEEEMETETEAEALQEKVRGQAGKVPWARRWGWREKG
```

947 - 966:	EEEEEEEEEEEEEEEEEEEE
948 - 967:	EEEEEEEEEEEEEEEEEEEE

A0A2R9C5J6 **A0A2R9C5J6_PANPA** (709 aa)
YTH domain containing 1. *Pan paniscus (Pygmy chimpanzee) (Bonobo)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESADTKRQKPSVHSRQLVSKPLSSSVSN
NKRIVSTKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEE
EEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSAS
ESYADQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVILIFSVRESGKFQGFARLSSE
SHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLLFPPDESI
DLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQRPGYLKDPRYQEVDRRFSG
VRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHHPVPHEARYRDKRVHDYDM
RVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDRGERGRYRR
```

230 - 249:	EEEEEEEEEEEEEEEEEEEE

A0A2R9C5K1 **A0A2R9C5K1_PANPA** (536 aa)
YTH domain containing 1. *Pan paniscus (Pygmy chimpanzee) (Bonobo)*

```
KYGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESADTKRQKPSVHSRQLVSKPLSSSVSNNKRIVSTK
GKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVDRRASRSSQ
SSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEEEEEEEEEEEEEEEEEEEEYEQDE
RDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSASESYAGSEKKHEKLS
SSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVILIFSVRESGKFQGFAR
LSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLLFPP
DESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRLETFFGLIIGTCIRIT
```

215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE

A0A2R9CG49 **A0A2R9CG49_PANPA** (735 aa)
YTH domain containing 1. *Pan paniscus (Pygmy chimpanzee) (Bonobo)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESADTKRQKPSVHSRQLVSKPLSSSVSN
```

```
NKRIVSTKGKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEE
EEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSAS
ESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVILI
FSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEI
ELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQR
PGYLKDPRYQEVDSFTNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQA
HPPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERL
CDRDRDRGERGRYRR
```

230 - 249:	EEEEEEEEEEEEEEEEEEEE

A0A2R9CG54 **A0A2R9CG54_PANPA** (727 aa)
YTH domain containing 1. *Pan paniscus (Pygmy chimpanzee) (Bonobo)*

```
KYGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESADTKRQKPSVHSRQLVSKPLSSSVSNNKRIVSTK
GKSVTEYKNEEYQRSERNKRLDADRKIRLSSSASREPYKNQPEKTCVRKRDPERRAKSPTPDGSERIGLEVDRRASRSSQ
SSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEEEEEEEEE
EYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSASESYAGSEK
KHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNLAFRSARSVILIFSVRESGK
FQGFARLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQL
CLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQRPGYLKDPR
YQEVDSFTNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHH
PVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDRG
ERGRYRR
```

222 - 241:	EEEEEEEEEEEEEEEEEEEE

A0A2S2N6C3 **A0A2S2N6C3_9ZZZZ** (130 aa)
Splicing factor, arginine/serine-rich 19 (Fragment). *bird metagenome*

```
GTAGGAASSSSPGKEAEGRQDQKYDPFDPTGSNPSSSRSSPSPGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEQPALP
DVSHSISRISETLAGIYDDNSLSQDFEKDPEPAPPKTPPNAPGADSTLPE
```

45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE

A0A2S2QC02 **A0A2S2QC02_9HEMI** (587 aa)
Ankyrin repeat domain-containing protein 17 (Fragment). *Sipha flava (yellow sugarcane aphid)*

```
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVPVKVLVEMKKKVDLKKKGKVTVLSSVILADVEEGDSGIDANSQGSCSS
TDAKNAAAARLAAQTQNPTSIKKEKKKKGKEAAVEVKINPSNAKLTTNSAATQTNATKVNSTQIKSNKEKKNQTNTTQNK
VASVLPTKTETISQIVVKSTQLKTKVQQPNNNLSNVTTRKESVKTNNYKGNNKVVNNMVFESTQNPAAREDFEATGSENF
IVKLKKQQQTEEYTNVNAKTSNVSPVKQTRGREEGWKEVVRTRYLASPYRSKKVSVPLNAISRVIGRGGSNINAIRASTG
ALIEVDNQSKGQGERIITIKGSTDVTKQAHDLIAMLIKDPEVNIMSVIAKNPKVTSAWDKSVNNAKAKTAAALPQKSIVS
QPITITASKVTSAPIVASMTIKPTITVNGPWPTVAAVAAGEKKITSTVKPTMSYTNAIISSSDPIPKSSQQTPTPVNPKV
VQSVSVTPETTAVTVSVTPTTASSASTTVMTKSINPLPLAQPKPQQEPSVTHHPVAIVSPMVSSAPVPPQSQIKPQVVDA
SEYSLFDSFSKVIKILITTDSYKISFF
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE

10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE

A0A2S3I2S0 **A0A2S3I2S0_9POAL** (682 aa)
G domain-containing protein. *Panicum hallii*

```
MAKPLPIPALTVARLPFRILSPSARPLCLLPFLPPPFVPQKRSLSASAVSTSRRGRPLAPVISEGSDGEEAAVGRPVCPG
CGVFMQDADPNLPGFFKNPSRSSQDKMRESGEGLLTADTDAFLEGEEARVAKDALMSESDDELEYLDSDIDEFPEEIEED
EEDESAVKAGTDIDGFDSDWDSDWEEMEEDEDEKWRKELDGFTPPGVGYGNITEETIERLKKEKLSKSERKRRAKEAKRA
EAEEDLAVVCARCHSLRNYGLVKNDKAENLIPDFDFDRFISSRLMKRSASTPVIIMVVDCADFDGSFPKRAVKSLFKALE
GRRNSKVSETPRLVLVGTKVDLLPWQQMGVRFDRWVRGRAKAFGAPKLDAVFLISVHRDLAVRNLISYIKDSAGPRSNVW
VIGAQNAGKSTLINAIAKKQGVKITRLTEAAVPGTTLGILRVTGVLPAKAKMYDTPGLLHPYIMAMRLNNEERKMIEIRK
ELRPRSFRVKIGQSIHIGGLTRLDVLKSSAQTIYVTVWSSSNIPLHLGKTENAGDLREQHFGIRLQPPIGPERVNELGHW
TERRIEVSGESWDVNSMDIAVSGLGWYSLGLKGTATVSLWTFEGIGVTERDAMILHRAQFLERPGFWLPIAIANAIGEET
RKNSERRKAEQRRKEEEEEEEEEEEEEEEEEEEEELLLEEMVE
```

655 - 674:	EEEEEEEEEEEEEEEEEEEE

A0A2S4UJV9 **A0A2S4UJV9_9BASI** (1819 aa)
SH3 domain-containing protein. *Puccinia striiformis*

```
MPQQQQQQQQQHHIRQSEYEEDEEEEEEEEEEEEEEEEEEEEENHYREHQQNQNEVTQDDEADRASDSSFSDSVSLSSTPS
IPCSDDIDFTLVYALHTFLATVDGQASVVKGDQLTLLDDSNSYWWLIRVLKTQAVGYIPAENIETPFERLARLNKHRNVD
LSSATPVDVQAGAASSLAQTRFTQRIPSAGDPVRSRSPQDRRKGPGPPPMVGPGYFSPPPVAPAPGTGKGKTVVFTAPTY
FENSGNEWSEDEEGESGNEHMMDGEEVADGDWDGEGEFEEGEEGFEDEEEESEDDEEEEEEEEEEDKHSETNNTPQRPERA
PVLDVDSNNPKPNTTIDSQRQLEDQLAQEHKQQQRQHQLQQQIQHQVASEQSLSRQISAESEEAIKSPSGWTRLVWPPKH
LQTLYEVVQVIRVRMTHAANSEKQQAGARNITHASLSNGPKSSSSLSVDRIASTSALQLNPSALTETKKLTLTPNIARDS
ALYALDGSPPNSARSINPTRQRSLSASSTEGPYRHSTSKPQTRINGGEPSPVSLEGNSIYSTDSHNGTAEETKPLKLSSS
TKKEETESKKKKAGGILSGLFSRKKDKKPKNDHTTDELRSSSLDNDRHRSASPLSPSENSIRSLNSPQHVEGSPGRRVAV
EQDDMFSTDAALRKQQEEAQEVMHRQYGISRETTDLNGTQRKPSYPPINANVPSASLSSHSPFSPGSSTGHSPAGGRVRP
GSLIGSPGINGLDVPMLNVLRIFAGDNVDCEATFKTVLLSAATTAQDGEETVLNDHPQTPLKLFEMMNESLGQHSLSLPS
VKRSSVGSISSISSNLSLNPAISRLGMNDFSDDSAVKFYINRYPDGHQAQRNNPSIQSTRKHERSGSLAPIQEDGSGPHK
GSDERVTLLWSLQIHPPSHLNTTPKIRRALSTLTTSSPSLRFAMRVRMHSNDLPEGLVFDPQSNAIIPKTVLIERGQRAA
LNPPSSPLNSGASYREKVIIFPRNIHVSDAIEHTLEAFGIADGVVDGGDDIDDKLSKRRNSAKIRYGLSMLSHDSTSEVP
VNLISKVLDSYQVPPILRPADRTSKEARRRSQEYHPFVLGTIQDLQPTDPIFSLRRALHHHPVTRRDSYRTSTSNHNGLV
GAVADELSALQNTRKNSLTGSPVVTSPPPPHLSTLASRPPAPSTQASFRTASESLYSSTENESIPTTVSSSNPVAVVSTH
PNSEEGIDINLENNARIRSIRRNHDNNNGDDDDDGSQEKKRAISQSYRYSYFDPSGEEYDISELIERELTTPQDDYLQQE
QREEFKGKNGETHQRNISLDRSTTHTHHHDDEDEDSAIEALRAADLTIDQDLVPTSSHLQNQNHREAPGKSIPQNKDLLA
WTVRKQQHHSDHSDSHRSSPSSSDHISSQPRSSPFSNETLDQRIARVLSQVNNPNQKSLNNNNIRPLAPTHSDSNSSSTT
YKTTSSQQHHPTTTTSLFNTSFETPPNATRSKGHPHPTIIPLNEELQQQSSTIDQQERTYQLNDDQDQAQTRRSLDSSGS
NSSNEDEDGSISPVTPLTATSPTGESGSSYTPISSATRGIGIDSRQSMNREQAGLGILPSGGNARHLGSFGGNHRGWLPL
LFPPASSSSSTSTTGNNLTNPSNGDDSGMMVSRQNENGGQAGLDILMNLIHHSAATSSSTIGLSSSSSFIDSSSTTTTSS
SSVHLPIKDIKFLWNSDSDPYLSQLFNERPNPSPLNSDPSSINGFHHHSPSSSLSNYETNETGGAGEISTTEDSKSINQF
IDPLSSSTDIRTFFNSSLHTFNHIDNKLDRLLDDLLKVPFNNKINSGSDPSVITSTTTD
```

23 - 42:	EEEEEEEEEEEEEEEEEEEE

A0A2S4UP00 **A0A2S4UP00_9BASI** (448 aa)
Uncharacterized protein. *Puccinia striiformis*

```
MANQKQKTNKIACPVEPPPPASPLPPSNQGISGRLFGLFKKFPMQITSPTKEIRPPSPQEKDNDHTQSEEQSDSEQEDED
EDEEEEEEEEEEEEEEEEEEEEGETDEQEIVTESEEEEDPLGEEQCKAIMENYLLETSTRTNLLRNRVETHFRPALRRRL
DFELSRITPSIANVTALDYHQRDQGVLRHTMEFVARQAIELKSISIGIKRSQSQQDQFWDEQEKNHHHKRKRQLTNNTES
QQAGTDPKPNSRSGSSSRSKPPRSRSKQSVLQAQERKNSSTSSLEPTELNPRLPSTPLISDFKPVRLARRNESLLSVNGS
PVISYGTTATTTNQEDENHRIPISTSSTTIASKFSELFPPSSISSSSLIDQHSSSHPNPLFGNSRSTNLVNTTSSDSQLS
LNSVNQFTFVEKSKWKELEVQLNSLEIDQIQKKKLDDLLKGCLNFGDS
```

83 - 102:	EEEEEEEEEEEEEEEEEEEE

A0A2S4UVE0 **A0A2S4UVE0_9BASI** (938 aa)
Uncharacterized protein. *Puccinia striiformis*

```
MNLAAVQSQQAFPSTPLPDPEPQQQAIHYAACQSQQAFPLTPLPDPQPQPQAIHFAAQAFSSTPLPNTQPISQPQQQAIN
FAACHSEQLFTSTHLPNPQPQQRALDQGSCQSLQAAVNQATRQSLQRLSSTPLSNGHPPPHATNQTSRQSLQAFSFLSTP
AADGHPLTDSTSRPASPQPRKSRANPNRPSQTSSTQASQTGTSKSNPSARSKKATQSQATDPTQPRFAALPSLQAELRRA
IDANAKTTKAKAANAAKAAERATAKALALAEEAKAAEAAEEAVQANERGQPALTILQLTAESPTTTSRNSAFNATHAPEL
DLNLDFSGLRSVPASPKATLHAIEDFPIDHSDRPGGHDADDACNEDDGHHHEDDDHHHDDRRYEDDGQPRDDGRDADDGQ
LPDQQAMDTSVHDHDEDSVDDINCDVVRLVNGNTRLRLKPQTVQRLEGMALDELRERCYKHEHYSRLVAEDKADLDEATD
EYDKHILRIACRNKLKLKTVEAYLGQGHRARGTNRYSEFCRYNLEARIATADGSKPMHQRWVESGRLWRQLTKEEQEQYD
DPDFLAQHANPFEELELEDGQILPACKRPTGPNGVNLAKPSKFDATRWCKSIQTTMVNLAKSHGVEGVVFVVYPTKKGRA
LLTGGSRLGQAYVNILPDEGNPAQDFLAFSDGQLSTQRLARCEVALPKKVRQPKAAKNRMENCEFSLGTLKANRPPICEQ
LGWAIHKASKGKWCNGWPGADTVNQLKLLKLSLRVDENPLQVGPEEFCKPISNMQIGEQERILTAIGKGWVHLERRDTSN
PTRAIGDVEEEADEAAPDVQVVSVTVGPVPPGESVPKKPSVKLKAGKGKGNGKGKGKGKGKGKGKGKGKGKAVRVQDETDDE
EEEEEEQEEEEIEEEEEEEEEEEEEEEEEEEEEEERGRGRGRGRGRGRGRGRGRGTAGRA
```

893 - 912:	EEEEEEEEEEEEEEEEEEEE
894 - 913:	EEEEEEEEEEEEEEEEEEEE
895 - 914:	EEEEEEEEEEEEEEEEEEEE

896 - 915:	EEEEEEEEEEEEEEEEEEEE

A0A2S4W641 **A0A2S4W641_9BASI** (1042 aa)
Uncharacterized protein. *Puccinia striiformis*

```
MINPYGGDAPRRLQDQSPLPPGQRLSPSDLQHYRNIQPHRSSGHHPIHSQPDPLVLGLVSHQSPFPSLYPSLPAHHQHTN
YRSPHLNKPVHPPRPPQAMNLAAVQSQQAFPSTPLPDPEPQQQAIHYAACQSQQAFPLTPLPDPQPQPQAIHFAAQAFSS
TPLPNTQPISQPQQQAINFAACHSEQLFTSTHLPNPQPQQRALDQGSCQSLQAAVNQATRQSLQRLSSTPLSNGHPPPHA
TNQTSRQSLQAFSFLSTPAADGHPLTDSTSRPASPQPRKSRANPNRPSQTSSTQASQTGTSKSNPSARSKKATQSQATDP
TQPRFAALPSLQAELRRAIDANAKTTKAKAANAAKAAERATAKALALAEEAKAAEAAEEAVQANERGQPALTILQLTAES
PTTTSRNSAFNATHAPELDLNLDFSGLRSVPASPKATLHAIEDFPIDHSDRPGGHDADDACNEDDGHHHEDDDHHHDDRR
YEDDGQPRDDGRDADDGQLPDQQAMDTSVHDHDEDSVDDINCDVVRLVNGNTRLRLKPQTVQRLEGMALDELRERCYKHE
HYSRLVAEDKADLDEATDEYDKHILRIACRNKLKLKTVEAYLGQGHRARGTNRYSEFCRYNLEARIATADGSKPMHQRWV
ESGRLWRQLTKEEQEQYDDPDFLAQHANPFEELELEDGQILPACKRPTGPNGVNLAKPSKFDATRWCKSIQTTMVNLAKS
HGVEGVVFVVYPTKKGRALLTGGSRLGQAYVNILPDEGNPAQDFLAFSDGQLSTQRLARCEVALPKKVRQPKAAKNRMEN
CEFSLGTLKANRPPICEQLGWAIHKASKGKWCNGWPGADTVNQLKLLKLSLRVDENPLQVGPEEFCKPISNMQIGEQERI
LTAIGKGWVHLERRDTSNPTRAIGDVEEEADEAAPDVQVVSVTVGPVPPGESVPKKPSVKLKAGKGKGNGKGKGKGKGKG
KGKGKGKAVRVQDETDDEEEEEEEQEEEEIEEEEEEEEEEEEEEEEEEEEEEEEEGKGKGKGKRKRKRKRNCRTRIISNR
VE
```

991 - 1010:	EEEEEEEEEEEEEEEEEEEE
992 - 1011:	EEEEEEEEEEEEEEEEEEEE
993 - 1012:	EEEEEEEEEEEEEEEEEEEE
994 - 1013:	EEEEEEEEEEEEEEEEEEEE
995 - 1014:	EEEEEEEEEEEEEEEEEEEE
996 - 1015:	EEEEEEEEEEEEEEEEEEEE

A0A2S4WNK7 **A0A2S4WNK7_9BASI** (488 aa)
Uncharacterized protein. *Puccinia striiformis*

```
MASGDSTKSDAPLYHNNSHKTKEVRFQDFQESYLQMFKLIREEVASYPKPDPEDEYEEPSSIEKNDIPYRLEKKLLPELK
ETLEKLSSITDPANVKDESTSKHLAFFEFLSQLTERLVELRETTDKMSDGIVSEQLLPDSQDVKPLSAFKRQRILEKVHH
LFVVTLSKLLSESGVFLWSFDPSNKTADDQLILKRRQELEQLFIPANKEIDEIIKWLQKPLLSVTRQGWQRLVVRIEERL
DTLLHNRNHKEDNYKSPERLRCIQAGIIFLQFSRLFFNKLSRPENSQDMFFTDSLMDPEVDRLQELIEVTETVPAALERF
LDSILSPCSPRGISRPAAMLHHHLDKLVQILRQHFISLNVNKNPAIDPVQIDNASRWLEFWVSQLRYVKRRMERATDRVI
DWSYEPKDSDDSAISSDTAMEESEEESEEEEKEEEEEEEEEEEEEEEEEEEEEEEEESEDEIYRVNDCSCFNCVNRAFKNRW
ESGRWGDC
```

433 - 452:	EEEEEEEEEEEEEEEEEEEE
434 - 453:	EEEEEEEEEEEEEEEEEEEE
435 - 454:	EEEEEEEEEEEEEEEEEEEE
436 - 455:	EEEEEEEEEEEEEEEEEEEE

A0A2S6UR88 **A0A2S6UR88_9PROT** (73 aa)
Uncharacterized protein (Fragment). *Alphaproteobacteria bacterium MarineAlpha2_Bin1*

```
MARRKNDEKLEKINEQEEDDDSSSDKMDLHVKNEKHDVNEDEEQGEEEEEEEEEEEEEEEEEEEQLEKKKFF
```

46 - 65:	EEEEEEEEEEEEEEEEEEEE

A0A2S6US09 **A0A2S6US09_9PROT** (392 aa)
FecR domain-containing protein (Fragment). *Alphaproteobacteria bacterium MarineAlpha2_Bin1*

```
MVESLTFGKGEMGDVRPGTPASSAQEYNLVIDASGHSSLTIPFGVLLLKADFVREGTDLLLVGPNGEQILVRDYFTMDPP
PDLLTEGGAMLTADTVEALAGPIAPGLFAQAEEGAEASPIGSVESVEGEVTVTRADGTEIKLNEGDPVFQGDVLETGEEG
TVGIVFIDDSTFALDEDGRMVLDELIFDPQSTEGKSSLTVVQGAFTFVSGKIAQSGPDSMKVSTPVATLGIRGTKVAGQA
AQEGEENTIVLLEGEILVTNQSGVALTLNQPNQSVQVTSAFTPPQAVQLTPDQVQQRFGGVLESLPPSPAATQETQETEG
PAATEEAVEEEEEEEEGEEEEGEEGAAEEGEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEEEGEGEEEEGEEEE
```

352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE

A0A2S7XXM5 **A0A2S7XXM5_BEABA** (594 aa)
Uncharacterized protein. *Beauveria bassiana (White muscardine disease fungus) (Tritirachium shiotae)*

```
MPLKDTISSPLEAGPSLLDAHHIPPQLVPALEYTSSRLARKSLHLTLVVARRDYQLPPSPVLCSPPPSPPSTCGSPASPS
RSRSFTRHLHLPRWGRRRHHDHQPSPSPASPSYSSSSSAAASSMPTSPRSIFSLPAYTPISPQFPRAQQGSMSPKSPIWP
LTPMTPLSPRLPTTPSTMKSSVPTESSSSYGFPMTPQHGVRLIHHGNLPAKAERTLQSALAKAGRKSGGDGRTHIAPALG
APACGLSSALFNDSVAQNDVLFSSDGLSLIALDRLYSLKAALSSYSKTGSPLRLEDAVDELRRYVLATGGKVSKMHLLRS
YDSLNVSRSALADLDRMYRRAYGGVEMQGGIDGMYFAPVPETTSSVWSDDEEDDNQDEEDDDDEMGREEAYNDQDSGVYV
EGLPDSPTVDPATVGMSDSATPVPTQPKLSPSSSASASSRKTPPLRVQTSMIHTPAHQTVDKTHAIDERQNATPIVPQEE
```

```
EEEEEEEEEEEEEEEEEEEEAEAVATARPDDESGLAAVARDQLWCSTQSASIDEVLSPGADLETPARDRNDDNDDDGPMTP
NGYDDISPITRGEWGFLLVDRDFRNARTVAVTTC
```

479 - 498:	EEEEEEEEEEEEEEEEEEEE
480 - 499:	EEEEEEEEEEEEEEEEEEEE

A0A2S7Y955 **A0A2S7Y955_BEABA** (1248 aa)
Uncharacterized protein. *Beauveria bassiana (White muscardine disease fungus) (Tritirachium shiotae)*

```
MASPVTTPQNPAPRRRGRPPGTTNAVRAARAAEAARLAELGQTVSSRKRRYVPGGPGGGGRYVDPESLLNASTPRTGAAP
PSSRRRAVASRDISYAVSPVPLPRRDRSTRTRATAGDDFEEIEWGSAAAVAASVKQAEDYKPREERSWEEFHPNLDIEQR
FVVFSADEVDGVVAMRETPSTPSRQTPGTPFNGAATPMLHANPVSTGNTPNSQFQFDVNSQPDSQPAAGALTPSRRSRRT
ARESVSFYGLRNTPMAGTPRTPRILPISNQTPKEKLDLKQPSFRKTNRIEPFESKTFGQARYVDKAMSNVGYQESDNFLR
PDETMLRAIDIGAEDDAEQSLALIPNKSEEHSIGSHVPHAQKLGRVEYDMDEQDDMWLEYYNAQRKQADLEPITREVFEI
TMTKIEKEWHALERRIPKPNPKPPQTHRPRSSSAAAVNGEVQSGGAGGAGSGDEPDSKCVICDDGDCENTNAIVFCDGCN
LAVHQECYGVPFIPEGQWLCRKCQLCGRGVPTCIFCPNTDGAFKQTNSSKWAHLLCAMWIPEISLGNHTFMEPVMDVEKV
PKTRWRLNCYICRQKMGACIQCSNKNCYQAFHVTCARRSRLYLKMKTSHGALAVLDSSMVLKAFCHNHCPPDYTIENNVH
QATRTAKKFYKRNMRGRIWADNQAMANVLAAQHRVAITEHPASESQTPSAKNLTMLGNGVDEQTGQGQPPKNLWKLPSGA
PIIPQAVYDVVEASIQRFPFRKRKDFLGEACRYWTLKREARRGAALLKRLQLQMEAFSSMELTRRDFASMGSNGRTRLAR
RIEFAENVVKDLEQLKELSEDVVRREQLRVEAAELENDFVDECYFPVAKLLEPAIEKAVFLDKDLFETDLQGISKRVSKR
HYATVMPFAQDLCKVISKGIRTPRAEVSDDVSSAGSRFEGANVSLSKPSFADIRERRKLGKRILKSVQPFLESALRVEAE
INSKSAETLATELEALIEASLDTTKPAEANEDTVMADAPDASEITVKGPVVDGNGADSAETDAMDTAEDDVVQDHIEVAT
SGLGIVDVTTLVAAAKSDKAAATRAAGSSSASPDDGGGGGGGDYAVLAQQQQQQQQQKGPPTPPQSNGSLGRDPPTDPL
TEGGILWHLKSFEPWGTSALLEQTAAVEVPGGFDAARLLSEDLTDLDEVELKGLGAHGSGALLAGGGEEEEEEEEEEEE
EEEEEEEEEEEAEEEEEEAEEAQAQAQEAATKTKTSKARARRVSARLR
```

1188 - 1207:	EEEEEEEEEEEEEEEEEEEE
1189 - 1208:	EEEEEEEEEEEEEEEEEEEE
1190 - 1209:	EEEEEEEEEEEEEEEEEEEE
1191 - 1210:	EEEEEEEEEEEEEEEEEEEE
1192 - 1211:	EEEEEEEEEEEEEEEEEEEE

A0A2T2ZRZ3 **A0A2T2ZRZ3_9PEZI** (225 aa)
Uncharacterized protein. *Coniella lustricola*

```
MLFLYQKHWRIDPAVGRCVFLSFNFLIFLSLFSFLSFWSRRTKSIVAERERETLLLATTKTTGQDKENPQDGRACPGGLQ
HLSIILCSSIMRPNGLGLAWLGFCVWCPVVVARHVRAVTGGVFMCVSCLFVCIRLADPSAETNVHGSPLWEKDSTTQELQ
YYSTWTRNGPKTQQRMVEEEEEEEEEEEEEEEEEEEEEGEEEEDLKIEVQDRIHRHIKKRNRTD
```

178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE

A0A2T2ZVG8 **A0A2T2ZVG8_9PEZI** (752 aa)
ANK_REP_REGION domain-containing protein. *Coniella lustricola*

```
MPSSSSSSSSSSSSSPLPAISSQNTSIQVVESAAPPPADATSAGGLGAVHLAVLQNRPTYLHRLLSQGEHGVDQRTPKDG
VTPAMLACLFGFAKVLTVLLRHGASLEKRDKQGRCPYDYLAARRQQSVNNGTGAGAGGWREMDVLVVEYLPFARQKPKPH
GQTYIAMMMKWHRKEMRKADSRHRRSNTAVNADHSDMAINDDSGIDNGKNDNSIHVSHPDNNQSTDVEMKDAAVHAQLEE
EEEEEEEEEEEEEEEEEEEEEEDRTRQPVSQATSGSSNDDDNDNNANNNNINNNNNTQNRTIFLRKGKVLEICEVRVVAS
VALDHDLGRKSLGAIRGKDNAHFSTFALSGWRGDQWKEKINFETVLNNKMYYGRSRHACEVFDQKLRANWLDNRFRGASS
DKVGAFEACHAEKQLAVWTVEEAAGLLLGSRAITTESLDQIRSRCHELPPSLQHSVIHLDHEPCVSCIGLLRRIRKKTGL
LIEWKPTEWFVWGKRSQLRRQDGRRVFTLGDHEAFENELEDGEDIDNDVLMDDDSAPPQDEDEIQEATTEQSGATEEDQS
QPEAGQTRAFCDRHKKNRVSSRHLKKGSPVLFDPVEKESPKNQPKAHRLPLPSRRRRRALRQARHRDRAERDKLLGRMAD
HAGKGDETGTADSPASTENDLSPVQPLTPFRPLPSHMPSPPMTKASKGVKIPIKEPPTAAVAAMLTAEEAGDDKNNKNEE
MEEHQEQPHQQPYQLQPDEQRHIEEPFPGAAL
```

239 - 258:	EEEEEEEEEEEEEEEEEEEE
240 - 259:	EEEEEEEEEEEEEEEEEEEE
241 - 260:	EEEEEEEEEEEEEEEEEEEE
242 - 261:	EEEEEEEEEEEEEEEEEEEE
243 - 262:	EEEEEEEEEEEEEEEEEEEE

A0A2T3A3P1 **A0A2T3A3P1_9PEZI** (652 aa)
Uncharacterized protein. *Coniella lustricola*

```
MSTLFPDSQLFKHNGAAARPETMMDASRAQRAFSSLRDPVRDVSPMPIVSDIIMTSAAPARTPLPALKPTDPERRPADQL
KPSSKAKGKKRAHSPLGSGSTPATKKRKGEKREIPCVKCVRRMANDPQWTCCDAVVGQTGSTKYTGNRCSSCVSMHVSCR
VVRLPQRYPPWPKTGAAYQNLTHYLQIPPQAEGPVRALVRAAADMVASNGHDKIVLRAVFEAAIGPALQAIVRTSLPDMP
PKKRRKTKKPSNGASPTHRPATTAAAAATALDPTHRTVLRPNKTPARAQSPQRGLNGRFSATAGAPTRLPQAQDNSHQNA
AQGPSQFSMHNTHYPADTVTSDFERLEHQALRRRKVEALESIAHTAALFLAEFMTFTKQYPSTATAAAASSSSTPLDMPN
RMNRGRGSDDRMHAELSHSHEVDFAAAAAASTAAAEMATTIFRPLLAQNWRDRTVSEDKPNPKHDEISCNDHDKNNAKRD
NDNFSGEEGANEDQLREDDDNDSDTGSESTNHSVARSLVTNSRLVVHYDDDDDNANHSNNGGQEERDSQLRNDESTDAEE
TDSSDADDDGDNEEEEEEEEEEEEEEEEEEEEEEGDSGPEAGSTNGGRLSVSAGARQQYNNEQLNSPAEAPQPQERDVTDA
ARESSVKVEDEE
```

573 - 592:	EEEEEEEEEEEEEEEEEEEE
574 - 593:	EEEEEEEEEEEEEEEEEEEE

A0A2T3A481 **A0A2T3A481_9PEZI** (329 aa)
Uncharacterized protein. *Coniella lustricola*

```
MLWWACVGELWEAASLDAKQCCRLRACIHRDDIFGSCTLYTYTSAAHALNRITDAPLLRPWAHMAAASLLIYQFLAPCSH
PRPEKPATHDGWIRPGTLSRFLPLLSTDTDTIRSGLSTRMPRRYVWKTLSKHVLFQENQPPSPRTSSLPQPRRGYEPSCA
PDPLAYSASAQLGSAADSGTPDSVRRVSRLCLVPLDPSDCVSAYRPRVASVLGVLLAVPLRWHYSIAIPQASQSGPRGLL
VSCQFGRSRGDRSRSRGGVPNAETQDEKRNEAEGTWTGAQQGGRRRGEEEEEEEEEEEEEEEEEEEGEGEKQHAAFPRC
GPGQGEPRA
```

288 - 307:	EEEEEEEEEEEEEEEEEEEE

A0A2T3AIH5 **A0A2T3AIH5_9PEZI** (768 aa)
ATPase. *Coniella lustricola*

```
MNTPKTTENIVQNDFAEEGKVKENASLIETGTESSAVETPTSDDDQEYQEDAVKNGAVEGSNGKNKAQSKAQGKAKTAKR
LKKDEEEEEEEEEEEEEEEEEEEEEEEEEEEEDKSNEDDDNNERNGDDEDEEEDEEEKSDLPVGSVSAVKNIYRSAKDA
DGNWTWVKKFPVDAEEPAENAITDTYAVLVRNMISRSGRKKLEAHSIVIQSPWLREALGKVILADYPGVACELERLTFEA
PFKPFVHRWTRLVDYLNREDLDEKLREHLVLLHDVLKYEIGDNIKAYEDYVQNGVITFQHLWMIFQPGSVVLAAHKGPLS
AFEILETEYLENKCGQFLQLRADCVDYSGKEFGRHTEHISVPEFIGTKKITGLNAFPLDFHEARDDVVDQLVRRGQTFEA
LAGHHYKAYDGIAITWDRQGEEQPISISGRIVIDIASFNRSNMWKRRWLGEWNAKDLERLQEHKKENGAIPEGAAYHLRL
TPYHQMLARSRTRGYSLKRKEWLESYVDQVGDIEWNTDAFDKLVLPEDQKELIMAFSESQIQGNADFDDLISGKGRGIIC
LLSGPPGVGKTLTAEAVAENLRVPLHTLSSGDLGSEAWEVETGLSQILELVARWKAILLLDECDVFLEARTTADLQRNKV
VSIFLRTLEYYEGILFMTTNRVDNIDAAFQSRIHVSLEYPDLTTQSRKQIWQNFLAGFKEAQKPEISDRDIEELAELHLN
GRQIKNILKTSQLLALRRKSVLRRCFIDTVLAIEKRRPAVNKGFTGTQ
```

85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE

A0A2T3AKG2 **A0A2T3AKG2_9PEZI** (315 aa)
WSC domain-domain-containing protein. *Coniella lustricola*

```
MLLTVLLLTVPATLAVASGAPDIYIGCFREGTDSRALDSASLTASNMTLQGCKSYCEGHRYYGLEHGTECYCGYRTISNP
HQVPESSCNLPCAGDLTQTCGGSNLISLYRARFTSQSPRYHWNNLGCIKEPPKSRALDRVLSTDSMTTNKCLVICSYGNY
QWAGLESGSECWCGNSLAAGIQSIDQICSMPCSGNATDTCGGPMALNLFSRNQTSLVLPPNSRTEIVEEEEEEEEEKEEE
EEEEEEEEEEEEEEEEEEDSDEETEADEDSDSSSDEEEEPADEENDQNADNEEHGDDGFVEAERKAIRKESPEGR
```

238 - 257:	EEEEEEEEEEEEEEEEEEEE
239 - 258:	EEEEEEEEEEEEEEEEEEEE

A0A2T4B9A0 **A0A2T4B9A0_9HYPO** (224 aa)
Uncharacterized protein. *Trichoderma citrinoviride*

```
MSPREHVRLPLLGDGPLFALTSDALAAAAAAGGVVYNNDDDDDDEGVLVLAAEDAAQFDELGGASSPWPEEEDSDDDDDE
PDSSSEDEQLLRFRGYAAVIRRAARMAPPHGDEAMHVYLMLILPLLFDKDDTEDEDEDAVVEQDSADDADADDEDEKEEE
EEEEEEEEEEEEEEEEEEEESYILLYLAGEAMAADMDPPDWTDPASELFLEAYAFPPLQRQNQR
```

158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE

A0A2T4GJI9 **A0A2T4GJI9_FUSCU** (1294 aa)
Importin N-terminal domain-containing protein. *Fusarium culmorum*

```
MQQALEIVHNPYATSGDRRTAQDYLEEVKDHDEAPMQGFNLASDKSQSPVVRHYALSLLEHAIRYRWSTYTTEQTEAVRQ
WVLNLGQAIAKEDPAYIRNKTAQLWVEVAKRCWGAEWMDMDSMLYQLWEVPDSAVHKELVMFILENLSDEVFTGDDSVVA
MREGVLSKACVEIFTPTSVLVEAFPNRQPGPPVRYGDDGWLSRLSQFLGYCLNSAHSDNDEVKLCIHKGLSALLSLMPWA
IPKAISSAHCVEVLCVGLASSHASIQKAALEALHALYCRTNFNDEEFRELVAPMYNRESIDLCRRLFEWSAVDPEDVDED
```

```
KYQTLKKLSEMLSCLGDYFDRKFAKLPAEAAKDEFLGLLVQIVQHQSLMVSIPVLVTWTRLLSNRLIGPGEHVSPLIPPL
LETCSSRLVRYENLPEDTQDPTFLYLMEDTDTVPERHAFLGNYRRYSSQIIEAVVQLKLVDAIPHILNRTEELLQHLYDG
QPPLDKQNYFKHSMPVLRVDAQFTVIEATLKGYTKWRKHRPQDHQQRGPEMEANLETWCNKILEMTFEDPMIRKRTLQLL
VYFSTTALNKNATFMLKVLEHILLTWPALEPEYRAFNDSIKDLQGESMVELQRLASEMPDHLLGVYDQIENKVNEMMSSG
SLDEKRSIAYRSFLFIIIHRATGVGADAKIQKLREFIDPVKAQWQDENVRNSLKSYGSFCELLGLDKAQAYMANHRAHEI
HDWGTRELDAEGLALQSELEERLKLLPLRSTKSFLAFSVERLDKNSDAFKASYALWEDGFSNILADLLEFLSFAHACHNP
DNWAGLPSEMRSTVNRILSDRFWQAGISEGSKDDFYARVMDKKNTMEGLASTIRGSVRFVRETAYAIIYCMSRLERQFYG
FQGLSAPLSKALFADSVWLSTHQQSNLLNLVRYLVDDCPVDCREHFLPQVLAACFQQMDAKINGEWDKMERQQQVAADGE
AGLKEEMKAESILRQVTYTAVLMVADFLDPTKLSKLRYVWFPQADYANGCTDGPIEDGESTSDSDQAKNYPTLRRFCLTH
HEIVEPLLVFCAHGIRMRDTRCCSMILRLFVSLVPEFHLVDGQLPKSVVQSPMEAHLASDKFPIPSSISSAIREYISLHV
LKACITSFHEPYFVELQKDLAALIAAIIVYYSPVTSTPSDVLLSLPNVSESSLERLSTYMAKPGAHTRQQRALVLDLLKD
LKGVSVSEMGKLPKSSGFDNSRGKRSNRSKMAQQFMNDPQAGQNATRAGMNVGRQSTPDGLEGVSNLFEGENEEEEEEEE
EEEEEEEEEEEEEE
```

1273 - 1292:	EEEEEEEEEEEEEEEEEEEE
1274 - 1293:	EEEEEEEEEEEEEEEEEEEE
1275 - 1294:	EEEEEEEEEEEEEEEEEEEE

A0A2T4GLI0 **A0A2T4GLI0_FUSCU** (1785 aa)
ATP-dependent DNA helicase II subunit 1 (EC 3.6.4.12) (ATP-dependent DNA helicase II subunit Ku70). *Fusarium culmorum*

```
MADKQDWRREDEDDGEQEVDENSYKAQKDAILLAIDVSKSMLEPPPPSDSKKADRDSPVQAALKCAYHLMEQRIISNPKD
MMGILLFGTEKSKFQESGDGRGSLGYPHCYLFTDLDVPAAEDVKALKALVEEGEDEDEVLTPSDEPVSMSNVLFCANQIF
TTKAANFGSRRLFIVTDNANPHASDKQAKSAAAVRAKDLYDLGIMIDLFPITRGDGTFDVHKFYDDIIYRDPVGEANMSE
VRTSKSGDGLTLLSSLISNVNSKQTAKRALFSNLPFEIAPGLRISVKGYNIVHRQVPARTCYIWLDGEKAQIASGETTRI
AEDSAKVIEKGDIKKAYKFGGEYVYFTPDEQKSLKDFGSPVIRIIGFKPRSSLPIWASTKKSTFIFPSEEDYVGSSRVFT
ALWQKLLKDDKMGIAWCITRANAQPMLAAIIPSRERSDDDSGTPYLPAGLWIYPLPFQDDLRNINPQARILQALALQEEV
PEKADDATEPKYKAISKRAGGYLEDWSECLAQEAGKVANSKATKRETDDEDVERPAKKSRGASEKASGSSFSMEQLKAAI
NGGGINKMTVVQLRDLLATKGMSVKMDVTKDPAAFMHTPPSASASDRRDSFQWAARQDSGNNQDILPVTGVRAQSPTSLV
GWPSHPTSSIKSVPFSSSASAQLFARPQTPGAGAGCRNRASTDSSPQKEPWADDYISRLLRRVRHRPVMADFLASLGFGG
AQTTAVSNNSQCDSVEQLQNQLRGILDAKVTSTRAEHVAITTELRATVRFQLTASELENGNHDNPNNLDPALGGAQSTEV
NGDQDAGQPSRVVFANDTIMNQPQDDPALQRSVAKHIISTISSADGSTWTVREVSRGAQGWTFTYLCKDSFQHWSRQTAK
NPLKTIVGEFSQREPDPTLHTRPAFDCRGSIVIAFNRSSRSISVKYDHTPLHKTVAELAAHFKPPPRQLGPGAQKLQEQQ
QKAKEKTPKKPRGEKKDKKERKKRDSVKAQDENGNPRKRKRKTNGASQPETTDGSMMPLDYPGASVVGGQTDPSYMNGGQ
APDNTGHQGFNDYPQGLMGDAPGATNGTGSQQAGGQPGSVTFPVNVSAAEAARRREAATAMLSNAGVDPTTLSPEQFGIF
SNQAPELQRESLNMLVKYGAERLRIVHPSNREGSAQASGSTAQSSQSSTGPRTTKELVPQSGAHDSPNTDSEAQAASQTA
DDTSSPKRKARKMGKSRIACFSCKVRKTKCPRERPTCTECSNHGTACEYAPQKPRNRGKKTKKSEEIVIDEEEEEEEEEE
EEEEEEEEEEEEEQQEDAEDAEDVEAEGDEEEDDDDEQAASQDYSHPQMNIGNMVTNTDATTQDSHATQNNYYQSTSSLAM
PQANPYPKKPQSLTTAASQRNNYSHALPEVTQPVHHVPPLIPAPVGTIAPSETRRWTAFGSGGLNGASDSSKARRGLPSE
PPRPTAQSPSTTNVQPSSWGQSSNTTMPAVSATTMATVSPQMSYDSRSNHRSRQKNQSLSNDSAQQAAAMASTAMQQAQV
QVHAQAQARQSPVAAAAMMAQARKSPYQQVAVPRTTSRTSQRNQSRTPVTEQARGYQPPPPVDMGQQQSVRPGAHYDTSS
SHMPSGSGYNDYGRYGGANTAANHQAAMSAASATPSTMGTSCQSKPATANQWSGSSSRNDRSYGSNSSYQTPNIYTKTPA
AKSVSASGQNFKMRPGTQQQQQPPPPPQHQQQPQHAHGSSNSYSQQQQANYPAYSGSTHQNQQGQTSNQQQQQQPPSWYF
QNSHNPSMHPGGQSSGYNYESWSGV
```

1271 - 1290:	EEEEEEEEEEEEEEEEEEEE
1272 - 1291:	EEEEEEEEEEEEEEEEEEEE
1273 - 1292:	EEEEEEEEEEEEEEEEEEEE

A0A2T4HAA0 **A0A2T4HAA0_FUSCU** (87 aa)
Uncharacterized protein. *Fusarium culmorum*

```
MVRDLVLILKKKQVHESVFSVSADINYGPIPRNQPHEEQEEEEEEEEEEEEEEEEEEEEWGNEQYPRGQTRRSDKHEHV
HMGNARG
```

40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE

A0A2T5LMV1 **A0A2T5LMV1_9EURO** (763 aa)
Fungal_trans domain-containing protein. *Aspergillus ochraceoroseus IBT 24754*

```
MGQGIVETYTKHGFIAGAECKRHKIRCEFRTGESSCTKCLRSGIKCVVNDFSQKFVDDDGIWKSQASATIQQLQAAVSHL
LRQNALPDLSTYSVGDSQNGPSPVPATYHVGGRPSSSLNSSPPDGKPDEPGLVLTREGSQDPDLQDRELVPAPMRSLYEV
TKLRDLRNNHIEEPKSTLLEEDFLSRGLLSIHEAEELFAYFSRTMNQLLWGGIILVHRDLTSVRRASTLLAAAVLTVAAL
HIPNRTETLNRCYGEYVSLVSSMSLTRAHTLDDVRALCIGAFWLSELSWKLSGHAVRIATELGLHQSYQKMIRGHGDQYE
RAQLWYLLYVCDHHFSIAYGRPPVIHEDLAIKNYETFLQSALVVPGDIRLIAQVALFMILTEAYRMFGSDTEQALTEEDF
GQLRVYNVAVDQWRLLWQPRSADSPYVRTYPSKGVVLHYHFAKFQLNSLSLRALSPTNTPVFSMDRKESANIAISSAMAC
LNMVLEEQDIRDAIVGVPIFTHTMVTFSAVFLLKVAVNWNSAYLSLDRRQVRGLVERVIALLTCVSAGERHLTRHIARGL
SKMLERLDSGTVGDRRRGGSDVPGGANAMAQGFPPPDLIYDMVGTSLPPDTMSTRKRKQDAEEDEELQALPSDESEEEDE
YESTDLGESEGSEEEEEISDEEFDEEEEEQVPQGPPVAKKRKTAAPVAADEEGVKANGANGHGPAEEYDEEEEEEEEEEE
EEEEEEEEEEDDADEAEESAKTSATKVKAAGGNAPGSATAEATA
```

710 - 729:	EEEEEEEEEEEEEEEEEEEE

A0A2T6IFP1 **A0A2T6IFP1_TOXGO** (2812 aa)
Tyrosine kinase-like (TKL) protein. *Toxoplasma gondii TgCATBr9*

```
MGGGVGRAPRAGRGASVSDSEALSMPALLPPLSPLSSPSPALGDSACFPFIGLEPLKPPAGGRGSPASPVRSLSSILIVS
SASAAAFVRSASSSFASSLSSRASSSSAPVPVYIHPVSGTVHPYPAQPAPPPPTHLVLAVPASASYAPPASSSSSSFLEG
```

```
LSVGFSGVSGRPSARATAQEKPDASFFAALQTSVVQLLKRSRSIRSVVLRGDGDWLEVLREALQNHVSVSSVSLEAVTNL
SEKELTSGYARLLSGLSKCTSISIRGCGLTSRGLKSLLRSLGKQSDFVEHLQEIDLAHNDLDDEAAAVLLSLFSSSSPRR
LASLRLDANPCSLSALEPLLALLASCDGASSEEESGLNLLSLGGLTNVSESTLSSLSLFSSLSSLSLSRCRSDSPHTLRL
LPSLASSLTAASLTSKSAFLSTLTHLDLSHVPSLLSDDDVALLVEILFPRESLPRLQTRGGRDERGKSPACTRKPQTAKG
RDRSVSAVSSISSLLSLSLAGDGLTGGCLRALALGLLSPSCRLQHLDLSRNSFGKKPSIDGDAGSDSHAPERKDKDKRRA
KGRPGARKRPEEKEEEALPIEPLVDALQQGYEEAPHAPCGLRFLSLAFCELSLEAMQQLAAALLTNGENLVFLDLRGNLR
SAEGPDGGEEQRKGDRRDELRLARCAFDTVAGMCGLQVLLLEEETKKRRQETEETEETEETQETGRKRQKRGTRQPKGRR
RDKATEEANEEEGTVEEGEDEEDEEEDDEKHGEEGTRGVRGGRAAEIERRRCGGKGGRGRRSEKSESKKRKAEMAEEDSG
RSSVRTRRQRKDDEEEEEEEEEEEEEEEEEEEEEEDDEEEEEDDEEDESFDELDAMEAEQKADESSEDEGGEDGEEKEEDE
DEEEEEEDETTRTSLRKRGRHSGMRSEKEQENLSKATEPRQRTMESENGGKTTPRRGRPTRRTSADSSRRKKSKKDESEE
EEEEEDEEEEEEEEEEEEDDDDEEYEEGESVTGRKGRRRRHPQRGRDQVVSAHVRKRRKTTAEEKEAGEERLEKREQVDEQ
VEENLKNNAVLPSPSPQKEGRRRRTVCAVPSARASRPRKTRADPEDETSFPETAGDQESCMLSGQTSASPSLPLRSRQKS
RWIEEDSVSGPLPHPRASRPSSFFVAETGRIGVGGAQPRRSCSALMSTTSVDLEGGGELFGNRERGPPRRRQSASFLAAP
AAPAIVVHQVSPAPGAGERPRKKESLVVNKKSEATFSSSVVSAATPVDTPFLMYFDMKREYPATSALRDPEANGDLRPGE
EDALPRGGVYVQPSAGAPSEAGEALGRVRVREEEARRVESSRGFAVLPPVPAAPEEQRDIRVFLNRAGIHLLNLFFPRDS
HSYVGKTPLQPLLRSYPQELLLGLKYILSSHYLPLLSFPDVYTLQELSLSPHLSPPLQLLLSIIFEELARTNLTYKYQQY
GELGFDENLCHPGKVLFDGGPGCQAIHAAEFRVFWMRRHGRRLGRRRPGWGSRAQLAVGSRADDAPVAPFQSPPPPLPLA
SPQASGLERERLFSGKKFERRDPRDAFSGACTLDGLDHDSPPGASPCTSPKQAEFPPPTPQFVETPDRVRGLAGLFEGSP
RSAFSAAENGDHSASLSTVFDLLEPARLHPLAASFDGDTFGAAGPEKGLLKISGKAPENGRPLQCTCGRDEAERRRQLPG
ERPSKPPLREKKPLDAETKKNSADGSRTADGAPAPELSEVPTGQPPPLPNAEKSGAEVFATPAPFRWMKKALGAVRSQGI
SGLKKETVPRNLDFYFRLNRRASDDAAQLQAKADSAKRGETSTARAESAGGLNAAGPLAAGEEFQGLSDAGKDETDVASK
NRETPGGGVSRSSVDSRSLSERRDSEVSVSAPADDRDSQDEVVAVSRPSALTGRGGLYSAVSSPALSASDFAEELSENEA
RPVVLRTNGHRPEVRPAEPRREEEGDTFGPSAWAPKGEAPGSEEGKATRDDEEKAGREKAPVPRCASTPQDRFVVSWDDD
EWLGSIECFLDDLSLCPSAVSTRACSFESSSTHGASCPLASRGAPHTRSLPADFVLHPPLLPPSLSPSAPPSSVSLSAVS
APLVPASPCVGGAGVQTPGPCSCREVIVVDVQSDAQLRKRIWDVQTLFTGSELSVHRKIELLRRMVLRSIKSAATGYGEQ
KDEVKRLAAEHDGFVYLGDVNYGFSRHMALLFKVLCDASQIPCRVMRAGLLGEETVGDNGDTSARSPELGGGAPGEGEKR
LAGPRARRDGLERQERRRREEEEFVYNVVLVKDATKSELEQLIPIIWTQNAAAGLWRRHLSPGVEKGARGEDRERKRGRH
SSLTDFLASGVVRLNPPTLSSIPLPRRLRALQRRLAVSSASFSSCGQERSSERSRCVGRDLETETGRGATAGNERCGDTA
GDLGGDRELPPLGRARSPRPFDYFKHGWVDRRRETSHCCCCASRSLPSLEAETGGDRAETRGDNGRDNRVGRDSAPGGDV
TSRNERREKTEKENWGTKPSEDGPLHRQHADLDRLLLAASGASAFCGCGGAPASVAATELDLDAFFDFREKLGKGSFGEV
WRVRIKSEGRAVGAARRKPRERKRSREEQDAGVREENAVSEEEERGKEVHSGEERAEAPWRRETDEDGEADEAGERGEAD
EACRGDSGEPAEPEYALKLVPKSEENLPEAEIMRSYSHPRVVPFLGVFEGFQMLEDRSKKKVKNTSLCFLMDIADQSLES
LLEEHEKANTCLDVEFILTILLDTARGMNYLHSPSATKPHLLHRDLKPANILLKVKKVNLEKKEFSPIHLGNTETEITVI
SSRLQKYLYRYI
```

814 - 833:	EEEEEEEEEEEEEEEEEEEE
815 - 834:	EEEEEEEEEEEEEEEEEEEE

A0A2T6IHM6 **A0A2T6IHM6_TOXGO** (834 aa)
Uncharacterized protein. *Toxoplasma gondii TgCATBr9*

```
MRGRRPSQQRKKAASLGASSLLSSLPSSLPSSLFSRGDSVGRRLGKRRGIEEEGGKRKRARGGRSARHNFPEVDQQGGSD
LDELPSSEADPREAQQDGEGSFGHEQELAETLKKSKRAVLERKRRRHEERRQKKQIHRKQQQLWKLERQKALLERQLDMQ
KAAISGIRVNQGTGSGVRTPCGPEADSEDEEEDVSPRREKKTPSSLSSSLSSSLSSLDVRGSVLSALSAKDKKHTASGEV
LLLSGVSSRSTEEQRKAEERRLALDAAGRQLDAELAFLESKLGIGKDSSKAGEKKKKKLAQELLDDGFDEDLQTLLDDIL
GGKAENRKRKTKTDYDHDEGEMEGEETQEGAHEELGRVEAEEDEEDEEEEDDEEDEEDDEEENEEEEEDEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEKEEEEEEEEDEGDEEDEEEGEDLKLKTEHYSTCASASAGKYLPPHLRNRAQRDLS
NEAEFDGDNPGRNSTRQHGAAPASEASDKANFVASKLPLSCLEKARQTATDAGRGLTQRLRGSLNRVSEGNVEVILQQIS
QEVKAALTQVLSGALPVPATSPALTPRDVRGLRREQEMSFFQEVNCIIVRLLMQSMVESKFSTASLVATQTALCCGLSCL
LDASLCSQLLAALGEAFRKFFPLALAQADRRTETGEPVGLYVRHTLMALCFLFDFNVVQPAVFLGLLQRLSGKVATTKEK
GGAKNGERNEPLVEFQVECLLMVLRLGGGKLRNDNPVLFKEAWNFLMTRVKGGEGEREVQVHSGREERPFEEQTREEQRA
RLARVSTSFSGALRQRQEGEQPATTGEDAGQPGG
```

390 - 409:	EEEEEEEEEEEEEEEEEEEE
391 - 410:	EEEEEEEEEEEEEEEEEEEE
392 - 411:	EEEEEEEEEEEEEEEEEEEE
393 - 412:	EEEEEEEEEEEEEEEEEEEE
394 - 413:	EEEEEEEEEEEEEEEEEEEE
395 - 414:	EEEEEEEEEEEEEEEEEEEE
396 - 415:	EEEEEEEEEEEEEEEEEEEE
397 - 416:	EEEEEEEEEEEEEEEEEEEE
398 - 417:	EEEEEEEEEEEEEEEEEEEE
399 - 418:	EEEEEEEEEEEEEEEEEEEE
400 - 419:	EEEEEEEEEEEEEEEEEEEE
401 - 420:	EEEEEEEEEEEEEEEEEEEE
402 - 421:	EEEEEEEEEEEEEEEEEEEE
403 - 422:	EEEEEEEEEEEEEEEEEEEE
404 - 423:	EEEEEEEEEEEEEEEEEEEE
405 - 424:	EEEEEEEEEEEEEEEEEEEE
406 - 425:	EEEEEEEEEEEEEEEEEEEE

A0A2T6IJK4 **A0A2T6IJK4_TOXGO** (2218 aa)
Ribonuclease type III Dicer. *Toxoplasma gondii TgCATBr9*

```
MDMPSSLVRFVQAKGRARKKPAEFVVLCPDSGPCGASWPDASLPFSSSFSSSSSFFPFSSSLQSQTPDCTVSSPSLLLSL
QSVSSLAVSSSSLPAPLSVSLRSRTGEAPTTPAFAAQGFSAAGGAACYLQAVSPSVNFELARLQLCEAKVAALAADVEAT
ERFGLLGPFRCMRKVCSLDDLLLTHTGAMVHSAFAPALLREIVDACTAGKTAERTERGADERGEEGRWAEDTEDEGREER
```

```
ERGNAELRTGREKALGTCCSNAPFSSSLSSSGMRRVSDLCETRRQRTPSALRLLSTQDGKWILSVPSLQGFRSSPLPPFS
IEFSPTGSAPTRASAAAGVLAVRVLRRLVQEGVVDSFLRCRDRDSVEKDLRDEKERRRRENCGGVGAVDLLWRELPACLL
PPRSWRNARRASGDRHGDSEETLHTSAKTREEAARAEEAVSGSNEERRRSRDHKEGTIEGDAGAQEVEENAEEGRKEEEG
DQLKRLPSGTGKKDETSTSNAKSETHREKTRTPAPPPGITRLFLHRVWCTPLTAREAALERLWEPNEKQRRRRRRVLKKL
AESRGFLPSPLYESGGFCGLWRIFADAEAPLQAADLALDGASRRRQEKAKETEQIEPDAGDGEGDEDGLWWTGNRRQREA
CFEKREREGGDGKHDQCKEDEKCRAEKEEEEEEEEEEEEEEEEEEEEEEEEEEKKWSWQEEEKNRQRREILELIRSRIDA
VVEGRRGPDSVLQPLCLLLAHPIPATVAFHALHPEASEKAALHRGRRPRTGRTSFSLRASKAEKASNAWTELEADEEGEE
GDEEGDEEEGEEEGEEEEGEEEDGEEEDGEEDVPGLMRVEVEKPAKTMFIDLPTEYVEKVLLRFTHIHLFRLLQLSNFSP
NGTCNSLLLTVLQFLSALPFRRFPFRTVPSSSSLSSSASASASASCLGGDGEPRSRFVSLPLPACASASRLLPSHALSLF
ALPPSLFSLLSLLSLAVEEAEESTESTLHSQSPPSSPRSSSPRSSSLSSSSPSTSAEQLKRQMVEACSSLAKAGVVDLQR
VMFPFFVLAPLSPLDAKSVDLDFIHRLASLRLFLRSGQRRSSGFLEAGACPPSLMLQHDRRLLRGAVESLHCLPSLSAVA
RLFCAGNSARKLDYEGGRSLQKAERRSARKEQNEGDAAEEKGAFNWPRSLLGTLPSSDRESESAKDTKEKRTPGSEKGER
GEADGERREEDGEKGATKEDGLFSKEEQFFRRLQSYKGSIFSRGGDAANAWTTEEQKLLTFFQQRNENALSVKEALRAEG
MEIFYHLRSRGFEPVALRMTHQFGRSFRFYRLQTIHRNLTPRNVVINSDAGFTLGTLCRVYLSRFKQRLAEPHPDSQQGP
RGNCFLVQGVKRRQEISWMPAILYQLEVQGKHCDLVRRLRQEMRPFLFTAEENISPPLELDFRLVSRALTAPQSRQVGAV
DAAGVDWHGQRLEFLGDAVLKFVVSCYLFFHVHEGKPAESRADAERKETEKEETGLESGEPGDAEAAEEVEEQVEEPESK
ETGGEREEREEEGEEEEARWKFLFSLLTQEEAGRFFGGVDEGVLSRLRQHYVANDYLRFAMRRFRLQAYLVNFPFVSHKK
SLLDLREQPVSEKAQADVIEALLGAVYLSNADSALFGAQPGKRSGGKETTGKTEDREATEKRGGTEENEREGERREKERE
GRGRDVGENVSKKETEGRVDKRQAVHRRPREMRHRGLDKETTEEREEQAVVGSSSGCMAAAAFFDAYLLLPSAVNNAVLL
FDEEVEREKGRRETGERDNKLKEREESEEDRLSHEGVALAPDGAGEQREVPDRQEKETLEHWKALLVDCLEEALRRRDRG
VSVSDLGEDRHKEENAFPCSAKDINRDAWMLLPDRLAKQTEDLRALARLPHMSETFLLLSRATNRQRTPHNGLSHDDEET
EEEEDETEEEEEDGTEEEGDETEEEEEDETEEEEEDEIEEDESGVWREEPSRREVEASQRVWMSKIFSRYDTDGGRGDLD
RVMAVDSVQLIYRGPRQSLLSSLQEGKKRANLETSGDRDHLRRCLLLLSETVRGCASNASVLRMWSSTGNATREERRAQK
VGEKGRVEKKKKTERTQNEEEEQKEQSLHRKEGNAGGTAKAQTNRRTEGSPSCVSSTSFASSLSSSSSSLSSPSSSLSSS
SSSSSPPASSSLSSFCGRRREREFPLKGLLTAARNRDVCCILGVVLSSLLARRLSAVYG
```

668 - 687:	EEEEEEEEEEEEEEEEEEEE
669 - 688:	EEEEEEEEEEEEEEEEEEEE
670 - 689:	EEEEEEEEEEEEEEEEEEEE
671 - 690:	EEEEEEEEEEEEEEEEEEEE
672 - 691:	EEEEEEEEEEEEEEEEEEEE
673 - 692:	EEEEEEEEEEEEEEEEEEEE
674 - 693:	EEEEEEEEEEEEEEEEEEEE

A0A2T6IME5 **A0A2T6IME5_TOXGO** (660 aa)
WD domain, G-beta repeat-containing protein. *Toxoplasma gondii TgCATBr9*

```
MFTSCLYTPFFSFMSSSGASDGSLAVWHAATGRCLAQVPPGHHGGAINAVAFQQKEWLRPSPLFKKSMREGVLAASGRKE
KKESSDLSVPLCACDCRGINASTPHALLFAAASSGDHAVKVWKAEISPSFLSGKVRGDDEPGASGKKKKTADTGHPQILV
TSLASVVAHRKEINDVKISPNDALLCTVSQDKTGKLFSFPSLVYVGELRGHSRSIFACAFPKREKIVATASADSTVKLWN
VDTCACIKTFQIWCLDVCGPAMVTGGSGGQLCLWEDVTNLVRHKAELAQQRETQQLAALKLLAAEGRGDEVFSLLLRLRR
RAGMREFLENQCGKILLQAFQRGLELQRRIALYSGQPLARSGSDQDASASTFGRLSAFLESLEEERVAAREDEDDRRGGQ
ESKAELGASKKRKGEKKVKGEETEAGARGRPDAPLRSAWLRDLNGDLSLPQLLKKMKKKDVATLLEFAAAWNTNSHTSWL
AQGLVRLLLEARGEDIFEGAEKAGRNVSDVENMISSFCAYTARHDRRLTALIEKTFLLDLLQGCESGDTRDLGDRWSGET
RREPHREKTLDPRDATTFTRLCLYGDESEQTEMSQGKKTKNEPKRDSDERSTQEEEEEGEGEEEEEEEEEEEEEEEEEEE
EEEEEEAEEEEAEEEEEADA
```

622 - 641:	EEEEEEEEEEEEEEEEEEEE
623 - 642:	EEEEEEEEEEEEEEEEEEEE
624 - 643:	EEEEEEEEEEEEEEEEEEEE
625 - 644:	EEEEEEEEEEEEEEEEEEEE
626 - 645:	EEEEEEEEEEEEEEEEEEEE
627 - 646:	EEEEEEEEEEEEEEEEEEEE

A0A2T6IY40 **A0A2T6IY40_TOXGO** (1418 aa)
Putative DNA mismatch repair protein MSH6-1 (EC 3.4.21.72) (Fragment). *Toxoplasma gondii TgCATBr9*

```
ASVGDSTAARSSSGNEEDPGSEDVRKLKRLRRRLALSDDEEKMETPPSIRRRRQAEQTKKIEKEAARRAKPEEEEEEEED
EEEEEESEPSAFSDESYEDESEEESEDDSEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVRGKKRPAPKKEKRVEEGSQT
TWTTASSSASSSSRAKLKDLVYSASSEKPGTTSSLTPPPVTSPPSSSPPAAPEPTSSSSSLSSSLSSSSLSSSSVSSSSV
SSSSVSSSSVSSSSVSSSSRLPCSTGRKATDAVDEAELRRRLLASPAAQNCHYFRHYIEDFYMYHRQFSFPPWADPARMR
DISGRRAIDCGEDYDFSSLWIPSPDSQLARAHARPHMTPGMAQYWEIKKEHFDKLILFKIGKFYELVYGDACAAHRILDL
KWMGGGGADAKPHCGFPEQNLHFQARQLVQAGYKVVVVEQMETPKELEKRNSQAAAGAKDKAVRREVCEVYSAGTVRHAD
MLGQAARYLLVLYFGEEDEEVDVDTEVATEKQVAAGRRGADIMAADRRETGERASTEAGDRGDPEMRQSLDAAEKATVGM
DSSTRDARDTSEKRRELKPGFAACLVDVSTCRVSLVRLSDDPTAAWPSLRLLLAQTVPVEVVYSPTNIPASVLKLLKFLP
SPPQLSPLTSFPDLLGAHTEVDRYITSRLDALTSKSNASSSSSSSSSSSSSPASGSSSLSSSSSSSPAQSLELCRTLCD
RWPSLHCAVGGLCVYLRECRLDASVLPLCQFESFRPRDASVLVLDAHALRQLEILQTQDGCAKQALLGYLDRTVTAFGHR
LLRRWLVAPLRNVAELTRRLDAVDWLCNSPESVADIRKALQACPDIERLSAKICAQGLQGERRAVYFDHFHQKLLADFFA
LLDAFLSVESLAKRLAQRLATSHGQEGAEEREAAEEREGEEGRGGRLLDLCADREHGGLFPPLGELVASLKSKVAINADG
HKIPAKGVLAAYDDTVTEMQEVQQKLENLLDDLRSSWKMKSLQFVHSKFKYEVECPDTVSKELLRTHECDITSSRKGFFR
FRTPEICELVAELEDLEQKQKDTFYPFFSILFNAFYSHFTHTFGRAIQVAAELDCLQSLATVVATHPGRNRRLPIVKGTE
RHPVAETLMDNFVPNDVYLNCGPHESKRTLLITGPNMGGKSTLLRQAALCVVMAQVGCFVPADSCTLSPVDRIFTRLGAE
DSILQGASTFLVELKDISELMTYGTRHSLAVIDELGRGTSTFDGTAIALASLEHITDNLQCRCLFATHYHLLCYEMQGHP
HVVNVHMKAAINEEQQSLAFLYKLTKGVCPKSHGIHVARLAGIDPRILECAEEKSLRLQQEVVRQQRHWRLLGVAKTLEA
ADPATLQSLFARKESVLEDLIQEEEAEAGEEEAKAGEEEAKAGEEEAVPNEREVEMEG
```

112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE

114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE

A0A2T6J0E9 **A0A2T6J0E9_TOXGO** (1745 aa)
IgA-specific metalloendopeptidase. *Toxoplasma gondii TgCATBr9*

```
MTSARTREGLVGAEAPLGEGEEDLQDSIACSVPRAPTNSFEEEYEVECVDECPYIKFQHASKLPLSPLLFDASSSPAPLP
ERLLAARCTDSLCLLHCCGVLLLPGLDSILAVDATEAACGSPISRGRLPLHASKEGETKDAFPSLLLLSPDARFLAVAVD
CQVKLVQLGGCGGPSCSKSAGEASREGNAEARLGGQQGGDSCISEKTQVLSLAGFASPVKDISWIWPSGDRTETWCEGDT
RGDAERLIGLAVLTESGEAFILSPRGAQAFPLPAHGLAIHALPRRSPAAAKSEGAGPGGLAPLTAVVSCCAPASLWLVGL
QETALLPEGSGQGESLYDFGHRRPDVSRETAKEEKRKGRRKIRVEGLADIPGYEDEAQALHKGRGRFVGVHCLGASLDSA
AGESPLPLALAWFVPDADLSTGEDDWEKPELESDSAEPRLDPLRQAPASAEDCGDSWSCFILFGFLARRPYTPSDARALR
GDIGEAESADEKEELVFRIYAASRNEMFLRSVAASTVCRFRWIPQWHCLWVFSNACTQVICFALPHSFSRNGDPLPSPRS
SSFLGSGEVPWRCFTMPEGRALETADEDAFPQGLALFFNFKESMFREHSTTDTPPLEHPPVFFLLQSDGQVCVHLADCCE
CYVDDAGIGKEKRLLPRLEWTPVSPPSSFLLTSWTEPRRRACGEQPATPVPKVSPPALSPSSSSLASPLFASLQQGKPTP
SLFGTPSTNAASAPLFSSSSGTSLFPSSASSASSLFTPAKSEEEARKTGWVVPTTHLKVTSASSPANDPSASNGASASNN
LSALDGSSPRPLSSSRKDCVDQARPAAKETREEAPTRRLPAKSSSRDPQRRGHCVHCGAVDVGDRRGGREAERRRREKKL
RRRVEAKNASLRQAAAAANEVIEATLQAARGTKAEPAREKNAKKRILLTEEQSEVKALLDEFEEKKHAFCSFSRFLPSSL
FRPLLLSARCFENALRHEERRDVLLESSPVSSSASSSSSSSSSSSASSSSSSSSSSPGSLFVSRCGEKDAPVDCGAEQEK
STAALLPAAAAGLARTGRLADKLKDEQRNVRTKQETETEVVETLQEAQQHLVAWRSCLEAVRDQLLLRMQFAEKKSENPT
ERNGEQTDAAGREEGRGDREADGREEKRERQAERGNSVTEEDVIACMQKIQSESGARRNLFEALQTLLPADAEHAQLNTD
THTKCVLTHLESGLLRAERRLLLLLQRFRFYTSFQTRFPSSLDPESGSPVRRPAASGWPGSWKINSGLSSLSSYGDKGVS
SLPLAHGKDSDRDARTKRGSVHTPDTACGRGRPGGCYGLRFEWLEEDEFPDKREESVVDSHRRVSSTTHPVSEGTPGARP
SLAFSLSASPPSAFHLSLFGSPGGARDSRIACSQGPGGSVKDGGLAGSRSGAASGDFLLDMHAEHRAAGLVAELEAAVSE
FLSSVRQLEIDLAKLEWKATDLQSPARQSPSSSSSTSSFAASLSLLSSSVFGEPLPPSGPSGLPDVVGAEKPAKDGEQRF
PVSSLREQRERFDERRKLRRQLLEVWRATTSTDPQQEGEEETETDADEEEEEEEEEEEEEEEEEEEEEEEDEEEEDEEEEE
EDESDAFEVLEDSSSVSYDEESDEWEPVGSASPENPQTPPRQSVVSRRLGASLRSGRRTSRSKQRAKFAPLSGDEDSSEN
ACSSSPSSPDDVSPRRRGAELSDSEGAPEDGASRSNSHDESASLPSVRSRTHFVLIRVKFFLASS
```

1568 - 1587:	EEEEEEEEEEEEEEEEEEEE
1569 - 1588:	EEEEEEEEEEEEEEEEEEEE
1570 - 1589:	EEEEEEEEEEEEEEEEEEEE

A0A2T6J5R5 **A0A2T6J5R5_TOXGO** (257 aa)
Uncharacterized protein. *Toxoplasma gondii TgCATBr9*

```
MTTSAPSSRRARPEAASAAAAAITEAAAAAPDKVEGTEDEKEKEEEEEDEEEEEEEGEEEEGEEGEEEEEEEEEEEGEEEE
GEEGEEEEEEEEEEEEEEEEDEEAEGEEEEEKDGTRSTDCARATNVCRGEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEE
DEEEEEGEEEEEEEEEEGEEEGAEEGEEEEEEEEEEGEEEEEAEEEADEEEVDSSAACVRFWMPVCPPSVRAVEAEVREG
RAGARQLKEKEKWSASK
```

136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE

A0A2T6ZPM9 **A0A2T6ZPM9_TUBBO** (131 aa)
Uncharacterized protein. *Tuber borchii (White truffle)*

```
MLFALALELIASGTTPGWGSLPGSGCILGSVIWVGMKKAERADIAKTREVDEEWMEMGDRADAWRLNGGAGGEDDEDGEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDKDGDESG
```

79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE

88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE

A0A2T7A3S6 **A0A2T7A3S6_TUBBO** (907 aa)
Uncharacterized protein. *Tuber borchii (White truffle)*

```
MANPSSGDGAGSTGTSPTGPSPSPVKPSPKSSSSNAPASATPTSAQAQFHRFRLSEFNRAESSPTSASPGGHCSRFRVTD
FVPWASQTDPPPPPPPPPPPGVATNGGRSASDGSPSSATTPRAGSFSVMHMDVDNSGPQQTSTSVAAAAGSTRGVLQKITV
PSAQAQGLKQALPIHPRPLAPSPIMTNGMVPYNPATVPQEAVWELSRVLNILRNTAPEMVVKIISDALISWPSVLEGSLL
RRIGEIFPPLPAPSPAGVPGPSNSAASPQEPPKKKRGRPPGKKAKLNDGSSATVPIAANLAAMPPPPLPYIAPGPQAQIA
PVAPPPQPPPTAAKRSQTDGGKLLQCTRCLKYFNPTWRATPASDPSSEATCAVKHPFKDFPSGLEVVTPARRKNNYKTTW
KWKCCGREVQSTSNELLMWPRKEDDRTGGWCFVGKHTTEAGVREKLGLKPGKGRKIHGDGDKKHKGGQGAEDHSQANGEQ
EDPKEEGWTMLPGGGRSIAGPAGGAQQYGGHPQQQQPLQQPPPPSPQGQQSAYQQQQHPRHQQQQQPQPQQPQQPQQPQQ
QVEDSPDSPPKRKRGRPKGSKTRSKAMPIPTSTASSSPATVTAKDPTASTPTQQHPHPHQQQQRAHPQDQSSFWTQYTEP
ASTSNASPRHQPPTTLPTASPSTTATSPATPQTPHHPHHAHHSHQHSHHPLEDPAISTADLTLLASATAAMAGTSNNPSS
GQPSTSNAGTTTTDTPEKRKRGRPKGSKNGGKTLDTGGTTTSGNRGLRMKEQQQQQQPQQQQPQPQQKKVERTVISAVPE
EIEVIDDDDEEEMEEEEEEEEEEEEEEEEEEEEEEEEDAVGEDDVDVDANNTPANATTTSTAVPATGSNTAEVGGEVEFGG
VGVGVGMGISGIDGYTGLGASDGGGWF
```

814 - 833:	EEEEEEEEEEEEEEEEEEEE
815 - 834:	EEEEEEEEEEEEEEEEEEEE
816 - 835:	EEEEEEEEEEEEEEEEEEEE
817 - 836:	EEEEEEEEEEEEEEEEEEEE

A0A2T7DHU6 **A0A2T7DHU6_9POAL** (191 aa)
Uncharacterized protein. *Panicum hallii var. hallii*

```
MDEATKKKVEATVLEILRGSDMDSVTEYKVRSAAADRLGIDLSVPDRKLFVRGVVEGYLTSLSSQEAEEEQQQGGAGEEA
KGDEEEEEEEEEEEEEEEEEEEEEEEEEEGGARKREYDDQGDLILCRLSTKRRVTLSEFKGRTLVSIREFYLKDGKELPTS
KGISMTVEQWEAFRNAVPAIEDAIRKLEDSD
```

84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE

A0A2T7DM57 **A0A2T7DM57_9POAL** (327 aa)
Uncharacterized protein. *Panicum hallii var. hallii*

```
MADVRRIYWDAEGYAHTDCLYWEGFPRILWDTLCIYHYPNPPRYKGREFTEVGVPRYRGTITIPQHPTLEWQSIEIEVVG
YHLVDAFKAAALKAITTFCEQHPNAVAAYPIRLFPVVFAHDAEWTFRTTYLGRLVGDLAEETLSAVIRYMNAQYRLQSLT
QRCMDDLVNLAQDFHRDLTLKDDQIHSLGQGIAGRDTTIGHLEVQILEGDAQILQRNTVIDFLQEQVHDLNQELGDALRH
IEMLQEQQMPPLVPNELEEEEEEEEEEEEEEEEEEEEEEEEESEEIEGVSEIDSEHGDPEPNPQPDHSSSGSHSSSGSQSS
VGNLDDF
```

258 - 277:	EEEEEEEEEEEEEEEEEEEE
259 - 278:	EEEEEEEEEEEEEEEEEEEE

260 - 279:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE
262 - 281:	EEEEEEEEEEEEEEEEEEEE

A0A2T7DNN7 **A0A2T7DNN7_9POAL** (297 aa)
Uncharacterized protein. *Panicum hallii var. hallii*

```
MASPLTEASPPPTIRDVIGRDDDDDDNFIAEEEEEEEEEEEEEEEEEEEEEEWDMSKRLSRLAMEGSDGGDADDEDGGDG
EDEEDDEFEVRSDVNAATYGGAWPPPYDVQAPSSASLPGTPDRGARAAAARSSSSPPWWPGTSGGKEYASETEARWPPGA
GRRQRYHHRERMAREVWLERAWRARKQRQEAAAAVPVVVLGGGGGESPAAGRGGVAMDMEEVRACRDLGLGLPCDWTVEI
PCHALSGVDTASSGGNSPASGSWRISSPGDDPKDVKARLKVWAQAVALASAASRLGS
```

31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE

A0A2T7EME2 **A0A2T7EME2_9POAL** (144 aa)
Uncharacterized protein. *Panicum hallii var. hallii*

```
MARRGVNSDKAWLRRHDNPLRPISKFLERKAVAYRRHHFPGGEVKATGQHAAGYSYYNPPRQVYLQEDQAPRKVYLQEDP
PYLFRFLDVKCKEKEEEEEEEEEEEEEEEEEEEEEEEEEEQLELMRRFTCNMSPAFRFVNLKRQ
```

95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE

A0A2T7FDQ7 **A0A2T7FDQ7_9POAL** (110 aa)
Uncharacterized protein. *Panicum hallii var. hallii*

```
MHFIINPLHPSCNYLLNSSTDTASCQIYAAALILFNEEEEEEEEEEEEEEEEEEEEEEEEEEVLLPLFIRSPNERDFGGV
LLHACHPACPVPCIEPLIDRWLGDYASDAR
```

37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE

A0A2T7NTN0 **A0A2T7NTN0_POMCA** (622 aa)
Uncharacterized protein. *Pomacea canaliculata (Golden apple snail)*

```
MLTVGYPFDRQFSSSCRLSSTYFSCQEEERRREERRRKKKKEERRKKKEEEEEEEEEEEEEEEEEEEEEEEEEKKKKKK
KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKEERKKKKKKKKKKKKKKRRRRRRRRRRRRRRNLMRKSEPPYVPGHFLWGNSA
QFSKHLVRFLQTSQKQLGDIFTIRLLYHYFTVIMDPNCYEMFVKEKNFDFSLVTKQVISNVFGLEVKSRRKLFSETAKRL
KGVYLNTTMDNFAKHVQNSFTDLTKTSAMTNSDCNANINTDGNTSVDWRRETLFTLMSRTVFASLFYTMFGCSVDPSGEN
TTKNFCPKVFHDNFDIFHKYFTYLWIGLPLKLFPKAAEAFAVLLQQPTSHNMLQRDGVSEQVKVSINHFHQHGHSEQDIA
VYNLILVHVNYNIFRVTFWCVYKLAEDPRVLKDLERELHEAIEMKRADGEESVAFTLAEIDEFPLLDSFLKETLRMYSSA
LVVRYITEDTEFEMPSGHKYTVRKGDRVAISAAAVHMDPEIFQDPEVFKHKRFVNTTFYKYGKEVKKLILSFGSACVGQR
FALMQVKWFVVSLINSFSLHLPEGQKTEPNTESYGVEILPPVNDVQVDFRPKEGAPVLVYSE
```

49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE

A0A2T7NXL4 **A0A2T7NXL4_POMCA** (678 aa)
SH3 domain-containing protein. *Pomacea canaliculata (Golden apple snail)*

```
MFSESSCFDLQQQIKVLLSAVNGLKEENETEKIKYFETKKNNEVKRLETFMRVSRSLEQSMASDFENFNWYLVTVSNSPA
KVPRQSDEKEEEEEKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEERKTQETNEVAPKNVGKANIKEKRKDPLRHQFI
TVDDYEGEEGDLSFKRGEVITVIETREDGWWMAENDRGDTGLVPSTYLQLHNKHRDVQQDDEEEEGADSEQGDGDTVRRT
KKLWSGIKKAITETTVSDVLHAMGAVPSGFRQSTLAKKHAEGVTYRTVSYLAIKLSPSNLIYKDLFFDPSSNRIRPRMVR
IERIVTISACRQIPVPSAGIDVLDRTVRICLFDGNNILSNIHCVKVSSIDKSQNTWSFTTKVTDTMDLASHAEVFVRSNN
TVDNIGILFELCITTFRASTKERTEMSCGWAHLPLLGENGTATQNKSFDLHVNGGTPYEKGVEVDPRISRRTTSNALMSL
ISGNRQPRLVVRLSIPKKEFKDQMDTLPEPLVGNTILLPFYSYYRQILADVLLRDRLDLDSTELIHNPLLSLFPTAAEQM
DLMQLLRASWLEKQRSAHRVEKRDEEYMKDLFKQAVMDTVYPVLHIAALPSYQPGDYDNVQSRFEEVHRFRELRQTRQST
LAVLLSSDIIFQPFEMDEMIFSMLGPHCLQKSVPIPDD
```

97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE

A0A2T7NZM4 **A0A2T7NZM4_POMCA** (1260 aa)
Uncharacterized protein. *Pomacea canaliculata (Golden apple snail)*

```
MCEVAVFGDDEIDPSAGEAVATPVSHDYIAVRLTEVVAKLGEGKQVPHKKGFCIIKSAMTEKRPATDCGSSSGDYSSASK
RPKTNDCREECSLNADSAGESCGSAQGTLEYEMWDPLDQDDAEKSTQQLKCSINSLSVTGNIIPSFTECSRQAGIENNCH
ESNIYLSDEVGASLGESQASSSTLPPTLWKSTSLEGDARTIKSVFPNANLHLVYETLAKHRTNPDRLDITTEALLDISDG
DKSPTGVINATNRATTNLAENVLNQDVKKVVQLIQEHSPVIILDLTEVYIMLQQYAKNEDRVKTVAETFLTRAKRENGDY
NHFAQGDSIFDNAIKLIAEFPDIHPSVIYEMLEREGDNKDELDSLRKTLANMVEGVGSKGLLEELPQGLDNSQSDDSLYR
DDPVYRDMRTISKVFPHRDQNEIYALVEAHYYKKDRIQVVIDELTMLERGSQTEADMYSPASSLEKRPSEIAFDTSASLE
DLQSEIDSLQEIFPDCDPNYIYHRLEGAKHMKDRVKMIAEDMFERKDYPRLKDLVEKQTKLSHKQRLQRLDFTVEDFLAK
FPDPQGTFMDEGKEMKENYTSHVWAQLNYDFYTFRHSFVKKVVKKHKYHFLPIVQELEATMADILTRGGQSKKLRKSPMF
LPLEYPQEPDEYFFYELWYTKNEHIVRDYLDQKEKMRTAKINAARDKNELYECPCCFEEECLFEEMSCCADGHLFCQNCI
VFSAKTSFNEGKTKFPCLTGYCKHEIPLSVLKSLLPASIFSKMLKKLQEEEVRSAGIEDLVDCPFCSFATIMPDKNDRVF
KCLNPECLKDSCRLCREPNHIPLKCSEVEKQKETDMRTFIEKRVTEAMIRKCHQCGKQFVKESGCNKMTCVCGATSCYVC
RARDIDYSHFDRTRCYDEDMNALHQREMEEAAAKAKAEYLQKYPDAADIQLKHDPLQHLKNEEEEEEEEEEEEEEEEEEE
EDGRIGRGYEMLPNQHFDDEEDEDERSFAYYQVIKASFNYVVRLTATYVDIEHVAGCTKDYISIYDGNSSSAALLGEYCS
YWCTPLESSGLQMFIRFVTDTNVTDEGFQLTYTAVRPPTVPQITPSVEIPSSAAVSIATPDSSSSRQDLQLAIIGAVVAV
VCVFGLLITVCYVVTVKKNTSARVGAMPSRAGGGLTRAGRRVAEDFVEYDNSLFMVPVPFPPHYSSAPPPEYSSDPPPTD
SVESSPPAASDARNEVSAAASPGNEASVEVSASPSTGVTSEPHRLASSTSSVQVVDATVA
```

942 - 961:	EEEEEEEEEEEEEEEEEEEE

A0A2T7PDU7 **A0A2T7PDU7_POMCA** (146 aa)
Uncharacterized protein. *Pomacea canaliculata (Golden apple snail)*

```
MVDKLIGTWMSVSSENFNTFLDAAGASQALKAVAIKKSTVTISREDGGWKLVRTVGDNTIQMVYPLGQEVEITSFSGKKM
KIRHPFKNLKSLPDDDSITHAITNNTSMYKRNRNDDDDDDEEEEEEEEEEEEEEEEEEEEEEEAEQE
```

121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE

A0A2T7PPX5 **A0A2T7PPX5_POMCA** (499 aa)
Uncharacterized protein. *Pomacea canaliculata (Golden apple snail)*

```
MDGRWNCSVPHWPDFRLHFPCNLVSDCVGGEDEVDCPYTSHVCGPGFQSANGTCLQLVKTDQKVSWETALETCESRGMVL
MTANTLAEWEATRVLLLRYFTDSDYLLYGLKPASSSLPYMYRHVLTGVDGIANYLLPITRMLEKYECLAVLIHSGDHLGT
STGNCNGNYWSWFVCKFVVSGDDTLPQMPVSLTANWSCIPDQFLCDGFWHCPDGSDENKCINNKYLSIRKESFLPPAIID
IDSHGFLNTVKQLTRTNQPLCPETHFQCPGLDIYCLPVYVRCNGVFDCPGKQDETACDTYTCPGYYRCRSSHVCLHPDHV
CDGWSQCPEGDDELLCDLSCPDTCVCHGLAFTCTARFAASSYLELRFLDASGSGMTPRDVVNNTMIVYLSFNNCSISVLG
EMYFVNLQILELRDNYITSFRSSIFEKLHNLRSLRLAGNPLTSLHPTDKHYHPELGQKKKKEEEEEEEEEEEEEEEEEE
EEEEEEQEQEQEQLVEEKQ
```

462 - 481:	EEEEEEEEEEEEEEEEEEEE
463 - 482:	EEEEEEEEEEEEEEEEEEEE
464 - 483:	EEEEEEEEEEEEEEEEEEEE
465 - 484:	EEEEEEEEEEEEEEEEEEEE

466 - 485:	EEEEEEEEEEEEEEEEEEEE
467 - 486:	EEEEEEEEEEEEEEEEEEEE

A0A2T7PVD2 **A0A2T7PVD2_POMCA** (184 aa)
Uncharacterized protein. *Pomacea canaliculata (Golden apple snail)*

```
MTDDMLPATVDDSDCYINYSALEVTQHRCHAPLQMTDDMLPATVDDSDCTRDDTAQVSCLTDVGLTGFDLLHRQIQGESH
HPPGAPGSRGRCRVKPSLRPLLNHCPPGHLGHRALQWRRCGTSSAAGVNERCHSERLRAHTQEHEPWRNSREEEEEEEEE
EEEEEEEEEEEEEEEEEEEEIPVR
```

152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE

A0A2T8IKF9 **A0A2T8IKF9_9POAL** (186 aa)
Uncharacterized protein. *Panicum hallii*

```
MDEATKKKVEATVLEILRGSDMDSVTEYKVRSAAADRLGIDLSVPDRKLFVRGVVEGYLTSLSSQEAEEEQQQGGAGEEA
KGDEEEEEEEEEEEEEEEEEEEEGGARKREYDDQGDLILCRLSTKRRVTLSEFKGRTLVSIREFYLKDGKELPTSKGISM
TVEQWEAFRNAVPAIEDAIKKLEDSD
```

84 - 103:	EEEEEEEEEEEEEEEEEEEE

A0A2U1MLZ6 **A0A2U1MLZ6_ARTAN** (1082 aa)
Zinc finger, RanBP2-type. *Artemisia annua (Sweet wormwood)*

```
MAMTNYFLTLATIVCIISCTCGTGSAAESLAEECSKQLPQVMTCVAFASGKESTPQQKCCDSVTQMKNSNPACLCFLIQQ
IHNGTNPALKQMNIQESKLLQLPSACKIANASISNCPKLLNLPPNSPDAAIFNNVSSTVTPTTGGTTTSSQSTSGSLGFK
HEAPVLLGSVMIDNRNSSAVKRARTDGGRREDDWTCPSCGNVNFSFRTTCNMRNCTQPRPADHNSKSAPRQMPTPQGYSS
SSPYAGSGAPSSMYMGVTPYAASPFNGTSMPPYDGSAYHYNYNSRMPGGNPYRPLQLSATPAYSGGPMIGTGALYGLLQL
MEQFGLRLPIAQAAMDFSMQPPAQELVARDLHDYQWTFRHIFRGQPKRHLLTTGWSLFVGGKRLAAGDSVRTGGSVANDE
ILGFAKPLTDKLTLDNISRGTFSSLPDKVVGVTSLPSEDSASERQEELSKEKEEQAKKKQSIECNKDVALEETTNATAAD
AQQQARAIALDKQQQLCKTSEALPVLASASINLCHSMMDKEGNGEQDITKAYKAAHEEIDDSSDGASSARINRDYDGKVT
SEELDSATTNLKDAMAKDKAAGVLHGDEDEDHFPPVFEQVSESNVEEEEEEDHFPPVVEDGESSSRVVDEEEEEKEEDSP
PVTQATSEERPTGVSVSDVEEDEEEYEEEEDEEAASPPVIQGLNKYNDLLRTTTTQEEEEEEEEEEEEEEEEEEEEELL
VREQNVRVRVRGSTNLFVDALEPLGPERRKMLEDTPFHKLLVMDRNIQNNFIIKKLATIFNTQDHSIELKGERHVVTAQD
VTKIMGIEDGEEEEIKLPLRGQKTDVPTHLKKDFVKIRQKVICMEKVKTKLRESLDEDTVKRAYMLLVLRYIVYPPSAHD
YLPESCLDLVRDVNKKKRWATFVITSLVNGIEKYNNYKGNKEIFIGGCALFLQLYATKGSITTPPQKKTRDKERTDCFEN
ALLVKNIMQQRNESMVTALQKEQKKHLSKVKNKKAKDFLKKDGEDVMFEFVSMLDAKMAIIDSILECGARIEEEGISQKR
KAENELETDASEGKRKETERKVIEPKHTMQTRSRRTRKPVGD
```

697 - 716:	EEEEEEEEEEEEEEEEEEEE
698 - 717:	EEEEEEEEEEEEEEEEEEEE
699 - 718:	EEEEEEEEEEEEEEEEEEEE

A0A2U1PW88 **A0A2U1PW88_ARTAN** (567 aa)
Zinc finger, LIM-type, Ubiquitin interacting motif, Protein DA1-like protein. *Artemisia annua (Sweet wormwood)*

```
MGWLTKIIKGSSSGSSHRVSEGRDQESYENDEIWEEPPATVDASSDFDYEEIDRAIALSLVEEDERSLLSLVEDDKKSAH
SSVKEEEEEQEEEEEEEEEEEEEEEEEEEEEEEDEEGSVSSLEDQKNAVSSPKEHNRGSSSTSEEDHKGKKVIDDKSYLEED
EELAKAIQLSLNTDSPPRISRGSLFPRLPNIFQGIYRVCAGCNKQIGHGRFLSCMGGVWHPECFCCHACGLPIDDYEFSL
SENRPFHKSCYKEHHHPKCDVCKNFIPTNAGGLIEYRAHPFWLQKYCPAHERDGTPRCCSCERMEPRDTRYLLLDDGRKL
CLECLDSAIMDTHECQPLYLEIQDFYEGLNMKIGQQVPLLLVERQALNEALEGEKHGHHHMSETRGLCLSEEQTISTIMR
RPRIGAGRIIDMFTEPYRLVRRCEVTAILILYSLPRLLTGSILAHEMMHAWLRLSGYSNLPPDVEEGICQVVAHMWLDSE
IMAGSSASTVASSSSSSSSTPIPAPASSKKGKRSDFEKKLGEFFKHQIESDTSAAYGDGFREGNKAVLKYGLRSTLDHIR
LTGRFPC
```

91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE

A0A2U1PWA7 **A0A2U1PWA7_ARTAN** (568 aa)
Zinc finger, LIM-type, Ubiquitin interacting motif, Protein DA1-like protein. *Artemisia annua (Sweet wormwood)*

```
MGWLTKIIKGSSSGSSHRVSEGRDQESYENDEIWEEPPATVDASSDFDYEEIDRAIALSLVEEDERSLLSLVEDDKKSAH
SSVKEEEEEQEEEEEEEEEEEEEEEEEEEEEDEEGSVSSLEDQKNAVSSPKEHNRGSSSTSEEDHKGKKVIADDKSYLEE
DEELAKAIQLSLNTDSPPRISRGSLFPRLPNIFQGIYRVCAGCNKQIGHGRFLSCMGGVWHPECFCCHACGLPIDDYEFS
LSENRPFHKSCYKEHHHPKCDVCKNFIPTNAGGLIEYRAHPFWLQKYCPAHERDGTPRCCSCERMEPRDTRYLLLDDGRK
LCLECLDSAIMDTHECQPLYLEIQDFYEGLNMKIGQQVPLLLVERQALNEALEGEKHGHHHMSETRGLCLSEEQTISTIM
RRPRIGAGRIIDMFTEPYRLVRRCEVTAILILYSLPRLLTGSILAHEMMHAWLRLSGYSNLPPDVEEGICQVVAHMWLDS
EIMAGSSASTVASSSSSSSSTPIPAPASSKKGKRSDFEKKLGEFFKHQIESDTSAAYGDGFREGNKAVLKYGLRSTLDHI
RLTGRFPC
```

91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE

A0A2U3V031 **A0A2U3V031_TURTR** (531 aa)
histone H4 transcription factor isoform X1. *Tursiops truncatus (Atlantic bottle-nosed dolphin) (Delphinus truncatus)*

```
MPPPGKVPRKENLGLQCEWGSCSFVCSAMEEFCEHVTQHLQQHLQGSGEEEEEEEEEEEEEEEEEEEEDPLEEEFSCLWQ
ECGFCSLDSSADLVRHVYFHCYHTKLKQCGLQALQSQADLSPCVLDFQSRNLIPDIPDHFLCLWEHCESSFDNPEWFYRH
VEAHSLCCEYQAVGKDNHVVLCGWKGCTCTFKDRFKLREHLRSHTQEKVVACPTCGGMFANNTKFLDHIRRQTSLDQQHF
QCSHCSKRFATERLLRDHMRNHVNHYKCPLCDMTCPLPSSLRNHMRFRHSEDRPFKCDYCDYSCKNLIDLRKHLDTHSKE
PAYRCDFENCTFSARSLCSIKSHYRKVHEGDSEPRYRCHVCDKCFTRGNNLTVHLRKKHQFKWPSGHPRFRYKEHEDGYM
RLQLVRYESVELTQQLLRQPPEGSGLGASLNESSLQGIILETVPGEPGPQEEAEEEEEGGGGEGTALSASQDTSSSVIHV
VNQTSAQGEREIIYYVLSEAPGEPPPASEPRSGGVMEELQGVAEEPQVQIV
```

49 - 68:	EEEEEEEEEEEEEEEEEEEE

A0A2U3VE43 **A0A2U3VE43_ODORO** (712 aa)
YTH domain-containing protein 1 isoform X4. *Odobenus rosmarus divergens (Pacific walrus)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDIKRQKPSVHSRQLISKPLSSSVSN
NKRIVSTKGKSVAEYKNEEYQRSERSKRLEADRKIRLSSSASREPYKSQPEKTCLRKRDPERRTKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEEE
EEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGS
SASESYADQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSARSVILIFSVRESGKFQGFARL
SSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLLFPPD
ESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYAPEFHQRPGYLKDPRYQEVDRR
FSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMAPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHHPVPHEARYRDKRVHD
YDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDRGERGRYRR
```

229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE

A0A2U3VE67 **A0A2U3VE67_ODORO** (738 aa)
YTH domain-containing protein 1 isoform X1. *Odobenus rosmarus divergens (Pacific walrus)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDIKRQKPSVHSRQLISKPLSSSVSN
NKRIVSTKGKSVAEYKNEEYQRSERSKRLEADRKIRLSSSASREPYKSQPEKTCLRKRDPERRTKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEEE
EEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGS
SASESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSARSV
ILIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDG
QEIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYAPEF
HQRPGYLKDPRYQEVDSFTNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMAPYPGMEQPPHHPYYQHHAPP
PQAHPPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERER
ERLCDRDRDRGERGRYRR
```

229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE

A0A2U3VE72 **A0A2U3VE72_ODORO** (730 aa)
YTH domain-containing protein 1 isoform X3. *Odobenus rosmarus divergens (Pacific walrus)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDIKRQKPSVHSRQLISKPLSSSVSN
NKRIVSTKGKSVAEYKNEEYQRSERSKRLEADRKIRLSSSASREPYKSQPEKTCLRKRDPERRTKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEEE
EEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGS
SASESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSARSV
ILIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDG
QEIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYAPEF
HQRPGYLKDPRYQEVDRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMAPYPGMEQPPHHPYYQHHAPPPQAHPPYS
GHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDR
```

DRGERGRYRR

229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE

A0A2U3W488 **A0A2U3W488_ODORO** (980 aa)
peroxisome proliferator-activated receptor gamma coactivator 1-beta isoform X2. *Odobenus rosmarus divergens (Pacific walrus)*

MAGNDCGALLDEELSSFFLNYLADTQCGGSGEEQLCADFPELDLSQLDASDFDSATCFGELQWCPENSDTEPSHYSPDDS
ELFQIIDSENEALLAALTKTLDDIPEDDVGLAAFPALDGGDALSCTSASPATSSAPPSPSPSLERPQAPTPEVDELSLMD
GTQDKKAPMMQSQSRSCTELHKHLTSVPSCPQTKARSPDRSLQPPPTLSPQLPAKEEEEAGEDCPSPQPAPASPQDSPAP
GRAGPGAQGSREDMQAMVQLIRYMHTYCLPQRKLPPQAPEPAPQPCGSPSKQVKPRSRSQHPSKGSWAEFSILRELLAQD
VLCDVSKPYRLATPVYASLTPRPRPRDSQASPGHPSPVEEVRITASPRSTGPRPSLRPLRLEVKGHAGRSARLQREEEEE
EEEEEEEEEEEEEEEEWGRKRPGRGLPWTKLGRKLENTVCPVRRSRRLNPELGPWLAFSDESLVPAEPQGALPSLRLTPE
AYDMAGALGSPTDEDSGQDQQLPRGPQIPALESPCESGCGDTDEDPSCPRLPSRDSPRCLMLALSQSDPPFGRKSFEQTL
TVELCGTAGLTPPTTPPYKPTEEDPFKPDIKHSLGEDRAPSLPSLEGLQLGAAPVAAHKLPKKHPERSELLSHLRHATAQ
PASQTGQKRPFSCSFGDHDYCQVLKPEGALQRKVLRSWQPSGVHLEDWPQQGAPQAAGPASDREEDRSCDGGAPAKDSVL
LRDHEIRASLTKHFGLLETALEDEDLASCKSAEYDTVFEDSNSSSGESSFLLEEEEEDAEDDSGLSPPRSDHCPYQSPPS
KASRQPCSRSRSSSGSACRSRSPATRRTFRCESRGPCSDGTPSVRHARKRREKAIGEGRVVYVRNLSSDMSSRELKRRFE
VFGEIVECQVLTRSRRGEKYGFITYQCSEHAALSLRNGAALRKRNEPSFQLSYGGLQHFCWPRHTDYDSNSEEALPAAVK
NKYEAMDFDSLLKEAQQSLH

396 - 415:	EEEEEEEEEEEEEEEEEEEE
397 - 416:	EEEEEEEEEEEEEEEEEEEE

A0A2U3W495 **A0A2U3W495_ODORO** (1019 aa)
peroxisome proliferator-activated receptor gamma coactivator 1-beta isoform X1. *Odobenus rosmarus divergens (Pacific walrus)*

MAGNDCGALLDEELSSFFLNYLADTQCGGSGEEQLCADFPELDLSQLDASDFDSATCFGELQWCPENSDTEPSHYSPDDS
ELFQIIDSENEALLAALTKTLDDIPEDDVGLAAFPALDGGDALSCTSASPATSSAPPSPSPSLERPQAPTPEVDELSLLQ
KLLLGTTYPTSSSDTQKEGTAWRQAGLRSRNPRPCVKMDGTQDKKAPMMQSQSRSCTELHKHLTSVPSCPQTKARSPDRS
LQPPPTLSPQLPAKEEEEAGEDCPSPQPAPASPQDSPAPGRAGPGAQGSREDMQAMVQLIRYMHTYCLPQRKLPPQAPEP
APQPCGSPSKQVKPRSRSQHPSKGSWAEFSILRELLAQDVLCDVSKPYRLATPVYASLTPRPRPRDSQASPGHPSPVEEV
RITASPRSTGPRPSLRPLRLEVKGHAGRSARLQREEEEEEEEEEEEEEEEEEEEEWGRKRPGRGLPWTKLGRKLENTVCP
VRRSRRLNPELGPWLAFSDESLVPAEPQGALPSLRLTPEAYDMAGALGSPTDEDSGQDQQLPRGPQIPALESPCESGCGD
TDEDPSCPRLPSRDSPRCLMLALSQSDPPFGRKSFEQTLTVELCGTAGLTPPTTPPYKPTEEDPFKPDIKHSLGEDRAPS
LPSLEGLQLGAAPVAAHKLPKKHPERSELLSHLRHATAQPASQTGQKRPFSCSFGDHDYCQVLKPEGALQRKVLRSWQPS
GVHLEDWPQQGAPQAAGPASDREEDRSCDGGAPAKDSVLLRDHEIRASLTKHFGLLETALEDEDLASCKSAEYDTVFEDS
NSSSGESSFLLEEEEEDAEDDSGLSPPRSDHCPYQSPPSKASRQPCSRSRSSSGSACRSRSPATRRTFRCESRGPCSDGT
PSVRHARKRREKAIGEGRVVYVRNLSSDMSSRELKRRFEVFGEIVECQVLTRSRRGEKYGFITYQCSEHAALSLRNGAAL
RKRNEPSFQLSYGGLQHFCWPRHTDYDSNSEEALPAAVKNKYEAMDFDSLLKEAQQSLH

435 - 454:	EEEEEEEEEEEEEEEEEEEE
436 - 455:	EEEEEEEEEEEEEEEEEEEE

A0A2U3WEQ9 **A0A2U3WEQ9_ODORO** (1767 aa)
Histone acetyltransferase (EC 2.3.1.48). *Odobenus rosmarus divergens (Pacific walrus)*

MVKLANPLYTEWILEAIQKIKKQKQRPSEERICHAVSTSHGLDKKTVSEQLELSVQDGSVLKVTNKGLASYKDPDNPGRF
SSVKPGTFPKSTKGSRGSCNDLRNVDWNKLLRRAIEGLEEPNGSSLKNIEKYLRSQSDLTGTTNNPAFQQRLRLGAKRAV
NNGRLLKDGPQYRVNYGSLDGKGAPKYPSAFPSSLPPVSLLPHEKDQPRADPIPICSFCLGTKESNREKKPEELLSCADC
GSSGHPSCLKFCPELTTNVKALRWQCIECKTCSACRIQGKNADNMLFCDSCDRGFHMECCDPPLSRMPKGMWICQVCRPK
KKGRKLLHEKAAQIKRRYAKPIGRPKNKLKQRLLSVTSDEGSMNAFTGRGSPDTEIKISIKQESTDINVIGNKDTVTEED
LDVFKQAQELSWEKIECESGVEDCGRYPSVIEFGKYEIQTWYSSPYPQEYARLPKLYLCEFCLKYMKSKNILLRHSKKCG
WFHPPANEIYRRKDLSVFEVDGNMSKIYCQNLCLLAKLFLDHKTLYYDVEPFLFYVLTKNDEKGCHLVGYFSKEKLCQQK
YNVSCIMIMPQHQRQGFGRFLIDFSYLLSRREGQAGSPEKPLSDLGRLSYLAYWKSVILEYLYHHQEKHISIKAISRATG
MCPHDIATTLQHLHMIDKRDGRFVIIRREKLILGHMEKLKTCSRTNELDPESLRWTPILISNAAVSEEEREAEKEAERLM
EQASCWEKEEQEILSSRANSRQSPAKVQSKNKYLHSPESRPVAGERGQLMELSKDSSEEEEEEEEEEEEEEEEEEEEEEE
EEEENIQSSPPRLTKPQSVAIKRKRPFVLKKKRGRKRRRINSSVTTETISETTEVLNEPFDNSDEERPMPHLEPTCEIEV
EEDGGKPVLRKAFQHQPGKKRQTEEDEEKDNHCFKNADPCRNNMDDDTDNLKDSSRDNPEPLKCKQVWPKGTKRGLSKWR
PNKERKTGFKLNLYTPPETPMEPDDQVTVEDQREALEDKTSPIPARTEEEVKETAEPLLPRDENRRDETCAPVSPNKSPG
EKPEDDLIKPEEEEEEEEDDDDEEEEEEEENVEKDLGGAKSQEQEEPAVCMDKEDPVPLDEHEEEEEEEEEPSHNEGHD
ADDEDDSHMECTEAEKEERPREAFKEVLENQEAFLDLSVRPSHSNSEVLMDCGVDLAAACNSEPKELAGDTEAAPESDEE
SPEEQAQKQDRKSSEEVDAEFKERNTATMEIDSETVQAVQSLTQENSEQDDTFQDCAETQEACRSLQNYTHADQSPQIAT
ALDDCQQSDHSSPVSSVHSHPGQSVRSVNSPSVPALENSYAQISPDQSAISVPSLQNMETSPMMDVPSVSDHSQQVVDSG
FSDLGSIESTTENYENPSSYDSTMGGSICGNGSSQNSCSYSSLTSSSLTQSSCAVTQQMSNISGSCSLLQQTSISSPPTC
GVKSPQGCVVERPPSSGQQLAQCSMAANFSPPMQLAELPDTGSANLGLYERMGQSDFGAGHYPQPSATFSLAKLQQLTNT
LIDHSLPYSHSAAVTSYANSASLSTPLSNTGLVQLSQSPHSVPGGPQAQATMTPPPNLTPPPMNLPPPLLQRNMAASNIG
ISHSQRLQTQIASKGHVSMRTKSASLSPAAATHQSQIYGRSQTVAMQGPARTLTMQRGMNMSVNLMPAPAYNVNSVNMNM
NTLNAMNGYSMSQPMMNSGYHSNHGYMNQTPQYPMQMQMGMMGTQPYAQQPMQTPPHGNMMYTAPGHHGYMNTGMSKQSL
NGSYMRR

778 - 797:	EEEEEEEEEEEEEEEEEEEE
779 - 798:	EEEEEEEEEEEEEEEEEEEE

780 - 799:	EEEEEEEEEEEEEEEEEEEE
781 - 800:	EEEEEEEEEEEEEEEEEEEE
782 - 801:	EEEEEEEEEEEEEEEEEEEE
783 - 802:	EEEEEEEEEEEEEEEEEEEE
784 - 803:	EEEEEEEEEEEEEEEEEEEE
785 - 804:	EEEEEEEEEEEEEEEEEEEE

A0A2U3WER0 **A0A2U3WER0_ODORO** (1876 aa)
Histone acetyltransferase (EC 2.3.1.48). *Odobenus rosmarus divergens (Pacific walrus)*

```
MVKLANPLYTEWILEAIQKIKKQKQRPSEERICHAVSTSHGLDKKTVSEQLELSVQDGSVLKVTNKGLASYKDPDNPGRF
SSVKPGTFPKSTKGSRGSCNDLRNVDWNKLLRRAIEGLEEPNGSSLKNIEKYLRSQSDLTGTTNNPAFQQRLRLGAKRAV
NNGRLLKDGPQYRVNYGSLDGKGAPKYPSAFPSSLPPVSLLPHEKDQPRADPIPICSFCLGTKESNREKKPEELLSCADC
GSSGHPSCLKFCPELTTNVKALRWQCIECKTCSACRIQGKNADNMLFCDSCDRGFHMECCDPPLSRMPKGMWICQVCRPK
KKGRKLLHEKAAQIKRRYAKPIGRPKNKLKQRLLSVTSDEGSMNAFTGRGSPGRGQKTKVCTTPSSGHAASGKDSSSRLA
VTDPTRPGATTKITTTSTYISASTLKVNKKTKGLIDGLTKFFTPSPDGRRSRGEIIDFSKHYRPRKKVSQKQSCTSHVLA
TDTEIKISIKQESTDINVIGNKDTVTEEDLDVFKQAQELSWEKIECESGVEDCGRYPSVIEFGKYEIQTWYSSPYPQEYA
RLPKLYLCEFCLKYMKSKNILLRHSKKCGWFHPPANEIYRRKDLSVFEVDGNMSKIYCQNLCLLAKLFLDHKTLYYDVEP
FLFYVLTKNDEKGCHLVGYFSKEKLCQQKYNVSCIMIMPQHQRQGFGRFLIDFSYLLSRREGQAGSPEKPLSDLGRLSYL
AYWKSVILEYLYHHQEKHISIKAISRATGMCPHDIATTLQHLHMIDKRDGRFVIIRREKLILGHMEKLKTCSRTNELDPE
SLRWTPILISNAAVSEEEREAEKEAERLMEQASCWEKEEQEILSSRANSRQSPAKVQSKNKYLHSPESRPVAGERGQLME
LSKDSSEEEEEEEEEEEEEEEEEEEEEEEEEEEENIQSSPPRLTKPQSVAIKRKRPFVLKKKRGRKRRRINSSVTTETISE
TTEVLNEPFDNSDEERPMPHLEPTCEIEVEEDGGKPVLRKAFQHQPGKKRQTEEDEEKDNHCFKNADPCRNNMDDDTDNL
KDSSRDNPEPLKCKQVWPKGTKRGLSKWRPNKERKTGFKLNLYTPPETPMEPDDQVTVEDQREALEDKTSPIPARTEEEV
KETAEPLLPRDENRRDETCAPVSPNKSPGEKPEDDLIKPEEEEEEEEDDDDEEEEEEEEENVEKDLGGAKSQEQEEPAVC
MDKEDPVPLDEHEEEEEEEEEPSHNEGHDADDEDDSHMECTEAEKEERPREAFKEVLENQEAFLDLSVRPSHSNSEVLMD
CGVDLAAACNSEPKELAGDTEAAPESDEESPEEQAQKQDRKSSEEVDAEFKERNTATMEIDSETVQAVQSLTQENSEQDD
TFQDCAETQEACRSLQNYTHADQSPQIATALDDCQQSDHSSPVSSVHSHPGQSVRSVNSPSVPALENSYAQISPDQSAIS
VPSLQNMETSPMMDVPSVSDHSQQVVDSGFSDLGSIESTTENYENPSSYDSTMGGSICGNGSSQNSCSYSSLTSSSLTQS
SCAVTQQMSNISGSCSLLQQTSISSPPTCGVKSPQGCVVERPPSSGQQLAQCSMAANFSPPMQLAELPDTGSANLGLYER
MGQSDFGAGHYPQPSATFSLAKLQQLTNTLIDHSLPYSHSAAVTSYANSASLSTPLSNTGLVQLSQSPHSVPGGPQAQAT
MTPPPNLTPPPMNLPPPLLQRNMAASNIGISHSQRLQTQIASKGHVSMRTKSASLSPAAATHQSQIYGRSQTVAMQGPAR
TLTMQRGMNMSVNLMPAPAYNVNSVNMNMNTLNAMNGYSMSQPMMNSGYHSNHGYMNQTPQYPMQMQMGMMGTQPYAQQP
MQTPPHGNMMYTAPGHHGYMNTGMSKQSLNGSYMRR
```

887 - 906:	EEEEEEEEEEEEEEEEEEEE
888 - 907:	EEEEEEEEEEEEEEEEEEEE
889 - 908:	EEEEEEEEEEEEEEEEEEEE
890 - 909:	EEEEEEEEEEEEEEEEEEEE
891 - 910:	EEEEEEEEEEEEEEEEEEEE
892 - 911:	EEEEEEEEEEEEEEEEEEEE
893 - 912:	EEEEEEEEEEEEEEEEEEEE
894 - 913:	EEEEEEEEEEEEEEEEEEEE

A0A2U3WES6 **A0A2U3WES6_ODORO** (2059 aa)
Histone acetyltransferase (EC 2.3.1.48). *Odobenus rosmarus divergens (Pacific walrus)*

```
MVKLANPLYTEWILEAIQKIKKQKQRPSEERICHAVSTSHGLDKKTVSEQLELSVQDGSVLKVTNKGLASYKDPDNPGRF
SSVKPGTFPKSTKGSRGSCNDLRNVDWNKLLRRAIEGLEEPNGSSLKNIEKYLRSQSDLTGTTNNPAFQQRLRLGAKRAV
NNGRLLKDGPQYRVNYGSLDGKGAPKYPSAFPSSLPPVSLLPHEKDQPRADPIPICSFCLGTKESNREKKPEELLSCADC
GSSGHPSCLKFCPELTTNVKALRWQCIECKTCSACRIQGKNADNMLFCDSCDRGFHMECCDPPLSRMPKGMWICQVCRPK
KKGRKLLHEKAAQIKRRYAKPIGRPKNKLKQRLLSVTSDEGSMNAFTGRGSPGRGQKTKVCTTPSSGHAASGKDSSSRLA
VTDPTRPGATTKITTTSTYISASTLKVNKKTKGLIDGLTKFFTPSPDGRRSRGEIIDFSKHYRPRKKVSQKQSCTSHVLA
TGTTQKLKPPPSSLPPPTPISGQSPSSQKSSTSTSSTSPQSCSSQSSVPSFSSLTKNSQLKALFDGLSHIYTTQGQSRKK
GHPSYAPPKRMRRKTELSSTAKSKAHFFGKRDIRSRFIAHSSSSSWGMARGRIFKAIAHFKRTTFLKKHRMLGRLKYKVT
PQMGTPSPGKGSLTDGRIKPDQDDDTEIKISIKQESTDINVIGNKDTVTEEDLDVFKQAQELSWEKIECESGVEDCGRYP
SVIEFGKYEIQTWYSSPYPQEYARLPKLYLCEFCLKYMKSKNILLRHSKKCGWFHPPANEIYRRKDLSVFEVDGNMSKIY
CQNLCLLAKLFLDHKTLYYDVEPFLFYVLTKNDEKGCHLVGYFSKEKLCQQKYNVSCIMIMPQHQRQGFGRFLIDFSYLL
SRREGQAGSPEKPLSDLGRLSYLAYWKSVILEYLYHHQEKHISIKAISRATGMCPHDIATTLQHLHMIDKRDGRFVIIRR
EKLILGHMEKLKTCSRTNELDPESLRWTPILISNAAVSEEEREAEKEAERLMEQASCWEKEEQEILSSRANSRQSPAKVQ
SKNKYLHSPESRPVAGERGQLMELSKDSSEEEEEEEEEEEEEEEEEEEEEEEEEEEENIQSSPPRLTKPQSVAIKRKRPFV
LKKKRGRKRRRINSSVTTETISETTEVLNEPFDNSDEERPMPHLEPTCEIEVEEDGGKPVLRKAFQHQPGKKRQTEEDEE
KDNHCFKNADPCRNNMDDDTDNLKDSSRDNPEPLKCKQVWPKGTKRGLSKWRPNKERKTGFKLNLYTPPETPMEPDDQVT
VEDQREALEDKTSPIPARTEEEVKETAEPLLPRDENRRDETCAPVSPNKSPGEKPEDDLIKPEEEEEEEEDDDDEEEEEE
EEENVEKDLGGAKSQEQEEPAVCMDKEDPVPLDEHEEEEEEEEEPSHNEGHDADDEDDSHMECTEAEKEERPREAFKEVL
ENQEAFLDLSVRPSHSNSEVLMDCGVDLAAACNSEPKELAGDTEAAPESDEESPEEQAQKQDRKSSEEVDAEFKERNTAT
MEIDSETVQAVQSLTQENSEQDDTFQDCAETQEACRSLQNYTHADQSPQIATALDDCQQSDHSSPVSSVHSHPGQSVRSV
NSPSVPALENSYAQISPDQSAISVPSLQNMETSPMMDVPSVSDHSQQVVDSGFSDLGSIESTTENYENPSSYDSTMGGSI
CGNGSSQNSCSYSSLTSSSLTQSSCAVTQQMSNISGSCSLLQQTSISSPPTCGVKSPQGCVVERPPSSGQQLAQCSMAAN
FSPPMQLAELPDTGSANLGLYERMGQSDFGAGHYPQPSATFSLAKLQQLTNTLIDHSLPYSHSAAVTSYANSASLSTPLS
NTGLVQLSQSPHSVPGGPQAQATMTPPPNLTPPPMNLPPPLLQRNMAASNIGISHSQRLQTQIASKGHVSMRTKSASLSP
AAATHQSQIYGRSQTVAMQGPARTLTMQRGMNMSVNLMPAPAYNVNSVNMNMNTLNAMNGYSMSQPMMNSGYHSNHGYMN
QTPQYPMQMQMGMMGTQPYAQQPMQTPPHGNMMYTAPGHHGYMNTGMSKQSLNGSYMRR
```

1070 - 1089:	EEEEEEEEEEEEEEEEEEEE
1071 - 1090:	EEEEEEEEEEEEEEEEEEEE
1072 - 1091:	EEEEEEEEEEEEEEEEEEEE

1073 - 1092:	EEEEEEEEEEEEEEEEEEEE
1074 - 1093:	EEEEEEEEEEEEEEEEEEEE
1075 - 1094:	EEEEEEEEEEEEEEEEEEEE
1076 - 1095:	EEEEEEEEEEEEEEEEEEEE
1077 - 1096:	EEEEEEEEEEEEEEEEEEEE

A0A2U3WHG2 **A0A2U3WHG2_ODORO** (1315 aa)
tau-tubulin kinase 1. *Odobenus rosmarus divergens (Pacific walrus)*

```
MQCLAAALKDETNMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTRENVALKVESAQQPKQVLKMEVAV
LKKLQGKSHVCRFIGCGRNEKFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESIEAIHSVGFLHRDIKPSNF
AMGRLPSTYRKCYMLDFGLARQYTNTTGDVRPPRNVAGFRGTVRYASVNAHKNREMGRHDDLWSLFYMLVEFAVGQLPWR
KIKDKEQVGMIKEKYEHRMLLKHMPSEFHLFLDHIASLDYFTKPDYQLIMSVFENSMKERGIAENEAFDWEKAGTDALLS
TSTSTPPQQNTRQTAAMFGVVNVTPVPGDLLRENTEDVLQGEHLSDQENAPPILPGRPPEGLGPSPHLAPHPGGPEAEVW
EETDVNRNKLRINIGKTPCVVEEEQNRGVGVPSSPVRAPPDSPTTPVRSLRYRRVNSPESERLSTVDGRVELHERRSRMD
LPGSPSRQACSSQPAQMLSVDTGHPDRQASGRMDVSASVEQEALSNAFRSVPLAEEEDFDSKEWVIIDKETELKDFPPGA
EPSTSGTTDEEPEELRPLPEEGEERRRPAVEPSVRPRGRGMQTLAEEDPRQTPFQPLPPPLSQAEGRSETSQPPTPGSPS
HSPLHSGPRPRRRESDPTGPQRQVFSVAPPFEVNGLPRAVPLSLPYQDFKKDLSDYRERARLLNRVRRVGFSHMLLTTPQ
VPLATVQPQANGKEEEEEEEEEEEEEEEEEEEEEDEEEEEEEEDEGEEEGEEGEEAVALGEVLGPRSGSSSDGSERSTDR
SQEGAPSTLLADDQKESRGRASMADGDLEPEEGSKTLVLVSPGDMKKSPVTADLAPDPDLGTLAALTPQQERPQPTGSQL
DVSEPGTLSSVLKSEPKPPGPGTGPGAGAVTAGAGGVAVTSSPFTKVERTFVHIAEKTHLNVMSSGGQASRPEELGAGGE
LGLEAPSDGRAVEEGASVPLENGIAQAGLESCAPTGPPGDTPLEVATDSLPNGPALANGPAPASPLEPGPEKLATISPSR
HAMAGPRPRSRIPVLLSEEDTGSEPSGSLSARERWGKRVRPQQDLARLVMEKRQGRLLLRLASGASSSSSEEQRRASETL
SGTGSEEDTPASEPAAPRKAGRAAATRSRIPRPISIRMPTPAAAQQQSAGRPHGAAPASDTAITSRLQLQKPPGSTVAAD
LRPKQPPGRGPGPGRAPAGTRPAAPRSPGSSASAAPRHPNASPRSQSLSRKESSSPSHQARPAGPPPRGAPQARAQPDGT
PSPGGPKKGPRGKLQTQRAATKGRAGVAEGRAGAR
```

734 - 753:	EEEEEEEEEEEEEEEEEEEE
735 - 754:	EEEEEEEEEEEEEEEEEEEE

A0A2U3WLE7 **A0A2U3WLE7_ODORO** (831 aa)
C-Jun-amino-terminal kinase-interacting protein 2. *Odobenus rosmarus divergens (Pacific walrus)*

```
MADRAEMFSLSTFHSLSPPGCRPPQDISLEEFDDEDLSEITDDCGLGLSYDSDHCEKDSLSLGRSEQPHPICSFQDDFQE
FEMIDDNEEEEEEEEEEEEEEEEEEEEEEEEEGEGEGKEGGGPGSEAPAPEALIPSPSLEEPHKNRPTTLHLTTLGAQDSL
NNNGGFAPAPPASWQETVLCSPPQEPLRESPASLQPTDASPCGAQSPVRSGCDCEGNPPAAGPPAPCGASPSSDPGIEAD
LGSRSSGGRGGRRSSQELSSPGSDSEDAGGARLGRMISSISETELELSSDGGSSSSGRSSHLTNSIEEASSPASEPEPEP
EAPCEPPRRPAFLPVGPDDTNSEYESGSESEPDLSEDADSPWLLSNLVSRMISEGSSPIRCPGQCLSPASRPSGEPASPA
GGTTEAPEAAAGPGGVELVDMETLCGPPPPAPSAPRPGPAQPGPCLFLSNPTRDTITPLWAAPGRSARPARACSAACSEE
DDEDEDEDDADDKVGPPGGRGVGPAAPLDASLVYDAVKYTLVVDEHTQLELVSLRRCAGLGEDSSEDSGGEASEEETAAT
LLGGGQGPEDASPDSPDLTFSKKFLNVFVNSTSRSSSTESFGLFSCLVNGEEKEQTHRAVFRFIPRHPDELELDVDDPVL
VEAEEDDFWFRGFNMRTGERGVFPAFYAHAVPGPVKDLLGSKRSPCWVERFDVQFLGSVEVPCHQGNGILCAAMQKIATA
RKLTVHLRPPASCDLEISLRGVKLSLSGGPEFQHCSHFFQMKNISFCGCHPRNSCYFGFITKHPLLSRFACHVFVSQESM
RPVAQSVGRAFLEYYQEHLEYACPTEDIYLE
```

88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE

A0A2U3WLV5 **A0A2U3WLV5_ODORO** (1324 aa)
splicing factor, arginine/serine-rich 19. *Odobenus rosmarus divergens (Pacific walrus)*

```
MEEEDESRGKTEESGEDRGDGPPDRDPTLSPSAFILRAIQQAVGSSLQGDLPNDKDGSRCHGLRWRRCRSPRSEPRSQES
GGTDTATVLDMAADSFLTGLVSVLDPPDTWVPSHLDLRPGESEDMLELVAEVRIGDRDPIPLPVPSLLPRLRAWRTGKTV
SPQPHSSRPSCARHLLTLGTGDGGPAPPPAPSSASSSPSPSPSSSSPSPPPPPPPPAPPAPPAPRFDIYDPFHPTDEAYS
PPPAPEQKYDPFEPTGSNPSSSAGTPSPEEEEEEEEEEEEEEEEEEEEEEEEEGLSQSISRISETLAGIYDDNSLSQDFPGD
ESPRPDPQPPQPTPAPGTPPQVDSTRVDGATRRRVFVVGTEAEACREGKVSVEVVTAGGAAIPPTLLPPGDSEIEEGEIV
QPEEEPRVAVSLFRGGGGGGGGRAVRPPPAVAAPPAAQPPPPPPAARAPEGDDFLSLHAESDGEGALQVDLGEPAPAPPA
ADTRWGGLDLRRKILTQRRERYRQRSPSPAVAAAAAAAAAAAAAAPAGPPTRKKSRRERKRSGGEAKEAASSSSGAPPAP
PAPASPWDSKKHRSRDRKPGSHASASARRRSRSRSARRRSRSADRRRGGSRRSRSREKRRRRRRSASPPPATSSSSSSRR
ERHRGKHRDGGGSKKKKKRSRSRGEKRSGDSEKAPVPTQPPSGSSSLGGERDSRRRGAVPPSIQDLTDHDLFAIKRTITV
GRPDKSDPRGPSPAPASSPKREVLYDSEGLSAEERGGKSSEKDRRRSGAASSSSSSREKGSRRKALDGGDRDRDRDRDRD
RDRSSKKARPPKESAPSSGPPPKPPVSSGSGSSSSSCSSSSRKVKLQSKVAVLIREGVSSTTPAKEAASAGLGSIGVKFS
RDRESRSPFLKPDERAPAEVAKAAPGSTKPKKTKVKAKAGAKKAKGTKGKTKPSKTRKKIRGGGSGGGGGGPVTLKKSKA
DSCSQAAGAKGVEETSWSGEERAAKAPSTPPPKAAPPPPALTPDSQTVDSSCKTPEVSFLPEEATEEAGVRGGAEEEEEE
EEEEEEEEEEEQQPATTTATSTAAAAPSTAPSAGSTAGDSGAEDGPATRVSQLPTLPPPMPWNLPAGVDCTTSGVLALTA
LLFKMEEANLASRAKAQELIQATNQILSHRKPPSSLGVTPTPVPTSLGLPPGPSSYLLPGSLPLGGCGSTPPTPTGLAAA
SDKREGSSSSEGRGDTDKYLKKLHTQERAVEEVKLAIKPYYQKKDITKEEYKDILRKAVHKICHSKSGEINPVKVSNLVR
AYVQRYRYFRKHGRKPGDPPGPPRPPKEPGPPDKGGPGLPLPPL
```

269 - 288:	EEEEEEEEEEEEEEEEEEEE
270 - 289:	EEEEEEEEEEEEEEEEEEEE
271 - 290:	EEEEEEEEEEEEEEEEEEEE
272 - 291:	EEEEEEEEEEEEEEEEEEEE

A0A2U3WMI6 **A0A2U3WMI6_ODORO** (1097 aa)
myelin transcription factor 1. *Odobenus rosmarus divergens (Pacific walrus)*

```
MSLENEDKRARTRSKAPRVPPEPTGADLSCPTPGCTGSGHIRGKYSRHRSLQSCPLAKKRKLEGAQAEHLASTRKSHPLK
LALDEGYSVDTDGSEDAEVKDASVSDESEGTLEDEAEMSGQEEIHRPEPAEGRAPAKSHFGPKPIGSSAGPAKGSYSSYQ
EIIATSLLNLGQIAVETLVGEDLGQVAKPGPGVVHLVQEEAEEGATSDEGERDTFLPLEDAEGVAGVVRERSQELCPQAV
EGVASEESRKMKVALGEEEEEEEEEEEEEEEEEEEEEEEEEVAAPEVICQEDAPLAPTQKAPELRHPASPSPKPEYSVIV
EVHSDDGRDEDARSQKSAVTDESEMYDMMTRGNLGLLEQAIALKAEQVQAVCEPGCPPTEQGQLGPGEPGKAVRPLDAAR
KNYCSKDPSRAEKREIKCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRIPPEILAMHENVLKCPTPGCTGQGHVNSNRNTH
RSLSGCPIAAAEKLAKSHEKQQPQAGDPSKNSSNSDRILRPMCFVKQLEVPPYGSYHPSVAPATPRANLAKELEKFSKVT
FDYASFDAQVFGKRMLAPKIQTSETSPKAFKCFDYAHDAEAAHMAATAILNLSTRCWEMPENLSTKPQDLPSKAVDIEVD
ENGTLDLSMHKHRKRESAFPSSSSPGVKSPEASQRQSSTSAPSSSMTSPQSSQASRQDAWDRPLDYTKPSRQREEEPEES
EPAAHSFASSEADDQEVSEESFEERKYPGEVTLTNFKMKFLSKDIKKELLTCPTPGCDGSGHITGNYASHRSLSGCPLAD
KSLRNLMAAHSADLKCPTPGCDGSGHITGNYASHRSLSGCPRAKKSGARVTPTKDDKEDPELMKCPVPGCVGLGHISGKY
ASHRSASGCPLAARRQKEGSLNGSPFSWKSLKNEGPTCPTPGCDGSGHANGSFLTHRSLSGCPRATFAGKKGKVSGDEVL
STKFKTSDVLENDEEIKQLNQEIRDLNESNSEMEAAMVQLQSQISSMEKSLKNIEEENKLIEEQNEALFLELSGLSQALI
QSLANIRLPHMEPICEQNFDAYVSTLTDMYSNQECYQNPENKDLLESIKRAVRGIQV
```

257 - 276:	EEEEEEEEEEEEEEEEEEEE
258 - 277:	EEEEEEEEEEEEEEEEEEEE
259 - 278:	EEEEEEEEEEEEEEEEEEEE
260 - 279:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE
262 - 281:	EEEEEEEEEEEEEEEEEEEE

A0A2U3X003 **A0A2U3X003_ODORO** (1234 aa)
histone-lysine N-methyltransferase EHMT2 isoform X2. *Odobenus rosmarus divergens (Pacific walrus)*

```
MRGLPRGRGLMRPRGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWAPQLPTGLTSPPIPCVPCQGEAPAEMGA
LVLEKEPRGVTERVHGSLGDTPRSEETLPKASPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDEPENLEGDGDLH
GGRILLGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAATAGPEPPVATPSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSMGKMTSEVAKRRKLNAGGGLSEELGSTRGSGEVTVEKGDPGSLEEWE
TVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKA
KKKWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGEL
SGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHC
GEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLAQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGG
CLSAVGLPPGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKG
SVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQV
DVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLH
IAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAVRTEKIICRDVARGYENVPIP
CVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFE
CNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEV
YCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCK
HSAEAIALEQSRLARLDPHPELLPELSSLPPVNP
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE

A0A2U3X004 **A0A2U3X004_ODORO** (1177 aa)
histone-lysine N-methyltransferase EHMT2 isoform X4. *Odobenus rosmarus divergens (Pacific walrus)*

```
MAAAAGAAAAAAAEGEAPAEMGALVLEKEPRGVTERVHGSLGDTPRSEETLPKASPDSLEPAGPSSPASVTVTVGDEGAD
TPVGATPLIGDEPENLEGDGDLHGGRILLGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGA
ATAGPEPPVATPSPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSMGKMTSEVAKRRKLNAGGGLSEEL
GSTRGSGEVTVEKGDPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEE
EEEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAP
KIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDF
RVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLAQDAPGRADTSQPSARMRGHGEPRR
PPCDPLADTIDSSGPSLTLPNGGCLSAVGLPPGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDN
LDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGST
CLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAI
AEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGN
RAVRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIR
CWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELIS
DAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFD
YGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELSSLPPVNP
```

300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE

305 - 324:	EEEEEEEEEEEEEEEEEEEE

A0A2U3X006 **A0A2U3X006_ODORO** (1211 aa)
histone-lysine N-methyltransferase EHMT2 isoform X3. *Odobenus rosmarus divergens (Pacific walrus)*

```
MAAAAGAAAAAAAEGEAPAEMGALVLEKEPRGVTERVHGSLGDTPRSEETLPKASPDSLEPAGPSSPASVTVTVGDEGAD
TPVGATPLIGDEPENLEGDGDLHGGRILLGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGA
ATAGPEPPVATPSPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSMGKMTSEVAKRRKLNAGGGLSEEL
GSTRGSGEVTVEKGDPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEE
EEEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGT
LSPNHAGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMV
LCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAG
TAAPAPPPLAQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPPGPGREALEKALVIQ
ESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQR
TPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIE
VIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPEL
RNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAVRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCET
STMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVR
LQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNI
IPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELL
PELSSLPPVNP
```

300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE

A0A2U3X024 **A0A2U3X024_ODORO** (1268 aa)
histone-lysine N-methyltransferase EHMT2 isoform X1. *Odobenus rosmarus divergens (Pacific walrus)*

```
MRGLPRGRGLMRPRGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWAPQLPTGLTSPPIPCVPCQGEAPAEMGA
LVLEKEPRGVTERVHGSLGDTPRSEETLPKASPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDEPENLEGDGDLH
GGRILLGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAATAGPEPPVATPSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSMGKMTSEVAKRRKLNAGGGLSEELGSTRGSGEVTVEKGDPGSLEEWE
TVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKA
KKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEE
LPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCT
AGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLAQDAPGRADTSQPS
ARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPPGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGE
LQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGG
CVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICL
HWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQ
LNRKLRLGVGNRAVRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSS
SNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGT
FICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSR
DIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELSSLPPVNP
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE

A0A2U3XD16 **A0A2U3XD16_LEPWE** (712 aa)
YTH domain-containing protein 1 isoform X2. *Leptonychotes weddellii (Weddell seal) (Otaria weddellii)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDIKRQKPSVHSRQLISKPLSSSVSN
NKRIVSTKGKSVAEYKNEEYQRSERSKRLEADRKIRLSSSASREPYKSQPEKTCLRKRDPDRRTKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEEE
EEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGS
SASESYADQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSARSVILIFSVRESGKFQGFARL
SSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLLFPPD
ESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYAPEFHQRPGYLKDPRYQEVDRR
FSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMAPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHHPVPHEARYRDKRVHD
YDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDRGERGRYRR
```

229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE

A0A2U3XD39 **A0A2U3XD39_LEPWE** (730 aa)
YTH domain-containing protein 1 isoform X1. *Leptonychotes weddellii (Weddell seal) (Otaria weddellii)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDIKRQKPSVHSRQLISKPLSSSVSN
NKRIVSTKGKSVAEYKNEEYQRSERSKRLEADRKIRLSSSASREPYKSQPEKTCLRKRDPDRRTKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEEE
EEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGS
SASESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSARSV
ILIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDG
QEIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYAPEF
HQRPGYLKDPRYQEVDRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMAPYPGMEQPPHHPYYQHHAPPPQAHPPYS
GHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDR
DRGERGRYRR
```

229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE

A0A2U3XDY4 **A0A2U3XDY4_LEPWE** (1109 aa)
sodium/potassium/calcium exchanger 1 isoform X1. *Leptonychotes weddellii (Weddell seal) (Otaria weddellii)*

```
MGKLIRMGTRKRRLLWPKRLLWSRLFFLLGMLIIGSAYQHLRSPRGLPSLWAAVSSQHPVKLASRDLPNNDMMMVSSDPP
RASSEMMGDTRVPQTTVGKDEATRGITMENTPNPPRRTANITPTMPKNNYSLTAADTERTKEDTTITPSRVLNHYTPTSK
RPTVKNHTPTTSPRVEMQSYHPTQAGRKVMKYTPSPLGRLVSTYAPSTLMTMTESHGITPRTTVKDSETMTTTKILETNP
SKRIVEETTPTTLKGIINKTPTSLINDMETNILTSPRSMTEENTLTTPRRVNNNRSTKPRGLVGKNKLTAPLGMGLEHTT
AISEGRVTIRTTPTGSGPTETKASTATWSISNPLSGTSVSTSGISSATFRGLAKKSSMAPRPSSPSKVRANPTIQVRHCV
VVEPAPAVPPAPSPSLTTAMIPEAPSSNPSALPPGWPDLHSKAEYPPDLFSIEERRQGWVVLHIFGMMYVFVALAIVCDE
YFVPALGVITDKLQISDDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCALFSREILNLTW
WPLFRDVSFYILDLIMLILFFLDSLITWWESLLLLLAYALYVFTMKWNKQLEVWVKEQLSRRPVAKVMALGDLSKPGNGA
AAVDELQENTKLKVVLPAVLTRGSSSASLHNSTIRSTIYQLMLHSLDPLGEARPSKDKESLSQEAKAKLHANAENKPEEE
EPAQLPAVTVTPAPDPDVKGDQEEEDPGGQEGDVPGAESTGDVIGEEAETPDRGENGQQGGGETQLEGEGEIEAEGEGGE
DEGEIKAEGGEGEHEGEDEGELQAEDGEMKADEGENEEQELNAESQGEAKSDEKGRDGEGGGEGGGSEDEEEEEEEEEEE
EEEEEEEEEDEAEDEEEEEEEASEEPLSLEWPETRQKQAIYLFLLPIVFPLWLTVPDVRRLESKKFFVLTFLGSIMWIAM
FSYLMVWWAHQVGETVGISEEIMGLTILAAGTSIPDLITSVIVARKGLGDMAVSSSVGSNIFDITMGLPVPWLLFSFING
LQPVPVSSNGLFCAIVLLFLMLLFVISSIASCKWRMNKILGFTMFLLYFVFLIISVMLEDRIISCPVSV
```

870 - 889:	EEEEEEEEEEEEEEEEEEEE

A0A2U3XEE2 **A0A2U3XEE2_LEPWE** (1093 aa)
sodium/potassium/calcium exchanger 1 isoform X2. *Leptonychotes weddellii (Weddell seal) (Otaria weddellii)*

```
MGKLIRMGTRKRRLLWPKRLLWSRLFFLLGMLIIGSAYQHLRSPRGLPSLWAAVSSQHPVKLASRDLPNNDMMMVSSDPP
RASSEMMGDTRVPQTTVGKDEATRGITMENTPNPPRRTANITPTMPKNNYSLTAADTERTKEDTTITPSRVLNHYTPTSK
RPTVKNHTPTTSPRVEMQSYHPTQAGRKVMKYTPSPLGRLVSTYAPSTLMTMTESHGITPRTTVKDSETMTTTKILETNP
SKRIVEETTPTTLKGIINKTPTSLINDMETNILTSPRSMTEENTLTTPRRVNNNRSTKPRGLVGKNKLTAPLGMGLEHTT
AISEGRVTIRTTPTGSGPTETKASTATWSISNPLSGTSVSTSGISSATFRGLAKKSSMAPRPSSPSKVRANPTIQVRHCV
VVEPAPAVPPAPSPSLTTAMIPEAPSSNPSALPPGWPDLHSKAEYPPDLFSIEERRQGWVVLHIFGMMYVFVALAIVCDE
YFVPALGVITDKLQISDDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCALFSREILNLTW
WPLFRDVSFYILDLIMLILFFLDSLITWWESLLLLLAYALYVFTMKWNKQLEVWVKEQLSRRPVAKVMALGDLSKLPAVL
PAVLTRGSSSASLHNSTIRSTIYQLMLHSLDPLGEARPSKDKESLSQEAKAKLHANAENKPEEEEPAQLPAVTVTPAPDP
DVKGDQEEEDPGGQEGDVPGAESTGDVIGEEAETPDRGENGQQGGGETQLEGEGEIEAEGEGGEDEGEIKAEGGEGEHEG
EDEGELQAEDGEMKADEGENEEQELNAESQGEAKSDEKGRDGEGGGEGGGSEDEEEEEEEEEEEEEEEEEEEEEDEAEDEE
EEEEEASEEPLSLEWPETRQKQAIYLFLLPIVFPLWLTVPDVRRLESKKFFVLTFLGSIMWIAMFSYLMVWWAHQVGETV
GISEEIMGLTILAAGTSIPDLITSVIVARKGLGDMAVSSSVGSNIFDITMGLPVPWLLFSFINGLQPVPVSSNGLFCAIV
LLFLMLLFVISSIASCKWRMNKILGFTMFLLYFVFLIISVMLEDRIISCPVSV
```

854 - 873:	EEEEEEEEEEEEEEEEEEEE

A0A2U3XF77 **A0A2U3XF77_LEPWE** (549 aa)
ran GTPase-activating protein 1. *Leptonychotes weddellii (Weddell seal) (Otaria weddellii)*

```
MAKDVIKEIEDFDGLEALRLEGNTVGVEAARVIAKALEKKSELKRCHWSDMFTGRLRSEIPPALTSLGEGLITAGAQLVE
LDLSDNAFGPDGVRGFEALLKSSSCFTLHELKLNNCGMGIGGGKILAAALTECHRKSSAQGKPLGLKVFVAGRNRLENDG
ATALAEAFGIIGTLEEVHMPQNGINHPGVTALAQAFAINPLLRVINLNDNTFTEKGAVAMAKTLKTLRQVEMINFGDCLV
RSKGAVAIAEAVRGGLPKLKELNLSFCEIKRDAALAVAEAVADKSELEKLDLNGNTLGAEGCEQLQEVLDGFHMAKVLAS
LSDDEGEDDEEEEEEEEEEGEEEEEEEEEEEEEEEEEEEEEAQQGPGEQSTASRKILDPNSGEPAPVLSAPPPADVSTFL
AFPSPEKLLRLGPKSPVLIAQQTDTSDPEKVVSAFLKVSSVFKDEATVRTAVQDAVDALMKKAFSSPSFNSNAFLTRLLV
HMGLLKSEDKIKAIANLYGPLMVLNHMVQQDYFPKALAPLLLAFMTKPNGALESCSFARHNLLQTLYKV
```

341 - 360:	EEEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEEE

A0A2U3XVK4 **A0A2U3XVK4_LEPWE** (831 aa)
C-Jun-amino-terminal kinase-interacting protein 2. *Leptonychotes weddellii (Weddell seal) (Otaria weddellii)*

```
MADRAEMFSLSTFHSLSPPGCRPPQDISLEEFDDEDLSEITDDCGLGLSYDSDHCEKDSLSLGRSEQPHPICSFQDDFQE
```

```
FEMIDDNEEEEEEEEEEEEEEEEEEEEEEEGEGEGKEGGGPGSEAPAPEALIPSPSLEEPHKNRPTTLHLTTLGAQDSLNN
NGGFAPAPPASWQETVLCSPPQEPLRESPASLQPTDASPCGAQSPVLPGCDCEGNPPAAGPPAPCGASPSSDPGIEADLG
SRSSGGRGGRRSSQELSSPGSDSEDAGGARLGRMISSISETELELSSDGGSSSSSGRSSHLTNSIEEASSPTSEPEPEPE
APCEPPRRPAFLPVGPDDTNSEYESGSESEPDLSEDADSPWLLSNLVSRMISEGSSPIRCPGQCLSPASRPSGEPSSPAG
GTTEAPEAAAGPGGVELVDMETLCGPPPPAPSAPRPGPAQPGPCLFLSNPTRDTITPLWAAPGRSARPARACSAACSEED
DEDEEEEEDADDKVGPPGGRGVGPAAPLDASLVYDAVKYTLVVDEHTQLELVSLRRCAGLGEDSSEDSGGEASEEETAAT
LLGGGQGPEDASPDSPDLTFSKKFLNVFVNSTSRSSSTESFGLFSCLVNGEEKEQTHRAVFRFIPRHPDELELDVDDPVL
VEAEEDDFWFRGFNMRTGERGVFPAFYAHAVPGPAKDLLGSKRSPCWVERFDVQFLGSVEVPCHQGNGILCAAMQKIATA
RKLTVHLRPPASCDLEISLRGVKLSLSGGPEFQHCSHFFQMKNISFCGCHPRNSCYFGFITKHPLLSRFACHVFVSQESM
RPVAQSVGRAFLEYYQEHLEYACPTEDIYLE
```

88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE

A0A2U3Y450 **A0A2U3Y450_LEPWE** (1211 aa)
histone-lysine N-methyltransferase EHMT2 isoform X2. *Leptonychotes weddellii (Weddell seal) (Otaria weddellii)*

```
MAAAAGAAAAAAAEGEAPAEMGALVLEKEPRGATERVHGSLGDTPRSEETLPKASPDSLEPAGPSSPASVTVTVGDEGAD
TPVGATPLIGDEPENLEGDGDLHGGRILLGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGA
ATAGPEPPVATPSPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSMGKMTSEVAKRRKLNAGGGLSEEL
GSTRGSGEVTVEKGDPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEE
EEEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGT
LSPNHAGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMV
LCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAG
TAAPAPPPLAQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPPGPGREALEKALVIQ
ESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQR
TPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIE
VIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPEL
RNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAVRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCET
STMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVR
LQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNI
IPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELL
PELSSLPPVNP
```

300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE

A0A2U3Y459 **A0A2U3Y459_LEPWE** (1268 aa)
histone-lysine N-methyltransferase EHMT2 isoform X1. *Leptonychotes weddellii (Weddell seal) (Otaria weddellii)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWAPQLPTGLTSPPIPCVPCQGEAPAEMGA
LVLEKEPRGATERVHGSLGDTPRSEETLPKASPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDEPENLEGDGDLH
GGRILLGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAATAGPEPPVATPSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSMGKMTSEVAKRRKLNAGGGLSEELGSTRGSGEVTVEKGDPGSLEEWE
TVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKA
KKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEE
LPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCT
AGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLAQDAPGRADTSQPS
ARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPPGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGE
LQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGG
CVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICL
HWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQ
LNRKLRLGVGNRAVRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSS
SNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGT
FICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSR
DIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELSSLPPVNP
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE

A0A2U3YHJ6 **A0A2U3YHJ6_LEPWE** (984 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Leptonychotes weddellii (Weddell seal) (Otaria weddellii)*

```
MFQQHCVSWLRSIQQVLQSQDPPPTMELAVAVLRDLLRYAAQLPTLFRDISMNHLPGLLTSLLGLRPECELSALEGMKAC
MTYFPRACGSLKGKLASFFLSRVDALSPQLQQLACECYSRLPSLGAGFSQGLKHTESWQQELRSLLASLHSLLGALYEGA
ETAPVQYEGPGVEVLLTPAEDGDAHALLRLRQRFCGLARCLGLMLSSEFGAPVSVPVQEILDVICRTLSISAKNISLLGD
GPLRLLLLPSIHLDALDLLSALILACGGRLLRFGGLVSRLLPQVLNAWNMGRDTLSPGQERPYSTVRTKVYAVLELWVQV
```

```
CGASAGVLQGGASGEALLSHLLSDIAPPADALKLRSPRGSPDGGLQSGKPSAPKKLKLDLGEAMAPPSHRKGDSNANSDV
CAAALRGLSRTVLMCGPLIKEETHRRLHDLVVPLVMGLQRGETLGSSPYTSSRCRRELYRLLLALLLAPSPRCPPPLACA
LHAFSLGQREDSLEVSSFCSEALVVCAALTHPRVPPLQPAGPPCPTPAPVPPPEAPSPFRAPPFHPPAGPLPPARPGPPA
TANHLGLSVPGLVSVPPRLLPGPENHRAGSNEDPVLAPSGTPPPALPPDETFGGRVPRPAFVHYDKEEASDVEISLESDS
DDSVVIVPEGLPPLPPPPPSGTTPPPVAPAGPPTASPPVPAKEEPEELPAAPGPLPPPPPPPVPGPVALPPPQLVPEGTP
GGGGPPTLEEDLTVININSSDEEEEEEEEEEEEEEEEEEEEEDFEEEEEDEEEYFEEEEEEEEFEEEFEEEEGELEEEEE
EEDEEDEEELEELEEAEFGPAGGPAEEGGPAPPSPAPALPPAQSPTVQPEPEGEPGLLLEVEEPGAEEEPGAQAAPTLAP
EVLPSQGEGPRATGSPPAGPPPQELVEEEPLAPPTLLEEGTESGGDRVPPLPETPAAEDGEAEAEAESAALQEKEQDDTA
AMLADFIDCPPDDEKPPPAPEPDS
```

742 - 761:	EEEEEEEEEEEEEEEEEEEE
743 - 762:	EEEEEEEEEEEEEEEEEEEE

A0A2U3ZAX4 **A0A2U3ZAX4_ODORO** (767 aa)
LOW QUALITY PROTEIN: lipid phosphate phosphatase-related protein type 3. *Odobenus rosmarus divergens (Pacific walrus)*

```
MIATKEKNKTPKDSMTLLPCFYFVELPIVASSVVSLYFLELTDLFKPAKVGFQCYDRTLSMPYVETNEELIPLLMLLSLA
FAAPAASIMVGEGMLYCLQSRLWGRGGGPGGAEGSINAGGCSFNSFLRRTVRFVGVHVFGLCATALVTDVIQLATGYHAP
FFLTVCKPNYTLLGTSCEANPYITQDICSGHDTHAILSARKTFPSQHATLSAFAAVYVSVSPGPPXARAQARPPAGNHAL
TRPALPCPQMYFNSVISDTTKLLKPILVFAFAIAAGVCGLTQITQYRSHPVDVYAGFLIGAGIAAYLACHAVGNFQAPTA
EKPMALAPAKDALRALTQRGHDSVYQQNKSVSTDELGPPGRLEGVPRPVARETKSLGSLKRASVDVDLLAPRSPMGKENM
VTFSHTLPRVSTPSLDDPARRHMTIHVPLDASRSKQLISEWKQKSLEGRGLGLPDEASPGHLRAPAEPMAEEEEEEEEEE
EEEEEEEEEEGEEGGPAPPSLYPTVQARPGLGPRVILPPRAGPQPLVHIPEEGAQAAAGLSPKSSAAVRAKWLMMAEKSG
AAAAAAAAASAQPRMANPPRLLQVIAMSKAPGGPGPKVAETASSSSASSDSSQYRSPSDRDSASIVTIDAHAPHHPVVHL
SAGNGPWEWKTAGGAAKGVEGEGGYELGDLARGFRGGPKPPGVSPGSSISDVDQEEPRFGAVATVNLATGEGLPPLSVTD
GALGPASRESTLRRKASGLVLGERETAGEAEAEGYYRKMQAARRFKD
```

471 - 490:	EEEEEEEEEEEEEEEEEEEE

A0A2U3ZC06 **A0A2U3ZC06_ODORO** (2917 aa)
WD repeat-containing protein 87. *Odobenus rosmarus divergens (Pacific walrus)*

```
MSSTRLIPLWKDFKYLVNDIIHKSKQTSEDPKNEVVVLSDQSQILFRESRHPQNMPLICYYFSDANFFASLSWVTSTKEI
QAVVWMKSKTEDMVEKRTFSMTEKLPPIQSMVHTGSFHILVAYCGDLILRLFGDHFRSFKPLGIVPCRFNINCLCYDPEM
KMLLSGILGAVVTWIIERSGKGLQVAHMVPMPGEELVQDIRLNGPNGSLLALCETVVRVLERQGHGQLGEVQRFTSTTSG
SSITCCFTCFDQGFLYAGNKTGEIQVWSLVRGNSLHSFKAHFSSVTCIRSRPEAHTLLTAGKEGLIKEWNLTLGNLLRRL
ELGEELYELEFIDNTTFFCQTMHTFSLRRLPCFYSLFSVCGSAPQQLRRVRCGDNWFRILCTTEDGLLRFVSPLTGDLLV
LTWPFTILDRAVDWAYDPEKEELFVATGNAEVLVFDTTRCPCPAKYLLCTSPNSQDWVQCLAYGHFHLGRGLQGLMFSGH
QSGVIRVLSQNYCARIEKFMHFGAILALSTLPGGLFGSRENSLLCSYGMDDYVHLSEAVLEGRKVHLKPLASILSSCHLR
HLILLPMSVGAITETNCLRLWKFHDFLSSESQEDSVFIETLPLHQCTITSFDVCLSLSLFVTGGIDGSVRVWNFHGRLIA
MLDSSLHFGPLCFANDRGDLLVSFNQSLYLVSCLKLLHPTLLARLSFMSMTDEVLESPKPFTPSFFFSFETMFVPKYIYL
GKGQQELVSLEKLVNKRAIAFDHTVPHVIEEDKQGSPMVLPAFRHGFLYKEETDGMEVGKPPHYVIPPQLQLTAWDGLNP
YQILRCYFGHGRKWLLAPDGYIPNSVIRARLWPEGSPIYLQCNLHSPVWETDWDKSQQFFFWHSRVTSLSDAGEYSQEKE
DEDFIEMRLSKDITYSVLTDSAKCSWLGKKMSEIAINSLVETILNIMIHASPLKYQCCIGALGQIFASYEVSSSLRSETA
HRLLDDTTNSKPLIRELAWEGLKHLGMITHLFAMPLAQGLMDKDQRVRSKALNLMADTGIHSKSSLLNLIQHRETFQEMQ
QEMIGEESLDHLLGMRATDLQILHTQVEQRLNENLTLSEGQEKPAFSLEVSRISERISLSKQPDVIPKESEATVKSGKGQ
RRGRAGGKKHVRKLWRALKKIKEAGKQPGPLEGEIDQREAAPVLVEDTAAHSRMSSTISVLKISKDGEQQPPEKDTSKDN
FALNLKMLRKIHDRKSKKRTVQKPKKRHKKTKEAEVTTEESLSAVKEEPVVKQLKAKGRGATGAPGRKTIPEDSSSWRDD
LCRLMTLRISGSQTKMSEALNMELVATAQEVLADQQPSWELFQEICPLLEKKSEVLLEDLNWDIAWPEEKPIFIHEGAIR
DDIMTIRREDEIPEEQEQVQKEAEEMPYLQETQVIPKKGKKKKAIFLGPSGLTKRKRISKKEETKSFTKPFKQERKEVQQ
EIKVDKKETVSKTERDVSQAVEEVAKPEEEVVKQEERPVMDERKLSWQERKKSWDEWKQAQGETKIAWDEWKKAWDKKHL
EEEEKQQTDERKPLPEEEKLDVDKKKLRWDEWLEFWEQTVARSGEEHKDDEELTLKGEELPQEWGEEEQEELMSKEQRQI
QKEYNQAWMERKRAQAERKRAQEERKLAQEEEKLVQEERKLAQEERKLAREYGKLAQRDRTMVQSERKFVHNEEKLAKRE
EKLSQEAEKLAQKRKKLAKQFEELAREEEKIAKKGGKLAEVKKILAQKMEKLTQKEQELALQEKELARELEELMWEEEEL
ARKEEELIQELKDLAEEEEGLAQEDKTLAWQEQKLIKEEKTLALEEELLIQEEKKLAHDKEKLPEEEEKLAQRRKKLMEN
KLKLAQEKEKLAQDKEKLTKNKTILDWREKSLAQERENLLQEKVKLAQRKENFLQVKENLAQNKNKLDQAKEKLDVYKKK
LAQVEKKLMEEKEKLSQKKEKLDEAEKKLTQLEESLAQKQHNLAQDKMELAMEKRAVFQELKMLRGEWDGAKEEKALGTE
MKKLAQEKVRLSEEKQILSAGETEETLKQIRLTKNELELIKRKLSLEEKILRYEDRILATEQRDIAKRKLEFTRGRRVYA
QEERKLAKVVRKLIKEKEGTSKASKVSSKVLKALRELTKEEMKLTQEEIEMTKMKRNFFVKERKLSKEKNKLDAKEWDFS
EEQPEVTKDEKKLAKKQRKLAKEMKRMIKKEKKITEEESRLARQQREVIQEEEEEGLTKDEEVIPLLKQRSRKRKELKTV
DTPQEKLPSREESRESLSEEMEGLLDQVEQESLSEEEEEEEEEEEEEEEEEEEEEGKVVEEVEVEEKRKKEKEKEKEEKE
KKEKKKKKVQEEEEKEEEEEKESISEEESESLSEEESESLSEEESESLSEKEKGKSSLKKEADKKKEISKKEKLFKSQAE
REKDQRREIIPSIGKRIPDIKDSDIQLKVLKVPSKKVITIALRRQETIPVPVSTKQVSWEEKARALEASRILPESRFMDR
QGEPLKKYKPKPLQLLDTVLESPEQDLKTPYLPHILRKTMEAHKLQGEPLEPKWQWILQHHPTLMRKTEVPVPQIWTKEI
GAQVGLSDIEWIRHVLEQMEAGEQLTRDSFHRLCQLLKDLTSKGNLEWLHLAQLEAIVYRHKQVLESRSAHISKPSKEPM
GPKYLKVIPPIKGKESWLKPFTVPTLKSPLGTKGIPTPKGINWHLLEEPYRSAWAEQISTALKEMEVQHFHPATGDSFTG
AQASVDKQTLALMFQKDFWAFKDKGRSPRLPKLEKKAQAVSKKKEEVPLWETFVALYHVLRMLQQRYAKDSTAWMEQFYQ
LMDLYQLKSPRIQKLLQELLLRDERQSQEITYEEALKAMELVPGERLFYHLFCGGSQNPKGPLEFQEVVSLPGQNNVRTM
NPMGITQYGILELAWRSLPQADTHHTKEMPHIIASTP
```

2275 - 2294:	EEEEEEEEEEEEEEEEEEEE
2276 - 2295:	EEEEEEEEEEEEEEEEEEEE

A0A2U3ZCG7 **A0A2U3ZCG7_ODORO** (441 aa)
protein FAM43A. *Odobenus rosmarus divergens (Pacific walrus)*

```
MLPWKKHKFELLAEAPPRQASKPKGYAVSLHYSALSSLARACPEGALSRVGSMFRSKRKKLHITSEDPTYTVLYLGNATT
IQARGDGCTDLAVGKIWSKSEAGRQGTKMKLTVSAQGIRMVHAEERALRRPGHLYLLHRVTYCVADARLPKVFAWVYRHE
LKHKAVMLRCHAVLVSKPEKAQAMALLLYQTSANALAEFKRLKRRDDARHQQQELVGAHTIPLVPLRKLLLHGPCCYKPP
VERSRSAPKLGSITEDLLGEQQEQELQEEEEEEHTEGCLEEEEEEEEEEEEEEEEEEEEEDRAEDRHPAVEEAKAQRAL
VVAMHLECGDLLDTLESGREEALGGGGVSLGPGAGPSPLLMGSAPDMKAELSQLINDLGELSFGNDVRSLQADLRVTRLL
SGESTGSESSIEGGGPDATSATAGDRSGPADGANPEEPHSG
```

280 - 299:	EEEEEEEEEEEEEEEEEEEE

281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE

A0A2U3ZLL7 **A0A2U3ZLL7_ODORO** (737 aa)
YTH domain-containing protein 1 isoform X2. *Odobenus rosmarus divergens (Pacific walrus)*

```
MLNGNDFSLFLIFWLSDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDIKRQKPSVHSRQLISKP
LSSSVSNNKRIVSTKGKSVAEYKNEEYQRSERSKRLEADRKIRLSSSASREPYKSQPEKTCLRKRDPERRTKSPTPDGSE
RIGLEVDRRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEEE
EEEEEEEEEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPI
VFDRSGSSASESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAA
FRSARSVILIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKP
VKIGRDGQEIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPR
IDYAPEFHQRPGYLKDPRYQEVDRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMAPYPGMEQPPHHPYYQHHAPPP
QAHPPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERE
RLCDRDRDRGERGRYRR
```

236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE
239 - 258:	EEEEEEEEEEEEEEEEEEEE
240 - 259:	EEEEEEEEEEEEEEEEEEEE

A0A2U3ZVW0 **A0A2U3ZVW0_ODORO** (988 aa)
histone-lysine N-methyltransferase EHMT2 isoform X5. *Odobenus rosmarus divergens (Pacific walrus)*

```
MGALVLEKEPRGVTERVHGSLGDTPRSEETLPKASPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDEPENLEGDG
DLHGGRILLGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAATAGPEPPVATPSPEGQPKV
HRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSMGKMTSEVAKRRKLNAGGGLSEELGSTRGSGEVTVEKGDPGSLE
EWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGR
RKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERG
FEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGY
FCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQD
SGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARES
YHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAVRTEKIICRDVARGYENVPIPCVNGVD
GEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACS
CWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDAR
YYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAI
ALEQSRLARLDPHPELLPELSSLPPVNP
```

280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE

A0A2U4BEB5 **A0A2U4BEB5_TURTR** (1873 aa)
Histone acetyltransferase (EC 2.3.1.48). *Tursiops truncatus (Atlantic bottle-nosed dolphin) (Delphinus truncatus)*

```
MVKLANPLYTEWILEAIQKIKKQKQRPSEERICHAVSTSHGLDKKTVSEQLELSVQDGSVLKVTNKGLASYKDPDNPGRF
SSVKPGTFPKSAKGSRGSCNDLRNVDWNKLLRRAIEGLEEPNGSSLKNIEKYLRSQSDLTSTTTNPAFQQRLRLGAKRAV
NNGRLLKDGPQYRVNYGGLDGKGAPKYPSAFPSSLPPVSLLPHEKDQPRADPIPICSFCLGTKESNREKKPEELLSCADC
GSSGHPSCLKFCPELTTNVKALRWQCIECKTCSACRIQGKNADNMLFCDSCDRGFHMECCDPPLSRMPKGMWICQVCRPK
KKGRKLLHEKAAQIKRRYAKPIGRPKNKLKQRLLSVTSDEGSMNAFTGRGSPGRGQKTKVCTTPSSGHAASGKDSSSRLA
VTDPTRPGATTKITTTSTYISASTLKVNKKTKGLIDGLTKFFTPSPDGRRSRGEIIDFSKHYRPRKKVSQKQSCTSHVLA
PDTEIKISIKQESTDINVIGNKDTVTEEDLDVFKQAQELSWEKIECESGVEDCGRYPSVIEFGKYEIQTWYSSPYPQEYA
RLPKLYLCEFCLKYMKSKNILLRHSRKCGWFHPPANEIYRRKDLSVFEVDGNMSKIYCQNLCLLAKLFLDHKTLYYDVEP
FLFYVLTKNDEKGCHLVGYFSKEKLCQQKYNVSCIMIMPQHQRQGFGRFLIDFSYLLSRREGQAGSPEKPLSDLGRLSYL
AYWKSVILEYLYHHHERHISIKAISRATGMCPHDIATTLQHLHMIDKRDGRFVIIRREKLILGHMEKLKTCSRTNELDPE
SLRWTPILISNAAVSEEEREAEKEAERLMEQASCWEKEEQEILSSRANSRQSPAKVQSKNKYLHSPESRPVAGERGQLME
LSKESSEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEENIQSSPPRLTKPQSVAIKRKRPFVLKKKRGRKRRRINSSVTTETIS
ETTEVLNEPFDNSDEERPMPQLEPTCEIEVEEDGGKPVLRKAFQHQPGKKRQTEEEEGKDNHCFKNADPCRNNMDDDANN
LKEASRDNPEPLKCKQWPKGTKRGLSKWRPNKERKTGFKLNLYTPPETPMEPDDQVIVEEQKETPADKTSPAPTRTEEEV
KEAVEPLLPGDENRREETCAPVSPNKSPGEKPEDDLIKPEEDEEEEEEEEEEEEEEGNVAKDPCGAQSQEKEEPEVCTDK
EDPVRLDDHEEEEEEDEEPSHNEGHDADDEDDSHVESAESEKEERPREGFKEVLETQEAFLDLSVQPSHSNAEVLMDCGV
DLTASCNSEPKELAGATETAPESDEEPAGEQAQEQDQKNSEEVDSEFKEGNTATLEIDSETVQAVQSLTQENSEQDDTFQ
DCAETQEACRSLQNYTHADQSPQIAASLDDCQQSDHSSPVSSVHSHPSQSVRSVNSPSVPALENSYAQISPDQNAISVPS
LQNMETSPMMDVPSVSDHSQQVVDSGFSDLGSIESTTENYENPSSYDSTMGGSICGNGSSQNSCSYSNLTSSNLTQSSCA
VTQQMSNISGSCSMLQQTSISSPPTCSVKSPQGCVVERPPSSSQQLAQCSMAANFTPPMQLAEIPETGNTNLGLYERMGQ
SDFGAGHYPQPSATFSLAKLQQLTNTLIDHSLPYSHSAAVTSYANSASLSTPLSNTGLVQLSQSPHSVPGGPQAQATMTP
PPNLTPPPMNLPPPLLQRNMAASNIGISHSQRLQTQIASKGHVSMRTKSASLSPAAATHQSQIYGRSQTVAMQGPARTLT
MQRGMNMSVNLMPSPAYNVNSVNMNMNTLNAMNGYSMSQPMMNSGYHSNHGYMNQTPQYPMQMQMGMMGTQPYAQQPMQT
PPHSNMMYTAPGHHGYMNPGMSKQSLNGSYMRR
```

887 - 906:	EEEEEEEEEEEEEEEEEEEE
888 - 907:	EEEEEEEEEEEEEEEEEEEE

889 - 908:	EEEEEEEEEEEEEEEEEEEE
890 - 909:	EEEEEEEEEEEEEEEEEEEE
891 - 910:	EEEEEEEEEEEEEEEEEEEE
892 - 911:	EEEEEEEEEEEEEEEEEEEE
893 - 912:	EEEEEEEEEEEEEEEEEEEE
894 - 913:	EEEEEEEEEEEEEEEEEEEE
895 - 914:	EEEEEEEEEEEEEEEEEEEE

A0A2U4BEE6 **A0A2U4BEE6_TURTR** (2056 aa)
Histone acetyltransferase (EC 2.3.1.48). *Tursiops truncatus (Atlantic bottle-nosed dolphin) (Delphinus truncatus)*

```
MVKLANPLYTEWILEAIQKIKKQKQRPSEERICHAVSTSHGLDKKTVSEQLELSVQDGSVLKVTNKGLASYKDPDNPGRF
SSVKPGTFPKSAKGSRGSCNDLRNVDWNKLLRRAIEGLEEPNGSSLKNIEKYLRSQSDLTSTTTNPAFQQRLRLGAKRAV
NNGRLLKDGPQYRVNYGGLDGKGAPKYPSAFPSSLPPVSLLPHEKDQPRADPIPICSFCLGTKESNREKKPEELLSCADC
GSSGHPSCLKFCPELTTNVKALRWQCIECKTCSACRIQGKNADNMLFCDSCDRGFHMECCDPPLSRMPKGMWICQVCRPK
KKGRKLLHEKAAQIKRRYAKPIGRPKNKLKQRLLSVTSDEGSMNAFTGRGSPGRGQKTKVCTTPSSGHAASGKDSSSRLA
VTDPTRPGATTKITTTSTYISASTLKVNKKTKGLIDGLTKFFTPSPDGRRSRGEIIDFSKHYRPRKKVSQKQSCTSHVLA
PGTTQKLKPPPSSLPPATPISGQSPSSQKSSTSVSSTSPQSSSSQSSVPSFSSLTNNSQLKALFDGLSHIYTTQGQSRQK
GHPSYAPPKRMRRKIEFPSTAKSKAHFFGKRDIRSRFISHPSSSSWGMARGRIFKAIAHFKRTTFLKKHRMLGRLKYKVT
PQMGTPSPGKGSLTDGRIKPDQDDDTEIKISIKQESTDINVIGNKDTVTEEDLDVFKQAQELSWEKIECESGVEDCGRYP
SVIEFGKYEIQTWYSSPYPQEYARLPKLYLCEFCLKYMKSKNILLRHSRKCGWFHPPANEIYRRKDLSVFEVDGNMSKIY
CQNLCLLAKLFLDHKTLYYDVEPFLFYVLTKNDEKGCHLVGYFSKEKLCQQKYNVSCIMIMPQHQRQGFGRFLIDFSYLL
SRREGQAGSPEKPLSDLGRLSYLAYWKSVILEYLYHHHERHISIKAISRATGMCPHDIATTLQHLHMIDKRDGRFVIIRR
EKLILGHMEKLKTCSRTNELDPESLRWTPILISNAAVSEEEREAEKEAERLMEQASCWEKEEQEILSSRANSRQSPAKVQ
SKNKYLHSPESRPVAGERGQLMELSKESSEEEEEEEEEEEEEEEEEEEEEEEEEEENIQSSPPRLTKPQSVAIKRKRPF
VLKKKRGRKRRRINSSVTTETISETTEVLNEPFDNSDEERPMPQLEPTCEIEVEEDGGKPVLRKAFQHQPGKKRQTEEEE
GKDNHCFKNADPCRNNMDDDANNLKEASRDNPEPLKCKQWPKGTKRGLSKWRPNKERKTGFKLNLYTPPETPMEPDDQVI
VEEQKETPADKTSPAPTRTEEEVKEAVEPLLPGDENRREETCAPVSPNKSPGEKPEDDLIKPEEDEEEEEEEEEEEEEEG
NVAKDPCGAQSQEKEEPEVCTDKEDPVRLDDHEEEEEEDEEPSHNEGHDADDEDDSHVESAESEKEERPREGFKEVLETQ
EAFLDLSVQPSHSNAEVLMDCGVDLTASCNSEPKELAGATETAPESDEEPAGEQAQEQDQKNSEEVDSEFKEGNTATLEI
DSETVQAVQSLTQENSEQDDTFQDCAETQEACRSLQNYTHADQSPQIAASLDDCQQSDHSSPVSSVHSHPSQSVRSVNSP
SVPALENSYAQISPDQNAISVPSLQNMETSPMMDVPSVSDHSQQVVDSGFSDLGSIESTTENYENPSSYDSTMGGSICGN
GSSQNSCSYSNLTSSNLTQSSCAVTQQMSNISGSCSMLQQTSISSPPTCSVKSPQGCVVERPPSSSQQLAQCSMAANFTP
PMQLAEIPETGNTNLGLYERMGQSDFGAGHYPQPSATFSLAKLQQLTNTLIDHSLPYSHSAAVTSYANSASLSTPLSNTG
LVQLSQSPHSVPGGPQAQATMTPPPNLTPPPMNLPPPLLQRNMAASNIGISHSQRLQTQIASKGHVSMRTKSASLSPAAA
THQSQIYGRSQTVAMQGPARTLTMQRGMNMSVNLMPSPAYNVNSVNMNMNTLNAMNGYSMSQPMMNSGYHSNHGYMNQTP
QYPMQMQMGMMGTQPYAQQPMQTPPHSNMMYTAPGHHGYMNPGMSKQSLNGSYMRR
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1070 - 1089:	EEEEEEEEEEEEEEEEEEEE
1071 - 1090:	EEEEEEEEEEEEEEEEEEEE
1072 - 1091:	EEEEEEEEEEEEEEEEEEEE
1073 - 1092:	EEEEEEEEEEEEEEEEEEEE
1074 - 1093:	EEEEEEEEEEEEEEEEEEEE
1075 - 1094:	EEEEEEEEEEEEEEEEEEEE
1076 - 1095:	EEEEEEEEEEEEEEEEEEEE
1077 - 1096:	EEEEEEEEEEEEEEEEEEEE
1078 - 1097:	EEEEEEEEEEEEEEEEEEEE

A0A2U4BEN7 **A0A2U4BEN7_TURTR** (1764 aa)
Histone acetyltransferase (EC 2.3.1.48). *Tursiops truncatus (Atlantic bottle-nosed dolphin) (Delphinus truncatus)*

```
MVKLANPLYTEWILEAIQKIKKQKQRPSEERICHAVSTSHGLDKKTVSEQLELSVQDGSVLKVTNKGLASYKDPDNPGRF
SSVKPGTFPKSAKGSRGSCNDLRNVDWNKLLRRAIEGLEEPNGSSLKNIEKYLRSQSDLTSTTTNPAFQQRLRLGAKRAV
NNGRLLKDGPQYRVNYGGLDGKGAPKYPSAFPSSLPPVSLLPHEKDQPRADPIPICSFCLGTKESNREKKPEELLSCADC
GSSGHPSCLKFCPELTTNVKALRWQCIECKTCSACRIQGKNADNMLFCDSCDRGFHMECCDPPLSRMPKGMWICQVCRPK
KKGRKLLHEKAAQIKRRYAKPIGRPKNKLKQRLLSVTSDEGSMNAFTGRGSPDTEIKISIKQESTDINVIGNKDTVTEED
LDVFKQAQELSWEKIECESGVEDCGRYPSVIEFGKYEIQTWYSSPYPQEYARLPKLYLCEFCLKYMKSKNILLRHSRKCG
WFHPPANEIYRRKDLSVFEVDGNMSKIYCQNLCLLAKLFLDHKTLYYDVEPFLFYVLTKNDEKGCHLVGYFSKEKLCQQK
YNVSCIMIMPQHQRQGFGRFLIDFSYLLSRREGQAGSPEKPLSDLGRLSYLAYWKSVILEYLYHHHERHISIKAISRATG
MCPHDIATTLQHLHMIDKRDGRFVIIRREKLILGHMEKLKTCSRTNELDPESLRWTPILISNAAVSEEEREAEKEAERLM
EQASCWEKEEQEILSSRANSRQSPAKVQSKNKYLHSPESRPVAGERGQLMELSKESSEEEEEEEEEEEEEEEEEEEEEEE
EEEEENIQSSPPRLTKPQSVAIKRKRPFVLKKKRGRKRRRINSSVTTETISETTEVLNEPFDNSDEERPMPQLEPTCEIE
VEEDGGKPVLRKAFQHQPGKKRQTEEEEGKDNHCFKNADPCRNNMDDDANNLKEASRDNPEPLKCKQWPKGTKRGLSKWR
PNKERKTGFKLNLYTPPETPMEPDDQVIVEEQKETPADKTSPAPTRTEEEVKEAVEPLLPGDENRREETCAPVSPNKSPG
EKPEDDLIKPEEDEEEEEEEEEEEEEEEEGNVAKDPCGAQSQEKEEPEVCTDKEDPVRLDDHEEEEEEDEEPSHNEGHDADD
EDDSHVESAESEKEERPREGFKEVLETQEAFLDLSVQPSHSNAEVLMDCGVDLTASCNSEPKELAGATETAPESDEEPAG
EQAQEQDQKNSEEVDSEFKEGNTATLEIDSETVQAVQSLTQENSEQDDTFQDCAETQEACRSLQNYTHADQSPQIAASLD
DCQQSDHSSPVSSVHSHPSQSVRSVNSPSVPALENSYAQISPDQNAISVPSLQNMETSPMMDVPSVSDHSQQVVDSGFSD
LGSIESTTENYENPSSYDSTMGGSICGNGSSQNSCSYSNLTSSNLTQSSCAVTQQMSNISGSCSMLQQTSISSPPTCSVK
SPQGCVVERPPSSSQQLAQCSMAANFTPPMQLAEIPETGNTNLGLYERMGQSDFGAGHYPQPSATFSLAKLQQLTNTLID
HSLPYSHSAAVTSYANSASLSTPLSNTGLVQLSQSPHSVPGGPQAQATMTPPPNLTPPPMNLPPPLLQRNMAASNIGISH
SQRLQTQIASKGHVSMRTKSASLSPAAATHQSQIYGRSQTVAMQGPARTLTMQRGMNMSVNLMPSPAYNVNSVNMNMNTL
NAMNGYSMSQPMMNSGYHSNHGYMNQTPQYPMQMQMGMMGTQPYAQQPMQTPPHSNMMYTAPGHHGYMNPGMSKQSLNGS
YMRR
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778 - 797:	EEEEEEEEEEEEEEEEEEEE
779 - 798:	EEEEEEEEEEEEEEEEEEEE

780 - 799:	EEEEEEEEEEEEEEEEEEEE
781 - 800:	EEEEEEEEEEEEEEEEEEEE
782 - 801:	EEEEEEEEEEEEEEEEEEEE
783 - 802:	EEEEEEEEEEEEEEEEEEEE
784 - 803:	EEEEEEEEEEEEEEEEEEEE
785 - 804:	EEEEEEEEEEEEEEEEEEEE
786 - 805:	EEEEEEEEEEEEEEEEEEEE

A0A2U4CL52 **A0A2U4CL52_TURTR** (603 aa)
major centromere autoantigen B. *Tursiops truncatus (Atlantic bottle-nosed dolphin) (Delphinus truncatus)*

```
MGPKRRQLTFREKSRIIQEVEENPDLRKGEIARRFNIPPSTLSTILKNKRAILASERKYGVASTCRKTNKLSPYDKLEGL
LIAWFQQIRAAGLPVKGIILKEKALRIAEELGMDDFTASNGWLDRFRRRHGVVSCSGVARARSRSAAPRPPAAPASPPTV
PSEGSGGGTTGWRAREEQPPSVAEGYASQDVFSATETSLWYDFLPDQAAGLCGSDGRARKATQRLSVLLCANADGSEKLP
PLVAGKSAKPRAGQAGLPCDYTANSKGGVTTQALAKYLKALDTRMAAESRRVLLLAGRLAAQSLDTSGLRHVQLAYFPPG
TVQPLERGVVQQVKGHYRQAMLLKAMAALEGQDRSGLQLGLMEALHFVAAAWQAVEPSDIATCFREAGFGGGPNATITTA
LKSEEEEEEEEEEEEEEEEEEEEGEGEEEEEEDGEEEEEGGEGEELGEEEEVEEEGDVDDSDEEEEEEEESSSEGLEAED
WAQGVVEAGGSFGGYGAQEEVQCPTLHFLEGEEDSESDSEEEEEDDEEEDEDDEDDDEDGDEVPVPSFGEAMAYFAMVKR
YLTSFPIDDRVQSHILHLEHDLVHVTRKNHARQAGVRGLGHQS
```

404 - 423:	EEEEEEEEEEEEEEEEEEEE

A0A2U9BB08 **A0A2U9BB08_SCOMX** (556 aa)
Putative SH3 and multiple ankyrin repeat domains protein 2 (Fragment). *Scophthalmus maximus (Turbot) (Psetta maxima)*

```
KCMRFNPDATVWVAKQRILCTLNQSLQDVLNYGLFQPASDGRDGKFLDEERTLREYPQPISKGVPCLEFRYKSRVYRQPS
VDEKQIAKLHTKANLRKFMDLLQHNQVDKVAKLLERGFDPNYHDSETGESPLTFAAHLDDVVDAIKVLRNGGAHLDFRAK
DGMTALHKAARSKNQVSLTTLLELGASPDYKDSRGLTPLYHSAVVGGDPGCCELLLSHHASVCCQDENGWHEVHQACRHG
HVQHLEHLLFYGADMSAQNASGNSALHICALYNQDNCARVLLVRGADKDVKNYNSQSPFQVAIIAGNFELAELIKNHRET
DIDPTADGASFSSRRTFTTDRLGPNKMAAPESETFYLRVCSTRGRRDASSILVYSLWSRLTLSMREYQLAVGTTEEEEEG
EEEEEEGEEEEEEEEEEEDEEGEEEEEEEEEEEEEEEEGEEEEEEEGGGEEGGGGGEGEEEGGEGEEEEEEEEEEEEGEE
EEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEELCDQNKKYGKKYIYIYRYTEIDKYIYLTHDLTVTADTPVFAHP
```

490 - 509:	EEEEEEEEEEEEEEEEEEEE
491 - 510:	EEEEEEEEEEEEEEEEEEEE
492 - 511:	EEEEEEEEEEEEEEEEEEEE
493 - 512:	EEEEEEEEEEEEEEEEEEEE
494 - 513:	EEEEEEEEEEEEEEEEEEEE

A0A2U9BPT8 **A0A2U9BPT8_SCOMX** (807 aa)
Putative B-cell lymphoma/leukemia 11A-like. *Scophthalmus maximus (Turbot) (Psetta maxima)*

```
MSRRKQGKPQHLSTREFTPEPLSGVLPEEDSQDSPRLGVAPGDPLKGDQDLLTCGQCHSRFPLADILLFIEHKRRQCHGS
LCTDKPLDRPPSSPLASPLSTSSSHSRTHHQHPRRACRPVEVAVQVSPRDEDCLSAPLQGIIPKLENITDKDEPSSYTCT
TCKQPFTSAWFLLQHAQNTHGFRIYLESEPGSPLTPRVATAPGMGGDCVSSQPPLHAVHLADGSPYSLLRMPGSGSGRDS
ASTPREGRYPRTPPLFSPPPRHHLSPDDLALATHHPSAFDRVMRLNSVPLEPPPSMDFSRRLRELAGNATGASPPLSPNR
PNHMQRLLQPFQPGSKPPFSATPPLSTSQSPSGSRSTPNTVSNAVQPSTPLKAKSCEFCGKTFKFQSNLIVHRRSHTGEK
PFKCHLCNHACTQASKLKRHMKTHCQSKSSALNAKSDDGLSTASSPEPGTSELMGSATDALKSVVAKFKSENNGLMNGEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEIESKPGVEEEEGRNEYRFSLRLEGARHHENSEALHPRRRSSSQEPGDEDSAM
ESDRADDGTTTTMNGLGPLSTDSLSRKLLGGGVSPGSLSPISKRIKVEKDLDPPTPTIPNTENVYSQWLAGYAASRQLKD
PFINFTGGDSRQSPFASSSEHSSENGSLRFSTPPGELDGERATSGRSGTGSGASTPHGGSGNGRPSSKDGRRSDTCEYCG
KVFKNCSNLTVHRRSHTGERPYKCELCSYACAQSSKLTRHMKTHGQMGKDVYKCEICHMPFSVYSTLEKHMKKWHSDRPL
ANDIKTE
```

479 - 498:	EEEEEEEEEEEEEEEEEEEE
480 - 499:	EEEEEEEEEEEEEEEEEEEE
481 - 500:	EEEEEEEEEEEEEEEEEEEE
482 - 501:	EEEEEEEEEEEEEEEEEEEE
483 - 502:	EEEEEEEEEEEEEEEEEEEE
484 - 503:	EEEEEEEEEEEEEEEEEEEE
485 - 504:	EEEEEEEEEEEEEEEEEEEE
486 - 505:	EEEEEEEEEEEEEEEEEEEE
487 - 506:	EEEEEEEEEEEEEEEEEEEE
488 - 507:	EEEEEEEEEEEEEEEEEEEE
489 - 508:	EEEEEEEEEEEEEEEEEEEE

A0A2U9C271 **A0A2U9C271_SCOMX** (4088 aa)

Non-specific serine/threonine protein kinase (EC 2.7.11.1). *Scophthalmus maximus (Turbot) (Psetta maxima)*

```
MSNGGFPGCRTISQHLNDLKKENFSLKLRIYFLEEKIQQKFEESSDGVHKRNIELKVEVESLKKELEDKQQLLDEALLTA
DSLSNQNEAELQRRLAERQHEICHMQEILETKVQLLQEEAELARGEAERMASLADVESRRCLALEREMVERTEQSGGAAA
AFTQQPLADKDRAIEQLTQEKLSLRLRVEELEVRVHDLSSSVGRKGAEEEEEEEEEEEEEEEEEEEEEEELVQREMIDPR
DPNTRGREERLMDEQQDQLSRYESGAGRCVSELQEARLQVRSLQATIREGESGNQKLQQRLGEMELELRSAREEAQQHER
SIQNIADNFSSKEAEAADLYTVIEEQNKMLCSLKELVDRHQLLPQVSGAESARGPVEVLALQASLFQAQLELQAGERSQR
QAARAQEDLSRALQRLETDLQGALQHRRETETHNQELQSVLDQARSALQEREEQLREGEREKEREREEREKRIRELMTSL
QTKEQLLEDYCELLDDPQKEKRDSLLQKLRQRVRERDRALERALDEKFLCIEEKEEETRRLQLLLREKERDMERQRSVLV
NNEETINSLELLLRGKAVELQQVRDAWTSVQRRQRQSDERQSRALSERDDIISQLQAALLARSQEAQDLRCSLLAQIQSA
PGDVLEELKVRLRLKDSLFQEVLADRTHQAQQHQDQVQALLTALGSRDQYIQESARRLGDVMSEQTSRLQELRRQLCSGS
GSGTDQDQDLELELQAAREELRLALRREKENQERSGRREAELDSLSRALRVKEGVIRDFQRQMADPSGLPLVERLTQEVQ
ELREGLVRPGVGQQPEIGVSESQCLSVSVSLCLSVSVSESQCLCVSVSLCLSLRVSVSQSQCLSLSVSVSVSESQCLSLS
VSVSESQSQSDVKTKPSSEDEDEDLNSEDVDEEEEELRGPTLRTTKSGLYLCMSGSSAASDSSQGSGAAGEAAGLGPAVE
GHGLTEVKQLVEQKRAVERELAELKAQLEKCGFSSLSQMRKALISLRAENQDLTHQLTEGEHAEEDEELDVTIEEEEQEE
EEEQEEEEEEESSEMWEAWDSELPLSPTGEDPRAEGDTRHEASSSQELSPCSPLRTCPRYPASVPQQQLHVAGRGRHRAGE
RDQEPGRERPLGPGATVRDQAEQLIAETTVPRDTKQIQVDLQDPGYETCGRSETEAEREDTSSPEFDDLEMCTSLDCGSQ
WWPATSGGSPFTKAAAQSSALGDEASSLQRLVEDLRSQLSRSQAVIRGLQSRLRSLSTSSDVGPAAPRKVNWCFQASQSG
TEDDEGWQSSDGGPLASPRHPRPDTGLQELSSRVDALENQLRKGGKKSVDQDGKSATGPGKFDSLIQAQARELSHLRQRL
REGRGVCSILTQQLGDTTKAFEELLRANDVDYYMGQSFREQLAQSGALAQRVGAKISGRDHPEDPDEKTELLAIRLSKEL
QQKDKIIESLRTKLNQHHPHHHHSHRSDTPCSSHALSDATDQSDRISYVSDEQGSTNEDLELCSDVDAASELGAEETSSS
TRVGTDCPSHMSHHMSGPPSIASSHKTPSCLSCPSMHCPGSPLKPAVMQSQTAPASVFTSAPLYPPPSARTAPSPLHPHP
STPRTRLHGGGGGGVGFTLAEVHQELQMLQRQLDRFSTPQSKPPGFLFARQQTDPSSFLPLSLHGYQASPYGSGLDAGLA
MKAGASLLESSALWDTTYNLGRPARLGADLSSGSSGYQSGTSHAGSDLMKEHLREVRSLRQRLEDSIQTNERLRQQLEDR
LTRNNSEKGAPTNIYIQGLDSVGQLSSEIRLLKEENVRLLNQLRQASAEGAKEAELLREAALSDRARLKEAELEVERWAE
QSRKSQAEAEAHNGEIAQLKQDRQRSQETINRLQHEVNILQQQLLESRSLVRSLQCELQVCHGGGGATSNTHSGPVGGIT
FDPRQLHVQLEPQLIGRPRARRLLFNDNARSPPVRDTGLGGVPSSPLRSLHKHETGDVDAASTLQGQVPDGSFASRHGRH
AVGHIDDFQALQQQVVEGGTLLCRMEVALRPLLAPPARQEFSPRQDPDAGSARTLLSDAQTLRQILEEADALLGMFWRAT
LPNPEETKQTDEVVSLRLRLSEQEQALKDVMERMRSCDRTRDNMENFIVSQLDGEVEGMRRTENKNKRKLCNMEPRGSGA
EDKDVKEFAAPPPLLFRKLSNPDLSPAATAATKSKLHRQLSQDESRARRSSVAMTGKQLLPLSCSLHAGVSQLTWQGPCG
GFGGPGAVGGAPAGGGAEVNNLVRMRSQTLGQSAPSLTGLKELSLPRRGSFCRTSNRKSLIVTSSTSPTLPRPHSPLHGH
TGTSPLDSPRNFSPNTAAHFSFIPARRTDGRRWSLASLPSSGYGTNTPSSTVSSSCSSQEKLHQLPFQPTPDELHFLTKH
FSSESITDEEGRRSPAMRPRSRSLSPGRSPISFDHEIVMMNHVYKERFPKATAQMEERLAELLCSFSDPARVCPLADGVL
SFIHHQLTELSRDCLEKSREGVITSRYFYELQENLERLLQDAHERSESVEVTFVTQLVRKLMIIIARPARLLECLEFDPE
EFYHLLEAAEGHAKEGQGIKCDIPRYIISQLGLTRDPLEEMAQLSSYDSGNPETPETDDSVDNRGTPVPAAPPQTKTKPP
REEDFETIKLISNGAYGAVFLVRHKETRQRFAMKKINKQNLILRNQIQQAFVERDILTFAENPFVVSMFCSFETRRHLCM
VMEYVEGGDCATLLKNIGALPVDMARMYFAETVLALEYLHNYGIVHRDLKPDNLLITSMGHIKLTDFGLSKIGLMSLTTN
LYEGHIEKDTREFLDKQVCGTPEYIAPEVILRQGYGKPVDWWAMGVILYEFLVGCAPFFGDTPEELFGQVISDEIIWPEE
EEALPQEAQDLICKLLRQNPLERLGTGSAFEVKQHLFFKELDWNSLLRQKAEFIPQLESEDDTSYFDTRSDRYHHVDSEE
EDDTNDDEHVEMRQFSSCSPRFSKVYSSMERLSLHEEKRTPPPTKRSLSEEGGDRIDSLSGLKSRDRSWLVGSPEILRKR
LSVSESSHTESDSSPPLTVRRRCCSAIIEMPRFAISSEEEGAQGQGAAGSRKSPSLLGLSAARGPRGDELPLAIPELPLE
RELKLDESPTTPSSTCSQLSRATLTPGSSGDVCERATGGTGVNAKSDSDSPSTPKAISDLAARRARHRLLSGDADKHAAP
PSSRPLNKVIKSASATALSLMIPADHYGASPLASPMSPHSLSSNPSSRDSSPIRDLSPAVSCVKPAIVIHRAGKKYGFTL
RAIRVYMGDSDIYSVHHMVWHVEDGGPAHEAGLREGDLITQVNGEQVHGLVHTEVVELILKSGAKVSICATPFENTSIKV
GPARKTSHKSKMARRNKKTKTKEGQDSKKRTSLFRKITKQASLLHTSRSLSSLNRSLSSGESGPGSPTHNLSPRSPTQGY
RSTPDSAHSVGGNSSQSSSPSSSVPNSPASSGHIRPSSLHGLAPKLQRQYRSPRRKSAGNIPLSPLARTPSPTPQSSSPQ
RSPSPLSGHALGAQGATGQSFPVKLHSSPPLARQISRPKSAESPRSPLLKRVQSAEKLASSLSNPPSCPSGAAAAAGAAG
SRKHSLEILQREPSLQSLQESASEGLLSSAGRGVETGSLQKHASSSSRKLGRQEGDGSLVPVSGPLGLAPGKSKLKDKLS
AIRQDRAERRESLQKQDAIHEVDSSEDETDEGSEDSQDGRRGATFTPPPLLRPTTVRTGPGGTLPSLCLSPFTHTGRPTP
SHTSLPSVTETRPGQSSAASSADDGVVRREKKVLEQSATRPLPFSTPGSAFISVCKDTFLKPAPPPDPRSARAKTSESRA
EDRTLVSPRTTGPPTSTTSTTSTSDFRTTSTTSVTTDQTTETPRPSCSSPGVPKEKKEADNRRLCAVAVASSLSTTSSSS
SSSSSSSSSSSSTSSSNSTSSSPVPPPDSGVDKVVSQLAIVATSVLGPVKLKSAAAADESVKERKPSGGVVSDVPPPAAP
QSQRSSKPSTQKDCTAPRLPPSCKDVPERPTSGSSRENAASSAARPERNTSLATAAASDPQCKRSEPQTATNAASASSQQ
DKATNKKT
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208 - 227:	EEEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE

A0A2U9CCY7 **A0A2U9CCY7_SCOMX** (831 aa)
Putative B-cell lymphoma/leukemia 11A-like. *Scophthalmus maximus (Turbot) (Psetta maxima)*

```
MSRRKQGKPQHLSKRDFSPVVSSEELSERCSEHSEESGSLNGHHPGSTVGRLARLGHAAHPSLEQDLLTCGQCQATFPLA
DILLFIEHKRKRCHGPPCLAVGRGLDKPPSPSPGLALTPSPALGALRSRRPVEVGVQATLADDDDDRFSLPRAICPKQEP
LPGKEEPTTYTCTTCKQSYGSAWFLLQHAQNNHGFRIYLESEHGSPLTPRMGGPSSLGGGADCPSQPPLHGLHLPPDASP
FNLLRIPGSGSGGRDSIGAGIGVGPAGTAVGGHHQRFPPTPPLFSPPPRNHLDPHHLSPEELALAAHHPSAFDRVLRLNP
PLALDPPATMDFSRRLRELAGNTSGSSPPPSPSRPSPMQRLLQPFQTGGGSGGTVGAGGSKPPYLATPPPLPGSLQSPVG
SQTTPTTPLPSAGTTPSSTNPLKSKCCEFCGKSFKFQSNLIVHRRSHTGEKPYKCHLCDHACTQASKLKRHMKTHMHKSS
SPNTGKSEDGLSTASSPEPGTSEHMGSASNALKSVVAKLKSENARMLRENGEEEEEEEEEEEEEEEEEEEEEEEEEEEIE
EEDHSGERAPRRNNSYHFGLNLETARQHENNGGIGSRLEGLTDEGSIPRSLPEVMQGMGLAASMQHFSEALHAHKRNAMA
QENHLHHHLNRDHHHIREMCDGNSVLETDRGEEGAVSTVNGRGASPNESASVGLSKKLLLGSPSPLSPFSKRIKLEKEFD
LPTPTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRFSTPPGELDGGMSGRSGTGSGGSTP
HLGGPGRPSSKESRRSDTSSWWCSRLRSQYI
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532 - 551:	EEEEEEEEEEEEEEEEEEEE
533 - 552:	EEEEEEEEEEEEEEEEEEEE
534 - 553:	EEEEEEEEEEEEEEEEEEEE
535 - 554:	EEEEEEEEEEEEEEEEEEEE
536 - 555:	EEEEEEEEEEEEEEEEEEEE
537 - 556:	EEEEEEEEEEEEEEEEEEEE
538 - 557:	EEEEEEEEEEEEEEEEEEEE

A0A2U9CU76 **A0A2U9CU76_SCOMX** (975 aa)

Putative B-cell lymphoma/leukemia 11B-like. *Scophthalmus maximus (Turbot) (Psetta maxima)*

```
MPCDETIISLEFKKGVNTGERSQIRVPIAAGVHRTSSVTAVAAAEVLRPAKTQSDLVGRAALQPLIALPSAPSRPERAPE
RQSRTANCGGNKEGRGESWSPCDPEQTDTTVQADSKCRSPGDARVNAGAMSRRKQVNPQHLSLTHRETIQAEANHDSGAG
SPSPVPSTPSPRRAGPGEHDLLTCGQCQTNFPLGDILVFIEHKRRLCRGPRSGPGSFSKPGERGGVTGLPIPPRVRSLEL
GRGSLPVEIGIQVTPGGEGNEERRLTPAKGICPKQERGDKNEPSSYICTTCKQNFTSAWFLLQHAQHTHGIRIYLDNHPV
NCSLTPRMALPPPPGVEALPRSPLPTFLGDTNNPFHLLRMAAPLLREHPPPPGYMETRLPATPPFISPPPPPRPPLERLG
PEEMGLLSQHPSAFERVMRMTPMEPPSMDFSRRLRELAGNTTNNGGPTPPLSPNRVPPMHRLLSPTLFQPGAKPPAFLTY
APQPPTSQGGHGSTSPPDTQGQNQTPGKSKSCEFCGKIFKFQSNLIVHRRSHTGERPYKCHLCDHACSQASKLKRHMKTH
MHNKSGSMSGSPEPGNRGEGEEKSREGDSRVIGLDNEEEEEEEEEEEEEEEEEEEELRNGSRPDSNLSEDSQEFGPKREN
GPRQSPEEKPLNRDRVSDSGGVGIMHQYNHMDNHLRLNPHKRILERQPNGDGGERGEAERERERHEREQERERERERERER
ARERDEQEDQRPVMNGRISLSEADSFPGLFQRRPTPITSPNPSNNKRIKIEKEHLELPPTLPLISPENVYSQLLAGYAAS
RHFIREPFLGFTDSRQSPFGTSSEHSSSETGSLRYSTPPGELMEAGSASGRSGSSTPHLLRGPGPGRPPSSKDRRNDTCE
YCGKVFKNCSNLTVHRRSHTGERPYKCDLCSYACAQSSKLTRHMKTHGQFGKEVYRCDICHMPFSVYSTLEKHMKKWHGE
HLMASEVKLEEADRG
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597 - 616:	EEEEEEEEEEEEEEEEEEEE

A0A2U9CW95 **A0A2U9CW95_SCOMX** (960 aa)
Triadin. *Scophthalmus maximus (Turbot) (Psetta maxima)*

```
MQGEFSTGDYQSITDMPQGMLTASWKRFYVFVGGNTNNAHESFVRRITASGHTEVGSFEECDYCLAFCPIASRVGTDVDY
VLRRIPADKPTVLVLMYHTFRGDYVVPESGRLVDARNVGLTVSCLFHEGELLKCSCNDIAWFDIQRFLGLPQDNDDSRIE
SVFRRGTDTGSFGCVVALDKLVADPWARSSSTTTTTMVIEGKGGGGAAPPPSSIQTPKKTFSEDLSSTFSSPLAWILVLA
LVVTWSCVFVIMFDLMDYKTISGMDVFFHPLSPLSVSDTGFLCFSLTIGSDPMRAVNDAMEESSSAIGALFKFASGLIAP
EDDEGTLYAVRKKGEFLPSRSKVVGMQAKTKPPAVEAMEEEEEVGDKGDEVGAVEEEEDEGYAEEEQQLEEEEEEYEEEY
DEYEEYDEEYDEEYDEEYDEEYDDEYDEEEYEEEEEEGGVEDDGEEEDEGVGTVEEEEGEEEEEEEEEEEENEDDLEESAD
AEEDDDDEEVSPEPSSTSEDEESAASSDSESDAPVQDVTLPDDDDDDDDDDEKDAEDRDEGDTSDDAFTDSSDEEAVKTE
DHDEEEEEEEEEEEEEEEEEEEEEEEXXXXXXXXXKQREPDEDDEPTGEMQKSVDEPEDKKEEYDEDDEDEEKATVDVTRPL
PEPGEEDSEPAVCPCMNSAKSKESVAKTAEKKEKDAPRRVSATRRKRDREAVKSEPKRRALPRGASLEPKIRRIRRIPAL
LRVKKAEKTKTPRTEAETKKPQEVPESGEDVGPCRPAPVYCPSPPGWYVHHIVTDNPYPPPTMSAPSAPVLTVHPGAPPL
QPPLYQQQQPPPLMQPLHYQLYQPPLQPLTQPQXXXXXXXXXVPVPAPEPEEAPVQPELQTPAAAADDAQPAAAPVHAAE
KKTKAADSEKEKAVKEKSKTAVAAKKEPAAVRPKRKPASEETAKKRSETVAERKGKSEKTSKDDKAEKKSVKAAQGTVWN
```

564 - 583:	EEEEEEEEEEEEEEEEEEEE
565 - 584:	EEEEEEEEEEEEEEEEEEEE

A0A2U9R9T8 **A0A2U9R9T8_PICKU** (473 aa)
PWWP domain-containing protein. *Pichia kudriavzevii (Yeast) (Issatchenkia orientalis)*

```
MFEPKQLVLAKIKGFPDWPAIIVPIESIPAKLSSSRYQRQIDAYLKNDVCVKFYFDDQYSWTKLTNLKPLSLDMVEAFLL
QDHGGRRKKRIVEAFEKVKEVPVDEFLKWGSWGEPKPVVEDAEDVFEDGLDNKGGRKRKNNNGSKQTGKGKGKGKGKDKD
KDQDKDLGRETKRRRSGRATKVTEETSTPEFTEEEQIVDDEDVEYVEPEDEDLEEEEEEEEEEEEEEEEEEEEEEQTVEP
PAIVDDLSSKQPPDFNVDFSVIPHSSALTTEVQEMSQWCHDLRMELQTLIFPLRKQQPGEMEEEAVVPNEANGADNASNT
SVEVTGTNVDDAHQQHNESEVKAEDVEQVQPNYKDLNKQIEELISPLLNADLSKSIVKSTGLSKIILIILSKPEFSSACT
KRLSKWWVSNFDFSIKPDHHWSDEFTIADHLQEEKQRKAMEEERRRKKKEERRLASMSAVSQTPETEPQSSNV
```

214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE

A0A2U9RB40 **A0A2U9RB40_PICKU** (730 aa)
Uncharacterized protein. *Pichia kudriavzevii (Yeast) (Issatchenkia orientalis)*

```
MPTSDISGVASNVTSLSTVEATSTFDSTSPGNGDKGVYGLVRIVDSLINAVIQQSKESNKETRMFFSYWMSPYALMCMIT
AVIMNRIVILASTRHQRRLPLLSNAVLRGLAIYMLIRGSYGLFLSLRCYVKHPIVDFIFESSGEDFKFDENEYLKSKFLS
IPFGTKVYRSDETVGPTTSILRNFHLSLCISQILDTFTSVASGLNPSVETGITLFEYSLAFQEAQFESTVSTELLVFAMI
ALANQINTHLLGMFNLLKYKLVTSSIIGLFTLAYYTYKIFTINILKLPFSIIVGYFPHFCVLSIVLLSEGIYLLSGLARL
SFEDLAMSSLFEDWDSTDIPLSDDFYTALIRLGEFLINLSVNFYYLQETPSVLLPRNNYISEELLYMRKNCGYGEETENS
PDIKQLQIGLATRRKKSWAITNRIQMLSKITFNFFRLVLLKLKGGSKRIVPNGQSLEKISDNYNLVERNGKYYFAKKEDE
TRIDVNRIEEDVLDKIYPHLLLNMNLTENDESEDYRDDLGGDFERGEYEKNHGEEEEEEEEEEEEEEEEEEEEEEDDDH
YDHDGYDQDNDDHENEGPARQDKVCEREEINEVISDLITVGDLKDILNPSQELRVLSYHLRNLNLPTSRLTRSHFREYYT
DEMKLLDILIEKRKLSLHDFPNSQEHCEPLTHDELGTCVICHENTRQIILWPCKCLAICDSCRVSLLVREFATCVCCRRP
VEGYSKVYIP
```

534 - 553:	EEEEEEEEEEEEEEEEEEEE
535 - 554:	EEEEEEEEEEEEEEEEEEEE
536 - 555:	EEEEEEEEEEEEEEEEEEEE
537 - 556:	EEEEEEEEEEEEEEEEEEEE

A0A2V1AMK1 **A0A2V1AMK1_9ASCO** (550 aa)
CobW C-terminal domain-containing protein. *[Candida] haemuloni*

```
MANKSAKSNQKPIPVTLLSGFLGSGKTTLLEHILTKDHGLKIAVIINDMSQLNIDADLVQNHRVSQKEEKLVQLQNGCIC
CTLRGDLLEELVSLAKDSAFEYIVIESTGISEPMQVAETFTTEFTNMYLDNQEGITAEDEKILKEIKDLGGLEKVAKLDT
CVTVIDGKNFYHNLETTEFLVDRFGSSGQNEEERTICDLMVDQIEFADVIIVNKIDLVNKKQKKKIFKTIKSLNPVAKVI
RTNYSRVDVTDVVGTGLFDFEKASSSAGWLQSLHEMTKREAYGNKLTPKPETEEYGINNFVYKSRKPFHPERLYKLIRDK
FVVIESSGLADENGEEGQVEDGEEEEEEEEEEEEEEEEEEEEDDEIEIDGENFVDPSEEQIIKTKKNSKFGPVLRSKGFF
```

WLASRHIIRGEWSSAGPMLTMRGGIPWFAVAGKEFYPPEAQMLIDRDMQGRFGDRRNEIVFIGLSIDQEAITKELDKCLL
NDEEYKVYERLTRDKNLFKIEKALQNEFVDGFASWIAFDEPDAPEEEPKLAAPEIHNGHVHKPKAVAGKS

343 - 362:	EEEEEEEEEEEEEEEEEEEE

A0A2V1ARH6 **A0A2V1ARH6_9ASCO** (247 aa)
Uncharacterized protein. *[Candida] haemuloni*

MASYIPENWPYGESEYQISYFGKCRVSETETACVWNVWGDFPFVSWDMGLLIARNWTQNTKEQQEIAHAWERATLEALSS
SLETIQSVSRFSSPPESPKSTFNAEAIQVIQTLNIWNPNITNRLVSLFSLFFLGISALLLPCSYKPAFAFAQLSFFLLPF
LLWEPCGEGGDVEKVFDFGVTFCVVFGVAALEYLGLRREEEEEEEEEEEEEEEEEEEEEENTDVILIAQTVAARKSGLPY
LGQTSEQ

199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE

A0A2V1B0M2 **A0A2V1B0M2_9ASCO** (252 aa)
Autophagy_act_C domain-containing protein. *[Candida] haemuloni*

MSINTNEFPPGLSLEDVASKENIQLSKFDSDIAWKIGTLAKQRAIDYRLSRPILIDITTTDGTTYFHSPSRPSTVKDNDI
WVERKRRTVFRFGFSSYYMGQKLKSKDTKNLEEAFYISSIDYAVHGGSVPIRLKNFDGVVAALTISGLKQEEDHAFALQI
LEEVKISREPRYGNRHMDVSCISSALIVNSNIGQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEETSVKFR
VSFTYKCFYFVE

195 - 214:	EEEEEEEEEEEEEEEEEEEE
196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE
208 - 227:	EEEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE

A0A2V1CLZ8 **A0A2V1CLZ8_9HELO** (132 aa)
Uncharacterized protein. *Cadophora sp. DSE1049*

MELPRLLDILIELAISYSFDHLRAPLYATAGHSYGLIIDHLCGVFEAVRPGVQNLIIDHLEDRAEFYEAADAVHMRENGD
WSSGEEFTDEDEDEEDEDEEEEEEEEEEEEEEEEEEEEEEIQDPDDDISALH

99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE

A0A2V2UII9 **A0A2V2UII9_TRYCR** (219 aa)
Putative retrotransposon hot spot (RHS) protein. *Trypanosoma cruzi*

MNAGSYLLYQLLHYDAEQLPMVAYCFGDRTFLFDKITETVKKYSAASSIVDILDEFSDRGVKGYIIYDVALKGRQPSNTL
PCEGWGMIVVTPPDKKNYESWAKLVQAEQIIINCPDESDVRAMCIWMKHSGQVEEEEEEEEEEEEEEEEEEEEEEEEEE

EEEEEEEEEEAEEEEEEEEAEEEEADYWKKVKDRMDKVGPLLRCVFNQRNYKDRIDSCKSKV

134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE

A0A2V2UPI3 **A0A2V2UPI3_TRYCR** (278 aa)
Mucin-associated surface protein (MASP). *Trypanosoma cruzi*

MMMMTGRVLLVCVLCVLWCGVCGGERVEASLPDSPGTQPEKSTHNDNATKAVAGGGDQSSKEVAPKEPTPKASKSPELPT
ESSQPPQQSGEGVSEKAIATMDNQDQKQEVKEEEEEEEEEEEEEEEEEEEEDDLKKQEEEDKKDQKEEGDEEEKEDEEGD
TKKEDAVTGTAEGISASGQEQPSLSSAAGGASNITNPNSTPTTGDDDPAADGAGTAEGKQNENKDANPKETPVEAAAMNT
TTATTGDSDSSTAVSHITSPLLLLVVVACAAAAAVVAA

112 - 131:	EEEEEEEEEEEEEEEEEEEE

A0A2V2VA57 **A0A2V2VA57_TRYCR** (642 aa)
Putative retrotransposon hot spot (RHS) protein. *Trypanosoma cruzi*

MYVLEGYYESVYNARWHHVMEVPDGEGMVMDVKEGEPKQSWTYKTVGRTLEKNDAVQQSGAPRPRLMVLTSDKGWPYTWE
QGVGEFIPDCYVNCEVERVWRIVKGDLTKWFSTHVKKKLSPRRRVLIGTPGIGKSMNAGSYLLYQLLHYDAEKLQMVAYC
FGDEASLFDKTSKRVSRYEGGTSIMNIVKDFSRRGVKGYIIYDVALKGRQPSNTLPCEGWGMIVVTPPDKKNYESWAKLV
QAEQIIINCPDESDVRAMCIWMKHSGQVEEEEEEEEEEEEEEEEEEEEEEEEEEAEEEEEEEAEEEADYWKKVKDRMDKV
GPLLRCVFNQRNYKDRIDSCKSKVKKMKLFDTKYYSILGSNEVCDDSHSSHKLVKVVRVRGGKKSELPLNALVSSYLGNL
VTCKLAELMAPNDFILLVLAMKDDLLSKPLEKYSVFTFLSEDFVSAIIPKLKELKLQEDAPPHDCALRVRLNERPLKTCI
LQCLENFKKKIKIEYRVLYKPVAQNFPLVDGFFFLKPPQKTLVGLQITTAGEHRTIPSTVKLFKERMAAYFNGWEKFSQE
LSWEIIYIQHADSTPMNDWQRCHVVDSNNVSKKENQKIAAFWNEKVRQYQVSISSREIRKKALRGVKNKNKNKKGNRLGN
EK

269 - 288:	EEEEEEEEEEEEEEEEEEEE
270 - 289:	EEEEEEEEEEEEEEEEEEEE
271 - 290:	EEEEEEEEEEEEEEEEEEEE
272 - 291:	EEEEEEEEEEEEEEEEEEEE
273 - 292:	EEEEEEEEEEEEEEEEEEEE
274 - 293:	EEEEEEEEEEEEEEEEEEEE
275 - 294:	EEEEEEEEEEEEEEEEEEEE

A0A2V2VDS5 **A0A2V2VDS5_TRYCR** (643 aa)
Putative retrotransposon hot spot (RHS) protein. *Trypanosoma cruzi*

MYVLEGYYESVYNARWHHVMEVPDGEGMVMDVKEGEPKQSWTYKTVGRTLEKNDAVQQSGAPRPRLMVLTSDKGWPYTWE
QGVGEFIPDCYVNCEVERVWRIVKGDLTKWFSTHVKKKLSPRRRVLIGTPGIGKSMNAGSYLLYQLLHYDAEQLPMVAYC
FGDRTFLFDKITETVTKYSAASSIVDILDEFSDRGVKGYIIYDVALKGRQPSNTLPCEGWGMIVVTPPDKKNYESWAKLV
QAEQIIINCPDESDVRAMCIWMKHSGQVEEEEEEEEEEEEEEEEEEEEEAEEEEEEEEEEEEEAEEEEEEEEEEEEEEEE
EEEAEEEADYWKKVKDRMDKVGPLLRCVFNQRNYKDRIDSCKSKVKKMKLFDTKYYSILGSNEVCDDSHSSHKLVKVVRV
RGGKKSELPLNALVSSYLGNLVTCKLAELMAPNDFILLVLAMKDDLLSKPLEKYSVFTFLSEDFVSAIIPKLKELKLQED
APPHDCALRVRPNERPLKTCILQCLENFKKKIKIEYRVLYKPVAQNFPLVDGFFFLKPPQKTLVGLQITTAGEHRTIPST
VKLFKERMAAYFNGWEKFSQELSWEIIYIQHADSTPMNDWQRCHVVDSNNVSKKENQKIAAFWNEKVRQYQVSISSKDVP
RRF

269 - 288:	EEEEEEEEEEEEEEEEEEEE

304 - 323:	EEEEEEEEEEEEEEEEEEEE

A0A2V2VSV8 **A0A2V2VSV8_TRYCR** (475 aa)
Putative histone deacetylase. *Trypanosoma cruzi*

```
MLQHYACPVFSHKKSGDAMNTVSSDVFEWVLEPFPVVGVEDMTAFHDRAYLNYLSIREALSEVDERASTVKRSRAEGIQP
PVSRRSSAQTQPPLRVLPDLVPIPADEEYGLVNENMPFVGMWRTIQATVSGTLLAARLLAQPGRFAAIHWFGGRHHAKKS
TAGGFCFANDVVLGVLELKKLLSSDKNGILVVDVDAHHGDGTQSAFLHDNSVLTLSMHAHGVGIFPGTGGIEEIGAGLGR
GFTMNVPLPEGATDILAVTLMYRSIHFAFKKLGEGLAAIVIVCGSDALSGDPLGALNLTVGGMQSIIRLLLKEAARRSLK
VLLLGAGGYVDTSCARLAGVVTKDVLSCAAAMRLGKTEYFGDSANLGDNLGVAVPEGCEYFTRYGPSFLMHGLPPARVSK
LYRLPYGSPLFMRMQRAATKEALRRRLNQEQDEEEDAEDDEEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEP
```

447 - 466:	EEEEEEEEEEEEEEEEEEEE
448 - 467:	EEEEEEEEEEEEEEEEEEEE
449 - 468:	EEEEEEEEEEEEEEEEEEEE
450 - 469:	EEEEEEEEEEEEEEEEEEEE
451 - 470:	EEEEEEEEEEEEEEEEEEEE
452 - 471:	EEEEEEEEEEEEEEEEEEEE
453 - 472:	EEEEEEEEEEEEEEEEEEEE
454 - 473:	EEEEEEEEEEEEEEEEEEEE
455 - 474:	EEEEEEEEEEEEEEEEEEEE

A0A2V2VT05 **A0A2V2VT05_TRYCR** (631 aa)
Putative retrotransposon hot spot (RHS) protein. *Trypanosoma cruzi*

```
MHVLEGHYESVYNASWHHVVEVSDDTEMGMEVKEGKPAQSWMYKAVGDTLEKDDGVEQSGAPRLRLMVLTSDKGWPYTWE
GGVDEFIPDCYVNCEVERVWQIVRKDLTAWFSGHCKKKLSPRRRVLIGTPGIGKSMNAGSYLLYQLLHYDAERLQMVAYC
FGDRKFLFDKTAKTVKKHRAASNIVDILDGFSGRGVKGYIIYDMALKGHQPSNTLPCEGWGMIVVTPPNKNNYESWAKLV
GAEQIIINCPDQSDVKAMCIWKEHNGQLEEEEEEEEEEEEEEEEEEEEEAEEEEEEEEADYWKKVKDRMDKVGPLLRYVF
DQRKYYDRIDSCESTVKSMNLFDTKYYSILGSNEVCDDNRISHKLVRVVRVRGGKKSELPLNALVSSYLGNLVTCNLAEL
MAPNDFILLILALKDDLLSKALEKHSVFTFLSEAFLSAIIPKLTELKVEQNAPPHLCALREHPNERPLKPFLLRCLKNLK
KKINIERRVLYKPVAQNFPLVDAFFFVNSNPKTLVGLRMTTASEHHIIPSTVRQFNERMAKYFNGWEKFSRQLSWDIIYV
QHADSTPMNGWQRCGPVNANDLSDAEKKIVAFWKEKVRQYQVSVSSRDLIRKKALRSVKEQQKQKKKQIRK
```

269 - 288:	EEEEEEEEEEEEEEEEEEEE
270 - 289:	EEEEEEEEEEEEEEEEEEEE

A0A2V2VWE7 **A0A2V2VWE7_TRYCR** (564 aa)
Uncharacterized protein. *Trypanosoma cruzi*

```
MARPKDDKLLREEEEEEEEEEEEEEEEEEEEEEELEEWTELNDIDELQDGPSTFYVGGFSTIKKLQDALNVVKYRDDIVLVY
PGLYAEKEVCMDESRLDGLSVMSVPLAMGPKGGYRKKIRIPKDERRLGPWYAPFGSDAPKTDAVTPTTTDATQFPVFEGK
LILRSTAPFTPQGEPKTVYPIKQYDPREDDEEDEEQEKEAEEEGEENETQKENVKRSRLELQGFSFLEGAVFEPLSRATV
RHCVFGRSEVEEKANKTQDSDVPLSSPLLETTVTAHPLTEVQVEFCVIYGNQKHGIYAFPRCALRFHSSMIIGPQFGIVH
ETQDFWSRAARHAQKNTYSQSVPRSRRPLQQAKIPEKAFCAVGVYLDDADVSIQDVFVAQSHVGILLVNGCRGTSVIASR
VESISSVGILFSGEDGAAKVKCSAVRWCGRECLLVKGPVPPLPPDPSLLMEIIHDASQDAEAREEEEQEEEEEEEEGDTA
ARALSRVPIPTQHPILRGNAFDGSVRLEGDVSSSAMCDNVIYVAKEGISSDVPTFTGPAAEKRFALKGFHVHVRGTTPRK
NDSD
```

12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE

A0A2V2W007 **A0A2V2W007_TRYCR** (362 aa)
Mucin-associated surface protein (MASP). *Trypanosoma cruzi*

```
MAMMMTGRVLLVCALCVLWCGACGGGRAETIPPAPPDSSDTTPEKNTQNDNATKAVVGELDQKAQQVAPKEPAPEASVSQ
ELPPESSQAQKSGGGASETIIAKMDNENQNPEEKKEELKKEEAKQKEQKKQQDEEDEEEEEEEEEEEEEEEEEEEEEEQE
VRDSKSDSLEEEAAEEQENEKALKNDKMGQKSPTETPGVPTNNEETQTATTQVNGQSSPEALEDVEQPEVQGEKDSNHNP
QTNSVASIAVNQQNEPPADHGESGPPSPTANGDATNNDFDKSTEDGISNSDPAADVAGTREEKQNENKDANPKETPVTAT
AMKNTTATTGDSDGSTAVSHTTSPLLLLLVVACAAAAAVVAA
```

137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE

A0A2V2WT40 **A0A2V2WT40_TRYCR** (563 aa)
Uncharacterized protein. *Trypanosoma cruzi*

```
MARPKDDKLLREEEEEEEEEEEEEEEEEEEEEEELEEWTELNDIDELQDGPSTFYVGGFSTIKKLQDALNVVKYRDDIVLVYP
GLYAEKEVCMDESRLDGLSVMSVPLAMGPKGGYRKKIRIPKDERRLGPWYAPFGSDAPKTDAVTPTTTDATHFPVFEGKL
```

```
ILRSTAPFTPQGERKTVNPIKQYDPREDDEEDEEQEKEAEEEEEENDTQKETVKRSRLELQGFSFLEGAVFEPLSRATVR
HCVFGRSEVEEKANKTQGSDVPLPSPLLETTVTAHPLTEVQVEFCVIYGNQKHGIYAFPRCALRFHSSMIIGPQFGVVHE
TQDFWSRAARHAQKNTSSQSVPRSRRPLQQAKIPEKTLCAVGVYLDDADVSIQDVFVAQSHVGILLVNGCRGTSVIASRV
ESISSVGILFSGEDGAAKINCSAVRWCGRECLLVKGPVPPLPPDPSLLMDIIHDAFQDAEAGKGEEQEEEEEEEEEDTAA
RALSRVPIPTQHPILRGNAFDGSVRLEGDVSSAAMCDNVIYVAKEGISPDVPTFTGPAAEKRFALKGFHVHVRGTTPRKN
DSD
```

12 - 31:	EEEEEEEEEEEEEEEEEEEE

A0A2V2XC17 **A0A2V2XC17_TRYCR** (379 aa)
Mucin-associated surface protein (MASP). *Trypanosoma cruzi*

```
MTMMMTGRVLLVCALCVLCCGAAMVMAEANVDKGTEMKKDESFDSSELISGIVGAEQHVTQDSVREGSENGNQSLGAQTG
NGINQDNGVIIASPASTVRGEEEEEEEEEEEEEEEEEEEEEEEEEGESVDAEGETEEIEELKGPIEGEETSQLTLPQEGVLL
PSEPLKTTLNGNPAGTLNATPAKGQPRSDDGSAQEEGLKLPTLQAPAAPAAPAAAAAAAEATTTQTKDENPSSADDPSVQ
HVEASQHDMELRSALRKEGTIPTTVTKTDGPTEVNAESTPTSPSASKGAITNDADEGNEEGIQKHDQAPDGEATKEAQQG
ENKEENTNKTATLEAAAITNDTATHGDSDGSTAVSCTTFPLLLLLLVVACAAAAAVVAA
```

101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE

A0A2V2XF79 **A0A2V2XF79_TRYCR** (511 aa)
Putative histone deacetylase. *Trypanosoma cruzi*

```
MAFTDAVAGKTSLPPPVAIIVGHNIDASAMPLTYERNRLVIDMLQHYACPVFSHKKSGDAMNTVSSDVFEWVLEPLPVVG
VEDMTAFHDRAYLNYLSIREALSEVDERASTVKRSRAEGIQPPVSRRSSAQNQPPLRVLPDLVPIPTDEEYGLVNENMPF
VGMWRTIQATVSGTLLAARLLAQPGRFAAIHWFGGRHHAKQSTAGGFCFANDVVLGVLELKKLLSSDKKGILVVDVDAHH
GDGTQSAFLHDNSVLTLSMHAHGVGIFPGSGGIEEIGAGLGRGFTMNVPLPEGATDILAVTLMYRSIHFAFKKLGEGLAA
IVIVCGSDALSGDPLGALNLTVGGMQSIIRLLLKEAARRSLKVLLLGGGGYVDTSCARLAGVVTKDVLSCAAAMRLGKTE
YFGDSANLGDNLGVAVPEGCEYFTRYGPSFLMHGLPPARVSKLYRLPYGSPLFMRMQRAATKEALRRRRNQEQDEEEEEE
EEEEEEEEEEEEEEEEEEEVEEEEGEGEEEA
```

475 - 494:	EEEEEEEEEEEEEEEEEEEE
476 - 495:	EEEEEEEEEEEEEEEEEEEE
477 - 496:	EEEEEEEEEEEEEEEEEEEE
478 - 497:	EEEEEEEEEEEEEEEEEEEE
479 - 498:	EEEEEEEEEEEEEEEEEEEE
480 - 499:	EEEEEEEEEEEEEEEEEEEE

A0A2V2XLG6 **A0A2V2XLG6_TRYCR** (565 aa)
Uncharacterized protein. *Trypanosoma cruzi*

```
MARPKDDKLLREEEEEEEEEEEEEEEEEEEEEEEELEEWTELNDIDELQDGPSTFYVGGFSTIKRLQDALNVVKYRDDIVLV
YPGLYAEKEVCMDESRLDGLSVMSVPLAMGPKGGYRKKIRIPKDERRLGPWYAPFGSDAPKTDAVTPTTTDATQFPVFEG
KLILRSTAPFTPQGERKTVYPIKQYDPREDDEEDEEQEKEAEEEEEENETQKETVKRSRLELQGFSFLEGAVFEPLSRAT
VRHCVFGRSEVEEKANKTQDSDVPLPSPLLETTVTAHPLTEVQVEFCVIYGNQKHGIYAFPRCALRFHSSMIIGPQFGIV
HETQDFWSRAARHAQKNTSSQSVSRSRRPLQQAKIPEKTLCAVGVYLDDADVSIQDVFVAQSHVGILLVNGCHGTSVIAS
RVESISSVGILFSGEDGAAKVKCSAVRWCGRECLLVKGPVPPLPPDPSLLMDIIHDASQDAEAKEEEEQEEEEEEEEEDT
EARALSRVPIPTQHPILRGNAFDGSVRLEGDVSSAAMCDNVIYVAKEGVSPDVPTFTGPAAEKRFALKGFHVHVRGTTPR
KNDSD
```

12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE

A0A2V5H0A1 **A0A2V5H0A1_ASPV1** (76 aa)
Uncharacterized protein. *Aspergillus violaceofuscus (strain CBS 115571)*

```
MGGGEERKRRVSDDESEKREEGEREEQKERREERIETSSLCVEASGEEEEEEEEEEEEEEEEEEEEAEQPAAGSRK
```

47 - 66:	EEEEEEEEEEEEEEEEEEEE

A0A2V5H0C2 **A0A2V5H0C2_ASPV1** (295 aa)
Zn(2)-C6 fungal-type domain-containing protein. *Aspergillus violaceofuscus (strain CBS 115571)*

```
MPVSRQLSPQPGLKREMRSRRRHAVGVCNACRRRHIKCDLARPTCSACKAIGALCERSNAQLTWTSTSGPSFQGNTRAHH
GPSTTTTTAVRRRYLYGEQDRVSTSISLLSSLHTASVDNSLQQIEDESWQTALHPGQSNFIGPFGVLSLPHDPVPLSSGS
QEEEEEEEEEEEEEEEEEEEEEEEEEEEARNSSSNSNQDQTHSLEIPPPLLAGSLGSLPTAEESLHWPDILEMDMSWPEL
FNFNDLPSPLPEQPVSLVAEGAEQSNEDAPLEGSVQTPGPGFSLEISKSRTPRCS
```

162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE

A0A2V5I7L4 **A0A2V5I7L4_9EURO** (122 aa)
Uncharacterized protein. *Aspergillus indologenus CBS 114.80*

```
MYPCGVSAARESEPKRPLGYYNIGLALRRQAVSPGEVLHGPLCSTRKENFIRKEEEEEEEEEEEEEEEEEEEEEEEEEE
EETKKYNFKPIHKIETACPNSDKTKNTNVSHTIGQKPLSAVT
```

54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE

A0A2V5JAB9 **A0A2V5JAB9_9EURO** (60 aa)
Uncharacterized protein (Fragment). *Aspergillus indologenus CBS 114.80*

```
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEEKEEEKE
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE

20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE

A0A2W4REX3 **A0A2W4REX3_9GAMM** (159 aa)
Uncharacterized protein (Fragment). *Candidatus Methyloumidiphilus alinensis*

```
MLIVDDILFFPVKGINWIFKQIHEIAEEELAGEGDRIRNSLTELYMMLETGQITEEEFDQQEKVLLDRLDTLEEDDDIID
NETGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE

119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE

A0A2X0LSB0 **A0A2X0LSB0_9BASI** (684 aa)
BZ3500_MvSof-1268-A1-R1_Chr5-3g08320 protein. *Microbotryum saponariae*

```
MTTRSGKTLMATPRTTRPSQLSRTPLNDVVQNGTTQEPKDLASNLRSVAKEGSEFDIESLFTPPKEIVTMQAATAAAAAN
TADLHMDVVTGGDGRPLQPGGNSLGNIGAYDEHDDDEDEEEAQEEEEEEEEEEEEEEEEEEEEEEEEDEDEDEDEEMDSR
SDGERDALRYEMHQLETMVPHLKDKYKLIDRLGEGTFSSVYKAIDLRHDEYDNSSWEASDKHGRPSCEGPNGQVYVAIKR
IYVTSSPVRIQNELDILNVLRGKDNIAYLIDAMRHDDQVIAIMPFSRHQDFRTYYRTASIPLMRSYFACLFRALAGTHVH
HIIHRDVKPANFLFDVTKGTGVLCDYGLAQKIGGDEWYEWKSECLHSLPGPSWGGLDGRHSSREMMEKLAPGVAPGLNAG
LHGVRMPRPVNLHDQVTKSQQDWKEWSKAYRAKIVEDPIIGGQMRTEALRRQPWWAPESWVEDLRLKAKERVGFYKGWRS
ALQSAPMPKDRIGFLKEDRRPSVRANRAGTRGFRAPEVLLKCPDQTVALDIWSAGIILLCFLTRRFPFFNSSDDTEALAE
IGTIFGKRKMERCAALHNRTFVTNIPHLESPPHPNLHALVKSLNPVIFVENSPTPYGPIPSSEGDDQKWYTDSPLYHAVD
LMKRCLELDCTKRWTAEECLEHPFFDGAFDSGMGVLCERDERFW
```

124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE

A0A2X0MHY7 **A0A2X0MHY7_9BASI** (1474 aa)
BQ5605_C019g08949 protein. *Microbotryum silenes-dioicae*

```
MRMISALILDICVFQEDRVSGRRTGKIDRHDRAETRLRQPDLEQVLKVVKRLRKAELTATEATEELCTINVFKNFMNKYE
DDDYDIFKTHLKRYAAALRPDTGIAFHETNRYAKKQRKPSTFSSIRSLLPTNAAGVVALPRLSPADSSIALNLLQPSTSH
GPTPPKNNFIEVGVFATRPFQKGEIIRLQGGIADLTDEDDDEMRENGGRSDFSILWSERKKCFCLLLGPARFVNHDCRNN
VEFYLVGNVMSFKVVEDIQPDEEIFTHYGIHYFERDNMGCMCATCEKFKRGFFTPKPARGAKKLSSQATQASLVNPPVIP
LSKLANTTTIVSDHEGGESSTSSPHPGSPRPESRYGTRRMSSVRATETDNHASTSLNGGGGVGTNSTPSTSVTNQLINAL
KVRSSTRTRSSSLPLNLHSNGANRSLTPTPISVTAGGTNSRHPSPSSSSTLNPNRLLSDLELRSGPRLIHPKMKPPPVYK
DDYAWDERKKIAIYTGLVRVPQKPKKKVLTARERKKERERMEEEMRREEEEKKRRSHRKGGAVEEVGKKGEGKGKQREKQ
VAEKPKRVRLRPSRSRASTEASTTVKPKPKRARVRKPKVVEEEPEEADEEASVEEKEEEEYDEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEELQKPAPRKRNRSTKIVTVTKATSSPRKRKSSTPAAATKNKLRGPPSKRRKVRSVSEEQPFVGIVVVK
GSQVTGGPRKRSKKDANGDDREVELGRFVPIALSMDEAGLHSTGGVSAVEDDAYGRVPETPLDSSSVASPYEKVGSEPMP
PSRKRFNHSIGPKGRQSLPPRDPTPLPPYLRRSTSGTTRASIPPRDSSTAELDSDMDSDSHSHKDVVRATISTSSFFGVP
IRIPKLRALVTTHAVNDASGSSASTTTTNGDDSKHASTSTSSSTSLAAGASAMQSFRLGSRPRKGGGGAGQNDDDDEDDE
DDERRRRRQNGIHGEKVDDVIMEDVKPKVEEGEEEGDEGGVAMMVDETLDEEMLGLGDGQAIDALDLRDTDTQEAAALLL
MLNFPQSSTNQDHSTNSAHSSNVPTPSAPGSSASGSSAQATRRPRVSTTSTKAAVSTSTQRKRSRMSVDGVAPSTSSASS
STSKTPVASANPRSTRRHSQLDEGQVLVASTNASSSKSKTKFGKSVAEPKPVIPPQPVKPGERGTRRSAPLAGNLSDILA
APAVLRVSGGYDAEKGRYIAKGAPVDIEGPLFALAPPKPVPSLSPQPPSQSMSASTSTSSNGAPRRSLPGRLIVNEPKQR
RYSDSKLADRKPHNLARTASVPRASKSPRASTSSAAAQQLLPPVVPPPRPRSVPTHSRATRLAAPLEGDLRALLDSESVG
AVTGIYDPTKGKYVSQKYLAAAAAKQAPASSSTIASPSTSSATNRLTEPSRPESVLVVDGSVGEGSERARGTRASRPIAG
SVADLLASPTVASVTGRFDAEKGKYVAATTARKG
```

623 - 642:	EEEEEEEEEEEEEEEEEEEE
624 - 643:	EEEEEEEEEEEEEEEEEEEE

625 - 644:	EEEEEEEEEEEEEEEEEEEE
626 - 645:	EEEEEEEEEEEEEEEEEEEE
627 - 646:	EEEEEEEEEEEEEEEEEEEE
628 - 647:	EEEEEEEEEEEEEEEEEEEE
629 - 648:	EEEEEEEEEEEEEEEEEEEE
630 - 649:	EEEEEEEEEEEEEEEEEEEE
631 - 650:	EEEEEEEEEEEEEEEEEEEE
632 - 651:	EEEEEEEEEEEEEEEEEEEE
633 - 652:	EEEEEEEEEEEEEEEEEEEE
634 - 653:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9D9M1 **A0A2Y9D9M1_TRIMA** (1165 aa)
myelin transcription factor 1. *Trichechus manatus latirostris (Florida manatee)*

```
MPLPFLTMWGEAFWSVSDATLAPDTRQAQAPPPPPSTAWLPGQLASFYGEHSPPEPRAPGFVTEESACTARHSSPDALTT
ELLRCGLNLEMRDMQWMSLENEDKRARTRSKTGRAPPETTGTDLSCPTPGCTGSGHVRGKYSRHRSLQSCPLAKKRRLGG
AEAEHLAAKRKPQPLKLALDEGYGMDSDSSEDAEVKDASVSDESEGTLEGDEAKMSGQEGTQHPEPAEGRSPATSHFGAS
PTGPSKGSYSSYQEIIATSLLNLGQIAEDTLAAEDLGQGTKPGPSVVHLVQEEAGEGATSDEGEKDVFIQPEDAEEVVEA
TGEQPRELGPESLEGMVSEESSRQKDALDPEEDEEEDEEEDEEEEEEEEEEEEEEEEEEEEEEEEATPDVICQDAPNASTQK
APEPPHPEPPRPEPEYSVIVEVRSDDDKDEDARSQKSAVTDESEMYDMMTRGNLGLLEQAIALKAEQVRVARGSAEQGPG
EGQAGKPLDAVRKNYYSKDPSRAEKREIKCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRIPPEILAMHENVLKCPTPGCT
GQGHVNSNRNTHRSLSGCPIAAAEKLAKSHEKQQPQTGDPSKMSSSSNRILRPMCFVKQLEVPPYGSYRPSMAPATPRAS
LAKELEKFSKVTFDYASFDAQVFGKRMLAPKIQTSETSPKAFKCFDYSQDAEAAHMAATAILNLSTRCWEMPENLSTKPQ
DLPGKAMDIEVDENGTLDLSMHKHRRRDSALPGSSSCSSSPGVKSPDVAPRQGSASTTSSSMTSPQSSQASRQDEWDGPL
DYTKPSRQREEEPEESEPAAHSFASSEADDQEVSEESFEERKYPGEVTLTNFKLKFLSKDIKKELLTCPTPGCDGSGHIT
GNYASHRSLSGCPLADKSLRNLMAAHSADLKCPTPGCDGSGHITGNYASHRRCPVPGCVGLGHISGKYASHRSASGCPLA
ARRQKEGSLNGSSFSWKSLKNEGPTCPTPGCDGSGHANGSFLTHRSLSGCPRATFAGKKGKLSGDEILSTKFKTSDVLEN
DEEIKQLNKEIHDLSESNSEMEAAMVKLQSQISSMEKNLENIEKENKLIEEQNEALFLELSGLSQALIRSLANIRLPHME
PICEQNFDAYVSTLTDMYTDQDCYQNPENKALLESIKQAVRGIQV
```

362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9DRC2 **A0A2Y9DRC2_TRIMA** (1325 aa)
tau-tubulin kinase 1. *Trichechus manatus latirostris (Florida manatee)*

```
MQCLAAALKDETNMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTRENVALKVESAQQPKQVLKMEVAV
LKKLQGKDHVCRFIGCGRNEKFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESIEAIHSVGFLHRDIKPSNF
AMGRLPSTYRKCYMLDFGLARQYTNTTGDVRPPRNVAGFRGTVRYASVNAHKNREMGRHDDLWSLFYMLVEFAVGQLPWR
KIKDKEQVGMIKEKYEHRMLLKHMPSEFHLFLDHIASLDYFTKPDYQLIMSVFENSMKERGIAENEAFDWEKAGNDALLS
TSTSTPPQQNTRQTAAMFGVVNVTPVPGDLLRENTEDVLQGEHLSDQENAPPILPGRLPEGLGPGPHLTPHPGGPEAEVW
EETDVNRNKLRINIGKTSCVVEEEQSRGVGVPSSPVRAPPDSPTTPVRSLRYRRVNSPESERLSMADGRVELHERRSRMD
LPGSPSRQACSSQPAQMLSVDTGHADRQASGRMDVSASVEQEALSNAFRSVPLAEEEDFDSKEWVIIDKETELKDFPPGA
EPSTSGTTDEEPEELRPLPEEGEERRRPVAELAVRPRGRSMQTLAEEDPRHTPLQPPLPQLSQADGRLETSQPPTPGSPS
HSPLHSGPRPRRRESDPTGPQRQVFSVAPPFEVNGLPRAVPLNLPYQDFKRDLSDYRERARLLNRVRRVGFSHMLLTTPQ
VPLAPIQPQANGKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAVALGEVLGPRSGSSSEGSERSTD
RSQEGAPSTLLADDQKESRGRASMADGDLEPEEGSKTLVLVSPGDMKKSPVTADLAPDPDLGTLAVLTPQHERPQPTGSQ
LDVSEPGTLSSILKSESKPPGPGVGPGAGVVTTGAGGVAVTSSPFTKVERTFVHIAEKTHLNVMSSSGQALRPEELGTGV
ELGLEVPSDGGAAWERALVPLENGITLSGLDGAKTESCALSGPPGDTPSEVARDSLPNGPALADGPAPVSPLEPGPEKLD
TISPSRQARPGPHLRSRIPVLLSEEDTGSEPSGSLSAKERWSKRARPQQDLARLVMEKRQGRLRLHLASGASSSSSEEQR
RASETLSGTGSEEDTPASEPAAPRKSGRAAATRSRIPRPISIRMPTPATAQQSPGRPQVASPASDTAITSRLQLQKPPGS
AISADLRPKQPSGRRPAPGRARAGARTPAPAPAPAPRSPGLTAAARNQSASPRSRSLSRKESASPSHQVRPAGPPPRGAP
QARAQPDGTPSPGGPKKGPRGKLQTQSAVTKGRAGVAEGRAGAKS
```

734 - 753:	EEEEEEEEEEEEEEEEEEEE
735 - 754:	EEEEEEEEEEEEEEEEEEEE
736 - 755:	EEEEEEEEEEEEEEEEEEEE
737 - 756:	EEEEEEEEEEEEEEEEEEEE
738 - 757:	EEEEEEEEEEEEEEEEEEEE
739 - 758:	EEEEEEEEEEEEEEEEEEEE
740 - 759:	EEEEEEEEEEEEEEEEEEEE
741 - 760:	EEEEEEEEEEEEEEEEEEEE
742 - 761:	EEEEEEEEEEEEEEEEEEEE
743 - 762:	EEEEEEEEEEEEEEEEEEEE
744 - 763:	EEEEEEEEEEEEEEEEEEEE
745 - 764:	EEEEEEEEEEEEEEEEEEEE
746 - 765:	EEEEEEEEEEEEEEEEEEEE
747 - 766:	EEEEEEEEEEEEEEEEEEEE

748 - 767:	EEEEEEEEEEEEEEEEEEEE
749 - 768:	EEEEEEEEEEEEEEEEEEEE
750 - 769:	EEEEEEEEEEEEEEEEEEEE
751 - 770:	EEEEEEEEEEEEEEEEEEEE
752 - 771:	EEEEEEEEEEEEEEEEEEEE
753 - 772:	EEEEEEEEEEEEEEEEEEEE
754 - 773:	EEEEEEEEEEEEEEEEEEEE
755 - 774:	EEEEEEEEEEEEEEEEEEEE
756 - 775:	EEEEEEEEEEEEEEEEEEEE
757 - 776:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9DXK1 **A0A2Y9DXK1_TRIMA** (1880 aa)
Histone acetyltransferase (EC 2.3.1.48). *Trichechus manatus latirostris (Florida manatee)*

```
MVKLANPLYTEWILEAIQKIKKQKQRPSEERICHAVSTSHGLDKKTVSEQLELSVQDGSVLKVTNKGLASYKDPDNPGRF
SSVKPGTFPKSTKGSRGSCNDLRNVDWNKLLKRAIEGLEEPNGSSLKNIEKYLRNQSDLTGTTNNPAFQQRLRLGAKRAV
NNGRLLKDGPQYRVNYGSLDGKGAPKYPSAFPSSLPPVSLLPHEKDQPRADPIPICSFCLGTKESNREKKPEELLSCADC
GSSGHPSCLKFCPELTTNVKALRWQCIECKTCSACRIQGKNADNMLFCDSCDRGFHMECCDPPLSRMPKGMWICQVCRPK
KKGRKLLHEKAAQIKRRYAKPIGRPKNKLKQRLLSVTSDEGSMNAFTGRGSPGRGQKTKVCTTPSSGHAASGKDSSSRLA
VTDPTRPGATTKITTTSTYISASTLKVNKKTKGLIDGLTKFFTPSPDGRRSRGEIIDFSKHYRPRKKVSQKQSCTSHVLA
TDTEIKISIKQESTDVNVIGNKDTVTEEDLDVFKQAQELSWEKIECESGVEDCGRYPSVIEFGKYEIQTWYSSPYPQEYA
RLPKLYLCEFCLKYMKSKNILLRHSKKCGWFHPPANEIYRRKDLSVFEVDGNMSKIYCQNLCLLAKLFLDHKTLYYDVEP
FLFYVLTKNDEKGCHLVGYFSKEKLCQQKYNVSCIMIMPQHQRQGFGRFLIDFSYLLSRREGQAGSPEKPLSDLGRLSYL
AYWKSVILEYLYHHHERHISIKAISRATGMCPHDIATTLQHLHMIDKRDGRFVIIRREKLILGHMEKLKSCSRANELDPE
SLRWTPILISNAAVSEEEREAEKEAERLMEQASCWEKEEQEMLSSRANSRQSPAKVQSKNKYLHSPESRPVAGERGQLME
LSKESSEEEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEENIQSSPPRLTKPQSVAIKRKRPFVLKKKRGRKRRRINSS
VTTETISETTEVLNEPFDNSDEERPMPQLEPTCEIDLDEDGLKPVMRKAFQHQPGMKRQTEEEEGKDNHCFKNADPCRNN
IDGDADNLKEGSKDNPEPLKCKQVWPKGTKRGLSKWRQNKERKTGFKLNLYTPPETPMEPDDQITVEEQKQTSEDKTSST
PIRIEEEVKETVGPLLPRDENRREETCAPISPNKSPGEKREDDLTKPEEEEEEEEEEEEEEEEEGNVEKDPDGTKSEEKEE
PEISMEKEDTVQLDDHEEEEEEDEEPSHNEDHDADDEDDGHMESTEVEKEELPRETFKEVLENQEAFLDLSVQPSHSNSE
VLMDCGVDLAASCNSEPKELAGDTETVPESDEEPPEEQAQKQDQKDSQEVDSDFKEGNTATMEIDSETVQAVQSLTQENN
EQDDTFQDCAETQEACRSLQNYTHADQSPQIATTLDDCQQSDHSSPVSSVHSHPGQSVRSVNSPSVPALENSYAQISPDQ
SAISVPSLQNMETSPMMDVPSVSDHSQQVVDSGFSDLGSIESTTENYENPSSYDSTLGGSICGNGSSQNSCSYSNLTSSS
LTQSSCAVTQQMSNISGSCSLLQQSSISSPPTCGVKSPQGCVVERPPSSSQQLAQCSMAANFTPPMQLAEIPETGNANIG
LYERMGQSDFGAGHYPQPSATFSLAKLQQLTNTLIDHSLPYSHSAAVTSYANSASLSTPLSNTGLVQLSQSPHSVPGGPQ
AQATMTPPPNLTPPPMNLPPPLLQRNMAASNIGISHSQRLQTQIASKGHVSMRTKSASLSPAAATHQSQIYGRSQTVAMQ
GPARTLTMQRSMNMSVNLMPAPAYNVNSVNMNMNTLNAMNGYSMSQPMMNSGYHSNHGYMNQTPQYPMQMQMGMMGTQPY
AQQPMQTPPHGNMMYTAPGHHGYMNTGMSKQSLNGSYMRR
```

897 - 916:	EEEEEEEEEEEEEEEEEEEE
898 - 917:	EEEEEEEEEEEEEEEEEEEE
899 - 918:	EEEEEEEEEEEEEEEEEEEE
900 - 919:	EEEEEEEEEEEEEEEEEEEE
901 - 920:	EEEEEEEEEEEEEEEEEEEE
902 - 921:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9DZ06 **A0A2Y9DZ06_TRIMA** (1771 aa)
Histone acetyltransferase (EC 2.3.1.48). *Trichechus manatus latirostris (Florida manatee)*

```
MVKLANPLYTEWILEAIQKIKKQKQRPSEERICHAVSTSHGLDKKTVSEQLELSVQDGSVLKVTNKGLASYKDPDNPGRF
SSVKPGTFPKSTKGSRGSCNDLRNVDWNKLLKRAIEGLEEPNGSSLKNIEKYLRNQSDLTGTTNNPAFQQRLRLGAKRAV
NNGRLLKDGPQYRVNYGSLDGKGAPKYPSAFPSSLPPVSLLPHEKDQPRADPIPICSFCLGTKESNREKKPEELLSCADC
GSSGHPSCLKFCPELTTNVKALRWQCIECKTCSACRIQGKNADNMLFCDSCDRGFHMECCDPPLSRMPKGMWICQVCRPK
KKGRKLLHEKAAQIKRRYAKPIGRPKNKLKQRLLSVTSDEGSMNAFTGRGSPDTEIKISIKQESTDVNVIGNKDTVTEED
LDVFKQAQELSWEKIECESGVEDCGRYPSVIEFGKYEIQTWYSSPYPQEYARLPKLYLCEFCLKYMKSKNILLRHSKKCG
WFHPPANEIYRRKDLSVFEVDGNMSKIYCQNLCLLAKLFLDHKTLYYDVEPFLFYVLTKNDEKGCHLVGYFSKEKLCQQK
YNVSCIMIMPQHQRQGFGRFLIDFSYLLSRREGQAGSPEKPLSDLGRLSYLAYWKSVILEYLYHHHERHISIKAISRATG
MCPHDIATTLQHLHMIDKRDGRFVIIRREKLILGHMEKLKSCSRANELDPESLRWTPILISNAAVSEEEREAEKEAERLM
EQASCWEKEEQEMLSSRANSRQSPAKVQSKNKYLHSPESRPVAGERGQLMELSKESSEEEEEEEEEDEEEEEEEEEEEE
EEEEEEEEEEEEENIQSSPPRLTKPQSVAIKRKRPFVLKKKRGRKRRRINSSVTTETISETTEVLNEPFDNSDEERPMPQL
EPTCEIDLDEDGLKPVMRKAFQHQPGMKRQTEEEEGKDNHCFKNADPCRNNIDGDADNLKEGSKDNPEPLKCKQVWPKGT
KRGLSKWRQNKERKTGFKLNLYTPPETPMEPDDQITVEEQKQTSEDKTSSTPIRIEEEVKETVGPLLPRDENRREETCAP
ISPNKSPGEKREDDLTKPEEEEEEEEEEEEEEEEEGNVEKDPDGTKSEEKEEPEISMEKEDTVQLDDHEEEEEEDEEPSHN
EDHDADDEDDGHMESTEVEKEELPRETFKEVLENQEAFLDLSVQPSHSNSEVLMDCGVDLAASCNSEPKELAGDTETVPE
SDEEPPEEQAQKQDQKDSQEVDSDFKEGNTATMEIDSETVQAVQSLTQENNEQDDTFQDCAETQEACRSLQNYTHADQSP
QIATTLDDCQQSDHSSPVSSVHSHPGQSVRSVNSPSVPALENSYAQISPDQSAISVPSLQNMETSPMMDVPSVSDHSQQV
VDSGFSDLGSIESTTENYENPSSYDSTLGGSICGNGSSQNSCSYSNLTSSSLTQSSCAVTQQMSNISGSCSLLQQSSISS
PPTCGVKSPQGCVVERPPSSSQQLAQCSMAANFTPPMQLAEIPETGNANIGLYERMGQSDFGAGHYPQPSATFSLAKLQQ
LTNTLIDHSLPYSHSAAVTSYANSASLSTPLSNTGLVQLSQSPHSVPGGPQAQATMTPPPNLTPPPMNLPPPLLQRNMAA
SNIGISHSQRLQTQIASKGHVSMRTKSASLSPAAATHQSQIYGRSQTVAMQGPARTLTMQRSMNMSVNLMPAPAYNVNSV
NMNMNTLNAMNGYSMSQPMMNSGYHSNHGYMNQTPQYPMQMQMGMMGTQPYAQQPMQTPPHGNMMYTAPGHHGYMNTGMS
KQSLNGSYMRR
```

788 - 807:	EEEEEEEEEEEEEEEEEEEE
789 - 808:	EEEEEEEEEEEEEEEEEEEE
790 - 809:	EEEEEEEEEEEEEEEEEEEE

791 - 810:	EEEEEEEEEEEEEEEEEEEE
792 - 811:	EEEEEEEEEEEEEEEEEEEE
793 - 812:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9EB74 **A0A2Y9EB74_TRIMA** (1340 aa)
apoptotic chromatin condensation inducer in the nucleus. *Trichechus manatus latirostris (Florida manatee)*

```
MPCDWFCITNATVVIEGLTKAVGGVSWVRSKGVGGNYRRCPKPSGRDPSTSRKMAELEEVTLDGKPLQALRVTDLKAALE
QRGLAKSGQKSALVKRLKGALMLENLQKHSTPHAAFQPNSQIGEEMSQNSFIKQYLEKQQELLRQRLEREAREAAELEEA
SAESEDEMIHPEGVASLLPPDFQSSRERPELELSRHSPRKSSSVSEEKGESDDERPRKGERRSPRVRQARAAKLSECSQT
AEEEEDQEAPSRNLRVRADRNLKTEEEEEEEEEEEEEEEEEEEENEVQKSREAPILKQFEEEEEEEEMSRAKPEEVMDER
PKTIRSQEEEGLEKGGRVTRSQEETRRSHLARHQQEKEMKTASPLEEKEREIKSSKGLEGNSKSPSPPQLTEDLEKVPLI
LQREQTASEEETLPPLLTKEPCSPSPNIQLRSEEEVDPVEGPAPPVLVQLSPPNADAEARELLVAQHTVRLVGGLSPLLS
PTDTKVESPAEKMPEESVLPLVHKSTLAESSIQKGLETEPEKSAQPLPLKIEELAPPKGITEESLKQPSLEQKESKRASH
TLRPSHSSKRSPDSSSSSRSSSSSSSTSRSRSRSPDSSGSRSHSPPRSKHRDGSRARSHSSPHSRLKMGSRSTSESRSRS
RSHSRSRSASSNSRKSLSPRISRDSNTSYTETKDPSSGQEVATPPVPQLQVLEPKERTATSSSSIQVRRVSQPEPPEKHV
RLQPEQGSPKKCEAEEAEPPAATQPQTSETQTSQQPESERIQHTVEEKEEVNMDTTENRPENEIPEPPMPIADQVSNDDR
PEGSAEDEEKKESSLPKSFKRKISVVSASKGVPAGNSDTEGGQPGRKRRWGASTATTQKKPSISITTDSLKSLIPDIKPL
AGQEAVVDLHADDSRISEDETERNGDDGTHEKGLKICRTVTQVVPAEGQENGQREEEEEEKEPEAEPPVAPQVSVEVALP
PPVEHEVKKVTLGDTLTRRSISQQKSGVSITIDDPVRTAQVPSPPRGKISNIVHISNLVRPFTLGQLKELLGRTGTLVEE
AFWIDKIKSHCFVTYSTVEEAVATRTALHGVKWPQSNPKFLCADYAEQDELDYHRGLLVDRPSETKAEEQGVPRPLHPPP
PPPAQPPQHPRAEQREQERAVREQWAEREREMERRERTRSEREWDRDKVREGPRSRSRSRDRRRKERAKSKEKKSEKKEK
VQEEPPAKLLDDLFRKTKAAPCIYWLPLTDSQIVQKEAERAERAKEREKRRKEQEEEEQKEREKEAERERNRQLEREKRR
EHSRERDRERERERERDRGDRDRDRERDRERGRERDRRDTKRHSRSRSRSTPVRDRGGRR
```

265 - 284:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9ECX0 **A0A2Y9ECX0_TRIMA** (1269 aa)
histone-lysine N-methyltransferase EHMT2. *Trichechus manatus latirostris (Florida manatee)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWAPQLPTGLTSPPVPCLPSQGEAPAEMGA
LLLEKEPRGATERVHGCLGDTSGSEETLPKANPDPLEPPGPSSPASVTVTVGDEGAHTPVGATPLIGDEPESLEGDGDLH
GGRILLGHATKSFPSSPSKGGGGVCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGVAAAGPEAPPATTSPEGQPKVH
RARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVVKRRKLNSGGGLSEELGSARGSGEVTLQKGDPGSLEE
WETVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRK
AKKKWRKDSPWVKPTRKRRKRDPPRAKELRGVNGVGSSGPTEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFE
ELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFC
TAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGMTPPASTAAPAPPPLAQDAPGRADTSQP
SARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPPGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQG
ELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRG
GCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENIC
LHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFAL
QLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCS
SSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQG
TFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSS
RDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNP
```

359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9ERN7 **A0A2Y9ERN7_PHYMC** (1315 aa)
tau-tubulin kinase 1. *Physeter macrocephalus (Sperm whale) (Physeter catodon)*

```
MQCLAAALKDETNMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTRENVALKVESAQQPKQVLKMEVAV
LKKLQGKDHVCRFIGCGRNEKFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESIEAIHSVGFLHRDIKPSNF
AMGRLPSTYRKCYMLDFGLARQYTNTTGDVRPPRNVAGFRGTVRYASVNAHKNREMGRHDDLWSLFYMLVEFAVGQLPWR
KIKDKEQVGMIKEKYEHRMLLKHMPSEFHLFLDHIASLDYFTKPDYQLIMSVFENSMKERGIAENEAFDWEKAGNDALLS
TSTSTPPQQNTRQTAAMFGVVNVTPVPGDLLRENTEDVLQGEHLSDQENAPPILPGRPPEGPGSSPHLAPHPGGPEAEVW
EETDVNRNKLRINIGKTPCLVEEEQSRVAGVPSSPVRAPPDSPTTPVRSLHYRRVNSPESERLSTADGRVELHERRSRMD
LPGSPSRQACSSQPAQMLSVDTGHADRQASGRMDVSASVEQEALSNAFRSVPLAEEEDFDSKEWVIIDKETELKDFPPGA
EPSTSGTTDEEPEELRPLPEEGEERRRPGPEPAVRPRGRGMHTLAEEDLRLTPAQPLPPQLNQADGRSEISQPPTPGSPS
HSPLHSGPRPRRRESDPTGPQRQVFSVAPPFEVNGLPRAVPLSLPYQDYKKDLSDYRERARLLNRVRRVDFSHVLLATPQ
VPLAPVQPQTNGKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAVALGEVLGPHSGSSSEGSERS
TDRSQEGAPSTLLADDQKESRGRASMADGDLEPEEGSKTLVLVSPGDMKKSPVTADLAPEPDLGTLAALTPQHERPQPTG
SQLDVSEPGTLSSVLKSEPKPPGTGTGPGVGAVTIGAGGVAVTSSPFTKVERTFVHIAEKTHLNVMSSGGQASRSEELSS
GGELGLEVPSDGRAAEEGASVYLENGIALSGLVSCVLSAPPGSSPLEVTTDSLPNGPALADGPALASLLEPGPEKLATIS
PSRHAMPGPRPRSRIPVLLSEEDTGSEPSGSLSAKERWVKRARPQQDLARLVMEKRQGRLLLRLASGASSSSSEEQRRAS
ETLSGTGSEEDTPASEPAVPRKAGRAAATRSRIPRPISIRMPTPAAAQQPPDRPQGAAPASDTAITSRLQLQKHPGTAIA
ADLRPKQPTGRGPGPGRAQAGTRPRAPRSPGLPASSAHHPSASPRSRSLSRKESPSPSHQARPGAPPPRGAPQARAQPEG
TPSPGAPKKGPRGKLQTQRATKGRAGVAEGRAGAR
```

734 - 753:	EEEEEEEEEEEEEEEEEEEE
735 - 754:	EEEEEEEEEEEEEEEEEEEE
736 - 755:	EEEEEEEEEEEEEEEEEEEE
737 - 756:	EEEEEEEEEEEEEEEEEEEE

738 - 757:	EEEEEEEEEEEEEEEEEEEE
739 - 758:	EEEEEEEEEEEEEEEEEEEE
740 - 759:	EEEEEEEEEEEEEEEEEEEE
741 - 760:	EEEEEEEEEEEEEEEEEEEE
742 - 761:	EEEEEEEEEEEEEEEEEEEE
743 - 762:	EEEEEEEEEEEEEEEEEEEE
744 - 763:	EEEEEEEEEEEEEEEEEEEE
745 - 764:	EEEEEEEEEEEEEEEEEEEE
746 - 765:	EEEEEEEEEEEEEEEEEEEE
747 - 766:	EEEEEEEEEEEEEEEEEEEE
748 - 767:	EEEEEEEEEEEEEEEEEEEE
749 - 768:	EEEEEEEEEEEEEEEEEEEE
750 - 769:	EEEEEEEEEEEEEEEEEEEE
751 - 770:	EEEEEEEEEEEEEEEEEEEE
752 - 771:	EEEEEEEEEEEEEEEEEEEE
753 - 772:	EEEEEEEEEEEEEEEEEEEE
754 - 773:	EEEEEEEEEEEEEEEEEEEE
755 - 774:	EEEEEEEEEEEEEEEEEEEE
756 - 775:	EEEEEEEEEEEEEEEEEEEE
757 - 776:	EEEEEEEEEEEEEEEEEEEE
758 - 777:	EEEEEEEEEEEEEEEEEEEE
759 - 778:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9EW05 **A0A2Y9EW05_PHYMC** (1177 aa)
histone-lysine N-methyltransferase EHMT2 isoform X5. *Physeter macrocephalus (Sperm whale) (Physeter catodon)*

```
MAAAAGAVAAATAEGEAPAEMGALVLEKEPRGATERVHGSLGDTPRSEEILPKANPDSLETAGPSSPASVTVTVGDEGAD
TPVGATPLIGDEPENLEGDGDLHGGRILMGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGA
TAAGPEPPPATASPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEEL
GSARGSREVTLEKGDPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEE
EEEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAP
KIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDF
RVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGEGVTPPAGTAAPAPPPLAQDAPGRADTSQPSARMRGQGEPRR
PPCDPLADTIDSSGPSLTLPNGGCLSAVGLPPGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDN
LDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGST
CLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAI
AEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGN
RAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIR
CWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELIS
DAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRAGEELGFD
YGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNP
```

300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9EW29 **A0A2Y9EW29_PHYMC** (1211 aa)
histone-lysine N-methyltransferase EHMT2 isoform X3. *Physeter macrocephalus (Sperm whale) (Physeter catodon)*

```
MAAAAGAVAAATAEGEAPAEMGALVLEKEPRGATERVHGSLGDTPRSEEILPKANPDSLETAGPSSPASVTVTVGDEGAD
TPVGATPLIGDEPENLEGDGDLHGGRILMGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGA
TAAGPEPPPATASPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEEL
GSARGSREVTLEKGDPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEE
EEEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGT
LSPNHAGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMV
LCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGEGVTPPAG
TAAPAPPPLAQDAPGRADTSQPSARMRGQGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPPGPGREALEKALVIQ
ESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQR
TPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIE
VIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPEL
RNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCET
STMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVR
LQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNI
IPVRVFMLHQDLRFPRIAFFSSRDIRAGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELL
PELGSLPPVNP
```

300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9EWL2 **A0A2Y9EWL2_PHYMC** (1268 aa)
histone-lysine N-methyltransferase EHMT2 isoform X1. *Physeter macrocephalus (Sperm whale) (Physeter catodon)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWAPQLTTGLTSSPIPCVPSQGEAPAEMGA
LVLEKEPRGATERVHGSLGDTPRSEEILPKANPDSLETAGPSSPASVTVTVGDEGADTPVGATPLIGDEPENLEGDGDLH
GGRILMGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGATAAGPEPPPATASPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEELGSARGSREVTLEKGDPGSLEEWE
TVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKA
KKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEE
LPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCT
AGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGEGVTPPAGTAAPAPPPLAQDAPGRADTSQPS
ARMRGQGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPPGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGE
LQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGG
CVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICL
HWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQ
LNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSS
SNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGT
FICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSR
DIRAGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNP
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9EXY6 **A0A2Y9EXY6_PHYMC** (1234 aa)
histone-lysine N-methyltransferase EHMT2 isoform X2. *Physeter macrocephalus (Sperm whale) (Physeter catodon)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWAPQLTTGLTSSPIPCVPSQGEAPAEMGA
LVLEKEPRGATERVHGSLGDTPRSEEILPKANPDSLETAGPSSPASVTVTVGDEGADTPVGATPLIGDEPENLEGDGDLH
GGRILMGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGATAAGPEPPPATASPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEELGSARGSREVTLEKGDPGSLEEWE
TVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKA
KKKWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGEL
SGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHC
GEDASEAQEVTIPRGEGVTPPAGTAAPAPPPLAQDAPGRADTSQPSARMRGQGEPRRPPCDPLADTIDSSGPSLTLPNGG
CLSAVGLPPGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKG
SVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQV
DVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLH
IAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIP
CVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFE
CNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEV
YCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRAGEELGFDYGDRFWDIKSKYFTCQCGSEKCK
HSAEAIALEQSRLARLDPHPELLPELGSLPPVNP
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9G313 **A0A2Y9G313_NEOSC** (1100 aa)
myelin transcription factor 1. *Neomonachus schauinslandi (Hawaiian monk seal) (Monachus schauinslandi)*

```
MSLENEDKRARTRSKALRVPPEPTGADLSCPTPGCTGSGHIRGKYSRHRSLQSCPLAKKRKLEGAQAEHLASTRKSHPLK
LALDEGYSVDTDGSEDAEVKDASVSDESEGTLEEDEAEMSGQEEIHRPEPAEGRAPVKPHFGPKPVSSSAGPAKGSYSSY
QEIIATSLLNLGQIAVDTLVGEDLDQVAKPGPGVVHLVQEEAEEGATSDEGEKDVFLPPEDTGEVVGVTRERSQEQLCPQ
SVEGVASEESSKMKVAPGDEEEEEEEEEEEEEEEEEEEEEEEEEVAAPEVICQEDAPLAPTQKAPELRHPASPSPKPEYS
VIVEVHSDDGKDEDSRSQKSAVTDESEMYDMMTRGNLGLLEQAIALKAEQVQAICEPGCPPTEQGQLGPGEPGKAVRPLD
AARKNYCSKDPSRAEKREIKCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRIPPEILAMHENVLKCPTPGCTGQGHVNSNR
NTHRSLSGCPIAAAEKLAKSHEKQQPQTGDPSKNSSSSDRILRPMCFVKQLEVPPYGSYRPSVTPATPRANLAKELEKFS
KVTFDYASFDAQVFGKRMLAPKIQTSETSPKAFKCFDYAHDAEAAHMAATAILNLSTRCWEMPENLSTKPQDLPSKAADI
EVDENGTLDLSMHKHRKRESAFPSSSSPGVKSPEASQRQNSTSAPSSSMTSPQSSQASRQDEWDRPLDYTKPSRQREEEP
EESEPAAHSFASSEADDQEVSEESFEERKYPGEVTLTNFKMKFLSKEIKKELLTCPTPGCDGSGHITGNYASHRSLSGCP
LADKSLRNLMAAHSADLKCPTPGCDGSGHITGNYASHRSLSGCPRAKKSGARVTPTKDDKEDPELMKCPVPGCVGLGHIS
GKYASHRSASGCPLAARRQKEGSLNGSPFSWKSLKNEGPTCPTPGCDGSGHANGSFLTHRSLSGCPRATFAGKKGKVSGD
```

```
EVLSTKFKTSDVLENDEEIKQLNQEIRDLNESNSEMEAAMVQLQSQISSMEKSLKNIEEENKLIEEQNEALFLELSGLSQ
ALIQSLANIRLPHMEPICEQNFDAYVSTLTDMYSNQECYQNPENKDLLESIKRAVRGIQV
```

260 - 279:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE
262 - 281:	EEEEEEEEEEEEEEEEEEEE
263 - 282:	EEEEEEEEEEEEEEEEEEEE
264 - 283:	EEEEEEEEEEEEEEEEEEEE
265 - 284:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9G9Z7 **A0A2Y9G9Z7_NEOSC** (1016 aa)
LOW QUALITY PROTEIN: zinc finger protein 316. *Neomonachus schauinslandi (Hawaiian monk seal) (Monachus schauinslandi)*

```
MAALRTTPGSPATQLAKVEDGLECGPAQEEEEEEDQGEEVEIEEEEEIVVEEGEDKQVVEDEEEGGRAGHVDQVEVELEE
DEDVEEVTAEEQSLTLGTQERCSRAADAKSPVLQGKALQAARVPATPRDEDLEEEEEEEEEEEEEEEEEEEEEDDDDSLTA
GSQGLVTFEDVAVYFSLEEWERLDTDQRDLYKDVMQENYGILVSLGYPIPRPDLIFRLEQGEEPWVPDSPRPDEGDIVTG
VYTGAWFWTDDLDDHEEEDDEDFLAEVAEEENEPPGLWSAAYGVGDVPGTWGPDDSDSAQTPEGWGPDPGSLGVLAEGSE
AKPFLPGREPGANLLAPWAFPATVAAPAGRPETTCDVCGKVFPHRSRLAKHQRYHAAVKPFGCDECGKGFVYRSHLAIHQ
RTHTGEKPFPCPDCGKRFVYKSHLVTHRRIHTGERPYRCAFCGAGFGRRSYLVTHQRTHTGERPYPCPHCGRSFSQSSAL
ARHQAVHTADRPHCCPDCGQAFRLRADFQRHRRGGGCAEPGGDGPRREPCDTVPAAGPEEAEVGPEGPEEAGAGEADVEA
EAEAREEAAAAVGRSPGRKEDPEPDRRFLELGNGLGEGEGPSSHPLGFHFPVHPKSWLHPDGFPMLGLPDFGERLQADGR
PLPGPLGGRLALVEGAGLACDPFGGGGRGGGGGGGLRAFAPAVGGLLAEPAPAALAEEESPWICSDCGKTFGRRAALAKH
QRYHAGERPHRCADCGKSFVYGSHLARHRRTHTGERPFPCPECGARFARGSHLAAHVRGHTGEKPFVCGVCGAGFSRRAH
LTAHGRAHTGERPYACGECGRRFGQSAALTRHQWAHAEEKPHRCPDCGKGFGHSSDFKRHRRTHTGEKPFRCTDCGRGFA
QRSNLAKHRRGHTGERPFPCPECGKRFSQRSVLVTHQRTHTGERPYACANCGRRFSQSSHLLTHMKTHRSAAGAPGSATA
APASKAEAPAKGPPGAGSGPGERGSTLLEFAGGTSFGSEPTATFAGPSGAYEESIL
```

133 - 152:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9GHI9 **A0A2Y9GHI9_NEOSC** (1314 aa)
splicing factor, arginine/serine-rich 19. *Neomonachus schauinslandi (Hawaiian monk seal) (Monachus schauinslandi)*

```
MEEEDESRGKTEESGEDRGDGPPERDPTLSPSAFILRAIQQAVGSSLQGDLPNDKDGSRCHGLRWRRCRSPRSEPRSQES
GGTDTATVLDMAADSFLTGLVSVLDPPDTWVPSHLDLRPGESEDMLELVAEVRIGDRDPIPLPVPSLLPRLRAWRTGKTV
SPQPHSSRPSCARHLLTLGTGDGGPAPPPAPSSASSSPSPSPSSSSPSPPPPPPPPAPPAPPAPRFDIYDPFHPTDEAYS
PPPAPEQKYDPFEPTGSNPSSSAGTPSPEEEEEEEEEEEEEEEEEEEEEEEEGLSQSISRISETLAGIYDDNSLSQDFPGD
ESPRPDPQPPQPTPAPGTPPQVDSTRVDGATRRRVFVVGTEAEACREGKVSVEVVTAGGAAIPPTLLPPGDSEIEEGEIV
QPEEEPRVAVSLFRAGGSRAARPPPAVAAPPAAQPPPPPPAPRAPEGDDFLSLHAESDGEGALQVDLGEPAPAPPAADTR
WGGLDLRRKILTQRRERYRQRSPSPAAAAAAAAAAAPAGPPTRKKSRRERKRSGGEAKEAASSSSGAPPAPPAPASPWDS
KKHRSRDRKPGSHASASARRRSRSRSARRRSRSADRRRGGSRRSRSREKRRRRRRSASPPPATSSSSSSRRERHRGKHRD
GGGSKKKKKRSRSRGEKRSGDSEKAPVPTQPPSGSSSLGGERDSRRRGAVPPSIQDLTDHDLFAIKRTITVGRPDKSDPR
GPSPAPASSPKREVLYDSEGLSAEERGGKSSEKDRRRSGAASSSSSSREKGSRRKALDGGDRDRDRDRDRDRSSKKARPP
KESAPSSGPPPKPPVSSGSGSSSSSCSSSSRKVKLQSKVAVLIREGVSSTTPAKEAASAGLGSIGVKFSRDRESRSPFLK
PDERAPAEVAKAAPGSTKPKKTKVKAKAGAKKAKGTKGKTKPSKTRKKIRGGGSGGGSGGPVTLKKSKADSCSQAAGAKG
VEETSWSGEERAAKAPSTPPPKAAPPPPALTPDSQTVDSSCKTPEVSFLPEEATEEAGVRGGAEEEEEEEEEEEEEEEEE
EQQPATTTATSTAAAAPSTAPSAGSTAGDSGAEDGPATRVSQLPTLPPPMPWNLPAGVDCTTSGVLALTALLFKMEEANL
ASRAKAQELIQATNQILSHRKPPSTLGVTPTPVPTSLGLPPGPSSYLLPGSLPLGGCGSTPPTPTGLAAASDKREGSSSS
EGRGDTDKYLKKLHTQERAVEEVKLAIKPYYQKKDITKEEYKDILRKAVHKICHSKSGEINPVKVSNLVRAYVQRYRYFR
KHGRKPGDPPGPPRPPKEPGPPDKGGPGLPLPPL
```

269 - 288:	EEEEEEEEEEEEEEEEEEEE
270 - 289:	EEEEEEEEEEEEEEEEEEEE
271 - 290:	EEEEEEEEEEEEEEEEEEEE
272 - 291:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9GM85 **A0A2Y9GM85_NEOSC** (750 aa)
Daxx (Death domain-associated protein 6). *Neomonachus schauinslandi (Hawaiian monk seal) (Monachus schauinslandi)*

```
MATANSIIVLDDDDEDEAAAQPGPSHPPPNPASPGAEAPGSSQPHGAGGSSSSGGKKCYKLENEKLFEEFLELCKTQTAD
HPEVVPFLYNRQQRAHSLFLASAEFCNILSRVLSRAQSRPAKLYVYINELCTVLKAHSAKKKLNLAPAATTSSEPSGNNP
PTDPSSDPTNAETTASEAPRTRGSRRQIQRLEQLLALYVAEIRRLQEKELDLSELDDPDSTYLQEARLKRKLIRLFGRLC
ELKDCSFLTGRVIEQRIPYRGTRYPEVNRRIERLINKPGPDTFPDYGDVLRAVEKAAARHSLGLPRQQLQLMAQDAFRDV
GIRLQERRHLDLIYNFGCHLTDDYRPGIDPALSDPALARRLRENRSLAMSRLDEVISKYAMMQDKSEEGERQKRRARLPQ
ATSSHTADPPKASLDSGEGPSGMASQECPTTSKPETDDEEDEESDEEEEEEEEEEEEEEEEEEEEEEATDSEEEEDLEQMQ
EGQGDDEEEEEEEEEEEEAGQDGDKSPMSPPRMSTENNLEPSKGISRSVGEQQNKGLMVSPSSLSEEPLAPSSVDAESNGE
HLEELPLEEESPMSQLFELEIEALPLDTTPSPEERDISSSRKQSEDPLTTVLENGAAMVTSTSFNGGVSPHTWGDSCPPC
KKSRKEKQTGAGPLGNSYVERQRAVHEKNGKKIPTLYSPPSPLTSMAPVADSSTRVDSPSHGLVTSSLCSPSPARLSQTP
HSQPSRPGTYKMSVATQCDPEEIIVLSDSD
```

446 - 465:	EEEEEEEEEEEEEEEEEEEE
447 - 466:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9GVQ5 **A0A2Y9GVQ5_NEOSC** (585 aa)
ran GTPase-activating protein 1. *Neomonachus schauinslandi (Hawaiian monk seal) (Monachus schauinslandi)*

```
MASEDIAKLAETLAKTQVAGGQLSFKGKSLKLNTAEDAKDVIKEIEDFDGLEALRLEGNTVGVEAARVIAKALEKKSELK
```

```
RCHWSDMFTGRLRSEIPPALTSLGEGLITAGAQLVELDLSDNAFGPDGVRGFEALLKSSSCFTLHELKLNNCGMGIGGGK
ILAAALTECHRKSSAQGKPLGLKVFVAGRNRLENDGATALAEAFGIIGTLEEVHMPQNGINHPGVTALAQAFAINPLLRV
INLNDNTFTEKGAVAMAKTLKTLRQVEMINFGDCLVRSKGAVAIAEAVRGGLPKLKELNLSFCEIKRDAALAVAEAVADK
SELEKLDLNGNTLGAEGCEQLQEVLDGFHMAKVLASLSDDEGEDDEEEEEEEEEEGEEEEEEEEEEEEEEEEEEEEAQQ
GPGEQSTASRKILDPNSGEPAPVLSAPPPADVSTFLAFPSPEKLLRLGPKSPVLIAQQTDTSDPEKVVSAFLKVSSVFKD
EATVRTAVQDAVDALMKKAFSSPSFNSNAFLTRLLVHMGLLKSEDKIKAIANLYGPLMVLNHMVQQDYFPKALAPLLLAF
MTKPNGALESCSFARHNLLQTLYKV
```

377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9H231 **A0A2Y9H231_NEOSC** (834 aa)
C-Jun-amino-terminal kinase-interacting protein 2. *Neomonachus schauinslandi (Hawaiian monk seal) (Monachus schauinslandi)*

```
MADRAEMFSLSTFHSLSPPGCRPPQDISLEEFDDEDLSEITDDCGLGLSYDSDHCEKDSLSLGRSEQPHPICSFQDDFQE
FEMIDDNEEEEEEEEEEEEEEEEEEEEEEEEEGEGEKEGGGPGSEAPAPEALIPSPSLEEPHKNRPTTLHLTTLGAQDSLN
NNGGFAPAPPASWQETVLCSPPQEPLRESPASLQPTDASPCGAQSPVRPGCDCEGNPPAAAPPAPCGASPSSDPGIEADL
GSRSSGGRGGRRSSQELSSPGSDSEDAGGARLGRMISSISETELELSSDGGSSSSSGRSSHLTNSIEEASSPASEPEPEP
EPEAPCEPPRRPAFLPVGPDDTNSEYESGSESEPDLSEDADSPWLLSNLVSRMISEGSSPIRCPGQCLSPASRPSGEPSS
PAGGTMEAPEAAAGPGGVELVDMETLCGPPPPAPSAPRPGPAQPGPCLFLSNPTRDTITPLWAAPGRSVRPARACSAACS
EEDDEDEEEEDDADDKVGPPGGRGVGPAAPLDASLVYDAVKYTLVVDEHTQLELVSLRRCAGLGEDSSEDSGGEASEEET
AATLLGGGQGPEDASPDSPDLTFSKKFLNVFVNSTSRSSSTESFGLFSCLVNGEEKEQTHRAVFRFIPRHPDELELDVDD
PVLVEAEEDDFWFRGFNMRTGERGVFPAFYAHAVPGPAKDLLGSKRSPCWVERFDVQFLGSVEVPCHQGNGILCAAMQKI
ATARKLTVHLRPPASCDLEISLRGVKLSLSGGPEFQHCSHFFQMKNISFCGCHPRNSCYFGFITKHPLLSRFACHVFVSQ
ESMRPVAQSVGRAFLEYYQEHLEYACPTEDIYLE
```

88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9H7T8 **A0A2Y9H7T8_NEOSC** (1326 aa)
LOW QUALITY PROTEIN: tau-tubulin kinase 1. *Neomonachus schauinslandi (Hawaiian monk seal) (Monachus schauinslandi)*

```
MQCLAAALKDETNMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTRENVALKVESAQQPKQVLKMEVAV
LKKLQGKSHVCRFIGCGRNEKFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESIEAIHSVGFLHRDIKPSNF
AMGRLPSTYRKCYMLDFGLARQYTNTTGDVRPPRNVAGFRGTVRYASVNAHKNREMGRHDDLWSLFYMLVEFAVGQLPWR
KIKDKEQVGMIKEKYEHRMLLKHMPSEFHLFLDHIASLDYFTKPDYQLIMSVFENSMKERGIAENEAFDWEKAGTDALLS
TSTSTPPQQNTRQTAAMFGVVNVTPVPGDLLRENTEDVLQGEHLSDQENAPPILPGRPPEGLGPSPHLAPHPGGPEAEVW
EETDVNRNKLRINIGKTPCVVEEEQSRGVGVPSSPVRAPPDSPTTPVRSLRYRRVNSPESERLSTADGRVELHERRSRMD
LPGSPSRQACSSQPAQMLSVDTGHPDRQASGRMDVSASVEQEALSNAFRSVPLAEEEDFDSKEWVIIDKETELKDFPPGA
EPSTSGTTDEEPEELRPLPEEGEERRRPGTEPSVRPRGRGMQTLAEEDTRQTPFQPLPPPLSQAEGRSETSQPPTPGSPS
HSPLHSGPRPRRRESDPTGPQRQVFSVAPPFEVNGLPRAVPLSLPYQDFKKDLSDYRERARLLNRVRRVGFSHVLLTTPP
VPLATVQPQANGKEEEEEEEEEEEEEEEEEEEEEEVEEEEEEEEDEEEEDEEDGEEEEEEGEEGEEAVALGEVPGPRSGC
SSDGSERSTDRSQEGAPSTLLADDQKESRGRASMADGDLEPEEGSKTLVLVSPGDMKKSPVTADLAPDPDLGTLAALTPQ
QERPQPTGSQLDVSEPGTLSSVLKSEPKPPGPGPGPGAGAVTAGAGGVAVTSSPFTKVERTFVHIAEKTHLNVMSSGGQA
SRPEELGPGGELGLEAPSDGRAVEEGASVPLENGIAQAGLESCAPTGPPRDTPLEVATDSLPNGPALANGPAPASPLEPG
PEKLATISPSRHAMAGPRPRSRIPVLLSEEDTGSEPSGSLSARERWGKRARPQQDLARLVMEKRQGRLLLRLASGASSSS
SEEQRRASETLSGTGSEEDTPASEPAAPRKAGGAATTRSRIPRPISIRMPTPAAAQQQSVGSPHGAAPASDTAITSRLQL
QKPRGSAVAADLRPRQPPGRGPGPGRAPAGARPPAPRSPGPSASAAPRHPNASPRSQSLSRKESSSPSHQARPAGPPPRG
APQARAQPDGTPSPGGPKKGPRGKLQTQRAATKGRAGIAEGRAGAR
```

734 - 753:	EEEEEEEEEEEEEEEEEEEE
735 - 754:	EEEEEEEEEEEEEEEEEEEE
736 - 755:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9HHB9 **A0A2Y9HHB9_NEOSC** (1023 aa)
peroxisome proliferator-activated receptor gamma coactivator 1-beta. *Neomonachus schauinslandi (Hawaiian monk seal) (Monachus schauinslandi)*

```
MAGNDCGALLDEELSSFFLNYLADTQGGGSGEEQLCADFPELDLSQLDASDFDSATCFGELQWCPENSDTEPSQYSPDDS
ELFQIIDSENEALLAALTKTLDDIPEDDVGLAAFPALDGGDAPSCTSASPATSSAPPSPSPSLERPQAPTPEVDELSLLQ
KLLLATSYPTSSSDTQKEGTAWRQAGLRSRNQRPCVKVDGTQDKKAPTMQSQSRSCTELHKHLTSGPSCPQTKARSPDRG
LQPPPSLSPQLPAKEEEEAGEDCPSPQPAPASPQDSPAPGRAGPGAQGSQEDMQEIVKLIRYMHTYCLPQRKLPPQAPEP
APQPCGSPSKQVKPRPRSQHPSKGSWAEFSILRELLAQDVLCDVSKPYRLATPVYASLTPRPRPRPPKDSQASPGHPSPV
EEVRITASPRSTGPRPSLRPLRLEVKGHAGRSARLQREEEEEEEEEEEEEEEEEEEEWGRKRPGRGLPWTKLGRKLENAV
CPVRRSRRLNPELGPWLALSDESLVPAEPQGALPSLRLAPEAYDMAGALGSPTDEDSGQDQQLPRGPQIPALESPCESGC
GDTDEDPSCPRLPSRDSPRCLMLALSQSDPPFGRKSFEQNLTVELCGTAGLTPPTTPPYKPTEEDPFKPDIKHSPGEDRA
PSLPSLEGLQLGAAPVAAHKLPKKHPERSELLSHLRHGTAQPASQTGQKRPFSCSFGDHDYCQVLKPEGALQRKVLRSWE
PSGVHLEDWPQQGAPRAAGQASDREEDRSCDGGAPTKDSMLLRDHEIRASLTKHFGLLETALEDEDLASCKSAEYDTVFE
DSNSSSGESSFLLEEDEDEDDEEDDSGLSPPRSDHCPYQRPPSKASRQPCSRSRSSSGSTCCSWSPATRRTFRCESRGPC
SDGTPSVRHARKRREKAIGEGRVVYVRNLSSDMSSRELKRRFEVFGEIVECQVLTRSRRGEKYGFITYRCSEHAALSLRN
GAALRKRNEPSFQLSYGGLQHLCWPRHTDYDSNSEEALPASVKNKYEAMDFDSLLKEAQQSLH
```

438 - 457:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9HLD1 **A0A2Y9HLD1_NEOSC** (1037 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Neomonachus*

schauinslandi (Hawaiian monk seal) (Monachus schauinslandi)

```
MCLLRLHGTVGGAQNLSAVGALVGLSNARLGSIKTRFEGLCLLSLLVGESPTEMFQQHCVSWLRSIQQVLQSQDPPPTME
LAVAVLRDLLRYAAQLPTLFRDISMNHLPGLLTSLLGLRPECELSALEGMKACMTYFPRACGSLKGKLASFFLSRVDALS
PQLQQLACECYSRLPSLGAGFSQGLKHTESWQQELRSLLASLHSLLGALYEGAETAPVQYEGPGVEVLLTPSEDGDAHAL
LRLRQRFCGLARCLGLMLSSEFGAPVSVPVQEILDVICRTLSISAKNISLLGDGPLRLLLLPSIHLDALDLLSALILACG
GRLLRFGGLVSRLLPQVLNAWNMGRDTLSPGQERPYSTVRTKVYAVLELWVQVCGASAGVLQGGASGEALLSHLLSDIAP
PADALKLRSPRGSPDGGLQSGKPSAPKKLKLDLGEAMAPPSHRKGDSNANSDVCAAALRGLSRTVLMCGPLIKEETHRRL
HDLVVPLVMGLQRGETLGSSPYTSSRCRRELYRLLLALLLAPSPRCPPPLACALHAFSLGQREDSLEVSSFCSEALVVCA
ALTHPRVPPLQPAGPPCPTPAPVPPPEAPSPFRAPPFHPPAGPLPPARPGPPATANHLGLSVPGLVSVPPRLLPGPENHR
AGSNEDPVLAPSGTPPPALPPDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDSVVIVPEGLPPLPPPPPSGTTPPPV
APAGPPTASPPVPAKEEPEELPAAPGPLPPPPPPPVPGPVALPPPQLVPEGTPGGGGPPTLEEDLTVININSSDEEEEEE
EEEEEEEEEEEEEEEDFEEEEEDEEEYFEEEEEEEEFEEEFEEEEGELEEEEDEEDEEDEEELEELEEAEFGPAGGPAEE
GGPAPPSPAPALPPAQSPTVQPEPEGEPGLLLEVEEPGAEEEPGAQAAPTLAPEVLPSQGEGPRATGSPPAGPPPQELVE
EEPLAPPTLLEEGTESGGDRVPPLPETPAAEDGEAEAEAETAALQEKEQDDTAAMLADFIDCPPDDEKPPPAPEPDS
```

795 - 814:	EEEEEEEEEEEEEEEEEEEE
796 - 815:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9HMB9 **A0A2Y9HMB9_NEOSC** (1268 aa)
histone-lysine N-methyltransferase EHMT2 isoform X1. *Neomonachus schauinslandi (Hawaiian monk seal) (Monachus schauinslandi)*

```
MRGLPRGRGLMRARGRGRAAHPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWAPQLPTGLTSPPMPCVPCQGEAPAEMGA
LVLEKEPRGATERVHGSLGDTPRSEETLPKASPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDEPENLEGDGDLH
GGRILLGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAATAGPEPPVATPSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSMGKMTSEVAKRRKLNAGGGLSEELGSTRGSGEVTVEKGDPGSLEEWE
TVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKA
KKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEE
LPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCT
AGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLAQDAPGRADTSQPS
ARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGE
LQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGG
CVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICL
HWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQ
LNRKLRLGVGNRAVRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSS
SNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGT
FICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSR
DIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELSSLPPVNP
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9HMJ0 **A0A2Y9HMJ0_NEOSC** (1211 aa)
histone-lysine N-methyltransferase EHMT2 isoform X2. *Neomonachus schauinslandi (Hawaiian monk seal) (Monachus schauinslandi)*

```
MAAAAGAAAAAAAEGEAPAEMGALVLEKEPRGATERVHGSLGDTPRSEETLPKASPDSLEPAGPSSPASVTVTVGDEGAD
TPVGATPLIGDEPENLEGDGDLHGGRILLGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGA
ATAGPEPPVATPSPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSMGKMTSEVAKRRKLNAGGGLSEEL
GSTRGSGEVTVEKGDPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEE
EEEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGT
LSPNHAGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMV
LCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAG
TAAPAPPPLAQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPLGPGREALEKALVIQ
ESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQR
TPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIE
VIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPEL
RNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAVRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCET
STMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVR
LQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNI
IPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELL
PELSSLPPVNP
```

300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9HWF2 **A0A2Y9HWF2_NEOSC** (822 aa)
disintegrin and metalloproteinase domain-containing protein 1a-like. *Neomonachus schauinslandi (Hawaiian monk seal)*

(Monachus schauinslandi)

```
MATSVAAPLRHFASSLSSLQKYQVVTCEAGRVLQTWVPQMKGSRRALVVPGPSCVRLGIMLVLVLIFLPSMYCDPGSVYY
SSYETVIPKGLTVKGREDPGEKASYMLLMQGQKQVIHLKAKRDYFVNNFPVFSYHNGVLGQETPFISYDCHYEGYIEGVP
GSFVSLNTCSGLRGILIKEGKPYGIEPMDTSKRFEHVLYTMAHQARVSCSVTSKGSQVVSTSQQQGSRKPRSLQALSSFW
SHTKYVEMFVVVNNQRFQMWGSNVNETVQRVMDIAALANIFSREINTEVVLAGMEIWTEGDLIEVPADLRVTLRNFNSWR
QEKLFYRVKHDVAHMIVGHHPEEDVGHAFLNGACSRGFAAAVEAFHHEDVLLFAALMVHELGHNLGIQHDHSACICKDKR
FCLMHENITKEGGFSNCSSDHFYQFLREHKGACLFNKPQPRGRLRRQATCGNGVLDYNEECDCGRDCGNNPCCDLTCRLK
EKAKCSPGPCCNDTCQYSVKGSMCRPSSGECDLPEYCDGTSDRCPTNTYKQDGTSCQRVHYCIQGVCKTPDFQCLSVFGF
PARSAPEDCYIHMNTKGDRFGNCGLLTSGNQEYVKCTGENIYCGKIICTNVKNVPLIKPMETMIQVPHKDDWCWSMDAYN
DTDIPDDGYVQIGTLCAPEKICMNNSCINHDVLNYDCDTKEMCNGRGVCNNLKHCHCEAGYAPPDCKTVGTGGSVDSGSP
VVQRETENTINVAKHEDGYLDYMIILFLILFSLILIIIIVCVIIMCKRSIEASAEPTEKGPEEAAVKPPEEAAEEAPPEE
EEEEEEEEEEEEEEEEEEESEP
```

799 - 818:	EEEEEEEEEEEEEEEEEEE
800 - 819:	EEEEEEEEEEEEEEEEEEE

A0A2Y9HYM7 **A0A2Y9HYM7_NEOSC** (546 aa)
leiomodin-2. *Neomonachus schauinslandi (Hawaiian monk seal) (Monachus schauinslandi)*

```
MSTFGYRRGLSKYESIDEDELLASLSAEELKELERELEDIEPDHSLPVGLRQKSLTEKTPTGTFSREALMAYWEKESQKL
LEKERLGECGKVAEEDKEESEEELIFTETNSEVSEEVYTEEEEEEEEEEEEEEEEEEEEGTTENEKGINGTVNYDGIDSD
NSKPKTFKSQIENINLTNGHSGRNTESPAAIHPCGNPTVIEDALEKIRNNDPDTTEVNLNNIENITSQTLARFAEALKGN
TAVKTFSLANTRADDSAAMAVAEMLKVNEHITNINVESNFITGKGILAIMRALQHNTVVTELRFHNQRHIMGSQVEMEIV
KLLRENTTLLRLGYHFELPGPRMSMTSLLTRNMDKQRQKRIQEQKQQESYDGGANLRTKVWQRGTPGSSPYASPRHSPWS
SPKLPKKVQTVRSRPPSPVAPPPPSPPPPPPLPPQRLPPPPLLAPPPLPEKKLITRNIAEVIKQQESAQRALQNGQKKKK
GKKVKKQPNNILKEIKNSLRSVQEKKMEESSRPSTPLRSAHENLMEAIRGSSIKQLRQVEVPEALR
```

120 - 139:	EEEEEEEEEEEEEEEEEEE

A0A2Y9I1T4 **A0A2Y9I1T4_NEOSC** (712 aa)
YTH domain-containing protein 1 isoform X4. *Neomonachus schauinslandi (Hawaiian monk seal) (Monachus schauinslandi)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDIKRQKPSVHSRQLISKPLSSSVSN
NKRIVSTKGKSVAEYKNEEYQRSERSKRLEVDRKIRLSSSASREPYKSQPEKTCLRKRDPDRRTKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEEE
EEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGS
SASESYADQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSARSVILIFSVRESGKFQGFARL
SSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLLFPPD
ESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYAPEFHQRPGYLKDPRYQEVDRR
FSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMAPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHHPVPHEARYRDKRVHD
YDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDRGERGRYRR
```

229 - 248:	EEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEE

A0A2Y9I2A5 **A0A2Y9I2A5_NEOSC** (720 aa)
YTH domain-containing protein 1 isoform X3. *Neomonachus schauinslandi (Hawaiian monk seal) (Monachus schauinslandi)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDIKRQKPSVHSRQLISKPLSSSVSN
NKRIVSTKGKSVAEYKNEEYQRSERSKRLEVDRKIRLSSSASREPYKSQPEKTCLRKRDPDRRTKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEEE
EEEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGS
SASESYADQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSARSVILIFSVRESGKFQGFARL
SSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLLFPPD
ESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYAPEFHQRPGYLKDPRYQEVDSF
TNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMAPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHHPVPHEAR
YRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDRGERGRYRR
```

229 - 248:	EEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEE

A0A2Y9I5C5 **A0A2Y9I5C5_NEOSC** (2924 aa)
WD repeat-containing protein 87. *Neomonachus schauinslandi (Hawaiian monk seal) (Monachus schauinslandi)*

```
MSSTRLIPLWKDFKYLVNDIIHKSKQTSEDPKNEVVVLSDQSQILFRESRHPQNMPLICYYFSDANFFASLSWVTSTKEI
QAVVWMKSKTEDMVEKRTFSMTERLPPIQSMVHTGSFHILVAYCGDLILRLFGDHFRSFKPLGIVPCRFNINCLCYDPEM
KMLLSGILGAVVTWIIERSGKGLQVAHMVPMPGDQLVQDIRLNGPNGSLLALCETVVRVLERQGHGQLGEVQRFMSTTSG
SSITCCFTCFDQGFLYAGNKTGEIQVWSLFRGNSLHSFKAHSSSVTCIRSRPEAHTLLTAGKEGLIKEWNLTLGNLLRRL
ELGEELYELEFIDNTTFFCQTTHTFSLRRLPCFYSLFSVCGSAPQQLRRVRCGDNWFRILCTTEDGLLRFVSPLTGDLLV
```

```
LTWPFTILDRAVDWAYDPEKEELFVATGNAEVLVFDTTRCPCPAKYLLCTSPNSQDWVQCLAYGHFHLGRGLQGLMFSGH
QSGVIRVLSQNYCARIEKFMHFGAILALSTLPGGLFSSRENSLLCSYGMDDYVHLSEAVLEGRKVHLKPLASILSSCHLR
HLILLPTSVGAITETNCLRLWKFHDFLSSESREDSMFIETLPLHQCTITSFDVCLSLSLFVTGGIDGSVRIWNFHGRLIA
MLDSSLHFGPLCFANDRGDLLVSFNQSLYLVSCLKLLHPTLLARLSFMSMTDEVLEAPKPFTPSFFLSFETMFVPKYIYL
GKGQQELVGLEKLVNKRAIAFDHTVPHVIEEDEQGSPMLLPAFRHGFSYKEETDGMEVGKAPHYVVPPQLQLTAWDGLSP
YQILRCYFGHGRKWLLAPDGYIPNSVIRARLWPEGSPIYLQCNLHSPVWETDWDKSQQFFFWHSRVKSLSDAGEYSEEKE
DEDFIEMRLSKDVTYSVLTDSANRSWLGKKMSEIAINSLVETILNIMIHASPLKYQCCIGALGQIFASYEVSSSLRSETA
HRLLDDTTNSNPLIRELAWEGLKHLGMITHLFAMPLAQGLMDKDQKVRSKALSLMADTGIHSKSSLLNLIQHRETFREMQ
QEMIGEESLDHLLGMRATDLQILHTQVEQRLNENLTLSEGQEKPAFSLEVSRISERISLSKQPDVIPGESKAAIKSGKGQ
RQGRAGGKKHVRKLWRALKKIKEAGKEPGPVEGEIDQREAAPVLVEDTAAHSRMSSTISVLKISKDGEQQPPEKDTSKDQ
FALTLKMLRKIHDRKGKKRTVQKPKKRHKKTKEAEVTTEESLSAVKEEPVVKQLKAKGRGATGAPGRKTIPEDSSSWRDD
LCRLMTLRISGSQTKMSEALNMELVATAQKVLADQQPSWELFQEICPLLEKKSEVLLEDLNWDIAWPEEKPIFIHEGAIR
DDIMTIRREDEIPEEQEQEQVQKEEEAMPYLQETQVIPKKGKKKKAIFLGPSGLTKGKQISKKEEKKSFMKPFKQERKEV
QQEIKVDKKETVSKRERDVSQAVEEVAKPEEEVVKQEERPVMDERKLSWQEWKKSWDEWKQAQGETKIAWDEWKKAWDKK
HLEEEEKQQTDERKPLPEEEKLDVDKKKLRWDEWLEFWEQTAARSREEHKDEEELTLEGEELSQEWGEEQEELMTKEQRQ
IQKEYNQAWMERKRAQAERKRAQEERKLAQEEQKLAQGERKLAQEERKLAREYGKLAQRDRTMVQSERKFVHNEEKLAKR
EEKLSQEAEKLAQKRKKLAKQFEEMAREEEKIAKKGGKLAEVKKILAQKLEKLTQKEQELALQEKELAQELEELMWEEEE
LALKEEELIQELKDLAEEEEGLAQEEKTLAWQEQKLIKEEKTLTLEEELLIQEENKLAHDKELPEEEEKLAQKRKKLME
NKLKLAQEKEKLAQDKEKLTKNKKILDWREKSLAQERENLLQEKVKLAQRKENFLQVKENLAQNKNKLVQAKEKLNVYKK
KLAQVEKKLMEEKEKLSQKNKNLDEAEKKLTQLEESLAQKQHNLAQDKMELAMEKRAVFQELKMLRGEWDGAKEEKALGT
EMKKLAQEKVRLSEEKEILSAGETEETLKQVRLTKNELELIKRKLSLEEKILRYEDRILATEQTDIAKGKLEFTRGGRVY
AQEERKLAKVVRKLIKEKEGTSKASKVSSKVLKALQELTKEEMKLTQEEIEMTKMKRNFFVKERRLSKEKNKLDAKEWDF
SEEQPEVTKDEKKLAKKQRKLAKEMKRMIKKEKKITEEESRLARQQREVIQEEEEEGLTKDEEVIPLLKQRLRKRKELKT
VDIPQEKLPSQEESRESLSEEMESLLDQVERESLSEEEEEEEEEEEEEEEEEEEEEEEGKVVEEVEVEERRKEKEKEKKK
EEKEKKEKKKKKKVQEGEEKEEEEEGEEEEVFEEEEKESISEEESESLSEEESESLSEKEKGKSSLKKEADKKKEIFKKE
KLFKSQAEREKDQRREIIPSIGKRIPDIKDSDIQLKVLKVPSKKVISIALGRQETIPVPVSTKQVSWEERARALEASRVL
PESRFMERQELLKKYKPKPLQLLDTVLESPEQDLKTPYLPHILRKTMEAHKLQGEPLEPKWQWILQHHPALMRKTEVPVP
QIWAKEIGAQVVLSDIEWIRHVLERMEAGEQLSRDSFHRLCQLLKDLTSKGNLEWLHLAQLEAIVYRHKQVLESQSAHIS
KPNKEPMGPKYLKVIPPIKGKESWLKPFTVPTQKSPLGTKGIPTPKDVNWHLLEEPYRSAWAEQISTALKEMEVQHFHPA
TGDSFTGAQASVEKQTLALMFQKDFWAFKDKGRFPRLPKLEKKAQAISKKKEEVPLWETFVALYHVLRMLQQRYAKDSAA
WMEQFYQLMDLYQLKSPRIQKLLQELLLRDERQSQEITYEAALKAMELVPGERLFSHLFCGGSQNPKGPLEFQEVVSLPG
QNNVRTMNPMGIAQYGILELAWKSLPQADIHLTKEMPHIIAPTP
```

2276 - 2295:	EEEEEEEEEEEEEEEEEEEE
2277 - 2296:	EEEEEEEEEEEEEEEEEEEE
2278 - 2297:	EEEEEEEEEEEEEEEEEEEE
2279 - 2298:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9I6P1 **A0A2Y9I6P1_NEOSC** (738 aa)
YTH domain-containing protein 1 isoform X1. *Neomonachus schauinslandi (Hawaiian monk seal) (Monachus schauinslandi)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDIKRQKPSVHSRQLISKPLSSSVSN
NKRIVSTKGKSVAEYKNEEYQRSERSKRLEVDRKIRLSSSASREPYKSQPEKTCLRKRDPDRRTKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEEE
EEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGS
SASESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSARSV
ILIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDG
QEIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYAPEF
HQRPGYLKDPRYQEVDSFTNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMAPYPGMEQPPHHPYYQHHAPP
PQAHPPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERER
ERLCDRDRDRGERGRYRR
```

229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9I8R7 **A0A2Y9I8R7_NEOSC** (730 aa)
YTH domain-containing protein 1 isoform X2. *Neomonachus schauinslandi (Hawaiian monk seal) (Monachus schauinslandi)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDIKRQKPSVHSRQLISKPLSSSVSN
NKRIVSTKGKSVAEYKNEEYQRSERSKRLEVDRKIRLSSSASREPYKSQPEKTCLRKRDPDRRTKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEEE
EEEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGS
SASESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSARSV
ILIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDG
QEIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYAPEF
HQRPGYLKDPRYQEVDRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMAPYPGMEQPPHHPYYQHHAPPPQAHPPYS
GHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDR
DRGERGRYRR
```

229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9INH3 **A0A2Y9INH3_ENHLU** (1126 aa)
myelin transcription factor 1. *Enhydra lutris kenyoni*

```
MSLETEDKRARTRSKALRVPPEPTGADLSCPTPGCTGSGHIRGKYSRHRSSQSCPLAKKRKLEGAPAEHLASTRKSRPLK
LALDEGCGADTDGSEDAEVKDASVSDESEGTPEEDEAELPGQEEIHRPEPAEGRSPVKSHFGSKPVGSSAGPAKGSYSSY
QEIIATSLLNLGQIAVETLVGEDLGQVAKPGPGVVHLVQEEAEEGATSDEGEKDVFLRPEDTEQVVGVTREHPQELGPQA
VEGVASEESSKRKVALGNEEEEEDEEEEEDEEEEEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEVAAPEVICQ
EDAPLAPSQKAPEARPLASPSPKPEYSVLGEERSDDGRDEDALSQKSEVTDASEMYDVMTRGNLGLLEQAIALKAEQVQA
VCEPGCPPTEQGQLGPGEPGKAVRPLDARKNYCNKDPSRAEKREIKCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRIPPE
ILAMHENVLKCPTPGCTGQGHVNSNRNTHRSLSGCPIAAAEKLAKSHEKQQPQTGDPSKSSSSSDRILRPMCFVKQLEVP
PYGSYRPNVAPATPRANLAKELEKFSKVTFDYASFDAQVFGKRMLAPKIQTSETSPKAFKCFDYTHDAEAAHMAATAILN
LSTRCWEMPENLSTKPQDLPSKAADIEVDENGTLDLSMHRHRKRDGAFPGGGPGVKAPDASQRQSSVSAAPSSSMASPQC
SQASRQDEWDRPLDYTKPSRPREEEPEESEPAAHSFASSEADDQEVSEESFEERKYPGEVTLTNFKMKFLSKDIKKELLT
CPTPGCDGSGHITGNYASHRSLSGCPLADKSLRNLMAAHSADLKCPTPGCDGSGHITGNYASHRSLSGCPRAKKSGARVT
PTKDDKEDPELMKCPVPGCVGLGHISGKYASHRSASGCPLAARRQKEGSLNGSPFSWKSLKNEGPTCPTPGCDGSGHANG
SFLTHRSLSGCPRATFAGKKGKVSGDEGLSTKFKTSDVLENDEEIKQLNQEIRDLNESNSEMEAAMVQLQSQISSMEKSL
KNIEEENKLIEEQNEALFLELSGLSQALIQSLADIRLPHMEPICEQNFDAYVNTLTDMYSNQECYQNPENKDLLESIKRA
VRGIQV
```

283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE
287 - 306:	EEEEEEEEEEEEEEEEEEEE
288 - 307:	EEEEEEEEEEEEEEEEEEEE
289 - 308:	EEEEEEEEEEEEEEEEEEEE
290 - 309:	EEEEEEEEEEEEEEEEEEEE
291 - 310:	EEEEEEEEEEEEEEEEEEEE
292 - 311:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9J329 **A0A2Y9J329_ENHLU** (2081 aa)
Histone acetyltransferase (EC 2.3.1.48). *Enhydra lutris kenyoni*

```
MVKLANPLYTEWILEAIQKIKKQKQRPSEERICHAVSTSHGLDKKTVSEQLELSVQDGSVLKVTNKGLASYKDPDNPGRF
SSVKPGTFPKSTKGSRGSCNDLRNVDWNKLLRRAIEGLEEPNGSSLKNIEKYLRSQSDLTSTTNNPAFQQRLRLGAKRAV
NNGRLLKDGPQYRVNYGSLDGKGAPKYPSAFPSSLPPVSLLPHEKDQPRADPIPICSFCLGTKESNREKKPEELLSCADC
GSSGHPSCLKFCPELTTNVKALRWQCIECKTCSACRIQGKNADNMLFCDSCDRGFHMECCDPPLSRMPKGMWICQVCRPK
KKGRKLLHEKAAQIKRRYAKPIGRPKNKLKQRLLSVTSDEGSMNAFTGRGSPGRGQKTKVCTTPSSGHAASGKDSSSRLA
VTDPTRPGATTKITTTSTYISASTLKVNKKTKGLIDGLTKFFTPSPDGRRSRGEIIDFSKHYRPRKKVSQKQSCTSHVLA
PGTTQKLKPPPSSLPPPTPISGQSPSSQKSSTSTSSTSPQSSSSQSSVPSLSSLTKNSQLKALFDGLSHIYTTQGQSRKK
GHPSYAPPKRMRRKTELSSTAKSKAHFFGKREIRSRFIAHSSSSSWGMARGRIFKAIAHFKRTTFLKKHRMLGRLKYKVT
PQMGTPSPGKGSLTDGRIKPDQDDDTEIKISIKQESTDINVIGNKDTVTEEDLDVFKQAQELSWEKIECESGVEDCGRYP
SVIEFGKYEIQTWYSSPYPQEYARLPKLYLCEFCLKYMKSKNILLRHSKKCGWFHPPANEIYRRKDLSVFEVDGNMSKIY
CQNLCLLAKLFLDHKTLYYDVEPFLFYVLTKNDEKGCHLVGYFSKEKLCQQKYNVSCIMIMPQHQRQGFGRLLIDFSYLL
SRREGQAGSPEKPLSDLGRLSYLAYWKSVILEYLYRHQERHISIKAISRATGMCPHDIATTLQHLHMIDKRDGRFVIIRR
EKLILGHMEKLKTCSRTNELDPESLRWTPILISNAAVSEEEREAEKEAERLMEQASCWEKEEQEILSSRANSRQSPAKVQ
SKNKYLHSPESRPMAGERGQLMELSKDSSEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDDDEEENIQSSPPR
LTKPQSVAIKRKRPFVLKKKRGRKRRRINSSVTTETISETTEVLNEPFDNSDEERPMPHLEPTCEIEVEEDGGKPALRKA
FQHQPGKKRQTEEDDEKDNHCFKSADPCRNNTDDDTDNLKDSSRDNPEPLKCKQVWPKGTKRGLSKWRPNKERKTGFKLN
LYTPPETPMEPDDQITVEEQKETPGDKTSPTPTRIEEEVKETTEPLLPRDENRRDETCAPVSPNKSPGEKPEDDLIKPEE
EEEEEEEEEDEEEEEEEEEEEEEEEENVEKDPGGAKNQEKEEPEVCLDKEDPVPLDDHEEEEEDEEPSHNEGHDADDEDD
SHMECTEVEKEERPREAFKEVLENQEAFLDLSVQPSHSNSEVLMDCGVDLAAACNGEPKELAGDPDAAPESDEELPEEQA
QKQDRKSSEEAGPEFKERNSATMEIDSETVQAVQSLTQENNEQDDTFQDCAETQEACRSLQNYTHADQSPQIATTLDDCQ
QSDHSSPVSSVHSHPGQSVRSVNSPSVPALENSYAQISPDQSAISVPSLQNMETSPMMDVPSVSDHSQQVVDSGFSDLGS
IESTTENYENPSSYDSTMGGSICGNGSSQNSCSYSSLTSSNLTQSSCAVTQQMSNISGSCSMLQQTSISSPPTCSVKSPQ
GCVVERPPSSSQQLAQCSMAANFTPPMQLAEIPETGSANLGLYERMGQSDFGAGHYPQPSATFSLAKLQQLTNTLIDHSL
PYSHSAAVTSYANSASLSTPLSNTGLVQLSQSPHSVPGGPQAQATMTPPPNLTPPPMNLPPPLLQRNMAASNIGISHSQR
LQTQIASKGHVSMRTKSASLSPAAATHQSQIYGRSQTVAMQGPARTLTMQRGMNMSVNLMPAPAYNVNSVNMNMNTLNAM
NGYSMSQPMMNSGYHSNHGYMNQTPQYPMQMQMGMMGTQPYAQQPMQTTPHGNMMYTAPGHHGYMNTGMSKQSLNGSYMR
R
```

1070 - 1089:	EEEEEEEEEEEEEEEEEEEE
1071 - 1090:	EEEEEEEEEEEEEEEEEEEE
1072 - 1091:	EEEEEEEEEEEEEEEEEEEE
1073 - 1092:	EEEEEEEEEEEEEEEEEEEE
1074 - 1093:	EEEEEEEEEEEEEEEEEEEE
1075 - 1094:	EEEEEEEEEEEEEEEEEEEE
1076 - 1095:	EEEEEEEEEEEEEEEEEEEE
1077 - 1096:	EEEEEEEEEEEEEEEEEEEE
1078 - 1097:	EEEEEEEEEEEEEEEEEEEE
1079 - 1098:	EEEEEEEEEEEEEEEEEEEE
1080 - 1099:	EEEEEEEEEEEEEEEEEEEE
1081 - 1100:	EEEEEEEEEEEEEEEEEEEE
1082 - 1101:	EEEEEEEEEEEEEEEEEEEE

1083 - 1102:	EEEEEEEEEEEEEEEEEEEE
1084 - 1103:	EEEEEEEEEEEEEEEEEEEE
1085 - 1104:	EEEEEEEEEEEEEEEEEEEE
1086 - 1105:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9JFB8 **A0A2Y9JFB8_ENHLU** (1316 aa)
LOW QUALITY PROTEIN: tau-tubulin kinase 1. *Enhydra lutris kenyoni*

```
MQCLAAALKDETNMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTRENVALKVESAQQPKQVLKMEVAV
LKKLQGKSHVCRFIGCGRNEKFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESIEAIHSVGFLHRDIKPSNF
AMGRLPSTYRKCYMLDFGLARQYTNTTGDVRPPRNVAGFRGTVRYASVNAHKNREMGRHDDLWSLFYMLVEFAVGQLPWR
KIKDKEQVGMIKEKYEHRMLLKHMPSEFHLFLDHIASLDYFTKPDYQLIMSVFENSMKERGIAENEAFDWEKAGTDALLS
TSTSTPPQQNTRQTAAMFGVVNVTPVPGDLLRENTEDVLQGEHLSDQENAPPILPGRPSEGLGPSPHLAPHPGGPEAEVW
EETDVNRNKLRINIGKTPCVVEEEQSRGVGVPSSPVRAPPDSPTTPVRSLRYRRVNSPESERLSTADGRVELHERRSRMD
LPGSPSRQACSSQPAQMLSVDTGHPDRQASGRMDVSASVEQEALSNAFRSVPLAEEEDFDSKEWVIIDKETELKDFPPGA
EPSTSGTTDEEPEELRPLPEEGEERRRPGTEPTVRPRGRGVHTLAEEDPRQTPFQPPPPQLSQVEGRSETSQPPTPGSPS
HSPLHSGPRPRRRESDPTGPQRQVFSVAPPFEVNGLPRAVPLSLPYQDFKKDLSDYRERARLLNRVRRVGFSHMLLTTPQ
VPLAPVQPQANGKDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAVALGEVLRPRSGSSSEGSERSTDR
SQEGAPSTLLADDQKESRGRASMADGDLEPEEGSKTLVLVSPGDMKKSPVTADLAPDPDLGTLAALTPQQERPQPTGSQL
DVSEPGTLSSVLKSEPKPPGPGTGQGAGAVTTGAGGVAVTSSPFTKVERTFVHIAEKTHLNVMSSGGQASRPEELGTGGE
LGLEAPSDGRAVEEGASLPLENGIAQSGLESGALASAPRDTPPEVATDSLPSGPALANGPTPVSPLEPGPEKLATISPSR
HAMAGARPRSRIPVLLSEEDTGSEPSGSLSAKERWGKRVRPQQDLARLVMEKRQGRLLLRLASGASSSSSEEQRRASETL
SGTGSEEDMPASEPAAPRKAGRAAATRSRIPRPISIRMPTPAAAQQPSAASRPHGAAPASDTAITSRLQLQKPPGSAVAA
DLRPKQPPGRGPGPGRAPAGTRPPAPRSPGPSASAAPRHPSASPRSQSLSRKESSSPSHQARPTGPPPRGAPQARAQPDG
TPSPGGPKKGPRGKLQTQRAATKGRAGVAEGRAGAR
```

735 - 754:	EEEEEEEEEEEEEEEEEEEE
736 - 755:	EEEEEEEEEEEEEEEEEEEE
737 - 756:	EEEEEEEEEEEEEEEEEEEE
738 - 757:	EEEEEEEEEEEEEEEEEEEE
739 - 758:	EEEEEEEEEEEEEEEEEEEE
740 - 759:	EEEEEEEEEEEEEEEEEEEE
741 - 760:	EEEEEEEEEEEEEEEEEEEE
742 - 761:	EEEEEEEEEEEEEEEEEEEE
743 - 762:	EEEEEEEEEEEEEEEEEEEE
744 - 763:	EEEEEEEEEEEEEEEEEEEE
745 - 764:	EEEEEEEEEEEEEEEEEEEE
746 - 765:	EEEEEEEEEEEEEEEEEEEE
747 - 766:	EEEEEEEEEEEEEEEEEEEE
748 - 767:	EEEEEEEEEEEEEEEEEEEE
749 - 768:	EEEEEEEEEEEEEEEEEEEE
750 - 769:	EEEEEEEEEEEEEEEEEEEE
751 - 770:	EEEEEEEEEEEEEEEEEEEE
752 - 771:	EEEEEEEEEEEEEEEEEEEE
753 - 772:	EEEEEEEEEEEEEEEEEEEE
754 - 773:	EEEEEEEEEEEEEEEEEEEE
755 - 774:	EEEEEEEEEEEEEEEEEEEE
756 - 775:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9JKQ7 **A0A2Y9JKQ7_ENHLU** (745 aa)
YTH domain-containing protein 1 isoform X1. *Enhydra lutris kenyoni*

```
MLNGNDFSLFLIFLLSDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDLKRQKPSVHSRQLISKP
LSSSASNNKRIVSTKGKSVAEYKNEEYQRSERSKRLEADRKIRLSSNASREPYKSQPEKTCLRKRDPERRTKSPTPDDSE
RIGLEVDRRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEEE
EEEEEEEEEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPI
VFDRSGSSASESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAA
FRSARSVILIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKP
VKIGRDGQEIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPR
IDYAPEFHQRPGYLKDPRYQEVDSFTNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMAPYPGMEQPPHHPY
YQHHAPPPQAHPPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRG
RDRERERERLCDRDRDRGERGRYRR
```

236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE
239 - 258:	EEEEEEEEEEEEEEEEEEEE

240 - 259:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9JL33 **A0A2Y9JL33_ENHLU** (712 aa)
YTH domain-containing protein 1 isoform X5. *Enhydra lutris kenyoni*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDLKRQKPSVHSRQLISKPLSSSASN
NKRIVSTKGKSVAEYKNEEYQRSERSKRLEADRKIRLSSNASREPYKSQPEKTCLRKRDPERRTKSPTPDDSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEEE
EEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGS
SASESYADQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSARSVILIFSVRESGKFQGFARL
SSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLLFPPD
ESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYAPEFHQRPGYLKDPRYQEVDRR
FSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMAPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHHPVPHEARYRDKRVHD
YDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDRGERGRYRR
```

229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9JM60 **A0A2Y9JM60_ENHLU** (730 aa)
YTH domain-containing protein 1 isoform X4. *Enhydra lutris kenyoni*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDLKRQKPSVHSRQLISKPLSSSASN
NKRIVSTKGKSVAEYKNEEYQRSERSKRLEADRKIRLSSNASREPYKSQPEKTCLRKRDPERRTKSPTPDDSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEEE
EEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGS
SASESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSARSV
ILIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDG
QEIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYAPEF
HQRPGYLKDPRYQEVDRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMAPYPGMEQPPHHPYYQHHAPPPQAHPPYS
GHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDR
DRGERGRYRR
```

229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9JQ30 **A0A2Y9JQ30_ENHLU** (738 aa)
YTH domain-containing protein 1 isoform X2. *Enhydra lutris kenyoni*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDLKRQKPSVHSRQLISKPLSSSASN
NKRIVSTKGKSVAEYKNEEYQRSERSKRLEADRKIRLSSNASREPYKSQPEKTCLRKRDPERRTKSPTPDDSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEEE
EEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGS
SASESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSARSV
ILIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDG
QEIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYAPEF
HQRPGYLKDPRYQEVDSFTNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMAPYPGMEQPPHHPYYQHHAPP
PQAHPPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERER
ERLCDRDRDRGERGRYRR
```

229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9JVD4 **A0A2Y9JVD4_ENHLU** (737 aa)
YTH domain-containing protein 1 isoform X3. *Enhydra lutris kenyoni*

```
MLNGNDFSLFLIFLLSDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDLKRQKPSVHSRQLISKP
LSSSASNNKRIVSTKGKSVAEYKNEEYQRSERSKRLEADRKIRLSSNASREPYKSQPEKTCLRKRDPERRTKSPTPDDSE
RIGLEVDRRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEEE
EEEEEEEEEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPI
VFDRSGSSASESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAA
FRSARSVILIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKP
VKIGRDGQEIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPR
IDYAPEFHQRPGYLKDPRYQEVDRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMAPYPGMEQPPHHPYYQHHAPPP
QAHPPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERE
RLCDRDRDRGERGRYRR
```

236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE
239 - 258:	EEEEEEEEEEEEEEEEEEEE
240 - 259:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9JYY8 **A0A2Y9JYY8_ENHLU** (1212 aa)
histone-lysine N-methyltransferase EHMT2 isoform X3. *Enhydra lutris kenyoni*

```
MAAAAGAAAAAAAAEGEAPAEMGALVLEKEPRGATERVHGSLGDTPRNEETLPKASPNSLEPAGPSSPASVTVTVGDEGAD
TPVGAAPLIGDEPENLEGDGDLHGGRILLGHATKSFPSSPSKGGTCPSRAKMSMTGTGKSPPSVQSLAMRLLSMPGAQGA
ATAGPEPPVATPSPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKMTSEVAKRRKLNAGGGLSEEL
GSTRGSGEVTMEKGGPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEE
EEEEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEG
TLSPNHAGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALM
VLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPWGDGVTPPA
GTAAPAPPPLAQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPPGPGREALEKALVI
QESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQ
RTPLMEAVVNNHLEAARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHI
EVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPE
LRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCE
TSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKV
RLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPN
IIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPEL
LPELSSLPPVNP
```

300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE
306 - 325:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9JZ85 **A0A2Y9JZ85_ENHLU** (1178 aa)
histone-lysine N-methyltransferase EHMT2 isoform X4. *Enhydra lutris kenyoni*

```
MAAAAGAAAAAAAAEGEAPAEMGALVLEKEPRGATERVHGSLGDTPRNEETLPKASPNSLEPAGPSSPASVTVTVGDEGAD
TPVGAAPLIGDEPENLEGDGDLHGGRILLGHATKSFPSSPSKGGTCPSRAKMSMTGTGKSPPSVQSLAMRLLSMPGAQGA
ATAGPEPPVATPSPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKMTSEVAKRRKLNAGGGLSEEL
GSTRGSGEVTMEKGGPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEE
EEEEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEA
PKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPD
FRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPWGDGVTPPAGTAAPAPPPLAQDAPGRADTSQPSARMRGHGEPR
RPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPPGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLD
NLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEAARYMVQRGGCVYSKEEDGS
TCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAA
IAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVG
NRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSI
RCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELI
SDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGF
DYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELSSLPPVNP
```

300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE
306 - 325:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9JZR3 **A0A2Y9JZR3_ENHLU** (1235 aa)
histone-lysine N-methyltransferase EHMT2 isoform X2. *Enhydra lutris kenyoni*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWAPQLPTGLTSPPIPCVPCQGEAPAEMGA
LVLEKEPRGATERVHGSLGDTPRNEETLPKASPNSLEPAGPSSPASVTVTVGDEGADTPVGAAPLIGDEPENLEGDGDLH
GGRILLGHATKSFPSSPSKGGTCPSRAKMSMTGTGKSPPSVQSLAMRLLSMPGAQGAATAGPEPPVATPSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKMTSEVAKRRKLNAGGGLSEELGSTRGSGEVTMEKGGPGSLEEWE
TVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRK
AKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGE
LSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPH
CGEDASEAQEVTIPWGDGVTPPAGTAAPAPPPLAQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNG
GCLSAVGLPPGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQK
GSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEAARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQ
VDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPL
HIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPI
PCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIF
ECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGE
VYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKC
KHSAEAIALEQSRLARLDPHPELLPELSSLPPVNP
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9K436 **A0A2Y9K436_ENHLU** (1128 aa)
sodium/potassium/calcium exchanger 1 isoform X1. *Enhydra lutris kenyoni*

```
MGKLIRMGTRERRLLWPKRLHWSRLLFLLGTLIIGSTYQHLRSPRGLPSLWAAVSSQNPVKLASRDLSNNDMMMVSSDPL
RASSEMAGDTLVPQATVGRGEATPGITMENTPNPPRRIANITPTTPKNNYNLTAADTERVEEDTTTTPSRVLNHYTPTSS
RPTVKNHTSATPPSREMQSYHPTQTGRKVKKYTPSPLGGIVDNYAPFTLMTMTKSHGITPRTTVKDSETMTTTKILKTNP
TKRMVEETTPTTLKGIIHTTPTFLVNDIETNILTSPRSMIEENTLTTTRRVDNNRSTKPRGLVRKNKLTAPLETVLGDTT
AISEGQVTIRTTTGSSPTETKTSTATWSISNPLSRTSALTTGISSTTFWGLAKRTSTAPRPSASSEARANPTIQVHHCVV
VEPAPAVPPATSPSLTTAMIPEVPSSSPSALPPGWPDLHAKGEYPPDLFSIEQRQQGWVALHIFGMIYVFVALAIVCDEY
FVPALGVITDKLQISDDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCALFSREILNLTWW
PLFRDVSFYILDLIMLIIFFLDSLIAWWESLLLLLGYAFYVFTMKWNKEVEVWVKEQLSRRPVAKVMALGDLSKPGYGAV
MVNELQENKRDKVVLPAVLTRERSLASLHNSTIRSPIFQLMLHSLDPLGEARHSKDKEEESLSKQAKAKPHAKAQNKPEE
EEPAQLPEATVTPAPAPEVKGDQEEDPGGQEGEVAEAESTGEVTGKEAEAPGRGENGQQGGGETQLEGEGEIEAEGEGEH
EGEIEEGKCINECDPGGELQAEGKATDDGGGELQAEDGDMKADEGENEEQELNAERKSEAKSDEKDRDAEGGGEGHGSED
EKEEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEANEEPLSLEWPETRKKQAIYLFLLPIVFPLWLTVPDVRRL
ESKKFFVLTFLGSVVWIAMFSYLMVWWAHQVGETVGISEEIMGLTILAAGTSIPDLITSVIVARKGLGDMAVSSSVGSNI
FDITVGLPAPWLLFSLINGLQPVPVSSNGLFCAIVLLFLMLLFVISSIASCKWRMNKILGFTMFLLYFVFLIISVMLEDR
IISCPVSV
```

888 - 907:	EEEEEEEEEEEEEEEEEEEE
889 - 908:	EEEEEEEEEEEEEEEEEEEE
890 - 909:	EEEEEEEEEEEEEEEEEEEE
891 - 910:	EEEEEEEEEEEEEEEEEEEE
892 - 911:	EEEEEEEEEEEEEEEEEEEE
893 - 912:	EEEEEEEEEEEEEEEEEEEE
894 - 913:	EEEEEEEEEEEEEEEEEEEE
895 - 914:	EEEEEEEEEEEEEEEEEEEE
896 - 915:	EEEEEEEEEEEEEEEEEEEE
897 - 916:	EEEEEEEEEEEEEEEEEEEE
898 - 917:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9K4B4 **A0A2Y9K4B4_ENHLU** (1112 aa)
sodium/potassium/calcium exchanger 1 isoform X2. *Enhydra lutris kenyoni*

```
MGKLIRMGTRERRLLWPKRLHWSRLLFLLGTLIIGSTYQHLRSPRGLPSLWAAVSSQNPVKLASRDLSNNDMMMVSSDPL
RASSEMAGDTLVPQATVGRGEATPGITMENTPNPPRRIANITPTTPKNNYNLTAADTERVEEDTTTTPSRVLNHYTPTSS
RPTVKNHTSATPPSREMQSYHPTQTGRKVKKYTPSPLGGIVDNYAPFTLMTMTKSHGITPRTTVKDSETMTTTKILKTNP
TKRMVEETTPTTLKGIIHTTPTFLVNDIETNILTSPRSMIEENTLTTTRRVDNNRSTKPRGLVRKNKLTAPLETVLGDTT
AISEGQVTIRTTTGSSPTETKTSTATWSISNPLSRTSALTTGISSTTFWGLAKRTSTAPRPSASSEARANPTIQVHHCVV
VEPAPAVPPATSPSLTTAMIPEVPSSSPSALPPGWPDLHAKGEYPPDLFSIEQRQQGWVALHIFGMIYVFVALAIVCDEY
FVPALGVITDKLQISDDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCALFSREILNLTWW
PLFRDVSFYILDLIMLIIFFLDSLIAWWESLLLLLGYAFYVFTMKWNKEVEVWVKEQLSRRPVAKVMALGDLSKLPAVLP
AVLTRERSLASLHNSTIRSPIFQLMLHSLDPLGEARHSKDKEEESLSKQAKAKPHAKAQNKPEEEEPAQLPEATVTPAPA
PEVKGDQEEDPGGQEGEVAEAESTGEVTGKEAEAPGRGENGQQGGGETQLEGEGEIEAEGEGEHEGEIEEGKCINECDPG
GELQAEGKATDDGGGELQAEDGDMKADEGENEEQELNAERKSEAKSDEKDRDAEGGGEGHGSEDEKEEEEKEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEDEEANEEPLSLEWPETRKKQAIYLFLLPIVFPLWLTVPDVRRLESKKFFVLTFLGSVVW
IAMFSYLMVWWAHQVGETVGISEEIMGLTILAAGTSIPDLITSVIVARKGLGDMAVSSSVGSNIFDITVGLPAPWLLFSL
INGLQPVPVSSNGLFCAIVLLFLMLLFVISSIASCKWRMNKILGFTMFLLYFVFLIISVMLEDRIISCPVSV
```

872 - 891:	EEEEEEEEEEEEEEEEEEEE
873 - 892:	EEEEEEEEEEEEEEEEEEEE
874 - 893:	EEEEEEEEEEEEEEEEEEEE
875 - 894:	EEEEEEEEEEEEEEEEEEEE
876 - 895:	EEEEEEEEEEEEEEEEEEEE
877 - 896:	EEEEEEEEEEEEEEEEEEEE
878 - 897:	EEEEEEEEEEEEEEEEEEEE
879 - 898:	EEEEEEEEEEEEEEEEEEEE
880 - 899:	EEEEEEEEEEEEEEEEEEEE
881 - 900:	EEEEEEEEEEEEEEEEEEEE
882 - 901:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9K8W5 **A0A2Y9K8W5_ENHLU** (1098 aa)
sodium/potassium/calcium exchanger 1 isoform X3. *Enhydra lutris kenyoni*

```
MGKLIRMGTRERRLLWPKRLHWSRLLFLLGTLIIGSTYQHLRSPRGLPSLWAAVSSQNPVKLASRDLSNNDMMMVSSDPL
RASSEMAGDTLVPQATVGRGEATPGITMENTPNPPRRIANITPTTPKNNYNLTAADTERVEEDTTTTPSRVLNHYTPTSS
RPTVKNHTSATPPSREMQSYHPTQTGRKVKKYTPSPLGGIVDNYAPFTLMTMTKSHGITPRTTVKDSETMTTTKILKTNP
TKRMVEETTPTTLKGIIHTTPTFLVNDIETNILTSPRSMIEENTLTTTRRVDNNRSTKPRGLVRKNKLTAPLETVLGDTT
AISEGQVTIRTTTGSSPTETKTSTATWSISNPLSRTSALTTGISSTTFWGLAKRTSTAPRPSASSEARANPTIQVHHCVV
VEPAPAVPPATSPSLTTAMIPEVPSSSPSALPPGWPDLHAKGEYPPDLFSIEQRQQGWVALHIFGMIYVFVALAIVCDEY
FVPALGVITDKLQISDDVAGATFMAAGGSAPELFTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCALFSREILNLTWW
PLFRDVSFYILDLIMLIIFFLDSLIAWWESLLLLLGYAFYVFTMKWNKEVEVWVKEQLSRRPVAKVMALGDLSKPGYGAV
MVNELQENKRDKVVLPAVLTRERSLASLHNSTIRSPIFQLMLHSLDPLGEARHSKDKEEESLSKQAKAKPHAKAQNKPEE
EEPAQLPEATVTPAPAPEVKGDQEEDPGGQEGEVAEAESTGEVTGKEAEAPGRGENGQQGGGETQLEGEGEIEAEGEGEH
EGEIEEGKCINECDPGGELQAEGKATDDGGGELQAEDGDMKADEGENEEQELNAERKSEAKSDEKDRDAEGGGEGHGSED
EKEEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEANEEPLSLEWPETRKKQAIYLFLLPIVFPLWLTVPDVRRL
VGETVGISEEIMGLTILAAGTSIPDLITSVIVARKGLGDMAVSSSVGSNIFDITVGLPAPWLLFSLINGLQPVPVSSNGL
FCAIVLLFLMLLFVISSIASCKWRMNKILGFTMFLLYFVFLIISVMLEDRIISCPVSV
```

888 - 907:	EEEEEEEEEEEEEEEEEEEE
889 - 908:	EEEEEEEEEEEEEEEEEEEE
890 - 909:	EEEEEEEEEEEEEEEEEEEE
891 - 910:	EEEEEEEEEEEEEEEEEEEE
892 - 911:	EEEEEEEEEEEEEEEEEEEE
893 - 912:	EEEEEEEEEEEEEEEEEEEE
894 - 913:	EEEEEEEEEEEEEEEEEEEE
895 - 914:	EEEEEEEEEEEEEEEEEEEE
896 - 915:	EEEEEEEEEEEEEEEEEEEE
897 - 916:	EEEEEEEEEEEEEEEEEEEE
898 - 917:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9KA49 **A0A2Y9KA49_ENHLU** (1269 aa)
histone-lysine N-methyltransferase EHMT2 isoform X1. *Enhydra lutris kenyoni*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWAPQLPTGLTSPPIPCVPCQGEAPAEMGA
LVLEKEPRGATERVHGSLGDTPRNEETLPKASPNSLEPAGPSSPASVTVTVGDEGADTPVGAAPLIGDEPENLEGDGDLH
GGRILLGHATKSFPSSPSKGGTCPSRAKMSMTGTGKSPPSVQSLAMRLLSMPGAQGAATAGPEPPVATPSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKMTSEVAKRRKLNAGGGLSEELGSTRGSGEVTMEKGGPGSLEEWE
TVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRK
AKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFE
ELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFC
TAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPWGDGVTPPAGTAAPAPPPLAQDAPGRADTSQP
SARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPPGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQG
ELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEAARYMVQRG
```

```
GCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENIC
LHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFAL
QLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCS
SSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQG
TFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSS
RDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELSSLPPVNP
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9KA55 **A0A2Y9KA55_ENHLU** (989 aa)
histone-lysine N-methyltransferase EHMT2 isoform X5. *Enhydra lutris kenyoni*

```
MGALVLEKEPRGATERVHGSLGDTPRNEETLPKASPNSLEPAGPSSPASVTVTVGDEGADTPVGAAPLIGDEPENLEGDG
DLHGGRILLGHATKSFPSSPSKGGTCPSRAKMSMTGTGKSPPSVQSLAMRLLSMPGAQGAATAGPEPPVATPSPEGQPKV
HRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKMTSEVAKRRKLNAGGGLSEELGSTRGSGEVTMEKGGPGSLE
EWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSG
RRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETER
GFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCG
YFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQ
DSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARE
SYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGV
DGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQAC
SCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDA
RYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEA
IALEQSRLARLDPHPELLPELSSLPPVNP
```

280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9KJ54 **A0A2Y9KJ54_ENHLU** (813 aa)
disintegrin and metalloproteinase domain-containing protein 1a-like. *Enhydra lutris kenyoni*

```
MSAAASLRQSASSSSSLQKYQVAACGAGRVLPAWAPQMKGWRRAPEVPGPSCVRLGIMLVLVLIFLPGLYCDPGSVYYSS
YETVIPKSLTVKGREDPGEKASYTLLMQGQKQVIQLKVKRDYFVNNFPVFSYHNGVLGQEVPFISHDCHYEGYIEGVPGS
FVSLNTCSGLRGILIKEGKPYGIEPTDTSERFEHVLYTMAPQARVSCSVTSRGSQVVSTSRQQGSRKPRSLQALPSFWSH
TKYVEMFVVVSNLRFQMWGSNVDETVQRVMDITALANIFTRGINTQVVLAGMEIWTEGDLIEVPADLRVTLRNFNSWRQE
KLFPRVKHDVAHMIVGHHPEDDVGQAFLNGACSRGFAAAVESFHHEDVLLFAALMAHELGHNLGIQHDHSACTCKDKRFC
LMRENITKESGFSNCSSDHFYQFLREHKGACLFNKPQPQGRLRRQATCGNGVLEMYEECDCGPDCGNNLCCDETCRLKAT
ALCSSGPCCNETCGFVEKGIMCRSAFGECDLPEYCDGNSDRCPTNTYKQDGTPCERVHYCIEGLCKTADFQCVNVFGYPA
RSAPEDCYISMNTKGDRFGNCGLPTSDNQEYVKCTAENIYCGKIICTNVKHVPVVKPMHTMIQVPHRDDWCWSMDAFNNT
DIPDDGDVDAGTRCAPEKICLNYSCIDHAVLNYDCEPRRMCNGRGVCNNLKHCHCEAGYAPPDCTTIGTGGSVDSGSPVV
QRESESAFNVAKHEHLTDNMIIIFLIVFFLLLILVTAFISLLCKHSRKAPPEPKEKGSEEAAEEVQPEEEEEEEEEEEEE
EEEEEEEEEESEP
```

788 - 807:	EEEEEEEEEEEEEEEEEEEE
789 - 808:	EEEEEEEEEEEEEEEEEEEE
790 - 809:	EEEEEEEEEEEEEEEEEEEE
791 - 810:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9KSQ4 **A0A2Y9KSQ4_ENHLU** (366 aa)
Sodium/potassium-transporting ATPase subunit beta. *Enhydra lutris kenyoni*

```
MRRQLRSRRAPASPYGYRSRLDDQDEVNQNYLADEEEEAEEEARVMVVPDLEEEEEEEEEEEEEEEEEEEEEEEEEAKAEE
KGQGQPAGNAWWQRWQIVNEYLWDPEKRMSLARTGQSWSLILVIYFFFYASLAAVVTLCMYTLFLTISPYMPTFTERVKP
PGVMIRPFAHSLNFNFNVSEPDTWQHYVISLNGFLQGYNDSLQEEMNVDCPPGQYFIQDGDEEEDKKACQFKRSFLKNCS
GLEDPTFGYSTGQPCILLKMNRIVGFRPELGDPVKVSCKVQRGDENDIRSINYYPESASFDLRYYPYYGKLTHVNYTSPL
VAMHFTDVVKNQAVPVQCQLKGKGIINDVINDRFVGRVIFTLNIET
```

52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE

54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9KYP0 **A0A2Y9KYP0_ENHLU** (362 aa)
Sodium/potassium-transporting ATPase subunit beta. *Enhydra lutris kenyoni*

```
MRRQLRSRRAPASPYGYRSRLDDQDEVNQNYLADEEEEAEEEARVMVVPDLEEEEEEEEEEEEEEEEEEEEEEEAKAEE
KGQGQPAGNAWWQRWQIVNEYLWDPEKRMSLARTGLILVIYFFFYASLAAVVTLCMYTLFLTISPYMPTFTERVKPPGVM
IRPFAHSLNFNFNVSEPDTWQHYVISLNGFLQGYNDSLQEEMNVDCPPGQYFIQDGDEEEDKKACQFKRSFLKNCSGLED
PTFGYSTGQPCILLKMNRIVGFRPELGDPVKVSCKVQRGDENDIRSINYYPESASFDLRYYPYYGKLTHVNYTSPLVAMH
FTDVVKNQAVPVQCQLKGKGIINDVINDRFVGRVIFTLNIET
```

52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9L299 **A0A2Y9L299_ENHLU** (1131 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Enhydra lutris kenyoni*

```
MAAAVLSGPSAGSAAGVPGGTGGLSAVGSGPRLRLLLLESVSGLLQPRAGGAVAPVHPPVRSAPHLPGLMCLLRLHGTVG
GAQNLSAVGALVGLSNARLGSIKTRFEGLCLLSLLVGESPTEMFQQHCVSWLRSIQQVLQSQDPPPTMELAVAVLRDLLR
YAAQLPTLFRDISMNHLPGLLTSLLGLRPECELSALEGMKACMTYFPRACGSLKGKLASFFLSRVDALSPQLQQLACECY
SKLPSLGAGFSQGLKHTESWEQELRSLLASLHSLLGALYEGAETTPMQYEGPGVEMLLTPSEDGDAHVLLRLRQRFCGLA
RCLGLMLSSEFGAPVSVPVQEILDVICRALSISAKSISLLGDGPLRLLLLPSIHLDALDLLSALILACGGRLLRFGALIS
RLLPQVLNAWNLGRDTLSPGQERPYSTVRAKVYAVLELWVQVCGASAGVLQGGASGEALLSHLLSDISPPADTLKLRSPR
GSPDGGLQSGKPSAPKKLKLDMGEATAPPSHRKGDSNANSDVCAAALRGLSRTVLMCGPLIKEETHRRLHELVLPLVMGV
QQGEALGSSPYTSSRCRRELYHLLLALLLAPAPRCPPPLSCAVQAFSLGQREDSLEVASFCSEALVTCAALTHPRVPPLQ
SVGPACPTPAPAPPPEAPSPFRAPPFHPPGPMPSVGPMPSVGPMPSAGAMPPTGPLPPAGPMPPPRPGPPAANHLGLSVP
GLVSVPPRLLPGPENHRAGSNEDPVLAPSGTPPPTIPPDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDSVVIVPEG
LPPLPPSGTTPPPVAPAGPPTASPPGPAKEEPEELPAAPGPLPPPPPPPVPGPVALPPPQLVPEGTPGSGGPPGLEEDLT
VININSSDEEEEEEEEEEEEEEEEEEEEEEDFEEEEEDEEEYFEEEEEEEEEFEEEFEEEEGELEEEEEDEEEEEEELEEL
EEVEFGPAGAPAEGSGPPPPSPPPELPPAQSPKAQPEPEVEPGLLLEVEEPGAEEGPGAEAAPTLVPEVLPSQGEGPRDA
KSPPAGPPPQELVEEEPSAPPTLLEEGTESGGDEVPVPPETPAAADVEAEAEAETAALPEKEQDDAAAMLADFIDCPPDD
EKPPPAPEPDS
```

889 - 908:	EEEEEEEEEEEEEEEEEEEE
890 - 909:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9L5C6 **A0A2Y9L5C6_ENHLU** (768 aa)
phospholipid phosphatase-related protein type 3 isoform X4. *Enhydra lutris kenyoni*

```
MIATKEKNKSPKDSMTLLPCFYFVELPIVASSIVSLYFLELTDLFKPAKVGFQCYDRALSMPYVGTNEELIPLLMLLSLA
FAAPAASIMVGEGLLYCAQSRLWGRGGGPGEAEGSISAGGCSFNSFLRRTVRFVGVHVFGLCATALVTDVIQLATGYHAP
FFLTVCKPNYTLLGTSCEANPYITQDICAGHDTHAILSARKTFPSQHATLSAFAAVYVSVSPGPPPARPRPALCPAPPGG
GRALTRPAPPRPQMYFNSVISDTTKLLKPILVFAFAIAAGVCGLTQITQYRSHPVDVYAGFLIGAGIAAYLACHAVGNFQ
APTTEKPTALAPAKDALRALTQRGHDSVYQQNKSVSTDELGPPGRLEGGPRPVAREKTSLGSLKRASVDVDLLAPRSPMG
KENMVTFSHTLPRVSTPSLDDPARRHMTIHVPLDASRSKQLISEWKQKSLEGRGLGLPDEASPGHLRAPTEPMAEEEEEE
EEEEEEEEEEEEEEEGEEGGRAPPSLYPTVQARPGLGPRVILPPRSGPQPLVHIPEEGAQAATGLSPKSSATVRAKWLMM
AEKSGAAAAASAQPRVANPPRLLQVIAMSKAPGGPGPKVAETASSSSASSDSSQYRSPSDRDSASTVTIDAHAPHHPVVH
LSAGNGPWEWKTAGSTAKGVEGEGGYELGDLARSFRMGPKPPGVSPGSSVSDVDQEEPRFGAVATVNLATGEGLPPLGTA
DGALGPASRESTLRRKAGGLVLGERETAGEAEAESYYRKMHVARRFKD
```

475 - 494:	EEEEEEEEEEEEEEEEEEEE
476 - 495:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9L656 **A0A2Y9L656_ENHLU** (734 aa)
phospholipid phosphatase-related protein type 3 isoform X3. *Enhydra lutris kenyoni*

```
MIATKEKNKSPKDSMTLLPCFYFVELPIVASSIVSLYFLELTDLFKPAKVGFQCYDRALSMPYVGTNEELIPLLMLLSLA
FAAPAASIMVGEGLLYCAQSRLWGRGGGPGEAEGSISAGGCSFNSFLRRTVRFVGVHVFGLCATALVTDVIQLATGYHAP
FFLTVCKPNYTLLGTSCEANPYITQDICAGHDTHAILSARKTFPSQHATLSAFAAVYVSMYFNSVISDTTKLLKPILVFA
FAIAAGVCGLTQITQYRSHPVDVYAGFLIGAGIAAYLACHAVGNFQAPTTEKPTALAPAKDALRALTQRGHDSVYQQNKS
VSTDELGPPGRLEGGPRPVAREKTSLGSLKRASVDVDLLAPRSPMGKENMVTFSHTLPRVSTPSLDDPARRHMTIHVPLD
ASRSKQLISEWKQKSLEGRGLGLPDEASPGHLRAPTEPMAEEEEEEEEEEEEEEEEEEEEEEGEEGGRAPPSLYPTVQARP
GLGPRVILPPRSGPQPLVHIPEEGAQAATGLSPKSSATVRAKWLMMAEKSGAAAAASAQPRVANPPRLLQVIAMSKAPGG
PGPKVAETASSSSASSDSSQYRSPSDRDSASTVTIDAHAPHHPVVHLSAGNGPWEWKTAGSTAKGVEGEGGYELGDLARS
FRMGPKPPGVSPGSSVSDVDQEEPRFGAVATVNLATGEGLPPLGTADGALGPASRESTLRRKAGGLVLGERETAGEAEAE
SYYRKMHVARRFKD
```

441 - 460:	EEEEEEEEEEEEEEEEEEEE
442 - 461:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9L7V0 **A0A2Y9L7V0_ENHLU** (1312 aa)
splicing factor, arginine/serine-rich 19. *Enhydra lutris kenyoni*

```
MEEEDESRGKTEESGEDRGDGPPDRDPTLSPSAFILRAIQQAVGSSLQGDLPNDKDGSRCHGLRWRRCRSPRSEPRSQES
GGTDTATVLDMAADSFLAGLVSVLDPPDTWVPSHLDLRPGESEDMLELVAEVRIGDRDPIPLPVPSLLPRLRAWRTGKTV
SPQPHSSRPSCARHLLTLGTGDGGPAPPPAPSSASSSPSPSPSSSSPSPPPPPPPPAPPAPPAPRFDIYDPFHPTDEAYS
PPPAPEQKYDPFEPTGSNPSSSAGTPSPEEEEEEEEEEEEEEEEEEEEEEEEGLSQSISRISETLAGIYDDNSLSQDFPGD
ESPRPDPQPPQPTPAPGTPPQVDSTRVDGASRRRVFVVGTEAEACREGKVSVEVVTAGGAVIPPTLLPPGDSEIEEGEIV
QPEEEPRVAVSLFRPSGGRAARPPPAAAAPPAAQPPPPPPAPRAPEGDDFLSLHAESDGEGALQVDLGEPAPAPPAADTR
WGGLDLRRKILTQRRERYRQRSPSPAATPAAATAPAGPPTRKKSRRERKRSGGEAKEAASSSSGAAPAPPAPASPWDSKK
HRSRDRKPGSHASSSARRRSRSARRRSRSTDRRRGGSRRSRSREKRRRRRRSASPPPATSSSSSSRRERHRGKHRDGGGS
KKKKKRSRSRGEKRSGDSEKAPVPTQPPSGSSSLGGERDSRRRGAVPPSIQDLTDHDLFAIKRTITVGRPDKPDPRGPSP
APASSPKREVLYDSEGLSAEERGGKSSEKDRRRSGAASSSSSSREKGSRRKALDGGDRDRDRDRDRDRDRSSKKVRPPKE
SAASSGPPPKPPVSSGSGSSSSSCSSSSRKVKLQSKVAVLIREGVSSTTPAKEAASAGLGSIGVKFSRDRESRSPFLKPD
ERAPTEVAKAAPGSTKPKKTKVKAKAGAKKAKGTKGKTKPSKTRKKIRSGGSSGGSGGPVMLKKSKADSCSQAAGAKGVE
ETSWSGEERAAKAPSTPPPKAAPPPPALTPDSQTVDSSCKTPEVSFLPEEAAEEAGVRGGAEEEEEEEEEEEEEEEEEEQ
QPATTTATSTAAAAPSTAPSAGSTAGDSGAEDGPATRVSQLPTLPPPMPWNLPAGVDCTTSGVLALTALLFKMEEANLAS
RAKAQELIQATNQILSHRKPPSSLGVTPAPVPTSLGLPPGPSSYLLPGSLPLGGCGSTPPTPTGLAAASDKREGSSSSEG
RGDTDKYLKKLHTQERAVEEVKLAIKPYYQKKDITKEEYKDILRKAVHKICHSKSGEINPVKVSNLVRAYVQRYRYFRKH
GRKPGDPPGPPRPPKEPGPPDKGGPGLPLPPL
```

269 - 288:	EEEEEEEEEEEEEEEEEEEE
270 - 289:	EEEEEEEEEEEEEEEEEEEE
271 - 290:	EEEEEEEEEEEEEEEEEEEE
272 - 291:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9LCY4 **A0A2Y9LCY4_ENHLU** (755 aa)
phospholipid phosphatase-related protein type 3 isoform X1. *Enhydra lutris kenyoni*

```
MIATKEKNKSPKDSMTLLPCFYFVELPIVASSIVSLYFLELTDLFKPAKVGFQCYDRALSMPYVGTNEELIPLLMLLSLA
FAAPAASIMVGEGLLYCAQSRLWGRGGGPGEAEGSISAGGCSFNSFLRRTVRFVGVHVFGLCATALVTDVIQLATGYHAP
FFLTVCKPNYTLLGTSCEANPYITQDICAGHDTHAILSARKTFPSQHATLSAFAAVYVSMYFNSVISDTTKLLKPILVFA
FAIAAGVCGLTQITQYRSHPVDVYAGFLIGAGIAAYLTALAGLLPGEKSGLQPPPHPQACHAVGNFQAPTTEKPTALAPA
KDALRALTQRGHDSVYQQNKSVSTDELGPPGRLEGGPRPVAREKTSLGSLKRASVDVDLLAPRSPMGKENMVTFSHTLPR
VSTPSLDDPARRHMTIHVPLDASRSKQLISEWKQKSLEGRGLGLPDEASPGHLRAPTEPMAEEEEEEEEEEEEEEEEEEE
EEGEEGGRAPPSLYPTVQARPGLGPRVILPPRSGPQPLVHIPEEGAQAATGLSPKSSATVRAKWLMMAEKSGAAAAASAQ
PRVANPPRLLQVIAMSKAPGGPGPKVAETASSSSASSDSSQYRSPSDRDSASTVTIDAHAPHHPVVHLSAGNGPWEWKTA
GSTAKGVEGEGGYELGDLARSFRMGPKPPGVSPGSSVSDVDQEEPRFGAVATVNLATGEGLPPLGTADGALGPASRESTL
RRKAGGLVLGERETAGEAEAESYYRKMHVARRFKD
```

462 - 481:	EEEEEEEEEEEEEEEEEEEE
463 - 482:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9LID6 **A0A2Y9LID6_ENHLU** (740 aa)
phospholipid phosphatase-related protein type 3 isoform X2. *Enhydra lutris kenyoni*

```
MIATKEKNKSPKDSMTLLPCFYFVELPIVASSIVSLYFLELTDLFKPAKVGFQCYDRALSMPYVGTNEELIPLLMLLSLA
FAAPAASIMVGEGLLYCAQSRLWGRGGGPGEAEGSISAGGCSFNSFLRRTVRFVGVHVFGLCATALVTDVIQLATGYHAP
FFLTVCKPNYTLLGTSCEANPYITQDICAGHDTHAILSARKTFPSQHATLSAFAAVYVSMYFNSVISDTTKLLKPILVFA
FAIAAGVCGLTQITQYRSHPVDVYAGFLIGAGIAAYLPPPHPQACHAVGNFQAPTTEKPTALAPAKDALRALTQRGHDSV
YQQNKSVSTDELGPPGRLEGGPRPVAREKTSLGSLKRASVDVDLLAPRSPMGKENMVTFSHTLPRVSTPSLDDPARRHMT
IHVPLDASRSKQLISEWKQKSLEGRGLGLPDEASPGHLRAPTEPMAEEEEEEEEEEEEEEEEEEEEEGEEGGRAPPSLYP
TVQARPGLGPRVILPPRSGPQPLVHIPEEGAQAATGLSPKSSATVRAKWLMMAEKSGAAAAASAQPRVANPPRLLQVIAM
SKAPGGPGPKVAETASSSSASSDSSQYRSPSDRDSASTVTIDAHAPHHPVVHLSAGNGPWEWKTAGSTAKGVEGEGGYEL
GDLARSFRMGPKPPGVSPGSSVSDVDQEEPRFGAVATVNLATGEGLPPLGTADGALGPASRESTLRRKAGGLVLGERETA
GEAEAESYYRKMHVARRFKD
```

447 - 466:	EEEEEEEEEEEEEEEEEEEE
448 - 467:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9M5M4 **A0A2Y9M5M4_DELLE** (738 aa)
YTH domain-containing protein 1 isoform X1. *Delphinapterus leucas (Beluga whale)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLISKPLSSSVSN
NKRMVSTKGKSVTEYKNEEYQRSERNKRLEADRKIRLSSSASREPYKSQSEKTCLRKRDPERRVKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDDDGEEEEEEEEEEE
EEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGS
SASESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSARSV
ILIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDG
QEIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYAPEF
HQRPGYLKDPRYQEVDSFTNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMTPYPGMEQPPHHPYYQHHAPP
PQAHPPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERER
ERLCDRDRDRGERGRYRR
```

229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE

233 - 252:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9M6R0 **A0A2Y9M6R0_DELLE** (730 aa)
YTH domain-containing protein 1 isoform X2. *Delphinapterus leucas (Beluga whale)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLISKPLSSSVSN
NKRMVSTKGKSVTEYKNEEYQRSERNKRLEADRKIRLSSSASREPYKSQSEKTCLRKRDPERRVKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDDDGEEEEEEEEEEE
EEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGS
SASESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSARSV
ILIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDG
QEIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYAPEF
HQRPGYLKDPRYQEVDRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMTPYPGMEQPPHHPYYQHHAPPPQAHPPYS
GHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDR
DRGERGRYRR
```

229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9M8K6 **A0A2Y9M8K6_DELLE** (720 aa)
YTH domain-containing protein 1 isoform X3. *Delphinapterus leucas (Beluga whale)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLISKPLSSSVSN
NKRMVSTKGKSVTEYKNEEYQRSERNKRLEADRKIRLSSSASREPYKSQSEKTCLRKRDPERRVKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDDDGEEEEEEEEEEE
EEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGS
SASESYADQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSARSVILIFSVRESGKFQGFARL
SSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLLFPPD
ESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYAPEFHQRPGYLKDPRYQEVDSF
TNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMTPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHHPVPHEAR
YRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDRGERGRYRR
```

229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9MED2 **A0A2Y9MED2_DELLE** (712 aa)
YTH domain-containing protein 1 isoform X4. *Delphinapterus leucas (Beluga whale)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLISKPLSSSVSN
NKRMVSTKGKSVTEYKNEEYQRSERNKRLEADRKIRLSSSASREPYKSQSEKTCLRKRDPERRVKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDDDGEEEEEEEEEEE
EEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGS
SASESYADQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSARSVILIFSVRESGKFQGFARL
SSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLLFPPD
ESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYAPEFHQRPGYLKDPRYQEVDRR
FSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMTPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHHPVPHEARYRDKRVHD
YDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDRGERGRYRR
```

229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9MIB0 **A0A2Y9MIB0_DELLE** (1032 aa)
histone-lysine N-methyltransferase EHMT2 isoform X5. *Delphinapterus leucas (Beluga whale)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGTHRGRGRPRSLLSLPRAQASWAPQLPTGLTSSPIPCVPSQGEAPAEMGA
LVLEKEPRGATERVHGSLGDTPRSEEILPKANPDSLETAGPSSPASVTVTVGDEGADTPVGATPLIGDEPENLEGDGDLH
GGRILMGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGATAAGPEPPPATASPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDLHSLGKVTSDVAKRRKLNSGGGLSEELGSARGSREVTLEKGDPGSLEEWE
TVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKA
KKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEE
LPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNSAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCT
AGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLAQDAPGRADTSQPS
ARMRGQGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPPGPGRETLEKALVIQESERRKKLRFHPRQLYLSVKQGE
LQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGG
CVYSKEEDGSTCLHHAAKIGNLEMVSLLLGTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICL
```

```
HWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQ
LNRKLRLGVGNRAVRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQDT
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9MIQ9 **A0A2Y9MIQ9_DELLE** (1268 aa)
histone-lysine N-methyltransferase EHMT2 isoform X1. *Delphinapterus leucas (Beluga whale)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGTHRGRGRPRSLLSLPRAQASWAPQLPTGLTSSPIPCVPSQGEAPAEMGA
LVLEKEPRGATERVHGSLGDTPRSEEILPKANPDSLETAGPSSPASVTVTVGDEGADTPVGATPLIGDEPENLEGDGDLH
GGRILMGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGATAAGPEPPPATASPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDLHSLGKVTSDVAKRRKLNSGGGLSEELGSARGSREVTLEKGDPGSLEEWE
TVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKA
KKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEE
LPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNSAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCT
AGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLAQDAPGRADTSQPS
ARMRGQGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPPGPGRETLEKALVIQESERRKKLRFHPRQLYLSVKQGE
LQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGG
CVYSKEEDGSTCLHHAAKIGNLEMVSLLLGTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICL
HWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQ
LNRKLRLGVGNRAVRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSS
SNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGT
FICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSR
DIRAGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNP
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9MLQ2 **A0A2Y9MLQ2_DELLE** (1234 aa)
histone-lysine N-methyltransferase EHMT2 isoform X2. *Delphinapterus leucas (Beluga whale)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGTHRGRGRPRSLLSLPRAQASWAPQLPTGLTSSPIPCVPSQGEAPAEMGA
LVLEKEPRGATERVHGSLGDTPRSEEILPKANPDSLETAGPSSPASVTVTVGDEGADTPVGATPLIGDEPENLEGDGDLH
GGRILMGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGATAAGPEPPPATASPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDLHSLGKVTSDVAKRRKLNSGGGLSEELGSARGSREVTLEKGDPGSLEEWE
TVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKA
KKKWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGEL
SGCNSAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHC
GEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLAQDAPGRADTSQPSARMRGQGEPRRPPCDPLADTIDSSGPSLTLPNGG
CLSAVGLPPGPGRETLEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKG
SVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLGTGQV
DVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLH
IAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAVRTEKIICRDVARGYENVPIP
CVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFE
CNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEV
YCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRAGEELGFDYGDRFWDIKSKYFTCQCGSEKCK
HSAEAIALEQSRLARLDPHPELLPELGSLPPVNP
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9MSD8 **A0A2Y9MSD8_DELLE** (1247 aa)
histone-lysine N-methyltransferase EHMT2 isoform X3. *Delphinapterus leucas (Beluga whale)*

```
MARKCVVAPLRLLLARLLAHVTRGGRAPARPPAQAAMAAAAGAAAAAAAEGEAPAEMGALVLEKEPRGATERVHGSLGDT
PRSEEILPKANPDSLETAGPSSPASVTVTVGDEGADTPVGATPLIGDEPENLEGDGDLHGGRILMGHATKSFPSSPSKGG
ACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGATAAGPEPPPATASPEGQPKVHRARKTMSKPGNGQPPVPEKRPPE
VQHFRMSDDLHSLGKVTSDVAKRRKLNSGGGLSEELGSARGSREVTLEKGDPGSLEEWETVVGDDFSLYYDSYSVDERVD
SDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKRE
PPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAG
HKCMATESVDGELSGCNSAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKAC
```

```
VSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLAQDAPGRADTSQPSARMRGQGEPRRPPCDPLADTI
DSSGPSLTLPNGGCLSAVGLPPGPGRETLEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQ
SKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGN
LEMVSLLLGTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCD
LHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAVRTEKIIC
RDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLL
QEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDD
SYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRAGEELGFDYGDRFWDIKS
KYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNP
```

336 - 355:	EEEEEEEEEEEEEEEEEEEE
337 - 356:	EEEEEEEEEEEEEEEEEEEE
338 - 357:	EEEEEEEEEEEEEEEEEEEE
339 - 358:	EEEEEEEEEEEEEEEEEEEE
340 - 359:	EEEEEEEEEEEEEEEEEEEE
341 - 360:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9MXN9 **A0A2Y9MXN9_DELLE** (1177 aa)
histone-lysine N-methyltransferase EHMT2 isoform X4. *Delphinapterus leucas (Beluga whale)*

```
MAAAAGAAAAAAAEGEAPAEMGALVLEKEPRGATERVHGSLGDTPRSEEILPKANPDSLETAGPSSPASVTVTVGDEGAD
TPVGATPLIGDEPENLEGDGDLHGGRILMGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGA
TAAGPEPPPATASPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDLHSLGKVTSDVAKRRKLNSGGGLSEEL
GSARGSREVTLEKGDPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEE
EEEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAP
KIDRISERAGHKCMATESVDGELSGCNSAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDF
RVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLAQDAPGRADTSQPSARMRGQGEPRR
PPCDPLADTIDSSGPSLTLPNGGCLSAVGLPPGPGRETLEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDN
LDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGST
CLHHAAKIGNLEMVSLLLGTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAI
AEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGN
RAVRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIR
CWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELIS
DAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRAGEELGFD
YGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNP
```

300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9MYQ4 **A0A2Y9MYQ4_DELLE** (2027 aa)
Histone acetyltransferase (EC 2.3.1.48). *Delphinapterus leucas (Beluga whale)*

```
MVKLANPLYTEWILEAIKKVKKQKQRPSEERICNAVSSSHGLDRKTVLEQLELSVKDGTILKVSNKGLNSYKDPDNPGRI
ALPKPRNHGKVDNKQNVDWNKLIKRAVEGLAESGGSTLKSIERFLKGQKDVSALFGGGAASGFHQQLRLAIKRAVGHGRL
LKDGPLYRLNTKATNVDGKESCESLSSLPPVSLLPHEKDKPVAEPIPICSFCLGTKDQNREKKPEELISCADCGNSGHPS
CLKFSPELTVRVKALRWQCIECKTCSSCRDQGKNADNMLFCDSCDRGFHMECCDPPLTRMPKGMWICQICRPRKKGRKLL
QKKAAQIKRRYANPIGRPKNRLKKQNTVSKGPFSKVRTGPGRGRKRKITLSSQSASSSEDGYLEQIDGLDFCRDGSVPLK
FNKKTKGLIDGLTKFFTPSPDGRKPRGEVVDYSEQYRVRKKGNRKSSTSDWPTDNQDGWDGKQESEERLFGSQEIMTEKD
MELFRDIQEQALQKVGVTGPPDPQVRCPSVIEFGKYEIHTWYSSPYPQEYSRLPKLYLCEFCLKYMKSRTILQQHMKKCG
WFHPPANEIYRKNNISVFEVDGNVSTIYCQNLCLLAKLFLDHKTLYYDVEPFLFYVLTQNDVKGCHLVGYFSKEKHCQQK
YNVSCIMILPQYQRKGYGRFLIDFSYLLSKREGQAGSPEKPLSDLGRLSYMAYWKSVILECLYHQNDKQISIKKLSKLTG
ICPQDITSTLHHLRMLDFRSDQFVIIRREKLIQDHMAKLQLNLRPVDVDPECLRWTPVIVSNSVVSEEEEEEEEEEEEE
EEEEEEEEGEQEEPQSQEGELEPSVGKSASREKKEQDSYSSVESEKKPEVTAPASSTRLNKQVLPRDSLPANNQPSRRGR
WRRKNRKAQERFGDEDSKLLLEETSAPPEQYGDCEEKSETCQEEYTEGQEQSAASQEQPSQDAKPDGPKRRPSEGLELWR
GPLKKSPEPLKCGLPESHDRLPRRYSEGRYSDGDRALLRGCSESSEEEGEPESPRSSSPPVLTKPTLKRKKPILHRRRRV
RKRKHHNSSVVTETISETTEVLDEPFEDSDSERPMPRLEPTFEIDQEEEEEDENELFSQGYFRHLSSQDVLRCRPASKRK
SKDRDEDEDSDDADDTPILKPVSLLRKCDVKDSPLEPDTSTPMKKKKGWPKGKSRKPVHWKKRPGRKPGLKLNRELAAVC
TRECVVEPVVPLPEPGREPQVQENQEAVGPREDLPLREERKEGEELPLEAEEGEEGEEEEDTTSSDVRAASPADSCSPET
GAKGPEVGEEEEESRAPVGQPPSEEGSQDLAQRAREEEEEEEEEEEEEDAAAETQQSEDRDADDEDDGHLESTGKKGPEE
QPAGGDAQEAHGGQESFLDPDVHSSREHAKDKEETEPDSEEEQTSHEASVVSEHMPGSEDDHEEDSHSKEELLQLKEEAE
IPHSDLDLETVQAVQSLTQEESSEHEGAYQDCEETLAACQTLQSYTQADEDPQLPLVEDCHASEHNSPLSSVQSHPSQSV
RSVGSPSVPALEGGYTQISPEQGSLSAPSMQNMETSPMMDVPSVSDHSQQVVDSGFSDLGSIESTTENYENPSSYDSTMG
GSICGNSSSQSSCSYGGLSSSSSLTQNSCVVTQQMAGVGGSCSLMPQSSVPPAAATCSIKSPQSCAVERPPSTQQPPPPQ
PPPQAPPAPPPAPPPPPPPPAPQPPPPPPQPQPPAPTPQQQQPPLSQCSMNSSFTPAPMIMEIPESGSTGNISIYERIPG
DFGAGSYSQPSATFSLAKLQQLTNTIMDPHAMPYSHSPAVTSYATSVSLSNTGLPQLAPSHPLAGTPQAQATMTPPPNLA
STTMNLTSPLLQCNMSATNIGIPHTQRLQGQMPVKGHISIRSKSAPLPSAAAHQQQLYGRSPPAVAMQAGPRALAVQRGM
NMGVNLMPTPAYNVNSMNMNTLNAMNSYRMTQPMMNSSYHSNPAYMNQTAQYPMQMQMGMMGSQAYTQQPMQPNPHGNMM
YTGPSHHSYMNAAGVPKQSLNGPYMRR
```

787 - 806:	EEEEEEEEEEEEEEEEEEEE
788 - 807:	EEEEEEEEEEEEEEEEEEEE
789 - 808:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9N1I2 **A0A2Y9N1I2_DELLE** (2020 aa)
Histone acetyltransferase (EC 2.3.1.48). *Delphinapterus leucas (Beluga whale)*

```
MVKLANPLYTEWILEAIKKVKKQKQRPSEERICNAVSSSHGLDRKTVLEQLELSVKDGTILKVSNKGLNSYKDPDNPGRI
ALPKPRNHGKVDNKQNVDWNKLIKRAVEGLAESGGSTLKSIERFLKGQKDVSALFGGGAASGFHQQLRLAIKRAVGHGRL
LKDGPLYRLNTKATNVDGKESCESLSSLPPVSLLPHEKDKPVAEPIPICSFCLGTKDQNREKKPEELISCADCGNSGHPS
CLKFSPELTVRVKALRWQCIECKTCSSCRDQGKNADNMLFCDSCDRGFHMECCDPPLTRMPKGMWICQICRPRKKGRKLL
QKKAAQIKRRYANPIGRPKNRSKGPFSKVRTGPGRGRKRKITLSSQSASSSEDGYLEQIDGLDFCRDGSVPLKFNKKTKG
LIDGLTKFFTPSPDGRKPRGEVVDYSEQYRVRKKGNRKSSTSDWPTDNQDGWDGKQESEERLFGSQEIMTEKDMELFRDI
QEQALQKVGVTGPPDPQVRCPSVIEFGKYEIHTWYSSPYPQEYSRLPKLYLCEFCLKYMKSRTILQQHMKKCGWFHPPAN
EIYRKNNISVFEVDGNVSTIYCQNLCLLAKLFLDHKTLYYDVEPFLFYVLTQNDVKGCHLVGYFSKEKHCQQKYNVSCIM
ILPQYQRKGYGRFLIDFSYLLSKREGQAGSPEKPLSDLGRLSYMAYWKSVILECLYHQNDKQISIKKLSKLTGICPQDIT
STLHHLRMLDFRSDQFVIIRREKLIQDHMAKLQLNLRPVDVDPECLRWTPVIVSNSVVSEEEEEEEEEEEEEEEEEEEEE
EGEQEEPQSQEGELEPSVGKSASREKKEQDSYSSVESEKKPEVTAPASSTRLNKQVLPRDSLPANNQPSRRGRWRRKNRK
AQERFGDEDSKLLLEETSAPPEQYGDCEEKSETCQEEYTEGQEQSAASQEQPSQDAKPDGPKRRPSEGLELWRGPLKKSP
EPLKCGLPESHDRLPRRYSEGRYSDGDRALLRGCSESSEEEGEPESPRSSSPPVLTKPTLKRKKPILHRRRRVRKRKHHN
SSVVTETISETTEVLDEPFEDSDSERPMPRLEPTFEIDQEEEEEDENELFSQGYFRHLSSQDVLRCRPASKRKSKDRDED
EDSDDADDTPILKPVSLLRKCDVKDSPLEPDTSTPMKKKKGWPKGKSRKPVHWKKRPGRKPGLKLNRELAAVCTRECVVE
PVVPLPEPGREPQVQENQEAVGPREDLPLREERKEGEELPLEAEEGEEGEEEEDTTSSDVRAASPADSCSPETGAKGPEV
GEEEEESRAPVGQPPSEEGSQDLAQRAREEEEEEEEEEEEEDAAAETQQSEDRDADDEDDGHLESTGKKGPEEQPAGGDA
QEAHGGQESFLDPDVHSSREHAKDKEETEPDSEEEQTSHEASVVSEHMPGSEDDHEEDSHSKEELLQLKEEAEIPHSDLD
LETVQAVQSLTQEESSEHEGAYQDCEETLAACQTLQSYTQADEDPQLPLVEDCHASEHNSPLSSVQSHPSQSVRSVGSPS
VPALEGGYTQISPEQGSLSAPSMQNMETSPMMDVPSVSDHSQQVVDSGFSDLGSIESTTENYENPSSYDSTMGGSICGNS
SSQSSCSYGGLSSSSSLTQNSCVVTQQMAGVGGSCSLMPQSSVPPAAATCSIKSPQSCAVERPPSTQQPPPPQPPPQAPP
APPPAPPPPPPPPAPQPPPPPPQPQPPAPTPQQQQPPLSQCSMNSSFTPAPMIMEIPESGSTGNISIYERIPGDFGAGSY
SQPSATFSLAKLQQLTNTIMDPHAMPYSHSPAVTSYATSVSLSNTGLPQLAPSHPLAGTPQAQATMTPPPNLASTTMNLT
SPLLQCNMSATNIGIPHTQRLQGQMPVKGHISIRSKSAPLPSAAAHQQQLYGRSPPAVAMQAGPRALAVQRGMNMGVNLM
PTPAYNVNSMNMNTLNAMNSYRMTQPMMNSSYHSNPAYMNQTAQYPMQMQMGMMGSQAYTQQPMQPNPHGNMMYTGPSHH
SYMNAAGVPKQSLNGPYMRR
```

780 - 799:	EEEEEEEEEEEEEEEEEEEE
781 - 800:	EEEEEEEEEEEEEEEEEEEE
782 - 801:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9NUF3 **A0A2Y9NUF3_DELLE** (1311 aa)
tau-tubulin kinase 1. *Delphinapterus leucas (Beluga whale)*

```
MQCLAAALKDETNMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTRENVALKVESAQQPKQVLKMEVAV
LKKLQGKDHVCRFIGCGRNEKFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESIEAIHSVGFLHRDIKPSNF
AMGRLPSTYRKCYMLDFGLARQYTNTTGDVRPPRNVAGFRGTVRYASVNAHKNREMGRHDDLWSLFYMLVEFAVGQLPWR
KIKDKEQVGMIKEKYEHRMLLKHMPSEFHLFLDHIASLDYFTKPDYQLIMSVFENSMKERGIAENEAFDWEKAGNDALLS
TSTSTPPQQNTRQTAAMFGVVNVTPVPGDLLRENTEDVLQGEHLSDQENAPPILPGRPPEGPGSSPHLAPHPGGPEAEVW
EETDVNRNKLRINIGKTPCVVEEEQSRVAGLPGSPVRAPPDSPTTPVRSLHYRRVNSPESERLSTADGRVELHERRSRMD
LPGSPSRQACSSQPAQMLSVDTGHADRQASGRMDVSASVEQEALSNAFRSVPLAEEEDFDSKEWVIIDKETELKDFPPGA
EPSTSGTTDEEPEELRPLPEEGEERRRPGPEPAVRPRGRGMHTLAEEDLRLTPAQPLPPQLNQADGRSETSQPPTPGSPS
HSPLHSGPRPRRRESDPTGPQRQVFSVAPPFEVNGLPRAVPLSLPYQDYKKDLSDYRERARLLNRVRRVDFSHMLLATPQ
VPLAPVQPQTNGKEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEEEEEEEEEEEAVALGEVLGPHSGSSSEGSERSTDRS
QEGAPSTLLADDQKESRGRASMADGDLEPEEGSKTLVLVSPGDMKKSPVTADLAPDPDLGTLAALTPQHERPQPTGSQLD
VSEPGTLSSVLKSEPKPPGTGTGPGAGAVTIGAGGVAVTSSPFTKVERTFVHIAEKTHLNVMSSGGQASRSEELSAGGEL
GLEVPSDGRAAEEGASVYLENGIALSGLVSCVLSAPPESSPLEVTTDSLPNGPALADGPAPASLLEPGPEKLATVSPSRH
ARPGPRPRSRIPVLLSEEDTGSEPSGSLSAKERWGKRARPQQDLARLVMEKRQGRLLLRLASGASSSSSEEQRRASETLS
GTGSEEDTPASEPAVPRKAGRAAATRSRIPRPISIRMPTPAAAQQPPDRPQGAAPASDTAITSRVQLQKPPGTAIAADLR
PKQPPGRGPGPGRAQAGTRPPAPRSPGLPASSAHHPSASPRSRSLSRKESPSPSHQARPGAPPPRGAPQARAQPEGTPSP
GAPKKGPRVKLQTQRATKGRAGVAEGRAGAR
```

734 - 753:	EEEEEEEEEEEEEEEEEEEE
735 - 754:	EEEEEEEEEEEEEEEEEEEE
736 - 755:	EEEEEEEEEEEEEEEEEEEE
737 - 756:	EEEEEEEEEEEEEEEEEEEE
738 - 757:	EEEEEEEEEEEEEEEEEEEE
739 - 758:	EEEEEEEEEEEEEEEEEEEE
740 - 759:	EEEEEEEEEEEEEEEEEEEE
741 - 760:	EEEEEEEEEEEEEEEEEEEE
742 - 761:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9P3P0 **A0A2Y9P3P0_DELLE** (1308 aa)
splicing factor, arginine/serine-rich 19 isoform X2. *Delphinapterus leucas (Beluga whale)*

```
MEEEDESRGKTEESGEDRGDGPPDRDPMLSPSAFILRAIQQAVGSSLQGDLPNDKDSSRCHGLRWRRCRSPRSEPRSQES
GGTDTASVLDVAADGLLAGLVSILDPPDTWVPSHLDLRPGESEDMLELVAEVRIGDRDPVPLPVPSLLPRVRAWRTGKTV
SPQSHSSRPTCARHLLTLGTDGGPAPPPAPSSASSSPSPSPSSSSPSPPPPPPPPPAPPAPPAPRFDIYDPFHPTDEAYS
PPPAPEQKYDPFEPTGSNPSSSAGTPSPEEEEEEEEEEEEEEEEEEEEALSQSISRISETLAGIYDDNSLSQDFPGDESP
GPDPQPLQPTPAPGTPPQADSTRADGATRRRVFVVGTEAEACREGKVSVEVVTAGGAALPPPLLPPGDSEIEEGEIVQPE
EEPRMALSLFRAGGRAARPPTAAPAPAAAQPPPPPPAPRAPEGDDFLSLHAESDGEGALQVDLGEPAPAPPTADARWGGL
DLRRKILTQRRERYRQRSPSPAAAPASAAPTGPPTRKKSRRERKRSGGEAKEAASSSSGAQAAPPAPASPWDSKKHRSRD
RKPGSHASSSARRRSRSRSARRRSRSTDRRRGGSRRSRSREKRRRRRRSNSPPPATSSSSSSRRERHRGKHRDGGGSKKK
KKRSRSRGEKRSGDSEKGLAPAQPPSGSTSLGGERDSRRRGAVPPSIQDLTDHDLFAIKRTITVGRPDKPDPRGPSPAPA
SSPKREVLYDSEGLSAEERGGKSSEKDRRRSGAASSSSSSREKGSRRKALDGGDRDRDRDRDRDRDRSSKKARPPKELAP
SSGPPPKPPVSSGSGSSSSSSSSSSRKVKLQSKVAVLIREGVSSTTSAKEATSAGLGSIGVKFSRDRESRSPFLKPDERA
PTEVAKAAQGSTKPKKTKVKAKAGAKKAKGTKGKTKPSKTRKKIRSGGGSGGGGSGPATLKKSKADSCSQAAGAKGAEET
SWSGEERAAKAPSTPPPKAAPPPPALTPDSQTVDSSCKTPEVSFLPEEAAEEAGVRGGAEEEEEEEEEEEEEEEEQQPAT
STATSTAAAAPSTAPSAGSTAGDSGAEDGPAPRVSQLPTLPPPMPWNLPAGVDCTTSGVLALTALLFKMEEANLASRAKA
```

QELIQATNQILSHRKPPSSLGVTPAPVPTSLGLPPGPSSYLLPGSLPLGGCGSTPPTPTGLAAASDKREGSSSSEGRGDT
DKYLKKLHTQERAVEEVKLAIKPYYQKKDITKEEYKDILRKAVHKICHSKSGEINPVKVSNLVRAYVQRYRYFRKHGRKP
GDPPGPPRPPKEPGPPDKGGPGLPLPPL

269 - 288:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9PLI7 **A0A2Y9PLI7_DELLE** (2055 aa)
Histone acetyltransferase (EC 2.3.1.48). *Delphinapterus leucas (Beluga whale)*

MVKLANPLYTEWILEAIQKIKKQKQRPSEERICHAVSTSHGLDKKTVSEQLELSVQDGSVLKVTNKGLASYKDPDNPGRF
SSAKPGTFPKSAKGSRGSCNDLRNVDWNKLLRRAIEGLEEPNGSSLKNIEKYLRSQSDLTSTTTNPAFQQRLRLGAKRAV
NNGRLLKDGPQYRVNYGGLDGKGAPKYPSAFPSSLPPVSLLPHEKDQPRADPIPICSFCLGTKESNREKKPEELLSCADC
GSSGHPSCLKFCPELTTNVKALRWQCIECKTCSACRIQGKNADNMLFCDSCDRGFHMECCDPPLSRMPKGMWICQVCRPK
KKGRKLLHEKAAQIKRRYAKPIGRPKNKLKQRLLSVTSDEGSMNAFTGRGSPGRGQKTKVCTTPSSGHAASGKDSSSRLA
VTDPTRPGATTKITTTSTYISASTLKVNKKTKGLIDGLTKFFTPSPDGRRSRGEIIDFSKHYRPRKKVSQKQSCTSHVLA
PGTTQKLKPPPSSLPPATPISGQSPSSQKSSTSVSSTSPQSSSSQSSVPSFSSLTNNSQLKALFDGLSHSIPLRDSLAKR
DXPSYAPPKRMRRKIEFPSTAKSKAHFFGKRDIRSRFISHPSSSSWGMARGRIFKAIAHFKRTTFLKKHRMLGRLKYKVT
PQMGTPSPGKGSLTDGRIKPDQDDDTEIKISIKQESTDINVIGNKDTVTEEDLDVFKQAQELSWEKIECESGVEDCGRYP
SVIEFGKYEIQTWYSSPYPQEYARLPKLYLCEFCLKYMKSKNILLRHSRKCGWFHPPANEIYRRKDLSVFEVDGNMSKIY
CQNLCLLAKLFLDHKTLYYDVEPFLFYVLTKNDEKGCHLVGYFSKEKLCQQKYNVSCIMIMPQHQRQGFGRFLIDFSYLL
SRREGQAGSPEKPLSDLGRLSYLAYWKSVILEYLYHHHERHISIKAISRATGMCPHDIATTLQHLHMIDKRDGRFVIIRR
EKLILGHMEKLKTCSRTNELDPESLRWTPILISNAAVSEEEREAEKEAERLMEQASCWEKEEQEILSSRANSRQSPAKVQ
SKNKYLHSPESRPVAGERGQLMELSKESSEEEEEEEEEEEEEEEEEEEEEEEEEEEEEENIQSSPPRLTKPQSVAIKRKRPF
VLKKKRGRKRRRINSSVTTETISETTEVLNEPFDNSDEERPMPQLEPTCEIEVEEDGGKPVLRKAFQHQPGKKRQIEEEE
GKDNHCFKNADPCRNNMDDDANNLKEASRDNPEPLKCKQWPKGTKRGLSKWRPNKERKTGFKLNLYTPPETPMEPDDQVI
VEEQKEAPADKTSPAPTRTEEEVKEAVEPLLPGDENRREETCAPVSPNKSPGEKPEDDLIKPEEDEEEEEEEEEEEEEGN
VEKDPCGAQSQDKEEPEVCTDKEDPVRLDDHEEEEEEDEEPSHNEGHDADDEDDSHMESAESEKEERPREAFKEVLETQE
AFLDLSVQPSHSNAEVLMDCGVDLTASCNSEPKELAGATETAPESDEEPAGEQAQEQDQKNSEEVDSEFKEGNTATLEID
SETVQAVQSLTQENSEQDDTFQDCAETQEACRSLQNYTHADQSPQIAASLDDCQQSDHSSPVSSVHSHPSQSVRSVNSPS
VPALENSYAQISPDQNAISVPSLQNMETSPMMDVPSVSDHSQQVVDSGFSDLGSIESTTENYENPSSYDSTMGGSICGNG
SSQNSCSYSNLTSSNLTQSSCAVTQQMSNISGSCSMLQQTSISSPPTCSVKSPQGCVVERPPSSSQQLAQCSMAANFTPP
MQLAEIPETGNTNLGLYERMGQSDFGAGHYPQPSATFSLAKLQQLTNTLIDHSLPYSHSAAVTSYANSASLSTPLSNTGL
VQLSQSPHSVPGGPQAQATMTPPPNLTPPPMNLPPPLLQRNMAASNIGISHSQRLQTQIASKGHVSMRTKSASLSPAAAT
HQSQIYGRSQTVAMQGPARTLTMQRGMNMSVNLMPSPAYNVNSVNMNMNTLNAMNGYSMSQPMMNSGYHSNHGYMNQTPQ
YPMQMQMGMMGTQPYAQQPMQTPPHSNMMYTAPGHHGYMNPGMSKQSLNGSYMRR

1070 - 1089:	EEEEEEEEEEEEEEEEEEEE
1071 - 1090:	EEEEEEEEEEEEEEEEEEEE
1072 - 1091:	EEEEEEEEEEEEEEEEEEEE
1073 - 1092:	EEEEEEEEEEEEEEEEEEEE
1074 - 1093:	EEEEEEEEEEEEEEEEEEEE
1075 - 1094:	EEEEEEEEEEEEEEEEEEEE
1076 - 1095:	EEEEEEEEEEEEEEEEEEEE
1077 - 1096:	EEEEEEEEEEEEEEEEEEEE
1078 - 1097:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9PZL4 **A0A2Y9PZL4_DELLE** (602 aa)
major centromere autoantigen B. *Delphinapterus leucas (Beluga whale)*

MGPKRRQLTFREKSRIIQEVEENPDLRKGEIARRFNIPPSTLSTILKNKRAILASERKYGVASTCRKTNKLSPYDKLEGL
LIAWFQQIRAAGLPVKGIILKEKALRIAEELGMDDFTASNGWLDRFRRRHGVVSCSGVARARSRSAAPRPPAAPASPPTV
PSEGSGGGTTGWRAREEQPPSVAEGYASQDVFSATETSLWYDFLPDQAAGLCGSDGRARKATQRLSVLLCANADGSEKLP
PLVAGKSAKPRAGQAGLPCDYTANSKGGVTTQALAKYLKALDTRMAAESRRVLLLAGRLAAQSLDTSGLRHVQLAFFPPG
TVQPLERGVVQQVKGHYRQAMLLKAMAALEGQDRSGLQLGLMEALHFVAAAWQAVEPSDIATCFREAGFGGGPNATITTA
LKSEEEEEEEEEEEEEEEEEEEGEGEEEEEEDGEEEEEGGEGEELGEEEEVEEEGDVDDSDEEEEEEEESSSEGLEAED
WAQGVVEAGGSFGGYGAQEEVQCPTLHFLEGEEDSESDSEEEEEDEEEDEDDEDDDEDGDEVPVPSFGEAMAYFAMVKRY
LTSFPIDDRVQSHILHLEHDLVHVTRKNHARQAGVRGLGHQS

404 - 423:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9RPF7 **A0A2Y9RPF7_TRIMA** (2063 aa)
Histone acetyltransferase (EC 2.3.1.48). *Trichechus manatus latirostris (Florida manatee)*

MVKLANPLYTEWILEAIQKIKKQKQRPSEERICHAVSTSHGLDKKTVSEQLELSVQDGSVLKVTNKGLASYKDPDNPGRF
SSVKPGTFPKSTKGSRGSCNDLRNVDWNKLLKRAIEGLEEPNGSSLKNIEKYLRNQSDLTGTTNNPAFQQRLRLGAKRAV
NNGRLLKDGPQYRVNYGSLDGKGAPKYPSAFPSSLPPVSLLPHEKDQPRADPIPICSFCLGTKESNREKKPEELLSCADC
GSSGHPSCLKFCPELTTNVKALRWQCIECKTCSACRIQGKNADNMLFCDSCDRGFHMECCDPPLSRMPKGMWICQVCRPK
KKGRKLLHEKAAQIKRRYAKPIGRPKNKLKQRLLSVTSDEGSMNAFTGRGSPGRGQKTKVCTTPSSGHAASGKDSSSRLA
VTDPTRPGATTKITTTSTYISASTLKVNKKTKGLIDGLTKFFTPSPDGRRSRGEIIDFSKHYRPRKKVSQKQSCTSHVLA
TGTTQKLKPPPPSLPPRTPISGQSPSSQKSSTSTSSPSPQSSSSQSSVPSFSSLTNNSQLKALFDGLSHIYTTQGQSRKK
GHPSYAPPKRMRRKTELSSTAKSKAHFFGKRDIRSRFISHSSSSSWGMARGRIFKAIAHFKRTTFLKKHRMLGRLKYKVT
PQMGTPSPGKGSLADGRIKPDQDDDTEIKISIKQESTDVNVIGNKDTVTEEDLDVFKQAQELSWEKIECESGVEDCGRYP
SVIEFGKYEIQTWYSSPYPQEYARLPKLYLCEFCLKYMKSKNILLRHSKKCGWFHPPANEIYRRKDLSVFEVDGNMSKIY
CQNLCLLAKLFLDHKTLYYDVEPFLFYVLTKNDEKGCHLVGYFSKEKLCQQKYNVSCIMIMPQHQRQGFGRFLIDFSYLL
SRREGQAGSPEKPLSDLGRLSYLAYWKSVILEYLYHHHERHISIKAISRATGMCPHDIATTLQHLHMIDKRDGRFVIIRR
EKLILGHMEKLKSCSRANELDPESLRWTPILISNAAVSEEEREAEKEAERLMEQASCWEKEEQEMLSSRANSRQSPAKVQ
SKNKYLHSPESRPVAGERGQLMELSKESSEEEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEENIQSSPPRLTKPQSVA
IKRKRPFVLKKKRGRKRRRINSSVTTETISETTEVLNEPFDNSDEERPMPQLEPTCEIDLDEDGLKPVMRKAFQHQPGMK
RQTEEEEGKDNHCFKNADPCRNNIDGDADNLKEGSKDNPEPLKCKQVWPKGTKRGLSKWRQNKERKTGFKLNLYTPPETP
MEPDDQITVEEQKQTSEDKTSSTPIRIEEEVKETVGPLLPRDENRREETCAPISPNKSPGEKREDDLTKPEEEEEEEEEE
EEEEEEGNVEKDPDGTKSEEKEEPEISMEKEDTVQLDDHEEEEEEDEEPSHNEDHDADDEDDGHMESTEVEKEELPRETF

```
KEVLENQEAFLDLSVQPSHSNSEVLMDCGVDLAASCNSEPKELAGDTETVPESDEEPPEEQAQKQDQKDSQEVDSDFKEG
NTATMEIDSETVQAVQSLTQENNEQDDTFQDCAETQEACRSLQNYTHADQSPQIATTLDDCQQSDHSSPVSSVHSHPGQS
VRSVNSPSVPALENSYAQISPDQSAISVPSLQNMETSPMMDVPSVSDHSQQVVDSGFSDLGSIESTTENYENPSSYDSTL
GGSICGNGSSQNSCSYSNLTSSSLTQSSCAVTQQMSNISGSCSLLQQSSISSPPTCGVKSPQGCVVERPPSSSQQLAQCS
MAANFTPPMQLAEIPETGNANIGLYERMGQSDFGAGHYPQPSATFSLAKLQQLTNTLIDHSLPYSHSAAVTSYANSASLS
TPLSNTGLVQLSQSPHSVPGGPQAQATMTPPPNLTPPPMNLPPPLLQRNMAASNIGISHSQRLQTQIASKGHVSMRTKSA
SLSPAAATHQSQIYGRSQTVAMQGPARTLTMQRSMNMSVNLMPAPAYNVNSVNMNMNTLNAMNGYSMSQPMMNSGYHSNH
GYMNQTPQYPMQMQMGMMGTQPYAQQPMQTPPHGNMMYTAPGHHGYMNTGMSKQSLNGSYMRR
```

1080 - 1099:	EEEEEEEEEEEEEEEEEEEE
1081 - 1100:	EEEEEEEEEEEEEEEEEEEE
1082 - 1101:	EEEEEEEEEEEEEEEEEEEE
1083 - 1102:	EEEEEEEEEEEEEEEEEEEE
1084 - 1103:	EEEEEEEEEEEEEEEEEEEE
1085 - 1104:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9S6J4 **A0A2Y9S6J4_PHYMC** (602 aa)
major centromere autoantigen B isoform X3. *Physeter macrocephalus (Sperm whale) (Physeter catodon)*

```
MGPKRRQLTFREKSRIIQEVEENPDLRKGEIARRFNIPPSTLSTILKNKRAILASERKYGVASTCRKTNKLSPYDKLEGL
LIAWFQQIRAAGLPVKGIILKEKALRIAEELGMDDFTASNGWLDRFRRRHGVVSCSGVARARSRSAAPRPPAAPASPPTV
PSEGSGGGTTGWRAREEQPPSVAEGYASQDVFSATETSLWYDFLPDQAAGLCGSDGRARKATQRLSVLLCANADGSEKLP
PLVAGKSAKPRAGQAGLPCDYTANSKGGVTTQALAKYLKALDTRMAAESRRVLLLAGRLAAQSLDTSGLRHVQLAFFPPG
TVQPLERGVVQQVKGHYRQAMLLKAMAALEGQDRSGLQLGLMEALHFVAAAWQAVEPSDIATCFREAGFGGGPNATITTA
LKSEEEEEEEEEEEEEEEEEEEEGEGEEEEEDGEEEEEEAGEGEELGEEEEVEEEGDVDDSDEEEEEEEESSSEGLEAED
WAQGVVEAGGSFGGYGAQEEVQCPTLHFLEGEEDSESDSEEEEEDDEEDEDDEDDDEDGDEVPVPSFGEAMAYFAMVKRY
LTSFPIDDRVQSHILHLEHDLVHVTRKNHARQAGVRGLGHQS
```

404 - 423:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9T5G6 **A0A2Y9T5G6_PHYMC** (1120 aa)
Histone deacetylase (EC 3.5.1.98). *Physeter macrocephalus (Sperm whale) (Physeter catodon)*

```
MNSPTESDGMPGREPSLEILPRTPLHGLPVAVEVKPVPPGAMPSSMGGGGGGSPSPVELRGALAGPVDPALREQQLQQEL
LALKQQQQLQKQLLFAEFQKQHDHLTRQHEVQLQKHLKQQQEMLAAKRQQELEQQRQREQQRQEELEKQRLEQQLLVLRN
KEKSKESAIASTEVKLRLQEFLLSKSKEPPPGGLNHSLPQHPKCWGAHHASLDQSSPPQSGPPGTPPSYKLPLLGPYDSR
DDFPLRKTASEPNLKVRSRLKQKVAERRSSPLLRRKDGTVISTFKKRAVEITGAGPGAAAVCNSAPGSGPSSPNSSHSTI
AENGFTGSVPNIPTEMLPQHRALPLDSSPNQFSLYTSPSLPNISLGLQATVTVTNSHLTASPKLSTQQEAERQALQSLRQ
GGALTGKFMSTSSIPGCLLGVALEGDTSPHGHASLLQHVLLLEQARQQSALIAVPLHGQSPLVTGERVATSMRTVGKLPR
HRPLSRTQSSPLPQSPQALQQLVMQQQHQQFLEKQKQQQLGKILTKTGELPRQPTTHPEETEEELTEQQEAFLGEGALTI
PREGSTESESTQEDLEEEEEEEEEEEEEEEEEEEEEEDCIQVKDEEGESGAEEGPDLEESSAGYKKVFADAQQLQPLQVY
QAPLSLATVPHQALGRTQSSPAAPGGVKSPPDQPTKHLFTTGVVYDTFMLKHQCMCGNTHVHPEHAGRIQSIWSRLQETG
LLSKCERIRGRKATLDEIQTVHSEYHTLLYGTSPLNRQKLDSKKLLGPISQKMYAMLPCGGIGVDSDTVWNEMHSSSAVR
MAVGCLVELAFKVATGELKNGFAIIRPPGHHAEESTAMGFCFFNSVAITTKLLQQKLNVGKVLIVDWDIHHGNGTQQAFY
NDPSVLYISLHRYDNGNFFPGSGAPEEVGGGPGVGYNVNVAWTGGVDPPIGDVEYLTAFRTVVMPIAHEFSPDVVLVSAG
FDAVEGHLSPLGGYSVTARCFGHLTRQLMTLAGGRVVLALEGGHDLTAICDASEACVSALLSVELQPLDEAVLQQKPSVN
AVATLEKVIEIQSKHWSCVQRFAAGLGRSLREAQAGETEEAETVSAMALLSVGAEQAQAAAGREHSPRPAEEPMEQEPAL
```

576 - 595:	EEEEEEEEEEEEEEEEEEEE
577 - 596:	EEEEEEEEEEEEEEEEEEEE
578 - 597:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9T9V6 **A0A2Y9T9V6_PHYMC** (730 aa)
YTH domain-containing protein 1 isoform X2. *Physeter macrocephalus (Sperm whale) (Physeter catodon)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLISKPLSSSVSN
NKRMVSTKGKSVTEYKNEEYQRSERNKRLEADRKIRLSSSASREPYKSQPEKTCLRKRDAERRVKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDDDGEEEEEEEEEEEE
EEEEEEEEEEEEYEQDERDQKEEGNDYDTQSEASDSDSESISFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGS
SASESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSARSV
ILIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDG
QEIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYAPEF
HQRPGYLKDPRYQEVDRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMTPYPGMEQPPHHPYYQHHAPPPQAHPPYS
GHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDR
DRGERGRYRR
```

229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9TBV3 **A0A2Y9TBV3_PHYMC** (712 aa)
YTH domain-containing protein 1 isoform X3. *Physeter macrocephalus (Sperm whale) (Physeter catodon)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLISKPLSSSVSN
NKRMVSTKGKSVTEYKNEEYQRSERNKRLEADRKIRLSSSASREPYKSQPEKTCLRKRDAERRVKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDDDGEEEEEEEEEEE
EEEEEEEEEEEEYEQDERDQKEEGNDYDTQSEASDSDSESISFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGS
SASESYADQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSARSVILIFSVRESGKFQGFARL
SSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLLFPPD
ESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYAPEFHQRPGYLKDPRYQEVDRR
FSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMTPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHHPVPHEARYRDKRVHD
YDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDRGERGRYRR
```

229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9TE41 **A0A2Y9TE41_PHYMC** (2057 aa)
Histone acetyltransferase (EC 2.3.1.48). *Physeter macrocephalus (Sperm whale) (Physeter catodon)*

```
MVKLANPLYTEWILEAIQKIKKQKQRPSEERICHAVSTSHGLDKKTVSEQLELSVQDGSVLKVTNKGLASYKDPDNPGRF
SSVKPGTFPKSAKGSRGSCNDLRNVDWNKLLRRAIEGLEEPNGSSLKNIEKYLRSQSDLTSTTTNPAFQQRLRLGAKRAV
NNGRLLKDGPQYRVNYGGLDGKGAPKYPSAFPSSLPPVSLLPHEKDQPRADPIPICSFCLGTKESNREKKPEELLSCADC
GSSGHPSCLKFCPELTTNVKALRWQCIECKTCSACRIQGKNADNMLFCDSCDRGFHMECCDPPLSRMPKGMWICQVCRPK
KKGRKLLHEKAAQIKRRYAKPIGRPKNKLKQRLLSVTSDEGSMNAFTGRGSPGRGQKTKVCTTPSSGHAASGKDSSSRLA
VTDPTRPGATTKITTTSTYISASTLKVNKKTKGLIDGLTKFFTPSPDGRRSRGEIIDFSKHYRPRKKVSQKQSCTSHVLA
PGTTQKLKPPPSSLPPATPISGQSPSSQKSSTSVSSTSPQSSSSQSSVPSFSSLTNNSQLKALFDGLSHSIPLRDSLAKR
DXPSYAPPKRMRRKIEFPSTAKSKAHFFGKRDIRSRFISHPSSSSWGMARGRIFKAIAHFKRTTFLKKHRMLGRLKYKVT
PQMGTPSPGKGSLTDGRIKPDQDDDTEIKISIKQESTDINVIGNKDTVTEEDLDVFKQAQELSWEKIECESGVEDCGRYP
SVIEFGKYEIQTWYSSPYPQEYARLPKLYLCEFCLKYMKSKNILLRHSRKCGWFHPPANEIYRRKDLSVFEVDGNMSKIY
CQNLCLLAKLFLDHKTLYYDVEPFLFYVLTKNDEKGCHLVGYFSKEKLCQQKYNVSCIMIMPQHQRQGFGRFLIDFSYLL
SRREGQAGSPEKPLSDLGRLSYLAYWKSVILEYLYHHHERHISIKAISRATGMCPHDIATTLQHLHMIDRRDGRFVIIRR
EKLILGHMEKLKTCSRTNELDPESLRWTPILISNAAVSEEEREAEKEAERLMEQASCWEKEEQEILSSRANSRQSPAKVQ
SKNKYLHSPESRPVAGERGQLMELSKESSEEEEEEEEEEEEEEEEEEEEEEEEEEEEEENIQSSPPRLTKPQSVAIKRKRPF
VLKKKRGRKRRRINSSVTTETISETTEVLNEPFDNSDEERPMPQLEPTCEIEVEEDGGKPVLRKAFQHQPGKKRQTEEEE
GKDNHCFKNADPCRNNMDDDANNLKEASRDNPEPLKCKQWPKGTKRGLSKWRPNKERKTGFKLNLYTPPETPMEPDDQVT
VEEQKETPADKTSPAPTRTEEEVKEAVEPLLPGDENRREETCAPVSPNKSPGEKPEDDLVKPEEEEEEEEEEEEEEEEEE
GNVEKDPCGAKSQEKEEPEVCTDKEDPVRLDDHEDEEEEDEEPSHNEGHDADDEDDSHMESAESEKEERPREAFKEVLEN
QEAFLDLSVQPSHSNPEVLMDCGVDLTASCNSEPKELAGATETAPESDEEPAGEQAQEQEQKNSEEVDSEFKEGNTATLE
IDSETVQAVQSLTQENSEQDDTFQDCAETQEACRSLQNYTHADQSPQIAATLDDCQQSDHSSPVSSVHSHPSQSVRSVNS
PSVPALENSYAQISPDQNAISVPSLQNMETSPMMDVPSVSDHSQQVVDSGFSDLGSIESTTENYENPSSYDSTMGGSICG
NGSSQNSCSYSNLTSSNLTQSSCAVTQQMSNISGSCSMLQQTSISSPPTCSVKSPQGCVVERPPSSSQQLAQCSMAANFT
PPMQLAEIPETGNTNLGLYERMGQSDFGAGHYPQPSATFSLAKLQQLTNTLIDHSLPYSHSAAVTSYANSASLSTPLSNT
GLVQLSQSPHSVPGGPQAQATMTPPPNLTPPPMNLPPPLLQRNMAASNIGISHSQRLQTQIASKGHVSMRTKSASLSPAA
ATHQSQIYGRSQTVAMQGPARTLTMQRGMNMSVNLMPSPAYNVNSVNMNMNTLNAMNGYSMSQPMMNSGYHSNHGYMNQT
PQYPMQMQMGMMGTQPYAQQPMQTPPHSNMMYTAPGHHGYMNPGMSKQSLNGSYMRR
```

1070 - 1089:	EEEEEEEEEEEEEEEEEEEE
1071 - 1090:	EEEEEEEEEEEEEEEEEEEE
1072 - 1091:	EEEEEEEEEEEEEEEEEEEE
1073 - 1092:	EEEEEEEEEEEEEEEEEEEE
1074 - 1093:	EEEEEEEEEEEEEEEEEEEE
1075 - 1094:	EEEEEEEEEEEEEEEEEEEE
1076 - 1095:	EEEEEEEEEEEEEEEEEEEE
1077 - 1096:	EEEEEEEEEEEEEEEEEEEE
1078 - 1097:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9TFU9 **A0A2Y9TFU9_PHYMC** (738 aa)
YTH domain-containing protein 1 isoform X1. *Physeter macrocephalus (Sperm whale) (Physeter catodon)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLISKPLSSSVSN
NKRMVSTKGKSVTEYKNEEYQRSERNKRLEADRKIRLSSSASREPYKSQPEKTCLRKRDAERRVKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDDDGEEEEEEEEEEE
EEEEEEEEEEEEYEQDERDQKEEGNDYDTQSEASDSDSESISFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGS
SASESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSARSV
ILIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDG
QEIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYAPEF
HQRPGYLKDPRYQEVDSFTNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMTPYPGMEQPPHHPYYQHHAPP
PQAHPPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERER
ERLCDRDRDRGERGRYRR
```

229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE

A0A2Y9TIJ0 **A0A2Y9TIJ0_PHYMC** (1512 aa)
splicing factor, arginine/serine-rich 19. *Physeter macrocephalus (Sperm whale) (Physeter catodon)*

```
MKFVFSFSKWRTGFVAHSIIVPSSVCKYILLGPSPSRRIDAFLGSGVLFEAHPAHWHVSRFGKGGFMRLRDAVFEITTQQ
KRVLAPVKAGSCEVLKFGCGGRCGNWGGVCGNRPGRPPFGRGGNKFRQGKRVTPPVPLVSALGLVLARAWDAVEERRDAE
RDTVLEAPEVFMSVLSFHHLAPPWPAHLPLLQTLPPFHHQVTMEEEDESRGKTEESGEDRGDGPPDRDPTLSPSAFILRA
IQQAVGSSLQGDLPNDKDGSRCHGLRWRRCRSPRSEPRSQESGGTDTASVLDVAADGLLAGLVSILDPPDTWVPSHLDLR
PGESEDVLELVAEVRIGDRDPVPLPVPSLLPRVRAWRTGKTVSPQSHSSRPTCARHLLTLGTGDGGPAPPPAPSSASSSP
SPSPSSSSPSPPPPPPPPAPPAPPAPRFDIYDPFHPTDEAYSPPPAPEQKYDPFEPTGSNPSSSAGTPSPEEEEEEEEEE
EEEEEEEEEEEGLSQSISRISETLAGIYDDNSLSQDFPGDESPGPDPQPLQQTPAPGTPPQADSTRADGATRRRVFVVGT
EAEACREGKVSVEVVTAGGAALPPPLMPPGDSEIEEGEIVQPEEEPRMAISLFRAGGRAARPPPAAPAPPAAQPPPPPPA
PRAPEGDDFLSLHAESDGEGALQVDLGEPAPAPPTADTRWGGLDLRRKILTQRRERYRQRSPSPAAAPASAAPTGPPTRK
KSRRERKRSGGEAKEAASSSSGAQPAPPAPASPWDSKKHRSRDRKLGSHASSSARRRSRSRSARRRSRSTDRRRGGSRRS
RSREKRRRRRRSNSPPPATSSSSSSRRERHRGKHRDGGGSKKKKKRSRSRGEKRSGDSEKGPAPAQPPSGPTSLGGERDS
RRRGAVPPSIQDLTDHDLFAIKRTITVGRPDKPDPRGPSPAPASSPKREVLYDSEGLSAEERGGKSSEKDRRRSGAASSS
SSSREKGSRRKALDGGDRDRDRDRDRDRDRSSKKARPPKELAPSSGPPPKPPVSSGSGSSSSSSSSSSRKVKLQSKVAVL
IREGVSSTTPAKEATSAGLGSIGVKFSRDRESRSPFLKPDERAPTEVAKAAQGSTKPKKTKVKAKAGAKKAKGTKGKIKP
SKTRKKIRSGGGSSGGSSGPVTLKKSKADSCSQAAGARGAEETSWSGEERAAKAPSTPPPKAAPPPPALTPDSQTVDSSC
KTPEVSFLPEEATEEAGVRGGAEEEEEEEEEEEEEEEEEEQQPATSTATSTAAAAPSTAPSAGSTAGDSGAEDGPAPRVSQ
LPTLPPPMPWNLPAGVDCTTSGVLALTALLFKMEEANLASRAKAQELIQATNQILSHRKPPSSLGVTPAPVPTSLGLPPG
PSSYLLPGSLPLGGCGSTPPTPTGLAAASDKREGSSSSEGRGDTDKYLKKLHTQERAVEEVKLAIKPYYQKKDITKEEYK
DILRKAVHKICHSKSGEINPVKVSNLVRAYVQRYRYFRKHGRKPGDPPGPPRPPKEPGPPDKGGPGLPLPPL
```

471 - 490:	EEEEEEEEEEEEEEEEEEEE
472 - 491:	EEEEEEEEEEEEEEEEEEEE

A0A2Z5D4I7 **A0A2Z5D4I7_PASAR** (1019 aa)
Acetyl-CoA carboxylase carboxyltransferase beta subunit. *Passiflora auriculata (Passion flower)*

```
MLSLSKEQLSKRPTTYFLSSMFLCKRKKKVEKGLFQSFCKKNQNPDFDIPDDHSFESDLEGSFVKYFEFGYRENLLSDYL
ENPMNTNMILRNYILEKCVDVYFDTKTGMYRSTNDFGDVSPSNNPNSEEPLSDVSPSNNPNSEEPLSDVSPSNNPNSEEP
LSDVSPSNNPNSEEPLGDGEEEEEEEEEEEEEEEEEEEEEEEEGEEEEEEEPEEEKPKDFSPFWVNCDECYAPNYKRYFF
QTRLYVCEYCGCHLKLPSSLRIQLLIDPGTWVPLDHIMKDFDSKPALDPWTWDEHEARENLANPLGETGDFQKEDNDDLA
NPLEETGDFQKEDNDDLANPLEETGDFQKEDNDDLANPLGETGDFQKEDFGVYGPQNEGHTRGLNSSDLNFGNNKEGSLS
YDQTKKSKQTKKAENDESANAKKTTNENHKNIDGTWQEKQIDKKETSHNGASDCFGGNGSASHLPLSNHSFDGGRKEPIA
DLEGNLDTNPDDPNDGEYLGGNDFTAPEKSLADGIAKHISDLTNGNAPLVPDHFKAPTPINGYPLPGMQNILGLHNDHFA
GPSDNENLDIAEENRPFEEDSALDLESGGHGDNIQPPNNDNLAPGPRREDPSSRREGQEAQKNLESAGYDDLPYPNLFGE
GCASIDMENGPFENISSSDGMVQSLVVRRQRSLGLFKIDQNSPLVYDSDSDFESESDHESDDKQEKELGPFLCIPFFIKN
GELDMDGELDMDSPCIPLIPTFFPNGEHQINTEGEDEAQRTDEWYSDKVKDVCHQLAEVDWWRSWTQEDWDRDEIKELLA
DVEFVVEIEEEAEAKPYVSRIFSDQDETELSEAIQTGLGQLNGIPVALGVMDFSFIGGSMGYVVGDRIIRLIEYSSRLEI
PLIIVCASGGARMYEGSLALMQMAKISSSLYYFKKNNKKPFYISMLASPTTGGVTASFGMLGDIIISEPDAYIAFAGKRV
IEDTLKIPVPEGSQVAEVAFEKGLLDSIIPREMLKGVLTELLQLHDFLPLTPKIKGLLN
```

180 - 199:	EEEEEEEEEEEEEEEEEEEE
181 - 200:	EEEEEEEEEEEEEEEEEEEE
182 - 201:	EEEEEEEEEEEEEEEEEEEE
183 - 202:	EEEEEEEEEEEEEEEEEEEE
184 - 203:	EEEEEEEEEEEEEEEEEEEE

A0A2Z5U6F4 **A0A2Z5U6F4_9GAMA** (426 aa)
LANA-1. *Rhinolophus gammaherpesvirus 1*

```
MPGTRMHPLGPGGPCTRASCKEQIKWPPSDPPDTRKRKQPETSSPGETGKKRRRLHHRPGRQPEPEPEPEPEPEEEPEPE
EEPEPEEEPEEEEEEPEEEPEEEEEEEPEPEPEPEPEPEPEPEPELEPEPELEPEPELEPEPELEPEPEEEPEEEPEEE
PEEEPEEEPEEEPEEEEEEEEPEEEEEEEEPEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEHHQDHTYCMPWGHSSHPQISI
TSSDHTYAKQQIGEPGEPGEPGEPGEPGEPGEPGEPGEPGEPQPGPSRTNIYPRFPKPKKQHEPGAPIPRKYRSRWNFMNRYM
RDFVYDPSKGWQYGLMIQCGDPYSLYLLSRSLEQDCLLPTGVQANPQAREAVRTVFNVTVFFQDPSVGRALESAITAYTV
RYSTWVDLCRVRTSGPIDDGRDNVSQ
```

192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE
194 - 213:	EEEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEEE
196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE

A0A2Z6M279 **A0A2Z6M279_TRISU** (167 aa)
Uncharacterized protein. *Trifolium subterraneum (Subterranean clover)*

```
MSFCCELDDRDPIGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEIAIDVSFLAVAVVSF
VDSEHSK
```

15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE

63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE

115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE

A0A2Z6MJR5 **A0A2Z6MJR5_TRISU** (65 aa)
Uncharacterized protein. *Trifolium subterraneum (Subterranean clover)*

```
MCFNRPFELRFRLGFWVLLEGMICDMEEEIDKEDEEEEEEEEEEEEEEEEEEEEEEGIDGWKRRNR
```

35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE

A0A2Z6PB62 **A0A2Z6PB62_TRISU** (61 aa)
Uncharacterized protein. *Trifolium subterraneum (Subterranean clover)*

```
MLYVNGLERGPLMSSHLSRLLPSFYCWLLVIWSEIEEEEEEEEEEEEEEEEEEEEEEEESN
```

36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE

A0A2Z6PJD0 **A0A2Z6PJD0_TRISU** (521 aa)
Uncharacterized protein. *Trifolium subterraneum (Subterranean clover)*

```
MATSISPWFSSISISCSNTRNRRYRVPSHTKSKPPPNPKLNSPPQPPLLSAGDAITYTRLPLKEDYSSPFSPSSSEIKLS
DSTPIHQFLYKLKHDSDEEEEEEEEEEEEEEEEEEEEEEEEEEEINANFEVIVDSDSEDDEELGFTDDDDEDEEINNEDE
EIDEGEEVWSEGTEGEVKEKGLPAVMRCFDQAKIYAKAGDGGNGSMAFRREKYVPFGGPSGGDGGRGGNVYVEVDTSMNS
LLPFRNEIHFRAGRGSHGAGRLKIGAKGEDVVVKVPPGTVVREADKDEILLEMVYHGQKALLLPGGRGGRGNAAFKSGTN
KAPKIAENGEEGPEMWLELELKLVADVGIVGASNAGKSTLLSVVSAAKPEVANYPFTTLLPNLGVVSFDYDSTMVHVVDG
SSPQPDLEFDAVRLELKLFNPELAEKPFIVAYNKMDLPEAYENWESFKEKLQSRGITPFCMSAAKREDGQNMVNISHVAH
ALQKQRSASIGDFEIFHDSDSNAWNVVGSGLQRFVQMTNWR
```

98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE

A0A2Z6RC04 **A0A2Z6RC04_9GLOM** (121 aa)
Uncharacterized protein. *Rhizophagus clarus*

```
MKRTNVINYSINRESIIDLPDIHHSLIIIPDTVYENTDITITNSGNKSTIITPTYKIEEEEEEEEEEEEEEEEEEEEEE
TVKSNDEKFVESNDKETKSREINDEKSKMFTDIDLSETKQK
```

58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE

A0A2Z6V0Z8 **A0A2Z6V0Z8_MICAE** (395 aa)
DUF262 domain-containing protein. *Microcystis aeruginosa Sj*

```
MKNSTNDITYEQLTSQETELQEEEEEEEEEEEEEEEEEEEEEEESSDFFDPTKIRITTKQITMDLLIKRIEYKEINLNPDFQ
RNANIWTDKAKSRLIESLLIRIPLPAFYMDATKEDEWLIIDGLQRLSTFKSFILDQKLVLKDLEFLKELEKNKYSDLSRN
YKRRINEAEFIVYLIEPGTPPKVKYNIFRRINTGGLPLNLQEFRQAINPGQAIKILKELANIPEFQKLTSFSQKRKNRMV
DHEFILGFIAFTLISYNCYSSDKGRDDFLDQAMKKLNKIDENRVQEIKNKFIFAMKAANNIFGEDAFRKIRKITEDGKRK
YPINKALFESWSVTLSDLSEQELETLIERKENVKEVFIKKMEDDSNFLESVSQAATKVPYRFDTIKEIIKEVLSC
```

22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE

A0A2Z6ZZY9 **A0A2Z6ZZY9_9LAMI** (284 aa)
Uncharacterized protein. *Dorcoceras hygrometricum*

```
MSLFDLQDVRIAIGSIATLDLPMVVDLIGIYGLKGLYCTLTTKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEVLGDESTPPSPPK
```

44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE

82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE

134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE
180 - 199:	EEEEEEEEEEEEEEEEEEEE
181 - 200:	EEEEEEEEEEEEEEEEEEEE
182 - 201:	EEEEEEEEEEEEEEEEEEEE
183 - 202:	EEEEEEEEEEEEEEEEEEEE
184 - 203:	EEEEEEEEEEEEEEEEEEEE
185 - 204:	EEEEEEEEEEEEEEEEEEEE

186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE
190 - 209:	EEEEEEEEEEEEEEEEEEEE
191 - 210:	EEEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE
194 - 213:	EEEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEEE
196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE
208 - 227:	EEEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEEE
225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE

238 - 257:	EEEEEEEEEEEEEEEEEEEE
239 - 258:	EEEEEEEEEEEEEEEEEEEE
240 - 259:	EEEEEEEEEEEEEEEEEEEE
241 - 260:	EEEEEEEEEEEEEEEEEEEE
242 - 261:	EEEEEEEEEEEEEEEEEEEE
243 - 262:	EEEEEEEEEEEEEEEEEEEE
244 - 263:	EEEEEEEEEEEEEEEEEEEE
245 - 264:	EEEEEEEEEEEEEEEEEEEE
246 - 265:	EEEEEEEEEEEEEEEEEEEE
247 - 266:	EEEEEEEEEEEEEEEEEEEE
248 - 267:	EEEEEEEEEEEEEEEEEEEE
249 - 268:	EEEEEEEEEEEEEEEEEEEE
250 - 269:	EEEEEEEEEEEEEEEEEEEE

A0A2Z7AGL0 **A0A2Z7AGL0_9LAMI** (195 aa)
Uncharacterized protein. *Dorcoceras hygrometricum*

```
MNPSTVAIPEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDFIYKCL
SSLLRRLISRIATNLSLEASRSRRYGVLVLLDPMVPAVVIFVANVEVDIHRRSVLEFRVFHISTGSYDTFLECVLRLEIS
VPLQHRRVGLVGRLEVGLFPVQPQRLGVLQPRGSF
```

10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE

44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE

A0A2Z7AN55 **A0A2Z7AN55_9LAMI** (96 aa)
Uncharacterized protein. *Dorcoceras hygrometricum*

```
MFSSWFDAFKESAVGLAMETSRVDSVSQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEDFVYKYC
```

29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE

65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE

A0A2Z7AXS7 **A0A2Z7AXS7_9LAMI** (358 aa)
Uncharacterized protein. *Dorcoceras hygrometricum*

```
MRIRPPELETSICDVKYHVSLVNGFAVTLAMSLFDLQDVCIDIGSLATLDLPMVVDLIGIYVLKGPYCTLTTTNWFLQAL
SVIPRGSWGDVARRFTMIRWATSNLTRAAPSPSTTSRSPPLRRRDRTCSDCLFEDLPPPTFQEPEFPVNLVGARRLDASK
SQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDFVYKYC
```

163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE
180 - 199:	EEEEEEEEEEEEEEEEEEEE
181 - 200:	EEEEEEEEEEEEEEEEEEEE
182 - 201:	EEEEEEEEEEEEEEEEEEEE
183 - 202:	EEEEEEEEEEEEEEEEEEEE
184 - 203:	EEEEEEEEEEEEEEEEEEEE
185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE
190 - 209:	EEEEEEEEEEEEEEEEEEEE
191 - 210:	EEEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE
194 - 213:	EEEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEEE
196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE

203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE
208 - 227:	EEEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEEE
225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE
239 - 258:	EEEEEEEEEEEEEEEEEEEE
240 - 259:	EEEEEEEEEEEEEEEEEEEE
241 - 260:	EEEEEEEEEEEEEEEEEEEE
242 - 261:	EEEEEEEEEEEEEEEEEEEE
243 - 262:	EEEEEEEEEEEEEEEEEEEE
244 - 263:	EEEEEEEEEEEEEEEEEEEE
245 - 264:	EEEEEEEEEEEEEEEEEEEE
246 - 265:	EEEEEEEEEEEEEEEEEEEE
247 - 266:	EEEEEEEEEEEEEEEEEEEE
248 - 267:	EEEEEEEEEEEEEEEEEEEE
249 - 268:	EEEEEEEEEEEEEEEEEEEE
250 - 269:	EEEEEEEEEEEEEEEEEEEE
251 - 270:	EEEEEEEEEEEEEEEEEEEE
252 - 271:	EEEEEEEEEEEEEEEEEEEE
253 - 272:	EEEEEEEEEEEEEEEEEEEE
254 - 273:	EEEEEEEEEEEEEEEEEEEE

255 - 274:	EEEEEEEEEEEEEEEEEEEE
256 - 275:	EEEEEEEEEEEEEEEEEEEE
257 - 276:	EEEEEEEEEEEEEEEEEEEE
258 - 277:	EEEEEEEEEEEEEEEEEEEE
259 - 278:	EEEEEEEEEEEEEEEEEEEE
260 - 279:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE
262 - 281:	EEEEEEEEEEEEEEEEEEEE
263 - 282:	EEEEEEEEEEEEEEEEEEEE
264 - 283:	EEEEEEEEEEEEEEEEEEEE
265 - 284:	EEEEEEEEEEEEEEEEEEEE
266 - 285:	EEEEEEEEEEEEEEEEEEEE
267 - 286:	EEEEEEEEEEEEEEEEEEEE
268 - 287:	EEEEEEEEEEEEEEEEEEEE
269 - 288:	EEEEEEEEEEEEEEEEEEEE
270 - 289:	EEEEEEEEEEEEEEEEEEEE
271 - 290:	EEEEEEEEEEEEEEEEEEEE
272 - 291:	EEEEEEEEEEEEEEEEEEEE
273 - 292:	EEEEEEEEEEEEEEEEEEEE
274 - 293:	EEEEEEEEEEEEEEEEEEEE
275 - 294:	EEEEEEEEEEEEEEEEEEEE
276 - 295:	EEEEEEEEEEEEEEEEEEEE
277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE
287 - 306:	EEEEEEEEEEEEEEEEEEEE
288 - 307:	EEEEEEEEEEEEEEEEEEEE
289 - 308:	EEEEEEEEEEEEEEEEEEEE
290 - 309:	EEEEEEEEEEEEEEEEEEEE
291 - 310:	EEEEEEEEEEEEEEEEEEEE
292 - 311:	EEEEEEEEEEEEEEEEEEEE
293 - 312:	EEEEEEEEEEEEEEEEEEEE
294 - 313:	EEEEEEEEEEEEEEEEEEEE
295 - 314:	EEEEEEEEEEEEEEEEEEEE
296 - 315:	EEEEEEEEEEEEEEEEEEEE
297 - 316:	EEEEEEEEEEEEEEEEEEEE
298 - 317:	EEEEEEEEEEEEEEEEEEEE
299 - 318:	EEEEEEEEEEEEEEEEEEEE
300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE
306 - 325:	EEEEEEEEEEEEEEEEEEEE

307 - 326:	EEEEEEEEEEEEEEEEEEEE
308 - 327:	EEEEEEEEEEEEEEEEEEEE
309 - 328:	EEEEEEEEEEEEEEEEEEEE
310 - 329:	EEEEEEEEEEEEEEEEEEEE
311 - 330:	EEEEEEEEEEEEEEEEEEEE
312 - 331:	EEEEEEEEEEEEEEEEEEEE
313 - 332:	EEEEEEEEEEEEEEEEEEEE
314 - 333:	EEEEEEEEEEEEEEEEEEEE
315 - 334:	EEEEEEEEEEEEEEEEEEEE
316 - 335:	EEEEEEEEEEEEEEEEEEEE
317 - 336:	EEEEEEEEEEEEEEEEEEEE
318 - 337:	EEEEEEEEEEEEEEEEEEEE
319 - 338:	EEEEEEEEEEEEEEEEEEEE
320 - 339:	EEEEEEEEEEEEEEEEEEEE
321 - 340:	EEEEEEEEEEEEEEEEEEEE
322 - 341:	EEEEEEEEEEEEEEEEEEEE
323 - 342:	EEEEEEEEEEEEEEEEEEEE
324 - 343:	EEEEEEEEEEEEEEEEEEEE
325 - 344:	EEEEEEEEEEEEEEEEEEEE
326 - 345:	EEEEEEEEEEEEEEEEEEEE
327 - 346:	EEEEEEEEEEEEEEEEEEEE
328 - 347:	EEEEEEEEEEEEEEEEEEEE
329 - 348:	EEEEEEEEEEEEEEEEEEEE
330 - 349:	EEEEEEEEEEEEEEEEEEEE
331 - 350:	EEEEEEEEEEEEEEEEEEEE
332 - 351:	EEEEEEEEEEEEEEEEEEEE

A0A2Z7CX91 **A0A2Z7CX91_9LAMI** (154 aa)
Uncharacterized protein. *Dorcoceras hygrometricum*

```
MVRNISISSGLVFMESAVELAMETSRVTSAVQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEIAVARVV
LQCKIFSTADVMSVEIVEAEYDGDVMMSGVFLWLTSSNPLRQTMSCLTVYEKLSIDTCTLFKNNTVARSDITSR
```

33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE

54 - 73:	EEEEEEEEEEEEEEEEEEEE

A0A310S8I7 **A0A310S8I7_9HYME** (406 aa)
Troponin T (Fragment). *Eufriesea mexicana*

```
EFWKILRDLSEDERQELKRVTFVFAPAYIRESGENIEFMKRQEQKRSDLDEQLKEYIAEWRKQRAKEEEELKRLKEKQAK
RKITRADEEKRLAQKKKEEEERRQREIEEKKQRDMEEKRKRLEESEKKRQAMMQAMKDQASKKGPNFTITRKDLAGNLTS
AQLERNKTKEQLEEEKKISLSIRIKPLEIDGLSIEKLRSKANELWDTIVKLETEKYDLEERQKRQDYDLKELKERQKQQL
RHKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGLTEQQKEIIEKQWTQQKEQFLGRQKTKLPKWFG
ERPGKKPGDPESPEGEEDVKAAAEDEELEEPQFEEEEEEEEEEEEEEEEEGDKKEGEGEGEEEEEEEEEEEEEEEEEEE
EEEEEE
```

381 - 400:	EEEEEEEEEEEEEEEEEEEE
382 - 401:	EEEEEEEEEEEEEEEEEEEE
383 - 402:	EEEEEEEEEEEEEEEEEEEE
384 - 403:	EEEEEEEEEEEEEEEEEEEE
385 - 404:	EEEEEEEEEEEEEEEEEEEE
386 - 405:	EEEEEEEEEEEEEEEEEEEE
387 - 406:	EEEEEEEEEEEEEEEEEEEE

A0A310SFR0 **A0A310SFR0_9HYME** (52 aa)
Uncharacterized protein. *Eufriesea mexicana*

```
MSTFLRTVGFSPEPISMRNNNEEREEEEEQEQEEEEEEEEEEEEEEEEEEEE
```

33 - 52:	EEEEEEEEEEEEEEEEEEEE

A0A310SKA7 **A0A310SKA7_9HYME** (758 aa)
NAD-dependent histone deacetylase Sir2. *Eufriesea mexicana*

```
MFDINYFGQDPRPFYKFAREIYPGQFKPSPCHRFIKMLDKQKKLLRNYSQNIDTLEQVAGIENVIECHGSFATASCTRCK
YQVKADDIREDIFSQRIPLCPKCRINILPPISEINLNESYKDLVTQGIMKPDIVFFGEGLPDAFHDAMAKDKDECDLLIV
IGSSLKVRPVALIPSSIPSHVPQILINRESLPHLKFDVELLGDGDIIINQLCHLMENIYKEVCWNGTILKEATQLLPIHY
LADDTWEQSQDTTSNTVLSRDSMETDFKPHDLCSIESQDSLMVHNNVVERYVENMNARISPFCTDHTNSIEEKLSILGES
PKRRLGESSVESSPKRMNFGSNCMLNFSLGSSKIDAISNTSIGYKFHAVSIESTSKDIGKIYSLGECQVFPRIIEISSEN
TLLDSTLKPNHHVENRASLKMNDVYPTSIPIEAEKINFKPRQASIDSALDSGVGDSCNSVDSQEDKNNKEELKNGRLGRH
YWHAKIRKSLAMRLPENSYYQLASGKYIFPGAEVYSDLEEYDHCSLSINSESSDSDCDSSSVEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEDEEEEEEEEEEEEEEEEEEEEVEVEEEEEEEEEEEEEEEEEEGEGKGDHDDEGEEE
EEEIEAAEGEEEHDSVEKEEEEEDEMKDKEKQIQINEDEDEMNVRKEDVKEEENKEKKVKEQKEVLKEQRKGEPKDNKMA
KETEKEKNQQITIKEEDERRNMSKLKNENILEDQRNGN
```

543 - 562:	EEEEEEEEEEEEEEEEEEEE
544 - 563:	EEEEEEEEEEEEEEEEEEEE
545 - 564:	EEEEEEEEEEEEEEEEEEEE
546 - 565:	EEEEEEEEEEEEEEEEEEEE
547 - 566:	EEEEEEEEEEEEEEEEEEEE
548 - 567:	EEEEEEEEEEEEEEEEEEEE
549 - 568:	EEEEEEEEEEEEEEEEEEEE
550 - 569:	EEEEEEEEEEEEEEEEEEEE
551 - 570:	EEEEEEEEEEEEEEEEEEEE
552 - 571:	EEEEEEEEEEEEEEEEEEEE
553 - 572:	EEEEEEEEEEEEEEEEEEEE
554 - 573:	EEEEEEEEEEEEEEEEEEEE
555 - 574:	EEEEEEEEEEEEEEEEEEEE
556 - 575:	EEEEEEEEEEEEEEEEEEEE
557 - 576:	EEEEEEEEEEEEEEEEEEEE
558 - 577:	EEEEEEEEEEEEEEEEEEEE
559 - 578:	EEEEEEEEEEEEEEEEEEEE
560 - 579:	EEEEEEEEEEEEEEEEEEEE
561 - 580:	EEEEEEEEEEEEEEEEEEEE
562 - 581:	EEEEEEEEEEEEEEEEEEEE
563 - 582:	EEEEEEEEEEEEEEEEEEEE
564 - 583:	EEEEEEEEEEEEEEEEEEEE

565 - 584:	EEEEEEEEEEEEEEEEEEEE
566 - 585:	EEEEEEEEEEEEEEEEEEEE
567 - 586:	EEEEEEEEEEEEEEEEEEEE

A0A314KLG6 **A0A314KLG6_NICAT** (2033 aa)
Uncharacterized protein. *Nicotiana attenuata (Coyote tobacco)*

```
MGVELLEIGVQMRRVVMFSIKGCYKTVLNHPFLASMLCFITFLYRSFPFLFSILVAISPVLICTAILLGTLLSFGQPNIP
EIEREEKTTHDIVPLKTGLLCDTTHIESEDSYYVERYTDNERNVVEQSIDKVSHLSPLLEERSREFQFGNGVFDEAAREF
YEQNNEKSEEKHSDGEHTEDLYSPIPTVDGDFEEAEREFYEQNDEKNEEKHDDDELMESQYPPIPMVDEGFEEAEREFYE
QNDEKNEEKHDDGELIESQYSPIPTVDNESIDFDFDRSDSFDSKRVNLNSLPGSPWKKEESDKEEEQEEEDDESFDSESD
RAESSSPDASMADIIPMLDELHPLLDEDTPQHVSLSHDDGFDAASDSSGKFSASDNESDDGCENQEEVEVAHDENEEETR
DKEDKSKSAITWTEEDQKNLIDLGSSEVERNQRLESLMARRRALKKMRLMMTEKNLIDLDTADLPFNIPPISTARNNPFD
VPKDNYELGLPPIPGSAPSILVPRRNPFDLPYDSSEEKPDLMEDSFEEEFMAFRPKEPVLRRNETFSARPSLFGMNRQDS
HFRPYFVPERMASEGTSYSPFQRQSSELSDSKVSSVPETDSLGSVEDLIEEVNVRHKSLDEEELEHKDLIDEHISEEPEL
ISKMEHTSEHVRNGSESSEEVESLEQLGAVEIHHEVEETLLQEGRVSDALELNPTEIQSKSETSDQIYSNQSSSSSLEVS
ERVFAYKEEEEEEEEEEEEEEEEEEEEEEEEEETMSSLEETMGDVEQNGISRQTSFNGSDFHITSTSAEQTSHWEPIYDTS
PSAIMENTFSASLSSDQLEESETGFSPILVKRSVSFLERESEESSQDIERSISTNEEISAPVDDQESLSRNEVCKRELDV
GKAEISQHDEFFGSASAPPVPEFVVGQASTDSKLSANEDIGYEEGTIEHALQQIYSSGFNADTCIVPQHAVDQTVEFLSK
SSEHENIHQLDEQHSLIAEEVPLVQPDVRSLERDSVDDAAQKEEAIISEINDLPSSNNVVNLVTDAHSELDEKLISSEHQ
FASVEKSSSLCEEDTACSDKSMDEESSEDHNVMEPPVILVESIEEASTTENLNVPEIHDLGDGIPIINSPRTPDSFSNLH
EVDEAPRGAGLSGLRNNILDELENDNQIKVLENYVLPLEAADFHHDEQYIVEETDGISDIDEVFLSELDTVGDFSIKGSS
QNEFERQINSSAEDLSPFHAVDSVTTEVYEGACAEVHERKLPLHPEILNASTFEEIDEHEEKECASDIQNYGLISIDHID
VVYPRSIEGGLPEDSETGPSDPSVKHNVDAQEIVPEMPIVEAQNSVFEVENLQSTQTGVTEEETDSGMPVLEAQTIQDIE
SAFWQVYEKETEKSNVLEQSDGEDSGMPVLEAQTIEDIELAFRSTSEKEIEHSDVLELPNSELVTEQSGCSNNDAAVEMS
SSVQEDSGMPVLEAQTVENIELAFRSTSEKEIEHPNVLELPNAELVTEQSGSSNNAAAVEVSSSVQEDSGMPVLEAQTVE
DIEFAFRNIWDKEIENSDALELPNAKVVTEESGSSDNAAVFEVSSSVQKNSGMPVVEAQTIEDIESAFRSTSEKETENSN
VLELVTEESGNNTAAVEVSSSALEDSGMPVLEAQTVEDIELAFRNIWEKEIENSDVLELPNAKPLTEESGSSDNSTVFEV
SSSVKEDSGMPVLEAQTIEDIELAFRQISEDETENSNVLELPTAELETEESGNNVAAVEVSSSVLEDSGMPVLEAQTIED
IELAFRQISENETETENSNVLELPNAELVTEESGNNAAAVEVSSSALEDSGMPVLEAETVEDIDTVFRRISEKEIEKSNV
LEQPNAELATDISGNFDNAAVLEVSSVTRAMQLPILETRQTEYFDLDHEDLSEGDGDEHTEKSRDIGASSDSQNFETDLA
LKQVLEANLERPLKSTSEGELAEVKPSGAGSSNMESSARGSDVSGFGEGETGKGDHEVVVKEAKELTAEKPDHVVDMPTT
ADVKSKKDKHQKSGSSSSSSSSSDSSSSDSERE
```

728 - 747:	EEEEEEEEEEEEEEEEEEEE
729 - 748:	EEEEEEEEEEEEEEEEEEEE
730 - 749:	EEEEEEEEEEEEEEEEEEEE
731 - 750:	EEEEEEEEEEEEEEEEEEEE
732 - 751:	EEEEEEEEEEEEEEEEEEEE
733 - 752:	EEEEEEEEEEEEEEEEEEEE

A0A314Z1F2 **A0A314Z1F2_PRUYE** (961 aa)
Vacuolar protein sorting-associated protein 41 homolog. *Prunus yedoensis var. nudiflora*

```
MAPIPPDNGVEGDDEREEEGEEEEEEEEEEEEEEEEEEEEEEPRLKYQRMGGSIPTLLTSDVATCIAVAERMIALGTHGGT
VHILDFLGNQVKEFPAHTAAVNDLSFDIEGEYIGSCSDDGSVVINSLFTDEKMRFEYHRPMKAIALDPDYAKKSSRRFAA
GGLAGHLYYNTKRWLGFRDQVLHSGEGPIHAVKWRTSLIAWANDAGVKVYDTANDQRITFIERPRGSPRPELLLPHLVWQ
DDTLLVIGWGTSIKITSIKTNQSRAANGTVKHVSMPMSNMNQVDIVASFQTSYFISGVAPFGDSLVVLAYIPGEEDGEKE
FSSSVPSRQGNAQRPEVRIVTWNNDELSTDALPVHGFEHYKAKDYSLAHAPFSGSSYAGGQWAEGDEPLYYIVSPKDVVI
AKPRDAEDHIAWLLQHGWHEKALAAVEAGQGRSELLDEVGSRFLDHLIVERKYAEAASLCPKLLRRSASAWERWVFHFAH
LRQLPVLVPYIPTENPRLRDTAYEVALVALATNPSFHTELLSTVKSWPPVIYSSLPVISAIEPQLNTSSMTDALKEALAE
LYVIDGQYEKAFSLYADLLKPDIFSFIEKHNLYDSIREKVVQLMMLDCKQAVPLLIQNKDLITPSEVVKQLLNARDKCDS
RYFLHAYLHSLFEANPHAGKDFHDMQVELYADYDSKMLLPFLRSSQHYKLEKAYEICIGRGLLREQVFILGRMGNAKQAL
SVIINNLGDIEEAVEFVNMQHDDELWEELIQQCLHKPEMVGVLLEHTVGNLDPLYIVNMVPNGLEIPRLRDRLVKIITNY
RTETSLRHGCNDILKADIVNLLVKYYKEAIHGIYLSNEEDEARTKRNDSRASQVIEKSPGVRSMEVKSKPRGGARCCMCF
DPFSIQSLNVIVFFCCHAYHMTCLMDSTYTSGIKGTGATSSERVADNEYDDRVVEEDDDDTQSGDSRMRCILCTTAASRV
R
```

21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE

A0A315VS04 **A0A315VS04_GAMAF** (828 aa)
Uncharacterized protein (Fragment). *Gambusia affinis (Western mosquitofish) (Heterandria affinis)*

```
KEEPTTYTCTTCKQSYGSAWFLLQHAQNSHGFRIYLESEHGSPLTPRMGGPSSLGGGADCPSQPPLHGLHLPPDASPFNL
LRIPGSGSGGRDSVGAGGAIGSGVPGGHHQRFPPTPPLFSPPPRNHLDPHHLSPEELALAAHHPSAFDRVLRLNPPLPLD
PPPTMDFSRRLRELAGNTSGSTPPLSPSRPSPMQRLLQPFQTGGNGGAGGAGGSKPPYLATPPPLQGSMQSPVGSQTTPP
TPLPTAGPPSSSNTQLKSKCCEFCGKAFKFQSNLIVHRRSHTGEKPYKCHLCDHACTQASKLKRHMKTHMHKSSSPNTGK
SEDGLSIASSPEPGTSEHIGSASNALKSVVAKLKSENNRMLRENGEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEVQNG
ERPPKRNNSYHFGLSLEAARQHENSSSIGSRLGGVADETSIPRSLPEVMQGMGLAASMQHFSEALNAHKRNAMAQENHLH
HHLSRDHHHSRDMCDGDSVLETERVEEGTVSAVNGRGVSPHESSSIGLSKKLLLGSPSPLSPFSKRIKLEKEFDLPTPTI
PNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRFSTPPGELDGGMSGRSGTGSGGSTPHLGGPG
RPSSKDGRRSDTCEFCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQSSKLTRHMKTHGQVGKDVYKCEICQMPFSV
YSTLEKHMKKWHSDRPLSTEIKTKLLLLKAEVSKLLNVHLTEQSFPSLTSQSAVMTDGWKHNTRLAFSRVRKGPPSDPCL
HWLAELMENPRGLSWIKGCPGVQERHGL
```

366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE

368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE

A0A316E8I0 **A0A316E8I0_9BACT** (463 aa)
Papain like protease. *Arcicella aurantiaca*

```
MYNHQFTTMSLKFDQQGGSDREIKGYEYLAPSADAEKYKASSKLKNAEMPSKVDLRSYMTQVEDQQRLSSCTANAVAGAY
EYLAKKYLAKKAFDVSRLFIYYNARLRAGGTIKDAGSHIQYAVDSLMKIGACKESTWPYEAKMVNEKPHEKSYEVAADFK
IETKKFVPVKLEEWKKSLADGYPIVFGIALFPSFDSCTKNKGIVPMPSPDEASRSAHGLHAMLCVGYSEVDKMFIVRNSW
GEKWGDKGYCYMPYEYVINNKFNLGDCWIFGRTTPIPESDDTWINDKKSVIDNGRGYDRKDYIFYKENDYKTFDIWEFID
VYEYDEEVPEEYDELEYEGTGEYDDILAEYEDEYYEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEAGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAGEEEEEE
```

356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE
379 - 398:	EEEEEEEEEEEEEEEEEEEE
380 - 399:	EEEEEEEEEEEEEEEEEEEE
381 - 400:	EEEEEEEEEEEEEEEEEEEE
382 - 401:	EEEEEEEEEEEEEEEEEEEE
383 - 402:	EEEEEEEEEEEEEEEEEEEE
384 - 403:	EEEEEEEEEEEEEEEEEEEE
385 - 404:	EEEEEEEEEEEEEEEEEEEE
386 - 405:	EEEEEEEEEEEEEEEEEEEE
387 - 406:	EEEEEEEEEEEEEEEEEEEE
388 - 407:	EEEEEEEEEEEEEEEEEEEE
389 - 408:	EEEEEEEEEEEEEEEEEEEE
390 - 409:	EEEEEEEEEEEEEEEEEEEE
391 - 410:	EEEEEEEEEEEEEEEEEEEE
392 - 411:	EEEEEEEEEEEEEEEEEEEE
393 - 412:	EEEEEEEEEEEEEEEEEEEE
394 - 413:	EEEEEEEEEEEEEEEEEEEE
395 - 414:	EEEEEEEEEEEEEEEEEEEE

396 - 415:	EEEEEEEEEEEEEEEEEEEE
397 - 416:	EEEEEEEEEEEEEEEEEEEE
398 - 417:	EEEEEEEEEEEEEEEEEEEE
399 - 418:	EEEEEEEEEEEEEEEEEEEE
400 - 419:	EEEEEEEEEEEEEEEEEEEE
401 - 420:	EEEEEEEEEEEEEEEEEEEE
423 - 442:	EEEEEEEEEEEEEEEEEEEE
424 - 443:	EEEEEEEEEEEEEEEEEEEE
425 - 444:	EEEEEEEEEEEEEEEEEEEE
426 - 445:	EEEEEEEEEEEEEEEEEEEE
427 - 446:	EEEEEEEEEEEEEEEEEEEE
428 - 447:	EEEEEEEEEEEEEEEEEEEE
429 - 448:	EEEEEEEEEEEEEEEEEEEE
430 - 449:	EEEEEEEEEEEEEEEEEEEE
431 - 450:	EEEEEEEEEEEEEEEEEEEE
432 - 451:	EEEEEEEEEEEEEEEEEEEE
433 - 452:	EEEEEEEEEEEEEEEEEEEE
434 - 453:	EEEEEEEEEEEEEEEEEEEE
435 - 454:	EEEEEEEEEEEEEEEEEEEE
436 - 455:	EEEEEEEEEEEEEEEEEEEE

A0A316YH99 **A0A316YH99_9BASI** (919 aa)
ARM repeat-containing protein. *Acaromyces ingoldii*

```
MSSASASAALQYLSERAEDAAEAVKGFVGAGSSSTSSSRYTNFDESLVRSQLESDRDDQKLEGLRAVVAGLSSPMSATNA
SLLPSVLKLAASPNVEMRRLVYVVLRRYAHRQPDVALLCINSLQRDLSDSSPMVRAMSLRVLSGLRVPVVASVVELAISR
AIKDQSFYVRKVAALALVKVKPLIATSTLERFVKTLLQDRHPAVLACALVAFRSVSSMPPDYSLLHPHYRKLCHALTDMD
EWGQQVAIHVLGSYARRCLSRPKDEEDGNGQMDVDLKLLINKAEDLLASRNAAVVTAATRLLVAVAPSKQYHGSASRALT
HLVSSSSSLPEEVYVALLHCMLLLSSDTIADFAAEIDAFIPRSSFIEPGYVTVVKLQILARLAPSSSASARLVLTELSEQ
AQFHPNVDVARTAVDLIGQLSTVNDASACLDALLSLLGQRGAIVASAVDVVCRLVFARQQQQDDQTTSTIIAKLASLLFD
GQRPPAVAAKMAAQGKRPKLVASKGTVSQPTARAALYWMLGQYCRLTIKVRDQAGNSTMTATLAETVVADIVRRAALNFA
KEDKAARLQIITLSTKLDAFLPTISSMAILTPESRKALSLLHTYLLQLARYDADIDVRDRARLCKALCLSLQQQDNASSG
EEKEGKDKGDGAEEDGDDAMTMLGGVRLRRPQILHVLFEGRPSEDSSRVSNASAADVPQREAASLDVLSYLSRKKRGKDT
SISSSSSHHTEKRAEFDHFDFPPWNEGGDGALPPTSVREPQIEGPSVLALNTGKSFSSAAVGNAAASGSGNREKLIPVES
VDEDETKERQRVGGSGSKYKDLDAFLDEESEEEEEEPAPALRATRTLQAKEEELEEEEEGGEEEEEEEEEEEEEEEEEEE
EEQSEEESDEEEGLSSGRNIPATSSTATPTLALTNEWAD
```

862 - 881:	EEEEEEEEEEEEEEEEEEEE
863 - 882:	EEEEEEEEEEEEEEEEEEEE

A0A316YI02 **A0A316YI02_9BASI** (1686 aa)
Mediator of RNA polymerase II transcription subunit 13 (Mediator complex subunit 13). *Acaromyces ingoldii*

```
MAPLSQGRHGLSSSRKSTHAPGPSSSSSLNGAGSSGFGLGGTSGTGHSRRAQYSLPPPLVPDCLTSLSRISTPADDALLR
WRRFSGSSEELEAGQEALCRLSAEEVRAKGRESLLPGYDCQGRGTLDKILDGILWAPEHAAAGPLIALWLFEFGTQEGER
KFGLERLTCTWGSTQLSSFYEPLSSENISSPDILRPQQPNLDQAQRLFLLAIEEKAMSRWIYTRAREKKLASESSSRDGD
DDISVPTVPNQESHQDASEQGPILNEVLDKHTAHTPAYWKRAGRRDAIRFGRSILLASRRGQGLIRLGLRATLSDGGKLF
LETRPLVSQHLKPIFSQASAPSGTRVMLSPLASEARLIDWVGGLIDQDAEGEAAARLKQARSELLSRIGDRGVNVESLSS
DWVLCETDSPPVDQKQEGEENASSTRRFLWPADLVFACESNPLQALEPQRPKMQPHGAMEIVSMCTTELAQRTVDMMRGI
PIETAKRAKEAGTDPGSVTGRRHSNDTSEGDEEEEEADEGERVKKEEEVEEEKEEEEEEEEEEEEEEEEEEEEVEEEEGE
EEGDSTLPRRRVGENGDDGAPVEDGEEDNDVDVGDDTIRSARLEERENEGKAAALAPAQGPAIASGEVLQEGEQAVAESS
KSKEDADMDLWGDFVYEGESRQRQPSSSPAKQTNDDDDGGMFGLVTEDDFSFFDDAAAAAAAAASAAFDVETPTASVTGD
DEEMRFSEIDNSEQRQDEITSGPMAVDSLPRSNGNSSSSFSTSTIVDHPSVPGFTPSSLSASSPAAHGAHAAKTPRTPYS
PTQDMADAHVTIEGEHQGDMYRHSSRISAGGGAPPSAYSAAGGEGEGLEYDDTGSTPFSIQEPGSKEPDSPRKNFDLSSK
YEMGKYAISQRPFRRRASRRGPLAGIRSNQLLNMTGISQKRRLNRRGGAEQEDETMVDGEGMTPATASERSSLLAEDSEV
DSSRKSELGDEDDEEGIEFDMDGFGQDSDDAASGSDDETDTSIDSAQQAEILAHERHALLKAALTISQAAQARRESQNDT
EMAVREHQKKPWPAAATLDVLVSWALDIVTFRDAIVQFFQKYETRPLCLDSRDSFELLTPLESTSACSLGTIFKETRVLE
EPSILVGCQGSVTSIKPPAISFWDKLGLTPVSGQKQATAFALQVADASEGWAREVRSYFDRMQQAFRSYGLGSHELADDG
LLGIGFPGESTISEALASIHNSTDRWDDSMDSLLSRFKPYLKSGSTILVYVVGEPSSPPPFWAMVLLQTSLQTRVKERLG
LPMQRLLVRPLLWRWTSSSGPSLSTTVGQSSSLFGPGRQSFNMSGQARSIYDSLQVTVVPRVNEEPFLPQLPNDKGLPVR
FPHLTLAPSAHLTRSRSTSTGRAASEQRFDLRWPTTYVDVVHRSVLLHVGYYIATSEEELTIVTVMDELAQGYDIKAWPG
GRGAQKDIDDIWSFACHFARKAKIGWKVVICRGAGGLQFEEVEMWSRLLSKPSSFVGLEHVVDVSLALADDQSNLAIVAP
TSMARRTQTEVPTSQEGRLKHSIDTSRVSYVLHPAARIGVTISDGEDVDSQILALRSSLTVTLFQQTNMSTSIAQPSCLF
HSALCPHQLWIHLLQVYPNPLSRLEKGTNDDLEHSLDERMRRMANSFHDLEGVARYRHQILEVGQHLPWHLAMLTLLLHG
SQLFRR
```

534 - 553:	EEEEEEEEEEEEEEEEEEEE

A0A316YKG7 **A0A316YKG7_9BASI** (1219 aa)
Uncharacterized protein. *Acaromyces ingoldii*

```
MRRQYVAQPASTGGGGAGGPDAVRTPSRARVSSGERASGGRVASTSAAAAAAAAASAGGSQRRGRRSAYDSFDSVGFLND
MTERMRRELQRPFGHGASTSSNGYHSPDDGGGDEGWRGSKAAARRSDEGRVDAATQTEGSYDDDEEAPMILGIDRTQTEQ
LKRNAQSFLRMAAQAGAPLDAHQGAFDLFGPEDEDDEDEQEAQGEEEEEDEEEEEEAGDAVHDRIASMLAAPADGKPAPA
AAKMLIQVRGILNSRRGVVLTVLHPSFQELGGAEKEHGAADSSEEEDEDEDDEEDDDDDDEEEDEEDEEDELAEKEEKEE
EEEKEEEGEEWRAEFGTEPVRVGQDDAISLSDSSEDQDDGEAGQWAEHDEQRDEVDEDDDDEEEEDEEDEGEDEGEQHRA
DDDALQPPPSYSGAVWPDAPSSAAPIREWVPSSSDDAAASPSNLFDQLSAAVSSGADFSWALPASTMADAAVADSAREGE
GNAAAHFDAGSFFSEMAGPLAIAVAAQQQQQASDAPAQGEAQPGADSAASDLHRLRGLVAEAQQQAEAAATAAAASLADT
NAATLAPATEPALESAHTSSHLAPQTHPLPHTLQRLHSEGSIAGAVPASNVATPGGGSSVGGDDEHVQPSSPAAKLFDAS
GDGAAQPAAVPLVENARDLLELKVEARAGAHGEQLRLQSPTGSVQAEAGSAYGANTPRRGGAGAGAGEDGAVARTASKLR
SALEAEQQADVDDVEPAPAGEEQNGALDGMSEPGDSAGGGDGDGDNSEGEGVMEEEEEEEEEEEEEEEEEEEEEEEEDD
DDDGIALIESRAARQAAQSASTDAQEAAPVGLAEGEERRAASATPVLDEAAADDDGDEDAEKADVVEDALVADAATEREE
EEAPMIVTRAMSRALDEEAAAAAEEQVSAELDPPSFAFSEGPGGQEHRRKRSRSKSRRSDPNGDMADYVPVPSSSSSDSS
GEAGRSGRRVRARTQEAEEEQEKGKEDEADLSVAVLEELVSDGQQPGDGRSEVALEEEAGAGEEEEEEEEEEVVVEKEEE
KAAAPVAEEEEGEEEGEEEEKEAQSQATTRRKAKAATRASTKRTSKRASPARATTRAKGRSAAGTTPAASTAPAARRAKS
ERRTRSTTPANRGELDEEEGGDAPGDKKRKRTAAPTRQSPRRAPTGRGRGAGAEEAAEEKGPEKEEKEQEQEQEQEQEQE
QERPKTRRRSARTSSRAPV
```

774 - 793:	EEEEEEEEEEEEEEEEEEEE
775 - 794:	EEEEEEEEEEEEEEEEEEEE
776 - 795:	EEEEEEEEEEEEEEEEEEEE
777 - 796:	EEEEEEEEEEEEEEEEEEEE
778 - 797:	EEEEEEEEEEEEEEEEEEEE
779 - 798:	EEEEEEEEEEEEEEEEEEEE

A0A316Z7K0 **A0A316Z7K0_9BASI** (1927 aa)
Uncharacterized protein. *Tilletiopsis washingtonensis*

```
MAAPAPEPTLLEAAEQEAPYLTLRQLALGVTLRLSAALSAEQSEDATRTALGALAVSARKDLLAARTKGGFAVHRLSSLR
TTFQTSTRNTSPDVSASALRTVATPAEVAFLRIADSDAALVVGLENGTVLVWGTEALEGEPRFTIAPPSPAGLLDIVAQP
GEQASLCACAYASDGAAGRVALLDVRSGAWQSELSAPAAAASVCWSVRGKQLALGLADGSIAQMDPTDALKDTVARPPDL
PEGHALIALRWLENHVFLATYNAPPSADEPAPHDESTYAIARAGGALTYTRFGEPAPAFGDAARRTQRYMTAVRGWAPTK
HLVFVAASASTDIGALALAESGWQNLELEETSRPVLPFAAHDRASDTAPVALELDTGATEEIDDPLAAARGDDKKLPAAP
ILLCYTNDGVLMAYHIINTEEPACPAMLSATETSAQQAATPAAAPATPAAAAAPSALAFGASSSAAPAFGTPSAFASPAA
PAFGAPSFGTPSTPGAPPAFGASSFGKPSTPGAAPAFGASSFGAPKTPATPFGASSSGSGSGGGFGAFASKPVGFGAAAG
SSTGFSFGAPKDAKKPDSVFASPSPAPSSTAPTSAFGAPSTPAFGPPSPAPSSTAPSSAFGAPSAFGKSPFGTPSAPATS
SPSSAFGSTTASTPPAFGATSSASAVSAFSAPTGFGSSTSSTPAFGSTSALTAAPAFGSSSAFGTGPRSSATPPFSTAGA
FSAFSAPSSTGSPSAFSAFATAKPAFGASSDAPGGSVFGSGGKLAGAAAPPDAPPSGFQTSGFRTGSSVTPAPAASASSA
QPSPSTPAASGSGSFGFGSMSAMLGEESDSKQTTPAAAEQPVPETSTPEKQSSTGENATPAPKASEPPAAPSPKPFSFAP
SSTPSSAGQAPAKPFSFAPSASADSPATSAASSAPAAKPFSFASPAASAAKPAAPSAFASTSAFGGSSAFGGTSAFGSAS
KPGSAFGGTSFSFGAPASPAEKPASPAEKPSAADASVSADRSAEQADETQDQLEDEEDEEDEEEKYSVEHDDEEDEDEQE
QDEEETFDESGAEEDAEEDDEAQDESAGSEAHGEPQRSTTPPSPAAPIKVKEEPVSPPRAPSRSPPASPAKPPPSKPFSF
ASSGDKPSFSFGTPAAASQAKPAEASGSKSSFSFAGAALAPAAPAGKAPFSFANAGDAPKAADKPQQSSAAPASKPAFSF
AGPSSVPAPPPPASTPSAQPSFSFGSPSKPAAPAAAAASKPTFSFGPAPTTSSSSDASESPSSSSAPTRAPFLGNFNSRA
PRSSSPLTSTPVNRADLSPSPEKAKAKPAQQGSRPPQPLFGQAAEAPKAAPRDVSPSPAPLPPPVTNAFANAQPPRLGAT
VSSLGPNDVQETGVAGEFLRTFLTIEQELRVLRSNVQRCDAFQAELRQASGGAFDGTPWTFGDLPSMLTLARELGGEVAT
FDERTETQRRRAAEVQSLLLKAEAKREEAARYVRAHADPQLARLLRVRELGPEHAENQTKLRRATQAVRTRLAELEEHVT
ALRRRVVDDRAGRAPPMKGPSLDSMRRAVRNISSMAAARILDLDALQTQLELAAGPRGGSTKRGVSRAHSVLDSIGDLSS
ALPSPPMPQRRHGGSASALAASAIASQRGAADLRQAFTAQRREPILSRAPGLRSSSSSTAAEAKTARRFAASDLEIAFAR
GPAHVSAPVLAAPAQPAPVKAVPVPASAAPAPTAAPAPFAASASFGTPPTRAGPSAAPVLSAAAASAASGSRAAAAAPFA
GFSFGPAASLPPSLFSAPAGAGADDGDTFAPGARAPSHSPSARQAPRASKRSSTAVHLPQGHVPPAAAAAAASSFFARPD
AAAPAPQFTTFKGLEAPKRVVPLVVEEDSSSEEDRRALSDGEDEEDTERGEEEEEEEEEEEEEEEEEEEEEEEGLSPVEE
DEEDDGE
```

1891 - 1910:	EEEEEEEEEEEEEEEEEEEE
1892 - 1911:	EEEEEEEEEEEEEEEEEEEE
1893 - 1912:	EEEEEEEEEEEEEEEEEEEE
1894 - 1913:	EEEEEEEEEEEEEEEEEEEE

A0A317VR43 **A0A317VR43_9EURO** (177 aa)
Uncharacterized protein. *Aspergillus heteromorphus CBS 117.55*

```
MPTITQPIRSITPPQKGRRAASVSSEESFISEEEEEEEEEEEEEEEEEEEEEEVLMESDSEPEPDSPRHGKQPVAAVQRRQQ
DSTQPRALQRTRQRQKQQELQPYRRTGADQAADEEGQSLTSVRGRHGDLQAKGESSAGQGVQEEGKDGLKLRLDLNLDIE
VELKAQIHGDITLSLLQ
```

32 - 51:	EEEEEEEEEEEEEEEEEEEE

A0A317VWT4 **A0A317VWT4_9EURO** (111 aa)
Uncharacterized protein. *Aspergillus heteromorphus CBS 117.55*

```
MTTGREACQTASGHVEQQSGSQFIEEEEEEEEEEEEEEEEEEEEEEKKNLGNRQSIHRSSSSQVEALRILLSRTNGFEDWRR
RGEEMDGWIMDAFHFLACHPSRPGRYSTVLY
```

25 - 44:	EEEEEEEEEEEEEEEEEEEE

A0A317WQ89 **A0A317WQ89_9EURO** (953 aa)

Ent-kaurene synthase. *Aspergillus sclerotioniger CBS 115572*

```
MSDRAAASMDVRAARIIASLAESLETPYQGSSSMTPTVYDTAWASMVAKDGEWLFPECFQVVLDSQSPGGGFGVDEGAPP
PPQLDGILSTMAAVLALCKYRKSPSSSIRGGPHCILPPSSSDLQDRIDRARAYLDQALQCWNVHSTVQVGFEILVPSLLR
LLHEEGLHFDFPGRKALMALHRCKIDKIRPALDTPHPPQTTLLHSLEGFIGCMELGNMAPCLANGSMMGSPSSTAAYLIH
SPEWDKEAERYLRFVVARNNGNVPSAFPISVFEISWVLSTLLDSGFEADVLGTENVCTLAAYLESRLAEDNGITGFAPGM
LADADDTAKSIYSLSLLGRSTDCAAMLQAFEGHTHFKTYNLEAKESFASTAITWESGKWSDKWNIESQYAIMLLADALAS
LIDRWQDGALGDLDPNFLADHVPRVTLQIVVRTLSAQSEDSGSWKQSPEITAYGLLTLKALVSFPWVRTAIGAQVIDEHI
DRAIKYLRAHEDRWNDPEMIWVEKVNYGSSILSETYCLAALRRKATCPSRWGEPVGDLCKVPKERLDRFCRFFARLPIFK
GEPTWRLRASILEGDLLAPVLRRAALELAIFPFPQGDGMKTAKYLEYIPLTWTTSNNAAASFGLSTATMVEMMVLSLLNF
QVDRWFEETTEDPRLQGDWAALRSVIGELFTDDDDPKERKTPNGHHNHKRRQRGDLTGHGPAMVADEEEKAAFLAEAKRT
LARFVQGGVLQKVSVRSAPPALRRRVRQELRTFLLAQVTQGEDNNKNHDSKATPIMTRTYYEWVHTTSADHTSCPYSFEF
FRCLVSSGAGGDCFVGPRAQYLAQDFCRHLATMCRQYNDYGSMARDQEERNLNSIDFLVLGKEDDDGDDDDHAKEEEEEE
EEEEEEEEEEEEEEEEKKLLLLGIAQYERECLELAVQRLQPQVSKPAWKAWRVFLAVTDLYGQIYVAQDINSR
```

875 - 894:	EEEEEEEEEEEEEEEEEEEE
876 - 895:	EEEEEEEEEEEEEEEEEEEE
877 - 896:	EEEEEEEEEEEEEEEEEEEE

A0A317X3Z1 **A0A317X3Z1_9EURO** (727 aa)
Uncharacterized protein. *Aspergillus sclerotioniger CBS 115572*

```
MSESMQIPVRSAKSGIPSIFWRPEVARFIFNNLPRHSLKNVRLTCKCLNDLVVSPLSHLFSRVYMSAQREDLKVFARISQ
HPRIAACVRELIWDVSIFYGIDDDLYWLSWIGRDFRVLTWALPQLTGIKHATLTSLMSRWITMDSDNTSPAPALFGHLVD
ESQINHLHPTRPYICSVESPAMRHWNPRARSWRKAPEWNEAVRPLMNSDDDEIYHYITQLLHSPEDIDCRGEAFSNIHDR
HDRAQILLLTACRRANINLLSYTVDAPHISCDRTDEKPSIEPFPGIAFSPPVCSALMKAGLSEHLRSLRHLSLSLDAGTW
SKWYHAFYTEDLQTLELRVYKEAFVDREIFKAPFSKLKRLVLGNFKISGEGYGFLLNWCTENKVQTLHLIDPVFESEKRC
PARKRFLDLLNRDILYRNKSFVFNTDRPGYKNWKRRERFMKEVHDIRTRYSKKGRSMDFDAMPVVQDISLNQESESGSGG
GDHISDCSSEGDDTSESDKSMETGDSDASDDSDVMEDSGGEEGEEEEGEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEGEGEEEPNQGSEEEDSEEEDSHGDDESDAMDDSQEDDKYDECEDSSDE
MDIDLTSKFESLAIQPSDSDYSESDTDDSSESDDDEIDIQHEIPFPRLRPDVAYDLLSIEGESFEVRIAQWRSEPLRVLI
DGYRTKC
```

534 - 553:	EEEEEEEEEEEEEEEEEEEE
535 - 554:	EEEEEEEEEEEEEEEEEEEE
536 - 555:	EEEEEEEEEEEEEEEEEEEE
537 - 556:	EEEEEEEEEEEEEEEEEEEE
538 - 557:	EEEEEEEEEEEEEEEEEEEE
539 - 558:	EEEEEEEEEEEEEEEEEEEE
540 - 559:	EEEEEEEEEEEEEEEEEEEE
541 - 560:	EEEEEEEEEEEEEEEEEEEE
542 - 561:	EEEEEEEEEEEEEEEEEEEE
543 - 562:	EEEEEEEEEEEEEEEEEEEE
544 - 563:	EEEEEEEEEEEEEEEEEEEE
545 - 564:	EEEEEEEEEEEEEEEEEEEE
546 - 565:	EEEEEEEEEEEEEEEEEEEE
547 - 566:	EEEEEEEEEEEEEEEEEEEE
548 - 567:	EEEEEEEEEEEEEEEEEEEE
549 - 568:	EEEEEEEEEEEEEEEEEEEE
550 - 569:	EEEEEEEEEEEEEEEEEEEE
551 - 570:	EEEEEEEEEEEEEEEEEEEE
552 - 571:	EEEEEEEEEEEEEEEEEEEE
553 - 572:	EEEEEEEEEEEEEEEEEEEE
554 - 573:	EEEEEEEEEEEEEEEEEEEE
555 - 574:	EEEEEEEEEEEEEEEEEEEE
556 - 575:	EEEEEEEEEEEEEEEEEEEE
557 - 576:	EEEEEEEEEEEEEEEEEEEE
558 - 577:	EEEEEEEEEEEEEEEEEEEE
559 - 578:	EEEEEEEEEEEEEEEEEEEE
560 - 579:	EEEEEEEEEEEEEEEEEEEE
561 - 580:	EEEEEEEEEEEEEEEEEEEE
562 - 581:	EEEEEEEEEEEEEEEEEEEE
563 - 582:	EEEEEEEEEEEEEEEEEEEE
564 - 583:	EEEEEEEEEEEEEEEEEEEE

565 - 584:	EEEEEEEEEEEEEEEEEEEE
566 - 585:	EEEEEEEEEEEEEEEEEEEE
567 - 586:	EEEEEEEEEEEEEEEEEEEE
568 - 587:	EEEEEEEEEEEEEEEEEEEE
569 - 588:	EEEEEEEEEEEEEEEEEEEE
570 - 589:	EEEEEEEEEEEEEEEEEEEE
571 - 590:	EEEEEEEEEEEEEEEEEEEE

A0A318YL69 **A0A318YL69_ASPNB** (642 aa)
Uncharacterized protein. *Aspergillus neoniger (strain CBS 115656)*

```
MSRNFHPVNANSPSTTTLTSDPDINPSLEDNSNNNTIIQPYLFPPGVPTNTSFNSNDQTLVDNCSNIEVSQLVTEANRFW
GNCSTTIPNIETGPAAEYPTTYMMGNYDHGYGDQNMHETSVPYGPCDHFQVAGTGIDMGMRMTGTKGEDEDDMYNANQAS
MLAALGMTHLDEGESHAVDDDAKTSSSVTVDDDPEWKEWKNWNETDANGGVRLLSEERMDRAGVAAWLDMNREEDHGVFQ
HEESDDYDEDDATSYGSDDDMMEMGEETEYEEEEEEVVNVVEGPSRQVLISSRTGAVAEYDTASFGCDFEEEEEEEEEEE
EEEEEEEEEEKQQNEERWGGDGQPRPSPFPCFYDARSGLIIELSSSESDAEETMSDPSSDNDIEETMSDPSSSSTSSSSS
PTSEAPQAYALPWPTSPSNFSTTTTTTTSSTSTSTSTPSETTPPPSSQPVRPPSSTPFTLLADLHTNLSSAPDHRATHLR
NLANEISNTMYFVNSRTISGDFSAEDAAPVDRVMRIVREGELKMRYQERYERQKGKLVKRERRVAEREDRVSKREEMVSR
REMGVAGWWEVWRERGREVWEGVEGEMDGGIGDGDGIRRNAMDTLQRTVRVTREVVRRMDRLIDESEVDGDGDCDVEGGV
EL
```

310 - 329:	EEEEEEEEEEEEEEEEEEEE
311 - 330:	EEEEEEEEEEEEEEEEEEEE

A0A318ZZX3 **A0A318ZZX3_9EURO** (115 aa)
Uncharacterized protein. *Aspergillus saccharolyticus JOP 1030-1*

```
MKGENGEPRIDAMQVRIGEEAARWRRGKVYLNSITQGSQEGRRGEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEVICRKE
IRPGKVIERKPIPLLLRREGLEISRHRVAAGYAVN
```

47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE

A0A319ACK9 **A0A319ACK9_9EURO** (805 aa)
Putative ribosome assembly protein Noc2. *Aspergillus saccharolyticus JOP 1030-1*

```
MAGSQKKSTKKFEKKHLKDVLERRKATAKIKQRNHLKEKRKADNAKQRAERDEDEEESPEQVQKQKDFAEMNVDDFFAGG
FDIPESAAELTKKGRKKAVTPKIGKRKRSDKQKDEDEEAASASEEGGSDDEGSGPDDFEAHKDQLEALKEKDPEFYKYLK
ENDAELLDFGEHGDLAEVDQLSEEEEEEGPAKKKKKGSKAKAAEEDEDEATDNTLTLAMVKKWQQLMEEQHSIRAMRQAV
LAFRAAAYVNEGNDEQEHKYTISDSNVYHQVLVTALNNIPRVLAHHLPVKESASGKVRVSMDSKKFKTLTPLIKSHTSSV
HQLLTNLSDEPTLKLTLSSIEPMLPYLLQFRKLLKVLVKTIVSIWADVSTTEATRITAFLILRRLMVIGDAGLKEAVLKA
SYEGVVKGSRNTTVHTLAGVNLMKNSAAELWGIDQNVSYTTGFSFIRQLAMHLRSSITNTSKESYKTVYNWQYVHSLDFW
SRVLSQHCDALVEAQAGKPSALRPLIYPVVQITLGAMRLIPTAQYLPLRFQLTRALLRLSRATGTYIPLASALLEVLNLA
EMRKPPKTSTLRQLDFATAIRAPKSYLRTRVYQDGVGEQVAELLSEFFVLWTKHIAFPELSVPVVVALKRWIKQASARTG
GNRNTKINQMILLLVQKVEANARWIEEKRLAVTYTPRNRAEVESFLKDVEWESSPLGAFVKSQRKLREEKAALLEQGRLE
EEKRRKEEKAEAAREAIRDEVISEGDESSEDDDEEAEEEEIEEGSSSDGEGSEEEEEEEEEEEEEEEEEEEEDEDEMEF
EEEED
```

773 - 792:	EEEEEEEEEEEEEEEEEEEE
774 - 793:	EEEEEEEEEEEEEEEEEEEE

A0A319AG02 **A0A319AG02_9EURO** (766 aa)
Lipin Smp2. *Aspergillus saccharolyticus JOP 1030-1*

```
MQYVRSISGSVSKTWNSINPATLSGAIDVIVIEQEDGTLACSPFHVRFGKFSLLRPYEKKVEFSVNGVKQDYAMKLGEGG
EAFFVFETTAEIPASLQTSPLVSPTSSPKMRSEENLSSSLSEPEYLDLDRSPSPSDNQADGKRSAELPILSRGMRASSDL
GTLTPLSRSPDESNMGRSRHGSFGEAPLKIDRIATDSVLMTKNRSNSIGVTDQTYAVNAAGDENSRDDRSRSPPPLSPEE
LMSRAVSLSKKLSGSNIPSRVTETGDLMLDMTGYKSSEEDALRAEVIARKILAEELEGNYDIGALIGADEHGNLWIYSSE
EAKEAADRRATFNAMRPGSAMSENAISDPGYHSDSDPSIHDKTVTARHYRTQSDVQPGFPTPPQSPTQDSLAMEPTRNYA
KTLRLTSDQLKALKLKPGPNNMSFSVNRATCTANMYLWNGNTPIVISDIDGTITKSDALGHVLNMIGRDWTHAGVAKLYT
DIVNNGYNIMYLTSRSVGQADTTRAYLYGVRQDGYRLPKGPVIMSPDRTMAALRREIYLRKPEVFKMACLRDILNLFNGK
ENPFYAGFGNRLTDALSYRSVNIPSTRIFTINSNTEVSLDLLSLNKYKSSYVSMGELLDHFFPPVSLLVQAGGEEYTDFT
YWREPPPDLEAFSCTDSEAEDEEAEEEEEEEEEEEEEEEEEEEEEEEEEEEEDELEEDEEYDGKLSDEDGSEALEEEIDEE
EDLGASYISQDSVDGSELADEQNVLPEDEVETVDVTQRSPRGSPSR
```

665 - 684:	EEEEEEEEEEEEEEEEEEEE
666 - 685:	EEEEEEEEEEEEEEEEEEEE
667 - 686:	EEEEEEEEEEEEEEEEEEEE
668 - 687:	EEEEEEEEEEEEEEEEEEEE
669 - 688:	EEEEEEEEEEEEEEEEEEEE
670 - 689:	EEEEEEEEEEEEEEEEEEEE
671 - 690:	EEEEEEEEEEEEEEEEEEEE
672 - 691:	EEEEEEEEEEEEEEEEEEEE

A0A319BTY5 **A0A319BTY5_9EURO** (522 aa)
Uncharacterized protein. *Aspergillus uvarum CBS 121591*

```
MSNLAQNTGLHNLPLEIFELTLTHLDLKSIKVLRLVDRKLAEKCIGPRFLRCIQQPVLDVSPQSLRSLHALACNPVLSKK
IHSLTFLATTMEPSELDKNIKSGKYVAQKLNKLGNVVSRTKVRFTPEELEKAKSDLCWLNEQQEARDQESPSEMMEVLQL
TLNLFGTLDVIRFDGGVLRGRTERKAPNSRDWQPLWARAAQIFLLVSKAMVQSRISVKSLDIFRDTDKCCIPIDKITDIA
LNLGSAQLGMLGKDLISLKLSISMAMEDSLQDEEEDEEEEEEEEEEEEEEEEEEEEEKEEEEEDTRPVLEDGTSGIASLFL
KSAPALRELNLAFRRTAYGRKLFHYYDRIVDSIAHKTQLPLLERCALSGFAVKGQSLLLFLKKHSNLRSLTLHECHLTSG
SWTPVFAYLECSMPRLENLSLKNLFGRHMQNLKDHALPDPTLGQETEDAEQEGKGLVVLLPIWDTNRPPRCTRYSHSNGL
AVHTRDFTREDLAKGLVFQPLRKGPGRALGSPELMRWNKSRT
```

277 - 296:	EEEEEEEEEEEEEEEEEEEE

A0A319CF70 **A0A319CF70_9EURO** (797 aa)
J domain-containing protein. *Aspergillus uvarum CBS 121591*

```
MSTPTSSTFIDCYATLNIHPHADLKEINSAYKRLALRYHPDKTEGGDAETFQKILYAVETLRDPNHRAVHDAALDEHRCR
NLKYNLHTTADAGAFFHRSYHRHHRQQQQQQQHRADDPYSQSRYEASYRHSVHMDPTAPESIEILKQMRREREYSEQLER
EREQEAREAEEAAAAAAAELFQEGGDGEGEGYDRGRAHVVDDELSSWSSSSEEPMGYYDESGFVVTRKKDKKKMGKGKGV
KEGEMNEEEEEKEETWIGYSDKTAYWSEEKQAKDLAQEDRHAKWMASLLDPDAAWKSTKYSWGRQQEEEEEEEEEKEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDDDDDEEEGEDEEDSEEEQSDEEDSADILSEGENDGQEESTSMGNLI
DLEDDAKDHAEMPTVTSKGSTGSATEVVLEDHHQSADLVDLVEDENSQAGVKADNDLGEGNEKMDLDGQPGCTQGQKDAD
WKENDECYGTPGAEVFHEMFCKEDIGPKRKEVCMCGRVEGIADDEEDWFRYPGQMPWGMSLPDKFSKDSTTGAGDDDDDK
DDDEDTDDEDNDSEGDEVDGDEGEDFEDDSVKDDSTVHNHNPHINHDDHDDHDHTQITPKTSASPIDTPFETNSLFATYH
FHDPRTEHPAAAEQSDSDFVTAYEDLAISTDSLTRPTIIAAPPHGLSAYLTPLLPYFESKLNRGDGQYTPDDMIVECRGI
ILETFCGWMEGVRRTFREAATRGCNEGHECHHLGYWDKAYGQAKCKICGQWEPIFTLTCPGCGLEACVACKFMAPAA
```

318 - 337:	EEEEEEEEEEEEEEEEEEEE
319 - 338:	EEEEEEEEEEEEEEEEEEEE
320 - 339:	EEEEEEEEEEEEEEEEEEEE
321 - 340:	EEEEEEEEEEEEEEEEEEEE
322 - 341:	EEEEEEEEEEEEEEEEEEEE
323 - 342:	EEEEEEEEEEEEEEEEEEEE
324 - 343:	EEEEEEEEEEEEEEEEEEEE
325 - 344:	EEEEEEEEEEEEEEEEEEEE
326 - 345:	EEEEEEEEEEEEEEEEEEEE
327 - 346:	EEEEEEEEEEEEEEEEEEEE
328 - 347:	EEEEEEEEEEEEEEEEEEEE
329 - 348:	EEEEEEEEEEEEEEEEEEEE
330 - 349:	EEEEEEEEEEEEEEEEEEEE
331 - 350:	EEEEEEEEEEEEEEEEEEEE
332 - 351:	EEEEEEEEEEEEEEEEEEEE
333 - 352:	EEEEEEEEEEEEEEEEEEEE

A0A319CFE9 **A0A319CFE9_9EURO** (908 aa)
Uncharacterized protein. *Aspergillus uvarum CBS 121591*

```
MASAKRKRNSTGLNATPNAGGRTGFVPQTPQTPLTNSSATHPAKRKKVKGSESSKKKQKREQQREESQELPYISSPVSAK
RTSTTIATNGHHHHRQHDAPPAVPEIPEPEIPIDPALRGEPVAIPKPQDQVMQDADQTETATPRPQKDVTRASSAPSALA
RQKKGRRVQADDDNDDDDDDDDSNSNKNKNPTGKTGFFSPDEIQKLEAFKLEFCTINGVEADTFDMMVQHSVRERQEQWP
VQTDIITKPDFWARIYEIIPDRAKRSVYRFMRRHFQCSSQKPHHWTHEQDEELISLHRLHGAKWAYIAKMIGRSDDDVVQ
RWKNRLQHRRTMNRGSWSEQEVQDMMDALQEVWHTMKATGVDVGQDVYELDEVYIAWGVVSDKMNNCRSRQQCADKWRKL
RAKVLNQRRKENPDAFHDSAVAKKSGGSRRSKSRAVSTPQQKPNQKFKSKEIVESEDEDVSQETQKAAEKKEAQEPEEEA
VEESDQEPEEEAVEESDQEEEEEEEEEEEEEEEEEEEEEEDESAEPEVPIKHERHSMELDDAHMSPPSKQPTGATRHITNT
GSREDSVADEVGDGLVDWAVKHERRQKSDSESEEESGEEEEEESPSPNAKREVKPNLGDKEAESESESGSESGSESNESE
EENYSTPPSGQKSTNLKVTSPSTVTKSSQQQQRGGNIKPRSPPAVAIKSRKSPSPTASASSSEDEEEEEEEESGGSDSET
SSTGGDWPAKPTATATNRKPSTNSSPITTAKRTITTTTEPTQKPQQPPTKPTVTHSKRSNPTPPESDPETASDDDASDED
ASDTTSSSSEESSRAPKQQSQPQPQPQRPSIPTRPSFGSSSQPTRSPGHRLSLKELRDASLSKANSKLKALKPNTLNDML
SDAKLRAKADSSSDDDDDESSDSDSDSE
```

499 - 518:	EEEEEEEEEEEEEEEEEEEE
500 - 519:	EEEEEEEEEEEEEEEEEEEE

A0A319CNG5 **A0A319CNG5_9EURO** (336 aa)
Uncharacterized protein. *Aspergillus uvarum CBS 121591*

```
MARVINTGPGDTGAKVAGTAQKRQTRPTTTTQKTAQTTTGPLTGTMPTAGKQAAQPTGPVAGPSTTKVPAAAKQATQPTR
SVAGPSTGKVPAATKQAAQPTTSVVGPSTAKVAAKTAAKKKKKSTRGRPRKACSPCRRAKKKCIHMGEEDENDEEEEEEE
EEEEEEEEEEEEEEEEENDDGQKKLSEKAKGKQKIKSADNDDGDDGDDGDDDDDDGDDDQKQLFEKAKGKQKRKRANDDDD
DDAPGPKPAKTRGRPAKNQATVAGPSGSAPATPTNLSNPLTAAGHIVTHQYMSQRLGQRLDNAEKKWEDAMDAMMEAKEA
LDAWKDFYLKHKESPS
```

154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE

A0A319CWX0 **A0A319CWX0_9EURO** (398 aa)
Uncharacterized protein. *Aspergillus ellipticus CBS 707.79*

```
MAEYRGDRVDVSPTSFTSINEDASPVQSKLDPEDTEEDILMEQAEVVKTPTKRRKPTPGTSSSNPKSTPTMGTFYPSNSS
RPFSSAASPTPALKPNPRATLGASPSDEDAEGEEYPDEEALAQTPSKKVRIAEPEATSKVTPKSTPKGKGKGKAKGKVNP
NVKIEKAFSLSDMDDVVDNNDENDVVTAPVSTTPSKKPRKSIFERPPAPASKSTSIKHESSDSDNDDSDHEEEEEEEEEE
EEEEEEEEEEEEEEEKNPIPVFTPTLTSNPVPKHEPTPTPTPTSPAETSASASPKASASIPEKKAKPTPTPKPGKKTKTK
TIGAANATKKIKTTPIPTSYALATPPDKLILRMRDIEGASWPDITAAWSAMTGVTVGGTTLRMRYRHMKDNFEGGCFF
```

231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE

A0A319D6Z0 **A0A319D6Z0_9EURO** (164 aa)
Non-heme 11 kDa protein of cytochrome bc1 complex. *Aspergillus ellipticus CBS 707.79*

```
MGLADFFSDVVSSLGFPEAQAEAPAESVEQSSSQEAEVEEEKPAVTEEKTEESSEESAEETPAEESAEEEQPEEEEEEEE
EEEEEEEEEEEEEPEDIKPQLEEECANSAQCAPYKHHFDECVERVTSQQEDADYKGPKEDCVEEFFHLSHCATQCAAPKLW
KSLK
```

73 - 92:	EEEEEEEEEEEEEEEEEEEE

A0A319ECY6 **A0A319ECY6_ASPSB** (320 aa)
Non-structural maintenance of chromosomes element 1 homolog (EC 2.3.2.27) (Fragment). *Aspergillus sclerotiicarbonarius (strain CBS 121057 / IBT 28362)*

```
DNQETAPEEITQDDLETYIAASNSAISPFDLEIRSLLPQLELDNTPDSSNAAAPERVYALVNTTSDALTQLATTHSADEI
AFVKRLLDAMFETYNTRRQEAMVVSGIQALQLAKVSGEARRESLQGTQSGGGGGGAAQSLTMTQAETVLRQLVEEGWLEK
SRKGYYRLSPRGLMELRGWLVATYNEEGEGVRKIKFCEACRDVITAGQRCGERDCPGRLHDHCMRNFFRMQKAEVCPVCK
IPWPGDRFVGERAITREQGAQRSRRTTTTTNTQQVDAGPSTQVELEGLDVDLEGEGEGEEEEEEEEEEEEEEEEEEEGE
```

299 - 318:	EEEEEEEEEEEEEEEEEEEE

A0A328D9I1 **A0A328D9I1_9ASTE** (859 aa)
Uncharacterized protein. *Cuscuta australis*

```
MSSSSSFSSPLRHYCCSSSPRSPLPKLYLINGDQQGFTPRLQQHCKAIRKPRTQEVVVLQNGLTAGGGGGGRLKVDELPR
LQEEDHGSFLENHTHHHEAAMKEIKGRVEVVRSKLRTMGDGEITVSAYDTAWVALVKDDVVAGGRGDRPQFPSALEWIAG
NQLADGSWGDGDIFLAHDRVLNTLACVIALKSWNVCPIHVQKGMMFLRENMRKVEEEDGEHMPIGFEVAFPSLMAMAKKL
GIHLPHHDHDHDHHHDSRPLFQNIYAHRNLKLTKIPKEVMHQVPTTLLHSLEGMEGVVEIDLDWEKLLPLQCHDGSFLFS
PASTAFALIHTKDPNCLRYLSNAVRQFHGGVPNVYPVDLFERIWVVDRLQRLGISRFFKPEIADCIAYVHRYWSDERGIC
WARNTRVEDIDDTAMAFRLLRLHGYPVSPEVFKNFKKGREFVCFAGQTNQAVTGMYNLYRASQVRFPGEEILEDAMEFSS
LFLQHKRASNQLLDKWIITKDLPGEVGYALDLPWYASLPRLETRFFLEQYGGEEDVWIGKTLYRMPLVSNNLYLELGKLD
YNNCQALHQQEWKSIQKWSEDCKLGVSKRSLLLGFYLAMASIFEPERSKERLAWAKTAALAAAIRAEFCLDHHHHHKRAF
TREFTNATSRASSRHTTREQTLVGALNETLNQLSRDALLTHGRDVRPYLRRAWEKWLLAWEKDDGEGEAELVVRTLNAFN
GQGTLEELWFSHPRYQQLMEITNRVCHGLSLYRHAQSYEREVDERPQERMTKAEVEREMQSLVKIVLTDDDDDEEEEEEE
EEEEEEEEEEEEEEEEEDLISPEVKQTFLTVTKAFYYAAFCNPGTIDSHIAKVLFQRVL
```

794 - 813:	EEEEEEEEEEEEEEEEEEEE
795 - 814:	EEEEEEEEEEEEEEEEEEEE
796 - 815:	EEEEEEEEEEEEEEEEEEEE
797 - 816:	EEEEEEEEEEEEEEEEEEEE
798 - 817:	EEEEEEEEEEEEEEEEEEEE

A0A328DPV8 **A0A328DPV8_9ASTE** (95 aa)
Uncharacterized protein. *Cuscuta australis*

```
MVNPSADTVHSGTCRAEFLRSGPNPNSLKKKMKNPKKKTKNLKKKKEEEEEEEEEEEEEEEEEEEEEEEEEEKRRREKKK
GREEEEIWKKKEEKR
```

47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE

A0A328DW67 **A0A328DW67_9ASTE** (208 aa)
Uncharacterized protein. *Cuscuta australis*

```
MEKKKSCDADWNARRKGDEEYEEEEESEEEDAKSEGEDTESEGEDVDFEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEVVVVVVESEEEEEEKEEEEEEEEEEEEEEVVVVVVVESEEEEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEIREEKRRRPGKKEEEEIWNRGTEIEKERTKKRKRRKERRKKMEKS
```

51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE

137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE

A0A329S201 **A0A329S201_9STRA** (876 aa)
Uncharacterized protein. *Phytophthora cactorum*

```
MVRINHTQRFPLGTRVSKYFNGFAEPFQGIVDKHSDVTDFYHITYEDGDSEEMTEDDVATHFLEVPGSKRSPKSRKNLNL
TKPSKPSTLSMKRANSDSSINMSSPSAVAPSSKGKSRQKPKVLSLNANAPGLMRSNSFTGTSNSHDEARESLSLTIPAKT
IESEEEEEEEQEEEEEEEEEEEEEEEEEEEEEEEEDDDDEVMADKVTELIGKSVEKTVTKEGCGIDVVQGAVASYFPAT
KMFRVMYFDGECCDLTYQEVFNSIPADLRPVDIGGKRKRNAEGTPRNGEKDSTSSAPSASPKRLKTLDLNAKGMAPSKRS
SSPSSPVSLVIRESDMLMVDNVEFNIVRKVLFIIVSTVNNAVMEAQLEVLSSADLKDKEALEVFVRKDGLASLAELLSKW
EDEVETEQGVLLILKVLAVLPGITKDTIIDSRIGKKVRGVEKRGSYRDSSISGLAAWVIKKMKADFAVQGEAQVPSKSVN
GKSAGGTANRRRGSNSPRRSIPSPRDDEKRDDRLTTPKLAGSPRSNKPKTPSTSNGSGPAAKRSNSVNHLQNLMNSRNGR
DTSTARRDRDIFGNLVTPQNKRRLGTAHNWRARRSTVVLDQVTKRVTENAQEVETMKTKEVEEDDWQPSKIKFAEKESVC
PFEKEVEVSKLLVFRPAGSTKAPERPPVKRHTGPLRSILRVRFPPRPTQENTPQPGAGDSSSAPPTVHATGRPAVDPIVV
PSERPSLTSEVSEDGAAESPMFDTSKLSKVVSPTEKRKQGFSPPPCIPTSEHPPLDFTEEGEEDEASGDGVESDAKTEAP
LEKSERSEPAEAGVIVLSPIVSEDEASEEGEVSSNDAGAGIPKAEAAAPPSLSTGPKDGDAANVKSAAQQATTISA
```

172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE

A0A337SCY8 **A0A337SCY8_FELCA** (1126 aa)
Phospholipid phosphatase related 3. *Felis catus (Cat) (Felis silvestris catus)*

```
MRGRPYPPPPRPGASRRAPWEPGEGPGGPQSGPGGGARAEGEGAEGGAGGGGGDGRESTPPPTPGSFVSGLRRRSAPSPW
KRAPGSGGPREGDDTGGDPGRHEDSRGPRGPDAQPPPPPSTGLPRPSREGRGAAQTPVPARPYGGPRPPDSPGPREREPR
ARRAHAGGPARRGTRAAPRTRRDKEPPPLAPHAGRGGRGVSGRAGPPPLPALPLAAPPAPAGEGPRFVLAAPQPPPRAPA
GSALRAPARQVRGLRAEGRGRTPLPAAGTLPSLPRPPAAGLPTVQTPGNGPRPGTPKPGRPRPLPGPSRPPIWGAGVPGS
WVVGQGRSARRGGRGDTPLPQPQFPWAVRRIFARPSPAGAGHRVPPGLRLRLPSSSASLSPPTTACGARGTMIATKEKNK
TPKDSMTLLPCFYFVELPIVASSVVSLYFLELTDLFKPAKVGFQCYDRTLSMPYVETNEELIPLLMLLSLAFAAPAASIM
VGEGMLYCVQSRLWGRGGGPGGAEGSINAGGCNFNSFLRRTVRFVGVHVFGLCATALVTDVIQLATGYHAPFFLTVCKPN
YTLLGTSCEANPYVTQDICSGRDAHAILSARKTFPSQHATLSAFAAVYVSMYFNSVISDTTKLLKPILVFGFAIAAGVCG
LTQITQYRSHPVDVYAGFLIGAGIAAYLACHAVGNFQAPTAEKPMALAPAKDALRALTQRGHDSVYQQNKSVSTDELGPP
GRLDGVPRPVAREKASLGSLKRASVDVDLLAPRSPMGKENMVTFSHTLPRVSTPSLDDPARRHMTIHVPLDASRSKQLIS
EWKQKSLEGRGLGLPDEASPGHLRAPAEPMAEEEEEEEEEEEEEEEEEEEEEGEEGGPAPPSLYPTVQARPGLGPRVLLP
PRAGPQPLVHIPEEGAQAAGGLSPKSSAAVRAKWLMMAEKSGAAVAVASAQPRVANPPRLLQVIAMSKAPGGPGPKGAET
ASSSSASSDSSQYRSPSDRDSASIVTIDAHAPHHPVVHLSSGNGPWEWKTAGGTAKGAEGEGGYELGDLARGFRGGPKPP
GVSPGSSISDVDQEEPRFGAVATVNLATGEGLPPPGMADGALGPGSRESTLRRKAGGLVLGEREATGEAEAEGYYRKMQA
ARRFKD
```

832 - 851:	EEEEEEEEEEEEEEEEEEEE
833 - 852:	EEEEEEEEEEEEEEEEEEEE

A0A337SEG8 **A0A337SEG8_FELCA** (1281 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Felis catus (Cat) (Felis silvestris catus)*

```
MPRAACIRVCRARTAVPDSRREAGSQDAGRAESGGAASPGHSPRRPGTLAPFVPTTWSAPRARRPAVRACSLAARAASPT
SARPARGDAAPSSRPLPTRRPSRCVCVIAPRHHGARVKMAAAVLSGPSAGSAAGVPGGTGGLSAVGSGPRLRLLLLESVS
GLLQPRAGSAVAPVHPPVRSAAHLPGLMCLLRLHGTVGGAQNLSAVGALVGLSNARLGSVKTRFEGLCLLSLLVGESPTE
LFQQHCVSWLRSIQQVLQSQDPPPTMELAVAVLRDLLRYAAQLPTLFRDISTNHLPGLLTSLLGLRPECELSAMEGMKAC
MTYFPRACGSLKGKLASFFLSRVDALSPQLQQLACECYARLPSLGAGFSQGLKHTESWEQELHSLLASLHGLLGALYEGA
DTAPVQCEGPGLDVLLAPSEDGDAHTLLRLRHRFSGLARCLGLLLSSEFGAPVSVPVQEILDIICRTLSISAKNISLLGD
GPLRLLLLPSIHLDALDLLSALILACGSRLLRFGALISRLLPQVLNAWNLGRDALPPGQERPYSAVRTKVYAVLDLWVQV
CGASAGVLQGGASGEALLSHLLSDISPPADALKLRSPRGSPDGGLQSGKPSAPKKLKLDMGEATAPPGHRKGDSNANSDV
CAAALRGLSRTVLMCGPLIKEETHRRLHDLVLPLVMGVQQGEVLGSSPYTSSRCRRELYRLLLALLLAPSPRCPPPLACA
LQAFSLGQREDSLEVSSFCSEALVTCAALTHPRVPPLQSMGPACPAPAPAPPPEAPSPFRAPPFHPPGPMPSVGPMPSVG
PMPSVGPMPPAGPMPPTRPGPPATANHLGLSVPGLVSVPPRLLPGPENHRAGSNDDPVLAPSGTPPPAVPPDETFGGRVP
RPAFVHYDKEEASDVEISLESDSDDSVVIVPEGLPPLPPPPPTGSTPPPAAPAGPPTASPPVPAKEEPEELPAAPGPLPP
PPPPPVPGPVALPPPQLVPEGPPGGGGTPALEEDLTVININSSDEEEEEEEEEEEEEEEEEEEEEDFEEEEEEEEEYFEE
EEEEEEEFEEEFEEEEGELEEEEEDEDEEEDELEELEEVEFGPAGGPAEEGGPPPPSPAPALPPAQPPEVPPEPGVEPG
LLLEVEEPGPEDEPGAEAAPTLAPEVLPSQGEGQREAGSPPAGPPPQELVEEEPSAPPPLLEEGTENGGDKVPPPPETPA
AEEMEAAAEAETAALQEKVRRAGGGCGCPGDLGRPALPRVAASNGVSLPRKEQDDTAAMLADFIDCPPDDEKPPAAPEPE
S
```

1005 - 1024:	EEEEEEEEEEEEEEEEEEEE
1006 - 1025:	EEEEEEEEEEEEEEEEEEEE

A0A337SHG0 **A0A337SHG0_FELCA** (1210 aa)
Euchromatic histone lysine methyltransferase 2. *Felis catus (Cat) (Felis silvestris catus)*

```
MAAAAGAAAAAAAAEGEAPAEMGALVLEKEPRGATERVHGSLGDTPRSEETLPKASPDSLEPAGPSSPASVTVTVGDEGAD
TPVGATPLIGDEPENLEGDGDLHGGRILLGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGA
AAGPEPPPATPSPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKMTSDVAKRRKLNSGGGLSEELG
SARGSGEVTMEKGDPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEE
EEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTL
SPNHAGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVL
CETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGT
AAPAPPPLAQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPPGPGREALEKALVIQE
SERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRT
PLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEV
IRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELR
NKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETS
TMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRL
QLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNII
PVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLP
ELGSLPPVNP
```

299 - 318:	EEEEEEEEEEEEEEEEEEEE
300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE

A0A337SK88 **A0A337SK88_FELCA** (460 aa)
BTB domain-containing protein. *Felis catus (Cat) (Felis silvestris catus)*

```
MLLVEKTTDSPAAEFSLVEDVALHFACLMGRLNEQRLFQPDLCDVDLVLVPQRSVFPAHKGVLAAYSQFFHSLFTQNKQL
QRVELSLEALAPGGLQQILNFIYTSKLLVNAANVHEVLSAASLLQMADIAASCQELLDARSLGPPGPSAVALAQPATGCA
PAAPPYYCDIKQEADAPGLPKIYAREGPDPYSVRVEDGAGAAGGTVPAAIGPAQPFFKEEKEGGVEEAGGPPGSLCKLEG
GEGLEEELGGSGTYSRREQSQIIVEVNLNNQTLHVSTGPEGKPGTTPGPATMVLGREDGLQRHSEEEEEEEEEEEEEEEE
EEEEGGGSGGEEEEEEEEEEEGGSQGEEEDEEEGHSEQEEEEEEEEEGHSEQDQESSQGGGCVVWSRGCAGAGGGGGER
HGQSPLPTGAWPLGPERTPGAGAPLSLRRPGHGVGRGPSPRREPLRRPEGHRPLTGWGPR
```

305 - 324:	EEEEEEEEEEEEEEEEEEEE

A0A337SL86 **A0A337SL86_FELCA** (1278 aa)
SR-related CTD associated factor 1. *Felis catus (Cat) (Felis silvestris catus)*

```
MEEEDESRGKTEESGEDLGDGPPDRDPTLSPSAFILRAIQQAVGSSLQGDLPNDKDGSRCHGLRWRGCRSPRSEPRSQES
GGTDTATVLDMAADSFLAGLVSVLDPPDTWVPSHLDLRPGESEDMLELVAEVRIGDRDPIPLPVPSLLPRLRAWRTGTVS
PQSHSSRPSCARHLLTLGTGDGGPAPPPAPSSASSSPSPSPSSSSPSPPPPPPPPAPPAPPAPRFDIYDPFHPTDEAYSP
PPAPEQKYDPFEPTGSNPSSSAGTPSPEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGLSQSISRISETLAGIYDDNSLSQDFP
GDESPRPDPQPPQPTPAPGTPPQVDSTRVDGATRRRVFVVGTEAEACREGKVSVEVVTAGGAAIPPTLLPPGDSEIEEGE
IVQPEEEPRVAVSLFRAAGRAARPPPAASAPPAAQPPPPPPPAPRAPEGDDFLSLHAESDGEGALQVDLGEPAPAPPTADT
RWGGLDLRRKILTQRRERYRQRSPSPAAAAAAAAAAPAGPPTRKKSRRERKRSGGEAKEAASSSSSAQPAPPAPASPWDS
KKHRSRDRKPGSHASSSARRRSRSRSARRRSRSTDRRRGGSRRSRSREKRRRRRRSASPPPATSSSSSSRRERHRGKHRD
GGGGKKKKKRSRSRGEKWSGDSEKAPVPTQPPSGSSSLGGERDSRRRGAVPPSIQDLTDHDLFAIKRTITVGRPDKSDPR
GPSPAPASSPKREVLYDSEGLSAEERGGKSGEKDRRRSGAASSSSSSREKGSRRKALDGGDRDRDRDRDRDRDRSSKKAR
PPKESAPSSGPPPKPPVSSGSGSSSSSCSSSSRKVKLQSKVAVLIREGVSSTTPAKEAASAGLGSIGVKFSRDRESRSPF
LKPDERAPAEVAKAAPGSTKPKKTKVKAKAGAKKAKGTKGKTKPSKTRKKIRSGGSGGSGGGPATLKKSKADSCSQAAGA
KGVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEQQPATTTATSTAAAAPSTAPSAGSTAGDSGAEDGP
ATRVSQLPTLPPPMPWNLPAGVDCTTSGVLALTALLFKMEEANLASRAKAQELIQATNQILSHRKPPSGLGVTPAPVPTS
LGLPPGPSSYLLPGSLPLGGCGSTPPTPTGLAAASDKREGSSSSSEGRGDTDKYLKKLHTQERAVEEVKLAIKPYYQKKDI
TKEEYKDILRKAVHKICHSKSGEINPVKVSNLVRAYVQRYRYFRKHGRKPGDPPGPPRPPKEPGPPDKGGPGLPLPPL
```

268 - 287:	EEEEEEEEEEEEEEEEEEEE
269 - 288:	EEEEEEEEEEEEEEEEEEEE
270 - 289:	EEEEEEEEEEEEEEEEEEEE
271 - 290:	EEEEEEEEEEEEEEEEEEEE
272 - 291:	EEEEEEEEEEEEEEEEEEEE
273 - 292:	EEEEEEEEEEEEEEEEEEEE
274 - 293:	EEEEEEEEEEEEEEEEEEEE
964 - 983:	EEEEEEEEEEEEEEEEEEEE
965 - 984:	EEEEEEEEEEEEEEEEEEEE
966 - 985:	EEEEEEEEEEEEEEEEEEEE
967 - 986:	EEEEEEEEEEEEEEEEEEEE

968 - 987:	EEEEEEEEEEEEEEEEEEEE
969 - 988:	EEEEEEEEEEEEEEEEEEEE
970 - 989:	EEEEEEEEEEEEEEEEEEEE
971 - 990:	EEEEEEEEEEEEEEEEEEEE
972 - 991:	EEEEEEEEEEEEEEEEEEEE
973 - 992:	EEEEEEEEEEEEEEEEEEEE
974 - 993:	EEEEEEEEEEEEEEEEEEEE
975 - 994:	EEEEEEEEEEEEEEEEEEEE
976 - 995:	EEEEEEEEEEEEEEEEEEEE
977 - 996:	EEEEEEEEEEEEEEEEEEEE
978 - 997:	EEEEEEEEEEEEEEEEEEEE
979 - 998:	EEEEEEEEEEEEEEEEEEEE
980 - 999:	EEEEEEEEEEEEEEEEEEEE
981 - 1000:	EEEEEEEEEEEEEEEEEEEE
982 - 1001:	EEEEEEEEEEEEEEEEEEEE
983 - 1002:	EEEEEEEEEEEEEEEEEEEE
984 - 1003:	EEEEEEEEEEEEEEEEEEEE
985 - 1004:	EEEEEEEEEEEEEEEEEEEE
986 - 1005:	EEEEEEEEEEEEEEEEEEEE

A0A337SU21 **A0A337SU21_FELCA** (1354 aa)
Euchromatic histone lysine methyltransferase 2. *Felis catus (Cat) (Felis silvestris catus)*

```
MLRGCNGAGGPGRDLQQSGGPAPGADEGTRGWEVGGVGTEARVQPPAAPEWAAGAGAPGARARGTRGRPPGWGAAGAGGV
GARGPRGLGDKGGAARAAGRRGRGRGAEAPPPPPPLFSAPEMRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRP
RSLLSLPRAQASWAPQLPTGLTSPPLPCVPCQGEAPAEMGALVLEKEPRGATERVHGSLGDTPRSEETLPKASPDSLEPA
GPSSPASVTVTVGDEGADTPVGATPLIGDEPENLEGDGDLHGGRILLGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPP
SVQSLAMRLLSMPGAQGAAAGPEPPPATPSPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKMTSD
VAKRRKLNSGGGLSEELGSARGSGEVTMEKGDPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEE
EEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLET
ERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPG
CGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLAQDAPGRA
DTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPPGPGREALEKALVIQESERRKKLRFHPRQLYL
SVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARY
MVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDN
EENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSD
VWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTC
VDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQ
TIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRI
AFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNP
```

477 - 496:	EEEEEEEEEEEEEEEEEEEE
478 - 497:	EEEEEEEEEEEEEEEEEEEE
479 - 498:	EEEEEEEEEEEEEEEEEEEE
480 - 499:	EEEEEEEEEEEEEEEEEEEE
481 - 500:	EEEEEEEEEEEEEEEEEEEE
482 - 501:	EEEEEEEEEEEEEEEEEEEE

A0A337SWY8 **A0A337SWY8_FELCA** (1314 aa)
Tau tubulin kinase 1. *Felis catus (Cat) (Felis silvestris catus)*

```
MQCLAAAIKDETNMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTRENVALKVESAQQPKQVLKMEVAV
LKKLQGKSHVCRFIGCGRNEKFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESIEAIHSVGFLHRDIKPSNF
AMGRLPSTYRKCYMLDFGLARQYTNTTGDVRPPRNVAGFRGTVRYASVNAHKNREMGRHDDLWSLFYMLVEFAVGQLPWR
KIKDKEQVGMIKEKYEHRMLLKHMPSEFHLFLDHIASLDYFTKPDYQLIMSVFENSMKERGIAENEAFDWEKAGTDALLS
TSTSTPPQQNTRQTAAMFGVVNVTPVPGDLLRENTEDVLQGEHLSDQENAPPILPGRPPEGLGPSPHLAPHPGGPEAEVW
EETDVNRNKLRINIGKTPCVVEEEQSRGVGVPSSPVRAPPDSPTTPVRSLRYRRVNSPESERLSTADGRVELHERRSRMD
LPGSPSRQACSSQPAQMLSVDTGHADRQASGRMDVSASVEQEALSNAFRSVPLAEEEDFDSKEWVIIDKETELKDFPPGA
EPSTSGTTDEEPEELRPLPEEGEERRRPGAEPAVRPRGRGMQTLAEEDPRQIPTQPLPPQLSQADGRSETSQPPTPGSPS
HSPLHSGPRPRRRESDPTGPQRQVFSVASPFEVNGLPRAVPLSLPYQDFKKDLSDYRERARLLNRVRRVGFSHMLLTTSQ
VPLAPVQPQANGKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAVALGEVLGPRSGSSSDGSERSTDR
SQEGAPSTLLADDQKESRGRASMADGDLEPEEGSKTLVLVSPGDMKKSPVTADLAPDPDLGTLAALTPQQERPQPTGSQL
DVSEPGTLSSVLKSEPKPPGPGTGPGAGAVTTGAGGVAVTSSPFTKVERTFVHIAEKTHLNVMSSGGQASRSEELGAGGE
PGLEAPSDGRVVEEGASVPLENGIAQSGLESCVLSGPPMDSPLEVATDSLPNGPALVNGPAPASPLEPGPEKLATVSPSR
HAMPGPRPRSRIPVLLSEEDTGSEPSGSLSAKERWGKRARPQQDLARLVMEKRQGRLLLRLASGASSSSSEEQRRASETL
SGTGSEEDTPASEPAAPRKAGRAATTRSRIPRPISIRMPTPAAAQQSPGRPHSAAPASDTAITSRLQLQKPPGSAVAADL
RPKQPPGRGPGPGRAPAGTRPPAPRSPGPSTSAAPRQPSASPRSQSLSRKESSSPSHQARPAGPPPRGAPQARAQPDGTP
SPGGPKKGPRGKLQTQRAATKGRAGVAEGRAGAR
```

734 - 753:	EEEEEEEEEEEEEEEEEEEE

735 - 754:	EEEEEEEEEEEEEEEEEEEE
736 - 755:	EEEEEEEEEEEEEEEEEEEE
737 - 756:	EEEEEEEEEEEEEEEEEEEE
738 - 757:	EEEEEEEEEEEEEEEEEEEE
739 - 758:	EEEEEEEEEEEEEEEEEEEE
740 - 759:	EEEEEEEEEEEEEEEEEEEE
741 - 760:	EEEEEEEEEEEEEEEEEEEE
742 - 761:	EEEEEEEEEEEEEEEEEEEE
743 - 762:	EEEEEEEEEEEEEEEEEEEE
744 - 763:	EEEEEEEEEEEEEEEEEEEE
745 - 764:	EEEEEEEEEEEEEEEEEEEE
746 - 765:	EEEEEEEEEEEEEEEEEEEE
747 - 766:	EEEEEEEEEEEEEEEEEEEE
748 - 767:	EEEEEEEEEEEEEEEEEEEE
749 - 768:	EEEEEEEEEEEEEEEEEEEE
750 - 769:	EEEEEEEEEEEEEEEEEEEE
751 - 770:	EEEEEEEEEEEEEEEEEEEE
752 - 771:	EEEEEEEEEEEEEEEEEEEE
753 - 772:	EEEEEEEEEEEEEEEEEEEE
754 - 773:	EEEEEEEEEEEEEEEEEEEE
755 - 774:	EEEEEEEEEEEEEEEEEEEE
756 - 775:	EEEEEEEEEEEEEEEEEEEE

A0A340WL22 **A0A340WL22_LIPVE** (734 aa)
LOW QUALITY PROTEIN: YTH domain-containing protein 1. *Lipotes vexillifer (Yangtze river dolphin)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLISKPLSSSVSN
NKRMVSTKGKSVTEYKNEEYQRSERNKYLEXRKIRLSSSASRESYKSQPEKTCLRKRDPERRVKSPTPDGSERIGLEVDR
RASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDDDGEEEEEEEEEEEE
EEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSS
ASESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSARSVI
LIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGXXXXGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKI
GRDGQEIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDY
APEFHQRPGYLKDPRYQEVDRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMTPYPGMEQPPHHPYYQHHAPPPQAH
PPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLC
DRDRDRGERGRYRR
```

228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE

A0A340X8J3 **A0A340X8J3_LIPVE** (2087 aa)
Histone acetyltransferase (EC 2.3.1.48). *Lipotes vexillifer (Yangtze river dolphin)*

```
MVKLANPLYTEWILEAIKKVKKQKQRPSEERICNAVSSSHGLDRKTVLEQLELSVKDGTILKVSNKGLNSYKDPDNPGRI
ALPKPRNHGKVDNKQNVDWNKLIKRAVEGLAESSGSTLKSIERFLKGQKDVSALFGGGAASGFHQQLRLAIKRAVGHGRL
LKDGPLYRLNTKATNVDGKESCESLSSLPPVSLLPHEKDKPVAEPIPICSFCLGTKDQNREKKPEELISCADCGNSGHPS
CLKFSPELTVRVKALRWQCIECKTCSSCRDQGKNADNMLFCDSCDRGFHMECCDPPLTRMPKGMWICQICRPRKKGRKLL
QKKAAQIKRRYANPIGRPKNRLKKQNTVSKGPFSKVRTGPGRGRKRKITLSSQSASSSEDGYLEQIDGLDFCRDGSVPLK
FNKKTKGLIDGLTKFFTPSPDGRKPRGEVVDYSEQYRVRKKGNRKSSTSDWPTDNQDGWDGKQESEERLFGSQEIMTEKD
MELFRDIQEQALQKVGVTGPPDPQVRCPSVIEFGKYEIHTWYSSPYPQEYSRLPKLYLCEFCLKYMKSRTILQQHMKKCG
WFHPPANEIYRKNNISVFEVDGNVSTIYCQNLCLLAKLFLDHKTLYYDVEPFLFYVLTQNDVKGCHLVGYFSKEKHCQQK
YNVSCIMILPQYQRKGYGRFLIDFSYLLSKREGQAGSPEKPLSDLGRLSYMAYWKSVILECLYHQNDKQISIKKLSKLTG
ICPQDITSTLHHLRMLDFRSDQFVIIRREKLIQDHMAKLQLNLRPVDVDPECLRWTPVIVSNSVVSEEEEEEEEEEEEE
EEEEEEEEEGEQEEPQSQEGELEPSVGKSASRENKEQDSYSSVESEKKPEVTAPASSTRLNKQVLPRDSLPANNQPSRRG
RWRRKNRKAQERFGDEDSKLLLEETSAPPEQYGDCEEKSETCQEQYTEGQEQSAASQEQPSQDAKPDGPKRRPSEGLELW
RGPLKKSPEPLKCGLPESHDRLPRRYSEGRYSDGDRALLRGCSESSEEEGEPESPRSSSPPVLTKPTLKRKKPILHRRRR
VRKRKHHNSSVVTETISETTEVLDEPFEDSDSERPMPRLEPTFEIDQEEEEEDENELFSQGYFRHLSSQDVLRCRPASKR
KSKDRDEDEDSDDADDTPILKPVSLLRKCDVKDSPLEPDTSTPMKKKKGWPKGKSRKPVHWKKRPGRRPGLKLNRELAAI
STRECVVEPVVPLPEPGREPQVQENQEAVGPREDLPLREERKEGEELPLEAEEGEEGEEGEEEEDTTSSDVRAASPADSC
SPETGAKGPEVGEEEEEPHAPVGQQPSEEGPQELGQCAREEEEEEEDAAAAETQQSEDRDADDEDDGHLESTEKKGPGEQ
LAGGDVKEEHGGQESFLDPDVHGSREHAKDKEETEPDSEEEQTSHEASVVSEHMPGSEDDHEEDPHSKDELLQLKEEADI
PHSDLDLETVQAVQSLTQEESSEHEGAYQDCEETLAACQTLQSYTQADEDPQLPLVEDCHASEHNSPLSSVQSHPSQSVR
SVGSPSVPALEGGYTQISPEQGSLSAPSMQNMETSPMMDVPSVSDHSQQVVDSGFSDLGSIESTTENYENPSSYDSTMGG
SICGNSSSQSSCSYSGLSSSSSLTQNSCVVTQQMAGVGGSCSLMPQSSVPPAAATCSIKSPQSCAVERPPSTQQPPAPQP
PPQAPPAPPPAPAPRSAPACDPASRSALRPVHRPQLQFEIRPQARSSSCPAQSRPVQQPRPQLVHWSDFDPISTNGPPRL
TRGERRPQRPQQQQQQQQQQQQPPLSQCSMNSSFTPAPMIMEIPESGSTGNISIYERIPGDFGAGSYSQPSATFSLAKLQ
QLTNTIMDPHAMPYSHSPAVTSYATSVSLSNTGLAQLAPSHPLAGTPQAQATMTPPPNLASTTMNLTSPLLQCNMSATNI
GIPHTQRLQGQMPVKGHISIRSKSAPLPSAAAHQQQLYGRSPPAVAMQAGPRALAVQRGMNMGVNLMPTPAYNVNSMNMN
```

```
TLNAMNSYRMTQPMMNSSYHSNPAYMNQTAQYPMQMQMGMMGSQAYTQQPMQPNPHGNMMYTGPSHHSYMNAAGVPKQSL
NGPYMRR
```

787 - 806:	EEEEEEEEEEEEEEEEEEEE
788 - 807:	EEEEEEEEEEEEEEEEEEEE
789 - 808:	EEEEEEEEEEEEEEEEEEEE
790 - 809:	EEEEEEEEEEEEEEEEEEEE

A0A340Y1H1 **A0A340Y1H1_LIPVE** (602 aa)
major centromere autoantigen B. *Lipotes vexillifer (Yangtze river dolphin)*

```
MGPKRRQLTFREKSRIIQEVEENPDLRKGEIARRFNIPPSTLSTILKNKRAILASERKYGVASTCRKTNKLSPYDKLEGL
LIAWFQQIRAAGLPVKGIILKEKALRIAEELGMDDFTASNGWLDRFRRRHGVVSCSGVARARSRSAAPRPPAAPASPPTV
PSEGSGGGTTGWRAREEQPPSVAEGYASQDVFSATETSLWYDFLPDQAAGLCGSDGRARKATQRLSVLLCANADGSEKLP
PLVAGKSAKPRAGQAGLPCDYTANSKGGVTTQALAKYLKALDTRMAAESRRVLLLAGRLAAQSLDTSGLRHVQLAFFPPG
TVQPLERGVVQQVKGHYRQAMLLKAMAALEGQDRSGLQLGLMEALHFVAAAWQAVEPSDIATCFREAGFGGGPNATITTA
LKSEEEEEEEEEEEEEEEEEEEEGEGEEEEEEDGEEEEEGGEGEELGEEEEVEEEGDVDDSDEEEEEEEESSSEGLEAED
WAQGVVEAGGSFGGYGAQEEVQCPTLHFLEGEEDSESDSEEEEEDEEEDEDDEDDDEDGDEVPVPSFGEAMAYFAMVKRY
LTSFPIDDRVQSHILHLEHDLVHVTRKNHARQAGVRGLGHQS
```

404 - 423:	EEEEEEEEEEEEEEEEEEEE

A0A341B1E9 **A0A341B1E9_NEOAA** (1872 aa)
Histone acetyltransferase (EC 2.3.1.48). *Neophocaena asiaeorientalis asiaeorientalis (Yangtze finless porpoise) (Neophocaena phocaenoides subsp. asiaeorientalis)*

```
MVKLANPLYTEWILEAIQKIKKQKQRPSEERICHAVSTSHGLDKKTVSEQLELSVQDGSVLKVTNKGLASYKDPDNPGRF
SSVKPGTFPKSAKGSRGSCNDLRNVDWNKLLRRAIEGLEEPNGSSLKNIEKYLRSQSDLTSTTTNPAFQQRLRLGAKRAV
NNGRLLKDGPQYKVNYGGLDGKGAPKYPSAFPSSLPPVSLLPHEKDQPRADPIPICSFCLGTKESNREKKPEELLSCADC
GSSGHPSCLKFCPELTTNVKALRWQCIECKTCSACRIQGKNADNMLFCDSCDRGFHMECCDPPLSRMPKGMWICQVCRPK
KKGRKLLHEKAAQIKRRYAKPIGRPKNKLKQRLLSVTSDEGSMNAFTGRGSPGRGQKTKVCTTPSSGHAASGKDSSSRLA
VTDPPRPGATTKITTTSTYISASTLKVNKKTKGLIDGLTKFFTPSPDGRRSRGEIIDFSKHYRPRKKVSQKQSCTSHVLA
PDTEIKISIKQESTDINVIGNKDTVTEEDLDVFKQAQELSWEKIECESGVEDCGRYPSVIEFGKYEIQTWYSSPYPQEYA
RLPKLYLCEFCLKYMKSKNILLRHSRKCGWFHPPANEIYRRKDLSVFEVDGNMSKIYCQNLCLLAKLFLDHKTLYYDVEP
FLFYVLTKNDEKGCHLVGYFSKEKLCQQKYNVSCIMIMPQHQRQGFGRFLIDFSYLLSRREGQAGSPEKPLSDLGRLSYL
AYWKSVILEYLYHHHERHISIKAISRATGMCPHDIATTLQHLHMIDKRDGRFVIIRREKLILGHMEKLKTCSRTNELDPE
SLRWTPILISNAAVSEEEREAEKEAERLMEQASCWEKEEQEILSSRANSRQSPAKVQSKNKYLHSPESRPVAGERGQLME
LSKESSEEEEEEEEEEEEEEEEEEEEEEEEEEEEEENIQSSPPRLTKPQSVAIKRKRPFVLKKKRGRKRRRINSSVTTETISE
TTEVLNEPFDNSDEERPMPQLEPTCEIEVEEDGGKPVLRKAFQHQPGKKRQIEEEEGKDNHCFKNADPCRNNMDDDANNL
KEASRDNPEPLKCKQWPKGTKRGLSKWRPNKERKTGFKLNLYTPPETPMEPDDQVIVEEQKETPADKTSPAPTRTEEEVK
EAVEPLLPGDENRREEMCAPVSPNKSPGEKPEDDLIKPEEDEEEEEEEEEEEEEEGNVEKDPCGAQSQEKEEPEVCTDKE
DPVRLDDHEEEEEEDEEPSHNEGHDADDEDDSHMESAESEKEERPREAFKEVLETQEAFLDLSVQPSHSNAEVLMDCGID
LTASCNSEPKELAGATETAPESDEEPAGEQAQEQDQKNSEEVDSEFKEGNTATLEIDSETVQAVQSLTQENSEQDDTFQD
CAETQEACRSLQNYTHADQSPQIAASLDDCQQSDHSSPVSSVHSHPSQSVRSVNSPSVPALENSYAQISPDQNAISVPSL
QNMETSPMMDVPSVSDHSQQVVDSGFSDLGSIESTTENYENPSSYDSTMGGSICGNGSSQNSCSYSNLTSSNLTQSSCAV
TQQMSNISGSCSMLQQTSISSPPTCSVKSPQGCVVERPPSSSQQLAQCSMAANFTPPMQLAEIPETGNTNLGLYERMGQS
DFGAGHYPQPSATFSLAKLQQLTNTLIDHSLPYSHSAAVTSYANSASLSTPLSNTGLVQLSQSPHSVPGGPQAQATMTPP
PNLTPPPMNLPPPLLQRNMAASNIGISHSQRLQTQIASKGHVSMRTKSASLSPAAATHQSQIYGRSQTVAMQGPARTLTM
QRGMNMSVNLMPSPAYNVNSVNMNMNTLNAMNGYSMSQPMMNSGYHSNHGYMNQTPQYPMQMQMGMMGTQPYAQQPMQTP
PHSNMMYTAPGHHGYMNPGMSKQSLNGSYMRR
```

887 - 906:	EEEEEEEEEEEEEEEEEEEE
888 - 907:	EEEEEEEEEEEEEEEEEEEE
889 - 908:	EEEEEEEEEEEEEEEEEEEE
890 - 909:	EEEEEEEEEEEEEEEEEEEE
891 - 910:	EEEEEEEEEEEEEEEEEEEE
892 - 911:	EEEEEEEEEEEEEEEEEEEE
893 - 912:	EEEEEEEEEEEEEEEEEEEE
894 - 913:	EEEEEEEEEEEEEEEEEEEE

A0A341B3F4 **A0A341B3F4_NEOAA** (737 aa)
YTH domain-containing protein 1 isoform X1. *Neophocaena asiaeorientalis asiaeorientalis (Yangtze finless porpoise) (Neophocaena phocaenoides subsp. asiaeorientalis)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLISKPLSSSVSN
NKRMVNTKGKSVTEYKNEEYQRSERNKRLEVDRKIRLSSSASREPYKSQSEKTCLRKRDPERRVKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGAEDVEEDEEVEDAEEDEEVDDDGEEEEEEEEEEEEE
EEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSS
ASESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSARSVI
LIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQ
EIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYAPEFH
QRPGYLKDPRYQEVDSFTNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMTPYPGMEQPPHHPYYQHHAPPP
QAHPPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERE
RLCDRDRDRGERGRYRR
```

228 - 247:	EEEEEEEEEEEEEEEEEEEE

229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE

A0A341B4C4 **A0A341B4C4_NEOAA** (2055 aa)
Histone acetyltransferase (EC 2.3.1.48). *Neophocaena asiaeorientalis asiaeorientalis (Yangtze finless porpoise) (Neophocaena phocaenoides subsp. asiaeorientalis)*

```
MVKLANPLYTEWILEAIQKIKKQKQRPSEERICHAVSTSHGLDKKTVSEQLELSVQDGSVLKVTNKGLASYKDPDNPGRF
SSVKPGTFPKSAKGSRGSCNDLRNVDWNKLLRRAIEGLEEPNGSSLKNIEKYLRSQSDLTSTTTNPAFQQRLRLGAKRAV
NNGRLLKDGPQYKVNYGGLDGKGAPKYPSAFPSSLPPVSLLPHEKDQPRADPIPICSFCLGTKESNREKKPEELLSCADC
GSSGHPSCLKFCPELTTNVKALRWQCIECKTCSACRIQGKNADNMLFCDSCDRGFHMECCDPPLSRMPKGMWICQVCRPK
KKGRKLLHEKAAQIKRRYAKPIGRPKNKLKQRLLSVTSDEGSMNAFTGRGSPGRGQKTKVCTTPSSGHAASGKDSSSRLA
VTDPPRPGATTKITTTSTYISASTLKVNKKTKGLIDGLTKFFTPSPDGRRSRGEIIDFSKHYRPRKKVSQKQSCTSHVLA
PGTTQKLKPPPSSLPPATPLSGQSPSSQKSSTSVSSTSPQSSSSQSSVPSFSSLTNNSQLKALFDGLSHIYTTQGQSRQK
GHPSYAPPKRMRRKIEFPSTAKSKAHFFGKRDIRSRFISHPSSSSWGMARGRIFKAIAHFKRTTFLKKHRMLGRLKYKVT
PQMGTPSPGKGSLTDGRIKPDQDDDTEIKISIKQESTDINVIGNKDTVTEEDLDVFKQAQELSWEKIECESGVEDCGRYP
SVIEFGKYEIQTWYSSPYPQEYARLPKLYLCEFCLKYMKSKNILLRHSRKCGWFHPPANEIYRRKDLSVFEVDGNMSKIY
CQNLCLLAKLFLDHKTLYYDVEPFLFYVLTKNDEKGCHLVGYFSKEKLCQQKYNVSCIMIMPQHQRQGFGRFLIDFSYLL
SRREGQAGSPEKPLSDLGRLSYLAYWKSVILEYLYHHHERHISIKAISRATGMCPHDIATTLQHLHMIDKRDGRFVIIRR
EKLILGHMEKLKTCSRTNELDPESLRWTPILISNAAVSEEEREAEKEAERLMEQASCWEKEEQEILSSRANSRQSPAKVQ
SKNKYLHSPESRPVAGERGQLMELSKESSEEEEEEEEEEEEEEEEEEEEEEEEEEEENIQSSPPRLTKPQSVAIKRKRPFV
LKKKRGRKRRRINSSVTTETISETTEVLNEPFDNSDEERPMPQLEPTCEIEVEEDGGKPVLRKAFQHQPGKKRQIEEEEG
KDNHCFKNADPCRNNMDDDANNLKEASRDNPEPLKCKQWPKGTKRGLSKWRPNKERKTGFKLNLYTPPETPMEPDDQVIV
EEQKETPADKTSPAPTRTEEEVKEAVEPLLPGDENRREEMCAPVSPNKSPGEKPEDDLIKPEEDEEEEEEEEEEEEEEGN
VEKDPCGAQSQEKEEPEVCTDKEDPVRLDDHEEEEEEDEEPSHNEGHDADDEDDSHMESAESEKEERPREAFKEVLETQE
AFLDLSVQPSHSNAEVLMDCGIDLTASCNSEPKELAGATETAPESDEEPAGEQAQEQDQKNSEEVDSEFKEGNTATLEID
SETVQAVQSLTQENSEQDDTFQDCAETQEACRSLQNYTHADQSPQIAASLDDCQQSDHSSPVSSVHSHPSQSVRSVNSPS
VPALENSYAQISPDQNAISVPSLQNMETSPMMDVPSVSDHSQQVVDSGFSDLGSIESTTENYENPSSYDSTMGGSICGNG
SSQNSCSYSNLTSSNLTQSSCAVTQQMSNISGSCSMLQQTSISSPPTCSVKSPQGCVVERPPSSSQQLAQCSMAANFTPP
MQLAEIPETGNTNLGLYERMGQSDFGAGHYPQPSATFSLAKLQQLTNTLIDHSLPYSHSAAVTSYANSASLSTPLSNTGL
VQLSQSPHSVPGGPQAQATMTPPPNLTPPPMNLPPPLLQRNMAASNIGISHSQRLQTQIASKGHVSMRTKSASLSPAAAT
HQSQIYGRSQTVAMQGPARTLTMQRGMNMSVNLMPSPAYNVNSVNMNMNTLNAMNGYSMSQPMMNSGYHSNHGYMNQTPQ
YPMQMQMGMMGTQPYAQQPMQTPPHSNMMYTAPGHHGYMNPGMSKQSLNGSYMRR
```

1070 - 1089:	EEEEEEEEEEEEEEEEEEEE
1071 - 1090:	EEEEEEEEEEEEEEEEEEEE
1072 - 1091:	EEEEEEEEEEEEEEEEEEEE
1073 - 1092:	EEEEEEEEEEEEEEEEEEEE
1074 - 1093:	EEEEEEEEEEEEEEEEEEEE
1075 - 1094:	EEEEEEEEEEEEEEEEEEEE
1076 - 1095:	EEEEEEEEEEEEEEEEEEEE
1077 - 1096:	EEEEEEEEEEEEEEEEEEEE

A0A341B4E6 **A0A341B4E6_NEOAA** (1763 aa)
Histone acetyltransferase (EC 2.3.1.48). *Neophocaena asiaeorientalis asiaeorientalis (Yangtze finless porpoise) (Neophocaena phocaenoides subsp. asiaeorientalis)*

```
MVKLANPLYTEWILEAIQKIKKQKQRPSEERICHAVSTSHGLDKKTVSEQLELSVQDGSVLKVTNKGLASYKDPDNPGRF
SSVKPGTFPKSAKGSRGSCNDLRNVDWNKLLRRAIEGLEEPNGSSLKNIEKYLRSQSDLTSTTTNPAFQQRLRLGAKRAV
NNGRLLKDGPQYKVNYGGLDGKGAPKYPSAFPSSLPPVSLLPHEKDQPRADPIPICSFCLGTKESNREKKPEELLSCADC
GSSGHPSCLKFCPELTTNVKALRWQCIECKTCSACRIQGKNADNMLFCDSCDRGFHMECCDPPLSRMPKGMWICQVCRPK
KKGRKLLHEKAAQIKRRYAKPIGRPKNKLKQRLLSVTSDEGSMNAFTGRGSPDTEIKISIKQESTDINVIGNKDTVTEED
LDVFKQAQELSWEKIECESGVEDCGRYPSVIEFGKYEIQTWYSSPYPQEYARLPKLYLCEFCLKYMKSKNILLRHSRKCG
WFHPPANEIYRRKDLSVFEVDGNMSKIYCQNLCLLAKLFLDHKTLYYDVEPFLFYVLTKNDEKGCHLVGYFSKEKLCQQK
YNVSCIMIMPQHQRQGFGRFLIDFSYLLSRREGQAGSPEKPLSDLGRLSYLAYWKSVILEYLYHHHERHISIKAISRATG
MCPHDIATTLQHLHMIDKRDGRFVIIRREKLILGHMEKLKTCSRTNELDPESLRWTPILISNAAVSEEEREAEKEAERLM
EQASCWEKEEQEILSSRANSRQSPAKVQSKNKYLHSPESRPVAGERGQLMELSKESSEEEEEEEEEEEEEEEEEEEEEEE
EEEENIQSSPPRLTKPQSVAIKRKRPFVLKKKRGRKRRRINSSVTTETISETTEVLNEPFDNSDEERPMPQLEPTCEIEV
EEDGGKPVLRKAFQHQPGKKRQIEEEEGKDNHCFKNADPCRNNMDDDANNLKEASRDNPEPLKCKQWPKGTKRGLSKWRP
NKERKTGFKLNLYTPPETPMEPDDQVIVEEQKETPADKTSPAPTRTEEEVKEAVEPLLPGDENRREEMCAPVSPNKSPGE
KPEDDLIKPEEDEEEEEEEEEEEEEEEEGNVEKDPCGAQSQEKEEPEVCTDKEDPVRLDDHEEEEEEDEEPSHNEGHDADDE
DDSHMESAESEKEERPREAFKEVLETQEAFLDLSVQPSHSNAEVLMDCGIDLTASCNSEPKELAGATETAPESDEEPAGE
QAQEQDQKNSEEVDSEFKEGNTATLEIDSETVQAVQSLTQENSEQDDTFQDCAETQEACRSLQNYTHADQSPQIAASLDD
CQQSDHSSPVSSVHSHPSQSVRSVNSPSVPALENSYAQISPDQNAISVPSLQNMETSPMMDVPSVSDHSQQVVDSGFSDL
GSIESTTENYENPSSYDSTMGGSICGNGSSQNSCSYSNLTSSNLTQSSCAVTQQMSNISGSCSMLQQTSISSPPTCSVKS
PQGCVVERPPSSSQQLAQCSMAANFTPPMQLAEIPETGNTNLGLYERMGQSDFGAGHYPQPSATFSLAKLQQLTNTLIDH
SLPYSHSAAVTSYANSASLSTPLSNTGLVQLSQSPHSVPGGPQAQATMTPPPNLTPPPMNLPPPLLQRNMAASNIGISHS
QRLQTQIASKGHVSMRTKSASLSPAAATHQSQIYGRSQTVAMQGPARTLTMQRGMNMSVNLMPSPAYNVNSVNMNMNTLN
AMNGYSMSQPMMNSGYHSNHGYMNQTPQYPMQMQMGMMGTQPYAQQPMQTPPHSNMMYTAPGHHGYMNPGMSKQSLNGSY
MRR
```

778 - 797:	EEEEEEEEEEEEEEEEEEEE
779 - 798:	EEEEEEEEEEEEEEEEEEEE
780 - 799:	EEEEEEEEEEEEEEEEEEEE
781 - 800:	EEEEEEEEEEEEEEEEEEEE
782 - 801:	EEEEEEEEEEEEEEEEEEEE

783 - 802:	EEEEEEEEEEEEEEEEEEEE
784 - 803:	EEEEEEEEEEEEEEEEEEEE
785 - 804:	EEEEEEEEEEEEEEEEEEEE

A0A341B6X0 **A0A341B6X0_NEOAA** (729 aa)
YTH domain-containing protein 1 isoform X2. *Neophocaena asiaeorientalis asiaeorientalis (Yangtze finless porpoise) (Neophocaena phocaenoides subsp. asiaeorientalis)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLISKPLSSSVSN
NKRMVNTKGKSVTEYKNEEYQRSERNKRLEVDRKIRLSSSASREPYKSQSEKTCLRKRDPERRVKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGAEDVEEDEEVEDAEEDEEVDDDGEEEEEEEEEEEEE
EEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSS
ASESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSARSVI
LIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQ
EIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYAPEFH
QRPGYLKDPRYQEVDRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMTPYPGMEQPPHHPYYQHHAPPPQAHPPYSG
HHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRD
RGERGRYRR
```

228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE

A0A341B7J8 **A0A341B7J8_NEOAA** (645 aa)
major centromere autoantigen B. *Neophocaena asiaeorientalis asiaeorientalis (Yangtze finless porpoise) (Neophocaena phocaenoides subsp. asiaeorientalis)*

```
MAAHPARRPGTAPRPAPLPAGHQTPERWPFKQAEAPPRAPRVAALPAFRSRASRSCPRPPPAARRPALRKGEIARRFNIP
PSTLSTILKNKRAILASERKYGVASTCRKTNKLSPYDKLEGLLIAWFQQIRAAGLPVKGIILKEKALRIAEELGMDDFTA
SNGWLDRFRRRHGVVSCSGVARARSRSAAPRPPAAPASPPTVPSEGSGGGTTGWRAREEQPPSVAEGYASQDVFSATETS
LWYDFLPDQAAGLCGSDGRARKATQRLSVLLCANADGSEKLPPLVAGKSAKPRAGQAGLPCDYTANSKGGVTTQALAKYL
KALDTRMAAESRRVLLLAGRLAAQSLDTSGLRHVQLAFFPPGTVQPLERGVVQQVKGHYRQAMLLKAMAALEGQDRSGLQ
LGLMEALHFVAAAWQAVEPSDIATCFREAGFGGGPNATITTALKSEEEEEEEEEEEEEEEEEEEGEGEEEEEEDGEEEE
EGGEGEELGEEEEVEEEGDVDDSDEEEEEEEESSSEGLEAEDWAQGVVEAGGSFGGYGAQEEVQCPTLHFLEGEEDSESD
SDEEEEDEEEEDEDDEDDDEDGDEVPVPSFGEAMAYFAMVKRYLTSFPIDDRVQSHILHLEHDLVHVTRKNHARQAGVRG
LGHQS
```

446 - 465:	EEEEEEEEEEEEEEEEEEEE

A0A341D4E4 **A0A341D4E4_NEOAA** (1975 aa)
Histone acetyltransferase (EC 2.3.1.48). *Neophocaena asiaeorientalis asiaeorientalis (Yangtze finless porpoise) (Neophocaena phocaenoides subsp. asiaeorientalis)*

```
MVKLANPLYTEWILEAIKKVKKQKQRPSEERICNAVSSSHGLDRKTVLEQLELSVKDGTILKVSNKGLNSYKDPDNPGRI
ALPKPRNHGKVDNKQNVDWNKLIKRAVEGLAESGGSTLKSIERFLKGQKDVSALFGGGAASGFHQQLRLAIKRAVGHGRL
LKDGPLYRLNTKATNVDGKESCESLSSLPPVSLLPHEKDKPVAEPIPICSFCLGTKDQNREKKPEELISCADCGNSGHPS
CLKFSPELTVRVKALRWQCIECKTCSSCRDQGKNADNMLFCDSCDRGFHMECCDPPLTRMPKGMWICQICRPRKKGRKLL
QKKAAQIKRRYANPIGRPKNRLKKQNTVSKGPFSKVRTGPGRGRKRKITLSSHSASSSEDGYLEQIDGLDFCRDGSVPLK
FNKKTKGLIDGLTKFFTPSPDGRKPRGEVVDYSEQYRVRKKGNRKSSTSDWPTDNQDGWDGKQESEERLFGSQEVMTEKD
MELFRDIQEQALQKVGVTGPPDPQVRCPSVIEFGKYEIHTWYSSPYPQEYSRLPKLYLCEFCLKYMKSRTILQQHMKKCG
WFHPPANEIYRKNNISVFEVDGNVSTIYCQNLCLLAKLFLDHKTLYYDVEPFLFYVLTQNDVKGCHLVGYFSKEKHCQQK
YNVSCIMILPQYQRKGYGRFLIDFSYLLSKREGQAGSPEKPLSDLGRLSYMAYWKSVILECLYHQNDKQISIKKLSKLTG
ICPQDITSTLHHLRMLDFRSDQFVIIRREKLIQDHMAKLQLNLRPVDVDPECLRWTPVIVSNSVVSEEEEEEEEEEEEEE
EEEEEEEEDGEQEEPQSQEGELETSVGKSASRENKEQDSYSSVESEKKPEVTAPASSTRLNKQVLPRDSLPANNQPSRRG
RWRRKNRKAQERFGDEDSKLLLEETSAPPEQYGDCEEKSETCQEEYTEGQEQSAASQEQPSQDAMPDGPKRRPSEGLELW
RGPLKKSPEPLKCGLPESHDRLPRRYSEGRYSDGDRALLRGCSESSEEEGEPESPRSSSPPVLTKPTLKRKKPILHRRRR
VRKRKHHNSSVVTETISETTEVLDEPFEDSDSERPMPRLEPTFEIDQEEEEEDENELFSQGYFRHLSSQDVLRCRPASKR
KSKDRDEYEDSDDADDTPILKPVSLLRKCDVKDSPLEPDTSTPMKKKKGWPKGKSRKPVHWKKRPGRKPGLKLNRELAAV
STRECVVEPVVPLPEPGREPQVQENQEAVGPREDLPLREERKEGEELPLEAEEGEDTTSSDVRAASPADSCSPETGAEGP
GVGEEEEEPRAPVGQQPSEEGPQDLAQRAREEEEEEEEEDAAETQQSEDRDADDEDDGHLESTEKKGPEEQPAGGNVKEE
HGGQESFLDPDVHSSREHAKDKEETEPDSEEEQTSHEASVVSEHMPGSEDDHEEDSHSKEELLQLKEEAEIPHSDLDLET
VQAVQSLTQEESSEHEGAYQDCEETLAACQTLQSYTQADEDPQLPLVEDCHASEHNSPLSSVQSHPSQSVRSVGSPSVPA
LEGGYTQISPEQGSLSAPSMQNMETSPMMDVPSVSDHSQQVVDSGFSDLGSIESTTENYENPSSYDSTMGGSICGNSSSQ
SSCSYGGLSSSSSLTQNSCVVTQQMAGVGGSCSLMPQSSVPPAAATCSIKSPQSCAVERPPSTQQPPPPQPPPQAXXXXX
XXPQXPMIMEIPESGSTGNISIYERIPGDFGAGSYSQPSATFSLAKLQQLTNTIMDPHAMPYSHSPAVTSYAASVSLSNT
GLPQLAPSHPLAGTPQAQATMTPPPNLASTTMNLTSPLLQCNMSATNIGIPHTQRLQGQMPVKGHISIRSKSAPLPSAAA
HQQQLYGRSPPAVAMQAGPRALAVQRGMNMGVNLMPTPAYNVNSMNMNTLNAMNSYRMTQPMMNSSYHSNPAYMNQTAQY
PMQMQMGMMGSQAYTQQPMQPNPHGNMMYTGPSHHSYMNAAGVPKQSLNGPYMRR
```

787 - 806:	EEEEEEEEEEEEEEEEEEEE
788 - 807:	EEEEEEEEEEEEEEEEEEEE
789 - 808:	EEEEEEEEEEEEEEEEEEEE

A0A341D4W7 **A0A341D4W7_NEOAA** (1313 aa)
tau-tubulin kinase 1. *Neophocaena asiaeorientalis asiaeorientalis (Yangtze finless porpoise) (Neophocaena phocaenoides subsp.*

asiaeorientalis)

```
MQCLAAALKDETNMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTRENVALKVESAQQPKQVLKMEVAV
LKKLQGKDHVCRFIGCGRNEKFNYVVMQLQVSPRGLSSLHRSQPRGTFTLSTTLRLGKQILESIEAIHSVGFLHRDIKPS
NFAMGRLPSTYRKCYMLDFGLARQYTNTTGDVRPPRNVAGFRGTVRYASVNAHKNREMGRHDDLWSLFYMLVEFAVGQLP
WRKIKDKEQVGMIKEKYEHRMLLKHMPSEFHLFLDHIASLDYFTKPDYQLIMSVFENSMKERGIAENEAFDWEKAGNDAL
LSTSTSTPPQQNTRQTAAMFGVVNVTPVPGDLLRENTEDVLQGEHLSDQENAPPILPGRPPEGPGSGPHLAPHPGGPEAE
VWEETDVNRNKLRINVGKTPCVVEEEQSRVAGLPGSPVRAPPDSPTTPVRSLHYRRVNSPESERLSTADGRVELHERRSR
MDLPGSPSRQACSSQPAQMLSVDTGHADRQASGRMDVSASVEQEALSNAFRSVPLAEEEDFDSKEWVIIDKETELKDFPP
GAEPSTSGTTDEEPEELRPLPEEGEERRRPGPEPAVRPRGRGMHALAEEDLRLTPAQPLPPQLNQADGRSETSQPPTPGS
PSHSPLHSGPRPRRRESDPTGPQRQVFSVAPPFEVNGLPRAVPLSLPYQDYKKDLSDYRERARLLNRVRRVDFSHMLLAT
PQVPLAPVQPQTNGKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEEEEEEEEEEEAVALGEVLGPHSGSSSEGSERSTD
RSQEGAPSTLLADDQKESRGRASMADGDLEPEEGSKTLVLVSPGDMKKSPVTADLAPDPDLGTLAALTPQHERPQPTGSQ
LDVSEPGTLSSVLKSEPKPPGTGTGPGAGAVTIGAGGVAVTSSPFTKVERTFVHIAEKTHLNVMSSGGQASRSEELSAGG
ELGLEVPSDGRAAEEGASVYLENGIALSGLVSCVLSAPPESSPLEVTTDSLPNGPALADGPAPASLLEPGPEKLATISPS
RHARPGPRPRSRIPVLLSEEDTGSEPSGSLSAKERWGKRARPQQDLARLVMEKRQGRLLLRLASGASSSSSEEQRRASET
LSGTGSEEDTPASEPAVPRKAGRAAATRSRIPRPISIRMPTPAAAQQPPDRPQGAAPASDTAITSRLQLQKPPGTAIAAD
LRPKQPPGRGPGPGRAQAGTRPPAPRSPGLPASSAHHPSASPRSRSLSRKESPSPSHQARPGAPPPRGAPQARAQPEGTP
SPGAPKKGPRVKLQTQRATKGRAGVAEGRAGAR
```

736 - 755:	EEEEEEEEEEEEEEEEEEEE
737 - 756:	EEEEEEEEEEEEEEEEEEEE
738 - 757:	EEEEEEEEEEEEEEEEEEEE
739 - 758:	EEEEEEEEEEEEEEEEEEEE
740 - 759:	EEEEEEEEEEEEEEEEEEEE
741 - 760:	EEEEEEEEEEEEEEEEEEEE
742 - 761:	EEEEEEEEEEEEEEEEEEEE
743 - 762:	EEEEEEEEEEEEEEEEEEEE
744 - 763:	EEEEEEEEEEEEEEEEEEEE

A0A348PM23 **A0A348PM23_9FLAO** (294 aa)
Uncharacterized protein. *Flavobacteriales bacterium*

```
MNRNNYLILALILGLMFTNCKKEKVPEEDTTEQSENEGEGEEEEEEEEEEEEEEEEEEEEEEEEQANPPEISKFELDCY
SNNSANLYIKINTVKHATATIGLLYSKTENAGWNGTKIQQSDPSSTYYPRMSDLEEGTTYYIMAYAIDGTDTGYSQQYNF
TTRAQAFGYEIGDFYQGGIIVGFDCSGIHGLIVAEQEFGNPFAWSVAKDICESYTHNGYSDWVLPSVYDLRAIYSNLHNP
NIKKYSDKYFWSSRNRKEGASGQFGYSYAKNFLDGAENEYDEYYKYRVVAVRYF
```

41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE

A0A364N9K4 **A0A364N9K4_9PLEO** (1000 aa)
Major facilitator superfamily transporter. *Stemphylium lycopersici*

```
MSTDDGAMQFAYCSMSKQVNRKMDIALLPFLSLLYLFNGLDRSNVGNAETQGFTTDIGATPDDLNLAVSLFFITFIGWGL
FTLAHAFIHGRNALIGVRLMIGAFEAGFYPTAVAYLSTFYSRYDLAVRIGLFYGQYAVAGAFSGSIAFGIFHLNGTTLYN
WQYLFIIEGTLTILIAFVAWFWLPHGPGTAWFLSADEQVFASQRVAKDHAAYVLHYGHDGLPRKRLMQRDAVETFKDWKL
WFLLMFNICASVPSQAFSVFMPMVVQGLGYSSVEANLMSVPPFVCGAAGLYLFALSSDRRQERGYHILAGISVSLIGLIV
TVTTQSHSTQYVGLCILLFGSYVSAPLTVVWLSGNNPEPGKRFLVMGVNGFGNLAGVIGSQLYKKQYAPRYLTPFYATLG
FVAAALVGYAAYKYILKRVNERKLKLMEGKSEEQIEAERLDETRYADAKWTFLYGFHMLPSTELNPLNRVVQKVRPDNPI
AMFQFSSLVPNPFASRSTPRQQPSGPPPPPTVAEDPEAPLAPPFPFLRLPLELREQIYSHYFDPADHLAKSPVHESKGFF
GGIYEWDFDIFLANKQVYRESKKVWRREIVFVKIATPWPSAVNHISSEGLVPIVCHDAKATAFTEHHAVVQISAPFHGVV
PEHMVVVLVDDLHLFTKTWYYSALSYPMLNERLSTTFVLRNPSREEHDSDDEAEQHREEEEEEEEEEEEEEEEEEEEEE
EGLGVPIALQKKLLLPFEHVKGLHGTRIHGYSRSVQSELARLQALPIPSLQQSLESATDFMLAGDAALATPDAEDTAALE
ALELYNKAFHAIHILIHGRTRRVMADVFFHESITQGRYAGQTGITVRVILRLKLVSRTIAAYNKLAKWDEAAYWGMRSIH
ILHESLNPDFEAFLTEVLGGADVGLIYLRTGIAFWQMESQRMNWLGELIHYADEAMAQSESLWKTSRRFLRDLPRGHVRA
ELVQYGVPRETVALFADVKKEDAVQSSVVADGESSSTSEE
```

698 - 717:	EEEEEEEEEEEEEEEEEEEE
699 - 718:	EEEEEEEEEEEEEEEEEEEE
700 - 719:	EEEEEEEEEEEEEEEEEEEE
701 - 720:	EEEEEEEEEEEEEEEEEEEE
702 - 721:	EEEEEEEEEEEEEEEEEEEE

A0A365N4S1 **A0A365N4S1_GIBIN** (368 aa)
Uncharacterized protein. *Gibberella intermedia (Bulb rot disease fungus) (Fusarium proliferatum)*

```
MAASSFDPFPRLPTELRLQIWITACVSYPSDDRGVHYIDVEPISTGSMLSSSPTLTARLADGDKNSACLRNGGLWTACKE
```

```
SRDFMIQHSRVDALDCARISICGNGEGWSSPVNPTRDIFCVKSKAWKTPDDHGQEWEILLPYFSPNGSYPTDVKNVALEF
DESRNKDLPKSYYDLMSETSARGFLSRLLYNRFLNDSDTPQIWVIVKNGQWVLEPGLACTPNPYRDHDKDYIPAWPYFSC
RHCHRTHDFDGVFKNVKNFLHTLDDLGEACKEDHPDYKEREDYDEWYGSWEEAFDIATDVQFLAHRDMLIDLCTGPEPEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDIDMGI
```

319 - 338:	EEEEEEEEEEEEEEEEEEEE
320 - 339:	EEEEEEEEEEEEEEEEEEEE
321 - 340:	EEEEEEEEEEEEEEEEEEEE
322 - 341:	EEEEEEEEEEEEEEEEEEEE
323 - 342:	EEEEEEEEEEEEEEEEEEEE
324 - 343:	EEEEEEEEEEEEEEEEEEEE
325 - 344:	EEEEEEEEEEEEEEEEEEEE
326 - 345:	EEEEEEEEEEEEEEEEEEEE
327 - 346:	EEEEEEEEEEEEEEEEEEEE
328 - 347:	EEEEEEEEEEEEEEEEEEEE
329 - 348:	EEEEEEEEEEEEEEEEEEEE
330 - 349:	EEEEEEEEEEEEEEEEEEEE
331 - 350:	EEEEEEEEEEEEEEEEEEEE
332 - 351:	EEEEEEEEEEEEEEEEEEEE
333 - 352:	EEEEEEEEEEEEEEEEEEEE
334 - 353:	EEEEEEEEEEEEEEEEEEEE
335 - 354:	EEEEEEEEEEEEEEEEEEEE
336 - 355:	EEEEEEEEEEEEEEEEEEEE
337 - 356:	EEEEEEEEEEEEEEEEEEEE
338 - 357:	EEEEEEEEEEEEEEEEEEEE
339 - 358:	EEEEEEEEEEEEEEEEEEEE
340 - 359:	EEEEEEEEEEEEEEEEEEEE
341 - 360:	EEEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEEE

A0A366QNK9 **A0A366QNK9_9HYPO** (3273 aa)
Uncharacterized protein. *Fusarium coffeatum*

```
MPINGTGRNANRRLPSWLTSSPLPSSDSQKERRRPNDDLISDPASDTLIDFNSNQGFYEAAKKPKKAKAPAAPPPPPPPP
AAPPADDGQKDDNTGGDGGASGGSAAGGAGDGNGNGGGGAPQKPPTTFDNISLGGSKLDLGLSPPEGKSISSWGAKLGFG
GGGWGWGGGAKNEPAPAPAPPPPPEPKDEENPWDKPKDQPGGLGMKDDDDAWGFGTKKDKKQSTLWGAEPDEGPKDGDDP
WGWGGQKKKGKPGGILEELALDPEPAPPPGSKKDIWDTWGISKKDRAKKKGIMEEVALAAAPDPPSMDDQWGGWSGKKDN
PPQSSLWGAQDPIPAAPDPPSFEDKDGDDFWSTFGSGKPKPAEENPPGWGSWGVEPPKIEDDGWDLWGTGKKKKKAGDLI
QLEDEIPPPAPDPVEAVGTDDFLDSWGFDKKPKKPAADPFDFKTSGAHDPNDAFWGSIDNQRPSANDFLIDTTDPEQAAR
EAEEQAAREAEDAEAAREDEEIASLMDKRAKRGGRLLKSDRERLTLLEGNAARRAEVRAAREAEAAAAAEAAQAAADAQA
AADAEAAALQAAADAEAAKENEEIEQLLAKKQKRGGKLLRKDQERLTVLEGNASRRAEAQAAREAEAAAAAAEVDIIEEI
PLDEPPPEAPEEDAAAQAAAEAEAAFAAEVAQEEAEMESLKSKKAKKGKLLKKEQERLNILIDNATKRAEDAIAKEADEQ
AAKDAADAAAAAAAEAAEAEAAAQAAAEAEAAAQAAADAEAEEAAKEEEEMAALKAKKAKKVKLTKAETTRLMTLVGNSV
KRAQVKTAKEAEEAAAAQAAKEAEESAAREVEEKAAREAEDAAAREAEAALAAEEDKELAALDALKKKRGGNLIKKKDVE
RYNVLTLRAKERAAKKAEAAPTEATPELPDEPTESVPEPVPEAPPADADPELVVPEPVPGPDAAIIAEEEAELASLEAKK
AKKGKLGKKDTDRYNLLNENAAQRQAAKEAEETAARDAAEAAAAEEAAAAETAGADAVTASEAEAILIADEEAELAMLTA
KKAKKGKLVKKDLERFDILTENAAQRQASKDAEEAAAAAAAEAEAQAEKDAEEAAAAEAAEAEATAAREAEAAAIAEEEA
ELSALAAKKAKKGKLIKKDAERFAILTENADRRAQEAAMAVEQPDDPAPPAEVDVEEPAPEPPVEEELVEIDDPDANAAN
EAEAAAIAEEEAEMAALVAKKERKGKLGKKDTDRFNLLTANAASRADKAAEEEAAAAAAAAAAEEEAAAAEAAAIEEAAA
REAAEAAEAEAAVIAEEEAELAALTAKKNKKGKLGKKDNDRFAILTENATQRAEKAAAAAAAEVEPEPEPEPEPEPEPEP
EEVPPEVEDPPIDDFDDAAASEAGDEEAAIAAEAAAIAATIAAEEEEELEALIAKKTKKGKLGKKDSDRLAVLTENAAQR
AEKAAQEEAAALAEPEIVDDALVDIEDPTPEDAPEEPPEEEVAPEEEDAAAAEAAALIAAEEQELADLDAKKARKGKLGR
KDTDRYNILTENAVKRAEERAARESEEAAAAEAAAVAEAEEIAAREAAEAEAAAIAEEAEKEAADAEAQAAIAQEEEELA
ALEAKRERKGKLGRKDTDRLNALMDNKAARDARAEEEQAAKEAEDQAAQEAEDAAAAEAAAAAEAEETAAKEAAEAEAAA
IAAEEDAELAALTAKKTRKGKLGRKDTERFDQLTLNATRRAEEQAAREAEAAAEEIPVEDEPAPEEPEEPVPDAIEPVEA
PVEEPPEAQAPDLDDEAAAEAAAIAAEEEAELASLEAKKARKGRLGNKDTQRFNFLTENITRRAEEQAAKEAAAAEAVVD
EVEAEDIPEDVPEDDEAAVQAAADAEAEAAAAAIAAEEEAELSALVAKKARKGKLGRKDTERFDILTENAARRADEQAAK
DAQAAEAEAEVEEPVPEPIEDAAEPEPDEEPEDEDAAAKEAAEAEAQAVAAEEEAELAALNKKKAKKGRLGRSDTERFKV
LTDNAAKRAEAQAAKEAEEAAEEAAEEAEEEAQPAEEEEEDDFVDAEDGEDDLIEEPEPEAEEAAVPEEEGAAAAAAAEA
EAQAAAIAEEEEAELASLTKKKIRKGKLGRTDTQRFQVLTDNAARRAEEAAAREAEDAAAAEAELEAEPEPEPDNEPEPE
ADQEPDDGAINEVDEAEAAVIAEEEAELAALTKKKIRKGKLGRTDTQRFQVLTDNATRREEERSAREAAAVAEAEAAEAD
AEAEAAEDAEDADAHADEEEEEEDDIVEVEDDEMAAREAEEAAIAEAEEEELESLKAKRARKGRLGRKDTERFAVLEENA
IRRAEERAAKEASAAAEPEEPPEGDEPDDGEDAAEEEEQDEEDAAAAAEEDAAAREAEEEAAREAEEAAIAEAEEDELES
LKAKKARKGRLGRKDTDRFHMLEENAARRAEERAVKEAAAAAAVDEAEAEEAPENEEEEEEEEEEEEEEEEEEGEEEEEE
EEEEEEEEEEEEEEEEDDNGAVDEEAAAAREAEEAAAREAEEAAAREAEAAAIAEAEEAELDSLKFKKSRKGRLGRKDTD
RLRFLEENAAKRAEELAEKEAAAAAEAKAEEAPEDKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDAAAEADPPEEEPAEV
ANKDIADESDEEEAEAVPEEAPEEPEPEVPADDEIVEVVDLSPKRERRSRKGKSRRDAPPPPPVPDPPLTPPPEPKHSRR
PKLGREGTSWGKWGATPREERDEYPQEKSGRHRRREEKTSSKGSTSDKVEKPSSRTAALFGKTPLGRSASTREKRDGLGS
KRRHSEAARGIVSPPPEEMLMQEDPSSRRKSRKPRSREDEDAMMSGAAPVPDRYERRHSHKTRSREDDDVVMVDPDLAND
RRERRRSHKPRSREDEDMVMPDDMAVPGPRDRRRRDRRSRDDEPIMVEPDVPADQPLPRGSKKGFGGIFSGLRTPKNERP
DPLRRRSTYATTDDEALRTARMDGDAVVVDADREARRAARKAKRADPEEEARRAKDEARRERRRQREKGADAPRQDQDAR
RAERRAARQRGEEERRAQEEQQAEEELQRAQEAKEAQRAERRRLRREQEAAAAAEQEEQEARRAAKRDRRRPRQADVSED
EHERRRRREARRAARAAEEGAEGHHRRPRHEEPQQPAWPHLGTSSWVKEHVDAPPPPEIPQAGDVNGGQTEDDEMARREA
```

RRAQHRSKYSDETPDEAEERRKRRARREERERGGRHRDRRSEGSDERHHARRASNFAENAAAPRTSWWKKIKG

2475 - 2494:	EEEEEEEEEEEEEEEEEEEE
2476 - 2495:	EEEEEEEEEEEEEEEEEEEE
2477 - 2496:	EEEEEEEEEEEEEEEEEEEE
2597 - 2616:	EEEEEEEEEEEEEEEEEEEE
2598 - 2617:	EEEEEEEEEEEEEEEEEEEE
2599 - 2618:	EEEEEEEEEEEEEEEEEEEE
2600 - 2619:	EEEEEEEEEEEEEEEEEEEE
2601 - 2620:	EEEEEEEEEEEEEEEEEEEE
2602 - 2621:	EEEEEEEEEEEEEEEEEEEE
2603 - 2622:	EEEEEEEEEEEEEEEEEEEE
2604 - 2623:	EEEEEEEEEEEEEEEEEEEE
2605 - 2624:	EEEEEEEEEEEEEEEEEEEE

A0A366R375 **A0A366R375_GIBMO** (547 aa)
Uncharacterized protein. *Gibberella moniliformis (Maize ear and stalk rot fungus) (Fusarium verticillioides)*

MPSDSELSDFWAGVNHSDAVDFLAMSWEKLDESPEDAESAAAETEGNQEPQGSDTEEQHVKPLEETQAQSFLNDPRKVKA
CAVFLLCGCNTPDAEPRPSPYYLIRFSPALNCSGVDLFTAIPTLPDAASVEKHWQTHSRVQRLLRSFMDNPSYGSKYFYC
HRAVADGVLVSFPNATPGSPMTRAVTFPVEWDHYYSGTRFSENQDINMNGPQGGEYGGLSDVEEEGLDANFVYGRLSPVP
APQQDSKTLSELNGYLPGYRFVGNRDAEMDEGDVTYDGSFHEFTLEYPFFPAEGFEGFSGCWQEDDYEADVSESCFEESS
QESSDTCGSSGDDSVSYTILRRDSDIEDSCSGLRKRKFDEHEQGQIEADEFEEEKFDEDESEDVRLEEQCSDPSDDEVDL
EDVLECGCCSDFYFNPTDAPQDYGCFLEDFTFQGDDVKIEEFPRRLQTIPEVDEPGSPVPYGYAEHAPNATYVPGGSGAE
DDAHHGKLRYIILEQESSHPWPVWPDEIVLSVEEEEEEEEEEEEEEEEEEEEEYGNGPYFNDAQLD

513 - 532:	EEEEEEEEEEEEEEEEEEEE
514 - 533:	EEEEEEEEEEEEEEEEEEEE
515 - 534:	EEEEEEEEEEEEEEEEEEEE

A0A366RRC7 **A0A366RRC7_9HYPO** (425 aa)
Uncharacterized protein. *Fusarium coffeatum*

MFENSPLMVFPSASSPTGTSFIDTLAMNAEEYGVANDLQGPSSWKSDRMQTPIDYGSGSIDLEESVEYIDESHQTSPASE
EGEYRQHSVSLEDGASSVQRSSQADTEAMIVPRERGKRRKVTPQSAGSEEVFEEYTNDADRTVALPKRGKVSEVTSGMSG
SRERFSRNGATRNPRGRPPGRRKTDPWGGTTVQHKVRTVTRPPGIVKTRSGRASVTPKAQDTIRAPESVRTNERIKPRRT
RPLQRQTVTELVADNSQETWEMTSGYKAVGCWERRPQKEVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGDKNWL
YLHRKVAFSSVMTLGSNLPRNKFHWGKVKVDGLNEFGQMVIPPGGSKERSRMQEFNLLFIILQGPVTVEINDQCFKINTR
SMFVVPKGWSQGTTIVSLTKTKNLL

281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE
287 - 306:	EEEEEEEEEEEEEEEEEEEE
288 - 307:	EEEEEEEEEEEEEEEEEEEE
289 - 308:	EEEEEEEEEEEEEEEEEEEE
290 - 309:	EEEEEEEEEEEEEEEEEEEE
291 - 310:	EEEEEEEEEEEEEEEEEEEE
292 - 311:	EEEEEEEEEEEEEEEEEEEE
293 - 312:	EEEEEEEEEEEEEEEEEEEE
294 - 313:	EEEEEEEEEEEEEEEEEEEE
295 - 314:	EEEEEEEEEEEEEEEEEEEE

A0A366RYC6 **A0A366RYC6_9HYPO** (577 aa)
Uncharacterized protein. *Fusarium coffeatum*

MEQQSCQLPRFSPELIFMIVGYNDPPDLLALSLACSDLHHRCRSLLVKHQGAYSKYRITSDLSPETAVDLLKDTLTAEIN
RYHVRELEFWGSRLRWEDWRSWNPALSGNYEVAEEEPSRSAWDAREIEEYIQKGIRLWDLTEEKIEELQMSLDRGMEAWL
KLLLICLCPRLHSVRFVKRRGDSYNILAWISEVISWSVEDGCHWPPGFESLRSISVGVSIGQLPHEEEEEEEEEEEEEE
EEEEEEEYYDGFEEFTKLFYIPNLKNIYFNGFSCHEDEWEDHFWDEDLLPNGTSNVESLFLDGVEGGWADFYYWLSGASR
KLDTVVLRAIDSRRGGMLDASSLVDSLAVMNKTMERLVLYHPAAVQHGMFPIEIYKHKSVKQITIMALDIDCRFDYTGRD

```
RTSDIALAFPPNIEAVYLWGELNDLGKPGRRCLRNLDSFLAELIESGVYKHLKAVYVEDVELTYRQRLKSASPFRIREWK
RPAFLKATAAGQRAGVHVGTLMNRDDGGHWKNFPARPDRFNIKTGPFAAERPEEWKLNLYTGQWGPDCSGCGECEECLAV
YPSELWKESAAQRSNSP
```

226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE

A0A367IRL4 **A0A367IRL4_RHIST** (531 aa)
W2 domain-containing protein. *Rhizopus stolonifer (Rhizopus nigricans)*

```
MNLRNDFHNMIDLIDPVDMEYYLQNSSPRTVPICIAAAVYRISAGNCMPNANNQKRSFLSPWQSYRRKRAEDTSSLESTC
SSRSDSPEPKSTKKRSTHLLLREIHRLRGENTALKNSVSLLKNDLRDITLARQDTDASHRRFYEEYLDKNAQLEIDVMDR
DDEIARLKKQIEQLKSRNTSYDTAYEKNGFGCFEFDDDESELSCQPVAHESALPEVDIKMDELKTEDEHIDDYFHKRYLD
DSNPHYFSQQSDEEEEEEEEEEPFENVASSYIQQAMLSRLSSARVRLEFDDLICKYEPSSDTITTCLADAFVTWMGSLIT
NNNKTSQPMSIPRVFTSKIQAGIVEFWESILQYYTTDDQAQRQLLDHIEQLLQIVPFGLAIADHFDRLVLMLYKYHVIDD
DALISWWQTSSFDHQISQKIRKVTTRFIEWVQDSEEEEEEEEEEEEEEEEEEEEEEEEEDDDESDVFSFVESPLPEEEED
LNSSIDDLLNTNTRNYCVCHDTNNNSSECTCSTYTPPQVPEKKKKSVRIAM
```

435 - 454:	EEEEEEEEEEEEEEEEEEEE
436 - 455:	EEEEEEEEEEEEEEEEEEEE
437 - 456:	EEEEEEEEEEEEEEEEEEEE
438 - 457:	EEEEEEEEEEEEEEEEEEEE
439 - 458:	EEEEEEEEEEEEEEEEEEEE
440 - 459:	EEEEEEEEEEEEEEEEEEEE

A0A367IXA4 **A0A367IXA4_RHIAZ** (281 aa)
Uncharacterized protein. *Rhizopus azygosporus (Rhizopus microsporus var. azygosporus)*

```
MRYNILSLGLIATTLIASISARALPVGSLPDTTSSVGNAVAADGDVVTTALGRRSLYTNDKKRAAVSFQRREEEEEEEEE
DEEEEEEEEEEEDEEEEDEEEEEEEEEEEEGGEGNAADQSSLARRHWQKNKGTSNDDTEAANDGDAEELEPVTEELDTATE
DIDNIYPDDTDAAEDEVVYGGEDDDEDDEDEDDDDSDDDSDSDDDSDSEDEDEEDSKLARRQNTEEAAVDQPTDTSAVNT
TEQPVDATSGEGEGEEEEEEEEEEEEEEEEEEEEEEEEEEDE
```

255 - 274:	EEEEEEEEEEEEEEEEEEEE
256 - 275:	EEEEEEEEEEEEEEEEEEEE
257 - 276:	EEEEEEEEEEEEEEEEEEEE
258 - 277:	EEEEEEEEEEEEEEEEEEEE
259 - 278:	EEEEEEEEEEEEEEEEEEEE
260 - 279:	EEEEEEEEEEEEEEEEEEEE

A0A367J8F1 **A0A367J8F1_RHIAZ** (932 aa)
CBF domain-containing protein. *Rhizopus azygosporus (Rhizopus microsporus var. azygosporus)*

```
MGSKADHKKNKKTVEKSKNVAKSDDAFEQAVLELGGTKGDIKYLKDIDDDNEEDLQTTATKDEEALKNELKSFMANIGLS
ASTYEQDIDTDEEQPEDKEDEEEDVSSEEEEEEEEEEEEEEEEEEEEEEEEEPMKIHTPKSSSGLLIEPTPFWYNVSLPAI
SIENVQRLSTLQTQEKLNYAKQLLKDENAKAETHPMLTSSNRSFMSNIIQSGTLNDKVSALTLMFRESPLHGIKTLDTLI
SMSRKKGRNEAVMAITSLKDLFIGSVLPDRKLIYFADRPLAAKEVSDTHLLVWAFEDYLKKTFLEYLRIIEELSRDTLMY
VRNNMVTCIHDLLANKPEQEQNLLKLLVNKLGDSDNKVAAKTSQLIIELLIQHPGMKMIVIRELEQLLFLPSTNEKAQYY
AMITMNQTILTAKEKDVANKLIEIYFIFFKKLLKIQEKEDNSKKNEENEEVKVEEENDKKKSKKQMKKEKQQEQKKLELD
DHKTKMIAAVLTGVNRAFHFADISDKIVEDHLETLFKITHASTFNAAIQALSLIFTISISKPNIADRFYRVLYESLLDPR
IHQSSKQSMYLNLLFKAIRADNDMRRVMAFVKRLVQIAARHQPAFVCGIFFLISQLMESKPGLKTLLMPPEDDEEEHFED
VEEDDAPKKEDNKSSRVEYDGRKRDPRFSNAEKSCLWELLPFKLHYHPSVVKYVESLFAGELITNQPDLHQFTLMHFLDR
FVYKNPKKESVPKGQSIMQPLSGSRRDGGVLFTKSAINEIPVNSEQFIRKKEEEVAADEVFFHKYFTQKAASQPAKAKKE
KSGEDSEEEEDEVWRAMMASIPGGLDDEDDNDEDAALYDDDDEDDEEMKALLAENEEEEENEGDEDEEDIEFGSDEEDIE
LLNASDMEEELQAKRELSDDEEEEQPKKKKSKKERLPTFATYEDYAKLIEQE
```

108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE

A0A367JJW5 **A0A367JJW5_RHIST** (209 aa)
Uncharacterized protein. *Rhizopus stolonifer (Rhizopus nigricans)*

```
MTEHKEWPSERERIDVVGFYHQILWTSQQEPSKSDRKVSFSANPPTVYEYEAEYSKSFLINYQSIFQKAKIYRKESYHMC
DHSLDEEEEEEKEEEEEEEEEEEEEEEEEEEEEEEEDDDDDDDDEVDKNRLQKTKSFVDLAAVSHTCLAKLVNTNNSSDT
TLQDHPVEEFPSYQKNNDCKTVRKRGLFQRITHRAISISLHFVKCDFQQ
```

93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE

A0A367JYG3 **A0A367JYG3_RHIAZ** (874 aa)
Suppressor of glycerol defect. *Rhizopus azygosporus (Rhizopus microsporus var. azygosporus)*

```
MPHKRGPTPGSVLPKAMKEEVDAAEKDDRKFGKKFVNKIANRKELRKQKRAEKGKRKAIHQQTRDQQNKKRLLSEKQPQP
NKRQKKEDLPKDQSKDQPKKQVTNSEEAEKRLSKKNPALYKMLAADNLVGKNSTTDEDFEEDDKEIAYWEKKLGLNKKKK
KKLGKEFENDGLLDVLGNVDNVNNEMDDIEYLKQKRSKQAQLKEQKSLEENAERAVDQLFEDFPSDEDDDDMDASVDEDM
SDILNDEQESGEEEEVSDALEDEQDDDDDDDDEEEEEEEEEEEEEEEEEEEEEEENDEENDEENKKEEQVVVKEPPKSSVL
TKYVPPHLRKPVSTGKSEQQLRLQKQLQGQLNRLSELNIESILVEIEKCYGTYPRHDVTSTITELIINSISQRSNLLDSF
VITYATIVASLYRLVGVEFAAHFVQTVIEMFETEHKKYKKAKQQTIDDEQEGYKETRNLLTLILELYNFQVISCILVYDI
VRMLINELDEGNVELLLRIIRTAGAELRNDDPTSLKHIIDEIQKETAKRDPSTISLRHKFMLETIANVKNNKIKNKQTAA
GHGDKELVQKMKKFIQGLSKKRSTRSTEALRVSLDDIHNVHTKGKWWLVGASWKDNLVGTESKYKTTNVPEDLKKDQSMQ
EALLKLARKQGMNTDIRRTIFITIMSAEDYLDAFEKLMKLGLNEVQQREICRVMLQCTGNEKTFNPYYMLVSRRLCEIDH
SFKVTFQYCLWDFLRECGESEVGGLERSASESFSGSKEVRLSKIVNMAKFYASLITEGALTLAVLKSINFMNLQKNGRIF
LELLFVNILLQLHAGGAQAIANVFGKIRDQRILAQGCIFFIVGTVTHCKHSGLEEDDIEKVQWGCKIAKEVLNK
```

273 - 292:	EEEEEEEEEEEEEEEEEEEE
274 - 293:	EEEEEEEEEEEEEEEEEEEE
275 - 294:	EEEEEEEEEEEEEEEEEEEE

A0A367KHG9 **A0A367KHG9_RHIAZ** (291 aa)
Uncharacterized protein. *Rhizopus azygosporus (Rhizopus microsporus var. azygosporus)*

```
MRYNILSLGLIAATLIASISARALPVGSLPDTTSSISSAVAADEDVVTTALGRRSLYTNNKKRATVSFQRREEEEEEEEE
EEEEEEEEEEDEEEDEEEDEEEEEEGEGDEEGAADQSSLARRHWQKNKEASNDDADAANDGDAEELEPVTEELDTATEDID
NIYPDDTDVAEDEVAYGGEDDEDDEDDDDEDSDDDSDSDDDSDSDEDEDEDEDEEDSKLARRQNTDEAAVDQLADTSAVD
TTEQPADATSGEGEGEGESDEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDE
```

261 - 280:	EEEEEEEEEEEEEEEEEEEE
262 - 281:	EEEEEEEEEEEEEEEEEEEE
263 - 282:	EEEEEEEEEEEEEEEEEEEE
264 - 283:	EEEEEEEEEEEEEEEEEEEE
265 - 284:	EEEEEEEEEEEEEEEEEEEE
266 - 285:	EEEEEEEEEEEEEEEEEEEE
267 - 286:	EEEEEEEEEEEEEEEEEEEE
268 - 287:	EEEEEEEEEEEEEEEEEEEE
269 - 288:	EEEEEEEEEEEEEEEEEEEE

A0A367KS63 **A0A367KS63_RHIST** (698 aa)
Uncharacterized protein. *Rhizopus stolonifer (Rhizopus nigricans)*

```
MSVNTRHSSVEALKEKYQKSRQRAIENKQSSPATVYEEEEEEEEEEEEEEEEEEEEEEEEEEEKEDDNDSFYSSTSSIPDE
DINFDLVYALHTFVATLDGQASVVKGDAMTLLDDTNSYWWLVKALKTSEVGYIPAENIETPFERLARLNKHRNVEVTLPA
HLPEYTKNSNKKQASKKKVKMSRKLACQLQVVFTEEDDIEPIYERWEEEMSIESLVEEEEEEEVENKSPLLNPEFNKSIQ
SHEDQPSEIPKNKPKPLVQFEPSELNKGPPVQKPVSGLKRLFSIGNKKESPTEEEEENRQFHVLRIFAGNINVGAMFATV
AVTPEMSADQLLKIALEKFHIPLLTTDKSNSIEYYLTVKSMDSDELTMLPQDKPLAIFQSLSDHLTTPMPSLTYIKRLSI
EQPTIKVTRVGVSKARQRAKAHFGEDSVIRFALHKRIKRTLDGQTYVKISYYGDCDKKKSSSLIKKSSLLRKDSQPKKSK
KERMDKLVAISALTPISELTTTALEKFHLSPGESETYYMTLLINGRNEKTLPADKLLTDIFNDPSWIPKGTIEKFFVLRK
NHFVPSTSQSEPISPTDSNRRSVVRKLLKQQDNSGKSSLSNTDNVIKRLDEAIQSLENDKNKMAKNEDFTRRAPVRSNSL
SAYYNKGSKNDSDAYKKSTPTRSTSLKLVGDAFDTLNNNGLSNMDDLELELHRIATSS
```

37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE

43 - 62:	EEEEEEEEEEEEEEEEEEEE

A0A367L0V6 **A0A367L0V6_9HYPO** (70 aa)
Uncharacterized protein. *Ophiocordyceps polyrhachis-furcata BCC 54312*

```
MAEAGMADTRRIGLEVEVEEVEEEEEEEEEEEEEEEEEEEEEAWGLNAKEEEKRDGGNRSINIYIRTTKG
```

22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE

A0A367L7G6 **A0A367L7G6_9HYPO** (59 aa)
Uncharacterized protein. *Ophiocordyceps polyrhachis-furcata BCC 54312*

```
MEEEEEEEEEEEEEEEEEEEEEETTQGGIVFAFGRRRKMDASSSHAHKMMQRTKLGSEGV
```

2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE

A0A367LNS2 **A0A367LNS2_9HYPO** (378 aa)
Uncharacterized protein. *Ophiocordyceps polyrhachis-furcata BCC 54312*

```
MTWLGINDTSKLSRAGRMVFLSKADAMICRLDRLMTRAIKRAPPEAIIAAKELMERRHMVEGPDRDWQTEAVAEEGKEEE
QTPNESRGGEHGQMWESELSSTLTQESEATATRLTQEETEEEEEEEEEEEEEEEEEEEEEEEKEEEEEKEDKVTTQQTQR
HDSRQDQASQQLPADAAAAVDQQLPAEKTDQQPSCEEAISFNENNHVLFDRWNTTFAGQVEAYLDREEENTEVMLSGRHL
SRLQDDIELATYYRARLCDTIRWMDIHNERSSRKWKSTRPSPGCVASLMVSRGLGSLLAEREGGEADDGTTSPPPPPKGS
WEEKGRCRRRSRLCGQQARNKVKGCYDEDESSYDNVTCVGYDFFVGGRVMLILERWIW
```

120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE

A0A367XXS1 **A0A367XXS1_9ASCO** (1654 aa)
DNA polymerase (EC 2.7.7.7). *Candida viswanathii*

```
MNTTNDSTASTTFNASSVNWTNNQVNSSSNLRVQINDYDTYQTFATRLDQYCTRVTQVPIIRIYGSIAIDHEAVLCEVSP
RKKKQKIEAHSSVFNVVIHVHNFYPYIYVNCHETDYAKLQDEKFIELVMSYLEAALKVSFQNRRGRKKGGDDEEDEEEED
DSDPLPASSKVRKYIASVAVCKGVPIYGFQVGYQLFYKISLLSPLYKSRLTKLFQDKKISLYRFGAEEKENVIYQSEPHY
VYEGHIPYLLQFLTDFNLFGCGWLNIDKDFIADGDAKTRGLYFRSPILTDLHKSGYDPKQIDQLSRYLSMFVTADNVLRS
GESKTGHSLPFNRIGKSILEMDITSGSIVNRSWLVPRDLHDDFTERDEYNLYKEAADSGQLKHGYKYDNEGHPRIYLSSL
KQIYNDLKFQCRSRHSPFDVSTDALQTSKVSYFGTGTSTWSNEQLNKDLLDYVVKLNGQLKLDLRLFSSKVLKSRRLLED
KDPFDQFPTSFQLVDIEKNKEYHKFGMRFDKELIKWDNYDGLFTSQPPIQTIDESHVTELVLSDVLSSDIEFSDLDVNNL
LHMDKDQKPEPKDEVSDEHEEEEEEEEEEEEEEEEEEEEEEEEEEEDEHDDTIDDQAELTQLHQFDENIVKEMSQLKPT
AMLNHLGVDQLSFIEDFSFPPTLEQPVMKNLKVTENTYEIPVPEQLKPENCDQAFQDSGILKINYDDPFYDNVTDVPPRP
LIFANQKIIVPLKDQSLVPSLEMSKLIQGEVGNTGAIKSGEFRTWQYLPEPPSKNEVKTWLRTEESNAMRKYLKYRSQIE
PGKSQGNEFKCSYNSEKVSRKPDEFNYLTSFHVEIHANPPNEKLSVDPLRDPVSLIVYSFDDANHMFGHCTFKSGILMFN
RSGGDKKLIERLSVLLGRHFEVFDNEMEMLVKLVTLVELFDPDILSGYEVNSMSWGYLVERSREIFDLNLMANLSRGNFK
SNGKFGDRWGYTHTSNIEISGRHMLNVWRILRSEMSLTSYSLENVTYHLLHHTLPKFPNYQLSQWIKSGKFGDLSTVLSY
YIQKVETILKIINVRELITKNVEHSRLIGIEFNSNFYRGSQFKIESILSRIAKPESLLLNSPSKQDVHEMRPIECIPLIL
EPQSNFYKSPLVVLDFQSLYPSIMIAYNYCYSTLLCKMHNYTPGKNDIGYLRNLKLAPGLVDLLIKEDGVNISPNGFVFV
KSHIRKSILAKMLEEILNIRIKVKEVMKLFKDDAELTRLYNARQLALKLIANVTYGYTSATFSGRMPNSDISDAIVSTGR
EILNKSIELIEAGNYGAKVVYGDTDSLFVYFPGKSKSEAFKLGKAIAKDITDFFPDPVKLKFEKVYHPCMLLAKKRYVGY
SYEYEDQETPKFDAKGIETVRRDGIPAQLKMTEKTLRILFETKNLSKVKKYTVDQFFKIIFNKVSVKDFCFAKEVRYGTY
KSEKHLPPGALIASKMAEEDPRKEPQYRERVPYVVYKDSSKPRIKDRCITPEEFIRSYQTNKPYELDAEYYITRVLIPPL
ERIFNLIGVDVRGWYKQMPKSKHGARHHAACAGVCVVCGRSVDLGGGICLACLEDEQQLWTDVNMTHHETETKIIEIENL
CRDCVHNFVRPGTMISECADYCTNGDCSVYYNKSKLENESKQMFATRDKILLEW
```

580 - 599:	EEEEEEEEEEEEEEEEEEEE
581 - 600:	EEEEEEEEEEEEEEEEEEEE
582 - 601:	EEEEEEEEEEEEEEEEEEEE
583 - 602:	EEEEEEEEEEEEEEEEEEEE
584 - 603:	EEEEEEEEEEEEEEEEEEEE
585 - 604:	EEEEEEEEEEEEEEEEEEEE
586 - 605:	EEEEEEEEEEEEEEEEEEEE
587 - 606:	EEEEEEEEEEEEEEEEEEEE
588 - 607:	EEEEEEEEEEEEEEEEEEEE

A0A369GKD7 **A0A369GKD7_9HYPO** (754 aa)
Uncharacterized protein. *Ophiocordyceps camponoti-leonardi (nom. inval.)*

```
MNGLVPPCARGCFQSFLSFNYGSSSSSSSSPSSSSFSSPSEDDDKLLCAREGSSEYTLGEGAVQCIVAERSVGSCSAEEA
SPMVVYRALRMCDGLPGAIRPSHRSTTTTALSSSPNSSTASQPPLSTGQKAAIAIGILGLLSLLIGTIALFRHYRRRQRK
QANQGKPPSSRQKTSRHHHHHHQSWGYKVEDDNVNNSWLPLNHDPTPTPPPPPPPPPPPPPPPPASAKPYSRSSWRPSAI
GLAIPNNHQTRPVSRLLPERPDEQHHRQQTTTIPAWPQVRLVEASPPPQPQPSRQNNRIEEEEEEEEEEEEEEEEEEEE
EEKEVMMMARNNLHRSDSTLTEFEEDDGGLALALAINNANDDDPRLGGPASVVVVANNNSGSEPPKSPSPPRIWRPPSGL
PQYYVSDPSGNWVLGEAEGEQRPSRRRRCSPPISAPTRNLTPTPTPTPTPASDPDSDPYRRPPSSIDVTTAFNRPSPITS
STTATTTTKIPSYPPIIPNGPRAQGTVRHGNRQPPPPPPPPPPPRQPHLQPANANANVNVNDRSLSWSSSASSPWSHASR
FRSALASMSLFFFRISCHRVRPPSSRTFIRRFFPVGLPIMHGCHARSSSIIARASSGIDARRVLDRRLTSTSRSIASDLH
LGMICTSANRTSTTSSISVSTIRIPATTPVATCWPSVRVTSPPRAVAPAARMKASPWIAAKPAVTRGNDESEQSNVSITS
PLHSAMARHERKPTAPAKTVGTATCIGGPDDTAA
```

300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE

A0A369S412 **A0A369S412_9METZ** (1886 aa)
Bromodomain adjacent to zinc finger domain protein 2B. *Trichoplax sp. H2*

```
MESNQKHSATDPVTGGTVDDAAASGVHPIRNVSSSHVSSTNSDWLPSADDSQNCSDAGVSSFPNTDMHNSAFPSETLNGN
ALSEKYRSSSKTANTLEEVRLPSNVDKINSKEKLVGDEGTGLNQAISSASDSVEVNTLKSQKNIANGKGVRPAAKRTVDQ
SDANSRSKQPPAKKSKSEVVPRQQVRPRIITRLPNMKYKKKKMESSEESSSDNESSDDTGDSDNSEEDDDDNEKEGVEDE
IEEEEDDDDDEDDNEVEEEKEDNDEQTTEDDEEEEDVEVDDDGVEMEDEENDVDSQDREDENEEGDDDENDEDEDDEEEE
SSDSESESEEESSDDDDTSSSSSDDSEEDGSSSSSTTTSTSSSSSDSDGSDETTSSSDSDSSSTSDEEELPPVRSRGRGK
YKARGRRGRGNMNFSRTGRRINGVRKLKGPSKPTPRKRLQSVDEDDIQLPLDQGWRRQTRLRRVGRNLRGDVYYFTPCGK
KLRIYPDVTKYLRKNSISDLNLENFSFSTKLYIGDFQIYNEDSGTFEPMDEDELHRRRQEASTKKNQKLEKLRKRDERKR
LAAEKAKKVQEAKLQRKMEKQRAAADKREEKKERAIKAAMERKAARDQAKMEKLREKMARHEKIKQEKKKKKEALIQARN
KKKEDAEKKRYQEALQRQKERELKKQQAKILKTKEKERRKQQMLLVRSLEIQRKAEERNRVKEEKKLRKRLVKERKQEQK
RLEMAVLRDLKMPAEDMKLSHDHDIPSLKTVPGLLSGNCFADMLLVIQFIQTFAEPLQLDSDDFTSLRDLQESILCRSDP
DEDVYTYLCQQLFYNALKDPGCTGPQSYTALGTPLISVEITNSNVSELLRRYMWSKLSKEHELVKTLEVTPLQALSASDK
LKILVFLVNELLCSKLICKEIESNMEEISNLRRDKWIIEGKARKLRAVHAKRFPAVNSKSTEAKTRGNSQLNSSRDESGS
EGSNMDVEVDVNVGSEKKVQKGKARNGKEGEDVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEVEEVEEVEEEEEEEEEEEDDDEEEDSADDSESGEDENYMDIDQNCEDLSKEDLERAIEKLEKQQKVYKFNLSKIHTTL
KGLLLGQDRYRRRYWVFHNIQGILVEGMLEIEHEDVEVVDTETECEVANINENVEPVTEVEDRKEAATAIDNTKHSTELK
VDPKKETVNSTNSDCDTKRTNKMNLQNLENMLKQREEEEKQKTELENGQNKDVNPEDENAVFHWFDLLPRLPCTRGSIVA
PVKIESKCQVEDEIETKVQEKLAKLQAPRTADPILNDSNVEDEIAVDMSFLTTLTREAFVELLKRIPDHKRRKELQDLLI
LPSAKEIKAAVAAKLGLEEKMITVDDLEKRKAQSIPNCKPKLDESIKRVYFLFLKAIPFIALDFQNKWWHVKDLKEIKTL
IKSLNPRGVRERQLIKSLTKYSENFNDVDGNADAAIGLITIDGEDDMECNYSHGIEAEFPEQRFKAEIALLQEIENMEEK
VSSASLQVKGWKAPSKASKSLRFNNTDVQPLEIARERLQALEAALERRYVKPPLKESSKANNQSNSGSVNGDEPVDDNSE
RSDSGKSDISPGLHNWREAVVSATSAAQLTLCQLQLHSSIAWEKSVMKVFCQICRKGDNESLLLLCDKCDCGTHTYCCTP
KLTSVPEGDWFCPKCASECDKDYCCICEIDDNEKAIACERCNSVYHLACLDPVIKRYPKTGWYCRDCRKRIYKRQPKKGY
VMNESDMEDEDSDTEDSKLSTRNFGVCRIILNELEQHEDGWPFNEPVSDKDCPTYHEVISNPMDLRTMKNKLRDLQYSSH
SDFLVDIGLIFSNCKLFNEDDSEVGIAGQNLSKFFEERWAELCKDV
```

994 - 1013:	EEEEEEEEEEEEEEEEEEEE
995 - 1014:	EEEEEEEEEEEEEEEEEEEE
996 - 1015:	EEEEEEEEEEEEEEEEEEEE
997 - 1016:	EEEEEEEEEEEEEEEEEEEE
998 - 1017:	EEEEEEEEEEEEEEEEEEEE
999 - 1018:	EEEEEEEEEEEEEEEEEEEE
1000 - 1019:	EEEEEEEEEEEEEEEEEEEE
1001 - 1020:	EEEEEEEEEEEEEEEEEEEE
1002 - 1021:	EEEEEEEEEEEEEEEEEEEE
1003 - 1022:	EEEEEEEEEEEEEEEEEEEE
1004 - 1023:	EEEEEEEEEEEEEEEEEEEE
1005 - 1024:	EEEEEEEEEEEEEEEEEEEE
1006 - 1025:	EEEEEEEEEEEEEEEEEEEE
1007 - 1026:	EEEEEEEEEEEEEEEEEEEE
1008 - 1027:	EEEEEEEEEEEEEEEEEEEE
1009 - 1028:	EEEEEEEEEEEEEEEEEEEE
1010 - 1029:	EEEEEEEEEEEEEEEEEEEE
1011 - 1030:	EEEEEEEEEEEEEEEEEEEE
1012 - 1031:	EEEEEEEEEEEEEEEEEEEE
1013 - 1032:	EEEEEEEEEEEEEEEEEEEE
1014 - 1033:	EEEEEEEEEEEEEEEEEEEE
1015 - 1034:	EEEEEEEEEEEEEEEEEEEE
1016 - 1035:	EEEEEEEEEEEEEEEEEEEE
1017 - 1036:	EEEEEEEEEEEEEEEEEEEE
1018 - 1037:	EEEEEEEEEEEEEEEEEEEE

1019 - 1038:	EEEEEEEEEEEEEEEEEEEE
1020 - 1039:	EEEEEEEEEEEEEEEEEEEE
1021 - 1040:	EEEEEEEEEEEEEEEEEEEE
1022 - 1041:	EEEEEEEEEEEEEEEEEEEE
1023 - 1042:	EEEEEEEEEEEEEEEEEEEE

A0A371EXY3 **A0A371EXY3_MUCPR** (665 aa)
Basic helix-loop-helix protein A (Fragment). *Mucuna pruriens (Velvet bean) (Dolichos pruriens)*

```
MAAPLGCRLQSMLQAAVQSVHWTYSLFWQLCPQQVILVWGDGYYNGAIKTRKTVQPMEVSAEEASLQRSQQLRELYESLS
AGETNPPTRRPCAALSPEDLTESEWFYLMCVSFSFPPGVGLPGKAYARRQHVWLTGANEADSKTFSRAILAKTVVCIPLL
DGVVEFGTTDKVQEDLNFIQHVKSFFIDQLNTLPPKPALSEHSTSNPTSSSDHIPAVMYTVADPPAANPSQNDDMDEEEE
EEEEEEEEEEEEEEEEEEEEEEEESGSDEETGGRIGRRGSTPNMAAEASELMQLEMPEEIRVGSPNDGSNNLDSDFHLLAV
SQGGNAAGQAESTRRWGTSQDALQVQLPASALHPLEDLTQEDTHYSQTVSNILQNQSNRWPASPTSVGYIACSTQSAFSR
WSTRANHHFLPAVDGSNQWLLKYILFTVPYLHAKNPGETSPQTAPDPKLRGKGTPQDELSANHVLAERRRREKLNERFII
LRSLVPFVTKMDKASILGDTIEYVKQLRRKIQELEARNHRTEAEQRSKVLEVTVQRTNSGSSKEQQRSGVTTMEKRKVRI
VEGVAAKAKAKAVEVVAAATSVQVSIIESDALLELECPHREGLLLDVMQMLREVRIEIIGVQSSLNNGVFAAELRAKVND
HANGKKVSIVEVKRALNQIIPHAVD
```

237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE
239 - 258:	EEEEEEEEEEEEEEEEEEEE
240 - 259:	EEEEEEEEEEEEEEEEEEEE
241 - 260:	EEEEEEEEEEEEEEEEEEEE
242 - 261:	EEEEEEEEEEEEEEEEEEEE
243 - 262:	EEEEEEEEEEEEEEEEEEEE
244 - 263:	EEEEEEEEEEEEEEEEEEEE

A0A371FSN3 **A0A371FSN3_MUCPR** (855 aa)
PHD and RING finger domain-containing protein 1 (Fragment). *Mucuna pruriens (Velvet bean) (Dolichos pruriens)*

```
MVRGGKFSGKRSFRKRVRSKEGCSDDSDEDYVVSDEGREASDYYCSSLDGCASEESFGSLMEEEEEEFQRVRNFNRSKAK
KGIAGQRKNASNNSHKRGRVAYEEEEEEEEEEEEEEEEEEEEIQEVRIFNRSKAKNGVCSKKKRAGKISPKRGRKIRAEQ
LEEEEEEEEEKQEEKEKVERHGDEAEEEEGDRDGEDEDFDYDDEDEDDEFLPEEEDYSDEEEEMRGRKKKNDGMKIDKVL
QKKRASVVSTRGRKRRSSRPSKKPLRNKRGKNGRLRKKEICDDEDDFIDNGPAIGTTSRRRRGQKRRRVLLSDSDYACSG
SSDFEFTISEEEREQVREAKRLCGSLRNNLRSSSNLINNEEVGVHEDQHQQRKPPGRKGKEKIEEPQGRKGKEKVEGLKS
EVGKQMCGICLSEEDKRRVRGVLNCCTHYFCFACIMEWAKVESRCPLCKQRFKTISKPARSTTGIDLREVVIQVPERDQV
YQPSEEELRSYIDPYEYVICSECHQGGDDGLMLLCDICDSPAHTYCVGLGREVPEGNWYCDGCRPVALGSSSSQVQEGVA
DPRVTIQNLPVRPPPVLHVRESIDLNLISSPRAAFNQGFGHLSSSRFSGRSVEGASPVSGGAPTLSERRWIHRQIQQLLS
SGGAPGRTNGISATSSTSNLYSSQVDQSRGNAILHARTQDVGTSYHTFFDERLCNNTSPLMQNGPLWPGLMGTPPVPDCE
QVHQFGRSNIVPDGGLSPAVREESNFHIAKEQLQSMVKNHLKSLSQNIDLGHSTFKDIARSSMHTILAACDLEHKKSEVC
SVPPPSACPHMELMAGGQTSLIKGCCSSCFDSFVGDVVKRILDTRISSQWLRLGL
```

103 - 122:	EEEEEEEEEEEEEEEEEEEE

A0A371GRV5 **A0A371GRV5_MUCPR** (84 aa)
Uncharacterized protein (Fragment). *Mucuna pruriens (Velvet bean) (Dolichos pruriens)*

```
MVVDKQYKDEILYGVVPMKATHVLLGRPWQFDRKVTHDSVINKLSFVHKGNKNQIDMKEEEEEEEEEEEEEEEEEEEEEP
NYLK
```

59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE

A0A371H7D3 **A0A371H7D3_MUCPR** (579 aa)
Heterogeneous nuclear ribonucleoprotein Q (Fragment). *Mucuna pruriens (Velvet bean) (Dolichos pruriens)*

```
MDRGGVEGPAQGKIPLDTAEQQLFYVAKSFNGNHLVKFPCKLAFLDAKMPGTRQRDVTAQNPESPEGNSEPEKPTDSDEQ
VDFDEDNDQDDTMEEEVEYEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEETKPSDGEDETRVADTKDEVEKKKHAE
LLALPPHGSEVYIGGIPQKVSEEDLRVFCQSVGEVSEVRIMKGKESSEAKGYAFVTFKTKELASKAIEELNNSEFKGKRI
KCSTSQAKHRLFIGNVPKDWTEEDMKKAVAEIGPGVISVELLKDLQSSGRNRGFAFIEFYNHACAEYSRQKMSNSNFKLD
SNAPTVSWADPRNSESSATSQAVIYDLHYADISIEIIVVDRLAWLYCYDYGIKFPVVKAVYVKNLPGNITQDRLKELFEH
HGKITKVALPPAKAGQEKSRFGFVHFAERSSAMKALQNTEKYELDGQTLECSLAKPQADQKSSGAANSQKPVVLPTYPPH
LGYGMVGGAYGTIGAGYGTAGFAQPLMYGPGANPAGMAMMPMLLPDGRLGYVLQQPGFQQPAPTMPVSRHGRSGGGSSSG
WKHSNDNNRNRGHGRYHPY
```

100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE

104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE

A0A371I0Q6 **A0A371I0Q6_MUCPR** (201 aa)
Uncharacterized protein (Fragment). *Mucuna pruriens (Velvet bean) (Dolichos pruriens)*

```
MGEKYIFQDLKPKKEDKLPLEKTGRDGLDWLGELTVGRCLGQSRPAITYGSLSFLGGVTNRLPLVGLGNLGSHWPTSSLS
FLGGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEART
```

85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE

120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE

172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE

A0A372RYR5 **A0A372RYR5_9GLOM** (235 aa)
Uncharacterized protein. *Rhizophagus sp. MUCL 43196*

```
METTKSADAGSKNWLKERAAISAAHRRQKTDPAAARLIEKADQLHKERTQKNLRETVDEDDEAVDEVPETTVKKNEGRDR
PEDEDLEDIDAIVSVPPPEEIVVKIAQKPAEEDTIASNHGKETSEDVYRSFAESVLEQGLTTKSELELSFDLKPEDIKIK
EEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEETQEDLNEADITEGKVQEKLKDADVDINHNEENKGDVKDQGKMN
```

161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE

A0A376B1W1 **A0A376B1W1_9ASCO** (768 aa)
PHD-type domain-containing protein. *Saccharomycodes ludwigii*

```
MNEINDQQMENVDKLKQKTYEVEFRYTPPSKQSRRKNTSDVLTNNEFSPVKQTEPFKNIAALREEGEKQQQKSNHVSLGT
ENVEIFLQPNLMDTSKKSVYTDDFNKEYHTEQKEESVIIQNEGREIEEGKDENEEKKVVEEGEEGEEGKEVVEEEGERQK
ESTNNQTDGNSNISTKHNEEQNGTRTRQTQQQEPVTEEPPKKLHSKIEKNDDGQKENSTEEQEIQENYNNQTKEDIQEEK
IYHDHETKEVHGEQKNDEEEEEEEEEEEEEEEEEEEEEGETRCVCGEFDPPDDSGLYIQCDNCSCWQHGVCVGFTNESEVP
EKYWCEVCKPEFHSLFINARGLTQSHYSSDTPSPDSASFHQRKKNRNNNSSEELSSSSKRLTEKASTKISVSNGSHASNE
YSKKLNVSSEETDTASVEADTKQSINANASIPTNLDAVHESETDAYNKRKLEPFGETKNVSMEDEHENDDTDSQLKMEDD
YSGAKGSRKRKKRKTQTFTGNDSKKATSIKRIKSPRVKNSVRTRATSYARGEIQYQIMLEQAIRESKKEVDENGEETLDE
EDVVDDEREDEEEEEEEHANLQHLNENDCSKAPPRYTKNSNDTSNKNKQPTVDESDTKESDDNDASKFIKPKLRAGKPIG
RRKKGGRSVRSNTPTKKVASSPASSSNNKQKANNIELGTDKPIKPRIPSPRVSLAEMRRRANAILEFISRTQIELVTDRS
QKDDLLKFVESSAFIERVNGIFSNYDSALSDMDSLTSKLLHWEEKYSN
```

258 - 277:	EEEEEEEEEEEEEEEEEEEE

A0A376B365 **A0A376B365_9ASCO** (1062 aa)
Probable ATP-dependent helicase NAM7. *Saccharomycodes ludwigii*

```
MPEDELENICAKSNNDEVVSSNNTESNVIIKSIYNSIDANNNKNDKSNNETIDKEEEKEEEEEEEEEEEKEEKEEEKEED
DDDDDDDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDDDDDDDDEEEEEDDDEELFLSDPHIRTDYCAYCGIDA
PECLIKCNMCNKWFCNSKQKSASSHIVNHLVLTHHNHVSLHENSDLGDTVLECYNCGCKNCFILGFVSAKSEAVVVILCR
LPCAQQKNLNWVTDQWQPLIENKQFLSWIAEPPNEEQILKAKLITPSQIAKLEAKWRSNKDATINDLDLPDDSEEEVLPI
LMRYSDAYQYQRSFAPLVKLEADYDKQLKESQALEHISVTWSTDGARTLASFALSTYESNALKVAVGDEMILRYSGLQHT
DWEGRGYIIRLPNSMKDEFTLELKPSASSSKQTPTSLNTGFTAEFVWKGTSYDRMQDAMKKFAIDKKSISGFLYYNILGH
DIPSIKYEVDLPEQFSIPNFAQLNISQAHAVRHVLQRPLSLIQGPPGTGKTVTSATIVYHLSKLHKERILVCAPSNVAVD
HLASKLRDLGLKVVRLTAKSREDVESTVSELGLHNLVLKSADGSFKKLLDKKRNGEELSAKEAKKFVVNVRKYEAGILKK
ADVVCCTCVGAGDKRIDFKFKTVLIDESTQATEPECLIPIVKGAKQVILVGDHQQLGPVILDRKAGDAGLKQSLFERLIT
LGHVPFRLEVQYRMNPHLSEFPSNMFYDGSLQNGVTMEQRLLPNSNFPWPIHDVPMMFWANYGREEISSNGTSYLNRIEA
MNCERIITRLFKDGIKPEQIGVITPYEGQRAYIVQYMQMNGSMDKDAYLSVEVSSVDAFQGREKDFIILSCVRANDQQTI
GFLSDPRRLNVALTRSKYGLIILGNPASLSRNILWNNLLVHFRSKGCLVEGSLDNLQMCAVQLMKPVQNNNKKNNANNNN
NTNNITNKGNSYINDFTNNYNSSIHNMNNFINNANNNYYNNNINSSSSHFDTQSIVSFNQVQDPSSLFVQDTDLSSFLHK
QFMNNDGPTDYVQEAFSNLNVK
```

88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE

95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE

A0A376B3C5 **A0A376B3C5_9ASCO** (377 aa)
SHNi-TPR domain-containing protein. *Saccharomycodes ludwigii*

```
MSDSTTKTKSTKELNHLLTEASKYYANKDYNKSVENYGKLNELYYDLNGENSPDYLFLYGKSLFQLALDNSDIFGGNPGV
DLDGEENEVDEEGLREESGTVCKKKSKMFQFDTEIEEDEEQGEEKEKEEEEEEEEEEEEEEEEEEEEESKEKHNKQEYED
LQNDFENAWDVLEVSRKLYENRLKKEPLQSSSDIILRLSEVHDILGEISLENENFEQASIDFEQSLNYRKQYFENNKDRK
DPTNRLIIESYYKLSLSYEFQPKRGPDCEKNLGIAIKLLKDRIDQGKSEEGDSSLLQDLETKLKETKESIKLNANMENQQ
IEMMKSLLSGGAVTSHSTVNSSHANVHDLSSIVVKKNKKRPAGNGANDDNSQKKAKK
```

128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE

A0A376B410 **A0A376B410_9ASCO** (429 aa)
HMG box domain-containing protein. *Saccharomycodes ludwigii*

```
MTMSLSLEVKDQPRKKREEKQQQTGNNPNGETNKDLKDKIIKLQESNEVLALTVQRTRLSVRRLRFQYASLLERLQDRID
RDPILSCEEPLPTLQNFKEQLKKAQFPNMQNGANGTTGTTNRISLYSKRKLARAKRDPNMPKRPTNAYLFFCEMNKEKLR
EKYGATSDMSKCLTDAWKSLDEEARKPYYDMYNEDKKRYQKAMSIYMANKENSENVKGGDHKEEKITQTTKTEPMDSNFT
DNTVSLNGKGIEEDGDIEMNDDEEEAEAEEEEEEEEEEEEEEEEEEEEEEAEEEEAEEEEAEEEEAEEEEAEEEEADEKV
EEEGGDDTGTDVETRPENGSSIGDNEKEKKEEEEEEEEGEKEKNNDNINDKGDMEGQREEDNIGVKEKVDIIRQDIKGTT
KGEEEEEHKEEKKQDKTSNEIIEEEEKKG
```

269 - 288:	EEEEEEEEEEEEEEEEEEEE
270 - 289:	EEEEEEEEEEEEEEEEEEEE
271 - 290:	EEEEEEEEEEEEEEEEEEEE

A0A376B4M4 **A0A376B4M4_9ASCO** (612 aa)
U3 small nucleolar ribonucleoprotein protein MPP10. *Saccharomycodes ludwigii*

```
MTHLVEVLNADPTALFNKEYLQNNISINDVKEHLDRTIKLYKTQLSVKVPLDEVTVDGLDANQVWWQSKIILDNIQSSLL
EKINDLKKLLDRQEGISEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKKTNGLSEINSDENTSDSSVPEDQFQD
ARDISSIIEKNKNESNEDEDKEDSKDDEFFNAEDFARKMEDAEAKGEDIFGNNKTHDEEEKEDIDYFGDMPSDEDEEALY
YNDFFDEPTKNKKKNRKIQNQAKKDTLDTLKEKDLDEEEYDNIMNTVKLDLFDDAKAASSDGEGEGDTRDSKYLTTFERQ
QLEIQRQIAQLEKEAVAEKKWALKGEVKAKDRPDDALLAEDLEFDRTSKPVPVITSEVTESLEEMIRRRIKEYNFDDLPK
RLLTDVAKFNPKPLLELSDQKSSKSLAEIYEDDYKGITEETEITEEMQKAHDEINNMFKDLMYKLDSLSSAHFVPKPVEK
SLEVKVQTAAITMEDAQPLTLSSASTLAPQEVYKVGKSQNTNEITLKDGTVMSKEELSREDKRRLRRAVKRKRAKSFATN
SKEPPKKTKKQNVIETLSKAKNVTVINKKGEKTDVHGNVQKSFTKNTNDLKL
```

98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE

A0A376B8N0 **A0A376B8N0_9ASCO** (1008 aa)
5'-3' exoribonuclease (EC 3.1.13.-). *Saccharomycodes ludwigii*

```
MGVPSFFRWLSRKYPKIISPVIEQDSTTVDDGNVYSSENPNGELDNLYLDMNGIVHPCSHPENKPPPENEDEMLVAVFEY
TNRVLNMARPRRILMIAVDGVAPRAKMNQQRARRFRSAKDAALEREKLEMDYIKEGKNLDDALLKKKSWDSNAITPGTPF
MDKLAQGLRYWISFKLSTDPGWENLQVIISDATVPGEGEHKIMNFIRSQRQDPEYNPNTTHCIYGLDADLIFLGLATHEP
HFKILREDVFEQTINRKHGSNNSRYDKRRELTEEEKKELQEKDKKKPFLWLHISVLREYLKEELFVPGLSIEFDLERSID
DWVFMCFFCGNDFLPHLPSLDVRESSIDLLVEIWKTVLPQTKGYMSLDGRLNLSGVELLLKGLGTREPGIFVEKRQQELR
KLENEQRRKLLNLRRQEQNNLSSFADNGAVNHVRSETPISSAGSIHLTEEKEEEKKKEEEEEEGKEGEEEEEEEEGKEEE
EEEEEEEEEEEEEEEEEEEDSYDPTPSSNINDINKTNLTVASKFKEKLLLKRKRLVIEKESINTTTAGNSHKIIKLDKSQ
EVSLNTSSSGPTSGTYDSNLAVKLYEPGYHDRYYITKFGCPNNKEEIAALSKKVVKAYVEGISWVLLYYYQGCASWNWYY
PYHYAPFASDFMNIAGLDIKFEKGEPFAPFEQLMSVLPASSGHTLPKIFRPLMSELTSPIIDFYPTEFPIDMNGKKMSWQ
GIALLPFIEEKRLLETVRKKYAELSKEDLARNSRKNDILLISHKNINYKKFVKTLYQTESSDNVRLKVTAYKNRISGEVS
VVANDGDDVGRFDLKGELTCPVSGGYPNLNNSKYLKLTYKMLNIYDDKNKAVILNGYIPHKQVLNIQDKNNIRYGQGHSQ
GNNNKRNNGYYNFQRNFHFTMQNNFVETGPFGSTQYKPRFGGYKSFVSSELEKKSNQANFQNYYYNDNYDNYGNNNDTYY
GRNYNNNYNSHGARNYGYNNYGSNNYNNGYNNSKGGNRGIRPNRQGTL
```

478 - 497:	EEEEEEEEEEEEEEEEEEEE
479 - 498:	EEEEEEEEEEEEEEEEEEEE
480 - 499:	EEEEEEEEEEEEEEEEEEEE

A0A376B9N9 **A0A376B9N9_9ASCO** (1472 aa)
Uncharacterized protein. *Saccharomycodes ludwigii*

```
MTNSTSSKKSSSNTGTLNPEDRRKIYNFYVALNQYYQITSDSKVDRSGNQRAKKARAKLLKLSSPQFFELGTDVHDELER
RLNESQQQPAYLLPNEKFHIKRNQARQKLANLSASRFNDLVDDILYEIRRRNYDVDPIFETSAANNSVPMGDAQQQRNNI
KEASSLDKSIMNNDNGIKKNSNNNSKGPSTTATGIQATKVIPKKASLDWSSDEEEKEEGAESHFSNYNHSAQKKANTTNV
NNNGEQEINNNTNTNVEIAAASTDVEFKQQEQQQQNIPRGFVKQGLRIRELNPSSNVRNTGITDNISANSMTDESSSSKP
KNNKDISKLEAELNETNQKFNELENLNFILSSKANKFEKEAYDLRQTNETLSIEVASLKEEKMTSDKIITNLKSELTMTE
TQLKEVNNKYLENEAAVHNLGKSMDSNFQKEVSALSREISALSIENENLKLAISELELKLKQANNKSPTNGNANTNEAPN
VTMIEQEAKLWKSRYESVIKSNNDNINTPVKLPSTFDSVKSTDILRYISPDGLIPLVLVQSLQNKVIKSFQHLQNTTDTN
NCNNNKNNIGDVLFEDIAQISDDVSSIISYCEKFEDFTGHAILLRASVSHAITTIRYYAIYHSLLPRITVESALCEILFT
ICNLLNVAHINEAIECVTKSLPQATKSTTTRSVANSKVDTDVKEASISKDLNNGSTEYAKPIVNFNKNQNSFGNLSHNNN
TNIDGHADDDNDFGVSSPVRPLKLAQKLASSENLTSPTASTAPRKPANTGLFNYLQKESNNHISSKKKFFFNNNTSLLSK
NNRIGNIKSNNVAENGKNINLLKLNLNENSDNTSANDVNNNEKIDNTESSAVATDNNIDDLKNKETNVTPNTKKHEKSNS
LASTISKQSGSDISRSPGTIKSKVLQFENKTVNSNSISSNSSSTEASPLNSTLFLKNNESVTSTDNILQNSKNGGSLSKK
NSFASIEERVKSFQDPNVSLTKKSSLLSLNKSSISNNSIEEEEEEEEEEEEEEEEEEEEEEGGEKKKEEGEGEVEERQAR
EKEIPSHNGKNLDAETKCTPTVSSEASTIKLTEEKLANTNEINHKTDASFFNNTFDINKPPPSLATSKLASALEDIPSSS
VPTSTDDDDYNDDEEEEEEEEQKKQIAQETLRNEQAYQKIQASLLNGHGTNNNGDGIKSLSESKLSNNTVSDSKSDLGLD
KYPLISSDTSNIGDNISVRDSLNSRDSIVAFDSKPVNLMSSIDPTSPIKKVLPTMHSNKTNTSPLNNLVSRQSNEIPQTD
EPVSKPATNTEVAGTMDHSRLSILEETFDVGGFDIENPDNTLSELLLYLEHQTVDVINTIQSLLSSIKRPKAKTGELRGE
SFDINHVIGQMVEATSVSMQQSRNFALKEHGTWVVQSLDDCKRRMTLLCTLGSEFELLETDDDFADKHFKQRLAGIAFDV
AKCTKELVKIVEEASLKEEIEYLNNRLNPNNV
```

1000 - 1019:	EEEEEEEEEEEEEEEEEEEE
1001 - 1020:	EEEEEEEEEEEEEEEEEEEE
1002 - 1021:	EEEEEEEEEEEEEEEEEEEE

A0A376B9R9 **A0A376B9R9_9ASCO** (339 aa)
Alkyl transferase (EC 2.5.1.-). *Saccharomycodes ludwigii*

```
MITTSEEYYASAKGPLSMLGKCRFWVDSILKKNFGKMIRVSGHSPQHVAFIMDGNRRYAKKKNMQIKQGHENGFLSLCQI
LELCYESGVKTVTVFAFSIENFKRTKYEVNALMELFKKRIDQVIANGDICSQYGIKFRTLGDRSLIPSDVMVKILEAEKL
TENNTRACLNLCFPYTGRQEIYHSIKETIRDSLNNKITINEQTIDGNLYTKDDPPLDLLIRTSGVSRLSDFLLWQVDKKG
VTIELLDCLWPEFTPWNMACILLKFAYKKTILSEEEEEEEEEEEEEEEEEEEEEEEEEEEGDEKEEEKQEEEEEEEKEK
EEEKEKDANAVSNERLDKN
```

274 - 293:	EEEEEEEEEEEEEEEEEEEE
275 - 294:	EEEEEEEEEEEEEEEEEEEE
276 - 295:	EEEEEEEEEEEEEEEEEEEE
277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE

A0A376BAU4 **A0A376BAU4_9ASCO** (838 aa)
Uncharacterized protein. *Saccharomycodes ludwigii*

```
MLNHHLPVFGAPSFGSIATNSNAESPFGKPAFGTSTATDENKESPFGKPVFGAPSFGSIATNNNAESPFAKPPFGTSTTI
DENKESPSAKPAFGNNLFPSYSTSLGDKPLFGTVTTEVKDSPFASLSLNGNSGSTFSKDSLFEDITKENNTVKEHKEEEE
EEEEEEEEEEEEEEEEEEEEGEKEEGREKEKEKEKKKEKEEHDGEEDKDTESFEIISEPEREEQGEKSVSDAIITNVKAP
DDENFFQGKENKQETESEPFKKDVSQNIQKIEPNADSVEHLNPPFKTEISNNEQSEEIIGKTENGFMKVESDKKDIESNA
HFHLNDDISTLSERIIKKASTNKTPLPSLLQEKTLGTVKESSPFDSFSNILKPPAEETKKVSDTSDLKPSFSFTDVIDKA
HSKKDEFGNEHSINKPNDEALTIKDQVEDTLARELNKSTTEEKEKEDESVAGSTGNPKNVDTNTFQEAPSILNKNDQSST
```

```
SNIERDTKTETKLEKADASSQTSNENTTEIHVQTDSISVREQEVNATPVLKTAEQQTVQPEIVDNSIFSFENDKRYLASQ
YPVLKMKPYYYNNASNLTSKYQNPILKTIDELYQLVESELTVLNENLRNFDAVIIDQLNVPFDKDITCLSMDYSWRLSEV
SVLNKIIFQAARTGDVKIVNNLANKIDDLEGAQSHFSLEIKQLNKSYDILQLESKVSKTDEETLTASQLQVKLKLEKKIK
ELSIQFNKISQLLQVLKLFSIDLEGGGACLSPHSKTHIQQLFEGKVDRDTLLNEVRNLRQEVSALTIGSTNTNDKYKRKE
NSRREVALIANESASIVRVASKINFKSKLGAAFRNKKL
```

157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE

A0A376BBI0 **A0A376BBI0_9ASCO** (1096 aa)
Related to DNA polymerase V. *Saccharomycodes ludwigii*

```
MDNTTNKVNRDLFFKLASDLEKERVESAISIIKQLNLLKEDSASLFTSEYSYVLDRLTKGLASNRSGARLGYSLCLTEVI
NLGLETRELSSIDEYIDNILFKTLSGNSTNKEERQNLFGLLFGLQCLLNEPLFSKIFFIPSNGDSKAINMQFSIAFVNHL
IHISLRKTWISEPCLFTVYNFITKLTPLIVDISHIEEILSALDENSLTLTKEGLAVYLWFIYECPTTSILIKNNDGLKHI
TFKNKNNTNNLKWKNNDPLSHGNLKTLALVMKEALNNTTVDGNSSTSKPKGFWSPRLHFVWGHLLKVLSSNASNDDGKRA
HKKRKIAKGSSKKQKSNSASNSMGIIQISDFWKPVVDEIFFAEKASNERKYIGLLIFKKSLEILPADSIPVLFSNNLIRT
IINQSSDKERMLYKLCHSVFDDIIKILRLNGNCSKIIPILENLWFTRGLVNFDQLTKSNFTSSLLNNKQLDNDNLCCLTQ
MILKNIMNNSANEESDADEGKMVNFGLDCLLHIVRSHRSKALSIDGGGIEWVKLILEKLVDVAFFKADNENEKSTKNIRD
QEHEISTDAESSINYKALQKLYSVLGDLISTNNVSSGYDTKNQDNLQWPYFVLQLTVTKEEDGNKPLVYKPDESLINIKL
NSLSVLTEIKELLNADISTETNVQRGVFQGLELLLTINLLQLYSGDTESLSILDDLTTFFAEYTHDTQEDISFVGITEIL
LSLLAQQKSFLKKISIIVWRLFMPVIKQKEIDVLLNSLSTRENKKGFTLLFESDYELQEEEEEEEEEEEEEEEEEEEEE
EEEEEEDIENQNHEEIGKIDKEATSALAKALNLPENILNSNGEIRFDDLDDSDDDISDDDDEDEDLDDEKMMELDEHLSS
IFKHRKEALERINTGNQRKVEVQNARETVTSFKQKNVDLLEEYIKCVEHSAINDIGISSQHLMLLLSMCKPFIQCIRNTL
SRQLAEKVTKLIKTRICKVKIGNAAKKDSKNLIKYSTALLDDIHELVLKPKIGQFPNLYLSVASTTSLFLCKIIHTLKTN
GDNDNEVGLFDDIIDRYSNTMKKWSSDPSVKITQNFFTEYVNWIAAKKKQQTSQEK
```

779 - 798:	EEEEEEEEEEEEEEEEEEEE
780 - 799:	EEEEEEEEEEEEEEEEEEEE
781 - 800:	EEEEEEEEEEEEEEEEEEEE
782 - 801:	EEEEEEEEEEEEEEEEEEEE
783 - 802:	EEEEEEEEEEEEEEEEEEEE
784 - 803:	EEEEEEEEEEEEEEEEEEEE
785 - 804:	EEEEEEEEEEEEEEEEEEEE
786 - 805:	EEEEEEEEEEEEEEEEEEEE
787 - 806:	EEEEEEEEEEEEEEEEEEEE

A0A379QNJ4 **A0A379QNJ4_SALER** (1035 aa)
Putative hydroxymethyltransferase. *Salmonella enterica (Salmonella choleraesuis)*

```
MTISIHASKFDVNSWYQKITLTLINESGNPVDMNHAAIAFSASGHMDPWGNFGGTLKGNLPLTLNDVSQGTLEANEIIIN
NSDELLLQPGESGTLFFSLAATQVPVKMSAITLTLASSEEKIPEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEPATDELPVVPDAPENETKDNDLPQGSGLTLSVSELNTASWYQRVTFTLTNLYAQAVDLNQLQLNFTASAHP
DPYSPFKGTMLGNQAVTLASDGGWPIEKNTITINHDGALMLAAGDIAELQCYLAATQTPVVISDLSAMLAHDPARQGKIC
VHFPAMAQTVALKPAIELLFPAGEARRFVGEWGEVLTIGDLSAGTYQLTVPVLANDEMQIAPVESSFTVTLQSGDDAAQI
QVSCLPIVHYASARLMIDAPALGNAKLTVKIADATQADERTVMLIANQPQLITRLLAGRHYTVNLQPAMVNNCFISAPVQ
LTGFIPAVAQVAEVSVAYQQSAIDTASFVTVDATILGLPDGVAPQRYLFSSGKYQYSLMLESGSDRQTLALRFAPGLYDV
QTDDIFIDSVPWRCEQAGPLRLLQKINHVALEFLPGVTLQVKGWPDYLAHGGVTVNAPETVSLYRDIPFSALFKYDGFDG
GGDPVPASEVDVNGDGFLDYATLPIHKTVALVRQIEKEAGRSVMPVMVIYTANASGGSALADLQDAQKLRNHFGNFITQC
LAAQSYKDETHPVPATFVLNPDFLGALQQGPYGYTVVRQKNSVPVNAQLAAAIQALPAMAGFIAPSLPTFSDDLYGYIQA
VNYLVRQFAPDVAFGWQTNVWATGTADWVLRDTADPVAEGQAIAGFIHELGVYSGEYAPDFIAFDKFERDCFSPDALAHY
GWNATCWLNYLAMVKQVTKALLTPAMLWQIPGGHMPTVEEGVSKITAAHFASGGTFFMGDARIGSDPDTLSLQLLNTALN
SATYGVPTVGDFLRKDKGYDWSQMQALNLPDFNVFSILWGGGSTISITTIHSNGEDGGWLADKMVEYYASPRYFR
```

124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE

136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE

A0A383YUS0 **A0A383YUS0_BALAS** (1875 aa)
Histone acetyltransferase (EC 2.3.1.48). *Balaenoptera acutorostrata scammoni (North Pacific minke whale) (Balaenoptera davidsoni)*

```
MVKLANPLYTEWILEAIQKIKKQKQRPSEERICHAVSTSHGLDKKTVSEQLELSVQDGSVLKVTNKGLASYKDPDNPGRF
SSVKPGTFPKSAKGSRGSCNDLRNVDWNKLLRRAIEGLEEPNGSSLKNIEKYLRSQSDLTSTTTNPAFQQRLRLGAKRAV
NNGRLLKDGPQYRVNYGGLDGKGAPKYPSAFPSSLPPVSLLPHEKDQPRADPIPICSFCLGTKESNREKKPEELLSCADC
GSSGHPSCLKFCPELTTNVKALRWQCIECKTCSACRIQGKNADNMLFCDSCDRGFHMECCDPPLSRMPKGMWICQVCRPK
KKGRKLLHEKAAQIKRRYAKPIGRPKNKLKQRLLSVTSDEGSMNAFTGRGSPGRGQKTKVCTTPSSGHAASGKDSSSRLA
VTDPTRPGATTKITTTSTYISASTLKVNKKTKGLIDGLTKFFTPSPDGRRSRGEIIDFSKHYRPRKKVSQKQSCTSHVLA
PDTEIKISIKQESTDINVIGNKDTVTEEDLDVFKQAQELSWEKIECESGVEDCGRYPSVIEFGKYEIQTWYSSPYPQEYA
RLPKLYLCEFCLKYMKSKNILLRHSRKCGWFHPPANEIYRRKDLSVFEVDGNMSKIYCQNLCLLAKLFLDHKTLYYDVEP
FLFYVLTKNDEKGCHLVGYFSKEKLCQQKYNVSCIMIMPQHQRQGFGRFLIDFSYLLSRREGQAGSPEKPLSDLGRLSYL
AYWKSVILEYLYHHHERHISIKAISRATGMCPHDIATTLQHLHMIDKRDGRFVIIRREKLILGHMEKLKTCSRTNELDPE
SLRWTPILISNAAVSEEEREAEKEAERLMEQASCWEKEEQEILSSRANSRQSPAKVQSKNKYLHSPESRPVAGERGQLME
LSKESSEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEENIQSSPPRLTKPQSVAIKRKRPFVLKKKRGRKRRRINSSVTTETIS
ETTEVLNEPFDNSDEERPMPQLEPTCEIEVEEDGGKPVLRKAFQHQPGKKRQTEEEEGKDNHCFKNADPCRNNMDDDANN
LKEASRDNPEPLKCKQWPKGTKRGLSKWRPNKERKTGFKLNLYTPPETPMEPDDQVTVEEQKETPADKTSPAPTRTEEEV
KEAVEPLLPGDENRREEACAPVSPNKSPGEKPEDDLIKPEEEEEEEEEEEEEEEEEEGNVEKDPCGAKSQEREEPEVCTD
KEDPVRLDDHEEEEEEDEEPSHNEGHDADDEDDSHMESAESEKEERPREAFKEVLENQEAFLDLSVQPNHSNPEVLMDCG
VDLTASCNSEPKELAGATETAPESDEEPTGEQAQEQDQKNSEEVDSEFKEGNTATLEIDSETVQAVQSLTQENSEQDDTF
QDCAETQEACRSLQNYTHADQSPQIAAALDDCQQSDHSSPVSSVHSHPSQSVRSVNSPSVPALENSYAQISPDQNAISVP
SLQNMETSPMMDVPSVSDHSQQVVDSGFSDLGSIESTTENYENPSSYDSTMGGGSICGNGSSQNSCSYSNLTSSSLTQSS
CAVTQQMSNISGSCSMLQQTSISSPPTCSVKSPQGCVVDRPPSSSQQLAQCSMAANFTPPMQLAEIPETGSASLGLYERM
GQSDFGAGHYPQPSATFSLAKLQQLTNTLIDHSLPYSHSAAVTSYANSASLSTPLSNTGLVQLSQSPHSVPGGPQAQATM
TPPPNLTPPPMNLPPPLLQRNMAASNIGISHSQRLQTQIASKGHVSMRTKSASLSPAAATHQSQIYGRSQTVAMQGPART
LTMQRGMNMSVNLMPSPAYNVNSVNMNMNTLNAMNGYSMSQPMMNSGYHSNHGYMNQTPQYPMQMQMGMMGTQPYAQQPM
QTPPHGNMMYTAPGHHGYMNPGMSKQSLNGSYMRR
```

887 - 906:	EEEEEEEEEEEEEEEEEEEE
888 - 907:	EEEEEEEEEEEEEEEEEEEE
889 - 908:	EEEEEEEEEEEEEEEEEEEE
890 - 909:	EEEEEEEEEEEEEEEEEEEE
891 - 910:	EEEEEEEEEEEEEEEEEEEE
892 - 911:	EEEEEEEEEEEEEEEEEEEE
893 - 912:	EEEEEEEEEEEEEEEEEEEE
894 - 913:	EEEEEEEEEEEEEEEEEEEE
895 - 914:	EEEEEEEEEEEEEEEEEEEE

A0A384A1K8 **A0A384A1K8_BALAS** (661 aa)
Potassium voltage-gated channel subfamily A member 4 (Voltage-gated potassium channel subunit Kv1.4). *Balaenoptera acutorostrata scammoni (North Pacific minke whale) (Balaenoptera davidsoni)*

```
MEVAMVSAESSGCNSHMPYGYAAQARARERERLAHSRAAAAAAVAAATAAVEGGGGSGGGAHHHHHQLRGACTSQDPQSG
RGSRRRRRQRPEKKKVHHRQSSFPHCSDLMPSGSEEKILRDLSEEEEEEEEEEEEEEEEEEEEEGRFYYSEDDHGDECS
YTDLLPQDDAGGGGYSSVRYSDCCERVVINVSGLRFETQMKTLAQFPETLLGDPEKRTQYFDPLRNEYFFDRNRPSFDAI
LYYYQSGGRLKRPVNVPFDIFTEEVKFYQLGEEALLKFREDEGFVRDEEDRALPESEFKKQIWLLFEYPESSSPARGIAI
VSVLVILISIVIFCLETLPEFRDDRDLIMALSTGGHSGLLNDTSAPHPENSGHTIFNDPFFIVETVCIVWFSFEFVVRCF
ACPSQALFFKNIMNIIDIVSILPYFITLGTDLAQQQGGGNGQQQQAMSFAILRIIRLVRVFRIFKLSRHSKGLQILGHTL
RASMRELGLLIFFLFIGVILFSSAVYFAEADEPTTHFQSIPDAFWWAVVTMTTVGYGDMKPITVGGKIVGSLCAIAGVLT
IALPVPVIVSNFNYFYHRETENEEQTQLTQNAVSCPYLPSNLLKKFRSSTSSSLGDKSEYLEMEEGVKESLCAKEKCQGK
GDDSETDKNNCSNAKAVETDV
```

124 - 143:	EEEEEEEEEEEEEEEEEEEE

125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE

A0A384B1M2 **A0A384B1M2_BALAS** (736 aa)
YTH domain-containing protein 1 isoform X2. *Balaenoptera acutorostrata scammoni (North Pacific minke whale) (Balaenoptera davidsoni)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLICKPLSSSVSN
NKRMVSTKGKSVTEYKNEEYQRSERNKRKLIGKFVRKIRLSSSASREPYKSQPEKTCLRKRDPERRVKSPTPDGSERIGL
EVDRRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEDDAEEDEEVDDDGEEEEEEEEE
EEEEEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDASDEKKKERKRARGISPIVFDR
SGSSASESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSA
RSVILIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAXXXXXXAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPV
KIGRDGQEIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRI
DYAPEFHQRPGYLKDPRYQEVDRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMTPYPGMEQPPHHPYYQHHAPPPQ
AHPPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERER
LCDRDRDRGERGRYRR
```

232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE

A0A384B1S0 **A0A384B1S0_BALAS** (744 aa)
YTH domain-containing protein 1 isoform X1. *Balaenoptera acutorostrata scammoni (North Pacific minke whale) (Balaenoptera davidsoni)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLICKPLSSSVSN
NKRMVSTKGKSVTEYKNEEYQRSERNKRKLIGKFVRKIRLSSSASREPYKSQPEKTCLRKRDPERRVKSPTPDGSERIGL
EVDRRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEDDAEEDEEVDDDGEEEEEEEEE
EEEEEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDASDEKKKERKRARGISPIVFDR
SGSSASESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSA
RSVILIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAXXXXXXAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPV
KIGRDGQEIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRI
DYAPEFHQRPGYLKDPRYQEVDSFTNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMTPYPGMEQPPHHPYY
QHHAPPPQAHPPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGR
DRERERERLCDRDRDRGERGRYRR
```

232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE

A0A384B1V9 **A0A384B1V9_BALAS** (718 aa)
YTH domain-containing protein 1 isoform X3. *Balaenoptera acutorostrata scammoni (North Pacific minke whale) (Balaenoptera davidsoni)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLICKPLSSSVSN
NKRMVSTKGKSVTEYKNEEYQRSERNKRKLIGKFVRKIRLSSSASREPYKSQPEKTCLRKRDPERRVKSPTPDGSERIGL
EVDRRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEDDAEEDEEVDDDGEEEEEEEEE
EEEEEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDASDEKKKERKRARGISPIVFDR
SGSSASESYADQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSARSVILIFSVRESGKFQGF
ARLSSESHHGGSPIHWVLPAXXXXXXAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLC
LLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYAPEFHQRPGYLKDPRY
QEVDRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMTPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHHPVPHEARYR
DKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDRGERGRYRR
```

232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE

A0A384B369 **A0A384B369_BALAS** (1268 aa)
histone-lysine N-methyltransferase EHMT2 isoform X1. *Balaenoptera acutorostrata scammoni (North Pacific minke whale) (Balaenoptera davidsoni)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGLHRGRGRPRSLLSLPRAQASWAPQLPSGLTSSPIPCVPSQGEAPAEMGA
LVLEKEPRGATERVHGSLGDTPRSEEILPKANPDSLETAGPSSPASVTVTVGDEGADTPVGATPLIGDEPENLEGDGDLH
GGRILMGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGATAAGPEPPPATASPEGQPKVHRA
```

```
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEELGSARGSREVTLEKGDPGSLEEWE
TVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKA
KKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEE
LPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCT
AGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLAQDAPGRADTSQPS
ARMRGQGEPRRPPCDPLADTIDSSGPSLTLPSGGRLSAVGLPPGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGE
LQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGG
CVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICL
HWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQ
LNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSS
SNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGT
FICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSR
DIRAGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNP
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE

A0A384B377 **A0A384B377_BALAS** (1279 aa)
tau-tubulin kinase 1. *Balaenoptera acutorostrata scammoni (North Pacific minke whale) (Balaenoptera davidsoni)*

```
MQCLAAALKDETNMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTRENVALKVESAQQPKQVLKMEVAV
LKKLQGKDHVCRFIGCGRNEKFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESIEAIHSVGFLHRDIKPSNF
AMGRLPSTYRKCYMLDFGLARQYTNTTGDVRPPRNVAGFRGTVRYASVNAHKNREMGRHDDLWSLFYMLVEFAVGQLPWR
KIKDKEQVGMIKEKYEHRMLLKHMPSEFHLFLDHIASLDYFTKPDYQLIMSVFENSMKERGIAENEAFDWEKAGNDALLS
TSTSTPPQQNTRQTAAMFGVVNVTPVPGDLLRENTEDVLQGEHLSDQENAPPILPGRPAEGPGSSPHLVPHPGGPEAEVW
EETDVNRNKLRINIGKTPCVVEEEQNRVAGVPSSPVRAPPDSPTTPVRSLHYRRVNSPESERLSTVDGRVELHERRSRMD
LPGSPSRQACSSQPAQMLSVDTGHADRQASGRMDVSASVEQEALSNAFRSVPLAEEEDFDSKEWVIIDKETELKDFPPGA
EPSTSGTTDEEPEELRPLPEEGEERRRPGPEPAVRPRARGMHTLAEEDLRLTPAQPLPPQLNQADGRSETSQPPTPGSPS
HSPLHSGPRPRRRESDPTGPQRQVFSVAPPFEVNGLPRAVPLSLPYQDYKKDLSDYRERARLLNRARRVDFSYMLLATPQ
VPLAPVQPQTNGKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAVALGEVLGPHSGSSSEGSERSTDRSQ
EGAPSTLLADDQKESRGRASMADGDLEPEEGSKTLVLVSPGDMKKSPVTADLAPDPDLGTLAALTPQHERPQPTGSQLDV
SEPGTLSSVLKSEAKPPGTGTGLGAGAVTIGAGGVAVTSSPFTKVERTFVHIAEKTHLNVMSSGGQASRSEELSAGGELG
LEVPSDGRAEEEGASVYLENGIAISGLVSCVLSAPPGSSPLEVTTDSLPNGPALADGPAPASLLEPGPEKLATISPSRHA
MPGPRPRSRIPVLLSEEDTGSEPSGSLSAKERWSKRARPQQDLARLVMEKRQGRLLLRLASGASSSSSEEQRRASETLSG
TGSGEDRPASEPAVPRKAGRAAATRSRIPRPISTRMPTPAAAQQPPDRPQGAAPASDTAITSRLQLQKPPGTAIAADLRP
KQPPGRGPGPGQTQAGTRPPAPRSPGLPSSSAHHPSASPRSRSLSRKESPSPSHQPKLHAPTLSERQPQIPEVEAPASH
```

734 - 753:	EEEEEEEEEEEEEEEEEEEE
735 - 754:	EEEEEEEEEEEEEEEEEEEE
736 - 755:	EEEEEEEEEEEEEEEEEEEE
737 - 756:	EEEEEEEEEEEEEEEEEEEE
738 - 757:	EEEEEEEEEEEEEEEEEEEE
739 - 758:	EEEEEEEEEEEEEEEEEEEE
740 - 759:	EEEEEEEEEEEEEEEEEEEE
741 - 760:	EEEEEEEEEEEEEEEEEEEE
742 - 761:	EEEEEEEEEEEEEEEEEEEE
743 - 762:	EEEEEEEEEEEEEEEEEEEE
744 - 763:	EEEEEEEEEEEEEEEEEEEE
745 - 764:	EEEEEEEEEEEEEEEEEEEE
746 - 765:	EEEEEEEEEEEEEEEEEEEE
747 - 766:	EEEEEEEEEEEEEEEEEEEE
748 - 767:	EEEEEEEEEEEEEEEEEEEE
749 - 768:	EEEEEEEEEEEEEEEEEEEE
750 - 769:	EEEEEEEEEEEEEEEEEEEE
751 - 770:	EEEEEEEEEEEEEEEEEEEE
752 - 771:	EEEEEEEEEEEEEEEEEEEE
753 - 772:	EEEEEEEEEEEEEEEEEEEE
754 - 773:	EEEEEEEEEEEEEEEEEEEE

A0A384B3W1 **A0A384B3W1_BALAS** (1234 aa)
histone-lysine N-methyltransferase EHMT2 isoform X2. *Balaenoptera acutorostrata scammoni (North Pacific minke whale) (Balaenoptera davidsoni)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGLHRGRGRPRSLLSLPRAQASWAPQLPSGLTSSPIPCVPSQGEAPAEMGA
LVLEKEPRGATERVHGSLGDTPRSEEILPKANPDSLETAGPSSPASVTVTVGDEGADTPVGATPLIGDEPENLEGDGDLH
```

```
GGRILMGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGATAAGPEPPPATASPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEELGSARGSREVTLEKGDPGSLEEWE
TVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKA
KKKWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGEL
SGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHC
GEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLAQDAPGRADTSQPSARMRGQGEPRRPPCDPLADTIDSSGPSLTLPSGG
RLSAVGLPPGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKG
SVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQV
DVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLH
IAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIP
CVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFE
CNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEV
YCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRAGEELGFDYGDRFWDIKSKYFTCQCGSEKCK
HSAEAIALEQSRLARLDPHPELLPELGSLPPVNP
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE

A0A384BUN9 **A0A384BUN9_URSMA** (746 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Ursus maritimus (Polar bear) (Thalarctos maritimus)*

```
LCLRFRHQNLSAVGALVGLSNARLGSIKTRFEGLCLLSLLVGESPTEMFQQHCVSWLRSIQQVLQSQDPPPTMDSMNHLP
GLLTSLLGLRPECELSALEGMKACMTYFPRACGSLKGKLASFFLSRVDALSPQLQQLACECYSRLPSLGAGFSQGLKHTE
SWEQELHSLLASLHPLLGALYEGAETAPVQYEGPGVEVLLTPSEDGDAHVLLRLRQRFCGLARCLGLMLSSEFGAPVSVP
VQEILDVICRTLSISAKNISLLGDGPLRLLLLPSIHLDALDLLSALILACGGRLLRFGALISRLLPQVLNAWNFGRDTLS
PGQERPYRLRSPRGSPDGGLQAGKPSAPKKLKLDMGEAMAPPSHRKGDSNANSDVCAAALRGLSRTVLPLIKEETHRRLH
DLVLPLVMGVQQGEVLGSSPYTSSRCRRELYRLLLALLLAPSPRCPPPLACALQAFSHGQREDSLEVSSFCSEALVTCAA
LTHPRVPPLQCRGPLTVININSSDEEEEEEEEEEEEEEEEEEEEEDFEEEEEDEEEYFEEEEEEEEEFEEEFEEEEGELE
EEEDEDEEEEELEELEEVEFGPAGGPVEEGGPPPASPAPALPPAQSPKVQPEPEGEPGLLLEVEEPGAEEEAGAEAAPTL
APEVLPSQGEGPRDTGSPPAGPPPQELMEEEPLAPPTLLEEGTESGGDKVPPPAETAVAEDVETELETATAALQEKEQDD
TAAMLADFIDCPPDDEKPPPAPEPES
```

505 - 524:	EEEEEEEEEEEEEEEEEEEE
506 - 525:	EEEEEEEEEEEEEEEEEEEE

A0A384BUW6 **A0A384BUW6_URSMA** (1167 aa)
LOW QUALITY PROTEIN: myelin transcription factor 1. *Ursus maritimus (Polar bear) (Thalarctos maritimus)*

```
MSLCRAFLENEFRGELLSQRWTQGDKASNCRTSRLLLGRRGKMSLENEDKRARTRSKALRVPPEPTGADLSCPTPGCTGS
GHIRGKYSRHRSLQSCPLAKKRKLEGAQAEHLASTRKSHPLKLALDEGYSVDTDGSEDAEVKDASVSDESEGTLEEDEAE
MSGQEGIHRPEPAEGRSPVKSHFGSKPIGSSAXAKGNYSSYQEIIATSLLNLGQIAVETLVGEDLGQVAKPGPGVVHLVQ
EEAEEGATSDEGEKDVFLRPDGTEEVVGGTKEHSQELCPQSVEGVASEESSKMKVALGNEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEGEEEEEEEEEEEEEEEEEVAAPDVLCQEDAPLAPTQKAPELRHPASPSPKPEYSVIVEVRSDDGKDED
SRSQKSAVTDESEMYDMMTRGNLGLLEQAIALKAGQVQAVCEPGCPPTEQGPCEPGKAVRPLDAARKNYCSKDPSRAEKR
EIKCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRIPPEILAMHENVLKCPTPGCTGQGHVNSNRNTHRSLSGCPIAAAEKL
AKSHEKQQPQTGDPSKNSSNSDRILRPMCFVKQLEVPPYGSYRPSVAPATPRANLAKELEKFSKVTFDYASFDAQVFGKR
MLAPKIQTSETSPKAFKCFDYVHDAEAAHMAATAILNLSTRCWEMPENLSTKPQDLPSKAADIEVDENGTLDLSMHKHRK
RESAFPSSSSSSSSPGVKSPEASQRQSSTSAPSSSMTSPQSSQASRQDEWDRPLDYTKPSRQREEEPEESEPAAHSFASS
EADDQEVSEESFEERKYPGEVTLTNFKMKFLSKDIKKELLTCPTPGCDGSGHITGNYASHRSLSGCPLADKSLRNLMAAH
SADLKCPTPGCDGSGHITGNYASHRSLSGCPRAKKSGARVTPTKDDKEDPELMKCPVPGCVGLGHISGKYASHRSASGCP
LAARRQKEGSLNGSPFSWKSLKNEGPTCPTPGCDGSGHANGSFLTHRSLSGCPRATFAGKKGKVSGDEVLSTKFKTSDVL
ENDEEIKQLNQEIHDLNESNSEMEAAMVQLQSQISSMEKSLKNIEEENKLIEEQNEALFLELSGLSQALIQSLANIRLPH
MEPICEQNFDAYVSTLTDMYSNQECYQNPENKDLLESIKRAVRGIQV
```

300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE
306 - 325:	EEEEEEEEEEEEEEEEEEEE
307 - 326:	EEEEEEEEEEEEEEEEEEEE
308 - 327:	EEEEEEEEEEEEEEEEEEEE
309 - 328:	EEEEEEEEEEEEEEEEEEEE
310 - 329:	EEEEEEEEEEEEEEEEEEEE
311 - 330:	EEEEEEEEEEEEEEEEEEEE
312 - 331:	EEEEEEEEEEEEEEEEEEEE

313 - 332:	EEEEEEEEEEEEEEEEEEEE
314 - 333:	EEEEEEEEEEEEEEEEEEEE

A0A384BWI9 **A0A384BWI9_URSMA** (2895 aa)
WD repeat-containing protein 87-like. *Ursus maritimus (Polar bear) (Thalarctos maritimus)*

```
MSSARLIPLWKDFKYLVNDIIHKSKQTSEDPKNDVVVLSDQSQILFRESRHPQNMPLICYYFSDANFFASLSWVTSAKEI
QAVVWMKSKTEDMVEKRTFSMTERLPPIQSMVHTGSFHILVAYCGDLILRLFGDHFRSFKPLGIVPCRFNINCLCYDPEM
KMLLSGILGAVVTWIIERSGKGLQVAHMVPMSGDELVQDIRLNGPNGSLLALCETVVRVLERQGHGQLGEVQRFTSTTSG
SFITCCFTCFDQGFLYAGNKTGEIQVWSLVRGNSLHSFKAHFSSVICIRSRPEAHTLLTAGKEGLIKEWNLTLGNLLRRL
ELGEELYKLEFIDNITFFCQTTHTFSLRRLPCFYSLFNVCGSAPQQLRRVHCGENRFRILCSTEDGLLRFVSPLTGDLLV
LTWPFAILDQAVDWAYDPEKEELFVATGNAEVLVFDTTRCPCPAKYLLCTSPDSQDWVQCLAYGHFHLGRGLQGLVFSGH
QSGVIRVLSQNYCARIEKFMHFGAILALSTLPGGVFGSRENSLLCSYGMDDYVHLSEAVLEGKKVHLKPLASILSSCHLK
HLILLPTSVGAITETNCLRLWKFHDFLSSESQEGSTFIETLPLHQCPITSFDVCWSLSLFVTGGIDGSVRVWNFHGRLVA
MLDSSLHFGPLCFANDRGDLLVTFNHSLYLVSCLKLLHPTLLARLSFMSMTDEVLEAPKPFTPSFFFSFETIFVPKYIYL
GKGQQELVGLEKLVNKRAIAFDHTVPHVIEEDEQGSPTLLSAFRCGFLHKEETDGMEVSKPPHYMFPPQLQLTTWDGLNP
YQLLRCYFGHGRKWLLAPDCYIPNSVIRARLWPEGSPIYLQCNLHSPVWEMEWDKSEQFFFWHSREKALSDAGEYSQERE
DADFIEMRLSKDITYSVLTDSANRSWLGKKMSEIAINSLVETILNIMIHASPLKYQCCIGALGQIFASYEVSSSLRSETA
HRLLDDTTNSNPLIRELAWEGLKRLGMITHLFAMPLAQGLMDKDQRVRSKALSLMADTGIHSKSSLLNLIQHRETFREMQ
QEMIGEESLDHLLGMRATDLQVLHTQVEQRLNENLTLSEGQEKPAFSLEVSRVSEHVSLSKQPDVIPEETEAATKSGKGQ
RRGRAAVKKHTRKLWRAFKKIKEAGKEPGPLEGESDQREAAPVLVEDTATHSRMSSTISVLKISKDGEQHPPEKDTSKDH
FALTLKMLRKIHDRKGKKRTVQKPQKRHKKKTKDAEVTTEESLPAVKKELVVKQLKAKGRGAAGAPGRKTIPEEGSSWRD
DLCRLMTLRISGSQTKMSEALNMELVTMAQEVLADQQPSWELFQEICPLLEKKSEVLLEDLQWDIAWPEERPIFIHERAI
REDMMVRREDEIPEVQEQVQKEAEDTPYLQETQVIPKKGKKKKIIFLGPSSLTKGKRISKKEEKNSFKKPQQEIKVDKKE
TVSKGERDVSQEIEEVAKPEEEEVVKQEERPIMDERKLSWQEWKKSWDEWKQAQDETKISWDEWKNAWDKRHLEEEEKQQ
TDERKPLPEEEKLDVDKLRWDEWLDVWEKIEARSREEHKDEEELTLEGEELSQEWGEEEQEEVMSEEQRQIQKEYNQAWI
ERKRAQAERKRAQEERKLAQEEEKLAQEERKLAQEERKLAREYGKLAQRDRTMVQAERNFVHNEEKLAQREDKLSQEAEK
LAQKRKKLAKQFEELAREEEKTAKKGGKLAEVKKILAQKMEKLTQKEQDLALQEKELAQELEELMWEEEELVRKEEELNQ
ELKDLAEEEEGLVQEEKTLAWQEQKLIKEEKTLALEEELLIQEEKKLAQDKEKLPGEEENLAQKRKKLMENKLKLAQEKE
KLAQDKEKLTKNKNILAWREKSLAQEKENLLQEKVKLAQRKENFLQVKQNLAQNKNKLVQAKEKLDMYKKKLAQVEKKLM
EEKEKLSQKKEKLDEAEKKLTQLEESLAQKQHNLAQDKMELATEKRAVFQELKMLRGEWDSAKEEKALGTEMKKLAQEKI
RLAEEKQILSAGETEETLKQIRLTKNELELIKRKLSLEEKILRYEDRVLATEQRDIAKGKLEFTRGGRVFAQEERKLAKV
VRKLIKEKEGTSRAQSKVSSKVLKALRDLTKKEMKLTQEEIEMTKMKRNFFVKERRLSKEQNKLDAKEWDFSEEEPEVTK
DEKKLAKKQRKLAKEMKRMMKKEKKITEEESRLARQQREVIQEEEEEGLTKDEEVIPLLEQRSRKREEKGRKELKTVDTP
WEKLPSQKESRDSLSEEMESLLDEIEQESLSEEEEEEEEEEEEEEEEEEEEEERKEEEEKEEEEKEEEEEEEEEGEEEEG
SEEEEEESISEEESESLREEESESLSEKEEGESSLKKEADKKKEILKKEKLFKSQEERQKDQRGREIIPSIGKRIPDIKD
SAIQLKILKAPSRKVIPIALGRQEKIPVPVSMKQVPWEEKARAPEASRILPESRFMDRQGELLKKYKPKPLQLLDTVLES
PERDLKTPYLPHILRKTMEAHNLQGEPLEPKWQWILKHHPALMRKTKVPVPQIWAKEIGAQVGLSDIEWIHHVLERMEAG
EQLSRDSFHRLCQLLKDLTSKGNLEWLHLAQLEAIVYHHKQVLESQSTHISKPSKEPMGPKYLKVIPPIKGKESWLKPFA
VPIPKSPLGTKGIPTPKGVNWHLLEEPYRSAWAEQISTALKEMEVQHFHPATGDIFIGAHASVEKQTLALMFQKDFWDFK
DKGRFPRLPKLEKKAQAISKKKEEVPLWETFVALYYVLRMLQQRYAKDSAAWMEQFHQLMDLYQLKSPRIQKLLQELLLR
EEPQSQEITYEEALKAMELVPGERLFCHLFCGGSQNPKGPLEFREVVSLPGQNNVRTMSPMGIAQYGILELAWKSLPQAD
IHLTKEMPHIIAPAP
```

2272 - 2291:	EEEEEEEEEEEEEEEEEEEE
2273 - 2292:	EEEEEEEEEEEEEEEEEEEE
2274 - 2293:	EEEEEEEEEEEEEEEEEEEE
2275 - 2294:	EEEEEEEEEEEEEEEEEEEE

A0A384C731 **A0A384C731_URSMA** (981 aa)
Nuclear protein MDM1. *Ursus maritimus (Polar bear) (Thalarctos maritimus)*

```
MSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTRENVALKVESAQQPKQVLKMEVAVLKKLQGKSHVCRF
IGCGRNEKFNYVVMQLQSNFAMGRLPSTYRKCYMLDFGLARQYTNTTGDVRPPRNVAGFRGTVRYASVNAHKNREMGRHD
DLWSLFYMLVEFAVGQLPWRKIKDKEQVGMIKEKYEHRMLLKHMPSEFHLFLDHIAGLDYFTKPDYQLIMSVFENSMKER
GIAENEAFDWEKAGNDALLSTSTSTPPQQNTRQTAAMFGVVNVTPVPGDLLRENTEDVLQGEHLSDQENAPPILPGRPPE
GLGPSPHLAPHPGGPEAEVWEETDVNRNKLRINIGKTPCVVEEEQSRAVGVPSSPVRAPPDSPTTPVRSLRYRRVNSPES
ERLSTADGRVELHERRSRMDLPGSPSRQACSSQPAQMLSVDTAFRSVPLAEEEDFDSKEWVIIDKETELKDFPPGAEPST
SGTTDEEPEELRPLPEEGEERRRPGAEPTVRPRGRGMQTLAEEDPGQTPFQPLPPQPSQAEGRSETSQPPTPGSPSHSTL
HSGPRPRRPRPRRRDSDPTGPQRQVFSVAPPFEVNGLPRAVPLSLPYQDFKKDLSDYRERARLLNRVRRVGFSHMLLTTP
QVPLAPVQPQANGKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAVALGEVLGPRS
GSSSDGSERSTDRSQEGAPSTLLADDQKESRGRASMADGDLEPEEGSKTLVLVSPGDMKKSPVTADLAPDPDLGTLAALT
PQQERPQPTGSQLDVSEPGTLSSVLKSEPKPPGPGPGPGAGAVTTGAGGVAVTSSPFTKVERTFVHIAEKTHLNVMSSGG
QASRPEELGAGGELGLEAPSDGRAVEEGASVPLENGIAQAGLESRALSGPSGDTPLEVATDSLPNGPALANGPAPASPLE
PTHAAELSLQRVRAVLLHERI
```

655 - 674:	EEEEEEEEEEEEEEEEEEEE
656 - 675:	EEEEEEEEEEEEEEEEEEEE
657 - 676:	EEEEEEEEEEEEEEEEEEEE
658 - 677:	EEEEEEEEEEEEEEEEEEEE
659 - 678:	EEEEEEEEEEEEEEEEEEEE
660 - 679:	EEEEEEEEEEEEEEEEEEEE
661 - 680:	EEEEEEEEEEEEEEEEEEEE
662 - 681:	EEEEEEEEEEEEEEEEEEEE
663 - 682:	EEEEEEEEEEEEEEEEEEEE
664 - 683:	EEEEEEEEEEEEEEEEEEEE
665 - 684:	EEEEEEEEEEEEEEEEEEEE

666 - 685:	EEEEEEEEEEEEEEEEEEEE
667 - 686:	EEEEEEEEEEEEEEEEEEEE
668 - 687:	EEEEEEEEEEEEEEEEEEEE
669 - 688:	EEEEEEEEEEEEEEEEEEEE
670 - 689:	EEEEEEEEEEEEEEEEEEEE
671 - 690:	EEEEEEEEEEEEEEEEEEEE
672 - 691:	EEEEEEEEEEEEEEEEEEEE
673 - 692:	EEEEEEEEEEEEEEEEEEEE
674 - 693:	EEEEEEEEEEEEEEEEEEEE
675 - 694:	EEEEEEEEEEEEEEEEEEEE
676 - 695:	EEEEEEEEEEEEEEEEEEEE
677 - 696:	EEEEEEEEEEEEEEEEEEEE
678 - 697:	EEEEEEEEEEEEEEEEEEEE
679 - 698:	EEEEEEEEEEEEEEEEEEEE
680 - 699:	EEEEEEEEEEEEEEEEEEEE
681 - 700:	EEEEEEEEEEEEEEEEEEEE
682 - 701:	EEEEEEEEEEEEEEEEEEEE
683 - 702:	EEEEEEEEEEEEEEEEEEEE
684 - 703:	EEEEEEEEEEEEEEEEEEEE
685 - 704:	EEEEEEEEEEEEEEEEEEEE
686 - 705:	EEEEEEEEEEEEEEEEEEEE
687 - 706:	EEEEEEEEEEEEEEEEEEEE
688 - 707:	EEEEEEEEEEEEEEEEEEEE
689 - 708:	EEEEEEEEEEEEEEEEEEEE

A0A384CFJ4 **A0A384CFJ4_URSMA** (838 aa)
LOW QUALITY PROTEIN: pleckstrin homology domain-containing family G member 5. *Ursus maritimus (Polar bear) (Thalarctos maritimus)*

```
MHYDGHVRFDLPPQGSVLARNVSTRSCPPRTSPAVDLEEEEESSMDGKGDRKSTGLKLSKKARRRHTDDPSKECFTLKFD
LNVDIETEIVPAMKKKSLGEVLLPVFERKGIALGKVDIYLDQSNTPLSLTFEAYRFGGHYLRVKAKPGDEGKVEQGVKDS
KSLSLPILRPARAGTPSLERVDPQSRRESLDVLAPGRRRKNMSEFLGDTSIPGQEAPTPSSCSLPSGSSGGSDSWKNRAA
SRFSGFFSSGPSASTFGREVDKMEQLEGKLHAYGLFGLPRLPRRLRFDHDSWEEEGDEEEEEDDSCLWLEDSWRELIDGH
EKLTRRQCHQQEAVWELLHTEASYIKKLRVITNVSVGPHLAQSHPAPHSLRLGALEQTLGLCRRNRGRKGRKAAPQGGGG
GDSHRPDNPWRRAWPRRARGNRACSVPGQFGSLFKPYVRYCMEEEGCMEYMRGLLRDNDLFRAYVTLTNYPLLLKSVLRK
TDEPRAKEAVVTMIDSVERFIHHVNACVRQRQXGAGGGVSRIDAYEVVEGSNDEVDKLLKEFLHLDLTAPIPGASPEETR
QLLLEGSLRMKEGKDSKMDVYCFLFTDLLLVTKAVKKAERTKVIRPPLLVDKIVCRELRDPGSFLLIYLNEFHSAVGAYT
FQASGQALCRGWVDAIYNAQNQLQQLRAQEHPGSQQHLQSLEEEEEEEEEEEEEEEEEEEEEEGGESSTSAASSPTVLRKS
SNSLNSQHCASDGSTETLAMVGEEPGVSPQEAGPSWVRRGTPSPGRGPEPSELEGRTSCPAGEPERPARRSKELPLGASP
RVQPEPPPGISAQHRKLTLAQLYRIRTTLLLNSTLTAS
```

682 - 701:	EEEEEEEEEEEEEEEEEEEE
683 - 702:	EEEEEEEEEEEEEEEEEEEE

A0A384D288 **A0A384D288_URSMA** (658 aa)
C-Jun-amino-terminal kinase-interacting protein 2. *Ursus maritimus (Polar bear) (Thalarctos maritimus)*

```
MKKLGSIGLSNLPMSRKLITGKDWDHSLSDPKADDFPFVLWGQIEDFTAPISTLGENSSFSTDPHVLGRSLRRPNQHPEA
DSSCSPLGRTASPASGQHPGREGVQGWWLSWEPCPCFLTLVPSPRPPQDISLEEFDDEDLSEITDDCGLGLSYDSDHCEK
DSLSLGRSEQPHPICSFQDDFQEFEMIDDNEEEEEEEEEEEEEEEEEEEEEEGEGEGKEGGGSGSEVPAPEALIPSPSLE
ESHKNRPTTLHLTTLGAQDSLNNNGGFAPAPPASWQETVLCSPPQEPLRESPASLQPTDTSPCGAQSPVRPGCDCEGNRP
PGEPPPPPRASLSSDTSALSYDSVKYTLVVDEHAQLELVSLRRCAGLGDDSSEDSGGEASEEETASTLLGGGQGPEDASP
DSPDLTFSKKFLNVFVNSTSRSSSTESFGLFSCLVNGEEKEQTHRAVFRFIPRHPDELELDVDDPVLVEAEEDDFWFRGF
NMRTGERGVFPAFYAHAVPGPAKDLLGSKRSPCWVERFDVQFLGSVEVPCHQGNGILCAAMQKIATARKLTVHLRPPASC
DLEISLRGVKLSLSGGPEFQHCSHFFQMKNISFCGCHPRNSCYFGFITKHPLLSRFACHVFVSQESMRPVAQSVGRAFLE
YYQEHLEYACPTEDIYLE
```

191 - 210:	EEEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE

A0A384DIN8 **A0A384DIN8_URSMA** (726 aa)
LOW QUALITY PROTEIN: YTH domain-containing protein 1. *Ursus maritimus (Polar bear) (Thalarctos maritimus)*

```
SREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDIKRQKPSVHSRQLISKPLSSSVSNNKRI
VSTKGKSVAEYKNEEYQRSERTKXXXXXXXXKICFSSSASREPYKSQPEKTCLRKRDPERRTKSPTPDGSERIGLEVDRR
```

```
ASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEEEEE
EEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSAS
ESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSARSVILI
FSVRESGKFQGFARLSSESHHGGSPXXXXXXXXXXXMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIE
LECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYAPEFHQRP
GYLKDPRYQEVDRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMAPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHHP
VPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDRGE
RGRYRR
```

227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE

A0A384DSS0 **A0A384DSS0_URSMA** (1231 aa)
histone-lysine N-methyltransferase EHMT2. *Ursus maritimus (Polar bear) (Thalarctos maritimus)*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWAPQLPTGLTSPPVPCVPCQGEAPAEMGA
LVLEKEPRGATERVHGSLGDTPRSEETLPKASPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDEPETLEGDGDLH
GGRILLGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAATAGPEPPVATPSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDMHSLGKMTSEVAKRRKMNTGGGLSEELGSTRGSGEVTVEKGDPGSLEEWE
TVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKA
KKKWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGEL
SGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHC
GEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLAQDAPPTLAQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGP
SLTLPNGGCLSAVGLPPGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTP
LHAAAQKGSVEICHVLLQVSTDLRAGRGRGSRPGLRCQQGLTCPHLPQEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVN
AQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAA
RESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGGGNRAIRTEKIICRDVARGYENVPIPCVN
GVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQ
ACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCI
DARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSA
EAIALEQSRLARLDPHPELLPELSSLPPVNP
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE

A0A384J9T5 **A0A384J9T5_BOTFB** (113 aa)
Uncharacterized protein. *Botryotinia fuckeliana (strain B05.10) (Noble rot fungus) (Botrytis cinerea)*

```
MRDEGGGIFLGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEYRYVMW
```

12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE

31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE

83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE

A0A384JM15 **A0A384JM15_BOTFB** (187 aa)
Uncharacterized protein. *Botryotinia fuckeliana (strain B05.10) (Noble rot fungus) (Botrytis cinerea)*

```
MDFSKVPKAKPISAKKAAQYNKIFDDPQKMKEIFEQCEASGRWAAGGCRVDGRGAPMYRGTKPEGIVEKEEEEEEEEEEE
EEEEEEEEEEEEELIASKYFKKGAGTKLKDPEKKMEKFGAGVRIPNLLVLRNEEEGSVLSTKNTTTPRTPTAESGTKNTQQ
HDEEACHYQSAITIMFSKHIVDAYNHE
```

70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE

A0A384JQB4 **A0A384JQB4_BOTFB** (849 aa)
Uncharacterized protein. *Botryotinia fuckeliana (strain B05.10) (Noble rot fungus) (Botrytis cinerea)*

```
MKKSKSKSTPEFALQTGLGGNGDQVAALQGLNRRGNTKEQRKKAPAIGPKNTSPLKKGVAIDAFQKKLSSVLPSSSSSTS
FTPIITKTISPKIEGGAKSKVFQASKNKLGRSKENLQRQCIENSPNDKARNSKEKNVASPAICVVDSKSFPGKGKGKERE
KSPEENGIQDTIFYPHQLNENKLSIFHLPTTTSKTPSTSSPPKTAQLLSKSAPKGQSQSKKHHSPTLTTSLTISLPLPLT
FQSPLLVPVAPKLLKRFYEALILLTVFGSNRGSRILEEEIPTDSLDDETLEIDISISVLDVNKKHEMDEISRTKLRRSFT
RHLAYLCDYEKGGDSTTAIALQQIEGGIVYHVAWNKISRPENGVEFLRKVLGLLGCAGCDVIRDSEEKRKEIVDKIFDLS
VKHAEKRISSYASFLARDIRFLLGEWKMDGEDNQDEDSSTHLHTWLQGLLTLTKNLSQLCRFCHKTCTTVSQEFAYLELL
IQLGSPFATRFAQIRHTIGRLNHTSKAIQILLPTRILLPHLFTQITISLLPSSKSFPPPLQERNPTLSALIGRTMSDPTA
ISFYRAALTEMDHKYQLSTHLSSHCTNPNWRPKIHAELLLLQHFSSRNLLFVDEDRYIACSKPACYCCYHYIRVHPGNFV
VPGSHCNHYLKWRAPDVEEGDKRGEKIREGVLIEMSRVFRMEVLKQIGEMRGPEVWKPDSLTEISEVRWGRMEGRGDFVE
NEMGGGGGEGDDVEEDCKSLVGDDVQEEDCESLVGEYDKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDDDEQMIK
PHHDRNEYFDLSQASRENKKAPHQQDQDMSEADYNSTSEEEEGGVSLYI
```

760 - 779:	EEEEEEEEEEEEEEEEEEEE
761 - 780:	EEEEEEEEEEEEEEEEEEEE
762 - 781:	EEEEEEEEEEEEEEEEEEEE
763 - 782:	EEEEEEEEEEEEEEEEEEEE
764 - 783:	EEEEEEEEEEEEEEEEEEEE
765 - 784:	EEEEEEEEEEEEEEEEEEEE
766 - 785:	EEEEEEEEEEEEEEEEEEEE
767 - 786:	EEEEEEEEEEEEEEEEEEEE
768 - 787:	EEEEEEEEEEEEEEEEEEEE
769 - 788:	EEEEEEEEEEEEEEEEEEEE
770 - 789:	EEEEEEEEEEEEEEEEEEEE
771 - 790:	EEEEEEEEEEEEEEEEEEEE
772 - 791:	EEEEEEEEEEEEEEEEEEEE

A0A384KDP7 **A0A384KDP7_PLAKH** (1904 aa)
Uncharacterized protein. *Plasmodium knowlesi (strain H)*

```
MHVLCAYKDRNTPFGNASPLEGRLSTKERVKSKNKDVYRGIMKKMKNQERRSSNDSSVKSKSGGRLGGNSWNIEGEVTHS
RTESLSRRKSEKGGDKNIEEGKSKSSSNTRSKMDTAKMNEKKEDLKNVKMFKNNTSESLKNKGSNSRESVKSNRSRSEKG
ATIEDKKKDESSHSNGEKKRKDSYNEKQEKNDLKVNNKLISKGTKSKNVNGKGNSSSASSTNHSRISASRAGDEKGASSK
GLPSKGSSLKNTPSKSSSAKSTPSKSGSSRSIASRNDTLKNDTPKNEARRNNSTRSLSKNASQESVNSENVKKEKRASTS
SSSSKGAQRSSEDASELMSNHTASSKEEGSRISRSVGKTEKKVKSERYKKGEREKSISGSDSEESKQKSSKKKSGADTRR
SDVVKNSLSGRGKSGVSETTKRKDITKKGSADQKKKKNNSKGGSGKDRQADSKSRKSKGGSRSKGGKDDEEDDDEDDEED
EEEEEVVEEEEEEEEEEEEEEEEEEEEEDDDDDNDDEDEEDDEDDDDDDEDDDEEDEESDPKRRSSSSSKKVTKGSVTKKK
KKRMSFSLKKRNRNRKGTQEDGKKGGNKNSGKSVNKSISKSTSKTSGKSSSKSKKAVKNEKKKNNNNSSNRNSKNNVKDE
NASEDEEEENPYFDPNDYTVDARRSVLEERERKRNLKESYIKQMKVPTYADDESILFINNPNYVMVLLFLTVYKDVLKMS
WNFKDIDEMFQNKETTEFGRNFILKLFFFLGRYFNSKSIFMYRYISRIFEDKQSSLMRVINFNELFPVMEIKRGKKSKSG
GGGGTSGGGNSFKKKKKNDKRKRKGKAEEDVNADAIDDANDDAIDDANDDVNEEVIDEVIDDVNEEVIDDAIDEEEEPDP
EDDENDSENENEVDETIEGDDAEDPPLNEANEVRKKSRNHGKAEQLSSDKLVKEGEEPQGMEEAPLGVAKDGAKREDSGT
TFIVRNENPDGSSTQQGVTTIANTSVADGANTFGGTEENDESANNPNGDHLIDSVKNEELQENRRLSKKLFLEWDDLSVI
SKLRIIRMLLNLVLCESNNLKKMLMEEKVDYSSGYLGKVNKEKYWLILNDTINIEFKLYVEKEEEGTFEFLCDNDDVLYT
IGYNLLKDTETKVMGETIIERYNKICRERRNRSRILKQQKKLCSDFNLNGGSLVTSKKRQHKQVEHFNFDNDKIRRKKNE
GANMHGVGASGYTSGLNASNPYALQKNNYQKNDRSFRLAARNAQKGNGLLVGELLDGMGNQEYVQGGGSVVGVEGALLNN
VDGTGVGGVVGTLSNLQGQNAGALGAGGVVVKVPQKRGRKKKSEKKKRGRKKKILTEGGALIPGASLGGEGGSLAAGLVV
DPNNPLATITQGKETKKATSTSTRGRRAPYAKRNTKPTVSIKYGTRSHSISKNRNETSDFSDFALTHGVNSETLYKNGNL
DEKYFNPNMHVNNFIPPSMNTPYGMQTNVLTMRRNKMEAPPGGYNFPYMYNPQMYGQYYMYNGSMYMLNNGGGGMFNQSG
ASGGGSGGGNGKEMKNEGVFMAKGGGSSGSGTTINNANNLNKNSVGPGGSGGSKGPVSGKDAEGEGSNEMSGSGVAGQMS
```

```
GPMTMMNSVGGPDGGLNSGMGGGLNYMDPMNKYQSYVLNRNAMNNMPTNPMYNNLYNIKFPYMNNDMMNYNYNMNNFQNM
NYEKMNKVGPGGPTGQSGGASSSPPSGGGMFKRYPNFLGGAFPPSYNNMNNPYANFNAYNMGYPRNEGGYASIPPGGTGT
GASPSSGGTSGASSFKSKLVDLNASESSSGVTGGTTGTVHSSGAGVSGYHMGNVKSRSGNNDVHGASAIYEKPTQLISSG
ASSGVNPGTGEANQKGETHRIDNLMNYMIMHSGSNADIHHGSNGKNNSSMANTENNVVQNGLNG
```

488 - 507:	EEEEEEEEEEEEEEEEEEE

A0A386AY39 **A0A386AY39_9CHLO** (2574 aa)
Cell division protein FTSH. *Pseudochlorodesmis sp. HV01306b*

```
MAFGRGIEDKMKKKNRWKFSFEFLSYWKYPFFKFGQRTSQQLTNWSIFLSFFVLSFSLTQKSFEKRNFTFFQNYPAFFQN
KKIPKKFETLYLQLPSAQYPLQELEKKVHQQNRENAIDLWYQNPLLDEDVKLFMDFHKYLKKPDPIYPTTFDNIHSPRQK
QDAINIYHRFEQIAPLLLSESVREKDEQNKTPEELQQEKEAIFILGGHALDQNWSSKTKNFYKEQEQEQIWSPRMSIFNT
FTNPWALVFERPLDDKEIVIHDYKKDKNSEINKHFNRSVDFIQKFIADYQDFLKNNKDDRKFYMHQRIFPFKKAEISQNN
AKITLPTFSENYKKKVGLPPKWQLNQKISQLLNPFISLVLVEAKSTEGDKFDEFDLFKTFFSKKTPKKTPTQKKDIPLDQ
RCFPLETLGVDPGWLHLKEKTKRVKQHYDNAKRVLTYLRIKLQPREIWLDPSHNSTQQQLDRMNYKLFSGRQSSEISKIV
LATIKRRKWKGIKYYLERKRLLRYGYKTKPLKCKRIFMDCKYQLYENLENRVDKVPPRVRVPSQFAQHRAAIRELERSVE
VPPKHRQKVSRLNEFKEAFYAIPKFKDRIPKKLEEFRLGSLKKKRKASIFIKDTEYEKKKVEIMVHSKKSLQHFKDQVSI
VHYAYPFAKKNEDGIVEKAKTVFIRDLPKYKRLFPFSKRISGLPWNQNEHNHNNAMNSLWQFIELIEKQYPEFKETPLGL
ARRDVAKLKKWLPHVLSLRERVIESTKGRTVEIIPLKEMEGIMNRDPDVLRKYQYLATEIKEKITHTKQSNSIYMDDFKI
YLTYPIPADASAGYYQDPTPISLVHLVDFMRWRAETEEKTIDLYFHQFSDILKKLNQNPFFDFYFSAEDYLLEAMLMKAP
HVFKEFEKKRQDEQKELKQKHKAQQEERERKYKAQQEEREQKRKARQEEREQKRKAQQEEEEEQEEQEEQVADASLDEQN
ISPQEQEKATFKIQQEEEEEEEEEEEEEEEEEEEEEEEEEQQALQSISISPKKLKKIIVKIQKKKQAADASLDKQSISPRK
REKVEKKSLISSTAYKIIDFIYNEQRLRNRLFQESEILFKQADDSENKQDIQMAVSEFLFKQIYLEKYYKDIQTAEKFSR
AILKDVFANEVQELKYMNIIDDFAALPSLLRTLQINLQLKKMLSFKEKSLEKIQLKSVNVKIQTTIVKLLCRYVNRKKLL
NHAPGRTEFFRIFSNLVKYRCLDYPFTNPFPLDRFKGQWVYKFPRSKFYSYKRGFTIFYLDKNNCPSQRNSFPFENQLLW
FQNLEPLTSTIFKKVRRCLPKLPKFEDEFYVVRRVLPKIPKNKDALCIFGNTDRFFKKTKKKPYCFNLINVSLQRPWKLN
KFEVFNELVNYLRSRYCFLQYMQCFRTFYDEFCIYLQENNPKLFNYYLEIDGFSEIEGDIYSGITLLNSSHSDLIEEEKL
RQQERQDKKEKITNWIQIYRSEIDQKKIDAQTKEKELERKKKEEKKKKRNPNPTHTQTQSDPTQTQSDPTQKEKEKEKKK
RKAKKKGKNSKDTTQQKNQKEVVYKGEIPISNKVLYDLVGDLLNDANTTCKDIIKRRRQLNTQKRIYELSFVRGMSGYYF
PDLDSQNFDRLFQRDAILQILLSNKDMPLSDFAQKFEQDQITHIYPRKDQSPGFHFFHHRHKFSQIKFWDSQFFDSRETV
QNASWSVIFFFSSGWIFVNLFKNIYKRYAKEFVESALDIFKRAGFLGDVKWIKEELGLAPIDKGYRGIRQHGQKLRHIIG
INQKQKILEISEIVLYLKTKKLLTSTTFDPFLKMIILVNRSQFFIKTKMRLLLERVPRYGLPFSLYQILLTLQTRTKTRS
ILSRTSRSFLPQMALGQSPTEEEAKINKKLDENKRRKRNIQPTKVLRPLRFRFRKARLMTIPWKKNPTANETVKIKPKAY
ILTGPPGTGKTLLVQAIAGETGVPVVTQSGGLLQNPRLGLEGCGTGAKTLHKLFLRAREIAPCMIFIDEMDGIGKRRQFL
DDRGHDPFEWLESDQLLIPPNPYHPKLKRRAEFLDDHDVYWREPEFTQTVESTAMPTDVLQDMQFSRGARSEQLSILIQL
LIELDGINSLDDIVVLGATNRLEILDPALLRPGRFQKILRFYLPNYGARMNLLKFYTHQSKIGVDSFSWEYFVKRTNGLS
SADIASIVFASELTAIEKGQKHSFETLERGIDLITSFPSDPIRFRLQKVLNFFEDAVQKLYAHNGFYRSFHSPSRGTQVP
NRPAVQELSTLIRHSYYSIGKMVLLFYLEQEKMPLAYISLWERPKNFRFFFFTKNFYEFEEFDQKRLSKREIEKRLLALF
GGKAGESFLIFLPLRTFTDETCLQFDATFGVLNNSVEQSNLGFDGDIQSAQRLLKLMVEEWYLYLERVATEKFHPILENV
NLWEYMSPEAEKDLLFGQTLVDEMLITLDMRNRLSQTDQKHAYRTWWMKKVATQLNYQESWRSYLQWSRLHLSDANYSAQ
NIEWVPPDEFYHTMYRTCPACMAWSHYLENRRFIIANVLLLQSFNSALKMLRPFLEFMDFLSDYFLRQGCIRETDFQSKM
TQFFSEFADFRSIS
```

976 - 995:	EEEEEEEEEEEEEEEEEEE
977 - 996:	EEEEEEEEEEEEEEEEEEE
978 - 997:	EEEEEEEEEEEEEEEEEEE
979 - 998:	EEEEEEEEEEEEEEEEEEE
980 - 999:	EEEEEEEEEEEEEEEEEEE

A0A387L8R2 **A0A387L8R2_PSECS** (1247 aa)
Euchromatic histone-lysine N-methyltransferase 2. *Pseudorca crassidens (False killer whale)*

```
MARKCVVAPLRLFLALLLAHVTRGGRAPARPPAQAAMAAAAGAAAAAAAEGEAPAEMGALVLEKEPRGATERVHGSLGDT
PRSEEILPKANPDSLETAGPSSPASVTVTVGDEGADTPVGATPLIGDEPENLEGDGDLHGGRILMGHATKSFPSSPSKGG
ACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGATAAGPEPPPATASPEGQPKVHRARKTMSKPGNGQPPVPEKRPPE
VQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEELGSARGSREMTLEKGDPGSLEEWETVVGDDFSLYYDSYSVDERVD
SDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKRE
PPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAG
HKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKAC
VSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLAQDAPGRADTSQPSARMRGQGEPRRPPCDPLTDTI
DSSGPSLTLPNGGCLSAVGLPPGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQ
SKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGN
LEMVSLLLGTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCD
LHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIIC
RDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLL
QEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDD
SYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRAGEELGFDYGDRFWDIKS
KYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELGSLPPVNP
```

336 - 355:	EEEEEEEEEEEEEEEEEEE
337 - 356:	EEEEEEEEEEEEEEEEEEE
338 - 357:	EEEEEEEEEEEEEEEEEEE
339 - 358:	EEEEEEEEEEEEEEEEEEE
340 - 359:	EEEEEEEEEEEEEEEEEEE
341 - 360:	EEEEEEEEEEEEEEEEEEE

A0A388JJ66 **A0A388JJ66_CHABU** (236 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MVKEEEVEEEEEEEEEIDMVGEGGGGGGEEEEEEEEEEEEEEEEEEEEEDREGEEVEEEKGEVVEEEEEEEAWATTTTGGG
GEGDNGGSRDPDREEEEGEEEEEEEEEEEEEEEEGLGEDDDDVKDGEEEDEKRTTRGGGGGGGRGGAGQLEGGGLSDDDD
DDVKEEEEEEEEEEEEEEEEEGVEEEEKEEEGKEEEEERATMTTTTTTTTTKKKKKKKKKKKKKKKKKKKKKKKKKKKR
```

28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE

A0A388JJG9 **A0A388JJG9_CHABU** (438 aa)
Uncharacterized protein (Fragment). *Chara braunii (Braun's stonewort)*

```
MASAVGVDTFASLEGRKAVHQYSKALEEEEERLAQLKQYVADNDSLARLVVELPDRVDHKVMVPFGKKAFFPGRLVHTNE
FHVLIGEGYYVERSARQTIDILQRRRGYLTSKVNAVQLQVNDLRMQHSFVAETVNADGLGVVEIREPYDEAAERTESSRT
GSSGARNGISDGVTTAPREAKGAGSNDGQARSSEGAAAMGEGTAGKTREEDEIEHKRLMARLDELEKLEAKAAEEDEDTE
EDEAVEEEDEDGNRETYLRPGWWAKEANADAHRSGKKLSKRPDAQEVEEDADASDMEEDYDSQEEQEDWEGEGKADEAEE
EEGEDVEEEEEEEEEEEEEEEEEEEEDTEEEEGTEEAEEEEEDVEDENQDEAVAAAAELGWNGRERIEGEDLTSDAENVA
AVSGQLKVLDVAQHNPQVSGMDRQTTVERTDSTGRSRQ
```

327 - 346:	EEEEEEEEEEEEEEEEEEEE

A0A388JJR2 **A0A388JJR2_CHABU** (104 aa)
Uncharacterized protein (Fragment). *Chara braunii (Braun's stonewort)*

```
LVDDLPLDIFLRCDNQPSTRVLSRMLEPHLLWSTCTELDGDNCVYPSQALFLEIDVTNLTVWDPIIRQGKAWQEEEEDEE
EEEEEEEEEEEEEEEEEEEEEEE
```

79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE

A0A388JKN8 **A0A388JKN8_CHABU** (326 aa)
Uncharacterized protein (Fragment). *Chara braunii (Braun's stonewort)*

```
MEKGWKEGRGGGEGVGGGGGEEEEEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEEEE
EEEEEEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
DEEEEEEEEEDDDDDDDEEEEEEEEEEEEEEEEEEEEEDEDDEVEEVEEEEEEEEEEEEEEEEEEEEEDEEKKRRRRRRRG
KKKKRRREEEGRRRRRGRRRRRRRRGGRGGGGEEEEEEEKKRGEEEEEGRRGKKKKKKKKKKKKRKTKRKKKKKKKKKKKK
KRRRRR
```

29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE

49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE
208 - 227:	EEEEEEEEEEEEEEEEEEEE

A0A388JKR6 **A0A388JKR6_CHABU** (126 aa)
Uncharacterized protein (Fragment). *Chara braunii (Braun's stonewort)*

```
KKKKRRNTTKKKTKTTKMKKKTIKKKTTKKKMKKKMKKKMKKKKKKKKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEDEEEEDEEEEEEEEEEEEEEEEDEEEEEEEEEEEEEDE
```

50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE

A0A388JKV9 **A0A388JKV9_CHABU** (131 aa)
Uncharacterized protein (Fragment). *Chara braunii (Braun's stonewort)*

```
VWKRSKKKTTKKKKKTMMKTTTTKKKKKKKKKKKKKKKTRTKKKKKKKKKKKKKKKKKKKKKTMTTTTTTTKKKKKKKKK
KKKKKRKNKKRREEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE

104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE

A0A388JL47 **A0A388JL47_CHABU** (45 aa)
Uncharacterized protein (Fragment). *Chara braunii (Braun's stonewort)*

```
EEEEEEEEDEEDEEVEDDDEDDEEEEEEEEEEEEEEEEEEEEEAEE
```

23 - 42:	EEEEEEEEEEEEEEEEEEEE

A0A388JL59 **A0A388JL59_CHABU** (309 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MGAIAVLHALDLQNNNKNHNSNKQTKKTKKKRRKKKKKNKNKKNKKNKKKKKKRKKKEKKNKKKKKKKKKRCGGHTCKRE
EEEGIRRWKKKKEEAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEKEEEEEEEEEEEEEEEGEEEEGEEEEGEEEE
EGRRRGGGRRRGRRRGKKKRRKKRRKKRRKKKKKKKKKKKKKKKKKKKKRRRKRRKSGRKKRGRTKRGRKKRGRKTRRKKKRR
KKKRRKKKRRKTRRRRKRRKKKKKKKKKKKKKKKKKMKKKKRKRRRKKTRKKKKKKKKKKKKKKKKKKKAI
```

96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE

A0A388JLC5 **A0A388JLC5_CHABU** (153 aa)
Uncharacterized protein (Fragment). *Chara braunii (Braun's stonewort)*

```
IMATRLQCGGGRELGGWRRRWRRRKKRTRRKRRGRRGRRWRRRRRRRRRRKEEEEEEEEEEEEKEEEEKEEEEMDKEDDD
DDEEEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEENEETEEEDEKKEEEEEEEKCRSRRGSR
```

89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE

103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE

A0A388JLD3 **A0A388JLD3_CHABU** (1848 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MEKRELIKQAKMLALVEEQEAKKKQMEEELQKWTREQEEKMAAIQAEVEKEEEEEKKVEEEVSLVRRRGEANTSMEEEIE
KTTQEWTANLELGEDREVELAIPQEEREAARRELEAERDLVRRRAKEEEQQRAWKWRLSQEKVRRLEAAERAERDLKAAK
ARMGKIRVETELATKRRHLMKTDSSAQCRPRMQTVLTIEVWAPNFEGMDDGEKVLLIGGMVHLHEDELLARKCDRIFAEW
SPRVGGGILDGGGVRDVAGEVLGQDGSNSKASQGTHNAQSESGVSILFTNADLVEATLEVDLCEVLGSMEAIKKLGDVRQ
GVLVLDCDPNEGAVVCAHAEFGGSAFLDEKATCTEGGGAWLNESFFKEVIELSLHFFSLWNGELVGWSAWRSVTGFQTND
ILDEAVGGGVLAKPAKLVDIVVDCLLRAEGGGEEGGPLEEGEGNRDVLVRREGGKVCDGGVKVEEVEGGVELLEDGVVDD
DKGGGEVQGGVVVEVGVEEVGGSDVEGGGVVLNTVMAWACCSKAVMRSERAEIVACMSVREVWTVENIWRMAERSVAMAG
PARCWPANSQARLPTDWVCVGDMLILEESAMGVVGGDAVKAAMEVAAEDEVTAAAVVEVAAADEVAAASATLLEWVWFPM
GICNAPAMFQRAMNVTFQNFVNKTRLNQGMINFCVIVYMNDILVYSETYHGHAQHIKWTLGALRDAGFKITLEKSEFFLS
EISFLGYVVTRGGLQPDSRKVAAVKDAPVRTSLTYPSHAEYLNPRGIIGFLFFSPRTTVEERAVAEEAEVEDESEEGIAE
EEGSYTFDGRDVNILPFHFSLIADYMTHPGAIVKHNVFGYKEFLGHCSIKAPFSVACYQDPGRAFLDAAAKGIQESPLLS
QAKSGLGGKVPFGTGGYFDIMMETKRTSDFPDVSRRNRSTSNTESEVPSPGIELGSKVEEAYRNLQAAGDEEENDVSLST
AHDCPIDDFGFQDAPPVMHRRGADLDICSPSSSGAGLSAVQGNGGYQNRGNPNPSQRHISSNDKDQPKDSEAEWSTVTGQ
RDQNFTQTSGNQVDRHALAVQLRQILRNWKFGPEVMLAKATKVDEELGRQSMKAAKRFEREEAEAHDRGTEFAKCNLREE
EEEEEEEEEEEEEEEEEEEEKEDDANRWGRRTRMCPNGVSVQMKDLVKRSQSKHEKMQKVHINRDQGDHGLEGQVRRPSTR
RKHIGHAHREKRWVKRRDARPPPAHGIVNVKSMKREKEMKEMRPAKDIQSKKEVFIADFTRTSRILNDRYQQGEFLSEDD
QEFILNAVLPYHPKLCEKITAGVDMIQQLEQRPVAAPDDSSSNTFDHLNALEIDVGALKDDTQLQQTARQQLEQQICAAA
TNPSSAPRETTPRFDDQKIFCDSTKTDPIPWFRKFELKLQLHHISEDKHHAYLYSRSGGACQSWLDNLLSKYGVVAVDLY
TKISWDDLKATWHKRFQVEPPEIKAMDKLMTFEQGMLSSIDWIAEYQRLTSVPDIQMGFKVVKHYIFRSCPALGNALTHV
EDTLMTTVELFDKAAQIIVTDKEAKNLHRSSATGPSRDQHRAKVVVVVAATPTDESSEAVPVNEGDRLAAARDGGCPGKG
RGRGKTKTNTISIRPNDRYKSAFKTWYGHFEWVVMRLMPFGLTNARATFQAAMTNKLCAMLDRFVLVYLDDILVYNRTLE
DHLEHLRRVLETLRRAKCKANRDKCKFVRQELEYLGHFVTLEGTSPLILPRKKSPRTKVNVLTEIRSYIVDSVDDSEEVK
DEAEKLIEAIEKRNKGKRATTDKHVEAASTRKKISPMKGKEKQVEDEGFVTPLRKPFAAFCLSEGMVDYALAQVRLLNNL
KLQEIRKI
```

1119 - 1138:	EEEEEEEEEEEEEEEEEEEE
1120 - 1139:	EEEEEEEEEEEEEEEEEEEE

A0A388JLE6 **A0A388JLE6_CHABU** (273 aa)
Uncharacterized protein (Fragment). *Chara braunii (Braun's stonewort)*

```
KKKKKRKKKEKKKKKKKKKKKKKKKKKKKKKKKKRGGGHTCKREEEEGIRRWKKKKEEAEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEDEEEKEEEEEEEEEEEEEEEGEEEEGEEEEGEEEEEGRRRGGGRRRGRRRGKKKRRKKRRKKRKKKKKKKK
KKKKKKKKKKRRRKRRKSGRKKRGRTKRGRKKRGRKTRRKKKRRKKKRRKKKRRKTRRRRKRRKKKKKKKKKKKKKKKKM
KKKKRKRRRKKTRKKKKKKKKKKKKKKKKKKKAI
```

60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE

A0A388JLL9 **A0A388JLL9_CHABU** (1412 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MHQGPLRARSSQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEEEEEEEEEEDEKEEEEEEDDEDEEGDD
EEEALREAEENLKSAMDQLRSKQAQLAAVEDQVAMLRKQLSDAEAELKSLKDQAELTSGRLTRAGKLTAALGDEEVRWTE
TAALILSRTELLVGDVFLSSASISYCGAFTGPYRKTMLDRWIARCQDLAIPVSKDASLRATLSNPVEVREWNIWGLPSDD
VSIDNGILVARGKRWPLMIDPQAQANRWIKSMEAKNGLRIIRLSDNNFLRTLENSIRIGNPVILEDVGEVLDPVLDPILQ
KQIQNRKGRLLIRVGDNDVDYDPSFRFYITTKMSNPHYLPETCIKVTIVNFTVTSIGLEDQLLGDVVRKERSDLEEQKDR
LVVSISNDKKQLKDLEDKILKLLKESEGNILDDEVLINTLNNSKLTSGVIQARVKEAEVTEKDINEAREQYRIVANRGSI
LYFVIADLALIDSMYQYSLSYFAQLFNYCIDVAAQSEDLDMRLSNLINYTTEFMFLNVSRGLFEEHKLLFSFLMATSILR
SSGDIGAEEWSFFLRGVAASKVTDDQGGSGAGRAALAVQESANPVSAWASDSVWVNLRALEKAIPSFVGLSAAVSANQAQ
WKAFAQSPEPHNAPLPGEYGQREVAATAAADAEAAAFAADVAAAAVAAAAAAATAAAVAPAAAGSPDILQAPVDDDHDAD
RHREPDPTKIKRVRRSRMGSLIHPQKSKCCFQRLNLVKVFREECLGFACARFVTDILGRRFAEVVPFQLDDVYKDTTCTS
PIIFILSSGADPTVLLQRFAEKLGRRPGEQLHMISLGQGQGPVAETLISKASKQGDWVCLQNCHLATSWMAVLERTVERF
QAESAEIHPDFRLWLTSMPSPDFPIPVLQTGVKITNEPPKGVRANLLRSYSGFTDAFLDSCSKKTVWKKLVFAISFFHAI
VQERRKFGPLGWNVRYEFNSSDLDCALQQLHMFLEEQPEIPWPALLYVTGEITYGGRVTDFLDRRCLASILNQYYCPFVL
EEDYTFTPSGVYRAPPEGGLESYVEYIKSLPLTEDPSVFGMHDNAAITFQTQETTRFIETILNIQPRQAATTAKGAPSQD
```

```
DLVLNLADDILKGLPQLLVRDEESAASSAFLPDANGRLPSLSVVLLHEAERFNRLLNRVGSTLKELQRAIKGLVVMSSDL
ERMFSSLLNNQIPALWTQVAYPSLKPLASWVKDFQARIEFMHTWMRKGQPSCFWLPGFFFPQGFMTGVLQTHARKYSVPI
DTLSFRFEVQDVYEAEEVQMPPEDGVYINGLFLDGGFWDQRYRALTEARPGIMYSPLPVVHFDPVVQYKTDNTNFMKDYE
CPLYKTAVRAGVLTTTGASSNYILNVSLPIRSDTTPDFWILQGVALLCQLSK
```

13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE

A0A388JMJ3 **A0A388JMJ3_CHABU** (216 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MRRDEDEEEEEEGEEGEDREDKEEEVEGEEKEEEEEEEEEEEEDEDEEEEEKEEEEEEEEDDEEEEEEGEEDEDEEGEEE
EGEEGKDREDKEEEEEEEEEDDEEVEYEDEEEEEEKEEEEEEEEEDEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEDDDDE
SEEEEEEDEEEEENEEEEEEKEGRRRWRGVKGDDVCYLETRLPAMASKGGGDGSRR
```

133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE

A0A388JMR0 **A0A388JMR0_CHABU** (535 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MARCGYGREGGIARWRGREDSRGVWQDVEMGRTMVRWEEGRNGEMAREGGTMVRWEGGRDVLWKMRGGRRRREVQEVTEG
RKKRKKKMAAAAGRDGMAAGCGGGRRRRRRRRGRRRQRGRRRQKGRRRRRGGRKRRGGRKRRGGREMGGREGCTMEDEG
GAEEERSTRSNRREEEEEEEDGGGGRAVWYGGGLWRRSKKTKKKTRRRKKKRKKKRKKKRKKKRKKRRSRRRRRRRRRK
EEEEEEEEEEEEEEEEEEEEEEEEEEEVDEEEDEEEEEEEEEEEEEEEEEEEEEEEDGEEEEDGEDGGGEEEEEEEEEEE
EEEEEEEEEEEEGGEGGGGEGGGGGEAEGGEAGGGEGGGGEEEEEEEEEEHDDDDEDDDDDEEEDEEEDADDEEEDADEE
EDADEDKEKKKKKKKKKKKKKKKMMMMMMMMMMTMSGAVFFFFFEEEDDDDDDDDDDDDDDDDERSSFLFFFLTCRLSR
DLSLTNVEKKKKNKIVRRGRGGEKNKKKKMRGRKYKKKKKKKKMRGGGGGGEKKK
```

241 - 260:	EEEEEEEEEEEEEEEEEEEE
242 - 261:	EEEEEEEEEEEEEEEEEEEE
243 - 262:	EEEEEEEEEEEEEEEEEEEE
244 - 263:	EEEEEEEEEEEEEEEEEEEE
245 - 264:	EEEEEEEEEEEEEEEEEEEE
246 - 265:	EEEEEEEEEEEEEEEEEEEE
247 - 266:	EEEEEEEEEEEEEEEEEEEE
248 - 267:	EEEEEEEEEEEEEEEEEEEE
274 - 293:	EEEEEEEEEEEEEEEEEEEE
275 - 294:	EEEEEEEEEEEEEEEEEEEE
276 - 295:	EEEEEEEEEEEEEEEEEEEE

277 - 296:	EEEEEEEEEEEEEEEEEEEE
310 - 329:	EEEEEEEEEEEEEEEEEEEE
311 - 330:	EEEEEEEEEEEEEEEEEEEE
312 - 331:	EEEEEEEEEEEEEEEEEEEE
313 - 332:	EEEEEEEEEEEEEEEEEEEE

A0A388JMV5 **A0A388JMV5_CHABU** (306 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MAGGWQSVGDGRIGGRRDGGGGGGGGGGGGGKGNDGGRGGGRGADDGGGVGGVGGGVGRDDEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEKKTLEGEEEDEEQTTEVESEEELEEEEEDEAMKKKKNKKKKKNKKKKKKKKKKKKKKKKKKKKKKKKK
KKKRKKKKKKKKKKKKKRRRRRRKRKRRRCRGRRGNDDDDDDDDDDDEEEEEEEEEEEEEEEEEEEEEEEEKELEEEEE
DEAKKKKKKKKKKKKKKKQKKKKKKSRRVEEEEEEEEEEEEEDEDEEEEEKEEEKQEEEEELEEEE
```

62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE

A0A388JN90 **A0A388JN90_CHABU** (3412 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MAEGNGANLAEEEDEEEEEEEKKEEEEEEKGSLVGDREGEHESRKSGEEGEHVSDSTNYGGGGDVVGGTKKREEKDVHVG
DRRLGSEAVAAADVEDERRGEGGGGRPSIEVFDRGRDTDDAGDGDVIRCERKERDRGDIVAIGLDERLRVDAVIADKEME
RQWGDGGGDSGEGMDGCRDEGKGKEGPDDDNARKEREEEDAGDGGFVSKVKDVLIGVGDGGEDLQQAAVIAEGGGQGRKG
DCACDNGVGDGDEDAVDEGRKCKSAGYGDGSQGKGVCAYDSDGGDGYAVSERRKHKNGGYGYGYGGVREMEGTLAVGEIG
CCREKKEQWCEGGGGQDPDACCDGAEYGDDEAGSRKKNEKKNKEEEEDEDGLYDAIGVCEVEQWLAGEVVAENENESNHQ
QFTRGGRQSAGASCDGTRQDGDYAGEDGGKRRKERDGGVDGGLGRMDGGVADDEGMMQVRREEGKSDVWERENEREGGRD
QGVGGVEGVGAADGGVVNVVSDVSNVNDYAKDMSATMDEVGDGGHVSVVEDKVLLHSRASVDRCVTAAHRCTGVFAGVIP
PSLQERLGKEGGGGEMGEEGKEGENELEDDDDEDDVDFTPGSLCSLSPLPSDFSSVILSDTEDEITDKGGEKGCEDDEEG
GDNERNLIGGWEMDVRTGVSSVLSGGGGDAFAGQSAAIFSHGLLENRQQDVGRLAVERREDEVDLGRGGGDAADLDGDAT
THAHGDKWGKTGGKGVELLSGRKGEHDSNDENAVTESSTGGTMMLDAISKRTRARLSLNDMTLEELEAFLRDSDEDEDLV
GADVEEEVAVYREFLASVIGGIQGEGGGNESREGDGGGGEGGGGGGRGGEEGKEPVVATGGREEEDDESDVDFTIEDLF
DSEGEHGEGDEDDEDDEDEDDDEEEEEEEEEEEEREGADEEEEMVGGESERGREQRAGAGSRKRKSSARSLPRTAFPCGS
RKKGKTGGGGGHTEAEICQDSLVADKAAKKWRPLLPRQQANHPMLMSWGSRSMAGPGPDFQPPHMMSYWPGGLGSQPPPI
HAAVATPGHQFTAHQIGQLYCLVHEHVQLLIQVATLGQLDKESMEAALAARKLLAELQSRREWILSWKKTAFPDACFKPP
YVHPTATLVRTAGCDGSQGCACGCAQPSPGTRQHRQSPATANSGNPNAADDQRMEVEEVSSASVPLPRTAVGTQTTSGMM
MMMMMAEAAGTRSSNDGVDLRSGSGFTQVQADVDAIWAPTVSGPVHSLLDVAPLRVLPQFLLQLDRAAVAGGDPDPDAHQ
SQAGRETQQGSSAAEGGEERCPMFTCCSHSQVATAPWPPRMSWLWCRNEAAAAPGASSCLPAVGSHAPGNIPVAEKNDEH
RGDNDAAGRGRGGRTAGGGSVLKEVDSIGGKAKDNNGPSGGKSSSRTAATGGGGGGGGGGVGGGGVVLVPGRYAQAMKVF
ERVFNPAVFPRCPPASYIAKRTLFTENEDLLLAMGIEIFNTDWPAIQKRFLPSKTAQQVFIRQKNRCAARAPVNPIKLVR
QLKQAPLSKEEKQLISQGLQIYKHDWLLVCSMCVPHRDPQTLPRLWKMALSSSSCSTTREGEANQPRRAQRPRHRDGRKR
GAQAVVSAASMSAEGQGETTVTAVDTGKWDRNRRAPSDGSRKENSRAHTVASAGEGEGVRAGGPSSETGGSVLSHSARPP
VAGSGMHKYDQTVLEGISAQPVGPQHSGTPVLQPSTAKAGHSQHLSAGLASSGMPHVSAAAPSIPGNQVQTVGAVPSGPS
VRLPGQTVLQSQVSPSNEVQTVAVTPAEPSVDLPGQTVSQTVLQGQTVLQSQGSVHRDRQTVAVVPASPVGLPGQTVVQC
QTVLQPQVSGGIEDHCGKSPERAAPRQALTVAGVPMGLTQNRKEHVPISDQEFEPSCHEVGAHMEADAGVMDQNGGVVPT
EGTGVTLLCDESYATFIQREDYMELAGMQHDSGDAGDEARRGCGPVADLQSAMEVEGGSTSSWPDAHVAVSSNQNPQVFV
AAATTGPPATNRRASLSPVGSEQGAELALGTRTSSFDEHKSASSLFASSDAGGQVVADTAEHSSDQDLVQDPPVGGRLSA
CETRLAGVPNGAKRLRPMSGPCVLSCASHLQASALSYHNRESVSGLPSLSRHSSPVPIRLIQRVSTPPDVNEFAAVQLTP
ALDRQIDLPDASCRVNSSASVSAASGQPRHPRTAAEPTAKEHRKQAGAQPADLRPMKKVTTGAKTNKKSGSRSSTCLRMG
QPVQQVSSQREAPNRTDSLSRPSPQLAVSLSGVGKPMHVVVATDMRPPNSAVRNMQPQHPPASSGDVVFHRESEALRGGT
ASGTAGRRVNDACSPPGQQSRTYKHSDAGQPALGLLTSEEGSESKLTQGTASHGQKKAVDTRTSQRPPRSQSAVGIDASL
FLRTAPAATQNRAKAVTQTANPMQLVSCTGKQAPPIAARKKQPSRKRVHVTENGSHHSLGVECSLQGQTDLAGCSTLILP
NANARRHMQCKGQRTLTVPCAQDEAGPDRLAGLHPSSTMTPTGSRQDLMRKPAKHPHNAPRQKDWHEKARASVAERHLCP
SGKEKAPSSAVQEPEERATSSERRVGNPIALKSHARAGKSHDPMLAEGAITLGKVSQGRYLAANGMQGTSIDAPRQQQKQ
QQQHRGQQQQQQRQHQQQQQQQQQHQRQQQQKQQQKKHQHQHQHQHQHQHQQQHQQQQQQQLQQQQRQMPAGLFGHVQGS
GSNHGVGEAAAEDTLGRNLDSGMPSQRGLRTSLGQGSRSIVLREGMVSIHHGSMWQKLDARRHLSRFGVQSNQNGESGAV
RAGVIINGVRVWGLPEGRRHEAEEASGCHTVQSMEFEQQRQMASAEQKVHPEKDQQECEERELGCSGHESVRLEEDVQAV
GEVQRTDDVLCIPVDHQMETQNEKDIEDVQKLRNTSEVDEGGDVLCIPVDNQMEMQNVEGIEDIQKWRSTSEVEEGGSKP
CIAAGEEVGNDPDGMSEDGFQSDEEEIDMEQEEISDSDDDDDDDDGDGDGDGDEDDDDGGETRMEIGNREGGGANDGRMQ
VSFPGTDSRGRVELPHDEVMESDVEFEKEEIEDSDDEMTESDPEVAGAERAEDGCDDAEVENIEFEEEEMLSEEDELDYV
PPCHGITESRNPNQVVVPPMGGSMEEVTCSKFENNQQVWQPEMRTPAKGRRVVCRNRARLDRKVGGICSLRTQKRCEIRV
```

```
ARGIGIKSAESLNAKRDAWETVNGEGLQSCRRKRPVKSGGGTGGAGWLRGRNIVGMYQLLWRGASGKELGGCEGRWNKIS
MAGKAAEQGTLLKSETKDNVDEEEEEEEEEEEEEEEEEEEEEEEEDDDNDDDGDDDDDDDEEEEEEEEEEEEEEEEEEEE
EEEDDDDNDDDDDGDDDDDDDDEEEEEEEEEEEEEEEEEEEEEKEETISQIFV
```

3302 - 3321:	EEEEEEEEEEEEEEEEEEEE
3303 - 3322:	EEEEEEEEEEEEEEEEEEEE
3304 - 3323:	EEEEEEEEEEEEEEEEEEEE
3305 - 3324:	EEEEEEEEEEEEEEEEEEEE
3306 - 3325:	EEEEEEEEEEEEEEEEEEEE
3341 - 3360:	EEEEEEEEEEEEEEEEEEEE
3342 - 3361:	EEEEEEEEEEEEEEEEEEEE
3343 - 3362:	EEEEEEEEEEEEEEEEEEEE
3344 - 3363:	EEEEEEEEEEEEEEEEEEEE
3383 - 3402:	EEEEEEEEEEEEEEEEEEEE

A0A388JNB8 **A0A388JNB8_CHABU** (1457 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MSFHFNSNERRLQEKIIRRNDDDDDGDDDDDDEEEEEEEEEEEEEEEEEEEEEEEETATATMTNDDDDNDDDDDDDDDEEE
EEEEEEEEEEEEEEGEKEREGEGEGEGEEEGEGEEEDAEKGEGEGEGEGEGGEEEEEEEEEEEEEEEEEGGGGGGGGG
GGGGGGEEEEDKLNQCHLPLNTPIIIIFPVIISYIILFIITNGRGLDQEEEEEEEEEASADDSDAIRQREYQNQTFDRNN
WMPKATFSLQGPQRRSNMISSKQPASVDIPFQNSGSSLSALSENGSEGVGMGSCFAMPGAHGQDAAIPQEELLTPSQPAP
LSNGKADQTSSRGDCPPLPALVDDSAPTATVWQRPAADVHQKRTVAAGLDLHSLSDGGDNRDMLDDGNRYPADSFPRFDV
LNRQLEALLADDQLEDGVKLLREIRASGGVPTSRNYSRIVAKLVHRRRDSFAIEIVSEIADAAALDEDAQGLLVMACLRS
RKVKQAVDLLHTMTRDGCRPRVAVWSAVVHQLSKFPATAAQALTLFHSMLSMLPNVHGKGKDEGVLSTPSSGGSVESDSV
DKHVVWTDKAADTVREPSAESSLCDMQDEDTRSEATHSGMEGKATKVDHVVARISTSAMPRTGNRMAPDVAAFNAALNAC
AMLGDPQQGEVLISKMVEELGLQPDVLSYNIMLKAYARVGDVISMHDLFEKMSKGTVNAQPDEVTYNTLVSAYVAAGNLE
RAEGIVEQMSNAARAAGAAVGVGVGAEVSSEKQEKEVVQKADASQASGRLGGQRVHQQRDLNRCKPTVQTYAILTKGYVK
AGRLGKAIHLLEMLEQSADKCVHPNEYIYTTVLDGCFCAGRVDVAYQIVQKMSQQSSTTFMTNRGERTIAPIYLSSSSSS
SSSSPSSSLPYSSSSSSKTAADGRSDASTSRLLLNNSANGNIRSKDGEDARSLKSSSSSSSSSSLPYSTFSKTAADGSSD
ASSSRLLLNKSVNGNIPSKDGEAARSVDSSSSSPSSSLRYSSSTLSKTAADGSSDASSSRLLLSESVNRNIRSKDGENAR
SANSDGRWILPDTVSYNAALKGLCHAGKMAIALAVYNDMQRARVSPCAVTFNTLIDGYVRCRNMDAAMAMLQEMEAVNLN
PTVATYTTLMKGAAHAGQVRMAAEIFCEMRADSTVHADRVAFNIMIDVYSRSGLMDEARGLFLEMKGELGMTPDIATYGS
LMKGYAKVGSAGEALVLWREIAARAAKDRAATLGGGGRPVDGTMSEESARRRRRGDGQEFPKWGSSSSSKDSLSVARTVN
MVDGSIGETLKSKFSGIRALDEGVENKKNTKVPTRKSRWGRRESGEEEEEEEEKRRLSRRMIMGMSNCQQERDLVPDKRL
LWPLLRVCIAAGYFQRAHQIVDEVGELGVPEHLVVQCQSYLRTQMKRAQQRRKGGRTPSIKQNPTPRSPSGPRGLEAVKF
WLGLPNSYYQSDWDWQK
```

33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE

A0A388JNC4 **A0A388JNC4_CHABU** (228 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MVDLRSGTSTTPYSQEQEERAAATLQERKERMEKWELIKQAKMLALLEEQEAKKKQMEEDLKKWTKEQEEKMAAIQEEVE
KEEEEEEEEEEEEEEEEEEEEEVEEEEPLERRRGETSTSKEEQVERMTQEWAAHLELGEDREAELAIPQAEREAARRELE
AERDPVRRRAKEEEQQRAWKWHLSQEKVRHLEAAEKAERDLKVAEARMGMIRAETELATKVESLTQSV
```

82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE

A0A388JNJ6 **A0A388JNJ6_CHABU** (1053 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MAVGERRINGGRRPRFKPFNRRAAAAAGGGGGGGKGGKGGGKGSKGAHHRRRMPTALQREVEEIRQLETKIEAGAPPPG
SNPLAIDLGPSTDRDGGRDVAVAKDLADQANKTQKESLIGQKRKAVSPRGGGGKEEREVGVGSGSCSKPYAGAKRFEDLP
ISEKTKKALREAKLVAMTAIQRAAVPHALCGRDVLGAAKTGSGKTLAFVIPLLEKLYRMRWSTMDGAGALVISPTRELAV
QIFDVLKTVGKYHLMSGGLLIGGKDVKAEKDRVNRLNIIICTPGRLLQHMDETPNFDCSNLQMLVLDEADRILDLGFAKT
LNAIIANLPKSRQTLLFSATQTKSVRDLARLSLRDPEYLSVHAESSAATPSKLRQSAIICPLHKKLDILWSFIKSHLRGK
ILVFLTSCKQVKFVYEAFRRLQPGVPLKCLHGKMKQMQRMIVFYEYCESKSAVLFATDIAARGLDFPAVDWVVQVDCPED
VAAYIHRVGRTARFTNTGRALMFLEPSEVAMLPLLKDAKIPVNVIKPNPTKLQPVTPALVSLLSKEQEIKYLAQRAFVTY
LRSIHLQGNKEVFDVAKLPVEEFAASLGLPNPPRIRFLRKGAGKTATDGGKEKNERKAGVGVAKEEEEEEEEKEEEGEED
EEEEEEEEEEEEEEEEEEEEEEERGGAMVDSGGKKITESGSEIESEEENDGPTAKRRRRLQESSNEEEEGKATSTSATKK
TKKTKMDKLFGKKNMNVLSEKYDKLRARNEDADDDEGGKTDSRRGGEEEEEGDELLRVKRKDHQLDGEEQEGRTTVPDGA
VVAAAGKPKKKKKKMKIDPSNTGGSNRLIFDDKGNALPPLAALGVRRGESSCEDDEESDGSDGDDDGGHGKATGTAAAAA
APTHLIKERFSRLREEMRERDKEDRCIERAKLREKRWKLKQKLKELEGSHGGRVAVLGRDGDESNDDDDDDGDDDDDDDD
DDDDGDSDGGHEKRGGRDDDSGSSGEEDTAGETDLEEEESSDGREAAFGKKAATSRRRTGVASLRGKTEQKDDIIESDSE
VSIDLNSDSEDSD
```

641 - 660:	EEEEEEEEEEEEEEEEEEEE
642 - 661:	EEEEEEEEEEEEEEEEEEEE

643 - 662:	EEEEEEEEEEEEEEEEEEEE
644 - 663:	EEEEEEEEEEEEEEEEEEEE

A0A388JP23 **A0A388JP23_CHABU** (3779 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MSDTGDTGEDDRRILRSARGPLTHVSLGPEGDRELFRRQRERRARAVEASKTLIGEAGATAAMATTAMSTSAQQTSQAGS
SGTAGSTVAQAVSQSSGLMASQPAVLTPEDVAIQQAALQEAQLQQALGQIKREKEMMIRRKTRLQRRVADIEELETMDLT
HMDEDVKVVRRALLGVIEMQEHQTTILQDIQQSLAVLAGHAQAAPSPAGPGAWPVPYPPFSVPPVTGVSPYVAPSTVAIV
SLGMPLSGGVTAGSSLQVPVQTVFTPSPPQVAVTTQPAVSQSVQPQGTQPQQLAQQPVSSGPQPGVVQGPGQNQWVPKTT
VAAPKPFTGDKKGEDLDTWLRAVSVYVRCKLTLPHEEVLVAASYLEGSAARWLSGLVQLQGYGHDFRSWAASQKLEDFLK
MVEERWHDPQEAQKATDAILTLHTRQFKSVRDATDAVEHLICVPWVRYDPQVLLTSYLRCLSQPLRNQLAKEANINMHNF
PSFSKVALDLEAKIGHGQTPTTEGRKKTLPPNWKAKGRIMFVDNDGSTIELDGNFQEGVGAEAGGETSEGGVVATVTQQK
GKGTGRRPRGSRSKSQTDPNAPPWEKAGLSEDVWRDRWARQACIKCGQYGHSMYKCRNRKVTEKIPPTMGPAVGSSTPVG
SNVASSSGSAPGNTYGLYEFVVMPFGLCNAPGTFQHAMNRIFHDYLDKFVIVYLDDILIFSKTVEEHVAHLDKVLGLLRQ
HKFKINGEKCEFGRTCVLYLGHEISAEGLKPDDAKVANIRDWPRPQSVTEMRSFLGMTGYYRTFVKNYNIVVAPLTDLTR
LDTPWEWTDKCEAAFIHLKHALTHYEVLELPDPDKPFIVTTGANQYGIGAVLGQQDGPKLRPVEYMSKKMPSHKLAKSTC
EKELYAVYKALTHWRHYLLGRIFILRTDHQTLRWMRTQSVLSDAIKRWIEVIEQYDFDPQYLKGEYNKVVDALSRRPDFS
GALITEFDLTDDVTQSLVEAYRQDQFMSEIIRRLEAKDKKTSAEFDLKKKKKKKKKKKKKKKKKKKKKEMKSEEEEEEEE
EEEEEEEEEEEEEEEEGRDGRGGEGGEEEGTGPWREEKRSSPPGTCPAAVEAAMAACQAQLLSQPQHQQATGLQPTQPPP
TSEGGTSPAQDQEMEPVSLTDGPHVAGPLPHLEENPGIHPALDLDMITVSQEEGSDEGTLHQALQETASEEEMPGGMAEA
ETIPSQGKPAQTNMIRDKAVRAQLKELTDWILQNSLSPTGAPICDLVTPLHWEKLRRRIMAKQQIKQAVNKYHNIDEIDW
GQVSKVTISTVSALFMELYSKTAGSRLSSQLVQASSSGIVGSTVAQTVSQSTGVMASQAAVLTPEDVAIQQAALQAQLQR
ALGERKAEKEKMIRRRARMQRRGADIEELETMDLTNTDDDVRVVRRALLGVIEMQEHQTTILQDIQQSLAILAGRSQAAP
SPPGLGAWPVAYPPFSVPPETGVSPYVAPSSVAIVSLGMPLSGGVLVGTSLQVPVQTVFTQTPSQVAVTTQPVVSQPVQP
QGTQPQQLAQQPVSPGPQPGVVQGPRQPQWVPKTTIAAPKPFTGDKRGEDLDTWLRQCSGKHVGPVGIVAVPARVEVVET
PSPSREMAQATDSSVVPQTHSDSSSLYSMNVFESLEELEVEWSRSDMLAFWTALVKALKGEMLVNEVVIGGRKAGAYYDT
CSTRNFISHACVERLRLQGRVQRLSRPVELTCANKQRMVVNDYLQDVECCFPYAGGELRHHVSFLVSDEFPMDMLLGMYY
LSVAQPQFDWDRKVVKHTLPGGGTARLHKFKASSLIESYGCMCAAAFYNYYKQNQEEGMYLVYASAAGEPVKMPPEIEGV
VAKYPDLFQEPTGVVEREVVHAIEIIPGSSIPKGRIYRMSLAELDEFRHQLKELVEKGWIRPTVSPYGSPVLFVPKKKEG
TLRMCIDYRGLNAITIKNREPLQRIDDLLDRVQGCRYFSKIDLKSGYHQIAIRPEDQHKTAFQTRYGLYEFVVMPFSLCN
APGTFQHAMNRIFHDYFDKFVIVYLDDILIFSTIVEEHVAHLDKVLSLLRQHKFKINGEKCEFGRTLVLYLGHEISVEGL
KPDDAKVANIRDWPRPQFVTEMRSFLGMTGYYRTFVKNYIIVAAPLTDLTRLDTPWEWTDECEAAFRHLKHALTHYEVLK
LPDPDKPFVVTTDASQYGIGVVLAQQEGPKLRPVEYMSKKMPSQKLAKLTYEKELYEVYKTLTHWRHYLLGRFFILRTDH
QTLRWMRTQPVLSDALKRWIEVIEQYDFDPQYIKGEYNKVADALSRRPDFSGNKRLCIPNSESLRSLFLGECHDATGHFG
CKKTAANLLQRFWWPTMMPDAQLYVETCEVCQTDKPRTQAPLGLLKPLPIPERPGESLSMDFMDTLITSKSGMRHIFVIV
DRFSKYARLVAMPETAKTEYVIRMFKENWVRDFGLPKSIVSDRDVRFTSELWKAAAAEQGTQLQMTFGNHLEANGQAEQL
NRVVQHLLRHYIKPNQVDWDEKLALIASLYNNVVHSAMGVGDKVWVKSSELGQEHGISRKLMPQYFGPWEVLDIVGTDPD
GPSYVIRIPGHLRTYPVFHASKQAPFKETDQFPSRRSMLPPTMDGEVDIDDIVDHRELPVSRPAGRGRPPKPKLKYRVRF
RHYTDPKEDRWFTGEELMQTAPQVARTITKYEETLKSLHACLDVLEKDDVPHRHTASSSIDPRIRELEERLDHLVALVGN
LNSFRHPTTISQQIAALQADLRQLQQQPTGTCNNVMPKRFKMPKFSIDKFDDYHKADPISWWQGFTNELSIHLVPLESKI
SALYLCSTGASQVWLNHLAQTEGVEVSKLHTKITWEAMTEKWWKRFIVDDAQGKGMNRIFSMHQGSQLTREWLTEWQKIV
TIPNLDIPFVHLRREFFQRSVDALSMALGERSLCTDFDQIVENAREVIQTNRWAANERRSQLTLWKRAKTRGRSKSLLSK
QELEYLGHFVTPQGISPLADKIKAIQDWPEPTNTTEVHSFMGLAGELEAIEDPLDRQALEDEKRLEWKLRLAREKKRRRE
EANRMGREVEKIQSCKQEVGAQQDIPTKLDKILSYLEILGQAWTEQYQANEGQEVTLHSIRTGFREVARVVVTHVGTEVK
RLKEGEEKFCAGAIEGAKVVATAEAETPPRKESVKPKFPDSYCGKKDDNFDNWEASINTYVYLQHIAPEEQVLLAFHALT
DEAASFVWSLAHAADCEHNMVAYSRLTPLSTFLKLLRERFTNVTRGVRASDKLKTIHSRQWKSARALKAVMDDLVAIPDR
GVTETQLVNLFYRAMPEPLQGHFFDKTQQANITYDALSREVVLFAAKSMPVSTFWHKDLDKGKKWKGRTISGWCKVFVKI
DLKSGYHQIEVDPADQRKTAFKTRDGLYEFTVMPFGLTNAPTTFRSLMDKGFRNQINRFVVVYLDDILIFSKSMEEHMRH
LEEVLQILKDAQLHLNWRNLIAREVEDEKWKTRDAIEEAKKKDVGESSGASAARSKKKDRKKNSSEMERSEERIKSWISS
EFGTSLRRINQKLDETEKMNKKIVELEGEVKGKGKVKESGSSEKRKRAVNSPAFSKVKSKSRSGGVRVRQPRIMISSDEE
DQKEKGLSNKVGGAKKDNDGKLEEILSLLGALVQKTNVKEEEGTNAGDEEGNTVKIEKSTQEKENEKSNEEKEDSEASDS
ATDVEEQGKARDGDVIEYMKDRLDHYMGLTYKEVCALCTKRDLKCARKDKGAWELAKQDMEQFTKLVNKVDDDDTDPSKP
SDDDDATQRSDDEDNVAGN
```

1033 - 1052:	EEEEEEEEEEEEEEEEEEEE
1034 - 1053:	EEEEEEEEEEEEEEEEEEEE
1035 - 1054:	EEEEEEEEEEEEEEEEEEEE
1036 - 1055:	EEEEEEEEEEEEEEEEEEEE
1037 - 1056:	EEEEEEEEEEEEEEEEEEEE

A0A388JPC7 **A0A388JPC7_CHABU** (540 aa)
Reverse transcriptase domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MVLFPRKTGSIHICIDYRKLNDITIKDVYPLPRIDDLLDAIGCANYFSKFDIRNGFHHILVKEEDRPKTTFVLFKGTWQW
VQCPMGICNALATFQRAMHMTFHNSVNKTQLTQGMVNFCVIVYMNDILVYSESFNRHAQYIEWTFGALRDAGFKIALEKS
EFFLSEISFLGYVVTRGGLRRDSRKVAAVRDAPTPTSLAQVRAFLGLASYYRRFIKGFAAIARPLTNLLRKDQPLRLKWT
RDSEHPAVNEDIELLIIQAWRTGVEGDLLGFVFGSVEAGHRQQIVGELLILLTQLLDDLPIDVVSHFDENPAPHILLRSL
MPYLQWLACLEGDWDSRSYPSYGNYLSPAEIIDLLFLDRGEPTLEEEEEDEEEEEEEEEEEEEEEEEEEEEEGDGSEDT
SEEGAYYSEHSEHSEHSEHESGATSEEEEEEEQASEEEETEQAGTKGEDPAEAERRRAEIVKGKQPLEQSVGTELPVLDD
PTRDPEPPTEEDERRAAETSSAPTQRQRSRSPSPSPRPSVRARANAGHRASSPVIIPLSP
```

371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE

A0A388JPI8 **A0A388JPI8_CHABU** (1242 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MSDRDDTREDDRILRSARRPIAHLALGPESDRYLFRQRRERLQQQSRVRAVEASRALVSEAGVSKAMATSAQQTTQASSS
GSVGSSVAQTQSQSAGVMASQPLVLTPEEVVVKRAAAREAQLQQALGEIKAEKERMIRRRARMQRREADVSELEGMNPAK
```

```
MDDDVRTIQSVLLSVLEMHDHQTDILQNIQQSLAVLVGQMQASPSPSGCISRADAGVTITVRARYGLYEFVVMPSDLRNA
PRTFQHAMNRIFYDYLDKFVIVYLDDILIFSKTVEEHVAHLDKVLSLLRQHKFKIDGEKCEFGRTRVLYLGHEISAEGLK
RDDAKVANIRDWPRPQSMTEMRSFLGMTGYYRNFMKNYLIVAAPLTVLTRLDTRWEWTERCEAAFRHLKHALTHYEVLKL
PDLDKPFIVTTDASQYGIGAVLAQQERKKLRPVEYMSKKMPSQKLAKSTYEKELYAVYKALTPWRHYLLGRFFMLRTDHQ
TLRWMRTLPVLSNALKRWIEVIDQYDFEPHYIKGEYNKVVDALSHRPDFSGALITEFNLAENVNQSLVEAYREDPFMSEI
IRRLEVKDKRDGRCAGRGTEPRAEVSRGGGEVAEAERKEREDMARGGGQRLRGDWRSQWREGGGQRRTESQRWPRGGGHA
PCFFVFLLKGGERDGGCADSGTEAERRWREAYGRWQRWRGDGRRSQRRWRRWTRDGGRRRTGGGGWEVAEAERRWXEQIT
GESGQEMAEGGRWRWAETERRWSKRSGRGEEEMTGGDGEESGRRPTGGWRHRAEAEGRWTEVPGVGLAEVGGGSGRRRWA
EADRRADRRWAEVGGGSGRRPRGAWRAQRDVQRDVGRRRTRGGQRARGDERSQWQKGGLARTAGCAAGWREGADARWGEG
KGRWEIPMAEGRGMADVRTAERRLRGDGGRRTGGGRGGEEMAGGVKGGGGGGQEMAGGGEREVAEAERRWWEQITGEGGR
EMVEGGRWRWAKTERRWSKLEMGKGPADQVYSGYGWLVFKEGVVRSEQAAGKTEPRRLASTRRRQEGGLGGGENERTCRR
PNIDNEDKGGAVLSRRGGANEEEEEEKEDKETDDAEVEGEEEEEEEEEEEEEEEEEEEEEEEEEDYEDEEGEEEGEDRG
GEDGQGGGEEEKMEKRKGEEEGEREKEKTGKEEEEGXXXXXXXXXXXXXXXXXXXXXXRRGRWTRRGRGRRRRRRGWKRG
RGRRRGEREKEKRRKEEEKVEEDDARTSEAYVETIVYDELHA
```

1080 - 1099:	EEEEEEEEEEEEEEEEEEE
1081 - 1100:	EEEEEEEEEEEEEEEEEEE
1082 - 1101:	EEEEEEEEEEEEEEEEEEE
1083 - 1102:	EEEEEEEEEEEEEEEEEEE
1084 - 1103:	EEEEEEEEEEEEEEEEEEE
1085 - 1104:	EEEEEEEEEEEEEEEEEEE
1086 - 1105:	EEEEEEEEEEEEEEEEEEE

A0A388JPL5 **A0A388JPL5_CHABU** (165 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MLKLWKDIFPAKRREQGRRRRSKKQEARSKQEEGGGGGGRRRRRRRRRRRRRRRRRRRRRRREEEEEGGGEEEEEEEEEEEEE
EEEEEEEEEDDDDDDEEEDEEDDNEDEDDDDDNDGDGDDDEEEEEEEEEEEEDEDEEAKDDEEDEEEEEEEEEEEEEEEEE
KEEEE
```

68 - 87:	EEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEE

A0A388JQ36 **A0A388JQ36_CHABU** (421 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MKTNFQEEEEEEEGGGGGEEGEGGKKGEEGEDEEDEEDEGEAGEEEEEEDEDEDDDEEEEDEDEAGEAGEEEEEEEEEEE
EEEEEDEDDEDCEDEEDDEEDDEEDDEEDDEEDEEEVGEKKEKEEDEEEEEEEDEEEEEEQGEEEEEEEEEEEEEEEEEE
EGRSRKKKKKKKKKRRRRRRRRRRRRRRRKKQEEAGRRRRRRRRMDGRMERGREGWRDGRSRDGDRLLTNVEEELEEEEE
EDGWMDGWRGGGMARWEDGRRLLNNIQEEEEEEEEEEEEEEEEEEEENGWKDGGKEGGXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXRRDGGRLLNNVQEEEGDGWMDGQGGSIARCEDGGMDGGRDGEMGGWRDGGR
LLNKVQEEEGDGWMDGGGEVW
```

268 - 287:	EEEEEEEEEEEEEEEEEEE

A0A388JQB3 **A0A388JQB3_CHABU** (4131 aa)
ULP_PROTEASE domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MAKDVFFRWNDHLCGSIEASDEAVRIYPRGRRLARSCALWSSVICAQIDDHFGVSGEKSREQEEEDGERVVGGRQWSRVG
GNDKVGENGVDEVEVLRGGFVGIERSHTEEEEEEEEEEEEEERRMKERRVQGKERREEREEREEEEEEEEEEEGREGGRG
RKKGREGGKGGRGGGGGGGGLRTTMMELTSSSDDEEREVDLARFVEEECDGDGRGGGAADERGAGGGGGGCGGGQGWIFR
DTLERRVRGHGIMYPEREDPWAVEVRGEDLSRLNPDQYLNDTIIDFYMRYIQRQEDISREDLDRCHFFNSFFFKKLSQSL
TAQKRSKRGGRGRRGGGGGAGGGGGGGGEGGGGAGGGGGNVGGGAAGAGCAGGAAGAGVGGNQKKREDDVYKMWKWTKGV
DLFAKDFVFVPIHDQLHWSLAIICWPGQMDLTFVLHLDSLKSSGHKTQTVKRALTYYLAKEWSRKLMMGMLAGDGGGGGG
GGGGEVGGSARPSAAGGSINTSARRRCDIKCKRLSVPQQENDSDCGLFLLHYLETFVRDLPKRFTIETAETAMGSGWFRP
EEASALRRRIRELILGLFSDANIPLPISPLSGPPPPAAPHPLSPPPSCSPTSCRDVNLVTTPEEGDEGGQNDEDGDVDGE
EDDSSDVVETVMAPQRRRLPAAPPPPPPPPPPPPAAAAAGITSPTAGTSSRAPTPGGGAGGVARSRSERRSLAHREFGGG
GAEMEVGERKVESLPAMPMPPCSGALIRPSRGAEGPATRGQEMPTTPMSANSNCFTALNANGGEVDGVLRGDRRRQRQQQ
QQQQHELLLIQEREVGREGKEEEGGCAVVQACTKGTPSSSRKRTRGKSRKSRPAAVRASCGGIMPAGEQGYSREEEVEEV
GEEEEEVRQEGKEEGVVSEVVHRHQEGMDGQEGRGGGGGGGVGGVGGGRGAGGLGKLRREGKGRAPRGGGKRRGEVWQQI
GTNKRPKKRARREQHQDQQHPHHQRRTCQQAQLTENGNLYLRKAAAAILDDEEEGRRRLKDLREIERMDEERRAAFEVES
EVSNEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEQGEEDEEEVELVEEVEEVKLVGERRRRQRRVLAKDKRVQIA
THDDGMGARREDSGRAMSDRLGMEGDRAAPVVKARRMEHHLQRHCDIDLVGDDAKSGRNSAEEEEVNLVVNDGDGGYGAK
GAGGGSLMAIRAPSSGSRRGAGRRAEERERKAKEKPSPLSRPAEEGVVTKIGSRSGRVVAMDCCWEIRGEEGGGEEEEEE
APGGRGKEKRELRGTCAAASGRGMLLRRPHLSFPVTVGGGGVLSEKEVIVVEGGGGRTHSSCATASGMRYVDLAIDGDVG
DVGDVSSRAMASRAHDGGSVGEREGDAVAVASVETWGGGESATRWLAGSGGYQAYPSRSRSTTTKRLDMAAAQERERGSA
MEVKSGGAAAKRRAMVDAREMTAGGMEDDHRSTLDKARVGKKRRLVSMGLDMAEGRRAEEGGIQEEEEEEESMAVGAQNPR
GKSLVLMTKEESSSRAADGHPPPCYGHSNETDEGVVGKEGNLIVRLKLTGHRKRGGGGEGGGRDRKHVQQQEEQEDLTTD
EGCMVAAAGRSGAGREGVGAITGSELGGEEVQLDQRDHPAGRAGHDTGVGLAWVARQCHSEGVGGGGGGGVGDESGVTPS
RKDAERWLANTSGRGGKGKGSCHEDLGRSDVAARGLSRQSARAKERERSSVVVDVAALATLGSADRTAAMDSRRAKGESV
MSEGGEGRRGGDKVVGRGGGTDGGNEDAEKDEQQQQPGEEAEPMKVRIFKSGGVWKLDRNRGKGNAGEMVGSEISGLGGG
KGGGGESNEREDKEGTAGDGGSMDLRSRDSLVGGNVLGSSAAVEGKWENDESEVVKTTTSSSQIVSVRLPQRLEEGSGET
SRRSSRSVVVDDDETPKRSEGGGEVMLLTPARKEASGLTHGGVRGKRKEGVESVVEEGGGGGGGGGLAGKESRERRGAQH
LFGGVDKKKKGIRREARGETSLPSSPIQGDVGFLTDLAGDEGRAEEDGVGMTLPVMPFSLCLEDDGADVARGEETGLSTR
VDLSLEEGREHRSVEEVPVGATEEAMVVGSPALFPTTYGRSEGRDLVVGPRYGEGVSAGEGQAQGVSAWMEVSWEEAFAD
RSDMEGHGREKGGEDEEGRRADEDDRRQRQKCAEVMDVADTDGLQLADLFSSDGYGCGDVGKKDLITSGVEKDDGVDKKR
EEKPQSTEGQLQDTKMEEPRGEGEEKEEGEEVRRGYGLVETDPTTTSGRHSPEDVEPEHKGLEERPKGVAAAASAAAEEE
EEEAEGEDAEEAEEGEGADDGETKKTRESDNGGTGVGMEPNESDVRDEEEGGNGLLACKAVEREEVMEKDGQSWDTAKVI
DLVSGTPRNEAFTGIAVGKIPRKDQANLGGVPKEEVEAGVIPGCSSAAIAVGILCPVAVEGTEEMPSRVFVDEKTISDGK
TAPGGKTRGHLAGKQLCERKGAETERSGGACGGDLLGRNAQESTSGGGLPRHDDDQHLREEEEAEGGESAREEGPNMADA
```

```
APLRLELQPDDGEPGRLSPDPLCSELDGGVVVPEAEDLQLRGSRQQLQEEKETVEGESALWEGGGNLSTYASLRLELQPE
EKSPASYGRLLMGVHNRDSEDRSENDSPLGGRCEPKTGEQADEERGGRESDKIHASSLPYGEALLSATYPRNVDPASAGG
DTDRGTERKGAVPDLSSVSGEVRKRPAGRQDDGEKQGSSSSSSLHTLQCLFENKVDGSTSPEGTPTQGAATGCLSVKDES
LCVQKADVLVVFPASLQKPKEEAGVATTSVVKNDSREMVAMAMVEDDTAAEEKEAGKQQSIVAIAKGEQEEGKLMAMKEE
GSMGGEQKMHGGGTAVTLSSEKLDKEKAEKDGSRVAFEEGVGIFCTNSQHDCGVSEEVTQTDTEKEGAILFVERQKDHDI
SETPTSGSQGVAKSVDEDRQPPQTQKEKEGGILSVGRQKDRDSSETRASRSGVAKSVNEDRREGDPCVTDAEARATVGIL
HRETAVGTEGLPLSPSPSREGDRSTLILHRETAVATESLPLSASPSCEVDVAGRRSTLRSGRGTGGEAGPQSPQQHGRGH
SVDPTKYLASTQIENVGSRDLGSENDRGRIVSASLPPPPPQGIDSLAVAIDMLSSDKRKTPCSSQLEGASGTLQDLSSRA
PWKVPQDDETTAGPKTLEAMSSSCIQREEAHTKVEEEGVISGSGQAGHNSSAICGSRGDAEMADEDASRPHAHANANAGN
PPVRANSVKSSAVLDGEWHVVCAAVSTSDRMAGVDRQVFQAKERQSELRMPGLNLEKREKKEEMETGRALRNGDARRELR
SKGRRVIDDDGAISNTEVRMRRSGGRGRGRGTKKVELQETWQQRSASVLDEQPGASRAEAKDDVGGVREPTALPLEIPNK
DGLGRGHGRGRGRLPKMSRQKVSGEQGLLGGTVIDAAVGGAPAVGNKPDAGLGELSAAPSRKEASRGGRRGRQKRQRLEK
ADEKGAMETEYTEEEVAGMKKADEKAAMETEYTKEGVAGTDTTSKNEDEVKETKQREGGEVVVVSTSKNAKQAGEAEKRE
DGKAVVRRSKVAEDASTGLGRVTRASRALYTEAKSRNEIGAEPSGTKGKSVLGAGGRARRRDAHKDSVGKEDDPASISAL
QGTPAEVKAEPVNRLEDAALKEVPAEQHYGSRGRGRGRGRGRGRGRKRPPPRPKEVPMVAGVVNTGVAGPAPQLGEPAKS
IGAGGKMGRGRGGRRGKNQGEVLQEEARMEDPSRALDTMMQDGQALTVNHQEQEAAAMETPADRSPTDPTVFDDAQREGA
QGMVGMPQVEPAKSSLVLAERGEASRGQEGLRIYERKQQRLRQQQQQQQQQLHKQSSQCPEKDDNSGEYEVCMTELGNMW
EEGGERKLLNMRDRRGAVRSSSRGNTHTWQTYLQTLFEAGSGTFGRVVQDSGGTSQGWRHLGEMKRDLGAVIVFRRRSKR
SRGETVAGSNRQSELERGGKTGRMKQPKRQRRSRAQEEAKGAVNRFSALAQSGTKPDIGSSLKQIDRLTHDYLKEKSLLL
PSVATSDLVTMDERELLTAEDMMEVSLLDWPEYNASRGAGTSEGDFSVLKR
```

1049 - 1068:	EEEEEEEEEEEEEEEEEEEE
1050 - 1069:	EEEEEEEEEEEEEEEEEEEE
1051 - 1070:	EEEEEEEEEEEEEEEEEEEE
1052 - 1071:	EEEEEEEEEEEEEEEEEEEE
1053 - 1072:	EEEEEEEEEEEEEEEEEEEE
1054 - 1073:	EEEEEEEEEEEEEEEEEEEE
1055 - 1074:	EEEEEEEEEEEEEEEEEEEE
1056 - 1075:	EEEEEEEEEEEEEEEEEEEE
1057 - 1076:	EEEEEEEEEEEEEEEEEEEE
1058 - 1077:	EEEEEEEEEEEEEEEEEEEE
1059 - 1078:	EEEEEEEEEEEEEEEEEEEE
1060 - 1079:	EEEEEEEEEEEEEEEEEEEE

A0A388JQE2 **A0A388JQE2_CHABU** (1353 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MGKDTVQRESVEVLGGRICDDSDRKMEMEIGHENDHSMEESTSAFLLRKERSWNSSCPRVEESHEVSTDCVTQQSGSGSA
AVTATMTMAMAFSSAGPFGIKWGLFLIANVAISLAALGVLAGAEFYPRNRRELIILGVSSGSIAGTLRSSPPSFSSPSSS
VSSSSSSSSPSSFSSSSLLLLPSPPSFSVSSSSSCFFEEEEEEEEEEEEEEEEEEEEEEEETEEEEEEEEEEEETRQLS
ESHLRTDATQRQTYKNDITTLTTGIRTEAIQQQQQHQLLNSTITRVNSIEANASAAPGCTTDVTKQLNERIXHVVTIIGD
ISSFNGPDSISSTVAAIKTDITKLRTRPEAATKTFKMPHFDISKFDDYNKSDALSWWQRFLTEASCRMVLADDMLKALYL
QLIGGAQGWMNHLAATHKCTIAELHTHITWKEFEQLWFTRFMVRNVVKAAMNEVYTCSQGNMPTRDWTTKWQKIVTRAGF
DLTFSNQRSEFFSRSCAGFRSALGNEYDYTTFQAILDRANLVIQTDDKAANERQSQPHYVAKQTYQRPTHNNAVFSEEID
DHHTAAASSSDGGIVAALPPKDPKRVRKNKATQGTAATGAGQQPWTAYKITKEVYDLRQKYAYCLWCNNMALSLLLFSTS
KSEVAAGGEDKVNGKASATMRSYWSCCWKAKSTGVCVKRAPSAPSDVEFSSRQSAKGNRSSKVVSMVSSGIRRCFWRYHR
ACVGSEVDAGPGGAYIALLCVNLTLATLSCTLAAACDFYTHWGLLAGSLPGPISALFSWGADISISNPGMAAVSKVAGLG
SMGAAAVGAAVGTMGSAAGVAIGNAAAQVTVAKAVVALFCAACLCIVVPLTHGLGGRLRNRHLPWAFWQPFVGGLKFVVI
QAVAWSLFAAALVAFGAAAYCAMFVTGTAIGQGLMAYAGFSGLASEILLAVSLVCFQPSSQQEAAKVAAAPTVPVLRKCI
SMPVLRQAEDAEMKTSLAATAGPVLSKCMSMLLWRQAEHAEMKRSGDQKAETKKEETDAFFDVGVAAADDCVEEVVYPQH
WSKETLCAALRGPWNMQSLPPQDYLTWALLRVKCWASLTLLYCPHYLFLGVVLLPFMLLPSVLSVPLLTLLAAVYLPTYL
GQPHRTDRRTWEASKGFFVGLLEEVSVHHFGGLRIVRDSTDPFPSNGKYMFAYHSELVYHCPREKKQVVLCSRKRGFIRE
AMEAGASLVPVFCFGEAFALRNFFEWRVAQALQRLTYRRLGFPVPFMPVGVAGLLPLPRPEQIAIVVGKPIPTAPQISEE
ATALSNSSNDDVAEHKVPDTGKKVYGCPAVRELTDADIETMRAKYFQALQELFEKHKAQYGYGDVQLILKDTP
```

198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE

A0A388JQL8 **A0A388JQL8_CHABU** (86 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MALPQKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEKEEEEEEEEGGGGEGGGGGGGGGGG
GPKQSY
```

7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE

11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE

A0A388JQY3 **A0A388JQY3_CHABU** (277 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MQQYYEELEEGQDLCATLEDRCYDADNIIMEGANNINPIAKDAININSKNNDNLTAVALIDAVNSNDNNNNDIGNNDNNN
NNNNSNNNNNNNNGEDGALREDDQDVRIQVANRDGNIADNNCNIDSDGGNRRVRQASPTIVAMFHGGRPLWEGMSLCMFM
CSWRCSCGRNSTAALPWDPGGRVAGWGRGLDLRSFDVYNNNNNINDNKNDTTHEVITLRQKHWSEIRREYEEEAEAEAAA
AAAAAAAEEEEEEEEEEEEEEEEEEEEEEEELSLIHI
```

248 - 267:	EEEEEEEEEEEEEEEEEEEE
249 - 268:	EEEEEEEEEEEEEEEEEEEE
250 - 269:	EEEEEEEEEEEEEEEEEEEE
251 - 270:	EEEEEEEEEEEEEEEEEEEE
252 - 271:	EEEEEEEEEEEEEEEEEEEE

A0A388JS08 **A0A388JS08_CHABU** (184 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MRRKKKKKKKKKKKKKKKKKKKTKKKKKKKKKKKTREEEEEEYEQEEEDDEEEDEEEEDEEEEMEEEEQKVEEEEEEEEE
EEEEEEEEEEAEEEEEEEEEEEEEEEEEEDDEEEEKVEEEEEEKKVEEEEEEKKVEEEEEEEEEEEEEEEEEEEDDEED
EEDEEEEEEEEEEDKEDEEYEEEE
```

136 - 155:	EEEEEEEEEEEEEEEEEEEE

A0A388JSH4 **A0A388JSH4_CHABU** (474 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MQVWMSYCWSARGATLVCSVVGKKGVQPSTLAMVEELRRRRRRNGGRGGGSEEEEEEKKKKKKKKKKKKKKKKKKKKKR
WKRRRRRTKRRRIRRGGGEEEEEEEEEEEEEEEEEEDEEEDEEDEEEEEEEEEEEEEEEEEEETVEEEEDEEEEEEDPKKT
KTKKKKKKKNKKKKKKKKKKKKKKRRRNGGGGGGRGGGGGEEEEEEEEEEEEEEEGEEEEEEEEEEEEEKEEEEEEEEEDEE
EEEETVEEEEEEDLKRRRRIRRGGGGGEEEEDDEEDDEEEEEEEEEEEEEEEEEEEEEEEEKEEEEEKEEEEEETVEKEEE
EEEEEEEEEDPKRRRRRRKEEEEEEEEEDDEEEEEEEEEEEEEEEEEEEEEETVEEEEEEEEEEEEEEEEDAKKKNTKTKT
NTKTKTKKKKKKKKKKKKKKKKKKKKEEEEEEEEEEEQKKKKKRRRRRRRRRRRRRRRRRRRRRRRRRSGGLRQ
```

278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE

352 - 371:	EEEEEEEEEEEEEEEEEEEE

A0A388JSK5 **A0A388JSK5_CHABU** (791 aa)
CCHC-type domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MLTRSQRKQHTGSRMSAVWRAVEDAEGGEVQDDEVELLIAQAWRTDTERELLEILFGKVEEGHLDTTTDELLVFLAPLVD
DLLLHILSRCDEKPGTDVLTRTLAPHLLRSTCTELDGITTFTRPRASISKSTSPISHCGTLLSGEETRKESVTKTKKKKK
RSQRRKSRALIGMILITLGQRKKKRRREREVDRENQVVVPGEAKRRKKLKLKGGGRKRRASGQSKAATTATVRWQILSSL
DYNVEDDVNNFPEVRAYNDQCRKLPAPGNGGGWNGGNGGNGGGNNWNGAGGNIGYGGGSNNGNGGSNGGNGGGGNGVNGG
GGNWGGRNGNGGGRNEGNGGNWNGGSQGNWNNSGNWNNRGSGGNGNGGNSGDWRKSARCYNCNQFGHIAQECNAPRQNQG
GGNWNNDSNGGGGGWNGGRNSNGASSSSSTGEATNMIGISRELEESLKAVSLFSQRHIEMEERRETEQREAVERNKQQEE
EKRVREEKNRIELEKKKAKEKKEADREWKLEILLAKQKATLREEFEKMFDKKLQKAVVSEKVVKGKAAMAKMSSNEEEED
PAEERLEKRKRQPPALACQASPPGESPSKVGRASTSEPPSTPRQDKSPCLRSCITMSREDDDMSLIVLTTMAVTAIATSS
ISSSRRPCPQPRTSISYNRSASTAEEERATTTIRTTTTSATRTKGVRTAIDVEEKKIRTHRHRGGGRGGRRGGSEGREEE
EEEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEEEEERSLRTLARGERK
```

727 - 746:	EEEEEEEEEEEEEEEEEEEE
728 - 747:	EEEEEEEEEEEEEEEEEEEE
729 - 748:	EEEEEEEEEEEEEEEEEEEE
730 - 749:	EEEEEEEEEEEEEEEEEEEE
731 - 750:	EEEEEEEEEEEEEEEEEEEE
732 - 751:	EEEEEEEEEEEEEEEEEEEE
733 - 752:	EEEEEEEEEEEEEEEEEEEE
734 - 753:	EEEEEEEEEEEEEEEEEEEE
735 - 754:	EEEEEEEEEEEEEEEEEEEE
736 - 755:	EEEEEEEEEEEEEEEEEEEE
737 - 756:	EEEEEEEEEEEEEEEEEEEE
738 - 757:	EEEEEEEEEEEEEEEEEEEE
739 - 758:	EEEEEEEEEEEEEEEEEEEE
740 - 759:	EEEEEEEEEEEEEEEEEEEE
741 - 760:	EEEEEEEEEEEEEEEEEEEE
742 - 761:	EEEEEEEEEEEEEEEEEEEE
743 - 762:	EEEEEEEEEEEEEEEEEEEE
744 - 763:	EEEEEEEEEEEEEEEEEEEE
745 - 764:	EEEEEEEEEEEEEEEEEEEE
746 - 765:	EEEEEEEEEEEEEEEEEEEE
747 - 766:	EEEEEEEEEEEEEEEEEEEE
748 - 767:	EEEEEEEEEEEEEEEEEEEE
749 - 768:	EEEEEEEEEEEEEEEEEEEE
750 - 769:	EEEEEEEEEEEEEEEEEEEE
751 - 770:	EEEEEEEEEEEEEEEEEEEE

A0A388JTA6 **A0A388JTA6_CHABU** (462 aa)
CG-1 domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MAPPHHESGSSSSRRRSAGSSQGRDSAIDVGKVLEEAKRRWLRPREVEYLIRNYRVHAFSLAMEPADRPESGTLYLFDKK
KCRYFRKDGHDWQKKKDGRTVKEAHEKLKVGSVDILHCYYAHCSENELFQRRSYWLLERKGQESFVVLVHYLEVTEESGR
PPRSLSESARRYCSAASASLSASSEEEEEEEEEEEEEEEEEEEEEEEDEEDEENVGEFESTCELLSLDALPLSPPPILWGE
KEDRDPDSHLVSPHDYLQPRHHDNYQEYAAYSYYQEPCSSAHDRTHHSPPSHSHSYGRFRSPRQQHDDPKTHHNHYDHHR
QQHHQPAPSPPLPPQQKERQSSSAYWQGPTSSNSGSTMLDKQSWQSSSVSGSLLDWTTSSTQRSMSQLSMTATSQTSTLP
NPAMVFSQAMLASAGGYGGSHRSTTIGGDFDDDDDDGDDDGDGDGDGGSDGKEGGGKEIHDY
```

185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE

A0A388JTI0 **A0A388JTI0_CHABU** (186 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MDSTDLYSIKIRRGGGGRRGGGGKGEGGGGRRGGRGGGGRRRGGQRRDKEEDEEGENEEEEEEGAYEEEEEEKEEEEEEE
KEEEEEEEEEEEEEEEEEEEEEEEEEEQEEDEEEEEDDKEEEEEKEEEDDDREEDGEEAKEEEAKEEENRREEEEDKVGS
GEGAGRQESERPIVSPQPPLTYRPTP
```

82 - 101:	EEEEEEEEEEEEEEEEEEEE

83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE

A0A388JTJ3 **A0A388JTJ3_CHABU** (1595 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MCIRDRREGEEEEEEEEEEEEEEEEEEEEWGSGQGKRRRRGTRRRGRIGKMTQWGQRSFGERMRNLWVAGSGEDESLDDLA
FISAQSTWSRSCLKHSSAEEVGWEERTGLQWAAGWDGGFRQWQMEAKPRREMGGKAEKISRDASVEPSPHDGSKNEAEDN
EEEELWGMTENWPPREDVKGALGYGGPLVKGGDWEREEREESEEREEREEREEREETEERGKKRKSMMHSFISIGSRDED
GQERQESGDSAVAVVSGTVSWRSEHTRIGKGMTVQRWALKGNEENGEKEDERGINVAAAAGGLDICRSAAAERKPVGGGS
GRSSCYCQSYSDSSQLLTEDRTTVSFPVDRSPSSCNTKHGWKAYLPVRSENDNVSHARCSEELISEKEKELTIIATSTSS
TCHSPHSRALTDIEPSSQEKHWTRWNYLAEGEYQSPRRVRTLANSYEEGVREQERGIDVGAGGGLRKCRATAKKDALFRR
TLNEKGILKSEGIPREMRRWDPPRAMEVRKRASLMVKRGGMGAVERIASMVAGFSAKGGGDMGDQAAMGRSKKLPDQQEA
VKIDRGCRAGGGGGGRGGGGGGGGGGMRREEGDEDEWGSQPYSMTMERSEKLPDQQEAVKVDKGCGGGGGQGVRRKEGEK
GEWSTQPYSTFQAETWNRTKRHYQVPSCAKLGAEVTHCEPPPRWMCATSRMPVASPSAYEDANMPICRTGGQVIKSKDQC
RMHNVQTSEQGVEDTDHVDGGMGSRFGKSGGCGRANVKGQMGKGAWWVPFGTGRKLEVQSKGKGANGVSNGVYSIEKKKA
GKRVPHGGVERTSVTNDRRKARVISSSESGRRELVGGWVGWVMLGKGNPVWVRKTGTIRSHNRLSPVVGAPATIDCEGLL
EGGFKLDPEATIRRDVGARAGRRPMEISTWVEAKGGCKWDVCWRSAADGLEAGNPMEERRRQHDEHHGRNDEGNGLCSPR
CELPKVPASWLDGQGGLALSPLQHNLKVQNNGDDVRLNIPLGESGQSANTGVDDSVLTQPADSSAHSNNEEVEIGSYRVK
GGEGTRCLERGEHNELNPGSSDVRWRQSEANKEPKEVLFGYQRYRCRNALIDRCFKCEDSEEVHRRNGRFQSNDLQLGGN
CAGTGLIAGHQGTAWCSVPRSNGPTGKVSSRGTEALQHSPGQLKLHPQLSRASMSVWSIADDVDLGCNAANQAEEPVQPQ
WLGSHSRVPRAVAMQRAERGCKSPKIKQSSSARHVRGKCEPTTGEGGGVQVAHIHQGRRDRLLAKIEGWEKEPGHEHLWM
KQRENAEKVLQQERQLFDGILLENGVGDETDRLSCSTRKVREMKNGTVNCFTSEGNTYKGEGDSVLKTEVLNQRSKHSSL
QIVQSNLEIMKSMLKELTGNTSLSIPNGLNKPLCQGGGAEEEEEEDVEQEQEQEEEEEHEEEESNDNEVEEDGDCLSAGE
GKEGNSMSEDCVHRVEVGAERRRSEIVTCSTAGPMKPRCLVGPMKPRCLVERKGEGNPLKEEQAELDSDGLSETKKWCWF
VDLPETMDRLEVEEVEALLEGTEEEEEEEEEEEEEEEEEEEEEKEEEEKGAEEEEEEKEEEEEEEEEEEEEEEKV
```

1543 - 1562:	EEEEEEEEEEEEEEEEEEEE
1544 - 1563:	EEEEEEEEEEEEEEEEEEEE

A0A388JTJ4 **A0A388JTJ4_CHABU** (1704 aa)
Reverse transcriptase. *Chara braunii (Braun's stonewort)*

```
MKWKKEKEEEEEKEEKRNESKKIGQSFIYHIMENTDVLRIMARPINEAKEFPHLPIRGGGCGDGGGGGGGGGCSNGGGGRG
GRGDGGERGAEIPTRTRTSPPRWRTRKRRRRRKKRRRRRRRRRLLGRRRRCRGGGRRNGGGGSGDWGGRGDAEGEADTME
EDEEEAAVIGEEEERPGKRPTQWRRRRRRRRGRGGGRRNGGGGGGGCGDWGGGGEAEEKADAMEEEEAEEADAMGEEEEE
EAAAIGEKDRGGGCGDRGRGGGRVRGGGGRRGDGAKGGGGRGGRGDGGRGGGGGGGGGGGGRDMDKEEEKEKVVMEEEEE
EEEEEEEEEEEEEEEEEEEEEATAMEEDETMEDEEEEKEEEEKVAAMEEDEATEEEEEEEEEEEEEEEEEEEEAEEGEED
EEDKEEEEEEEAAVMEDEEEKEEEEEEEEEGEEGEEEVEEVEEVEEEEVKEMRRRTKRSKRCKGKRKEKIRRRILKCEREK
MRKGRRRRGEEEKQAEKEEEEKEEEEEEEVANREVGGDGASGCGGRHQSSAKVTPNSNDIMDQRAGETDEAYQARMLAWC
TETKKRADDXAAAAKRKAXEAEQARLLADEQRRQQAEAAARAADEERHQXRXKIFTGEPAILNMAAAWRTEAEEGKLEDS
ANKIALLLSHLTDLLATCITQQEEIHGLDNSVADLQDRLQRLEQRPVAAADASSSNTADRLNALEMDVGSLKDGVQSQQT
ATQQLQQRLCATATTSSSEPRETTPKFDGQEIFCDATKTDPIPWFRKFELTLQLANLKEHKHHAYLYSRSGGACQAWLDN
LLSKYGVVAADLHTKISWDDLKAAWHKRFQVEPPEIKAMDKLMVFEQGSLPSADWIAEYQRLTFVPDIQMGFKAIRHYFI
SRSCPALSNALTHVEDTLTTTAELFDKAAQIIITNKEAKNLRSSASGPSRDQHRPRVVVVAAATPVDQSSEAASASEGDR
FAAAREGGRPGRGRDAGLPIERQGQTWKPSTAESDATTLSTPSELVSSRVTSLHSEAHAEVDSPPPLLSFEDYAAPLDPT
LGSQAQGQGLCVVSSPSGNSDNSSSSGDSRDSAREFNIEALDLLTSEDFAWLPLPTTGCLPGPQCAALSAHLHTYLSFYA
PPTSPTDDEVAVGDILAYITKVARKFRTQRYDNNNAPLMYVRTQVGQASCSALLDSGASRNFMSQSFMQRAGLGAQVRRK
ANPTAIKLADGKTQQLLDRYIEAVPVYFAPHACEPVTFDILDTDFDIILGMPWLASADRTVNFHRWTLSVRDAFGAEVAC
TIPHLPAAMTNEFRAMLDRFVLVYLDDILVYNRSLEDHLGHLRRVLETLRRAKYKANRDKCEFVRQELEYLGHFVTPEGI
SPLSDKIQVVQEWPEPRNVTDVRSFLGLTGYYQRFIKGYSKIAAHLNKLQCEDRPFDFGEEARGSFLALKAALLSAEVLR
IYDPLAPTRYLSKKVPLVHSIDDAHKKEFLAFVHTLKRWRHFLLGRSQFRWVTVNNPLVFYKTQDTINSTIARWMAFIGQ
FDFFPDHIPGKSNRFADALSRRPDHCTAVYSTFEIDDDLRNSFICGYQPDPEFRDKYANCSSPNPAPSHYRIQEGYLLVH
TRGKDLLCVPSDPHLCTRLLGEFHDAPATGHFEVNRTIGQLRQRFWWPGLLSNVTRYCESCEVCRRCKSHNHRLYDELRP
LPVPLRRREAIAMDITSPFPKHKT
```

316 - 335:	EEEEEEEEEEEEEEEEEEEE
317 - 336:	EEEEEEEEEEEEEEEEEEEE
318 - 337:	EEEEEEEEEEEEEEEEEEEE
319 - 338:	EEEEEEEEEEEEEEEEEEEE
320 - 339:	EEEEEEEEEEEEEEEEEEEE
321 - 340:	EEEEEEEEEEEEEEEEEEEE
322 - 341:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE

A0A388JTR6 **A0A388JTR6_CHABU** (663 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MSRGDDQKAGETTSTGAAGGDGSLRDRCIEEEEGRERVVGTDQRSCPPGHGSGEEGERVNGAQSMADEGILKDVGAKEVD
DVLGEETADLPVTQTRDGAEVEEEAAEVKRTVEGGLEPSATSGIAQEEIITPLFVVVDVQGNAEEGEEEEEEEEEEEEE
QVEAAGVGGAEAAGVGVEEGESGLLLIVQVQTHDETQEEEEEEEEEEEEEEEEEEEEEQAEMQKGEEKEEAFGGPSGE
RWGTTKDYDDVEANHWRGKSPRGGYDDWMLSSGVPRMRRSFLRRGGERWEREMVSCSSADPACSRLPDLPPSVIEVILSS
SSLGPADIAHVAACCKSLYRIASSDCIWSGFFRQRWGRVGGRKARNAIVQAWYSDKTVVPEISQSAMALFSIFERGLYSF
```

```
PAQVRNREQEDGWLLSAYDAIVKYDRKTDTFTATYVENVPAPTVETGITWHRIRPSLLDSDPFRVYGKDDLLSVQPGDHV
EVQWRLGSPMPYGWWYGIVGHLDRCPFATVSAEEESNGRSNGNAEESSDDVEGRRRSLEGGNSTAIGGGGRGGRGGEGGG
RGGEGGGRGGEERSGRCRGSRSDCVCCKADEVKLCFNQFTRVSQWRVGVVLRSKRGKKQPFPRWDTAHCFGYIGGVRRLD
EVEDKEEIKTWLSFMPGQLIGDE
```

198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE

A0A388JTT4 **A0A388JTT4_CHABU** (99 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MCIERTTRVKILTFYWKKKTGKKMEGGGEEEEEEEEEEEEEEEEEEEEEEEDEEEEEEDEEDDDDDDDDDDDEEEEEEEE
EEESGVQDEEEQEEEDKRT
```

29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE

A0A388JU84 **A0A388JU84_CHABU** (140 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MSLRIKAVVEKFIHELKEALEADLQDRAMRDREMRSYIEEREKEVAEREAAWKAELARREAEVVKQEQRLKIERENLEKE
KNLLMGTASKQDNQDGALEITVSGEQYRRQCKSEEEEEEEEEEEEEEEEEEEEEEEENYS
```

114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE

A0A388JV61 **A0A388JV61_CHABU** (1046 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MQKLKTPHQKKTQGPDHEESSSTDDISGFEEQECEEEMPSEREWKHLVDLFEHKTPEKFRMIPIAARTFHPEDGTLAPME
TQVSSSIFLGEPILQISYLADDLDPPHTLYEGTLSLRGRYQQAKQYLDISVSPPRSLLTTGATIALIKQDAEAPVDDVPD
LMQEMVDLTGLTVEGTSADSKTDAEAKETEMISPVESQMIATVFSVRTSNSIFSSVHNRRDRPADWIDMPLEIPNQPTVT
LPDHVPLEFRRSLISVLNGYAEVLSVCDNDIGLSNVIEHVIIMGDHPPISCVPYRYSPAQRAAAFQRIKEFEANGWIEPT
IGPWSFPVVIVPQKAGGIHICIDYRKLNDITIKDVYPLPRIDELLDAIGSAQFFSKFDVRHGFRHLLVREEDRPKTAFVL
FEGTWQWSRCLMDICNAPATFQRAMNMAFQNFVRKTRLTHSIINYCVIVYMDDILVYSSFYEGHVQHIEWTMHALRDAGF
KVALEKCQFFLTIISFLGHLVTDQGLRPKLQKVAAVRDAPVPTTITQVRAFLGLASYYRRFIKGFAAIAGPLTNLLKKDK
LLIWTPECDQAFSKLKATLISAPILIRPDPTKPFVLITDWQLEAISVILAQVEPDGLECVVEYASKSVPACKRNYAAPTG
ECYAALWGISHFRAFLYGRKFTLATDHEPLLALKKSKDYSGMIGRWATVLQSMDFDIRHRKHERHENADGLTRLHRPEKV
LKSEEVIPWNEPKEKNGPRYGQMTWTRTSEQTTCIEYLELLIIQAWRTDVEGDLLGFLFGSVRPGHSQPIVQELIVPIVQ
LADDLPLDIVSQSDDSPAPHVITRALTPYLQWIACLEEPGSDNTLPSRKEYLKSYGIIDRALYPREPEEVFQGEEEATEE
EGDVDEETSKEGSYKEYSEGEQSEEEELEEEEEEEEEEEEEEEEEEEEEEEGTGSEWEDLSEEAARTGTEAKDPEAAR
RREEIASGKNQLEIISGASLCINNDPTRDPEPPEPEDGGSATAAPGTSRRRRSRCPSPSTPTRPPVRPHTDAGNRSSSPV
VIPPSP
```

909 - 928:	EEEEEEEEEEEEEEEEEEEE
910 - 929:	EEEEEEEEEEEEEEEEEEEE
911 - 930:	EEEEEEEEEEEEEEEEEEEE
912 - 931:	EEEEEEEEEEEEEEEEEEEE
913 - 932:	EEEEEEEEEEEEEEEEEEEE
914 - 933:	EEEEEEEEEEEEEEEEEEEE

A0A388JVC7 **A0A388JVC7_CHABU** (331 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MSDATEILNLRSLCGAKLHRSIIKKAEEEEEAKEEEKKKKKKRRRRGERTEKKKKKKKKKKKKKLTPKMKKRKKSLWLLL
YLNVEGSRGGGGGHEEEEEEEEEEEEAEEEESDMKDEKTKGGGQEEEEEEEEEEEEEESDTKDEKTKTNCYGYGYGSTGS
EAEEEEEEKRTWREKDEEEEDEEKNKKKRRREKDDEDEDKEEDEKKKRRRKEEEEEEEKKKKKKKKRRRRRTRRGGGGG
GEEQEEEEEGKYDEGEDKEEAEKKKKKKKKKKKKKKKKKKKKKKKEEEEEEEEEEEEEEEEEEEEEKKKKRTRRRREDEE
AEEEEEEERVV
```

285 - 304:	EEEEEEEEEEEEEEEEEEEE

286 - 305:	EEEEEEEEEEEEEEEEEEEE

A0A388JW65 **A0A388JW65_CHABU** (352 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MVEETNGAVSAAVVAEEAAKLIPLDQLISVRYLGLGMIGAIQPANEKREVSECRPSPSEMESGGPAFITGEIDVLDIIRA
LDHRIPLPIGHLLSISEQANRRMLQHCKANRNVPLIKPVQWQRWSRTYATLSLCLVEIELKSTRDSEHNDVIEDVKLFTI
QAWRMEVEGDLLGFIFGTVEVAHWQSIVGELLILLTQLLDDLPIDIVSHYDESPAPHILSRSLTSYLHWSACLEGNWDNR
NYPSYGNYLNPAEIIDILFFDRGEPTSEDEEEEDEKEKDEEEEDESEDTPGKDKYYSEHSEHESGAISEEEEEEEEEEEE
EEEEEEEEAEGASEGEEVGQAETQREDHAEAE
```

309 - 328:	EEEEEEEEEEEEEEEEEEEE

A0A388JWF6 **A0A388JWF6_CHABU** (1269 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MPTLGKSNKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAAAAAAAAAAEEEEEEEEEEEEEENDMWKEFCAALLTLQGPME
MVVVAVLIGLEIGWTAMIAGMATIIVLIPIQLLLGRMFTKQRVQSVKETDARVKMTGEVLDGILAVKMFAWESTFKRKIQ
ATRKAEGKIIEKAAMIRGFNEATYFCNSSLAAMVTFLVSQASGRRLQTSTVLYVITLLHLPRLWMGSFFSQGIERLAEVL
VCFSRLEKFFQLAHDGIIHRTPEKRESIEHNSPSSVAINISAATRGGRGGGGGGGGGGGGGGERGANGQDQLNPRLALKI
RNGAFCWRIPEGQATHSRLVAVYHDGRHHSKQTIRTDGVHGLPPSYGDGEQAKDSHISLKNVTFEMAKGEILGVMGKVGA
GKSTLIAAIMGELHSVGGAVRSNCSKLAYAPQKPFILTGSVKSNIILWEPWDEEKYRRVVHACALKGDFASFPDGDATIL
GERGANLSGGQRARVGLARAVYRDADLYLLDDPLSAVDPAVGRHLFEQCILGYLKGKSVIIITHQLQYLPKCDRVLLLQD
GEMKDIGTFEELQKRVDIQGFMYLEEEADREQEVTAKLQNKEVDNEKKMVATNKNHGGTRRIKGDDGSSNKGIVVKEIGK
TGAVSWGVYWGYTKCFGRLAALASLALLCIGQAVSVLSDWYLAIWSMKKDQEGHSKFIYMGLVFGTCILSYSRAALFFHF
MLVASSNIHKFMLGAVLGSPLQFFHSNPIGRILNRFSADQGILDDMLPQTSYNAIQCVFMTLGTVVMIAIGVPWIAVVLL
PVILIFVRIQRFYATTSREVKRLEAISRSPVYAHFSETIQGLPTIRVFGIQRNFEDGFMEKLDQHTRSYFAWLICGRWFG
FQLDSICAGVVFIASMAAVASKGRLSPLLVGLGLTYSTQLSGLFQWTVRQCTEVENMFTSVERCLEYKDLRQEGREWLGL
SLQKPPAGWPRWGAIRFDKLTIRYRDGLAPVLKRLTFTIQGGEKCGIVGRTGAGKSTLMLALFRLVEAAEGRILFDEVDI
AELRLEDVRRKVSAIPQDPVLFGGSVRFNLDPFSEYNEQELWDALEAVQLKEKVMNLHGGLNASMAEFGGNFSVGERQMC
CLARAILQKSKILIMDEATANVDLETDALIQATLRARFKNSTVLIIAHRMDTIIDTDKIIVLHYGRLEELGSPEELLERE
DGMFTSMVRRTGSAGEAHLRQLAKQHALARRGHRPHAWSSSSKDILTSSSLKGVLSSHVTAPPTDRNDR
```

10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE

A0A388JX20 **A0A388JX20_CHABU** (198 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MSVQEEEEEEEEEEEEEEEEEEEEEEEEGGGGGGEGGEGGEGEGGGGEGGEGGGEEGGEEGGEGGEGGGEGGEGGGEEEEE
EEEEEEEEEEEEEEEEEEEEEEGGGGGGEGGGEGGEGGGEGGGEEKEKEKKEKKKKKEEEEEEEEKEEKEKEEEEEKEKEE
EEEERKEERKEESEEEREEEREEKEKEKEEEEEEEKEK
```

5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE

A0A388JX64 **A0A388JX64_CHABU** (1745 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MFNVCKISTNSSATIARRRRRRRRRRRRRGGGRQRKRRRRGRGREKEEEEEKEEEQEKEKEEEEEEEEEEEEKEEEEEEEE
EEEEEEEEEEEEEEQQQQQQQQQQDEDDEEEERTKTKTTRKNKEKKKKKKNKKKKKKTEKKKKTKKKTDEDKEEEEDEDE
NENENENENENENENANANENENEDEDEEDDDEDEDEDDEEDKDDDDDEEEDEDEEEEEDMTTTKKTKTKKTKTKTKTK
TKTKTKTKKKKKKKKKKKKTKKKTKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKRTTTTKTKTATKKTTTRTRTRTTKKTK
```

```
TTTTTKKIRRRRRRRRRRRRRRRHDDNEEDEDEEDEDEDEDEDEDEEEEEEEEEEEEDKEEDKEEEEEEEKEEEEEEEEEE
KEEEEEEEEEEEDNDNEDEDGDEEDEDDDKEDTMTKMKTTTTTKKIRRRRGRRRRRRRRRRQEEGEEEEEEEEEDEEKE
EEEEEEEETKKKRKKKKNKKKKKKKKKKKNKKKKTKTKKKTTKTKMTMKTKTTTTTTTKKKKKKKKKKKKKKKTTTKKK
KKKKKKKTTTTKKKKKKKKKKKKKKKKKKKKKTKRKTKKKKEEKKTTTTKKRTTKMTTKKTTKTTKTTKTKDKKAK
KNKAKKAKKAKKAKKKEAKKAKKKKEKKKKAKKKKAKKKKVKKKKKAKKKAAKKKKAKKKAKAKKKAKKKAKKKAKKTAS
EEECEGEEEGEGEGEEEDEEEEEEEEEETAKKAKKKTKAKKKKAKKKKAKKKTKAKKKKKKKKKKKKKKKKKKKTMMK
KTKTKTKTKTKTATTTTTTTTKTKTKTKNKKKRKKKKKTKTRKKXKRTTSNTTKTKTTKKTKNTTTTKKMTTTMKKKKK
KKDKAKKKKKKKKKKKKKKKKKKKKKKKKTMKTTTTTTTTTTRKKTTKKKATKKKMAKKKTAKQAKKAKKKKKKKKKK
KKKKKKKKKKKKKKKEREEEEGNDDDDEDDDEGGEGEEEEGEEGEEEEEEGEEEEGEEEEEEEEEEEEEEEEEEEGEQEEE
EEKEEEEEEEEEEEGEGEEKDEEEEEEEEEEEEEEEEEDNDDDNQDEEDEDQDQDEDDDDDDDEEEENEDEDEDEDDDDDD
DDEDDEDQDEDEDEEEEDEEEEEEEEEEEEDRDDDDEEEEEEEEEEEENRDDDDEEDDEVEEEEEEEEEEEEEKKTTKTTTMK
TATKKTTTKKTTKKKTAKKKTTKKANTAKKAKKAKAKKVRGRSEGEGEEEEEGEEEGEEEGEEQGGEEEEEEEEEEEEEEE
EEKEEEEEEEEEEEDEEDDDEEEEDEDEEHEDDEEEEEEEEEEEEEEEEEAEEQQVEEEEDEKEEDDDDNDEEEEEKGRRRR
RRRRRRKRRRRRRESEEEEEEEEEEEEEEEEDEDEDEDEDEDEHDDDDHDDDDDDEEEEEEDEDEDEDEEEEEEEEEEEEE
EEEKEKDEDENDEHEEEEEEEEEEEEEDEDEDDEHEEEEEEVEVEEEEEEEDEDEDDNDDEEEEQEHEEEHEDDEHEAEEE
EEEEEEEEEEEEEKDGDEDDDDEDDDDDDEEDEKDDDDDDDDEEEEEEEEEEEEEEKRGRRRRRRRRRRRRRKGENEEE
EEGEEGEKKKKKKKRTETKTTTTTTTTTTTKKTKKTTTTTKKKNKKTKKKTKTKTNTKTTNTKPKKKKKKKKKKKKKKK
KKKKKKRTETKTTTTKTTTTATKKTKKTTTTTTKKKKKKKKKKKKKKKKKKEEEEEEEEEEEEEEE
```

73 - 92:	EEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEE

A0A388JYH2 **A0A388JYH2_CHABU** (680 aa)
Integrase catalytic domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MVVPHPLMWYDRVKTAHEETAAHFAVRITESAIDKNEWYWSNIRDDVKYIIANCQVCAADKAPIQPPRSIVPTVVERSFQ
RVSMDTTDIMVPPGPNSCEYSVLLVFVDHFSKWIEAYPFRTRQATKIARYVNRFLLGMHQDTEEILTDNGAEFRGKVLRS
LVLHGVAIRNTAPHMSQSNGLVENANRVIKTALQRNIAARDPRPWPDIVDHFLAVHRGTPHESTRLSPFQLRTNSVACVS
IPSLPDETTLNRRPTTATAQDKAKRHLELMERSLPRLARKRQKMTELAQGRQVRSYEARNGNVGPWPQYKLEDVVQVRKC
ARQEFVELSFCLLQVDLNWTWEGDQRFALEIVELLVIQAWRTNVAGDLLGFIFGAVDRGNRLQIVRELTIVIARLADELP
LDIVSQSDEEPVPHTLSRTLAPSLQWSACIEERWADDRFPSRSEYLDVHNLTNPRFFRQPTAFEWAALRAEEEDEEESEG
ELRREAGEAAVRLAEDEEEEREAGEESAEEEEEEEEEEEEEEEEEEEEEEEEEEEDAEEETSEEEKEAYSEYSEGEQSEEE
EDDEEVESEDNQEPTHDELEWVPGPDRREENPEAAAQRKKEIAEGKRLAIDPALNNPFKNPEPPKPEHGDLAATTSGAAT
TRRRSRSRSRSPSASVRPPIRQRVNEGLNPSSPIHIPPSP
```

509 - 528:	EEEEEEEEEEEEEEEEEEE
510 - 529:	EEEEEEEEEEEEEEEEEEE
511 - 530:	EEEEEEEEEEEEEEEEEEE
512 - 531:	EEEEEEEEEEEEEEEEEEE
513 - 532:	EEEEEEEEEEEEEEEEEEE
514 - 533:	EEEEEEEEEEEEEEEEEEE
515 - 534:	EEEEEEEEEEEEEEEEEEE

A0A388JYM4 **A0A388JYM4_CHABU** (424 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MPTHIGFIMDGNRRFAKRSNLDRHVGHVMGFDRLMETLKSCLSLGVQYISAYAFAIDNFSRSPEEVSALMTLMKEKLESL
MEHQSAIKEGGVRINVLGDLSLLPEDVRQAAERVMTATAHNTRLVFNVLIAYSGKAEIVSAVQSLCSEVLEEEEQEKKKQ
EEQEEEEEEEEEGEDCCNDTCNGTHELQGNGHYANDLCESPPPRLRQKVTEVGEGRIKRGVQSTAVECNGHQGVRRKLSCS
DNCAVQCAVGEVNGLSASALSTCGVEGEEEEEEEGEEEGEEEEEEEEEEEEEEEEEEEEGEEEGEEEEEERGGRCLGKVP
WAETGRCSSSRVEGLTEDAFDQWMYTSGCPYPDLIIRTSGEIRLSNFLSWQSCDAHLIFCKVLWPAFSWYHLLWAILQFQ
LAYPQLIKQRDLRLASRNGACSSP
```

280 - 299:	EEEEEEEEEEEEEEEEEEE

A0A388JZN5 **A0A388JZN5_CHABU** (949 aa)
Reverse transcriptase domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MSPGELDELRRQLKELVEKGWIRPSVSPYGSPVLFVLKKRGALRMCIDYRGLNAINVKNREPLSCIDDLLDRVQRCRYFS
KIDLKRGYHQIAIRPEDQHKTTFQTRYGLYKFVMMPFGLCNAPGTFQHAMNRIFHAYLDKFVVVYLDDIVIFSRIVEEHV
AHLDKVPSLLQQHKFKINGEKCEFGRTRILHLGHEISAQGLKPNDAKVASIRDWLRPQSVTEMRSFLGTTGYYRNFVKNY
SILAAPLTDLTRLDTPWDWTDRKMPFQKLAKSTYEKELYAIYKVLTQWRHYLLGRFFYVRIDHQTLKWMRTQPVLSDVLK
RWIEVIEQYDFEPQYIKGEYNKVADALSRRPDFSGALITESGLADDVTRSMVEAYREDPFMSEIIRRLEAKDKATSAEFE
LVNGSLFLEKAKNKRLCVPNRESLRSLFLGECHDATRHFGYKKTTANLLQRFWWPTRPTMMKDAKLYVETCQVCQRDKPR
TQAPLGLLKALPIPERPGESLSMDFMDTLVTSKSGMRYVYVNVDRFSNCRTGNTAADDTREPSRGEWANRAAEPRSAAAE
AAAEAEPQAAAEAEAEAEAAAEAEAAKAAAAAAEAAEAAAEAAAEEEEAAEEEEAAEAEEEAEEAEEEAEAEEEA
EEEAAEEAAEDVAAAEAEAEAAEAAATSAEAAAQAAEAAATSAEAAAQAAEAAAEAEEAEAEAEAEAEAEEEEAEAKEA
EAEAEEEEEEEEEEEEEEEAEEEEAEEEAGAAGAAEEEEAEAEEEEEEEEEEEEEEAEAEEAAEEEEAEEAAEEEEAEAA
AAAEAAAAAEAAEEAAAAEAAEEEAEEAAEAAEEAEEAEAAAAEEEEEEEEEGGGGGGGGGGGGGEGGGGGGGGEEEEEE
EEEEEEEEEEEEEEEAGVVGGGGAAATTGEGAGEEDAGGGDADDNDEGGRGRRQDEGGEEEEEEEEVGA
```

875 - 894:	EEEEEEEEEEEEEEEEEEE
876 - 895:	EEEEEEEEEEEEEEEEEEE

A0A388K005 **A0A388K005_CHABU** (1119 aa)

BZIP domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MSRGAFDGKEDASWGTVRRSSGETTPLFQGLDQGGPSGSTARPPRSSQIPFHPTVSPRRGGGRGRGRGGRGEKEEEEEEE
EEEEEEDEDEEEEEEEEEEEEEEEEEEEKEKEEEDKDNDEDDEDEDNDDDDDDEEEEEEEEEEEEEEDEEEEEEEQEEEE
EDDDDEEEEEEDGEEEKEEKEEEEGEEEGEEEDRAEEEEEGEEEEEDVRRRRRRRRRRRRRRRRRRRRRKEEEEEEEEEE
EEEEEEEEEEAEEEEEEEEAEEEEEEEEEEEEEEEEEEEEEEEEEDEENDNDKDDEDDNDDDVDGEEEEEEEEEQEEEEE
QEEEEEEDNDENDDDDDDEDRDEDEDEDEDEDEDEEEEEEEEEKDKDDDDDEDAARTTTTTKKRKKKKKEKKKKKKKKKK
KKKKMKKKKKKKKKAKKKKTKKQKKRGRRARGRGRGRRGRGRREEEEEEEEEEEEEEEEEEEEGEEEEGEEEEGEEEEEE
EEEEDEEEQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEEEEEEEEEEEEEEEEEEEKEEEEEEEEEEEEEEEEEEE
EEEEEEEEDEDDEDDEDDEDDEDDEDDEDDEDDDDEGDEEEEEEEEDGAEEQEEGEEEEEEEAEEEDEEEEEEEEEEEE
EEEEDEDDDNDKDDEDDNDDDDDGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDNDENDDDDNDDDEDDDDNEEDGDDKDK
DEEDDKDDNDDKDEDEDEDEDEDEDEYEYEYEYEYEDEDEDEDEEEKEEEEEEEDNEKEEEEKKKKKKKKKKKKKKKKKK
KKKKKKKKRKERKRERKREEMKRKERKRMRKRKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKXKKKKKKKKKKKKKKKKK
KKKKKKKKKKKKRKKKKKKNNNNNNKKKMEEEEEEEEEEEEEEEEEEEEKEQEEEEEQEEEEKEEEEEEEEEEEDEEEK
EEEEEEEEEEEEEEEEEDEEEKEKEEEEEEEEEEEEEEEEEEDEDDDSDEHDEDEDSDDNEEEEEEEEEEEEEEEDDEEE
EKEEEEEEEEEEEDDDDDDDEDEDDDDENVEEDEEEEEEEEEEEEEEEEEEGEEDDEEEEEEEEEEEEEEEEEEEEDEE
```

231 - 250:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE
262 - 281:	EEEEEEEEEEEEEEEEEEEE
263 - 282:	EEEEEEEEEEEEEEEEEEEE
264 - 283:	EEEEEEEEEEEEEEEEEEEE
265 - 284:	EEEEEEEEEEEEEEEEEEEE
266 - 285:	EEEEEEEEEEEEEEEEEEEE
490 - 509:	EEEEEEEEEEEEEEEEEEEE
491 - 510:	EEEEEEEEEEEEEEEEEEEE
492 - 511:	EEEEEEEEEEEEEEEEEEEE
493 - 512:	EEEEEEEEEEEEEEEEEEEE
494 - 513:	EEEEEEEEEEEEEEEEEEEE
495 - 514:	EEEEEEEEEEEEEEEEEEEE
496 - 515:	EEEEEEEEEEEEEEEEEEEE
497 - 516:	EEEEEEEEEEEEEEEEEEEE
498 - 517:	EEEEEEEEEEEEEEEEEEEE
499 - 518:	EEEEEEEEEEEEEEEEEEEE
500 - 519:	EEEEEEEEEEEEEEEEEEEE
501 - 520:	EEEEEEEEEEEEEEEEEEEE
541 - 560:	EEEEEEEEEEEEEEEEEEEE
542 - 561:	EEEEEEEEEEEEEEEEEEEE
543 - 562:	EEEEEEEEEEEEEEEEEEEE
544 - 563:	EEEEEEEEEEEEEEEEEEEE
545 - 564:	EEEEEEEEEEEEEEEEEEEE
546 - 565:	EEEEEEEEEEEEEEEEEEEE
547 - 566:	EEEEEEEEEEEEEEEEEEEE
548 - 567:	EEEEEEEEEEEEEEEEEEEE
549 - 568:	EEEEEEEEEEEEEEEEEEEE
665 - 684:	EEEEEEEEEEEEEEEEEEEE
666 - 685:	EEEEEEEEEEEEEEEEEEEE
667 - 686:	EEEEEEEEEEEEEEEEEEEE
668 - 687:	EEEEEEEEEEEEEEEEEEEE
669 - 688:	EEEEEEEEEEEEEEEEEEEE
670 - 689:	EEEEEEEEEEEEEEEEEEEE
671 - 690:	EEEEEEEEEEEEEEEEEEEE
672 - 691:	EEEEEEEEEEEEEEEEEEEE
673 - 692:	EEEEEEEEEEEEEEEEEEEE
910 - 929:	EEEEEEEEEEEEEEEEEEEE
1097 - 1116:	EEEEEEEEEEEEEEEEEEEE

A0A388K0D7 **A0A388K0D7_CHABU** (167 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MRQPSPIPFRNAVIITFAGGGGTGGGEGKTERRRREEDQEAEEEEEEEEEEEEEEEEEEEEEQEEKVEENEEEEEEEEEE
EEEEEEEEEEQEEEEEEKQEEQVEENEEEEEEEEEEEEEEEEEEKEEEKEEEEDEGKEGEEGEEKAEGEERRGNLNQKKTQ
```

CFHCSAA

42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE

A0A388K0G6 **A0A388K0G6_CHABU** (163 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

MGVGDDEEGEEEEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDMDGGDRKKKKRRRRRRR
RRRRKKKKKKKKKKKKKKKXEEEEEEEEEEEEEEEEEEEEEEEEEEEEVDEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEE

21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE

141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE

A0A388K117 **A0A388K117_CHABU** (950 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MARKARIDDEHEKHVSTMTRKARIDDEHENHVSTMARKTRIDDEHENHVSTMSTEHDEHRPPKARIENEHWVQCPMRICN
APSTFQRAMNMTFQNFINKTRLTQGMINFCVIVYMDDILVYSETYHGHAQHIEWTLSALRDAGFKIALEKSEFFLSEISF
LGYVVTRGGLRPDSRKVAVVKEAPVPTSLTQVRAFLGLASYYRRFIKGLAAIARPLTNLLRKDQPLSWDAECQQTFATLK
DALATTPILIRPDPSKQFILITDWQPEAISAILAQKGNDGREHVIEYASRTVPDERRNDSAPQGECYAVVWGIQHFHPYL
YGSKFRLVTDHEPLLALKKLTNYTGMIGRWAVRLQEYDFDIIHRKTERHDNADGLTRLHQPVKWAALRPEEEAEEESEGE
LRREAGEAATRLAEDEEEKREVEEESAEAEEEEEEEEEEEEEEEEEEEEEEEEEDLEEETSEEEEEAYSEHSEGEQSEEEE
EDKEDDEGVESEHNQEPTHDELERGGGPIGGKGGEKGEGDKASEGGGKKGPSPTKDGAHPEEVRVKEKEKEGSSKWVVKK
GKARDWEETSKGPGGKGDSTGSRKENDDVTEKGEELRENRPERREKGKEQTVSNTRDGSGLPGLKDVDRMEGDIILFREK
CKRDEGDCPTEEVVLSSPKDSDPGNALVLYDATKARKAAGRLSPRSSGEDSEDDEDGFLEPLFGAKDGRGNSPIKTYDNE
SFDWTLTGNISIEELTTPITACRPLPVPAREFHSSNSKEFFEATEENTDERRTGGKKGHLKSLARSKSPMNDPRKGIASP
AKKSKKVLFQAKTGAQSSGKNDALVDQGSEGKEKKVTRRKLTSSLSSAPPMKTLSKAEKKKGVKAALAVPLICTLSPHGI
MVLTNKLPDETLAFPCFPSAGPPGDVQQTGWAAESVLKGYASCSILSKPKMGDMYTQPQMGMYILFIFPF
```

430 - 449:	EEEEEEEEEEEEEEEEEEEE
431 - 450:	EEEEEEEEEEEEEEEEEEEE
432 - 451:	EEEEEEEEEEEEEEEEEEEE
433 - 452:	EEEEEEEEEEEEEEEEEEEE
434 - 453:	EEEEEEEEEEEEEEEEEEEE

A0A388K155 **A0A388K155_CHABU** (800 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MSAFRELAAGPAAARSSFKCPIFPSHVYTPSPHSSSHASSSSSSSSGPMKILVMFSERSSTVRSSFRSADIFSSSSSSPS
PTQLRRAVPSLKKQPPFLRSVSQTSTVRSSEGTCPAEKWHAFLVGSNLMGTTRRWGGSTRVPCAPSSSSSSSSSSSRHPC
LSSDFLGCRLLSTSPRHTARHQAGEAGDDGEDGLQKKREVIRRGPGGKWRGRGGSTLLDGHVPTEEDLAMSNVTAAFGNN
KKVKRVKDVYLDRIIEAEKKTRALGRAWEFLSKEPGYRISLKKLGKVRRRAGFADRKLKSFFLQYPDIFVVTQERDGLYV
QFTPEAAAEVQKYRVALAALEPRAVENLRKLLLLTDKKFLLIERLSHVRRELLLPDNFEIDFVHRHPDAFRYVDTWGGPA
VILAEAADEPEKYIAEPTAAAAALPRANSLEAEIRRVQMVRQLLLLTRGKRLLIDQITHFRKDLRLSQSVKGLLLRHQDV
FYVSHKGVRNTVFLREKYGIPSGPGRRGNSAWLIEVDPVEAVMLGLDPDATIQQADRVRSIRTAGSGLLWKPTDVFTAWN
DDDDDDDSEEEEEEEEEEEEEEEEEEEEEDVVDDGIKKAEKVEEEEEEEEDREFIRGRIGGDGSMADLWDGFDEEDGGRGR
NGGGWSKKGRDAAVNSTAAARAKAARGRADRMAISNSHVASSSSSSSSAYTSSSFAASSSFSTSSSSSPDPTSFEDTRGS
PEDLAASDHDRDDEKGGLPEDFDAIGRAVQPATCNEEGGHHTGQSDPAGESESPSVNDIAGKDSSTIFRTELNLANATRL
```

569 - 588:	EEEEEEEEEEEEEEEEEEEE

A0A388K1R8 **A0A388K1R8_CHABU** (1480 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MTYDALSREVVAFEAKSVSVSTFWHKDLDKGKRWKGRTISGQVKTKDSLILTLDEGSVDEIPYDQIEWGLEDVDSGASQG
RTYATVAAGGRPQGGGRGQGQGGRASGNRSQGDQGVGDRGGNRQAGGRGQGEVREDGGEGEGDEGDGDGEEGKEDKENES
EEEEGGDEEGREEKEEGGSEEEEEEEEGGEEEGEEEEEEEDEEEEEEEEEEEEEEVEDGGEEVFEPLRPTRVLGPGHLVHL
DLAVMPVSTDGYKYILDARDNLIGFVEAVALKKKTGRSVADWIEDFYLRHPFVRRFIADNGTKFVNQEVLGMLKRLCVPI
KLIEPYHPEANAPVEKGHRTLKNTIAKLAADHLGNWPRYLKQAVFAKNMTPKRTTGCIPAELWYGREIDFPVEALVPTWN
RLDDDPQMTTEELIEARCQQILKNEEVMEDIANRVLDSSMRDKTRWDQTEDEEDAEEDVREVIEISSGDERDEISRHREE
GRPPMHQSGDGAFRWEDEFGPTPSHWFQQWTNVIRHEWIMKTRELARAGVEATPLDFFNEAGLRKIVRMKREIETYGLGL
ESLSRNRVDKELGKTRHKAAIGTRCEVREDGGEGEGDEGDGDGEEGEEDKENESEEEEGGDEEGREEKEEGGSEEEEEEE
EGGEEEGEEEEEEEEEEEEEEEEEEEEEEEEDGGEESVDAKVAGKHREDAKVGDEDRLREDGAAAIPNIAMHRCDDAAIAL
DLPKTDSAEVMAGTQIGSDDHISAIDENSNANDGDDDVVAALPDNSKGPQSPDSARGDGDRDSIRESPTRAVTLLHQGSI
ALTHEEMEVLLTDYLRCLPAEVRTKLVDEAYVEQHSFATFSKKALEIEAKLGSAHQASHDGRKRLPHDWKKKGQLMFVDH
DGQTTEIDDFLDLGEVTEQDGATETSDGGVVAPIKEKARGTGKKTVVRSTGQGAQGTPEWVKLGLEYEVWRDRVARGTCM
NCGNYGHTSRTCRGKKVLTRVASPTVVGLSSNPRGVVEREVVHAIEVVSGSKVPRGRIYRMSLAELDELRRQLNELTEKG
WIRLSTSPYGAPVLFVPKKGGTLRMCIDYRGLNAITVKNAEPLPRIDDLLDRVQGCRYFTKIDLKSGYHQIAIRLEDQHK
NAFQTRYGLYEFVVMPFGLCNAPGTFQHAINRIFHDYLDKFIVEYLDDIFIFSRTVEEHSEHLKTVLGLLRQHQYKVNLE
KCEFGRTKILYLGHEISADGLRPNDAKVASIRDWPIPQTVTEVRSFLGMTDYYRLFVKNYSTIASPLTDLTRLDTPWEWT
EECEAAFRKLKYALTHYEVLKLPDPDKPFVVTTDASQYGIGEVLAQKEGPKLRPIEYMSKKMPSRKLAKSTYEHAAAGVE
HIRKSQDALIAFENKHRWPSNFQLRDRVWVKSSELGQEMGISRKLMPQYFGPWEILDIVGDQPDGPSYVIRIPAHLRTYP
VFHASKLAPFVATEQFPSRRSMLPPTMDGEVDIDQIVDIE
```

648 - 667:	EEEEEEEEEEEEEEEEEEEE
649 - 668:	EEEEEEEEEEEEEEEEEEEE
650 - 669:	EEEEEEEEEEEEEEEEEEEE
651 - 670:	EEEEEEEEEEEEEEEEEEEE

A0A388K274 **A0A388K274_CHABU** (837 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MVGELSLRSYEEPEDVGGAISLAGWVKNMADDMLDIIWELEEGPDPQLESCIDWTRAHGMMSSCYTLFTEGRNLRYKLEE
RLIGNGDKEDENWQENGAQEDKANSDVNTDNNNNNNINNNNDYNNNSDNDNNNGLSNKNNDNNNISNDNDFNNNNDNNNG
```

```
HSDNNNGHSDNDVSINNNNNVNNYINNDKDYNGSDDHGNSDAVGIGADNNNNDDGDDNNNNCDDGSNGDGGGSDDGDRDV
RIGDDNSDGDDNNNNRDRDENNNNYKDGGNDDGGGSGYDSGNNDHGSSRAESINTTGKKPHADVVGSGVDTDKRVICGVM
CLVDETIPYGLLGGDEIPEWAARSAAITVELNTFVWKPNYLEKRIEPKAIPLLDPKHWQVWRETFVDLSVCLARVEVTWT
RIDEHQVCIEYLELLIIQAWRTDVEGDLLGFLFGSVRPGHRQPIVQELVVPLAQLVDDLSLDIVSQSDESPAPHVLTRTL
APYLQWSACLEEPGSESTLPSRQEYLKPSGVIDLAFYPKQDTSEEAVEEEEEEEATKEEGDVEEETSEEGSYSEHSEGEQS
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAGSEWETLPEEAARTGTEAEDPEVARKREEIAAGKSQLEFAREANLRI
NDDPIRDPDPLKPEDGEPAAAAPSASRRRQSRSPSPSTPVRPRTDAGNRPSSPVIIPPGSSPSKAILCALQSQVTERERQ
FAKFEVYVRHLWGIYQTNDYFPKSIRQRKITEELKRNRIQDFLKLLARDPRQTIGPESPPWKLFDDDEDHGGNDYNTNDV
NKSYNHKPLLHKPFDCQELRYCIHLLTPNKPPPNVNA
```

561 - 580:	EEEEEEEEEEEEEEEEEEEE
562 - 581:	EEEEEEEEEEEEEEEEEEEE
563 - 582:	EEEEEEEEEEEEEEEEEEEE
564 - 583:	EEEEEEEEEEEEEEEEEEEE
565 - 584:	EEEEEEEEEEEEEEEEEEEE
566 - 585:	EEEEEEEEEEEEEEEEEEEE
567 - 586:	EEEEEEEEEEEEEEEEEEEE
568 - 587:	EEEEEEEEEEEEEEEEEEEE
569 - 588:	EEEEEEEEEEEEEEEEEEEE
570 - 589:	EEEEEEEEEEEEEEEEEEEE
571 - 590:	EEEEEEEEEEEEEEEEEEEE
572 - 591:	EEEEEEEEEEEEEEEEEEEE
573 - 592:	EEEEEEEEEEEEEEEEEEEE

A0A388K282 **A0A388K282_CHABU** (1173 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MALGPTPNLRAPGRNGYPRLLKKKKKKKKKKKKKKEEEEAEAAAAAAAAAAEEEEEEEEEEEEEEEEEEEEEEEEEEEK
EKEKKKKTKKKEEEEEEEEEEEEEEEEEEEEEEEEEDNDDDDVDDDDDDDEGEEDDDDDDVVHEDDDDDDDDDDDDDDDDD
DDDDDIPLCPGLNSTRHAIEAVFGVLSDASAVGRVVLTRGYTSRVVRRALPGVIEMQEHQTTILQDIQQSLAVLAGRAQA
TPSPTGPGAWPVPYPPLSVPPVTGVSPYVAPSSVAIVSLGMPLSGGVTAGSSLQVPVQTVFTQSPLQVAVTTQPAVSQPA
QPQGTEPQQLAQQPVSLGPQPGVVQGPGQNQWVPKTAIAAPKSFIGDKRGKDLDTWLRAVSVYVRCKLTLPHEEVLVAAS
YLEGSAARWLSGLVQLQGYDHDFRSWAASHKLEDFLKMVEERWHDPQEAQKGRIYRMSPGELDELRRQLKELVEKGWVRP
NVSPYGSPVLFVPKKKEGTLRMCIDYRGLNAITVKNREPLPRIDDLLDRVQGCRYFSKIDLKSGYHQIAIRPKDQHKNVC
QTRYGLYEFVVMPFGLCNAPGTFQHAMNRIFHDYLDKFVVVYLDDILIFSKTVEEHVAHLDKVLSLLRQHKLKINGEKCE
FGRTRILYLGHEISAEGLKPDDAKVASIRDWPRPQSVTXMRSFLGMTGYYRTFVKNYSIVAAPLTDLTRLDTPWEWTDEC
EAAFRHLKHALTHYEVLKLPDPDKPFIVTTDASQYGMGAVLAQQEGPKLRPVEYMSKKMPSQKLAKSTYEKELYAVYKAL
THWRHYLLGRFFILRTDHQTLKWMRTQPVLSDALKRWIEVIEQYDFDPQYLKGEYNKVADALSRRPDFSGALITEFSLTD
NVTQSLVEAYREDQFISEIIRRLEAKDKKTSAEFELVNGLLFLEKAGNKRLCVPNSESLRSLFLGECHDAIGHFGYKKTA
ANLLQRFWWPTMMQDAQLYVETCQVCQRDKPRTQAPLGLLKPLPILERPGESLSMDFMDTLVTSKSGMRQIFVIVDRFSK
YARLIAMLETAKTEYVIRLFKENWVRDFGLPKSIVSDRDVRFTSELWKAAAAEQGTQLQMTSGNHLEANGQAEQMNRAVQ
HLLRHYIKPNQVDWDEKLALVASLYNNAVHSATGEGDHQDEVFSLRVGSLKRM
```

52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE

A0A388K2J2 **A0A388K2J2_CHABU** (163 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MFSPLLFFAECLLVLSHPGGLSPVAEEAEEAEAEAEAEAEAEAEAEADAEAEAEAEQTEAEAEAEEEGEAEAEAEEAEEAEEA
EAAAEEAEEAEEAEEEAEEAAAAEKEAEEEEEEEEEEEEEEEEEEEEEGEEVEKAHSQQCSCVGAFTCKSEDEEVNASTF
VLE
```

108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE

A0A388K2P3 **A0A388K2P3_CHABU** (129 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MTSPVSCQQLSAATSAFASVGVVGGTAVTGEIEGGGISCGEEEEEEEEEEEEEEEEEEEDEEDEDEEDDEDEEDEEDE
DDEDEDKEEDEEEEKEEEEEEEEEEEEEEEEEEEEEEEEDEEEKEEEEEK
```

96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE

A0A388K309 **A0A388K309_CHABU** (1019 aa)
RRM domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MAPTGDQTAEMALAAGNERGEAREGGGGIDRGKVGDRPREAMETSGGSDGGSNSESDPDSDSSDSDGDLDNESEVQHLQS
VLAANPSDYNAHMQYIGALRRRGMLERLRAAREGMNAIYPLTADMWREWAQDEARIVTDEKSYKMVEQLYERAVQDYLSV
SLWNDYLQFVEEKNAAAAACLPDGIPIMRNLFEKAITAAGLHLTEGGKLWSAYRQYEAKVLKAMAMAMADKGPEECAKQA
ERVRSLFHRQLSVPLADHADTLSQYVEWETSWRRESVGGLGSGDDGVVTLSPSLESAYAKAVAMVNARLPLEELVAQGKA
VDGGDHLASYYAYIGLEDQGGDPARVHLMYERAVSAFPLTAELWEKYALFVDTVLKIPSLARAVHARAVRNMPWVGLFWV
NYMLALERGHGEESEICQVFEQALQSGLQTAEEYLDLFLARVDGLRRRMVQEGEGGGGEGQQKGYALEKLRETFKRAVNY
MSDYDPNGVIRLYTYWADIEARVGKDDLARARAVWDGCVYGSSLAEAWLGYIQMEKALGKIKECRSLYRRCYSRKFDGNG
AEVVCDSWLRFEREHGSLEDYDSAFQKVRPRLVEIRALRWQQQVTTAVEPDQTSGGKSQLDRKGAAAVKAGAVKGGVKGG
RGVTAAAGAGVVGGGGEKRKTGPGGSGGGEAAGSSLKKQKMESEGGGVAGASDKGGLTGGLTDGQGARRGEEGKEEGEEK
KKKTKKQEEEGGMDQDGEDRGASATHVATRRAYSDQCTAFVSNLSQDATEKDLQELFEPCGGVEDIRLVRDRWTGRSKCF
AYVEFSDAKGLEAAIALNKTKLLGRAVSVARSAPPTDRGGRGRGRQGFAGGGAALNPQRGRGRGRGRGGGGGEPAELLQT
AADEGSTPTSAERQQREMRPPVLLSSHRRAGHVDLTGRSSATIFGVPRSVAVAGRGGGGGGRGGGGXMAKNRWEEEEEEE
EEEEEEEEEEEEEVLAKETKCLLKRKRMATGITKLWGGGGTTPQNRMKIFGKCFKRHKS
```

954 - 973:	EEEEEEEEEEEEEEEEEEEE

A0A388K3E4 **A0A388K3E4_CHABU** (115 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MEAEKEEEEEEEEEEEEEEEEEEEEEEEEQDEERREEKMYEEGGIEGDVGGGGGRGRRREEEGGGERGGRREEEKEEGGIE
GDVGGGGRGRRREVEKEEEGGGKEEQGEGEEDEED
```

6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE

A0A388K3X2 **A0A388K3X2_CHABU** (1129 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MGTLCSHDVASFPATIMDGRRKADSEERERKLWGEEEEEEEEEEEEEEEEEEEEEEEEEWTETKGKRTGRKTQSSLSDPLN
GRSTDVIESISETNGTNQERTIQDGANQAATHVDRARQCGATQAERIRRQRKSVADFRVNPPEFAYVDLKKHFANAKERV
IKLETHKEIPATPYERGPRRSLTGYIPSRLSINAGDPGGGQHRPRASIVEGDPTMLMFLEASLAAQAHEQSQMEGHLSEA
QPGVSPRMSINRRFSSISHSSEPTDARRLSQRVGGSQSSPGDPTGRRESGSSSGFTAADQHGKKGERRLSAASSSSLEQR
KRQSVSISEDRPYEGQLSVSGHPVEQAGEPSRRSSSTSTASKKRVSILMGSTQQAAAGDSADARDNPPTRVHKDDWGSTQ
PSLLLEQSDATPSHLLERIDRNSAEGLLLSPQHVSQRMAALPPDLIDNTIASINRSVPSWSPQPSSSVAGPSVSPGSSPD
DPAIPSRRSLQPSGGILRKTSQGDNLHPNAAKSSPPTDSAVRRPSNAKPGASKAEGSADHPAGSSQQKRLSSHSEGGSGG
AHQKSSTQSGGAGPNNRQDRVTIEDGITSSTPQSNLSQGLIGHGLFGEEDDGKDPTSQASKTIRRLRKAEKRAAEAKANH
DLDTALVLRMEVLAWAKICTSSPLRPLAELIGRSHLNLACAYYDKGLAEQAFLHCVKALQQCDNFREDPRAHALMVLVLT
ALARAKLLLGRSDCAADCLKYLDRAMSTNRVLYGEEVLSNYPIHNALAEVYIFMGDAKARGESGDGKAAEAHASSEGGAG
GPSRGQAGEGSTQKGGDNPEGPQPTGSGDPNDAEKLYAKAIRELQKALELLGHAYGGYHPEMGPIYAKLAQTKVKKREDR
DAASMYLNALKCYETEKVVDQRAVVQLRYEHGILLSRQERYSEALEELRKARVYCEKICGPEDQATFRVMKQIGLVQFKY
GELQDSLATYQTILERQKLRYGSKSMQVAETLKYIGNVQVGLELMEEACESYETAIKIMVTHVGNNHVRVREMRKRLDDV
RSLWKSLKQLSAPQTQQVASGQKRYRDRNSETVDAKAPRGVSASTSAPPGKVNNPQQSGPGTTNAGAPSSGPHQQGTSHQ
SNKTKGCNR
```

35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE

A0A388K3Y5 **A0A388K3Y5_CHABU** (1452 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MGTLCSHDVASFPATIMDGRRKADSEERERKLWGEEEEEEEEEEEEEEEEEEEEEEEEEWTETKGKRTGRKTQSSLSDPLN
GRSTDVIESISETNGTNQERTIQDGANQAATHVDRARQCGATQAERIRRQRKSVADFRVNPPEFAYVDLKKHFANAKERV
IKLETHKEIPATPYERGPRRSLTGYIPSRLSINAGDPGGGQHRPRASIVEGDPTMLMFLEASLAAQAHEQSQMEGHLSEA
QPGVSPRMSINRRFSSISHSSEPTDARRLSQRVGGSQSSPGDPTGRRESGSSSGFTAADQHGKKGERRLSAASSSSLEQR
KRQSVSISEDRPYEGQLSVSGHPVEQAGEPSRRSSSTSTASKKRVSILMGSTQQAAAGDSADARDNPPTRVHKDDWGSTQ
```

```
PSLLLEQSDATPSHLLERIDRNSAEGLLLSPQHVSQRMAALPPDLIDNTIASINRSVPSWSPQPSSSVAGPSVSPGSSPD
DPAIPSRRSLQPSGGILRKTSQGDNLHPNAAKSSPPTDSAVRRPSNAKPGASKAEGSADHPAGSSQQKRLSSHSEGGSGG
AHQKSSTQSGGAGPNNRQDRVTIEDGITSSTPQSNLSQGLIGHGLFGEEDDGKDPTSQASKTIRRLRKAEKRAAEAKANH
DLDTALVLRMEVLAWAKICTSSPLRPLAELIGRSHLNLACAYYDKGLAEQAFLHCVKVVSRLKRYSTPSNMEGTFWIFCK
GWSKRGRRGEEEGEEDSASSLYWARILKIWEEIFPARVRKPRSKEEVLRQPLFCNPWLKDSQGKPRTLTARDTRWGNWVE
HGVWQIKHLWSQEEGRWKTGRELRVSMKGCHRLTENLNDILISIPQEWTQLLRAPHKWIWGDWAAWSNSTTPEHAFRIHQ
EVGPDNQWLEGEMFPILSPGATVSPLDXAAKVAVAIRKNGLRKIRVIEDDXLTAFAPTXAIQELEIDPAEWAWNIKGRVS
GITTKVNILRYTTKLGYKLRGGSIQTDQPLAIRWEKREGIPSGRVEQLPWSRLQAIRLGKALQQCDNFREDPRAHALMVL
VLTALARAKLLLGRSDCAADCLKYLDRAMSTNRVLYGEEVLSNYPIHNALAEVYIFMGDAKARGESGDGKAAEAHASSEG
GAGGPSRGQAGEGSTQKGGDNPEGPQPTGSGDPNDAEKLYAKAIRELQKALELLGHAYGGYHPEMGPIYAKLAQTKVKKR
EDRDAASMYLNALKCYETEKVVDQRAVVQLRYEHGILLSRQERYSEALEELRKARVYCEKICGPEDQATFRVMKQIGLVQ
FKYGELQDSLATYQTILERQKLRYGSKSMQVAETLKYIGNVQVGLELMEEACESYETAIKIMVTHVGNNHVRVREMRKRL
DDVRSLWKSLKQLSAPQTQQVASGQKRYRDRNSETVDAKAPRGVSASTSAPPGKVNNPQQSGPGTTNAGAPSSGPHQQGT
SHQSNKTKGCNR
```

35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE

A0A388K4B1 **A0A388K4B1_CHABU** (314 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MKQELVQIKQKKGMKQEEEEEEEEEEEEEEEEEDEEEEEEEEEEEEEEEEEEEEEDEEEEEEEEEEEEEEDEEDEDEEDD
DDEGDGEGGEGGGGGEGDDDDGGGGGEEEEEEEEEEEEEEEEEEEEEEEEEEEEXKKKRRRRRRRRRRRRRRRERERE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEIVMC
IFQRSREGVLPRERNEGKERPNSWKGNSETMEEREAEGKTQNHTGRRQDRRGGEEGDDQVERQSTIKTLVDEET
```

34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE

178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE
180 - 199:	EEEEEEEEEEEEEEEEEEEE
181 - 200:	EEEEEEEEEEEEEEEEEEEE
182 - 201:	EEEEEEEEEEEEEEEEEEEE
183 - 202:	EEEEEEEEEEEEEEEEEEEE
184 - 203:	EEEEEEEEEEEEEEEEEEEE
185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE
190 - 209:	EEEEEEEEEEEEEEEEEEEE
191 - 210:	EEEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE
194 - 213:	EEEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEEE
196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE
208 - 227:	EEEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE

A0A388K516 **A0A388K516_CHABU** (166 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MNIGPEEEEEEGRKKKKKKKKKKKKKKEEEAEEEEEEEEEEEEEEEEEEEEEEEEEEGGGGGGGGGGEEGGGREEEEEE
REEEEEEEEEEEEEEEEGGGGGGGDFPRHLHSXKKKKKKKEEEEEEEEEEEEEEEEEEEEEEDEEEEEEEEEEEEEETIAG
HTTQGA
```

32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE

39 - 58:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE

A0A388K5W3 **A0A388K5W3_CHABU** (502 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MQALTSKCRTPTSTASSPTKTHSAPHSWKQTSHHCHLLDLTRTRAGIFEEDEDEEIEERGGRRGRKEEEEEGGKRRKEEE
EKREERGGRRRGKRRKEEEKERGGRRKKRKEGEEGGGGGGEGEGEEGEEGRRGRKEEEEEEERGGRRKNKRGRKEEEEEE
RGRGRRRWRRRRRRRRRRRKKREERGGGRRGKRRKEEEEMREERGGRRRGKRRKKRKEEEFGPYHLEGGGGRRKKKKKEK
GGGGEGGRRKEEEEEEEGGRKKEKGGGGEGGRRKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGRRR
RKKEEEEEEEEGEGEKEEEEEKGERRKKEEEKEEEEEEEEEEKEGEEEKKEKKKKKKKKKKKKKKKKKKKKEDERRKKEEEE
EEEEGERRKEKRERRKEKGEGGGGGEGRKEKKGGGEGGGEGGGGGGEGGGGGGEGGEGGGEEGGGGVEEGEEEGEEEGEE
EEGEEEEGKGGEEEEEEEEEEE
```

275 - 294:	EEEEEEEEEEEEEEEEEEEE
276 - 295:	EEEEEEEEEEEEEEEEEEEE
277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE
287 - 306:	EEEEEEEEEEEEEEEEEEEE
288 - 307:	EEEEEEEEEEEEEEEEEEEE
289 - 308:	EEEEEEEEEEEEEEEEEEEE
290 - 309:	EEEEEEEEEEEEEEEEEEEE
291 - 310:	EEEEEEEEEEEEEEEEEEEE
292 - 311:	EEEEEEEEEEEEEEEEEEEE
293 - 312:	EEEEEEEEEEEEEEEEEEEE
294 - 313:	EEEEEEEEEEEEEEEEEEEE
295 - 314:	EEEEEEEEEEEEEEEEEEEE
296 - 315:	EEEEEEEEEEEEEEEEEEEE
297 - 316:	EEEEEEEEEEEEEEEEEEEE

A0A388K654 **A0A388K654_CHABU** (104 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MTAEEEEEEEEEEEEEEEEEEEDKDEEEEEKEEEEEEVEMEEDEEAMEEDKEEEEDEEVEDEEEDEEEDEEEEEGADEKEE
EEEEEEEEEEEEEEEEEEEDQIKK
```

79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE

A0A388K6C8 **A0A388K6C8_CHABU** (1290 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MSREEDDEEEEEEEEEEEGEKEEEEDEEEEEEEEEEEEEDEEEDDDEEEDDNDDDDDDDDEEEEEEEEEEEEEEEEEEEEEK
EEEKAYLRGDGSRQHSRESAGRQQEDDDGAAAGRQRLASRTMATVQDDDELGEGRDGGGRRPKWATGGADRPRIRIRILE
ATAAGTSRGASNRQSSAGCVAKQAYDPTLYAHLPSHEIPLPPSDDEGEELRSTTVPLGSGSTQHWAATQSYGARRAEATR
SYTSLLNDGLCEDEGNAPVDLSFRLSSSSGAAATHTRIVDPYPDGGWAEQSSAAPCGRGDDGLSQASGGGGNRNVASTQG
GGRGDVRQRPDWMRLSPASRSGPGTPPGRQREDDGSASGAQVERHGRQSWADARQALRQAGADTITRGVQELHVDEGGEA
AAEEPFNCDDVDDEEDCNSDELPDVRPLGRKVWGGGASAKKGSTTSNRRNKRRDDDTGGSDGEGGRNFWPVGDTVTLVRA
KRDQDLYFAGMGHNFGCMKTREWRWEDVRQRLVKLGVQRKAVDCGKLMQQFKKVHKYQNLSGGKDYFKLASSARRSEGFS
FVMDRSVFDEMEAMTKGDHTIHPKNLADTGAPGGVQMPAGMRAVGDDIGSEGGGEPVDEVQGSMKDSRFSAGSGVATGKR
KNMRQQSFEVVTDVMKEHGTLMTTTMDNASKRQCSMMLRQCQVLESELELQRGHYAAADAANTMMCNALLEIAKAIRDRS
VVGETSFDDRRVTSSKSDRSANVTSSRLRHVIMSTRGNTLGKKRDALPEDGEGRLKKGRHVPKGKRLRPEEASGSAPSRI
AQGWVAAAQRDDDDEYASGEERAEGTTSAVRESGRQRSSDHSTSKGMTTPPPDALRVQGRDTRTEKVPVVDVVDPSDDEP
LEKRRLRTAAASTPGTPTLPRQPRPDDEGGSAQRVAAHAVVAARGAAGAEAEGAAGGATPSEKNPGREGDDPSSSRHRQG
VMTKDLLERALLWVDDTAFWTTGEGRRLYNIVHESREYFVAIASVLPAPTVPRSAVMPKSSAKVARISDQSQLQQATKRA
TTFENVVMRILHGWVFKSGNRPRGYHLAFQYTLESFATDLARVMWCGEEWSNAISAAVCAHTIDLGMDLSLWFVGASVED
RPDNDDMAAYQESTIICIAHAFRAAIQMGATIDGGFISYERLCRVSDCFKLLLAASMWLMRMAGDDQRSHYEAFYFAKLV
AKSTLVASMHRAFEHRKKVLHAVNVVTERLGKANATLGEYPKYIPDWTDCGISFGHDASITGPDEAKKLDWLGSGPPDDD
```

DGEADGKKET

59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE

A0A388K7L2 **A0A388K7L2_CHABU** (803 aa)
PseudoU_synth_1 domain-containing protein. *Chara braunii (Braun's stonewort)*

MMIRAGSVAASGVVRAASARCALGHRRDPDVAECILRTRAGQPIEARCEGVQSEARCGGVQSEARCEGVQSVRCRGRNLA
VQGGDVSRVGDPRVSNRELSRHGFPPPCRPSLSLSKARCLDGHGFPRDSQPPDLALVVMEIWAAKKEDRYGGGGGGQRGE
VGGKWWMSCRGRPRGRATRRLFLSSSVCRGGGDGLSSRPVAASVVRRAIASGSAAAQAGGKVNLAGKHVSAAEKEVNLAR
RAVIGQHEGWKSGAAADTWRRDLPIRREWSCASSVFTAALPSGVAAAAAAADYMGELQCTGGGGGASGSPRTVFGSGQKR
RAGERLHGGRCRLRILRAKLCPDCGGLVGDSGGWTTIRPGRAIEPTRRRGSGTKRPGSSSSSGDPARRRDPDDGGLLCLD
IAARAKTPSHRRPETAIAMKRRRRRRRGEGAALLASVGGAGEEAGRREEEEEEEEEEEEEEEEEEEEEEEDERNDPRREE
QALIGYQWEGRRVGNHRSVDQGGEDVDDEKLYNYRLVIAYDGTNYGGWQRIGDYVSVQQTVEEAISAAIRTTPNQLPIRV
AGSSRTDRGVHAKGQVAHVRLPVALTNLHRFHLSVNGILADDIRLLEVGAAPWGFDARRCALSKVYHYHVVNRPIMDPLR
SRYALYEYHLLDLQAMREAAMDLVGVHDFSAFGNRGRGKDNFRPCPVRWLMRFDIVEQEDGVRFEVEGTGFMYKQVRNMV
GFLLEVGKGSVAVSFGRELLTTLRRRDKAPRSAAAHGLCLMEIKYPARMLLPPPGAPETSYGRLKDGAKTRRQRKREAAM
VQR

448 - 467:	EEEEEEEEEEEEEEEEEEEE
449 - 468:	EEEEEEEEEEEEEEEEEEEE
450 - 469:	EEEEEEEEEEEEEEEEEEEE
451 - 470:	EEEEEEEEEEEEEEEEEEEE

A0A388K7P9 **A0A388K7P9_CHABU** (1669 aa)
Nuclear pore complex protein Nup85. *Chara braunii (Braun's stonewort)*

MLLRSQTAVMDQKAGETDEAYQACMLAWSTETKKRADDAAAAAKKRAEDAEQARLLAVEQQRQHDEAAARAADEERTQRC
EKIFTGERALLTMAAEWRSEAENSQLEDSANKIALLLSHLTDLLATCITQQAEILALDNSVAHLQDRLQRVEHRPVAAAD
AVSSNTADRLTALEMRVGSLQDGTQLQQTATQQLQQRICTTATTPSSEPRETAPKFDGHEIFHDSIKTDPIPWFRKFELT
LQLHNVKENKHHAYLYSRSGAACQAWLDNLLSKYGVVAADLHTMISWDDLKAAWHKRFQVEPPEIKAMDKLMIEVLDPLT
SEDFAWLPLPTTDCLPGPQCAALSTHLHTYLSFYAPPTSPTDDEVAVGDILAYVTKVAREFRTQRYDNNNALLMYVRIQV
GQASCNALLDSCATRNFMSLSFMQRAGLGAQVRRKANPTAIKLADGKTQQLLDRYIEAVPVYFAPHACEPVTFNILDTDF
DIILGMPWLASADHTVNVHWRTLSVRDAFGAEVACTIPLLHSSIRCQVVTAKSFRATCAYEQPEEIDICFLRTVAVADSS
PTDLSSDPRVVRLLDEFADIFESPTGVVPGRPISHEIILEAGVVPPKGCIYRTSKEELEAAMTNEFRAMLDRFVLVYLDD
ILVYSRTLEDHLGHLRRVLETLRHAKYKANRDKCEFARQELEYLGHFVTPEGISPLSDKIQAVQEWPEPRNVTDVRSFLG
LTDHYQRFIKGYSKIAAHLNKLQCEDRPFEFGEEARGSFLALKAALLSAEVLRIYDPLAPTRVTTDAFICGYQADPDFRD
KYANCSSPNPAPFHYRIQEGYLLVHTRGKDLLCVPSDPHLRTRLLGEFHDAPATGHFGVNHTIARLRQRFWWPDLLGDVT
RYCESCEVCRRCKSRNHRPYGELRPLPVLLRRREAIAMDITGPFPKHKTGVDGILTVVDRLTKFAMFLPCRYHAKAPELA
EVLYAGWIRTKGYPKDIVCDRDTQFMSGFWLALIKRWGSSLKPSSARHPQTDGQTERAHQTAQVLLRTLIRPDQKDWVER
LPDVELAYNSSIHPAIGISPFEFEHGSPVTSPLDTITPRTAESDDYLLFLCRMQELLVKARDQMAKTQQRMCQQANRQRL
PCPIRAGDLGWVSAAEFSLEQDISRKLLPKWMGPWPIIEPAGDTPEGPSFTIQVPSHLPVYPVFHCSKLALYTPAEHDDF
PGRRTQDPPSMDGFQEVGDIISQRCYDNKPTECLVHFAYCTYRADRWLTRAELQATAPDVLAAARQPLAHFGIGKSCLLG
LLAVEEEDDEEEGGQEEEEEEEEEENAVEEGREDDEEEEKKKKKKKKKKKKTQGRGEEEEEEEEEEEDKDDEEEGGEEE
EEEEEEEEEEEEEEEEEERKPMAKRGGLEEEEEEVEEEEGKAEDGYGLRARRVSTKKKKKKKKKKKKKKKKKKQTWGCDGVA
CWRGGAMLRLAGRGDDGDAAPCGDLPTMPRLQRVMARLVGGGDDGVAGCRRRRRSGCTDWSSYDEGHYLDKEEENGVVEA
AAVLLSKMPRMSPALDVVQPASGFTSLPEFIKARQKWLTQVEKLETVQFWEMCGAATQRGLRKVLSVVLGKAWALEEATS
HWIELLVAELLHLYPTHKALDGLKDKAVKCMKRRPAPSNQEVLDKLLLAIMDLDTEVVLAECSKTFDAW

1358 - 1377:	EEEEEEEEEEEEEEEEEEEE

A0A388K8H7 **A0A388K8H7_CHABU** (289 aa)
RT_RNaseH_2 domain-containing protein. *Chara braunii (Braun's stonewort)*

MCGFYRNFVKNYSTVASPLTDLTRLDTLWDWSDECEGNIKRLKHALMNHEALMVPDPQKPFIVTTDASQYDIGAVLAQQD
GKKLRPIEYMSKKMPSKKLAKSTYERELYALYKALVHWRYFLLGRFFYLRTDHQTLKWIKTQPALSDALKRWIEVMDQYD
FKLEYLKGEYNKVADALSRRADYLGALVSDFGVSEEVTQSLVGAYQEDPVTMDIIRKLQVKDKATENEFVMVDGLLYLDK
AGVKSNEENEEKEVKEEDKEEEEEEEEEEEEEEEEEEEEEVVSVTYLLS

260 - 279:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE

A0A388K8K8 **A0A388K8K8_CHABU** (187 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

MALATRWLCGGTVDDDEGPWQHADAFCAPGIADETLPPVYPADVAHATADQECIDDDDVDKGEVEEEEGDDEEGREEEEE
EEEEEEEEEEEEEEEEEEKEAAEKGWMTGGNVAEDVGGGAGGGGGDDGGGGSEDDGGGDCGSVGSDDGGGGGGEEGGGGGD
DGGGGGGGRDGGDCGSEGGTFSVATAA

76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE

A0A388K8N6 **A0A388K8N6_CHABU** (3163 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MNVRNCDNNWLYAPDPPALFPSLDCELSNDESGGDHNKSRFTPGSRAQGRLRSPMSLNSVNARRRFRGDTSPSSNMSWRA
SLPMASEALGQSTMRGAAGGSGSLSSVVDSSHSSLSSHSGSGSSGLRRTYSGNAKLMTSSTGNRRPVSMSPGSGGQPKFT
PGTPGRSSVDQRRRSVSPHLLGGIAKQKALSASSTNLLSLAMSTKTPPNLRTTATLSSSSRGSSGPDRPVSSGRPPGLTS
SSTRCSSRRGSLTSSFWPLGEEYYGNSNKLMGWRASLPLESRRPTSVDRDDSDGMESGKKEYYSDDVEGPALSSDDGQQS
AEEGAEADAELDSDSQMDTVRDSAATSQTIPRGGPRTGPGEHGTVVRECENADADCMRARNEASDSREEEARRRDAATAS
FTRAERQKGVSLIPSLRQKHVLGVEGPVKNVHGDGNAETQGVDEGADDSAFSGCCDKKELNRSVGGGSVEEELAGTENNG
APDDLRLPMKRKLRAVTGAAPYRGGGETSMPGEGEGEGEGEGEESPFSSPLRHIIMNDSSLEIPRTDSGTLLNQEDVDWD
LSLLDGTEAPELLTSTAMEGEDGQASEKWSDGEEAHRGSERGPGGVSAPRPIRGNSSATERASGYGSHDHGAWVSEEQSS
HSHAASYGVGALSSPFAPAHDSNKMGVVGSALPPSYSRPLPAAMWNNPHTSEAAMGNSQTCQAAIGDEMADVWEGGFQAC
IEKPSENAQRDGEEVQQESLCSRSGSDTDDDEPEVPSLRGGEEQAMVLPHQTTAPCNSAPISRYDNSASGLPLTGGCDQS
RPSPLESRVEDVSFSFLTSAAAHMDPWYGPDESPDGRTCLAPPSGLSGDCGFGAEEEPHQLVRNPEYVGSMVQEGDTFQQ
GRWHGQSGRPQEMRGSTAQSPDGGMMGPVAEEEYKRGSADVVDGDRKAYTAAEDVMTLSEAIEREKRSSAYSMKGSLQDN
LEKVVMMNVDTWAEIAGSEGSPQEADQMARDDVLTQTVRVASSQNAGPPEDNKLLGKNKGNAKKGQKEGSGEALRQRSKE
MEKARDDRDIGNIHNAVKNPEKGDKQKQARNGVERAELMERRETEKRENGRGGAEAGGKEGGKKGKKSGLLERGTFFRDV
RSTRLTSGSWDKNEKSVEVPAENVQLTEGLMTARPDCGGDFESAALGDAATDQGSGKRRPAKKGVFGSAKSADATAKLKR
PQELTKQGAMVGMLGKMVDDNAGLERSQERDSLSSDSRERVMSAPKSRDGFQKRRGESGAELVVTDYENQAKAKDWLTQE
RLESPEEWLMLRKQQEEEEGEEYMKQENLMLREHEEEARQHEMRILEEKKLRQDMELREREELRLREEEQRLQEQHRLQE
EYRLEQERRLEEQSRLQEELRQQEELRIQEQRRLEEERRIQEELRVQEQQRLQEEHRLKEELKRQEEIRQQEEIRQQEEL
RLQKELRRKEELKRQEELKRQEELKRQEEXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXLKRQ
EELKRQEELKRQEELKRQEELKRQEELKRQEELKRQEERERKRQEERKRQEERKRQEERKRQEERKRQEERKRQEELKRQ
EELKRQEELKRQDELKRQEELRRQAEVRRQAEVRRQEELRQQEERRLQEERRLEEERRREEERKLLEERRLQEERRLQKE
RKLEEERKLLEKARLEEEHRLLEEHRLEEERRLEEERRLEEERRMEEEHRLQEELQRQEEVRQQEELRQQEECRRQEEIR
RQEELRQQEELKREEELKREEELKRKEELKREEELKREEELKREEELKREEELRRQEALRLQEQQRLEQEHRLEEERRLV
EERRLEEERRLQEFRLEEERRLEEERRLEEERRLEEERRLEEERRLEECRLEERRLEEERKLAEYRREEECRLEEERRLE
EERRLEEERRLEEEHRLQKQHRLEEQRRLEEQRRLEEECTIDEEHRLKDRMHEEERRGGEESRVEEKHRLEAKHRVERGF
DKEQRLEEKSNAEDENRLKKKCWLEDAHRLAVDHSLEDACSLEEELVVEHRLPAVLRKPKEQRLPEQQDAAGAMIHQLDR
VEVERNGEKEWLRGLDCPSGQEEGEKKEEDEEEEKEEEEEEEEEEEEEEEEEEEELTYASVIRQLGELQRLQVNKIPEVE
MAGERRKRQESKTKKDARTPHNAAGREPEDSEGQEEELVTGLIRWAETAPLKEWEADVRQRPKQEVMKAGEEQKPEGVRH
AGGDLQMYKEQVVLDNYTAVTDESRKVDELRMSHEDNRGQSEGGHLKGMTDLGAANLDGTPWLKQRKEKDNYSSDAEDHT
RSENEPAQNHGIVDTRYIEPDSREVGHQMQLAHARVVGGRMNCELTSGKQGEEAGERDNIGGGGNEQTPTILMVKPEAAT
FVEQRLKSREGTQSQVREGEDVEHSLRESKGSAKSLLGLETTEDQQELDVWVLHDDYRLSNKLSLSCGQVDGGKEGGNNK
ERGRKLSLDNDMFVDGTILADNIDVDSPKKRNQQEHQQRVQLPEPRLSSTFRGALPFLSLRTHSHTGGSSASALLSSQSS
QSVGSSSAVSSGQRRSLSGRGSSRSGPPSENYEWEKCSSIADETYSDVSTPSTTASRHLTLEEATQAVLLCSSIVHDVIY
KAASIAQEREEELGEMGHMGELAAADRRLGHQREAVCQFGGSLNAVVVDGPDDRSFISDAFSLPDPLSDYPDPRICDHDP
IRRRNPGLPTNPEGLEVEGRGNFDVDLARPVYRNSPPLSSPQEECLRLGVLRCRLPLEIDCNHNAGKLCPAFKSSPAFEP
SADILDAIPALHPNHTPVMQPAAESNDDSSVFDLEPAGKIPPRLLFNDDPEPCLHRQTSEQETGQASAVIEQQVDADTRR
DALETCSFSRTMSKSSASLAGEDSEALSTDGSQSFSSRMAGEETGKGRRRAADRRAEGPAPVPERVGEVQRPEVGPETGV
QKGSSSDASEEGPGSRSRRALRFIRRSWGTSGSGRSNAEIGAASGDLSTPGALSPKESKLSGALSPPAKSSEKPAGNTTT
PPQLTMADEAADEGARAWNKASRVSDEEKKMNKKAPGDDKDSGKVSVKGKSKVEHERGATPKYRVTGKFPRPTEQLGRKT
EKDGVHARRKRNPSCGCVMMMTPFTCWRKGPEREESAFFETKS
```

2116 - 2135:	EEEEEEEEEEEEEEEEEEEE

A0A388K8R2 **A0A388K8R2_CHABU** (157 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MEEDKEEEEDEVEDEEENVAETRRKRTDEEEEEEEEEEEEEEEEEEEEEEEEEEEEXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEEEEEEEEVEEEDEEEDEEEDEEEDEEEDEE
```

29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE

A0A388K8V3 **A0A388K8V3_CHABU** (191 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MMPCGPPRVLPEEEEEEAEGRPTKHSTKRLRIRKSTYAEEKLTSSSCGRRRRIRWGGRKKTRRKKTRGKRGQEQDEGTRRK
TNEEQEEEQEEEEEEEEEEEEEGGRGRGGRGGGRGGRKRTRRKRTRRKRREEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEAEEEEEEEEEEEEEERIVEEKRDEAREGG
```

130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE

A0A388K978 **A0A388K978_CHABU** (497 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MANMGGMGMGVGMGVQGMVSPNMGNQNMSPTMVNPNMVPMGLGGQPNSAAASPFGTVTCHICGKNEHYARNCWQAQAVGK
QKIDEETLEMKELFKKLVQKEQEEQERKQREVEEAKKAAEERREGEKICEEEAREVRLEATILRILAQKRESLVAEVKLV
HGDDSRKPSPRSKARLLCEIRGYIAESEDDSDEVRLEVDKLVEVLEARKKGGRTRCVRCTDDLKTTLTKVVAALSKTGDT
IVARCYDIKDMFAKLPHEDIVSSVAWLIGNLRRRGLVAVKAATKKKKAAKKAAAKKKKKKKVAAKKAAKAAQEKAAKAGK
KKAAEKKKAAKKKKKKEEEEEEEEEEEEEEEGEEEEKEEEEEEEGEEEEEEEDEEEGEGGGEGEEREEREEREEGEEGEE
HEEGEEEEGGEEEENEEEEKEEEEEEEEEEGGGGGGGSKEGGGGGGGGGEEEEEEKEEEEEEEEEEEEEEEEEEEEEERR
RRRRRRDPPKHRLRTHC
```

457 - 476:	EEEEEEEEEEEEEEEEEEEE
458 - 477:	EEEEEEEEEEEEEEEEEEEE
459 - 478:	EEEEEEEEEEEEEEEEEEEE

A0A388K9A0 **A0A388K9A0_CHABU** (1186 aa)
Integrase catalytic domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MSDREEQQPDDRILRSARRPVAHLALGPEGDKHLFRQLRERQQHQRRARAAEASRALVSEAATSEAMATPAQQSSQAGSS
GSVRSTVSQTQSHSTGVMASQPLVLTPDEIAIQQAALQEAQLQKALGDIKAEKDRMIRRRVRMQRRQADVSELEKMDLTH
VTDDVRIIRSVLLNVVEMQDKQTTILQDIQQSLALLVGRAPATSPMSGPGAWPVVHPPPYVPPVTRVSPYIAPSLGMPLS
GGVSTGASLQAPVQIVYSQSPLQVAVTTQPAVSQPVQPQGTQPQQLAQQPVSQGPQPALMQGPGQTQWVPKKAIATPKPF
TGDKRGEDLDTWLRLVPVYVRCKLTLPHEEVFVAASYLEDSAARWLSGLVQLQGYGHDFRAWAVTQKLEDFLKMVEERWH
DPQEAQRATDAILTLHTRQFKSVREATDAVERLICVPGVRYDPQVLLTSYPRCFSLPLRNQLASQANINMHNFPSFSKMA
LDLXAKIGHGQAPTTDGRRKTLPPNWKAKGRIMFVDNDSALITEFDLTYNVTQSLVEAYREDQFMSEIICRLKAKDKKTS
AKFELVNGLLFLEKAGNKRLCVPNSESLRSLFLGECHDATGHFGYKKTAANLLQRFWWPTMMRDAQLYVETCQVCQRDKP
HTQAPLGLLKPLPIPEWPGESLSMDFMDTLITSKSGMRHIFVIVDRFSKYARLVAMPETGRTEYVTRMFKENWVRDFGLP
KSIISDKDVRFTSELWKAADAEQGTQLQMTSGNHPEANGQAEQLNRVVQHLLRHYIKPSQVDWDEKLALIASLYNNAVHS
ATGVSPNSLLLTFKPRLPLDFLLPENQSTAAPGTLEFAYRFEQKMQQVVEQMQKAQAAMIESANKHRRESSFQVGDRVWV
KSSELGQEHGISRKLMPQYFGPWEVLDIVGTDPDGPSYVIRIPGHLRTYPVFHASKLAPFKETDEFPSRRSMLPPTMDGE
VDIDDIVDHRELPAQRPAGRGRPPKPKLQYRKKTTTTRRRRKRRRKKEGGRRGGGGGGEGGGRKKRRKKRRRRRGGGKEE
KKERRRRREEEDVGGGGAEGGAGEAEEGEGDAEEAEEAEEGEGEAEEEAEAEAEAGGGGGGGGGGGGGEGARKEQEGEEG
EEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEEEQEEEEEEEE
```

1124 - 1143:	EEEEEEEEEEEEEEEEEEEE
1125 - 1144:	EEEEEEEEEEEEEEEEEEEE
1126 - 1145:	EEEEEEEEEEEEEEEEEEEE
1127 - 1146:	EEEEEEEEEEEEEEEEEEEE
1128 - 1147:	EEEEEEEEEEEEEEEEEEEE
1129 - 1148:	EEEEEEEEEEEEEEEEEEEE
1130 - 1149:	EEEEEEEEEEEEEEEEEEEE
1131 - 1150:	EEEEEEEEEEEEEEEEEEEE
1132 - 1151:	EEEEEEEEEEEEEEEEEEEE

1133 - 1152:	EEEEEEEEEEEEEEEEEEEE
1134 - 1153:	EEEEEEEEEEEEEEEEEEEE
1135 - 1154:	EEEEEEEEEEEEEEEEEEEE
1136 - 1155:	EEEEEEEEEEEEEEEEEEEE
1137 - 1156:	EEEEEEEEEEEEEEEEEEEE
1138 - 1157:	EEEEEEEEEEEEEEEEEEEE
1139 - 1158:	EEEEEEEEEEEEEEEEEEEE
1140 - 1159:	EEEEEEEEEEEEEEEEEEEE
1141 - 1160:	EEEEEEEEEEEEEEEEEEEE
1142 - 1161:	EEEEEEEEEEEEEEEEEEEE
1143 - 1162:	EEEEEEEEEEEEEEEEEEEE
1144 - 1163:	EEEEEEEEEEEEEEEEEEEE
1145 - 1164:	EEEEEEEEEEEEEEEEEEEE
1146 - 1165:	EEEEEEEEEEEEEEEEEEEE
1147 - 1166:	EEEEEEEEEEEEEEEEEEEE
1148 - 1167:	EEEEEEEEEEEEEEEEEEEE
1149 - 1168:	EEEEEEEEEEEEEEEEEEEE
1150 - 1169:	EEEEEEEEEEEEEEEEEEEE
1151 - 1170:	EEEEEEEEEEEEEEEEEEEE

A0A388KA34 **A0A388KA34_CHABU** (1716 aa)
Integrase catalytic domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MILGISWLRSADHPVNFHDRTVHICDRNGVLVPCTXATPHTSIACHVVSVARIRDAIARNDVEEMGLVFLHALPSPDGPA
ASPPDPRISHLLDEYRDIFEAPTGTAPCRPIRHGITLEAGVVPPRGCIYRMSEKELEVLRAQLNDLLDKGWIRPSCSPYG
APVLFVRKKNKDLRLCIDYRKLNAQAVKNVGPLPWIDDLLERLGGATYFSKLDLKSGYHQIEIQPQDRYKTGFKTRYEHF
EWVVMHFGLTDAPATFQAAMTTEFRDLLDRSVLIYLDDILVYICHRNKGRSRVPFDELKPLSIPRAPRLSIAMDVTGPFP
HDRHGHDGILTVVDRLSMYARFLPCKYHAAALELTRLLHTGWITNQGVPEDIVSDRDTRFMSAFWTSLMAESGTTMKPSL
AWHPQTDGQTERAHQTAQMMLHTLIRPDQKDWVDRLPDIEFAYNTSVHPAICVTPFELHHGGEKARIFADLLLPQAADID
VPCSPASVQKYLDLLIKARANMQKAQIRMQQQANRRRPSCPFREGDLVWVLSEEFGLEQDVLRKLLPKWFGPWEVTSAVG
DDPAGPSFVVNIPPHLLENGGGERGGKRIGRGEDVEIPDGDTVDLLGKMEIMARNIERVAQVQEEQYLFRRGQDIALRSI
RLGLRDFARALATKVGSEVRARLKGTKRYCTGAIEGARLTAPKEEEACPRRAPVKVKFPDSYSEKKEENFDNWESNVKTY
VHLQKVSPDEHVLIAIHALRDEAASFARSLYRAASYNDDLVAYSAFTPLTDFLKLLREWFAGVSQSVKASDRLQTIHSRQ
WKSARALKGVMDELVAIPDHGVTKTQFVLEKLRGANFKINAKKCEWAKTQVLYLGHVLDGDGIKPEDNKIATIRDCPTPR
TLTELRSFLGLANYYRKFVRNFSTIAAPLRRLSKKEAIWKWDKDYTPAMKKLKQALIEYPVLKVADPSLPFVVTTDASQY
GIGVLLQQNDGNGYRPVEFMYARMPSEKVTTSTYERELYALRQALEHWKHYLLGRHFKVYSDHETLRWLKTQAKMTPKLT
RWAAELDQYDFELKPVKGKYNVVADALSRRAEYLGAIVHYLDIGRDLQQKVREAYAQDPMYSDVLKKVKEAPESELDYST
TDGLLFEKTNVVDRLCFPNSEEIRSLILGECHDTEEVGWQKSLANLMCASGMKADCIEYVRSCKPKRKRKRKTKRRRRKK
KKRKRRKKRRKKRKRKRKRKKRRKKRKRKRKRKRKGKRKKRKRKKRKKRKKKKKRKRRKKRKRKRKRKRKAKRRKKKKRK
RKRKRKTKRKTKRKTKTKTKTKRRKKKKKRKRERRKRRKRKRKRKRKKTKKKKKKKKKKKKKKTKKKTMQKKTTTTTTKTTKK
KKKTTMTTTTTTTTKKKKKKKKKKKKKKKKKKKKKKKKKTKKKKTQNKTMRKKTTKKKTTTTTTTTKKTTKKKTKKKTKKTT
TTTKKKKKKKKKKKNKKKMTTTTTTTKKKKKKKKKKKKKKKKEKKKKKKQKKKKQKKKKKKKKKKKKKRRRKKKKKKRRKKRK
KRKKKRRKKKKKRRKKKKWKKKKKKRRRRRRRRRKKHKKKKRRKRKEEEEAEEEEAEEEEAEAEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEMEEEEEEEEEEEEEEEEEEEEXMEEEEEEEEEEEEEEEEEEEEEKAQEEEEEEE
EEEEEEEEEEEEKLKEEEEEKNRKKDKDEAKEEWRK
```

1584 - 1603:	EEEEEEEEEEEEEEEEEEEE
1585 - 1604:	EEEEEEEEEEEEEEEEEEEE
1586 - 1605:	EEEEEEEEEEEEEEEEEEEE
1587 - 1606:	EEEEEEEEEEEEEEEEEEEE
1588 - 1607:	EEEEEEEEEEEEEEEEEEEE
1589 - 1608:	EEEEEEEEEEEEEEEEEEEE
1590 - 1609:	EEEEEEEEEEEEEEEEEEEE
1591 - 1610:	EEEEEEEEEEEEEEEEEEEE
1592 - 1611:	EEEEEEEEEEEEEEEEEEEE
1593 - 1612:	EEEEEEEEEEEEEEEEEEEE
1594 - 1613:	EEEEEEEEEEEEEEEEEEEE
1595 - 1614:	EEEEEEEEEEEEEEEEEEEE
1596 - 1615:	EEEEEEEEEEEEEEEEEEEE
1597 - 1616:	EEEEEEEEEEEEEEEEEEEE
1598 - 1617:	EEEEEEEEEEEEEEEEEEEE
1599 - 1618:	EEEEEEEEEEEEEEEEEEEE
1600 - 1619:	EEEEEEEEEEEEEEEEEEEE
1601 - 1620:	EEEEEEEEEEEEEEEEEEEE

1602 - 1621:	EEEEEEEEEEEEEEEEEEEE
1603 - 1622:	EEEEEEEEEEEEEEEEEEEE
1604 - 1623:	EEEEEEEEEEEEEEEEEEEE
1605 - 1624:	EEEEEEEEEEEEEEEEEEEE
1606 - 1625:	EEEEEEEEEEEEEEEEEEEE
1607 - 1626:	EEEEEEEEEEEEEEEEEEEE
1608 - 1627:	EEEEEEEEEEEEEEEEEEEE
1650 - 1669:	EEEEEEEEEEEEEEEEEEEE
1651 - 1670:	EEEEEEEEEEEEEEEEEEEE

A0A388KA68 **A0A388KA68_CHABU** (535 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MPLWSPSAACTEHIFGHYSVYIRTSVHIWWDHGAARGKLIVRDTGKQTYIWGISGMCADEEEEEEEEEEEEEEEEEEEEE
EEEEEEEDEEEEEEEEEEKRKTKRKKKKTTKRKKKTTKRKKKEDEDEEEKEEEKRKTKRKKKTTTKRKKKTTTARTTRTTK
KTTTKTTTTTTMTTTTTTKKKKKKKKKKKAKTTTTTKKKKKKKKKKKKKKTTAKKKKKKKKEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEGGGGGEEEGEGEEEGEEEEEEEEEEDGEEDYRVGCWSTPGRRRGGTNVKEQQEAAAAERLRLAEQAAAQ
TRRQAEADRLAIDQLNAGSAERVSANQAQWTAVLNGMRYVPVPGSEPTTVQQERQDLADILLHTMRAVIWKSTMGELHSQ
STLQLQHDLSHNVKILAAAVKVADNQLKQLDARIATLEARPPQAAPGCTTEMTDTTKQLNGRIDHVVNLIGDIGVINGPD
TISSTVAAIKTDITKLQTKPDDATKNSTTTTRRTLWHGGNVSSRKHHAALSRPTT
```

60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEEE
225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE

A0A388KA89 **A0A388KA89_CHABU** (323 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MSWKTDALATTHKVTSKKTAKKKKEEEEEEEEETTMTTTTTKKKGKRKKGERKKAEEEEEEEKKTTTTKTATTKKGKGKK
KKGKKKKGKKKKGKKGKKGKGKGKKKKGKKGEGEEGEEGEEEEEEGEEGKEGKGEEEEGEEEEGEAGEGEEGEEGEEGEEEE
EEEEEEREEEEEEEEEEEEEEEEEEEEVWEGEEEEEEEGGGGEEEEGGEAEEGEEGEGEEGEEGEGEEGDEGEEGEEEGE
EGEEGEEEGEEEGEEEEEEGEEEEGGGEEEEEEEEGEEEEEGGDEEREEEEEGEEEEGGDEEREEEEEGEEEEEGREEEG
QED
```

168 - 187:	EEEEEEEEEEEEEEEEEEEE

A0A388KAF3 **A0A388KAF3_CHABU** (431 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MLERTFVPVELPVRWSWYAAHRGGAGSSKPTTTVTTATKKMKEQRSTDVGGGGQAWSGGRGRSAEVGGGEAEVGGGGRRS
AEVERRSLEVGGGRRRSAEVGGGRRRWSGDGPTCAEVGGGGQVERRWAEVGEGRRRWAEAGGGDRDRDREAEAEVVNLPR
GDLRTWEGEVVNFPRGDLATWQSCHVGGGGGELVSWRTCHVEILARGRGRWQTCHVAILSCGRGMKRKQGGKPGDSKSKG
GSRGTAKARGEAGGQQKQGGKPEEEEEEEEEEEEEEEEEEEEEEEEEGGRGADDAGARGAEGYEEEVGKPTEAEVEEDTQ
GEAEAELKPEVEAEEARKSAEAHVEEDMEGEAKAEPEPEAEVGKSTEAEVEDGRQGPLAMWVTWHVAILPRVELPRKRDR
DDRDNSRGRRRRRRRRRRRRRRRRRRRRLID
```

263 - 282:	EEEEEEEEEEEEEEEEEEEE
264 - 283:	EEEEEEEEEEEEEEEEEEEE

265 - 284:	EEEEEEEEEEEEEEEEEEEE
266 - 285:	EEEEEEEEEEEEEEEEEEEE
267 - 286:	EEEEEEEEEEEEEEEEEEEE
268 - 287:	EEEEEEEEEEEEEEEEEEEE

A0A388KAS6 **A0A388KAS6_CHABU** (841 aa)
Uncharacterized protein (Fragment). *Chara braunii (Braun's stonewort)*

```
ERRGRERRGRGRGRRGRRRGRGGRGGRKGGRRRGRGGAGGGRGGEEEEEEEDEEGEEDGEEQEEEEEEEEEEKEEEEQEE
EEEEEEEEEEEEEEEDEEEDEEEEEEEEEEEEEEEEGEEEEEEQEEEEEEEEKKRKKKKTKRRKRRKRRKRKRKRKRRR
RRRKRKRGRGRGGGGGRGGRGGEVEEEEEEEEEEEEEEKEEEEDEEEEEEEEEEGEEEEDEEEEEEEEDEEEEEEEEGRE
EEEEDEEEVEKRKKKKRKRWRRGRGGEEEEKEEEEEEEEEEEGGRGRRRTGTRRGRRRTGGRRGGGRGGGGRRRRRRRRR
RRRRRRGGGRGRRRGRNQEEEEERKRKKRKRRRKKRKRKKKKRKKRMKRKKKKKKKKKKKKKKKKKKKWKKNRKKKRKK
KKKRKRRKKKTKKKKGKNMRRKKKRRKKKRRRKKKRKTKKAGPGGGGGGGEESRRRSSRRRRRRKMRRRRGWRRRRRRGR
GRKGGGGGRGGEEEEEEEGEEEEEEEEEEEEEEEEERGRGRSGVGRGRGGGGRRRGGRRGRGGGGGRGRRGGGRGRGRG
GIGGGRGRGRGGRGRGRRGGGRGRRGGGRGGGGRGSGRGGGRGGRGEEEEEEEEEEEEEEEEEKEEEEEEGDEEEEEEEEE
KEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERRRKKKKKRKRGRRRGRGRRRRGRGGRGRRGRKRG
GGKGRRGGRWEEEEEEEEKRGGSGGRGRRGRRGGGGGGGEEEEDEEEEEELEEEKKRKKKKKRKRKKRKKKRRKKRKKRRK
RRRRKRRNRKKRRKRKRRKRKRRKRRKRKGRKKKKRKKRKK
```

642 - 661:	EEEEEEEEEEEEEEEEEEEE
643 - 662:	EEEEEEEEEEEEEEEEEEEE
644 - 663:	EEEEEEEEEEEEEEEEEEEE
645 - 664:	EEEEEEEEEEEEEEEEEEEE
646 - 665:	EEEEEEEEEEEEEEEEEEEE
647 - 666:	EEEEEEEEEEEEEEEEEEEE
648 - 667:	EEEEEEEEEEEEEEEEEEEE
649 - 668:	EEEEEEEEEEEEEEEEEEEE
650 - 669:	EEEEEEEEEEEEEEEEEEEE
651 - 670:	EEEEEEEEEEEEEEEEEEEE
652 - 671:	EEEEEEEEEEEEEEEEEEEE
653 - 672:	EEEEEEEEEEEEEEEEEEEE
654 - 673:	EEEEEEEEEEEEEEEEEEEE
655 - 674:	EEEEEEEEEEEEEEEEEEEE
656 - 675:	EEEEEEEEEEEEEEEEEEEE
657 - 676:	EEEEEEEEEEEEEEEEEEEE
658 - 677:	EEEEEEEEEEEEEEEEEEEE
659 - 678:	EEEEEEEEEEEEEEEEEEEE
660 - 679:	EEEEEEEEEEEEEEEEEEEE
661 - 680:	EEEEEEEEEEEEEEEEEEEE
662 - 681:	EEEEEEEEEEEEEEEEEEEE
663 - 682:	EEEEEEEEEEEEEEEEEEEE
664 - 683:	EEEEEEEEEEEEEEEEEEEE
665 - 684:	EEEEEEEEEEEEEEEEEEEE
666 - 685:	EEEEEEEEEEEEEEEEEEEE

A0A388KBA5 **A0A388KBA5_CHABU** (1631 aa)
Reverse transcriptase. *Chara braunii (Braun's stonewort)*

```
MKLTMTSGRHPEANGLAEEINQTVIQLLRALIVPDQNSWDEELPIVQGLYNSSIHSSTGITPNRLHPGWKIRNPLSYLFP
EQPPGLTPGQPGYSAKYDWLLKVVVAAMERRRSAMIKHANKKRQPAPFTVGSYVWVKMSEFSEEEGVSRKLLPQYYGPWK
VLNQVKEQQEVAAAERLRLAEEAAAQTRRQAEADQLAIDQLNAGSSEVVSANQAQWTAVLDGMRYVPAPGSEPTTVQQER
HDLADILLHTMRAVIWNSSMGELHSWSTLQLQHDLSHNVKILAAAVKVADNQLKQLDARIATLEARPPQAAPGCTPDMTD
TTKQLNGRIDHVVNLIGDIGVFNGLNTISSTVAAIKMDITKLQTKPDATTKSYKMPHFDISKFDDHNKTDALAWWQRFLT
EASCQQVPDDYLMKALYLQLIGGAQAWMNHLAATHTCTIAELHTHITWKEFEQLWFTRFMVRNVVKAAMNEVYTCSQGNL
RSYLHTTVLAPLTDDGVAVVDLRSYLAKIDREYATQRYAETDAPLLYIRIQIGKATCSALIDCGASRNFMSQAFMARAGL
GPRVRRKTQPTQVTLAFGRSQKSIDRCVDGVPEYFAPLACEPVSFDILDTKFDMILGMSWLRSADHPXNFHDRXVHIRDR
NGVLVPCTVVTPHTSIACHVVSVARIRAAIARNDVEEMGLVFLHALPSPDGPAEPPPDPRITHLLDEYGDVFEAPTETVP
DRPIRHGITLEAGAIPPRGCIYRMSEEELEVIRAQLDDLLDKGWIRPSCSPYGAPVLFVRKKNKDLRLCIDYRKLNAQTV
KNVGPLPRIDDLLERLGGTTYFSKLDLKSGYHQIEIQPQDRYKTAFKTRYGHFEWIVMPFGLTNAPATFQAVMTTEFRDL
LDRSVLIYLDDILGYSRTLDEHIVHLHVVLDRLRLAKYKANLDKCEFAKQELEYLGHFCHEDGWHPVEYFSQKVPLINTL
DDARKKELLAFVTVLKRWRHFLLGRRRFKWNTDNNPLTFYKTQETVTSTIGRWMYYIDQFDCDPCQIPSPANRAADALSR
RPDFCAIVTTAFDLDDDLQPHFVKGYKSDPTYSXLYAELSSDHXPASHYRISDGFLLLHTRGKDLLVVPQDRILRTHLLG
EFHDARLSAHLGGNRTLARLRQRFHWPEVLHDVTRYIESCAVCHRNKGRSRVPFGELKPLSIPRAPRLSIAMDVTSPFPR
DRHDHDGILTVVDRLSKYARFLPCKYHAAAPEHARLLHTDWITNQGVPDDIVSDRDTRFMSAFWTSLMAESSTTMKSSST
RHPQTDGQTERAHQTAQMMLRTLIRPDQKDWVDRLPDIEFAYNTSVHPAICVTPFELHHGGEKARIFADLLLPQAADIDV
PCSPASVRKYRDSLIKARANMQKAQIRMQQQANRRRLPCPFSEGDLVWVLSEEFALEQDVSRKLFPKWFGPWEVTSAVGD
DPAGPSFVINIPPHLPVHRVFHTSKLAIYTPPSADEFPGHQSQDPPSMDGHQEVDRVITHRKYGNKPMQFKVTFKQCTPD
DTRWISSTDLQTSAPLIFADYEKRRLAKEAAQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEE
```

EEEEEEEEEEEEEEEEEEEEMQSSDFVTRSK

1553 - 1572:	EEEEEEEEEEEEEEEEEEE
1554 - 1573:	EEEEEEEEEEEEEEEEEEE
1555 - 1574:	EEEEEEEEEEEEEEEEEEE
1556 - 1575:	EEEEEEEEEEEEEEEEEEE
1557 - 1576:	EEEEEEEEEEEEEEEEEEE
1558 - 1577:	EEEEEEEEEEEEEEEEEEE
1559 - 1578:	EEEEEEEEEEEEEEEEEEE
1560 - 1579:	EEEEEEEEEEEEEEEEEEE
1561 - 1580:	EEEEEEEEEEEEEEEEEEE
1562 - 1581:	EEEEEEEEEEEEEEEEEEE
1563 - 1582:	EEEEEEEEEEEEEEEEEEE
1564 - 1583:	EEEEEEEEEEEEEEEEEEE
1565 - 1584:	EEEEEEEEEEEEEEEEEEE
1566 - 1585:	EEEEEEEEEEEEEEEEEEE
1567 - 1586:	EEEEEEEEEEEEEEEEEEE
1568 - 1587:	EEEEEEEEEEEEEEEEEEE
1569 - 1588:	EEEEEEEEEEEEEEEEEEE
1570 - 1589:	EEEEEEEEEEEEEEEEEEE
1571 - 1590:	EEEEEEEEEEEEEEEEEEE
1572 - 1591:	EEEEEEEEEEEEEEEEEEE
1573 - 1592:	EEEEEEEEEEEEEEEEEEE
1574 - 1593:	EEEEEEEEEEEEEEEEEEE
1575 - 1594:	EEEEEEEEEEEEEEEEEEE
1576 - 1595:	EEEEEEEEEEEEEEEEEEE
1577 - 1596:	EEEEEEEEEEEEEEEEEEE
1578 - 1597:	EEEEEEEEEEEEEEEEEEE
1599 - 1618:	EEEEEEEEEEEEEEEEEEE
1600 - 1619:	EEEEEEEEEEEEEEEEEEE
1601 - 1620:	EEEEEEEEEEEEEEEEEEE

A0A388KBR9 **A0A388KBR9_CHABU** (1587 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

MAGADGSCPAQVEANENTIGAIPVVREEAHAVALSIVGCNKVEVATANSKEEREAEEEVMRFYRGEAASPSEETPSPDQS
SSPPKLDLGPPALTGEVVAFGIEEEEHHDGDVEDVKALAAVEEEEDEEDEDMKALAVEEEEDEEDEEDELEEEPKKQEEH
CQEGGDHAAETQGGLTSTSVPANGPEPPIPSLSATAAAEAEVEHAIDESDTAVVGESDLQTTDEGPGKACEVGEAEPPGI
QEWSFIEQTGLTASMMESEERVAIGSNQILVDYDSQAILLDRESKIDGHDVREEGEHVWAEERERPADVMMVDEDQSQVY
EQQAEKDRSAIAVGEDALPSAGESRTIVEGIGATGKATCDTQAAGDEEEMEIAATGEETCTAKVEEEEEEEEEEEEEEEE
EEEEEDDDVEVAIEGEGEEDVEEVDWEMVSVEDTIASRSPEIARKDQVGNQTGVEEMAREESSFVTIGLVLSSVGDREES
RMVEEEREITNISEQVKWTDLEEAIECRQEDGERGAEDMECEVGHAQTEHAESVGTQVTTGSHLDNASAAIGASIEVGNH
VREGWGMEEQNDEAREDEQDEEDEEEEDDIDEAVHMLPPEEPDADRFDQDGVESVDADIGEIGVGNESELDQSYQALSTR
DVAVQADETEGAGFVSEGPSAGGWSNGILSEGAPVGSPSDSLSERTVSSSEDFDLGSIVASSPVLEAVAQSTQTYDHLGD
GAGTTLSCMTAARILYHMAEQKGQVQPEDNVSSNIPACTDAESNTSLPLRPDTLASSSQVGELLAGDLKITPPSVIAAVE
NVGSVGLESTVRDTDDVLVDNSVPMDFSQVDGLHAAVSVGVVAGVLAERGVGDQGVLASTNEADADDKKSFERRDDDGDA
SRKSGIGQPEMGQSPSSDLKGAEDFLCMSEQASAALSLEAAEDGEEVGPQPHDQEEEDQQEEEDDDDDSDVVDDDEEEEE
VAFPPAYVHVVGAEREELAMETQSSSPRVAYRMDRSLVRMYGEGRRQRGRGFIREEDDDAESEEVVFELRDDEIEDIIYE
DADFKHDSEEGTSGGETEAEGEMDDEEDEDGDEEVVLPPVFRQPDMVEIEEELEASSSFEELQKLLLKAARERIQYQYHN
GRQAVRRVDDEKVVIRSGNRSGERGSMSEPEIQVASVSSWGKQLHDEDNAVASTSNLVQGRGEYDADSHAHRGSAPSPVD
INPRIPADRYLEPIPICFDSPSTNVPDDLTLPSAAKAGRERHRDSIGDGSFIKSTIVQEELWSPSRWRERGGQGLLYAYE
GLLEAKSSGQQRFQQALDGLRARRRKSGEGLSGEREGSVGEDGNEVRSTVPEQWKAVSPAAWKDKATQGVQYAYVGLTEA
RARGGQKLSEALEALRARASAAVSPAVSKGTGTKGAAGDASVPADDILDSDKSGATFKVKSACPYSGFKVERVLDVGGAR
SKGAGAGASEKPGRNREGEQTVFHTLSKDCKTVCSRSWQRVSTWTDTILKRKATTNRSERELSAPTSSSSSAPSDSAEAR
EGSGMAAAMFALFVFIVGMLFAVIMPVLYRLPVGRATAMPASKIQDSNLFMPIKQPAGSGDFHNEAW

385 - 404:	EEEEEEEEEEEEEEEEEEE
386 - 405:	EEEEEEEEEEEEEEEEEEE

A0A388KBS5 **A0A388KBS5_CHABU** (165 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

MEEKEEVEVEDEEKEEEDEEGGEQDHDKEEGEEEEKDEEEGPRPTRREESTTLMRRRGGEEEEEEEEEEEEEKEEEEEEE
EVEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEDEDEPEEERSEEQKEEEVEENDVNDDEREEEEEEEENDEKQKEEEEA
EMEGV

89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE

A0A388KC87 **A0A388KC87_CHABU** (5043 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MRSKSSVTAHQVSGPRIGPGTSGGVDYEPWSLEFDDVFPQVCPMLSQCPGSSTHSGLEYASLHGPGNEPGTTLDAGADNR
NGDGQSDFFYSSYDMGISEIDCTYPDLVNILSLGKLTCREEEEEEEEEVEKELRILESPIMVLFADEEKREGGGRKEDED
EEEVTAAVTGIVPGFPLSSTAHVTSNSMLDNGAARAPNANAADGENAEDLRERKGREECPVIMLFADEEKREGGGSKEKE
EVTAAATGIDPRFPLSSTAYDTSNSMVENGATRAHDANAAVPAERENTEGIQEREGREEVTLGVHSPSDREVDTEAGSER
GDGQGSMIGCHVVPIIVLEEEREVEVEEEEEEEEEEEEEEEGGGNILRWKTKGANMSEGGKESNKEEEEEEEEEEEEGVQE
EMMSLSTVTSSRTYNLSSSEEEEKKGCEGSEDREGEKKLLMLSVSSDGYERNEESKAGEGKETQERTLTCPAVPVLEEKK
KRDWEQKAREDEADTAKIENRLSKCRMASMVSQSLDSSHKQEKGEEDREGEEDGEVGEGGEDGKDGEGEKKKDAQKEAAK
VVRVGERTNEEEEEEEWMSRCPMLQAVIGDCPEGPEQWAESEERKQSVGDSGKGIRYAMLPDIEPLPSRNEERKGSVCEE
EEEEVQVPLQEVGEAERCVPNYPTMVAQSRIVDDVAERQHGVHPSKAEGKEGEEEKGRGCGKEGEDGEEGEEEKVGSAEK
HLIMPGLSERLGVKEDKQGTEERKERMGAKVDRQEEEWEEEDEREESVWQSLTEGLEDKTVSPLTFPMPSLPGDTSLPSL
HELSVGKEDKEEDKEEEKEEDKAGEKEKTVSPLKFPMPSLRGHTSVQDLHQRWSLGKEEKEEEKVEKEEEEEEEEKEEEE
KKGKEEKEGEEKEKVELISWESLADQHSYCYNHDYQLRAHYPSFEMVALVGGSILDADADDAGYESYDDGSVLQSSAIFS
HTSGTIVTLSDEDRGPPVEAEGLLKDQQTIHDYLDSTTFDMTSTNVPGIGFGPYGAGLEISYSDCLGPLVNPPTATSANG
HKRSENSSAVVLSEQSEPTGRASTICSEVTANLVHFHPACSGDSGEPQARALNWSLSRPDPPVNCHPADGCDKQTCSTYL
SDLEHCQATTSRSAEPRSWTSSRTAAAGLVHCQSSSTREGLSHTRFKDTGGLGLGRCRTSAQSAEDSEEHGSPNVSSRGI
ADVVRSKTSDEDQKQWKTWAWPGNLSDLCDGPSSDSPHAECSSPTWMSARALAELLCCDSAAVAQCQPEKLACPTYKFDQ
SCSQLSEEVYYFHKDQNSSPGSWAMFTHRDGLQSAPGPYQLGYHSDTCDEVLYQVAVPSRDRVPGAGLQSGPGPYQLGHH
NDTWLGHHSDTCDQVLYQVAVPSPDRPPGAGLQSGPGPYQLGYPGEMCHRGPYQVAVPSPDRSPGAGVVPPQGALWPAAP
SSSQPQDVCWSNHANLPITTRNDSESLTIVLSRAMNCASRDCSELSFPLTALPCYATLAAAATSVAIPPPRQNYGTHPDH
SQTRTHLPLTATEIHEEVGRSQRSCTLSYLTPSDCSAGTTSLSVDVTTTSARGTDSVDVTAANARGTNSVDVTAQTAANL
KGTISVDVTTVNARGTKSVDVSHVTAANARVTDSVEVTAASSKGTNSVGFRTVNARGTESTDGVELTAASSRLGLGCAGP
EQFVVPGPDTAAGSGQEPLKECLSLEQPQEDSGSTFKHDWSSSLDPTGSLFIPNGWNLGDTSHLNDKWDNMSDKWDHISD
KWDNMSAMLEMQQLQLQVDEQVSAQGRDMDDDEDLSVFVSSLLEDYENELGQQECQENRFLDFQSIRPGTHEGHDSIIAA
TSELSELALRTHAYFDSRDNRPNYGDVDRIPLSLAADLALSEALLSPNCQRVPNTSPNPSPIPIPIPNSSSSCSPQDSVC
GASLWPNSRSILSTTCVPDDPDPDPKPDPVLDPKPSHGSDRSLTPTLDPKRHPRGLSPNPRPIPKQTQSLNASRRGSLTP
TMGPCGKSAIGSFNHSNPSFTLDPGSVLEPDLCPNPNGYPGITSNGSSYSVPGPITGSKASSGSNPRLRAFSRSIPSSIP
GPISGPKVSPSPSGTLEPKFGGRTHRVGCFDPNPFSPGPAQSHASLCSQTAGTSSIQKDVNVISAPQTVKPEVGWCREGS
HVIHGNGVIGTPDRLGAVELSGTVQRWRHCRGTTGTRKRKVEVQDQYFWARAICKVLADTPPVSASWGVDQQEGERAPIE
HDTQAQAAQQQSPIGGCEVGDGGSTGRESKFNELDLRQAETVKGTTRRGRGGKRTKSMQSRSDVDGLESSNPKKMPQVSV
QATYLKLNYGLGPTESGERVKGRKTRKPRQCSGKRINFKDAHDKNKGNTSVMRQCSGVSVPSDPSACRQFREKPLPGVSV
PFTCRRFRPEPLPRQACGISMERRSAAPHDGPGPRLDFQRESVSVGTEPLPCQACGTLLGSLSAAPHDGPGLEVQREHVF
AEVSGPPSGPEFDPGAVRADASSPCQEHGVTVHIGREGRHKKTSLHGAAAKVWCICQRTSSLESGVHPELNPATCGRSDQ
TDPEPEGDVLDEMVAEASGRTQVCGPSDEQTGSKPGPETVPAPGSNRDKQVEQQQSDNLPSPPPPQAALLVARGSNPPKE
LLPDARQAAHADNVDVNAAFSKQIIVPEPEASVCSAAVQQQLDNANRGSSSTSRSGQQLTSTSSRPYCGASSATPDSRSQ
EDTGHTAAAAPRPAAVDVQTDPDTSVVADVANIKNVDKLLMATALSNRFTGSQPRCCDLSSVSTGARRHDEGEAGVREKE
LPARKSSGVTGVSVTGTPACTSDLTCATLASASAGTAACGSAAVAAEIGTSASIIAGEQAPPRGRLNDGQDEDREGPPST
SVFPRSQRTLIMDEYKLLSLVGQQHRVSAHHSPKATNLLNEPRRRASPDTFKMLTFGEWCGEADSHDELVLCSGEDGLDG
RPLISNRNQSALTEEGEEEEEEEEEKLTAHQTAGKADLDAHYGGALAEAGDFNVRKLHASRGSGYGVTSKTDSKAHHHDR
DQGHDDDDDGALEEDVDVHLKSHRHGVPREWVDVSLKTPHNHATNPGSNDAPPGSACEWSGRGDRGSECRDSGKTLEGRET
DMLNRLSTLGLPASTSFSQPTSNLVTSAVSTFSHPVLVELPPCPSALHGLKSGGDAVEMKSHSEENDRTNRRWEGRTNNN
INNNNNNNNNNNNNNNNNCSSSSSNKNNTGETSLVWSIACETTGTGDVVTCARTRESGGLGEAECVHTDFTLVLVPEPP
AFALRHEMGQRGAEAKDDVNAGASSGEEIAREGGGGGGGGGGGSSLRESDGLAETLRLRTDACADHALAVACSSSRDAR
SVECVRIVDDVNGLNMNEGSVEPPTKPEISAASLGHQEEGSQTSTQGPNLGGIPDRIPNRDPGQIPNRNPSQIPNWNPDQ
KEATGPSSHLARSAHGTRSCDSSLQDELAGRLRVLRPRTCLHWEEPNGNPDRKEAAGPCPHLGESDGTRLCDSSLQDDEL
AGRLQRKKPRTCSHWEEPDRHPNWKEAPGPRSHLGESDDTRITRSCDSSLQDELAETLPRKKTRTCSHCEEPSFGTFGQC
HKLSMQGEDLPDNSKWKHWKGVETPIPAATQLVETREEIDHHHGMESRARHAGCVLNFEEQKGEAHRRVQGGEVGGWDRG
EEGGSGNLGPEKIGESSRSQRVVSKESCGIKEMDVAVKAIGISPHREDDNDSESRGTRGLGQSKEVSLKEMEEGRGKLGN
CSTAGKGAITLHCLERGGDADIAESVLLFLQQQEEEGDGLVGQGERVDVVERSYGGELASLEAIARSSREEEEDGRRRLQ
PEEAAVTAVVIELGERGEGSLSSHQEEEGGGSCRSVREVRAVGVEALEGLRRREEDCLEAIGRVDSMEREEDEHGRKLQL
GEGCGKRSLERGGACWKVGLQPGAACGIISVHEGGACRKVGLHEGGACGKVSLNEGGAVEDVGLQGVEAFGEASLQRREL
DNMGLEVGGGISEAEVVGENSPEGEIPCGSLQRGERAVGRRQGGEPHGSPLVVLPTGVAEGVGLSKGKEVTLTQGGEPHN
RMDALVTAKPGAATGVSLSPASSPRGEVAERYADAEDDHSAGVSSRGEVARVGVGAGGVIGGGGGRGGGGSSLGQNPLEP
AAEVQDAGLRKGPASLGPSQVQDPAVTEGPASLGPVRKGEHLHSEDVHVVPASVPLGNPDPLQHGVRRRLSHRNGCSSYH
KGGQEEEEEEEEEEEEEEEEEEEEEEEEEADQRRREVVEEESPGGKWADSERVLPSSEQTRRKRTRAVCDDGSLCRAKRRRQG
NRPSTATTSILSSPSVLAHEETVFQSQRRGKQYSEIERCEHCHTTEGTPFQSTPVAVQVKEPVLRQVPGPAAEGDAVGGV
KVERGTQEQLDDVNKTFWKSISSALRRLLLRTREGVDVNNKGTRCQPLSAGARGRNENDEIRCEFELFNTENSVLSRGLP
VGLDRHQEFESWILRMEEMVDKVMGEEERYLHKIDQLWSELQGTTMDQGATGRRKAIQALRRAVSASFHRLRFQILKHFA
KVFSAHSTSAGGVSCSSSPLDRPTRVTDPTCVRSWPGPGGLNRGGGPVKRLKTSVEPGLPVGPRADQNHRPGAVEPVSGQ
YLGAQCGPAGVYLAAGPKRRCGVVKPGFPEPSLPVRPGAGQDQRPGAVGPGSRRYLGAQCGPAGAHLAPGLKLQARSDTG
LPLTQRPGRDLRPGPAGDILLMGPGPVHQVHQPAGPAPLGPARQHFTPIYTTAPETAGLGLGRGPEPAGRVRRPGVACGP
WQHTCERAWQPVGAHATGGTAPELNQSEGSLRLVSGPDFEACSVPGLGGLPVEFEPGLAPGVETGHTFERNLDSLREGVS
RVSNWFINARVRLWKPMLECIYQELTEERQQQETCGSRQFDRRLFSAKKRKRECQSSSSATVHPFASASENEADDNEEDD
DEEEEEEEGGGEVHMKEDEQEDRKDEGEEEEKEHIVKRNEEPKGQSKEEEEARVWDDAADVSDMLGCFTTRPENNLGVAM
IGF
```

4245 - 4264:	EEEEEEEEEEEEEEEEEEEE
4246 - 4265:	EEEEEEEEEEEEEEEEEEEE
4247 - 4266:	EEEEEEEEEEEEEEEEEEEE

A0A388KCE8 **A0A388KCE8_CHABU** (2439 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MGQKLSAEEVAAQAGAGQHTVGMFDWQAMGLDENTMCDPDLWQKFEVNGQRVFVEGENGAAGGSSRKEMVMPRGRREDDP
RLASCQTRGAAAAAAAAGAAGGGGGGGGGGVARQLSIGKVSREETMSLNDGMCFPLSPRVQPPPTEGFNRTLLERDCDRD
PSWDEAMGEEEILEAKEWVTSPTSGNTKVLMKRLSVKKDGTVRESIVGEVREGVLHRYASADIKHVNNEGKSDDGYCVLD
RCTFLKGKLTNIGLLLIFYQPETGVTQAATALACARLSVDDTQHMMMDCTESGRSPRPLAKRKREKPKETGLLRAVEEDA
EGSRTEVVVATKRASQHDWHSLSSQLAEEEEISSDAWERYRKRVQRPTHEEVQLPDQQQQSTTSSDVGVINDEQMSIAMM
```

```
EDLRPAGIGCLLETGVLSMEDGNDDGQSGTEQVQAADSATHKSSEDEDEPRPLLEDEAMVAEVVGDLAAVRSISMPGGET
EDISQRNGGGVSSAEKEDHSFGISQRIITCSGEDSSVDDLLAIAMPAELQQPVSESTVEQLDVETVAADPSHAPINAQES
DQEFLSGHDAASSGVLTENPLGAPEMQVIPALPQGEETEIVTRANEEEEESDVQCEPFSNLLEKKEDEKLLPPILSTDLD
LSAREVDFEFVARHAPVDEVERNMAADFALQTVEVAKRAEAGKEEKLQDEAHTAEEETAKLIDENLPLVVDETEAVETGM
VVSTEQELVHVEAAQRVVDDAPPMIERSALEVDVNVSDSHNHVLDTAETTVPAGELEHEIPSASAEDEPRVHEENVMAEE
APVKEDNEEADLPVKEEDQVESKCTAYEAEPSPAMEEEELEEDDKETAQEDEGDGSGKEEDEVLVEDKDRIASKSVMCDA
GTLLMTEEQEKEGKEVLEEKMVEREEEVVTEEEEGEVEIKETQKDEEGVMVEDEDQTTSKGVMCDASTLLLAGEEEKDEK
EAKEEKVEAREEDVMMEEAQKDEEAVMVEDEDQTTSKGPGVMCDAGTLLLTEKQDKDVQEAEEDKGKKSEEEVVMQRTDT
FTILNLSEGEEAASVVAQEAASVVAQEAAPVVAQEAASVPAVDFSENHQTEDVILPVNVDDKEREANDVAHGSLGIELSL
FGVSVLDFEMDEDDSDEMIELSKMLVQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGESDDGNLAASGEKETFDMEPM
PEEPNPNHLPSETEGNETVARILRDAECQATQTDHAVKEGHTGASCSPETASIHERPEMDDQLMTVCPHIAISCQNHAEV
SHVTESIIQEVVMEEEVVMEEEVVMEEVAHATESTTIQELMTASREDLQTENQSDTAIADEVEVQAAPAMLPSESVFVEQ
SVERESQVIAGMLNTEHGCESIVMEMASEELCATAGGSVSECSQEERPIPSTTPGPDVGPDSREVTVARIKSDNDRTEED
GGLRVGCSSFHRKSEKRVDENGLLSVRQETGSCALEKEENETYELERTEDDVDRVCGSSVEEQMLQLAAEQTQLADGMTC
IHAEAVIVSADEAEAAVAPALRSREENDSEEVHLLGQAVAADDTKDVQNEEPVILDDREGGSERSCLSVEHGLEDEEEGM
EATSAVRLVHDVNEGKKGEDGLQVSAVCVQQREEVMLSHKNGTDSDTKEVGDGVLLSLLDVNEASEAAPHQGSPLGNSEA
MQIDTSSPRSRTCLNRQPQDMDIWPGCSYEMMQMESVRKQQITCTDEASSAQDPGEVVEAEDAGKERRRLPLRISVSSPH
RQGLACCEIPIEYLVDDGEDRVAKDNSKVGSLGMSMDAVPVLRHPESIEVLDHLHEVARSWSESGFAGFDDHRMQPGLIM
QNGRRGLSDISGSIDIFDEAEMFSEAWSDKWEQRWGIAESEGRRARTKPRTSDLSVAQLSGRSSSSSFCAPSEDDSEQVI
ASGTVLAKVQEFTRKVREKQQAANSGHSPSASSTTSSSGAQDFQFSADGSEHETAALLSCGDASSKLSTWKAKCRASGTS
KSGGLCVSVGKPKESESLPAEVGGVLARQTQKKQESNVLSAIGRSTEGERPAGHRRQFSSGSGKGKENAILRDGNTQACA
RPCAPLEACSGSKNAVVIYGLFDEEDDPMLNPHDENKQPVVRTPTRVGVNVRSLVKVPHQVQHQVPDQIPHKVPDRVALN
KIPNRLRGQDQVPGPVPDPVPDPVPDPVPDTVPKKVPDPVPNPVPDQVPDQVPDGIHQVPDGIHQVPDGIHQVPRSRCQV
LGSRLQVPGPIPNPIPDPVPDQVPDPIPEKVPEIQFQIRFQIRFQIRFQISFQMAFIRFQIRFQIRFQIRFQVPRSRFQV
PGSRSDSKSDSRSCSWIQFQIRFQRRFQRFSSRSGSRSGSKSGSRSSSRFRVPGSRFQVPGQIPNLIPDPVPHPVPDPIP
EKVPEIQFQIRFQIRSQMTLICLNEVPNWICGWLHEIDR
```

1148 - 1167:	EEEEEEEEEEEEEEEEEEEE
1149 - 1168:	EEEEEEEEEEEEEEEEEEEE
1150 - 1169:	EEEEEEEEEEEEEEEEEEEE
1151 - 1170:	EEEEEEEEEEEEEEEEEEEE
1152 - 1171:	EEEEEEEEEEEEEEEEEEEE
1153 - 1172:	EEEEEEEEEEEEEEEEEEEE
1154 - 1173:	EEEEEEEEEEEEEEEEEEEE
1155 - 1174:	EEEEEEEEEEEEEEEEEEEE
1156 - 1175:	EEEEEEEEEEEEEEEEEEEE
1157 - 1176:	EEEEEEEEEEEEEEEEEEEE
1158 - 1177:	EEEEEEEEEEEEEEEEEEEE
1159 - 1178:	EEEEEEEEEEEEEEEEEEEE

A0A388KCR2 **A0A388KCR2_CHABU** (724 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MRGAVGGGGGGGGGGGGGFASRDGSRKRPAGGSAVSGNVSTEVKLSIQRGGGGRGEGGGGGGGGRGSVRRDHGGDYGLP
MPMVDAKRQRSDNAATGRSRSPSSHQHHQYQHHHHHHHQPPPASQPIKRGGQSSADVVGDGSESYDHNQNHNRRMAAAAP
RSPRYVNRTGHTASGHGRMRNSHMAPPADPDPTQAESSETESDSKGKMVGGGDLGRVEDYRRRVEGSAAGGGAGGRKAGG
GRGGGRLPSRSPGRSSPSMNVGGGGGGKGLMMGELGWRGGRERYDGGGGGGGMRMRGALRERAGDAAIAAAAVAPRAGAG
RRAGVGPGAGPGDRDYSGTETEARTEGEEDEEQEVGEGEEVGGREEEEERQEEEEEEEEEEEEEEEEEEGLHVGHAGDVPG
GRRRDLASRASAFPRRAEQRAEEGGQQEEEEEEEEEEEEEEEEEEEEQDRGVRVEEEEERGEEAQRQEEQEDEEEEEDLR
DVVRVRKGGGGGGGGGGGGGGERGEKVAIARMKQQKDLASWYRAECVSCCRELLGMQRKWEQELRSPIAGYEDREVFFNL
QRPPAPPAPPPPPPPPAAPLPLPPLSSSMANRMQQQVSSAVPLGGSTRRHQSTPSPKTVLDYNAGRGGGGGARVGGVRAG
GGGGGGAGGGGGGNQADTAAAPTGPLPHVDPPRVRHSNLQSHSSRVHAPLSSASHVAPPPLRQVVRVKTEPYSPVVRVKN
EPYV
```

428 - 447:	EEEEEEEEEEEEEEEEEEEE

A0A388KCZ2 **A0A388KCZ2_CHABU** (218 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MAHASIVDSQRGERAEEHAWRNRDGRAERRWAHERGRHTKEEEEEEEEEEEEEEEEEEEDEKEEEEEEEEEEEEEEEEEEE
EEEEAEGGGGGGVTSFAIDGGDVPGVGSGTVYSSFEKLLNTLRVVSSLRETGESFSGVRANIFAAPRGPLVISLGGLSRQ
LAFTGGGRDCRGFSMPWCWVVDRYVHPRSSRRCREERLQLGCGVIFVSALTTALSQRC
```

62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE

A0A388KDK7 **A0A388KDK7_CHABU** (381 aa)
CCHC-type domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MFLTNGPGGGGQGSANATPVFGNRGNQNVVTGQGYVDTNGFARGGGGMGGGGGVCYNCGKPRHIARDCWAGRSRSLGNQQ
VDQELEEMKEHFRQIRRERREMEERRKLEEEKKAREEDELRRSQDFARKAEEFKLQLRAELMEEWRRNNARNRGQNDVHM
HMKDDTETDAEPRTPLTGGFKGLAAGCSQKVLIEYCISAHKIYSSKKADVLKKLCDQKGLKYTKKPKAVELLARHQVELA
YEDYEEDRQTNKETTKTKASGTPRKEFTKDRTTTEKKTQKAVPVIISGTCGAYKRGLPIVRTRLIEALEDYVRDTIEPMH
```

FMIGFVRGELPELSSLQMEEEEEEEEEEEEEEEEEEEEEAGGGQTLENKRGEWAEQEGFLDG

339 - 358:	EEEEEEEEEEEEEEEEEEE

A0A388KDT2 **A0A388KDT2_CHABU** (1274 aa)
Reverse transcriptase domain-containing protein. *Chara braunii (Braun's stonewort)*

MDDYPMYGLLVGFSLWGTLWRLLFPLGFWPTFTCRVGLRGGTSTQPYTKEEEEKMAAILRERKEKKEAKKKALQEEHATK
LKKIEEEMAREKERLKKEEEEKLKEVDEEEEEDETPLQRKRGQYSGSKDDEMEKRISEWVANLSLGEEEEVAIYIPKDEQ
EAAMKKWDAEEDVLKRQALEDEKRMEWKLAVMREKKRRVDVAAEAAEELEEVKKIEEQLAAQDELPKKMEVIARNVARLA
RIQAEQYDFSRSQHIAVRSIRFGFRDFARELVGAVGTEVGHRLDKTERFCAGAIEGVKAAVPKEEEARPRREPVKVKFPD
SYSGKREENFDNWEANVKTYVHLQQVSPDQHVLIAIHSLRDEAASFARSLVRAANSNDDAVAYSSFTPLIDFLKLLRERF
ADVAQSVEASDKLLTIHACKWKSVRALKSTMDELVAVPDHGVTDTQSVALFYRAMPEAFRGHFFAKSEDPATTYDSLSRE
VVTFEAKSVSVSSLWHKDLDKGKQWKGRTISGQVKTKDSLVLTLDEGSVDEIPYDQIEWGLEEEDSCVGQGRTYAAVAAG
ARPQGGGRGQGQGGRASGSRFQGDQGVGGRGGNRQAGGRGQVKREQLEEQVLVVYVRPVTEPKEEKPIDPAIAKLLEEFK
DLAESSTGTVSRPIQHRIEIEPGSRTPKGVVYRMSPWELEEIRKQLDELLEKGWIRPSSSPCGAPVLFVPKKEGELRMCI
DYRGLNAITVKNVEPLSRIDDLLDRVQGCKYFSKIDLKHGYHQIEVHPDDQYKTAFRTRYGHYEFIVMPFGLTNAPATFQ
QCMNDLFRPWLDSFVVVYLDDILVFSKTLEEHQGHLRQVLEKLREANFKINAKKREWAKTQVLYLGHVLDGDGIKPEDSK
IATIRDWPAPLLKVVDPSLPFVVTSDASQYGIGVVLQQDDGHGYRPVEFMSARMPSEKVATSTYERELYALRQALEHWKH
YLLGRHFKVYSDHETLRWLKTQAKMTPKLTRWAAEIDQYDFELKPVKGKYNVVADALSRRVDYFGAIVHYLDIGSDLQQK
IREAYAQDPIYSDLLKRVKEAPETEPNYRTTEGLLFEKTNVFDRLCIPSSEEIRSLILGECHNTEGHFGWQKTLANLMRA
YTWPGMKNDCVEYVRSCKEEESEENEEEDNEEDNDVEDDEEKEEEEEEEEEKEDGEEEEEEEEEEKEEEEEEEEEEEEE
EEEEEEEVEDKGKQTHLAWAGDGAWVAAVGRRSSATATSNSTDRAGRSHVRESAAVPQNSNLKSARSGSSITEI

1188 - 1207:	EEEEEEEEEEEEEEEEEEE

A0A388KDT6 **A0A388KDT6_CHABU** (1575 aa)
WD_REPEATS_REGION domain-containing protein. *Chara braunii (Braun's stonewort)*

MAVGGARQLFLCRLPKASVLGSRPPGDPSAGADPLPPPTSWQTDPNDPSQVAIADGSGILRLVRVVDQDAGPGFARAFRC
SDDDRERWQYLGGHCQEDQLRVSACAAYRLFMVCSTGQEDHGTSVSAAGRPGSSAGLASGPGPGSPAHAHRTQYDRQCNG
HVQPNGRMEEVDNARSRPQGHLVPILRPWGAFSYVRNKPGEIFFHQQGSNKILFARLPGAGEGEGDCGGKDLEDAGQLYG
GQRFGRQARDGDPPAGLGDRSGGERVQGGAEGGGEKITVRGGELCHPQRLMSNSSSMVYSLGNHPASVACFAVSPKGSWL
VSGGIDGSLRLWRLEDGVLISRFDAIEGKGGGSLSHQPGRTTADHVARSSGTIGRDAGTNGAEMVGVAVLERAAPVAVSS
WTDGTVVLWDAKTPHMRACKWLSSMGTLAITAMALHEVGGVSERNGHLPSNQNALQHSSVMQQRSGNLTHCSIPMIDDLG
AVTRSAVTAANPTVEALGAVCVLAIGTEEGEIHTWVGREKKTKLGGNRTRGRGGIPNEGVGGYRRRQEGEEEEDEEEEGE
EEEQMWDRARRPEEGECQPGHNIGNANGCSDSRIRGQDGRPTSAASVLRMHVISAESKRETRAYDWEHVSVTPLPLPVPW
ERSRGRAARRVLSICFTSCGRSLVALLGGRGNENRTDREEIGEEKGEEKGGKGMRRTHGVEPLALPSLPPLMLCVYDSSR
LLQSSRSRGKGGTSSSLRLCGASLLDGTKENIMLPMRGLAGWRLLLQPVQLRRQLPHEEEEEEEEEEEEEEEEEEEEER
EAVDDLAEDRKTGGASWNASYVGVREGEGAKIQCGGRRAHHHVPHRHLGNWNAGGGGGADVLLAVVVIGTSGCVAKGILG
WEKIPRPAFGESNDRSPTRNRATVPSQREIDWHQDMCATQSRFPNGHKHTQGTAVSEEGNGTRNVTSRHGTGSQGEDVSA
LVGYKDTTGTGAVVRESSMAWEGILSETTSGTARTTAAAKVGTMSPVDGIAEGKQIAVHRAELVEREQATDKRGRNLQSR
FSDRGGSGVGSLHARGDAASATAGREEEGGGGGKGGVQRGGGQAPFAEDRGEIQASAGGRGGARRPGAGEGGGGGGGGG
GGGGGVGGGNNWEQVQWSGGVGAFAGRGVMLRSTGAGRRVHEASLTTAIGGNTGRQDDLAKGTARGLGNAERKENSVGTN
SFRERLTAAEEETEEKEIPVPAIPPLHVREALMRLKKTAGGGDGTISAGGELQSTTSKKQFATSLSRKKMSKGGGGGGGG
GGGTAGEAGLTSRSRSGVWFQPGIASAKDRGDAAASASLLSRQQKRMSTLPEVDGEVENSRHGGEGTGRKEDRRNPSAPC
SDDISAYFDRRAGGMAGDMSRGKSQWNCLQEGGREGSSHLDSRDCDRGRREGGGGGQVGGGFLGQTSQSGGMAKGLADQG
NDRLGPKINSTLQLIQKLQKLKTKVRDESNNLGKEKKESKQCEASSSRVPSMGDEGRGGGEGSTKGRAEEQGLTDGGGPR
RQECLERSASEQGNGDSLGKRKGDQSAAGARKGHGHTYNDLTPLDDPVDCDVKPK

778 - 797:	EEEEEEEEEEEEEEEEEEE
779 - 798:	EEEEEEEEEEEEEEEEEEE
780 - 799:	EEEEEEEEEEEEEEEEEEE

A0A388KDY2 **A0A388KDY2_CHABU** (369 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

MVNTRSGASTTPYSKEQEEIVASLLLERKERMEKRELIKQAKMLALLEEQEAKNRQMEEEMEKWTKEQEEKMAAIQAVVE
KEEEEEEEEEEEEEEEEEEEEEEEEEEEEVKKEAALERRRGEASTSKEEEIEKITQEWAAHLELGGDREAELAISQEEREAA
RRQSEAERDPVRRRAKKEEQQRAWKWRLSQEKVRRPEAAEEAERDLKAVEARMGKIKAETEIATKVETLTQSVESLLIAH
RDQMQYLRSQDIKLEAIRTGFKDFARDMMKYLVEQVHLAISKTKEFCIGAIEGAKLAAAKEEELAPPRHKKVKGCKYFSK
INLKSGYHQIEVHPNDQYKTTFRTRCLERKWAVKKTVAIANQRGGRRRP

82 - 101:	EEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEE

A0A388KEC9 **A0A388KEC9_CHABU** (359 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

MNWHRLSPFGLPSNLPTFWQSAMDAPLSFRVRQLDVSILDADKRTEWWNVYYVALSFCFLEVIFHWAEPANKDEEDEVPD
DDVEMLIIQAWRTDTEGELLGILFGKVRGGHLEPITSEVLVLLAQLLDDLPLDILSRCDERPTPATLTRTLIPHLLWSMC
TKLDGDNGYYPSLGHYLVIDVTDLTLWDPITRRVEAEEEVDEEEEEEEEEEEEEEEEEEEEEEEEENSGAESDDPDYNESQ

```
ESESGRSGSDGSGSPSERSKEEDEAATQKRRERAEGKWPVEESDGPTMRLLKGDPTPNPEPPQEELGGDSVTATEGSRSR
RRRRSPSPAQSSPPPRPTVRIRGDAGARASSPVVIPPSP
```

202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE

A0A388KEM1 **A0A388KEM1_CHABU** (1080 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MFHKCFEDCVFHSERIMLKCATTRSDGSECSLSVGEEEHSHDVERKRLWRKRRDGDGDDNSRLQSAYSHASPSNHTMGDS
LLEYLRMKVHPDVERKWLWRKIIVVGRHDRSSSSRISTREKTKKRFNWQRPTSRISVFTGGNHYAGVDESGDDICVAANA
KCHHPPDHNDAGFDDRAAAVYLDCSGKAEHEDGGGSGDDGAGYGGDRNRDRDRDESSSSSRQPQEDEHAEEEEAIASMNR
HVSVSRHEREGEGEGDEGERDGERGGGQGGEEEEGMEGFKLEQTELESVDVVRIDGTTGSHPKATLILQCFPGKDYVFH
YAAMVATYLKLTSSDRHSYGYGYGYDVPSFSLSSLTSLASGGNAQLTPPPPLPARNPAFCKIAPPLPQAFCTIAPPPVFY
KIPSIDECSQAIATSNLALMPCVDIVVMGVVDRLPSVVRDGDGWDGGERRRRRRRPEKERYGVDDCGCGRLPPRFPAVPA
TSGQHIDDSEVEEEEEEEEEEEEEEGQVFSWYIRTLREDDDGYGARRSSSRHSQERRLGGGKDDVDNITHPTLLQGSGPN
PAAALGVHHNPLWESSVPIHDDHDEEEDEEEEEEEEEEEEEEEEEEEEGDRFFSAERRGISEEESDNAFGYGCRFPLRRP
DCHERPRTVAFLGCRSSFWGEIAGTIIRFLAGDRRRCCSCRTRSCRGGMTKDGYGGQAKESNSLENKRKKEKKKKKKKKK
KKTMMVERSSEKNIRKNDDHVVDVDKPATPTAMVITMGEGEGDDDELEDGGDGDQLPDDRDAEIETKKKEKKEKEKEKMTGV
AMHHVDEAKEKAKEKAKEKAKEKAKEKGGGGDDRRCCSCCLQAVIYLGKLGSLRENHLPNRCLATGDVSFVEGKMVTWHN
LLADVVAGCEDVVYGRHITLPSVLMETKEWLAHVESKYQQQQQEEQEEEEEEEGLQQHQQELQTVTDVHNRDDRGEEEDM
HDDLGKGKVRERKEEQKEEKEEKEEEEENQKTDVCVSFVDPEIGHMAQAANEKGIGFSYLHVVSDNLRRKFEEDLANERR
EEVVLARQNLYRRMDEILEAYFVDVIRRWSVVPTKRKKET
```

589 - 608:	EEEEEEEEEEEEEEEEEEEE

A0A388KEV0 **A0A388KEV0_CHABU** (724 aa)
Integrase catalytic domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MHTCTLGQDVRIKHGWTTCCPHPRAVSELHNFINWTNRTAAWQKRFQVEPLEHQAMDKLLTFSQNNMPSGDWISEFQRLA
SMPKLPMTFDDIKLYFIKRSCPALQNVLTQVVENLNRSEELFNKAAHIIVTNMEAKNIGRSARARISIDRKWEAIAMDII
GPFPKQKPGVDGILTVVDRLTKFAMFLPCRYHAKAPELADNLYVGSIRTKGYPKEIVCDHDTRFMSDFWLAFIKRWGSSL
KPSWARHPQTDGQTTRASQTTQVLLRTLIRPDQKDWVERLPDAELAYNSSIHPAIGMLPFEFEHGSPVNSLFDTIILRAA
ESDDHLLFTCRMQERLVKAHNQMSKTQQRMCQQANLQRLPCPFCVGDLKKKKKEKEKKKKKRKKKRKKKRKKKRKRRRKK
TSGGEGEDEEEEERLWRKMKTRGGRKEDEEDERRRRREEEEEEEEEEEEEEEEEEEEEEEEPRRGGRVNPSQREECQEEERDD
KREEEGREEKGRTATTRRMNGRKKAEGGGGEDGKREWKEEGKITRGSGMRRGKTSRSKRTTNRRGRTQKIYSHVAHLVSS
GAKLSELEQQQEEAGWDDKRDEEKDEEGEDYEGEENEWQEKEWKEEGEDGEWEQKGDEQEWHEEHNEEGEDDEWEEEDGE
NDEREEVDGELEEAEGEDDKQEKEVDGQEEEEIGGLREGRRRRRRWAIRRAKREADSQAENTEYSQGSGSWVHRKESQLH
QLKG
```

438 - 457:	EEEEEEEEEEEEEEEEEEEE
439 - 458:	EEEEEEEEEEEEEEEEEEEE

A0A388KFM0 **A0A388KFM0_CHABU** (1285 aa)
Reverse transcriptase domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MVGDTMGENHEESKMTMGLEKMVGDTMGENHEESRMTMGLEGDIDGHGVPVYYILYSDPGLCLFLVGWLEVLWAIWGRRHV
RAGVYVEEEQEQEQEQEQEQEQEEEVLEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDQWLRGIQRWQDITCSADEGALT
REQATSTVTRQLQCHVSSATTDTVPRKQCHVRHIATSDTVPRQQCHVSNMTGLPGQLANEPIADYKKRFQAQLAVIEAEE
QRQLAAKAAQLQAEEAATAEKLQLQAEADAYAQARRKEAQDLLQRHEATSIENSSSGTLNQTAKTEHRKSSIRSSSPNSQ
NQELQQQYKDLKTQHRELANLRRMVQSHEDATRALNSRVLDLEQAVPGPDAGASSSAPSSRQLEERVDHVVAMLGDICTF
AAPTTISSQLDTLKTEVQQLQPTNTDGNPKQYKMPTFQLEKFDDYTHQDAVLWWEAFTTQLRILPVAKHAYIGALFMNSK
GGCQIWLTHLAATHSVDVADLKDKITWEELTRLWKKRFIVDDAPALAINRLFTMSQGNTATRDWLTEWQKIAALPDLDLP
FTHLRPEFYNRSCAALSQALGDREHYASFPEIIDKEREIIKTNRAAAHEKSTWQPTYVEKVRTGPRQQQFAAVQSDSGED
PAATPASREAREDHPVNFYLRTVHIRDRNGVLVPCTVAPPHPSVSCHVVSATSMRASIIRDDIVEMGVCFLHALLPQDAS
STDSSSDPRITELLDAYSDVFEGPHVIVLDRPIRHEIILQDGAVPPRGCIYRMSEEELSVLRAQLDDLLEKGWIRPSSSS
YGAPVLFVRKTNKDLRLCIDYRKLNAWTIRNVGPLPRIDDLLERLGGAKFCSKLDLKSGYHQLEIWQKDRYKTAFKTRYG
HFKWLVMPFGLTNAPASFQAAMTTEFQHMLDRYVLIHLDDILVYSRSFEGACGTHVYRFGAATTSQVQSQPRQVQIRATV
AGVLGTLRDAARHPEAAATVEKLRLQAEANADAQARHKEAQDLLQLHEATRIEKLKFWHFEPNGDDGTPEEKHKEFLSKL
VARFLYACNYQRSELERQNLELQQHFLDLKTHPHELANLRRMVQSHEDATRALNSRVLDVEQAVPGPDVGASSSAPSSRQ
LEERVDHVVAMLGDISTFAAPTIISSQLDMLKTEVQQLQSTNMDGNPKKYKMPTFQLEKFDDYTHQDPVLWWEAFTTQLR
ILPVAKHAYIGALFMNSKGGCQIWLTHLSATHSVDVANLKDKITWEELTRLWKKRFIVDDAPTLAINCLFTMSQGNTATR
DWLTE
```

108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE

116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE

A0A388KFR3 **A0A388KFR3_CHABU** (210 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MTNAVDVVEQAAGKTKKLKEPHRLPSIRRREGGGLGGGENERACRRPNMDNEDKGGSGLSWRGEEEEEEEEEEEEEEEEE
EDEEEGEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEEEEEEEKEKEEEEEEGGRGGEEEGGGGDDKEEEDAGNEG
GEGEGGGGGEGEEGRVYIVKQRGCDREWLRGRRGQTVSAEREKRTTKERL
```

91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE

A0A388KFS4 **A0A388KFS4_CHABU** (407 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MRRCQLINGCMLGGKVQTQTARIYVRNRTDAPQNRRSQDHKALFKKKTKKRKRKKRKKKKRKRKKKKKKRKRKKKKKRKK
KKKKRKRKKKKKRKRKKKKKKKRKKKRKKKKRKSNKKKKKRKRKKKKRKRKKKKKKKKRKRKKKKRKRKKKKKKRKRTR
SSRQQKRKRKRKRKRKRKRKRKRKRKRKRKRRRKKKKKKKKKKKKKKKKKKRSSRPQQAAEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEDEEEEEEEEEEEEEAEEAEAEAEVEAEEEEEAKEEEEEEEEEAEAEE
EEKEAEEEEAEAEEEEEEEEEEEEAEEEEXEEEEGEEEEEEEEEEAEEAEAEAEEAEAEEAEAEAEAEEEEEEAEAEEEE
EEAEVGA
```

221 - 240:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEEE
225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE
239 - 258:	EEEEEEEEEEEEEEEEEEEE
240 - 259:	EEEEEEEEEEEEEEEEEEEE
241 - 260:	EEEEEEEEEEEEEEEEEEEE
242 - 261:	EEEEEEEEEEEEEEEEEEEE
243 - 262:	EEEEEEEEEEEEEEEEEEEE
244 - 263:	EEEEEEEEEEEEEEEEEEEE
245 - 264:	EEEEEEEEEEEEEEEEEEEE
246 - 265:	EEEEEEEEEEEEEEEEEEEE
247 - 266:	EEEEEEEEEEEEEEEEEEEE
248 - 267:	EEEEEEEEEEEEEEEEEEEE
249 - 268:	EEEEEEEEEEEEEEEEEEEE

250 - 269:	EEEEEEEEEEEEEEEEEEEE
251 - 270:	EEEEEEEEEEEEEEEEEEEE
252 - 271:	EEEEEEEEEEEEEEEEEEEE
253 - 272:	EEEEEEEEEEEEEEEEEEEE

A0A388KHJ5 **A0A388KHJ5_CHABU** (2138 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MKLKLIHVVGDSEQKITRLQDTLQQATLKAERMRSQLVDIADAMGEFVVDDDVLDLKSVLSEATAAISQPSTLVDNSMSL
REAICWGTAGMGHGKASLPMEPRSQMGQLPRSKEGEDPRTATWSRENEAALPPPLFPAGLDVPLSSGGTTVLKNLFRDGR
STFSSLLSKEDWQEAEIESQKLMGVADRAAYHALQQDTREATNNTLTGRVDFGTGYHPDRLNLQRVMAGGLWAYSKQLPS
YQKGVGSPRCGANRGRNGRRSQRRQCKKPSNGPDRSEAPRKPTGLLKLAETIRNFRTEKDDLEMRLRVAEAANAKLAEQT
SIADKMGNKLVLENRALTLSLEKINREKEALQVRMAMTESIVREVAKLGDQDLTMFGLSEDPRSNQMFLLRGSGPKGVRR
GNGTNVQGGARVPTTAKGAPLPVQGAGPKGIGGGTGVEEVSNSQGGVTDDQADEEHAWRAELERLRGVKLLFLTLARNFK
VSLNSLAEAIAEKDKFKSKLQGLVKDISGVSLEDLDQLQTSDDGEDDAEEEAQRPNDSAVMASSEGAATKRKRGPKRKTA
LTVEEIAWVIKGLRNDNKKLQAKVEKLQVRLESSEVQRRRAQAAIMTLEKELSDPLWSTDGQGKSEEGPFSIADSMSPSR
LVERQLKELGRSTSVKEPVIGDVAPVDEPDSEQYVRYNAEQLQSRFTWILTRLREQRVFQKERVAELEVLLSRVSKDAES
AKSKLLASESLLQLYEDEVMTHGENRSSEDTRVPTEGGTKAGRSPSQRWKGRIRTSVLARLQSKGFSKDSKASMVSRSKK
QSSDAETDNNDDEEAITANDDNDDDDGKEEEEEEEDDDDDDIKEEEEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEKHGMAKTKTKTKTKTKTKTKTKTKTKTKKTKTKRKKKKKKKKKTKKKKKKKKKKKKKKKNMALQKTK
TKTKTKTKTKTKTKMKKKKKKKPVVVVVSDLEKRERFELFTVETLDQLLRGMTAIYNADVTSWSDPTTMRPSLENHLSVI
EQNSTIVASSVKKDGDDQTRAKVFSEAEPQSGPLAEVLHESSLYGNVSSDAVSPKPPATGKQGEVWSMKDPPDWMMGQLT
LKMLGKASNRLHKLTMKWKDLEDSKAQLQSSLSETEKRLTSALQNVERSAQECGHLLQLISQAEDIIKGDRVNSPVPVKP
TGFRRHSRISPHGSQTELRTFMAQSNEHGTDHSRQNAEKRDGNVLGGTSSGTPTSSHVHPPTPSFLERVRGLHSAYEKGK
EENKDLRRDHVELKKQFSLANKHLAEMLAFMDEMEGSSGGREEDKTSDVAADTSHSGAVDTEGEADGEQSAVEGGATWKR
ASKSVEKMKKLKEELQAVKLDVAARVRERDGFRVQVESLQEERRNMRTSVNTLQKQLETQTAANEKLKSETNLLMSKSKE
LTGERDALLLQKEQLESRTRSEMERIKGERISLETELGSLQGRQRSLKAERDSLIAERDSLKVERDDLKTQRETLLSKVA
LTALGAIGAGEEGSGIRAQLPVHSSFQDGEGPGGHKRISGGAEGTAHMGADGEAKLQSPSEMAKEQKQVIELGSGEAGKG
GKALVSLQVGEDAYEQVSGKVDGDTSTSGRSSRRESLVEVAGSVAARIQQLRFEKQQLEKERDDAKAKLKEAMQEVELLH
KQTEGMRLPNTKSARNPREDRSVREIDRASHRPREVIAIPSGQGDGSSTSQVSGLADVLGMGISKETSMEEGGAKGESEA
AAKQRNQESTEAKELGKIQGKDVDKTDVKAAKTRANATDESKDSKPETEPVAHARESQEKKLQVLLDYVRHVKQILVTAE
TWCESHSLGDGAASGPRQMDGTLSEAPHKTGVSQGPDAHPSPRADRSAAAAHKDVNSSGVEGGGGNNQPHLQKTTSRKVS
ANKGAHVTGPKAEERDEGETLLIEVKRFVEIVRTCVERKEQQLKQEREKAAQLEQDKVNLDSESGKIYQRLEFFKTEVLR
AGGLDLDDPIEQERLEAAKLKVKAHLASLKPLKTGKSPEPGKPAAEAGRTPGKRTRAGSVYRHNLAAASIVNPLNQLARY
QVALLLNDQVSFDTMIPPGSQSSNMIVDLVLVGAAPACSLVGGLSTDVAATGFPVILQ
```

852 - 871:	EEEEEEEEEEEEEEEEEEEE
853 - 872:	EEEEEEEEEEEEEEEEEEEE
854 - 873:	EEEEEEEEEEEEEEEEEEEE
855 - 874:	EEEEEEEEEEEEEEEEEEEE
856 - 875:	EEEEEEEEEEEEEEEEEEEE
857 - 876:	EEEEEEEEEEEEEEEEEEEE
858 - 877:	EEEEEEEEEEEEEEEEEEEE
859 - 878:	EEEEEEEEEEEEEEEEEEEE
860 - 879:	EEEEEEEEEEEEEEEEEEEE
861 - 880:	EEEEEEEEEEEEEEEEEEEE
862 - 881:	EEEEEEEEEEEEEEEEEEEE
863 - 882:	EEEEEEEEEEEEEEEEEEEE
864 - 883:	EEEEEEEEEEEEEEEEEEEE
865 - 884:	EEEEEEEEEEEEEEEEEEEE
866 - 885:	EEEEEEEEEEEEEEEEEEEE
867 - 886:	EEEEEEEEEEEEEEEEEEEE
868 - 887:	EEEEEEEEEEEEEEEEEEEE
869 - 888:	EEEEEEEEEEEEEEEEEEEE
870 - 889:	EEEEEEEEEEEEEEEEEEEE
871 - 890:	EEEEEEEEEEEEEEEEEEEE
872 - 891:	EEEEEEEEEEEEEEEEEEEE
873 - 892:	EEEEEEEEEEEEEEEEEEEE
874 - 893:	EEEEEEEEEEEEEEEEEEEE
875 - 894:	EEEEEEEEEEEEEEEEEEEE
876 - 895:	EEEEEEEEEEEEEEEEEEEE
877 - 896:	EEEEEEEEEEEEEEEEEEEE
878 - 897:	EEEEEEEEEEEEEEEEEEEE

A0A388KHU3 **A0A388KHU3_CHABU** (2168 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MKLKLIHVVGDSEQKITRLQDTLQQATLKAERMRSQLVDIADAMGEFVVDDDVLDLKSVLSEATAAISQPSTLVDNSMSL
REAICWGTAGMGHGKASLPMEPRSQMGQLPRSKEGEDPRTATWSRENEAALPPPLFPAGLDVPLSSGGTTVLKNLFRDGR
STFSSLLSKEDWQEAEIESQKLMGVADRAAYHALQQDTREATNNTLTGRVDFGTGYHPDRLNLQRVMAGGLWAYSKQLPS
YQKGVGSPRCGANRGRNGRRSQRRQCKKPSNGPDRSEAPRKPTGLLKLAETIRNFRTEKDDLEMRLRVAEAANAKLAEQT
SIADKMGNKLVLENRALTLSLEKINREKEALQVRMAMTESIVREVAKLGDQDLTMFGLSEDPRSNQMFLLRGSGPKGVRR
GNGTNVQGGARVPTTAKGAPLPVQGAGPKGIGGGTGVEEVSNSQGGVTDDQADEEHAWRAELERLRGVKLLFLTLARNFK
VSLNSLAEAIAEKDKFKSKLQGLVKDISGVSLEDLDQLQTSDDGEDDAEEEAQRPNDSAVMASSEGAATKRKRGPKRKTA
LTVEEIAWVIKGLRNDNKKLQAKVEKLQVRLESSEVQRRRAQAAIMTLEKELSDPLWSTDGQGKSEEGPFSIADSMSPSR
LVERQLKELGRSTSVKEPVIGDVAPVDEPDSEQYVRYNAEQLQSRFTWILTRLREQRVFQKERVAELEVLLSRVSKDAES
AKSKLLASESLLQLYEDEVMTHGENRSSEDTRVPTEGGTKAGRSPSQRWKGRIRTSVLARLQSKGFSKDSKASMVSRSKK
QSSDAETDNNDDEEAITANDDNDDDDGKEEEEEEEDDDDDDIKEEEEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEKHGMAKTKTKTKTKTKTKTKTKTKTKTKKTKTKRKKKKKKKKKTKKKKKKKKKKKKKKKNMALQKTK
TKTKTKTKTKTKTKMKKKKKKKPVVVVVSDLEKRERFELFTVETLDQLLRGMTAIYNADVTSWSDPTTMRPSLENHLSVI
EQNSTIVASSVKKDGDDQTRAKVFSEAEPQSGPLAEVLHESSLYGNVSSDAVSPKPPATGKQGEVWSMKDPPDWMMGQLT
LKMLGKASNRLHKLTMKWKDLEDSKAQLQSSLSETEKRLTSALQNVERSAQECGHLLQLISQAEDIIKGDRVNSPVPVKP
TGFRRHSRISPHGSQTELRTFMAQSNEHGTDHSRQNAEKRDGNVLGGTSSGTPTSSHVHPPTPSFLERVRGLHSAYEKGK
EENKDLRRDHVELKKQFSLANKHLAEMLAFMDEMEGSSGGREEDKTSDVAADTSHSGAVDTEGEADGEQSAVEGGATWKR
ASKSVEKMKKLKEELQAVKLDVAARVRERDGFRVQVESLQEERRNMRTSVNTLQKQLETQTAANEKLKSETNLLMSKSKE
LTGERDALLLQKEQLESRTRSEMERIKGERISLETELGSLQGRQRSLKAERDSLIAERDSLKVERDDLKTQRETLLSKVA
LTALGAIGAGEEGSGIRAQLPVHSSFQDGEGPGGHKRISGGAEGTAHMGADGEAKLQSPSEMAKEQKQVIELGSGEAGKG
GKALVSLQVGEDAYEQVSGKVDGDTSTSGRSSRRESLVEVAGSVAARIQQLRFEKQQLEKERDDAKAKLKEAMQEVELLH
KQTEGMRLPNTKSARNPREDRSVREIDRASHRPREVIAIPSGQGDGSSTSQVSGLADVLGMGISKETSMEEGGAKGESEA
AAKQRNQESTEAKELGKIQGKDVDKTDVKAAKTRANATDESKDSKPETEPVAHARESQEKKLQVLLDYVRHVKQILVTAE
TWCESHSLGDGAASGPRQMDGTLSEAPHKTGVSQGPDAHPSPRADRSAAAAHKDVNSSGVEGGGGNNQPHLQKTTSRKVS
ANKGAHVTGPKAEERDEGETLLIEVKRFVEIVRTCVERKEQQLKQEREKAAQLEQDKVNLDSESGKIYQRLEFFKTEVLR
AGGLDLDDPIEQERLEAAKLKVKAHLASLKPLKTGKSPEPGKPAAEAGRTPGKRTRAGSVYRHNLAAASIVNPLNQLARY
QVALLLNDQVCQEFDVGSSTGGVYQAAIHYFTVDVNTGEVSFDTMIPPGSQSSNMIVDLVLVGAAPACSLVGGLSTDVAA
TGFPVILQ
```

852 - 871:	EEEEEEEEEEEEEEEEEEEE
853 - 872:	EEEEEEEEEEEEEEEEEEEE
854 - 873:	EEEEEEEEEEEEEEEEEEEE
855 - 874:	EEEEEEEEEEEEEEEEEEEE
856 - 875:	EEEEEEEEEEEEEEEEEEEE
857 - 876:	EEEEEEEEEEEEEEEEEEEE
858 - 877:	EEEEEEEEEEEEEEEEEEEE
859 - 878:	EEEEEEEEEEEEEEEEEEEE
860 - 879:	EEEEEEEEEEEEEEEEEEEE
861 - 880:	EEEEEEEEEEEEEEEEEEEE
862 - 881:	EEEEEEEEEEEEEEEEEEEE
863 - 882:	EEEEEEEEEEEEEEEEEEEE
864 - 883:	EEEEEEEEEEEEEEEEEEEE
865 - 884:	EEEEEEEEEEEEEEEEEEEE
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867 - 886:	EEEEEEEEEEEEEEEEEEEE
868 - 887:	EEEEEEEEEEEEEEEEEEEE
869 - 888:	EEEEEEEEEEEEEEEEEEEE
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872 - 891:	EEEEEEEEEEEEEEEEEEEE
873 - 892:	EEEEEEEEEEEEEEEEEEEE
874 - 893:	EEEEEEEEEEEEEEEEEEEE
875 - 894:	EEEEEEEEEEEEEEEEEEEE
876 - 895:	EEEEEEEEEEEEEEEEEEEE
877 - 896:	EEEEEEEEEEEEEEEEEEEE
878 - 897:	EEEEEEEEEEEEEEEEEEEE

A0A388KI38 **A0A388KI38_CHABU** (240 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MRGRTTTRGGEKRKKKKKRKKTRKKRKKKKRRKRRKRRKRRKRRKRRRRRKRKRKKRRKRKKRRKRKKKKRKKRRGRPKGG
GGGGGGRRERKKRKKRKKRKKRKKRKKRKRRKEEKEGEEEEEGEEEDGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDEDEEEEDEDEDDDDEEDEDDDDKKRKKTSRKKKKTRKMTRRRRRRRRR
```

129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE

133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE

A0A388KIN8 **A0A388KIN8_CHABU** (742 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MGGGGEAGGARGRAGEGATGGTGERAGEAVGEEEEREEQQENERERGYGGIFVTLFGGGGSGGGRGGRGGGVGGAGEGAR
GGVGEGAVKEREWGYGAGRGEGGGGGGTGGKAGEAAGGAGGAATEEAGEGEGGGAGEGARAGLRQDLFLEEGQALCAVSV
ECWYAHFDVEDEDNLPSSPSTPMQVVGCPCIGENRNNKININNNDNNNNIDAAAAGPFDGDSCIGEIGGINNYNNTTNNN
TNNDIDSVISRSCVGESDNNDNSNNNNNNNNNNNNNNNNNNDDYNNNKNTNNNINNKNNDNAVDASSSDGDSDTGAIGG
SISFNNNNNTDGGKNNDNNNHKDNSNERFIDRVTGKIDIHNNNNDNNDNNAPYTLNSARVVFLNQRPQPRPGKCPGNACE
TCDRGLQDPYRYCSVACKVDAILNEGRDCSSFLQRCSLSSMDYASATVAATSSPLRTIKRPKLEMEDPPSQTSSGSAASM
FNDRFCECTRHMWKTRKERTALHMPRCVLPLTCLVNWELLISLSSHSSHSSFLYGQEEEEKEEEEEEEEEEEEEEEEEE
EHGLSAYSYDKHSVVFCKVLSRRLNPRLNPRLNPELNPELNPELNPELNPRLNLGRNPRLNQSAAVKLSYCMHLQSCCTQ
KQGCDVKLPQALLKDCSHFGNLKFARSEEENNNNNDNDNDKEAKEEKDEKKHSVDEEEEKEKEEEEEEEDEEEREEEEE
EEEEEEGSHLKAMWQTSGWMAV
```

542 - 561:	EEEEEEEEEEEEEEEEEEEE

A0A388KIP4 **A0A388KIP4_CHABU** (633 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MLQSLLHIITKLEEGPASYLARFIYLRQAAILMRHCHAVLEEGQALCAVSVECWYAHFDVEDEDNLPSSPSTPMQVVGCP
CIGENRNNKININNNDNNNNIDAAAAGPFDGDSCIGEIGGINNYNNTTNNNTNNDIDSVISRSCVGESDNNDNSNNNNNN
```

```
NNNNNNNNNNNNNNDDYNNNKNTNNNINNKNNDNAVDASSSDGDSDTGAIGGSISFNNNNNTDGGKNNDNNNHKDNSNERF
IDRVTGKIDIHNNNNDNNDNNAPYTLNSARVVFLNQRPQPRPGKCPGNACETCDRGLQDPYRYCSVACKVDAILNEGRDC
SSFLQRCSLSSMDYASATVAATSSPLRTIKRPKLEMEDPPSQTSSGSAASMFNDRFCECTRHMWKTRKERTALHMPRCVL
PLTCLVNWELLISLSSHSSHSSFLYGQEEEEKEEEEEEEEEEEEEEEEEEEHGLSAYSYDKHSVVFCKVLSRRLNPRLN
PRLNPELNPELNPELNPELNPRLNLGRNPRLNQSAAVKLSYCMHLQSCCTQKQGCDVKLPQALLKDCSHFGNLKFARSEE
ENNNNNDNDNDKEAKEEKDEKKHSVDEEEEKEKEEEEEEEDEEEREEEEEEEEEEEEGSHLKAMWQTSGWMAV
```

433 - 452:	EEEEEEEEEEEEEEEEEEEE

A0A388KJ22 **A0A388KJ22_CHABU** (95 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MSDDSDHDDGQMETTERSQDGHGSGGGGGAEEEEEEEEEEEEEEEEEEEEDEEEEEEVKRRGGGSGGDSNRGKERNSYGW
NCETRSRELFGERTT
```

31 - 50:	EEEEEEEEEEEEEEEEEEEE

A0A388KJG8 **A0A388KJG8_CHABU** (222 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MEIHMRMESKRIDDKGEKRGKEAKDEEQEQENEQKEKGDDEMDLETANVKQIRSDSETEGEQAAESRGNRSHGSKKDEED
EKKRQKKEAEEEEEEEEEEEEEEEVEEEEEEEEEEEEEEEEEEEEESKGSCVWEGGGEDEGSCSGGGLEEEEEEEEEEEE
EEEEEETAGGRLRRGGRAAAAARRGGGGGGEEEEEKEEAAGGGGRRRRRRGRVAASAGEEEE
```

105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE

A0A388KJM0 **A0A388KJM0_CHABU** (188 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MHSKTKAQKEKSKNKGKERRRSRRKGREGEAERGEEEYEETSSGTRRRRSKRRTRRRRRSTSGSGIRKRMNTGEQRAGGG
KKGSSGTWKRRKRGEGGGEGGEGGGEGRVAVTEAVAVAEEWNEEKEEEEEEEEEEEEEEEEWDEEKEEKEKKEEEEEEEE
EEEEEEEEEEEEGKEQEKRRVRAKQQDE
```

153 - 172:	EEEEEEEEEEEEEEEEEEEE

A0A388KKE2 **A0A388KKE2_CHABU** (285 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MSRSQCCARAVTDPGGLLSWPGGGGGGGEERGGGRRGEEGEGEGERGVGVRGGVGGGGGRLASVFEKKTEEEEEEEEEEE
EEEEEDRTSISGSHSRSFVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEREGEEGEEEEEKEEEKGEE
EGEEEEGEEDERTSISGRHSRSFVKVEEEEEEEGEEEEEGEEEEEGEEEEEEEEEEEEEEEKGEEGEGEEDNEEEEERTSI
SGSHSRSFVEVEFFLILSKVKIGDGVLPARSHRSSVVGSAHRANG
```

100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE

120 - 139:	EEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEE

A0A388KKK3 **A0A388KKK3_CHABU** (215 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MVPTSRTMSRRWRNRRTARWRRRRRKMRRWRVRRGGGRGATDGGGVGGGLGRRGGRRRGDDDDDDEEEEEEEEEEEEEEE
EEEEEEEEEEEEEELEEEEEEEKETMEKKTRRQRIRRRRRRRRRRRRRRRRRRRRRRRRGVGGGGGRGRGDEEEEAEEEED
EEDEEKKETMEGEEEDEEQTTEMGLEEKEEDETAKKKKKKKKKKKRNKKKKRKKR
```

66 - 85:	EEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEE

A0A388KKS6 **A0A388KKS6_CHABU** (257 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MNRHRFSLFNLPSDLPTFWQSAIDPAFSFQIRELSVQILDEDKWNGWWDAYVELNFCLVCLVFHWAEPAPEAEGGEVPDN
EVELLIVQAWRTSTEGELLGILFGKVEERHLEAITDELLVFLVQLVDDLRLDILSRCDGKPGTDVLARALAPHLMWSTCT
ELDGDICFYPSPTLYLDINVTDLTLWDPFVWRGNTLEAGEKEEEEEEEEEEEEEEEEEEEEESGEEESGTDRDDPDYIG
LEEEEESASGEPSSRPP
```

202 - 221:	EEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEE

A0A388KKS8 **A0A388KKS8_CHABU** (1928 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MSISSKEEEEEEEDEEEVDVEEEEDEEEKANDEEEEEMGEEVDEVEEEEEDEEEEKVEEVDEVGEEEDEEEKVEEVDEVE
EEGEDKEDELEALEGALNEEDMAGYESADEDEEEEEEEEEEEEEEEKEGGEEDATWWFLTWEVMETTTATMTTTTTPRVG
DWRGRVSLSSGRRGGDSLIKGHEDSQRVFDGKAEERRALLQSPEREILPTKGDRILTALGRRRSHGEGEGGGGGGGGGGG
GGGGRERGGRGGGEEVGGESISLEEGVGEAELAGKRSSTTGYRRVRVGDPENSEELAGNLAGNAIRMRKNSEELAGNAIR
MRTNSEELAGNAIRMRTNSEELAGNLAGNAIRMRKKSEEEQEEEELAGKASGTGCRRVWVGDPDKSNASAENLAGNAIRT
SKYTLWTFLPRNLFEQFHRLAYVYFLTIVVLNQIPQLAVFGRTASLFPLLFVVSVTAIKDAYEDWFRHKSDREENARECL
VLGEGEGEGVGVGVGGVSKDPPSFPLKRVVKGRVIKDLGGWFKSRVRSLRRSIFFLKGVIIARGKRWRGGYNTQKEEDEG
LNEEDGCKEVEEEEEEEEEEEERSFYPKQWRDVRAGDVIKLYADEMVPCDIVLLQTGNETGSCHVSTLNLDGESNLKTRN
ASVGSRRVPIISQQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGKKEEEKEKEKEEKKEEEEEEKKKKDCKSGFHVS
AAQWLSSLLVCEAPHKNIYEFVGYLELSPDWSSESSGESSSVDWSPDSGKKEKGKSKRKRKRKRIETHHSRPDLDRGDVG
GDMEEEENEEEEEKKRKDGRRRRRRRRRDLSSLRIPLSIKNVALRGCQIKNCPWVIGVAVYTGSHTKMMLNSCPTPSKNS
RLERLMNVETIWLTVILILLCLISATSSYLFIANKDLEQIPYYYLDLERETSSSSAAGGGGGGGGGGGGGERRMKVEMTM
AVFFSFIIVFQVIVPISLYISMELVRLGQSYLMVRDRRMFDEDSSNSTPLHCRALNINEDLGQITYLFADKTGTLTENRM
IVRRCSIRGADYRILAEVEEEEEEEEEEQRKEEEEERVLEEEEEEEEEGRIEEEEEGRGKHSFFGMDGNSKASATDESGL
KSSSGQKSRSRHSHYYYNNKAETKVEDHRGAQMGDGSGVGAVVGVGVVVGGGGGHKLSASTSAKALKLTVNFQEDEAKAI
DDFFLVLAVCNTVIPARGGGDLVVPGTGGQPVRNVNQKQKQKQKQKQKQNQDQDQLSKQTGNQRTIGCLQNGYGGQVIDY
EGESPDEVALVRAAALHGYVLVQRTAEFILLAVCGEVRRFGILGLHEFDSTRKRMSIVLKCPDGTVKVLCKGADASVLPL
LQPSNLDGDDREQPSTTDTVDRSLDGRVEALEAPTLTQLTCQHLDEYAGNGLRTLMAASKTFNGAEYAEWLSKFELAGRA
IDGRARLLRDAAASAERYLTLLGAVGIEDKLQEGVPETIALLRSAGMKVWILTGDKQETAIAIAFSCRLLMEDMTQIIVN
EKTKEGCKRALLEAKAVDAELKHSTGEVRPMDYGGGKNRKHLALIIDGDSLAHALDEDLEHQMADVGVGISGQEGRQAVM
ASDFSIARFKYLGRLLLVHGHWNYHRIAYMILYNFYRNAFFVFLLFWYVFHNAWSPQMSISDWNLIFFTLVYTSAPTIVV
GILDQDLDDRTLLRIPGLYGFGRRDEGYNKRLFWVMMADVLWQSLVVFYAAYFAFVESTEGLWELGSFFTLAGTLVCTFH
LACDTWHWTWINHLFLWGSVIVCIVCLLTFDSLQSMPQYMVTFVAMHDAQYWLLLLLVVVAALLPRFVVKAVLVRWWPSD
LQIAKEQERLFETQDNKGVCAASTAAETGILSAIVFSPGNSVQEDPASPGTDMKRRGRKRSWSLSKRSGSGLLYSDFQPL
EVEMPARV
```

655 - 674:	EEEEEEEEEEEEEEEEEEE
656 - 675:	EEEEEEEEEEEEEEEEEEE
657 - 676:	EEEEEEEEEEEEEEEEEEE
658 - 677:	EEEEEEEEEEEEEEEEEEE
659 - 678:	EEEEEEEEEEEEEEEEEEE
660 - 679:	EEEEEEEEEEEEEEEEEEE
661 - 680:	EEEEEEEEEEEEEEEEEEE

662 - 681:	EEEEEEEEEEEEEEEEEEEE
663 - 682:	EEEEEEEEEEEEEEEEEEEE
664 - 683:	EEEEEEEEEEEEEEEEEEEE
665 - 684:	EEEEEEEEEEEEEEEEEEEE
666 - 685:	EEEEEEEEEEEEEEEEEEEE
667 - 686:	EEEEEEEEEEEEEEEEEEEE

A0A388KL03 **A0A388KL03_CHABU** (257 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MIGRWATVLQSMDFDIRHRKHERHGNADGLTRLHRPEKVLKSEEVIPWNKSKDENGPRALPSRQEYLKLAGIINLAFYPK
QDSSEEAGDEEVTEEEDDAEEETPEEGSYSEHSEGEQSVEEGEEEEEEEEEEEEEEEEEEEEEEEVGSEWEALPEEAART
GMEAEDPEAERRKEEIVVGKSQLEFASEANLRIVNDSTRDPEPPEPEDGGPATAAPSASRRRRSRSPSPSAPARPPVRPR
TDAGDRPSSPVIIPPSP
```

123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE

A0A388KL17 **A0A388KL17_CHABU** (1942 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MSISSKEEEEEEEDEEEVDVEEEEDEEEKANDEEEEEMGEEVDEVEEEEEDEEEEKVEEVDEVGEEEDEEEKVEEVDEVE
EEGEDKEDELEALEGALNEEDMAGYESADEDEEEEEEEEEEEEEEEKEGGEEDATWWFLTWEVMETTTATMTTTTTPRVG
DWRGRVSLSSGRRGGDSLIKGHEDSQRVFDGKAEERRALLQSPEREILPTKGDRILTALGRRRSHGEGEGGGGGGGGGG
GGGGRERGGRGGGEEVGGESISLEEGVGEAELAGKRSSTTGYRRVRVGDPENSEELAGNLAGNAIRMRKNSEELAGNAIR
MRTNSEELAGNAIRMRTNSEELAGNLAGNAIRMRKKSEEEQEEEELAGKASGTGCRRVWVGDPDKSNASAENLAGNAIRT
SKYTLWTFLPRNLFEQFHRLAYVYFLTIVVLNQIPQLAVFGRTASLFPLLFVVSVTAIKDAYEDWFRHKSDREENARECL
VLGEGEGEGVGVGVGGVSKDPPSFPLKRVVKGRVIKDLGGWFKSRVRSLRRSIFFLKGVIIARGKRWRGGYNTQKEEDEG
LNEEDGCKEVEEEEEEEEEEEERSFYPKQWRDVRAGDVIKLYADEMVPCDIVLLQTGNETGSCHVSTLNLDGESNLKTRN
ASVGSRRVPIISQQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGKKEEEKEKEKEEKKEEEEEEKKKKDCKSGFHVS
AAQWLSSLLVCEAPHKNIYEFVGYLELSPDWSSESSGESSSVDWSPDSGKKEKGKSKRKRKRKRIETHHSRPDLDRGDVG
GDMEEEENEEEEEKKRKDGRRRRRRRRRDLSSLRIPLSIKNVALRGCQIKNCPWVIGVAVYTGSHTKMMLNSCPTPSKNS
RLERLMNVETIWLTVILILLCLISATSSYLFIANKDLEQIPYYYLDLERETSSSSAAGGGGGGGGGGGGGERRMKVEMTM
AVFFSFIIVFQVIVPISLYISMELVRLGQSYLMVRDRRMFDEDSSNSTPLHCRALNINEDLGQITYLFADKTGTLTENRM
IVRRCSIRGADYRILAEVEEEEEEEEEEEQRKEEEEERVLEEEEEEEEEGRIEEEEEGRGKHSFFGMDGNSKASATDESGL
KSSSGQKSRSRHSHYYYNNKAETKVEDHRGAQMGDGSGVGAVVGVGVVVGGGGGHKLSASTSAKALKLTVNFQEDEAKAI
DDFFLVLAVCNTVIPARGGGDLVVPGTGGQPVRNVNQKQKQKQKQKQKQNQDQDQLSKQTGNQRTIGCLQNGYGGQVIDY
EGESPDEVALVRAAALHGYVLVQRTAEFILLAVCGEVRSMPTGMGSCGDKGAGFGILGLHEFDSTRKRMSIVLKCPDGTV
KVLCKGADASVLPLLQPSNLDGDDREQPSTTDTVDRSLDGRVEALEAPTLTQLTCQHLDEYAGNGLRTLMAASKTFNGAE
YAEWLSKFELAGRAIDGRARLLRDAAASAERYLTLLGAVGIEDKLQEGVPETIALLRSAGMKVWILTGDKQETAIAIAFS
CRLLMEDMTQIIVNEKTKEGCKRALLEAKAVDAELKHSTGEVRPMDYGGGKNRKHLALIIDGDSLAHALDEDLEHQMADV
GVGISGQEGRQAVMASDFSIARFKYLGRLLLVHGHWNYHRIAYMILYNFYRNAFFVFLLFWYVFHNAWSPQMSISDWNLI
FFTLVYTSAPTIVVGILDQDLDDRTLLRIPGLYGFGRRDEGYNKRLFWVMMADVLWQSLVVFYAAYFAFVESTEGLWELG
SFFTLAGTLVCTFHLACDTWHWTWINHLFLWGSVIVCIVCLLTFDSLQSMPQYMVTFVAMHDAQYWLLLLLVVVAALLPR
FVVKAVLVRWWPSDLQIAKEQERLFETQDNKGVCAASTAAETGILSAIVFSPGNSVQEDPASPGTDMKRRGRKRSWSLSK
RSGSGLLYSDFQPLEVEMPARV
```

655 - 674:	EEEEEEEEEEEEEEEEEEEE
656 - 675:	EEEEEEEEEEEEEEEEEEEE
657 - 676:	EEEEEEEEEEEEEEEEEEEE
658 - 677:	EEEEEEEEEEEEEEEEEEEE
659 - 678:	EEEEEEEEEEEEEEEEEEEE
660 - 679:	EEEEEEEEEEEEEEEEEEEE
661 - 680:	EEEEEEEEEEEEEEEEEEEE
662 - 681:	EEEEEEEEEEEEEEEEEEEE
663 - 682:	EEEEEEEEEEEEEEEEEEEE
664 - 683:	EEEEEEEEEEEEEEEEEEEE
665 - 684:	EEEEEEEEEEEEEEEEEEEE
666 - 685:	EEEEEEEEEEEEEEEEEEEE
667 - 686:	EEEEEEEEEEEEEEEEEEEE

A0A388KL35 **A0A388KL35_CHABU** (831 aa)
Pectinesterase (EC 3.1.1.11). *Chara braunii (Braun's stonewort)*

```
MNTEQIESPAGVQKNTEKTEEGGEKSGEVPGDEPGNKGDQAQKMDIDPFQAAFGPEPMEVDPLPANAGESPEGLSPGGEP
AAGVEGAPPPQMPVEQKLIVIADWLMTKLKAKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDQTGSPRRQAAVDAGREQ
HDDGRRGATGHGDGDGDGDGDGDGLRATALPGDGDDSQLLRRRTDAMTKAGGWRTGPANEKALGTPRSQRFGFGNMDPSKES
DRTPFGVQDGQGQRRGRPGRKRLKMIMVVALIIAVLIVIIVVPIAVVGDRRRGRAYARRRTPKTMSAASEQYCSTADNIT
LCKSTVMLGVNDNTPFGPSDLPDFPIKVINATKAPMNVLLSAMQVLKQSNLSVAAAEACNRTLYDGPESLDEAVGLIASG
```

```
NIRDAQIVLAAVRTFNTDCADQLLLLENLTGDGSATLAEGLPATELVAFHLGNALALTDEILADARGGEKLSGRRRKLLR
RRLLAEAEKVRRDLDAHFTVGSNGTGEFRNLTSAISKALTKRATTKERIVIRVRAGVYTEQVLIPKDLWGLTLIGEGAER
TRISYHDFGILGGNLEASSFVVEARGFLAIDLTFANDPVKNDRQNPAVAMRVSQRTSAISGADIPGSVGMAAFVSCKFQG
YHSVLYAHTGWQFYYDCDIMGSEDYIFGNAAAVFEQCKVHSQPDFNGTSIISAQGRTSAHEPTGFVFRKCGVEGELETNS
SVFLGEPQPYRKVFLRPAWKPFSRTALLLSVLGRVELAGWREWRYGAGDANLYKTVEFYEYLNSGPGSGRSARVPWSREL
PDKDAEAYTVDRFVSGDTWLPSLGIPSATWL
```

113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE

A0A388KLA9 **A0A388KLA9_CHABU** (335 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MHNIWSGRWEIWCEHYLTLSLCLVEKQLTWTRDSEHRPARESVALLIIQAWRTEVEGDLLGFVFRAVEPGHRQTIVWKLT
VPFAQLIDDLPLNIISRCDESPVPHVLSRRLTPYLQWSACLEDRTGGGSYPSCAEYLNPRGIIDVLFFSPRTVVEERAVA
EEAEVEDESEEETSEEEASYSEYNEEESGEKEEEEEEEEEEEEEEEEEEEEEEEEEEEENELEEEGGSEWKTLEEEADRAEA
QEEDLEAATRRREEITAGKQPVEHASGADLPILNDPTTDPEPSKNGDGDPTAETSGALARRRQSRSRSPSPRTPVRARID
AGHRALSPVVISSSP
```

192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE
194 - 213:	EEEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEEE
196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEEE

A0A388KLC9 **A0A388KLC9_CHABU** (876 aa)
Myb-like domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MSVAHPFVRYDWVKSAHEEIAAHFAVRITKAAIDKKPAPEAEGGEVPDDEVDLVIVQAWQTRMEGELLGILFDKVEDGHL
NTITDELLVFLAQLVDDLPLDILSRRDEKSGTDVLTRTLAPHLLRSTCTELDGDNCVYPSLSLYLEIDVTDLTHWDPFIQ
RGNAIEASYEEEEEEEESEGKESEENFKEEEEEEEEEEEEEEEEEEEEWEENEEEEGGEEVKEEEKEEEEEASMEAHLDG
DDGGGGGSWRGSSDGGDGSSSRTMGQRDRSHGRPPPKGRPVVCPAASARCHPVLRIFCSLRRLPESRSRKSKKKATRRMA
GGEGSERFTYGIGSRLTEGAPHVTPPRFDPALYAHLPPHQQPLPDDETWEPPTPAFPLAYGSTQSMSEGLATPMHGCGGD
GSMTSLLFSKDGDVAGPALDLHLSSGGGRSVTRTLLVNQQGQSEGEPSVGVFGGRSNHLRSPGVGGERALRSPGVGGAPP
AQGVGYGDRTALSAGRGRPSAGGGGHHATADVAESPVSGCVERIIARVSTMRASSDGDRTDNGEMYGEGDGLDDDDMAGG
REDDANVQPPPPAEGRIDGGAGRGKGRGKAKASGGDAGVASGGGRTYWSLDESLVLVRCKRDQDEAMAAAGSTFARIKTR
EWKWTDISKRTTAYGVHKEWDACMKRWENVIGWYRKVWDREKESGMQSFFTMTPKERAEKGYKFQMDRRLYDSVHAMQHR
SQTAHPPNLVDTGASQQQQGGGAGGDGVLGGETSASDNCEGGVGDTNGVRPPGGPKILKRKSARQNAFEAVTDVMQSHSK
VVAESVDRASKRQCEVLQRQCDIMEREVEAQEKQCYVWESGQRMLAPKDCPGSLQGLTIPQGGRVIGVVMRLSKQW
```

189 - 208:	EEEEEEEEEEEEEEEEEEEE

A0A388KLN4 **A0A388KLN4_CHABU** (3957 aa)
ATP-dependent DNA helicase (EC 3.6.4.12). *Chara braunii (Braun's stonewort)*

```
MMGRRRREWSRDWRDNEVEEKRARRRRRRTTMKKKRARRRTKKRWRRRREVVAMEKNEEDDGEGGGRGGGGDLDDGGGGG
GGRRGGGGGGGGGGEGGRRKGGGGGGRAKRARRRRGRRRRMTKKKRARRWTKKRWRRRREVAAMEKNEEDDGEGGGGGGG
GLDDGRGGGERRGGKGGRRGGGGRRGGGGERRGGGGGGEGGRRRGGGGGGHEEEEEEEEEEEEEEEEEEEEADNEEGEE
EEEEEEVEEKEDDEEEEEEEEEEATVNEEDEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEGPTMEELAHLAWAGNG
SWEGRNLLPRNERCAPFAVVTIAEKNTLSSDSAVRHSSIRLGENECGVPTGATTHWRGGKVLDTGHSLPRGHASFVEERG
REWALNEDLGRTQGQRAALSEASSRSYDFGACHGWLDGGSLGGVVPVPCSVSWPGTDNVAFESGEAGGVAPDVDSTVFGD
GRVFQLPLEMEQEPSCVPQCVRAACCAAGSLDGLDPQGKSVPVEGGVGGGSCEPVRKDRASDGPVSGDNSGRSVGQGLAS
SMATARAARRLRVSSRRKRRASTPGEGAQHRSDLERHAPAIEEGGEGAEERHVDTGSRSGVDVAMLRFGSVSLASDAVAD
YPTLPKATPTTSPNNFMRSICMRGVVSVPPCFVRSDCFKSTAAWHTPRLRLKEKMRCERYKELRRAVQENEHRDGVGTKV
FLPSTFTGGPHYMAEKYYDAMAVVQKLGRPDLFITMTCNSNWPEILDAVMPGQVPSDRQELLPRVFRGHLKQLIHEIKDK
RVFRAVSAVFYTVEFQKRGLPHAHILVILDRGQKLSNPDAMDEAISSEIPSDGELREKVSKFMIHQLCGAAKPSAACTTN
KRCTKHFPKPFVRKTTFQTGKGYPLYRRSSPDAGGCTLCEGGVVYDNGRVVPYNGYLLLRFNSHINVESCANILACKYLY
KYILKGNDKVMVAELERQHSVNEIRMSHEVDGVDELNKELQRCGCNRLPLYADITETHMWHKTEKRWKLRLSAGRSGAFP
KIGRLQRAYPAQGDLFYLRILLGHEHSRGATSFXALRTVEHGELATFREVCQRLHLLDDDFEYDKDMETAALHYMPHQIR
QVFAMLLAYGPVSDPMALFFKHWQPMCEDYVRKLRSMSVAPGVLQALALLDIHVQLLDMKTTMGGVGLAFPDPEAQRVAE
ELRARILLEGLPELIQEELMYDRADMERQWGANYPLLRPSRKELVDGVMSAVLNRSPLCVFVDAPPGTGKTFCINTILAG
VRRHENCIALAVASSGIASLLLPGGRTFHSRFQAPLRPDAKKAFPIRRQGELVRLIRMCSLIVWDEASITHRAQLEALNI
```

```
TLQDICQTDEPFSGKVLLLAGDFRQVLPVVRRGSRPKQIRASIKSSPLWAHFKTHRLHENMRVLRRGDDEVERKFAAFLL
RVGDGEHDVVDPADPETIELPPEICMALDLGALIDWTFPDLGRHLHDPDYLTGRFVLCPKNDAAYVINNLILDGLPQRDI
LYRSLHSAPTDSYGLNVPVEYLNSLSCSGLPPHVLRIKEGVPIMLLRNISVQMGMCNGTCLIVNKSVSGRLIEATILPSH
KIAVIPRMTLDSDDSDGFLWKRRQFPLHLAFAITINKSQGQSVSRAGLYLEKPVFGHGQLYVGLSRAGHPDDICVALPAD
STRTKNGRAPPASNAAHGSALETGSTPACGSRNQSLLASAFSPDDEDFLDYDYDEVPATLDAPSEPERCGRTPTESVRAR
SPLAIHTPMGSLLLDIYQAGVDIGDLSGDESTDSWEWDRSSPAELRGGSDGAPARYVGQSSPYGVSAGRSPLPPTTPVAA
AQMNADCARAHGVSKQACEIDAGTDNLQTPFTASTKRVRTSQPDGTSTFVPYIRPSQSSAPAVHDGAPPLRPFGSTPACG
NCGPVSVFAKLPREVVVGPSLTSDAAHRPDASSSLARRGATDSGQSENVVMGPMITPSYGRNGFRPGTTLVYHDINSYDP
PIWVDAKRTVILDGKKQRIVESWTDVLDRVGRRRIVNWMLFGLFLDGDRVEPTEHIWLDFLLARGRIERGFVPHRDKFLC
DNGSLDDAHELIEAILRHEHATRPGFDVPSLCEKVAKFEDDYVPFEIYRYARLDEIASRLPDVPRVSRPYAKACHGDCLI
ATYAPPVQWVSQAYIRTRTRRIAEASAARDYAHGRSPLTFSKPAANSPMTPAFTAPAARRVQRSLFLPATPPPFPLPAAD
REAGSSACKHCSAQLSAGPSALRQIGAVMAAKNEAVEDCSAVEAVMFVDYCRQGYNKVASFEQYKTAAASYIAKDDPSIS
LLSFGLHHHVCFFCHLLLYPHAKMSPKNRGAAKDPHPLLAKSIEEEESVRWRIAELNEKLVKLRSRGYDDTDVRWLRVEE
KIDEAEEKRQRAASRAERMRNIIDAGDIYSDADYRSGDEWIEEQEEASDSTDPEEMVTDYDVSDLEAAVDTDYADADDDT
DDDNSSSDDSTEEGDGSTNLSTLCFSVLFSALSYSRLSYPLNGITSHDDLGTFRFRVGLSGSAGHMAIRGPLITSSCPSP
QLPPTAFTLPHVLHVETASQIKERLEREYLTPRLDHKEGDSVVQCGLTWDVDWLSDWTRAEPTPCRDVVEPVWRPHLKTP
KLVNEADCNHHEDDRPCRCDRPDSFEQQPTPEIPEFREVEIATFNETASNSSSLLRRMGRPEDFVRGSKSSQPFQPGGFD
GGGGDEGRPRAPPDAENGGWLHEVLHQTGPWQTVPPGFKHGIRFDDEPQPEDSKKEEADKAIRMGDQHQQVSTLSFGSIF
QKAWETSYGGEEGEEEEEEEEDEEEEGENVKMRRDASGAEASVARTAFSGRAQGEAVVELPARPAETGVVGVGGGGGGAGV
GGGGGGGEEEAVPRIKDQDELLDKLLSRTPGQLDMLSQKGISDKERKEEVWAIMDGMHGIDKRFKELVPEMAMEFPFELD
TFQKEAIYRLENYESVFVAAHTSAGKTVVAEYAFALVTKHCTRAIYTSPIKTISNQKFRDFSGKFDVGLLTGDISIRPEA
PCLIMTTEILRSMLYRGADLIRDVEWVVFDEVHYVNDAERGVVWEEVIIMLPDHINMIMLSATVPNTKEFADWIGRTKQK
KIFVTGTTRRPVPLEHNLFYSGKLYRICDRETFLPEGHREAMVAHKAKNEKKAPAGGMGQGRGGAGAGGRSRTGASGQTK
AAAAQAARAIGSAMTGGGGGGWRSETSQWYNFLDMLKKQSLLPVVVFCFSKNRCDQIADSLTASDLTTSQEKSEIRVFCD
RAFSRLKGTDRQLPQVLRIMELLKRGIGVHHAGLLPIVKEVVEMLFCRGVIKILLSTETFAMGVNAPARTVAFHGLRKHD
GKTFRQILSGEYTQMAGRAGRRGLDKVGTVIILCWDDIMEEGDLRRLLTGKATKLESQFRLTYNMILNLLRVEDLKVEDM
LKRSFAEFHGQKTMPLHMQELIKREGVLNGMNTEINCILGSPTIEEYYEMAVEADRVGEQLMETGLQSRVAQQALVPGRV
VLVRTAAESPSLGVIVRGSSGEGQSRPYIVLALHRGPVPASAQAMLAPAGQDVVGGGGSGGNNFPTTLPGDSPLDGMAMM
RVHRKGQKDVDYSVFSGGSKKGPEVVTIALPRYGEVGGSGYVVMNVDKRGILSICKARVKVDTSAILEQPRPVAYASAVQ
QLEQLERENPGQDPAALDPVKDLKLNDVETIERYRRRQALQAAMARNQCHRCPKLQEHYAEVRKRALLREHVRDLKFIVS
DANLQQMPEFRQRLAGGGDDGDAAPWKDLPTMARLHRVMVQLVGGGDERAAGCRRRRQSGCTDWRLFETACRIGAVQGSC
GLQVSPAEYAHGALKFGLMEVVYEWAKGTPFADICDLTNVPEGTVVRAIVRLDELCREFRDAARVIGDATLFQKLEVASA
SIKRDIVFAGSLYITAGQFPMLIRSGDMLAVAIRVQI
```

213 - 232:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE

A0A388KN80 **A0A388KN80_CHABU** (647 aa)
Reverse transcriptase domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MGICNAPATFQQAMNMTFQNFVNKTRLMQGMINFYVIVYMDDILVYSETYHGHAQHIEWTLGALRDVGFKIALEKSEFFL
SEISFLGYVVTRGGLRPDSRKVAAVKEAPVPTSLTQVRAFLGLASYYRRFIKGFAAIARPLTNLLRKDQPLSWDAECQQA
FATLKDALAMAPILIRPDPSKQFILITDWQPEAVSAILAQKGNDGREHVIEYVSRTVPDERRNDSAPQGECYAVVWGIQH
FHPYLYGQKFHLVTDHEPLLALKKLTNYTGMIGRWAVRLQEYDFDIVHRKTERHGSADGLTRLHRPAKAWRTNVAGDLLG
FVFGAVDRGNRLQIVRELMIVIARLADELPLDIVSQSDEEPVPHTLSRTLAPSLQWSACIEERLADGRFHSRSEYLDVHS
LTNPRFFQQPTAFEWAALRAKEEPEEESEGELRREAGEAAARLAEDEEEEREAEGESEEEEEEEEEEEEEEEEEEEEEEE
EEEEEDAEEETSEEEKEAYSEYSEGEQSEEEEDDEEVESEDNQEPMHDELEWVSGPDRREENPEAAAQRKKEIAEGKRLV
IDPAPNDPFKDPEPPKPEHGDLAATTSGAAMTRRQSRSRSTSPSASARPPIRQRVNEGLSPSSPIHIPPSPQLSLFQSVF
PSHRLPL
```

458 - 477:	EEEEEEEEEEEEEEEEEEEE
459 - 478:	EEEEEEEEEEEEEEEEEEEE
460 - 479:	EEEEEEEEEEEEEEEEEEEE
461 - 480:	EEEEEEEEEEEEEEEEEEEE
462 - 481:	EEEEEEEEEEEEEEEEEEEE
463 - 482:	EEEEEEEEEEEEEEEEEEEE
464 - 483:	EEEEEEEEEEEEEEEEEEEE
465 - 484:	EEEEEEEEEEEEEEEEEEEE
466 - 485:	EEEEEEEEEEEEEEEEEEEE

A0A388KNG0 **A0A388KNG0_CHABU** (209 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MLAFPPCVAHHDCHEQEMQQNRRRRKKVMKKVVHIIYSWYTLPSSSSAAAATAAAAAAAEEEEEEEEEEEEDDDNEEEEE
EEEEEEEEEEEEEEDEDEDEDEDEEEEEEEEEEDDDEEDDDNEDDDNEDDNDDDDDDDDDDDDDEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEMVGMHMVCCRGSATKTSGPLLKLLPTDIIAS
```

146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE

148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE

A0A388KPU0 **A0A388KPU0_CHABU** (2592 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MVGNDFRLKSNFPRINKTSSSFKLSRQAGGNGEAARGDNISSCQTRPGNDGDHQKEPEVGKPDGQEPLPSFGRHLHLYLD
IYAAVLQTLKALEVNNVVHYDLKCDNILLEPTDPSISEADFWDPPCNVQSRSTMEAMPPDCKGEMGKAGREVTRNAGHLS
CVLPFRVCIADFGQSKIGRKSDWDGEYEGVITAGNRGTECVKSPEMLLISNASFKSRSTYDRRKKFSPMTARERELREIQ
QVERLRQQLEEDLKKATDREKEIKSRAARLDTLEADKAALEGLDESSLSDTLKVLRDNMLSLHAHIDSRMDFMQSTLDQI
LDALTKPGFRPPAQSPLSLTAMSGPFAVQVGTQPSGTFATAAQTVASSSSSPVVIVASPQQPVQQSGQPQGHWYPKTLMK
PPLAFSGERKDEELNTWLRTVPVWVKAKRTLPEDEVVTAASYLEGKAAKWLDGVVVKARYGRRMADWAKSLTLDQFMEMV
EARWHNPQEAQRATDAINKLDQRKFRSVRELMTTVESLILVPGINYSDQFLLTTFVRCLPENVRNLLANEARTEYHSFET
LSRKALDLEATLGNAQPTSGNDSKKKKSPQEWKKKGAKLMMVESDGTQTEIDELADLMDYSEYDGEEELITKEKASKVGN
LRPIIDFLEWVLVRDPKRRPLMADLSVRLNHLKRTLFYDCIGPIERPPSPLRPDPEDKSKAMVLSHSPSKRPTDEELTKC
ALQHQISDRDHSSTPVTAPSMGSTPEGRVGASRNEEETGIDRSSALEGPSRSPFQPWSAGDTVESSSPIRSTMGRPVNRP
SQSGGVADATRISTSATTITRTELRKPRDEDCSSPADTFQASHSAVNDGSETSFHLLKPRTWRWLPLSQRNSSGFHQQCE
RNVNLGCECDGLGGQEGCSSVSDPHLNCRDPGSRTKESDVCLSPFKHHLGAVTISESKLESRSIIDGKPAVVRPKESALP
LMRRGAGAQRTEEVTMMNDSAAHPSRTLLQSLSSSVTPPQTGALGILKIRWRRRLPGTQSTKGKLTRSSGRRWSMPATTT
GSSRRDVKLFSWLPSKLPAMLSSILGGSRASRRLAMAAGTGIGGIPGHKRILPDPQGKDRIGLSGRVKGGDLPFESGRTT
GSHIVATVTESAPGHTGSESSPKTAVSHAPPSPPHQTSEERAPELESLGAIQPDRPLGEPSAFRRKHGLDGEPSTSQHLE
CAINGNNIGENTTAAANDRLQADGRRTKQPPPNRTASNTTVTGNYTRSRKVRSQSEPSITISRRIMRRQTSAESADQVDD
KLAMLSLLSRPVLLSHLMSRFPTRITDELWVGSYATLSDPDTLLELGITHILVCHPPPTIESTRFPFPYPSSSSASSSSS
SSSSSSSSSSSSKTTPAVESDPFDRPLFVSPPGTSGEQVFSSSQSRASAADGHGIRCSSNHSRCSSRVLQGQSGPEAWYE
SPQILTYQRQPQPAFTPLPAVPWLPVKNSLSWHSSRIADDPLRLPSFRCPWLSNSQRQDHRRYSTPGLPVSRGGEMSIPI
LVRAASSPRPSPSCGAHSTTEKGLANIPHPNNLPSAAVNFYWCWIGCDLDAPPPTPAFPDLLTCPSRSEHRWPCHTKTSP
QPQDSVTRTNSRAVQTRKPGHTSWAGPDVKQRQELVDHRCQSQGCSCCNASWRGDFPSNPDRYSPGGTAAATVPSTISSS
GYNNNTNTFKLSSSCPALSAKQASVSSSSPPRSSSCPPPPPPYLIQALRALYCAAHLGGTVLLVFPSSPTLGSCAIAVVL
SHLLVVSPQGRELQGVYGAYTYLRNQFPPASLFSPQPSSTFRWILGVAKTHGAVRRPVFHQDHQRQPGTGRPERATSAAT
VHPGAMSGTPAMLATTTAMDSPDELRKQVVGSAGLHTQPPHDADSSSKYLQGSHSRSQTNQTCFDADNCTWVQCKCRLWR
AVVIGIGTAPAVRTTTSRVEVGSGEPSSSRSSGKPHGAQTVRKDVRISSRMRRERCMHLSDSEANLRRGGDGSSLVNQSS
AKVSSSSTSEPHKLLVQSDDRNGKLDSITSGSSAAEDPSTRCSTIEDDEDEDDEGDGDDGDDVDDDEAGAAAATDDVDDD
DYYYHFDDDDDQEEEEEEEEEEEEEEEEEEEEDGEDEEYSAEDRRSRGTPSGTTTRGHYRADDNSAAALPAQLDRKVSLM
KQLTVSERQGIECFVPSACGCWPALSSSGICHEEDRQKDDDPRKAGPGRNRWKKTKRKMPLPCTQGVCSLQVRLEGHEEA
IYSNNCRGVISRQSRCSSSRSSASSSQWLVVKGENLVIDPVSPLCVPFTMTRPSARHHLPSLSAEASKPGKGDLGVEADD
QVQEEDRPKHSSGPPGGRSSDQRTAMQSSVFSEASSCRSLESPRPLTSCRKLGERQSDPEEEENKEVTLRTRRRRIRGES
SSRQEQKQRKKRERERREEDEVVDWERRQRSVVSGSGSLWHVFSCPACHAITYAVLREKTVGSAPAHPTTSPSVLAQENQ
KESEEVAPQQRGGFAAWKVPCSSPSSSAAVAESSASSSSSSSSSSSCLSRKEPLPREKTQKDMPCSLTRETLCEMAEFN
RLFILPSNGLDGNDKIALSIHSLFTTQRCEVQ
```

2093 - 2112:	EEEEEEEEEEEEEEEEEEEE

A0A388KPU7 **A0A388KPU7_CHABU** (3499 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MGVHRGPLVMGEKSLGELPEETKEKACQCRLGSLHTAEEYCHHQTLKMGKMHHTASGRYFEFVSFVHLMPYHWLQLSDVF
LVHQYVIAMDGLDFIFVSIGGDTKMGHYASLHVDWMEGKFFVRQGIGVTLDGENCLRVKIQWGTWRELAVKVDEDGILHV
GMEGLGHCTCRWQGLVTWLLIHVVHLNVATTSPSQVVTSGGKEESEEGEGKSSSVLPCSHSEKRSDPCGGRKSSVEGLGQ
ELRSPGHGRGRRQEEGITSPLHGGFDQSGHNQSPRERLLQGVRLGTARPDCNGDENCNSKKAYDGCRVSGSGRTCDMPAL
TSRERCAMSQIRSSMLNVRRRGLKTLLDLLVRSDIEDDVVDAPDAVVSDTTHRSVAGSTRQETYRCSAPLHVQSNTCERE
CSFQRGTANEGRGQRGVGVEGKENRVPSGNRNVDLNCEDVINNNCVGSGGFASSRCRRQRVPLLKMPVTQGSSDRKADRK
TRQLLEVHNASITDVGVLERSPCSVKNNNSQFAGSQESADTGGKKSSAGGRVDSAAEGRGTLLVGVDIRQNESMTRTVLT
TGEKNQYQEIVDGSNQRPTSGTRHEIEHCHDLQKSEEFATEQEEEEDLEEEDGEEEEEEEEEEEEEEEEEEEEEEQEEEE
EEEEEEEEEEEEEEEQQPQQQQQHQELIRESRTAKQDVASRDVKKRERSLSKNGCGKGPNHESGKQLWGEPFPSQCRDLK
LCKRPIFLTVRHLVRWVEGGFVSALVYEIAGCTVLKSGGEQQIIVDCNGKWDSGIAFSQVKAAIMLLVETIPQIVVRLFV
KAAIKSLSAWSSFLEKDCECEGITDRGSACKETCTYSRLSCVNVQQSSYADGWGGQGFAGVGGHQVCEDQHTHLRAVSQL
RAANANGEAGRIRRPAYNDGERCKGLLQVCELLYAVSKRSLMSNREIVCRSGVGLLLQVYGWLSQIKYDCGKSLLSYRAR
ENIGVALGNRGKDQPRNNGLCDEECTGSIPGQVGRMAGGKGSPAGAAAAGGEGFKNVMPEVCDKQEKLLSDRVEKCQHDV
STKNGSVSVGTREPLSLAATAARPAVLPEASAMSPRGDEAWPSSPKFLLTSNQLPNKIGSPASRNRQGQRHPSISPPVHR
DVAAAGETGRMASDVMIASHPESGLHNHMRTMGTNDNVVTSSSDFFVRHNAGPQAALLSSPSSFSSDFDQWDGSHECILT
AQHGPTASFEGCIPVGFFSPVGNRGAGGRWFPTPRIGPRSHLSAMGTQVVSGADDRATSPTRGQMSTPMFKKRAMSEVLP
DTWRYPVEDFNTKGLSVLSKVAAESDVHVDNLEEENYHSQGAVSRGGSTVRIAPVEKFGLMAESASQVVGGEGPNRGSLR
VPKLTLPPQPLIGAQTRSSRRSSTTTDRSRVGTPLPIGWAAGEGVVSVRGRLTAPGWGPSVPAASAAVPKLVLARPGSGW
VGVGSKNARLMSGTANISNFQKENQLNSPTRLAQVSSPERMVNSTCLAQRWSGAAGQGAWDGENHPMVAKRAQGQLAQLG
RELGEALMMCDLTSMILHKRMREGTRILADMLGGPFVSEMGGNAGSTVMRHGGDGAVFVVQDFQVGQRKQARSRMTESAC
DPGMSNKWEKEQRKGVLDPVSPNTLTRIEPNDISPSARRQGQQRDELCCHNGTGSARIELVPDSGKSGSLGMATSLSRAG
VAELVVPRSGRWRENDGVAGRDTGNRADSTNTLSPKPDRTALSDRAVNQESVDVRAAGLSNWDCPSTLRSEKQMICLCAV
KVAVLRALKLVLTSTLSHSSREVFVGQTEAVGLQALVENVILDMRCDKRKCCRDEEEERRLAYAILHYVECRGELPDYLR
QNTFCGHTTTGLGKRARLCATSSVMYWNPSNYCDVRHVEVLLQAVSQGLERLVVSVLESRSKRAKISRRKMSQVATGTMP
KDLEEACIDIIHLLGVLEECLCASPLQRCISSILVQICGSSLGRLVNLIREEVFGGEKLADGPLVIDIGWGSLWPAVMVM
WLSLMSALVSRGGTSTRALSFRCECKGCGQLLSLQSVRAICGGNEEGKSRCRYDQLNDNMTHTANVTDARATGKKGEPNI
EAERNSTDGGKQEEAPEALEQELGEEDGRAGESHLLRCKDTTTLMENGDAVKGRCMGEGVNVVHRFLAKTLFGKGQGECI
QLIESFANWAFLQMTAGCDGQKTHCSVGGESEEVSSARQRVTHERGTSIGGYGARNPSRSVPTDSCAMQTSETHCLALLR
```

```
WYRSVLPLIRHWATNLDELCNLIVVDRGESHNKEGGITSAQLGFQVGQLLSSDWLMEPENGWLSRILARGGVGGGSNDNL
CKEYRNSKISTPLSIGGKHAKGGSSGGKHRRERGGGDLQQTGRGWNTADSPGGGELWHARTTASNIWIPMHYDSVSIEAL
HLIIDTFDWFPAMSGEGREGCASPASLGILGQEKKRASNIGAAESEKLGMGGVVCNSGGREPSGDADTLQSAVVSDAGGT
TEEKKGKVHYHAWCQSSLNSCSGRLLRKWDVVNGPGIHSCAGLLGGHCLTSNPFLTKHYTDPFIYYHFLCFVKLYNSQGA
ADEQLRSPLLLVKEENHSSTTFRDCKSSSRIVRGTVLEGKGNVTRSGTASAYTRVEPQSPVHTSSSAHGEAWSTRLCTER
LVGRFDIEDAGRWGQESRRGRSRSTDEVPPDFASLSGGDKSSSRLCSTSNYGIIDGSTTFAGSELLAEDACELHIKALLA
IAQSRSESASWKLYQLRVMDFLVHEIALEYEVSKFDMGRTTPPPPQYQMAPTPALGSAPGIARETLHERGPRLGKSNDES
GSSRRQAQQQSYNSTAAQARKGAAAGQIISMAGNNDSGNLNCASQGQMEGSNWGTNDETMRRRPATPTGKTCSNISESPT
DKHWGDVTSPSMKVRIPRLELRDCSSSSFSIGGGGGGGGGRSDERCCSMRFGCLKPVDSKADVSHAAIGASDSRSMVDLL
TFSDCNLRHVDEQNYGYSSTDGVANGGANDDKKEETIEKKRSSGHQSCKGNPSAGREDPSQQPVVDSPAVHESRGSPVGS
DESTLKLQRKCSTQLTTTRVLSNPRAAGCAEQSREPCFPSSSKFPDGEAVVKKTATGMIVIPKLGISRLGNRRESLKSNL
LLCGVMEGEREGEEEEHKDSPDQPMHPQAAAAAAAGGGGGGGGGVGVQATLITNSDREDSMAASGSRENCYTISDGSMNR
EIGDTEDASIQGIELKYAGRWVDLNDEVEKEEMAIPSGGDQVCMVPHTNLNLGSESRPMSGERDYGPCSGASARVGASEP
SRASEDKDHCSYEEEQVYREEDVVEEEEEGDKDENRTKLEPYPEETTPSNHRKRDEWRSTVLSEVGRVSAGWHPGRDSIE
RNDLKAGLKKDVVPPLKLSLIDRPGEGWDSRMTAEVEVQGEEQKVAKHKMSERKGEGAPGLLSSSDRKSSSRRKQLGMMM
RKDFERQLGNETPTISGAEDNDKQPSSAIAKEAWSAHKHPWQVLGCKVTMMGDKDGSWK
```

614 - 633:	EEEEEEEEEEEEEEEEEEEE
615 - 634:	EEEEEEEEEEEEEEEEEEEE
616 - 635:	EEEEEEEEEEEEEEEEEEEE

A0A388KPW0 **A0A388KPW0_CHABU** (2522 aa)
Protein kinase domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MYFHDVHHVLRLLKYCVQLKALEVNNVVHYDLKCDNILLEPTDPSISEADFWDPPCNVQSRSTMEAMPPDCKGEMGKAGR
EVTRNAGHLSCVLPFRVCIADFGQSKIGRKSDWDGEYEGVITAGNRGTECVKSPEMLLISNASFKSRSTYDRRKKFSPMT
ARERELREIQQVERLRQQLEEDLKKATDREKEIKSRAARLDTLEADKAALEGLDESSLSDTLKVLRDNMLSLHAHIDSRM
DFMQSTLDQILDALTKPGFRPPAQSPLSLTAMSGPFAVQVGTQPSGTFATAAQTVASSSSSPVVIVASPQQPVQQSGQPQ
GHWYPKTLMKPPLAFSGERKDEELNTWLRTVPVWVKAKRTLPEDEVVTAASYLEGKAAKWLDGVVVKARYGRRMADWAKS
LTLDQFMEMVEARWHNPQEAQRATDAINKLDQRKFRSVRELMTTVESLILVPGINYSDQFLLTTFVRCLPENVRNLLANE
ARTEYHSFETLSRKALDLEATLGNAQPTSGNDSKKKKSPQEWKKKGAKLMMVESDGTQTEIDELADLMDYSEYDGEEELI
TKEKASKVGNLRPIIDFLEWVLVRDPKRRPLMADLSVRLNHLKRTLFYDCIGPIERPPSPLRPDPEDKSKAMVLSHSPSK
RPTDEELTKCALQHQISDRDHSSTPVTAPSMGSTPEGRVGASRNEEETGIDRSSALEGPSRSPFQPWSAGDTVESSSPIR
STMGRPVNRPSQSGGVADATRISTSATTITRTELRKPRDEDCSSPADTFQASHSAVNDGSETSFHLLKPRTWRWLPLSQR
NSSGFHQQCERNVNLGCECDGLGGQEGCSSVSDPHLNCRDPGSRTKESDVCLSPFKHHLGAVTISESKLESRSIIDGKPA
VVRPKESALPLMRRGAGAQRTEEVTMMNDSAAHPSRTLLQSLSSSVTPPQTGALGILKIRWRRRLPGTQSTKGKLTRSSG
RRWSMPATTTGSSRRDVKLFSWLPSKLPAMLSSILGGSRASRRLAMAAGTGIGGIPGHKRILPDPQGKDRIGLSGRVKGG
DLPFESGRTTGSHIVATVTESAPGHTGSESSPKTAVSHAPPSPPHQTSEERAPELESLGAIQPDRPLGEPSAFRRKHGLD
GEPSTSQHLECAINGNNIGENTTAAANDRLQADGRRTKQPPPNRTASNTTVTGNYTRSRKVRSQSEPSITISRRIMRRQT
SAESADQVDDKLAMLSLLSRPVLLSHLMSRFPTRITDELWVGSYATLSDPDTLLELGITHILVCHPPPTIESTRFPFPYP
SSSSASSSSSSSSSSSSSSSSSKTTPAVESDPFDRPLFVSPPGTSGEQVFSSSQSRASAADGHGIRCSSNHSRCSSRVLQ
GQSGPEAWYESPQILTYQRQPQPAFTPLPAVPWLPVKNSLSWHSSRIADDPLRLPSFRCPWLSNSQRQDHRRYSTPGLPV
SRGGEMSIPILVRAASSPRPSPSCGAHSTTEKGLANIPHPNNLPSAAVNFYWCWIGCDLDAPPPTPAFPDLLTCPSRSEH
RWPCHTKTSPQPQDSVTRTNSRAVQTRKPGHTSWAGPDVKQRQELVDHRCQSQGCSCCNASWRGDFPSNPDRYSPGGTAA
ATVPSTISSSGYNNNTNTFKLSSSCPALSAKQASVSSSSPPRSSSCPPPPPPYLIQALRALYCAAHLGGTVLLVFPSSPT
LGSCAIAVVLSHLLVVSPQGRELQGVYGAYTYLRNQFPPASLFSPQPSSTFRWILGVAKTHGAVRRPVFHQDHQRQPGTG
RPERATSAATVHPGAMSGTPAMLATTTAMDSPDELRKQVVGSAGLHTQPPHDADSSSKYLQGSHSRSQTNQTCFDADNCT
WVQCKCRLWRAVVIGIGTAPAVRTTTSRVEVGSGEPSSSRSSGKPHGAQTVRKDVRISSRMRRERCMHLSDSEANLRRGG
DGSSLVNQSSAKVSSSSTSEPHKLLVQSDDRNGKLDSITSGSSAAEDPSTRCSTIEDDEDEDDEGDGDDGDDVDDDEAGA
AAATDDVDDDDYYYHFDDDDDQEEEEEEEEEEEEEEEEEEEEDGEDEEYSAEDRRSRGTPSGTTTRGHYRADDNSAAALP
AQLDRKVSLMKQLTVSERQGIECFVPSACGCWPALSSSGICHEEDRQKDDDPRKAGPGRNRWKKTKRKMPLPCTQGVCSL
QVRLEGHEEAIYSNNCRGVISRQSRCSSSRSSASSSQWLVVKGENLVIDPVSPLCVPFTMTRPSARHHLPSLSAEASKPG
KGDLGVEADDQVQEEDRPKHSSGPPGGRSSDQRTAMQSSVFSEASSCRSLESPRPLTSCRKLGERQSDPEEEENKEVTLR
TRRRRIRGESSSRQEQKQRKKREREREEEDEVVDWERRQRSVVSGSGSLWHVFSCPACHAITYAVLREKTVGSAPAHPTT
SPSVLAQENQKESEEVAPQQRGGFAAWKVPCSSPSSSAAVAESSASSSSSSSSSSSSCLSRKEPLPREKTQKDMPCSLTR
ETLCEMAEFNRLFILPSNGLDGNDKIALSIHSLFTTQRCEVQ
```

2023 - 2042:	EEEEEEEEEEEEEEEEEEEE

A0A388KQ39 **A0A388KQ39_CHABU** (526 aa)
Dimer_Tnp_hAT domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MHADAAAAALAALAAAGPAAAAATAAAGLVAAAAAPRPAVAAAAAAAPPRPAAATRHPHAHPAAGSRAAAPCAAAARAAA
PPAAAAPPAAGPPAAAPRAAAPYAAARVAAPPVAPRATACAAAVAAPAARAAAVAAPAARAAAAPTAAAPVATARAAAAP
AAAAAPAVAAPAAAAPAVAAPVVVAAHRAPHPPPHHHHHHVVPRVVGPLAGLEHSVMQSGDVGDKPWAKDVIKKANMVVK
FFRNHRWPRSMLRTELMAQKGVKTMSLRDVGKRTDMLLSPVHVVARLLNPRLRDITVFSNLDLMAQFNSVVDRLVAKNGS
QKFTDCKDQLYDFQFGRGIFGGAAALRRANKDNAVLWWEARGGGHPELKMLAMKTLSIWTTSSPAERNWSTWSLVQTKTR
SQLKHKRTEKLVYSHWNLRLKSRGEDGPTVKGGWLGLEQDWVDEDIEGEAVDMLNVEDDDAVRHGATGSERGSTNIITAR
CATQSTTHGPDVFEEEEEEEEEEEEEEEEEEEEEEEEEEDEGGVIH
```

494 - 513:	EEEEEEEEEEEEEEEEEEEE
495 - 514:	EEEEEEEEEEEEEEEEEEEE
496 - 515:	EEEEEEEEEEEEEEEEEEEE
497 - 516:	EEEEEEEEEEEEEEEEEEEE
498 - 517:	EEEEEEEEEEEEEEEEEEEE
499 - 518:	EEEEEEEEEEEEEEEEEEEE
500 - 519:	EEEEEEEEEEEEEEEEEEEE

A0A388KQB8 **A0A388KQB8_CHABU** (278 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MNVCQEEEDEEEEGADEEEEEEAEEEEEEDEEEEEDDEGEEDDEGEEDDEGEEDEEEEDDEEEEDEEEEDEEEEDDEGEEDD
GGEEDDEGEEEDDDGEEDDDGEEDEEEEEEEDEEEDDEEEEEDEEEEDEEEEEDEEENDEEEEDNEAEEGDEAEEDDKEE
DGDEEGEGEEEDEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAEEEEEEEEEEKEEEEEEEEEEEEEAEAEAEKERRRRR
RRRRRRRRRRRRRRRRRGRRRRRRRRRRRRRNLLCFSS
```

175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE
180 - 199:	EEEEEEEEEEEEEEEEEEEE
181 - 200:	EEEEEEEEEEEEEEEEEEEE
182 - 201:	EEEEEEEEEEEEEEEEEEEE
183 - 202:	EEEEEEEEEEEEEEEEEEEE
184 - 203:	EEEEEEEEEEEEEEEEEEEE
185 - 204:	EEEEEEEEEEEEEEEEEEEE

A0A388KQC8 **A0A388KQC8_CHABU** (482 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MPVTEQHKAKKNAKKKKKKKKKKKKKKKKKAKANAKKKKAKKKKFKKAKAKKAKAKKARKKAKVKANAKKAKAKAKKAEG
EGEGGEGEGEEGEGKGEGEGEEAKKAKKAKKKAKKKAKKAKKAKKAKKRAKKKAKKKPKKVKNAKKKNKKAKKKKKKAKA
AKMKKKAKKKAKAKVKANAKKAKKAKKAQKAQKANANAKKATAKGKKKAKAKKKAKKARKAKKAKKEAKKEAKRRRRRRR
RRRRRRRRRRRIRRRRRRRRRQEGGEEGGKEEGEEGRKEEGEEEGEGEEEGEEEGKEEGKEEGKEEEEGGEGGEGGGNE
GEGEGEGEGEGEEEEEEEEEGEEGGEEEGEEGEGEEGEGEEGGGEGEGEGGGGGGEEEEEEEEEEEEEEEEEDEEDEDDEE
EDEEKGEEEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEGGGGGGGGGGGEGGGRTAIPQWVLRPPKRLERERERELESCR
DF
```

416 - 435:	EEEEEEEEEEEEEEEEEEEE
417 - 436:	EEEEEEEEEEEEEEEEEEEE
418 - 437:	EEEEEEEEEEEEEEEEEEEE
419 - 438:	EEEEEEEEEEEEEEEEEEEE

A0A388KQJ0 **A0A388KQJ0_CHABU** (632 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MIGTIRPAQEQREVAEWRPSPGEMKSGGSTFVTGEIDVLNVVRALDHRIPLPIGHLLSISEQDNERMLQHYKANRKRFVI
ARTTNTKGKGPAQENIPNHANTSEPIRLGLIRKDNHFLRIKAIPWKFAECDIEVWGIPYNTIIDSGVVVLAISLRVVERA
GKRKNMIMLAEKDHLVSADEKKNKTVWRMTNVVFRLGKVHALGDVVVLDSAHAPTLYFCIKPLSVPILNEDEWSDWWDAY
LELSFCLVEVIFHWSKPVPGGEGTEVPNNEAELLIVQAWRTETEGELLGIIFGKVEEGNLALITSELLVFLVQLVDDLPL
DILSRCDSKPGPDVLPRTLAPHLLWSTCTELDVDNCLYPSQDLYLEINVTDLVLWDPVIRRASVCAAANDDDDDDDDDD
DDDDDEEEEEEEEEEEEEEEEEEEEEEEEESCTDPDDSDYLSEEETEEELERGEEEEESEPEEPSDRPRRSEEGEEAEAQR
RREKAEGKRPIKEGPPLELLLGDPLLNPETPREEPEDDGAAAEGSAAAGGVNRRLHPFPHPTLPFAFVEMRAIGLRPRSL
SRRPHDYMMVRQLPGRPPFPDGWCPFQPTLFHQLYATRLLITIVPHSTTRSLVDSFLLRVLLFSATGGNTIT
```

406 - 425:	EEEEEEEEEEEEEEEEEEEE
407 - 426:	EEEEEEEEEEEEEEEEEEEE
408 - 427:	EEEEEEEEEEEEEEEEEEEE
409 - 428:	EEEEEEEEEEEEEEEEEEEE
410 - 429:	EEEEEEEEEEEEEEEEEEEE

A0A388KRC0 **A0A388KRC0_CHABU** (800 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MLNVVCVTILVISRGGGGGGGGGGGEEEEEEAEEEEEEEEEEEEEEEKRRRRGEEEEEEEEEEEGGGKEAEEGEEEEAGG
GGEGEEEEERGGGEGEKEEERGGGGGGGGGGGGEEEEERTKKKRKKKRKGKRNRKRNRKRRKRRKRKKRRRKGKTRKRK
KRTRRRRRRRRRRRRRKRKRKRKKKKKRREEEEKRRRRRRRRRREGGKEEDEEEEEEEEEEEEEEEEEEKEEEEEEEEEEEE
EGGEEEEEEEEEGEEEGGGGKEEEENRRRTGAAAAGRRRGKRRRRGGGRGEEEEEEEEEEEEEEEEEEEEEEEEEEEEAEDED
EEEEEEEEEEEEEEEEEEEEEEEEEEGGGEEEEEEEKRKKKRKEERGGGGEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEKMRRGRGGEEEEEEEERGGEEAALISSVLVKCLEVEEEVEEEEESSVLVKCLEVEEEEEEEEEEEEEEEEEEEDEE
EEEEKEEVEEEEEEEEEEEEEEEEKEEEEKEEEEALQDEALHFVIDTFWAGSGIRLWAEAVGRLAGVMCLRAPRPSLLDKK
KKKKKKRRRKRKRKRKRKTKRKTKTKTKKKRKKKRKKKKKKKKKKRKRKKKKKRKKKKKKKRRFLKEEEEEEEEEEEE
EEEEEERSSSSSSSSSSSSSSSSSSSSSSSRSSRSSSRSRRSSSRGSNSFTGLAIRETGGGGRRRRRRRNWRRRRRRRKRK
WKKRKRKKKKKRRKRGKEEEEEEEEEEEEEEEEEEEEEEDEDEDEDDDNDDDDERRRRRRRKKKKKTTKEEEEEEEEEDQQHQ
```

290 - 309:	EEEEEEEEEEEEEEEEEEEE
291 - 310:	EEEEEEEEEEEEEEEEEEEE
292 - 311:	EEEEEEEEEEEEEEEEEEEE

293 - 312:	EEEEEEEEEEEEEEEEEEEE
294 - 313:	EEEEEEEEEEEEEEEEEEEE
295 - 314:	EEEEEEEEEEEEEEEEEEEE
296 - 315:	EEEEEEEEEEEEEEEEEEEE
321 - 340:	EEEEEEEEEEEEEEEEEEEE
322 - 341:	EEEEEEEEEEEEEEEEEEEE
323 - 342:	EEEEEEEEEEEEEEEEEEEE
324 - 343:	EEEEEEEEEEEEEEEEEEEE
325 - 344:	EEEEEEEEEEEEEEEEEEEE
326 - 345:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE
379 - 398:	EEEEEEEEEEEEEEEEEEEE
380 - 399:	EEEEEEEEEEEEEEEEEEEE
381 - 400:	EEEEEEEEEEEEEEEEEEEE
382 - 401:	EEEEEEEEEEEEEEEEEEEE
383 - 402:	EEEEEEEEEEEEEEEEEEEE
384 - 403:	EEEEEEEEEEEEEEEEEEEE
385 - 404:	EEEEEEEEEEEEEEEEEEEE
386 - 405:	EEEEEEEEEEEEEEEEEEEE
738 - 757:	EEEEEEEEEEEEEEEEEEEE

A0A388KRF7 **A0A388KRF7_CHABU** (316 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MSSLLLRIYCSQQENAHHPRRVSARLCSRPSSGGFSRNRLAAPPNFPTKYLRIKEGVEDEEADEEGDEEEEEEEEEEEEE
EEEEDEDEDDEEDEEDDEDEEDEEEDEEDEEDDEDDEEEDEEEEEEEDEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEDEEEKDEDDDDDDEEEEEEEEDEEEKDEDDDDDDDDEEEEEEEEEEEEEEAEEEEKEEEEEEEEEEEEEEEEDEAEEE
EEEEEEEEEEEEEEEDEGKEEEEEEEEEEEEEEKEEEEEEEEEEDDDEGKEEEEKWKRKERERERERERERERERERG
```

133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE

A0A388KRP3 **A0A388KRP3_CHABU** (284 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MEVSSKTERRSYVSEEEEEEEEEEEEEEEDKDDEKEEDGDEDDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDKDDEKEE
DGDEDDEEEEEKEEEEEEEDDDEEEEEEDDDEEEDKEMEGKEEEEDEEKEGKEEEEDGWRGGGGGGGRGGGGGGGGGG
VGRQRRRIRRRGGGGGGQLISQSTFNLSVIKINKKAKNKKEEEEEEEEEEEEEYREEEEEEEEEEEEEEEDKDDEEEE
DGDEEEEEEEEEEEEEDEEEEEDDDGCDGRRRRGGGGGLGGGRR
```

43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE

48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE

A0A388KT39 **A0A388KT39_CHABU** (92 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MKREERKKREEEEEREEEEKREEGEEEEEEEEEEEEEEEEDEEEDEAEDEVEEEEEETEEEEEEEEEDEEEEEEEEEEEE
EEEEEEEEEALI
```

69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE

A0A388KTE7 **A0A388KTE7_CHABU** (177 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MRMAKKKEEEEVVEEQETAPTEEEDEEDEEEDEEEEEEKEEEEEEDGEEENDVAQKEEEGGGRGLKDDEEEEEEEEEEEE
EEVEEEEDEDEEQKEEEEEEEEEEEDEEEKGEQEEEEGEEGEEEEEEEEKEEEEEEEDEEEEEEEEEEEEEEEEEEEEDVE
EEKEDKDEEEKEEEEEE
```

138 - 157:	EEEEEEEEEEEEEEEEEEEE

A0A388KTM1 **A0A388KTM1_CHABU** (1063 aa)
Reverse transcriptase domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MQAQVMDAEADLWGRWAWIKAVIGGEEWVLTTVYAPTTVYVPTNWWERAKFFLKLKTIVPKADRLLVAGDWNVSLDEALR
PGAASADRGDVQDLLDLSAEMMLSEPFPVLNPEDPGYTWFSNLFRNRQDITRRPLDYFLLSEEILERVTTVRQFCHPMSD
QKPVVVEISLVAGAERGKGFFRLNSQVLEDPGIGEWVKDHMSRWEAARPFFETPAEWLDGGIAIASGMLDACSRILPKAR
NSKEAECLRRIEEAEDRMEGHPISVMVWAAERERRMTKWNGLQEEREKRWVEIPRLKGVETQDKMTRATFQKLQPRRSQQ
QMVELRHPFNAAAPPACSPLGMLQYARLYYSNILTSRRPHDSVDTNLSLTSDMWENTTTRLHAGGRLDLDRPLTLEEISQ
TLKTMAKGKSPGVDGLTVEFYAANWGVFGPLLVCVRAGPLDLQQHSDGNRNTRGGANENLDYAVLLLDLEKAYDKVGWTF
VLTTLHWIGFGEGFCAWVIALYTFSTASVMINGHLSEPFPLARSLTQGCPLAPLIFVIQLEVLLNKIRAQPVIRGLQLHT
GNECKVKALADDLFAVCKNSVPALSAMKRVLGEYSVLSEASVNWGKSTYLLPAQFELKVEWGMKRVAKGEEERFLGIMIS
LKVEASSQGFHLQQRIASRLRVWDSAWDLSLIGRALAANVALFSILWFVTTVYELADGAARAIRRLVARFIWKPKAQNSE
SFISKVALDTLSFPSDKGGLGLVYPARKNKDQLCWIKKVAGLGVAEHWVALAERILMVEWELSHPKDVWSCWFMPSFKEK
ETQIGFLGTHQKSLEEDAARLKDLNPTTKEEVLNQMLFENPAVVDSTEEEEDEEEEEEEEEEEEEEEEEEEEEEEDDDDDD
DKEEEEEEEEEEKDIGKEEGEGEGGGEGKEGGGEVEGEVEGEVEGEVEGEEGRGGGGGEEGGSGEEEREDRGGEDGQEGGW
GGGGGGEDGKEEGGRGGGGRRRSGRKRRRRWKRMMHGPAKHTSKPLCKTSYMYRLSALASTNAISPSSGQSRRSTATGKQ
TADKHGCRSYEIMPIITNLLKPT
```

853 - 872:	EEEEEEEEEEEEEEEEEEEE
854 - 873:	EEEEEEEEEEEEEEEEEEEE
855 - 874:	EEEEEEEEEEEEEEEEEEEE

A0A388KTZ7 **A0A388KTZ7_CHABU** (863 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MPKKQHRRATRGDIILNFPKGDGNPLEEEKTTKGKTTNPYPYSKSVAVRERDTMEKEEKHGLPALQSQRQAQAECGLSGN
SMPSESTQARQLLQEWDLDAEEWKQHQHQQEQEQQQQQQQEQMREGEGEGEEEEEEVVVWEGQEIWERTEMGMRRLRGLV
PVPACGACKVHMQEEEESIEPILDGIGMTRGGGGGGGGGGGGGGGLLNPSFLVRLISTVQSLAFSMDDVKGKLLECSSV
MDKRMRAMESSMSGMKGMSLEETIRRAIRQETSASAPDSVSRRETASTSDSTLTCRHCHMQSGVVARELRKLRAELRQLE
NRVRKLDKAMNTSAMPSLSATLPNTVTIEAAAPPQDATATDTQIRSTATSRRRKHPRGPPSVNNSQYRNSTNGHEDGNSY
NSSRNVDSRRNSYSNRSAKHGVNSISKMKSQLVTPKLDCTKNSNGNSNGNSNGNSNGNSNGNSNGNSNGNSNGNSNGNSN
SNSNRRANGGGNRSPKTESQSGKPRPEFGRWLIEVERFFEAVGGPEERKLIICRPLLGGLYHAWLLHGDDDMEHRTAMNL
EFAFTWDELKHAMWARYPTRKPERKARHLLDRCKQNGRPIQDHIQEFEKILGMAEKTYPEEIIIEKFVDSLDARLRKQVR
PKEDEVETFDAIATFAQKLANPNSGPGNRAISFASFHFQFWFWFWFWFWFWFQFRFRFWFRFRFQFRFQFQFRFRFQFRF
WFRFRFWFQQKGATVSFNELAPDNRSPYGMQRIQHPTHVDINIEDDSLPSQPSPADGHKKKSKKKREEEVEEEEVEEEVE
EEVEEEEEVEEEVEEEEEVEEEEEEEEEEEEEEEEEEEEEREVGGVPMGSEARHRSSDQSIH
```

820 - 839:	EEEEEEEEEEEEEEEEEEEE
821 - 840:	EEEEEEEEEEEEEEEEEEEE
822 - 841:	EEEEEEEEEEEEEEEEEEEE

A0A388KU08 **A0A388KU08_CHABU** (186 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MSAAAVSVSFPKDEDESATAVSYTHLDVYKRQEEEEEEEEEEEEEAEVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EGEDEEKEEEEEEEEEEEEEEXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXKLSTGVRMVLQMSIAWACMVLAW
ENIVLLDRDHGDHRLFAVGSRLALPL
```

49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE

A0A388KVH1 **A0A388KVH1_CHABU** (430 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MQPILVYMSKVDGKFLFTPVSVNFLTEITKVFFAMLMLFLQAMKANILLVVPSFLYAINNYLKFTMQLYFKPVTVKMLSN
LKVLSIALLLKVIMKRRFSVLQWEALCLLLIGISVNQIPCGQDNSSTLGGLSTMALVYTLMSVTVPSMASVYNEYALKSQ
HDTNVHLQFLFLFGYGAAFNFMGIILMTLIKDTAIMTVSCIRGKEEEEEEEEEEEEEEEKEGEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEGRRTRRRKRRRWRKRRRRKKRRRKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKEEEEEEEK
EKKKKKKKKKKKKKKKKKKKKKKKKERRVVFGVSLDTAIMTVSCVWGKEEEEEEEKKKKKKNEEDEEEEEEEEEEEEEEEE
EEEEAEEEEEEEEEEEEEDGRRRRKRRGGG
```

223 - 242:	EEEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEEE
225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE
384 - 403:	EEEEEEEEEEEEEEEEEEEE
385 - 404:	EEEEEEEEEEEEEEEEEEEE

A0A388KVJ4 **A0A388KVJ4_CHABU** (157 aa)
TFIIS central domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MKEEEKEEEEEEEEDEEEEEEEEEEEEEEEEEKEEEEEEEKEEEEEEEEEEEEEKEEEEEDEEEEEEEEEQEEEEEEEE
QEEEEKEEEEEEEEEEEEEEEEEEEEEEGEEEEEEEEEEEEKEEEEEEEKEEEEKEEEEEEEEEEEEEEEEEEEEEE
```

87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE

138 - 157:	EEEEEEEEEEEEEEEEEEEE

A0A388KVN5 **A0A388KVN5_CHABU** (681 aa)
Integrase catalytic domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MMMAKEKEGEVAEEEEEEEGGGGGRGRRRRRRRRRRTRRRRREEEEKKKEGGGGKGIDIGRCRYNDDGERERRRSGRGG
GGRRRRRRRRKREKKKKQEEEEEEEEEEEEKEEEKKKEGGGGEEEEEEEEEEEEEEEEEEEEEEKEDEEEEEEEEEEEEE
EEEEEEEEEEEEEEDEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEDEEEEEEEEEEEEEEEEEKEEEEEEE
EEEEEGASSVGWARPLAVGAPIWGLIHKGPFISANHISYHLVSSPLHLILLLHSILLHLILLISVSSRLVSSRTPPYSSI
SXLLHSILLHLILLISVSSRLVSSRTPPYSSISSYSLILLHLISHPIILISSHLSKSYLISSCLVSSPSHLTPPFHLTPS
HLTRLVSSRLVSPRLVSSRLVSSRLVSSRLISSISSRLVSSRLVSLSRLISSVSSRLVSSRLVSSISSHLLCLVLSHLVS
YYSVVDVDDFKLDLLKGEYNKVVDALSRRADYLGVLVMKFGISDEVSRSMVEAYEEDPIMYEIMHKLDAKDKATSDEFVP
VDGLLFLEKAGNHPESNGLAEQMNRVVQHLLWHYIRPSQDDWDEKLPLIASRYNNVVHSTSSMTPNQPHLSWKPRSALDF
LLTENQPTAAPGSIEFAVKYEQLLQPAVEHIKKTRDAMVAS
```

121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE
180 - 199:	EEEEEEEEEEEEEEEEEEEE
181 - 200:	EEEEEEEEEEEEEEEEEEEE
182 - 201:	EEEEEEEEEEEEEEEEEEEE
183 - 202:	EEEEEEEEEEEEEEEEEEEE
184 - 203:	EEEEEEEEEEEEEEEEEEEE
185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE
190 - 209:	EEEEEEEEEEEEEEEEEEEE
191 - 210:	EEEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEEE

A0A388KW32 **A0A388KW32_CHABU** (203 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MSSRGLVAIQTCKSFVEEEEEEEEEEEEEEEEEEEEEEEEDGEKVEDEEEEEEEEEEEDERENDEETCQSFVEEEEEKKEE
EEEEDEREDDEEEVDEDEEEREEEEEYESRREEVEKRRIGQQTVLGQKPSSFITQDAFWEFFTSESVARSRRRRGGCCAT
AQAASSGMGWMRMLEIVFQDHAVKWFAVNISWMASQAVLLRSS
```

17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE

A0A388KWI1 **A0A388KWI1_CHABU** (179 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MRALGGGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXEPNGEAEEEEEDIDIDEEEEMKDDDAEEEEEDEEEEDEEEKDEE
EEEEEEEEEEEEEEEEEEEEKEDDDDEEDNEIEEEEEVKNDDAKEEEEDKEEEDEDDKDDEEEEEDGEAKEGEEKEDEEE
KEEEDEEEKDEDEEEFDED
```

79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE

A0A388KXH7 **A0A388KXH7_CHABU** (73 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MRRTRRKDDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDQDEEEEKEEREEDDAEKVEDEERRREKADREEGSTQ
```

10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE

A0A388KYV7 **A0A388KYV7_CHABU** (560 aa)
Ig-like domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MEVGYQGGGGGGRRGGHGGGTEGGGGRRGGHRGGAGGGGGGARAGEGGRRGGGGREGGGRGGREGREGEQEEEEEGEEE
EEEEEEEEEEEEEEEEEEEEEKEEEEKEEEEGGDQEEEVGSGSPEGNLHLFINRPLIVLALLDAVHDGNAGGKKGFVPRG
TSVLDKLPDLDAPDERSNIIEASKADAGGMASTDPPLADSFANWQKRRSLASGRQKKNHEDERSPQDVGGCESSTSEALE
TRRVERFLRNVGFLLRVQDLKRGKIAFVNNRSELLSDGKRRLLMVVEFITDLLVKLAPDPEDEHGQEYIQQAADFVRGSV
REAEETGNFGERSRVYAIIDDLVFKLLQGIMTPASAKSDEDAISWLRRQRNICSQREEILLKISRVASVGQRVLLSATNQ
IAEKAKALLRCHGVSFPLSGSAFAPPAFAAQSTEGEGHPLLRCQSFESLHHLLEIVETILDNYSMKWFEEGSIDKAMLEK
WVAQQLELQGFVQCCVDRGSLVRMYVTRISAKVVRQLQIVAKAGEGEAAAIPSAYGSVADKAASHLTRSALSILPQQQRF
```

78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE

A0A388KYW1 **A0A388KYW1_CHABU** (3049 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MKLAELARRIWSGGKMGGGGGGGGGGDQPHPSTVSGMGKQQEEGDKENGKEEEEEEEEEEEEEEEEEENLKEEKVGSKQL
PWIRRMLPNPPPMNPRGLVKRVMIGSGRQEREESEEEEEEEEEDEREEEEEEEEEEEEEEEEEEEEEDEEEEEEGREE
EGEENAHVFNRVRKDMNVHVSNGGRTRLFAYPKMLPNPTAMTSTAMARADVARTSSSREESRVTQPRVSSHSSPKLMGFM
HSPNLLPQRRSNGGGVPSHRQASASAYKQQEENGFHGIDTARRHRPVGSSLGRDRSVYRPAPNSSKEHHFVNVRRDSGRD
PDGHNLPSTDEEGDLLVGIPRHRRLNASTKPDPDGDRRQSGVDGDGHRYHRDRCCSDRDRRHRLDGRPDDDRRRDADLEH
RYLDDDRHRDPDVEHRYRGDDRVPPDRAVVEHRCRGSRSAGNRSTIYHQVDDRGEVRKGGRGSVGAVRVGGGNNGGDRGG
DTSTTTGCYVQSSTAIPKSMASEPDGRHSLRTKVAQPTAKVAQSAGACQRITTATTTATTTTTTTVRGPRRASPIPPSRD
RFEWGGGANGSTAAAAKIGTDGRRPVVDGGTGAGAGGGAGAGAGGGVGGVVSLSARHSFAGIGTLPPSGQAPMMTSSSGR
SAAPPSAAEISPRTPKKAAEAMGKAAMMRQSARESGETRLHAVEEDKWTSSPRRTTAADSAPRPRRAGDRLEAERERRSN
YWSRQTTAAVVGGKASDPFEARVPDETVLSCSDDEEDEEEKRAAPDEKGAAAAVDTDTDEVGQDNSHAAATVSRQSRQFL
GSDRRKSGWCYETGSKEQELSLRGREGRGVMREGDEAKGEEQGEGAKEEGKGSVRASAPHCLFDRPTAGGDRDRGERERD
KHGVSVRGRGDPTLPKAYGSPRLRQSDLQNAGEERIRIEEEEEEEEEVEEEVEEDGQQGVLVSGRGDRTLLKCYGLPRRP
GPRGAIAKQHYIGKKQSLDATEDDPNHWEREEAKGEGKKKAISEEERVQGGRIAMVDQEKKTTESRFDAERCHVSKGHAH
AHVVQVGFENPTGDPVKGREMQRGLSAWGGWNGWCPGGHQREWPRGKTGVVLTERDDKSPRVGAEDRSSARGQNVEDEVR
SSLRKLWKQAEAARNLRAEEEWKATRRKDRRHENHRERSDNKQMTGPNSRNDVRYTRRRQDGRSDGGGGGVHRGNNGREY
DRVHAQHRHRDDNRHEGRDEIRKKKMWGNNNNNNVQKETASRSIGRSGTMGRRAHMPPPPQHLGTSKPGMAGRRDPAKKG
FFPRPPPPPPPPPSNAPYPTTSPAQESRAESLTAASPGRTSPEVPKVKSVRVTSRSGLFWMRGTNSSYYYGEEDDDDLVI
GYGGGGGYVGVQGRRGRGRGGGRESDMEDSDRDDEQEWWNDDSKLDLEEKDTHDHHAERGSESGSGSGSESGKSYVRDEE
EQPSCDDTGSVNDDETEAEAEVEAATAAAAEEEGEEEDYDEFGSERTWSSPVYDEDDEVDRRRDGSCDDSDPSLSSCGSL
SSGGRSSGGSDEDESAKARRKAERRRKRAEEGTSLPWSAWVKNDDSTTGHGQSDKRNDEEGGDAGNDVEDEYSALYAAFD
LLKQGKEAELLLAKQSAVGGETVVAPDDDADNRVPCPDQGLEHTPILIENKGYICTRCEMVIYDLETWSRLFTRYRYAPD
GKRLNATKANDGCDPTVGGGGASEEEAGEDKRGEAAAAAATAMASSPKDVSRSRTRMIKPHPWIYNRMHPHQKEGFQFLW
RNLVMGVHLPSHQDLDKQVHDALQARETSSPTMGKGQVTEEEVNVEVKGTATPNGGNSGPCTTSSSPATTILTSLCNTAN
EETKSEKTGEGGVRRRDREGRGEEVGKKTTSTCTSVESTEVGGCILAHAPGTGKTLQIIAFMERYFKYHPETLVRALLIV
PANMLTTWKSEFGRWTNCTDRRLGRMRRVEVSVIDEKTDKHWQQAFRRKQKRLGPASVSGCSPRTGFGSRTAGPVPASRP
SSRRGSRPRTGSGPRTPAPVPASGLNRTGSGPGTPAPVPASGLNSRCGSGGPGLIILPDDSTDPSEDIDHHAYDHRDRDE
VKWRDGSTAGRKRTWHGLSSREGPGMNRKRQQKGLGRGRAGPGRPFTGPPGGKRRKLDRGFWARNARRPQKQPQQCGWVQ
GKDQKAAEVAAEADGKRDPLCPPKKGSQNVIELWNERGGVLLISHTKFSMMMSDRKRKNTVEEEPVLCDGNVAAVAAAGS
EEKAELGGPSGGPGVKNDNLQDPQSLGEGTAADRHDFITEQRRSQALLENATIIVVDEGHRMKDSTTRLFDSLMKMKTRL
RISMTGTLVHNNLEELFNQLSFVRDEYITDICTSWARSNCENMPNASEGEEMEEEEEEEEEEEEEEEEEESGEGEQPKQKRK
KTAVSEGQSNGLSSRAQPTCDGHSDSSESECMILEEEDWKQAKATKEEEKRVAKEKKEAKEDKEKKEKVKSNANGNSSHT
RNKRVHNGKQREAEGEEEVHEKIEARESQENEEEGRESRKGKSERNQGPQGEDDGTSDTDTSGCAMVMDWKPGKATKEET
KSKGEEEGKVEEDQNEKMKSNANGNNCSKTRSEQLRNGRHGEAEDEGLQKVAGIEKKEEVKEGITPEKGKCEAKRRGRRV
RRRRVTMKEARQGFLKAVEVPIMAGLEMKSVAEKRALEPVLFRLHKLMEPFVHFHNGSQVLKSRPHGLDDYTIKIYLTPL
QRWMYNKIKGVRRIDACTNPESFCYAEFATLALDPYDLIANPKKKNIAACLSEPDGKQLLDPLRHGKPRIHDSCKIWFIF
ELIKACQSTNERILVFSTYIRPLQALARMITSEQSPKETRGWREGVEVVSILGSMSQADRSQEIKIINDPCNQTKICLLS
RKACGEGIHLIGASRVVFLDVSWNPCDTIQAISRAYRLNQTRRVIVYRLISCDTWEEKAYNYSRVKELVSALVEHIPMGS
KPVPLFYEQSHPGSATPRLVPHRRDGQNFKSTFLDAIVETDEMLAQKGLRGKMIDSVLEHNGILTHFVVRADKALWQSVG
AQPQQGEQQ
```

128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE

A0A388KYX0 **A0A388KYX0_CHABU** (633 aa)
DDE Tnp4 domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MSFSTEQVISARLLAPRGRISTIRQVQRPRLSADLLRFAAFFSTTTIHAAAEFRIKQAAATRVLTEISAFQRLSPPGISH
ITVIVVFVGNLALITSELLVFLTQLVDGLPLDILSWCDNQPGTHVLSRTLKPHLLRSTCTELDDDNCVYPSQALFLEIDV
TDLTVWKPIVRRGNARQGEEEEEDDDDDDDDDEEEEEEEEEEEEEEEEEEEEESSEDRDNADYVQGEEEEDEEGEPAEE
EAVAAAAVALVRRFQLERAAGRMKVTLSRRRQRLLLQRVLDAPDCVSSSEAVLQLCFAIGCGVLPRSTPRWWMRRRTGGT
WEDLQLCDDTTDDYFWEKLPMSRRVFMEISEACAPLLQRQVTFYREPLPSEQIVAYALHRISWPTGVRKHVVLRAFLDKG
FPNCHGAVDCTRIYVDKPMNAPGENCFDCKHRFSVMAQVVVDLDLRVLDMFVGYPGSCHDIRVIQLSSLSRRAEEGVFFR
GPPVTLPGGGVRTNGYILGDNGYPPSEWVVVPYEGINQHPYEERFDTKQKVARGAVERAFGRLKRMWRLFLRTHKTNLET
LPQQFTTVCILHNILLDAGVEFDENLLWEVDENGVRRRVDLGIHRPLQLVSMLTSTGPALALRNTLAERMKHM
```

194 - 213:	EEEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEEE

A0A388KYZ9 **A0A388KYZ9_CHABU** (147 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MKKNKKKKTETDDEEVEVEEEEEEEEEEEEEEEEEEEEEEKEEEEEEEEDAGKKEGEGEGGGEGGGEGGGEGEEGGGEVEG
EGGGGGGGGEEGGSGEEEGEDRRGEDGQEGGGGVGGGGGEDGKEEGGGGGGEGEGEAKERGGEGRRG
```

19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE

A0A388KZU1 **A0A388KZU1_CHABU** (1202 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MCQVIRARARAIELERRMAVVASGGDLTVSEQVHQYESTMEREQSKIRKATLARARMRRAMSCRERNLSGSEAGSLWSDH
HLSAAGEGLTATAPGLAGPDSRRTSCGSSAWGIPEGFKDIGRSQSQVKGGIGGGRGLRFAGEAASGGWSSSSGRELIRSS
LTGSIGRKLSPVFRGRAQNEKCLEMLQRSTSSGVRGSCSSIGGDLESSSASPARPWSMSPAHFSLPGGAVLTRKVRGKGR
GRKKRNRSGDKGKDKENMERAEIILQDMVVAVEEMERGGKQVAAVRRTLATSTASDRKTETNNLLQQHQQHNEGQRTLSW
RQDVERDSEKRLQSEGTAGKDLEARKAAKFQQEMECVLKQRLEARNQGNPNHKGCSSQREEDTSLMRNQKKVSYGTGNGV
AEEPSRFVLAQHKTQPQWAEERKREVERVLKKRLEARKLEETGEHGSKTGGEYGVKPLPGRFACEVSIEKHADETAKSGH
VAAKSSSVQQKLHLQWADERKQEVENASKQHSKAKDAEKITGNTQRAHPEGRAKPVAGKTEDKKVVRACLEADRCVAAAE
GKLNIERDMDEKCTKAKMGFSSKRVNVIDGPHQPVEGQEDERKRETVRGTSELWDRPAVHLKEQVSERRKKHESSEDQAA
KCMQWDIHQTIEVRRQLQRAEEEPQRRDVEGSHDHQGAKYMQLCLRQAIEFERRMQKVKKEKQEAEEKEEKQREAQRAAE
LRHLAEKAAMLCAAKTPERSDGLVLGKGWSKTSHQTESWRQEVAAEQWKGGANLMAAEREADVRRESMRAAERQREAERV
AGFRRQAQWFQDKMDNCKRLDLEKRDLEKEAIAQAQAERAAEVRRRAERAEELRRLAEKAEEEWREAERLDEIRRKEEMK
```

```
GLTRGMETADEKQERGEERAKDLQEMEQARNSRKEAARVAELHRQAQQMEKRRWEAKRIANLRGEADWAAQERREAERAE
ELQRQSYRMLEVQNEAKRAAELQKQHEQVMVDRRKSGRAVMEQHEIQAHLRLRKIIKDSVCQGGTDALGQVGQGESLQAN
VVRLKEEQDEDEGEEQQQQQGEEEEEEEEEEEEEEEEEEEEKDEEEEEENVEVEVVGEGWGACFLRRNRFGSWLDSELG
ERLAGVDFHHIDLASLLKEMLHLVEELTETQRAWRRGMLEARHEWLMKWGTKEGIEAWLRESQTLKGVFIKGSRLVREDR
GR
```

1062 - 1081:	EEEEEEEEEEEEEEEEEEEE
1063 - 1082:	EEEEEEEEEEEEEEEEEEEE

A0A388L118 **A0A388L118_CHABU** (267 aa)
DEAD domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MESVVLVSDNSDGDDGCTVRGQGYAGVPADVSLLEDELYCVEAELQRIQEEIGRLLEQQDQLDTRRTAIQKCLKLAKKSA
AASAQSDSKFGLHSEGQVAPSSASGESNWLRPFQWDEEVEKLRKNLFGLPSFRTHQREIINSVLSGRDVFVIMPSGGGKS
LCYQLPAVLRPGVSLVISPLLSLIQDQVCHIGSLSYMYTSRTSHLCGMHLTNGVKIRATDLPCSSKIASGMHAYEACFTM
GPEEEEEEEEEEEEEEEEEEEEEEKKE
```

243 - 262:	EEEEEEEEEEEEEEEEEEEE
244 - 263:	EEEEEEEEEEEEEEEEEEEE
245 - 264:	EEEEEEEEEEEEEEEEEEEE

A0A388L122 **A0A388L122_CHABU** (346 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MATMGDYVPSMDEMLHAEGFLPDGDNGAELLRRMEHPERSGDARHEEEEEEEEDSEEEDSEEEEEEEEEDDDEEEDDDEE
DDDEEEDELDEEEEEEEEEEEEEEGEEKEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEEVSLYMGRWTRGGRRKAEEEE
EEEEVKEEEEEEEEEEEERNERKKRKKRKKKRKKRKKRKKRKKRKKRKKRKKEEEEEEEEGGRRGRRRRRRKREEEEEEE
GGGGRGRRRGGRRKKKRRKKEEKEEEEEEEEEEEEEEEEEEEEEEDEEEEEEEEEEEEEEEEEGRRKKKEEGRTKKEEEE
GRRRKKKEEEEEGRKVRRSSFPSSSP
```

109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
264 - 283:	EEEEEEEEEEEEEEEEEEEE
265 - 284:	EEEEEEEEEEEEEEEEEEEE
266 - 285:	EEEEEEEEEEEEEEEEEEEE

A0A388L1S9 **A0A388L1S9_CHABU** (277 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MNDEKEEEDNDDGEEEDEDHDDDDDDEEEEDDDEEEDDDEEEEEEWKEEEEKEEDDDDDDEEDGDDRPPDLARWRRAAEG
AMTEMLLGSILTAIALAAMVLSVVVSLDEPQLAPDETSAPDEEDEKEEEDDDDEEEEEEEEEEEEKEEEEDDDDDDEEEE
EVKDDDAEEEEEEEEEEEEDNEEYNDDEDEEEEGEEEEQEKEKNEDGEEEEEEMEEDDNEEEDNDDEDDEEEEEEEEEEE
DGEEEEGEEKEEEEEEEEEEEEEEEEEEEEEVEEEVEQ
```

251 - 270:	EEEEEEEEEEEEEEEEEEEE

A0A388L2F4 **A0A388L2F4_CHABU** (119 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MMEEGEDTKGQKEEEEDTEEEGNEEKDDDEEGGGGEGGPSDREGGGNREAPGGRGRRKKRGRGGGDKEEVVEEAMMMEEE
ERENLDEEEEEEEEEEEEEEEEEEEEEEEEEEEKGLGRG
```

87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE

A0A388L2H4 **A0A388L2H4_CHABU** (1143 aa)
PPR_long domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MSAADVSSFFGVHVRATPRLRQCRRVFRIDIPSCRFPNDYKGTQHESSRNLLRSMGSYHHRDTSAAKSVANHRGCWLCLF
EGDIDRWRSGSKRSRSASLQCKGARGDDKSSSRHGSFHHHHGFVEEGEEETKEKGKLDEVGEGRQRDPSPSFREKRPQQQ
ALQRRSPSRNDTRQETTRPATMTKPRRSLPPLYPTPPSPYRTQHMLQMVDEALSLRQTSSSSSSSSFSSSSREAAGYKNR
RYGEKKAGTIPEKRGNVSRPRSNDDEWNATEQGDENDVKRAAGGGGGGGGGGGRGGIGGSGREERKRARGILKGGWGSPV
MRHGEAYISILKQAVGQLRVDQVEEVDAILARFEKLTYSPLDCATASAVVIDLCRCGRWHQAMRVCLWVHRREQQVIEAD
VDATSRFPEVEEAQGRGGGDYRRGKDGGGVTGAAARGKKDGSVGEILPGNRHLDVVAYNSLIAAFSRNGPFEQSLRVYRM
MRKAGLEPNLYTFTSVMQALSRAGRWKDAMSVFRDLVRHGNQPDVVVYNTLITGLAGAGKWYQVEKVWREMQEGQVRKSL
GTYSLFMSSFVKARRCDLALDVYWEAVKEGVNITSPMIRGLVCVCAYAGRWALALDFYHMLRQQAAEESSTSSDVPRAQS
GSVRSKTVLSAERSAEPSSKPANWSSDWSSEPPFALAGCTSEPRLKPMEDSLDPWSRPTEESSDDEEDFDIDGSHAVERG
KGEQYQQVEEEEGEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEVVKYRDSVSQKQREDDDDGNVYSDGPSEKGRVLSSDEGM
EEERGGGEDGRFPERSIGRQLESIDTDRRGVSVSGNQSSSVVENTLIDCLGRAGRWDLANGVFKQMAYAGCEPDAYTWSA
MINAAVNSKKERRFERAMRVHKRMTRRGIRPNVEVYNIAISACRHAEEEGWLWAVGLINEMKEVGIKPDVVTYSAAIRVC
EKDGEGRMVALLWDEMGRAGCTPNHFTYAAGIRGFGKIGQRKRALALFQDMIIRGIKPDVNVYNAVILANGANGKPWLAR
DVYRQMRRRGCLPNETTERLIQEFGTVEPVQQKLTKAQRRKRRKKMAEERKNAMERGQQFVYYSKGAGLKGNKGPSRGHG
EEKGDKEGGSAASTDVHSQFSSV
```

739 - 758:	EEEEEEEEEEEEEEEEEEEE
740 - 759:	EEEEEEEEEEEEEEEEEEEE
741 - 760:	EEEEEEEEEEEEEEEEEEEE
742 - 761:	EEEEEEEEEEEEEEEEEEEE

A0A388L2M3 **A0A388L2M3_CHABU** (621 aa)
MYND-type domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MTSSGLDLPPDQAGGLRERENGDEEEEDDEEEEEVLLGHCVEPVDPDDFAPVRFPSKVGGAPVWLDPVNMPSGDCICCQV
CGKPLDFLLQVYAPVDSVASAFHRSVYVFACRNLQCLLEHSRMQNKDETVQEERSGEGGGSAASSASPCLPKKKSVRAFR
CQLPRANQFYPYDAPKPADEEPVSLPALATPPLCEWCATWKAEKRCGGCRRSHYCSRCHQVDHWKGGHAPECRHFQAQAK
ESQQPGASGRATDSITSAHVMAPWKRGAVARVKPVNPRVWPEYALEVEPEPLESADGDVLNDTANGKDDGNTQCSTTRDR
IAALLADYERRLKEGDADYPTEELRETEEGVASLHEGQKQWAEFESRVARAPQQCLRYCYAERAKPLWPQLSYRPTPSRI
AACGRCRSPRIFEFQVLPQILYFLKVDSSDENALDFSTLAVYTCANSCDTLVAGDGSAGKEGSYVEELVWRLIAGVYVEE
EEDEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEETRTRRGEEEEEEEEEKEKKKKKKKKKKKKKKKKKK
KKMMFGDGGWHPRGGHETWAKKKKQKQRKKKKKKGGGGWWAEGHEMVAKKKKKKKKKKKKK
```

487 - 506:	EEEEEEEEEEEEEEEEEEEE
488 - 507:	EEEEEEEEEEEEEEEEEEEE
489 - 508:	EEEEEEEEEEEEEEEEEEEE
490 - 509:	EEEEEEEEEEEEEEEEEEEE
491 - 510:	EEEEEEEEEEEEEEEEEEEE
492 - 511:	EEEEEEEEEEEEEEEEEEEE
493 - 512:	EEEEEEEEEEEEEEEEEEEE
494 - 513:	EEEEEEEEEEEEEEEEEEEE
495 - 514:	EEEEEEEEEEEEEEEEEEEE
496 - 515:	EEEEEEEEEEEEEEEEEEEE
497 - 516:	EEEEEEEEEEEEEEEEEEEE
498 - 517:	EEEEEEEEEEEEEEEEEEEE
499 - 518:	EEEEEEEEEEEEEEEEEEEE
500 - 519:	EEEEEEEEEEEEEEEEEEEE
501 - 520:	EEEEEEEEEEEEEEEEEEEE
502 - 521:	EEEEEEEEEEEEEEEEEEEE
503 - 522:	EEEEEEEEEEEEEEEEEEEE
504 - 523:	EEEEEEEEEEEEEEEEEEEE
505 - 524:	EEEEEEEEEEEEEEEEEEEE

A0A388L2R3 **A0A388L2R3_CHABU** (1355 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MRKCWTPFDTDGGGCNRDNVDGIGDEFRSQDAPHIEDKGGADLSQRGGANEEEEEEEEEEEEEEEEEGEEEEEEEEEEEEE
EEEEEEEEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDDEDDEDEEEEEEEDAGKEEGEGEGGGEGEEGG
GETIVCVAVQNGVLEIGTTQMVPEDLPLVLLLRSVFNGKKDVRQLAEANDRLFAPAASLHASAVFAAAIAAAVAAHAGST
ETESQTQHTKAVPEALLLEGKSETGSSTDKDSRSQSVTSKTTSACRSPCLSSMSENRLQSLVDRTRSMLTIVAEESKSRA
GEDTSAETACQVSANQGSQTLRASVDSVVPVSGDAPHGSDLPVSSTWWDELPESIVYNLPLHKEPAACPSGPSCTPREDS
RWISEDRSDQDNAKESVNGDVACEWVRITASEERGDGGQEKGLVKEGDLLMDLPDLELSYAKDSLDLLSMNPLSDPLRDW
PWDEQQVRIGDEDPYLTSLMAPDQVSPVPVTSPESQYVACTAPLHTTASACYSAATEPRSDSCRSESVNRDGVPSSEKPN
AKLAQSSSVTFRSDGDSSSGVSVSVSEAPNLLAHTNGVPKLSTTNHPILAQTKGSHSYSHHTGLDGLDHTRRGADITNGV
QSVHRSVHQEDQQRNSNDPVRSMKRKQKESSGNMDWNANSLLATKPETEKRTCNKHPARHAAPEPEPELRHRQGPEIAAL
LPPSIHRSRSGTHGSGSMSSYLQPAKLGEDSVGMVVNGSGPRQVANGDEPALKRLKRETKLAPKSFPKLEGNDCITFVGP
IDSSTADPLVRTTMRPSPLFVAPQQPRLSPQPQAQSLQQPPSFLKTPDLATNEVLGPTSASYVHPVSQPHPGERRDDLSF
FTSTLLTSSSLTLPGSNRHGERCLPGGDSLAGCGGIAAGAPFTTRFSAARGVGPDSRSNMGSSAVLHADDANLVARTEAV
SDRIKESQAGPLTLEQEARLPPATFSSLPLRPPQQLVLNSGGGEVQSSLNQLVSTPAPFSSRWEGDLRAMTMSAVTSSTT
```

```
TWDDRSGKRMDGHNSNVRLASNLPSSLTCPSFDCTPRLDSRGDVWKSEITTRHETSYSNQGWCCLSVSDGMQRSNDCSLA
ETVAQPAGEVSARGKGGRCREGNWSQREAIPSLSSVDITQFHQASSSPAKNSIGTKPIVDGVRLDTPSHVHHTRQKAPLR
SNQTEASTAALQNFHKGDLEQSSMVPFNVQAEQQLSPSTEMRDGAEASLVSFLGGLHNFHPRCQEGNGTRPFTDILNKDI
LPIDMPTGADNYADWPWEVAGINNREALPQGVKRKWTAEALTRAILKTTSPSQSLAPSWLPNLWWSADDIPVTTR
```

68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE

A0A388L5L2 **A0A388L5L2_CHABU** (1854 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MGRSEVLVGSNIDRDTVCSDIAAGPTDRWSGVDPSARRRGGSGFVDDESLEEGEVMENALISPSSRRRGSSQSQRHVIDP
SSGLRSRGTKPTISRRSSRASPPTAGEPYGELMTGVASLMGMAKATKQVKKRAGEGRETGEQTPTLFDGSEAGETKLRTE
PRKSRSQSQPLIRRGSKLSIHSHGSGALWDNESGGRVRKGEVGKRAPWDDRFVVPDNRRSTGRGRNENQAMQHRQKPLGS
GGGGDDGGDGRRRSLERAGKVLEGVPGTRALAVALYLLGSKAETEGEPKEMAMAGEGAAERRRRSHGENQADSLNGLLQG
IHGSSQEGKDGGEQVRRILLGLQMTKQELKKMRKRTSNANGWEKGDREGEGIEVDLPRNDAGLAAGLRLGREEEARAARA
TKAGKRPEGAAGTLDRVMAGTTTTSQLLIEEGRKQSQRKDPSFGDDFVDINRAAVDADAEAEVDDVTNGIVLQKLLRVQG
SITAQSQQFAQLLKQHFAQDTEQYTKLVNKKEEEDTTPSEPSDEDEADQTSDEEDDVLENRFGNRRGFGREPSGDCRDML
DILWELEEGPAPQFYAYMDRRGVEARMGVWQALFREGQDLRYRLEDHLAMDDKAVDGELLLCHLGSGFRTAGGIDNHLRL
EGDSVYTEDVTDYTYTEDVTHPTGTTSTPMGRSDRSEPVEHHHKGTKAMREQERRDRRGPRDPRDKSSSVPGVSGKPRSS
HHSVGSDPGSNITTTASLPAGSMAGITFEHAEPPAVSFFPVTGSRSHSTEDAIVPGTLPHSGGQGGGSEPAVPGTRSAYP
GPRFAVPGPRRAAPGARSAILGPGSAMVSQLSESSLATLTDPTNHQASARSLLHSRAPSEDEHVHDQGQGRLAAAIRIPS
AEIMYRTSSVPNLAPQELAAAALQEADSDSSALESGGSLVIDSRRDDFYDRTTDISARGKAHQQQRMSARIAGGASSDHL
ASSSDVSHAGKLEHSSGLRNPTSPQGSENVSQQGKLMTRTDFGQQSLQKGEGLEANQGFAVNNRVLRGMVEPTTQELQYD
QMGKHRNGSDMLAAQSIVQCWTRFYTVFLSELSSNFTQEEEGEEEGGEEGGEEGGEERGEEGEEGGVEGEEEEEGEEEQE
GEGEGGGGGEEEKEEEEEKEKEKEEDKVKEKEEEKEKKKEEKEKKEKAKEKEKAKNAKKKKKNAKKKKKKKKKKKKKKKK
KKKKKKKKAKKKKKAKKAKKAKKAKKAKNAKKKKAKKKKKAKKKKKAKKKKKAKKAKKKAAKKKKVKKKKAKKAKKKKEKK
RKKKKKKKAKKKKKAKKKAKKKAKKKAKKKTWEIQDVQGPPTTLANRAKDPKKKKKKKKKKKKKKKKKEKKKVKKEKKKK
AKKEKAKKKAKKKKKKKKKKKKKKKKKKKAKKKKKAKKAKKKKAKKKKKAKKKKKAKKAKKKAAKKKAAKKKAKKKAKKKAK
AKAKAKKKKKKRKKRKKKKKKKKKKKKAKKKKKKKKKKKKKKKAGEEEGEEEGEEEEEEEEEEEEEEQEEEGEEEGEEG
EKEEGEEGEEEEEEEEEEEEEEEEEEEEEEKEKEGEEEEEEGEKGEEEGSEEEEEEEEEEEEEEEEEEEEEEEGEEGK
EGEEEGEEEEGEEEGEEEGEEEEEEXEEEEEEEEEEEEEGEEEEEEEEEEEEEEEEEEDEGEGEGEGGDGEGKGTGGEEG
GEKAKKKKTVKKKAKKKKVKAKKKAKKKAKKKAKKKAKKKAKKKRAKKKAKKKKKAKKKKKKKKKKKKKKKKKKKKKK
KKKKKKAKKKAKAKKKVKKAKKVAKKAVKKAVKKTVKKTVKKTVKKAKKKKKAKKAKKAKAKKKAKAKKKANKKKAKKKK
KAKKKKKAKKKAKA
```

1529 - 1548:	EEEEEEEEEEEEEEEEEEEE
1530 - 1549:	EEEEEEEEEEEEEEEEEEEE
1531 - 1550:	EEEEEEEEEEEEEEEEEEEE
1571 - 1590:	EEEEEEEEEEEEEEEEEEEE
1572 - 1591:	EEEEEEEEEEEEEEEEEEEE
1573 - 1592:	EEEEEEEEEEEEEEEEEEEE
1574 - 1593:	EEEEEEEEEEEEEEEEEEEE
1575 - 1594:	EEEEEEEEEEEEEEEEEEEE
1576 - 1595:	EEEEEEEEEEEEEEEEEEEE

A0A388L5V5 **A0A388L5V5_CHABU** (170 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MGRRMFKYKCIAPLCPKGGGGGGGRGRGGRRGGVEEEEIEDDNEDEDEKGKEEEEEEEEEEEEEEEEEEEEEEEEEEE
VEEEEEEEEEEEEQEDKEEEEEEEEEEEEDVEEEEDEEEEEEEEDKKVEENEVEEEEEEEEEEEEEEEDDEDKKEEEEEE
EEEEDGDEEK
```

52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE

A0A388L6B0 **A0A388L6B0_CHABU** (130 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MDNKDKGGSGLSRRGEEEEEEEEEEEEEEEEEEEEEEEGEVEEEEEEEEEGEEEEEEEEEEEEEEEEEEEEEEEEGGGGGGG
DDKEEEDAGNEGGEGDGGGEGEEGRGEAEGEGRGEKGRVVVPCQSWLVLR
```

16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE

A0A388L6S7 **A0A388L6S7_CHABU** (486 aa)
Reverse transcriptase domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MPTPSPTITVTSPRQFAQDDVTFFMLNVTDLLHYHPPCLDAELISLKPDPPSISMASISASLPLSFVESTQSSCADADAE
ERTRHTADLEPAICDLIREYHDLFPSSFSYANIPPMRDVEHSIQLVPDYLDGTLRLCIDYHSFNHYTVKDSYPMPRFDEL
FDRLADNHFFTRIDLRSGYHHIRVAAADQLKTAFRSRFSHHEFTVMSFGLTHAPATFQTAMNDIFRDILEQYVLIYLEDI
LIYSRTLEEHLRDLRDVRGHDFYAKLSKCHFAQRKVNFLGHYVSDHSLHMDDSKITAIADWPNPKSVKQLRRFLGLIKED
EEEEDEEEYDKEEEDEEEEGEEENDEEEDKEEENEEEEDEEEDEEEDEEEEENEEEEEDEEKDEEEEDDEEEDNEEE
DDEEVHDGEKEEDNEEEFDEEEVEDDEEEEVEDDDDDDVEEEEEEEEEEEEEEEEEEEEEKIEEEKMEVDYKDDDEEEVK
EEEQQI
```

440 - 459:	EEEEEEEEEEEEEEEEEEEE
441 - 460:	EEEEEEEEEEEEEEEEEEEE

A0A388L738 **A0A388L738_CHABU** (866 aa)
Reverse transcriptase domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MGICNAPATFQRAMNVTFQNFVNKTRLTQGMVNLCVIVYMDDILVYSETYHGHAQQIEWTLGALRDARFKIALEKSEFFL
LEISFLGYVVTRGGLRPDSRKVTVVKDTPVPTSLTQVRAFLGLASYYRHFIKGFAAIARPLTNLLRKDQPLSWDAERERA
FATLKDALATTPILIRPDPTKKFILITDWHPEAMSAILAQKGNGDREHVIEYASRTVSDERRNDSAPQGECYAVVWGIRH
FHAYLYGQKFLLVTDHEPLLALKKLTNYTGMIGRWAVRLQEYDFDIIHRKTKRHGNEDGLTRLHRPANVRKCARQGKIAP
RFFGRFRVIERGERHAPRVGGLGKPIGSTDRPPRVLSSSSPFLSISSCVCFLLRYRGGRRLFTALIPSCIFCPFSYPVPI
AIAISFLTERALGDHMLVPRGDISVIRQVHHPRFNPDLLRLAQFFCTTGVYVATEFRFTGHRQAIVLAEALAVRRLSAPR
VRHVSTIVIFGGDISTISPLRHKTIRTSFREWGQQLATEWNQWLTRRGDDLVPTDDIGVGGIRTSRHEPAVVLPELMTWT
RDIEHRAWIEYVELLIIQAWRTEVEGDLLGFLSGLVRPGHRQLIVQKLTIPLAQLVDDLPLDIVSQCDESPVPHVLSRTL
TWSACLEEQGGNNNPPSQREYQVPRRIIDLAFFQPRTASEDEGLILEEEEEEGVEEGDEEEEEETSEEAGSYSEYSEKES
GGGEEEEEEEEEEEEEEEEEEEEEEEEDQLEEEEESEWETLGEEAECAETREEDPEAARRREEIAAGKQPLEFASGVDLS
IPNNPAKDPEPPKNDNGNLATETSSAPARRRRSRSPSPSTSACPPVRARTDAGHRASSPVLIPSPP
```

724 - 743:	EEEEEEEEEEEEEEEEEEEE
725 - 744:	EEEEEEEEEEEEEEEEEEEE
726 - 745:	EEEEEEEEEEEEEEEEEEEE
727 - 746:	EEEEEEEEEEEEEEEEEEEE
728 - 747:	EEEEEEEEEEEEEEEEEEEE

A0A388L7B8 **A0A388L7B8_CHABU** (6263 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MAAADVDFAEDTASVRRLPASTSAASAGAAMSAGTSSVPIRPQYRLRSADKLVGVGTAQQVEEEEQKGLVDGNVKESGRA
GEDGGAAWGENAPVGRGKGEGGGRLRGQGTGIGGGGGEGRGAEQEQEQEQEHVPPPPDLPLPPGSQRHKARRERVIKKES
ALQASGDGGHGGHPGATEREGAVSGSGSGTTSRRGRTCKGAGAEDGRRTMPSPSPTDREPSKTQRVSIARRALSTKRGGS
PWMDSSARSERGKRVREDDPYAGALRKADDDDPDPNRDDDGEEEETGEDAVGEDEESSSSSDGSCDNDHEGDHIEHEEEE
EEEEEEEEGISRKFLKGRPMTAVVQDDDDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERVPILAEAVMSID
GLDVSPNGYGGRAASDAYGYGGRGGRRRRYGWSVKKKEDGWLEDNPFEDAAQDFARALRTVGLTSGVGGVGAAAGGGGGG
GGGSDTAAKLGGKQCRRRRGGGGGGGGGGGGGGGGGERAAADVTFAGEAAVDVDVSGGVDGDGLVQRVLSDEMLLGCLPR
RRGAGYGGPTAIAMAIVQEEDPLQKVPEPSQVVDMVAHQICKEDDLQSVSEACGWLVTPEKKKDNNQHNYSTQNKKSSCS
SSPVATVSAAAVRDDPRRSRSSGCGGRAGGIEARSDGGTVVDGDHDRVRAKDKRLPEESAALQEPFNAPGGNEQSNSCCG
GIEARSDGGTVVDGDRVKGKDKGLPEESAAFPELRSDGRLVFNAPGGNEQSNDGGLVDGRDGGFGGRDGVEDSKLRSDGG
LVDGNGGDGDGVGKGREPADEPMVLNEVAADAQHPCSRDCMPRGGGFELRSDGGGCVGDDDDDEGDGDGRGIHKGSEKRS
AEDYTQQVGKFFCKVTTDPPAPSSSLAAIAAASPAVIAAVVDVHSLQRHLTVAIENRRESLGEDNGEDNGDNKGAEESKR
KNGVQAAGGKLCNDGGKDVVRERERRAVVTPTRCGGEETVERPVTVPTLSEEETETVERPVTVPTLSEEDTETVERPVAA
APPLRTGGSSRACHGRKKLEDNVDGYGGTQSVKGDTWTRRGEDESIPAKNEVPAQNEAEEMREERRRRTSRRTERESVSL
LSRRGGCHVRKTMGREQAALGAEGEGEGGRELGEEEEKIGENAEKNKEERGVASPSVAARASCLADTCTPTSAPTTRTAA
AAKNRRQTDKTEEEEEEEEATASPKEDSTHARAVLNITASDACTPPSSAAAKESLLPAPRCEITASPTYSLYELGLSDDH
YAARLLANRPHDPNPDPDPDRKPYSRSPLPGRRSGRRRLVLKKKLEGLLDAAAPPPDGAASLLRCGDRVSSMSCSTEPSV
LAAAAGGVVVNNDEEAVTDPGTGTGRGDVGGTGTLVAGPARSPGAVPRSVGGTETETGSGLGSGTGMEAGSGTKSGTQTD
RATEKGTKRERETVGAGRRPGTETRTKRGREMAGAAAKHGTQIMDTGTETDTRTGTGSGTGTGTGAKRGRATRAEAGPKY
GAQKTGTETGNTAIRTGTATGTGMRRGRGTREDTGPKAGTQTDTGTETGAKGGRGTEPGSGTKPGKRTDAGRGITGTGPG
TDPRTGPSTNTGTHAGTETGAKGGRGTEPGSGTKPGMQTDTGTEAGIAGTVPGTVPGTVPGTGPGTDPGTAARARLSGSA
VLTSELVTGEEKGPGTEPKPGTETGPGTETMGPGTAMDARGTTSRAWSSPKRRSPAKRRLATLKSIAAIVTESVEGGGMG
GEVVGSGEAGGELEGRRRARAGAIKGRRGGGGARAAHGARGEPPTDGGGPLRSEDLPEESSERGRRGPLGALSVKRAGSS
PRLPRAGKNVDDAVNEQQQQQQEEEEEEEEEEEEEKESGCMGAVYLQGEEARGGRERLILLEGNELEKQGSVVIAALLVK
SDKRRKRKRVDGGREGKDVGGSGGYGGKGSVAAAGGGGVNQGRSPKQLPRREEIVDAARRNEEDEQGGGKVSSARQVLQS
RSRYGGKAGRGGRNLLLLPCPTSEASSRGGERPPPPPPPPSPLEAAAFARRQRADDGPPPPSPMPMQPPPSPRSSIQVLP
RLSLEARGYGGKRSMAERRAGEMNRGADGDCMRSAREQNDEEGKGREARSVDEERAGKLLDKDKRKEGGGSSRTAGHVFT
DRNGKSGGVGEGGGGGRELGSRRDGDDVSLKATLGPRAHGVGDLGDDDDDDEEEGDGGYLPRMRSLAPIALQQARVEEEE
EEDMAGKNEPGTRRVLLPGKKAGTISRPRPAADVVGAGGPSSPPARKKKGTAELAKLMRRQQMDDRQSKQQIGIRIGTRG
GGMRSTPRGSKSSPGSKSDPPTAPAPSPPLQRQQKQRSGSGVKRGGGSLLRFHDDDDDPPRDRFLDHRVNENEGDWKTKK
EKKEKKKTSPVSVAMAMAKAMAATRKDSQSPSVKRRKLESIAGCLEASQKKKVMAIAGSPPPMGARGHVAASDEASPGLA
QVSPGLAQVSPGLAQAAPSRRHPWLRSRKGDNANVGGDSCSQPRLMKTVGGGKDAEPLGAVGTEQGGRERGEEEAMAGTH
DALFRGYAAGDPDPSTPAAVRSGGTTDFPSVDEGERSRSQTIEKMQQQSQRRGSGDRYPYPVSAADAHDDVEKHDRIVER
PSARDRTARGRARARDLQQQQQQAPSRSPSSSAQEHLHHLRRRRRGGGGEGESMAEGDGLMMTEGGAAESRAVGPAPARQ
ADEDEDEDVGGGNVLRCARESPTARQADEDEDYKPXPTADDCNPTPAVEDYAPTNPPPPEEDHPIIMVINKRVGDGEAAK
PGHRKGGSNHGRKSSASLQIGIPPRILTNQHVAPIQAAKQQDEEEGQSSFSSSSDDEVAVKSGGKQKEKHQVRYTPAAKL
QLQHKQEEGEEGEEEEEEEEEVAVKQEQGQDDGKAVLEQDGIRSGKKSRGKQKEKHQVRYTPAAKLQLQLQHKEEVGKEE
EEEEEVCVQRKQNAVSCKWTGAAEEEVSLHRSPPSLWKGRSFKTAEVGLGEWRVKVERLKMNEDEHEGKGGRRQALPVVG
THEEERRVVGNGEKEDRRDGDRDHRSGSAMMMVERERMAGREEGGGEKKERTMTMRSALLLGSSVVAAAQCETPRGETRR
RRRRRRSEQEEEDDQHEAPPDGDGGEESIGMKTMKTMQSFSPSSPSLLPDRDKEREDDEPVMVKVASSTIDLPLASGRYR
AECTDPTEDKSAISLCTSIPAIAASSPVKGMAIEEEQRVRRDGKKEEEEEEEKEKDRMKDKSSISLGTAIAASHPVKGEGM
EKEQRVGGEGEEEKEEEEEEEEEEEKKRGISASPCPDPPPEGGDGVERVSGSIPASAASAPSSLAPEAQCKGETEHPAGW
SGQTPDAAEACHPDTDSHGGLGELKTNLESRDTADSSRSVQPSETPDLKSRYRRLNVDPSPTDPVTAALHTVGSSGFIHP
SKRLPPVTVAAAFAAAEAAAGVDGDHVSLAQQLMRDGHVLKEVGDGDQVDISEQQCRQLQEKGEEEEEEEEEEEKDEEEE
EEEKDEREEGCGGEIGKNLREGKLASQRQSAAAVDRAKKRGGGGGGGGGSQATAAQAVAATRPAAEDAAATCSPCLPVDD
RRDRVDDVYVAGMGGGRDGSISESSEKETPPRGASSATGAAEEGVAGDGGGAPVEAAEAKGATTWKEDRVGGGGGGRGGG
GASTSGTTANEPVESTPSSVCLPGPGPSSTDGQLGDRHRQQQEEDELVASDEEEGEEQATACSISTTAATGGSGSGCVGM
GGRSISALSAGHDQSVSNVATTTPPVFRLWGMDVRIQRREGEDEGGESRGVSADCASPQNREEDISMPAFSCWQASREKG
EEVDGQGREAVCMPQAIEQYGTSSAQSLEPWYGCRRGGGGGKGEGGNGNRKGGIWTEKMTGVEREGWNGGNSERPAAEGG
LVDRTNRSCSREEEGEVGGGGGEGSTAEAAAEKDVFVRDVSDGTTGAPLPARSSRSRAGGRSGIELVGGTRFAEKMGGQL
GGLRGLSTASSERGCRDTVRGGGAGGDQGGGGGSADRHGGLAAMSVPDAVFVCWEAGDANARLVAERRKVAERRKVAERR
KERDSTEEKLMKKDQRLTSSSGDGERGRGRWPVTGRELFGHPPFNESNSELQPRVASSSVIRGGEDDERGIVEEKQRQVV
TPPPTSAKTEREHRVDRDPDYHDKDEATTSCSSPLIAHDRRLCASYEFWDKPTRSSGSEPPAAAAEALSAAAAHHTTIAD
SSLAETTAMVISPPMGGGGGSNRSSSCGLGLDVLVAAANVSGDRVVEGGVGGGGGDVGSSACVSPSATESLAALSQPASG
SSREEGNLHGVFHATGGQDYHQHRVRRDDSLGSGSLSFAMAKAPSSSLHRVLPTPQLSVPALRDESGADGPLFSAAAAAA
AAQQPFYGADRLLSPARAPASCPSEAVGGGRRGRGGVESLSLSEMASDGDRAPLAASMMRTDMAAPPPSSSASSHLPSQQ
QMITAVRFTGHNPPPPPPAPPPPPPSSPPLHWHLPPPNQWAPSSSDRHHGQPGSVAVNAFDHSARSLGRAQEKGIPTECG
GSCDGRGGSWQSRSRTSSCDHLDSAGPAAAAGAQCLLAGQREQRESPALLHLRTSSAPITVSVCGGSSSSSSSSALDMAG
AVSIASARNGFDFVRQHHQRLSYERAADEGSAMGGRRGPMSRVDESGGGAGGGGDEASAASAASAASAVSAAGASGANAA
RSVGQRYGGARGPPAASQTCGVSSADAETLLGALRAPAVPAAMVVSTSERYPGAAGGGGGGGGGAVGLPAARVGWGVMPI
SQLHSRSHAFPLGMSAAGGGSATVTAETSTPTSRDIFSPPRAASAEAGGAIPSSSSLTSSPSPSSSPAHRYRPKGAASIP
PTPAIATRVPFIGAAAEEEESRRGHRVVTASCATAAATPFSPPSPAVAHFRSAVSLGAAHLYERPSMGGAERATALSPAS
TGGGGGGGGRSAGGGHCLGVGTGLHTGGRGLQGAPGPPAAGGATGAMAMAAAASSPSPRTSLSKINTSSGCAISAGRRSL
LSEEELRRIGYIPANPEASPVRGPPSSSSRAIPIPAASMTAAASSAICGPNRFLSSSLIDAQLGGAVRAAQAMANDNNKS
GGIGSAAAAAAAAAAYGRLSQPSMTAGFCPSSPPAVGGDRDLSPLGQQVRLHTHTGTAPGAPVPSFSCSTRGGGIPLTSS
IQAASARDHQQAAGEGSAGTPLPPSPSSSVQTLRSMEYHQGLMLSSRSAGGSAGGYSDKAGRETQQQRKVLSVQEERSQR
GGGGGEGGGGGGGGGGGAKGEGGAIEQQQRGGSIAQLRGDWREKDLIVIDDDDETEPPKKTREVGFPLTSAVKEGGRSTA
GGASGVSTCAAGGGGGGGGGMVRTGVVVRTSDYSQGIVPGSGPSTGLTSAGPWSFAKDRSSISTTEFERYRITQLPHPQS
GLAEGARGMAEAGRTAAAAAAAGGGGGGGGAGRNDGEVSVSGSLGRLMLDTILSGRVGFEASRSGRIDDSPSAGPSHLPA
NHLRREVGEGGGAGAAGGGGGGGGEGRGGGGGGGISHINSLSSPRPCATVIKAASTSRVATGLDTDRGTRPARAGTPPSV
VGHHWTPTSEVIGHSPLITTSSSDCRWLSTDRSFSARSPSAAASVAGEAALPSGTSLMAGLPVAAGPSATPNAAGIAAEV
IPVWTSTGGRRGGAGGRISGAGGGARDSPTPFSSSASSYSKRAVFMAAQETGMLPSPSPSPLHPPTGPCSSNRSSSAAAA
NDLSNDHHQRSLGHTITTPGGAGKYLWGPPPSGLSLPFSTPTLSNTTAAGGRTTQREGRDLVDVPRMIWHAAPGAGGERS
RHSGWVQSVHAADVGIASGSVIETRRLIGSVTAPASASMEWFDHFVSMGATGSQAGSMEMASRASMFRPRPGEDGCSSSS
TAALMGNCAPTMRNHDTATPGSSSGGYGGGLGQWWGPHQQQRTQGQVRQAEGEGEGEGHARRWGRAATSMATAGGVGFPR
DLSVDVSSYPAAAAAAGGGPGGGGGGGGGGGRGSILDMVLSDMFTDVLPSRFGLSPGGHTTASATGRPVSGPDLVPPGLA
SCSDGPHHCMGLPLCSAGARGTVGGGVGGLLGIPTELTAVGGESIESLNCGPTRVVAVPLRQPSAVCRDRDDAVLMAHRR
AKDEVEGGSTSSSSGSGARIALAMVGMIGQKSQAAQQPGGGGAPNGHFMSQSRPAAPAVETVSRKDGRDSSSTSASASVH
QHLASLQALLPHLDLNKTFNTVR
```

350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE

A0A388L7R4 **A0A388L7R4_CHABU** (241 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MKGREHVCREEEEEEEEEEEEKEEKEEEEEEEEEEDDDEEEVEDDEEEEDDQEEENDEEEDGEEEDGEEEDDAEEHDEEE
DEKEQKEEEAEEEKEDREEEDEEEDEEEDEEEDKVEENKEKEDEEEEDEEEKGEEEEDDEEEDDEEEDDREVQDDEEEKD
DEEEEVDDEEEVEDGEEEEVEDDDDEEEEEEEEEEEEEEEEEEEEEKEKEDEEEEEKILEEKIEEEKMEVDYKDDNDSEK
K
```

186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE

A0A388L948 **A0A388L948_CHABU** (322 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MKKRWFVTRQRRRRGKGEEEGGVEEGTERREEAEETTKTKTTTTKTTKTKTTKTKTAKTKTTKKKTRKKTKKKKTSTRTT
RRTRRRTTKNEDADKEKDDDIEEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEKEVVRLDNPKYRVEGGVGTEKEE
SSELRFYPVDTQTWMEKFVFKKDEWAEESVAERAEVTAKLEAAEDNAERELLTQEREHELHQRLLINKRAELEGKRRLKA
EGEEIDDELKEQKGLEEANYCHYWKDLQKGVRSKNNNQAAKGGDYSAAAAREKRDKEEEEVEKEVEEEDVAPKGVVAKVP
IT
```

111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE

A0A388L952 **A0A388L952_CHABU** (439 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MAGEGRKEMKVWSEVGNGRKEEGNRGWGVGGRWRRKEGNCKRKVGDQDGRGKRGVGDCRSGCGVGWRWRRKEGKGKRKVG
DQEGRGKRGVGDVGDCRSEVVRWQVGGGKWHEGGIWEIEIGRWRNGLNEGQRRQQKGGGREEAGGRRNASNFILFSCCGR
RERKEGGEEEQTRTKEDEVAAEERNRAGMDEEGGEEGEDGRRRRGDKEEQKRRPRRRTTTRRKRRKGKEKKTRRRRRGER
KEEEGEEEGEEEEKDEEKEEEEEEEEKEENEENDDEEEEEEEEEEEEEEEEEEGEEEEEEEEEEEEEEXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEDNDDNDEGGEDESKHEEDLVHGEGRRRSSRS
```

375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE
379 - 398:	EEEEEEEEEEEEEEEEEEEE
380 - 399:	EEEEEEEEEEEEEEEEEEEE
381 - 400:	EEEEEEEEEEEEEEEEEEEE
382 - 401:	EEEEEEEEEEEEEEEEEEEE
383 - 402:	EEEEEEEEEEEEEEEEEEEE
384 - 403:	EEEEEEEEEEEEEEEEEEEE

385 - 404:	EEEEEEEEEEEEEEEEEEEE
386 - 405:	EEEEEEEEEEEEEEEEEEEE
387 - 406:	EEEEEEEEEEEEEEEEEEEE
388 - 407:	EEEEEEEEEEEEEEEEEEEE
389 - 408:	EEEEEEEEEEEEEEEEEEEE

A0A388L9U1 **A0A388L9U1_CHABU** (323 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MDEEEGEEEEEEEEEEEEEEGEEEEEEGEGHYGRGGGGGEEEEEEEEEEEEEEEEEEEDNMIRGGGRTTRRRSQEGKEK
EEEEEEEGEHVKDVKEEERDMLEEKEKEEKNIVEEDDEEERDLAEGVEDDEEGEAKEEEEGEQVDEEKEEEERDMVEKEE
EERDMAEEDDEEEEEDEGEEEEEEDEGHYAGEEEEEEEEEEEEGARDMVVEGKDEEEKEEEDEEKEEAKEEEVGKQVEEE
KEEEERDIAAEEEEEERDIVENEEEKEGEEGEEERDMAEEEEEERYGGERGREGGRGGRGGGERRRRRGGGGRKSLWRAA
LGG
```

40 - 59:	EEEEEEEEEEEEEEEEEEEE

A0A388L9W1 **A0A388L9W1_CHABU** (6226 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MPYLCSIGVVLLVLIIVTIFASQACFLKSSMTRNFIVPIGMVMETAGIDNNVAATTSSEQSLQLERPSSHYCHSYFLSRP
ARHHYTSSASCGSYPNHFNADRVPSTRTEDRRDPRVGERGHTLEVPELANDSCEVRQSDKVIQLFGNQTKIPSSALAATA
VIGRGQGGGGRRKARTVKGGSRVKAGDEAGATAGEEVMQLFKKHTKQPSARLAAVAVAGQRQGGEGGKEGAGCVRDDNKV
EAAKRPGTSAGDLVPPSEVPPMLASSRHKPYATRSHIQSAQETSSISSCIRSLCVALNLTFTFNLPSGEEAASGLFTTVG
EGLNIGSDKMQWPSGVRVVADLVNEQPSRPLTSSNQSISASLCAALITPSLPAAPLLSSHVPSQARALSVLPVHSAAATA
RNRPSSPALCDGESLVNCDNCPPPHFAPGLTMTYSSSSQTADITSAASLAADAADTATTVQILTPSSSMLSTYGALPESK
SGSAVPYPTLTVAPSAYSDISDTQVTPYLLVADAESAAPDLLAAGASSAAETVQTITYTVPVSASELVVDSLSFPTPSSS
AVLPLSPFQRLGVALASSPPDTAGSIENALRVVKLSDAHVTQRSSTVTALDSLAQRRTLAELHSATLSPPACSPPLLSLS
SLCGNVVPSTSSSAQPQKISSGAAITHSTYAGHASSPAVLHFEMPLLFPAPAEIPRSATHATSVSLTPLTVCSMSVCSPT
SDQVGMSVATATSASLAPPPTSMSQAATMTPTFSSTPRRVPIAVPPATSPSMAAPSTSMTPSATVAPISSSAVDRISMSK
PTAASPSLAASLTSMPQAAANLTPTSSSLMTPMQRDLSSKTPRPSLEHLSSSLSKSLTSALTQAAGISSLPPQPVSGFPN
CEPRANPDTSFTCPGLSTSSHGRTELLFELMPEACSGVHPFLSAGLKHPGVAMEAAAILSSLPCIDPAILVDNFDGSVQF
VSSLTGPGAPTRREFMAQNLTEETVDYCPRTAMTLVAKKNVDSPPTSSSSAPLLKCGPRVPMTAKRHVSTEEALSLVPVS
VESKLGQHSLEIRKDYASDDDDNQYGADIESSGLSIDLLLKEVEELLPSLYGPTPESQENEADDLSPIFTTSKSKHYDSQ
LFMMSLRHPGAYAQESEHVRGGGGEREQEQEREQEQEQDLKRGDSVPAVLNTEKHIREGGGGDGGGGGEQEHKEKSGGRM
AALLRQLAIPICEVSQSSAQTLEEGEEEERERDDDLMTLWGQIPACKRVRVRRYSVEAEAEEEEEEEEEEEEAEEEEEEE
EEEEEEEEEEEEKKKEEEEEDRGEVEDWQERKREDSVPLLLGQIAFPATRRMFYGQHSAQAPIPVSPEGPVGCGNWLGED
WQGKQGPLVSCGTTILLADSATTTCCETTTLIASSPFIDRRRAQTLPVAIKLDCEHSEESEAKSSFCNFVLDPQELCESW
VNSDLGHGYGDNDTNRGHTGDWGWENQGHPSVLEAGKWRGGGGGGGAHGSIRRDGHDADNSVSECVAFGQGARNKQSRPT
QEVMVEGGGAGGGRGGQGRRGRAAHEIGDRVSELMAFAQGAWNQQPRASSQEGMLHRSALLPQLPRQSPASEGKDEEARK
FAEMLADDFIYRQQCCFSEGFPVASAIMAVAVSSTLEDGHCTDQPESNDQDWYLPGDVNNLARDGAEPGVEDSWQTGPRP
SDRKTSGPSGPSIAVAEVGGRPGNRGFTTRPTQSLEPGQKLCPEVQPEVRSGVRLDYRPLVRSEVRPEVWSQVRSEIQPT
VRPEVPPEIQPEGWPEVQPLVRSEVRPEIQPEGQSEVRPLGQSGFQPEVRPLVWSEVRPEVQPEGRSEVRPVGRSEVWPE
VWSEIRPEANSEGIEGWLNGSHSSGETTCGPGAPVRQAKEQLVSRGEGCTPMPTPNLPPSFEETGALAEALERTIALRAS
SEGLERVPTFLPCHGSTCIRSLAMDVGANSYRGSRSSALLEFMVTSAEALGTHVPPEKMLRITDKGLTGAGVENQSQNRE
PSDCRLELLGNGSDIRPERGSDLETPVTPLAEVAGAAQRGQCSLTSGRRSQYQAMRDVDPHNDQMLQNDPHRMIDPESDP
SGKMADLWQKADAPDDTRELVKPRNALRVMLHLQNAPRQTGEPPQTVDPQEMINPHLQQLKIAKQGLKRGVTASAHTLEK
NEESLCGFALKSKEGSPIVQIPEEGMAMAFQDAYLHGLQRADDHVTGSACGPCPGSTFGPRSVPNGDSSPPCSPAHAPAP
GLSSGPDSSPGHAPVSGRSCGPSYGPDALVPGPTYGPPSGSGHTPVSGLNYDHHSGPEDAPAPGHAPVPGLNCGPGYAPV
PGLDCDPTSSPGHAPAPGLSCDRDLSPDSIPGDGSRSGLHIHKAQANVNFERVPMSSPVTVNDPVTSTKSNSHGTLGIGT
FKSFDTSRSFQGPGSVQLPSQFSVQGSPVTLVYAKDDVLSPLLSSNSSFFSALTSQDSLVCSQPKPRFALGTSHKAWCNL
SWAPPFWTPSVPSFPPSCPSSLLAIPSLQTSQTNDRLQKGCAAFIAELPHHQQAPIASSHDPIESRTLRLQESLHDSFVS
SSLGEDLDEALREDPVFVSMAPTKQLDPSGTRSRSVSPQREVSRTDPSDHDRTVNEQVVLSRSAELSADLTACRAECQAV
DQAITPVPSYMPEMSPSSRSVRSVVLQGWWPALGSESCSHVLAHAPDLEGMLFSSAHPVDDEGLPCTTDGAPLSSAPISA
PPGPTGTVLSLTIPRAGTHMGETLMQSGANTFLGNAFPVAPGADSGTSPPSHAASSFAAGVPCLVMPGTETQRWENLVLP
GTHGGTGNSAAVGTNSVPLPQTHAAMSPASGAQAGQVPSPANPGGNPHRALVLPGTDALSGISVADGPDMYTVPLPQIHD
AVSPLLGAGAVQVSSRAILRQTFFTESDAGNSLSAARGTYAGPLPQSHSASSTALGGEAGQPSLLGIPGPHTHTRKTSAL
PDTDACAGNTFASAPGKMETALSTQSHAMRSPALGAEKTGHRPSIAILVTDTGKTIVLPAVPGTDAGAVHSLQVAAVPGT
DAGSLPPSHPGHSLAPGAETDAMRRLTTPEVYAHIGKFRVLPGADHCQGKSPPAAPGTDAALFALSDAERSPPPGTEAGP
VLSLTLTETLARTEESLPLPGPDSGPGYSLPAPSTTAAVPACLLASGTDIVSGQPFAPGTDAVPGQRLTPGTAAVPAHPL
GRGTGTDSGQPLGPGTDAVPWHHLTPRTDAVPDMVSGQPFAPGTDAVPGQHLPPGTDAAPAHPLGPGTDTVSGQSLAPGT
DAVPGQLLIRGTDEVSARLLGPGTGTDSRQPLAPAPGTDAVPQQRLTPGTDAVPGQPHIPGTDQWQSQAQSGRATDACLH
VMRFPEHPTKEDGGKLLAPAGSDRWESHAPHGTAEAKQSVAAISGTSADTRQFLALEIPYGNAGQSNEPTPGKDTDNPGL
LSSAPGTVLCPWESFPAATGTDAGAGTGTFLALPGAGAHAGGGSFPPAAAITAHKDTPQLHLLREPTSFAKTFGLPCTVG
YEVADARQLPAEILEADTNPGKLLAQALRTTSYAWRLHPAAPDTIENAESRPVLSADSAPGTNVGAGQFLAVVPGAAADH
LPCPAGTQRDLAQPSDVRDSLHTQLLSALCSQRTPDMAPSSPQRQSIDASQLLSSTSSLVQLSLQPSASCSTPAFSASDL
MTTPVPFAGQQSEPRSKSSALQMERSAKQETSQLSLIQPSTHQLLFSALATQPVALPSISLCTEEVAGWEMSLPSSIQPS
SANLSCSPSTSTLSAQKCPTQPSTSSPLSSVTYFSWEQLSEAIKELIAEHSRRSLSLHLSSSSSSEGFFSCTNLSSPALR
APSAALQPLARNVNPCLTTHSIERQLAPPFTPTEQSAFPSSSSSSSSSSSLSIADVAVCLSMSSSGTSSMCMMTSQLDTS
LLSQCLCSPLSLQELQPQQLWQSMSSLSAPSTTHSTLPSHPSSLTSPPLSSSGGILHTLGLSSCTVAAASQLEMQPVPPK
TVMVIDAQPSLQPSSYSHHSSGTTSHSAIQSIQTEAGVDLPASGNGNPSISSLTEVDVSAGDQCAHAQTLSETSVTLLSL
LHIPSPAVRTTPHIEIHSIQSAPGVDVTTTSQRSHIRIPSSHSAAEINTDSINQFVQVRSLLETSDPLPHLPYSAARTTS
YAGSLSIQYAPGVVVKTPSHIEIPSTKSVAEEGANSINQWDHSPSRTGKTSVTLLDLSSPVVGEVLQLSHSDVQYPPCSS
PSLPEMSVMLLDLSSPVVSQVLQLSHSDDRCPPCANPREATDSARDKFTGQTFENLVDEAACGLLSNPAETVQGLLQPAT
NHCLSLSPGQAFQSADSVITSLTQGQAFGLPVTAVTTHRKCLPPTLGESNNPLVFYDLAAQMIFPGDEVACISEVSTASL
TTALGELPSAGHEDPCAGKLPPPQPQSVENGPYGPQRDPESASPLLGFIVPPQPSSAGYLTAMSGWTLPAETLSHLRSDP
IHASQPYTRAITPDYQHKTESKEEGPTTSSPLPTSQSHQEGGCGGGGGGGGGGGGGVPRDRRSQDSFTVASECARLPRS
TCTPTQPIEAYDSLNLSDSHQLSSQCMEGGAYELPYLPSWQQNFTERIAWPVPTPSSLSSPAPLFSLSSPLCQDDLFVKS
PPPTTTTSSPILSLHLCSPSGTPYGELESPFSLSNVTRSVTQSVTHLTSSAPTTPSTEGCFFDTWDSLHVSERTAFSPLQ
RPDSQLICQRCAAVLVSRASQTVSRFSDLQRSAQQGLTLCSTVTVLNSTDPNTVSSSVGIRLPSYQAHPGGQELSLANHD
LPGSYGERIRASAPWNHSSQEEENHQLFTQFASAVRKEDVSCSTPGKIVSVGAKVESGNPVSSPGFVKESESLPLPQSGP
AIAPLLPPPPSTLATRHPQDAAPCSLSSWSCLHVSVSPPCPDQTALAHTYPCVAGLPPPLPPAAPHSAPSSPAPPLPPSP
SSSPLLPVSTSHPSCLSNAQQLPPTAALPQFPAVLHNRLTATTIDSSEVKVEIATISPPPPLPPPLFDPVSPRLPSVAQG
GRTVDEFGIPSTLMSSTCAWIEDHSAAADVRGGEGEGEGEGEGEGMQELSLTLHGCAEHHTATTSSSRSLFSSSSTSS
LLGLQSRSALPPSCSVIPIISKTAMQVYNHYSEEEDQEQEEKREYIDKGGGHITVKDEGQLCLSGKEKLPNSIRGRAWTL
AAWPPTTVVTHLRSCRKFHSTYEEKDARIKSCTRIDEDQKSRNRSKMSLEEEQRQGWRLCTSSTRFKEQQQANESPPTRS
EEDEQSRNQTWTRFKECRTRTRFKEQRRANELPPIRSEEKEQARNQTLTRFKESPVRKSEDEYGSNQIWTRFEECQTKTR
TRFKEQQRENESLPTRSEEEEEQARNQTLTRFEESPVRRSADEQRRNQTWTRFEESSARNISRTRFEDRGGGGRKKQSLA
RLELRQQQTSKKQNSELAWQSPISPSPISPMLPSVEQTERIEFELEVVTQQLIQRVSNGVGDMIECEGTSPANLASHILP
```

```
WSCAFGQDLIAAAAAEQELQAAKLQVTAVASPAVDPVPRRVENGGTLTRQEGASNQHQDKPRKGGQSIFRAYNSHNNQCE
DKPRKGGRSVSLAPNFHDHRDDGVFNEVEVNSSRESCSVRPPGQIYQKDDVFGSLLSEPSATVTHTSAAAAAAQLPRAWP
SHQHGQGHGNGDGDGHGTGTRTGTGNGTDSGTGTWDGTGTGDATGYGYGTKDGTGIGTGTDYGTGTCYETGTNDGTGNGY
GTKDGTGTRTGTGTATGTGTGTGTAAGDEDGTETEDGTGTGKGEGADDGRRKNHGIRDLQQLRGRPNPSSSHSVITVLFP
FRADEAGAYTAPPPVSPSSPSQARDSRYHMPRAWHSRPMTQSPDRDRDVRPTTSPSRSASWSSAVLSSSASLPLPSSRDT
EISDECSTASHHEQGERFSKKGNFVSRLFRSLWKKKAHKKDHDGQHGHGHGQAQSAIVGLREIVTEMNDPDPRGQVDQRG
SDIMISPHTTTSPPHLRKGALPGDGYGGKQGRHSTTLSSSSVIRGTRRRQLKGNGIHSQEKCSSRHYQGEKKVDYDVDDE
DGFGIRSGSGIGIGIGIETNDKPVSRSKASRGAAVVTIHERSRQSAVDRHIQAEVEEAEYEGEILEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEISQSPQLPHHSPRRWPPGFGSFRQGFVSSWSRKEKREEARKDAFKMLVDGE
```

6146 - 6165:	EEEEEEEEEEEEEEEEEEEE
6147 - 6166:	EEEEEEEEEEEEEEEEEEEE
6148 - 6167:	EEEEEEEEEEEEEEEEEEEE
6149 - 6168:	EEEEEEEEEEEEEEEEEEEE
6150 - 6169:	EEEEEEEEEEEEEEEEEEEE
6151 - 6170:	EEEEEEEEEEEEEEEEEEEE
6152 - 6171:	EEEEEEEEEEEEEEEEEEEE
6153 - 6172:	EEEEEEEEEEEEEEEEEEEE
6154 - 6173:	EEEEEEEEEEEEEEEEEEEE
6155 - 6174:	EEEEEEEEEEEEEEEEEEEE
6156 - 6175:	EEEEEEEEEEEEEEEEEEEE

A0A388LAB9 **A0A388LAB9_CHABU** (417 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MYVSIYLPMFLSPYPHTSLSTHLATHLRTCISPYVEGEEEEEEEKEEKDSEDEKVEADDGDEEEEEGEEEEEEDNDDEDE
EEEDEEEEEEEEEGEEEEEEDKDDEEEDGDEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDNEKEEDGDEDDE
EEEEEEEEDNGSDGRGERGGGGGGGGGGGGGGGGGGGGGGGQRRRIRRRGVVVVGGGGGRVGRQRRRIRRRGGGGGGGGGG
GGGERDGGKGGRGGVEKRGKRGGGGAAQVKEKEEDEEEEKEEEEEDGGDGRRLRGGGGLGGGRRGGGGGEGGGGGGEGRG
VQRREGGGGWRRWTTATRRRWRSTRRKKMRRRRRRRRRRRTTTKNKKTRRRRKKKKRRTTTTKKEEEDEEDEEDEEDGS
DGRRLRGGGGGLRGGRR
```

112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE

A0A388LAS8 **A0A388LAS8_CHABU** (365 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MGRRTTSRRTETGGTTRKNKKRGRRRPWIWIRTSRETKRWTRAKEEEEEEEEEDDEEYEDDEEKEEEEEVEEEETVATEE
EEGEGGRRGRRGGGGGEVGDEEEEENLGDEEEDEEEEEEEEEDEEEEEEEEEEEEVEEEDNEVQEKEEEEEEEEEEEDHE
EEQEEEEEEEGEEEEEKEEEEEEEEEEVEEDKEDDEEEEATVNDDDDDDDDEEEEEEEEEEEEEEEAVDVGGGGQGGGGGG
GGRMEKEVEEEKEGKEDDEEEEEEEATVNEEEEEEEEEEEEEEEEEEEEEEYKEEEEEEVEGPTMEDMAHLAWAGDGAWG
CGCRCRSSATTTPNSGSSAGAKMCGGEREGHPFFNFKIAQSGSSI
```

270 - 289:	EEEEEEEEEEEEEEEEEEEE
271 - 290:	EEEEEEEEEEEEEEEEEEEE
272 - 291:	EEEEEEEEEEEEEEEEEEEE

A0A388LAW8 **A0A388LAW8_CHABU** (260 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MDNEDKGGGGLSRRGEEEEEEEDKETNDAEVEKGEEEEEEEEEEEEEEEEEEEEEEEKEEEEEEEDEDDEDEEEEEEEE
EEEEEEGGAGGGEVEEEEEEDEEEEDEEEEEEEEEEEEEEEEEEDNDDEDDDDEDDEEEEEEEEEEKEEEEEEEEEKEEE
EEEEEEEEEEEEEEEEEEEEEEEEGDSFARLELGDGDGDGDGDGGGDGDGDGDGDGLMVPAMAKKKRKKKRKKKRKKKTK
TAHAMTEVEEEDDEPKRRRG
```

35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE

A0A388LB30 **A0A388LB30_CHABU** (502 aa)
DUF659 domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MRDGVTITDPVGRAMAARHLEVHEEELEMEDLQRAEEAAATTTGMPMHDDRVRGRGRQSAAQGSQTVRMDEGAVDGGSMD
DELSILRERVRVLEAEQGSTKVQNTARQPSRRKTDLSWLRTEGTRAPSGVVVPRDRRTLQTRLDSWAKGDLQQQYERLWV
RALYRAGVPFIFIQLETTQELHDFMVSLMRVTIGPTLVLPSYTDMRTRLLDEIYHEIAERVAPKKAKWKLTGCTMMTDGA
TTRLYKPIVNFIAASEDGPVLISTVDMSERDKTGVALAELWEEVIRDINIKHVNAYCTDNAYANKVAAQQLQDHPYGRYT
PGPRHVAVEEEEEEEEKNYKTMRRRNRRTRRKRRGRRRRRRMKKKKMRRWGTKRGRKEEEEEEEKEDEKKDEEVEDEEEE
EEEEEEEEEEEEEEEEDLPRCSSRGTLPVKAPAAVAMAPTAQQRGGGEMGQYVVNADSPSTQAAGGDEHQEPRRRRALHR
PAAGPIWAEFEFKKWPDLGRRC
```

397 - 416:	EEEEEEEEEEEEEEEEEEEE

A0A388LB83 **A0A388LB83_CHABU** (405 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MTFCSFARKNTKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVDEEEDDGDNGESENDEFGDSLDRD
WWDEEEEEEGEEEEDDDEEGEGEEEDEEEEDEEDVEESTAMEEEDDEEDVKEEEEEVEEEEEEEEEDWERDAEEAEERRG
RGGGGRRRGGGGGGHDDGGGGRRGGGGGGYGDGGGGREHRGGRRRGAHGDDEGVVGGGGPGDGGGGGNEGAGGGNGGAGG
GGGGGRRRGRGGGRRRGGGGGGHDDGGGRRGGGGGHGDGGGGRELRGGRRRRGGGGGGGLGRGRRRSGGGRRGGPDDGG
GGGGGGGGGGAHGDGEEGEEEEEEAPAMEEEEGPRMEEEEVVEVEATATEEEAPHEEHGEENEGPHFFLFFSFFWSYHSI
TQSIN
```

13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE

31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE

A0A388LBD7 **A0A388LBD7_CHABU** (863 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MDALHSPTRFWKRRRKRRRRRRRRRRRRRRRRRRRRGGGGGRRRRGRRRRRRRRRRRRRGGREEEEEKRRTRRGGEEEEE
KRRRRGGGEEEEEKRRSRRRRKKEGEGKEGKEGKKKTTTTKKKKKKKKKRKTKKKKTMTTKKAKPKAKKAKAKAKKAKKE
GEEGEEEEEEEEEEEEEEEEEEEEEEEEEGEEGEEGEEEDGEEGGEEKEESEEEEESEEEEEEEEEEEEEEEEEEEEGEE
EEGEEEEGEEEEEEEEEEEEEEEDEEEEGEEEEDGEGEGEEGEEGEGEEGEGEEGEGEEGENREEEEEEEEEEEEEEEEE
EEEEEEGEEEEEEEEEEEEGEGSEEGKGGSEGEGGEEGEGEGGEEGEGEGEEGEGEGEEGEGGQEGEGSGEGEGKGEGGR
GEGEGGGEGEGEEEEEEKEEEEEEEEEEEEEEEEEEEEGGGGEGKEGGGEEGSSQGKEGAGEGEEGGGEGEEGGDEGEEG
GGEGEEGGGEEEGGGGEEGSGGEEGGGEEEEEGGEEEEGGGEEGGVKKGGGGGGGGGGVGGGGGEGGEEGEGKGEGEGGG
EGEGKGEAEGEGEGGEGGGGEGEEGGGGEGEEGDGGGGGGEGGGSGGEEEGEGSGEGSEGEEGDGDEGGGEEEGYEEGGG
GEKAAEKKKAMKKEKEEKEKKKKKKAKAAVEKAKATAETQVVNGDPHFSALGNDVHQNFRIFRMINSTNSNNPNDTKFDT
QQACPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXKKKKEEEEEEEEEEEEKKKEE
KKEKKEKEEEEEEEKEEEKEEEKEEKEEEKEEEKEEKEKKKKKKKKKKEEEEEEEEVKAARFVQT
```

165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE
306 - 325:	EEEEEEEEEEEEEEEEEEEE
307 - 326:	EEEEEEEEEEEEEEEEEEEE
419 - 438:	EEEEEEEEEEEEEEEEEEEE

A0A388LBK1 **A0A388LBK1_CHABU** (1020 aa)
Chromo domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MEAEGPTFVTSEIDVLNVVRALDHRIPLPIGHLLLISEQANERMLQHYKANRKRFDLTRTAKDKSPTPNEHASGPSEPVR
LGLIQRDDHFLRIKPIPWRSAECDIQTWGVPYNAIIDSGAAVLAISLRVVERAGRKSDLIMLTEKDQLISADEEKIKTVG
RLTNVAFRLGKVHALGDVVVLDVNTYDVLFGLPTLVALRANLDFERRTIVLRNTGGRPYAVPMRLTLRTTVNTVPRVSPM
MAGTLRMISWDEPAEVKSSTDDIESSDEDDPKILKLWVRCPMGICNAPATFQRAMNMTFHNFVNKTRLTQGMINFCVIVY
MDDILVYLETYHGHAQHIEWTLGALRDAGFKIALEKSEFFLSEISFLGYITVVTRGGLRPESRKVAAVKEAPVPTSLTQV
RAFLGLASYYRRFIKGFAVIARPLTNLLRKDQPLGWDAGCQQAFTTLKDALAMAPILIRPDPSKQFILITDWQPEAIFAI
SAQKGNDGREYVIEYASRTVPDERRNDSTPQGECYAVVWGIQHFHPYLYGHKFRLLADHEPLMALKKLTNYTGMIGRWAV
RLQEYDFDIVHRKTERHGNADGLTRLHLRVEDQRGGRSSGIRLWSSGSWKPITDRARTYDRDCTIGQLPLHIVSQSDEEP
VPHTLTRTLAPSLQWSACIEEHWADDHFPSRSEYLDVRSLTNPRFFRQPTAFEWAALRAKEEAEEESEEELRREAGEAAA
RLAEDEEEEREVEEESEEAEEEEEEEAKEEEEEEEEEEEEEEEEEEEEEEEELSEEEEEAYSEHGEGEQSEEEEEEDDE
GVESRDDQGPTHDELEGVPEPDRREENPEAAEQRKKEIAEGKRPATDPAPDDPFEDPEPPKPEHGDIAATTSGAATTRRR
PRSRSTPSERFAGRPYERPPPIMVDGHKEFVVSDIVSRRVTDDTPPRIEYLVRWKGYPDEEATWETLEHLQHARMLVRAY
DRARRAETSASTQPTDPLPPPPAEEIAEDAPAPSEAVPQPQTVAFERPQRTHRRPSRYDD
```

748 - 767:	EEEEEEEEEEEEEEEEEEEE
749 - 768:	EEEEEEEEEEEEEEEEEEEE
750 - 769:	EEEEEEEEEEEEEEEEEEEE
751 - 770:	EEEEEEEEEEEEEEEEEEEE
752 - 771:	EEEEEEEEEEEEEEEEEEEE
753 - 772:	EEEEEEEEEEEEEEEEEEEE
754 - 773:	EEEEEEEEEEEEEEEEEEEE
755 - 774:	EEEEEEEEEEEEEEEEEEEE

A0A388LCA3 **A0A388LCA3_CHABU** (1078 aa)
Reverse transcriptase domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MQWMPKIPLMSPKPFSGDKKKEEDLDTWVRTVPTYVRHKLTRPEQEVVVAASFLEGSAARWLNGLVQQQGYGQDFDAWAQ
AQTLEQFVRAVYSRWHDPQGAQKATDAINNLCSRRFKDVRELTDTIERLLVVPGVRFDQQVLLTDYLRCLPTEVRTKLVD
EACVDQHTFASFSKKALDIEAKLGSAHKVPNDGRKRLPQDWKKKGQLMFVDHDGQNDGRRLLRSSGVHRAGWGWWHDPQ
EAQKATDAILTLHTRQFKSVRDATDAVERLICVPGVRYDPQVLLTSYLRTLSPPLRNQLHNFPSFSKVALDLEAKIGHGQ
```

```
APTTEGRKKTLPPNWKAKGRLMLVNNDGSTIELDGNLQEGVGAEAGGDTSEGGVVAAVTQQKGEPVKMPTEIEGVVAKYP
DLFEEPTGVVEREVVHAIEIIPGSSIPRGRTYRMSPGELDELRRQLKKLIEKGWIRPSLSPYGTPVLFVPKKEEGTLRMC
IDYRGLDAITVKNREPLPRIDDLLDRVQGCRYFSKIDLKSGYHQIAIRPEDQHKTAFQTRYGLYEFVVMPFGLCNAPSTF
QHAMNRIFHDYLDKFVVVYLDDILIFSKTVEEHVAHLDQVLSLLRQHKFKINGEKCEFGRTRILYLGHEISAEGLKPDDA
KVASIRDWPRPQLVTEMRSFLGMTGYYRTFVKNYSILAAPLTDLTRLDTPWEWTDECEAAFRHLKHALTHYEVLKLPDSD
KPFIVTTNASQYGIGAVLAQQEGPKLRPKKKKRKRKRKKKRRKRKRRRKRKSRRKRRRKRKKKRRRKRRRKRRRKRRRK
KKKKKKKTKRRKRRRKRRRKRKKKRKKKRRKKTRKKKRRKKTRKKKRRRRMKKRRRRKKRKKKRRRKKRKRKKKKRQ
KRKKKKKQKKRQKRKKKQKKQKKQKKKKKAEEAEEAEEAEEEKEEAEEEEEEEEEEEEEEEQQEEEEEEEEEEEEEEEE
EEEEEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVEEEEEEEEEDDEEEDDEEEEEEEEAEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEGERERERLLASIGKAER
```

945 - 964:	EEEEEEEEEEEEEEEEEEEE
946 - 965:	EEEEEEEEEEEEEEEEEEEE
947 - 966:	EEEEEEEEEEEEEEEEEEEE
948 - 967:	EEEEEEEEEEEEEEEEEEEE
969 - 988:	EEEEEEEEEEEEEEEEEEEE
970 - 989:	EEEEEEEEEEEEEEEEEEEE
971 - 990:	EEEEEEEEEEEEEEEEEEEE
972 - 991:	EEEEEEEEEEEEEEEEEEEE
973 - 992:	EEEEEEEEEEEEEEEEEEEE
974 - 993:	EEEEEEEEEEEEEEEEEEEE
975 - 994:	EEEEEEEEEEEEEEEEEEEE
976 - 995:	EEEEEEEEEEEEEEEEEEEE
977 - 996:	EEEEEEEEEEEEEEEEEEEE
978 - 997:	EEEEEEEEEEEEEEEEEEEE
979 - 998:	EEEEEEEEEEEEEEEEEEEE
980 - 999:	EEEEEEEEEEEEEEEEEEEE
981 - 1000:	EEEEEEEEEEEEEEEEEEEE
982 - 1001:	EEEEEEEEEEEEEEEEEEEE
983 - 1002:	EEEEEEEEEEEEEEEEEEEE
1029 - 1048:	EEEEEEEEEEEEEEEEEEEE
1030 - 1049:	EEEEEEEEEEEEEEEEEEEE
1031 - 1050:	EEEEEEEEEEEEEEEEEEEE
1032 - 1051:	EEEEEEEEEEEEEEEEEEEE
1033 - 1052:	EEEEEEEEEEEEEEEEEEEE
1034 - 1053:	EEEEEEEEEEEEEEEEEEEE
1035 - 1054:	EEEEEEEEEEEEEEEEEEEE
1036 - 1055:	EEEEEEEEEEEEEEEEEEEE
1037 - 1056:	EEEEEEEEEEEEEEEEEEEE
1038 - 1057:	EEEEEEEEEEEEEEEEEEEE
1039 - 1058:	EEEEEEEEEEEEEEEEEEEE
1040 - 1059:	EEEEEEEEEEEEEEEEEEEE
1041 - 1060:	EEEEEEEEEEEEEEEEEEEE
1042 - 1061:	EEEEEEEEEEEEEEEEEEEE

A0A388LCM4 **A0A388LCM4_CHABU** (1144 aa)
Reverse transcriptase domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MVDTHTGKSTAPSETEQARIATLLREKKEKKELLKQAKLKAIEEEQAAKKKRLEEEMLRFQKEKLMLLEREKEERRKAAE
EEAAAEEEEEEEEEEPLERRRGEERGEASGTKEDRWREKKISEWVANLSLGEDEEAHLYVPQEEREAFARASELIEDPLE
CQAKEDEKKLEPKRKSLPNKMIGFLEVLSEAWLEEHQARNGQEVTLQAMRSGFREFASDVVGHVGAEVRRLRDGVDKFYA
GVIETAKVVATTEATARPRKEVVKLKFPDPYSGKKEENFDNWEASINTSFFLQHTAPKEQVLVAFHALKDEAASFARSLA
RAADCEHNMIAYSRLTPLATFLKLLRERFADVTRGVRASDKLQTIHSRQRRSARALKAVMDDLVAVPDHGVTETQLVQLF
YRVMPKPLRGHFFDKTQQPNITYDALSREEVLFEAKSMPVSTFWHKDLDKGRKWKGRTISGQVRAKDHMILTLEEGGTDE
VPYSQIEWGLEEEDSNVGQRRSYAAVAAGGRPQGRGGGQGQRGQAMGGRGSGAQGVGGQGNRQVGEGVQAYFRLEKDGKV
DKVLHSLTLLVQDDLPFDIVLGMDWGEAAGGTLHLREHECRLPSPSGEVKTARLFHVSGDDNSLPHCCLSAPAFAQLVRK
EQLEDQVFVVYVRSVTETNEEDSSTDPAIAKLLEEFTDLSEPPTGVVSRLIQHRIEIEPGSRTPKGAVYRMSPRELEELH
KQLDELLEKGWIRPSSFPFGAPVLFVPKKEGELRMCIDYRGLNAITIKNAEPLPRIDDLLDRVQGCKYFSKRDLKSDYHQ
IEVHPDDQYKTAFRTRYGHYEFIGMPFGLTNAPSTFQRCMNDLFRPWLDRFVVVYLDDILVFSRTLQEHQRHLRQVLEKL
REANFKINAKKCEWAKTQVLYLGHVLDGDGIKPEDSKIAAIRDWPTPRTLTELRSFLGLDNYYRKFIRNFSTIAAPLRRL
LKKEALWQWDKDCTSALKKLKRALIEDLVLKVADPSLPFVVTRDASQYGIGAVLQQADGNGYRPVEFMSARMPSEKVATS
TQVLKKKSRRKRKRKKRKEEEEEEEEEEEEEQEEEEEEEEEEEEEEGEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEESEYHRDILRQIYQAIHKNVHS
```

1092 - 1111:	EEEEEEEEEEEEEEEEEEEE

1093 - 1112:	EEEEEEEEEEEEEEEEEEEE
1094 - 1113:	EEEEEEEEEEEEEEEEEEEE
1095 - 1114:	EEEEEEEEEEEEEEEEEEEE
1096 - 1115:	EEEEEEEEEEEEEEEEEEEE
1097 - 1116:	EEEEEEEEEEEEEEEEEEEE
1098 - 1117:	EEEEEEEEEEEEEEEEEEEE
1099 - 1118:	EEEEEEEEEEEEEEEEEEEE
1100 - 1119:	EEEEEEEEEEEEEEEEEEEE
1101 - 1120:	EEEEEEEEEEEEEEEEEEEE
1102 - 1121:	EEEEEEEEEEEEEEEEEEEE
1103 - 1122:	EEEEEEEEEEEEEEEEEEEE
1104 - 1123:	EEEEEEEEEEEEEEEEEEEE

A0A388LDG9 **A0A388LDG9_CHABU** (271 aa)
Uncharacterized protein (Fragment). *Chara braunii (Braun's stonewort)*

```
EEDGEEDGEEDGEEEEEEEEEEEEEEEEEEEEEEQGEGEEEDEEEEEDDDEEEEEEEEEEEEEEEEEEEEEEEGEAAAEEEE
DEKEKEKEQKEEEGGEEEEEEEEEEEEEEEEEEEEEEDEDGDDDDDDEEEEEEEEEEEEEGEGEAAEEEEEDEKEKEKEQK
EEEGGEEEEEEEEEEEEEEEEDEDDDDEEEEEEEEEEEEEEEEEEEEEEGEGEAAEEEEDEKEKEKEQKEEEGGEEEEEEEE
EEEEEEEEEEDEEEEEEEEEEEEEEGEEEEE
```

13 - 32:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE

A0A388LDI4 **A0A388LDI4_CHABU** (128 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MEEEVPMEEEEEVPTKEEEKEEEEEEEEEEVPRRIRPINGGGGGGGPDEEEDEVEVPTIEEEEEEEEEEEEEEEEEEEEE
KSEEVEEEEEVPTRRRTRFRRGGGGGGGGGTEGGGGGPDDGGGGGGR
```

60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE

A0A388LDU5 **A0A388LDU5_CHABU** (1273 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MLMPSRKRPAGVRPSTPTAETDGARVPHRGGGMSMMNGKKARCDGGGGGGGEGGGGILTAVGLPRRSELVSIDDRMDTLR
RGGDFESAAVETLARDRKRVRIVSSLAVPSGQRIEEEGEDEEREEGEEEEEEEEEEPEERGGIGVLLRDLGRENCCLCKI
YHTCHHADVFFECCAAKERSVVMAAKNRRKEEGAKDEEGTGVVDGSGGRRRRRKCATTGMMALTSSVGCNAASDPRGGAH
PHFAPPAAGREEGGVKGLRAYVGTLEMKVETLERELRDFKELFVLQTDQFKRVAEAAVRIGRRGCYRGGGEEGGGGGERG
GGGGESGGGGTGVAGVIKQRGRSGGIGRHCEEEEEEEEEEEEEEEEEEEEEENQDGDAVDRCLTNGRVRTPDVLIGDDDCSS
DDHDDGILGCMENGEREEKGCMENGEREEKGCMENGEREEKDDDTEDDIAEESDYDDDGEDGKENGGGAAEVAVGRTVVG
IDNAMTERHVAHGQLCLGGILTMSPINVGQTKEQSAAAAILGVAAPIKPVAGCIVRQLRNRTIYAPPPGSLPGGLTSSTA
ADDPDRGRTSDKHHRRSNVLVPPSSSSARNHHHHNRHHRHHHDHSSGTTGAGLAPGRSAGGPAAADAAACAGVAAIAKAR
MTTTTTNGREVTPGEIAVEDRGCGGAVDLACQEDSTFDRAPMVARRPCPSPSASDSDSDSAYDSASDSASADAHAAHAAS
AAADDDRAGGAHHNNLASANHTRSTWHYADEACSPFTLGKEPVCVAKFVREGEAVLAAGYDGSCHYFDVASGGEKMCLRV
PEGAAADVAADCWLVRAPGRDGQMAELAVVVSDWRPSFCSWDIGTGEAAGFYNSGGGGALARVGGGGGGGGLLSSGTGRL
CWARPDECLLGVARAGGRRVCFFDVRDGDLALDFDVEKRIASLPRCSPIQCLYNGHVMIAEQDGIAVWDVATTKVRKVGQ
VHCVDEGERVTAVLSSDEMFGGCGARYPRWHYQHQGVGSLLFSARHDGAFCTDSGSIYVMDWRVHGGLAQHMVSSEPGPV
DCLFGFGDSILAGYSGVRRSGGGRYLPPVVKEWDLGERREVSSFTLGSTGGCDGEGESAATGRSIHQLWGDESRVMALTE
EGLFVFGSGRTYLSPTSRSAMISSDGVEGKDDYFEEDDAAMMDMFEGPLIAVISGREACTSGAAADFNKSASTPRTGNSA
RREAATLGEKSSLLRSSSSSSSSSIGRGVEQQQQQQQQQVNSTSRHRSCFDASSGRLLLATGYRPACLYSCP
```

351 - 370:	EEEEEEEEEEEEEEEEEEEE

A0A388LDV6 **A0A388LDV6_CHABU** (196 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MDKEEEKEDGDDDHGVTMDEEDEEEEEEEEEEEEEEEEEEEEEEEYWEEEEKEEVEEEEYWEEEEEDGNDNEEEEEEEEE
EEEDCGKEEAEDDDDEEEVQGESAEEEREQEGATIMNANRDATTMDEDAEEEDGDGEKKEEDEGEEDEEEEEEEEEQEEE
```

EEEEEEEEEEEVEGEEDTDGGRGGRGGGGGRGRRRR

23 - 42:	EEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEE

A0A388LDW3 **A0A388LDW3_CHABU** (856 aa)
M16C_associated domain-containing protein. *Chara braunii (Braun's stonewort)*

MTPIFEDPVFLYYRQSLEVLYPDTCYRFDSGGYPAEIPKLNFAAYKEFHKAFYHPTNSLIFFYGDDDPMVRLKKLNEYLS
AFELNAQAKSKSYLKLQKPWSKPLEVESTYPTWEDNNAPSFMGIHWLIADEPKSIDSETYFALQVISDLMCNYVMLALEA
TSGSQDEPSCGIDQLTTVQPYAYIVVEEPSANLTKKNFKTAVSLGLQLMSTAFMPKWVYGMLNQMEIEMMSIDDKAMTTF
FAVEGSWKADLDPLRLLNATLALESIRSKVAALGGDAAGYFRPLLKKYLIDNPSQVFLDIKPDYGGLERQFQEEKDRLRH
IKERMSASEIQRIVDETLAIKEEMQPSPPSVINKFLKPISTSALTTPAPTTISQVRTLASVNLFQTKAFTNGVVYIDMLF
SLERLPEELVPYIGILRSVWQFLSTGDLSFSTRVLENTGGLDVFFEYLNNANEPNRTSRNAYLGFFGAARNSNVTELIDL
MKILVTQVDLDDKDTFLYVLDLLTADMDGDTAYGYVSSRLAAKDNVKGWFAEQVYGKRQVFFQLPVLESSAQKVFGRCVC
RRRRRRQKTEEEEDEEEDEEEEEEEEEEEEEEEEEEEEEGWLKMAGRGYGIAAEKKKEGGKRLWAAVEKDGQQEEEQEEET
TTTKKKKKKKKKKKKKKKKKKKKKKKKGGGGFQAGESGNLHKGGYLPSPGSVTADVVLNREIHWKVRAQGKAYGAYARLD
GDAGLLTLLSYRDPEVISTLDAYNESISNMLKMRPDKQTLDRRIVAAWGLLNPHMYPYDEAYFSFQKFLADAPPGVMDLI
NEQVLYTRVEELNWFANAALPTFLNGNSTVVIATSRDNIEEAMRESPELKLTVAAS

579 - 598:	EEEEEEEEEEEEEEEEEEE

A0A388LE12 **A0A388LE12_CHABU** (980 aa)
RT_RNaseH_2 domain-containing protein. *Chara braunii (Braun's stonewort)*

MDDLVAVPDHGVTEPQLVQLFYCAIPEALRGHFFDKSQQAGVTYDALSREVVLYESKSMLVTTFWHKDLEKGKKWKDRTI
SGQVKAKDHLILTLEEGGTEEVPYDQIEWGLGEEYNSVGQGKSYAAVAVGGRPQGRGGGQGQRGQAMGGREPGAQGVGGQ
GNRQAGGRGQGPPLNRQGNRSPQRGGGRAPQGGWHPGLPQGRPWEDLGLDQRVWQERVDRGLANYYRKFVRNFSTIAAPL
RRLLKKEAIWQWDKDCTSALKKLKRALIEYPVLKVADPSLPFVVTMDASQYGIGAVLQQDDDNGYRPVEFMSXRMPCEKV
ATSTQIVPATGTSGWNTWNPRQRGDSELMVLVREIAYDAREMREARRQENERRIREEQEKAARDAEEKRIEEAAWKEAEK
EARLAKMLDDRMKEMDSKREEDNKKIWEKLEKGKGTEVTEGEKTVTNGHNKKRGLEEIAGAAVGQPSTPRKKANEVGALD
AGLLLMNLDSVQRAQAQQNQLLEKVQAQNNLMFERMLNMMERFESQRRNQPVVAPAPSNTQNGSANPPMTAAASAAEAAA
VAESSQCPPPIRIIPSMAPPPNPIPQAHHHNPAHAQVGGGRRRRAEVERRSVEVGGGRRRKSGGRRRWAEVXXXXXXXXX
XGGWRSAEVGGGRRRWSGGGQRSVEVERRWAEVGEGRRRWAKVGGGDRDRDREVEAEVADLPRGDLRTWEGEAAEGPGNL
SLSLGGNHDDPSTPLSINRAELGIEEVVAWTADGPRCAEVGGGGQVERRWAKMDERWAEAGGGDQDRDQEAEAEVENLPH
GELAWRSCHGEVASENGRGGKRKQGGKLGEAEAGGQRKQGGKPGEEEEEEEEEEEEEEEEEEEGRGVDDASAHGAEGYA
AEVGKPAEAEVEEDTQVEAEVKPEPEAEAEEVGKSAEAEVEEDTQGEAEAELEPEAEAEEVGKSAEAEVEEDKQGPLATW
ATWHMANLARGDLATCRASP

845 - 864:	EEEEEEEEEEEEEEEEEEE

A0A388LEM5 **A0A388LEM5_CHABU** (555 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

MPRNSAGYDRCSAVDWRSCQDYGQCRHSRSGGAIGRYKATSKGGSQEDASSSYRDEEEEKTEKREERKKKGKEEEEGEGG
DEGGEEDEEEDDEEEEEEEEEEEEEGEEEEEGEEKEEEEEEGEEKEEEEEEEGEEKEEEEEEEEGEGEEEKEEEEEEEEE
EEEEEEEEEEEEEEKKKKKKKTKKKKKKEEEEEEEEEEDEEEEEVEEEGEEEEGEEEDKEDSFFPSCTNLVSVYFSRYGRA
EDGAGAMAPQGTSPVAIFERIGNLPWSHKNSRIKEELARIAAISIDLFGATEPSFWKLLLTNIVKLLEDSHIATREAAMT
CLEEMYRHGINFEEDLFQNYQIRPAQWRSAKALKGTMDDLVAVPDHGVTEPQLVQLFYRAIPEALRGHFFDKSQQASITY
DQLSREVVLYESKSMPVTTFWHKDLEKGKKWKNRTISGQVKAKDHMILTLEEGGTDEVPYDQIEWGLEDDGSSVGQGRSY
AAVVAGGRPRGGGGGQGQRGQAMGGRGPGAQGVGGQGNRQAGGRGQGPPSNRQGNRSPQRRGGRAPQGGWHPGLP

152 - 171:	EEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEE

A0A388LES0 **A0A388LES0_CHABU** (2642 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

MDSAAAAPPQGGYGGRGSQEEDDEVTLQKKRDIFSQDLAGSRSFFRSPLTGDGSMSADAGIHAKPGFRERKTATSSMTSM
SIKNSNNNEGSGGVGAGSLFGPGWTKASSAEIGRRVVTKFSEEIKTEVGDTDCNRLQGAGRISSAGGSSGIAFVRGGGAG
GGGGERGEWTERKEKEGREKGKGQQDDRKRQGGGGGDGSEVGEQYDEEEEWTWTEGSDSSEGTSGRGGSAAGGGTKQQSE
RKTKKKRRKKKKKEKGKGKSNGQQEETIATSSKTLGGLRQAGPSAAEAGGEAAGLNDFGSWTRTCNLDASGGIWGRAKSM
ESAKLEKLNILDSAAGNSAASYVSSSPFLGRSINRIQSTVKSKGQAGPVQGGSGLSGGGEALSGLLPSSGGEGVGGGGDT
LLVLQKARELIRSHSQARRPVAEGDGEGPEDEVVESKGRVRKVTTKRRSFKISSSSAQEDSKILKVKVVTWLEHILCEDI
PSTMPLEDILADGTLLIQVMRVIQERKEKAKTIGLAKAKALPREKRECPAIYKTGVGSKLTFLAYGNVDMFLKFLKRCGI
PESEHFSIADLVEKKSIWRVMTCLRWLSKKLRDERLEDYDIDNIFDLLNIHLGDNEQGEDMVSRRQAAELAVVDPKPDER
GRQKGQEVGSSERTTTTTSSSSSSSSSSEEKAEQQLQQEQENGCGKGKEGLSGKVKEVELAVPSSTPSTHRLGGVISPPI
PPRPPCVHLPPRSAPPPPAVVATVPCPLSSVVALSPMSLSSAGATPHSVDESLDVNEAGPMAVPPPPTSPAIGTHALLRE
AEEREKERLVEEQNGAGIDQHHQKHGQLLDEQKQEQERPQDRQQQEQGRQQQEQERKADKLLKPTWGMTLLTAARQSSGT
QQGHKKEEEGDAVTATDADAGNGDTLTAATASGASSASCAGEGGVASLEANLKARLRLLVEKHALKSPKAQWKRLMSQLP
PRERRAEKELLYSESFKQEDLEFLERKAKAWIEYTLCIRLAEGPPLIDYLADGNMLAQIMKKWHQKYDLPDVTRVLPRGP
NFSPVLFRTGSRLGFFAYSNVLAFLRFCKGLGLEQTEIFNPADLVEKKDPRRVYICLRAISKRLSVRGLETVDLDNAIAQ
RAAQTFKTEDRHWELMQQEPADEVDEVNDEDVATVEELVDNDNDNDEDHTADVDETCELDALRSEGQGEDNNKGKHTRPS
KALWGGLGMIARIAQMRQRQRQEVEKVGQPHEQCGQLAARHIDTDMDIVTLGKLDAALKGPVMEDEVRAWMERRRRWRKV
STMSSFIARSRSFSFKPSSLHGAAALALSSSGAMKGPTEEKVEKIEQMQGMRWLRKEEKEMGTVEKGELMQGMRQAKEMM
ENMRMXQGDGDGGEGGADAGDEASEGDDGEHEDEADARVREREGEDDGNKRTKKIERGTSEQIEEGGPSDAAAAKSRVNE

```
ERGEGEGREEVVRPESLEQTSQPMEEQDIDKRSATGVRGLAAGGLTEDLPATIELSEVEDEIEIEEKKLVWERVQSLMTS
IQQLRGLTEEQSPSGGNTISSGAPPAGLWENSVGTGEDQQQGRGQGKGVKWRKMKSLVSTGFLRSGLYDSLPLPTIKETQ
SYDSAKELLVQEEDNEHREEQAEKEPPVDESIEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDWNEFKPREVEEEKGQRN
DDPYFDGDAHEDKGSEVEAAAAAAAAAAAEEEEEEEGHMDMEEEDAGIQMEERKEEDARIEEGEKADFPIAMEQKGKVGA
ELAVQEGIVEREHMKIKMQEEEAEAAEKAIEDTEVKNTEVEEAKVEAKVEEAEVEAKVEEAEVEAKVEEAEVEAKVEEAK
VEAKVEECEVEAKVEEAKVEAKVEEAEVEAKVEEVELEAAVNEAEVEEAQTKAVKVKEPKVEASLWVEEAGKVDPDEPKG
QKVVVVQKEVREAEEGGEAEAGVEAKVLAAEVEAKVEETQVQAKEEETEVEANIAVEVKVNEVGKTEPEELKGQKHVVVE
ESGEMEQRELKRDKHVVMEEKSPSRLLDKEAQSSSSSSSSSSSAAAAAAASPSSLGAGLQAALVESGEDRYDGHHTTVV
KTESEDSPLPPGGGGDEIARAGLSALAMSDFNVSGPSELLPSIPVPSGTVADASCHLVGSLGSPSSSSSAPSAGIAATSS
SCPSSVAAIATDAACVSYSSVASIATAAAAMAMAAAVVAAASAASAAAAAAAAATPSTLTEGTADSLSNMLQEVSLCQDD
EKRVDSRGLSTTHPIVHQSGNPSFSAVMENSSGVLLTTIPAKGSSTRSPAALPVESKHSVSLQSNSLSFVSLGCAAGGDG
DNCHAVAPFPCPSPMVISESRSKEEVAPADPGLPAMEDAGLLREEKSVEQQRLLTEKRQIADPIPNNDPEMKTAALLRTR
SSPAVMTAAVLRTASSPAFFPLDSHPPPRELSPSAATSSSTSLSSSLRSQRFPGVRTLHGNGREFNAMSTSSKQAQIPDP
RSEAPAVTEEATSSGTRAPPGAGGLDTDSAADRSALIETTTAAVQPSLSLAAVYRSIPTRWSGMMTTQADVTRKNPTSVI
PTPVATPRTRPPVVITASILVVFVALLFSLSNDPLYATSLDSPHNAESGIGAVLFPGFSFVLKLLAIILSAAVLRLAFSP
PS
```

1633 - 1652:	EEEEEEEEEEEEEEEEEEEE
1634 - 1653:	EEEEEEEEEEEEEEEEEEEE
1635 - 1654:	EEEEEEEEEEEEEEEEEEEE
1636 - 1655:	EEEEEEEEEEEEEEEEEEEE
1637 - 1656:	EEEEEEEEEEEEEEEEEEEE
1638 - 1657:	EEEEEEEEEEEEEEEEEEEE
1639 - 1658:	EEEEEEEEEEEEEEEEEEEE
1640 - 1659:	EEEEEEEEEEEEEEEEEEEE
1641 - 1660:	EEEEEEEEEEEEEEEEEEEE
1642 - 1661:	EEEEEEEEEEEEEEEEEEEE
1643 - 1662:	EEEEEEEEEEEEEEEEEEEE

A0A388LEU6 **A0A388LEU6_CHABU** (324 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
METKTKTKTKTKTKTKTKTKTKTKTKTKTKTTTTTTTKGRKKEGRRKEDEDEDEEEEEEDGDEEDDDDDDDEEEEEEEEEEE
EEEEEEEEEEEEXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXDEEEDEEDDEEE
DEEDDEEEDEEEDEEEDEEVDDDDDDDEEEEEEEEEEEEEEEEEEEEGGGGGEEDEEGEGRRRRKKKKEEEEEDEEEEDEE
REEDEEGEGRRRRKTKKEKDEEGEHEEGEHEEGEEGGGGGGEEGEEEEEGRRRRRKKKKKEEEAPTVLPCLALYFIVVHG
PSGS
```

70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE

A0A388LEW7 **A0A388LEW7_CHABU** (2252 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MVDLCSGTSTTPYTKAQEEQAAFLLKERKEKEAKELIKQAKKLALLEEQAAKKKKLEEEMEKLQKEEEEKLMAMEEEEEE
EEEEEEEEEEEEEEEEEEEVEEEVPLNRRARRERGESNGTNKEDRWMEKISEWVANLSLGEQEKPMTCKLCQRNKTNTRA
PLGLLIPLPIPAGPEDSMSVDFMDVGIKSRHGKSQVMVKVDRFTGPAAPAASAAALDAAGPAAASAARAAGPDAATAGVA
EAAAAASATCAAAAAAAGDAASAAVVAAPGVAAAAAPAVSSAARGAAAAARAGAAATAAGGKKRKQNGKKKTKKKNGGGG
GGKRWMEEMDGEGGWRRWREVGERRAGGGGRGGRGGRGGGGRRRLETVEVGGRRGGGAEEKEEDEEEEEYEDEDEDEDE
EDEDEEEKEEGKEKDEDGKDEVKDEEQQEEGEEKEEEEKEEEKEKEKGEEEDEEEEEEEELMIGGRGERSRKAGVMAMSK
RRGGVATWERTLRRGGRVYGEGEGGKEEVEKEKEEDDEEKEDEQENEEENEEEEQDEEEEKENGEDEEEEEEEEETSRIR
SRGGKGGVVEAGRGGEAGKVEETRRTKRRRRRKRISDKEWEAAKEDIEWEGRSAMFIFSVSISEEEEDDEQDTEDEEQDK
EGDEQDEQEDEKEEEEKEKEKEERRRRRRTSGHTNILYVDESEVRRGGRGEGRRRGGGGGGRRRGGRGGRRKEEGEEVEN
QNDEDEEKEEGGEDDEQEEEEEEEEEEEEEEQQEEEEEEEEEEEEDDENETKEEDEGEEDEENEQEEEEEEEGEQEEVEE
DEEEEEAEEEEEEEEEEKEEEEEKEDDEDEMEEEEEQQAAEDKHTRNRRRRRRVSKEDDEDEEEEEEKEEEEQDKEEEEE
EEEEEEEEEEEEDEDEEEKEEEEEEEQSSGPIHRHARRYFCSSRVEGCLPVIQLMANMHRRLPLLVLVVAVFLFVVFLHVC
LSCRPWKQRRKRRAATKRQGGERPMAGMQARAVLAASQGGRRPATAEPRRRGSTQLLSQTVRAGGSASNEGDEFTSLLHQ
GLGDDDNGGLYLKFGLCSGGAREASRTFIIDVDPLPRGLQHVGSEHTEQSTLRRGASVTGGVGPSAAAQQHGSTAPSADR
LTSTWPARTGVTSGSLRIAGARPSMPNRTTPTQPDLRDEGARTPPVRPGPIVENITRGVSNMRAHSDGGDNDGGGGDDAD
EGLREDVEAGDDDDDIPIPPLGKTGRRGKGCSRGVVRGRSVGRGGRGGGSDDGGRSATYWSSEDQMLLVRCKREQEMHLA
GLGHNYGRMRTKEWKWDDIAKRIVNAGRPKDADDCKKKLSNEERKEHDFKFRMERVLYNETHVGMLGKHTIFPPNVADTG
NPDGVQLPSRGAVGGESVGSEAGGDDCPEERSSARDSDNNAGSGAGGEKRKNVRQQALESIADVMDRHGELMSATIDSSS
KRGELEGGFSYFWFLASKLTHVARAVEGSFRALGRIIMTQQDRQGGLTWHRRRCLFSPQRSDVVGDPSVALNSIVRIPTR
MNVVRMFPSQKPVAPAAHRLQRRESNTSLLASDKCRLLPADIFSIAEDHCRRLRSHLVTWRFFARVVVLLSYTWTSAVNH
SAAEHSHRRSFVLLAVNLFAAERSRWGRCPYVVHVYVVVYFPWRRDLLRRRGIRPPHATATWETFFSPDWWDFKRRSTKY
FPLIRSDCQARLQKSRRIMSTRGSTRGKKRDVVPDDSQGQGRGRRHVPKVKRARLDDASASVPPRRAQGWAAAAEGDYDD
DSTREEEQAEATAFAQLRARDTRIEKVAVVDMGGDDDEPLEKRRLRTLAQGTSAPPPTVHAAVDERRLTGRQPAMPSQPR
QRNPGDDGGSVQCGGGGEVVADARAVGGELVGAAGAGASGGVAPVATAREEAAVVATAREEARGENKTDRDGGEPGSSRV
RRGVMTKDLIDRVMLWVDEKTFWTTREGRRLYNIVHKTREYFVAIASGLPTPVVPRSVVLPKSSTKVARITDPSQLQQVI
SCAATMENIALHILHGWVFKSENRPRGYNVAFQYSLESVATDIARAMWYGEEWCNVVSAAVCSHTMDLSMDLPLWFVGAN
IEDRPEDDDMATYQESSVICIAHAFRAAVQMGAHIDDDFISYDRLCRVADCFRLLLAVCMWIMRMVGDDPRSHYEAFYFA
NLVAKPTLVAVMHRSFDHRRSIVHAAKVVTERLGKANAMFGEYPDYIPGWAPCDIGFRHDASITGXEDAKKLDWLGSGPP
DDDNNDDGKDDA
```

75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE

A0A388LEX1 **A0A388LEX1_CHABU** (626 aa)
RT_RNaseH_2 domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MTRRSMRMMKKKEEEEEVEEQETAATEEEEGEKEEEEDEEEEKQEEQEEENADAQKEEEYERDDEKEATAMEEGEEEEEE
EEEEEEEEEEEEEEEEEEEEGEEEEEEEEEEEEEEEEEKEEEEEEEENEEEAGPTKAARPIFRLPRNWGKFTQNQLAGEA
NINVHNFPSFSKKALDLDAKIGHVHQPTKDGRKKTLPPKWKAKGCIMFVDNGSTIELDNGFHEGVGAEARSVEASGGGAG
AASVQKGKPTGRRCGGSRSRSQVDRNAPPWEKAGLAEDVWRDCRTVEEHTGHLDKVLSLLRQHKLKINDMKCEFGRTRIL
YLGHEISAEGLKPDDAKVANIRDWPRPQSVTETRSLGMTGYYRNFVKNYSIVVAPLTDLTRLDTPWEWIDRCEAALKHMK
HALTHHKVLKLPDPDKSFIVTTNANQYGIDVVLAQLEGPKLRPIEYMSKKIPSQKLAKSTYEKELYAVYKALTHWRHYLL
GRFFYDRTDHQTLKWMRTQPVLSDALKPWIEVIEQYDFEPQYIKGEYNKVVDALLCRSDFLCALMTEFGFADDVTRSLVE
AYHEDPFMVEIIRRLKAKDKATSTKFELVNGLLFLEKVGNKRLCVPNRESLRSLFLVDVRQLMYDS
```

75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE

A0A388LF50 **A0A388LF50_CHABU** (425 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MAKRELIKQAKMLALLEEQEAKKRQLEEEMKKWTHEQEEKMAAIQAEVEKEEEEEEEEEEEEEEEEEEEEEEEEEVEEVE
PLERRRGEASTSKEEQIEKLTQEWTAHLELGEDREAELDIPQAEREAARRELEAERDPVRRKAKEEEQQRAWKWRMSQEK
VRRLEAAKRAERDLKAAKTGMGKIKEETEIATKLDTLTQSVESLLIAHREQTQYIRNLEVKIDAIRVGLKDFVRDMMKYL
VDQVHPAISKTKEFYTGTIEDAKLATPKEEEPTPPRREKVKVRFPEPFSGKKEEDFDNWEANVHSYLYLQGVTPEDHVLV
AFQALRDEATSFATSLARAANCENDMATYSSMGALGERRYTIAMERGVSTTPRHIARRGTTGSVGSGSHVGSSDAERRPY
TCIGDSRKDLGVNKTSRSIETKDRR
```

51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE

A0A388LGB5 **A0A388LGB5_CHABU** (2766 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MAAIRESRESLRRAGVGVGVGVLGVGVGVGVGVGVGGGIREKERRMVEEQDWWYGGGGGGQSDWSEESSELFDLPLLPPL
YARSTAEESRSLSSPSRPPPPRTPPPPPPPPPPPPPPPPFAHPPSPLQLNGNPRPPALESQQFSEVRQGFARGSGGPSR
SSSPSRSTAIRTNGPDNHRLRDGPGPDWTKPPSRDSKKKQTHTHTQKQKQKLKQTQTQKKQKEKEKEKKEKEKKEKKEKE
KKEKKEKEKIWGLAADSRNGSDAAVVALDDDDDDDDGDEVDEDDDDDDEDDGTSSSCDLVEDSLDEEEDSEEEKSALLGK
VQRRSTDGGKGEEEVDKKQRSNHVSGLGNNNVNFKVRIRMPGDEEGSQEGGGGVERRKRKWQRQKEQGEARRQGGGQQEA
TTAQPRALPSLPSKLEVGGNKAARGRESARTPRPRLEEDGDPQPQPQPQPSQEMPSWLTGVPYRQSSYYHGPFAPSDQ
SQADGPSTTGGSNQASRDTGHNSPLGAKDVNGKWPREKGTRIVASRAARVTTNQGGEADGGGGEGGGGGGGGEGEKQTCL
NSSAVPNTWVDTVSSPVRHSARRSLAVAPADLLTTKCSVMCVDGKIDEEEAIQAEEGVGEEEEEEEEEEEEEETRRGMGE
GISEGDEASTTSLSFPDKEQRDDDDYCSSSCRDDSLAMAPAVSRRGLHRHRHSAIWSHSGSSSFNGSSFTASPGHSHGGE
SSSFSFPYPPSPLRGNAPGTPSLELFTRTSTTNHSLAASTTTTTEDRVVETTSTTLTLRTAEEEGKEELQASFEQEGHIN
VDVTGGRVEERSVKAERRGGGATAMQRLEREQLSSSRASDAAPPFVRKPVSKAEEEEEGEEEEEEEEEEEEEEEEEEED
DVIVADIAVGREEGEEEEAADMPLTDATRNHARNAVGNGREPDTRSSKEHSSAAQSGGEIDACASVFGCASQDHEDYNSR
DVGCKGSSTLDERRWELEQAFSPPFDVGREGRNSLSNKGGGEGSEGGGSSCRAVPSQAQPMPPPQPQQEQQRQQQRLVAM
MMIRHASGGGGGGGGGGEGVGGAVWGGRNGAPLLLQTSGTTGGASARSSTHSSRSSTPSRAASSPSRMAGDAGRLLKSSA
TGAGGRGGGGGGEGEGEGGGGGGDLESDSDKSSYISISPRRYFAFPGHRDPFSSGFSSGSSSPGCDRATGRSRAAGAVAA
AAGVLLPPHVPFFSRAATWRTPSLNVHREQWLDAAAPTAPSSPAMPKVASPPPPPPPPHGDGGLERKRIPEAEHRTLNGS
LTYPSKCMEGGGGGEGGGEGGGGGGGEKGVSQIDVIHQNAPIASTSPFVSRNGHPLTLDLTGRHVAATGGAIEEEEEDAI
GTSSKEGVKEELIVNAKGEAAQNAHSLVLSSHSAALSRRMPSLSVVSQIGPRAALSTTGQKRASVLSQTDGRRLLMKYER
EGDHHHNHHHHHHPALSTNITDIGGAITLDAHSIIATWEQGKMVSYTSTRTEEGRGSHGATTTVRQRREMLLTNELSQKI
VQVPALLGGSRVLSCAAGTGPDTSTAGDHAQLSGTTCNLLLDGKWTSPDRRSGSADLASDSSISVSSSSATGATGAGDSY
SDCGFDPPPTLPESPVFYCVNGVDLHLRSAADGEDMMMVGDVRDANLLLLHRTAHKFSKIVSGLEGLLEYDDDNNNEDND
GCRSDCGEEQGGGEEADECEDQAAREMDEDESMVSISGVRVWLDAEHLARMPDNPPGHGDAIAAATVLSFPSASAAAAAA
GDSRRPPLILGAPCAARLDEEVTGHRGPTMVTSLQQQQQQEEEEEWHHETKRQEGDKRTKKKASSRLAASASSSSSAYQT
HSRSFSSVLSAALGWVSGALSRAHKGRRHVRDDEGANNPLSDIRPTAEKETAANAVRREDGERVGASPAPARWAPSRPGE
QGGRQSWERQPAAMTEKHPSPVRQYAGVPQPLPPVPLQSALSSTSSPTLHRAGSPPPRLPSAARSPNPPPSPLPPRERSN
SAAPAASREGAGAEEDDVASRGVCHGTGGFSPRSNAAGRGTWRATELLPAEGAGGGPPPGGPPPPVGDAPPANGSTLLVF
EGDGRGGGGPRPGAWTAHNNHDQTGSAALQWPSPRMTSSFSDSDPATATLPVHRPNSNSTSSPGQGRQSAGSPRGSIPVP
GVDAEDQPVRQLGTLPGPATTSPAGAATFTTTTPTVTTRATEENSRSQANNNNNSPIITPTPTGAPTSCGASGSAVAIPA
```

```
ESGGLPDDAPTTEDEPTVPSDDLQTGGCCMRMEEPNSSAATDGGGGSSSSGSGPAGGASSGRIDTDVATGTRAAAGEEEE
GSIGGSGGNTLGQMPVGTFHVEHERAPVVSPEQGSSCSAGGRGRRSGPSAWGERWWGGGQSTIESCKGGVGGCLNMAGPT
GAPAPSLAEMQDRSMSRDALQPDSDGWTGGCCWDRGGGRGYEPISMTRLCPPRNCGTLAAMAWWSAATGSRPLTLFFPGI
RIRDAVMTAASLRLLSFWLAVVGTAMLVLGLPIGFLPSLIKNKLFELSLGAFVLLGVPVRGASVVFSLYYRDLVMVLIDM
VMMMLDISLGVMLIVLGDLGRKVLTIALASWFIAKGIFEICAGVCTGSSSMSCWARSVVLFSALFNVVLGTMAVLLWPSS
QKWYLGLLVGVYVTTNAIPLLLVCSSDIHVDKGDESAEDPRNQDQSMAPDTALSPGRSWEVSKIASRDRLSIRYLVECFL
SCVRGAVGSLRDRFQDGPSIINLDGVLFRPAYAMTSTAQRRLGMPL
```

860 - 879:	EEEEEEEEEEEEEEEEEEEE

A0A388LGP0 **A0A388LGP0_CHABU** (289 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MYALLTGFSLWGALYHLFFPLGFWHTFSCATVTKSGRQTIPYTTEQEERGVAILCEQKEKKEKKAVQKEAKKLALLEEQA
AKKRELEEEMKWLLKEQEEKIAAIEEEEDDDDDDDDDEEEEEEEEEEEEEEEEEEKEEKEKEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEGGGGGRRRRRRRRRRRRSGGDPVKDNGKRGHKRKKSSGTSTEREEVGRMIGEWASKLEIGEEQEAKLLVP
QAEKEAVQRELEAEESPSQKKALEQEKTLEWKLRLAREKTRRLQAAERA
```

142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE

A0A388LGR0 **A0A388LGR0_CHABU** (617 aa)
RT_RNaseH_2 domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MVIVPKKAGGIHICIDYRKLNDITIKDVYPLPRIDELLDAIGSAQFFTSYYRRFIKGFAAIAGTFTNPLKKDQPLIWTQE
CDQAFLELKVTLISAPILIRPDREKPFVLITDCQLEAISAILAQVAPGGLECVVEYASKSVPACKRNYAALTGECYPALW
GISHFRAYLYGRKFTLVTDHEPLLALKKSKDYSGMIGRWATVLQNMDFDIRHRKHERHGNADGLTRLHQPEKVLNGEEVI
LWNEPKEENGPRYRHVEILSREHWRARREIFVDLSVCLARVEVTWTRTDEHQACIEYLELLIIQPWRTDVEGDLLGFLFG
SVGPGHRQLIVQELVVPLAQLVDDLSLDIVSQSDESPAPHVVMRTLAPHLQWTACLEEPRSESTLPSRQEYLKPAGIIDL
AFYAKQDSSEEAGEEEAIEEEDDTEEETPEEGSYSEHSEGEQSEEEEEEEEEEEEEEEEEEEEDEEEDEEEEEEEEEEE
EEHEDEEEEARSEWEALPEEAARPGTEAEDPEAARRREEIASGNSQLEFASKANLRIDDDPTRDPEPPEPKDGGPATAAP
SASRRRRSRSPSPSTSACPPVRPRTDVGDRPSSPVIIPPAHGDLMDHDGATWTISEV
```

444 - 463:	EEEEEEEEEEEEEEEEEEEE
445 - 464:	EEEEEEEEEEEEEEEEEEEE

A0A388LIZ7 **A0A388LIZ7_CHABU** (105 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MGQDNIGGGRRRQRKKNGAGQDRRRRPKTTTEKEWGRTTSEEENDNEDTDDDDNDEDNDDDDDADAAADDDDEKETEKEE
EEEEEEEEEEEEEEEEEEEEEEEE
```

79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE

A0A388LK76 **A0A388LK76_CHABU** (4283 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MLVALSDSLGWLARSARAPQGILDRLIWIGQAGVKIAMMESTFLSPELHSMLEFRSRGERIATVNCWAAVLQNAAWLGIK
LVEGALGLVWELENNGQGGEEKRPHLTAMLNKCIVMAVRVQRTAHHMRTHLKATTADLAEVLRVFGEGLFVLAQKERDMQ
QVEEEEEEERRQQRGSRLDFRKRQEEEPPGRHERRVDLTERQAAGMKQQVEEERHRRGSGTEFRKRRQGEMTEGRQSTGQ
TARKQVGKEWMEGKEPKTGQWRKEWGESEREGKSSLKRRRVGSGMLDTIPANLEEEPAVKTSGRSVQEHGVAVFCQQQKV
PGAKTSGVEEDAAIISRVHRGAKMPCHQGLSCVVAEKHECKTVRKRAVVSTSVSFSGHLNGPSQQWDAVGATADHIAASS
IVSAPVSMRVKEAGQEAGQEGLAPAAAARRQKCTGELAAALPRLSQTVSVRAEDQRAGWRGATVQTASTPVGCVDASTRI
GGRGQGSSVAQADRPHCKVLGASNKTDGLGQGGSGDARSDQQQAAVKQTASSGMSIPPIVEAPLRRLHSSATNGEPLRRL
```

```
HISATNLEHGSSRDVVGGLGKRVHGSSLPRTASCYGQAATAAQRTDQLVKRAGERTAAENDRLEXAASFARSKPPEPHVS
RTYSRPQLRQSDLGRKSDIAANICSXLPVEEEKEKDDDPMARSQCVAVKAHVIPVRNQSLXSSVEFIEQRTWKRTAEXWK
EGKKDRKAWXEQAEVGKTKTAGVVDAMRFRNQDKKGGTESNKGGAIGDAEAKYKTALGGRYAPHTGGXNAPXNVSASSQI
QGNKDRAELSEVRLDWRRKNCCNQEEDDSDQDAGRGERKKESTEQLTGRRGSTCITEERSGCLEAKEPPYQDGDTDAENQ
GPVVLDGRGLGYRNKQMSSARTSAKQQKQAVSSETQLWTNVVMQSNSCSRTGKKEVVSGVEHVNIGWARGNHHDWCWTEQ
GGGMTHKGRKSSTLRRTGAENGLRPRSDHKKTRKPGQTDGRMTSREEIATNQHVIAERDPSAQAVPASGNPFVKAAIKEQ
IKNGEYDGDDYSDLANFVVCKPGRDYDEFLSNYSPILPIRPRKALGSANYHAEDNGSGENEDEAYEVEGGSEDCESSEAY
EVEDESTDWKSCGDGGKVYKVEDENHEEEDSEIGGCSENDNLNEYSDDEEEEEEENEAAGVPSCRKDSGSRIVDMHKKGGE
KAEDTEDGDQLDSGEVEEVEEVEEVEEAEEAEEEESDEDVEPVEEEVEQDDDVEEEEEEEEEEEEEEEEEEEEEVLEEEE
EEVEAKTRATKKKASREGREGVEVEKTAFMTKALQKLVKEKMAAEMKALGKNDDLKRQGEKVEGVTRGQDKRVERQTRAP
SKKSIXRETEQSEVKMKGLPAKASEIKKETSAVSRGRHEDAEGKSSTLTKKDKSKEKERVEVKMGALTKKAVEIKEEEET
EASEKNAVTRTRATAKMKLPKEKERLGVKMKEVEMKALRKKAVKKEEEEAEAEAEAEAEAETETEMKIKNLEKNVKRRKA
EVVLTTERKTRAAKKKAAEEEQEREKTTAFIRKGSRKEKEAEIRSGTRDLEDEVMGMGEEVKGEAKTLRKKKGKEEKVGV
KVPKRGKKEKEKKVEVKQHQQPLRLQTDDDDDDDDDDDDNDDGDTGNDDDDDDDDDDDDDDDDDDDEDDDDDDDDDDDDDD
DFDDAQYLTSCTGEGALLDRHEYGCSYDGWVDTEKGPVGNGKDEGNKKKKMLTLMTDGDGDDDDDDDDDDDDDDDDDAAAAA
ADDDDDDDDDDDDGDDDDDGLIVVCGLVGSLSALLYLGILLANLVIALFALVAIESGIQQLGRAYVGFLSCMLLLAVIWL
MAFSSEISVIWPTVCCPGALSIQCEDSVEEVECGVWSVIGCTGLILTMVLCSRPACKGEGSAGPPGVLHGSKAVPERENR
YTDVRGEHSFSDVDEVCTWLVRLTSDRNPAKGGRLHSSDAAALAALLRRYHCDEYDKIWQVVEESSVSSLGTNHVLLRDT
LDDPGRIGGSAGSPGVSETMLVALSDSLGWLARSARAPQGILDRLIWIGQAGVKIAMMESTFLSPELHSMLEXRSRGERI
ATVNCWAAVLQNAAWLGIKLVEGALGLVWELENNGQGGEEKRPHLTAMLNKCIVMAVRVQRTAHHMRTHLKATTADLAEV
LRVFGEGLSVLAQKERDMQQEEEEEEEEERRQQRGSGLDFRKRQEEEPAGRHERRADLTERQAAAMKQQVEEERHRRGSG
TEFRKRRQGEMTEGRQSTGQTARKQVGKEWMEGEEPKTGQWRKEWGESEREGKSSLKRRRVGSGMLDTIPANLEEEPAVK
TSGRSVQEHGVVFFCQQQKVPGAKAAGVEEDAAIISRLHRGAKMPCHQGLSCVVAEKRECKTVRKRAVVSTSVSFSGHLN
GPSQQWDAVGATADHIAASSIVSAPVSMRVKEAGQEAGQEAGQEGLAPAAAARRQKCTGELAAALPRLSQTVSVRAEDPR
AGWRGATVQTASTPVGCVDASTSIRGRGQGSSVAQADRRQCKVLGASNKTDGLGQGGSGDARSDQQQAAVKQTASSGMSI
PPIVEAPLRRLHSSATNGEPLXRLHXSATNLEHGSSXDVVGGLXKXVHGSSLPRTASCYGQAATAAQRTGMTASVCAEAR
GQESRAATADWQQGSADLKLQTRMEQXGWGWNAAQGNLPXVGGVHTHMKEPDDRVRAWRCEAELRNANDRCFGSRGGAGT
SSNVFGSGGDDXRAVLGSREKPVAICSISPSHDEHWKPRNSTEARNAVDQLVKRAGERTAAENDRLEXAASFARSKPPEP
HVSRTYSRPQLRQSDLGRKSDIAANICSXLPVEEEKEKDDDPMARSQCVAVKAHVIPVRNQSLXSSVEFIEQRTWKRTAE
XWKEGKKDRKAWXEQAEVGKTKTAGVVDAMRFRNQDKKGGTESNKGGAIGDAEAKYKTALGGRYAPHTGGXNAPXNVSAS
SQIQGNKDRAELSEVRLDWRRKNCCNQEEDDSDQDAGRGERKKESTEQLTGRRGSTCITEERSGCLEAKEPPYQDGDTDA
ENQGPVVLDGRGLGYRNKQMSSARTSAKQQKQAVSSETQLWTNVVMQSNSCSRTGKKEVVSGVEHVNIGWARGNHHDWCK
SHGSRDCSMLCASEGTGVTQLLKGEDRSQVDMCRQAVTAGWTEQGGGMTHKERESRTFRRTGAENGLRPRSDHKKTRKPG
LTDGRMTSREEIARNQHVIAERDPSGQAVPASGNPFVKAAIKEQIKNGEYDGDDYSDLADFVVCKPGRDYDEFLSNYTPI
LPIRPRKTLGSANYHAEDNESGENEDEAYEVEGGSADCQSSEAYEVEDESTDWESCGDGGKVYKVEDENHEEEDSEIGGW
SENDNLNEYSDDEEEEEEENEAAGVPSCRKDSGSRIADMHKKDGDQLDSGEVEEVEEAEEEESDEDRDGSGWGVHPRPVAL
CYFHLILCYVDPVNKPVYFPRRYVEENDRRSKKIVKSSKINLKEIVSGLDPTKFLSAGDWVKKVLTMTEDEVISLAGLDS
AIFLRVFTFGLKLFIPICVFGIFVLIPVNVTDKSYRAVDLKYLDTLSMANVSKRSDRLVAHMFFAWIFSLWTYYRLYKEY
SEVTELRFKAIASSKRAPDQFTVLVRQVPESPSENVSVHVEHFFRVNHPNTYLSHNVVYATRNLDSMVANRQKLTDDLSF
AELRYEKKPTRRPTRKIGFLCWGKRVDTIDWCREELKKLNGEIAEELKHITTNESFIMPAAFVSFRSRYGAAIAAQTQQS
KNPLVWLTEWAPEPRDVYWPNLSIDYMQLTGRIWVMRVLLFGLVFFYLIPIGFVQSLANLESLNEKVPFFRHITNLPVVN
QVLTDFLPGLALKIFLAILPSLLMAMSTFQGYVSNSGIQRSAAEMYYYFMIVNVFFGSIFAGSALNLVNRFKDLVANPGD
IPMTFGREIPSRAPFFITYIMIEGWAGFPSEALRVSTLVVFHIKALLLFKSEKDKLDATKLDAVDYHVEIPRLMLFFLLG
LVYSITSPLLIPFLLTYFALGYVVFKNQIINVYESAYESHGSLWPYVHGRVVTALVVMQIMLIGVFMLKEKFKLVPLLIP
LPILTVFFTTYCTKRFYPAFQKYSMQEAMSKDTVDSVRNRGQDVRSFLTDAYLHPMLRAAKEDFEDIDVEDEESSRMQRQ
PGSPELVACKYYPKGTFTPRTGSKAGDTDTRSDHGKNSGSLRTGKFSANGGGPAAASGLMTPKGSGIGGVGPDGIKAPRV
GGLTGAGGATVSPRSAAWSPVIGNRGAVGPGPEGPYLNNNYRT
```

1254 - 1273:	EEEEEEEEEEEEEEEEEEEE
1255 - 1274:	EEEEEEEEEEEEEEEEEEEE

A0A388LKT3 **A0A388LKT3_CHABU** (312 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MWTRTSEHPACIEYLELLILQARRTDVEGDLLGFLFGSVRPDHRQPITQELVVPLVQLADDLSLDIVSQSDDNPAPHVIT
RTLAPYLQWTACLEEPGSDSTLPSRQTYLKPYGIIDRAFYPNEEPEEALEGEEEATKEEGDTDEETSEEGSYNEYSEGEQ
SEEEEEAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAGSEWEDLPEEAARTGTEAEDPEAARRREEIAAGKSQLEIASG
ASLCINDDPTRDLEPPETEDGRSATAAPSAYGANPPPPPPQPVPQFVHVPMRGIGLRPRSLSRRPLDYLTFS
```

168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE

A0A388LL72 **A0A388LL72_CHABU** (213 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MXCEPTKKKKKKKKKKKNKKKKKKNKNKNKKNKKKKNKKKKQEEEKQEEEEQEEQEQEQEQEQQQKEKEEEEEEEEE
EEEEEEEEEEEEEEEEEEEKEEEEEEEEKEEEDDEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGRWWTYL
CGYGGLLRRSGLAGRSSRTEMSMAGWRRGAGSVRLVAAHDVDMQAEWHDINVV
```

72 - 91:	EEEEEEEEEEEEEEEEEEEE

73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE

A0A388LME1 **A0A388LME1_CHABU** (137 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MQHIKEEEEEEEEEEEEEEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEGEEEEEETRRNMWHIEKRKDGNAMSR
```

23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE

47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE

A0A388LMH9 **A0A388LMH9_CHABU** (420 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MGYPAVQFHKEKEVRRVVIVDEVALEDEEDEMTEEEEYMRKKDDEVARTRVCHMTSKKKTFTNVRRNAFLPRASPSWVET
MSMGFSGKIWLLDTFNYLAPIDQRGYRLLASLTQEEMKAEYERALDMNTTPPKVKFPFNGDGIFLPPMSSMDVGKCPLPL
PNVLIKGNKPPQNSSALAEMERIWNIGRSYLKCRCSSEGKADCGTGPSWFDHVIWFLLYNMDILYPDAPTPRAKVSSLIK
CLSTCWKPLMLTSLSFGCGREVMMLLANKIVANPSLTIDSVLVRVNDVNRKAFKECAKLLLMSKYVKKRPRANEVCKGSL
VNGPLGRKRWEKLKAKEGSAHKFVHIHYVGRLMDPLGDDDDDDDDDDEEEEEEEEEEEEEEEEEEEEGEGEGEEEGKKG
EEEGERGGKEGERYSGRAQI
```

368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE

A0A388LN20 **A0A388LN20_CHABU** (806 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MGIRGFIPPDRIPDSPEYHVRADVRSGGSGSQSSDIFFPCHALLEVFGKIDWVDVLLKKAVEVTKFFMNHAKLRDLLLVY
SGGDVLVRPCATRFATNFIMLESLQKLYLLLRSCITDDDWKEAIVLPSQRRFFHTSMNEVLDNGFWAGVPKVKETTNDLL
HLLKFTDAAGPRINKVYGRMDKVVENLRKNEFLSETEKDELEEIMMRKWNMMTSPLHCAAMFLDLEFRTARLDKDVEVVD
GFRMWLYSWAKPMSYKVLDEEVNNWIEGTRKFNSEEAVASARGAQPARWWRRWCARVEEWRARLHHDLEEEESDDDDTDD
GSDTDCGSDDGNDANDEGRHRGHMSQQRALSNLLELERAINVEQQSWGKCTRPPKYLAHLHLAKSQRGAKNITVDHAEKY
VDGFSSPSEKDEVTQAEEGRGKEEMVELLDEAAAKREEVEVAVREEGEEEEGGGGGGGGEGEGGGGEEEEEEEEEEEEE
EEEEEEEEEEEGGGGGVKVEVEVENEKEKEKEGRWRWRWRMRRRRRRRRKKKKKKKKKKKKATKKATKKKEKKTEKKATK
TTKKATKKKKAGEKKKKKKKKKKKKKKKKKKKKKKATKKKKKKKKKKKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
EEEEEEEGDDDDDDDDEEEEEEEEEEEEEEEGNDDDEGEEAGRRSRKEEKEEEADDHTVVHPVHVQADAHRCMGHVLCV
PAHTAP
```

468 - 487:	EEEEEEEEEEEEEEEEEEEE
469 - 488:	EEEEEEEEEEEEEEEEEEEE
470 - 489:	EEEEEEEEEEEEEEEEEEEE
471 - 490:	EEEEEEEEEEEEEEEEEEEE
472 - 491:	EEEEEEEEEEEEEEEEEEEE

A0A388LNF8 **A0A388LNF8_CHABU** (3354 aa)
Integrase catalytic domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MLDRFVLIYLNYILVYSRSLDKHVEHLRTVLERLRQAKYKANRNKREFAQQELEYLGHYVTPRGIRPFADKIEVIHVWPE
PTNTTDVRSFMGLAGYYQRFITEYSRIAAPMTRLQSPKVPFVFDDDACRSFRALKTAMLMTPRPFIRGYESDPDFATLYA
QLSLDHPPASHYRIVGGYVLLHSRGKDLLCVPRDRRLRTRLLSEYHDSRLADHFGGNRTIARLRQRFRWPDLITDVTQYC
DSCEICPRSKPRNRNPYGELRPMPIPQEPGLSIAMDVTRPFPRDRLGHDDILTVVNRLSKNARFLPCKYYSTAPELARLL
HTGWICSHNVPEDIVSNRDTCFMSAFWTSLMQESGTKMKPSSARHPQTDGQTEPAHQTAQMMLRMLIRPDKKDWVDYLPD
IEFAYNTSLHPPIGVTPFELHHVGRKGHIFADLLLPRPADIDAACSPAFVRKYRELLAQARANMQKAQVRMQQQANRRRV
PYPIRAGDLVWVSQKSMHSSRMFRANYSPNGLDHGPKYEMAVQQEEELFKEEKRRIEMERKRIEETEQQQALEAAKRAKE
RQERMRKLEEEVVLEARRWIAANRIEQLRHALERGAADEVSAIFRAATKLKELQHNNNDRDDTMLAAASFLNQKSDEINR
NLMHYSKNGSFVSFQTTLNEAAKWGASMEIIEQAKNHFQRRKDEFLEKWRRRDNFDWRKSVLLNVLRMVEGAVCLGLEGR
EMAVAMDIAKLKMSTEEEESDGSEREGGGGEREILRVQKWMDRKKWGEIWEVVRVLEEWKIPEERVERVRMLAEEKRSGL
QERILWLSQGDQAAVDWDAEVMEELMREGRDMGLDDEVHELQSHLRRMKRRMTKRLRRIAKEGTQCEFEMCARKWRRVLK
AERVDSFRKVFNRRADWARESLRRACSEGSRLEIEVACKEGLRVGLRAEVVAGLRTVRERVEGVLCWEGEKEFKFSQKGK
RSGDGDEKRLHEEERVVLGVSPVAIEGIREARHAAQELRRWRLGEGDNRIDGSSYRGNLCEAGVVGDERPCLSDLSELDV
VARKVKKMGEEGGGGGENMAAKPTMLWPSELRWKEMEDMRLAWQWHMVMGEEQDGNHVLRRKHVAEGAVIARTRCQKSMG
GGECLLGMEKGRRRQTDGRQQGSWTNGHTAMVMTMTQEPDDDDYEDGVRNDAEEVLTAPHGNVDRNEHNSCLQRSPTGHS
MRQGMGGRRWPPAVHRPITEAYDDGDLEDLNATDAETESEEKKGGGDHNERMWSAADVPTVLTRTLLDEKRRLGDVGKLS
GLVVVDLSLEKLCSLGNGELGKWCPQLRWICLDMNSLTCLKSAFRGLEGVLEGVSIRHNDLKSIEGLQDLSHLRVLRLDA
NLLGHFGQPCMSGVPESRRSTSGIPSTVPGEQRGLWSWPKLRELGLSGNRIRVLYGLVGVCPTLEVLEISSNKLESFAGR
APFQNAMRGMRSLRVLDVEGNRLKSNGEGGLWEGVGYCDRIVNILASQNQLRNLPTHLGSGLLREIWLNGNRIRWFSCFA
WLPNLQRLYLQDNIIDVIEPMIGCCNSLEVLDLSFNCIADLESLWNLNCHRRLRSLQLNDNPVAELPSYTQGVIDAMPWL
RELDNEPLQEFVRDASLLHKSIERGIGGSLGWKFWRDSLSRNKLSYVLSDARRCQIARVEQRSALGYLGQGYSAWRYLCK
VMNWKRGWEAEREYSRRERECTKRWTGIGVTSGAPGGTGIQGRNENQTASSNRIGDDNYSALSAVRCRWRGATFFDMCAE
RRQRLQQASRRLPARGWEEIHGSADEEDGLERMLAADMSSEECAGWGETVARDGQDGEDLLSTEENQLHAENGRFSSGSR
AVQRTRSRNTDELRAALHDLVCFDPAKYQRVLSANPAYVAEERAWILEQVRFIQAAWRIAIARRKRKRERDRLRREEEER
RQRDMQSACVRVQAWWRGKRARRALVRKREQEREMELEREKEEARKMDFERRREEERAREKQRETDKQRTLAAICIQSTW
RGWRVRKKMRQAMEAAKFVDDDDFDYGGVDEVDYVFNEAALEEDLTFLEPMRCPSCGLDQDLHKVAAEATVRHADRAFWG
SDGHIGTKAVRTVGAVNDAYNRAYTASQRGMRRMTHGHEERRGAHTPLGYDHGICSDCRKMIDRFGPSSLSQAQSGGSPE
AKEPSVLLRTTTGDCCPQPSLAEPHDIPGPCERPRPIPRSLSRSGKGNSGAQGPLDDGSSSWTGKGMQTPSKHDAGDIDC
HDVSVSDKKSPYHSGDSVVGDESASESLWMEESEWSQYSSKAAEESSSGFGAGRFRNGRKTLEKKKETMAEIAKDWGFKT
KKTAEAFLRAKERVKNQIRSTQRKKLMHDPQQRLQVFKARQAHSEDPAISSARASRNIVTSVNGKRQMQMMAARHVQALK
QGMAVLIAIHALRDEAASFARSLVRAANCNDYPVAYSSFTSLTEFLKLLHERFADVARSVKASDRLQTIHARKWKSARAL
KSTMDELIAVPDHGVTDTQLVGLFYRAIPEALRGHFFAKSEDPATTYDSLSREVVAFEAKSASVSTFWHKDLDKGKQRKG
RTISGQVKTKDSLVLTLDEGSVDEIPYVPMAEVAGRCLDSCPETACVRVSLDTSLTGVAEELKERMPAWAKMKKENKGQL
ILPVTESMEEKSVEPAIAKLLEEFKDLTEPPIGVVPRPIQHRIEIEPGSRTPKGAVYRMSPRELEELRKQLDELLEKGWI
RPSSSPFGAPVLFVPKKEGELRMCIDYRGLNAITVLEKLRETNFKINTKKCDWAKTQVLYLGHVLDGDGVRPEDSKIAAI
RDWPTPRTLTELRSFLGLANYYKKFVRNFSTIAAPLRRLLRKETIWKWDKDCTSAMKKLKQALIEYPVLKVVDSSLPFVV
TTDASQYGIGAVLQQDDGNGYRPVEFMSARMPSEKVATSTYERELYALRQALDHWKHYLLGRHFKVYSDHETLRWLKTQA
KMTPKLTRWAAEIDQYDFELKPVKGKFNLSRWLEIEDDLLGLSYNKVKLSILDGSFSARISNIASKVLNFGVKLLRFALR
DVDKRSPIAEGEIVCSYVRYSNRKKEEKKKKEEKKEGEEEGGGEEEGGEGGGEGGEEGEEEEEGEGEGEEGEGGGG
EGEVEGEGEGGGGEEEDEEEEEEEEEEEEEEEEEEEEEEGRRRGRRRRRRRRRKKKRKKEEEEGGGRRRRRKKEKEEGGGR
RRMKNEKEEEEGRRKKQKEEEERRRRRRKKKKEKKERRRRKRRKMKEKEEEGGRRRRKEKEEEEGRRRKKKKEEEEEGRR
RRKKEKEKEKEEEEGRRRKKKKKEEGGRRRRRKEKEEGEGRRRRKKKKEEEEEGRRRRKKEKEEGRRRRRRRS
```

3138 - 3157:	EEEEEEEEEEEEEEEEEEEE
3139 - 3158:	EEEEEEEEEEEEEEEEEEEE

A0A388LNP6 **A0A388LNP6_CHABU** (100 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MQGAAQLAGERGRRGRSARGGRGIEVLEEDKRRIRGGRGGSGGRGGRGGSGGSGGSXXXXXXXXXXXEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEDS
```

68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE

73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE

A0A388LNR8 **A0A388LNR8_CHABU** (1959 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MAAICPPQLSSHPRDCSGDYLVNEGQKEEGWICHVYDRLGGDRLDGRVKEGEEVATVDVSKRRETAVLSLPLKAAAQEEA
QRVDELDLGQGAQGKRGRGVGGGQPWIVQSGRCGWCKSLLVPNVSCSVRILQERPRGGKSGRRPLGKRRCSSRRRGMGQR
RTRVRGYDDDDGGGDEGEVMEKIRGFVAALDLVQSENGKGNHHDGDNLCLSGRGKTVGGMKVIEWTKKTDEVVIADCGRG
EIWREGGEIAPEGIAAIRYDCFACGHSGRKKVGEGWAEVQATRTRTARAEEQGGTPCRRPIAGAVKSPPVNEEGVLPTAT
AAEEAVREGEAKEEKEWEGERGKEDGSNRGRRRQTRPFLRVSLEPVVDRKTSSAVVKNPTLMTLTQCGQACIASTSILSW
HAEKGIGTRNKEETKSVEQMKGGAAITHRSNRVRSSHDIVMGLGRKSGYGGGANGACLTVERPEPGRTGRLSEQRKLLRS
ESDGRKVDEQREVSKTCSRRHGCLGDAQRENVGGGGRGGGRGGGGGGGGEAMVPRSRGNPESVAGQLADSISFLYEAAYG
SNRYDGSRDEEGEDHRHAGDGGADQRSRDSSEDDYPADSQEDDSEEAQEGAGDGRDDGDDGDDGDDNDNDGHGECEDDDE
EEEDEEGTGDEEDEGRDGSSNVVLPRRQRWPSVEEIVEDDDDDAGDMEEEKGEVEEEEEDDEEDNAGQGEPAGSPNREVV
VVPPDDEDEDEGEAMDEHREVNQGSRMEVDDDEEDDVERGARRQRERSPTEWANGDGDGEVDRDERGGIVSMMGIDDASR
ARGDASASRGERSPRGMLISAGRAEISGAPVLVAAAGGGGGGGGGGGGGGGGGGGGEGGGGGSHGDGRNEDHGDGERTAG
DNDDRGDVGDADDGEAEGYRAGRGGGRNGGGERRREGGGLGNADGTERGDAGEVDEDCIVLAKDIPGVSAMASPEVGRGD
GEAGGGVTPPSSPPKMTNDVDVPAHPGPVPGSTSGEGERQNPMCAASASSPADDGGGGQMAAEGSAAAVPMEVEEVAVPS
AAAAAGAVATTATPAAAAPAAVVAPASASASTAALAGAGGGGGGGGGGGGGGGAVLRTIAPVAPPPATASVESARTSSQLV
ICVEDDVDVSKGEARRTRSAGGDAPAMMNITTVDELAPFVGESSKSDVAVAMATEGEGGKNGSVAFADGKKQRKAKKRPL
GLAGEKGKRKMEISAQRLEKLARNSWRGRVVSAARVYKLLVNARRSVKSLEEKLTAQKNTAEAMKEAETTCRKDVERALQ
DSRTEATNLRTIFASMEQKWAAERGRMEEQIRLGAERIYKADQMLMELGKRIQKSEEQNRELGEENAKLKMERTRLLGEQ
MKLDIDKKRLEEENRKCKMDREVALKTVSNNEKKSASEVQRADELLQAKNFLLQKLDHAERKLVRRDNRIKKLREKMDEL
QEQRGKWKKEAKRLKELVKKDKETAESRKELVGELEEERSKRLQVEETRNKEMELWREKEQEWQVEKQQLEESRLSDVKL
WEERLEEEKKISNKHARMCQTLKKIVKTLAHKDMKVKVKRDAPQKRPSGIAVEGEGREERRSGVNNGKVRTLSEGSQQQP
GARVREAPEAKVREMKPKARRQLDGAGAEGLVELKKATPSKIPKKNKKKEAKVVSALKERAGEKRAPPHQEPGQAGAVAS
AGKRKRSKEKKKVLKSVGKVLISCADGGTAPRSGLVLKSGQRKIMSKEYAVQTSTKRKGIARQRENLEEPVEEEEEEEEE
EDEEEEGQEEGEEEQEDEDGEEDEGEEEEAEEDDEEEDEEEEEEEEEEEEEEADEEEVEEDDEDDDEDAEEEDDDEEEEEE
EEEEEEEEEEEEEEEEEEDQMDVLYKYRNAACGRGRKDGWFIQHAASEGEKSLMGKAGKKRKNSGNLKGQKMNGGGSVSLA
KKPVPIPGPGRGPGFKRSSDACQAGQRKRRKQAHFASGF
```

1835 - 1854:	EEEEEEEEEEEEEEEEEEEE
1836 - 1855:	EEEEEEEEEEEEEEEEEEEE
1837 - 1856:	EEEEEEEEEEEEEEEEEEEE
1838 - 1857:	EEEEEEEEEEEEEEEEEEEE

A0A388LP58 **A0A388LP58_CHABU** (1085 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MTRSESVEDSKEEGRLGRTEYIYYSSLQRPTEDSYSRGLKRKASWPSPITQESALSVRPLWLMVSKSERYLLLEDNDTGD
VLLPLIYMKSVFEANYSRKLSSLKNRLVTLPENCNYCNSEDRQGFLYWQWAFESPHEVKVLVRKMLGEENTPQGHLRLVL
LPIVFNAMSQKAKLRQTPLFHEMYKAVRSSSYWPLLKQPPPDEYPGYSGNKGLVSQQLTSCGGDARLSGCSNGPNGAMSL
SSAGGGPLSKAGGVGSEGLTGGMAAAGLVPRGPRFDGNGTGGLANGTPGGRPMDGPAFNSLLCSPTSPSGSDDNVPDIDN
MPHRHGTPPLPYSAYSFTGLQAAGGGGGAGGGENTSLSPSSYLSPKTLQAGNGFACSRLHGDVNRKANGASTVGAGGGVM
GLANGTSAGGSYNTAGAATGSLHREIRRASSGADLMGNGCRNGKDGADLRLPLAGVRGGGGGGGGVSDTLELGMNSEHSE
SNGVNSESRGDSESTGKRERESEATCWSPCHPPLFTGPRDIQRTINKYCLTYEAAEETDISARRNRGISFVGRPSAEEVE
DAVELLRQQGEELNSEVKRLRVECESHMTLIYSELYNLKRWLVEVFTSLVPNSSMNLDTLASASLFPPTSSVTQREDDTS
GGRGTMGGGGGGGGGGVGVSGGGGGPGAVGSSLRSPSPCTVRGGNDVSPALPLASPIPSGIAVSSCLSRLSQDATTAGRA
AGPSSPIGMGGGGGGGGGQSSPSCYRGSPIGALALTSNPSGRGGGGGGRGGSGGGSGGSGGGGSGSTQHGGSGGSARGGG
STILTTVHSSQSVTSPSGMVDDHGGAEVKRATLALDPSAGPGSFWGGHGLSASTSAPPTSPCSLFGTINDGQHCSSSHWH
VGCLTGGAGADENVIQTQQFLPQGPLQSPTQADREEIDRWVERCMDVVQEQQEEEEEEEEEEEEEEEEEEEEEEREVEE
KKEEDEKKEEEEEEEECRSRRGSRDDDDDDDDDDGDSDMMVVDTFPAFSYLPLGQIMTMALFLPLGFAACTMLTMSFQSA
GPGSFSPFSSYNYDDEKRSTASSSLPPALLCITAALSRNEQRKSQ
```

933 - 952:	EEEEEEEEEEEEEEEEEEEE
934 - 953:	EEEEEEEEEEEEEEEEEEEE
935 - 954:	EEEEEEEEEEEEEEEEEEEE
936 - 955:	EEEEEEEEEEEEEEEEEEEE

A0A388LPC4 **A0A388LPC4_CHABU** (1648 aa)
Integrase catalytic domain-containing protein (Fragment). *Chara braunii (Braun's stonewort)*

```
VGLMRCLRGLKWYGAEDSADSFFPRCFDLKDASDVTEFRREFMWCAASSVLKRVLSDGFLVPEGAFGVDKQTLDIALAVS
TSHLKHMEHLVKEDYKDGTPSEHPCTSDQLVKLYGCPIFSGHSRFSPNIFSQSHSLSCLQGNPGAYSYAAVGPLSPNSCC
RMAHTMGMAGKSAPSAPPPPEERTRLTAEMRQSLDKLTNQLRSCCPQWDIDGMCNVWIVKPAGKSRGIGIRCFNCLEGIT
AYAGGQNAERYVVQKYVETPLLLQGRKCEYRQWVIVTDWNPLTIWCYDTGYFRFAAEDFTLDDIDNVFKHVSNNPVAKYS
RDAGSPNGPLTGHPAEPGRAQAAPSPSGPGAWPVIQPPPFVPPVIGVSPYASPASVQAVSLGMPLTGGFSAGPSVQVPVQ
TVYSQPPSQVVVTGQPAVSQSAQQQLVQQPTPQGLQPGVGQVPGQGQWVPKTAIASLKPFSGDKRGEDLDTWLMSVPVYV
KCKLTLPHEEVLVAASYLEGSAARWLSGLVQLQGYGHDFHAWAVNQKLKDFLKLVEERWHDPQEAQKATDAILTLSNRPF
KSVRDATNAVERLICVPGVRYDPQVLLTTYLRCFPMPLRNELVNEANINVHNFPLFSKKALDLDAKIGHVHQPTTNGRKK
ALPPNWKAKGRIMFVDNDGSTIELDDDFQEGVGSEVGSVEASGGGAVAASHAMNRIFHDYLDKFVIVYLDILIFSRTVEE
HVGHLDKVLGLLRQHKFKINDEKCEFGRTRILYLGHEISVEGLKPDDAKVASIRDWPRPQSVTEMRSFLGMTGYYRNFVK
```

```
NYCIVAAPLTDLTRLDTPWEWTNRCEAAFRYLKHALTHHEVLKLPDPDKPFIVTTDASQYGIGVVLAQQEGPKLRSVEYM
CKKMPCQKLAKSIYEKDLYVIYKVLTHWRHYLLGQFFYVRTDHQTLKWMRTQLVLSDALKRWIKVIEQYDFEPQYIKGEY
NKVADALSRRPDFSGALITEFGLADDVTRSLVEAYCEDPFMAEIIRRLETKDNTTSAEPGESLSMDFIDTLVTNKSGMRH
IFVIVDRFSKYARLVAMPETAKTEYVIQMFKEVRDFGLPKSIVSDRDVRFTSELWKAAAAEQGTQLQMTSGKHPEANGQA
EQLNRAVQHLLRHYIKPNQVDWDEKLALIASLYNNAVHSATGVSPNSLLLTFKPRLPLDFLLPENQPTAAPGTLEFAYRY
QQLMQHAVEQMHKAQAAMIESENKHRRPSTFQVGDRVWVKSSELGQEHGISLKLMPQYFGPWEVLDIVGDDLDGPSYVVQ
IPGHLRTLKTKLEQRRCSQQLTEEERWTPADMAKEPEQHIWKHVQRRLDLVSTCKLDEQVRLEEVERAIAEIPRLKAAGL
NGMPVELYRDLRNFFVILLTAAYDEALRQGSFPRGFTNAYGILLYKKGAKEDVRNWSPISILNALREDGEEVQPWRRGGR
EEEEEEEEEEEEEEEEEEEEKDQDGWRALAKNIRENISADTALGVYGLPPREMPIEGKMLDEPILTPFDPILVKLDEKAK
LSEGLTWRAWDTIKMLPHNVLNRRFSTTDIIADSLADIIRTHLLTSRTSLQDEATPIYVEMGNDEMDMENEEEEDFGLGD
DLSPGGEDEVLHPAIESSAGEYSMGTTSSKEDNRDSDSESSKAQAAAD
```

1441 - 1460:	EEEEEEEEEEEEEEEEEEEE

A0A388LPI2 **A0A388LPI2_CHABU** (243 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MTAFECSRTPPLSRVDGLEFTGGPNASRDVSKPVTQEFEESGEREEEEEEEEEEEEKEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEGEEEEEEEKEKEENEEEEEEEEEEEEEEEEEEEEDAEEEEEEDGEEEEEEEEEE
EGGGGGGGGGGGGGGGGEGEHEWVSPTAKIWKKKKRRKRKRKKRKKRKRKRKKRKKKKKKKKKKKHYGRSWQAPPFPWNI
SWD
```

58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE

A0A388LPK5 **A0A388LPK5_CHABU** (141 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MVRRRGGLGVRGGPTATHEEEEEEEEEEEEEEEEEEEEEEKEEDDKEEEEEEEEDQEAEEEEEGAQAMEEEEEEEQEEEEE
EEEEEEEEEEEEEGEEEEEEEEEGRRRNRPWRWRTPRRRRKRRTAGGGGGGGCLLFFHRNL
```

19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE

A0A388LPP6 **A0A388LPP6_CHABU** (3120 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MEGEEEHEEEEEEDEEDEKETMEEEEKEEEEEEEEEEEEEEEEEEEEEVEDKEEEEDEEEEEEDDGDEDGEEAHLSDSG
AAGQQAVGQRGGRGGGGEGRGGGGRGGGGGGGGGGREGGRGGGGRGGGGRGGGGVRWKMTRRSEVENDEEEEVKDEEEE
EEEVEEAKEEEEEEEEEEVEDEEKEDKEEEEEEWRKIKQAWTEDEEQRKNERLRFYKNWLLNNKIAECHVSNSAMSPTVP
HQQCHISNSATSAVPHQQCHVRSATSEVPRQKCHVRSATSEVPRQQCHVSNTTMTVSVLGMPGQLANESIAEYRQRFEAQ
LALTEAEEQHQAAAEAARLQAEAAAAAEKQRLQAEADTDTQAHRKEAQDLLQWHEAASIEKLKFWHFDPSEQHEDATPEE
QHKEFLAKLVTPLVYTCNHLQSELANLRQAVRNHKDLHEDATRALDSRVQDLEQVAPRPDAGESSSAPSTRQLEERVDHV
VAMLGDISTFAAPATICKQLDTLKTEVQQLHQRPNKDGNTSAQHYKMPTFQIENGATGMAAVIGATARQGGCSASHQLGK
LSCAGGEATPPLTPPDSAALLAASYTSGEDANVASPRFTYEDYAVHLVPLLDQPLHVQQSTACTVSLPSATDSAASPPSI
AGDSTTWSRLEELDPLTFADFQWMPLPPSGRLPKPHCNVLMAQLRDYLHTAVPTPLMDVGVEVVDLHDYVEKIDSEFKTQ
RYDDIDAPLLYIRIQIGEATCSALIYCGATRNYMSQDFMDPRISELLDAYGDVFEAPHGVVPDRPIRHEIILEAGAVPSR
GCIYRMSKEELSVLRAQLDDLLEEGWIRPDSSPYVAPVLFVWKKNKDLRLCIDYRKLNAQTVKNVGPLPRIDDLLERLGG
AKFFSKLDLKSGYHQLEIRQEDRYNTAFKTRYGHFEWLVMPFGLMNAPTTFQAAMTTEFRHMLDRFVLIYLDDILVYSRS
LDEHVEHMRTVLERLRQAKYKANCNKCKFTRQELEYLGHYVTPQGIRPLADKIEAIRVWSEPTNTTDVRSFMGLAGYYQR
FITGYSRIVAPVTRLQSPKVPFIFDDDARRSFQALKMAMLMAAVLSIYDPTLPMRVTTDASGYSIGAVLEQHHDDDWHPV
EYFSHKVPPINSLDDARKKELLAFVVALKQWRHFLLGRRRFTRVTDNNPLTYYKMRDTVSSTIGRWMYFIDQFDFTPKHL
AGLSHHAADALSRRPDLCAMTHHAFAFDEELQRHFIRGYESDPDFATLYAQLSSDHPSASHYCIIEGYLLLHSRGKDLLC
VPRDRRLRTRLLAKEKTTTVGDNISTKSATRKKIPAAMNLLEGSDSHTVQEAQDSRTPWKSLRRVSELFNEVSRALGSGD
TILLQRGGVYRGTLDLTSRRDVLENITISNYGNLYLPLPRIVGAVVVSAASHDAVTASLPDAEAEAAVGTITETGEDWKE
VLEVSLQSALGNKQEIKKPKPRVAQTLYMDQQVQPMTRFPDVSVNISMAMMKLSGDNQAYPWLGESFLHFSSCHGDVYQL
NFVVHDSMFTRAAAATHAVSDGGSYWSGAQFIFRSSPTTYSRGLVKNVTMTPGSDPSQYSTMSSTGPSSMDSKNGNEFGS
GSGYGSAQGVYVTVTDIEGPLPLARMCAEGGVGGGFFIQGVKGELNEPGEWAFNPYTSMLYVLRDRDSVQATESSTIYTM
QEEKTTSEEKARKEEEKGVIEVTVHDKGIAVSRTRFFTVQGIQVEKFSAVGIGTVPNTFSEDEDNYGFRIIDSTIEGIDG
TCIMLRAAKSMIERTYVSNCGKIGIDLAGNENVVSWSTVKNVGLRPDLLVGSPAGLLGRPTAVNLQISNNIFWKMGGAAL
ANLPRGSKVENNYITDTFLLLTMEEPLLGIGSVMASGEVMVSHNIIIRSFGNDDSLTKGWTTPLDAALRGTTNASSSAHE
AQDNYSPTTGSRISQSKRHLTSFMTPCIFMGEQARGSVVIKNTLAHCRFAVFSKGAAGMRIEGNVIFDSGSPAMQVIGGQ
SNIVEGNILYLVEGQTRFFGESLSPDQPSSESLSSASSSSGSQSSSSAVISSLAVEGGVTYIGNMLCSPYSTDAVIMFRE
MARGRESSNDVCKIRPKVTGRYQYTSNNLINSTWEAVAEDKQEPGLDLGSNSDSSSSSATGLVKHLENTWLVYPDNVVAT
VVGANQHCAGPCLKITPMSFESSHTIRIIAAANVAFDAGEQYLIRFEIAMENHSGWAVIQPGHGEYNMSPFNDDGYTILE
HVYREDSANGSVQNIELFLSRNSTVYVRSGTAHRVKPSTLPRDRLLVNAQARTQDFHLNPDEVNYKVDGEKVNGSVVTLQ
PWSSTILYREIADMFPTSQPRTDSWPTSYSLEKLDDQSSGRLDVVGLQPIPVRELNHLAEADVLPTLEGPGTQPGDNMLF
QVVEPPSVSLLPELFNATEQLSVTPTSSSSPLEGHLEGIPSPPEAATPPALPPAVSLPPEGLLPVDELPATSSEITPALS
PTDAPPTPPAPPLPPASPPPPLSPTLPASPPPAPPYNPPPGPVSIPEEWPPGDRTPSPQTPKSPNDTIPPDEGIDAPPTL
LNIGPVEAPSSTPEDSTDEPEKCKAKAGKSYSSGAAAGIGFVCALVVIAAFFSGLSLGRGVWKISCLQVQQRVPAPLMDA
GAEVFDLHAFIAKIDREFKTQRYDDIDAPLLYIRIQIGEATCSALIDCGASRNYISQDFMVRAGLGPRVRRKSPPTQVTL
ADGHTHKSIDRCIDAVPVYFAPHASEAVSFDILDTKFDIILGMSWLRSKDHLVNFFNRTVHVRDRNKVLVPCTVPFPHPS
INCHVVSAASMRVSIIRDDIEEMGVCFLHALPPHDASSTDSPSDPRITELLDAYSDVFEGPHGIVPDRPIRHEIILEDGA
VPPCGCIYRMSDEELSVLRAQLDDLLEKGWIRPSSSPYGAPVLFVRKKNKDLRLCIDYRKLNAQTIRNVGPLPHIDDLLE
RLGGTQFFSKLDLKSGYHQLEIRKEDCYKTAFRTRYGHFEWLVMPLGLTNAPATFQAAMTTEFRHMLDRFVLIYLDDILV
YSRSLDEHVEHLRTVLERLRQAKYKANRDKCEFAQQELEYLGHYVMPQGIRPLADKIEALRVWPEPTNTTDVRSFMGLAG
```

28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE

A0A388LPQ3 **A0A388LPQ3_CHABU** (1079 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MADVLRKLPLVVLVVILLVVVVFVQVCILGRLPSRTRRKRGVRKSVAMDGRRPNVATLSDTYAIHRPAICTGVDGRAAVV
HFPPPRRCPGRGTPPPGGSHIWPAEREPSSATRTVLVNPHPDDDAGQVTLVGRGTRGGSARQETSEKTTERPRVHATSGP
SIPRTTAGRPEWMNPPPPFSWGRDTVPRPVERGVSAEDFPFEGAREDGRRVWKESRREMRRQQEESITQGVQRLRVGERV
GQADAVGEGGDVWRDGDEVGCDAEEDDSGDVFPLRAPNMGGRGGRGRASTNAGRRRKRPLATSADAEGEGDGEGGRNFWS
VDHMVALIRAKRDQDAQLQAVGHAFARMRSREWKWLDVRERLLKEIKGANERSHAISPSNVADTGGAGGVQLPSAQSATP
KSVGDGDATGEGNDEDDNSAREASQTIGSPAGFGKRKNVRQQTFEALSECMEKHEALMASTMESASMRQCEAMESASMRQ
CEAMESASKRQCSIQIRQCEAIEAEVEVQKQHCAASNEVSKLMCQALMEIAKKTEVAGGVKRGLHQAKKPKASSGGALVI
GRSAREEWVNEASSGQDDDFESEADTFHGRKGTLREVSNARMVSGEEGVDGGKDGGHGVARGKGEATGDVGGGVAAREER
GQPTTPAMRGAMPLKDMQAAQDVGKHPPMREPSNPATPTAGQARRDEGVRVNVVVRGQVATHIPTKEAAAVGAVVGISTT
GPGGGGGNGRDDADDDDPLINRQRRSGNMAALEAKAKLWVDDLRFWNETEGHGMFKIIQETRLHLIAIAKGVKPPEIRKS
VLLPNATIPLQKLEDVSELGAAKERASRVQTIAKRGPTWRHEAEEVEYEDEREEEDDKEDEEVIDEEDKREDGQEDDEED
ENEEGGDKAMDKDEEEDEEEMGKDEDEEEDKEEDEEEEEEKEATQKDEYYEGEEGAMEKEDVEEEEEEEEEEEEEEEEEE
EERGRRGGRREERRHGGRIEEEDEEEEEEEEEEEDKEEEDEEEEEEEEEEDKEEDVEDSVEVEEVEEEVMEEEKGEDEEEE
EEAMEEEVDDDEEEGDEEGEEEEEEEEEVEEEMVSAYLP
```

943 - 962:	EEEEEEEEEEEEEEEEEEEE

A0A388LQ89 **A0A388LQ89_CHABU** (1861 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MAIVTGDRYLDQLADFVDQHGEELLDGRLVLKLNPVGLLYLHSRLGELKELEDLKVNAPVDYLRAFITNLGDNKKLEKLC
RVLQLLESLKVVSLTKNVRDPTPIKLLPFTRLRVLELRGCDLSTSNPRGLLELRPCLERLLCYDSASALDHILADRTKEL
EAALPWPRLTTLSCPENGMQVMDASLTLLPALQVLDLSRNRFAQVSNLNNCCRWRGRETGRTMARWEGGRDGEMATYQMM
DKMAAAAGQYGVMAGYGGGLCRRPYKKKKKKKKKKKKKKKKKKKKKMAVAAGRYGGGLWRRSYKKKKKKKKKKKKKKKKRM
MMRGEGGRGGDERRRNEEEEEEEEEEEEEEEEEEEEEEDDEKSREAEAEAEAEEEEEEEEEEEEEEEEEEDGGGGRAVSYGG
GVWWRAVATVLQEEEEEEEEEEEEEEEEEEEEEEEEDGGGGRAVRLVYLDLGFNGIKSVVSLNQMAKTLFNVTKVVLRSN
ALTCTRGLEELYRLEGLDLAFNLISCINEVARLGHLPNLKFLWFEGNPIAFLPSYRWQVSKRFHHPEKIVLDGQQLGNWR
FGGVASRQEGESSNVCTDAETVPLLSDESRNKVASGLVPSSSQRAAESSGVQRDAEVAPVFSDESQNGLENGLGLTSAAL
TSGVGANSGASASDRERNPMKGAGKRRVTRLAEIISDDDESADAFTGEQMGDDEVKCESYQRPFGRNTEQLSAGTRSVAT
AKKGLRKAKTAERGTSTLMCLKGDKLLEIAETLKKDGGNAWLKAYHDFVEKSHAEETCNEHGPYRSSTTQRGDDSDDVPS
GAVIKEARKVTDMETTAEEVRDGHGGCGEEKGRMEGPDSAREFILDSDNVVRSGDRDENGIEKMEKVSRGVMRDNGRND
VCRCSRDVEERVHISGHEESGLLEGIHQGSATGGLLSRTYDLSGDSEVQQLLPGGRTLKKCEGDRKMVGDGESVGEKERR
EEESNVQDMDGDANDAHICKGKCNMCEEGGQAILHGGDRGDKKLVGADMGTKRGLNSATDCVGGEIGTEGESGNCIQASP
MDSQACTDGASLQLQKRKQRQLIYGVHSNSMEMGISISSKHIQQTSGSMETGSAHPCQVQSAPPCRVRSGPPSSVDSQLS
AVDKQETSSESSSVEWTDESETDEVPVTGRSRVRIQEEESEGALPITVGDERGKPEGNCTKIRRKKAGRQVTAGQKIGRG
VQDEGECCRVDMEANVAKISSMDKAGMDGKKGAKNRSADAEQSCVGVKDHSDSSTAHVGIGMRYRSNGEGAAGQVESPSA
ALASGCRTWNERRSRRNRKHTKRIVNLSLVDEDENDWRKRIAWEVRLSSGAVVTATGPANDCAENSRLKADHDNGCERFL
FIGLKNSRQKTYESCDVQRSESAHGVEELSECQQVNDPEADVHSNRDANIHMRTIEEASGELSCWQLQGAAVERVQSSDG
ADTCEKGGSEKRIGMETDERMLEQFAAPVENDAREDDIGVCFKTAIADQERTEECMMYWRCGYLRLWGPATKERDVLLLI
```

```
STQQMLYFLNEESSRPGYYQTSYPVLRILASHCVGDVKRVVVGIGLQCLRLEIGIAASYLVVFRSASLTAEFIECITSAC
KSGRLQPRGTLEIASCEREQIEHMERELFGGKKTSIHFYAMLHCRFGQDKLWKSCSLILTSRQIVLCEEKLGAFGSGVCQ
GRDLCLQSNLSEKKRQQHTASSPAPKPEPYFTQLCSRTLNDVQRVESYEDGSSNVIRILFLPTASGASPRTPDQEEGSTS
LATMVSRRHRLPRLFGFRPHREDDGANMERTEAKKSQKQMLSDPSKLSGELQKGGDADPPHPCKDEESRNSQWELRFSDR
DSFVKLQMMVRAACKQTGQLR
```

337 - 356:	EEEEEEEEEEEEEEEEEEE
338 - 357:	EEEEEEEEEEEEEEEEEEE
413 - 432:	EEEEEEEEEEEEEEEEEEE
414 - 433:	EEEEEEEEEEEEEEEEEEE
415 - 434:	EEEEEEEEEEEEEEEEEEE
416 - 435:	EEEEEEEEEEEEEEEEEEE
417 - 436:	EEEEEEEEEEEEEEEEEEE

A0A388LQG6 **A0A388LQG6_CHABU** (318 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MRMMKKKEEEEVEEQENAAMEEEEGEKEEEEDEEEEEKQNEEEEEEEEEENGDAQKEEEHERDDEKEEPMTMEKKEEREE
EEEKEKEEEEVEAEEDDDEEQKKEEEEEEEEEEEEEEEEGEEEEEEKEGKEEEEEEEEDKEEEEEEEEEDEDDDDEEEDE
EEEEEENEEEENEEEEEKEKEEEEEEEEEEEEEENEEEEEEEEEEXEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEYEEDEEEEEEEEEEEEDNDEEEEEEEAEEEEENEEEEEEEEEGEEEEEEEEGEEEEVEEEKDKEEEEEDEEEE
```

207 - 226:	EEEEEEEEEEEEEEEEEEE
208 - 227:	EEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEE
225 - 244:	EEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEE

A0A388LQI2 **A0A388LQI2_CHABU** (91 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MCCALRPTGRLGPYEEEEEEEEEEKEEEGEVKEEEEERESEEKDEEEEEEESEGKEEEEEEEEEEEEEEEEEEEEEEEE
EEGGEEMGKRR
```

56 - 75:	EEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEE

A0A388LR09 **A0A388LR09_CHABU** (1185 aa)

Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MWSTMHFSAECANDEDVDDVAGGHTQEKVEPSRGPLQELEAQLGVSQWRVPQIDIRDGEPTGDISQEEVQESEREARPSA
QRRRAVEEVIEVGEDTPPQSPVHVPGSEPESEDVQEVEEELQRGDISLPPPDKTISPGVRVEMEREETGCRREALSTVNR
YLAAHAQEYPDLEGPPFIEPLQEHRQAEIEARPEVPSRDARGGTRRKEEEEDDEEEEEEEEEEEEEEEEEEEEEEEEEE
EENEIGDDVGRRRFSGGGGRTVQDDRRTGGGAAATSADTAEGDTAAATAGGATSAADTQLLQHPQLPRQQLHHVPRQPLH
QLPLQQLQRLPHQHTQQLPHSSCCTSAATEQLLHSSCRTTAATQQLPHQEVRHKLKYISSSRTAVATSAAPRQQPHSSCH
STTAAAPQQQPHSSCHNSTAPQQQHHSSCDISSSRSSFHVSSSTRIGSSTTAATSTSSGSTSAAAASSSWRREWTGTRKR
AYEHFLLKRSQCPYDTISIWKRLHKAGCDMAPDLLDRVQRALEKENSDVDEDAAMGGVVEGDGGGAEIGVDSEEPVCRRP
GSGPGELASGCVAVGPVAIGGAGGRRRMQQEVQTRGPAKQTSIARYAKNPRQEDIDDSCCEFFVENVIPFNVAKSKSFKE
FQLACYGSQPAARCPLVPTGYNPLRCRLLEQLRGRLEKEEHAIRDDWQVTGCTFITDGTTDICGRSLMNYILAGRSKPIF
VKCEDVSEGDKDAATVVAGWKRFFREWGVEKITAICTDSFAGNKSAARMLSREWAAEVINRANKVVNFFRVHKWPRSHLR
AQLLKYPELKATCLLRPASTRFGTHYVMLHRLQVCEKVLVRIVTGRPWENMMWRVDRTDEEPVRCAERGGQGCSLRHGLS
AQSIVRYGPLTVEEREVVIADVGKRTDMLLSPIHAVVRLLDPQLRDVAVFSNVDLMAQFDSVVERLIDKKGSKRFDDCKD
QLYDFQFGRGLFGDPAVVRRAAKDNPVLWWEAHGAGHPDIKELAVTVLSIWTTSSPTERNWSTWALVQTKSRKKLHHHRI
EKLVYSHWSLRLTNRGDNRPTIVGRWLGLEKDWANEDLEGDMANVTDAVDDNEVGVEGTGSVAGSTNIARDPPARSASVQ
RLEDVEEAIETDKAEDDVDDNLSDEDNIPGEEWVDERSDSDRSWTRREEILPYIEDTRFSHRLKD
```

214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE

A0A388LS25 **A0A388LS25_CHABU** (260 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MADGKEEGKEEEVGEEGEEDEEEGEKEKKRRGSRRKRTTRNGDGGGRGGGGGEGRGGGGGGGGDGGGWRDGGGGGGGGG
GRGGGDDGGRGGGRGAADGGGLGGLGGGGGGGDEEEEEEEEEEEEEEEEEEEEEEEEEEEELEEEEEEDKATTKKKKKKE
KKKKKKKKKKKKKKKKKKKRRRRRRKRRRWRERRRTRSRRQRWSRRRSLRRRRRRTRRRRRRRRRRREEEEEEEEEEEEE
EEEEEEEEEEEEEEEENEMM
```

115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE

A0A388LS66 **A0A388LS66_CHABU** (96 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MKVGGRDKEEDDEEEEEEEDEEDEEDEEDEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEITLVQ
```

34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE

36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE

A0A388LT44 **A0A388LT44_CHABU** (537 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MSENFIVKEMFNNSVAQELRDNDIEKEESRDDDEEEEKSSDDDDDEEELSEDEDSNDTDSEDDEGKEDEVVCEQRCHWDK
VDQDFRDRHSADVRIRKGGKCVHVLRDLPVVVPVRKRKGXMIRHRLRVLFLRFLALCLLLPEHMELKLLLLQNLLLLTAK
LGLPMQVQVLEQQMLMCQPILVLLLLILRQLCLEQPPEVLLTVILLHALLLLLSLVLHLHLRHNVVMLLLLRQVILLSRV
LLLEVALRRRGLDVVHELQLHLLLLQGQQRSRQVMVFLLLRAGKRLMVLCGTLLLVLAGLVLLLWVHPGLLPLLYMLLLL
LVMQLEGLMICKVVQLQRVGWIPRSLRRADPSAVLNGLLPLWSRGLLAKGRAKIVDRTHKEADTGSIEEKAMVDEEIGKV
EGRAGVWHGLRTVADEGIVKIEGDEEIGKVEKIEGRGCKTGKVTAEVKRAKLEVQEVLACISHVTVLWKRGPDTSKVGFP
TREEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEEEDMEEEEEAVPFHFLTSLGKYEP
```

483 - 502:	EEEEEEEEEEEEEEEEEEEE
484 - 503:	EEEEEEEEEEEEEEEEEEEE
485 - 504:	EEEEEEEEEEEEEEEEEEEE
486 - 505:	EEEEEEEEEEEEEEEEEEEE
487 - 506:	EEEEEEEEEEEEEEEEEEEE
488 - 507:	EEEEEEEEEEEEEEEEEEEE
489 - 508:	EEEEEEEEEEEEEEEEEEEE

490 - 509:	EEEEEEEEEEEEEEEEEEEE
491 - 510:	EEEEEEEEEEEEEEEEEEEE
492 - 511:	EEEEEEEEEEEEEEEEEEEE

A0A388LUX4 **A0A388LUX4_CHABU** (1293 aa)
Integrase_H2C2 domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MEGEVFDKNGRVIDPEIPGGTRDEALRVAALGPNALGMFQIWQEMEEPVVPVEDITNLEEKMNRMGIGEDKGDVPLVEEE
TEEEDVMANVRDTFDRMEDLVDKMQRLHLRLQGICKEAGKEGVGCPKVVTMGRRGTGIGPNEPNPRMLRANMAARNSGSQ
RSMRGTISFATRRPAGGNPQKEQAQASQPAGEEPPITVEGDEDEDEKIREEEERQAEIRAKRRKGEAKEGRSKGDTRPSK
KRKYQTSIEQGVDLEGLVNKLLEGHNEQLNLKEILASAPKLREMVKARLSRRRVASVRMGDVIPKEANWSVAGSKMDWKF
VGTGSIDVMIKGKMCPRMVDTEAEMNIVNGETAVKLGLEVDENDCGFLNGVSGKTGYTGVASNVIIEIGRVKVHMCFYVM
PSLDLPILLGRSFLCRYESLIMNKHDGTMFVILCDPACGNFEVITCRNTGPHNTKNRLNVGSYTFEESENRRRELQWEEE
EEESDDEEAKGLVLSLTNINDAVELVSAYRMADPDAVRALAERIQDDPKGGRVDLRMREDIQNGPCRIDDETEKELIIGE
PGFLTMQEEDLVKELIREKHGAYAFSDDQHGRLHVDKIEMIRIHTVPHEPWNIRGAKYPNPEDRKRVVEYLNGKIRTDVA
GYSSGPYASPWFCFVKPNGVLRWVQDLQRLNSVTVRDARVLPNADQLSEACAENYRIMDEPRTIEAGVQQADEQVAMMGR
MYYLTNSPLQVQANDERGIVKADEIIIGDDYEFDKEKEGEFEQEEISEEFREEEYDGFYLEIGLLLSEDKRERREVSEKTL
RVRDHYVVRGGHLFIRDKRGPPRHVVRGRNRQIDVIVELHDGIVGGHRSFAATYKKAMELYYWEGMFEMTRKYCEPCRDP
WKEEVMAQRGEVAGPSGPALRKEGQRREQRISRNLEELPIYRVGDSLRDFLRDLEEYAFRREWGDREKIANVSGAGMYKR
RIEGVVTGCTRWRVCKVRLWRDMGEFPRDGVEDDLRYDGTNLEDFIESLQLTAERGGWSEEEKRKQLIARSDKGEKEEIR
GIVEGSRTWKRITAELWIAYTQTRQDQTRKERLQKKGLWIGREAEEDEQEEEEAAEERKTSIGASMVPRKKKLGKKRVIE
SGRKEVQERVSEKGEGVEEDEEGKEVRGGSKTPKVKRTKEKRPIGDKEETSGIEKKEDEKDGQVKKLMRDMEEMRKEVRE
LKKEKEKLQKEMSQLRVTLNVRSRELEEEVATRGKMEIRVDGLVSESAAKEKFVKLYYEEEEEEEEEEEEEEEEEEEEE
GKGGEEGEGGEKE
```

1259 - 1278:	EEEEEEEEEEEEEEEEEEEE
1260 - 1279:	EEEEEEEEEEEEEEEEEEEE
1261 - 1280:	EEEEEEEEEEEEEEEEEEEE

A0A388LVD2 **A0A388LVD2_CHABU** (243 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MDFDIHHRKHERHGNADGLTRLHRPEKVLKSEKVIPWNEPKDENGPCDESLAPHVLTRTLAPYLQWTACLEEPGSESALP
SRQEYLKPSGVINLAFYLKQDTSEEAEEEEATEEGDDAEKETSEEGSYSEHSEGEQSVDDDDDDDEEEEEEEEEEEEEE
EEEEEEEEEEAESEWEALPEEAARTGTEAEDPEAARKREEIAAGKNQLEFASEANPRINDNPTRDPEAPKPEDGDPATAAP
STS
```

146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE

A0A388LVF1 **A0A388LVF1_CHABU** (569 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MTDMQLLRLHYTNLKVLCKMHDIRYKDKPQAISALRQVPRLIAYKGRDFNRDSDIETQIMPDPDNIRVSNKNAGDTSEDD
YESLSTRSSGSDEYDSSDKSSSAEDLSGRRRRRHSSSSSGSQGRKRSRRGRSKTPRDRRHKSKSPSSRRRRAESESPRWF
WRPLWEQRRNDFPPPGNRAWFTADLKEEIFKLRWEMDKVLKTLEQLTRKTSEKQPAPPYKEDTAKKPELTPDALKSIIDE
ALKPTEMNQGGQNQAGPSATGQKNAEAEGKVEWMVSEVQKEFNNLKLLKYDLAVVKGALQKINEPTRTCTPIVSSSVHPN
GYLTTRKLEQWMACMNQPSDMVDMVDNEFLLEMADVMKSVHPACITACPAMQEPKDWMTSTCTGAIWNVNGVTKNRQVTG
RMILLDGWSDRRNRPYLNVMVSSPIATILCKSVCVEGLDKYASAYFRILDVVIKETGPKSMIKSHHPQGDNTKGKEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAKRRRSSSSSSSSSXGGGGGGGGGGGGGGGGDKEEEDKGEEENDNQC
KIRKLVSRT
```

476 - 495:	EEEEEEEEEEEEEEEEEEEE
477 - 496:	EEEEEEEEEEEEEEEEEEEE
478 - 497:	EEEEEEEEEEEEEEEEEEEE
479 - 498:	EEEEEEEEEEEEEEEEEEEE
480 - 499:	EEEEEEEEEEEEEEEEEEEE
481 - 500:	EEEEEEEEEEEEEEEEEEEE
482 - 501:	EEEEEEEEEEEEEEEEEEEE
483 - 502:	EEEEEEEEEEEEEEEEEEEE
484 - 503:	EEEEEEEEEEEEEEEEEEEE
485 - 504:	EEEEEEEEEEEEEEEEEEEE
486 - 505:	EEEEEEEEEEEEEEEEEEEE
487 - 506:	EEEEEEEEEEEEEEEEEEEE
488 - 507:	EEEEEEEEEEEEEEEEEEEE

489 - 508:	EEEEEEEEEEEEEEEEEEEE
490 - 509:	EEEEEEEEEEEEEEEEEEEE
491 - 510:	EEEEEEEEEEEEEEEEEEEE
492 - 511:	EEEEEEEEEEEEEEEEEEEE
493 - 512:	EEEEEEEEEEEEEEEEEEEE

A0A388LVR6 **A0A388LVR6_CHABU** (767 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MMLLGERRAVGAVLAAAGRIRHQYGSTGAMWNRACGLAVSAAEDNGAVVEREREREEGGGEGGGGGGGGGAGEGEASVSA
HAHGLELSDVATGNDVRRGSLAGGNGRIQIPVVDAILGDGLSAGKGGGELFTESLLGGIGSSLGDDGAQQLAGRGRAWIR
AAGRGSGDGGGNGNGSVTFGAAGRLGGTGRGNGAGRGRRSGGEGSGGQKQLGLSSVGRGEGESAGIAETSSDLHKEKMAG
TTAAAARGAQKLAGTKVNLRPLPASSPPLPDLPDLPDLHVVDYSPSVPPREKVAPGDTLAQLLRRPAYSLGGGSKMNMEQ
ALRTDTAGRGGGGGRDTLGDRNGLHRTETAGRGGGGGRDTLGDRSGGTLRRIPGQGTVMGGSAFGGNRSRVGRGVGEAVP
GGGRSFPGAPPPSRNSSPGSQIGAGRRDGSPASLRSPGSGGVGRGGIEVAGEMDQSGKGSSRGGGGGGGAGGGGGSRFDR
RAVSPDFKRRETSVRMKGGGAGAGGMMEGFVLPEVPGGVSNGSEQRSRRRGERMRELNMVTDLPLRRGGGQGRSTGARSA
DRGGRTLDQRQRELRERAGTRGGERRGDRLQRTDTWQVQEQRMTPEERRNYEAWEKELMMVEKQEELFLEEEGEDEEEQE
EGEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERREKWRADELEKIVEKYAGPARMTAKEENEVLSKVVDAMPSDSS
PELLAFVKRAELTLKNNPQWALAQKQHLLSSIVDDFRAREDTVETLS
```

645 - 664:	EEEEEEEEEEEEEEEEEEEE
646 - 665:	EEEEEEEEEEEEEEEEEEEE
647 - 666:	EEEEEEEEEEEEEEEEEEEE
648 - 667:	EEEEEEEEEEEEEEEEEEEE
649 - 668:	EEEEEEEEEEEEEEEEEEEE
650 - 669:	EEEEEEEEEEEEEEEEEEEE
651 - 670:	EEEEEEEEEEEEEEEEEEEE
652 - 671:	EEEEEEEEEEEEEEEEEEEE
653 - 672:	EEEEEEEEEEEEEEEEEEEE
654 - 673:	EEEEEEEEEEEEEEEEEEEE
655 - 674:	EEEEEEEEEEEEEEEEEEEE
656 - 675:	EEEEEEEEEEEEEEEEEEEE
657 - 676:	EEEEEEEEEEEEEEEEEEEE

A0A388LVS7 **A0A388LVS7_CHABU** (348 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MSRPQVVRSRDPTNRKRVLQLFEWLLRRQADPQDGMALVRFFETALDTWPGDKRQKLGICLIVRGLVEKGAVVSERSAHS
ERRKGGVVPRSDIKTPEMLFDDQDLDDEGAELLQLLGGRQGGKTQFEHLHASPVDFNSHLAAERFMNFIPALMKIVKTES
VQERTRRMPTRLTSAAVDCILTITRAVSGGVEFIDQKSPEAPRSHSTQRRASKLISELGNEGHDAGKLLWHYLKDLCSLV
KELLEWYEGAGELGEVGGGGGGEEEEEEEEEEEEEEEEEEEEEGKKKKRRRRREKDEEEEGEEKNKKKRRRRERDDEDEE
EEEKKKRKKKKKKKKKKRRRRRRRRRRG
```

263 - 282:	EEEEEEEEEEEEEEEEEEEE
264 - 283:	EEEEEEEEEEEEEEEEEEEE

A0A388LW84 **A0A388LW84_CHABU** (956 aa)
Integrase catalytic domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MSGHDSEEERTDGRPVTRHSARRLSYMYQTLRPGGKRELRVESAARCQQRRREEAAAVAQARAATMVTAAATSGTFSILY
VSSSNGMSAGISVSQMAGSQYSRTAAGPATCAATGTSWTTAKVVSKDPDVSSRILLRGQEGGEPQHLVEDSSNMGKGQAD
ASRSGRDCGCLIPQGFGSKMAGWYSWTDSFGPKFNDWAQTQTVDSFLELVEQRWHNPQQAQQAIDALARLDLKKYKTAHK
LTNALKKLIVVPGVLYDLQILLTMYLRCLPPDIKNMLVIEESIDVHDFRSFSNEASDMEAKLGSAQRVAVNGRTKQSHKI
GRRRVMMIDSDGNQEEIHSIPDIGSEENVEGGTLAAATKGKAAGQRKGGQQKSQGKARVSLNEPAWVKAGLEHEHDVWKD
RYPKGACINCGQYGLTQYKCKKAKVSQKIPPTMGAGESSAHGVMAQHEGKKLRSIEYMGKKMSSHKLAKSTYKRKLYALY
KALIHWRHYLLGRFFYVRSDHPTLRWIKTQPTLSDALKRWIEVIDQYDCRLEFLKGEYNKVVGTLSHTAYFLGALITEFG
LSDNITRSMVHGYKKDLVMIDITRKLEAKDEVTTDEFVVVDGLLFLEKARNKRQSVSMDFMDTLVTSTSGKRHIFVVDRF
TKYARLVAMRETAKTEYAIQLFMDNWMLDFGLPKSIVSDRDVCFTIEMWKKAAEQLGSQLQMSSRNHPKANGQADQINHV
EQHPLRHYIKPNLEDWDEKLPHIASLYNNAVYSTTGVSPNELHLGWKPRSALNFLFPEKQRAAMPGTIEFGVQYEKELQQ
AVEHIKKAQEYMIASENRPEQQSTFQVGERVWVKASELGQEFAISRKLMPQYIGPWEVLDIVGSDPDGPSYVVRIRSSQR
RFRQNVMSAPPFFNYKKKDAEAEAEAEAEAEEGEEEEGEEEEEEEEEEEEEEEEEEEEAEEEEEEEEEEEEEEEEE
```

919 - 938:	EEEEEEEEEEEEEEEEEEEE

A0A388LWF2 **A0A388LWF2_CHABU** (707 aa)
Reticulon-like protein. *Chara braunii (Braun's stonewort)*

```
MLFLLECDCGAYNSDLARSITEILLWRRPSRTILAILCGSILYYHAQFRLRPMIAFLADAFLILSCVSVGVYHLAAVAAP
GWAVELSRKWEISTQSANCLVAFAVNLLGAAEAVLRVAASGSDIRLFLKVVVILYALSILGKLISGSTFLYACMWVGFTV
PAICTRLWGDGTAVGAEIGGGGVMGAGGRVGGGSCGGVRSSGKGVGGGAGVGGSAASRFLSEGDVLSGDRGHSPRTQSTG
```

```
MCTHAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEQGAKADPWADGHRQCVTPKILHSHRRCDLPCGAVRGVLID
VMSSEAASGMDVDGEAGRGGLMTAERTAIAAVVNAVLFRCQMASNDTNFKAAVRARRKLLALPTTGQCLDVAAISDAVLE
RRTGGTWEDLWQCDDATDDYFKEKLRMSPRVFREIVETLSPLLQRRVTFYRVPLQPDHIIAYALYRWATGETYDSGTCSF
GIGRASGITAVRDVTAALLTAYPDKISWPTGAQVVVDMNLRVLDVFVGYPGSVHDIRMLNLSSLWVRAESGQLFTGPHVM
LPFGVRTNGYLLGDNGYPQSEWIVVPYGGLAQHPTEARFDNKQKTARGAVERAFGRLKGMWRLFLRTHKCNMDSLPQQFV
AVCILHNILIDAGVPFDDNLLWEVGPNGVRRRVDLGMHQPLRPVCMESSTGDALILRDTLAERMIAQ
```

246 - 265:	EEEEEEEEEEEEEEEEEEEE
247 - 266:	EEEEEEEEEEEEEEEEEEEE
248 - 267:	EEEEEEEEEEEEEEEEEEEE
249 - 268:	EEEEEEEEEEEEEEEEEEEE
250 - 269:	EEEEEEEEEEEEEEEEEEEE
251 - 270:	EEEEEEEEEEEEEEEEEEEE
252 - 271:	EEEEEEEEEEEEEEEEEEEE
253 - 272:	EEEEEEEEEEEEEEEEEEEE
254 - 273:	EEEEEEEEEEEEEEEEEEEE
255 - 274:	EEEEEEEEEEEEEEEEEEEE
256 - 275:	EEEEEEEEEEEEEEEEEEEE
257 - 276:	EEEEEEEEEEEEEEEEEEEE
258 - 277:	EEEEEEEEEEEEEEEEEEEE
259 - 278:	EEEEEEEEEEEEEEEEEEEE

A0A388LWS5 **A0A388LWS5_CHABU** (1175 aa)
Reverse transcriptase domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MHWRSTSEPSRTTRSYNKPPHATTGATDLCCRRQPEFGTRETTPKFADQEIFCDSTKTDPIPWFRKFELKLQLHHVNEDK
KHAYLYSRSGGACQAWLDNLLSKYGVVAADLYTKINWDDLKAAWHKGFQVEPPEIKAMDKLLTFEQGTLLSVDWIAEYQR
LTSVAYIQMGFKAVKHYFITRSCPALGNALTHVEDTLTTTTELFNKAAQIIVTNKEAKNLNRSSATGLSREQHRLKVAVV
AAATPTDPSSEAVSANEGDKLAAARDVGFEVLDLKSGYPQISIRPNDRYKSAFKTQYGHFEWVVMPFGLTHAPTTFQAAM
TNGFRAMLDRFVLVYLDDILVYSQTLEDHRGHLRRVLETLRRAKYKANRDKCEFVQQELEFLGHFVTPEGISPLSDKIQA
IQEWPKPRNVTDVRSFLGLAGYYQRFIKGYSKIAAHLTKLQCEDRPFDFGKDARESFLALKAALLFAEVLQIYDPQLPTR
VTTDASGYGIGAVLKQHDGVDWHPVEYFSKKVSVVHSIDDARKELLAFVHALKRWRHSLLGRSQFQWVTNNNPLVFYKTQ
DTVNSTIARWMAFIDQFDFFPDHIPRKSNLFADALSRRPDHCTAVYSTFEIDDDLQDSFIRRYQANPEFRDKYANCSSPT
PTPSHYRIQEGYLLVHTRGKDLLCILSDSHLRTLLIGEFHDAPATGHFGVNRTIGRLRERFWWPGLLGAVTRYCESCEVC
RCCKSRNHRPYGELVPLPVPLRRREVIAMDITGPFPKHKTGVDGILTVVDRCTKFAMFLPGRYHAKAPELAEASLRLESQ
AEQKGIAEKNAVVVTGKDGDVDGSEIFIRIRNQHNFVIEDDSEEDDGLVAPAPMCPCSTTDSSEPSMSISPYLSQALASFP
PVQCLSPPSSCPTRSNGGAGRMRPPSSSAASSQVHVRSPSPLSAHGKPSSCTFLPNIAALLQPKLFANSSSTIHPEYPDM
HSQKSVSRLPPPRSAWSVPDDDSTVKMSTEGIDKENCNNGLLQENQSPDAHLRRHGEFNNGGREKQFSGDRMAESTSTSA
NSVLKNGNGDYMREKSSSARENLVRGALQKENEEQQTAIASQRNGIEQLEREGKALSECIQCLKKEQQQQQQEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEVPRHTVIVIEERKMNQQVVWHPCAGTVNE
```

1113 - 1132:	EEEEEEEEEEEEEEEEEEEE
1114 - 1133:	EEEEEEEEEEEEEEEEEEEE
1115 - 1134:	EEEEEEEEEEEEEEEEEEEE
1116 - 1135:	EEEEEEEEEEEEEEEEEEEE
1117 - 1136:	EEEEEEEEEEEEEEEEEEEE
1118 - 1137:	EEEEEEEEEEEEEEEEEEEE
1119 - 1138:	EEEEEEEEEEEEEEEEEEEE
1120 - 1139:	EEEEEEEEEEEEEEEEEEEE
1121 - 1140:	EEEEEEEEEEEEEEEEEEEE
1122 - 1141:	EEEEEEEEEEEEEEEEEEEE
1123 - 1142:	EEEEEEEEEEEEEEEEEEEE
1124 - 1143:	EEEEEEEEEEEEEEEEEEEE
1125 - 1144:	EEEEEEEEEEEEEEEEEEEE
1126 - 1145:	EEEEEEEEEEEEEEEEEEEE
1127 - 1146:	EEEEEEEEEEEEEEEEEEEE

A0A388LWZ0 **A0A388LWZ0_CHABU** (855 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MAVVKKWGKSGKGEKWENDEEEEEERKKKNRRKKKKKRKRKEEGGRRRGGGSGRRARRRRGGARGGGRRRRGGEEEEGGG
RRRRRKKKRRRSKRRSKRRRRKKKKKKKKKKKKKKKEEVEEEEQEEEEEEEEEEQEEEEEEEEEEEEEEEEEEEQEEEEEE
EEQEEEEEEEQEEEEEEEEEEEEEEEEEEEEEEEERRRKKEEEEEEEEEEEEGGGGRRRRGGRRRRRGRGRRGGEEEEEEGG
GGGRRRRRRGRRKKKRRRKKKKRRRKKKRRRKKRRRKKRTRRSKRRRKKKTRRRKKKKRSRKKKKKRRRRRRKREEXXXXXXXXX
XXXEEEEEEEEEEEQEEEEEEEEEEEEEEEEVLEEVRGRRRRGGGRRRGVRGGRRRRGGGRRRGVRGGRRRRGGGSRRRGGSR
RRGGSRRRGEGRGGGRKKKKRRGGGRERKKTKKKRKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGGRRRRGGEEE
EEEDDEEEEEEEEEEEGGRGGRGGSRRGGGRRRRRGRGGMRKKKKRRRRRKKQRRKKRVAPPRESVMERSCSRCGFFASF
VNVMHMPLGCLMSMTVLLVGLLVFMSPLPSTAVAAAAANAGTTHGFTALHPDPQIACSACEMVVGLVATLMKSPRRDLLR
```

```
RTIVETGLDGTEQTVPYVTSRAFVRDLLDVVCNSSALTGLRLGESWSGRKEYVVDRAPNYKRQPPVEPSLHKACNLMTTG
RYQFLLTQLLPKMITQRSTMNIQMTMCGYVFETCSWKRSRWTLLEVLVREALVYDWSLIPRLFPFLLIVLSLPFLIVPMF
RRRPQVAGLSGDQVDGNKSQSRQAVQGKGTSTKPHRGTRGAAAAAAAAVRRKKGE
```

172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
437 - 456:	EEEEEEEEEEEEEEEEEEEE
438 - 457:	EEEEEEEEEEEEEEEEEEEE
439 - 458:	EEEEEEEEEEEEEEEEEEEE
440 - 459:	EEEEEEEEEEEEEEEEEEEE
441 - 460:	EEEEEEEEEEEEEEEEEEEE
442 - 461:	EEEEEEEEEEEEEEEEEEEE
443 - 462:	EEEEEEEEEEEEEEEEEEEE
444 - 463:	EEEEEEEEEEEEEEEEEEEE
445 - 464:	EEEEEEEEEEEEEEEEEEEE
446 - 465:	EEEEEEEEEEEEEEEEEEEE
447 - 466:	EEEEEEEEEEEEEEEEEEEE
448 - 467:	EEEEEEEEEEEEEEEEEEEE
449 - 468:	EEEEEEEEEEEEEEEEEEEE
450 - 469:	EEEEEEEEEEEEEEEEEEEE

A0A388LX56 **A0A388LX56_CHABU** (907 aa)
Reverse transcriptase domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MHNFPLFNKKALDLEAKIGHGQTPTTDGRIKSLPPNRKAKGHIMFIDNDGSTIELDDDFQAGVGSKASSAEASRGGVVAA
VAQKGEPVKMAPEIEGVVAKYSDLFEEPTGVVEREVVHAIEIIPWSSIPKGRIYWMSPDELDELRRQLKEFIKKGWIRQS
VSPYGSPVLFVPKKGGTLRMCIDYRGLHAITVKNREPLPRIDDLLDRVQGCRYFNKIDMKSRYHLIVMRPEDQHKTAFQT
RYGLYLFVVIPLGLCNAPRTFQHAMNRIFHDHLDKSIIVYLDDILIFSRTIEEHAAHLDKVLSLLPQHKFKINGGKCEFG
RTRILYLGHEISAEDLKPDDAKVANIRDWPRPQSVSEMRSFFGMTDYYRNFVKNYSIVAAPLTDLTRLDTPWESTDRCKA
AFRHLNHALTHHEVLKLPDPDKPFIVTTEASPYGIGAVLEQQEGPKLRPVEYMSKKMPSQKLVKSTYEKELYAIYKALSL
GVVEQYDFEPQYIKGEYNKVADALSRGPNFSGALITEFGLADDVTRSLVEAYREDQLMSEIIRRLEAKDKVTSAEIELVN
DLRRKKNQNQKQQQQQKKKKKQQQKKQEEEQEEEEEEEEGEEEEEEEEEEEEEEGEQEEEEEEEEEEEEEEEQEEEEED
EEEEEEEEEEEEDEEEEEEEEEEEPEEEEEEEEEEEEEEEEEEEEEEEEEEELASETKEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEDEEDEEEEEEDEDEEDEDKEDEDEEDEDEDEDEDDEDEDEDEDEDEDEDEDDKEDEEEEDVAYQEEEEEEEEEE
EEEEEEEEQEEEEEEEEEDEDEEDEDEEDEDEEDEDEEEEEEDEDGEEEEEDEDEEDEEDEDKEDDEEDEEDNDEDEEEEE
EEEEEDEEEEDEGGEEEEEEEQEEQE
```

666 - 685:	EEEEEEEEEEEEEEEEEEEE
667 - 686:	EEEEEEEEEEEEEEEEEEEE
668 - 687:	EEEEEEEEEEEEEEEEEEEE
669 - 688:	EEEEEEEEEEEEEEEEEEEE
670 - 689:	EEEEEEEEEEEEEEEEEEEE
671 - 690:	EEEEEEEEEEEEEEEEEEEE
697 - 716:	EEEEEEEEEEEEEEEEEEEE
698 - 717:	EEEEEEEEEEEEEEEEEEEE
699 - 718:	EEEEEEEEEEEEEEEEEEEE
700 - 719:	EEEEEEEEEEEEEEEEEEEE
701 - 720:	EEEEEEEEEEEEEEEEEEEE
702 - 721:	EEEEEEEEEEEEEEEEEEEE
703 - 722:	EEEEEEEEEEEEEEEEEEEE
704 - 723:	EEEEEEEEEEEEEEEEEEEE
705 - 724:	EEEEEEEEEEEEEEEEEEEE
706 - 725:	EEEEEEEEEEEEEEEEEEEE
707 - 726:	EEEEEEEEEEEEEEEEEEEE

A0A388LXA4 **A0A388LXA4_CHABU** (264 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MGEITSGDQTPGSAYASAKVETVSNEMKRKRKRRRRRRRRRRKKKKKKKKKKKKKKKKKKKKRRRRRRRRIKRRRKKKK
KKKKKKKKKKKKKKKKKKKKKKKKXEEEEEEEEEEEEEEEEEEEEGEEEEEEEEEEEEEEEEEEEEEEEEAEEAAEAAPV
```

```
TAAAAAAAAAAAAAAAATVAAAVPAAAAAAATAETATAATAAAAAAAVAAATTAAATAAATEAVTAAAATGPTATAATAAA
AAAATATAAAAAVGAAVAAKAQQQ
```

106 - 125:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE

A0A388LXM6 **A0A388LXM6_CHABU** (360 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MIEQANKHGRPSQFVVGDLVWVKSKEFAPEENISHKLLPAYRGPWQVLDVIGDVDCPSYVIEIPLHLHTYPVFHASKLLP
CVTNELFPSRRLAIPPSMDGKYDVDKIVAESTLHTARRGRPQRQYKGPPTTLANLAKEEEEEDDDDDDDEEEEEEEEEE
EEEEEKAIPTCTFPREAEEEEEEEEEEEEEEEEEEEEEEAAAEAEAVAVAVAEEETGGMAKKKKTKKKTKTKTKKKMKKKK
NDEEDKAVHSCTFLLGHGVCDTETHEWSFVLPFDTGTHDWQRETAILDRSKPIKSLDVYCLLRGHRGTAWFDDISITEVK
RAACQCPFGQFYDPSPGQDCEACSKDDSCLMGIKFEKPFG
```

178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE

A0A388LXQ1 **A0A388LXQ1_CHABU** (257 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MIVAAPHVLTRRRWRRRRREEGSGGEEEGGEEGEKAAKKAKKKPKKKAAAKTKAKKKKAAKKKAKKKAEAAKAAAVAKEK
KKAAAKAAVKAVAKAEEDEGEGEEGEEGEEEGEEEGKEDGEEEGEEEEEEEEEEEEEEEEEEEEEKGEEEEDEEKEEEE
EEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEEEKEEGDAEEEEKEEEEEEEEEVEDEDEEDDDDDDDDEEEEE
EKRGGRGGRGGRRGRRR
```

125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE

A0A388LY61 **A0A388LY61_CHABU** (911 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MVDLRSGTSTTPYSKEQEEGAAGILRERKERMEKRELIKQAKMLAMLEEQEAKKKQLEEELKKEQEAKMATIQEEVEKEE
EEEEEEEEEEEEEEEEEEEEEEVEEEEPLERRRGEASTSKEIEIARIAQEWAAHLELGEDREAEMAIPQEEREAARRQIE
TKRDPVRRRAKEEEQQMAWRYRLSQERVRRLEAAERAEKDLKAAESKMGKIREETELATKLNTLTQSVESLLTAHHEQAQ
YIRSLEVKVDAMRVGFKDFASDMMKYLLAEVHNAISKTREFCTGAIEGAKLATPKEEEPSPPRREKVKAAGATLHLREHE
CRLPSVSGKVKQVRLCHESEVDNPLAHCCLSAPAFARLVRKEQLEEQVFLAYVRPISDQPKEEEKIHPTIASLLEEYKDL
SEAPTGIVPRPIQRRIEIEPGGRTPKGAVYRMSPKELEELRRQLDELLEKGWIRPSSAPFGAPVLFVPKKEGELRMYIDY
RGLNAITIKNAEPLPRTDDLLDRVQGCKYFSKTDLKSGYHQIEVHPGDQYKTAFRTRKFVRNFSTIAAPLRRLLKKETIW
KWDKDCTSAFKKLKKALIEYPVLKVVDPSLPFVVTTDASQYGIGAVLQQDDGNDYRPVEFMSASLPSEKVAASTYERELY
AVRQALDHWKQYLLGRHFKVYSDHETLRWLKTQAKMTPKLTRWAAEIDQFDFELKPVKGKYNVVVDALSRRVDYFGAIVH
YLDIGADLQQKITDAYAQDPICSELMKRVRETPDSESHYRTPNGLLFEKTNVDDRLCVPNSEEIRSLILGECHDTEGHFG
WQKTLANLMMSYTWPDMKADCIEYVRSCKVPGEEVGCEEDSVHSEPVRKTLAAIARRRKTTTAIAAQLLVQTDCTECEWL
CSVDIQGDPRTCVHARVWGSEAGGRDGVRRS
```

79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE

A0A388LYQ9 **A0A388LYQ9_CHABU** (518 aa)
Reverse transcriptase domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MEEAAELIPLDQYVTLEYPGLGMIGTIKPAPKQREVAEWRPSLGEMESGGPTFVMGEIDVLNIIRALDHRIPLPIGHLLL
ISEHANERMLQHCKANRKRFALTRTTNTKMKGPTPDENVADTSDPIRIGLIQKDDHFLHIKPIRWKSAECDIEFDIRHGF
HHILVKEEDRPNMAFVLFEGTWQWVRCPMGICNASATFQRAMNVTFQNFVNNTRLTQRMINFCVIVYMDDILVYSETYHD
HAQHIEWALGALRNAGFKIALENSEFFLSEILFLGYVVTRGGLRPDSRKVAAVKEAPVPTSLTQVRAFLGLASYYRRFIK
GFAAIARPLTNLRGVSDRRRRREEEEEEEEEEEEEEEEEEEEEEVEEDDEEETPEEGSYSEHNEEEQSEEEEEEEQGEEE
EELALEESEWGILAEEAEQTDAQAEDPEAARKREEIAAGKRQLEFASGANLQIVDDPAQDPEPPKPEDGDPVPETSSALT
WRRRSRSPSPSISDRPPVRARSDAGHRALSPVVIPPSL
```

343 - 362:	EEEEEEEEEEEEEEEEEEEE
344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE

A0A388LYS9 **A0A388LYS9_CHABU** (299 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MEVEQGFMAEAVVVVEERQGMGEIGEKGGMVDNNNNNFNNGGEQRMSQLGETGMKEDNNNNNNNNNNNNNNEMEERGDNAD
SNNNNNNNNNNNNNNNNNNNNNNNNNNNNSKAGENNEMVEMEEDNDNNNNNNNNNDGSVSHISLSLLSRSGVSTTPYSKEQ
EERAAALLRERKEKMEKMELIRQAKMLALLEEQEAKKRQMEEKEMEKWTKEKEEKMAAIQAEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEVVEEEVPLERRRDGASTSREDEIAKIAQEWATHLELGEDREAELAIP
```

222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEEE
225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE

A0A388LZB4 **A0A388LZB4_CHABU** (210 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MKGRNRTQIWWGRWRKKNGRGGGGGEIGGGGGLGDDGGSRDPDLISQLLGENDDEDDIKEEEEEEEEEEEEEEEEEEEE
GRAATGEVGIRVCRKRRRRRRRRRRRRRRRKKKKKTKKKKKKKKKKKKKKSRRRRRKKQNKRRMMMRRKDDNEDDGEEELDD
DDREEGEEEEEDDDDDGEEEEEEEEEEGGGGGGGELDTYPGDGVLPSRPQ
```

60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE

A0A388LZW3 **A0A388LZW3_CHABU** (781 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MQHRSGEAGGLGNGPCGEGYDGVVVRQVQGGVRGWGEVLVVRDGFSGGSAERVYNGVVVGQVQEEEDEWEEETWTARKGR
TRGRAGDKEAWQMRKYEDEEGQEEDEQEEDESEKTKRRREEETWRMRKGRRSKRDMLTVTEDICPKVTFPYIDGNPVKGP
KENDETLVDVRVRRFVWEHLQGVAKALERLAKYNLTASGPKSLLFHREVTILGFRCFLEGRSPDPKKADKILNWRMPLRT
VGEVRSFLGVCSFWRIFIPGFARIAEPLREMVRQGASLGWSDQREKVARTLQDKLRDGGVVLGVPYFDDERARPFTIEAD
DGPIALGGVFVQRDENGKERPLRFESRTLNSVERGYIQFRKELLAILHCLRVFKHYIMGRRFILRTGSTTVIGVVKRHQQ
VDTTTAIAAHELAESSKMVERRLNEIKDGSQDLEQSKDDEGRFREEEYDGEYKRIGMVMRSNHLNEFYHERTKRNFRLRR
GHLFVDAKEGLPPLRVVCGRERRLEVIVALHEGLAGGHRGVDATYYKVSRLYHWDGLRDMVMRYCTLQPNEDNGVWYDPT
VSGAEPADKEKGVWHYMSGGPRSEEVVGPSRGKGPVSYLGDGYSHLVGADFVIEAFRKPLYGDRFLEVSYDYIYGKGQIE
ILIGATGSISLAEELYLRSVADEEMARCMAYISKIDPAASFDISYVVPESMATQRGVGVGVGEEEEEEEEEEEEEDGEEE
EEEEEEEEEEEEEEEEEEEEEEDGEEEEEEEEEEEEEEEEEEGEEEKEEEEEEEEEEEEE
```

718 - 737:	EEEEEEEEEEEEEEEEEEEE
719 - 738:	EEEEEEEEEEEEEEEEEEEE
720 - 739:	EEEEEEEEEEEEEEEEEEEE
721 - 740:	EEEEEEEEEEEEEEEEEEEE
722 - 741:	EEEEEEEEEEEEEEEEEEEE
723 - 742:	EEEEEEEEEEEEEEEEEEEE
724 - 743:	EEEEEEEEEEEEEEEEEEEE

A0A388M0N8 **A0A388M0N8_CHABU** (944 aa)

Nudix hydrolase domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MKTMAIACANAAVAIATSKRARIPAATGSKRLRNRVGATAAVGKRSRGRSSSPSPVVPSTLVGRLHPDRLASAISAASGS
PSLGYGRLPSSLTDRRKTAAPALQLLAPSTVSPSSLLLGVSGVKKGRRDPGEGRGRFAPTFLIGNHFLAGTTGSLSTTVG
SAEVAPTFLIGNHFLPGTSGSLSTAGSAESMLSRFFKKHFSGNTSSRQNLGESSNLEKKIASHRWICGSATSVSPSSASP
TEQEMVPASLAASASPTDGGIFYSDAGLDRMAEHRTDTAWLKRALTDVATKRFCSSCGSRMFSSCAGFSLKCSGDGCRMS
SYPRLDPAVIMLVTCGDFLLLGRQARWDRGRYSLLAGFVEPGETMEMAVLREVKEESGVDVQPNSVRYAASQPWPFPSSL
MVGFISEVNPGPLLNAVPVSERPSSIIGYGDPEHERIVREQDCLPAVNADLTELEDVRWIHRDFLHQAVSSGASWPWLSA
SEFHVPGKFALARVIMEKWLSERSNEEAWAGCHVPCVEIDQGVFKYVLLRVSNEQGQEKLVVIGLFIGILAFSCAILYYV
REVGSCSGLHFYGGEEEEEEEGEEDEDDEEEEGEEEEEEEEEEEGKDEEEGREEEEEEEEGEEEEEEEEEEEEEEEKDKE
DNEEEGGKEEDSEEGGEDEEDGEEENNEKEGREEKEEEEEEEEEEEEEEEEEEEEEGEEEEEEEEEEEKDEEGGREEEEEE
GWEKKKKKKKKKKKKKKKKKIAKKREVKKKITKKREEKKKRTRKREEEEEEEEEEEDEEEEEEGEEEEEEEGEEEEEEEEEE
EEEEKDKEEGREEEEEEEGGEEEEEEEEEEDSEKEGGEEEDNKEEGGKEEEDAEEGGEDEENGEDEEEENNEEEGREEKE
EEEEEEEEEEEEEEEGEEEEEEEGEEEEEEEEEEEEKSEEEGREEEEEEEERRRRRRRRRRRGR
```

676 - 695:	EEEEEEEEEEEEEEEEEEEE

A0A388M152 **A0A388M152_CHABU** (598 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MEAGGDQGWLSVFSSIRSQQPHSIAALEYPNPVRRALPPPIPTKEVIGDGNGVTGEGVVPVSPKALGTIAAMRGNRCQLA
MPSVATDGSLVEYLDVEIPAAGDGVCGNLVEYLDVEIPSADQSSSSSSSSLLKSFLSADNPAAAAAEGTAPAILPLHQQ
ERVRSLQNDPPVGLLVEDAPGKYAALVNVFRLLPIHERMLTVPFVCREWVEAARDPSCYEDVAASSVIDAIAEGFAPEEV
PSRIGQFLEQVLRLANGEIKVLRLSRCSDGELRAVSRECPLLKNLSVKGSSTLVTNAGIVSIARHCGNLTQLELEGCLKL
TDAAIAEIAKHCHRVQRLGLSDCTRLTAAALNAIAQGVPDLRQLNVSGCVRIHDDGVVAVSLGCPNLLAIDLSGCEKITD
IALVSLAEKCKRLQEVKINGCYRVTDDGAIGLVEHCKDVSSLHVSECVKLTTRMLDAVAENLHGLRDLDISCFMNLTDEA
LVTVLRHCGKLTNLNISGCSHITDQGLAAIDRLCPWLGLLNVRGCREQQQEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
HLGIVRGGDKQETNCAVCRRIGGGGGGEGGGGNGSLAS
```

531 - 550:	EEEEEEEEEEEEEEEEEEEE
532 - 551:	EEEEEEEEEEEEEEEEEEEE
533 - 552:	EEEEEEEEEEEEEEEEEEEE
534 - 553:	EEEEEEEEEEEEEEEEEEEE
535 - 554:	EEEEEEEEEEEEEEEEEEEE
536 - 555:	EEEEEEEEEEEEEEEEEEEE
537 - 556:	EEEEEEEEEEEEEEEEEEEE
538 - 557:	EEEEEEEEEEEEEEEEEEEE
539 - 558:	EEEEEEEEEEEEEEEEEEEE
540 - 559:	EEEEEEEEEEEEEEEEEEEE
541 - 560:	EEEEEEEEEEEEEEEEEEEE

A0A388M1W9 **A0A388M1W9_CHABU** (146 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MDKHEDAMGAEEEEEEEEEEEEEEEEEEEEEEGGGGGGRRRRRRGRRRRRRGKKKKRKKKKKEEEEEEEEEEEEDDDEEEGG
XDEEEGGGGGGEGGGGGGRRRRRRRRKKKKKKKKKKKKKKKEEGRRRKKKKEGRRKKKEEEEKGG
```

11 - 30:	EEEEEEEEEEEEEEEEEEEE

A0A388M239 **A0A388M239_CHABU** (337 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MSAQLRQGKEEEEEEEEEEEEEEEEEEEEEEEEEKEEEEKDMVGEEEEEEEGEEDEEDEEDKDTAVLQEKNEEEQEKEENDM
AGEEEEEEEKETAALTKKRKQKTGRGGGRRRKGGGGGEEEDEEEEEEDEEEEEEEEEEEKDLAGEVEEEEEEDEEEEGEEK
EEDKDMARPRKKIKKRVPRGTCSEEGEEDEEEEEDDEEEEEVEGGGRRRRGGRRRGGRGGGGRREGRREGRRRRGGGGRR
SGGGLGRAGAGLHVGRAGGRGGQRYGGSERKKNVPRGNCSEEEKEEEEEEEEEEEEEEEEEEEEKGMAGEEEEDEEEKD
MAGWRKQKNKRGGSRTC
```

10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE

A0A388M358 **A0A388M358_CHABU** (1522 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MDGSWESSLKTPLLAATASGAPSSGGRAPQGYVAAATGRSFPASIGIAQQQQQQQQHPNPVSSLSGSQRSSRCASPHYAP
PVLPPSSLGPTHHHQPLQQQFATCPSYLSVSAPSAGAAAAGRRSGSRHHPAVAALSGAERRPLSRSSSPAPRGGRPFSTS
```

```
RSPPPSRGRPYSRSKSPGPFGRPLSGSRSPPPRLSALGSNFDKPRIAAGSWSTGGGGGGGGGGGGGGVSGTTLSLTRKK
ALAVRTWLRLDASGNVQVMEVDKGTIMRRCHIPARDLRLLDPLFVYPSTILGRDKAIVVNLEQIRALITNEEVWLLETSD
PCVRAFVRELGRRLAMPHSGNRGGTTAKTEQANHQINQGQQQQQQQQQQQQVPSSWQQQQQQPPSWQQQQQQQQQHVPSS
WQQQQQQQVPSSWQEQCYVQQSKRGDGHSPAAAESGWLPPVMVPTVAAGIPTGGAVGNLMPSTAATMAGSHVAIPPSTSM
SEAQSPTRRVDGSFFACGGGGGGGGGGGGWMPTAWPAPAAGRHDSDRSGVSPDMGSGWGEEPEARLAGAGPGGGGGGGGG
GGHQPPATTANAGAGGEGGEKGGGGEEGGDSESSIALGAWSSSAGGAAWDELPFEFRALELALEAACWLLDRQTTELQQE
SYPVLDELANKVSTLHLEHVRRLKSRLDALMRRVQRVRDEIEQLMDDDADMAEMYLTEKKVREEESILGRLGGGGGGGG
EEQYGNHYHHRRHLRSRRPSNRDRDRQNSSSDDLVERDRRSDVAVCGPISTSTMVASPAWSLDRDMDSLVDNTSMACPPS
AAAQRHTRPSSSPPFPPPPPPPPPSSRPGKKRKADVQQQQRQQQQQQQQQQQQQQQQQQQPHPGVGGVAAAAAATTTSTT
SILTPSRRSDFNLLSLNHPRAKDDDPEEEEEEEDDEEQQQQQEDDGGRSAVVRDGERPDHDGGDDGYGDGDEKKRRPRRI
RRNMSRRDRDRDRFHHRHRHHQAHGSAAADSSSSSPSPSPSLVYYTDDTLAGTSSLQPSSTSAVHTEELEMLLEAYFIQC
ESTLQKLGSLKEYIEDTEDYINIQLDQTRNQLILFELLLTSLTFVLTIYGVVAGIFGMNVPIGLENSPQAFGVVIVITGL
VGLAIFAAIMGYFRYKRLQWEEEEERKEEEEEEEEEEEEEEEEEEEEKEDEEEGEEEDGEEEEEEEGEEEEEEEEGEEK
EKEEGGEEEEEEEEEDKEGEKQKLLEKYQLSDQLLDLTDLSKVSWKSFGTTKQFLTKFERVAKLVPDLPDKDRCLIFLETF
TEVEQLKLVNGMKERYDWPKIRENLLAGDFDQILCRLLKQQKENRERLQLGTNKNKEVYKTLSDRREMMSSMKGEQLKLQ
VMMAKAKTGKRKGKEPVTKERSSESESEEEREPPRKLTKAERKALNQIRGGQGTSRKQRVSSKNGGNGSGERQVDQGQQN
QGQQTQPQGGRGRGRGRGNGDGRGNWQEYVCKYCDMKGHVIRFCQILAKDEKDHIVFTTIRGEVFDFEGNLIDQDIKGGM
RK
```

1148 - 1167:	EEEEEEEEEEEEEEEEEEEE
1149 - 1168:	EEEEEEEEEEEEEEEEEEEE

A0A388M404 **A0A388M404_CHABU** (702 aa)
Reverse transcriptase domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MRAEAGGGVGGGGERCGGGERCGGGERCGRMREETGGGGRRRREVVACEGGRRWRAEARGGGWRRLAGAGGGVQRWGEVR
VEAGAGRRRWHAEAGGGGGWRLAHTEACGGKERCVRRREEEAGGGGMQRREEVACRGGRRWRAEMGGCGGRRLAEADRDV
RRRGEEAGKGGRRWRAEVGGGGGRXXXXXXXXXXXXXXGGGGRMRVEKCWRRRAEAGGDVEELMRFTTYLEPIIRDLIREY
RDVFPPYFSYSGIRPMRGVEHPIQLVPDYRVHHQAPYRLSIPEATELKRQLEELLRLGFIKPSNSPWGAPVLFARKADGT
LCLCIDYRGLNRYTVKNSYPMPRADELFNRLAGNRFFTKIDLRSGYHQIRVAAEDQPKTAFRSRFGHYEFTVMPFGLTNA
PATFQTTMNDIFRDILEEYVLVYLDNILVYSRTLEDHIRHLRDVLQRFRKHGFYAKLSKCRFAQRKVDFLGHHVSDQGLH
MDDAKITAIAEWPVPTSAKQLRSFLDLTSYYSNFIQGYARYSYVLTSTLLRKNPPWFWTPLCEDAFRALKKAVTCTPVVR
LPDFDRPFIVTTDASDFAVGAVLSQGGRAGVGGCGRRGEKKKNEEGEGKGEGEEEEEEEEEEEEEEEEEEEEEVEEEDE
EEEEEEEEEEEVVEEEEEEEEEEEEEEEEEEEDEEEEVDDAEEEEDDEDEEDDEEEVDDETT
```

613 - 632:	EEEEEEEEEEEEEEEEEEEE
614 - 633:	EEEEEEEEEEEEEEEEEEEE
615 - 634:	EEEEEEEEEEEEEEEEEEEE

A0A388M432 **A0A388M432_CHABU** (324 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MTFSTKNSQQESSMSSCRGFFVYLTIDLLCGSCYVAAAVCADVAAAAAAEVAASAGADVGAGAAADVTRAAAAVLAAADV
VTADVATAVCLLLMSHLLMWQLLCRRKEEEEGGNEQEDDEEEDEEEEEKKEEEEDSEEREEEEEEEEEEEEEEEEEEGEE
KEDKEEEVEKEEDGGEEQEEEEEGEDEEEEEQEEEEKDSEEKQEEEEEEEEEELEEEEEEESTATDNVMEEEEGKTGADV
AATTDNDVEEEEEEEDKEEEKNEKEEEEEEEEEEEEEEEEEEKDEEEEEKEDEEEKEEEEEEEEEEEEEEEEEEEEFI
SSQV
```

298 - 317:	EEEEEEEEEEEEEEEEEEEE
299 - 318:	EEEEEEEEEEEEEEEEEEEE

A0A388M4K8 **A0A388M4K8_CHABU** (184 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MEKKVEEEEEEEEEEEEEEEMEEEEEEEEEKEVEEEYKEEEEEEEGDEEEEDDDDDEEEEEEEEEEEEEEEEEEEEEEEKEE
EKEDEDVEEEKEDDDNQEMEEEEEEETRRGEAEGGRHEKRKEEEEGGVKEEEEEEGEKEKEVDKGKLAHLAWAGDGAWGC
GRRRRSLAMAKPNSGDSSGAKTSG
```

55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE

A0A388M556 **A0A388M556_CHABU** (363 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MLRVDLNWTWEGDHRPASEIVELLVIQAWRTNVAGDLLGFIFGAVDRGNRLQIVRELTIVIARLADELPLDIVSQSDEEP
VPHTLSRTLAPSLQWSACIEERWADGRFPSRSEYLDIHSLTNPRFFRQPTTFEWATLREEEEAEEESEGELRREGGEAAA
RLAEDEEEECEAEEEPAGEEEEEEVEEEEEEEEEEEEEEEEEEEEDAEEETSEEEKEAYSEYSEGEQSEEEEEDDEEVKS
ENNQARTHDELEWVPGPDRREENPEAAAQRNKEIVEGKRLAFDPTPNDPFKDPEPPKPEHRDLAATTSGAGVRKPGEGHL
FAAEAKGNGAYHSSCPLQRSSAASRCGRERFVYFTPTKESLKG
```

186 - 205:	EEEEEEEEEEEEEEEEEEEE

A0A388M5F4 **A0A388M5F4_CHABU** (164 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MQLFCYDAANILDAKLNFGIMPSIANRGGGAAAAAAAAAAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEED
EEEEAEAEAEAESEEEAEEAEEEAAAAAAAAAEEEEEEEEEEEEEEEENEEEENEHKITPMSPPLLCPLPSAAAALSLTNA
SLLS
```

41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE

A0A388M5L7 **A0A388M5L7_CHABU** (3531 aa)
Non-specific serine/threonine protein kinase (EC 2.7.11.1). *Chara braunii (Braun's stonewort)*

```
MDGSAPTGGRQPQERCQAQMVMSFGPARRVWSKASEHERLQVRIQQFLGKIGGHGHLLVPTVHLDQMKGSGGLAWDTEER
VKFVLPFRDRKVDIWLDGILPRVVELAESASERQIKVAACELLHAICLLMLGTAAKGPVRRSSEESKQVYVFHRIYAKLF
PAILRLATDVDLVTRQLFEEFTKQLIRWMTGNVDKENPDTMALLDAILEGLVDSENGSLREFCADCFGEFLKWTVRHTPR
EADMFINVPSMLRRIHNRLDHPNPYHRLGAAMAVHRIHPVLRENQSIVDRHAFELAFHIIKSLQLAENDNEQIVPGRHGK
QKQKQKQKQKQKQKKKKKKKKKKKKKKKKNKNKKKKRKKKRKKKRKKTRRRRRKKKKKKKKKKKKKTTTKTKTKKKTKKK
KMKKEEEEERRRRRRRRREEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEGGGGG
GGGGGGRRRKEEKKKRRKEEEEEEEEEEEEEEELEEEEEEEEEEEEEEEEEADEEEEEEADEEEEEEEAEEEEEEEEEEEE
EAADKEEEEEEAEEEEEEEEEEEEEEERVKDPLRHERKDRRMFHTVDEFAEWLFVQTGRMEGCCRSKCMSLFIEISTLLK
GGDAVGWFRRKITPSSSLGSIVRPFQMRLHLPERWRYSSPLSLQPWLVDFARSLHWFRWSLSHGLILIHELHPVTGALEN
SPLHPCCALRTFMSGPAFARMEMDKTVWMALTPSEREAFHRLLHSAVLHGVKFLQTVVDASTHGDALSEEELRDFLPEND
EELARLICLSILRPWDLGLVVRTPRQADDVRTKSVKLLRKIVQLSGKFGESVTTSLQDLVRRQPDKYDLGKINLMGTAES
HGGPAAGALEALVLVKGYYDLHVSGILKALYRGGTDGKDRGRQLGEQLALSLFQIRKELAPTLTPLAMEMLSLSMALGLS
ARRILELVFDVATVEGREGPIIQGAADDSSLEKRASAGSFFFVNFREKIVEVCRFDYGLCLDMVLSKARDGNQTARLLLE
AIIDDYIRRGKDQITRAGFLSACSEQLWLIVAWSRPAASIGDKRLFLSILQKLFLLEDLMAKPVVLYKDGPSYNSVVEGF
LRFFVDQTEPRETQESVQTRTLLVQDALKLVPFFLRTGIDEQLRSRVVHQVSRLVTNRLLVREEHLIVGSSERQMYKGLL
QAVLDAFVKVRYAGVLEVLFPLLQNPNSINFQPVEDALFVFAEGLGVNSEPDGANAILDRCLEIFNDTSKPSRLRQAVIH
RLVVKVLGVMKEDALVEWYLERMNGFVQELQQLRSQPNLPDEETEEEWVVTRVSLYRLLQFLFDSLPLDVIEKNILPVVP
AAQVMRPAIEDSQAKKDPVLAGGMGVRSEQSADRMRKLHAAGYNCLAAVLMKTAKQERPFVALFKESGAGFKWQNLIDKE
KMLSVLPVETDSLSRQKNAVRSTKAKWRAQRESRPLGSSGVILATMSSQYLVSATLSQDAFVTGAGTPVGGKEGDNASSD
ANGKLGEGQKEGEEVIESTVLDDDMFDQNPAMGTVLRVIESLYNKFREHWTENMPDWMSSIHAIMDNPVTPLNVKLFFVK
VIVRARKVFAEYAKKWFQPLVQTVVSDPGKTGGFCFHYLLRDVCITLLEWGLPHPVDERLGSRFVNHLMAVIPHRNAQVT
RANLEIVRMFLERWNTHLAVNKEIIFNSLGSTEGLSGGKGAGRGGESTSMARVQRAVAIQLIGAMAIYGMPVFDPATDRF
VSEGGFYSRLLSNLEFNAKAIYEAAGEVIGLILCERGQKGDSISQTALETPLRVKLVKFCRECDDRFLYILNKITLRHPS
YGRDYVSFVVDRLGGQQGTFREISLDVLLRTCEALPEMNVQDLFDSMLPMLPGLISHRDEQAQARTLKLLLKMLTKGRDG
DVEGEPQTDVQVPRTLDVQRLTKFLLQGLCNTFTRHASVTCRELFFDILIVLYNKDEHLRENRLVFTSLLRGLFDDSDQV
RSKLQGFWHTELTKNIEHRLVQAMDRMYDPEVESSWALFTNVLLLKLCEDSVDYQRPIFDQPLSDCEFRAYPINTSFMAS
SLGMTPMFLTASQSQSALPASSSLTGQETVPDQDSAHGVVHGGAGMMVRATQTPSLSIDPSQFSLGTSSMTYGLTPTLAD
LSGSSLIASQRLRRGVRSDSDDGLGTLTIKDEAEPVKRRIERGRHMKPAQLRAIVSAQKRKEMRRVRQAADRANKVQMMR
HYRIALAGQFWRRGRVSQLEKDLWESERYTCLMELNQWRPIAEEVRGELQHEEFDDFVLLQSVWSCEGREQLLPLLMKSC
LKSAIDRSALLAFIQTSLEDPVKRAALIDEFSPEMAFLAALNDQPDRAQFYILETYRKFREKWGLLHPLATGVRHRQVQV
LQKITEVGEYLSASAVGNVKAQEAAGVAAVRSARGGRVIGTLPRLLSDWQMRCPSSIHDGALVWGDIVQQRSDFLDKIKR
EISSRSDHQTVDEKILSDVNPVDPLHRAISRHRPELYKAVARGLRKHGQYDVAELYLLEYLGQKPETAADTAMLDFGFIK
SLVKLRLRNARRVHQFRPEDAIKLLEEPMDWISKHTDLPGLRERRDHMHISQSLRMLEGDVHSELARLAMEQRTPIDLQA
VGESETPTNERVLALLGSAFELYSGVMRECWPEMLAVRRQVYASSAVEARHYTKSSLKYASFCNELLKLSVEGCVALPRL
AESLSEGDSAARLPGPAVDVYPQLIVRHVMRALAMGGTSTAQHIIPRVNALLGSYKVARSAFEKAWDNGKSSIPSWVFLP
WIPQMLSVIDQHEGVLYVPILLVIAKEYPQALYFPFRVSAEDFSPVARQRTAGIAQQLRSPTMDRFARALEDLTSPEQRI
KDGIESIQTYLERGDNRGALAAFKRMDDDCLDEEALHRRGAGDYNTTFARNWRSEFVDALGEGGSKLKTMSVADFVGATA
KIMRARQAAEGKQPKGRTDLSKFSKWLADYGQSRSTTPVTRSTGQQSSDKVSFPGGSDAIVGGDGGADEDKDMDFLDIGV
GIEIPGQYRSVGRPDPANHVRVTSFDQTIVTVSSKQRPKILTIRGSDEKEYRFIVKGGEDLRLDQRIEQLFEVMNTALGA
DGQCRQRGLKIKTFSVVPVTKRCGLLQFVESTCTLQELVERGLDTALAKSSIGRGSSRRPQVNSSHSLMTGVREEFMQWI
CRAAREKPPMRAGLYYPMYMRTDRAEVERKMQSFQGKLPWNALRSGLYQHAQGPESFLALRAKFARSLAVSSIAGYIAGV
GDRHLQNFLVDLSDGSLVPIDFGYSFGTGVMMLPVPELVPFRLTRQMQDVLAPLDALRLLRVDMTRVLNALREHKEALTA
VMDVFVKEPILEWKIEASRKRLMSRTMRGAAIQRGHARNEAQPGAGGPNQRDPDAESSRDHSDPQEGSNDWLVDDEDKRH
IEIKVESAHRKLSLWNPVDVMLEELHASVHANKPYFDHLEKIIRGDPRHNKRAQIQSKVCANAQEQVDCLIDQAVDLNLL
GRIWVGWTPWI
```

419 - 438:	EEEEEEEEEEEEEEEEEEEE
420 - 439:	EEEEEEEEEEEEEEEEEEEE
421 - 440:	EEEEEEEEEEEEEEEEEEEE
422 - 441:	EEEEEEEEEEEEEEEEEEEE
423 - 442:	EEEEEEEEEEEEEEEEEEEE
424 - 443:	EEEEEEEEEEEEEEEEEEEE
425 - 444:	EEEEEEEEEEEEEEEEEEEE
426 - 445:	EEEEEEEEEEEEEEEEEEEE
427 - 446:	EEEEEEEEEEEEEEEEEEEE
428 - 447:	EEEEEEEEEEEEEEEEEEEE
429 - 448:	EEEEEEEEEEEEEEEEEEEE
430 - 449:	EEEEEEEEEEEEEEEEEEEE
431 - 450:	EEEEEEEEEEEEEEEEEEEE
432 - 451:	EEEEEEEEEEEEEEEEEEEE
433 - 452:	EEEEEEEEEEEEEEEEEEEE
434 - 453:	EEEEEEEEEEEEEEEEEEEE
435 - 454:	EEEEEEEEEEEEEEEEEEEE
436 - 455:	EEEEEEEEEEEEEEEEEEEE
437 - 456:	EEEEEEEEEEEEEEEEEEEE
438 - 457:	EEEEEEEEEEEEEEEEEEEE
439 - 458:	EEEEEEEEEEEEEEEEEEEE
440 - 459:	EEEEEEEEEEEEEEEEEEEE
441 - 460:	EEEEEEEEEEEEEEEEEEEE
442 - 461:	EEEEEEEEEEEEEEEEEEEE
443 - 462:	EEEEEEEEEEEEEEEEEEEE
444 - 463:	EEEEEEEEEEEEEEEEEEEE
445 - 464:	EEEEEEEEEEEEEEEEEEEE
446 - 465:	EEEEEEEEEEEEEEEEEEEE
447 - 466:	EEEEEEEEEEEEEEEEEEEE
448 - 467:	EEEEEEEEEEEEEEEEEEEE
449 - 468:	EEEEEEEEEEEEEEEEEEEE
450 - 469:	EEEEEEEEEEEEEEEEEEEE
451 - 470:	EEEEEEEEEEEEEEEEEEEE
452 - 471:	EEEEEEEEEEEEEEEEEEEE
453 - 472:	EEEEEEEEEEEEEEEEEEEE
454 - 473:	EEEEEEEEEEEEEEEEEEEE

A0A388M706 **A0A388M706_CHABU** (301 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MWTRDEEHHTWVEYLELLIIQAWRTDVEGNLLGFLFGSVQPDHRQLIVQELTIPLAQLVDDLPLEIVSQSDESPVPHVLA
RTLTPYLLWSACLEEPRSDRNPPLQRGYLDSREIIDPAFFQDRTASEDEELAIEEEEEEEEEEEEEEEEEEEEAVEADDE
EETPEEGSYSEHSKGEQSEEEEDEELELEESEWEISTEEAEQTDAQAKHPKAARKREDIAAGKRHLEFASGANLQIADDP
ARDLESPKPADGDPAAETSSTPARRRRSQSPSPSTSDRPSVRAHTDAGHRASSPVVIPSSP
```

134 - 153:	EEEEEEEEEEEEEEEEEEEE

A0A388M781 **A0A388M781_CHABU** (189 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MDNEDKGGSGLSRRGEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEEEEEEGEVEEEEEEEEEEEEEKKKKRKKKRKKEKRRR
KKQKEKKKKKKKKKKKKKKKKKKKKKKKKEEEEMTKKKRMQAMREEKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XKEEGGRRGEEKVEEDDARTSEAYVETTM
```

16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE

19 - 38:	EEEEEEEEEEEEEEEEEEEE

A0A388M7U4 **A0A388M7U4_CHABU** (347 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MEGWRDGWMMEDGGWRDGMEGGRDGWEDGRMEKRREGVGKEGKKKRREEDLVNGAAAAAAAAAAAAAAAAAAAAEEEEEE
EEEEEEEEEEEEEEEEEEEKKKKKTRGRRGEEEKMKKMSGGGGGGRPSWGGGREGGMMEDGGWRMARWYGGREGGMDGWM
ENGGSRMEDGEMEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAEEEEAEEEEEEEEEEEEEEEEEEEE
EEEEEEDEEEEEEEEEKEEEEEGEEEEEEEEKEEEEEEKEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEAVGGRSFVLGPHVRRRWH
```

75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE
180 - 199:	EEEEEEEEEEEEEEEEEEEE
181 - 200:	EEEEEEEEEEEEEEEEEEEE
182 - 201:	EEEEEEEEEEEEEEEEEEEE
183 - 202:	EEEEEEEEEEEEEEEEEEEE
184 - 203:	EEEEEEEEEEEEEEEEEEEE
185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE
190 - 209:	EEEEEEEEEEEEEEEEEEEE
191 - 210:	EEEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEEE
225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE
287 - 306:	EEEEEEEEEEEEEEEEEEEE
288 - 307:	EEEEEEEEEEEEEEEEEEEE
289 - 308:	EEEEEEEEEEEEEEEEEEEE
290 - 309:	EEEEEEEEEEEEEEEEEEEE
291 - 310:	EEEEEEEEEEEEEEEEEEEE
292 - 311:	EEEEEEEEEEEEEEEEEEEE
293 - 312:	EEEEEEEEEEEEEEEEEEEE
294 - 313:	EEEEEEEEEEEEEEEEEEEE

295 - 314:	EEEEEEEEEEEEEEEEEEEE
296 - 315:	EEEEEEEEEEEEEEEEEEEE
297 - 316:	EEEEEEEEEEEEEEEEEEEE
298 - 317:	EEEEEEEEEEEEEEEEEEEE
299 - 318:	EEEEEEEEEEEEEEEEEEEE
300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE
306 - 325:	EEEEEEEEEEEEEEEEEEEE
307 - 326:	EEEEEEEEEEEEEEEEEEEE
308 - 327:	EEEEEEEEEEEEEEEEEEEE
309 - 328:	EEEEEEEEEEEEEEEEEEEE
310 - 329:	EEEEEEEEEEEEEEEEEEEE

A0A388M7Z5 **A0A388M7Z5_CHABU** (2225 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MAAVTLERGRDLQMESIAAMAGAVDDEEEEEEEEEEEEEGEEEEEEEEEEEEAEEEEEEEEEEDEEEEEEEEEEEEEEEE
EEEEEEEEEEEAEDYHRRFSSFSSSVSCPPSSSSSSSSSSTSTSFSSSSCLSSSSSSSPSSSSSPSSSSSSLSTGSDFL
MPLTSITTSPPSSSSSSSFCLSLSSSSPSSLSSSPSALTSQGCLSSCSSSSPCSCPSSESDPSSCPHSRISLPPSPPSPS
SSPSPSSSSSSFSSSSSTRSSSYSSASSSSSSPSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSAQALAKASVGSSHADDVGSE
GGDCLWSLLKNCPTCAICLDPLEKGKGRAIYTAGCGHVFHFDCLSCAVKFGTHVCPYCRARWDKVPLQLQVIRMEGSGPP
NIVFHLFFNQDTPPQLAPDQLVPGSTPGEYFYYQPLDTHSLIENPLFEQSQVIDPGEAEMNVESDQHLHGRGHQNRRHHQ
QEEEDEEEDDDDYYEEDNMGAMQGQGRADRHVAESPMYSHDAAAVAAIELQQQLSVSTMNEGIFLGGVEGEGGGDDEIRA
CQPVTLSLKPAVHAVACNDPPEKFRVLITVGASLPCPSSSHHRNSSACAATCDAPRLPVDLLICLHLGRSRSQRIFGAVK
RALMMVVHQMGPQDRLSLVGSSNAGQPRTIQPFIYMSEQSVHSVMEVIDSLEIHGTTEIMRLVKKGVESMRTRDNANPVS
AMVVISDGAGASVLSQRAHGEELRCLLDREELNLRVSDSTPVYAIGLGQNQDHFLLHMLAERTGGVYASPLDTRHVGEVL
QALVKGILQVVVYNAWLKMQLHIGHRIMEIHAGNSRHEIALDGWHGSVYLGSLSRGEKKHVLLELRLPRVPYSQNDPEST
VAHVACEYRDGILPGVQRMAPSQALSIRRLLQVTPDEARREREVEEHVVCMKVAVMLPKVAKRGRERDPTSVQRMLQEFR
RKVGEEHLAGGGCVSQSLASLLQDLDRCIDFFATRERFDSLGYPYALSCSSALLAGKPMVVNGPLLEVQHRHQQDPDDHD
PYHHHPSTLPGRAGGGGGDGEGGVGDGRVHEGFVGSRHFGVDDPADLHAEIDTEVVPSMEEEPAMQVNAMLVDIPEHGQR
GIVGGQLPFWSYPGWGEESPAAYMLPFPDFIIFPDNSPPMGDVPEYVRQQDVRPLADALEDEDDHNHGNDSEGDEGDEDV
GVDEETDDVEGGGSGGIGEGRDGDDGERNEEGGNSGEGGHGGHDDMGDEEEDDVEERLGDALRPGLVILEQLDSEEEEGD
RIGRVSPETHMCCDQNLEDMPSLGTLREDGEDGEDGEDGEDAHHEVEIGPEDAGQLDLEGEVDLRIAFDGSEHEDSGICR
NEHLADEDSDSAPCTDLPTMSSSDANEQLLRQPCPMSAQLHAQEPFGMAGISRPEEDGLSALQKLDQELREETQLVQAGL
SELGLGCDESQEFQEDIRFEVVEAGTMQVQQQIPLHEDADEDERDEEVEEEEQGGGEEEDEEEEDEEEEVEDDDEEEEEE
HCSGDRKLLSSCECQVEIPFEEDASSSSSSSSSNRSQHPLQHDEDLNVGGGTAQEADTFDIFGFGKAITEHEGCALLHGD
EEACAVVLHSDQGIQLSEEAEEADDAEDPDQLAGYQWPVTAGDGTTRQRVLLSEDEDVLPQWPVTGGDGASQQHLVSEEE
EDVAPFVEEDDSESEVVPSSSVAFTCASEPPPLTTIPALSDSFCKNAWDEIGNSSRRESSIPHVADPPFCMLEKNQPAAE
EGGEPPIPAPTFSDARVRYPGPVMPSQEPQDVADDLREEHSSSSTTVWAFQVPISSSSWLSHSSSAATPMSPTRRTNLSG
RQTTSLTTLFPGLFPSSANRHTPHTGLPPPWQSTTSSLCQAGPLAPPISGGQSSAWMATQPQLVTPNTLASWSNPASQSL
SASSSSFRPQMPAVSSPLAGSIPSSGSQWPPPSFTTPQINYYSSPSGSHVSPIGRLLSHPPPHLPILPPLPSPPSSSQPP
HLLPPPPPSPASVLASPSDSSLQLHLPSVMPHNNLPPALPQLSSSLLTPISSPLPPTPPSLSFAAPFCMGPSSDAQSTLL
ASSGCLPPSSSMLAPQFLPSTGTPPNILRRSTKPGAVPGGLPPTPAGSRLAAGERDDGCTPSPMGSAGCNTNSTVRMGTG
KFTCQQAITNSYSQNLANNAAAAIAAPGRKWAPVEGLPLMERDLSSSEEGGDERIRETEEISSSA
```

65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE

A0A388M872 **A0A388M872_CHABU** (1245 aa)
CCT domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MCIRDSRASCVTFATWRHCDNEIHNCNALAQRHHRVPVCLPSSSTPISSQSPSSAAPGAKVERAVPAPAPTATATMKTKG
KGGGGATTLSSIKVEAPTAGGSAGGGSHHRFVPRGAPVYPCLPSRLGPGPPPCEDDGGGGTGGGGGGGGGRGGGGGGGA
GGVAVVPSLAASVRTFGHHVPNKVFPKLERSSSGASSGGDNWAGSAVVPSSSCAARAEWAAKMCGGGSSAACAADATAAA
VCGAGAAAATAAASSAASTHAASANLATSVSSARRVNYVSAERPHCGMGIMYGGTAIGVPVMGLPRSQSLSGRSTTTTTT
TTHPSPVMIGSSCAPSAMVASAPNLVSGDAQRRPAGGAGMGNQDLIVVNLRASGRSSQAAAPERDQEEEEEEEENDDDDD
NNDADTEEDEGQNTASERRGRRTSAALREAAAAAAAAAGGGGGGGGEEEKAGEEDVLVGLRSGCEHSVLLSPLASCCTED
VAMANYTCSSTYPPQANPQRRAGEDGNGGAGNGENQQGQGGGGGGGGGGHHQGDLHRRRPSSCSAVLDCVDMEKALAMAA
ISRACDGEDDGEHGSTADFFNVEGEPGMRKIDSDIDLIGHVGGIVRLCSLDIDDEGMMQVPDGHVFAMELEAELSDCLRS
SEVGTTTTTTTTTATTTTNASLEAASSFVLDHRAAAIADSSPAMAAAAGRRSSSSIDFCQAAEAGTSPTTEQSVASFLTS
IAVVQVKEEPAEQDEATMAMEATLLSSTQMEQGDEERVVADRGWGAEEEAEEENDDDEDDDDDDDDEEDEDEEEEEEEEE
EEEEEEEEEEEEEGEQLAPTVSSSKPASTNASVGLQHYRYHHRPSPPPYLARAPTRDASIGTVPSRHHIRSHHRHNHLHHH
HSHNQHPYRHQHAQQQQKEPEKYPYRRTHGSAAQRGGGRQRNDEEAGHQQQSVPAHELNNARLVSAGSVPTLPRSRDRAN
```

```
SQHHHSRHHHHHLDSNHHHVPQLPAHYHHVPQLPAHHHHVPQLPAHHHHHSSTKGHHLRANVSNSQDQVCSVPVGEAWAA
AAAAGAAAGAAAGRGGGRAEEEAVVPEPLCDTGVTVFDSNQQNCNSTSMVTDLTCKEERSEEEEEPPRKQRKSSSFLRLD
YADVLSAWSGGNFWSDGKRPQTVPDADQMDFLVNLDFGLVPDLHLGSADEGGGTQAPEYGMVPNVMPPGDEGNSLAREAR
VLRYREKRRTRHFSKKIRYEVRKLNAERRPRIKGRFVKRSDCADF
```

792 - 811:	EEEEEEEEEEEEEEEEEEEE
793 - 812:	EEEEEEEEEEEEEEEEEEEE

A0A388M9J4 **A0A388M9J4_CHABU** (191 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MGKHEEEDEEEREDEQVVDEEEDKGGRQEEEEAMVEKDDEEDKDEEEEEDVEEEEKAMEEEQGEDGDEDDDEDEDEEEGE
RRGRRGGRREERRHGGRLEEEDEEEEEEEEEEEDEEEDVEDGVEVEEVEEEEAMEEEKDEDEEEEEEEAMEEEVDDDEEEGDK
KGEEEEEEEEEEEEEEEEEEEEEEMVSAYLL
```

163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE

A0A388MAS9 **A0A388MAS9_CHABU** (819 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MTQVNTKLVYILDETCWVGGGWSPSKGLLSFRQSSLDITVEEGGLISTWWPGRNGTGSRLVNTSCEDGARASSRDFVTGA
AIFGKQLFLSGYHGATPAGSWLTALSAETGNRSSLPLMIDYAAAIAFDPSLKNLYVASGAVPPFTIYSSPVTFDETGLPS
NKALALSQVFAANYSVQSIYFGPYSFDPQGACLYFLDRVGGAVWALDLVSKSVKSVAGGPITAADGVSNALNVSFGGLYD
LAVTDDGNNIFVSENDTGMVKRIQLESPCGLARRVSNVAEYRPRDGSEGYGLATGKYDEECILVIGTHDYQALRLAIDRA
ALQRETPLDPPPPSSSSSSSSSTSSSSYSSSSSSSSSSPHAPPSSSPSTCECRDRTGIPLVVGIPVGGVFAVVAAFAGAA
AAVMLIRKRERQSGNGIKIHSIEEFRWATLVKATKSWSYRIGEGGFGVVYLGELEREQGEEQERGVGRTGRGERQSRRFA
YQNLLNAPENVTVEQIAVKVMNAQGVNIDTQQSRDERNILKQFRTEPQEERKGQEQRDCKMTQEQQRREEKQRQESNWER
RQKEEEEEEGEEGEEAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKDEEKDEEEDEEEEEEEEEEDKEEEEEKDKEE
EEEEEEEEEEKNREDKEAKEEEEEEEEKDEEEEEEEKDEEEEEEEEEDGEEEEEEDEEKDEEEEEEEAGFVALALGDAHW
QRGSCPLPRGGIRTLVVVEQENLRACTLDRDFDLTTMVDPAIRRDITRPAFMGLTRQMLCLVAECVSTDPRMRPTITNAA
ARMETIMQGAGLTPNASGN
```

577 - 596:	EEEEEEEEEEEEEEEEEEEE
578 - 597:	EEEEEEEEEEEEEEEEEEEE
579 - 598:	EEEEEEEEEEEEEEEEEEEE
580 - 599:	EEEEEEEEEEEEEEEEEEEE
581 - 600:	EEEEEEEEEEEEEEEEEEEE
582 - 601:	EEEEEEEEEEEEEEEEEEEE
583 - 602:	EEEEEEEEEEEEEEEEEEEE
584 - 603:	EEEEEEEEEEEEEEEEEEEE
585 - 604:	EEEEEEEEEEEEEEEEEEEE
586 - 605:	EEEEEEEEEEEEEEEEEEEE
587 - 606:	EEEEEEEEEEEEEEEEEEEE
588 - 607:	EEEEEEEEEEEEEEEEEEEE
589 - 608:	EEEEEEEEEEEEEEEEEEEE

A0A388MAW6 **A0A388MAW6_CHABU** (260 aa)
BTB domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MWSLEPQVLEMLNKDCNRMSHPGGTPTKTRRLNDRRAVPCPSSWSSVEEEEEEEEEEEEEEEEEEEEKEEEEEEEEEEEE
EEDANLDDQLLSSVRTAPSHRESLNVKFVCADGRKVRANRALLASGSVVFSRLLDGDMNKSSMETIHLPGTTASGLQVVI
SFLHGHQFRWKDGTCWDEMVEAYCLAEQYQIDRMCQRISLRVSKLVSAHEFGRLLDVAIPRHAEELLEAAVKAMNKVLVF
NSTSFHGWSKDSIVYCLENV
```

48 - 67:	EEEEEEEEEEEEEEEEEEEE

A0A388MAZ4 **A0A388MAZ4_CHABU** (264 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MRKAARGRRKQESREPHASKAERGPTGAKRQRMQKGNTARKKWTCARYQHIGGGVGGIEGSVDRRARIQGEGEGEEEEEG
QRREKKKKKKKKKKKKKKNTKKDDEEEEEDEDEDEDEDEDDGDEDEDEDEEDEDEYEDDGDEDEDEDEDEDEDEDEDEDD
DDDNDDEDEDEDEDQDQDEDEDEDDDDDDGDDEDDDKDGEDDDDDDGEEEEEEEEEEEEDNDDDDDDDDEEEEEEEEEE
EEEEEEEEEEEEEEEEEEHASEDL
```

231 - 250:	EEEEEEEEEEEEEEEEEEEE

232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE
239 - 258:	EEEEEEEEEEEEEEEEEEEE

A0A388MBY1 **A0A388MBY1_CHABU** (554 aa)
Ubiquitin thioesterase OTU1 (EC 3.4.19.12). *Chara braunii (Braun's stonewort)*

```
MDGVVVRRVIDSDNSCLFNAVGYVMEHNRMKASELRQVIAAVVMSSPDVYNDAFLGKPNKEYSDWICGPDHWGGAIELAI
LSDYYRREIAAYDIQTRRCDVYGQGRNFPERVMVIYDGLHYDALAMAPFEGAPEEVDQTIFNVEKDGSIGYASHLAQKLV
DEAHRARRLFSALTWLGLGSTLGRIWLGFGSNMGRIWLGFGLNMRGEFGWDLARTCAANLAGIWLEHGSNLAGIWLELGS
DLAGIWLELGSDLAGIWLGFGSDLAGIWVGFGWDLGRTWVGFGWDLGRTWIGFGWDLGRTWVGFGYEPQYNNKQWRELLR
KRREERKVEHKLGRTRHSGLHAGKDYERSPKVNKQECTCTQKKKKKKKKKKKKKKRTRKKKKEKHKRRRKKKKKDKEEEE
EEEEEEGEEKEEKEEEEEEEEGEEEEEEEEEEEEEEEEEEEEEEGEAQEEEEEEERKRRRRGGGGRRRRGGGGGGGGRR
RRRRRRRRRRGRRRRRSTRGVRRRRKKKKKKRRRKKKERRRRRRRRRKKEKKKKKKKKKKKKKKRREEEEEL
```

423 - 442:	EEEEEEEEEEEEEEEEEEEE
424 - 443:	EEEEEEEEEEEEEEEEEEEE
425 - 444:	EEEEEEEEEEEEEEEEEEEE
426 - 445:	EEEEEEEEEEEEEEEEEEEE

A0A388MC94 **A0A388MC94_CHABU** (260 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MGISRQEEEEEEEEKEEEAEEEEEEEEEEEENHGHQQTRRRRGGGGGGGGSGGRGGGGGGGRGRGGRGGGGEGEGEGFNS
SSGHRYCTQLLRTGEYRFKEEEEEEEEEEEKEEDEEEEEEEEEEEEEEKEEDEEVEEEEEGEEEDNEEEEEDDEEEEEEE
GKEEEDEEEEKDEEEEEEDEDEEEEEEDEEEEDEGEEEEEEEEEEEEEEEEEEEEEEEEEAEEDDEEEEEEAEEEEAEEEE
EKTMKRKEGNDDEEEGRQRG
```

196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE

A0A388MCY3 **A0A388MCY3_CHABU** (2367 aa)
P/Homo B domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MCGVQQSRSDAAPRSFLSSGHDNTGAVPVAGVFASDPVHRTEERRSPIEAVQPTSCTPVSTNRARDVLSPSNDSEAGMSF
SPWPPRTRSSTPREGKPRWVRCRLDQQNRLGEIAKAMGKKLSTRTRGSKDKKKNHCSYEDVFDELLEWSSVHIDELISKY
DPGEQSYAHGGSCGQGSDATTTPKSRGGRPRSDVLKWRDGSRQWLQHVERVTKKSFDKVIARLRSSNDPVVVLVDGRYDS
SRDAQHCTVTAVDLKSGMIVGTETMLWGSESSWKLKTQCVEKLLHRLKDEKNLIIAEVVHDDCGAVDVILRRMNIDSQKC
MWHKAKTLVKRLREAVRGTKTVKPAVVRVCEHVREVKCFTKKELELWLEMKCVRVAGVSTKKNNELVEIVWGVFFPDEAG
KALPDDVVEIDALQTLHCDAAEEAKEWLYDACRLRERARDDDDDVLATHVQHLANHWAGDHSRCDKELSNLYKAGGDPDR
ESLYEAGGRVHLAIARCLEQFASNTKMTYYTRARMTFNDKCFHSVINKYCTKRLNFPNSYEARCDESPVPHVLSRTLTPY
LQWLACLEEQGGNNNPPSQEEYLNPRRIIDISFFQPPTISEDEVLALEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EGEEEEEEEEEEEEETPEEGNDVAANGVVANGLVANGLPADDVAEDDLAADDIAANGLAANGLAANGTARHFLEYESRGRD
FGLSFPQYQTALGLVHVDEDALPRGLEIPTEICCCPTSILMAMSGPLDSENGTSAAVPAAAMDAGVVNDNAGLTDITGLS
SDAPQPPAATSGKWNRGSGTMAVEPWQWNHSSGTMAVETLRGSGTTVKEPWMWKPFAAVEPWQWNPSRQWNPRSKGIAFR
GGGGLLQPGSRAMDSNRRTVGGEGAFGGGRDMQDGHLHARPLSCGPATTSMPLFNGGRQCASPAGRACFRATAPMQSSAF
HGAYGGQFSEHMHVGPVHGGPPAGELHQLDSYGVGDHVVHRHQPSDVYGGMSCAQGPTGGAGFGMPSLSAQSMGMGGRPW
SPQCGQNPGRLFGARVSPSPAVGDDGESTWTRPDPRPMSPDTRMDPPHDDGAGGSEAGDDDGVAEQGSVVPIRYQNDVLN
SGGAGEAGNGRPANARPPALKKQNVPWTLDEWIKLAMLMGEDDALMADAHGQHRFKQRKERYVWVNDRMKEAGFKHRSAE
DCRKKWSNMLQTAKLIVEKCEASGQPSYWDLSLEERKEKNLPLSFEKALWDAMQWQLDRPSMKCDKTLASENLMGGGGGS
ASMSGGSEERCADEPDSAAKIRQTEKGKARREEASTIATPLSRAMEDSTRSYCDGLDKAASSLAKATANAGSAIASRIGD
VAEAMRGGNSVLELLVGGVMVYEMRHERDGLWHRHFDFADGVTRRFRFYEVDVDGIPTMKMEVGLGFFGNLLVHVFIHIT
KGKSSCSTSPPWLTFLRSAWIRCRFGVASWNPHWLAGRICMGRYDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
DDDDDDDDDDEDDDCDDDDCHEDTVDGDISDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
DDEDEDEDDDVVHMGHNRAPILHPRQQQSRRMVQIFFLETSSKAHTTSQVSIMILLVDFNDQEAEIQKPLFEELFFSRGV
LPRGSVAEYYDVASLGKVSLDGEVHGWFRMPESYASYTNGAAGLGAYPANSQKLVEDAVKVALESGVPFGPELSFANAGF
VDGLVVIHAGEAAELQYDRAEQVQNVWSHSWIISSPLPATDLLSVYKYAMVSEYSTVGICAHEVGHLVFGWEDFYDAGGV
QGGQYWDGSRAWDLMGSGCWNGRNADCPALPAVLHRLEQNWIEVEEVSSTVRKLVIPPHSPTFSKTVKVVSPVYGPNQFL
LLETRSMKKGTIYDSALNGEGLLVWKVDLDQGQTSSRTLQFSPDTPRMRLVEADGRGSLLALGNYNSSTSGDPFPGSTRR
TTLDDNLGLVSTSFPGGAAAGVELQNISYNGRNGNVTLDVVFLEKGMMLQQATGGDSVDATTDATTPSQDEAVKRLGNRG
AGEVEDDSIPTQLHVAMQENSAEVQISNKNPAGALARVRIGMVGLVAAVEIEAMISHRRSKDLHMQLVSPGGKPVRIYHH
GHAAGGSIASTSVSSDQFKLSVSDPQVFKPLIGVQASGTWGLRVCDTRGGWGDGRLKMWRIVLTLVDSIRSVSETVIAKA
IILEGVGITSSIDIKQKGHVKEVGIEVGISHTVATHIHAELMAPSGAIVLLSGKLVNGKSGSMLLGADSANDLQLAPMIG
TSICGPWTLRLTDILGEGTSTLDAWNLNIQYVPLLPTREAVGLQTAG
```

608 - 627:	EEEEEEEEEEEEEEEEEEEE

609 - 628:	EEEEEEEEEEEEEEEEEEEE
610 - 629:	EEEEEEEEEEEEEEEEEEEE
611 - 630:	EEEEEEEEEEEEEEEEEEEE
612 - 631:	EEEEEEEEEEEEEEEEEEEE
613 - 632:	EEEEEEEEEEEEEEEEEEEE
614 - 633:	EEEEEEEEEEEEEEEEEEEE
615 - 634:	EEEEEEEEEEEEEEEEEEEE
616 - 635:	EEEEEEEEEEEEEEEEEEEE
617 - 636:	EEEEEEEEEEEEEEEEEEEE
618 - 637:	EEEEEEEEEEEEEEEEEEEE
619 - 638:	EEEEEEEEEEEEEEEEEEEE
620 - 639:	EEEEEEEEEEEEEEEEEEEE
621 - 640:	EEEEEEEEEEEEEEEEEEEE
622 - 641:	EEEEEEEEEEEEEEEEEEEE

A0A388MCY6 **A0A388MCY6_CHABU** (455 aa)
Uncharacterized protein (Fragment). *Chara braunii (Braun's stonewort)*

```
MRRKTCEEKEEEEGKEEDKEEKEEGEEEDKEERGGRRKGGRGGGGGGGGRLGKRRGGRRGSEGGGGRLGKRRGRGGGRGG
GGGRREEEEEAEEEEEEEEEEEEKEEEEEEEEEEKEEEEEEEEEQEQEEEEEGEEKEEKRERRRRRRRRRRGRRGGGGG
GGGGGGGGGGGGGRGRGGEEEEEEAAEEEDEDEEEEEEEEEENEDEEEEEEEEQEEEEEQEQEEEEEEEAEEEEEEEEE
EEEDEEDEEEEEEEKEEEEKEEEEEEEKEEEEDEEEEEQEEEEQEEEEEEEEEEERGGGRGRTGGRRERRGRRGRRRGRTG
RTGGGRGRRRGGRRRRGRKREQEEEEEEEKKAGGGGAKGGEEKKKDKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEL
EAAEAEEEAEEEEEEEEDEEKKEEEEAEAEEEEEEEEEEEEEEEEEEEAEAECGIL
```

368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE
379 - 398:	EEEEEEEEEEEEEEEEEEEE
380 - 399:	EEEEEEEEEEEEEEEEEEEE

A0A388MD90 **A0A388MD90_CHABU** (2516 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MQTRSKWEREVKEVAVENEGINGGGRLGRGCKVERGSGVEMSAGVRCSGRGGFRRESVRYLDADDSTADSDESEDSQVNT
MKLELTDIDGESNCNGYEDWENGSDEVAMTLTLLDHIPLDGENANGMLSELNFPCWASEMGPTIGEGNSKKDGCSHIVSP
KGYTKCLGGVLGATTGSSKRMGKVSTVLQDLPAQPDKNSRALPSHLAEVKALYESCTNLQTVESKTTKRSQRLSEEGKRD
NILSCQVAASLDGFPHNWHHERLSSGRNGRSRHTPQETENELALIARDPPLLNTSLLSSAGARRARSKRTSISGSGNKQE
DEEEGREKSAPEKNMERSVVGNESTAGDANKGAVVVKGSQGGSVGGDGTEQHYISNSKVLGQECSLDRDWDSWVGKGDES
DRLYCGGLGLSPRAISGGQEVEPQEEKKQAGKMEDRKGAKEAETGIATRGFTCLSSSEVEGNQSLLGRDDYGGAGGGRLS
TSPHEAQAQYVIDDAVIPCELERHGSGSVHEEEEEGISVEQSLILWRTTDPIIEPAGTGLPFSSSAPHGMLINPLRPCGD
GTVHDGTEEHYPHHNGRRVNPYKKGVDECSGERSMSGGQRACWDEQPSLKAAKANNKAEDEIGVRSTGDRLRTAESRHVQ
RCNSGSVCGEVPRISTVDTSGKFLRTVRSHGLYQLTCLQEDGRRSSQESQLTANAAVSKSLSASGLDSLGAADPMVQSLI
CEDIDEGSRYLFCSTQWKPCRSSIIPPFVNGKEEGTTATADLSQHAARPSMEVQPDGSVCAKRSNNGCYSSDDAEAMDLS
APGNAEISDGEHRKQIHRRHERRDTPGCSWKGGNQHGVFECRDSLVQAACPAAAAAAVSDQTINGDDGGGGSDDDDGYAH
DDGNEHKAGSYLHSEGKRGGGARGRMQTECRTREDAMKADCGSDLTTHNCKSDGRCKKEESVESAAKIHSTGRVEDNFEK
SKSLKEVKEMTEERKRKGVEQEEEEKGCKEKEEQEKADGKEECKEKKEDAKEATDKKSKREGDHKEEEEEEKREKEEEKG
ARESEEEGDQETRRIRRWPRVRIIQRNGEQVGGGTSPVCKEKLGCSESTYDGPRDEPSPKKEQRMGQRIDQVAAPSFGRI
GPSAGNLSFEGENETELGSLLHEELRHQEHRSAKGSSREMEEGWASTRHELSSGHGQFHDAARRDSPRRLLACSITDTKT
ETRTRDAVETPKSFRSIASRVSWESRDWRSSAAASDVVSALGAKRSPNGRLSEQLHAAHRTHNKHNEPHRIAVTQRRDQH
PNPHSTKGSVIEPVPSNRRIPNSRHLQDVTNKIVKADKTAKTDKITKTNKIVKTDNKVKTVNGGKETKKQKSGAEFRQVA
NRTTAKGGTGTPGSKSGPGLKVGGVRNVRSHARLSDDEQVTIGGPDTVRQSTTVTLREKEHQSAHTHMTGAMPPEQRLSV
SSELVVACPKDKTLANGISMPFIDGTSGVPRGPRSSPGSGPTAGQTLIDLLPIFDPQSTSTSIESQAQTCSGAQVASRSQ
FEMEQLSTRTLGYRSQANMEAARGMTGFGVRDEASTLSETPASTLLIDHIGPFSPQSSSGQGYGPGLVPASDESCNVVVE
DENTGSNSIPKPSSSVLLPSAAVGSEQLKDILEYLSKMTEIQLPKSHPWSPHLPASVNDFAAKSSQSEKPKGSTVDSLQI
ANPNGATVHPPRVQLQSAAHRHPQTAENQGHKDDGTTATNGCPRPGGHFNDQTKKEGSETGISNLHSQIASCNSNKRGVD
DSSNMAPATPFQLHQLPVDLATGGTAIVAIHDGCRSESSGCLLPVKGVAYGKFATSIHIPSSIETENVDSSVSRSDSMSV
LMGPDASILSLRGGGSNQSSEIQVGTDRSESCSSWTSRGGGGGGMYCLTQTADLDRSCSLAISVYDGVKARMKSLKDELL
KQEGYIQELKDERERLLRAHERDMMREREQHSLQMQNQKHENESTVQHHLALMDRLLRDKEELTAKCGQLTHDIRMAEIK
DDDDDDNDNDEEDDDDGDDNNNDDDDDDDDGDDDDDDDEEEEEEEEEEEEEEEEEEEGVVPPADHIVMAIAPQFIIFA
DVQGDDCCAPVLHFVQQKESWMIAEKAKREAWATNKAKELKEVTIRGLEPHIQRLMQRHRTEIERCEAKHETQLRIKLDE
LRQCCEKEKKEIESQLLKDHAEAVQRLESVNQSRLSEMEKRVKNQVTVQHMRVIKDLTAQIESMEASHRQDRKKLQMDLQ
ERMRESAQREEEMRAKVAATIQEISQQKEAEFEMRKGMWEEEKSKWKHSFEESMAVKLQQMENEMKERATAERDEEIDVI
```

```
ITRMEDENAEAKSQMLKEMQEATAELQKSHRLRMKEMEGEIAKLTSKYQEALEGKVNALQAKSAAEDHARDLKEELFAKD
EKVAELEKELDAERAKLRGLQASVQEEQRVQEIEKVQQIECLQMRLQACSKEIEQMKLQKADELAEVERRVKQVISQKDD
IINNLRQRMDATSQQLAFTEKVLYQQKKEILEHPNL
```

2039 - 2058:	EEEEEEEEEEEEEEEEEEEE
2040 - 2059:	EEEEEEEEEEEEEEEEEEEE

A0A388MDC9 **A0A388MDC9_CHABU** (550 aa)
Iso_dh domain-containing protein. *Chara braunii (Braun's stonewort)*

```
MALVARAAQCHAAVGSAAGGGIVAGSLSSEHSTAASLAAPRCRHVSAPREGPRLVGQCGKASHHLGLCDDSDTAISKTAV
VRPSSRRRDGLNGRICAVMVGTKATDSGVRLIRIGTRGRQIVQLRGHGAGQGLDFASSSQFGSGSSAMWYPADAAGRPWR
AAASSLTCKAAVEMQTRPKPTKIMDSYLITCLPGDGQGPAVMHEAKKVLRSLQDISGVTFKFQDGLIGNAAQLAVGNPLP
TETIELCKSCDAVLIGGLASTTSINGGTPLRSKVLMKLRADMGLYWQLSPAAAFPQMENDYPLSPSRVRGTDIMIVRELS
GGIYTGQQGRGELPNGDVRAFGTAEYTGKQVERIARSAFDIARQRSRRLTSVDLANYLEVSVLWREIVTKLAKEEYADVE
VNHELADYFATRLVQNPTRYDTVVAANLIGDVLVEVARGITGGVRFAPSAEFGDPGTPALFGFPGELGSRFTGTVNPFGL
IRSVSMMLRYQFGLVLKVTDITGKGEEEAEEEEEEEEEEEEEEEEEEEEKVFKYFQSFKVPGNPVEVGE
```

510 - 529:	EEEEEEEEEEEEEEEEEEEE
511 - 530:	EEEEEEEEEEEEEEEEEEEE

A0A388MDH0 **A0A388MDH0_CHABU** (129 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MIVMLVKEEEEEEADEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEKEEEKKKKLKKKKEGEEESKRVEKFNEEEEEEEEE
EEEEEEEEEGGGGGGGGGGGGEEEEEEGEKGKEGEGEEEEGGVYIFQL
```

16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE

A0A388MDI9 **A0A388MDI9_CHABU** (1950 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MASARNGARGGWRDLPQRTRRSGSPLSKGISKIFAAGRNGPHVDVRGPAVAAAGQTGQANHRGAPFTEVTREKGEGKESQ
KEERRRTGDTRMMHSEPGDSKHRSTSSSALASVQLATQTAARFTTSGAMTTTRIPAENGPQASPAAGGAAVGAGKLPRKS
LEGWTHDHDDNASCPEGEILERRRSGSMSQVPTPGLRVGRDQSKEDGKQRRPAEVLEPPSQKGSRSKGDLNAKVEHGSQL
VKNHAENGIAVPGWSRRGEIGVGKEGQWDASSGTHHLISARGGGRGVGGAGGGGERGGGGGAGAIAGGGARSLASTRIID
NRITSSSGSIWKEDKMDLKRTSRPWGPRGSILANPPNSSADRILTTSNSNSSTVSYSSAHSHSAVHRNRTQSNSNTNSNS
NSNSNSNSSGNAHGAGNILSLSISKSANSLSMSKSANQIHSSISSKRLFNSTAGFRTPKEGRRNERRTNNMSSSEVKKSP
RQPFTYSSRLFAVDPRGALNSRTGDALGLPTKGIAAPVNSLLRQRQLQRRKEGQYAFTNRLKAEPYAAGGSSNSATEDNR
LGENGVGPRKAIGVDHSHQPTVRFPSSSQGDDVPNGLHADHHDRWRQHQKQQPSLTLCRHEEPSQVKVGRQGLEEDKGKE
RSRSAEEGKASAVGHGHERSDLGYRERKAHPLRTQIDIYRTTAKNRHNQDEDDDNGYDNDDSDNDDDDDGDDGGDEEEDE
EEEEEEYEEVEEEEEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVEASEVKKCQVEKDEQESQDSEDGKN
GDCEDSEDGKNEDYVKVGNSIPEVVINASSGREKNHHEVGSVESPQTFSRASTTECTLAVESSPSDGRLLQVNDAFEKRL
DGDSYAKVCQSKKDEELPCHGKNRETPAAVRADAGLPTSGPCVCRSAAHCCDPCVCESGDCQAPSTAVAATACLGISGKT
ATTAGVEAFLQAEPRRALPSNCSLYSSLWLSKMSTTCCEPSIGPQKEVTVALAEVMQRKSNGQDVGLMLEERMTDLQKER
VRLAQKMQGLKRVRQVLGEKVESLGKTLREALLRRRRREQARTQVHSGVALSLETKNLVPTGAMSGETCRTREGLRRRER
ELLRTHARSATTELEDKVKVAALRTTQTLDSSTSPHSQRSYCGGGGEHGKGEVENGGIGMDSREEKDTCSSSLAHSVRDL
GDSNNNHADKAAASERCVNECSSDDAICREESEYWASTVTELEVETNDASDTHLPEGSAGSRVRKRAEEHAGNLTESAAV
NSVPSSCLRHEDGDGDGKARSYHLLPYDKKMVIVEETEVLECECGALQEWPNRGDGITRAEGEQETRLVTSAATHFKEDR
VIVGRIASWESSIHEKGYQKDGRKRLKREYPPACPSVTTRTSAGPDSEEGDGNTVAQKKERLDSGIHERRDEEDGVKTLK
RNKGGENAPTFPVASGATDLAGVEIASVKMTGMLESGIHERDGEEDGMVTSEVETAPTCPVASAAASFEGDCDVAARKTR
RSENHIHEGGGEEGMRGGGEENVPTQAEITTDLEDGNVVVDGTGITQSERCRAQIPQRSRDDGVSRTETEFALSCIEQMG
SGDEQPSRLLEAEPGGCGEASDRVGVADDDIGEQTGTWDSDGSAEIDGKVDPSEVGTVGHERGGLDGGLVGEGTEGSETS
TSESGGLGMGIREMDSNVSMAIINFLAAIKTELLTRKESLMEDVQNLRQVLASMSLYLATGAQGGIAKQEVVNGGDKSDF
ASQKEFLRCEMKLRDPDVVKLHRCPVGSNRCPEDWFVCSQEATGVLGITAWVRDCDRGRATARDHERDQERGRFGNKTRK
DAALATVDSTSGSLPESGRTTSPVSILETLRLVTSRSENKTSVNADNVPQLRHDPEGVVQLHQCSRCLSLEHKLAEAGSI
AQSLVKKLEAFDFSPIMLSIIHLCTAGKDM
```

743 - 762:	EEEEEEEEEEEEEEEEEEEE
744 - 763:	EEEEEEEEEEEEEEEEEEEE
745 - 764:	EEEEEEEEEEEEEEEEEEEE
746 - 765:	EEEEEEEEEEEEEEEEEEEE
747 - 766:	EEEEEEEEEEEEEEEEEEEE
748 - 767:	EEEEEEEEEEEEEEEEEEEE

749 - 768:	EEEEEEEEEEEEEEEEEEEE
750 - 769:	EEEEEEEEEEEEEEEEEEEE
751 - 770:	EEEEEEEEEEEEEEEEEEEE
752 - 771:	EEEEEEEEEEEEEEEEEEEE
753 - 772:	EEEEEEEEEEEEEEEEEEEE
754 - 773:	EEEEEEEEEEEEEEEEEEEE
755 - 774:	EEEEEEEEEEEEEEEEEEEE

A0A388ME27 **A0A388ME27_CHABU** (1574 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MSAQVASVEHGYGAQVASVERSYGAQVASVDHGYGAEVASVEHGYGAQVGNVEHGYGTQIASEEHGYGAQVASVEHGYGA
QQQPDEEEEEEEEEEEEEEEEEEEEEEEEEEQEEEEEEEEDKEEGEGEGEEEEKEEEEEEEEGQRPYPRHLPGRHSSNHA
VGLHNNNNNNNNNNNHYNNQNHNRLGAIAVLHIVDLHNNNKNNNSNNQTKKKRRKKKRKQKRKQKRKQKRRQKRKKKRKKK
REQEEGRRRGKKKREEEEEEEEEEEDEDEEEEEEEEEGRRKGGRRRGGRRRGGRRRGKKKTRKKRRRKKRRKKRKKKKK
KKKKKKKKKKKKKKKRKKKRTKRRRKRGRKKRGRKQRGRKKRGWKKREEDEEEEEEECNSQNHNHLGAIAVLHAVDLHNN
NKNNNSNNQTKKNRRKKKRKQKRKQKRKQKRKKKTKKKKKRKKKRKKNRGEEDEEEEGRRRGKKKKEEEGRRRGKKKREE
EEEEEEEEEEEEEEEEGEEEEGEEEEEEEEEDEEEEEEEEEEEEEGEEEEGEEEEGRRRGKKKRRRKKKREEEEEEEEEG
REKKRKNKREKEEGRRRGKKKKEEQEGRRRGKKKREEEEEKEEEEVEEEEEEEEEEEEEEEEEEEEQQEEEEEEEEEEEEE
EEEKEGRRPYLPVHNNDNNNNNNNNNNNNSNNHNNNQNHNQMGAIAVLHALDLQNNNKNNNSNKQTKKTKKKRRKKKKKK
KNKKNKKKKKKKKRKKKEKKKKKKKKKKKKKKKKKKKKKKKKRGGGHTCVTYLGAIAVIHAVDLHNNNNNNNNNNNHYNN
QNHNHLGAIAVLHTVDLHNNNKNNNSNHQTKKKRRKKKRKKRRKQKRKHKRKQKRKKKRKKKKRKKKRKKKRGEEEVEE
EGRRRGKKKNEEEEGRRRGKKKKKRKRKERKRKRKRKKRKRKRKKKRKKKRKKKRGWKKRGRKKRERKKRDEVEEEEEE
EGRRRGGRRRGKGRGKEEEEEEEEGTRRGKKNEEEEGRRRRKKKREEEEEEEEEEEEEEEEEEEEEEEEEKEEEEGEEE
EEEEEEEEEEGDEEEGEEEEGRRREKKKRRKKKRRKKKRRKKKRRKKKRRKKKRRRKKRRKKRRRKKKKKKKEKRRR
KRRRKRGRKKRGGKKWGRKKTEEEEGRRRRGGRRGGNQKRRKKKRRKKKREEEEEDEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEDEEEEEEEEEDEEEEEEEEEEEEEEEEERYMTSNCYSVAGSNLRVVFNTVHSNNQTKKRRRKKKRKQKRKK
KRKKKRQKKRKKKKKRKKKKMRRSKRKKKRKKKRGEEEERRRGKKTREEEEEEEEEEEEEEEEEEKEEEEQEEEEEEET
VCVFGLPRPRPLPGRPPSRAAANLSPSLADAASLDWSNGAAAATTATLGRCWSLLGPDADERSRAPHCRPAQQQQEQQQQ
QPDEEEEEEEEEEEEEEEEEEEEEGEEEEGRRRGKKKREEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGRRRGKKKSEED
KEEEEEEEEEEEEEEDEEEEEEEEVDEEDEEEEEEEEEEEESYMTCHCYSVASIS
```

86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
1006 - 1025:	EEEEEEEEEEEEEEEEEEEE
1007 - 1026:	EEEEEEEEEEEEEEEEEEEE
1008 - 1027:	EEEEEEEEEEEEEEEEEEEE
1009 - 1028:	EEEEEEEEEEEEEEEEEEEE
1010 - 1029:	EEEEEEEEEEEEEEEEEEEE
1011 - 1030:	EEEEEEEEEEEEEEEEEEEE
1012 - 1031:	EEEEEEEEEEEEEEEEEEEE
1177 - 1196:	EEEEEEEEEEEEEEEEEEEE
1178 - 1197:	EEEEEEEEEEEEEEEEEEEE
1179 - 1198:	EEEEEEEEEEEEEEEEEEEE
1180 - 1199:	EEEEEEEEEEEEEEEEEEEE
1181 - 1200:	EEEEEEEEEEEEEEEEEEEE
1182 - 1201:	EEEEEEEEEEEEEEEEEEEE
1183 - 1202:	EEEEEEEEEEEEEEEEEEEE
1184 - 1203:	EEEEEEEEEEEEEEEEEEEE
1185 - 1204:	EEEEEEEEEEEEEEEEEEEE
1186 - 1205:	EEEEEEEEEEEEEEEEEEEE
1187 - 1206:	EEEEEEEEEEEEEEEEEEEE
1188 - 1207:	EEEEEEEEEEEEEEEEEEEE
1189 - 1208:	EEEEEEEEEEEEEEEEEEEE
1190 - 1209:	EEEEEEEEEEEEEEEEEEEE
1444 - 1463:	EEEEEEEEEEEEEEEEEEEE
1478 - 1497:	EEEEEEEEEEEEEEEEEEEE
1479 - 1498:	EEEEEEEEEEEEEEEEEEEE

1480 - 1499:	EEEEEEEEEEEEEEEEEEEE
1481 - 1500:	EEEEEEEEEEEEEEEEEEEE
1482 - 1501:	EEEEEEEEEEEEEEEEEEEE
1483 - 1502:	EEEEEEEEEEEEEEEEEEEE
1484 - 1503:	EEEEEEEEEEEEEEEEEEEE
1485 - 1504:	EEEEEEEEEEEEEEEEEEEE
1486 - 1505:	EEEEEEEEEEEEEEEEEEEE
1487 - 1506:	EEEEEEEEEEEEEEEEEEEE
1488 - 1507:	EEEEEEEEEEEEEEEEEEEE
1489 - 1508:	EEEEEEEEEEEEEEEEEEEE

A0A388ME50 **A0A388ME50_CHABU** (189 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MPYLQWSACLEDRGERGSYPSRAEYLNPRGIIDIVFFQPRTTSEEEAVEEEAAEEDEEEETSEEEGSYNEYSEEEPGAVS
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEESGCESWGGEANQAEVREEDPAAAARREEIAAGKRPLEHSNGTNLPI
PDDPTRDPEPPMIEDELPPVETSSASAQR
```

81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE

A0A388MEJ7 **A0A388MEJ7_CHABU** (266 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MRRRRRSMKKKRARRRTTSKGKMTASRSTRMMKKKEEEEEEVEKEETAATQQEVGEQEEEDEEEEEEEKEEEEVEEEDED
SEKNDDAEKEEEEDKEKQKKRRKKKEEEKEEEEEEEGPTMEEEEGVEEEATTSEEEEEEEEEEEEEEEEEEEEEKKEDQN
VEEEKEDQNVEEEKKEDGNEEEDEEEENEEEEDEEEADEERRSERRKIGEVEGGGGGGGGVGGGRRGGGRREGGLLGVGK
RWRVGLRSSTLEFGNGNTELRRQCGG
```

134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE

A0A388MF80 **A0A388MF80_CHABU** (287 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MHLLGLALQKKKGGQSEGGRREEGGWEEGGRTSGGGRNGGRNGGRRSGRRSGREDIGRREEWREEVKVDMGPRKGGEERG
RGKEEVNANRAEEEGEGEDRGKEEVRRRLGERSGGRWPVGGRTKTKEGPISAGVGGQLKKKEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEDEEDDDDDEEEEEDAGKEEGEGEGGGEGEEGGGEVEGEGGGGGGEEKGEGERKRGKKEEGKMDKKGEG
EAEEEEKMEKRKGEEEREREKEKRRKEEEKVEEDNARTSEAYVETIV
```

142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE

152 - 171:	EEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEE

A0A388MFF4 **A0A388MFF4_CHABU** (281 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MEEEENKREVEEAMEEEGDEQEVEKEEGEEEEEEEEEEEEEEEEEEEEEEEEEDKEEEEEEEAMKGEEEHEKEEEKDAMD
EERGGGGGGERVDGGGGRGGGEGGGGGAREKDKQRRDEEEEEEEDKEDEGEDEEDEEDEEDEEDEEEEEDEAEEEEEEEE
EEEKGEVEEEEEDEEEGEEEEKDKEEEEEEEEDEEEDEEEEEEEAKDEDEEEEEEVEDEEEEEVKDDEEEEEEGRRRRKS
RKRRLTLVTGRGAAPGDGSSGGGYGTMRRGSRAASGGAAGQ
```

29 - 48:	EEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEE

A0A388MFN4 **A0A388MFN4_CHABU** (112 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MEEEDGEAMEEDKEEEEDKAEDEEENEEENEEENEEENEEENEEENEEKDGADEEEEEEEEEEEEEEEEEEEEEEEEE
EEEDEEEEEEEEEEEEEEEEDEEEEEEEDEE
```

55 - 74:	EEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEE

A0A388MFQ1 **A0A388MFQ1_CHABU** (359 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MYQRVQRMLKKKEGGEEVAPPEPETGEPEAARVAAISLVEKDYFVRARPMLWKSVECNCEVWGKPFNAFIDTESSAVAIS
LDTLGGPTWKVISSVFSSDRCGRNIALIAQELIVPIVQLADDLSPGSVSQSDDSPAQHVLTRTLDPYLQWIACLEEPGDE
GSLSSRQEYLKPYGIINHAFYPKAEEEAIEEEESDNDEETSEEGSSSEYSEGEQSEEEEEEEEEEEEEEEEEEEEEEEE
EEEEGEETGSEWEALPEEATRTDTEAEDPEAARKRKESATGKRQLEFASGASLRIGDDPTRDPEPPKPEDGDPAAAAPST
SWRRRSRSSSPSSPTRPPVRPRTDAGDRPSSPDLIPLSP
```

216 - 235:	EEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEE
225 - 244:	EEEEEEEEEEEEEEEEEEE

A0A388MFW9 **A0A388MFW9_CHABU** (148 aa)
Uncharacterized protein. *Chara braunii (Braun's stonewort)*

```
MRKRTRGGGGEEQDGKEKNKRKRKRKSGLRDDRGVCDATLRVDSGKGRLFSPGEKKKRKQRGLEERMRREEEEEEEEEE
EEEEEEEEEKRRRKRRHGGGEEEEEEEDEDEEDEEEEEEEEEEEEEEEEKERRRGGGGEGGDDKDDDG
```

70 - 89:	EEEEEEEEEEEEEEEEEEE

A0A388MG42 **A0A388MG42_CHABU** (641 aa)
Uncharacterized protein (Fragment). *Chara braunii (Braun's stonewort)*

```
VASVEHGYGTQVASMEHGYGAQVASVEHGYGAQVASMEHGYVAQVASEEHGYGAQVASMDHGYGAELSSADADRQRGARL
WRPGRQRGPRLCRPGRQRGARLWRPGKSPPWSTAITSRSPAWSTAMAPRSPALSDQVASVEHGYGAQIASVEYGYGAQVA
SVEHGYGAQVASVEHGIGLQVSTADAGMAPRYVPLTQVGPPRGRHNRAPRCRPAQQEQEQQQQQPDEEDEEEEEEEEEE
QQEEDEEKEEEEGEGEEEEEEEEEEEEEEEGEEEEEEEDEEEEEEEEEGRRPRAPRCRPAQQQQEQQQQQPDEEEEDEEE
EDEEEETEEEAEEEEEEEEEEEEEEEEEVEEEEEEEEGRRSGRRRGKKKREDEEVRRRGKKKREEEEEGEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEGEEEEGRRRGKKKREEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEGEEEEGRRRGEGRRGKKKRGEEEKEEEEEGRIRGGRRRGGRRRGKKKRRRKRRRKKRRKKRKKKKKTKKRK
KKRRKRRRKRGRKKKGRKKWGRKKRDEEEGRRRGGGRTGGKKKRRKKKRKKKREEEEEEEEEEEEEEEEEEAEEEEEEEE
E
```

391 - 410:	EEEEEEEEEEEEEEEEEEEE
392 - 411:	EEEEEEEEEEEEEEEEEEEE
393 - 412:	EEEEEEEEEEEEEEEEEEEE
394 - 413:	EEEEEEEEEEEEEEEEEEEE
395 - 414:	EEEEEEEEEEEEEEEEEEEE
396 - 415:	EEEEEEEEEEEEEEEEEEEE
397 - 416:	EEEEEEEEEEEEEEEEEEEE
398 - 417:	EEEEEEEEEEEEEEEEEEEE
399 - 418:	EEEEEEEEEEEEEEEEEEEE
400 - 419:	EEEEEEEEEEEEEEEEEEEE
401 - 420:	EEEEEEEEEEEEEEEEEEEE
402 - 421:	EEEEEEEEEEEEEEEEEEEE
403 - 422:	EEEEEEEEEEEEEEEEEEEE
404 - 423:	EEEEEEEEEEEEEEEEEEEE
405 - 424:	EEEEEEEEEEEEEEEEEEEE
406 - 425:	EEEEEEEEEEEEEEEEEEEE
440 - 459:	EEEEEEEEEEEEEEEEEEEE
441 - 460:	EEEEEEEEEEEEEEEEEEEE
442 - 461:	EEEEEEEEEEEEEEEEEEEE
443 - 462:	EEEEEEEEEEEEEEEEEEEE
444 - 463:	EEEEEEEEEEEEEEEEEEEE
445 - 464:	EEEEEEEEEEEEEEEEEEEE
446 - 465:	EEEEEEEEEEEEEEEEEEEE
447 - 466:	EEEEEEEEEEEEEEEEEEEE
448 - 467:	EEEEEEEEEEEEEEEEEEEE
449 - 468:	EEEEEEEEEEEEEEEEEEEE
450 - 469:	EEEEEEEEEEEEEEEEEEEE
451 - 470:	EEEEEEEEEEEEEEEEEEEE
452 - 471:	EEEEEEEEEEEEEEEEEEEE
453 - 472:	EEEEEEEEEEEEEEEEEEEE
454 - 473:	EEEEEEEEEEEEEEEEEEEE
455 - 474:	EEEEEEEEEEEEEEEEEEEE
456 - 475:	EEEEEEEEEEEEEEEEEEEE
457 - 476:	EEEEEEEEEEEEEEEEEEEE
458 - 477:	EEEEEEEEEEEEEEEEEEEE
459 - 478:	EEEEEEEEEEEEEEEEEEEE
460 - 479:	EEEEEEEEEEEEEEEEEEEE
461 - 480:	EEEEEEEEEEEEEEEEEEEE
462 - 481:	EEEEEEEEEEEEEEEEEEEE
463 - 482:	EEEEEEEEEEEEEEEEEEEE
464 - 483:	EEEEEEEEEEEEEEEEEEEE
465 - 484:	EEEEEEEEEEEEEEEEEEEE
466 - 485:	EEEEEEEEEEEEEEEEEEEE
467 - 486:	EEEEEEEEEEEEEEEEEEEE

468 - 487:	EEEEEEEEEEEEEEEEEEEE
469 - 488:	EEEEEEEEEEEEEEEEEEEE

A0A392M198 **A0A392M198_9FABA** (201 aa)
NBS-containing resistance-like protein (Fragment). *Trifolium medium*

```
VRMMGIYGAGGIGKTTFSVGSLENLSGEEDDDDDDVHHDDHNCDNIHHHDDRRDIHHHDDEEEEEEEEEEEEEEEEEEEE
EECTSRYFRNSNAQCGGVGSWDFAPVFGGGRWISNQYESELIEKIVKDTLAKLAPAPVQMNHKEVKSVLDIVSNDTVRMM
GIFGAGGIGKTTFAVGSLQNLSGKKKNKKKKKKKNKKNAHR
```

61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE

A0A392NP63 **A0A392NP63_9FABA** (44 aa)
Uncharacterized protein (Fragment). *Trifolium medium*

```
MNQRKELKSEKNERVEKGERRESLEEEEEEEEEEEEEEEEEEEE
```

25 - 44:	EEEEEEEEEEEEEEEEEEEE

A0A392T8Y4 **A0A392T8Y4_9FABA** (62 aa)
Serine/threonine-protein kinase 38 (Fragment). *Trifolium medium*

```
EEEEEEEEEEEEEEEEEEEEVIGSSLTMKKVEAAKKFIENHYRAQMKNIQDRIYGGGLIQNV
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE

A0A392U743 **A0A392U743_9FABA** (81 aa)
Uncharacterized protein (Fragment). *Trifolium medium*

```
VWSEFLIFTFVETVEVEEEEEEEEEEEEEEEEEEEEEEEEEEEAEEEEEEEEEEEEQQQQQQEAKEEAIEMEEEKEQETVV
E
```

17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE

A0A392U7N3 **A0A392U7N3_9FABA** (65 aa)
Uncharacterized protein (Fragment). *Trifolium medium*

```
QQRIGVPQRDWIGNEDFQEEEEEEEEEEEEEEEEEEEEEEGHDVEGKETVEVQNPFKLLFYFDF
```

19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE

A0A394DP76 **A0A394DP76_LUPAN** (864 aa)
Uncharacterized protein. *Lupinus angustifolius (Narrow-leaved blue lupine)*

```
MTLTYEQRLQAVTRIVLDNDARAADTPPCQAEELGLRATLKPHQLEGISWLVRRYKLGVNVVLDLFILLCLYMNHGQMGL
GKTLQAISFLCYLKVCQLSHGPFLVICPLSVTDGWVSEIVKFAPKLEVFKYVGDKEYRRSLRKKIHDHVKGQSIMLNVLL
PFDVLLTTYDIVLMDQDFLSQIPWQYAIIDEAQRLKNSKSVLFNVLKDRYIMPRRLLMTGTPIQNNLSELWALMYFCMPS
AFGTLDQFLSTFKDISDLTSVHAAPKVKGRLKILRSVLGAFMLRRTKSELIERGNLVLPPLTETTVYVIQLRKACSHPYL
FPGIEPEPYEEGEHLVQASGKLLILDQLLQKLHSSGHRVLLFAQMTHTLDILQDFLELRNYSYERLDGSIRAEERFAAIR
SFSSSSSNTGLNSEVDHNEAFVFMISTRAGGVGLNLVAADTVIFYEQDWNPQVDKQALQRAHRIGQMNHVLCINLVTEHT
VEEVIMRRAERKLRLSLNVMGDNILEDEDKETSGVGTGDLKSIIFGLHMFDPTDINNGKNKDMDLPEINAIADKVIALRN
EQTFDRDDRKFEVNPRNLLKEYDVKEGGSASFSRDLDLDEASYLSWVKKFEEVSKSSSDPIKELRSRRNLDEDNSVQLEY
AKKKAEEKKLSKWKALGYNSLSVKDPVIPLDGDDITSVTGSVNSVYGDCTTPSNICPSEPAIVFSCVDTSGHWGHGGMFD
ALTRLSTSISDAYERASEHGDLHLGDLHLIQLEDGSDEQNMDGNAPKWVALAVVQSYNPRRKVPRSEISLQHLESCLSKA
AFSAAQNSEEEEEEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

822 - 841:	EEEEEEEEEEEEEEEEEEEE
823 - 842:	EEEEEEEEEEEEEEEEEEEE
824 - 843:	EEEEEEEEEEEEEEEEEEEE
825 - 844:	EEEEEEEEEEEEEEEEEEEE
826 - 845:	EEEEEEEEEEEEEEEEEEEE
827 - 846:	EEEEEEEEEEEEEEEEEEEE
828 - 847:	EEEEEEEEEEEEEEEEEEEE
829 - 848:	EEEEEEEEEEEEEEEEEEEE
830 - 849:	EEEEEEEEEEEEEEEEEEEE
831 - 850:	EEEEEEEEEEEEEEEEEEEE
832 - 851:	EEEEEEEEEEEEEEEEEEEE
833 - 852:	EEEEEEEEEEEEEEEEEEEE
834 - 853:	EEEEEEEEEEEEEEEEEEEE
835 - 854:	EEEEEEEEEEEEEEEEEEEE
836 - 855:	EEEEEEEEEEEEEEEEEEEE
837 - 856:	EEEEEEEEEEEEEEEEEEEE
838 - 857:	EEEEEEEEEEEEEEEEEEEE
839 - 858:	EEEEEEEEEEEEEEEEEEEE
840 - 859:	EEEEEEEEEEEEEEEEEEEE
841 - 860:	EEEEEEEEEEEEEEEEEEEE
842 - 861:	EEEEEEEEEEEEEEEEEEEE
843 - 862:	EEEEEEEEEEEEEEEEEEEE
844 - 863:	EEEEEEEEEEEEEEEEEEEE
845 - 864:	EEEEEEEEEEEEEEEEEEEE

A0A395HBT6 **A0A395HBT6_9EURO** (165 aa)
Uncharacterized protein. *Aspergillus ibericus CBS 121593*

```
MFVGCCIGLAWCRVKEHLSLLQKDIYFIPRSNEVYTHYKVSRDYLATWSDGIGLDWFYSVDVWSELGPYTVVGEVPDGAQ
VTMYTSNTQRVIHMKEAPNKFIRPPIEQIECLCSLVMREEEEEEEEEEEEEEEEEEEEAEDTTGMSPVIPAHPTLSTVHR
GFPSP
```

119 - 138:	EEEEEEEEEEEEEEEEEEEE

A0A395HFR6 **A0A395HFR6_ASPHC** (161 aa)
Uncharacterized protein. *Aspergillus homomorphus (strain CBS 101889)*

```
MDWSHLPGSRKKKEEEEEEEEEEEEEEEEEEEEEEEEEAKVESQSLCFISIGCNRESPADRSTKPTVQIGIQVVVMNRSL
RWYCTSSIVLSKRRTRIWTRSAGPLQSDPSGAKWNGFRRSMIVQSGNSSRPVYSAGPCRVPPAMEARRSIRLSLPYFHRH
F
```

14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE

A0A395HKH4 **A0A395HKH4_ASPHC** (372 aa)
Uncharacterized protein (Fragment). *Aspergillus homomorphus (strain CBS 101889)*

```
MPQQIQNPQRKTRRFRPELVETSSRTSREVHLDNHPGRAQPARHECSGVRSIKSTPGENAMVFHDDTAGQHDPGCDTAQT
TCLAQNKAVVDLHDSNVQASGDSARLSRHAFVGPNSSTNESDPAKQSRPRKFAPQLMETGKRSFRRIHATHTTLREGRSL
NVIGEIPSITTAVGKATLNHRHMTPESRFSYMTLHQRQETRRHSFRIPDLPAIPSSCSETSETSDTPSAPASSFVSPHRL
EQKNSANVTARIGSQDDCSDYLSAIAVITVEKQLKEQALAAFPNEQDHQPVDHFAIDREEEEEEEEEEEEEEEEEEEEE
EEGTFNHEQSSSPDDISSPYIHRRTSSADLTWELEYMRRHKEEAEMSDRAMA
```

299 - 318:	EEEEEEEEEEEEEEEEEEEE
300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE

A0A395HL30 **A0A395HL30_ASPHC** (149 aa)
Uncharacterized protein. *Aspergillus homomorphus (strain CBS 101889)*

```
MGPSSSTADRLTMSSPSVPAAKKANVPPQNQVSHDFKVSLALFFDFILLYEELRLPLRDPKMKGPVLDQLVPEIEDARRI
ETFLTMSWHTLYLVAGPCFDEGEEEEEEEEEEEEEEEEEEEEEEEEEETKERSQKRERESRENEQRKK
```

103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE

A0A395HLT0 **A0A395HLT0_ASPHC** (440 aa)
Uncharacterized protein (Fragment). *Aspergillus homomorphus (strain CBS 101889)*

```
SCSETSETSDTPSAPASSFVSPHRLEQKNSANVTARIGSQDDCSDYLSAIAVITVEKQLKEQALAAFPNEQDHQPVDHFA
IDREEEEEEEEEEEEEEEEEEEEEEEEEEGTFNHEQSSSPDDISSPYIHRRTSSADLTWELEYMRRHKEEAEMSDRAMARTR
GSPFSLRSDTLFGARKLARHLDYRAKARDLAPPESNATPPMLGEDLIFPQSLSPESTVCEGSNIQHDVTRKRLCGCSGLW
YGTPRVDDRSNDGGLWKGTCKPGNMQEIQSRQTSIASPDSKVYAGPTLQSADTDWLRIKNQSLQRSSWSPTTSHFSQQIS
SRESLEMELHDGLVTQIYNYLSLGYPCVARYFDHELSRVSGISVADLRQDDLKTDAKGHVGVSDTTLIDKDLSEGGCMRW
RALQLYILDWANQRERSGFAELDGDHGAWGVCERKGSWAV
```

84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE

A0A395HPP9 **A0A395HPP9_ASPHC** (160 aa)
Uncharacterized protein. *Aspergillus homomorphus (strain CBS 101889)*

```
MIQDCTASVPNKEFCHSNNKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEESFIANRLLSSHQPSLSLTNKFSSASSGLAF
TESLPVCHAEVDQSDLTFPIIQRGMSPTICVWSARDLGGFLKWDKAQGHKLASHVSKDCDRSPAHQNQGAWLWENWELRL
```

21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE

A0A395IDF6 **A0A395IDF6_9HELO** (68 aa)
Uncharacterized protein. *Monilinia fructigena*

MMKMKKKKKKKKKKKEEEEEEEEEEEEEEEEEEEEEEKKRRRRRRRRSGTEAFRLLQKDGKRQAIFLV

16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE

A0A395IF39 **A0A395IF39_9HELO** (111 aa)
Uncharacterized protein. *Monilinia fructigena*

MDMNHVYLFGFKQLDESNDLNDAPLALWEPLPWRQNIWIWDEMDVVLYRYCIERSELWGKQTVKEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEKRKI

65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE

A0A395IT90 **A0A395IT90_9HELO** (97 aa)
Uncharacterized protein. *Monilinia fructigena*

MGHFLGDGQGLSDTISTESMIAMNGDGINEWNATNGADEMLIRGVYIVNAAIIGEEEEEEEEEEEEEEEEEEEEEKKKKK
KKKKKKKKKKKKKKKSIK

55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE

A0A395IU63 **A0A395IU63_9HELO** (90 aa)
Uncharacterized protein. *Monilinia fructigena*

MGLEGKRKRKRKRKRKRKRKRKRKRKREEERREEEEEEEEEEERGRGREREEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEGGMR

49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE

53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE

A0A395IV41 **A0A395IV41_9HELO** (590 aa)
Uncharacterized protein. *Monilinia fructigena*

```
MLNLLPYLTTDTVPVTHPYLLYLLYLAIPYIKHTKVVNFQFIFYGIIIRGNLIKSKSEKIVKAWKDLGRLERRVKRRRRR
REEEEEEKKKKKKKKREEEEEERKKKREEEEEEEEEERRRRRRRRRRKREEEEEEEEEEEEEEERRREEEEEEEEEEEEE
EEEEEEEEEERRRRRRRRRRRRRRRRRREEEEEEEEEEEEEEEKKKKKKKKKKKKKKKKKKKKKKKKKKKKKTTTTTTTT
TTTRENNQNQNQKKKKKTTRERTIRIRRRTRRESITATKLRLLNVNKINPTKNSFNSFHFLSSRIASKSFSPYSSSLPPP
LPTLNRKTRIISKTAFKFSIKNNNSYPANHINFSHANIISIHIMADNPPLDSMAPPGDSIDFATKDTSLSTESLTNDQIN
EAPKSPTSTKPPSLPSLRAAPDSETIATMTASSHLSVCWQMREDQDLVHQYQVPDLQHQKTTRWWFTYFHGGKNESISCI
KARHAHNSRPQVPSTVSTSGMPGSPVVDGLPGGLHLPPSMRPSPQNFVSAPVVPKNENGGGLSARRGMKLDLPPAPAPST
PGSETNVHQICQMRFYVQPIFKYVDTKNGH
```

147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE

A0A395IVC9 **A0A395IVC9_9HELO** (67 aa)
Uncharacterized protein. *Monilinia fructigena*

```
MFIFIIIRGVGEGNWLIWKSEGGEEEEEEEEEEEEEEEEEEEEEEEEEEEEKKGSGVVEQRSTIDLF
```

24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE

A0A395JAB8 **A0A395JAB8_9HELO** (97 aa)
Uncharacterized protein. *Monilinia fructigena*

```
MINDWTVLNEWIVREEKDNGDGDGDGDDGVDVEREEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEKEEEEEEEEDGDG
EGDEGNEKRLLYEVIMR
```

35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE

40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE

A0A395M6S7 **A0A395M6S7_9HYPO** (74 aa)
Uncharacterized protein (Fragment). *Fusarium flagelliforme*

```
KDAVDLIASPSRKQRGKQKALCVDDDELDIDESEDDEEIEEEEEEEEEEEEEEEEEEEEEDDDDISVKDTIEVR
```

40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE

A0A395M707 **A0A395M707_9HYPO** (3112 aa)
Uncharacterized protein (Fragment). *Fusarium flagelliforme*

```
GGGAKNEPAPAPAPPPPPEPKAEENPWDKSKDQPGGLGMKDDDDAWGFGTKKEKKQSTLWGAEPDEGPKDGDDPWGWGGQ
KKKGKPGGILEELALDPEPAPPPGSKKDIWDTWGISKKDRAKKKGIMEEVALAAAPDPPSMDDQWGGWSGKQDNPPQSSL
WGAQDPIPAAPDPPSFEDKDGDDFWSTFGSGKPKPAEENPPGWGSWGVVPEPPKIEDDGWDLWGTGKKKKKAGDLIQLED
EIPPPAPDPVEAVGTDDFLDSWGSGKRPKKPAADPFDFKTSGAHDPNNAFWGSIDNQKPSAHDFLIDTTDPEQAAREAEE
QAAREAEDAEAAREDEEIASLMDKKAKRGGRLLKSDRERLTLLEGNAARRAEARAAREAEAAAAAEAAQAAADAQAAADA
EAAALQAAQDAEAAKENEEIEQLLAKKQKRGGKLLRKDQERLTILEGNASRRAEAQAAREAEAAAAAAAAAAAAAAEVDII
EEIPLDDPPPEAPEEDAAAQAAAEAEAAFAAGVAQEEAEMESLKSKKVKKGKLLKKEQERLNILIDNATKRAEDAIAKEA
EEQAAKDAADAAAAAAAEAAEAEAAAQAVAEAEATAQAAADAEAAEAAKEEEEMVALKAKKAKKVKLTKAETTRLVTLVG
NSVKRAQAKSAKEAEEAAAAQAAKEAEESAAREAEEKAAREAEDAAAREAEAALAAEEDKELAALDALKKKRGGNLIKKK
DVERYNVLTLRANERAAKKAEVAAADAAPTEATPEVLDEPTEPVPEPVPEAPPADADPEPVVPEPASGPDAAIVAEEEAE
LASLEAKKAKKGKLGKKDTDRYNLLNENAAQRRAAKEAEETAAREAAEAAAAEEAAAAETAGADAVTASEAEAILIADEE
AELAMLVVKKAKKGKLVKKDLERFDILTENAAQRQASKDAEEAAAAAAAEAEAQAEKDAEEAAAAEAAEAEATAAREAEA
AAIAEEEAELSALAAKKAKKGKLIKKDAERFAILTENADRRTQEAAMAAEQPDDSAPPAEVDVEEPAPEPPVEEELIEID
DPDANAANEAEAAAIAEEEAEMAALVAKKERKGKLGKKDTDRFNLLIANAASRADKAAEEEAAAAAAAAAAAEEEAAAAE
AAAIEEAAAREAAEAAEAEAAVIAEEEAELAALTAKKNKKGKLGKKDNDRFAILTENATQRAEKAAEAAAAEVEPEPEPE
PEPEPELEPEPEPEPEEVPPEVEDPPIDDFDDAAASEAGDEEAAIAAEAAAIAATIAAEEEEELEALIAKKNKKGKLGRK
DSDRLAVLTENAAQRAEKAAQEEAAALAEPEIVDDALLDIEEPAPEDAPEESPEEEVAPEEDDAAAAEAAALIAAEEQEL
ADLDAKKARKGKLGRKDTDRYNILTENAVNRAEERAAREAEETAAAEAAAAAEAEEIAAREAAEAEAAAIAEEAEKEAAE
AEAKAAIAQEEEELAALEAKKERKGKLGRKDTDRLNALMDNKAARDAQAEEEQAAKEAEDQAAQEAEDAAAAEAAAAVEA
EETAAKEAAEAEAAAIAAAIAAEEDAELADLTAKKTRKGKLGRKDTERFDQLMMNATRRAEEQAAREAEAAAEELPAEDE
PAPEDPEEPVPDAIEPVEAPIEEPSEAQAPDPDDEAAAEAAAIAAEEEAELASLEAKKARKGRLGNKDTQRFNFLTENIT
RRAEEQAAKEAAAAEAVVDEVVAEDIPEDVPEDDEAAVQAAAEAEAEAAAIAAEEEAELSALVAKKARKGKLGRKDTERF
DILTENAARRADEQAAKDAQAAEAEAEVEEPVLEPIEDAAEPEPEEEPEDEDVAAKEAAEAEAQAIAAEEEAELAALNKK
KAKKGRLGRSDTERFNILTDNAAKRAEAQAAKEAEEAAEEAAEEAQPAEEEEEDDFVDAEDGEDDLIEEPEPEAEEAAAP
EEEDAAAAAEAEAQAAAIAEEEAELASLTKKKIKKGKLGRTDTQRFQILTDNAARRAEEAAAREADEAAAAEAELEAEPE
PEPDNEPEPEADQEPDDGAIDEVDEAEAAVIAEEEAELAALTKKKIKKGKLGRTDTQRLQVLTDNATRREERSAREAAA
AAAAAEAEAEAEAAEGDAEAEVAEDADEPADGEEEEEEEEEEEDDIVEVEDDEMAAREAEEAAIAEAEEEELESLKAKRA
RKGRLGRKDTERLAVLEENAIRRAEERAAKEASAAAEPEESPEGDEPDDGEEVAEEEEQDEEDAAAAAEEEAAAREAEEE
AAREAEEAAIAEAEEDELESLKAKKARKGRLGRKDTERFHMLEENAARRAEERAAKEAAVAAAIDEAEAEEAPENEEEEE
EQEEEEEEEEEEEEEEEEEEEEEEEDDNGADDAAVDEEAAAAREAEEAAAREAEEAAAREAEAAAIAEAEEAELDSLKFK
KSRKGRLGRKDTDRLRFLEENAAKRAEELAEKEAAAAAEAKAEEAPEDEDEDEEEEEEEEEEDAAVEADPLEEEPAEVA
NKDIADESDEEEAEAVPEEAPEEAEPEVPADDEIVEVVDLSPKRERRSRKGKSRRDAPPPPPVPDPPLTPPPEPKHSRRP
KLGREGTSWGKWGAAPREERDEYSQEKSGRHRRREEKTSSKGSTSDKVEKPSSRTAALFGKTPLARSASTREKRDGLSSK
RRHSEAARGIVSPPPEEMLMQEDPSSRRKSRKPRSREDEDVMMSGAAPVPDRYERRHSHKTRSRDDDDVVMVDPDLANDR
RERRRSHKPRSREDEDMAMPDDTAMPGPRDRRRRDRRSRDDEPVMVEPDVPADQPLPRGSKKGFAGLFSGLRTPKNERPD
PLRRRSTYATTDDEALRTARMDGDAVVVDADREARRAARKAKRADPEEEARRAKDEARRERRRQREKGADAPRQDQDARR
AERRAARQRGDEERRAQEEQQAEEELQRAQEAKEAQRAERRRLRREQEVAAAAEQEEQEARRAAKRDRRRPRQVDVSDDE
HERRRRREARRAARAAEEGAEGHHRRPRHEEPQQPAWPHLGTSSWVQEHVDAPPPPEIPQAGDVNGGQTEDDEMARREAR
RAQHRSKYSDETPDEAEERRKRRARREERERGGRHRDRRSEGSDERHHTRRASNFAENAAAPRTSWWKKIKG
```

2323 - 2342:	EEEEEEEEEEEEEEEEEEEE
2324 - 2343:	EEEEEEEEEEEEEEEEEEEE
2325 - 2344:	EEEEEEEEEEEEEEEEEEEE
2326 - 2345:	EEEEEEEEEEEEEEEEEEEE

A0A395RSY5 **A0A395RSY5_FUSSP** (341 aa)
Uncharacterized protein. *Fusarium sporotrichioides*

```
MSSQTFRFAFFCILMMASQHLNDKPAILNHPCKFCKVLEFNDSSFGGESKIGDGGTPYVDFGEVVQTQEDREAQHGARAL
RARMALSFAMEGVDATKPETVPKTELKVDYTRSDTLPELSGLARTATAGCSFCEVLRHDLMAAWEAIEDKEEEEEEEEEE
EEEEEEEEEEEEVTQQDENESDAGGEREKARNENDVSDDDGVEEDKEAGDDDAEDEEDACRSEDTNRATYEDIPTDSDAE
SEPDTEPDEQSDEGSDAKSVKEEDSKDQNKETQDQPTVKRAPRKAKLIITEVTYKLREHDPDHEQPQRTWLDALYVFFTI
ECEGKMRDYSIHYNIYADRAG
```

151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE

A0A395SS17 **A0A395SS17_FUSSP** (1587 aa)
Ccr4-not transcription complex subunit 4. *Fusarium sporotrichioides*

```
MAPQDSFIDDEEDTCPLCIEEFDLSDRNFQPCPCGYQVCQFCFNNIKNNMNGLCPACRRPYDEKTIKWKVVTQEEVAEFR
ANIQKNQKKRATDQRQKELQKREAEKENRKNLIGVRVVQKNLVYITGLAPTVREDELLKTLRKPEFFGQYGNIQKISISN
RKSSDGQHQSLGIYVTFEYPEEATRCIQAVHGSQNGDRVLKAQHGTTKYCSAWLKNEKCSNPGCMFLHEQGDEEDSYSRQ
DLSSMNSIASQRPLPAGGSRSASRQQAPHPTPPPVVSHPMTRSISKEGSENGVDGSALPSSANWARNPQRSRRGSLATSG
AASSPAISAAQPVTAEPVPEEAVEEEEEEEEEEEEEEEEEEEEEEEEPQPEEPVAGPSSSRAMEPESPAPSRNMAESGL
REILKVLGNCPWPVFPTAGADQYPPLFDPRGGEKRRAMREEEDSRLGGEQEERPEAREPSEGEPETGGSLALGGEPEDRD
ASNDNRGFDRRGSTQPPIQRLSTDGLFGPALTGASPFGQSPGNPGSRSMTPQQLFLRSQSGFGDAPPGIPNQSNAFQNQS
QGQGQGQGHNRQSSRFSFANDNASSTTNVKVSTNPRIMAQQSSMMPNTFQSQGNNQFYGASMPGPPPGLKSTGTPPNMFG
QFGGQGFGAPKDNSNELLQSLIGRSRAGNNQSHDAGKPPAPGLLPSLYGGTPSAYQDMSSKQKKKGKKHRHANTSSSGGS
GLVDLADPSILQVRMQHQSQGSAGVGQGLFGGQSQGGHELQAHFDSAHIREINAAQGDDELPSLDEATNSVDALVSDDPI
LSATTLEGRQSVPPGLGLPPGLAPISRPPSTTGHAKLSNILPALPKMPPPGLSQGVSTPDQSPRKSMPATPVSEAKKTSK
SLATESGLSKEITNQPQPKQTKAINLQDEEFPALDALKSKSRPATPTPKPTPKAKRNAERIVDRMMAKAGASKQSSTEES
KVQDAKTQELKLQETKVPEPKPMQFTPPIEKKPVSLKSQIEENSAPNQSTKTGGKTPISLNTQIEKNTVPKAGESSATTE
KPNTGNAAAFPPLPAPSSAATSSPVTRTGPKTLRVVATPKIEAPPPASPALTMASVALSGSRGVSASYRPDTPASSEAVS
DNASVVSASVTHSRASSPPPSRIGSAAVRTTTKSQQRKARKDVLKQETKMIAETPKVEAEVHAPIIGRKKKQKKEKPAKA
PQSDASTPAAPEAAKADVPTPEPPQPEPTKEPEQEPEEKPAKSKAAQKKAAKSKGKAKEVEPEPTPQPPSPAKEATPETQ
EATEKPGPNPASVFAEIKNALWASSVDKLQLFKPIASGSSRTDYSSAHNNANKAEHCKDCSCKCGEIQDDDLAALRAGKP
VRKQFHVDGSRMLITPNGDCIRGLNPEEEDAFLELQAAIADTAENPGSFIAPRHQPGSGAFSLIKGRAVPNGRPNIFPTT
AQLQSQDPIGKLQREDALSYINQYVLPRLNLGATNMGFPKGASPTKDAAAASLNSLAPYFYGPDAAAGVGIYSPPDGARA
MQDFSSAGMSSEERGKNFGMGVGGMPLMSVEDAEGALATARRETEKLEKGLNQVIRRNRRLVLGGNN
```

344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE

A0A396J5K4 **A0A396J5K4_MEDTR** (891 aa)
Putative transcription factor C3H family. *Medicago truncatula (Barrel medic) (Medicago tribuloides)*

```
MPNSDSSVEDDPSLQEEEEDEVDDDEEEEFEEVEVEEEEEDQEEEEEIEEVEQEEEEQEEVEEEEEEEEIEEEEEDEVEE
EEEEVEKEEVETVVVEEEEEEEEEEEEEEEEEEEEEEEEEAIESEHIKETIKVEEEEKEEEEEEEEEEEEEEEEEEKEEEE
EEEEEEEEEEEEEEMEDEEKQEKIVVEEKDKDKDEVPNSLPDADKHSKVEVEEEEEKEENEEAIDMEVEEEQETVVEKDKE
KDEVPDSLPDADKRSKDSSQHMELDVKEENLGSVSHVPDNPEVIRPSHYMEENDAMSKASVSLHEELTLKNEDYPLKQKV
ESPPKPSENLISAEDGKNQGLNVDVENPGHLQRKASEGCSEPDCNSKASLSDVMDIDSRATKPSSDTGKDVVTGIILRDN
FVEDADGDQNSKEKVMQSEMESTVDVKQKPSRTRIHSPSAEIKDGNKRPAIICAFFAKGWCIRGSSCSFLHVKDSVNNTD
QGAEGDVVTAHQKRELKLEKGVKENEEEASPSWHPSHEKEKFLMRDSLFPENKSAFNTSNNYFSSNLSSYSSRAEEMIAI
RNQHMYRGYTSTKDFSSPLGASALDSHAHKSSFSSDREDFHLVGSSRVAPHANGYTLKTRSNWEPSVPFRPSFFITSMNV
SSPRDLYDPLRNSIEIPNIGDGSLKASLLIRGSSVQASSQVRTYDDSAAVGKQMSDVNDDKSSVSSHHKFYENEPNRSSV
PRGKDCLATKAEITSGTCANYQNGDIGVGQYAFGVEDRIETLKKRTEHDARHHSDESEHKKNRVAKDNKFHEMEVDFQTD
GSVLKETKTLKIFHAVLVDLVKELLKPFWHEGRLSKDAHILIVKKSVDKVISTLEPRQIPTTEDTAKQYVSLCRPKIAKL
VHGYVNKHGKS
```

96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE

A0A397G1E0 **A0A397G1E0_9EURO** (373 aa)
Histone acetyltransferase (EC 2.3.1.48). *Aspergillus thermomutatus*

```
MASADRASSPHVKSPTERTVKQVVLGDLLFKTWYQSIYPEDLVSKDTDRLNVCCWCFCYSCDVNSHVKHMRLCEHRTTPP
GAKVYEHGGYSVWEVDGEEHKLYAQNLSLFAKLFLDHKSVFFDVATFLYYILTFTDPENPEKYHILGFFSKEKLSWDANN
LACILIFPPYQHKQLGKLLMGISYKISAWEEDGGFIGGPEKPLSDMGARSYSRFWQERIGRCLLSGDSDASVQETQLVKE
SRKRHSSTFMTIRDIGQATGMLTEDVITALKGMGVVQPETPSKRRKVKQAADEPGHYVTIRKSDLLRWMESRKVSLRDPV
RDEKFVGRWTLRETFDENNSSAGEEEEEEEEEEEEEEEEEEEEEEEKEGSHNV
```

344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE

A0A397IHP8 **A0A397IHP8_9GLOM** (1162 aa)
Uncharacterized protein. *Diversispora epigaea*

```
MNLSRLLYYKHRILVHNNKEYFINYQPVIKCIENLLSNPEISQLFVYDYKKLEIENEQSYGEQYTGNWWKKAKESIPSVA
YILSIILYSDATTTDTLGKGSLHPIYISLGNIPTWRRNKEDAKQLLGYLLILSAKDEREKKSSEFKKLVRETFHNSIKFL
LDPLFTNDDDDGDGIELKIDNEIFWFFPRVSTIICDWPEACTFSLTYKSTNSNYPCHFCLVSKENLNNTRLRDDQMVLRN
KENMLQYYNNGTTEKASLEPVFNYFWNIPNINVYVATVPDRMHHLDLGLYRYQIEFTKKLLFEAEERSLVDKMNRRITLI
PRHSELKIFSGGLQSIALLTADNYRNIMKVMVFVVDDLLNKDLSEVYVKWNEMYLLSRQKRLKKEAIEKWANLFIKLFGQ
FSNSDFKLPKLHSWVHHIVDTIREFGAINGYTTETYEALHKTYVKIPYRLSNKKDVEKQMMKTIRRKAIIKQNDFKKKFK
```

```
TPLKFNYSSKLFEFDISEAFEFIDKYKNETNLDEKMIKGLDHFIQSLDSYFDLLKISTAQGCHIKIYRSVTLENRAILRT
TNMFHKRPWFSNISVTMNDEELFEYQSDNGICYAQTLLITEVFLKKEKSLHLALVQWYDFISKRTPFVYGCPLLELTEVY
NFIEIEAIEDIVHIVPRFDKTNEYLDRKQSASSTTPTTPAATTPAATTPAATTPTATTPTTPTTPTMPIVLIELKEVAEA
SSRKKQKTVAGIIKNYYSDDDSPFTHKDANYFLNKFEEMNSRQIEMNNRQIKIEREISDIRKLLASSGIESDYTTENEFI
NVTTTPAATTPTATTPTTPTTPTMPIVLIELKEVAEASSRKKQKTVAGIIKNYYSDDDSPFTHKDANYFLNKFEEMNSRQ
IEMNNRQIKIEREISDIRKLLASSGIESDYTTENEFINASVYICYKASFIETFVINSNYLKSVAAGCAELEFCEYFGGWE
NKRWSSYYTKYIQSPLLAKHRSLRGSIANRVRSALFAVFGEHELPYIDTKSAPQEIKEWKDSEKLKNTYERLYQRIDSDK
EMTWCARIIQKTWPNFKKLTKEKIAFGMAVCQYMLNPKTESIKINDEEIRKIMKVKKKKLEEGQIIGLDNEEGEEEEEEE
EEEEEEEEEEEEEKEKEEREEEYENEVIFTGQSFRSRSNSLA
```

1114 - 1133:	EEEEEEEEEEEEEEEEEEEE

A0A397IK01 **A0A397IK01_9GLOM** (59 aa)
Uncharacterized protein. *Diversispora epigaea*

```
MTVVRSIHVSKIKNQKPDPGLIFNDPKINSETRNNPQEEEEEEEEEEEEEEEEEEEEEE
```

38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE

A0A397IST6 **A0A397IST6_9GLOM** (1262 aa)
Uncharacterized protein. *Diversispora epigaea*

```
MSTSYKCPYCNIRYFSNRNSYSQHVNRCINLYDVSTEESNTEVSEVTDMLLDNDDFNRIEERQSVQEIENLPSGSEITDL
FEYGDYDADASVSLEVISNIPERFEEILFESSRNEDSDVENLQNEDSNIERLQNEDLDVRSESSRNEDSDVEEFPNESYA
DLMTLVTKYNLNNKAGNAIIKFFNKHSNLSISPLPKNIETGRKYMDKMNLSRLLYYKHRILVHNNKEYFINYQPVIKCIE
NLLSNPEISQLFVYDYKKLEIENEQSYGEQYTGNWWKKVKESIPSVAHILSIILYSDATTTDTLGKGSLHPIYISLGNIP
TWRRNKEDAKQLLGYLPILSAKDEREKKSSEFKKLVRKTFHNSIKFLLDPLFTNDDDDGDGIELKIDNKIFWFFPRVSTI
ICDWPEACTFSLTYKSTNSNYPCHFCLVSKENLNNTRLRDDQMVLRNKENMLQYYNNGTTEKASLEPVFNYFWNIPNINV
YVATVSDRMHHLDLGLYRYQIEFTKKLLFEAEGRSLVDKMNRRITLILRHSELKIFSGGLQSIALLTADNYRNIMKMMVF
VVDDLLNKDLSEVYVKWNEMYLLSRQETFKESDLKNFQEAIEKWANLFIKLFGQFSNSDFKLPKLHSWVHHIVDTIREFR
AINGYTTETYEALHKTYVKIPYRLSNKKDVEEQMMKTIRRKAIIKQNDFKKKFKTPLKFNYSSKLFEFDISEAFEFIDKY
KNETNLNEKMIKGLDHFIQSLDSYFDLLKISTAQGCHIKIYRSVTLENRAILRTTNMFHKRPWFSNISVTMNDEELFEYQ
SDNGICYTQTLLITEVFLKKEKSLHLALVQWYDFISKRTPFVYGCPLLELTEVYNFIEIEAIEDIVHIVPRFNKTNEYLQ
LXKKDRKQSASSTTPTTPAATTPAATTPAATTPAATTPTATTPTTPTTPTMPIVLIEPKEVAEASSRKKQKTVAGAIKNY
YSDDDSPFTHKDANYFLNKFEEMNSRQIKMNNRQIKIEREISDIRKLLASSGIESDYTTENEFINKFVRKVANSAIDKRI
YPDESYLKSVAAGCAELEFCEYFGGWENKRWSSYYTKYIQSPLLAKHRSLRGSIANRVRSALFAVFGEHELPYIDTKSTP
QEIKEWKDSEKLKNAYERLYQRIDSDKEMTWCARIIQKTWPNFKKLTKEKIAFGMAVCQYMLNPKTESIKINDEEIRKIM
KVKKKKLEEGQIIGLDNEEGEEEEEEEEEEEEEEEEEEEEEKEREKREEEYEDEVIFTGQSF
```

1221 - 1240:	EEEEEEEEEEEEEEEEEEEE
1222 - 1241:	EEEEEEEEEEEEEEEEEEEE

A0A397IYD3 **A0A397IYD3_9GLOM** (1353 aa)
Uncharacterized protein. *Diversispora epigaea*

```
MSTSYKCPYCNIRYFSNRNSYSQHVNRCINLYDVSTEESNTEVSEVTDMLLDNDDFNRSEITDLFEYGDYDADASVSLEV
ISNIPERFEEILFESSRNEDSDVENLQNEDSNIERLQNEDLDVRSESSRNEDSDVEEFPNESYADLMTLVTKYNLNNKAG
NAIIKFFNKHSNLSISPLPKNIETGQNYKMYRKSFIKSGNFPAFCIENEQSYGEQYTGNWWKKAKESILSVAYILSIILY
SDATTTDTLGKGSLHPIYISLGNIPTWRRNKEDAKQLLGYLPILSAKDEREKKSSEFKKLVRETFHNSIKFLLDPLFTND
DDDDDGIELKIDNEIFWFFPRVSTIICDWPEACTFSLTYKSTNSNYPCHFCLVSKENLNNTRLRDDQMVLRNKENMLQYY
NNGTTEKATKESIPSVAYILSIILYSNATTTDTLGKGSLHPIYISLGNIPTWRRNKEDAKQLLGYLPILSAKDEREKKSS
EFKKLVRETFHNSIKFLLDPLFTNDDDDDDGIELKIDNEIFWFFPRVSTIICDWPEACTFSLTYKSTNSNYPCHFCLVSK
ENLNNTRLRDDQMVLRNKENMLQYYNNGTTEKASLEPVFNYFWNIPNINVYIVTVPDRMHHLNLGLYRYQIEFTKKLLFE
AEGRSLVDKMNRRIILIPRHLELKIFSGRLQSIALLTADNYRNIMKVMVFIVDNLLNKDLSEVYVKWNEMYLLSRQETFK
ESDLKNFQKAIEKWANLFIKLFGQFLNSDFKLPKLHSWVHHIVDTIREFRAINGYTTETYEALHKTYVKIPYRLSNKKDV
EEQMMKTIWRKAIIKQNDFKKKFKTPLKFNYSSKLFEFDISEAFEFIDKYKNETNLDEKIIKGLDHFIQSLDSYFDLLKI
STAQGCHIKIYRSVTLENRAILRTTNMFHKRPWFSNISVTMNDEELFEYQSDNGICYAQTLLITEVFLKKEKLLHLALVQ
WYDFISKRTPFVYGYEFYSGLLTGKSKFVKKDRKQSASSTTPTTPAATTPAATTPAATTPTATTPIATTPTTPTTPTMPI
VLIEPKEVAEASSRKKQKTVAGAIKNYYSDDNSPFTHKDANYFLNKFEEMNSRQIEMNNRQIKIEREISDIRKLLASSGI
ESDYTTENEFINKFVWKVANSAIDKRIYPDESYLKSVAAGCAELEFCEYFGGWENKRWSSYYTKYIQSPLLAKHRSLRGS
IANRVRSALFAVFGEHELPYIDTKSAPQEIKEWKDSKKLKNAYKRLYQRIDKKIAFGMAVCQYMLNPKTKSIKINDEEIR
KIMKVKKKKLEEDQIIGLDNEEGEEEEEEEEEEEEEEEEEEEEEKEREEREEEYEDKVIFTGQSFRSRSNSLA
```

1304 - 1323:	EEEEEEEEEEEEEEEEEEEE
1305 - 1324:	EEEEEEEEEEEEEEEEEEEE

A0A397J0U8 **A0A397J0U8_9GLOM** (1187 aa)
Uncharacterized protein. *Diversispora epigaea*

```
MSTSYKCPYCNIRYFSNRNSYSQHVNRCINLYDVSTEESNTEVSEVTDMLLDNDDFNRIEERQSVQEIENLPSGSEITDL
FEYGDYDADASVSLEVISNIPERFEEILFESSRNEDSDVENLQNEDSNIERLQNEDLDVRSESSRNEDSDVEEFPNESYA
DLMTLVTKYNLNNKAGNAIIKFFNKHSNLPISPLPKNIETGRKYMDKMNLSRLLYYKHRILVHNNKEYFINYQPVIKCIE
NLLSNPEISQFFVYDYKKLEIENEQSYGEQYTGNWWKKAKESIPSVAYILSIILYSDATTTDTLVRETFHNSIRFLLDPL
FTNDDDDGDGIELKIDNEIFWFFPRVSTIICDWPEACTFSLTYKSTNSNYPCHFCLVSKENLNNTRLRDDQMVLRNKENM
LQYYNNGTTEKASLEPVFNYFWNIPNINVYVATVPDRMHHLDLGLYRYQIEFTKKLLFEAEGRSLVDKMNRRITLIPRHS
ELKIFSGGLQSIALLTADNYRNIMKVMVFVVDDLLNKDLSEVYVKWNEMYLLSRQETFKESDLKNFQEAIKKWANLFIKL
FGQFSNSDFKLPKLHSWVHHIVDTIREFGAINGYTTETYEALHKTYVKIPYRLSNKKDVEEQMMKTIRRKAIIKQNDFKK
KFKTPLKFNYSSKLFEFDISEAFEFIDKYKNETNLDEKMIKGLDHFIQSLDSYFDLLKISTAQAPWFSNISVTMNDEELF
```

```
EYQSDNGICYAQTLLITEVFLKKEKSLHLALVQWYDFISKRTPFVYGCPLLELTEVYNFIEIEAIEDIVHIVPRFDKTNE
YLDRKQSASSTTPTTPAATTPAATTPAATTPAVTTPTATTPTTPITPTIPIVLIEPKEVAEASSRKKQKTVAGAIKNYYS
DDDSPFTHKDANYFLNKFEEMNSRQIEMNNRQIKIEREISDIRKLLASSGIESDYTTENEFINKFVRKVANSAIDKRIYP
DESYLKSVAAGCAELEFCEYFGGWENKRWSSYYTKYIQSPLLAKHRSLRGSIANRVRSALFAVFGEHELPYIDTKSAPQE
IKEWKDSEKLKNAYERLYQRIDSDKEMTWCARIIQKTWPNFKKLTKEKIAFGMAVCQYMLNPKTESIKINDEEIRKIMKV
KKKKLEEGQIIGLDNEEGEEEEEEEEEEEEEEEEEEEKEREEREEEYEDEVIFTGQSFRSRSNSLA
```

1139 - 1158:	EEEEEEEEEEEEEEEEEEE

A0A397J1M5 **A0A397J1M5_9GLOM** (1345 aa)
Uncharacterized protein. *Diversispora epigaea*

```
MSTSYKCPYCNIRYFSNRNSYSQHVNRCIKLYDVSTEESNTEVSEVTDMLLDNDDFNRIEERQSVQEIENLLSGSEITNL
FEYGDYDADVSVSLEVISNIPERFEEILSESLRNEDLDVESLQNEDSNIECLQNEDSDVKSESSQNEDSDVEEFPNESYA
DLMTLVTKYNLNNKAGNAIIKFFNKHSNLSISPLPKNIETGRKYMDKMNLSRLLYYKYRILVHNNKEYFINYQPVIKCIE
NLLSNLEISQLFVYDYKKLKIENEQSYRKQYTGNWWKKAKESILSVAYILSIILYSDATITDTLGKGLLHPIYISLGNIP
TWKRNKEDVKQLLGYLPILSAKDEREKKSSEFKKLVRETFHNSIKFLLNSLFTNDNDDGDGIELKIDNEIFWFFSRVSTI
ICDWPEACTFSLTYKSTNSNYPCHFCLVSKENLNNTRLRDDQMVLRNKENMLQYYNNGTTEKATEGRSLVDKMNQRITLI
PRHSELKIFSGGLQSIALLTADNYRNIMKVIVFVVDDLLNKDLSEVYVKWNKMYLLSRQETFKESNLKNFQEAIEKWANL
FIKLFGQFLNSDFKLPKLYSWVHHIVDTICEFGTINGYTTETYEALHKTYIRRKAIIKQNDFEKKFKTPLKFNYSSKLFE
FDILKAFEFIDKYKNKTNLDEKMIKGLDHFIQSLDSYFDLLKISTAQGCHIKIYRSVTLKNRAILRTTNINISVTMNDEE
LFEYQSDNGICYAQTLLITEVFLKKEKSLHLVYNFIEIEAIEDIVHIVSRFDKTNEYLKNKEIKKKKDEFYSGLLIGKSK
FVKKDRKQSASSTTSTTLAATTPAATTPAATTPTATTPTTPTTPTMSIVLIESEEVAEASSRKKQKTVAGAIKNYYSDSN
VSKVFENICNIQNFKTILFIDDSPFTHKDANYFLNKFEEMNNKQIEMNNRQIKIEREISDIRKLLASSGIESDYTTENEF
INKFVQKVANFAINKRIYLDESYLKSVAVGCAELKFHEYFGGWENKRWSSYYTKYIQSLLLAKHRSLRGSIVNRVRSALF
AVFGEHKLPYIDTKSAPQKIKEWKDSEKLKNAYERLYQRIDSDKEMTWCARIIQKTWPNFKKLTKEKIAFGMAVCQYMLN
PKTESIKINNEEIRKIMKVKKKKLEEGQIIGLDNEEGEEEEEEEEEEEEEEEEEEEKEREEREEEYEDEHKLPYIDTKS
APQKIKEWKDSEKLKNAYERLYQRIDSDKEMTWCARIIQKTWPNFKKLTKEKIAFGMAVCQYMLNPKTESIKINNEEIRK
IMKVKKKKLEEGQIIGLDNEEGEEEEEEEEEEEEEEEEEEEKEREEREEEYEDEVIFTGQSFWS
```

1158 - 1177:	EEEEEEEEEEEEEEEEEEE
1303 - 1322:	EEEEEEEEEEEEEEEEEEE

A0A397J3F5 **A0A397J3F5_9GLOM** (297 aa)
Uncharacterized protein. *Diversispora epigaea*

```
MAVCQYMLNPKTKSIKINDEEIRKIMKVKKKKLEEDQIIGLDNEEGEEEEEEEEEEEEEEEEEEEEKEREEREEEYEDK
VIFTGQSFRSRNLTHHKNIVQKYNVQERLYTLPSEVISDFKAHLVYIIQSKLKKHFSQLEIGDFTSEIIMYRNLSEIYVI
LRGNLHLTHHKNIVQKYNVQERLYTLPSEVISDFKAHLVYIIQSKLKKHFSQLGGQTISFPCLGIVHKFLDCDNMGRDVV
PLGEFMVWPGWFDKFHETDKDLIFISQRVNIESFEEIQNGGKSESFVAVVGQTVTSV
```

47 - 66:	EEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEE

A0A397J4I1 **A0A397J4I1_9GLOM** (1051 aa)
Uncharacterized protein. *Diversispora epigaea*

```
MSTSYKCPYCNIRYFSNRNSYSQHVNRCINLYDVSTEESNTEVSEVTDMLLDNDDFNRIEERQSVQEIENLPSGSEITDL
FEYGDYDADASVSLEVISNIPERFEEILFESSRNEDSDVENLQNEDSNIERLQNEDLDVRSESSRNEDSDVEEFPNESYA
DLMTLVTKYNLNNKAGNAIIKFFNKHSNLPISPLPKNIETGQKYMDKMNLSRLLYYKHRILVHNNKEYFINYQPVIKCIE
NLLSNPEISQLFVYDYKKLEIENEQSYGEQYTGNWWKKAKESIPSVAYILSIILYSDATTTDTLGKGSLHPIYISLGNIP
TWRRNKEDAKQLLGYLPILSAKDEREKKSSEFKKLVRETFHNSIKFLLDPLFTNDDDDGDGIELKIDNEIFWFFPRVSTI
ICDWPEACTFSLTYKSTNSNYPCHFCLVSKENLNNTRLRDDQMVLRNKENMLQYYNNGTTEKASLEPVFNYFWNIPNINV
YVATVPDRMHHLDLGLYRYQIEFTKKLLFEAEGRSLVDKMNWRITLIPRHSELKIFSGGLQSIALLTADNYRNIMKVMVF
VVDDLLNKDLSEVYVKWNEMYLLSRQETFKESDLKNFQEAIEKWANLFIKLFGQFSNSDFKLPKLHSWVHHIVDTIREFG
AINGYTTETYEALHKTYVKIPYRLSNKKDVEEQMMKTIRRKAIIKQNDFKKKFKTPLKFNYSSKLFEFDISEAFEFIDKY
KNETNLDEKMIKGLDHFIQSLDSYFDLLKISTAQGCHIKIYRSVTLENRAILRTTNMFHKRPWFSNISVTMNDEELFEYQ
SDNGICYAQKFVRKVTNSAIDKRIYPDESYLKSVAAGCAELEFCEYFGGWENKRWSSYYTKYIQSPLLAKHRSLRGSITN
RVRSALFAVFGEHELPYIDTKSAPQEIKEWKDSEKLKNAYERLYQRIDSDKEMTWCARIIQKTWPNFKKLTKEKIAFGMA
VCQYMLNLKTESIKINDEEIRKIMKVKKKKLEEGQIIGLDNEEGEEEEEEEEEEEEEEEEEEEKEREEREEEYEDEVIF
TXIFYLVLYFI
```

1005 - 1024:	EEEEEEEEEEEEEEEEEEE

A0A397YII9 **A0A397YII9_BRACM** (337 aa)
NAC domain-containing protein. *Brassica campestris (Field mustard)*

```
MPHCAVKVLADSDLQVTVSTNAWTAAAYPYFEKDEYWFFLHRKQQANDKKNVDRRLGDLGTWKARGRSTNIYIGAQLVGI
KQKYELMKGKVKTGWFQFEYTRFSNKFEKICVAHLIFAKKPEVDYPSDISEEEEEDEEEEEEEEEEEEEEEEEEEEEEE
EEEEESADEEEQGLQAQAHEAELVNEQQGLHEQVLNLEEEEAAASDEVEQTLANEEQRLQQVQAHEVELGNEHQGLQEQV
VNFAHEEALTFVNDFLDDDDDEDWARFLNTDDDGLAIDDLFEDGDSEKTLEHVNEQQSLQDQVLNLEEEAAAAADDEEEQ
TRVNEVEQQGGVAGTSS
```

137 - 156:	EEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEE

141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE

A0A397ZDW5 **A0A397ZDW5_BRACM** (412 aa)
Uncharacterized protein. *Brassica campestris (Field mustard)*

```
MVELEEKEEELEEDDDINDEQELEEEEDDDDEEEEEEEEEEEEEEEEEEEEEEEEEEEEDNDDDDDDEEKEEEDNDDDDDD
DDEEIEVLCKVICPRSHPDHPHTLSFRTGKAITCYSCGNQSGVYYYCTTCDVRFKKDCPFHSNKITHPYHLQHPLTYIRL
NTESEINNTIQTQSPFIFDACSWCGNKPDTWVYSCYICSFCLCVPCSKNTPPLTIANPKSHHHPLLFLPRPLLVPCDACG
LVRASEASYTCFQCNYMVHESCMSLPRVIKLTRHSHRLSFTPFLPPSVLSCGVCYRAVDVRFGQYSCDHEDCFYVVHSKC
ATHDEVWDGRELEWEPESQEEAEDDVASFKKVGGDLIKYFSHDHHLKLENYDGVRDAKKQCEACILPIDPRCFYGCTQCD
YSLHEWFQVQVH
```

32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE

A0A398AHJ2 **A0A398AHJ2_BRACM** (482 aa)
Uncharacterized protein. *Brassica campestris (Field mustard)*

```
MASRHHHACSQSHNHHNQIPLVPTSPHCCTHSNHPSPPPPDTLLHLLASYLQTHQQETHFPNQTCSCNQNNVPRQQHDQV
ILSCLLRKIDALESSLNKFAPFHDQRRDRHSTVRDSAARVIQTHFRSYLVRRSISFRHLKELAVIKSSFLSLKSSVSGKP
IFPYKVVSRKATDLLLQLDSIQGRVDPMIRSSKRSLSRDLVRFLQYVDDCVVRRYAADVSFVGSHSKRPQGFGVVEERRV
EKLRNRMGKVFVTCDEGEELDSTTDDSEEVSIDKRKSGSSKFRTGANVVKPTVRKTMVLDKNRTVYQDESVDSSEEETLV
VTRDNERKHHGLKTRKMVLVKEGGGKSRVVKTVRFDEDGNVYKVYGDTPEASSISEEGDDSTSGSNDGNGDKKGNEVEEI
KYVPKEKEGFEEEEEEEEEEEEEEEEEEEEEEETQSEKEVSSSEGSERDATGSNEHKKRQIQVQKGNLMVSPPLPLKM
EP
```

411 - 430:	EEEEEEEEEEEEEEEEEEEE
412 - 431:	EEEEEEEEEEEEEEEEEEEE
413 - 432:	EEEEEEEEEEEEEEEEEEEE
414 - 433:	EEEEEEEEEEEEEEEEEEEE
415 - 434:	EEEEEEEEEEEEEEEEEEEE
416 - 435:	EEEEEEEEEEEEEEEEEEEE

A0A398AIP5 **A0A398AIP5_BRACM** (318 aa)
Uncharacterized protein. *Brassica campestris (Field mustard)*

```
MLLRTTSAPILNSWLQQHCSRESSPEPESLLQPRNRSLSLLASKSIDEHTGEMLHQAFSEHRESVLKSSYNDHDSSNVLP
RRQRRSSLDESSHGTAYNGKILDPSSTLLTERLFSGSGLGEKVSDDEDHLEALVIGGAGGMGSSGVKICNGGDDSGSSGS
EDATDVYYREMINLTPGNSLLTGNYAKFLKEVRGDMKKAEEYCERAILGNTNDGNVLSLYADLILHNHGDRKRAHSYFQQ
AAKMSPEDCYVQASYARFLWDVEDDEYEEEEEEEEEEEEEEEEEEEEKEQLSDEIGHMPPTTIFRDFPKHARISTTS
```

268 - 287:	EEEEEEEEEEEEEEEEEEEE
269 - 288:	EEEEEEEEEEEEEEEEEEEE

A0A398BH04 **A0A398BH04_9BACI** (97 aa)
Uncharacterized protein (Fragment). *Peribacillus asahii*

```
EEESSGYEEESSGYEEESSGYEEESSSSGEEEETEEEEEEEEEEEEEEEEEEEEEEEEAEEEEEEAEEEEEEEEEEAEEEEE
AEEEEEEEEEAEEEEES
```

35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE

38 - 57:	EEEEEEEEEEEEEEEEEEEE

A0A3B0JWS9 **A0A3B0JWS9_DROGU** (396 aa)
Blast:Troponin T, skeletal muscle. *Drosophila guanche (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAK
RKISRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSS
AAMERNKTKEQLEEEKKISLSFRIKPLAIEGFGESKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQL
RHKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGFDEITKDSNEKIWNEKKDQYTGRQKSKLPKWFG
ERPGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE

A0A3B0JWU0 **A0A3B0JWU0_DROGU** (394 aa)
Blast:Troponin T, skeletal muscle. *Drosophila guanche (Fruit fly)*

```
MKSTPAPRRRRLSRRPERRRKKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAKRK
ISRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSSAA
MERNKTKEQLEEEKKISLSFRIKPLAIEGFGESKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRH
KALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGFDEITKDSNEKIWNEKKDQYTGRQKSKLPKWFGER
PGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE

A0A3B0JWW6 **A0A3B0JWW6_DROGU** (393 aa)
Blast:Troponin T, skeletal muscle. *Drosophila guanche (Fruit fly)*

```
MKSTPAPRRRRLSRRPERRRKKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAKRK
ISRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGLGLSSAAM
ERNKTKEQLEEEKKISLSFRIKPLAIEGFGESKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHK
ALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGFDEITKDSNEKIWNEKKDQYTGRQKSKLPKWFGERP
GKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE

A0A3B0JZP8 **A0A3B0JZP8_DROGU** (395 aa)
Blast:Troponin T, skeletal muscle. *Drosophila guanche (Fruit fly)*

```
MSDDEEYTSEEEEVVEETREETKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAKR
KISRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSSA
AMERNKTKEQLEEEKKISLSFRIKPLAIEGFGESKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLR
HKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGFDEITKDSNEKIWNEKKDQYTGRQKSKLPKWFGE
RPGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE

A0A3B0K1J9 **A0A3B0K1J9_DROGU** (395 aa)
Blast:Troponin T, skeletal muscle. *Drosophila guanche (Fruit fly)*

```
MSDDEEYTSSEEEEVVEETREETKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAK
RKISRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGLGLSSA
AMERNKTKEQLEEEKKISLSFRIKPLAIEGFGESKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLR
HKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGFDEITKDSNEKIWNEKKDQYTGRQKSKLPKWFGE
RPGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE

A0A3B0KE14 **A0A3B0KE14_DROGU** (372 aa)
Blast:Troponin T, skeletal muscle. *Drosophila guanche (Fruit fly)*

```
MSDDEEYTGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAKRKISRAEEEQKMAQRKKEEEERR
VREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGLGLSSAAMERNKTKEQLEEEKKISLSFRI
KPLAIEGFGESKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQV
ASKYERRVDTRSYDDKKKLFEGGFDEITKDSNEKIWNEKKDQYTGRQKSKLPKWFGERPGKKAGEPETPEGEEDAKADED
IVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE

A0A3B0KJ96 **A0A3B0KJ96_DROGU** (373 aa)
Blast:Troponin T, skeletal muscle. *Drosophila guanche (Fruit fly)*

MSDDEEYTGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAKRKISRAEEEQKMAQRKKEEEERR
VREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSSAAMERNKTKEQLEEEKKISLSFR
IKPLAIEGFGESKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQ
VASKYERRVDTRSYDDKKKLFEGGFDEITKDSNEKIWNEKKDQYTGRQKSKLPKWFGERPGKKAGEPETPEGEEDAKADE
DIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE

345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE

A0A3B0KN26 **A0A3B0KN26_DROGU** (373 aa)
Blast:Troponin T, skeletal muscle. *Drosophila guanche (Fruit fly)*

MSDDEEYTGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAKRKISRAEEEQKMAQRKKEEEERR
VREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSSAAMERNKTKEQLEEEKKISLSFR
IKPLAIEGFGESKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEALTGKYPPKIQ
VASKYERRVDTRSYDDKKKLFEGGYNTVYAETLEKTWQERQERFTQRTKSKLPKWFGERPGKKAGEPETPEGEEDAKADE
DIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE

345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE

A0A3B0KRJ7 **A0A3B0KRJ7_DROGU** (395 aa)
Blast:Troponin T, skeletal muscle. *Drosophila guanche (Fruit fly)*

MSDDEEYTSEEEEVVEETREETKPPQTPAEGEGDPEFIKRQDQKRSDLDEQLKEYISEWRKQRSKEEDELKKLKEKQAKR
KISRAEEEQKMAQRKKEEEERRVREAEEKKQREIEEKRMRLEEAEKKRQAMLQAMKDKDKKGPNFTIAKKDAGVLGLSSA
AMERNKTKEQLEEEKKISLSFRIKPLAIEGFGESKLREKAQELWELIVKLETEKYDLEERQKRQDYDLKELKERQKQQLR
HKALKKGLDPEALTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGYNTVYAETLEKTWQERQERFTQRTKSKLPKWFGE
RPGKKAGEPETPEGEEDAKADEDIVEDDEEVEEEVVEEEDEEAEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE

367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE
376 - 395:	EEEEEEEEEEEEEEEEEEEE

A0A3B1JPC7 **A0A3B1JPC7_ASTMX** (795 aa)
Uncharacterized protein. *Astyanax mexicanus (Blind cave fish) (Astyanax fasciatus mexicanus)*

MSRRKQGNPQHLSLSHRERAQHEPTHDADTDCHSPDPSLVSPVAGERDLLTCGQCQTNFPLGDILAFIEHKRRLCRGAGG
CYEKAGDRGSGPSSPRSQRAGPVEIGIQVTPGGEDEEKRLTPARGICPKQETIPTGKDEPSSYICTTCKQTFTSAWFLLQ
HAQNTHGIRIYLDNHPSSCSLTPRMALPPPLGADALPRSPLSSFLGDTSNPFHLLRLAAPLLREPPPAAYMETRIPSTPP
FVSPPPPPRHHLERLGPEEMGILSQHPSAFERVMRLAPMPMEPPPMDFSRRLRELAGNNNNSGGPTPPLSPNRVPPMHRL

```
LSPTLFQASSKPPAAFLSTPPQSMQAPSRSSSSPPLGQGGKVKSCEFCGKTFKFQSNLIVHRRSHTGERPYKCHLCDHAC
SQASKLKRHMKTHMHKSASLGSSPEQGSRDSMGEEAKCRDGNGMGEGHDNEEEEEEEEEEEEEEEEEEEEQQNGSSRPE
SNLSMDSEFSRNRENDSRPSPNEKPLSAERATESQYNNLDNHLRLPLGTRPREEMHEAETAAREADAECRPMVNGRGCGP
EDAIPGLFQQKPTPISSPSLSGSSAKRIKVEKDLELPPMPLISSENVYSQLLAGYAASRHFIREPFIGFGDSRQSPFGTS
SEHSSSETGSLRFSTPPGELLEGGALSGRSGSSTPHLHLRGPGPGRPPSSKESRRSDTCEYCGKVFKNCSNLTVHRRSHT
GERPYKCDLCSYACAQSSKLTRHMKTHGQFGKEVYRCDICHMPFSVYSTLEKHMKKWHGEHLMSNEVKLEEADQA
```

451 - 470:	EEEEEEEEEEEEEEEEEEEE
452 - 471:	EEEEEEEEEEEEEEEEEEEE

A0A3B1K9S1 **A0A3B1K9S1_ASTMX** (818 aa)
Uncharacterized protein. *Astyanax mexicanus (Blind cave fish) (Astyanax fasciatus mexicanus)*

```
MSRRKQGKPQHLSKRDFSPEPLSSVVSEERQEQHGLVQVAPEGDQDLLTCGQCQMNFPLGDILIFIEHKRKQCNGTPCMD
KAMDKPPSPSYSELRRASNPVEVGVQVTPEDDDCLSTSSRGICPKQENVTGKDEPSSYTCTTCKQPFSSAWFLLQHAQNT
HGFRIYLESERGSPLTPRVGAPSGMSAEHASQPPLHGIHLPEGSPFNLLRIPNSAREGPPLREGRFPPTPPLFSPPPRHH
LDPHRMEHLSPEELALATHHPSAFDRVLRLNPMPLDPPAMDFSRRLRELAGNTSGSTPPLSPNRPSPMQRLLQPFQSNAK
PPFLSTPPLPSVQSPSGSQSTPTPLPQQPNTPMKSKACEFCGKTFKFQSNLIVHRRSHTGEKPYKCHLCDHACTQASKLK
RHMKTHMHKSSPMTVKSDDGLSTASSPEPGTSDLVGSASNALKSVVAKFKSENDRMIPENGEEEEEEEEEEEEEEEEEE
EEEGEDEEELERERGRNSFHFGLNLEAARHHENSSGRLGVNEDSIPRSLPEVMQGMGLAASMQHYSEAFHQHKRGALNSD
SDAHRDMCDEDSALESDRAQEGCGSAINGRGSSPSESASVGLSKKLLLGSPSSLSPLSKRIKMEKDFDLPTPTIPNTENV
YSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRFSTPPGELDGGVSGRSGTGSGGSTPHLGGHGRPSSKD
GRRSDTCEYCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQSSKLTRHMKTHGQVGKDVYKCEICQMPFSVYSTLEK
HMKKWHSDRALNSEIKTE
```

462 - 481:	EEEEEEEEEEEEEEEEEEEE
463 - 482:	EEEEEEEEEEEEEEEEEEEE
464 - 483:	EEEEEEEEEEEEEEEEEEEE

A0A3B1KII4 **A0A3B1KII4_ASTMX** (371 aa)
BHLH domain-containing protein. *Astyanax mexicanus (Blind cave fish) (Astyanax fasciatus mexicanus)*

```
MMEKPKREEEGGQTACRGGGHEEEEEEEEEEEEEEEEEEEEGEEGVCERQEGTKLSRRRKRRRRKGAGSVILQRGGRVGG
AFVALGGALGAPVGGVRGIKGEAVEENSRLQCESRAPPGLCHIPPPHPPPSSLPHPAATPPPPHPPHSAPPAPAPAPPLL
LLLPHSEPRAARMVQLSPAALPPPARALLYGTMAQPLGHSGFAGEAEQYGMYPSHRVKRRPAPYEIEINDGSQPKIVRRI
FTNSRERWRQQNVNGAFAELRKLIPTHPPDKKLSKNEILRLAMKYINFLAKLLNDQDEVMVGSDGGPRIREGRDGLVRED
LLQDMLSPNSSCGSLLDGDGSPESFTEEQDSSPAGRGLHHPPMPLDGSNQR
```

22 - 41:	EEEEEEEEEEEEEEEEEEEE

A0A3B3HXX7 **A0A3B3HXX7_ORYLA** (1236 aa)
MYT1 domain-containing protein. *Oryzias latipes (Japanese rice fish) (Japanese killifish)*

```
MQLMEVDADDKRHRTRSKVPVDPALTELFSVYGCPLAKKRKSLDIEPLETSPKRSTLLDDMDNSTMEECYDTDGTEEMDD
REEEEEEGAMEGGGEVVEEEEDVGGYMDYNVEQMEHENEEGEERGEEEDIEEEDVEVEQEEEEDSDEVRVEEAEEEEEEA
IEEVDYEDDEEEEEEEQNMGQEDNQLSPGDSTSEGGGGDGYSKLGPAMEKDDNNNDEYENYDELVAKSLLNLGKIAEDAA
NRAMTESEMNSNSPNSAEDEGEEEEEEEEEEEEEEEEEEEEEDEEEEDEEEEEESELQRGDLSLDVESDVVRETVDSLKLL
AQGHGAVLSDSLDGQDFEGSARPGDQTNYSHNGGNGQMKTTNNGKIEGSDEEVCLSSLECLRNQCFDLARKLSETKSIDR
NGPSQQNHYSCGDPSQQPQHHGYGDFHNSQDSRRTLDRNYSDMDNLMKLEEQLSPRSKAFSSCAQDERYHTSHRDFDEDT
ASITSDRSEEVFDMTKGNLSLLEKAIALESERAKAMRDKLAAEAARRDGVRYAHEDHGPRHGYGVERKARLPDGMKKPFF
HKDPSRADKKESRCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRVPPEIVAMYENVLKCPTPGCTGRGHVNSNRNSHRSLS
GCPIAAAEKLAKAQEKHQSCDGPKSNQSSDRVLSTPRSNLAKELEKYSKTSFDYSAFDSTNNHHVYGKRAIAPKAHGQRD
ASPKGHDAKRYCKNSSSASSTTSTYAPSSSNSSLSCIGGGGGGGGGGGGGGSSASSTCSKSSFDYSHDMEAAHMAATAIL
NLSTRCREMPHGIGGKPQDLCSQSPGLDVDENGTLDLSMSKRLCGGGAGDAVLTPLEPMSPQRQAALLGSRCYGMGDAAD
CWDLPVDYTKIKHIDEDEKETDDLDPFQDLLDDRSYTTDVNMPSPKPKYVQCKETKKDLITLSGCPLADKSIRSMLANNA
QELKCPTPGCDGSGHITGNYASHRSLSGCPRARKSGIKIIHSKENKEDQEPIRCPVPGCDGQGHVTGKYASHRSASGCPI
AAKRQKDGYLNGIQFTWKSGKTEGMSCPTPGCDGSGHVSGSFLTHRSLSGCPRATSAMRKARLSGVEMLTIKQQHASNVL
DHEEEIKQLDEEIKDLSESNSQVEADMIKLRTQITTMESSLKSLEEENKKPLSHKEPLLRTSSCLQLHQQESLSEQNFDA
YVTTLTDMYTNQDQYQSVENKTLLENIKQAVQGIQV
```

262 - 281:	EEEEEEEEEEEEEEEEEEEE

A0A3B3I6E1 **A0A3B3I6E1_ORYLA** (1257 aa)
MYT1 domain-containing protein. *Oryzias latipes (Japanese rice fish) (Japanese killifish)*

```
MQLMEVDADDKRHRTRSKVPVDPALTELFSVYGCPLAKKRKSLDIEPLETSPKRSTLLDDMDNSTMEECYDTDGTEEMDD
REEEEEEGAMEGGGEVVEEEEDVGGYMDYNVEQMEHENEEGEERGEEEDIEEEDVEVEQEEEEDSDEVRVEEAEEEEEEA
IEEVDYEDDEEEEEEEQNMGQEDNQLSPGDSTSEGGGGDGYSKLGPAMEKDDNNNDEYENYDELVAKSLLNLGKIAEDAA
NRAMTESEMNSNSPNSAEDEGEEEEEEEEEEEEEEEEEEEEEDEEEEDEEEEEESELQRGDLSLDVESDVVRETVDSLKLL
AQGHGAVLSDSLDGQDFEGSARPGDQTNYSHNGGNGQMKTTNNGKIEGSDEEVCLSSLECLRNQCFDLARKLSETKSIDR
NGPSQQNHYSCGDPSQQPQHHGYGDFHNSQDSRRTLDRNYSDMDNLMKLEEQLSPRSKAFSSCAQDERYHTSHRDFDEDT
ASITSDRSEEVFDMTKGNLSLLEKAIALESERAKAMRDKLAAEAARRDGVRYAHEDHGPRHGYGVERKARLPDGMKKPFF
HKDPSRADKKESRCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRVPPEIVAMYENVLKCPTPGCTGRGHVNSNRNSHRSLS
GCPIAAAEKLAKAQEKHQSCDGPKSNQSSDRVLSTPRSNLAKELEKYSKTSFDYSAFDSTNNHHVYGKRAIAPKAHGQRD
ASPKGHDAKRYCKNSSSASSTTSTYAPSSSNSSLSCIGGGGGGGGGGGGGGSSASSTCSKSSFDYSHDMEAAHMAATAIL
NLSTRCREMPHGIGGKPQDLCSQSPGLDVDENGTLDLSMSKRLCGGGAGDAVLTPLEPMSPQRQAALLGSRCYGMGDAAD
CWDLPVDYTKIKHIDEDEKETDDLDPFQDLLDDRSYTTDVNMPSPKPKYVQCKETKKDLITCPTPGCDGSGHLTSNFASH
RSLSGCPLADKSIRSMLANNAQELKCPTPGCDGSGHITGNYASHRSLSGCPRARKSGIKIIHSKENKEDQEPIRCPVPGC
DGQGHVTGKYASHRSASGCPIAAKRQKDGYLNGIQFTWKSGKTEGMSCPTPGCDGSGHVSGSFLTHRSLSGCPRATSAMR
KARLSGVEMLTIKQQHASNVLDHEEEIKQLDEEIKDLSESNSQVEADMIKLRTQITTMESSLKSLEEENKKPLSHKEPLL
RTSSCLQLHQQESLSEQNFDAYVTTLTDMYTNQDQYQSVENKTLLENIKQAVQGIQV
```

262 - 281:	EEEEEEEEEEEEEEEEEEEE

A0A3B3I8X0 **A0A3B3I8X0_ORYLA** (937 aa)
Uncharacterized protein. *Oryzias latipes (Japanese rice fish) (Japanese killifish)*

```
MTWTFCSRRSSVMEETLTCSRSPFSQVFGRQGQLMRATVQSLNSLNDQIASFMVTGPKSPEEEEEEEEEEEEEEEEEEEE
EEEEKEEKEVQQPFPHPEKETLQKSMSLMRHLLVDAQAKILKMMDDNKQLAQRIDGAIQSASQEVTNLRSELSATSRRLA
ELGATDPSVNVLETLQHNHNDSPSHPRQKPSATDLCYKTEISSLMDFHSPDASLDKVLLREEVAQLQEEVHLLRQMKDML
SKDLEETQGGSSADVLSITELRVQLTQKEQELDRAKEALQAMKSDRKRLKAEKADLVNQMQQLYATLESREEQLRDFIRN
YEQHRKESEDAVKALAKEKDLLEREKWDLRRQTKEATEHTGMLRSQLDLKENRIKELEAELAMMSNCVNQRMEFRLFERL
GDRDYSPRFIAAKQSLATLTKDVPKRHSLAMPTEAVVNGNNQEWVMQADLPLTAAIRQSQQTLYVHTGHPTDRQVAAVRV
SPCHSRQPSIISDASAMEGDRSSTPSDINSPRHRTHSLCNSLEDLEEAKRKKKKEKMGLGSLSRVFARGKQRKSLDPGLF
DDSESLYSSAHLSLNLSDGSEDQLDRLQQVELARMTPMSQWRAGTVQAWLEVVMAMPMYIRTCSENVKSGKVLLGLTDED
LEQGLGVTNLMHRRKLRLAIEDYRDADNGKGLSKAADMDHHWVAKAWLNDVGLPQYSQAFQTHLVDGRVLNSLTRFDLEY
HLNVTKKFHQVSLLLGIELLHLLSFEKEALQARRAQCEHQNVDPLVWTSHRVMKWIRDIDLKEFADNLQNSGVHGAVLIL
DPTFNTDAMATALGIPTSKHMVRRHLVEEMRTLIPSARVDAKQEYECLGLGAPPTLLCQNSPGKLPSSNCKHTDEESLLK
RRAVKPPLGFSPKNHGGGDQSRHRTFGSLPREVRDHTPPRAEGSPIRGCTSIEVTNV
```

61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE

A0A3B3IBP8 **A0A3B3IBP8_ORYLA** (909 aa)
Uncharacterized protein. *Oryzias latipes (Japanese rice fish) (Japanese killifish)*

```
MTWTFCSRRSSVMEETLTCSRSPFSQVFGRQGQLMRATVQSLNSLNDQIASFMVTGPKSPEEEEEEEEEEEEEEEEEEEE
EEEEKEEKEVQQPFPHPEKETLQKSMSLMRHLLVDAQAKILKMMDDNKQLAQRIDGAIQSASQEVTNLRSELSATSRRLA
ELGATDPSVNVLETLQHNHNDSPSHPRQKPSATDLCYKTEISSLMDFHSPDASLDKVLLREEVAQLQEEVHLLRQMKDML
SKDLEETQGGSSADVLSITELRVQLTQKEQELDRAKEALQAMKSDRKRLKAEKADLVNQMQQLYATLESREEQLRDFIRN
YEQHRKESEDAVKALAKEKDLLEREKWDLRRQTKEATEHTGMLRSQLDLKENRIKELEAELAMAKQSLATLTKDVPKRHS
LAMPTEAVVNGNNQEWVMQADLPLTAAIRQSQQTLYVHTGHPTDRQVAAVRVSPCHSRQPSIISDASAMEGDRSSTPSDI
NSPRHRTHSLCNSLEDLEEAKRKKKKEKMGLGSLSRVFARGKQRKSLDPGLFDDSESLYSSAHLSLNLSDGSEDQLDRLQ
QVELARMTPMSQWRAGTVQAWLEVVMAMPMYIRTCSENVKSGKVLLGLTDEDLEQGLGVTNLMHRRKLRLAIEDYRDADN
GKGLSKAADMDHHWVAKAWLNDVGLPQYSQAFQTHLVDGRVLNSLTRFDLEYHLNVTKKFHQVSLLLGIELLHLLSFEKE
ALQARRAQCEHQNVDPLVWTSHRVMKWIRDIDLKEFADNLQNSGVHGAVLILDPTFNTDAMATALGIPTSKHMVRRHLVE
EMRTLIPSARVDAKQEYECLGLGAPPTLLCQNSPGKLPSSNCKHTDEESLLKRRAVKPPLGFSPKNHGGGDQSRHRTFGS
LPREVRDHTPPRAEGSPIRGCTSIEVTNV
```

61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE

A0A3B3IPQ6 **A0A3B3IPQ6_ORYLA** (1931 aa)
ATG_C domain-containing protein. *Oryzias latipes (Japanese rice fish) (Japanese killifish)*

```
MTSSMQLAQECLKDPPEASEDPPAPLEGLEMFAETIETVLRRIKVTLLDTIIRIEHQPLDLKTGVALEVHIKRLEYFDEA
VRDPASQTAVPVDIHQPPAFLHKILQLNAVQLFYDNTGTLQDPPEDEHQNLATAREGEEEEEEEEEEEEEEEEEEEEEE
EGEEDDKAKPLVAPPCPPSQPLPIGSCSGFIEMTVKLKQNDMLPGPKVCVCVVSPCVLKARENAFRHRSLSSFILAHQLE
LDGKVGCIHMLLSPDQITHLTDLLAALCIDIEPESKGGGVLSRPLDSDDLRMIEEDLGKQLGSSPRDGDWETETEPEDYV
TSLENGDMFYSMGPAGMSCSVTSIRSGSELSESDMESSTHSFSSFTQPAQGLAHVPRRYPVPGCLPSLPQTSRTRGRSYS
GQAEQLKPDALLRLTFGGLTLTLLTEDPLSKSDGASSLAQVSQVFFRELGFFKDSMFSNRGFHHLRGGFAKACPQSHFRL
TGAAVQVSCEMRSGKRRSRAVTSDLSFSRLEVLECLWEEGEPQYCELLQFQRAGLFTAGGTVGPCAKVHYSLTEKHLRKG
KQRVVHRDSVVQVELAELSAELDLDILSRLGSLNRAFSHCSTQTSTSGLMQAQSFELSSSFTLLSPHAVLRLRFPIADLR
PLHIRRPPSQRAVREETLVLELMELELKHQEAPDLQSNQATPGQPLVPCLTQLLEASFTDLHGSYEGWEGGSFPCIRVKK
SHDSVPRISVRVHGVEAQGPAAGLSGMNLSLMKDLGAAFFESHCEFNEKTSSPFSSNRTMFETEEMVIPAGPEEMLQFQE
QCVAQCQCAVDVIMPLAYILLPSKQAFQSIYNRINNDLLMWEPPPPPPPSAHSPERSSHQREEFQLCKSAFRLDSDSEEE
```

```
ETQFYLASEPSGRMQQSASRFNHNLSLLSLTVIIGKGRIQARTDRKEDQSHGEIALDLEGGKMFSVAQYLNDPNLSFLCL
ESRRVELYHQAVVKATTIPERLEMPSFSPPKHLDPTIYPTEVGVSSVSGREGEPQMLSTAIKITLDLQRNVKEFLVALQL
QGATMRHYVTQTHQSWHEQLVDFLDVIDDPILGYTAPAVITVLHTHLATCAIDYRPLYLPLRALFTAESFSLSSNIIVDT
ATFHLRFILDDSALYLSDKCEVDTVDLRRDYVCILDIDLLELAITTWKGNSTGKLSHPLFELRCSNNVVHLHTCADSCAA
LINLLQYLVSQGDLHPPPRLTSPTEIAGQILPLSESPASLVFCPPAETAEINQYDLADALIDTERSHREESTDQGSPSVP
SGSPVSVYLFPGEASKQIPSVLQRDKHELDGLVSTATEAQADLSDKDSEVSTDNDDFCILEAPGMGIPPRDGEPVVTVLS
QGPIKVKDSHFSRPRGSSDLLRAPSRFPVPQSRLMLREISVVWHLYGGKDFGGKPISIHAPSTNRGRSAPAGVRGSPSRA
VPSSRPQNSWRWAGGSGRQHSLLMEIQLTKVSLQHESYPVAVTGQDGDGAGAPGFGVGPAGEHPLSRQVFIVQELEIRDR
LASSQINKFLYLYTSESMPRRAHSNMLTVKALQVCPESGLGGPECCLRVSLLPLRLNIDQDALFFLKDFFSNLASYVNPY
LPVDTAAEAKPDPSHKEEDAAAGLGPDLTASVETTYSEQSSSSLGSSSSSSDQPIYFREFRFTSEVPIWLDYHGKHVVIE
QGTFAGILIGLAQLNCSELKLKRLCCRHGLLGVDKVIQYAVTEWLTDIRKNQLPGILGGVGPMHSVVQLFHGVRDLFWLP
IEQYRKDGRIIRGLQRGAASFGTSTASAALELSNRLVQAIQATAETVYDILSPTPPLNRYITEGRAPNSRSRRAIQPADL
REGVAKAYDTVREGVIDTAQTLCDVASRGHEQKGLPGAVGGVLRQIPPTVVRPLIVASEATSNLLGGMRNQIKPDARKED
FLKWRTEDAQE
```

138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE

A0A3B3SQC3 **A0A3B3SQC3_9TELE** (805 aa)
Cyclin-dependent kinase 11B-like. *Paramormyrops kingsleyae*

```
MGDEKDTWKVKTLDEILQEKKRRKELEEKSDAKRQKIVEEREAKRDTPEEGELRDNRMEITIRNSPYIREDSTEDRGEED
ESLAIKPPQQMARKDKSHHRKEEKRKDKRRRRSHSAEGGKHMRSKDKEKERENERRKRQREEQDKARRDWERQKRRELAR
AHSRRERDRLEQLERQRERERKLREQQQKEQRELKERERRAEERRKEREVRREVPSHHRGLPDEYGEKSRQSHRSRSPSR
PQRERLDHPDTRKPAVREDKPEDRDLLSDLQDVSDSERKTSTAESSSGSGSGSEEEEEEEEEEEEEEEEEEEEEDTSSQS
EGEEMESASNSQGSAQSADEVSEEEHSEEDYQDERENGNHVSADPVTAAVLFPPWRAVPESRFDRDTEGSVEEEEPEEGE
PTPPSHSRSPTPEESYIPDSPPISPVELKKELPKYLPALQGCRSVEEFQCLNRIEEGTYGVVYRAKDKKTDEIVALKRLK
MEKEKEGFPITSLREINTILKAQHTNIVTVREIVVGSNMDKIYIVMNYVEHDLKSLMETMKQPFLPGEVKTLMIQLLRGV
RHLHDNWILHRDLKTSNLLLSHKGILKVGDFGLAREYGSPLKPYTPVVVTLWYRAPELLLGAKEYSTAVDMWSVGCIFGE
LLTQKPLFPGKSEIDQINKIFKDLGSPSEKIWPGYNELPAVKKMTFTEYPYNNLRKRFGALLSDQGFDLMNKFLTYCPAR
RISADEALKHEYFRETPLPIEPSMFPTWPAKSEQQRVKRGTSPRPPEGGLGYSQLGDDDLKDTGFHLTTTNQGASAAGPG
FSLKF
```

294 - 313:	EEEEEEEEEEEEEEEEEEEE
295 - 314:	EEEEEEEEEEEEEEEEEEEE

A0A3B3UHL3 **A0A3B3UHL3_9TELE** (849 aa)
B-cell lymphoma/leukemia 11A-like. *Poecilia latipinna (sailfin molly)*

```
MSRRKQGKPQHLSKRDFSPEPLSTAVVSSEELSERCSEHSEDSGSLNGHHPVPTAGRLARLGPDSHPSPEQDLLTCGQCQ
ATFPLADILLFIEHKRKRCHGPPCLAIGRGLDKPPSPSPGLALTPSPALNSLRGRRPVEVGVQATLADEDDERFSSPRGI
CPKQEPLPGKEEPTTYTCTTCKQSYGSAWFLLQHAQNSHGFRIYLESEHGSPLTPRMGGPSSLGGGADCPSQPPLHGLHL
PPDASPFNLLRIPGSGSGGRDSVGAGGRFPPTPPLFSPPPRNHLDPHHLSPEELALAAHHPSAFDRVLRLNPPLPLDPPP
TMDFSRRLRELAGNTSGSTPPLSPSRPSPMQRLLQPFQTGGNGGAGGAGGTGPPSSSNTQLKSKCCEFCGKAFKFQSNLI
VHRRSHTGEKPYKCHLCDHACTQASKLKRHMKTHMHKSSSPNTGKSEDGLSIASSPEPGTSEHIGSAKNGEEEEEEEEEE
EEEEEEEEEEEEEEEEGEEEEVQNGERPPKRNNSYHFGLSLEGARQHENSSGIGSRLGGVADETSIPRSLPEVMQGMGLA
ASMQHFSEALNAHKRNAMAQENHLHHHLSRDHHHSRDMCDGDSVLETERVEEGTVSAVNGRGASPNESSSIGLSKKLLLG
SPSPLSPFSKRIKLEKEFDLPTPTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRFSTPPG
ELDGGMSGRSGTGSGGSTPHLGGPGRPSSKDGRRSDTCEFCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQSSKLT
RHMKTHGQVGKDVYKCEICQMPFSVYSTLEKHMKKWHSDRPLSTEIKSE
```

471 - 490:	EEEEEEEEEEEEEEEEEEEE
472 - 491:	EEEEEEEEEEEEEEEEEEEE
473 - 492:	EEEEEEEEEEEEEEEEEEEE
474 - 493:	EEEEEEEEEEEEEEEEEEEE
475 - 494:	EEEEEEEEEEEEEEEEEEEE
476 - 495:	EEEEEEEEEEEEEEEEEEEE
477 - 496:	EEEEEEEEEEEEEEEEEEEE

A0A3B3UHN3 **A0A3B3UHN3_9TELE** (896 aa)
B-cell lymphoma/leukemia 11A-like. *Poecilia latipinna (sailfin molly)*

```
MSRRKQGKPQHLSKRDFSPEPLSTAVVSSEELSERCSEHSEDSGSLNGHHPVPTAGRLARLGPDSHPSPEQDLLTCGQCQ
ATFPLADILLFIEHKRKRCHGPPCLAIGRGLDKPPSPSPGLALTPSPALNSLRGRRPVEVGVQATLADEDDERFSSPRGI
CPKQEPLPGKEEPTTYTCTTCKQSYGSAWFLLQHAQNSHGFRIYLESEHGSPLTPRMGGPSSLGGGADCPSQPPLHGLHL
PPDASPFNLLRIPGSGSGGRDSRFPPTPPLFSPPPRNHLDPHHLSPEELALAAHHPSAFDRVLRLNPPLPLDPPPTMDFS
RRLRELAGNTSGSTPPLSPSRPSPMQRLLQPFQTGGNGGAGGAGGSKPPYLATPPPLQGSMQSPVGSQTTPPTPLPTAGP
PSSSNTQLKSKCCEFCGKAFKFQSNLIVHRRSHTGEKPYKCHLCDHACTQASKLKRHMKTHMHKSSSPNTGKSEDGLSIA
SSPEPGTSEHIGSASNALKSVVAKLKSENNRMLRENGEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEVQNGERPPKRNN
SYHFGLSLEGARQHENSSGIGSRLGGVADETSIPRSLPEVMQGMGLAASMQHFSEALNAHKRNAMAQENHLHHHLSRDHH
HSRDMCDGDSVLETERVEEGTVSAVNGRGASPNESSSIGLSKKLLLGSPSPLSPFSKRIKLEKEFDLPTPTIPNTENVYS
QWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRFSTPPGELDGGMSGRSGTGSGGSTPHLGGPGRPSSKDGR
RSDTCEFCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQSSKLTRHMKTHGQVGKDVYKCEICQMPFSVYSTLEKHM
KKWHSDRPLSTEIKSE
```

518 - 537:	EEEEEEEEEEEEEEEEEEEE
519 - 538:	EEEEEEEEEEEEEEEEEEEE
520 - 539:	EEEEEEEEEEEEEEEEEEEE
521 - 540:	EEEEEEEEEEEEEEEEEEEE
522 - 541:	EEEEEEEEEEEEEEEEEEEE
523 - 542:	EEEEEEEEEEEEEEEEEEEE
524 - 543:	EEEEEEEEEEEEEEEEEEEE

A0A3B3VPY0 **A0A3B3VPY0_9TELE** (695 aa)
B-cell lymphoma/leukemia 11A-like. *Poecilia latipinna (sailfin molly)*

```
LERNNGVHFLSVPTGKEEPTTYTCTTCKQSYGSAWFLLQHAQNSHGFRIYLESEHGSPLTPRMGGPSSLGGGADCPSQPP
LHGLHLPPDASPFNLLRIPGSGSGGRDSVGAGGRFPPTPPLFSPPPRNHLDPHHLSPEELALAAHHPSAFDRVLRLNPPL
PLDPPPTMDFSRRLRELAGNTSGSTPPLSPSRPSPMQRLLQPFQTGGNGGAGGAGGTGPPSSSNTQLKSKCCEFCGKAFK
FQSNLIVHRRSHTGEKPYKCHLCDHACTQASKLKRHMKTHMHKSSSPNTGKSEDGLSIASSPEPGTSEHIGSAKNGEEEE
EEEEEEEEEEEEEEEEEEEEEGEEEEVQNGERPPKRNNSYHFGLSLEGARQHENSSGIGSRLGGVADETSIPRSLPEVM
QGMGLAASMQHFSEALNAHKRNAMAQENHLHHHLSRDHHHSRDMCDGDSVLETERVEEGTVSAVNGRGASPNESSSIGLS
KKLLLGSPSPLSPFSKRIKLEKEFDLPTPTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLR
FSTPPGELDGGMSGRSGTGSGGSTPHLGGPGRPSSKDGRRSDTCEFCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACA
QSSKLTRHMKTHGQVGKDVYKCEICQMPFSVYSTLEKHMKKWHSDRPLSTEIKSE
```

317 - 336:	EEEEEEEEEEEEEEEEEEEE
318 - 337:	EEEEEEEEEEEEEEEEEEEE
319 - 338:	EEEEEEEEEEEEEEEEEEEE
320 - 339:	EEEEEEEEEEEEEEEEEEEE
321 - 340:	EEEEEEEEEEEEEEEEEEEE
322 - 341:	EEEEEEEEEEEEEEEEEEEE
323 - 342:	EEEEEEEEEEEEEEEEEEEE

A0A3B3WE41 **A0A3B3WE41_9TELE** (374 aa)
Chromobox protein homolog 8-like. *Poecilia mexicana*

```
MELSAVGERVFAAESIIKRRIRKGRIEYLVKWKGWSPKYSTWEPEENILDSRLFAAFEQRERERELYGPKKRGPKPKTFL
LKAQAKGKTKSYEFRSEAVRGMHVTYPTPEPVFTPRAREGLRAVVPTIFPPSAVNRGESMRVRPSELSLHEHQRSSLQQT
DSDGHVQTPKKRGPKPKPRFVDDNFSPVVSEPRKRGTEEEEEEEEEEEEEEEEEEEEETRGPHKLSKFQGDEEMRLQKLA
HRHSENHKRHHHHHYYHHHHHTQKVSRGSSHKQLHSHRSMEPHRTKDGSGYLVAHFKQPHKASRGRPTELPPMEKPYFLD
RRSPTRLDDSQDQTAWRPCLSNVEKVLVTDVTANFLTVTIKESSTSKGFFKDKR
```

198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE

A0A3B3YNF3 **A0A3B3YNF3_9TELE** (914 aa)
B-cell lymphoma/leukemia 11A-like. *Poecilia mexicana*

```
MSRRKQGKPQHLSKRDFSPAEPLSTAVVSSEELSERCSEHSEDSGSLNGHHPVPTAGRLARLGPDSHPSPEQDLLTCGQC
QATFPLADILLFIEHKRKRCHGPPCLAIGRGLDKPPSPSPGLALTPSPALNSLRGRRPVEVGVQATLADEDDERFSSPRG
ICPKQEPLPGKEEPTTYTCTTCKQSYGSAWFLLQHAQNSHGFRIYLESEHGSPLTPRMGGPSSLGGGADCPSQPPLHGLH
LPPDASPFNLLRIPGSGSGGRDSVGAGGAVGSGVPGGHHQRFPPTPPLFSPPPRNHLDPHHLSPEELALAAHHPSAFDRV
LRLNPPLPLDPPPTMDFSRRLRELAGNTSGSTPPLSPSRPSPMQRLLQPFQTGGNGGAGGAGGSKPPYLATPPPLQGSMQ
SPVGSQTTPPTPLPTAGPPSSSNTQLKSKCCEFCGKAFKFQSNLIVHRRSHTGEKPYKCHLCDHACTQASKLKRHMKTHM
HKSSSPNTGKSEDGLSIASSPEPGTSEHIGSASNALKSVVAKLKSENNRMLRENGEEEEEEEEEEEEEEEEEEEEEEEEE
EGEEEEVQNGERPPKRNNSYHFGLSLEAARQHENSSGIGSRLGGVADETSIPRSLPEVMQGMGLAASMQHFSEALNAHKR
NAMAQENHLHHHLSRDHHHSRDMCDGDSVLETERVEEGTVSAVNGRGVSPNESSSIGLSKKLLLGSPSPLSPFSKRIKLE
KEFDLPTPTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRFSTPPGELDGGMSGRSGTGSG
GSTPHLGGPGRPSSKDGRRSDTCEFCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQSSKLTRHMKTHGQVGKDVYK
CEICQMPFSVYSTLEKHMKKWHSDRPLSTEIKSE
```

536 - 555:	EEEEEEEEEEEEEEEEEEEE
537 - 556:	EEEEEEEEEEEEEEEEEEEE
538 - 557:	EEEEEEEEEEEEEEEEEEEE
539 - 558:	EEEEEEEEEEEEEEEEEEEE
540 - 559:	EEEEEEEEEEEEEEEEEEEE
541 - 560:	EEEEEEEEEEEEEEEEEEEE
542 - 561:	EEEEEEEEEEEEEEEEEEEE

A0A3B4ATN7 **A0A3B4ATN7_9GOBI** (833 aa)
Uncharacterized protein. *Periophthalmus magnuspinnatus*

```
MSRRKQGKPQHLSKRDFSRKYNPLSQLSARRWKRGLADLLTCGQCQATFPLADIILFIDHKRKRCRGPSCLTMGGRGLDK
PPSPSPALALTPSPAVLRGRRPVEVGVQASLAEGHEDKMVSPRGICPKLEPIPGKEEPTTYTCTTCKEAYGSAWFLLQHA
QHSHGFRIYLDSELGSPLTPRMGGPSSLGGGADCPSQPPLHGLHLPPDASPFNLLRIPGSGSGGRDSRFPPTPPLFSPPP
RNHLEPHHLSPEELALAAHHPSAFDRVLRLNPPMSLDPPPSMDFSRRLRELAGNSSGPSPPLSPSRPSPMQRLLQPFQTG
GNGGNVTGASKPPYLATPPPIPNSMQSPVGSQTTPTTPVPSSGASNSTGTNMKTKCCEFCGKSFKFQSNLIVHRRSHTGE
KPYKCHLCDHACTQASKLKRHMKTHLHKSLSSPNTAKSEDGLSTASSPEPGTSEHMASNALKSVVAKLKSENGRLLRENG
EEEEDEEEEEEEEEEEEEEEEEEEEEEMEVTQNGDRLERRNNSFHFSLNLDGRPHENNGSVGNRLEESAIPRSLPEVMQGM
GLAASMQHFSEALSAHKRNALRDLCEAESILENERGDEMTTVNGRGASPNESASVGISKKLLLGSPSPLSPFSKRIKLEK
EFDIPTPTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRFSTPPGELDGGLSGRSGTGSGG
STPHLGGPGRPSSKDGRRSDTCEYCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQSSKLTRHMKTHGQVGKDVYKC
EICQMPFSVYSTLEKHMKKWHSDRPLSTEIKSE
```

486 - 505:	EEEEEEEEEEEEEEEEEEEE
487 - 506:	EEEEEEEEEEEEEEEEEEEE

A0A3B4AW40 **A0A3B4AW40_9GOBI** (691 aa)
Uncharacterized protein. *Periophthalmus magnuspinnatus*

```
LAQRKQRKEEPTTYTCTTCKEAYGSAWFLLQHAQHSHGFRIYLDSELGSPLTPRMGGPSSLGGGADCPSQPPLHGLHLPP
DASPFNLLRIPGSGSGGRDSVGTVGGGSRFPPTPPLFSPPPRNHLEPHHLSPEELALAAHHPSAFDRVLRLNPPMSLDPP
PSMDFSRRLRELAGNSSGPSPPLSPSRPSPMQRLLQPFQTGASNSTGTNMKTKCCEFCGKSFKFQSNLIVHRRSHTGEKP
YKCHLCDHACTQASKLKRHMKTHLHKSLSSPNTAKSEDGLSTASSPEPGTSEHMASNALKSVVAKLKSENGRLLRENGEE
EEDEEEEEEEEEEEEEEEEEEEEEMEVTQNGDRLERRNNSFHFSLNLDGRPHENNGSVGNRLEESAIPRSLPEVMQGMGL
AASMQHFSEALSAHKRNALAQENHLNHHHLNRDHHHLLQRDLCEAESILENERGDEMTTVNGRGASPNESASVGISKKLL
LGSPSPLSPFSKRIKLEKEFDIPTPTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRFSTP
PGELDGGLSGRSGTGSGGSTPHLGGPGRPSSKDGRRSDTCEYCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQSSK
LTRHMKTHGQVGKDVYKCEICQMPFSVYSTLEKHMKKWHSDRPLSTEIKSE
```

324 - 343:	EEEEEEEEEEEEEEEEEEEE
325 - 344:	EEEEEEEEEEEEEEEEEEEE

A0A3B4CHC4 **A0A3B4CHC4_PYGNA** (478 aa)
Kinase (EC 2.7.-.-). *Pygocentrus nattereri (Red-bellied piranha)*

```
MSPAIEGMETEQQQQQLYLGKGVLLEPFVHQVGGHSCVLRFGEQTICKPLIPREHQFYKSLPAAMRKFTPQYRGVVSVSF
EEDEEGNLCLIAYPLHSELGDLENVDPSADLEPKNKMKWSNKMLLDNEGYSKDRTRHSRKDKDKSLKREEELEWFQQAEV
LYYSLERSNAAGPQFKHNPWSLKCHQQHLQRMKENAKHRNQYKFILLENLTWRHRVPCVLDLKMGTRQHGDDASEEKKAV
QIRKCQQSTSASIGVRLCGMQVYQSASGQLMFMNKYHGRKLTLSGFKEALFQFFHDGRRLRLELLSPVLRRLREMQAALE
ACESYRFYSSSLLIIYDGDPPRSRRSPEEGLSDEEDEEEEEEEEEEEEEEEEEEEEEEEGGAFGFPRSAAGAGGSSSASSS
SSAISSSAGSSSNSAVSCRGTRLDIGPVVDVRMIDFAHTTCRHYREDSVVHEGQDSGYIFGLQNLITIISQLEDHSTD
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE

A0A3B4CXV5 **A0A3B4CXV5_PYGNA** (891 aa)
Phosphatase and actin regulator 4. *Pygocentrus nattereri (Red-bellied piranha)*

```
MGQSLSLETASQDSSTHTDDEGDHQHNTTGSEGGNTGEGTPPPKRKGKFSTLGKIFKPWKWRKKKSSEKFKETSEVLERK
MSMRRPRQELIEQGVLKELPENEVDEAHGPKLPYVKNGHTLPVGGSSGSGSRGLEPIRSRAEPDLRVNQAWLPQIEERRG
RVPSDGERRGMLGIRPTSHDEARRGGRSGGEEWKTNLAWQMDENRRGGRADEKRPGLIKAPSEDCRRTRPEPEWKPTLPR
HSSTEEGRGRRESDSSHYVPDSEALRDTLREPLPPKQSVMPPKWLMSSTPEPGMEGSPRTPAHSPATSFSSSSASSSSPP
SSATSAAGKPLRTASSAGANTQASSGALYTPSSVHSSSSVGTAPTQPVKQPPLPPPKPVNRTTNPAMLASTLHGGDPFPL
YWSCWKREGDYDVYLSLPVYLCRRAGGVRTAEFAQMTGGTNLVPAKPSPPMPPKRTTPVTKRNTEDSNLPISSLPSMLSP
EDRANIPGGFPLPPPPPSPPIPTHIPPSPPRGHTHHLLHQHSYPHPLPQPLPVHFDPPSPLQEPPARQAPVPLHIMIQRA
LTSPGPALPHPDGSQRAHSLLFETPPEYQGVRPLPVTIQPLKVGEDDYSDEEEEEEEEEEEEEEEEEEEEEEEEEDEP
SPEHLPLPQTQPELEPRSRRCLVGELSVSMIPEGPDSSEGEEGEEDQHAEESDSDGPVLYKEDESDEDEEDESPPSALAS
RVKRKDTLALKLSSRPSAPDRQAPERQARVEHTGLSWQSKEQWEAIRTQIGTALTRRLSQRPTAEELEQRNILQPKNEAD
RQAEVREIKRRLTRKLSQRPTVAELQARKILRFHEYVEVTLAQDYDRRADKPWTKLTPADKAAIRKELNEFKSSEMEVHE
ESRIYTRFHRP
```

611 - 630:	EEEEEEEEEEEEEEEEEEEE
612 - 631:	EEEEEEEEEEEEEEEEEEEE

A0A3B4CY03 **A0A3B4CY03_PYGNA** (877 aa)
Phosphatase and actin regulator 4. *Pygocentrus nattereri (Red-bellied piranha)*

```
MENRDDEGDHQHNTTGSEGGNTGEGTPPPKRKGKFSTLGKIFKPWKWRKKKSSEKFKETSEVLERKMSMRRPRQELIEQG
VLKELPENEVDEAHGPKLPYVKNGHTLPVGGSSGSGSRGLEPIRSRAEPDLRVNQAWLPQIEERRGRVPSDGERRGMLGI
RPTSHDEARRGGRSGGEEWKTNLAWQMDENRRGGRADEKRPGLIKAPSEDCRRTRPEPEWKPTLPRHSSTEEGRGRRESD
SSHYVPDSEALRDTLREPLPPKQSVMPPKWLMSSTPEPGMEGSPRTPAHSPATSFSSSSASSSSPPSSATSAAGKPLRTA
SSAGANTQASSGALYTPSSVHSSSSVGTAPTQPVKQPPLPPPKPVNRTTNPAMLASTLHGGDPFPLYWSCWKREGDYDVY
LSLPVYLCRRAGGVRTAEFAQMTGGTNLVPAKPSPPMPPKRTTPVTKRNTEDSNLPISSLPSMLSPEDRANIPGGFPLPP
PPPSPPIPTHIPPSPPRGHTHHLLHQHSYPHPLPQPLPVHFDPPSPLQEPPARQAPVPLHIMIQRALTSPGPALPHPDGS
QRAHSLLFETPPEYQGVRPLPVTIQPLKVGEDDYSDEEEEEEEEEEEEEEEEEEEEEEEEEDEPSPEHLPLPQTQPEL
EPRSRRCLVGELSVSMIPEGPDSSEGEEGEEDQHAEESDSDGPVLYKEDESDEDEEDESPPSALASRVKRKDTLALKLSS
RPSAPDRQAPERQARVEHTGLSWQSKEQWEAIRTQIGTALTRRLSQRPTAEELEQRNILQPKNEADRQAEVREIKRRLTR
KLSQRPTVAELQARKILRFHEYVEVTLAQDYDRRADKPWTKLTPADKAAIRKELNEFKSSEMEVHEESRIYTRFHRP
```

597 - 616:	EEEEEEEEEEEEEEEEEEEE
598 - 617:	EEEEEEEEEEEEEEEEEEEE

A0A3B4ECL6 **A0A3B4ECL6_PYGNA** (835 aa)
Phosphatase and actin regulator 4. *Pygocentrus nattereri (Red-bellied piranha)*

```
MENRDDEGDHQHNTTGSEGGNTGEGTPPPKRKGKFSTLGKIFKPWKWRKKKSSEKFKETSEVLERKMSMRRPRQELIEQG
VLKELPENEVDEAHGPKLPYVKNGHTLPVGGSSGSGSRGLEPIRSRAEPDLRVNQAWLPQIEERRGRVPSDGERRGMLGI
RPTSHDEARRGGRSGGEEWKTNLAWQMDENRRGGRADEKRPGLIKAPSEDCRRTRPEPEWKPTLPRHSSTEEGRGRRESD
SSHYVPDSEALRDTLREPLPPKQSVMPPKWLMSSTPEPGMEGSPRTPAHSPATSFSSSSASSSSPPSSATSAAGKPLRTA
SSAGANTQASSGALYTPSSVHSSSSVGTAPTQPVKQPPLPPPKPVNRTTNPAMLAEFAQMTGGTNLVPAKPSPPMPPKRT
TPVTKRNTEDSNLPISSLPSMLSPEDRANIPGGFPLPPPPPSPPIPTHIPPSPPRGHTHHLLHQHSYPHPLPQPLPVHFD
PPSPLQEPPARQAPVPLHIMIQRALTSPGPALPHPDGSQRAHSLLFETPPEYQGVRPLPVTIQPLKVGEDDYSDEEEEEE
EEEEEEEEEEEEEEEDEEEEEDEPSPEHLPLPQTQPELEPRSRRCLVGELSVSMIPEGPDSSEGEEGEEDQHAEESDSDG
PVLYKEDESDEDEEDESPPSALASRVKRKDTLALKLSSRPSAPDRQAPERQARVEHTGLSWQSKEQWEAIRTQIGTALTR
RLSQRPTAEELEQRNILQPKNEADRQAEVREIKRRLTRKLSQRPTVAELQARKILRFHEYVEVTLAQDYDRRADKPWTKL
TPADKAAIRKELNEFKSSEMEVHEESRIYTRFHRP
```

555 - 574:	EEEEEEEEEEEEEEEEEEEE
556 - 575:	EEEEEEEEEEEEEEEEEEEE

A0A3B4EEA8 **A0A3B4EEA8_PYGNA** (896 aa)
Phosphatase and actin regulator 4. *Pygocentrus nattereri (Red-bellied piranha)*

```
MLRTPQLPMACCLHTRRHGSWSPDDEGDHQHNTTGSEGGNTGEGTPPPKRKGKFSTLGKIFKPWKWRKKKSSEKFKETSE
VLERKMSMRRPRQELIEQGVLKELPENEVDEAHGPKLPYVKNGHTLPVGGSSGSGSRGLEPIRSRAEPDLRVNQAWLPQI
EERRGRVPSDGERRGMLGIRPTSHDEARRGGRSGGEEWKTNLAWQMDENRRGGRADEKRPGLIKAPSEDCRRTRPEPEWK
PTLPRHSSTEEGRGRRESDSSHYVPDSEALRDTLREPLPPKQSVMPPKWLMSSTPEPGMEGSPRTPAHSPATSFSSSSAS
SSSPPSSATSAAGKPLRTASSAGANTQASSGALYTPSSVHSSSSVGTAPTQPVKQPPLPPPKPVNRTTNPAMLASTLHGG
DPFPLYWSCWKREGDYDVYLSLPVYLCRRAGGVRTAEFAQMTGGTNLVPAKPSPPMPPKRTTPVTKRNTEDSNLPISSLP
SMLSPEDRANIPGGFPLPPPPPSPPIPTHIPPSPPRGHTHHLLHQHSYPHPLPQPLPVHFDPPSPLQEPPARQAPVPLHI
MIQRALTSPGPALPHPDGSQRAHSLLFETPPEYQGVRPLPVTIQPLKVGEDDYSDEEEEEEEEEEEEEEEEEEEEEDEEE
EEDEPSPEHLPLPQTQPELEPRSRRCLVGELSVSMIPEGPDSSEGEEGEEDQHAEESDSDGPVLYKEDESDEDEEDESPP
SALASRVKRKDTLALKLSSRPSAPDRQAPERQARVEHTGLSWQSKEQWEAIRTQIGTALTRRLSQRPTAEELEQRNILQP
KNEADRQAEVREIKRRLTRKLSQRPTVAELQARKILRFHEYVEVTLAQDYDRRADKPWTKLTPADKAAIRKELNEFKSSE
MEVHEESRIYTRFHRP
```

616 - 635:	EEEEEEEEEEEEEEEEEEEE
617 - 636:	EEEEEEEEEEEEEEEEEEEE

A0A3B4EEC8 **A0A3B4EEC8_PYGNA** (850 aa)
Phosphatase and actin regulator 4. *Pygocentrus nattereri (Red-bellied piranha)*

```
MENRDDEGDHQHNTTGSEGGNTGEGTPPPKRKGKFSTLGKIFKPWKWRKKKSSEKFKETSEEVDEAHGPKLPYVKNGHTL
PVGGSSGSGSRGLEPIRSRAEPDLRVNQAWLPQIEERRGRVPSDGERRGMLGIRPTSHDEARRGGRSGGEEWKTNLAWQM
DENRRGGRADEKRPGLIKAPSEDCRRTRPEPEWKPTLPRHSSTEEGRGRRESDSSHYVPDSEALRDTLREPLPPKQSVMP
PKWLMSSTPEPGMEGSPRTPAHSPATSFSSSSASSSSPPSSATSAAGKPLRTASSAGANTQASSGALYTPSSVHSSSSVG
TAPTQPVKQPPLPPPKPVNRTTNPAMLASTLHGGDPFPLYWSCWKREGDYDVYLSLPVYLCRRAGGVRTAEFAQMTGGTN
LVPAKPSPPMPPKRTTPVTKRNTEDSNLPISSLPSMLSPEDRANIPGGFPLPPPPPSPPIPTHIPPSPPRGHTHHLLHQH
SYPHPLPQPLPVHFDPPSPLQEPPARQAPVPLHIMIQRALTSPGPALPHPDGSQRAHSLLFETPPEYQGVRPLPVTIQPL
KVGEDDYSDEEEEEEEEEEEEEEEEEEEEEEEEEEDEEEEEDEPSPEHLPLPQTQPELEPRSRRCLVGELSVSMIPEGPDSSEGE
EGEEDQHAEESDSDGPVLYKEDESDEDEEDESPPSALASRVKRKDTLALKLSSRPSAPDRQAPERQARVEHTGLSWQSKE
QWEAIRTQIGTALTRRLSQRPTAEELEQRNILQPKNEADRQAEVREIKRRLTRKLSQRPTVAELQARKILRFHEYVEVTL
AQDYDRRADKPWTKLTPADKAAIRKELNEFKSSEMEVHEESRIYTRFHRP
```

570 - 589:	EEEEEEEEEEEEEEEEEEEE
571 - 590:	EEEEEEEEEEEEEEEEEEEE

A0A3B4FGZ5 **A0A3B4FGZ5_9CICH** (2173 aa)
Myomegalin-like. *Pundamilia nyererei*

```
MQQVLEAKIQLLQEEAQLARSEAERMASLAGSQSHASLLSLDAVMEEIPEEERPPNILSPSNNKDRLIEELTKELRTKEV
RITELCGEKTTLTLRVEELEGQVHELSNSLLQKDKDVEFYQEELGQERLRIEQEMQSLVEEQQSQLNQYECAAGQCVSEL
QKAQLQVQSLQAKIQESEANNMKLQEKLSEMECELRSLRQASQSQERTIQGLTESLSTKDSEAQELYQLIEGQNTTLCKL
QEIAHHSQLAQSKAPAGVSESLALAQLQGELVGVQSSLFSLGLELEASQRSLRQSQRQADDLMRFRERLNSDLQEALQHR
EVTEKHNQDLRCALHKLRTELQAKEAALKESEAEKHAVTQEKDRSVAQLKSALQDKEQQLQEYSEMVESTGSSKPNPRDA
LLEKLRERIKERDRALEQSIDDKFHCVEEREGQVRRLQLALREKERDLERLRCILSNNEETITSLDGLVRGKELELEQAA
EAYRNLQWLKQQSDEKERNSLREKDTIITQLQAALQTRSQEAQDLTAALVARVQAGPTEVVEELKARLALKEKLFQELLG
DRSRQSKEQQAQIQDLLSTLSSKDQYLQDYSYRLSLVISERTGQLQELRKQLSEREQELHELRWDKQRDTGGETEHLQSL
LKEKEAFIKELMKAQEEAMQPFSKESEAEIKALKEDMQLVLKKEAEAQKEISALRLSLAHQQSEGDATKDNTDHKHVLEQ
LVSEYSKLNDALRAEKRLYQNLTHIHKSDSSSEKIQALHMELDSVQALRRQLEEVLSRTRNTALLLDRAAKKQPDFGELS
TEEEEGDDEDGSSEEFTDSIEEDDDSVNARSLTSGQASVKAQGPECVTRGLVRGAQSQTADVKQLDEAKKTLEFELEEIK
SQLERDGYTSVAQMRSALQKLQRENQALKENQVRAGVVGTNTEKSLSPEEEQEEEEEEEEEEEEEEEEEEEEDTEEEDE
LETSPVPAGKRGPPCVSLSNEPGKRHCMRPCSLNLGTLTSHHLTHQPEAETAVAGDSSQVRALWRDKEDGLREQASRLHA
DLTLSQQENRELQERLMVSEATVQAQAEQLKEYRDLLTETSVQQANKQVQVDLQDLGYETCGRSENEAEREDTSSPEFDD
LEMCTSLSHPQDCEGGGWYAGRCSSSRGAYEMRDESASLQHLVQDLRSQLTRCHKVIRGLQLRVRSLSATSDYASSLERT
PRKVNWALERSPAPSGVEEDEGWLSDTQGARPASKPSRELQELMERVASLEAQLKTTRSEGKGQAEEGKCATWPGKYNSL
IQAQARELSHLRQRMREGQGVCHILTQHLGDTTKAFEELLRANDIDYYMGQSFREQLAQSTALAQRVVTKISGRERVESH
DDKTGHELLALRLSKELQQKDKIIESLHTKLQHRPETPSSCHALSETTDQSDRTSLVSDEYQTNEDLELCSDLDTREYQE
EHRLRQPGLGSDPEVRSSIPPPLPPPPLHGLLKSSSSCPNMLCTAAVGLTRALFSEPVSSSLSIPSGPDGWGHEVMFDPR
PRALSVMAVRPELDTLYKQMNEQNRGFPEPHDKALFTLSPDHHNQHGLSSYSQLSHHAFQPYQLGGIPTGHLMKSDSGLM
```

```
SGGPLWDMENFVGSYSGSSAHQPGSSQTGVNLIEEHLQEVRCLRQRLEESIRTNERLRQQLEEKLATTGRDGGAPTNIYI
QGLDTVTQLSNEIRVLKEENLGLQSRLQASTDTSEEVVQLREAVFTARARLKQSELEAEQWKEELRRLQAHSQEQGQQIH
TLRQERQAGQEKTNRLQHEVSLLQQQLCESRELIHSLQSELHVYDRVCSSTKANKGYLCEVPVLPVELGELLGEVRSLRA
QLQNSVQENSALKQLELHKQLEQKLGVGSPRTPSLSALTASPQRENFYRRQLLHDPAPSPPVRDIGLFNCGSPGPPYSDL
DDSHSTANDPLDPHSELEGDAPDGSFANRHGRHAIGHVDDFSALQQQVLEGRSLVQRMEMTLQACLGPPMLDVNQKQSSE
LIMDYGCVRSFLSNTKTLRQILEEATSLLKMFWRAALPSTDPSIQNLKKEQCMQEEILSLKLRVSEQEEVLKGTIQRLRS
TSRTKESMEHFIVSQLSRTRDVLKKARTNLETNKLRLSSLSSSSSSPYAAEEPGGAARERPADRSFLKAGGASGVTRASQ
RTAARKRSSQCLL
```

933 - 952:	EEEEEEEEEEEEEEEEEEEE
934 - 953:	EEEEEEEEEEEEEEEEEEEE

A0A3B4FKY8 **A0A3B4FKY8_9CICH** (2139 aa)
Myomegalin-like. *Pundamilia nyererei*

```
MQQVLEAKIQLLQEEAQLARSEAERMASLAGSQSHASLLSLDAVMEEIPEEERPPNILSPSNNKDRLIEELTKELRTKEV
RITELCGEKTTLTLRVEELEGQVHELSNSLLQKDKDVEFYQEELGQERLRIEQEMQSLVEEQQSQLNQYECAAGQCVSEL
QKAQLQVQSLQAKIQESEANNMKLQEKLSEMECELRSLRQASQSQERTIQGLTESLSTKDSEAQELYQLIEGQNTTLCKL
QEIAHHSQLAQSKAPAGVSESLALAQLQGELVGVQSSLFSLGLELEASQRSLRQSQRQADDLMRFRERLNSDLQEALQHR
EVTEKHNQDLRCALHKLRTELQAKEAALKESEAEKHAVTQEKDRSVAQLKSALQDKEQQLQEYSEMVESTGSSKPNPRDA
LLEKLRERIKERDRALEQSIDDKFHCVEEREGQVRRLQLALREKERDLERLRCILSNNEETITSLDGLVRGKELELEQAA
EAYRNLQWLKQQSDEKERNSLREKDTIITQLQAALQTRSQEAQDLTAALVARVQAGPTEVVEELKARLALKEKLFQELLG
DRSRQSKEQQAQIQDLLSTLSSKDQYLQDYSYRLSLVISERTGQLQELRKQLSEREQELHELRWDKQRDTGGETEHLQSL
LKEKEAFIKELMKAQEEAMQPFSKESEAEIKALKEDMQLVLKKEAEAQKEISALRLSLAHQQSEGDATKDNTDHKHVLEQ
LVSEYSKLNDALRAEKRLYQNLTHIHKSDSSSEKIQALHMELDSVQALRRQLEEVLSRTRNTALLLDRAAKKQPDFGELS
TEEEEGDDEDGSSEEFTDSIEEDDDSVNARSLTSGQASVKAQGPECVTRGLVRGAQSQTADVKQLDEAKKTLEFELEEIK
SQLERDGYTSVAQMRSALQKLQRENQALKENQVRAGVVGTNTEKSLSPEEEQEEEEEEEEEEEEEEEEEEEEDTEEEDE
LETSPVPAGKRGPPCVSLSNEPGKRHCMRPCSLNLGTLTSHHLTHQPEAETAVAGDSSQVRALWRDKEDGLREQASRLHA
DLTLSQQENRELQERLMVSEATVQAQAEQLKEYRDLLTETSVQQANKQVQVDLQDLGYETCGRSENEAEREDTSSPEFDD
LEMCTSLSHPQDCEGGGWYAGRCSSSRGAYEMRDESASLQHLVQDLRSQLTRCHKVIRGLQLRVRSLSATSDYASSLERT
PRKVNWALERSPAPSGVEEDEGWLSDTQGARPASKPSRELQELMERVASLEAQLKTTRSEGKGQAEEGKCATWPGKYNSL
IQAQARELSHLRQRMREGQGVCHILTQHLGDTTKAFEELLRANDIDYYMGQSFREQLAQSTALAQRVVTKISGRERVESH
DDKTGHELLALRLSKELQQKDKIIESLHTKLQHRPETPSSCHALSETTDQSDRTSLVSDEYQTNEDLELCSDLDTREYQE
EHRLRQPGLGSDPEVRSSIPPPLPPPPLHGLLKSSSSCPNMLCTAAVGLTRALFSEPVSSSLSIPSGPDGWGHEVMFDPR
PRALSVMAVRPELDTLYKQMNEQNRGFPEPHDKALFTLSPDHHNQHGLSSYSQLSHHAFQPYQLGGIPTGHLMKSDSGLM
SGGPLWDMENFVGSYSGSSAHQPGSSQTGVNLIEEHLQEVRCLRQRLEESIRTNERLRQQLEEKLATTGRDGGAPTNIYI
QGLDTVTQLSNEIRVLKEENLGLQSRLQASTDTSEEVVQLREAVFTARARLKQSELEAEQWKEELRRLQAHSQEQGQQIH
TLRQERQAGQEKTNRLQHEVSLLQQQLCESRELIHSLQSELHVYDRVCSSTKANKGYLCEVPVLPVELGELLGEVRSLRA
QLQNSVQENSALKQLELHKQLEQKLGVGSPRTPSLSALTASPQRENFYRRQLLHDPLDPHSELEGDAPDGSFANRHGRHA
IGHVDDFSALQQQVLEGRSLVQRMEMTLQACLGPPMLDVNQKQSSELIMDYGCVRSFLSNTKTLRQILEEATSLLKMFWR
AALPSTDPSIQNLKKEQCMQEEILSLKLRVSEQEEVLKGTIQRLRSTSRTKESMEHFIVSQLSRTRDVLKKARTNLETNK
LRLSSLSSSSSSPYAAEEPGGAARERPADRSFLKAGGASGVTRASQRTAARKRSSQCLL
```

933 - 952:	EEEEEEEEEEEEEEEEEEEE
934 - 953:	EEEEEEEEEEEEEEEEEEEE

A0A3B4FMD2 **A0A3B4FMD2_9CICH** (1304 aa)
Uncharacterized LOC102212400. *Pundamilia nyererei*

```
MDFWGQPRGSGACNFLGVPVLSSWDVDDDEGEVVIGIRPKSSPLPRRKSSVSDEDSEPEPPMCGSRRVSFADAKGLNLVQ
VKEFDTWDVPKLPGYDTSDGEGNDEDEYILSPLNFSLPLLTEELLTKVQEQKVELEKIELLPGTTIVKGVVRVLNISFTK
AIYVRTTLDCWSSHFDLLAEYIPGSSDGLTDCFSFTLTLWPPFREEGARVDFCLRYETPVGTFWANNANKNYVLSCFRRT
KENDQPQKENVNKKSCLKTASSNSSVENSSGKESSTQGNIAADVSNSGLEGDTLKSKNDQSGMSEEHGQKLLIESGVNDS
QRSRRKAARMARVKDYFAQRNGDANNADRDESPPGVPQAAREETPKESHTDVQLFAESNRKPEGSQAKCSKPLLSVSHVL
SPALDRTSENKPEKSESIAFTASVTLAEGESATDIQDDLFDNFAQAEQQHTKSQDSSQEADMGHEYISRTAVRNESLVGQ
TSSFTFGTVVAPLYHQVFGRVGSESQRGAGWENPAQATLNIGGLHPHTGMRQISCTVSTDIKSNNSKALRNVINNQKSNQ
ECTDIAPCNNRVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEASLSLTLNAETLQVLAGTENTDRRCTSTLKGSQTCLEDT
LSCPQTVNILSQADLLNPQIPAESLHPWGEAQEDSVTHDPQGQITAETTQCPLPENPCTHDKTNLDETHAKSNTHEVRTS
PQTSFVKPESSGDLLGHVNEEPDQQSADLEEKRHECELIKALCPGNASFSEVKPCEDLHKLNLHHNDNSVTKATVPDCKL
VEKSDFTTPETLLEARGETNNMGEGSRMTHGSLKDESKSSGETEVTGELAECVTTETQEKTEHCKIKAKEEALCLGEITE
VKDWEMMVKEEENNILIHEEERGIVYLNPGVCEVREKEIANEEFVKGRAVTGVEEDSETIGEAVSGEDGASTEVECAQVI
KMNKTGGREELTEENQVQETEGPVETQLHTKKHFAGKEVSIEWAHIQENKEIKGDGKINLNKEGEGGAEWEKEPKEGNGE
ELDPRYEFLNYRAAEAELVESHSRVAKQEQKDPELCLEEKLEITGSKDGEVLSALVHSGLKDGDESVPVKESIGEEQSAH
IQTEKQCLHTTKAQSEDGNGCAAAEGGALTDEPESDQTSQDSASAESDSGDEVELYMHCLRAVGTGGWSHEDKSTVSKRP
RLSRTKLLSATMPPITEYHDEEQHLSCLQEKLEDSNAAVSPAEERMGQSVLSWTDTFSCSNIAKSLLYATLLVVFLVVAY
HYDFFACLGLYLISLVWLCCQEEK
```

573 - 592:	EEEEEEEEEEEEEEEEEEEE
574 - 593:	EEEEEEEEEEEEEEEEEEEE
575 - 594:	EEEEEEEEEEEEEEEEEEEE
576 - 595:	EEEEEEEEEEEEEEEEEEEE
577 - 596:	EEEEEEEEEEEEEEEEEEEE
578 - 597:	EEEEEEEEEEEEEEEEEEEE
579 - 598:	EEEEEEEEEEEEEEEEEEEE
580 - 599:	EEEEEEEEEEEEEEEEEEEE
581 - 600:	EEEEEEEEEEEEEEEEEEEE
582 - 601:	EEEEEEEEEEEEEEEEEEEE

A0A3B4GQR5 **A0A3B4GQR5_9CICH** (620 aa)
Protein Ycf2-like. *Pundamilia nyererei*

```
MTAKHRKAKNNHKHEDNIFKNEVMETEVRPGGNNYTLLLVLFLIFVIGGATGVWFCFQQYQTLTYLTDNLMGIQMKIVKL
QSSHEEMRQSGNKQHISDNVEARLNALEESYSLAQKQVGMALATAEQLKTSDLPAQVLSLHTEMKTRLAEMQQATVSLEQ
LSLLQTMLKGKSEEFEDVKMKVEVLATLTGELAQKVDILTGGLEEAESKLEEKVGEIATVSAALDRQAAVMLRLKDQLDA
YQTQLKASVVEMTTVRELFEHEQSQWLHQARVQELNVSVAETKPETKPLEKTEGETIPTTEEEAETKEEEEAAGSEEKEE
ETPVEAEKRVETVETEEEALGSEQEVENVETDEEEEEEEEEEEEEEEEEEEEEEEALGTEKVEDIDTEEETPIAAGEEEV
AAPAESEEEETLPTADEKVTSTQEEEEAESDEPEELNTQDTAPVEKVESVTEETVPTQQAEAVEEDDAKQEKSVTVSEEE
KGHTTLTEEEGHNAQEQMPEDENRKGDEEEAPEREKGEDNSTVQDESLKARDEDETVLEKEESEDDEREKSEEHVPSGEE
EQLWKAVLEAEQPDVEEDVSEVEDEQQETADEEENHGAEDPQEADEEEEFLEFDALPEDK
```

353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE

A0A3B4H097 **A0A3B4H097_9CICH** (854 aa)
B-cell lymphoma/leukemia 11A-like. *Pundamilia nyererei*

```
MSRRKQGKPQHLSKRDFSPEPLSTAVVSSEDRLARLGHDAHPSLEQDLLTCGQCQATFPLADILLFIEHKRKRCHGPPCL
TVGRGLDKPPSPSPGLALTPSPAMGSLRSRRLEVGVQATLADEDEDRFSSPRGICPKQEPLPGKEEPTTYTCTTCKQSYG
SAWFLLQHAQNTHGFRIYLESEHGSPLTPRMGGPSSLGGGADCPSQPPLHGLHLPPDASPFNLLRIPGSGSGGRDSRFPP
TPPLFSPPPRNHLDPHHLSPEELALAAHHPSAFDRVLRLNPPLPLDPPPTMDFSRRLRELAGNTSGSTPPLSPSRPSPMQ
RLLHKPPYLATPPPLPGSMQSPVGSQTTPTTPLPSAGATPSSTTQLKSKCCEFCGKAFKFQSNLIVHRRSHTGEKPYKCH
LCDHACTQASKLKRHMKTHMHKSSSPNTGKSEDGLSTASSPEPGTSEHVGSASNALKSVVAKLKSENDRMLRENGEEEEE
EEEEEEEEEEEEEEEEEEEEGEEEEEQNGERVARRNNNSYHFGLNLETARQHENNGSIGSRLGGVADEGSIPRSLPEVMQ
GMGLAASMQHFSEALNAHKRNAMAQENHLHHHLNRDHHHNREICDGDSVLETDRGEEGSVSTVNGRGASPNESASVGLSK
KLLLGSPSPLSPFSKRIKLEKEFDLPTSTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRF
STPPGELDGGMSGRSGTGSGGSTPHLGGPGRPSSKDGRRSDTCEFCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQ
SSKLTRHMKTHGQVGKDVYKCEICQMPFSVYSTLEKHMKKWHSDRPLSTEIKSE
```

476 - 495:	EEEEEEEEEEEEEEEEEEEE
477 - 496:	EEEEEEEEEEEEEEEEEEEE
478 - 497:	EEEEEEEEEEEEEEEEEEEE
479 - 498:	EEEEEEEEEEEEEEEEEEEE
480 - 499:	EEEEEEEEEEEEEEEEEEEE
481 - 500:	EEEEEEEEEEEEEEEEEEEE

A0A3B4H3P4 **A0A3B4H3P4_9CICH** (836 aa)
B-cell lymphoma/leukemia 11B-like. *Pundamilia nyererei*

```
MSRRKQVNPQHLSLTHRETIQEANHDSGAGSPSPELSTPSPRRRASGEHDLLTCGQCQTNFPLGDILVFIEHKRRLCRGP
IGGLGSFSKPGAAGGVMGLPISPRARSLELGRGAVPVEVGVQVTPGGEEDQARRLTPAKGICPKQERGEKDEPSSYICTT
CKQTFTSAWFLLQHAQHTHGIRIYLDNHPVNCSLTPRMALPPPPGADALPRSPLPTFLGDASNPFHLLRMAGPQLRDHPH
PPGYMETRLPATPPFVSPPPPPRPPRERLGPEEMGLLSQHPSAFERVMRMTPMEHPPMDFSRRLRELAGNTTNNGGPTPP
LSPNRVPPMHRLLSPTLFQPGSQLSPFLAYPPQPPTSQGGHGSSSPPDTQGQNQAPGKSKSCEFCGKIFKFQSNLIVHRR
SHTGERPYKCHLCDHACSQASKLKRHMKTHMHNKSGAITGSPEQGNRGEGGEGEEKNREGDARGMGMDNEEEEEEEEEEE
EEEEEEEEELQNGSRPDSNLSEDSQEFTQNRENGSRQSPSEKPPSGDRVNDSGGVGIMHPYNHLDNHLRLNPNKRSLERQ
PNGDGGEGVEGERERENEREPDRQREEQEDQRPVMNGRISVSEAECFPGLFQRRPTPITSPSPSNNKRIKIEKEQLEIPP
TIPLISPENVYSQLLAGYAASRHFIREPFLGFTDSRQSPFATSSEHSSSETGSLRFSTPPGELMEGGSASGRSGSSTPHL
LRGPGPGRPPSSKERRNDTCEFCGKVFKNCSNLTVHRRSHTGERPYKCDLCSYACAQSSKLTRHMKTHGQYGKEVYRCDI
CHMPFSVYSTLEKHMKKWHGEHLMASEVKLEQADRS
```

470 - 489:	EEEEEEEEEEEEEEEEEEEE

A0A3B4TAT6 **A0A3B4TAT6_SERDU** (1423 aa)
PR domain zinc finger protein 2-like. *Seriola dumerili (Greater amberjack) (Caranx dumerili)*

```
MEDSPHLYFSEFGDNEDVEEEEEEEEEEEEEEEEEEEEEEEEDIYQEETNMEPDMIRSQNTDLHKHPNQDTERVWDSFPC
QHCERHFTSKQGLERHMHIHVLANNEAHAYKSNKSNMSFGSNVGQLQHEKMKPLDSVSPVMQRHTSSPTSSNTSSLSAED
HIAQPDKQGALDGHHACKYCEKIFTTYTNKRRHERRIHEQHLQLPSVEKTQLPQEESLQRIFPETSQQETQLVDNPAPAA
VENDGEHIEQYMLDISSNISENLSFYIDGKIVSTSTVSSCEAAEVHSGSSTLVGLDALILDPTQITQVLNTDSVTGKEIP
GQPLAKRRTATPPLLPQIKTELESEVVVSSSSSSLVSSLIENLLPQNTESTVVQKERTVYLSPKLKQLLEKQDGLKPTLA
LITDGQKPCSPVSLSVLPTATGRFKRRTGSPTSSPQQNPTSNEETPASDTGNFDAVNTGQMETQQISPVHLTASEKDDTT
PSVEDPAVKPVLTESWPPMTGGNSCNQQPLDLSNTIKRNEDVALADAVLDLSLQKKSLGESELTLNLVSQAALKEEQTNT
CMVEKALMNIGKQNESLGNPEAPLVTDFTIVSGSDMVTPVEPVAEGLVYGLALPPNSLTPSSASLTPVTLQPASPCTIAF
ASPASHTVVPSAPSLITVLAPPPPISNPSSQPIQVLAPNISPEPLVICSENTLNSSECDLTTAFATTNSANLVTLSQPLD
PTLNLPGHVFLTDQIALNPPIVDSAPVSEVPFSPTVTLNDSLINSYNITSNTVLIECTIALEAPGSVVPAAITLQENTPE
APAPTQMVVNHIEQQQIVSLPNPQTVDPTILVSSIAESVTLSTTTSVVSNCHSVGESSPIAEPVVNAEPPGTKEEEAADS
TVCIPEIPSNTSPPSEKAEEDESSNNTPNDAQQQTFTKNFICNVCDKLFHSMKELGHHVGDHADEWPYKCEFCVLLFGKP
SALLDHRSSLHGVGKTYVCSACTKEFVYLCNLKQHQEELHPGQQCTYTEEEKGKLRPQNYNNATKVNTESSVHDVPEEPK
KLVKKEEGEVDGAAEELFTTIKILASDGGKIKGPDVRLGINQHYPSFKPPPFPYHNRSPAGSVASATNFTTHNIPQTFST
AIRCTKCGKSFDNMPELHKHILACANASDKRRYTPKKNPIPLRHFAKTQNGVLSTTNSTNGLNASNRASQSNRSKPNQES
PVKMKFKVLNKRKKKLVQRVMPQRNKSVSSSNKVSSAPVHEQQEIFVCPHCSREFTMRRSRTKHMAVCPKKPKEAKKRKE
GGISVTKENDGHLHRGVSHVEEKQQRASPQHKTRFQTSGPAKRPAILPVQTVFSNKRSKIIIKESKQPTQETQTLNELPI
VRTFNPSMRQYSRVQQSVKGIPIKITIVKPQQTAPQKDELPPNQSQEEESGGVTSSSEQSATA
```

19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE

A0A3B4TQF2 **A0A3B4TQF2_SERDU** (505 aa)
Leiomodin-2-like. *Seriola dumerili (Greater amberjack) (Caranx dumerili)*

```
MSCFGYRRELSKYEDVDEDELLASLSPEELAELEKELADIDPDANVPIGLRQRDQTDKTPTGTFSREALMKYWENETRRL
LEDEIGGGSPKPVSDGKEEEEEQDEEDEDEEEQVEEEEEEEEEEEEEEEEEEEEEEDSEEAEEPIRLTPPPPPADPITT
GNPTVVDEALQRVLSNNPELTEVNLNNIDDISQETLIRFAEALRSNTHVRVFSLANTRADDPVALAIAKMLKENSSITSV
NIESNYVTGKGVMALVQALPGNNTLTELRFHNQRHMCGGQVEMEMVKILRENYTLIKLGYQFNLPGPRMSMTGILTRNQD
RQRQKRLQEQRQQQQGQQGGPEGVRGTPSSSPHSSPRASPWSSPKLPRSDLAKKQTPPAPPPPPPPPPPPPPPPPPPPL
QQEKKKPTRMIAEVIKAHEAGSKKVTKTKGKKGKKGKVKESGKEETGSILKELKNTLRPVSVEKRGEEGSRPSTPMRSAH
DQLMESIRNSSIRSLRRVQVPHHLR
```

115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE

A0A3B4TVB9 **A0A3B4TVB9_SERDU** (881 aa)
lm:7142702. *Seriola dumerili (Greater amberjack) (Caranx dumerili)*

```
MRWKLFGRHPGTHRHLEKRYLASDHHSRANHDSGAGSTSPEPSTPSPRRAGPGEHDLLTCGQCQTNFPLGDILVFIEHKR
RLCRGPGSSLGSFSKPGESGGITGIPISPRARSLELGRGSIPVEVGIQVTPGGEEDEERRLTPAKGICPKQERGGMETGT
HCRRMQLQEPISNSISPEGYNWSSFGCKTSNKHCVSPQTQSPFHCQSSLSFYKDEPSSYICTTCKQTFTSAWFLLQHAQH
THGIRIYLDNHPVNCSLTPRMALPPPPGADALPRSPLPTFLGDTNNPFHLLRMAAPLLREHPPPPGYMETRLPATPPFVS
PPPPPRPPLERLGPEEMGLLSQHPSAFERVMRMTPMEPPSMDFSRRLRELAGNTTNNGGPTPPLSPNRVPPMHRLLSPTL
FQPGAKPPAFLTYAPQPPTSQGGHGSSSPPDSQGQNQAPGKAKSCEFCGKIFKFQSNLIVHRRSHTGERPYKCHLCDHAC
SQASKLKRHMKTHMHKSGSMSGSPERGNRGEGGEGEEKSREGDSRGMGMDNEEEEEEEEEEEEEEEEEEEELRNGSRPDS
NLSDDSQEFGQNRENGPRQSPEEKPLSRDRVNDSGGVGIMHPYNHVDNHLRLNPNKRSLERQPNGDGGERDEHEDQRPVM
NGRISVSEADSFPGLFQRRPTPITSPSPSNNKRIKIEKEQLELPPAIPLISPENVYSQLLAGYAASRHFIREPFLGFTDS
RQSPFATSSEHSSSETGSLRFSTPPGELMEGGSASGRSGSSTPHLLRGPGPGRPPSSKERRNDTCEYCGKVFKNCSNLTV
HRRSHTGERPYKCDLCSYACAQSSKLTRHMKTHGQFGKEVYRCDICHMPFSVYSTLEKHMKKWHGEHLMASEVKLEQADR
G
```

532 - 551:	EEEEEEEEEEEEEEEEEEEE

A0A3B4U0J5 **A0A3B4U0J5_SERDU** (1725 aa)
Eukaryotic translation initiation factor 4 gamma 1-like. *Seriola dumerili (Greater amberjack) (Caranx dumerili)*

```
MNKPPQPITGPSSVPNPAPSPGLTQAAYGPGQPPSLVFATPPPPQMNSAPQPRPFAAGPRTLHQQSYYQNRPAMATSAPR
VQTSSGPRPVGPTHVYPPSSQMMMISQQQLSFAGSPQGYFIPPPGQYRAPYMPPTQQYPVTSGAPGFYAGTSPAEYPTYA
GAYYPAQAQYSPSVQPAPVMISPAQQQQQAPPPQQPPAQSQGPPKRERKPIRIRDPNQGGRDITEEIMSGGRSTTTPTPP
QASIAEVSPAQTNGEVVQSATTVMRKDEITEPPASAETPPPPATVNAEPVVEAKQETDSQVTPSAELAAQSVAPTAATEV
PSPSIKDQQTPASLPPAVASTATPAEAVNKDDTKVSDTVDAPVGPSASLAAQEAPVKMEEPQAAPAPAEKAPEKEEKKTE
EVKKIEKEEQVASSKLEPAVEVAAIVPPVKVAKEETATKTETEMSEPPPSAQEPAAPQTQTAAPSSAPEPEPTPAETAEP
PLPNGLPQHIEELSEDMAFPDTTPLDKPDASQSQESTPVAKTVTPAQEEEEEEEEEEEEEEEEEEEEEVVEVVEEKKGEEV
KEKSEDAPPASVSSIEESTMQAATSVPKKRKNMKELNKKEAIGDLLDAFTEEQDAKPASEPSSTQADPVPAAPAEPPAEA
ADETWEEKEDKQNADPDRAKATPEPTEQKYQYKEEQWKPIDPEEKKRYDREFLLGFQFISASMNKPEGLPIISDVVLDKV
NKTPLRPADPARMMSVGPDFTPSYLGNLGSRSVGGPRGPPPGPRRSQQGQRKEPRKIISSMSLNDDVQLNKAEKAWKPSV
KKSTRSRGAEEEEEGEGGVGGGAGGDTEQAKTQELFKRLRSILNKLTPQKFQELMKQVTELTIDTEERLKGAIDLIFEKA
ISEPNFSVAYANMCRCLMGLKVPTSDKPGVFVNFRKLLLNRCQKEFEKDQDDDEIFEKKQKEMEASKDDEERERLRVELE
EARDTARRRSLGNIKFIGELFKLKMLTEAIMHDCVVKLLKNHDEESLECLCRLLSTIGKDLDFEKAKPRMDQYFNQMDKI
IKERKTSSRIRFMLQDVLDLRRSNWVPRRGDQGPKTIDQIHKEAEMEEHREQIKVQQQLMSKKEGGGGGGGGRMGGNMG
GRGPHTPGGGRVTQPQDEGWNTVPISKNRPIDTTRLSKITKPGALDFNNQLLAPGGKGMWGSWGKGSSGGTGAKPASGEQ
DSGRPTTSTLNRFSALQQSGSLLSSSDSDRRVPQRSSSSRERGGDRERGDRERDRFDRFDRNEGREGRDDRSNRNQITKR
SFSRESQERGGRGGDSRASTEPVRRVASMTDDRERGSRDRGSRDRGSRDRGSRDRGPSKDLTAKRESAPTPPPSLPKAAL
TEEEVEKKTNAIIEEYLHINDLKEALQCVAELNSSALLYVFVRNGVESTLERSTIAREHMGLLLHQLVKAGTLPTQQYYK
GLQEILEAAEDMAIDIPHIWLYLAELITPMLHEGGIPMGQLFREISKPLVPLGKAAVLLVQILKLLCNGMTPKKVGAMWT
EAGLNWSDFLPKDEDVNKFVTEQKVDFTTGEETESKEVDKKKVLSGEELSKQLDRLLQDKANNQRIRDWVEANMDEQQMA
SNQFVRALMTSVCQSAIICDNPYRVDARQINQRASLLQKYLCDEQKELQALYALQALMVHMEQPANLLRMFFDALYDEDV
IKEEAFYKWESSKDPAEQTGKGVALKSVTAFFTWLREAEEESDKE
```

528 - 547:	EEEEEEEEEEEEEEEEEEEE

A0A3B4U0Z2 **A0A3B4U0Z2_SERDU** (1408 aa)
Eukaryotic translation initiation factor 4 gamma 1-like. *Seriola dumerili (Greater amberjack) (Caranx dumerili)*

```
MISPAQQQQQAPPPQQPPAQSQGPPKRERKPIRIRDPNQGGRDITEEIMSGGRSTTTPTPPQVRMLWLPLTYWNADPRQA
KQETDSQVTPSAELAAQSVAPTAATEVPSPSIKDQQTPASLPPAVASTATPAEAVNKDDTKVSDTVDAPVGPSASLAAQE
APVKMEEPQAAPAPAEKAPEKEEKKTEEVKKIEKEEQVASSKLEPAVEVAAIVPPVKVAKEETATKTETEMSEPPPSAQE
PAAPQTQTAAPSSAPEPEPTPAETAEPPLPNGLPQHIEELSEDMAFPDTTPLDKPDASQSQESTPVAKTVTPAQEEEEEE
EEEEEEEEEEEEEEVVEVVEEKKGEEVKEKSEDAPPASVSSIEESTMQAATSVPKKRKNMKELNKKEAIGDLLDAFTEDA
KPASEPSSTQADPVPAAPAEPPAEAADETWEEKEDKQNADPDRAKATPEPTEQKYQYKEEQWKPIDPEEKKRYDREFLLG
FQFISASMNKPEGLPIISDVVLDKVNKTPLRPADPARMMSVGPDFTPSYLGNLGSRSVGGPRGPVSDFPPGPRRSQQGQR
KEPRKIISSMSLNDDVQLNKAEKAWKPSVKKSTRSRGDTEQAKTQELFKRLRSILNKLTPQKFQELMKQVTELTIDTEER
```

```
LKGAIDLIFEKAISEPNFSVAYANMCRCLMGLKVPTSDKPGVFVNFRKLLLNRCQKEFEKDQDDDEIFEKKQKEMEASKD
DEERERLRVELEEARDTARRRSLGNIKFIGELFKLKMLTEAIMHDCVVKLLKNHDEESLECLCRLLSTIGKDLDFEKAKP
RMDQYFNQMDKIIKERKTSSRIRFMLQDVLDLRRSNWVPRRGDQGPKTIDQIHKEAEMEEHREQIKVQQQLMSKKEGGGG
GGGGGGRVTQPQDEGWNTVPISKNRPIDTTRLSKITKVTDAFTKTLWCLKLAAKIDPVLPSPKSSSSSRERGGDRERGDR
ERDRFDRFDRNEGREGRDDRSNRNQITKRSFSRESQERGGRGGDSRASTEPVRRVASMTDDRERGTKRESAPTPPPSLPK
AALTEEEVEKKTNAIIEEYLHINDLKEALQCVAELNSSALLYVFVRNGVESTLERSTIAREHMGLLLHQLVKAGTLPTQQ
YYKGLQEILEAAEDMAIDIPHIWLYLAELITPMLHEGGIPMGQLFREISKPLVPLGKAAVLLVQILKLLCNGMTPKKVGA
MWTEAGLNWSDFLPKDEDVNKFVTEQKVDFTTGEETESKEVDKKKVLSGEELSKQLDRLLQDKANNQRIRDWVEANMDEQ
QMASNQFVRALMTSVCQSAIICDNPYRVDARQINQRASLLQKYLCDEQKELQALYALQALMVHMEQPANLLRMFFDALYD
EDVIKEEAFYKWESSKDPAEQTGKGVALKSVTAFFTWLREAEEESDKE
```

315 - 334:	EEEEEEEEEEEEEEEEEEEE

A0A3B4U1B8 **A0A3B4U1B8_SERDU** (1714 aa)
Eukaryotic translation initiation factor 4 gamma 1-like. *Seriola dumerili (Greater amberjack) (Caranx dumerili)*

```
MNKPPQPITGPSSVPNPAPSPGLTQAAYGPGQPPSLVFATPPPPQMNSAPQPRPSYYQNRPAMATSAPRVQTSSGPRPVG
PTHVYPPSSQMMMISQQQLSFAGSPQGYFIPPPGQYRAPYMPPTQQYPVTSGAPGFYAGTSPAEYPTYAGAYYPAQAQYS
PSVQPAPVMISPAQQQQQAPPPQQPPAQSQGPPKRERKPIRIRDPNQGGRDITEEIMSGGRSTTTPTPPQASIAEVSPAQ
TNGEVVQSATTVMRKDEITEPPASAETPPPPATVNAEPVVEAKQETDSQVTPSAELAAQSVAPTAATEVPSPSIKDQQTP
ASLPPAVASTATPAEAVNKDDTKVSDTVDAPVGPSASLAAQEAPVKMEEPQAAPAPAEKAPEKEEKKTEEVKKIEKEEQV
ASSKLEPAVEVAAIVPPVKVAKEETATKTETEMSEPPPSAQEPAAPQTQTAAPSSAPEPEPTPAETAEPPLPNGLPQHIE
ELSEDMAFPDTTPLDKPDASQSQESTPVAKTVTPAQEEEEEEEEEEEEEEEEEEEEEVVEVVEEKKGEEVKEKSEDAPPAS
VSSIEESTMQAATSVPKKRKNMKELNKKEAIGDLLDAFTEEQDAKPASEPSSTQADPVPAAPAEPPAEAADETWEEKEDK
QNADPDRAKATPEPTEQKYQYKEEQWKPIDPEEKKRYDREFLLGFQFISASMNKPEGLPIISDVVLDKVNKTPLRPADPA
RMMSVGPDFTPSYLGNLGSRSVGGPRGPPPGPRRSQQGQRKEPRKIISSMSLNDDVQLNKAEKAWKPSVKKSTRSRGAEE
EEEGEGGVGGGAGGDTEQAKTQELFKRLRSILNKLTPQKFQELMKQVTELTIDTEERLKGAIDLIFEKAISEPNFSVAYA
NMCRCLMGLKVPTSDKPGVFVNFRKLLLNRCQKEFEKDQDDDEIFEKKQKEMEASKDDEERERLRVELEEARDTARRRSL
GNIKFIGELFKLKMLTEAIMHDCVVKLLKNHDEESLECLCRLLSTIGKDLDFEKAKPRMDQYFNQMDKIIKERKTSSRIR
FMLQDVLDLRRSNWVPRRGDQGPKTIDQIHKEAEMEEHREQIKVQQQLMSKKEGGGGGGGGRMGGNMGGRGPHTPGGGR
VTQPQDEGWNTVPISKNRPIDTTRLSKITKPGALDFNNQLLAPGGKGMWGSWGKGSSGGTGAKPASGEQDSGRPTTSTLN
RFSALQQSGSLLSSSDSDRRVPQRSSSSRERGGDRERGDRERDRFDRFDRNEGREGRDDRSNRNQITKRSFSRESQERGG
RGGDSRASTEPVRRVASMTDDRERGSRDRGSRDRGSRDRGSRDRGPSKDLTAKRESAPTPPPSLPKAALTEEEVEKKTNA
IIEEYLHINDLKEALQCVAELNSSALLYVFVRNGVESTLERSTIAREHMGLLLHQLVKAGTLPTQQYYKGLQEILEAAED
MAIDIPHIWLYLAELITPMLHEGGIPMGQLFREISKPLVPLGKAAVLLVQILKLLCNGMTPKKVGAMWTEAGLNWSDFLP
KDEDVNKFVTEQKVDFTTGEETESKEVDKKKVLSGEELSKQLDRLLQDKANNQRIRDWVEANMDEQQMASNQFVRALMTS
VCQSAIICDNPYRVDARQINQRASLLQKYLCDEQKELQALYALQALMVHMEQPANLLRMFFDALYDEDVIKEEAFYKWES
SKDPAEQTGKGVALKSVTAFFTWLREAEEESDKE
```

517 - 536:	EEEEEEEEEEEEEEEEEEEE

A0A3B4UA82 **A0A3B4UA82_SERDU** (1050 aa)
Deubiquitinating enzyme 15 (EC 3.4.19.12) (Ubiquitin carboxyl-terminal hydrolase 15) (Ubiquitin thioesterase 15) (Ubiquitin-specific-processing protease 15). *Seriola dumerili (Greater amberjack) (Caranx dumerili)*

```
MAEGGAADLDTQRGEVAALLKTQLRKGDTWYLVDSHWFKQWKKYVGFDSWDKYQMGDQNVYPGPVDNSGLLRDGDVLAIK
EHLIDELDYILVPTEGWNKLVSWYGLTEGQEPIARKVVEQGMFVKHCKVEVYLTELKLCEDSNMDNVITRRFSKADTIDM
IEKEMRKLFSIPDEKETRLWNRYMSNTFEPLNKPDSTIQDAGLYQGQVLVIEQKNEDGSWPRGSTAPKSSGASNLSALPK
ISPSSLTNNHNSSFNSRNVKNSSYSLPSYHPYSNSYDYSDQSRQSERSGLCGLSNLGNTCFMNSAVQCLSNIPPLTEYFL
KDKYTDELNEDNPLGMKGEIARAYAELIKQLWSGKYSYVTPRPFKTQVGRFAPQFSGYQQQDSHELLAFLLDGLHEDLNR
IRKKPYIQLKDANGRPDKVVAEEAWENHIKRNDSIIVDIFHGLFKSTLVCPVCSKVSVTFDPFCYLTLPLPMKKERTLEV
YLVRLDPLAKPTQYKLTVPKVGYISDLCTSLSSLSGVPAEKMIVTDIYNHRFHRIFATNENLSSIMERDDIYVFEVAVNR
VEDTDHVVIPVHLREKYKQSGYNHTSTPLFGQPFLIAVPRTLSEDKLYNMLLLRLCRFVRSSVEEDEEDCEETQPPKQHT
VNGNATNGLLEEGSPSEMETDEQDDESSQDQELPSENDNSQSEDSVGGDNELENGVVGPQNSTKGQQTAEHNRKRLFTFQ
FNNMGKTDFSLIKEDTRQIRFDEGHLRLSDRSYLSLDWEPEIKKKYFDETVVEDFDKHESMEYKPQKKAFFKLKDCIELF
TTKEKLGAEDPWYCPNCKQHQQATKKLDLWSLPPVLVVHLKRFSYSRYMRDKLDSLVDFPLRDLDMSEFLINPNAGPCRY
DLIAVSNHYGGMGGGHYTAYAKNKDDGKWYNFDDSSVSPANEDQIVSKAGYVLFYQRQDTVKGTGYFALDREEEEEEEEE
EEGEDEEEEENEDEERQERKAASSTQGASSAAAAAATAAQNDEEDLNENRRRKNDNEQEEEEEEEEEEEEEEEEEEEQA
RNRDVTMKTN
```

1019 - 1038:	EEEEEEEEEEEEEEEEEEEE

A0A3B4UA98 **A0A3B4UA98_SERDU** (1020 aa)
Deubiquitinating enzyme 15 (EC 3.4.19.12) (Ubiquitin carboxyl-terminal hydrolase 15) (Ubiquitin thioesterase 15) (Ubiquitin-specific-processing protease 15). *Seriola dumerili (Greater amberjack) (Caranx dumerili)*

```
MAEGGAADLDTQRGEVAALLKTQLRKGDTWYLVDSHWFKQWKKYVGFDSWDKYQMGDQNVYPGPVDNSGLLRDGDVLAIK
EHLIDELDYILVPTEGWNKLVSWYGLTEGQEPIARKVVEQGMFVKHCKVEVYLTELKLCEDSNMDNVITRRFSKADTIDM
IEKEMRKLFSIPDEKETRLWNRYMSNTFEPLNKPDSTIQDAGLYQGQVLVIEQKNEDGSWPRGSTAPNVKNSSYSLPSYH
PYSNSYDYSDQSRQSERSGLCGLSNLGNTCFMNSAVQCLSNIPPLTEYFLKDKYTDELNEDNPLGMKGEIARAYAELIKQ
LWSGKYSYVTPRPFKTQVGRFAPQFSGYQQQDSHELLAFLLDGLHEDLNRIRKKPYIQLKDANGRPDKVVAEEAWENHIK
RNDSIIVDIFHGLFKSTLVCPVCSKVSVTFDPFCYLTLPLPMKKERTLEVYLVRLDPLAKPTQYKLTVPKVGYISDLCTS
LSSLSGVPAEKMIVTDIYNHRFHRIFATNENLSSIMERDDIYVFEVAVNRVEDTDHVVIPVHLREKYKQSGYNHTSTPLF
GQPFLIAVPRTLSEDKLYNMLLLRLCRFVRSSVEEDEEDCEETQPPKQHTVNGNATNGLLEEGSPSEMETDEQDDESSQD
QELPSENDNSQSEDSVGGDNELENGVVGPQNSTKGQQTAEHNRKRLFTFQFNNMGKTDFSLIKEDTRQIRFDEGHLRLSD
RSYLSLDWEPEIKKKYFDETVVEDFDKHESMEYKPQKKAFFKLKDCIELFTTKEKLGAEDPWYCPNCKQHQQATKKLDLW
SLPPVLVVHLKRFSYSRYMRDKLDSLVDFPLRDLDMSEFLINPNAGPCRYDLIAVSNHYGGMGGGHYTAYAKNKDDGKWY
NFDDSSVSPANEDQIVSKAGYVLFYQRQDTVKGTGYFALDREEEEEEEEEEEGEDEEEEENEDEERQERKAASSTQGASS
AAAAAATAAQNDEEDLNENRRRKNDNEQEEEEEEEEEEEEEEEEEEEEQARNRDVTMKTN
```

989 - 1008:	EEEEEEEEEEEEEEEEEEEE

A0A3B4UZB0 **A0A3B4UZB0_SERDU** (864 aa)

B-cell lymphoma/leukemia 11A-like. *Seriola dumerili (Greater amberjack) (Caranx dumerili)*

```
MSRRKQGKPQHLSKRDFSQDLLTCGQCQATFPLADILLFIEHKRKRCHGPPCLAVGRGLDKPPSPSPGLALTPSPALGSL
RSRRPVEVGVQATLADDDDDRLSSPRGICPKQEPLPKEEPTTYTCTTCKQSYGSAWFLLQHAQNTHGFRIYLESEHGSPL
TPRMGGPSSLGGGADCPSQPPLHGLHLPPDASPFNLLRIPGSGSGGRDSVGAGGVGPPGMAGGGHHQRFPPTPPLFSPPP
RNHLDPHHLSPEELALAAHHPSAFDRVLRLNPPLPLDPPPTMDFSRRLRELAGNTSGSTPPLSPSRPSPMQRLLQPFQTG
GGSGGTGGAGGSKPPYLATPPPLPGSMQSPVGSQTTPTTPLPSAGAPPSSTTPLKSKCCEFCGKAFKFQSNLIVHRRSHT
GEKPYKCHLCDHACTQASKLKRHMKTHMHKSSSPNTGKSEDGLSTASSPEPGTSEHMGSASNALKSVVAKLKSENDRMLR
ENGEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEEQNADRAARRTNNSYHFGLNLETARQHENNGGIGSRLGGLADEGSI
PRSLPEVMQGMGLAASMQHFSEALNAHKRNAMAQENHLHHHLNRDHHHHNREMCDGDSVLETDRVEEGSVSTVNGRGASP
NENASVGLSKKLLLGSPSPLSPFSKRIKLEKEFDLPTPTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSE
HSSENGSLRFSTPPGELDGGMSGRSGTGSGGSTPHLGGPGRPSSKDGRRSDTCEFCGKVFKNCSNLTVHRRSHTGERPYK
CELCNYACAQSSKLTRHMKTHGQVGKDVYKCEICQMPFSVYSTLEKHMKKWHSDRPLSTEIKSE
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484 - 503:	EEEEEEEEEEEEEEEEEEEE
485 - 504:	EEEEEEEEEEEEEEEEEEEE
486 - 505:	EEEEEEEEEEEEEEEEEEEE
487 - 506:	EEEEEEEEEEEEEEEEEEEE
488 - 507:	EEEEEEEEEEEEEEEEEEEE
489 - 508:	EEEEEEEEEEEEEEEEEEEE
490 - 509:	EEEEEEEEEEEEEEEEEEEE

A0A3B4V7V3 **A0A3B4V7V3_SERDU** (715 aa)
Rho family-interacting cell polarization regulator 1-like. *Seriola dumerili (Greater amberjack) (Caranx dumerili)*

```
MFTGSTKLPPTKIPQPERLDEVYAALRRGLQSYLQVHQLELDSLGQQIKENKRNGRLGSLYEQDKQVKAIERFMRRLEFH
LSKVEELYDAYCIQRRLRDGASKMVAAFNSATGSKEARESLSEANKGYRECTEHMCSLESELESQMGEFHVKMKGLAGFA
RLCAGDQYEVLMRYGRQRWRLRGRVEVSNKQIWDSEEYIFLPLVTELLSIKVTELKSLANHVVVGSVSCEMLDLFCPLPQ
TLAVDINDLGTVKLNLEVTWSPFDKDDQTSSTSTVSKRLLSNQSPPDTPSMREQVFYSLLKRQGEMDNGTVWSNSSESSD
DSSSPALAHHAQRLTASNMLQSTLTSQLSFTPHKSSASTPSLSSNQEEDETEAGEVFSQRDAVPNGHLQTSCSHSHVSES
SPDCTVTDRASVPLADLSETSADLSCSCPDVSSAHPVLLVETAESHVSESGIPQVCVSAEDVKDDPCEDSSAQAEAETED
NTTEVGGGHQVEASEKHSQSHQSIQELKQSEDAPMVPFPTSSSFTQEVETALESFDFLNCSDLEEEEEEEEEEEEEEEEE
EEEEEEDEKEEKEEEEKEEEDEEEEEDEHQEEEEGEKEKEDGQHEEDQNKVEEEKTQEEEKVEENFYSGGSDVEEADGLE
ILMEAPEGFRNSDEDRFSESQESSVEDVQDLGQIEMPEEKEEPSEEKGDERHGKDASHDQEESPSTPSHLATTVF
```

544 - 563:	EEEEEEEEEEEEEEEEEEEE
545 - 564:	EEEEEEEEEEEEEEEEEEEE
546 - 565:	EEEEEEEEEEEEEEEEEEEE
547 - 566:	EEEEEEEEEEEEEEEEEEEE

A0A3B4VF23 **A0A3B4VF23_SERDU** (793 aa)
B-cell lymphoma/leukemia 11A-like. *Seriola dumerili (Greater amberjack) (Caranx dumerili)*

```
MSRRKQGKPQHLSKREFSPEPLSGVLPEEDSQDSPRLGVAQVDTLKGDQDLLTCGQCHSRFPLADILLFIEHKRRQCHGS
LCTDKPLDRPPSSPLHPRRVCHPVEVAVQVSPQDEDCLSSPLQGIIPKLENITDKDEPSSYTCTTCKQPFTSAWFLLQHA
QNTHGFRIYLESEPGSPLTPRVAAAPGMGGDCASSQPPLHAVHLAEGSPYSLLRMPGSGSGRDSASTPREGRYPRTPPLF
SPPPRHHLSPDDLALATHHPSAFDRVMRLNSVPLEPPPTMDFSRRLRELAGNATGASPPLSPNRPNPMQRLLQPFQPGSK
PPFSATPPLSTSQSPSGSRSTPNAVSNAAQPGTPLKAKSCEFCGKTFKFQSNLIVHRRSHTGEKPFKCHLCNHACTQASK
LKRHMKTHCQSKSSALNAKSDDGLSTASSPEPGTSDLMGSATDALKSVVAKFKSENNGLMPENGEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEIESKPGVEEEEGRNDYRFSLRLEGARHHQNSEALHPRHRSSSREPADEESAMESDRAEDGSTTTVN
GLGPLSTDNLSRKLLGGGVSPGSLSPLSKRIKVEKDLDPPTPTIPNTENVYSQWLAGYAASRQLKDPFINFTSGDSRQSP
FASSSEHSSENGSLRFSTPPGELDGERAASGRSGTGSGASTPHGGSGNGRPSSKDGRRSDTCEFCGKVFKNCSNLTVHRR
SHTGERPYKCELCSYACAQSSKLTRHMKTHGQMGKDVYKCEICHMPFSVYSTLEKHMKKWHSDRPLANDIKTE
```

465 - 484:	EEEEEEEEEEEEEEEEEEEE
466 - 485:	EEEEEEEEEEEEEEEEEEEE
467 - 486:	EEEEEEEEEEEEEEEEEEEE
468 - 487:	EEEEEEEEEEEEEEEEEEEE
469 - 488:	EEEEEEEEEEEEEEEEEEEE
470 - 489:	EEEEEEEEEEEEEEEEEEEE
471 - 490:	EEEEEEEEEEEEEEEEEEEE
472 - 491:	EEEEEEEEEEEEEEEEEEEE
473 - 492:	EEEEEEEEEEEEEEEEEEEE
474 - 493:	EEEEEEEEEEEEEEEEEEEE
475 - 494:	EEEEEEEEEEEEEEEEEEEE

A0A3B4WN49 **A0A3B4WN49_SERLL** (836 aa)
B-cell lymphoma/leukemia 11B-like. *Seriola lalandi dorsalis*

```
MSRRKQVNPQHLSLTHRETIQAEANHDSGAGSTSPEPSTPSPRRAGSGEHDLLTCGQCQTNFPLGDILVFIEHKRRLCRG
PGSGLGSFSKPGESGGITGIPISPRARSLELGRGSIPVEVGIQVTPGGEEDEERRLTPAKGICPKQERGDKDEPSSYICT
```

```
TCKQTFTSAWFLLQHAQHTHGIRIYLDNHPVNCSLTPRMALPPPPGADALPRSPLPTFLGDTNNPFHLLRMAAPLLREHP
PPPGYMETRLPATPPFVSPPPPPRPPLERLGPEEMGLLSQHPSAFERVMRMTPMEPPSMDFSRRLRELAGNTTNNGGPTP
PLSPNRVPPMHRLLSPTLFQPGAKPPAFLTYAPQPPTSQGGHGSSSPPDSQGQNQAPGKAKSCEFCGKIFKFQSNLIVHR
RSHTGERPYKCHLCDHACSQASKLKRHMKTHMHKSGSMSGSPERGNRGEGGEGEEKSREGDSRGMGMDNEEEEEEEEEEE
EEEEEEEEEELRNGSRPDSNLSDDSQEFGQNRENGPRQSPEEKPLSRDRVNDSGGVGIMHPYNHVDNHLRLNPNKRSLERQ
PNGDGGERGEEERERENEREQDRERDEHENQRPVMNGRISVSEADSFPGLFQRRPTPITSPSPSNNKRIKIEKEQLELPP
AIPLISPENVYSQLLAGYAASRHFIREPFLGFTDSRQSPFATSSEHSSSETGSLRFSTPPGELMEGGSASGRSGSSTPHL
LRGPGPGRPPSSKERRNDTCEYCGKVFKNCSNLTVHRRSHTGERPYKCDLCSYACAQSSKLTRHMKTHGQFGKEVYRCDI
CHMPFSVYSTLEKHMKKWHGEHLMASEVKLEQADRG
```

470 - 489:	EEEEEEEEEEEEEEEEEEEE

A0A3B4X8Z3 **A0A3B4X8Z3_SERLL** (809 aa)
B-cell lymphoma/leukemia 11A-like. *Seriola lalandi dorsalis*

```
MSRRKQGKPQHLSKREFSPEPLSGVLPEEDSQDSPRLGVAQVDTLKGDQDLLTCGQCHSRFPLADILLFIEHKRRQCHGS
LCTDKPLDRPPSSPLASPLSTSSTHSRTHHQHPRRVCHPVEVAVQVSPQDEDCLSSPLQGIIPKLENITDKDEPSSYTCT
TCKQPFTSAWFLLQHAQNTHGFRIYLESEPGSPLTPRVAAAPGMGGDCASSQPPLHAVHLAEGSPYSLLRMPGSGSGRDS
ASTPREGRYPRTPPLFSPPPRHHLSPDDLALATHHPSAFDRVMRLNSVPLEPPPTMDFSRRLRELAGNATGASPPLSPNR
PNPMQRLLQPFQPGSKPPFSATPPLSTSQSPSGSRSTPNAVSNAAQPGTPLKAKSCEFCGKTFKFQSNLIVHRRSHTGEK
PFKCHLCNHACTQASKLKRHMKTHCQSKSSALNAKSDDGLSTASSPEPGTSDLMGSATDALKSVVAKFKSENNGLMPENG
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEIESKPGVEEEEGRNDYRFSLRLEGARHHQNSEALHPRRRSSSREPADEES
AMESDRAEDGSTTTVNGLGPLSTDNLSRKLLGGGVSPGSLSPLSKRIKVEKDLDPPTPTIPNTENVYSQWLAGYAASRQL
KDPFINFTSGDSRQSPFASSSEHSSENGSLRFSTPPGELDGERAASGRSGTGSGASTPHGGSGNGRPSSKDGRRSDTCEF
CGKVFKNCSNLTVHRRSHTGERPYKCELCSYACAQSSKLTRHMKTHGQMGKDVYKCEICHMPFSVYSTLEKHMKKWHSDR
PLANDIKTE
```

481 - 500:	EEEEEEEEEEEEEEEEEEEE
482 - 501:	EEEEEEEEEEEEEEEEEEEE
483 - 502:	EEEEEEEEEEEEEEEEEEEE
484 - 503:	EEEEEEEEEEEEEEEEEEEE
485 - 504:	EEEEEEEEEEEEEEEEEEEE
486 - 505:	EEEEEEEEEEEEEEEEEEEE
487 - 506:	EEEEEEEEEEEEEEEEEEEE
488 - 507:	EEEEEEEEEEEEEEEEEEEE
489 - 508:	EEEEEEEEEEEEEEEEEEEE
490 - 509:	EEEEEEEEEEEEEEEEEEEE
491 - 510:	EEEEEEEEEEEEEEEEEEEE

A0A3B4XAT1 **A0A3B4XAT1_SERLL** (573 aa)
Cytosolic purine 5'-nucleotidase. *Seriola lalandi dorsalis*

```
MTTSWSDRLQNYADLPANMDGLTMKKYRREPYHRVFVNRSLAMEKIKCFGFDMDYTLAVYKSPEYESLGFELTVERLVSI
GYPQELLSFVYDPSFPTRGLVFDTMYGNLLKVDAYGNILVCVHGFNFLRGPEIRERYPNKFIQRDDTERFYILNTLFNLP
ETYLFACLVDFFSNCDRYTSCETGFKDGDLFMSYKSMFQDVRDAVDWVHFKGTLKEKTVENLEKYVVKDGKLPLLLSRMN
EVAKVFLATNSDYKYTDKIMTYLFDFPHGPKPGTSHRPWQSYFDLILVDARKPLFFGEGTVLRQVDTTTGRLKIGTYTGP
LQHGIVYSGGSSDIVCDLLGAKGKDIVYIGDHIFGDILKSKKRQGWRTFLVIPELAQELHVWTDKSSLFEELQGLDIFLA
ELYKHLDSSSNERPDISTIQRRVKKVTHDMDMCYGMMGSLFRSGSRQTLFASQVMRYADLYAASFINLLYYPFSYLFRAA
HVLMPHESTVEHTHVDIDTESPLATRNRTQCSDCKDLECKRNQLTRSFSEIKPPNLFPQTPQEITHCHDEDDDEEEEEEE
EEEEEEEEEEEEE
```

554 - 573:	EEEEEEEEEEEEEEEEEEEE

A0A3B4YPA1 **A0A3B4YPA1_SERLL** (918 aa)
B-cell lymphoma/leukemia 11A-like. *Seriola lalandi dorsalis*

```
MSRRKQGKPQHLSKRDFSPEPLSTAVVSSEELSERCSEHSEESGSLNGHRPGSTVGRLARLGHDAHPSLEQDLLTCGQCQ
ATFPLADILLFIEHKRKRCHGPPCLAVGRGLDKPPSPSPGLALTPSPAMGSLRSRRPVEVGVQATLADDDDDRLSSPRRI
CPKQEPLPGKEEPTTYTCTTCKQSYGSAWFLLQHAQNTHGFRIYLESEHGSPLTPRMGGPSSLGGGADCPSQPPLHGLHL
PPDASPFNLLRIPGSGSGGRDSVGAGGIGPPGMAGGGHHQRFPPTPPLFSPPPRNHLDPHHLSPEELALAAHHPSAFDRV
LRLNPPLPLDPPPTMDFSRRLRELAGNTSGSTPPLSPSRPSPMQRLLQPFQTGGGSGGTGGAGGSKPPYLATPPPLPGSM
QSPVGSQTTPTTPLPSAGAPPSSTTPLKSKCCEFCGKAFKFQSNLIVHRRSHTGEKPYKCHLCDHACTQASKLKRHMKTH
MHKSSSPNTGKSEDGLSTASSPEPGTSEHMGSASNALKSVVAKLKSENNRMLRENGEEEEEEEEEEEEEEEEEEEEEEEE
EEEGEEEEEQKADRAARRTNNSYHFGLNLETARQHENNGGIGSRLGGLADEGSIPRSLPEVMQGMGLAASMQHFSEALNA
HKRNAMAQENHLHHHLNRDHHHHNREMCDGDSVLETDRVEEGSVSTVNGRGASPNENASVGLSKKLLLGSPSPLSPFSKR
IKLEKEFDLPTPTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRFSTPPGELDGGMSGRSG
TGSGGSTPHLGGPGRPSSKDGRRSDTCEYCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQSSKLTRHMKTHGQVGK
DVYKCEICQMPFSVYSTLEKHMKKWHSDRPLSTEIKSE
```

537 - 556:	EEEEEEEEEEEEEEEEEEEE
538 - 557:	EEEEEEEEEEEEEEEEEEEE
539 - 558:	EEEEEEEEEEEEEEEEEEEE
540 - 559:	EEEEEEEEEEEEEEEEEEEE

541 - 560:	EEEEEEEEEEEEEEEEEEEE
542 - 561:	EEEEEEEEEEEEEEEEEEEE
543 - 562:	EEEEEEEEEEEEEEEEEEEE
544 - 563:	EEEEEEEEEEEEEEEEEEEE

A0A3B4YQA7 **A0A3B4YQA7_SERLL** (610 aa)
Cysteine/serine-rich nuclear protein 3-like. *Seriola lalandi dorsalis*

```
MSGILKRKLEEGPSPYLSLQGSDDDEVSCSDSGNSSDSLNHPVPSGLLDSSLQQQSKRLRGRNVHFESVTVYYFNRRQGF
TSVPTQGGSTLGMSPRHSGVKRFTLREFAMEQKRSHRNMLRDHLKEEKLNAIKLKLTKNGTVSSVEADTLTLDDISEDDL
DVDNTEVDDYFFLQPLTTRRRRALLRSSGVRRIDVEEKHELRTLRMSREECGCRCRGICDPETCACSLAGIKCQVNGTVV
DRMSFPCGCTKEGCSNTTGRLEFNPVRVRTHFLHTIMKLELEKSREEQHQQQQQQSEQQLVTNGNGYHGDSSLVQQQQQQ
QPNLQFPLMSSTPHIPIMHLQNTGDTDSHLDEEEEEEEEEEEEEEEEEEEEEEEDEEEDDDDEAYEEDEDGSSVCSGLSDC
STHSLDTIDPEEGEEDEEDEEDDDDEEEEDEEEEDWDCSLHGTSPPPYSVPLPSVLSYSNNTLMSLSNPFHNTPSMQHYQI
DSSVNDTPAFLSENVTVTPTLPTVETALESEINTELHCRTLSDPTDSLTPQTCSHADTRETDAAPAGAAAKQPLSTDRQN
NPDDHESQTEASAGSLEQTGEEIKEPLQERLQMQGALEDEKTDASFSESV
```

352 - 371:	EEEEEEEEEEEEEEEEEEEE
353 - 372:	EEEEEEEEEEEEEEEEEEEE
354 - 373:	EEEEEEEEEEEEEEEEEEEE

A0A3B4YWD5 **A0A3B4YWD5_SERLL** (1428 aa)
PR domain zinc finger protein 2-like. *Seriola lalandi dorsalis*

```
MEDSPHLYFSEFGDNEDVEEEEEEEEEEEEEEEEEEEEEEGEEEEEEDIYQEETNMEPDMIRSLNTDIHKHPNQDTERVWD
SFPCQHCERHFTSKQGLERHMHIHVLANNEAHAYKSNKSNMSFGSNVGQLQHEKMKTLDSGSPVMQRHTSSPTSSNTSSL
SAEDHIAQPDKQGALDSHHACKYCEKIFTTYTNKRRHERRIHEQHLQLPSVENTQMPQEESLQRIFTETSQQETQLGDNP
APAAVENEGEHIEQYMLDISSNISENLSFYIDGKIVSTSTVSSCEAAEVHSGSSTLVGLDALILDPTQISQVLNTDSVTG
KEIPGQPLAKRRTATPPLLPQIKTELESEVMVSSSSSSLVSSLIENLLPQNTESTVVQKERTVFLSPKLKQLLEKQDGLK
PTLALITDGQKPCSPVSLSVLPTATGRFKRRTGSPTSSPQQNPTSNEETPASDTGNFDAVNTGQTETQQISPVHLTASEK
DDTTPSVEDPAVKPVLTESWPPMTGGNSCNQQPLDLSNTIKRNEDVALADAVLDLSLQKKSLGESELTLNLVSQTALKEE
QTNICMVEEALMNIGKQNESLGNPEAPLVTDFTIVSGSDMVTPVEPVAEGLVYGLALPPNSLTPSSASLTPVTLQPASPC
TIAFASPASHTVVSTAPSLITVLAPPQPISNPSSQPIQVLAPNISPEPLVICSENTLNSSECDLTTAFATTNSANLVTLS
QPLDPTLNLPGHMFLTDQIALNPPIVDSAPVSEVPFSPTVTLNDSLINSYNITSNTVLIECTIALEAPGSVVPAGITLQE
NTPEAPAPTQMVVNHIEQQQIVSVPNPQTVDPTILVSSITESVTLSTTTTSVVSNCHSVGESSPIAEPVVNAEPPGTKEE
EAADSTVCIPEIPSNTSPPSEKAEEDEFSNNTPNDAQQQTFTKNFICNVCDKLFHSMKELGHHVGDHADEWPYKCEFCVL
LFGKPSALLDHRSSLHGVGKTYVCSACTKEFVYLCNLKQHQEELHPGQQCTYTEEEKGKLRPQNYNNATKVNTESSVHDV
PEEPKKLVKKEEGEVDVGAEELFTTIKILASDGGKIKGPDVRLGINQHYPSFKPPPFPYHNRSPAGSVASATNFTTHNIP
QTFSTAIRCTKCGKSFDNMPELHKHILACANASDKRRYTPKKNPIPLRHFAKTQNGVLSTTNSTNGLNASNRASQSNRSK
PNQESPVKMKFKVLNKRKKKLVQRVMPQRNKSVSSSNKVSSAPVHEQQEIFVCPHCSREFTMRRSRTKHMAVCPKKPKEA
KKRKEGGISVTKENDGHLHRGVSHVEEKQQRASPQHKTRFQTSGPAKRPAILPVQTVFSNKRSKIIIKESKQPTQETQTL
NELPIVRTFNPSMRQYSRVQQSVKGIPIKITIVKPQQTAPQKDELPPNQSQEEESGGVTSSSEQSATA
```

19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE

A0A3B4Z6D2 **A0A3B4Z6D2_9TELE** (550 aa)
Zinc finger protein 44-like. *Stegastes partitus (bicolor damselfish)*

```
MDGVSWSTTRSQESFSRSTTAADTLSRLASFISQAEAKQHTRSQRQLSNHLATFSCKECSKAFSCAADLLQHQELKHTLP
KPHRCPSCGQEFSLKSSLQLHKCDHDSTRCELCHGASRLGSPCAACTNRTSDPGRPQEKSLHRQPHLLDSSPYACAPCGR
GFSQKQALLHHQQAGCSEPPSPSDIADASSLPDDSPPVSEGDSTRSDCSDTPGPSGRAVNMCRLCSRTFRTEAGLQRHKL
MYHAAERQDTKADSARGEARKERDPKIDRHPNKSPKSQNKLLTCRSCDMVFRSTSKLYVHRKEKHSRDKTIGRESKPVIN
KRRVDTYPCQICGKVFFHHLSLRAHYRQHTARSFTTMKNKQSVRCPTKDSRSSENTPNKVAGNKTVKAGPGRPRKVPKVD
ESQTCREVPEVKEDEVEEEEEEVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEREFPCPSCAEVFSLQWQLKEHVE
LHQSSVKRRHCSVCKSDMDTCKWPGSKRQRLYHCVPCQQGFSALDSFLEHCQEHLRARVEEDRILEASKA
```

424 - 443:	EEEEEEEEEEEEEEEEEEEE
425 - 444:	EEEEEEEEEEEEEEEEEEEE
426 - 445:	EEEEEEEEEEEEEEEEEEEE
427 - 446:	EEEEEEEEEEEEEEEEEEEE
428 - 447:	EEEEEEEEEEEEEEEEEEEE
429 - 448:	EEEEEEEEEEEEEEEEEEEE
430 - 449:	EEEEEEEEEEEEEEEEEEEE
431 - 450:	EEEEEEEEEEEEEEEEEEEE
432 - 451:	EEEEEEEEEEEEEEEEEEEE
433 - 452:	EEEEEEEEEEEEEEEEEEEE
434 - 453:	EEEEEEEEEEEEEEEEEEEE
435 - 454:	EEEEEEEEEEEEEEEEEEEE
436 - 455:	EEEEEEEEEEEEEEEEEEEE

437 - 456:	EEEEEEEEEEEEEEEEEEEE
438 - 457:	EEEEEEEEEEEEEEEEEEEE

A0A3B4Z7B7 **A0A3B4Z7B7_9TELE** (812 aa)
Consortin-like. *Stegastes partitus (bicolor damselfish)*

```
MSQVRGGGVDLCDNLPSPDALTAQTRNLNETNTLTQTQSLPPSQNEEGRRCGLIQRSPLNNNGKEEEEEEQGKEGEEEDI
DAVMEEESEESSCLVRCQSPDTPMTDSSYSETGSLLETPYPFSPGTSPEPTSPVIPVLSPETTYPISSVILSQSDVKVDS
QISNTGSGASTTGSITCTQGPSFTTGPMDSTLQTLTSGTWPTSPAGPTCITEATDRIAKNTNSTTEQLTSSTELVFSGGP
TCTRGSATSYAETFTLTAATETLTFTTGPTTTGTEPTSTTGSVSLNREHVTSPPVTTCFSVSTCATGPIPSQALLESLEQ
LAQKGDDARLPHYLHQIAEAFVLHEDYQRALWCVQLERLYHQRVLDNLNALQEQWEGQCRRSSSHLATQHLDALKHICQT
HSRPRSGDAECESLDSLRPTFEESGALPSCTTAHQVEGGMEQRAEDSSCPVIPSINLPDRISSPEISVKDREDPDSFHGS
QLTDKQGNDREGGEAEGGVGYTISALENGLHPSTAGGMDQSNPAEQQGEDLGPAQEKEAKKEEEETDVEEAVEALEMEDE
EEEEEEEEKMKERGSPFAQKAVPVETLVSGAEFETPPLHQDALAQEKLHEDTQESTKSCLHQETHLPQEAHMKQQEERVA
EKEEDEEEEEEEEEEEEEEEEEEEEEYEVSQADIIREAPSLDDMAKLITVEELSPASGLVSILKKRSVCVDKESVSASPE
PRPEKTTAKRRVRFKVPDDSYDQDVGGGDSCLLLFLLCLVTVVISVGGTALYCALGDAQSSVCQDFSRNADFYIGQIQRG
IAQIQHWFGPGS
```

646 - 665:	EEEEEEEEEEEEEEEEEEEE
647 - 666:	EEEEEEEEEEEEEEEEEEEE

A0A3B4ZF42 **A0A3B4ZF42_9TELE** (325 aa)
Si:dkey-32e6.6. *Stegastes partitus (bicolor damselfish)*

```
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEATEPPSNQTETFSSFTASPLQCRTADGEISCRAIGMTHLPVFYN
LETTKLDMANNIRIITPLSFSGLPNLNTLDLSQNKLDDESFNLTFLKKLNLDGNQITAVPALPLSLEELKINNNKLNTLT
PHCFKLSNLLNLELEENLLHEGSVSPLAFKPLQRLLNVQLDNNHFRSIPLGLPASLQSLEALDLSYNQFTSVPMNLPRPL
RKLNLQHNNVSHIPAFTFRHMRPGLQSLHLSHNALSKEGIDRFSFVGMYRSLAELLLNNNRLREVPRCVRQFKNLQVLRL
DDNQI
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE

A0A3B5A7U5 **A0A3B5A7U5_9TELE** (775 aa)
Consortin-like. *Stegastes partitus (bicolor damselfish)*

```
MDHGGQFEREDSVMSQVRGGGVDLCDNLPSPDALTAQTRNLNETNTLTQTQSLPPSQNEEGRRCGLIQRSPLNNNGKEEE
EEEQGKEGEEEDIDAVMEEESEESSCLVRCQSPDTPMTDSSYSETGSLLETPYPFSPGTSPEPTSPVIPVLSPETTYPIS
SVILSQSDVKVDSQISNTGSGASTTGSITCTQGPSFTTGPMDSTLQTLTSGTWPTSPAGPTCITEATDRIAKNTNSTTEQ
LTSSTELVFSGGPTCTRGSATSYAETFTLTAATETLTFTTGPTTTGTEPTSTTGSVSLNREHVTSPPVTTCFSVSTCATG
PIPSQALLESLEQLAQKGDDARLPHYLHQIAEAFVLHEDYQRALWCVQLERLYHQRVLDNLNALQEQWEGQCRRSSSHLA
TQHLDALKHICQTHSRPRSGDAECESLDSLRPTFEESGALPSCTTAHQVEGGMEQRAEDSSCPVIPSINLPDRISSPEIS
VKDREDPDSFHGSQLTDKQGNDREGGEAEGGVGYTISALENGLHPSTAGGMDQSNPAEQQGEDLGPAQEKEAKKEEEETD
VEEAVEALEMEDEEEEEEEEEKMKERGSPFAQKAVPVETLVSGAEFETPPLHQDALAQEKLHEDTQESTKSCLHQETHLP
QEAHMKQQEERVAEKEEDEEEEEEEEEEEEEEEEEEEEEYEVSQADIIREAPSLDDMAKLITVEELSPASGLVSILKKRS
VSVDKESVSASSEPRPEKTTAKRRVRFKVPDDSYDQGMFISLLPTVGDLHLPINL
```

659 - 678:	EEEEEEEEEEEEEEEEEEEE
660 - 679:	EEEEEEEEEEEEEEEEEEEE

A0A3B5AQL1 **A0A3B5AQL1_9TELE** (811 aa)
B-cell lymphoma/leukemia 11A-like. *Stegastes partitus (bicolor damselfish)*

```
MSRRKQGKPQHLSKREFSPEPLAGVLPEEDSQDSPRLGVAQGEPLKGDQDLLTCGQCHSRFPLADILLFIEHKRRQCHGS
LCGDKPLDRPPSSPLASPVSTSSSHSRTQHQHPRRVRQPVEVAVQVSPQDEDCLSAPLQGIIPKQENITDKDEPSSYTCT
TCKQPFTSAWFLLQHAQNTHGFRIYLESEPGSPLTPRVAAAPGMGGDCASSQPPLHAVHLADGSPYSLLRMPGSGSGRDS
VSTPREGRYPRTPPLFSPPPRHHLSPDDLALATHHPSAFDRVMRLNSVPLDPPQTMDFSRRLRELAGNATGGSPPLSPNR
PNPMQRLMQPFQPGSKPPFSATPPLSTSQSPSGSRSTPNPVSSTVQPGTPLKAKSCEFCGKTFKFQSNLIVHRRSHTGEK
PFKCHLCNHACTQASKLKRHMKTHCQSKSSVLNAKSDDGLSTASSPEPGTSELMGSATDALKSVVAKFKSENNGLMPENG
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEIESKPGVDEEERNDYRFSLRLEGARHHQNSDALHPHRRSLSQEHGDE
DSAMESDRADDGTTTTINGLGSLPNDNLSRKLLGGGVSPGSLSPLSKRIKVEKDLDPPTPTIPNTENVYSQWLAGYAASR
QLKDPFISFTGGDSRQSPFASSSEHSSENGSLRFSTPPGELDGERAASGRSGTGSGASTPHGGSGNGRPSSKDGRRSDTC
EFCGKVFKNCSNLTVHRRSHTGERPYKCELCSYACAQSSKLTRHMKTHGQMGKDVYKCEICHMPFSVYSTLEKHMKKWHS
DRPLANDIKTE
```

481 - 500:	EEEEEEEEEEEEEEEEEEEE
482 - 501:	EEEEEEEEEEEEEEEEEEEE
483 - 502:	EEEEEEEEEEEEEEEEEEEE
484 - 503:	EEEEEEEEEEEEEEEEEEEE
485 - 504:	EEEEEEEEEEEEEEEEEEEE
486 - 505:	EEEEEEEEEEEEEEEEEEEE
487 - 506:	EEEEEEEEEEEEEEEEEEEE
488 - 507:	EEEEEEEEEEEEEEEEEEEE
489 - 508:	EEEEEEEEEEEEEEEEEEEE

A0A3B5B5G0 **A0A3B5B5G0_9TELE** (680 aa)
X-linked retinitis pigmentosa GTPase regulator-like. *Stegastes partitus (bicolor damselfish)*

```
MAGEAEDEIPDSGAVFTFGKSKFADNVPSKFWLKNDVPLKIACGDEHTALLTENGKLFMFGSNNWGQLGLGSKLTVNKPT
CVKALKSEKVQLVACGRNHTLVCTAQGKVYASGGNSEGQLGLGDCDERTAFHRVDFFNAHGPIRMLAAGSNTSAALTASG
RLFMWGDNTEGQIGLGKESQASSPQEVSVGRPVSWVSCGYYHSALVTVDGALFTFGERDSGKLGLGTDQLPGHRVPQLVK
SIKERVKQVECGGGHTVALTEDDVYTFGLGQFGQLGHGTFIFESRLPRPVEHFKKGRVCQVACGENHTAVITDGGLLYTF
GDGRHGKLCLGEENFTNQFKPTLCPRFLKYSVRAAACGGCHMVVLARPRDGSCSDVTLEDDDVTEDYLEKSYVELLGDSL
DSSTLQRSLSARVRRRERERSPDQFGALFRTLPAMTPGYLQPLPVCSQTAPPRLPPNRAVLFPEQAAADSDSAAESPTDT
DSVRGLGETTDFLNMTHVMKMDPGDKTLTLSPVQKSKEEEEEEEEESEEEEEEEEEEEEEEEEEKEEEEEEEEEEEEEKE
EEEEEEEGEEEKEQEEEENEEEEEEEEEKEESEEEDEESSKDDEEAEEEEEEEEEEEEEEEEEEEEEEEEEVVKKKKSK
EGKRQSAKSAKTRKSRVKGQAAAESEEFWDDVLPQYLNLK
```

607 - 626:	EEEEEEEEEEEEEEEEEEEE
608 - 627:	EEEEEEEEEEEEEEEEEEEE
609 - 628:	EEEEEEEEEEEEEEEEEEEE
610 - 629:	EEEEEEEEEEEEEEEEEEEE
611 - 630:	EEEEEEEEEEEEEEEEEEEE
612 - 631:	EEEEEEEEEEEEEEEEEEEE
613 - 632:	EEEEEEEEEEEEEEEEEEEE

A0A3B5K2S2 **A0A3B5K2S2_TAKRU** (908 aa)
Uncharacterized protein. *Takifugu rubripes (Japanese pufferfish) (Fugu rubripes)*

```
MSRRKQGKPQHLSKRDFSPAEPLSTAIVSSEELSERCSEHSEESGSLNGHHLGLTVGRLARLGHDAHPSLEQDLLTCGQC
QATFPLGDILLFIEHKRKRCHGPPCLTVGRGLDKPPSPSPGLALTPALSSLRSRRPVEVGVQATLADDDDDRFSSPRGNC
PKQEPLPGKEEPTTYTCTTCKQSYGSAWFLLQHAQNSHGFRIYLESEHGSPLIPRMGGPSSLGGGADCPSQPPLHGLHLP
PDASPFNLLRIPGSGSGGRDSVGTGGGIGPGVGLAGVHHQRFPPTPPLFSPPPRNHLDPHHLSPEELALAAHHPSAFDRV
MRLNPPLPLDPPPTMDFSRRLRELAGNTSGSTPPLSPSRPSPMQRLLQPFQTGGNGSVGGAGSGKPPYLATPPPLPGSMQ
SPVGSQTTPTTTLPSAGATPSSVTPLKTKCCEFCGKAFKFQSNLIVHRRSHTGEKPYKCHLCDHACTQASKLKRHMKTHM
HKSSSPNTGKSEDGLSTTSSPEPGTSEHIGSASNALKSVVAKVKSENDRMLHENGEEEEEEEEEEEEEEEEEEEEEEEE
EEEHNNENASRRNNSYHFGLNLEAVRQHENNGGIGSRLGGEEGSIPRSLPEVMQGMGLAASMQHFSEALNAHKRNAMAQE
NHLHHHLNRDHHHNRDMCDGESVLETDRAEEGAVSAVNGRGASPNESASIGLSKKMLLGSPSPLSPFTKRIKLEKEFDLP
TPTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRFSTPPGELDGGLSGRSGTCSGGSTPHL
GGPGRPSSKDSRRTDTCEYCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQSSKLTRHMKTHGQVGKDVYKCEVCKM
PFSVYSTLEKHMKKWHSDRPLSTEIKSE
```

536 - 555:	EEEEEEEEEEEEEEEEEEEE
537 - 556:	EEEEEEEEEEEEEEEEEEEE
538 - 557:	EEEEEEEEEEEEEEEEEEEE
539 - 558:	EEEEEEEEEEEEEEEEEEEE
540 - 559:	EEEEEEEEEEEEEEEEEEEE
541 - 560:	EEEEEEEEEEEEEEEEEEEE
542 - 561:	EEEEEEEEEEEEEEEEEEEE
543 - 562:	EEEEEEEEEEEEEEEEEEEE
544 - 563:	EEEEEEEEEEEEEEEEEEEE

A0A3B5KEU1 **A0A3B5KEU1_TAKRU** (808 aa)
Uncharacterized protein. *Takifugu rubripes (Japanese pufferfish) (Fugu rubripes)*

```
MSRRKQGKPQHLSKREFSPEPLSGVLPEDDSQDSPRLGVAQGEPLKGDPDLLTCGQCHSRFPLADILLFIEHKRRQCHGS
LCADKPLDRPPSSPLASPLSTSSSHSRSHHHHPQRPYHPVEVAVQVSPQDEDCLSAPLRGIIPKQENISDKDEPSSYTCT
TCKQPFTSAWFLLQHAQNTHGFRIYLESEPGTPLTPRVAAAPGMGGDCVSSQPPLHAVHLADGSPYSLLRMPGSGSGRES
ASTPHEGRYPRTPPLFSPPPRHHLSPDDLALATHHPSAFDRVMRLNSVPLETPPSMDFSRRLRELAGNAAGASPPLSPNR
PNPMQRLLQPFQPGSKPPFSATPPLSTSQSPSGSRSTPNVASNTIQPGTPLKAKSCEFCGKTFKFQSNLIVHRRSHTGEK
PFKCHLCNHACTQASKLKRHMKTHCQNKSLVPNAKSEDGLSTASSPEPGTSNLVGSATDALKSVVAKFKSENNGLVSENG
EEEEEEEEEEEEEEEEEEEEEEEEEEEGEKEEAESKAGVEEGEERNDYRFSLRLEGARHHQNSDALHPQRRNLSREPVV
DDESAVESDRAEDGTTTINGLGPLSTDLSRKLLGGGVSPRSLSPLSKRIKVEKDLDPPTPTFPNSENVYSQWLAGYAASR
QLKDPFITFTGGDSRQSPFASSSEHSSENGSLRFSTPPGEMDGERVASGRSSTGSGASTPHGNGRPSSKDSRRNDTCEFC
GKVFKNCSNLTVHRRSHTGERPYKCELCSYACAQSSKLTRHMKTHGQMGKDVYKCEICHMPFSVYSTLEKHMKKWHSDRP
LTNDIKTE
```

481 - 500:	EEEEEEEEEEEEEEEEEEEE
482 - 501:	EEEEEEEEEEEEEEEEEEEE
483 - 502:	EEEEEEEEEEEEEEEEEEEE
484 - 503:	EEEEEEEEEEEEEEEEEEEE
485 - 504:	EEEEEEEEEEEEEEEEEEEE
486 - 505:	EEEEEEEEEEEEEEEEEEEE
487 - 506:	EEEEEEEEEEEEEEEEEEEE
488 - 507:	EEEEEEEEEEEEEEEEEEEE
489 - 508:	EEEEEEEEEEEEEEEEEEEE

A0A3B5L967 **A0A3B5L967_9TELE** (896 aa)
Uncharacterized protein. *Xiphophorus couchianus (Monterrey platyfish)*

```
MSRRKQGKPQHLSKRDFSPEPLSTAVVSSEELSERCSEHSEDSGSLNGHHPVPTAGRLARLGPDSHPSPEQDLLTCGQCQ
ATFPLADILLFIEHKRKRCHGPSCLAIGRGLDKPPSPSPGLALTPSPALNSLRGRRPVEVGVQATLADEDDERFLSPRGI
CPKQEPLPGKEEPTTYTCTTCKQSYGSAWFLLQHAQNSHGFRIYLESEHGSPLTPRMGGPSSLGGGADCPSQPPLHGLHL
PPDASPFNLLRIPGSGSGGRDSRFPPTPPLFSPPPRNHLDPHHLSPEELALAAHHPSAFDRVLRLNPPLPLDPPPTMDFS
RRLRELAGNTSGSTPPLSPSRPSPMQRLLQPFQTGGNGGAGGAGGSKPPYLATPPPLQGSMQSPVGSQTTPPTPLPTAGP
PSSSNTQLKSKCCEFCGKAFKFQSNLIVHRRSHTGEKPYKCHLCDHACTQASKLKRHMKTHMHKSSSPNTGKSEDGLSIA
SSPEPGTSEHIGSASNALKSVVAKLKSENNRMLRENGEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEVQNGERPPKRNN
SYHFGLSLEAARQHENSSSIGSRLGGVADETSIPRSLPEVMQGMGLAASMQHFSEALNAHKRNAMAQENHLHHHLSRDHH
HSRDMCDGDSILETERVEEGTVSAVNGRGVSPNESSSIGLSKKLLLGSPSPLSPFSKRIKLEKEFDLPTPTIPNTENVYS
QWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRFSTPPGELDGGMSGRSGTGSGGSTPHLGGPGRPSSKDGR
RSDTCEYCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQSSKLTRHMKTHGQVGKDVYKCEICQMPFSVYSTLEKHM
KKWHSDRPLSTEIKSE
```

518 - 537:	EEEEEEEEEEEEEEEEEEEE
519 - 538:	EEEEEEEEEEEEEEEEEEEE
520 - 539:	EEEEEEEEEEEEEEEEEEEE
521 - 540:	EEEEEEEEEEEEEEEEEEEE
522 - 541:	EEEEEEEEEEEEEEEEEEEE
523 - 542:	EEEEEEEEEEEEEEEEEEEE
524 - 543:	EEEEEEEEEEEEEEEEEEEE

A0A3B5MNE3 **A0A3B5MNE3_9TELE** (909 aa)
Uncharacterized protein. *Xiphophorus couchianus (Monterrey platyfish)*

```
MAAPRSSRVTRSSVGLNGLDEKFCGRTLRNRSIAQPGETSVSPQPRARSPKKKQDTNKDNRQESKNIADSSIPAGDEDHS
TVSRKRGLSRLEKDLKQEKSENCDTGKEWRNTSPPIKRAKQCSLSGEFLGHEEDQGFLNPQSQVSVSEPCKDLICEDLPS
HNSCNAPPASSILSEHEGEVVGRQEKEDYCLDCDGPVFPQNSHKASNGLRETDAEETSTVTEYPSETPTSATSFPSLLNG
SQMEAPSSPDSSVPFRNSVAGQMAVSGSGESPASSALTFMGSVEDPVPELIVAKEQEVEEVEVDVVGDPLGLAHEEQVTV
SEGDTNGRSPSPVQEPAASSSNSGETMPTPTTPQSPTEPECNPSMSSMTPSFTELNEHRYTLRTSPRRVVSGGKASPSKP
CSPMTDNGPFREEGEVEDDCPMLEEPSCSDSVGLSSEPGSVNPSCRASEKDSDFMEDKETENGKELTRSEAVEEEEEEEE
EEEEEEEEEEEEPDVYYFESDHLALKHNKDYQRLLQTIVVLEAQRAQAILDLETLARQQREALSEPISFVEQLQKQVTLG
LPRPQRVVQLPDIAWEQYTSGLGEFEREFCDKKRKTRQLKLIFDKGLPLRPKSPVEPKKEGESSAVYSSLPTSDAPENGR
QTQMIRGRICHPNKPDTFNQLWTVEEQKKLEQLLVKFPPEEVESKRWQKIADELGNRTAKQVASRVQKYFIKLTKAGIPV
PGRTPNLCMYTKKASSKRQHHLNKHLYRPSTFLTSYEPPVYMEDEDERAAFYHSVQDPSADDSDEESVPVELRNLQEYKE
LLQLKRLKKQKLQEIREDNAGVQHMGYKCDVCGMDPIQGVRWHCQDCPPENSVDFCSNCSDCLFKTETHKPDHHLEAVYQ
PNTFLDRDYCLPQSAGYNYLDPNYFPANR
```

473 - 492:	EEEEEEEEEEEEEEEEEEEE

A0A3B5QBA0 **A0A3B5QBA0_XIPMA** (914 aa)
Uncharacterized protein. *Xiphophorus maculatus (Southern platyfish) (Platypoecilus maculatus)*

```
MSRRKQGKPQHLSKRDFSPAEPLSTAVVSSEELSERCSEHSEDSGSLNGHHPVPTAGRLARLGPDSHPSPEQDLLTCGQC
QATFPLADILLFIEHKRKRCHGPSCLAIGRGLDKPPSPSPGLALTPSPALNSLRGRRPVEVGVQATLADEDDERFLSPRG
ICPKQEPLPGKEEPTTYTCTTCKQSYGSAWFLLQHAQNSHGFRIYLESEHGSPLTPRMGGPSSLGGGADCPSQPPLHGLH
LPPDASPFNLLRIPGSGSGGRDSVGAGGAIGSGVPGGHHQRFPPTPPLFSPPPRNHLDPHHLSPEELALAAHHPSAFDRV
```

```
LRLNPPLPLDPPPTMDFSRRLRELAGNTSGSTPPLSPSRPSPMQRLLQPFQTGGNGGAGGAGGSKPPYLATPPPLQGSMQ
SPVGSQTTPPTPLPTAGPPSSSNTQLKSKCCEFCGKAFKFQSNLIVHRRSHTGEKPYKCHLCDHACTQASKLKRHMKTHM
HKSSSPNTGKSEDGLSIASSPEPGTSEHIGSASNALKSVVAKLKSENNRMLRENGEEEEEEEEEEEEEEEEEEEEEEEEE
EGEEEEVQNGERPPKRNNSYHFGLSLEAARQHENSSSIGNRLGGVADETSIPRSLPEVMQGMGLAASMQHFSEALNAHKR
NAMAQENHLHHHLSRDHHHSRDMCDGDSILETERVEEGTVSAVNGRGVSPNESSSIGLSKKLLLGSPSPLSPFSKRIKLE
KEFDLPTPTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRFSTPPGELDGGMSGRSGTGSG
GSTPHLGGPGRPSSKDGRRSDTCEYCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQSSKLTRHMKTHGQVGKDVYK
CEICQMPFSVYSTLEKHMKKWHSDRPLSTEIKSE
```

536 - 555:	EEEEEEEEEEEEEEEEEEEE
537 - 556:	EEEEEEEEEEEEEEEEEEEE
538 - 557:	EEEEEEEEEEEEEEEEEEEE
539 - 558:	EEEEEEEEEEEEEEEEEEEE
540 - 559:	EEEEEEEEEEEEEEEEEEEE
541 - 560:	EEEEEEEEEEEEEEEEEEEE
542 - 561:	EEEEEEEEEEEEEEEEEEEE

A0A3B5QCR0 **A0A3B5QCR0_XIPMA** (935 aa)
Uncharacterized protein. *Xiphophorus maculatus (Southern platyfish) (Platypoecilus maculatus)*

```
MSRRKQGKPQHLSKRDFSPAEPLSTAVVSSEELSERCSEHSEDSGSLNGHHPVPTAGRLARLGPDSHPSPEQDLLTCGQC
QATFPLADILLFIEHKRKRCHGPSCLAIGRGLDKPPSPSPGLALTPSPALNSLRGRRPVEVGVQATLADEDDERFLSPRG
ICPKQEPLPGKEEPTTYTCTTCKQSYGSAWFLLQHAQNSHGFRIYLESEHGSPLTPRMGGPSSLGGGADCPSQPPLHGLH
LPPDASPFNLLRIPGSGSGGRDSVGAGGAIGSGVPGGHHQRFPPTPPLFSPPPRNHLDPHHLSPEELALAAHHPSAFDRV
LRLNPPLPLDPPPTMDFSRRLRELAGNTSGSTPPLSPSRPSPMQRLLQPFQTGGNGGAGGAGGSKPPYLATPPPLQGSMQ
SPVGSQTTPPTPLPTAGPPSSSNTQLKSKCCEFCGKAFKFQSNLIVHRRSHTGEKPYKCHLCDHACTQASKLKRHMKTHM
HKSSSPNTGKSEDGLSIASSPEPGTSEHIGSASNALKSVVAKLKSENNRMLRENGEEEEEEEEEEEEEEEEEEEEEEEEE
EGEEEEVQNGERPPKRNNSYHFGLSLEAARQHENSSSIGNRLGGVADETSIPRSLPEVMQGMGLAASMQHFSEALNAHKR
NAMAQENHLHHHLSRDHHHSRDMCDGDSILETERVEEGTVSAVNGRGVSPNESSSIGLSKKLLLGSPSPLSPFSKRIKLE
KEFDLPTPTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRFSTPPGELDGGMSGRSGTGSG
GSTPHLGGPGRPSSKDGRRSDTCEYCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQSSKLTRHMKTHGQNAVMADG
WKRNTRLAFSRVRKGPPSDPCLHWLAELMENPCGLSWIKGCPGVQKTHGLSGHSS
```

536 - 555:	EEEEEEEEEEEEEEEEEEEE
537 - 556:	EEEEEEEEEEEEEEEEEEEE
538 - 557:	EEEEEEEEEEEEEEEEEEEE
539 - 558:	EEEEEEEEEEEEEEEEEEEE
540 - 559:	EEEEEEEEEEEEEEEEEEEE
541 - 560:	EEEEEEEEEEEEEEEEEEEE
542 - 561:	EEEEEEEEEEEEEEEEEEEE

A0A3B5RB42 **A0A3B5RB42_XIPMA** (1255 aa)
Uncharacterized protein. *Xiphophorus maculatus (Southern platyfish) (Platypoecilus maculatus)*

```
MAAPRSSRVTRSSVGLNGLDEKFCGRTLRNRSIAQPGETSVSPQPRARSPKKKQDTNKDNRQESKYDARKESKHDTSKDS
KQDSSQHANKVSKQESKPDTSRVSKQETKQDTSKNSKQESKQDNRKDSKQESKQDTSKDSKQEPKQDTSKDSKQESKQDT
SKDSTQESKQNNSKDSKQESKKDTSKDSTQESKQNNSKDSKQESKKDTSKDSTQESKQNNSKDSKQDFKRDTSKDSIKES
EQDAVKESKQDAVKESKQDAIKESKQDAVKESMQDAVKESKQDAVKESMQDAVKESEHDAVKESEHDAVKESEHDAVKES
EHDAVKESMQDTVKESEHDAIKESRQESNDNKQDNKQDTGEELNQDFELESKHAAKHDTKPQETSLQDSQQLDILQRNIA
DSSVPAGDEDHSTVSRKRGMSRLEKDLKQEKSENCDTGKEWRNTSPPIKRAKQCSLSGEFLGHEEDQGFLNPQSQVSVSE
PCKDLICEDLPSHNSCNAPPASSILSEHEGEVVGRQGKEDHCLDCDGPVFPQNSHKASNGLRETDAEETSTVTEHPSETP
TSATSFPSLLNGSQMEAPSSPDSSVPFRNSVAGQMAVSGSGESPASSALTFMGSVEDPVPELIVAKEQEVEEVEVDVVGD
PLGLAHEEQVTVSEGDTNGRSPSPVQEPAASSSSSTANVNCSSVNNSNSGETMPTPTTPQSPTEPECNPSMSSMTPSFTE
LNEHRYTLQTSPRRVVSGGKASPSKPCSPMTDNGPFREEGEMEDDCPMLEEPSCSDSVGLSSEPGSVNPSCRASEKDSDF
MEDKETENGKELTRSEAVEEEEEEEEEEEEEEEEEEEEPDVYYFESDHLALKHNKDYQRLLQTIVVLEAQRAQAILDLET
LARQQREALSEPISFVEQLQKQANLGLPRPQRVVQLPDIAWEQYTSGLGEFEREFCDKKRKTRQLKLIFDKGLPLRPKSP
VEPKKEGESSAVYSSLPTSDAPENGRQTQMIRGRICHPNKPDTFNQLWTVEEQKKLEQLLVKFPPEEVESKRWQKIADEL
GNRTAKQVASRVQKYFIKLTKAGIPVPGRTPNLCMYTKKASSKRQHHLNKHLYRPSTFLTSYEPPVYMEDEDERAAFYHS
VQDPSADDSDEESVPVELRNLQEYKELLQLKRLKKQKLQEIREDNAGVQHMGYKCDVCGMDPIQGVRWHCQDCPPENSVD
FCSNCSDCLFKTETHKPDHHLEAVYQPNTFLDRDYCLPQSAGYNYLDPNYFPANR
```

819 - 838:	EEEEEEEEEEEEEEEEEEEE

A0A3B6BX47 **A0A3B6BX47_WHEAT** (780 aa)
DUF4220 domain-containing protein. *Triticum aestivum (Wheat)*

```
MQLLPGGNYQPVILKLENEWLVRALVLASLATHLVLVLVAGTRRRRASGLCRGLLWFCYQVASWVGTHSISNLMLGAVTS
REKHLHALWTPFLLMHLALPDNISAYSLEDSALSGRQLASAIGQISGAIFILYKNFIFVRDADAGTLWQASYLMFTLGLY
KYVESVWALWQGSLGTIRGSIKEMKPKVLSPAECKVHGLDNEQALLFAHKLLHIGKGAFADYPIILKPVVRRQDEIRAFC
QSEGWQDMCRVVEMELSLVYDVMHTKAAIAHSWPGYCIRVMSPPFTAAALLLFWSDSKVGESGADVMVTYALLLVTLILD
VGWLLGTLGSTWTCAFLTHRPQHWLLHCSLGRCHRQLRSLGFVAGKDATKYRLWSGTMGQYNLLSENCRGRRASKLVKRL
SAEDAWMEYTYGCSEGIVLSPCVMDLVFQWVCEILEEAFPEEEEEEEEEEEEEEEEEEEEEEEEEGTSTDEEIAVPVTSK
ITAKAEIGMETGPDPSGALKRQAALGKVLGIGSEFPELVLKWHVATEIFLLCRPRPTASGSCIECKKHVEAIQGLSNYMMF
LVAVRPGMLPGLNLRSMLDATWMALDSLYRDRKGKCTSGRKTKRGLAEILQKKVAAATDHLHRKSAVLSDGTFYAEVMLF
RMGACCSWVWPHGKWSEEHQDRWTGPLRTLAPGLYHNVNKPLQMEEMLEIILYGWVRLLVHASTRCGPDSHAKQLSRGGD
LTTVVWMLAEHAGIYGIRADKTSDRPCWFPSPDPACDCVASFDRLIKQHYEAPGPQQTET
```

441 - 460:	EEEEEEEEEEEEEEEEEEEE
442 - 461:	EEEEEEEEEEEEEEEEEEEE
443 - 462:	EEEEEEEEEEEEEEEEEEEE
444 - 463:	EEEEEEEEEEEEEEEEEEEE
445 - 464:	EEEEEEEEEEEEEEEEEEEE
446 - 465:	EEEEEEEEEEEEEEEEEEEE

A0A3B6BZD5 **A0A3B6BZD5_WHEAT** (424 aa)
Uncharacterized protein. *Triticum aestivum (Wheat)*

```
MPQVSRARLCRRRRRPSQPANAGLDDDIESKSIYCEPTTEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEELAPES
SMEEQKEDFDQHRENWEISFGKGRFDFEALTMLSPMLFTHCSPSRIPGEAVLSKTLQIYSIKIAKTKHLKWPLQVYGVVA
ARDYVDHKRNILFFRRRGRSQTLTKKDPYLHLTGPSRALMCRDPVHIEFQLMVKGQSRSEDRTLFTLPVQMYNPSWHDWC
YRCFSNYLCKIELRFEQLDWSRQATILSARVTQGSPFKHGGQIVCRASPCEDDPNKEIVLFDSKYGTMNMESDETMSMDS
DGYLALLRRVVSVRGRLKIFIYTYSRSGAIAASGRVLFKAKDCQTSQATCVLHSCKPSRGKKTSSKGKDTKVKITVAWSR
LVRSINDMSQIPFDDRLLLGYADP
```

40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE

A0A3D8R8N1 **A0A3D8R8N1_9HELO** (146 aa)
Uncharacterized protein. *Coleophoma crateriformis*

```
MKGEEEEEEGEEKKEDEEEKKKKRKAKKKKGEEEEEEEEEEEEEEEDEEEEEEEEEEEEEEEEDEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEERREKEREEEEREKKEKKRSKEEGKKGRHGGIHQPRSKASSSSKHH
```

66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE

A0A3D8RGD3 **A0A3D8RGD3_9HELO** (821 aa)
Uncharacterized protein. *Coleophoma cylindrospora*

```
MASSPTPQPRRTTFAEPAERPQHSGSRSSSIVERPRTPCPMVKRQESFQTGFDSGYGRCDGEGSAGEEADVRGESGERLE
LGGDVANEPRRIVSDAEALMAVEIGAEEEEEEEEEEEEEEEEEEEEEEEEEDNAGHYDDDDNDDDDDGDTVVILNTQRQAK
```

```
EDQDDEDLKNAPQPSLTFSSDETSDKKESFQVDMGTCTQTLPLLRNNLAFEGPVVIMPGLSIAVEELTLYEDGTLAIDHR
LSSKIRSLLSYDNMLPDAEKATKKRKDSGYCSNTERTKSRTRNGDSGRNSQAHCEGKDHKLQASSHSSMGRLFQPACESS
SDKERKRKRKREYQLPSLPRITRSGHDFIAMCAPDCAEYHARFEIPETVLHRSDLKSRSPIVLKPVAAAEYLASAVLWIS
RDHAVLADASNLTSVPEKDDLDLLSPRSEDCYMPAPSINLVRKHFRSGQWVWVTEPGEFSTLGGEWGSDGYGESARDVNA
QIDLIWTAALAESRRRFFAGSLDFDAMVNFCHGRIPVPEERVDWLATALRARIEKHRRLHEDFRRALDRGAVSASLKRDL
KKLSYFSTGGDVGPLVRQASKKQAKKAAKEEMFLARSAIREQSSVLKRVVEFVKHPIYQYSDRRTSEKRELEKLRRLRFP
ELYAPASTAKSDTKREDNKEDLPSPPPDWIVNRNSLLQEQEVEGLERLKPGRDAFWSRASNRKALRFQKGKMKAVDLATS
YPCPSIQSRSSNLASHRTLSSDPSSDSRYPSPQTSSIRHLSSENQDGGDFKSRNGKMNKKSERWDPDHQSQPPPGTRAWL
RYFEEFEKHAPSDLLLDTCSM
```

107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE

A0A3D8S1M8 **A0A3D8S1M8_9HELO** (97 aa)
Uncharacterized protein. *Coleophoma cylindrospora*

```
MASYGDQTYGGRADSTAVRAVVPTPLPEEDEDNDITSGFDASPPPKAREEQSNFQARRAQLDVLEEEEKKKKNKEEEEEE
EEEEEEEEEEEEEEEE
```

75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE

A0A3E2H1G9 **A0A3E2H1G9_SCYLI** (219 aa)
Uncharacterized protein (Fragment). *Scytalidium lignicola (Hyphomycete)*

```
MTSWTLINRPRASTLAFDSSSASSILAVVMAPSSPAPEAPVAAVAPDFAGAVGPLLALLACPTGAMRSLAGLPPLRVFTV
REGCTLNTTRPVNMEALLGFLVGCVSGQLCTYCESGLGVWTDEGSRCSFYILVHNRYATPVVPVTLATSSASAPAGLSRA
LCSCALLVVGLVVTSSIAVVLLARLSLCPQPFAVDEEEEEEEEEEEEEEEEEEEEEEE
```

196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE

A0A3E2H706 **A0A3E2H706_SCYLI** (289 aa)
Uncharacterized protein (Fragment). *Scytalidium lignicola (Hyphomycete)*

```
MEKTSKTVFQLDSPYTTIQWPQISQETEAAILEHLCNFLSPIGKYRANHVSVSNGKRSKKRKRHQANVGEGAEGATIAPP
APEISQFVVIGLSHVTRRLELMSQRTRQLRSGNSTTEFTATKVGTDTSITKLPGSDISTTGDLTHAHFAAIFIPRSNQPP
ILHTHLPQLIATSSLAHPELPPTRLVQLPKGCDSQLCAALGLPRVSFCGILEGAPHSNALINLIRVAVADIKIPWLDDAR
KATYMPLRKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEXXEEEVYIH
```

250 - 269:	EEEEEEEEEEEEEEEEEEEE
251 - 270:	EEEEEEEEEEEEEEEEEEEE
252 - 271:	EEEEEEEEEEEEEEEEEEEE
253 - 272:	EEEEEEEEEEEEEEEEEEEE
254 - 273:	EEEEEEEEEEEEEEEEEEEE
255 - 274:	EEEEEEEEEEEEEEEEEEEE
256 - 275:	EEEEEEEEEEEEEEEEEEEE
257 - 276:	EEEEEEEEEEEEEEEEEEEE
258 - 277:	EEEEEEEEEEEEEEEEEEEE
259 - 278:	EEEEEEEEEEEEEEEEEEEE
260 - 279:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE

A0A3E2HD85 **A0A3E2HD85_SCYLI** (207 aa)
Uncharacterized protein (Fragment). *Scytalidium lignicola (Hyphomycete)*

```
MPTAGGEGGVVVVLAPIKDDWDGVVESLGAGDGFAEFDIFSVGGDEDMEKSSAGAYGGYSYGRSSVDDLWFQVDLERERE
RERERERREEXKRKRGRRGEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEGTLILQKQLTPATTPPILTANCSSTKSGPSS
NATNTSTNVHKGKSSLKIVSDMLTPKEDRGIFQERVKRLQLKITSSS
```

99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE

A0A3F2RCI7 **A0A3F2RCI7_9STRA** (411 aa)
Uncharacterized protein. *Phytophthora kernoviae*

```
MTEPSSASTDLSTRSAAEAFEGDSAEDLVDKETTLDDVLVSPVTKKGKLLDVDLPDVDDDEEFPQQDQEMDQELALELEN
CKDETEDQELQISQGGQDMDKIQSDVDALAPPEEDDLSEPPTSQNNEIDIVDVDEEEEDEEEDEEEEEAEVDSSGPGEYQ
QYSEEEDEDEQETVRAIARAQNQREARQLLQQLDNSARSKLCLTALEKYGEELFYGHEDARDAILVDACAQDSILSLMRD
AIRVRDLYLRGSSAAAPVELDDDDDEEDEEEMGGYEDEEEDEGDEEKRSASGQDDDDVVIISEEEEEEEEEEEEEEEEEE
EEGKSDSEAPDSTALSGSDGPAENGTHADDEMEEEDDEEEKEEEENGAANNAADKEVDVAEESKGYEDAAVGNVIVAGDL
AAEEPTTDTTT
```

303 - 322:	EEEEEEEEEEEEEEEEEEEE

A0A3L6P3L8 **A0A3L6P3L8_FUSOX** (3361 aa)
Uncharacterized protein. *Fusarium oxysporum f. sp. cepae*

```
MAAVDVLAFTDSWTRSAHGLPVFQCLSSAPVDRSLRHRLSLIARAWVGHKLHENVSSSPSHRKVAERPLIVPDHSPRWYC
RLPRSCDSSDPTDTTMPLNGTSRYAHMRTPAWLNPSPQPPSDAQKERRRPNDALLNDPNSDILIDFNSNQGFYEAAKKKK
TKTPSAPPPPPPPPAAPPADDGQKDDNTGGDGGASGGDAAGGAGDGNGDGNSNSPPKPPTTFENINLGDNKPDLGLSPPE
NKGISSSWGAKLGFGGGGWGWGGGGKSETAPAPAPAPAPAPPPPQETKAEENPWDKPKDKIGGIEEDDDGWGFGAKKE
KKKGSTLWGAEPDEEPKDGDDPWGWSGQKKKGKAGGILEELALDSDTAPPNGKKDIWDTWGISKKDRAKKKGIMEEVALA
AAPDPPSMEDQWGGWSGKKEHSQSSLWGAQDSIPAPAPDPPSFEDKDGDDFWSTFGTGKAKPPPEETSGWGSWGIGKKEP
PKTEDDGWDLWGTGKKKKKAGDLIQIEDDIPPPAPDPVEAVGTDDFLDSWGFGKKPKKPAADPFDFKTSGADDPNDAFWG
SIDNKKPNAHEFLIDATGDPEQAAREAEEQAAREAEEAEAAREDEEIASLLDKKSKRGGRLLKSDRERLALLEGNATRRA
EARATREAEAAAAAEAAQAAADAQAAADAEAAALQAAEDAEAAKENEEVATLLAKKQKRSGKLLKKDQERLTLLEGNVSR
RAEAQAAREAEAIAAAPVAPAAPADEPLSQETDRDGLATQAAAEADTALATEIAQEEAEMESLKSKKAKKGKLLKKEQER
LNFLIDNAAKRAEDQAAKEAEEQAAKEATDAAAAAAAAAAEAEAQAQAAADAEAAVQAAADAEAEVAAKEEEEMAVLKAK
KAKKVKLTKNETTRLMTLVGNSVKRAQEKSVKEAEEAAAAQAAKEAEETAAREADALAAREAEATAAREAEAVIAAEEEK
ELADLTAKKIKRGGNLIKKKDVERFNVLTQRAAERAERAAKQAEKIAAVEAQGELGEAAHGNAEVVVEAQPEPEPEQPLV
DIDAAFADPEPVTAPDAAIIAEEEAELASLDAKKTRKGKLGKKDTERYNILTENAAQRLAAKEAEEAAGAAAAEAEAEAA
KEAEEAAAAAEKAATAAAAAAAAAEAEAITASEAEAILIADEEAELATLAAKKAKRGKLVKKDADRFNILTENAAQRQAA
KEAEEAAAAAAAAEAEEQVAKEAEAATAAESAAAIEAAEAEAAAVREAEDAAIAEEEAELAVLTTKKAKKGKLAKKDADR
FAILSENAERRAREVAQIIEQPEDQTPEPETEVNEPSPEPAIDELSAEADDPDAIAAAEAEAAAIADEESELTALIAKKE
RKGKLGKKDTDRFNLLTVNSTARAEKAAQEEAAAQATAEAEAAAQAEAEQAAAAEAAALEEAAAREAAEAEALLIAEEED
ELAALTAKKNRKGKLGKKDNDRFATLTENATQRAEKAAASEVMKEAVLEVEDLPAENPADTEADAEAAEAAAIEAEAAAI
AATIAAEEEEELAALITKKDKKGKLGKKDSDRFAFLTENAAQRARNAMHEEAAEEDQEAAIAESEDINDHPADIEDSLFE
NALEPPVVEEEAPPEEDDAAAAEAMALVAAEEQEIADLEAKKARKGKLGKKDMERYTLLIENAAKRAEEQATKEAELAAA
AELVAIESAEAEAAAAEEEAVAREAAEIEAAAVIAQEEEELAALEAKKQRKGKLGRKDTDRFDYLLGNKVAREAQVAEER
AAKEAEEQALQEAEEAAAAAAAAATEAEEIAAREAAEAEAAAVADAEDEELAILAAKKVKKGKLGRKDTERFEQLSSNVA
KRAEKQAAREVEAAAEEAPAVEELLGEEELEEPTPEPEETVEEAPEAPEAPEAPVPDIDDEAAAEAAAIAAEEEAELASL
EAKKARKGRLGNKDTQRFTFLTENISRRAEEQAAKDAAAAAQALAQTTPEDVAEEEDITGQEDAEAAAIEAEAAAIAATI
AAEEEEELAALTLKKARKGKLGRKDTERFDLLMHNAAIRAEERAIKEAEPDGQAEELIPEEVDDIPEPEPEENPDAEEVA
AQEAAEAEAEAEAEAERAIAAEEEAELAALNKKKAKKGKLGRSDTERFNILVDNAAKRAEAQAAKEAEENLGDVPRAEE
EEDDDFVDAEDGEEDELAEELEPEAEELAEPEPEEDETATAEAMSAEAAAQAAVIAEEEAELAALTKKRLKKGKLGRKDT
ERFQALTENSAKRAEEAATRDTEDAAAEVEAELGEPEHEPEPEPEAAEPEPEDDGLKEAEQAVIAEEEAELAALMKKKAK
KGKLGRKDTERFIVLSENATRREQERAAVEAETEAVQEEPDIEGVEETGGEHGEEGGEEQEQEQEQERSEGQDEEAAARE
AEEAAIAREEEDELEALKAKKARKGRLGRKDTERFAILEENAARRAEEHAAADAATANPPEEEDGEGEEEEEEEPEADDE
DKADEEELAIQEAEEAAAREAEEVAIAEEEDELEALQAKKSRKGRLGRKDTERLRVLEDNAAKRAEERAAKEAAAVDENL
GVDDAEEEEEEEEEEEEEEEEEEEEEEEEEDEDIDNGKEGRGEDDADAEEAAAAAAREAEEAAAKEAAEAAAREVIAKEL
EELDSLQFKKARKGRLGRKDTERLRVLEENAAQRAAELAAKEEAAAAAEDEEEDVVEFGNPPEEEKSEIEAEDDDEEKEA
EAEDTADKESSDVENEAAVGEDEEKEPEVLPKDQVPEAPADDEIVEVIDLSPKKERKSRKSKSRRDAPPPPPVPDPPLTP
PPEPKQSRRPKIHREGTSFGRWAATPHEERDEPQEKSSRHRRREEKTSSKGSSSDKVEKTPSRSRGTALFSKPPLTRSTT
MREKKDGISSKRRHSTNARGLVSPPPEDMLMGEDELSNRRKSRKPRSREDEDAMMSGAAPVPDRYERRRSHKPRSHEDDD
LVMVDPDLAPDRRERRRSHKPRSREEEEVAVVDTERRRRARRSRDEEPVMVEPDVPFDAPPRSSKKSSGFAGLFSGLRTP
KTERPDPLRRRSTYATTDDEALRSAKMDGDAVLVDADREARRAARRAKRAAEGGPDPEEAARRTRDEIRRERRRQREEEA
DPLRQDKEARRAERRRQRDEDARRAQEERQAQEEQQRLQEEKEAQRAERRRLRREQEAAAAAEQAEDEEARRAAKRERRR
RDTKRAARGAEEEEGRQRRSQQSTDEYNQRRSHRREERPQAPAWPHSGTSSWVKEHSDAPPPPDLGDGGEANGGQTEDEM
ARREARRAHRSKYEEEPTEEVEDRRRRRARRDDRERGGRDKERHRDRRSEGSDERHHSRRASTFMEATATPRTSWWKKIA
G
```

2566 - 2585:	EEEEEEEEEEEEEEEEEEEE
2567 - 2586:	EEEEEEEEEEEEEEEEEEEE
2568 - 2587:	EEEEEEEEEEEEEEEEEEEE
2569 - 2588:	EEEEEEEEEEEEEEEEEEEE

2570 - 2589:	EEEEEEEEEEEEEEEEEEEE
2571 - 2590:	EEEEEEEEEEEEEEEEEEEE

A0A3L6QQ04 **A0A3L6QQ04_PANMI** (865 aa)
Uncharacterized protein. *Panicum miliaceum (Proso millet) (Broomcorn millet)*

```
MAPPRRPTTLPPPPPPSSWVMMGRRRWRSSLASGLRAALACTIVGLASLYAPPALRRHITFPAFSYVVTVIIVTDATLGT
ALRGAVSALHATLMGAVPSVLALWLAHRTGAAESVLATSAVVALTTFAVALPESVGPVAKRIALGQIIIIYVARFQQGER
PTRDFALMHPANVVACTALGVAAALLAVLLPGPRLATREARDKTRAYRELAAERVRVMADAAIVVIGEAAAACSRQRRWQ
MAARTSEANRLASVSTALLHRVNAIKEDVQWERGAAAAVDDGMAAMVEMPLTGMQMALAMMMDNKCKHQLLDHHHHADLI
MEMRDQIRLALLTPNNKQTAAAAAPGGGGFIRRSSSKPQISLCFPKTTTLQPQQLAPWLFLFSLYQLRGAASGLLVANNG
ANANKKVAPAATAAQESDLPGEEEEEEEEEEEEEEEEEEEEEEERQQAATTGEGKRLANNDGDCSTTTKNNHPCWFWLRL
VAAAKCGLSLGLAVLLGLLFSNDHGFWSGLIVATTITTGRESTWAVAAARAHGTALGSVYGALGCLLISQQRLLTMDLRF
LALLPWMVLATFLKRSRAYGPAGGVAAALSGIIIMGRRYDEPAMAFTVARLVETFIGISCAVLADIIFQPGARPSVQARE
QLTRCIAALAAADDPSQSQLKSLQSQLALLRRHAAEAGSEPSYLWLPPFPAACYDKIQGSLGRMAQLLHLYHQARMTVDV
GDDDMFQRRFRSLVSSSLRHCHRMLQAPADAIMSSSSSSPDHQEVDLEAGNAITSCCCCCFKEDDDREEEATTPEEVVDS
FLAHAGEAAALLDDDDDGDEAHAEEEKGLLVCCLASMGLCMGEIIREALRLEANIIDLNNLQRPH
```

422 - 441:	EEEEEEEEEEEEEEEEEEEE
423 - 442:	EEEEEEEEEEEEEEEEEEEE
424 - 443:	EEEEEEEEEEEEEEEEEEEE
425 - 444:	EEEEEEEEEEEEEEEEEEEE

A0A3L6RX90 **A0A3L6RX90_PANMI** (398 aa)
CCHC-type domain-containing protein. *Panicum miliaceum (Proso millet) (Broomcorn millet)*

```
MESYLMGQDLWKIVAGTETTPPLKENAKALRKWRIKACKAMFVLKSTIEKDLVEHIRDAVIPNETWEIFVKLFSKKNETR
LQLLEKELAGISQGTLSINKYFTKLKNICREISQLDPEEKVSEARMKRIIINGLRPEYSGFMAAVSGWPIQPSLVELENL
LANQEALAKRMDSITLEEKDEEEALFIRKKGPLKDRGEAKEWTRGDRYCLKKNNYSRGAQEDNDDEDDQELLKNERRRRG
ECFNCGKKGYFVRDCPSLRKHTEGNVATMKEVVHSGWLSEEEWDAEACITTEDDEAYFVEDLTEGEALSTRVAEEEEEEE
EEEEEEEEEEEEEEEEEAEASLSMEVRDPDISTRFIVFECDDDEDWEALSDKEEDNRDEKNEPSLHKDEKLQEYEENKD
```

314 - 333:	EEEEEEEEEEEEEEEEEEEE
315 - 334:	EEEEEEEEEEEEEEEEEEEE
316 - 335:	EEEEEEEEEEEEEEEEEEEE
317 - 336:	EEEEEEEEEEEEEEEEEEEE

A0A3L7GZE4 **A0A3L7GZE4_CRIGR** (330 aa)
Sulfotransferase (EC 2.8.2.-). *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MAQTPELRKQTKGKGIAEIAGIPLMADTVDNWSQIQTFKAKPDDLLICTYPKSGTTWIQEIVDMIEQNGDVEKCQRALIQ
HRHPFIEWARPPQPSGVDKANEMPAPRTLKTHLPTQLLPPSFWTSNCKFIYVARNAKDCMVSYYHFYRMSQLLPDPRTWD
EYFEFFINGKEEEEEEEEEEEEEEEEEEEEEEEEEPDSRLSVNWGSWFDHVRGWWEIRDRHQILFLFYEDMKRDPKHEIR
KVMQFMGKNLDETVLDKIVQETSFEKMKENPMTNRSTVPKSILDQSISSFMRKGTVGDWKNHFTVAQNERFDEIYRQKMK
GTSINFCMEL
```

171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE

A0A3L7H250 **A0A3L7H250_CRIGR** (313 aa)
FRMD8. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MRRSCVCCLFYEEAKGNVLTARYPCDLKDCEVLGALVCCAQLGPYQPDQPAACTLRENGAKTGLGEQGRLNAYRQVKEAK
GSDSEHETTLGCHYHAYLLKCYELPFYGCAFCHVWRRKEEEEEEEEEEEEEEEEEEEEEEPVLWLEFDGDSEGTPINKLL
RIYSKQIELMSGLIEYCIELTQARPKLLKLGSVVCSQIQHLSIIGYVEEGKGIKQVKPKCTTSVFSQQLSTSQGSYTMSY
QPTLLVTALVILTAVDDSRLATAASDVSPPDWLQLIGSYDATGEAETKGWKVTQHLRINLFTIRCLPDAGAIL
```

119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE

A0A3L7H2R5 **A0A3L7H2R5_CRIGR** (142 aa)
SETSIP. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MGLQVSPSATCANLGAAILVITSSDCWVLFRFRDSCVPFGARPLATPTGRRASVEELFAGSPPASPMGNAQRNLSGFIQQ
```

AGEVINDDIWPNPFQYYLVPDMDDEEGEAEDDDDDDDDDEEEEEEEEEEEEEEEEEEEEEE

120 - 139:	EEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEE

A0A3L7H3W6 **A0A3L7H3W6_CRIGR** (334 aa)
RPL5. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

MNNRIGFVKIVKNKAYFKRYQVRFRRQREGKTDSYARKRLVIQDKNKYNTPKYRKIVRVTERSSARLPVPIIEGDMIVCT
SYEHELPKYGVKVGLTNYTAAYCTSLLLARRLFNRFGMGKIYEGQVEVTGDEYNVESIDSQPGAFTCYLYAGLAQTTTGN
KVFGGLKGAVDGGLSIPHSTKRFPGYDSESKEINAEVHRKHIMGQNAADHMGYLMEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEDKKQFSQYIKNNVTPDMEEMYKKAHAAIPENPVYEKKPKRKNASYSSHNETYKYQEAAFRYNGLVQVTT
ATTLQCRLARSLFK

216 - 235:	EEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEE
225 - 244:	EEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEE

A0A3L7H414 **A0A3L7H414_CRIGR** (304 aa)
H2BFM. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

MTPLESRDTTPARTEKHNTQEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEPDLKNYFMKMIESPSLSSDLIHTEMSSWSLI
RHNGKCVTHLRIFGLVMAAIAGVSAMEAGEELTTVEMASVEEPIPVEEPVAVSEQASDAYEKIRRPKSATAKKRQKQLER
RRRFQSMTEEERRRAARLIKRRKDSFTIYFPRVLRNIHMGFTLSQESLNILDSFVKDMFERIATEASNLARYTRRSIINS
RDIQSAVYLLLPGELSKRATTEGTLALFRYISKQRTTSTSLKPKGSLSATTSKRAVASTRACPQ

24 - 43:	EEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEE

A0A3L7H5P4 **A0A3L7H5P4_CRIGR** (144 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

MGTGHSSFPIHRLITDQRLIRQEGIRHSSTNVFEQFFQGNSNRKDPIETIRDKERQTDRDRQKDRQKQRERERKKKKEVE
EGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVSVYQGRSRSVAQDTDIRAFQLSGVHTFV

83 - 102:	EEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEE

87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE

A0A3L7H6B8 **A0A3L7H6B8_CRIGR** (181 aa)
ADSL. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MQVEPLACRLMDLIMDPLKTVSNIIVAVDKTGSNQQDCHEKTRVLPQQAERSLLEHIWVDAYLSPIHSQVEHLLDPSSFT
IQAPQQVHTFTEEELHPLLKLNGNVMEEKKSRFLEQMFQDKLRSDSKGSAPPANVHTGTTVLGPNYTQKEEEEEEEEEEE
EEEEEEEEEEEEEEEELSSSS
```

150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE

A0A3L7H7T6 **A0A3L7H7T6_CRIGR** (160 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MSKDKNVHLIQKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKNSDMDFSSQNHPPHPCDCP
SSKKKKKEERIEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEIYSKSNLCCPYTPWIMFKLLAASPLKKTGLQYS
```

92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE

A0A3L7H872 **A0A3L7H872_CRIGR** (3589 aa)
WDR87. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MPGAYGGQKRASNSLELIVKMLVSHPVVYFALIDVPRASSIVLCKLFFPLQELIGDFSLSHMLRFEASDMECLLSHVKER
LNEDLTMSQRGSSLRFSFDSVKYEELELIAEQTGLPLSESEKIDGLNKRRKQVQDTARKIGVRTTVPARRTTVPEKDTTV
PEKDTTVPEKDITVPEKDVTVPEKDTTVPEKDTTKYERKLSHGLSGTPGRMSQLEKTSWRDDICQLLTSRIASSHPDMIR
DLGEELADLADAVLTNEPSWALFNELCPWRRASGMVPSELGKVDKKAIKEEVPGTATDEEVSLSKIKEMVIDFLESYLIL
EIERLKASGKQKGETVEDREEVISLEEEEERTHDKETPAAPGKLLTTGDEKQLRKEKRRKQITDEKEPTHPEETLMQAKE
IYNALQNMLAKAKLRQEEKLRGEKQATVSEEGRADLEKKEQEEKKWSWPSERTEEEEEDYDYWVLDRFLSSSEDEERSDE
```

```
ETEDEESEETWKKERLADQEDTEEGKEADRLVRGEGDQQELEGLAQDGESLEPGEKEWPTWKRGRKKGAQKETRMTQKER
RELWEKEKMRLAKKQRGEEEEEEEEEEEEEEEEEEEEDEETRKQKEAAKEEKKERAEKARLANIIRKLFPKVEEMLQRAR
PRQREQLVLVKGMAQEKGRHEMKKETEVVKDEKAPERRKRIRKKEKERLQSEKEEGQFQEEKEEQEEEEEEEEEKKEKEK
KEKKEKKEKKEKKKKEKEKEEKEEEKVVVEEEEEEEEEEEEEEEEEEEAKLLKEQRQAGELKEKGESLLTTEHLVKRDTS
EEKRAKSREKVRLERGKTEVTPKQEQIKKRQDKLPHSTRIKRKPVAKDKKTAIEEREQEAQEQAVKSPVHPEETEADDKL
WNKERQLLKVLASILKEPGLKPMEKRSSLAEESVPIMRVEGHGWEIFQKQDLKTEKGSLEEYCKLLRKNQEKIHLDRAQV
EALLTKLRQKQLLKENKLAELGKLIEESEPEKIQLKWLLDKIRKRLREKSPSEESLREKRLRKERLRAKSLREERLREKS
PSEESLREKRLRKERLRAKSLREERLREKSPSEESLREKSLREERLREKSPSEESLRKKSPREEHLRAKSLREKSPSEES
LREKSLREERLREKSPSEESLREKSLREEHLREKSPSEESLREKRLRKEHLRAKSLREERLREKSPSEESLRQKSLREER
LREKSPSEESLREKRLRKERLRAKSLREERLREKSPSEESLREKRLRKERLRAKSLREERLREKSPSEESLREKSLREER
LREKSPSEESLRKKSPREEHLREKSPSEESLREKSPREERLREKSPREKSPREKRLREKSPREKTLREERLREKSPSEES
LREKGLRKERLRAKSLREERLREKSPSEESLREKRLRKERLRAKSLREERLREKSPSEESLREKSPREEHRREKSPSEES
LRKKSPREEHLREKSPSEGSLREKSPREERLREKSPRAKSPREERLREKSPSEESLREERLREKSPKRLREKRPREERLR
EERLREKSPSEESLREKRLRKERLRAKSPREEPLREEHPREKSPSEESLRAKSLREERLREKSPSEESLREKSLREEHLR
EKSPREERLREKSPSEEILREKGLREEHLREKSLREEHLREKSPSEESLREKRLRKERQREKSLREERLREKSPSEESLR
EKRLRKERQREKSLREERLREKSPSEERPREERLREKRPSEEILREKGLREESLREKSPKHPREKSLREERLREKTPRAK
RLREKSLREKSPSEERLREKSPSEERLRERLREKSPSEESLREKRLREERLREKTPREKSLREEHLREERLREKSPSEES
LREKSPGEESLREKTLREERLREKIPSEESLREKSPREERLREKRLREERLREKRPSEESLREEHPREKSPREKRLRDKR
LREERLREKSLREARLGEKIPSEESPREKRLREERLREEHPREKSPSEESLREERLREKRLREKSPSEESLREERLRAKS
PSEESLKEERLREKRLREERLREKIPSEESPREKRLREERLREKSLREARLGEKIPSEESPREKRLREERLREEHPREKS
PSEESLREEHPREKSPSEESLREERLRAKSPSEESLKEERLREKRLREERLREKIPSEESPREKRLREERLREEHPREKS
PSEESLREEHPREKSPSEESLREERLRAKSPSEESLKEERLREKRLREERLREKIPSEESPREKRLREERLREKSPREKR
LREERLREKSLREARLGEKIPKKIPSEESPREKRLREERLREEHPREKSPSEESLREERLRAKSPSEESLKEERLRAKSP
SEESLREERLREKRLRERLREKIPSEESPREKRLREERLREEHPRERSPSEESLREERLRAKSPSEESLKEERLREKRLR
EERLREKIPSEESPREKRLREERLREKSPREKRLREERLREKSLREARLGEKIPSEESPREKRLREERLREKSPREARLG
EKIPSEESPREKRLREERLREEHPREKSPSEESLREERLREEHPREKSPSEESLREERLRAKSPSEEKRLREKTRRDKTP
REKSLRAKRLMEKILREKRPSEESLREERLREKSPREKRLREKSLREERLREKSPSEEILRVKSLREERLREKSPREKRL
REKRLREERLREERLREERLREKSPSEEILRVKSLREERLREKSPREKRLREKSLREERLREKRPSEESLREERLREKTR
RDKTPSEKSLRAKRLREKSLREKSPSEESLREKSPRKERLREKRRSEESLREERLREKSPSEEILRVKSLRVERLREKSL
REKSLREKKLREERLREKSLKRLREKSPSEEILRVKSLRVERLREKSLREKSLREKSLREERLREKSLREERLREKSPSE
ESLSVKSLREERLGEKIPSEESPREKRLREERLREKSPREKRLREERLREKSLREARLGEIPSEESPREKRLREERLREK
SPREKRLREERLREKSLREARLGEIPSEESPREKRLREERLREKSPREKRLKEERLREKSLREARLGEIPSEESPREKRL
REERLREKSPREKRLKEERLREERLGEKIPSEESPREKSLREKSRREKSLRGKRLREERLREKSPSEESSSEASSSEEEL
SFSEYESLSEEEEGEEEKEEKSKKEKKWRLKSRMVSKEDRVLERKAALPRPPTVAGDLAREKVVEQKMLPKKEGLLDGER
DSRFLDQSHLEMSLLASMRKKALMVLRALKEKWENRFLEILPTPSSRGPQEPAVSETRRKDFLQATGLEAQIRGPQVGLP
ASLQPRRRWWLVPLGDRVVPPAPTSSPTRLTGRDGGRASASEEEEEDWVTDALGRLVAGERLSRDSFHRLHQLVQDLCSR
SRREGLPLSRLRTVVQHLDVRDARGRRPPQDAFGKAMVPPIQRKEEPKVVAATRTPTPPALAWHPLAHEEKRARPLSSAL
REGFGDAYPLAGRKPPTLRFKDFADARARVGGLAATMPGPTPPWAPGRAAAPKAEPFLEVLECDTPLREEQCGYFPTCGH
RPVRVPRTGLEKLTSRQSFLGKKLPPVSPLTHTDRACCHGSQILPSGTEPGDLDFKPLDLFPASRRGPC
```

578 - 597:	EEEEEEEEEEEEEEEEEEEE

A0A3L7HBJ3 **A0A3L7HBJ3_CRIGR** (92 aa)
Coiled-coil domain-containing protein 72 (Translation machinery-associated protein 7). *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MDKEDKAFKQKQKEEQKKLKELKAKATGKEPLATKEEKKKKKKKEEEEEEEEEEEEEEEEEEEEEEEEEADILQTSGTLAP
LGTSDYQSNGEK
```

45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE

A0A3L7HD50 **A0A3L7HD50_CRIGR** (183 aa)
Down-regulator of transcription 1 (Negative cofactor 2-beta) (Protein Dr1). *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MIKETVPNVRVARHDARELVVNCCTEFIHFMSSEANEICNKSEKKTISPEHVIQALESLDFGSYISEVKECKTVELKKKE
RKKERKKERKKERKKERKKERERERRKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEPV
LVWRTWHSRRRIVETATGIICKS
```

108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE

120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE

A0A3L7HFS9 **A0A3L7HFS9_CRIGR** (647 aa)
OR5AL1. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MAKGNHSTVTEFILLGLTEDPELQVILFMILLIIYLFSVMSNLGLVFLIQISPQLQSPMYFFLSHLAFVDFCYTSCVTPN
ALVNFLREIKSISFYGCAAQVCFFTTFSVCEVFLLSVMAYDRYVAICNPLLYVIIMPRRLCFQIATTTYFYAFVTALIQT
VTTFLLSFCDSNLVNQFFCEDIPLMALACSSTQVKELMLLSMAGFNICCSLLIVLISYLFIVSAILKKHSGEGRQKVFST
CASHLSSIAIYYGTIIFMYLQPESSHSLNTDKFAAVFYVVVIPMLNPLIYSLRNKEVKNALKRSIDKIPLSINDPELRVS
LFAVFLVIYLTSVFGNIGLIVLIQVSPQLHTPMYFFLTHLAFIDFCFTSSVTPNTLLNFLREVKSITFYACATQLCCFVT
FVVCELYLLSIMAYDRYMAIWNPLLYAVLMPRKLCLQMIASTYIYGFTVGIAQAVATFCLSFCGSNVVNHFYCDDVPLVA
LACSDTHIKELMLLIIAGFNTLCSLVIVVISYVFIVFAILRIHSADGRRKAFSTCASHLTSITIFYGTVSFMYLQPKSSH
SLNTDKFASVFYVVVIPMLNPLIYSLRNQEDNQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEMMMMMMMM
MIRRNKT
```

594 - 613:	EEEEEEEEEEEEEEEEEEEE
595 - 614:	EEEEEEEEEEEEEEEEEEEE
596 - 615:	EEEEEEEEEEEEEEEEEEEE
597 - 616:	EEEEEEEEEEEEEEEEEEEE
598 - 617:	EEEEEEEEEEEEEEEEEEEE
599 - 618:	EEEEEEEEEEEEEEEEEEEE
600 - 619:	EEEEEEEEEEEEEEEEEEEE
601 - 620:	EEEEEEEEEEEEEEEEEEEE
602 - 621:	EEEEEEEEEEEEEEEEEEEE
603 - 622:	EEEEEEEEEEEEEEEEEEEE
604 - 623:	EEEEEEEEEEEEEEEEEEEE
605 - 624:	EEEEEEEEEEEEEEEEEEEE
606 - 625:	EEEEEEEEEEEEEEEEEEEE
607 - 626:	EEEEEEEEEEEEEEEEEEEE
608 - 627:	EEEEEEEEEEEEEEEEEEEE
609 - 628:	EEEEEEEEEEEEEEEEEEEE
610 - 629:	EEEEEEEEEEEEEEEEEEEE
611 - 630:	EEEEEEEEEEEEEEEEEEEE
612 - 631:	EEEEEEEEEEEEEEEEEEEE
613 - 632:	EEEEEEEEEEEEEEEEEEEE

A0A3L7HH39 **A0A3L7HH39_CRIGR** (603 aa)
OR4C3 (Fragment). *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
DSGHRGRWISEFEARLVYRESSTIILLTVMAYNRYVAICKPLHYTTTMTSSVLCWWQWLGWLPFCGPNVMNYFVCDLYPL
```

```
LELVCTNTYVIGLLVVANSGVICLLNFLMLAASYVVILVSQCREESESLVYVWGPLHGCCFVLCSLYIYLHEAIIYSVHR
QNCSCVLLYFDTHVQPPDLYSEKCRGDTALAYSLPLESMEISHNITEFFMLGLSQRPEVQRTLFVVFLIIYTVTVCGNML
IVVTITFSSSLASPMYFFLSNLSFIDTCYSSSLAPKLIADSLYEGTTLSYEGCLAQLFGAHFLGGVEIILLTVMAYDRYV
AICQPLYYTTTMTRHLCVVLVAVAWLGGFLHSSVQLFLVLQLPFCGPNVINHFVCDLYPLLELACTNTYVIGLLVVANSG
VICLLNFLMLAASYVVILCSLRSHSAEGRRKALSTCGAHFTVVTLFFVPCIFSYMRPSTTLPIDKSMAVFYGILTPMLNP
LIYTLRNEEVKNAMRKLITSSETGRAICGDSAKSTTSSSAGPGPFAMCPWQECIPSHYHRQAGLLCNGGKQLSLGHSSSI
YVQDGGGGEETTPLKDKKKKKEEEEEEEEEEEEEEEEEEESI
```

582 - 601:	EEEEEEEEEEEEEEEEEEEE

A0A3L7HHV1 **A0A3L7HHV1_CRIGR** (1141 aa)
MYT1. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MSLESDDKRARTRSKTLRGPPETTGADLSCPTPGCTGSGHVRGKYSRHRSLQSCPLAKKRKLEDAEAEHLVSKRKSHPLR
LALDEGYRMDSDGSEDAEVKDASVSDESEGPLEETEAEMSGQEEIHHPQPAEGKSLIKSHFGSNPTSSPSGFSKGSYSSY
QGIIATSLLNLGQIAEETLVQEDSVPVAKLGPTVVHQLQDEAAIAAPNDEDEKDLFIHPEDVEEVIEVTSERSQEPCPQS
LEDMISEESSKQKGVLGHEEEGEDDDEEEEEEEEEEEEGEEVEEEEEEEEEEEEEEEEEEEEEEVEEEEEEEEEEEEEE
ETTPNVIFGEDTSHTSAQKVSPEFRSPELSSPKPEYSVIVEVRSDDDKDEDSHSQKSAVTDESEMYDMMTRGNLGLLEQA
IALKAEQVRAVCEPGCLPAEQGHLGPGEPGKVAKPLDVVRKSCYSKDPSRVEKREIKCPTPGCDGTGHVTGLYPHHRSLS
GCPHKDRIPPEILAMHENVLKCPTPGCTGQGHVNSNRNTHRSLSGCPIAAAEKLAKSHEKQQLQTGDPPKNNSNSDRILR
PMCFVKQLEVPPYGSYRPNVAPATPRANLAKELEKFSKVTFDYASFDAQVFGKRMLAPKIQTSETSPKAFQCFDYSHDAE
AAHMAATAILNLSTRCWEMPENLSTKPQDLPSKAVDIEVDENGTLDLSMHKHRKRENTFPSSSSCSSSPGVKSPDVSQRQ
NTTSAPSSSMTSPQSSQASRQDEWDRPLDYTKPSRLREEETEESEPAAHSFASSEADDQEVSEENFEERKYPGEVTLTNF
KLKFLSKDIKKELLTCPTPGCDGSGHITGNYASHRSLSGCPLADKSLRNLMAAHSADLKCPTPGCDGSGHITGNYASHRS
LSGCPRAKKSGLKVAPTKDDKEDPELMKCPVPGCVGLGHISGKYASHRSASGCPLAARRQKEGALNGSSFSWKSLKNEGP
TCPTPGCDGSGHANGSFLTHRSLSGCPRATFAGKKGKLSGDEILSPKFKTSDVLENDEEIKQLNQEIRDLNESNSEMEAA
MVQLQSQISSMEKNLKNIEEENKLIEEQNEALFLELSGLSQALIQSLANIRLPHMEPICEQNFDAYVNTLTDMYSNQDCY
QNPENKGLLETIKQAVRGIQV
```

283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE

A0A3L7HNU1 **A0A3L7HNU1_CRIGR** (760 aa)
ACSBG1 (Fragment). *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
NPGSFDQTVLIFPLAEEALWTTRADGRVRLRLEPFCTQLPYTVHRMFYEALDKYGDLSALGFKHRNKWERISYYQYYLIS
RKVAKGFLKLTCLSAFDLELGLERAHSVAILGFNSPEWFFSAVGTVFAGGIVTGIYTTSSPEACQYIAHDCRANVIVVDT
QKQLEKILKIWKDLPHLKAVVIYQDPLPKKMPNVYTMDELMELGQEMPEKALDTIIDTQQPNQCCVLVYTSGTTGNPKGV
MLSQDNVGQMSRWITWTARYGSQAGDIQPAEVQQEVVVSYLPLSHIAAQIYDLWTGIQWGAQVCFADPDALKGSLVNTLR
EVEPTSHMGVPRVWEKIMERIQEVAAQSGFIRRKMLLWAMSVTLEQNLTCPSDDLKPFTSRLADYLVLAKVRQALGFAKC
QKNFYGAAPMTAETLRFFLGLNIRLYAGYGLSESTGPHFMSSPYNYRLYSSGRVVPGCRVKLVNQDADGIGEICLWGRTI
FMGYLNMEDKTCEAIDSEGWLHTGDMGRLDADGFLYITGRLKGEHPCPGEDGIEGRISAEISLLLTLLITIASPEPSVTA
IYLSLSASALGKRRRRRRRRRKEEEEEEEEEEEEEEEEEEEEEELIITAGGENVPPVPIEEAVKTELPIISSAMLIGDQR
KFLSMLLTLKCTLDPETSEPTDNLTEQAMEFCQRVGSRASTVSEIVEPRDEAVYQAIQEGIQRVNANAAARPYHIQKWAI
LKRDFSISGGELGPTMKLKRLTVLEKYKDIIDAFYQEQKQ
```

583 - 602:	EEEEEEEEEEEEEEEEEEEE
584 - 603:	EEEEEEEEEEEEEEEEEEEE
585 - 604:	EEEEEEEEEEEEEEEEEEEE

A0A3L7HTX8 **A0A3L7HTX8_CRIGR** (791 aa)
CDH13. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MTLLEGLELEKESTLTEFKVFSTKESRKSHKLSIKIIFGKKDKNDYDSPSKTLGSAEERYIKEVIAEVCYRNPGVLIKMS
PRKEAVAIVPEVWDIFKFARTSPVPRQKRSIVVSPILIPENQRQPFPRDVGKVVDSDRPEGSKFRLTGKGVDQEPKGIFR
INENTGSVSVTRTLDRETIATYQLFVETTDVSGKTLEGPVPLEVIVIDQNDNRPIFREGPYVGHVMEGSPTGTTVMRMTA
FDADDPATDNALLRYNIRQQTPDKPSPNMFYIDPEKGDIVTVVSPALLDRETLENPKYELIIEAQDMAGLDVGLTGTATA
TIVIDDKNDHSPKFTKKEFQATVEEGAVGVIVNLTVEDKDDPTTGAWRAAYTIINGNPGQSFEIHTNPQTNEGMLSVVKP
LDYEISAFHTLLIKVENEDPLVPDVSYGPSSTATVHITVLDVNEGPVFYPDPMMVTKWENISVGSVLLTVNATDPDSLQH
QTISYTEKPCLKEEEEEEEEEEEEEEEEEEEEEEEEEEAYASFLEIQLLSPHQCLTYLCEVERLMALTFTLTSYSLACQPG
LLADEASCLNCDDGVKELIQFPELVETLGERYSVYKDPAGWLNINPINGTVDTTAVLDRESPFVHNSVYTALFLAIDSGN
PPATGTGTLLITLEDVNDNAPFIYPTVAEVCDDAKNLSVVILGASDKDLHPNTDPFKFEIHKQSVPDKVWKISKINNTHA
LVSLLQNLNKANYNLPIMVTDSGKPPMANITDLRVQVCSCKNSKVDCNAAETLHLSLSLLLFFSLLSLSGL
```

493 - 512:	EEEEEEEEEEEEEEEEEEEE
494 - 513:	EEEEEEEEEEEEEEEEEEEE
495 - 514:	EEEEEEEEEEEEEEEEEEEE
496 - 515:	EEEEEEEEEEEEEEEEEEEE
497 - 516:	EEEEEEEEEEEEEEEEEEEE
498 - 517:	EEEEEEEEEEEEEEEEEEEE

A0A3L7HUA9 **A0A3L7HUA9_CRIGR** (93 aa)
Uncharacterized protein (Fragment). *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
TSGSCLKIGLRQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGRSSSSSSSSSRRRRRQDLIIWLYTWVHKHKPHI
ELARHSGKPECAL
```

13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE

A0A3L7HUH4 **A0A3L7HUH4_CRIGR** (526 aa)
OLFR147. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MDRDKTQRRMAPGNDSSVKEFILLGLTQQPELQLPLFFLFLAIYVVSMVGNLGLIVLIVLNPHLHTPMYYFLFNLSFTDL
CYSSVITPKMLVSFVKQNIISHAECMTQLFFFAFFVIDECYILTAMAYDRYAAICKPLLYKVTMSYQICHLMTVGVYAMG
FVGAMAHIVCMLRLTFCDNNIINHYMCDIPPLLKLSCTSTAINELVVFIVVGVNVTVPSLTIFFSYTLILYNILGIHSAE
GRSKAFSTCGSHVIAVSFFFGSIVFMYLKPSNVSGDEDKVSTIFYTIVGPMLNPFIYSIRNKDVHIALRKTLKKTYKTQR
RMAPGNDSSVKEFILLGLTQQPELQLPLFFLFLAIYVVSMVGNLGLIILIVLNPHLHTPMYYFLFNLSFTDLCYSSVITP
KMLVSFVKQNIISHAECMTQLFFFCLFVINECYILTAMAYDRYAAICKPLLYRVIMSHQKEKKEEEENGEEEMQLETAAA
AAAAAAAAEEEEEEEEEEEEEEEEEEEEEEEDDDDEEEDQAAAASL
```

489 - 508:	EEEEEEEEEEEEEEEEEEEE
490 - 509:	EEEEEEEEEEEEEEEEEEEE
491 - 510:	EEEEEEEEEEEEEEEEEEEE
492 - 511:	EEEEEEEEEEEEEEEEEEEE

A0A3L7HWW0 **A0A3L7HWW0_CRIGR** (382 aa)
TSPAN7. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MTLTFISVTCKLSSGEETESTGKAPVLLEQPRDADLKFIKKDRSASIFKTLMSQDARVQRWDVILGRKRFALPLRDKRMP
PSTVTYLQEEKTHSEEESDLDLKCNEAAKTKYISEYILAMSLLRRHVCFKGSEGKKNLKDEGPKKEQVCLRYFISISGLL
FHRGIKASFLNIYTNAVQNYNGNDDKSQAVDQVQYSLICCGVKNYTDWKTSPYFMDHGIPRSCCKDESDCNSQDLHNLTV
AATKVNQRGCYGLMMSFLEANMGTIIGVLFVVTFSQVIGLRLSCCLSRFIVAHQREMNVKRREFLHDVRVKDMNDLPIVT
VNDRRRRRKKKKKKKKKKKKKKKKKKKKKKKKKKKKKEKEEEEEEEEEEEEEEEEEEEEEEEEEVL
```

356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE

A0A3L7HXT6 **A0A3L7HXT6_CRIGR** (147 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MSAGQKRAPDFTTDGCEPPCGCWELNSGPLEELAMLLTTEPSLQPSKLHFYNVFFDTTGRDFVLAEEILSDRDLTGPPSL
IEKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERKKERKRGRKHTLKKENTHFWPECLGS
```

85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE

89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE

A0A3L7HZC4 **A0A3L7HZC4_CRIGR** (685 aa)
RALGDS (Fragment). *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MTASQKVPVLSLSEPSTLISPQAGKESAPEVPEEESGGLPHFNSMEEMVAHLVTSLQGGDTIFVLAFLCIYQRFLTTQQV
LDMLFKRYSSFRPGCEEDEQVKNTTCTLLEYWMDKFPAEFCRIEHLPILKRLKTYLIVNMPYSDLLVRVHNLQTQLLAEV
ASEEEEEEEEEEEEEEEEEEEEEEASGDACASSTFVSTLRPGEPHLLRRSRAASLPSSNEDGYSGARSSRGTRAGEQTTN
MAAAAGKESAPEVPEEECGGLPHFNSMEEMVAHLVTSLQGGDTIFVLAFLCIYQRFLTTQQVLDMLFKRYSSFRPGCEED
EQVKNTTCTLLEYWMDKFPAEFCRIEHLPILKRLKTYLIVNMPYSDLLVRVHNLQTQLLAEVASEEEEEEEEEEEEEEEE
EEEEEASGDACASSTFVSTLRPGEPHLLRRSRAASLPSSNEDGYSGARSSRGTRAGEQTTNMAAAAGKESAPEVPEEESG
GLPHFNSMEEMVAHLVTSLQGGDTIFVLAFLCIYQRFLTTQQVLDMLFKRYSSFRPGCEEDEQVKNTTCTLLEYWMDKFP
AEFCRIEHLPILKRLKTYLIVNMPYSDLLVRVHNLQTQLLAEVASEEEEEEEEEEEEEEEEEEEEEEASGDACASSTFVSTL
RPGEPHLLRRSRAASLPSSNEDGYSGARSSRGTRAGEQTTNMAAA
```

163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
385 - 404:	EEEEEEEEEEEEEEEEEEEE
386 - 405:	EEEEEEEEEEEEEEEEEEEE
606 - 625:	EEEEEEEEEEEEEEEEEEEE

A0A3L7I0F9 **A0A3L7I0F9_CRIGR** (180 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MEVRKGYWIPWNWSYLLMVVKCHVGAGNQTGVPSKSHKCSYQLSHLSSSQGMIFIGFELERKESEERKMMMFVLPACMPA
GQKRAPDLTTDGCKSPCGCWELNFGPLEEQQCSQPLSHPLPSSPPHPLPRKRRKEEEEEEEEEEEEEEEEEEEEKKKKK
KKKKKKKKKKKKKKKKKKHL
```

135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE

A0A3L7I0M1 **A0A3L7I0M1_CRIGR** (294 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MKSPVIVHSLGKLGSKSLRPKHTLLLGHCPAGLCNWNFQDCAPQVLLSADILASSASPSSFKIVSGTISNKGQSTGELPT
KSQGPIIHDSKPRVSCEKTVHVLQVTDMQDLMTSAGWILEEKLEVHHRNRDSTKIEKLSVLKTTPRYTAKLPQTNGWLMV
ITRPRCPENLWPKPALISTRHRHHMSQGLLSGVLAIASAEVPSLSVSVACQKHSIHSQFYHVLSRGTRFKMLTKGCLCKH
IKVPSAWWEDIYSLPDAIPLRRRSQKEEEEEEEEEEEEEEEEEEEEEEEEKS
```

267 - 286:	EEEEEEEEEEEEEEEEEEEE
268 - 287:	EEEEEEEEEEEEEEEEEEEE
269 - 288:	EEEEEEEEEEEEEEEEEEEE
270 - 289:	EEEEEEEEEEEEEEEEEEEE
271 - 290:	EEEEEEEEEEEEEEEEEEEE
272 - 291:	EEEEEEEEEEEEEEEEEEEE
273 - 292:	EEEEEEEEEEEEEEEEEEEE

A0A3L7I381 **A0A3L7I381_CRIGR** (106 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MLLLPRTQLLQMHASPAGMDSELCVAFVSPCLPKAPNWSNKKLNGQQLGRRGIGGAGRQREQVGGGSRLEREGGGGGREE
```

EEEEEEEEEEEEEEEEEEEEEEEERKE

79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE

A0A3L7I5R5 **A0A3L7I5R5_CRIGR** (872 aa)
3-hydroxy-3-methylglutaryl-coenzyme A reductase (EC 1.1.1.34). *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

MRGSRDRVATMLSRLFRMHGLFVASHPWEVIVGTVTLTICMMSMNMFTGNNKICGWNYECPKFEEDVLSSDIIILTITRC
IAILYIYFQFQNLRQLGSKYILGIAGLFTIFSSFVFSTVVIHFLDKELTGLNEALPFFLLLIDLSRASALAKFALSSNSQ
DEVRENIARGMAILGPTFTLDALVECLVIGVGTMSGVRQLEIMCCFGCMSVLANYFVFMTFFPACVSLVLELSRESREGR
PIWQLSHFARVLEEEENKPNPVTQRVKMIMSLGLVLVHAHSRWIADPSPQNSTTEHSKVSLGLDEDVSKRIEPSVSLWQF
YLSKMISMDIEQVVTLSLAFLLAVKYIFFEQAETESTLSLKNPITSPVVTPKKAPDNCCRREPLLVRRSEKLSSVEEEPG
VSQDRKVEVIKPLVVETESASRATFVLGASGTSPPVAARTQELEIELPSEPRPNEECLQILESAEKGAKFLSDAEIIQLV
NAKHIPAYKLETLMETHERGVSIRRQLLSTKLPEPSSLQYLPYRDYNYSLVMGACCENVIGYMPIPVGVAGPLCLDGKEY
QVPMATTEGCLVASTNRGCRAIGLGGGASSRVLADGMTRGPVVRLPRACDSAEVKAWLETPEGFAVIKDAFDSTSSGNYC
TDKKPAAINWIEGRGKTVVCEAVIPAKVVREVLKTTTEAMIDVNINKNLVGSAMAGSIGGYNAHAANIVTAIYIACGQDA
AQNVGSSNCITLMEASGPTNEDLYISCTMPSIEIGTVGGGTNLLPQQACLQMLGVQGACKDNPGENARQLARIVCEEKKK
KEEEEEEEEEEEEEEEEEEEEEEEIRRRRRREEERRRGGGGGRGGGGRRRRRRRRRRKERKKGPLDVSNVT

802 - 821:	EEEEEEEEEEEEEEEEEEEE
803 - 822:	EEEEEEEEEEEEEEEEEEEE
804 - 823:	EEEEEEEEEEEEEEEEEEEE
805 - 824:	EEEEEEEEEEEEEEEEEEEE
806 - 825:	EEEEEEEEEEEEEEEEEEEE

A0A3L7I676 **A0A3L7I676_CRIGR** (496 aa)
CCDC112. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

MSWALVTYALHKETLSRKTKTKTKEEEEEEEEEEEEEEEEEEEEEEEEERNEGACGTSAGTRPSQLQNWKQKVSRMKKAEF
IRTAEKLKNQVIVIEKDKHSHFYNQRGDFRTEHCMLEELENKLINSRKTEIVEKLREMMEEIENAINTFKEEQRLIYEEL
IQEEKATNNELSAISRKIDSWALGNSETEKAFRAISSKVPVARVIPSTLPEEVIEFERFLQQTGGRQGGWDDFDHQNFMK
LRNKHKGKPAFLKEVVEHLPGRTLDEVQQHEKWYQKFLALEERKKESIQNWKTKKQQKKEEILKLKEKADTAPMPSHSKP
EDNQKQKEEQRKKQKLAVEAWKKQKSIEMSMKHASQLKEEEERERKQQKERQRQCKLKLLLESYTQQKKEQEEFLRLEKE
IKEKTEKAEKRKTAADEISRFQERDLHKLELKILDRQSKEEEKAEKQRRLAKLKEKVENNVSRDPSRLYKPTKGWEERTK
KIGPSGSGPLLHIPHR

25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE

A0A3L7I6R5 **A0A3L7I6R5_CRIGR** (113 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

MAEDIKTKIKNYKIAPLTALAKPEPDQECWQKNYLNFHHCEKAVTTKNLAYPQPQDAFPDSRSWEKEEEEEEEKEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEIFSPWPF

75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE

86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE

A0A3L7I7A3 **A0A3L7I7A3_CRIGR** (337 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MSLEAFYLISSCIPGTFFKTLVPPCPRNPPIFHGTIQLYLLEDALLKPPVAHEKGYTCQHPAQILFYYGNLSGGQKITFS
ELVFSCHHVDQTQVIRDNGRLNTPTAPINELGREQGFVCLTPFTPTHNCTSELVLRYFVCGKQNPHDYNRPIRGEETRGR
CLMVLADSSPGWLYNAIIHHFTVAQVSHPLTTGVASRAPEVTRTLVGDVQDSCKEESWVLDGSETVVSLQDYWLCPLSNR
GFSVALEAFLERALVDHAGGLGNEQAEELPHKALDAVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVIGCVKMKLN
FTFPATGCLKLIEADDE
```

278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE
287 - 306:	EEEEEEEEEEEEEEEEEEEE
288 - 307:	EEEEEEEEEEEEEEEEEEEE
289 - 308:	EEEEEEEEEEEEEEEEEEEE
290 - 309:	EEEEEEEEEEEEEEEEEEEE
291 - 310:	EEEEEEEEEEEEEEEEEEEE

A0A3L7IC51 **A0A3L7IC51_CRIGR** (319 aa)
Inducible T-cell costimulator. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MSPPSGFLGKWAKVNKIRLATILICGCRQFCPRISSWFACCHSEGSGKFPLNNTKGTEKPSTDLIFCSRHKVWCSQTNVL
AQNRPRARQKPMQPHLFAREINDSAKHKMFSFYNGGIQISCVYPETTRQLKMQLFKGEEVLCELTKTNGNVGSSKNPRSC
PYQLSNDSVSFFLNNLDSSQSSYYFCSLLIFEPPPFRERTFPAEYLHIYESQRYCQLKPWLPIGCAAFVVVYIFGCMFIF
WFTKKKYGSSVHDSNSEYMIMAAVNTAKKSRLAEEEKEEEEEEEEEEEEEEEEEEEEEGEEEEEEEKATLEMFSTHW
```

278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE

A0A3L7IDP5 **A0A3L7IDP5_CRIGR** (154 aa)
LAMTOR2. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MTPLESRDSTPTRPEKHNTEEEEEKEGEEEEEEEEEEEEEEEEEEEEEEEEMDLKIYFMKIFETLKEGSCINKTDFKHT
LTSLMSQANTGGVQSTLLLNNEGSLLAYSGYGDTDALVTAAIASNIWAAYDQNGNQAFNEDISNLSSWTEWRAM
```

28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE

A0A3L7IDR4 **A0A3L7IDR4_CRIGR** (217 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MRSLAKKQKQNRPIRQWIWMKTGSKISTKEGGGRGGGGGGGRRRGREGEGEGEGVGEEEGAGEEEGKEEEGAGEEEEEEE
EEEEEEEEEEEEEEEEEEEEEDEEEEEDEEDEEDEEDEEDEEEEEDEEDEEDEEDEEDEEDEDDDDEEEEEEEEEEEEEE
EEEEGEEGEEGEEREEEEEEEEEEEEEEEEEEEEEEEEEEERRKKMTTTTTTFFLLAVAG
```

74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE

76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE
180 - 199:	EEEEEEEEEEEEEEEEEEEE

A0A3L7IDV0 **A0A3L7IDV0_CRIGR** (265 aa)
mTERF4. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MSPALFCKLTTVPGGESLRESSCVRPQKYVLAPEHRTHLVQCLHEDRGTSVEPKSLELEKVTSSLQDMGFDEAHVNSLLS
LQPSVHPQQLLDIISEFLLLGLHPEPVFVAVTKSPQLLKLSTMQMKRRSSYLRKLGLGEGILQLLWYAYFRMGLKHLDIV
RSDFFQYSVTKIKQRHMYLERLGRYQTPDKKGQTQIPNPLLKDILRVSEEEFLARTACSSAEEFGVFKKLLDREEEESKS
HASEEEEEEEEEEEEEEEEEEEELL
```

244 - 263:	EEEEEEEEEEEEEEEEEEEE

A0A3L7IIR0 **A0A3L7IIR0_CRIGR** (375 aa)
SLC23A2. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MNSAVISCESLFLSQQHAPHRLFHNFTKSSPDGCHFLQRDDGVLSSHTKGQAKNKDGQQKDPSRSHLAYGILDSPPWYLC
IFLGIQEEEEEEEEEEEEEEEEEEEEEENGGGPQFPVQRPHAHSPHFLTALGGLVAVPLILAKDLCLQHDPLTQSYLISTI
FFVSGICTLLQVFFGVSFGFGKSLSSPVWDALLVFCWLPSRKLAVSCANWTQGETTGNNVEKEMTPGLRITPGPLLLVSH
LAPPPGITPGPSSWYHTWSPPSVFSAHSCYLSNVARASRPLLGTQKSSLQLKEQGLLPILQGGTFAFVAPSLAMLSLPAW
KCPEWTLNASLVNTSSPEFIEEWQKRIREATASSPYIPLGSGLASAQPGKAHPKV
```

87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE

A0A3L7IJR2 **A0A3L7IJR2_CRIGR** (75 aa)
Uncharacterized protein. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MVVKTEKSKKKKEEEGEEDEEEEEEEEEEEDEEEEDEEEEEEEEKEEEEEEEEEEEEEEEEEEEEEEEEDDDDD
```

46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE

A0A3L7IK01 **A0A3L7IK01_CRIGR** (536 aa)
KCNC2. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MTLMTIGYMSKVEHNKLESLVVVDKPVEPNFIYTDTNEEEEEEEAEEEEEEEEEEEEEEEEEEEEEEEEERRRRRRRRRR
RRERERERKRRKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKNSLFAVLPLSLNFIAFASLFFILVSITTFCLETHEAFNIVKNKTE
PVINGTSAVLQYEIETDPALTYVEGVCVVWFTFEFLVRIIFSPNKLEFVKNLLNIIDFVAILPFYLEVGLSGLSSKAAKD
VLGFLRVVRFVRILRIFKLTRHFVGLRVLGHTLRASTNEFLLLIIFLALGVLIFATMIYYAERVGAQPNDPSASEHTQFK
NIPIGFWWAVVTMTTLGYGDMYPQTWSGMLVGALCALAGVLTIAMPVPVIVNNFGMYYSLAMAKQKLPRKRKKHIPPAPL
ASSPTFCKTELNMACNSTQSDTCLGKENRLLEHNRSVLSGDDSTGSEPPLSPPERLPIRRSSTRDKNRRGETCFLLTTGD
YTCTSDGGIRKGYEKSRSLNNIAGLAGNALRLSPVTSPYNSPCPLRRSRSPIPSIL
```

46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE

50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE

A0A3L7ILK1 **A0A3L7ILK1_CRIGR** (862 aa)
EHMT2. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MGALLLEKEPRGTAERALGPLGDAPRSEDTLPKADPDSLEPAGPSSPASVTVTVGDEGADTPAGAAPLLGDEPESLEGDG
GRVLLGHATKSFPSSPSKGGACPSRAKMSVTGAGKSPPSVQSLAMRLLSMPGAQGAATAGPEPPPATTTGQEGQPKVHRA
RKTMSKPGSGQPPVPEKRPPEVQHFRMSDDMHSLGKVTSDAAKRRKLNSGSLSEDFGSARGSGDVTLEKGEPRPLEEWEA
VVGDGFSLYYDSYSVDERVDSDSKSEVEALAEPLSEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAKKK
WRKDSPWVKPSRKRRKREPPRTKEPRGVNGVGSTGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFDELPL
CSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCEAHRARMVKHHCCPGCGYFCTAGT
FLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGGTPPAGTAAPAPLPLAQDAPGRADTSQPSARM
RGHGEPRRPPCDPLTDTIDSSGPSLTLPNGSCLSAVGLPPGPGREALEKALVIQESERRKKLRFHPRQLYVSVKQGELQK
VILMLRANINAVDKQQRTPLMEAVVHNRLEVARYMVQLGGCVYSKEEDGSTCLHHAAKMGNLEMVSLLLSTGQVDVNAQD
SGGWTPIIWAAEHKHIDVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARES
YHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAVRTEKIICR
```

276 - 295:	EEEEEEEEEEEEEEEEEEEE
277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE

A0A3L7IMT3 **A0A3L7IMT3_CRIGR** (611 aa)
Glycerol kinase (EC 2.7.1.30). *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MEASKETAVGPLVGAVVQGTNSTRFLVFNSKTSELLSHHHVELTQEFPKEGWVEQDPKEILQSVYECIAKTCEKLAGVNI
DISNIKAIGVSNQRETVVVWDKFTGEPLYNAVAWLDLRTQSTVEDLSKKIPGNSNFVKSKTGLPLSTYFSAVKLRWMLDN
LRPIQKAVEEGRALFGTIDSWLIWSMTGGVNGGVHCTDVTNASRTMLFNIHSLEWDKELCDFFEIPMNILPNVCSSSEIY
GLMTEGTLEGVPISGCLGDQSAALVGQMCFQEGQAKNTYGTGCFLLCNTGRKSVFSEHGLLTTVAYKLGKNKPVFYALEG
SVAIAGAVIRWLRDNFEIITTSEEIETLAKEAGTSYGCYFVPAFSGLYAPYWEPSARGIICGLTQFTNKCHIAFAALEAV
CFQTREIVDAMNRDCGIPLNHLQVDGGMTSNKILMQLQADILRIPVVKSVMPETTALGVAMAAGAAEGVNVWSLEPEDNS
AILMERYEPQIQDKESEVRYATWKKAVMKSMGWVTSKTPENVDGSSFCCLPLGFFISHGKKYDGLPKFKILKNSVLKENP
KKLLELGRAGGQNYQKEEEEEEEEEEEEEEEEEEEEEERKKERTESGITIS
```

577 - 596:	EEEEEEEEEEEEEEEEEEEE
578 - 597:	EEEEEEEEEEEEEEEEEEEE
579 - 598:	EEEEEEEEEEEEEEEEEEEE

A0A3L7IPB1 **A0A3L7IPB1_CRIGR** (880 aa)
Uncharacterized protein (Fragment). *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
VSGQQEKRDQQQVRQSPQFLSVWGGGTSVLNCTYENSAFDYFPWYRQFPGEGPALPIVSNEKEDGRFTVFFNERDKQLSL
HITDSQPGDSATYFCAAGTQCSPGTCSPLPTLQLRLQQNPAVGLSLAEVQSSFHLQEQVTGDTVNVRIRLIQPQTDQGSI
LGQKVTQVQSTASSQEGEEVNLDCSYETSQSFYHLFWYKQLHSGEMVFLIRQISSVTQSEKSDRYSVIFQKSAKSISLVI
SASQIEDSRALLHSPAFYLLSKIFTTCSHLSCSWLSFCKAVDFSHNRAAAFQVFSHVPDAPPSAGVTDKDSFAGDSRAQS
VTQPQARITVTEEASLQLRCNYSSSVPPSLFWYVQYPRQGLQLLLKYYSGEPVVRGLSGFEAEFSKSDSSFHLKKASVHL
GDSAVYFCALGAQCLGLQGELDINTHGSEESMAFDSKERGEGGKEMQQIWLSPQTMKTYGPTLFVFLWLQLDGLSHGKQV
EQLPSTLRVQEGDSTVINCTYTDSTSYYFPWYKQGPGEHPKLIIDIRSNEERKQDQRLIVLLDKKAKHFSLHITDTQPGD
SAMYFCAASAHCSPDTCSLSSNLPQGLEPHPHPVSQAFQCSLCQLFGELKNQVSLSSVNMLPDTCPVLLLLLMLGKSNGD
SVTQTEGLVTVTEGSPVMMTCTYKTTYSDISLFWYVKFLNKAPQLLLRTATDNKRTEHQGFHATLHKSNSSFHLHKSSVQ
LSDSALYYCALRDTVREMQGKLHTNQGAGGLRGVALRQRERQRDRERERERERERERERERCALWRQRQVDLCEFKASLV
SRASARIGSKATQRNPVSKKKKKKKKKKKKKKKKKKKKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKERKKDKGIAQ
```

839 - 858:	EEEEEEEEEEEEEEEEEEEE
840 - 859:	EEEEEEEEEEEEEEEEEEEE
841 - 860:	EEEEEEEEEEEEEEEEEEEE
842 - 861:	EEEEEEEEEEEEEEEEEEEE
843 - 862:	EEEEEEEEEEEEEEEEEEEE
844 - 863:	EEEEEEEEEEEEEEEEEEEE
845 - 864:	EEEEEEEEEEEEEEEEEEEE
846 - 865:	EEEEEEEEEEEEEEEEEEEE
847 - 866:	EEEEEEEEEEEEEEEEEEEE
848 - 867:	EEEEEEEEEEEEEEEEEEEE
849 - 868:	EEEEEEEEEEEEEEEEEEEE
850 - 869:	EEEEEEEEEEEEEEEEEEEE

A0A3L7IPD5 **A0A3L7IPD5_CRIGR** (649 aa)
KLHL38. *Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)*

```
MDKERRGRKQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEELRKKTWRRKTVKRMDEELPDGVVFKDDN
FSSDLLRQLNDLRQSKTLTDVSICSGAWEVPCHRNVLASSSPYFKAMFCSHFRESTEAKVWLKGINSSTLEQVVTYVYTG
EVHITAANVLPLMEAAAMLQYPRVFEACSSYLQSQLAPNNCLGLVRLAEILNCESLKKRAREVALTCFPEVAASADLKEL
CAMELRDYLGDDRLCGEEEKVFEALMAWVKHDLQARWPYMQELLQQVRLQYIHPAFFHHFIANDAVLQSSPACRAILEAA
RKQMFSLYSPSAQDCKLVWHEPPRSCYQDCLLVLGGQKDNQQTTRDVLLYSVHTGQWQSLAKLPARLYKASAVTLHRSVY
VLGGVAVREGKSAVSASVYVFSLKLNQWRRGEPMLAARYSHRSAAHRNFIFSIGGTGEGQQLLGSMERYDSVCDVWESMA
DMPVAVLHPAVAVKDQRLYLFGEKLTLKFGVMTLFPPQVYHISRNTWFKMETRMIKNVCAPAVVLGERIVIVGGYTRRIL
AYDPRANKFVKCADMKDRRMHHGAAVMGSKLYVTGGRRLTTDCNIEDSASFDCYDPETDTWTSQGQLPHTLFDHACLTLQ
CIRHTAGFT
```

11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE

A0A3L8DH48 **A0A3L8DH48_OOCBI** (2552 aa)
Uncharacterized protein. *Ooceraea biroi (Clonal raider ant) (Cerapachys biroi)*

```
MDARRKKETDVLDLDGEETQLFKQKIRQLAECDEIVSAEIINVVGEITKDVEMAEDNVPSSDEFDEDLEEEYRNLNVMLD
LPNDTYSLTEIKPELPTCVKYGVRSGLTHLNMPRFSPLSRGYQGSAIAIAAFATTTVHKSRGWNEAVIDQIIEDGDTFYC
ESYKDMNTGDRRTMTILDLKKNFLVQKKFNVTIKIDDPAYAGKFRSHDPTELHLAKALELFFERYDAGILTSPVLNIAIW
RDAKYYNIFDGQARQENGVSAADQVSGTAKLFLVRDLTEVLFIILEKSGVQNEPFVIHAIAVVCVEAVSPDDPEEAARTP
GRPQRRPSGYRIRRKHRAVVQGSYHLNHPALPKTLRNKGHLVIAIAALVYSRLIGANKWTTALLDLIFNHSNIYLIDLVR
VLGKKLDDAFELRLEDLMSDIILGVYSAKVKVDANVIPGHAQKRGKLDMDTGLCEFFETQEIGILEVKKIFYAVWKHGNV
YYFLDPFACDDEGFRIRYNDTEQTTIDSARYAACVTMNRTVKEVVETVLENTGTKDRDPFLIHGLKVLYVKTGMTLRGGP
FEKVIYREKGTNRRPRAPSPPMPIDTTIAKPIDTTPRARPESRRFADVSTQFPDIMQNAEEYMMTDDEPVTFLFAREQVK
REKRADEEEEEEYEDIKKEENEGEMEETLMDKDIDDEQMETDEKAQQKAPVNFITGYRMINAHRLLLRGTKNCLSEEYRA
RSRGRQGLIAALTTLAYRRLKDPTRWRNIDVDQIVDVSNKAYEQVITWIEQGRPEIKEAKAMEEELGEEEEEEEEEEEEE
IEEEEEEEEEEEVVARKLAVAPSHLDVSHLPPRLKLAEYDALFRTKPNVINGEADPLANLAEALERYFERYPELLLENKR
LTYAIWREDGKFFLFNPYGSDSEGWRLRDHPASFAVTDGLNELVDLLHGVLEYNDSSFALHFVTLDAIQPGKYASPVEIV
IPDEQTIKIFRTKFLPITDDDLLKLEEKKPDIVVEKIEEPAEEIEEEEEEEEEEEEEEEEEEEEEEEEAKEKKFKELEKP
LVDPLLEVEERMQPDAPHRLNLALLTSTVTIEEPTETELNGLHEEVVMEKMKYDHPPPYVMPPKRTLLILLKAKQASKSI
PSLVSRFSIDSRLEVKKRDGLVIDLPALAAIVSLPQDAKPSKMIKLSLRKYLYSRLPPIRIIPLRAIDESYIQDEETDKV
LDEKCLERGKSEEKYATLAELPVLPCLHRTELIPVGPIIKTPVVVTKHLTCLDERKRKSVSKNEKKVLAFKKNLCDAEKL
LFKLIFPKFHLDLQVNKLLFIKKFVYSENNRFILRCKVVDDNTEIIRGNWSLTDRSRVESSHFKPCYFSAILCILAKIAR
DADRFHSNTLNQLILLSNKINQRIGKLRYKEYRTFYNVDILDTNYNIVLKEIVRADPETVPSDQLDTVIKKFLERNQTGI
LVLTNCAYAFWTTDDKYYLFDPYPCDEKGNTNEEGYCCLMRFRELKPMLDRIKENAGETTRKPFRLYIMSITHVEIKRRK
RRQRKAVKRPTKIAEESVHSKEMQDVMTLPSAKSESSLIESVEWVTSDPELDPHRDVTSRGFTPMRHYSASMLEIAVLEN
YITTPTLAPFKESLKPDHDRGKTTVERMETLDRTFRNYTSVAIPIDLCVMAWSLIHDPASWSERTFRGLFEASVDYALDS
VLASEDTSVGDMTDALLPEFEIANYAFRAVFAPLHFGTLYATEGWNLAMTLCKIFETKIYTGAIIVCHYAHVGVTKKGNN
YFAWWTVTGTKNLRMITSRNMSEFLKLIVKEIDAPQKTGFVVRAITISYARKLAPDWSDIEGLHEPMAPTTSLAKIHRKE
SETRDIEAIFKPIESTPKPIFIHGTVALRDRDSLLEPRAKRCYFVALLAVVVKRDIVQSPLPAIIDKILEVAESLYREFS
EPKFHVEHILRNVPLMNRFFDLRDCASSLVTLTTNPRTGRNDFLMKVKKCLKCHFKMYTSGILHFTNCCYGFWYSRSTNC
YYYLDPYQCDARGRKTLSDGNACLCIFSSVCQMVKHMCLNQHEGTTGFFLHRIHVDSIDTPASEKFQEDPMWVYLDYHWN
FTHSIVRARKKRKVSDRSASSQIDRFWHNYVVEVTGLIYSIWGTIGAYDCRFGDRAGKNRTAICVAVLAIQNLCHPSRWS
PAILDSAVICGDTYYTESLRSLARECSQPTNRFGLRSSLRLFPHVWTVDFGTSVCGVLYDDRNRLTLTAALKLAFEEARN
IIVECNNITLAVSAAKNAYYVADPCWIGPPLFVKDRGAIYTLCCRNVYALVYAITKMINTNQRLGVRVTPVLFTFDREDS
REEPEPCPATAKILSRSLRRDPGRIDDPGMRIPGATAVPDESSYPQYLQRLARAVTGTGSQLEECQLSSRHTEPALNPEN
VNNTLVSAKWRLNLGQARPPKRPRPPLDLVWLKDDSTEFVDSATDLFEPRHSQVSITDLTACDYYPKPMDFASNIPAPGI
EFLECASERSFIREQSRTEFDKRAAEMSQDPYKSHPHRPPVIVIQKADEATENAELSEATTTDATEFTDSEF
```

1005 - 1024:	EEEEEEEEEEEEEEEEEEEE
1006 - 1025:	EEEEEEEEEEEEEEEEEEEE
1007 - 1026:	EEEEEEEEEEEEEEEEEEEE
1008 - 1027:	EEEEEEEEEEEEEEEEEEEE
1009 - 1028:	EEEEEEEEEEEEEEEEEEEE

A0A3L8DMQ8 **A0A3L8DMQ8_OOCBI** (383 aa)
Uncharacterized protein. *Ooceraea biroi (Clonal raider ant) (Cerapachys biroi)*

```
MSDDEEQYSGRASQKESGENPEFMKRQEQKRSDLDEQLKEYIAEWRKQRVKEEEELKRLKEKQAKRKVTRADEEKRLAQK
KKEEEERRQREIEEKKQRDIEEKRRRLEESEKKRQAMMQAMKDQSKAAKGPNFTITKKDALSGNLTSAQLERNKTKEQLE
EEKKISLSIRIKPLEIDGLSIEKLRTKATELWEAIVKLETEKYDLEERQKRQDYDLKELKERQKQQLRHKALKKGLDPEA
LTGKYPPKIQVASKYERRVDTRSYDDKKKLFEGGLTDQQKETMEKLWAEQKQQFMGRQKTKLPKWFGERPGKKPGDPESP
EGEEDVKAVADEDLEEPQFDEEEEEEGGEKEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE

A0A3L8DSI2 **A0A3L8DSI2_OOCBI** (4055 aa)
PHD-type domain-containing protein. *Ooceraea biroi (Clonal raider ant) (Cerapachys biroi)*

```
MASDNEASCASDPNFAVICSFLGCFGKSCGIIYPDMARLQEMLENTQEVSQELINLHIKLLRKTRKTVSPEKWERALVKF
CHTYSNQDGWELERFGYKKARIAVKLRLLKILLETQFDLNQKFKNEVNKLAADELRVEPLGRDKSGLAYWCQLDEECNIR
VYREDLDEENWELVAKDREGVANLINTLSNGEAGAIPINEDSNSLEISEKPIIDTGQVTTSPSLEDEENGVQENGVHTDE
MSDKQLPNGRTDEFEDEQEDDRVLNREQDRNQGQDQNNIVDEAENDEEEDIDGEEEEEEEQEEEEEEEEEEEEEEEEEEE
EEEEEEEDITNDESSKQITEEDDSQEMVQTPSTESRYTNASSLLPATHTKTLKVDAIPEDTCHKEAGNETSASLTSETKS
PVTHNALAITGVAKTEESMPLKSIETPVITSSPLKLVNIAELKQPEEKSVSAVTPIDVPLNAAKKHGASDETADPSAKPL
PDKLPGKNTLSFSSADSTPIGHSKLSVKPIDQLAANLVRIQSEKLEKPTAPKSLEKIAESLARSSGMLGSMVNGSEDDRL
PQDFCARNQSEKSATLRGHRGIDLSTSPRSWESANEQDRPMDFSGIDLSSRKLGKTVDLPSPGYRAQPDFQHREMDLSTK
KVSKPEVPNLPYDARSVMMRNHAMVADLSKRQMPFTAYEMSSTPYHNAARLPAKDEHRLPSYTVLPDPSKITALRINTAS
LKRPLEGDDAQQDMLKRIRADVIPIRGSMDKRPMMGGGNWREEVGEAIEEPMMMVQGEGSGSDCDAVNPGVGEAVEEPTI
FFHGEGSGAECETGNPGDDTSTDNKESNESKTEPDSATATLPQNKVLSEDETVSASTVLSNKPPVKLNRNYPQSNVSVND
NCQIVDSIQEKPKFKPTLGVQIIPESTTGPVKKLSRWDVGKPEEKVDCDNSIISNEEDISLKRTTDDDNEREDTKQTPLI
TDALTTKLGYEDTVGENQDIKIEESSVNAESATNEGSAKSQVSDVSLERTNTMEEERCSKLQEPMQCVSSVSTCQADTSQ
IPESCTMNPEPTVPITDMQSAKSDSDSVVSRESNVSGAVDDECKPAAASPPRFFFGPNCVAYTSKCDELESQSEHDLATS
ASDKTVDTVQYECVSSSKPADGTIYPCQTGDFDLAQTNNNSLKASPFASESDSALRGNGSEDAEKIEEPNKDTQWNQRAL
TVDSSRETNDTAEDNVTNSSIAQIEMDTKETVCTEKEMKEDVSLEVDTSSTSETATENENVNDESVTEEEPIKISSISES
SVVQPEESGSVEPPQCDRSDLEKPVNTVNQESFSPERIGAITSHVLDDKKNEDEISLADDCKNDCQVASNSDMFEDDQER
KESVTHSTSSSFVQNVQVEHRTGLEEFGDRDDDSSKLLDSTDAVECASYHRETSTPPKNDLDSAGESCDKQSDKNDNFSE
IDGQEDHSTDTDNEKMKGLTGSDADSVCVNYDKNSERTDALSDMGMQDDGSGDSEEIKEKGLNDAQINDAVFDIDSSTHL
AESSVVTSSETAQDGDNLVPTVSSSENICVQYSSSRESEPEQMDDEKTENRSSSADNLSTSDILPAVVPEMNTFEPSESP
IVEATRETNSSNLVQSTSEYADDVSENPSSCVDQDSNEEMVIDDRVSESNESSKETEEATCEQEQQPEENANQVTMKFAE
ERKEEVEEAPAVTATEQESRQTMMETEILEKERSEIVAENEGGNNLKEFIEDEENEDMEKDTCKDDKQDAVIVKDTVSGD
MESGEKNLEKSEIDSIDTVVAIEKSEMDCVISATSQELQEEVTNGNKLLTVMNYESESNDDDGSDDVFEPDLTQVSDSKD
DDVAIQEREMDKSMHENSAKEENLVKEAEVNITDLTCDVPHEQPPAQHEVDECPETKINEASNEKSTVVEQEDVKITAQE
YTDETQIKPTCNNIECLSNEPTMPLNTDRFQEETSDIRDIFINDQSEASEVSDATTPLADPVAEGTMESLLSKNSEIITG
DNEKGEEHPNNLIDNTKTAEETENVKMRTEKTECLISKSVGDRLNEDDASNREKSSFARDNLELNAIGGQATDAEDTFSA
REQHTDEKLNVSFDAEDTARQRDTSEHASEELPVPCKRLKEDLAEYDSKDTKWNVKSQLHEESLTKLPWKEEFMDVNIPI
HQAVCPPESNVMPSKLDSVLTEDKSQCKTESASLETVPSDTLYYANSVYTKIENVNNLDSSNDQNESLNTNVNISKITDN
SSKSSPLNTSDESAFLVQETISEIGTIKSDAKKEASKRLIDASDVEDIPPLKSKPQSPYVETVETLEKKTPEDTASTDVQ
ATKSLDTFHEIENFKSQLKDETKTAVICTTQLFQNDFDMVNDTASTAATSVEDSTKKESLEIQSVEMKPEAVLSDDSSGA
DNESGLNLDPAEDADPLACGNDDPLKIADIAENDASKISIRVKSVSEMVYEGWKLDSTTEAPKISRKRRNSAHESNSEDG
IAKEDEEMMGGKRMKLRAKRMPDKELRKSVEENREMAVSSEDEATKCGSDNVTEHPNKDGSDDPSIMQSMVIDKKIRGRP
RGRRRRGFRGGGRPNRPKLTDLQRDQISEVSSGVHPDGAPNDSGTTSMTQKTRKKRKMVLGLEIGRDISLEAQSAPKQDE
TPVRQSRRIAQLKIKEQADRRRIEEETMRELEEKKESEKKKRKKQKPESEDEIILYPKEIEKENKSKKKRRKRKKKKMLA
KFNEANPWQSSSGSSSDEENENEDEEEEEEEIESEGSLLFKSDHEFSPESDLEKDQESEPLRRARTAQKAQSDVEEAEDE
YACQKCGKADHPEWILLCDSCDKGWHCSCLRPALMLIPEGDWFCPPCQHNLLVIKLGETLKTFDQVSKRHENEVLRKKRL
AFVGISLDNVLHKGEPQRGSRGSKASSQESNNDSSDSSSSASSSETSSSEESEPVYQLRERRCANTYKFNEYDDMINAAI
QDEVEAVQGAGNQGRGKDIATIVNAEKEEAQAEALKMTQLEEDKDDVESKPEKESDDEYKIENDDMDNEEMEEEQSTARK
LLARKKHRKLNSLDISSEDDPESDEDFKGTSSEEDDFDDHHISSSDDSSLADVKRRRRKSDLRPVRRSTRARMTRAYDED
FINDDSEESDRPKRKKSRSLWGDSDSEDSDNSWRQRKKKSRTIPASRVRTIPKPKGKKKKKRKRIIESDNQSENDEEYEL
KIDGHQLQDVHNQFTELLNVDKQENLENNAGENNVEIKDEGGLQEVVSAEMTIQQSQEGVMPIQKIKKDIVPKPKKAIRR
KIIYGGLPDENRQKEDEILSRRTRGRKINYREEMASDSEEELKKALMMRKTGESEDEFVVNEADDMNDEGDKDSDSGDVY
IPKKNALKFKNKSPKAKKPRNSKSPAAKRKSLSDDVPKQRKKPGPKPGSKNRARKQKLKDDGDGDMIGAVMDNPIGDITT
KIDENLTDNVGLTGTTMSVASSFTGDVPEGSLTGLGAAELADLDDEQLEQMMMDEEYGRRQLELAAIEIAKKKKKEEREA
KKLEKARLKALEILAAERQRDPNAPEGTDSEAPKKKKRGRRSKAEIIAEQMRRDGAPNLGIAPAAVGGVVGIGGSGVGGI
GTPTNGAGNMHNMNSAALSAGLTPEIERNVEGGHMSLMTGPDAQLFNPDGMPVRPKRRGRGKGKKTLALEAARAAEAAKV
VVDVNLIAGMGTDSNPELKQNDIPNVLPTPGSSTSGSAPSTPPASAVPTPGPPSTQPSNVQPVYPSLPPGGQQSSVITRM
LQSQPVSSSPQSFTAAAAAMGHKYFGGPNTGGQIMGGPRTGYEMQPRARIPSPYRQAGQSSMPPHFAAVRSGTPPMRMRV
PGPQMYHTPHHPMDPSPSGGGPISINNRDRSSPLTPGGPAMIPPSAGSPLAKGGPTPPPPPPYVRGGPPMARFTENPMGP
RHQMPPFTNASPVNHNMQQPSPPPNRPPGNFSPYHPPPPPNYHYGAYPPPPPMTTADDAAAYQGSPYPSEHFSSPADSQP
PIQAPPPPQAPPPPPQQQQQQQQQQQSHPGDEEGTGEFGGLVSYFSSQREDDLDS
```

302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE
306 - 325:	EEEEEEEEEEEEEEEEEEEE
307 - 326:	EEEEEEEEEEEEEEEEEEEE
308 - 327:	EEEEEEEEEEEEEEEEEEEE

A0A3M0II26 **A0A3M0II26_HIRRU** (555 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MDKVAKEVFLVQTGGGDVGVQGIPLVALEDDSCAVGLLRVEEQQVPIATTTVHHWQYCTDRDSVIPIHEMIRKLESQGVV
SKVRSPFNSPISTVHKSSGEWRLTVDYRALNEVTPPLSAAVPDMLELQYELESKAAKWYATIDIANAFFSIPLAAGCRAQ
FAFTWKGVQYTWNRLPQGWKHSPTICHGLIQAALEKGEAPEHLQYIDDIIVWGNTAGEVFKKGEKIIQILLKAGFAIKRS
KVKGPAQEIQFLGIKWQDGRWQIPTEVIDRITAMSPPTSKKETQAFLGAIGFWRMHIPEYSQIVSPLYLVTRKKNDFHWG
PEQQQAFAQIKQEIAHVVALGPVRTGPDVKNALYSAAGNNGLSWSLWQKVPGETRGRPLGFWSRSYRGSKASYTPTKKEI
LTAYEGIQAASESKWIALITQHARIGNPNCPGILEIITNWPEGETFGLSEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
VTRAEEAPPYNELLETERQYALFTDGSCQIVGTNWKWKAAVWSPTRRVAQATEGQGGSSQVAELKAIQLALDIAE
```

450 - 469:	EEEEEEEEEEEEEEEEEEEE
451 - 470:	EEEEEEEEEEEEEEEEEEEE
452 - 471:	EEEEEEEEEEEEEEEEEEEE
453 - 472:	EEEEEEEEEEEEEEEEEEEE
454 - 473:	EEEEEEEEEEEEEEEEEEEE
455 - 474:	EEEEEEEEEEEEEEEEEEEE
456 - 475:	EEEEEEEEEEEEEEEEEEEE

457 - 476:	EEEEEEEEEEEEEEEEEEEE
458 - 477:	EEEEEEEEEEEEEEEEEEEE
459 - 478:	EEEEEEEEEEEEEEEEEEEE
460 - 479:	EEEEEEEEEEEEEEEEEEEE
461 - 480:	EEEEEEEEEEEEEEEEEEEE

A0A3M0II34 **A0A3M0II34_HIRRU** (831 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MLRNQTLHGVVQRLLEEEGKRNKCKTTASVSTQTVIEETGTASMQTVTEEKGTKNKATVSVSTQAVTEEKETKAAISIST
QTVTEAEQPKPVAVAPVQKKKSKSKSVRIVTDEDVAGPSHPAEETEPEIITRSLSLGELRDLRREFTRQTNESILTWLLR
IWDAAANDTILDGSEARQLGSLSRDVVIDQGIGRTQQTLSLWQRLLTRVRDRYLCKEDLQVHQGKWSTMEQDDSCAVGLL
RVEEQQVPIATTTVHHWQYCTDRDSVIPIHEMIRKLESQGVVSKVRSPFNSPIWPVHKSSGEWRLTVDYRALNEVTPPLS
AAVPDMLELQYELESKAAKWYATIDIANAFFSIPLAADCRPKFAFTWKGVQYTWNRLPQGWKHSPTICHGLIQTALEKGE
APEHLQYIDDIIVWGNTAGEVFKKGEKIIQILLKAGFAIKRSKVKGPAQEIQFLGVKWQDGRRQIPTEVINKITAMSPPT
SKKETQAFLGAIGFWRMHIPEYSQIVSPLYLVTRKKNDFHWGPEQQQAFAQIKQEIAHAVALGPVRTGPDVKNVLYSAAG
NNGLSWSLWQKVPGETRGRPLGFWSRSYRGSKANYTPTKKEILAAYEGVQAASEHARIGNPNRPGILEIITNWPEGETFG
LSEEEEEEEEEEEEEEEEEEEERRRRRRREVTRAEEAPPYNELLETERQYALFTDGSCRIVGTNWKWKAAVWSPTRRVAQ
ATEGQGGSSQIAELKAIQLALDIAEREKWPRLYLYTDSWMVANALWGRLNRWKKANWQRRGKPIWAAEIWQDIAARVEKL
TVKVRHVDAHVSKSRANESITTTSRWTKPPK
```

643 - 662:	EEEEEEEEEEEEEEEEEEEE

A0A3M0IL04 **A0A3M0IL04_HIRRU** (489 aa)
Reverse transcriptase domain-containing protein. *Hirundo rustica rustica*

```
MYPDAIKVCRNRVHFYFWGDRRVPEDDCIGGRNDSCAVGLLRVEEQQVPIATTTVHHWQYCTDRDSVIPIHEMIRKLESQ
GVVSKVRSHFNSPVWPVHKSSGEWRLTVDYRALNEVTPPLSAAVPDMLELQYELESKAAKWYATIDIANAFFSIPLAADC
RAKFAFTWKGVQYTWNRLPQGWKHSPTICHGLIQTALEKGEAPEHLQYIDDIIVWGNTAGEVFKKGEKIIQILLKAGFAI
KRSKVKGRAQEIQFLGVKWQDGRWQIPTEVINRITAMSPPTSKRETQAFLGAIGFWRMHIPEYSQIVSPLYLVTRKKNDF
HWGPEQQQAFAQIKQEIAHAVALGPVRTGPDVKNVLYSAAGNNGLAGVDVQGKVPSTHHATDTTWSKWIALITQRARIGN
PNRPGILEIITNWPEGETFGLSEEEEEEEEEEEEEEEEEEEEEEDTCRGSPMYNELPETERQYALFTDSSCRIVGTNWK
WKAAIWSPT
```

423 - 442:	EEEEEEEEEEEEEEEEEEEE
424 - 443:	EEEEEEEEEEEEEEEEEEEE
425 - 444:	EEEEEEEEEEEEEEEEEEEE
426 - 445:	EEEEEEEEEEEEEEEEEEEE

A0A3M0IPA7 **A0A3M0IPA7_HIRRU** (255 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MQRGRAGFIAQGADEMPREDEEEEEEEEEEKEKEEEEEEEEEEEEEEEEEEEEEKEKEKEKEKEKEKEKEKEKEKEEGG
GGGGGEGEGREEKEKEEEKEKKEEKEKEKEKGEGEGEGRKEKEEEEEEEKRRRRRRRRGGGGGRGGGGGGRGGGGGEGEG
EGEGEGEGRGGGGGRGGGGGRGGGGGGGGGGGGEGEGEEGEGEGEGRRRRRRRRRRRRRCSAKHCSQGRSLTKYTTRDTC
HRFTEQKSPLSAGIC
```

34 - 53:	EEEEEEEEEEEEEEEEEEEE

A0A3M0IPQ0 **A0A3M0IPQ0_HIRRU** (80 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MRDEKEGEEEGDEEEEEEEEEEGGGGEGWRARAMWDEKEAEVEEEEGRRRRRRREEEEEEEEEEEEEEEEEEEEEAKEDY
```

55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE

A0A3M0IQQ9 **A0A3M0IQQ9_HIRRU** (69 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MERAGEREEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDAHLGGVVDALTMANTSAQLLENWESSNAGG
```

8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE

13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE

A0A3M0IR71 **A0A3M0IR71_HIRRU** (761 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MDSVLHILDSLKSPARGGSPDTVAALGRGLEVCSTQGCWAVLDNPPWIPEHPLALTLSQWQLLIELLRHDLTTQELGAAL
APDGSMAALGPRLAGIEALGTSCLLAQGSDNNATTLGPPDPTLLGSRESPKLHFEGSPIPDPVAIGIMDGMVLGAQLARG
PLPVAKLLQGYYRTENGLEAGRPPSSYGCQDFEALAGQGQLKKEVAESLSPTMIIVIPGCWHPPQSLSTSMGLVIAPHWS
CHPHWFLSPLMGLVIVSPWSLSTSVVTVIILCFLVGSDRYLFEGQGWHWGGAHTNSYKTQGFGIGNVGDFMATLPDPNTL
ALVQDELLPCAIHSGHVWLDFTLGSHCQLSHTDCPGNAFFQIKNWLGFQGTPVALEFRAGGLVGLVGGATISEEEEEEEE
EEEEEEEEEEEEEEEEEEEAEEEVEKEEHHKCWKCEKSFSQRSHLICHWGINTGDWPYECGACGKRFKSSSTLIVHKRIH
TGERPYECDQCRKRFLRSSNLLLHQRIHTNERPFRCPDCKKGFKQNSALISHRRIHTGERPYKCSECGKSFIQRSTLNIH
QRSHTGERPYECGECGKSFRSSSALTIHQRSHTGERPYECGKCGKSFKTSSNLLVHQRSHTGERRYDCGKCRKRFQTISD
LLRHQQIHTDERPFRCHDCGKGFRDKSHLVRHRRIHTGERPYECSECGRSFSTSSHLISHQRMHTGERPYECPECGKSFS
QSSTLTAHQRIHTGERPYKCPECGKSFRHSSVLKKHQRRHH
```

393 - 412:	EEEEEEEEEEEEEEEEEEEE
394 - 413:	EEEEEEEEEEEEEEEEEEEE
395 - 414:	EEEEEEEEEEEEEEEEEEEE
396 - 415:	EEEEEEEEEEEEEEEEEEEE
397 - 416:	EEEEEEEEEEEEEEEEEEEE
398 - 417:	EEEEEEEEEEEEEEEEEEEE
399 - 418:	EEEEEEEEEEEEEEEEEEEE
400 - 419:	EEEEEEEEEEEEEEEEEEEE

A0A3M0IT11 **A0A3M0IT11_HIRRU** (153 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MGKLLWMGCQGTETPGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAQPLQSLGKPDFLPCCQGLCIFGNNREVRQ
EKDASVTAGLWQPGEERLCTGTDKVSMKSSLAARAHVRFVQPAEKIRQGRKNRKPCDGVFFVKLMEEVTKIFV
```

17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE

A0A3M0IT65 **A0A3M0IT65_HIRRU** (752 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MAPAGEAARREGLIELHGSFQELFEFFCKNSTIHGTVRLVCSGSNRMKTAFWTLLLLASLAMLYWQFALMLRQFWAHPVV
LTMSMHSEPKMFPAVTVCNLDPYRFELVSEHLAQLDRMAEESITFLYGINTSAKLFHLSDRKIHVQALANLSSSGFKLSQ
NFSLLRMSDLRSGKKHSSVGFRLCNSTGGNCFYKTYSSGMDAILEWYRFHYMNIMAQLPLIINISQHEEQIEDVVYSCQY
DGEPCRPSDYVHFHHPVFGSCYTFNSKGTDPFWTATKPGIPYGLSLILRAEQKDHIPLLSTVAGVKVMIHNHNQTPFLEH
EGFDIRPGIATTIGIQQDEVNRLGGHYGKCTRDGADVAVRLLYNSSYTLQLLHAAGTEPGLAKPGLAKPGLAKPGLGKPG
LAKPGLAKPGLGKPGLAKPGLAKPGLARLRLLYNSSYTLQACLHSCFQHTMLRECGCGYLYYPLPAGAQRCDYNKHPAWG
HCFYQLYSRLRNHHLNCFQQCPKPCRESLYKVSAGTAKWPSAKSQDWVRQALRHQNGYNSTSSRRDIAKVSIFYQQLNYQ
AVHEAPLLSENLLLSSMGSQWSLWFGSSVLSVVEMLELLVDTLALSLLFLVQRLRGGSGSGRVPGIGPAPRDSRQLQRCP
EVLLEGFGSDQEQDLGEERRAEGGEARNPPARNQTEEEQGGTDPDFYFQSFRRAEEEEEEEEEEEEEEEEEEEEEEEERR
```

RRRRRQSTARALGSYKGGTENIWFAGGAGARE

695 - 714:	EEEEEEEEEEEEEEEEEEE
696 - 715:	EEEEEEEEEEEEEEEEEEE
697 - 716:	EEEEEEEEEEEEEEEEEEE
698 - 717:	EEEEEEEEEEEEEEEEEEE
699 - 718:	EEEEEEEEEEEEEEEEEEE

A0A3M0ITB9 **A0A3M0ITB9_HIRRU** (150 aa)
Uncharacterized protein. *Hirundo rustica rustica*

MPSSQATANMTHVPDTAEGFTTMAKGQEWEEEEEEEEEEEEEEEEEEEEEEEGNPSEQYEETSMGWAVVARMAVDNTDGM
ATFPGTEKGTKSVWFLLSSHPPTGIGQGIALEVQLPSSRRQGVAPPSITIHHLVTECKNHSYMDNTICHF

30 - 49:	EEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEE

A0A3M0IVL4 **A0A3M0IVL4_HIRRU** (69 aa)
Uncharacterized protein. *Hirundo rustica rustica*

MENLAQKEKKEKEKEEEEGEEEEEEEEEEEEEEEEEEEEEKEEEEEEEREELSLPHWCSALGTHKLMS

20 - 39:	EEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEE

A0A3M0IW89 **A0A3M0IW89_HIRRU** (66 aa)
Uncharacterized protein. *Hirundo rustica rustica*

MPGFLEKLLPRLAVPRVHRDEEEEDEDKDEDEEEDEDEDEEEEEEEEEEEEEEEEEEEEEDEAGRG

40 - 59:	EEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEE

A0A3M0IYM2 **A0A3M0IYM2_HIRRU** (578 aa)
Uncharacterized protein. *Hirundo rustica rustica*

MGWELCGVSVCYSAEELEPQQEEEEEEEEEEEEEEEEEEEEEEEQEPTAGHKGSAKLGHEYTHLQDKQNKYSRVLAKAEE
PSEKIMGERFSSRAFTPMLAKRKYFTRAIVGALVALSIISLVLSLVRVEEVTLPPTVKYGMVFDAGSSHTSLFVYEWDSD
KENDTGVVSQTLSCDVQGQGISSYASNPPEAGNSLRECLDKALQVVPAEKQRDIPAYLGATAGMRLLREQNSSATEQVLA
EVAKTMQEYPVAFKGARILTGEEEGAYGWITINYLLDSFTKYSPKARTWLRPEAANIFGALDLGGASTQITFMPEGSVLS
QNEASEFTLYGYSYNIYTHSYLCYGQNEMLKRLAKELIVGYNETVSLSSFRGSPCTGGSEPRLALGDSTVTLEGRGNASG
CRAALRNLFNFSACGQSQDCTFDGVYQPPLRGRFIAFSAFYYNFKFLNLTEGQPLPVVREAIEAFCARSWEDLSSSYPKE
NPKRLPKYCANANYILTLLLDAYKFNETSWNNIIFQMKAGSADVGWTLGYMLNLTNMIPPQAPARLKGHRPSLWAAAITF
IILTLVLGLAALLLLLGA

22 - 41:	EEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEE

A0A3M0IZB1 **A0A3M0IZB1_HIRRU** (1293 aa)
Reverse transcriptase (EC 2.7.7.49) (EC 3.1.26.4) (Ribonuclease H). *Hirundo rustica rustica*

MGLYTRGAYPPGMDMKRGLKYDCQALPGLITWCKNHELDTTAGAALDFKMWDWAGRHILQALSIGDEVAIGIVKPWRLIM
GLLKQLQREQNTRVAEGEPWTPSEKDLDATVVIPVDLKQLFSCLLDSTEFKLWVAAWRQQLREALPSLLRDPETAVDDNR
NPLTLEYLMVTSSRHEPYRLRLTEALHLRTADWTFLSINIKEQGAWPVQGKELVIIGDCKYTLQEVEILPRVLVNDPGNL
VLWLRCTHPPTFLLKGQIIAQIIPTQGPNDTSKVPVACPVQAITEERPRVACKFTVGGETINISGLLDTGADVTVVPAQD
WPSHWALQDVAGHVQGVGGLQLARQSRSIVQIKGPKGQLANIHPFVLDYKEPLLGRDLMSQWGVKIDIPDPSVEISVASI
DERPTKKLNWLTNEPVWVEQWPLSKPKLKAIKELVKEQLAKGHIVETDSPWNSPVFVIQKPGKDKLRLLQDLCQINNVIE
DMGSLQPGMPSPTMLPQNWQLAVIDIKDCFFQIPLHPDDAPRFAFSVPTINREAPRRRYHWRVLPQGMKNSPVICQWYVA
SLLSPVRAAAGQAIIYHYMDDVLVCAPNDDMLSHVLGLTVDALVAAGFELQEEKVQRMPPWKYLGLEIGRRTIVPQKLAI
RTKVSSLADVHQLCGSLNWVRPWLGLTTNDLAPLSNLLKGGEELSSPRALTPEAEKALEKVQDAMSKRQAHRIDPELPFK
FIIMGKLPHLHGMIFQWRNIPKKDREGNDPLSIIEWVFLSHQRSKRMTRPQELVAELIRKARFRIRELASCDFECIHIPI
GLRSGQISKAMLEHLLQENEALQFALDSFTGQISIHWPAHKIFNSEVRFVLSLKEVRSRRPLKALTVFTDASGRSHKSVL
TWKDPQTQQWEADIAEVEGSPQVAELAAVVRAFEQFPEPFNLVTDSAYVAGVVSRADQAILQEVSNIALYDLLSKLVRLV

```
SHREQPYFVMHTRSHTDLPGFIAEGNRKADALAAPAEMAPLPNIFMQAKLSHQLFHQNAPGLVRRFHLTREQARAIVAAE
KAGDAIKHLIHAFSFMGIPRELKTDNGPAYKSRELRSFLQQWGVEHKTGIPHSPTGQAMVERTHGTIKRVLHQQQRVLKT
ESPSVRLARALFTINFLNCSYEVSIHPLSDTSARARCLGSKNDRRSWSEILGLEGQKGHTIWSRGDVVNHVTMPSEEDHE
EEGLELEEVLEGTPEDEERNPDEEEHGLGWMKEEEEEVVVEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKRRRK
KKWAHADHFKTLI
```

1241 - 1260:	EEEEEEEEEEEEEEEEEEEE
1242 - 1261:	EEEEEEEEEEEEEEEEEEEE
1243 - 1262:	EEEEEEEEEEEEEEEEEEEE
1244 - 1263:	EEEEEEEEEEEEEEEEEEEE
1245 - 1264:	EEEEEEEEEEEEEEEEEEEE
1246 - 1265:	EEEEEEEEEEEEEEEEEEEE
1247 - 1266:	EEEEEEEEEEEEEEEEEEEE
1248 - 1267:	EEEEEEEEEEEEEEEEEEEE
1249 - 1268:	EEEEEEEEEEEEEEEEEEEE
1250 - 1269:	EEEEEEEEEEEEEEEEEEEE
1251 - 1270:	EEEEEEEEEEEEEEEEEEEE
1252 - 1271:	EEEEEEEEEEEEEEEEEEEE
1253 - 1272:	EEEEEEEEEEEEEEEEEEEE
1254 - 1273:	EEEEEEEEEEEEEEEEEEEE
1255 - 1274:	EEEEEEEEEEEEEEEEEEEE
1256 - 1275:	EEEEEEEEEEEEEEEEEEEE

A0A3M0IZI2 **A0A3M0IZI2_HIRRU** (160 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MAKSWLKDGQTTYRDYVESVHRTQERTQHEEKREEREKRREEKRREEKRREEKRREEKRREEKRREEKRREEKKKKKKEE
EEEEEEEEEEEEEEEEEEEMTELVSMLPSAKPRFLMLLQLNSQHPFHPRHSSFSRKQQQLHPVKLWPLLYQMSTAPVAFH
```

79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE

A0A3M0J0G3 **A0A3M0J0G3_HIRRU** (190 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MSWITRGIPGHDLGFLDHIQDALAMLQGILDHPWDILTVFWDALDKSWDILYKSRDSLAIFWDILYKSWDILDKSWDILY
KSWDSLAILWDILDKSWDILYKSWDILYESRDILAVLREQRGWEEQEQEEEEEEEEEEEEEEEEEEEEEEQEEEKKAA
VELLGFPPIFSDFPVFPPLPVGLGPGLTGM
```

129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE

A0A3M0J1L4 **A0A3M0J1L4_HIRRU** (109 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MHDPTTQLFLLTEIALLKEKEKEKEKEKEKEKEKEKEKEKEKEKEKEKEKEKEKEKEKEKEKERRRRKKEEEEEEEEEEEEEE
EEEEEEEGKGKGKGKGKGKGKGKGKGKGT
```

66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE

A0A3M0J5U4 **A0A3M0J5U4_HIRRU** (99 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MNWACRMSYREKEKKKKKKREEEEEEEEEEEEEEEEEEEEEEEEEEEEMLSRKDKSTPCLPGNMAGVVCSELGSLWGKC
SFPDKANERIFICLVHFNM
```

21 - 40:	EEEEEEEEEEEEEEEEEEEE

22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE

A0A3M0J6U6 **A0A3M0J6U6_HIRRU** (352 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MVFFRCVTSQLLQNPCGTLGFKPAFPNGLFLKGKISLVLTFPSSFVTFICFVNDWEVLQWKFVLSSEYRDEKTFELRSRN
SDMKIYAPDIEEKLPLRIIPGRSWSWRVPSWKILVKIEENGKESTQSTESAISQIPACKKEENLAFIERNSEGALRHSSS
SSSAREEPFLIWPELIQREQLLLAKPGEPKFPEEMNQCSSQHSKLGQAEKKKKKQKKKKKKKKKKKKKKKKKKKKKKEE
EEEEEEEEEEEEEEEEEEEDPDKFGAATAPPSPLWSHPNLQKSAELSPGRQIKPPISTFAQNEKKEKEKEKEKEKEKEKE
KEKEKEKEKEKEKEKEKEKEKEKEKERIKENKGE
```

239 - 258:	EEEEEEEEEEEEEEEEEEEE
240 - 259:	EEEEEEEEEEEEEEEEEEEE

A0A3M0J7J5 **A0A3M0J7J5_HIRRU** (616 aa)
Elongation factor Ts, mitochondrial (EF-Ts) (EF-TsMt). *Hirundo rustica rustica*

```
MAAPGSHVGTGEGREGGEENGEEEEEEEEEEEEEEEEEEEEEEEEEEEQGEEAEAGAAGPWAEVTLTDRPPALPQLRDNA
RRNFPGGAGAPRVRALRWGRDQRRFPPKFHLILGSDIVYDPRAFSPLLGTLRHIVVPPAQALLSARLRGGDAGASRFLPP
DASPGRWFSAAPPALRELRELRARTGQPVMRCREALERAGGDLRQAEAWLEAESRRRGWARAAAPGAQRPREGLVGVLSE
GSAAVMVEVNCETDFVARTPDFQQLVEMAARGVLGHCQGASGTKHLLREDELAQLRAGDGGELLSDHLALAMGRLGERLA
LRRAGWLRAPGGFVATYAHGWVPPGPPVAMGTYGALVACGGPGPGPPPAELQELGRRVAQHVVGMAPTALGTPEDELGGD
TETRLLAQGSLLEPGVPLGRPSSRDKWDKLGIGVPWRSVQWQTGGGLGEDWDRTGRGLGEDWEWTGTGLGENWDRTGREL
GENWERTGRGLGEDWERTGSRLELECGQTGTGLGEDWEWTGSGLGEDWERTGRGLWADWNWTGTGSRLGGWMGLEMDLDW
DWTGSRLGLDWEQNEGGLDWNWTQTGLELDSDWTGNGLRLDLDSKRTGTGLGVDWN
```

22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE

A0A3M0J855 **A0A3M0J855_HIRRU** (135 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MPQNIYMNCKVKDCDRIPNLQLSNPQYQRTHLACTKAPEELFCGGEEEEEEEEEEEEEEEEEEEEEEEEEEEEKKEEKKE
EKKEEKEKKEEEKKEEEKKEKKEKKEKKEKKEKKEKKEKKEKKEKKEKKEKKAHL
```

46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE

A0A3M0J9K4 **A0A3M0J9K4_HIRRU** (1242 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MMEPLGEEEERVLKEFEFDSGKLVGELGQDFEGLGALLGWRRDPPRQPRVAWKEVVAPEESSSAAERPEVTMVQPLQPSL
AMAPSVQTRGLTWALLLSQNLKYCGPERRILGAGTWLSKILREEWLWLDPSPAADLSKPEIVLERCKEEENEEEEVEVED
```

```
GGGGGGGGRGKRRRRRPEQGQEQDQARTRSRTRSRTRKARTRRRMRRRRRRTRRGTRSRTRKDKDQEEEDEEEEEDEEEE
EEGGGGGQDQEEDQEGRRRRRRRTRRRRRRRRRRRRRRREEEEEEEEEEREEEEEEEEEEDRRRREEGREEEEGGRRRRRRR
RRGPGGGGGGGGGGGGRGREEEEDEEEEGDEEEEEEEEEEEEDGGGGEEEEEEEDEEEDEEEEDEEEEEEDGGGRGRGGG
GRGGGGGGGGDEDEEEEEEDEDGEEEEEEEEEEGRGGGGGGGGGRPGGRREEDEEEEDEEEEEEEEEEEEEEEDEEDEEEE
EEEEEEEEEEEEEEEEGGGGGGEDEEEDGRRRRRRRRRRRRRRERRREEEDEEEDGGEEEEEEEEERRRRTRRRRTEEEEED
EEDEEEEEEDEEEEEDEEDEEDEEEERRRRRRRTRRRRTRRRRGGGRGGGRRRTRRRRRRRRRRRRRRTRTRRRGGRG
GGGGRGGREEEEEEEEEEDQEGGGDEEDEDEEEEEEEEEDEEEEEEEDEEDEEDEEEEDEEEEERRRRRRRRRRRTRTRR
EEDGGEEEEGGPGGGQGRGGRGGGGGGGGGRGGGRGGGGGRGRGGGGGGRGTEEEEEEEEEDEEDEEEEDEDQEDEEDEE
EEEEEDGGGGGGGGGEEEEEEEEEGEEEEEEDKEQDRTGQDQDRSRSRSRTRTRTRTRSRRTGPGPGTRRRTRRTRRRRR
RRRRRTRTRTRTRPGPGAGGGGPGGPGPGPGPGGRTRTRRSRTRDQDQEDQEEDRRRRRRRTRTRRRRTRTRREEQDQEEE
EEDQDRDQDQDRTRTRRRTRRRTRTRRRRTGPGQEDQDQDQDQDQDQDHEEEEEEDQDRYRTRTRTRTRRDQDQDQDQDQ
EEEEEEEEEEEEEEEEEEEEEEEEEEEDKDKEDRSRTGGQDQDQEQEDRTRTRTRTRTRTRTRTRSRSRSRSRRTEDQDQ
DQEEDQDQEEEEEEEEEEGGGGGGGGGGTGTRSRTRPGPGPGSGPGPGPGAGPGPGPGPGKTRPRRRWMRTRKRQRTSRK
WRRRRTRTRRRRKMRRRMRKRKRRRKTNVFSTNPFLCRKREK
```

477 - 496:	EEEEEEEEEEEEEEEEEEEE
1041 - 1060:	EEEEEEEEEEEEEEEEEEEE
1042 - 1061:	EEEEEEEEEEEEEEEEEEEE
1043 - 1062:	EEEEEEEEEEEEEEEEEEEE
1044 - 1063:	EEEEEEEEEEEEEEEEEEEE
1045 - 1064:	EEEEEEEEEEEEEEEEEEEE
1046 - 1065:	EEEEEEEEEEEEEEEEEEEE
1047 - 1066:	EEEEEEEEEEEEEEEEEEEE
1048 - 1067:	EEEEEEEEEEEEEEEEEEEE

A0A3M0JC30 **A0A3M0JC30_HIRRU** (294 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MTAMLLEITPHASTSSTGTTKARNTAHFGISGQEYYLQNRKVIFGKLNVSCVIKPIWVKKKKKKKKEEEEEEEEEEEEEE
EEEEEEEEKKKKKKKKKKKKKKKKKKKKKKKKKKKQNKTPKTNTDCLNLFWTENPEEQQELTPGAQRGLDVLRDCFLIAPRILS
DLDTSSEISLSKPRSLERHSALRVLWKGVGWLQGLGIVPVCGIICCRLLRQAEGGEERRGEERRGEERRGEGGEERRGEE
RTGQDRTGQDRTGQDRTGQDRTGQERTGQDRTGQDRTWLGGQETLANHFSLVWV
```

67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE

A0A3M0JF45 **A0A3M0JF45_HIRRU** (248 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MQRAKGFTEQWPSPLVRAKWNTRNKGARSPPVPPWCSQQGLRWSLQQAETPDLFCPHRKSTSSICVLSLRYEEGEGEGEG
EGEGEGEGEGEGKGKEKEKEKEKEKEKEKEKEKEKEMEKEEKEKEKEKEKEKEKEKEKEKERKFIQNSNFVIGKQKKLTEKN
REEEEEEEEEEEEEEEEEEEEEEEEEKKEEEKKKKKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDAFML
RLHVQDSM
```

162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE
208 - 227:	EEEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE

211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE

A0A3M0JFK6 **A0A3M0JFK6_HIRRU** (403 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MGSTEEYGEMAQLRSWTHPKSEFTVEAAFGQKKKKKKKKKEEEEEEEEEEEEEEEEEEEEKMRCPVGEEEDKNPYEYDCL
YSENEKPVGEIELKDDDDDDEFYPVVFHTLKPLSQFWDTYRSSRVVPRLVYEASALYQEMTAAKTYFGFAGQQRTGTRLK
SNFLVPQTTFGQKVILVYGVGKRGCYSLNLMSEASSSSQEKAVRNFTLNEEGVMPLYSHQGQTASRGIPLEISKIMETGH
HKLALYFHSNYCHMFGSRLFHERSRAEIFRSGEKVDELFALYPERIFDDASLKTDMCEGLPVSLAVEQLTGEANAAPDQE
NRRLRQVQRLPLPAGQFWLEPIWDTDPSGETCRACQDDQNSDGKSEWQNSPSSFVYCSWFEEINNQVGYEEKFLDCKSGL
ALE
```

41 - 60:	EEEEEEEEEEEEEEEEEEEE

A0A3M0JH20 **A0A3M0JH20_HIRRU** (596 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MALPGMGPFSLLSLGVLVLALALPADAGLSQKHVSDVVDDSKDNITIFTRILDRLLDGYDNRLRPGLGAAMPELLFPPGC
CRRELKRARAEAAQERLVQPQPAPDSVTEVKTDIYVTSFGPVSDTDMLVFHTHPERGRLWVIAREFGDATRSWNCVLEER
QVKLPWEAGESTCLPSVEEEEEEEEEEEEEEEEEEEEEDMETFSLKCSKGLPVPVREYTIDVFFRQSWRDERLKFDGPMK
ILPLNNLLASKIWTPDTFFHNGKKSVAHNMTTPNKLLRLVDNGTLLYTMRLTIHAECPMHLEDFPMDVHACPLKFGSYAY
TKTEVIYTWTLGKDKSVEVAKGGSRLNQYDLLGHVVGTEMVRSSTGEYVVMTTHFHLKRKIGYFVIQTYLPCIMTVILSQ
VSFWLNRESVPARTVFGVTTVLTMTTLSISARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNYFTKRSWAWDGKKV
LEAQEMKKKEPVALAKKTNNTYNIVGTTYALNMAKEPGLPTISKSAAVTATAASVPPKMPRLEEKLPESKKTYNSVSKVD
KMSRIVFPVLFAIFNLVYWATYVNRESAIKGMIPKQ
```

178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE

A0A3M0JH29 **A0A3M0JH29_HIRRU** (192 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MDSYYNAASQDTEGSSPFRAFQASDKFSPTFLASKGQGFGDSSTKCRSRYSQQECQSLDGSVQAPGSAGSPASFNKYPPQ
QQPPHLYMQRGPCKTPPDSNIKLQESSGHNGALQVSCYVIFGQREESVRNRVTGWREEGEEMNEERQGKKKKKKKEEEEE
EEEEEEEEEEEEEEERRRRKEEEGIPWMGNKQ
```

156 - 175:	EEEEEEEEEEEEEEEEEEEE

A0A3M0JJF1 **A0A3M0JJF1_HIRRU** (80 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MAKKIERQKEEKLRDTQKQLGEEDEDGDEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERRPLFLEMKMIS
```

32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE

48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE

A0A3M0JJS5 **A0A3M0JJS5_HIRRU** (253 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MGKKKIKTSKAEGRKREKRKKKRKKGKGGKKGRKRKRKRKRKRKRKRRGRGRGRGRGRGEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEERKRGVPYKPSPRAGSGMSQGALGTTASPSPSALTQRACVTKGHPGSPSTAKGTGSGLEQPRP
WGLAALCAEPLLEMIRNSWARVKLAMVKRELESFVREKSDRCGAKAWCLKPLVWCPSARPKEPGVEHAEWGPDFMQARVQ
KTWPIHTGRDLSG
```

60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE

A0A3M0JJT1 **A0A3M0JJT1_HIRRU** (87 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MSQAWAKPPHAASAVSKLGLSPTGGGEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGSWTKDGAPVLPVGRTL
FDLNPSL
```

30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE

A0A3M0JJU5 **A0A3M0JJU5_HIRRU** (209 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MENIPAVGRRRRRRKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGAPRALAGGGILSWGPPGRRREDEEDEEEDDDEE
DEQDEEDEDGKEKDELDEEDEDEEDELDEEDEDEDNNDEEDEEDEEGEEDEDEEDEDEEEDEEEGEEGEEDEEDEEDEEG
```

EEGEEDEEDEEDEEGSTNSHSLSLSWSSKPFPVPRADPEGPSRSLFSPG

16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE

A0A3M0JK61 **A0A3M0JK61_HIRRU** (292 aa)
Uncharacterized protein. *Hirundo rustica rustica*

MISKHATGLPELSGIQVTPSPVQPGLGHFPGMGHATASVDKCPVLHLKQSSLRIWYLGKHRKWMRLMLWIQQVALFHPQP
GPAVFYNPQGVLQSQRRRKRRRRRRRREEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEERRRRRRREEEEEEEEEEEEEKRRREEEEEEEEEEEEEEEEEEEEEGGRGGDGEGLYLLPVLFLRSKMHLNVPS
DIQLFVFETILLSIFKNLEITTQRGEGQDLSSCSKPHAMLCVITVIMALMEQ

108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE

140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
191 - 210:	EEEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE

A0A3M0JLM6 **A0A3M0JLM6_HIRRU** (302 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MEPRMGWEEAGVRCWGWGGGREGAAEEELVDVFMWRGRALFLKGTMVSFLEVLLYTNSATNPSACAFQLVCLKMSSISTS
SFQQEITRDKDGEKDLRLRNCNSVQSLFQLSLPKASLKLSSSTDTPPLRSLRLEKVGNVECGIPICPEEITVSTVRRRRR
RRKEGEGEGEEEEQNKKKSKKKKKTLKKEEIEEEEEEEKKKKKKKKKKKEEEEEEEEEEEEEEEEEEEEQEQEQEVIKSV
VSTFKSGTVIRIFHRKYNYGFFSPSVLGAFFPPPFYVIKADFFLSPSNLLYACLPEELLFHS
```

210 - 229:	EEEEEEEEEEEEEEEEEEEE

A0A3M0JP01 **A0A3M0JP01_HIRRU** (86 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MMHSCDKPKMDLRCLSYCPDDWEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGGGEFVCWDEQHTGNVDVEFGRVQFI
GAVSSN
```

23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE

A0A3M0JQP2 **A0A3M0JQP2_HIRRU** (158 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MLTCWSCSGKGHQDDPRIDIPCWRDPQDQLPNCAPKKSARSLQQACKTQGLVLQGLIPNQSGALPGEEEEEEREEEEREE
EEEEEEEEEEEEEEEEEEEEEEKKKKRRKRRKRRKKRKKRKWKKKRKKKRKKKSHTKRRGLKATALCLFPGTGSNNMS
```

79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE

A0A3M0JRJ5 **A0A3M0JRJ5_HIRRU** (357 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MVEFSRKKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVEEEEDSMPTDGHMIFLTNHALIKPPVPNNKDKHWHYGE
IHSCETAAGSCTIPTVNKENFYQNILKIHLKNPIFWNNADNSIANIMPAEGISFTSSTKLYKCLCWVSLTALPAAGAAKP
CGGAHEKGSQEEGLPHMEPSSKDITSLLENAQGLLNVKDTTFLVFHLVSFLYIVCSFSRMSQTLLNTVGQQIEAGEQGDK
SVTQAAANPTATRVAAKPDSEAKTLAAAAVKKGKKRMHKTDRPVDDDSGEGSSMPPDIQSGAESTDTQSEAETTGTKSET
QPTGTRSGAQPAATRSGDTIESFSLKDLWGLRKDYTR
```

10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE

A0A3M0JRU6 **A0A3M0JRU6_HIRRU** (131 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MKKEKEEEEEEEEEEEEEEEDQDRDRTRDHDQPGTRTGAGSGAGPGSGPKPGDKDEEKEEEEEEEEENRTGTQGDLDEDQ
EQDNDQDQNQEDEDEEKEEEEEEEEEREEEEEEEEEEEEEEEEEEEDQDR
```

108 - 127:	EEEEEEEEEEEEEEEEEEEE

A0A3M0JUH5 **A0A3M0JUH5_HIRRU** (140 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MSKSREAKVSTEEEEEEEEEEEEEEEEEEEEEKKEEEKKEEGRKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKRRR
RRGRRRRRRRRRRRGRRGRREEEEEERRKRRGRRREGEGKQQQLQGESLIINDHGDSPCC
```

12 - 31:	EEEEEEEEEEEEEEEEEEEE

A0A3M0JUZ3 **A0A3M0JUZ3_HIRRU** (174 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MDLKDSLSPLIYMRVNQPTVTTTPHELEQSQTQAKPHSTPNSYSHSRHIKVAQIEMDKTQSLNKPRVWQKMEKEEKKRRR
RRGEGEEGEGEGEGEGEGEGEGEEEEEEEKREEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEETPPKIFHLALI
YLYTKTSKLQIFTL
```

114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE

A0A3M0JV41 **A0A3M0JV41_HIRRU** (590 aa)
Receptor_IA-2 domain-containing protein. *Hirundo rustica rustica*

```
MEVMRAQELCCDPAQPLDTNRDNWVARAGLVRGFTWRDDYTQHVIGQELSTIHKIHSRRPDVFAPEGSDTGRTLGQNEDN
ERNYDVENDVNLAKSLQQYLKYLRILSQSASKNLYPRKTSDKASVKSYIYNDPMKYYTRQNPKEPSPPLAHASKSHQEFP
```

```
PRGRTLSQLQPDQLSPESGTGLDQRSLMAALHSYITQNLSAQSSDRSPHSRTKGSQVYAERLYSTQVSPFDGTFAKGKAE
DFKMRKLFQPRPGVLRPTPEILSHKSASQDDPKDPLSVVDETLIKNVLKDLEKHQVNVENLSSAELDEIADTIATAIQSV
DIQEETGKKAGKTKGDKTETQTKKGDAQGRPELQTGLMENSVNIPDNGVHEASVRTDKEENTAKLIRFLNENALDENMHK
DLIPEEPTKTETKKSEESDLSSSEETNAGVENVKSETFSRELTTAKNSESDSKDPSQTSYWIKNALMQEGNSYENPQKNT
GQGLQLEVKSSEEKEYGYIVTVKDPLSVEKGLELIKEVADLLKLQMSVFDDVNVLGPAVTFRVHSNLQNISTADVAKEAE
EEEEEEEEEEEEEEEEEEVNLIRLYSLFK
```

560 - 579:	EEEEEEEEEEEEEEEEEEE

A0A3M0JV89 **A0A3M0JV89_HIRRU** (117 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MEEEEEKKRRRRKRRRRRRREEEEEEEEEEEEEEEEEEEKKKKKKKKKKKKKKKKKKKKKKRRRRRRRREEEEEEEEEK
KKKEDFPKSSVLLSSISILKPQNYKFSPCDKLNHYLF
```

21 - 40:	EEEEEEEEEEEEEEEEEEE

A0A3M0JXC2 **A0A3M0JXC2_HIRRU** (227 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MTYEMLSIVRSTPRSRAHWEEEEEEEEEEEEEEEEEEEEEEEEEKKKKKKKKKKKKKKKKKKKKKEKEKGKEKEKEEKEKE
KEEKEKKKKTKKKKKKKDPQGSFSFRILIRRLLLLLLLLLLLPSTSPSPSPSPSPSPSPPSPSPSPSSLISFSFSSFSSF
SPSPPSPPSPPSPPSPSSPSSPSSDNPKVSPSGQLVIISRIPGQTGFPIRACCVMRAIHLLHVVSVA
```

20 - 39:	EEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEE

A0A3M0JZ52 **A0A3M0JZ52_HIRRU** (909 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MEGSRSAECDRASETSSFIGDEEEEEEEEEEEEEEEEEEEEEEAMDPEEAEELTNSLKDLIQSEDVKPKLQYIMTNPSFSMV
TCQSEDSGIHWETSSSRCSTPWTSETSTASDLYSMESSPVGSPPGKVIFIMDEGKIVRKRTRKSSNRVPMATRPKGGQCN
KKRDSSGMQRQEPRTVLGDVQASMLNVEQVEAQDRDEEMLDNKEDLENIAEEPVKRAPIRSIFRESRLRKVGPILGGPVQ
ARIQLFNSIFGGTGPAPETLENNRIRRSSSASGDSEKCLETSVKERLQKFGALSEATRPKHFQGARSKILETPSERRRKQ
RQQLTEQANQSFSSPTPPLEKQLTKKNDVSSENIEPYKTKESTLQHEERKERQSLLETPNQVSGHLLKNEEEARKQQSHS
AAAGTSITESKTSISLKADEKRVLLPSAENANKKPDQSPVTASDHRDEVKKQEVQPNSAPQSVSADSVSELNRPSSQHIL
PKESMSEHLERETEKSYLPDVPSAKSKYSASTEVRQEDIIPQSSETAQSESEHVLLAHSGNETEEQDTKHPPSTTESSES
ATSGLMYSAERDEGQKTTSSETQNTHLESQTKSEEDFSLQEAEKQRMKLKPPIPENVDSKYFGISYPVHTETEETQKTSA
INKAVDFDHSDFSIEENKQGGEMEMEHPDLSYSTEGTGESEETQMETEHLDFSSPKEETEELKGEQMEMEYPDFSFSREE
IEEPGSAQLETELPDFSYSKEETEGSESAIPDTDYPEQLFSTEGIEKSGRSQPESEHPEFYFKKETKEPESAQLEMEHPD
FSFSREEMEESDSTQLETEHSDLSSSREEMVESESAQLEMGHPDSSLTRKQSRKCKVHSWKRNTRFPFPRKRQKTKHSVL
LNWKSLIPLKKKNKKKKKSLQWHIQSYHV
```

22 - 41:	EEEEEEEEEEEEEEEEEEE

A0A3M0JZS6 **A0A3M0JZS6_HIRRU** (163 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MNTDCKSLHNKTIRIKYGQRKGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEGEGEEEGEEEEEEEEEKRK
KRRRKRRKRRKTNHQPCDYVILLNQIFGEECNQQASFVFLMCERENSEDAPTYISPCISRLKKVQHGSNIFHRRMRVLVF
QVH
```

23 - 42:	EEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEE

35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE

A0A3M0JZU7 **A0A3M0JZU7_HIRRU** (67 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MFFLITADAFETTQGIMHLEKGIQVTEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEESS
```

27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE

A0A3M0K058 **A0A3M0K058_HIRRU** (143 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MSLRGEERRGEERRGEERRGEERRGEERRGEERRRGDETRREETRRDETRRDETRRDETRRDERRDERERETRREREKKK
KKKKKKKKKKKKKKKKKKEEEEEEEEEEEEEEEEEEEEKKKKKKEKKKKKKKKKKKKKKKKKE
```

99 - 118:	EEEEEEEEEEEEEEEEEEEE

A0A3M0K0I4 **A0A3M0K0I4_HIRRU** (363 aa)
Neur_chan_memb domain-containing protein. *Hirundo rustica rustica*

```
MNWSLDPKVMCAYPRLSLSFRLKRNIGYFILQTYMPSILITILSWVSFWINYDASAARVALGITTVLTMTTINTHLRETL
PKIPYVKAIDMYLMGCFVFVFLALLEYAFVNYIFFGKGPQRQKKLAEKTTKANNDRSRFEGSRVDTHGNILLTSLEIHNE
VASNEVTTSVTEARNSTISFDNSGIQYRKQSSHRESLGRHVGFNSHDCRNSKCHLLKETCNILNADDSFDIHKDSSVNLQ
VHTLYIRGSQKGYTFPIPHLPLGLSSGDHLTTQLRQRRKEFIEEERRKKKKKEEKKKEEKKKEERRKKKEERRKKKEERR
KKKRKKKERRKKKEERRRKEEEEEEEEEEEEEEEEEEEEEEL
```

340 - 359:	EEEEEEEEEEEEEEEEEEEE
341 - 360:	EEEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEEE

A0A3M0K1A9 **A0A3M0K1A9_HIRRU** (133 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MQFKKLQAKGLLNLFWRVLDLFSPPSPSKDLWLELTDTAKSIDSTFAVLDNRHLLCMSRDRGKSKRERVEGGGEREKKKV
EEGEGEGEGEGEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGGKGHQP
```

94 - 113:	EEEEEEEEEEEEEEEEEEEE

95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE

A0A3M0K1L4 **A0A3M0K1L4_HIRRU** (222 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MKIHCCFAYDFIRWRRRRRRRRERRREEEEEEEEEEEEEEEEEEEKKKKKKKRKQKKQKKKKQRRSRRSRTEEARRSKE
IEAEEEVRRSSRRRSRKAEEERRSRKEAEAAEAEEAEEAEAEEEAEEAEAEEAEEEAEEEEAERRRRRRRKKKQKKKKKK
KEAEEEAEEAERRSRRSRSRRSRRRRSRRSRRSRRRRKKQKKKKKKKEARRRRRRRRRRRRR
```

27 - 46:	EEEEEEEEEEEEEEEEEEEE

A0A3M0K208 **A0A3M0K208_HIRRU** (100 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MDFAVDDDDDDDDDDDEEEEEEEEEEEEEEEEEEEEDHDHYHCHHPLNSGDILAHSAAELRFSLAGKVVDAPSLEQSKFQ
WRFEQPDLVKLSLPKLEGLD
```

17 - 36:	EEEEEEEEEEEEEEEEEEEE

A0A3M0K2A5 **A0A3M0K2A5_HIRRU** (283 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MCGEGCNTWWSGQSGDLASEEEEEEEEEEEEEEEEEEEEEEEEEEEEVEVNLQNFAKKELNDLEQWKKEHKPGPITLVPQR
LGGSKSEAQVRQNQQMILMQSKYQKKHKREEYVKAKKAAEEAEILKKKATQREKMPDLENEEYVLTFYQKLLTHEMESFL
LSYGILDAFCIIGLIVFLSECIKSKTNELLNRLDVGLPKSDSCQIAKPGPESTAWAELMEFKQKQEDEARTRALKNEQRR
SQTTWNKGGASSDTSMSAETLLLGLETFEASSGYCRNIHFYLA
```

20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE

A0A3M0K2I3 **A0A3M0K2I3_HIRRU** (84 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MLKHNGGEEEEVEEEEEEEEEEEEEEEEEEEEEEEEEERRRGRRRGRGSRGRRRRMRRRRRRRRRRSGTEWAIRVYLPSPAS
STHP
```

13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE

A0A3M0K2L9 **A0A3M0K2L9_HIRRU** (1767 aa)

Uncharacterized protein. *Hirundo rustica rustica*

```
MDLQQKPLLLPYLGEMKQLESHIPSGNVGCNKKYFKKKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEKKKKKKKKKKKKKAAPPEELSSPSRCEGKANQGAADEGEAARSADGDSSVALSYPSLCLHAYSIENMTTFPNGCGN
GTTVTCIVMDNKEPQHQTTCASHNGGHNTSNGLEEEFQEDKLSPSKIMRFFTTPRKRANSSSDRPRSLVLMGNSSTWNAF
SSIRKMGSFKKLKSSGQQGIQTRECSDILNENSIGKHGSNGAVVRVQNNRYSYSGPLHDVQNAVDGLASDCSDVEESDES
FLRNTHRSRSIRRAYGAGRINLLDADKVQSRHNCARPASPVITEPKICEILVKDSGNNRIIYWRSKSSDNLNFLKKSSFK
RKSTSNLADLKVANEKQMPARTVSVASADSDKSGGNPERRSKRWKSPIRAKDFDRVLKLVSNVTDVARKKDGPKTMAPSP
SELSQRTRSNSRLHDDYSRRVSSSTDHDRKRCASSVSSPDSSLPGTPCLQSPVIAQDKEAEMHVAVTEDKSLRTSSGIPN
SDSFSPTLSDVSPFPNEVFYSDSDEPKATQQCTDEAENLHVPVRPTTPKPQSPTAGKVKCSMDFQCPNHHSTLSLSSSES
EERVEVPGLKLGRNPVCFQDSVQTVYYDDGNEDSGISSHSQLSLNLASGTEEKKEEVVSDDHWKRSTSQDEEKADSQKVT
SRKWGSGKRSRPRPLSDYGQMLIRSFSIPEDAVAVESQKTDCTDGDNQPGLAPVGSVIQSNTVGCHRGRKRRPISVIGGV
NFYGDDQVEERENLLTQPVARPPVPAHKVPPYKAVSARFRPLTFSQSTPIGLDRVGRRRQMRTSNVAADGGTESSALVDD
NGSEEDYSYEELCQAAPRYLQPGGEQLAINELISDGTVVYAEALWDHVTMDDQELGFKAGDVIRVLEASNKDWWWGRNED
KEAWFPASFVRLRVNQEEVPENCSNIQDEEQDPDISKHRQKIAENRDQMRTNVIQEIMKTERVYIKHLKDICEGYIRQCR
KHTGMFTTAQLSTIFGNIEDIYKFQRKFLKDLEKQYNKEEPHLSEIGSCFLQHQEGFAIYSEYCNNHPSACIELSKLMKQ
GKYRHFFEACRLLQQMIDIAIDGFLLTPVQKICKYPLQLAELLKYTTQEHSDYGNIKAAYEAMKNVACLINERKRRLESI
DKIARWQVSIVDWEGPDVLARSSELIHSGELTKISKQGKSQQRTFFLFDHQLVFCKKDLLRRDILYYKDRIDMDEMEIVD
TEDGRDKDFNISVKNAFKIINRTTEEIHLFCAKKQEDKKRWMEACESERRRVREDKEMGMEISENQKKQAMQNARKSRQG
KIKGVSYNGCPVPPPHQTLHPLHQRHITVPTSIPQQQVFALAEPKRKPSLFWHTFNKLTPFKKMKIWIVLLAIVVSTAAT
QNQGICTQGYPGIPGNPGHNGIPGRDGRDGSKGDKGEAGEPGVPGSPGKDGINGEKGEQGTNGTVEEKGNKGDKGERGPP
GKLGPKGFMGSVGYKGQKGELGLQGQKGLKGDIGPIGPKGTKGEIGHPGRVGFPGPIGPIGNPGPKGNTGAIGPQGNPGV
QGERGLKGDRGDKGNVGAPGVLPRSAFSVGLTANTKFPPPNRPIRFDKVLYNSLNDFNSATGKFTCKHPGVYYFTYHITV
YSRNVRVALVKNGIKMLHTVDRYQSGEDQASGAAILELQGGDEVWLQAHQGEAFNGLFADGDDDTTFAGFLLFSTADPLE
TLLPPTP
```

40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE

A0A3M0K3H4 **A0A3M0K3H4_HIRRU** (83 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MVADKNRRHLPGTDQLDGLAEEEEEEEEGGEEGEGGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERREPCN
GTL
```

37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE

44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE

A0A3M0K4J0 **A0A3M0K4J0_HIRRU** (66 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MEVHVGAGINVQFLGELDPTLEQDLVCPRSTRKEEEEEEEEEEEEEEEEEEEEEEEEEEERKEREKR
```

34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE

A0A3M0K4U8 **A0A3M0K4U8_HIRRU** (187 aa)
BZIP domain-containing protein. *Hirundo rustica rustica*

```
MCVRKREEKRREEKRREEREKKRREEREEEKRRREEKRREEKRRLLSHAQCIPEVFSSPSCLDEVLVPDPFSSGLFLGMK
DSDGSMARKGDRKGERRRRRRRRRRRRRRRRRRRTRTRTRRRRREEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEDE
EEEEEEEDEEDEEEEEEEGAEHHWKAF
```

131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE

A0A3M0K506 **A0A3M0K506_HIRRU** (75 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MEKSKDSKVTVQQKMEEEEEEEEEEEEEEEEEEEEEEEEEEEEKEEEKEEGGEEEEKEEEKEKMERRRRWRRRRRR
```

16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE

A0A3M0K6A5 **A0A3M0K6A5_HIRRU** (66 aa)
Uncharacterized protein. *Hirundo rustica rustica*

MKKKKEKEKEKEKREEKKEEEEEEKKKEEEEEEEEEEEEEEEEEEEEEEEEEEKEKKKREVLSGF

28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE

A0A3M0K745 **A0A3M0K745_HIRRU** (83 aa)
Uncharacterized protein. *Hirundo rustica rustica*

MEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEECVNDFGEIIIICIFITGKSMNMAEEKCNDIS
EAG

2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE

A0A3M0K762 **A0A3M0K762_HIRRU** (2407 aa)
Uncharacterized protein. *Hirundo rustica rustica*

MASGLPKTTPTPRLLFRERLKSISLLPSKFMREKFLNVKNASTGGNILPRIGPSLDTGQKLSSVAPKQSLFQVSPPEMVF
QNVPAHVTSDMVVSITNKGKRSQLVKVSMASSPYFQLDCPNGVCHIVPAGMSTPVRVLFTPKENKDYSHELVCMSGSEWI
VVPIRAIAARAILDFPDQLDFPVCPVKCSTQKTLLVRNVGNRAARYQLSTQSPFSVVPATGTLGVGDTMQVTVGFHPLTA
GDHSGSLVVGCTGEESIHTNLQGKAEDVNIELNTNFVKVEKTFVNMSNHTTMFIKNSSNITAHFQWKAFPTEEHENEEKR
RQCSLLQPSAKVWLEAYKKDKKMEKEKGFVKIAPSSCPISRESRLPLCLRGEGQGPLVELCSDTLNLGSISVNTPHNCEV
KLINQGAIDAPFTYIPSTTHVGSCFKFAPEEGIIAPGEIQTIQISFNATVVGCFEEQFQFSVAGSPTPVILTIKGRVTGP
TLHFDVDELDFGDISFGFPFTKTCRLTNTSPEPLTFKLRVSDDGTQPAVSSFDQIRSDSDPSWRKGIHFVVEPREFTMNP

```
SQGTILPQGHQDIEVTLCPNTVMEFCRKLLVDLEEIGEGVASLIIQARCFVPKLQVYPPILCIDDCRLKVPFERTLFITN
NTHLPGCYGLIPQKRKEDSPVFYSSPKPCGIVQPHSTAEIPLVVKVQTLGKHRTRVRIGVFGDERNPLGIQLQSYGKLSE
IYPSPRLIEFGMIPVLQPNSQSFTLFNEGFLPRGFRMEIACKPHCYVIEPREGVIPARGAVPVTVTATLDDTGVFDDAIR
LFIGNSLGSTFMLQALGTGTTIVIDKPFTPELNLGYQFSLLPCIRRFKLTNGGHHFHRLFWKVECNSPAEEEGQSTSALS
SPKAKDDSQSPKRPCPVFGLEPPSMHLQPGESVDMVLRGFSPVPQVVRDYVRCEAVIGTGSVTKKIIETIITCEFIDPSI
EVSTRQFSFRVEKKPSDVLTLHYQPLTIKNTCSLPLDLMLSLERPFHVCNANRQPLPDGQPVTVDVKQTCHLYIAFDPAY
KLDFNSWKEKKVLKIEMVRGHPSVEQITLWGEVHFPNLQIQPSTLEFGCVMAGTEEVHSLEMTNCSSLPVKYHWAFQTDS
QANGLTYELHPLKFKPEPPKGMSIYVDHPATQWRRFKIRNVEEPATTLEESRDLAQSPGAEVPPHTREKRYIPPGLRQFR
YSMDLPHKVVKAFSILPLSGVLQPGERQQVSLTFSGRLNTIAGVRALCCVEGGPTYKVELTGGASRVSYSLSPRKIDCGL
QIFNEIHHSTVTLENTCNVKFNWVINPSTADRHLPGVFLVNPVIGSLAPGKKQVLNFSYMPVLPGAFSRTYLLQVGDLNP
ESISLKGEAFFPMITVNLPWNIKGNEKYEKSPKQLGKPLQQYTGRNKSVVGKKTQTPKTQTLKIQNLKTQNQKPRLLGSG
IVPDNQVQVEMVKVLMEKAALELQQKLTSHLPKNRFPNKQLCQSLLKVELPEYVLDMGSVLKGCTERRILEITNPAQIYL
SFQMGVSVLQDTGFSVDLDQVKGLPPRQSMEFDVSFESARWPQGDVDVLLPIKVAECLTYNIRLHATVLELSLNISKSTL
EFSDVLVGQCQLETVRLYNWFQVPCKWSITAIKPVMKKNQRKYTTPDGRQKQLALKHELCPFKVTPSEGTLDAGSWQNLQ
IQFTPKEERSYKKELKFKICGSSNHLKLHLSGQGLEPRLEFSPPALEMGWVLVDSDGVEATVVVKNPCNFPIEFYSLDFD
EQYLEEEKILRMAVGSEYQKNFFMPPRAVGGTLPPELLEDYEAQKRPKAQRAGLKAVAEAEATAEAEAKAMGKAAPAHHR
AVPLYAEPMVKATGNPISRAVMRHLGIDPSSERREARQQKGIVVVVHGPPRAGKTEIAAALCRYYDGACLSIDTVVKEAI
ANDGSQAGLCARDLCTKAAMELKGKEEGYAGKKLQLTAQTSEEKINENAKGKNPPAKKKKEPASKPDIQDTKWSTLQFTV
STAPAPQQLNITSSCGEELNCLSCVLPEDVLVDILCERLKEEEEEEEEEEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEERGGGGGGGGGGGGGGGGGGGGGGGGGGGGFGGGGGGGGGGGAVSPCVQWLTYSSLYSQCKDCYKGAVFDGLE
SLFASSLESSLLCVLKAVKNRRHIFVVNLHQDYASWKAKDEAERQRKEAQREKEGCVGKSCESLQLTQSSQAYLQSLKVS
PLVCAKELQREEALQRNIERVSQMDEDEYDALPEEEKAEVDKILLEWNRMRRERELKRLAPKLEEKAKALEEEERQKKEK
KGVSLEKQPAKPEKGKTKTPEKKETKAPEKKAKPPEKKETKIPERKETKAPEKKGNQKPREEGNQKPREEGNQSHREESQ
ASREEGN
```

2058 - 2077:	EEEEEEEEEEEEEEEEEEEE
2059 - 2078:	EEEEEEEEEEEEEEEEEEEE
2060 - 2079:	EEEEEEEEEEEEEEEEEEEE
2061 - 2080:	EEEEEEEEEEEEEEEEEEEE
2062 - 2081:	EEEEEEEEEEEEEEEEEEEE
2063 - 2082:	EEEEEEEEEEEEEEEEEEEE
2064 - 2083:	EEEEEEEEEEEEEEEEEEEE
2065 - 2084:	EEEEEEEEEEEEEEEEEEEE
2066 - 2085:	EEEEEEEEEEEEEEEEEEEE
2067 - 2086:	EEEEEEEEEEEEEEEEEEEE
2068 - 2087:	EEEEEEEEEEEEEEEEEEEE
2069 - 2088:	EEEEEEEEEEEEEEEEEEEE

A0A3M0K7T4 **A0A3M0K7T4_HIRRU** (265 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MEGLSVGSVLLTGCDGGLGLALLKGFLEQPSPPRHLFAACLDPQGKAVNEVALGFPNVVILPLDVTDPNSIKAAVGKVRE
AVGSAGLNLLVNNTSATRRSTLATETAENMSLVYATNTIGPLQTSQAFLPLLKEAAEAEGQREMSCSRAAIINISSILGS
IEVAEAWEERQDISYRCSKAALNMLTKCLALEYGSRGILCVSVDPGHVTPPLEQGMESPLGMKGGEEEEEEEEEEEEEEE
EEEEEEEENVPPLMPQCPWTEEPKP
```

226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE

A0A3M0K900 **A0A3M0K900_HIRRU** (124 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MEFQPRMKAGHLCWANINFIESKVIKMQLGLCPGGGEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERRKKKK
KKKKKEEEEEEEKKKKKVEVEVEVEVEVEEEEEEEEEEEEEEGS
```

40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE

51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE

A0A3M0KBA2 **A0A3M0KBA2_HIRRU** (314 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MPGTVCDPPKQRIIAPINMEAYKVGLKYELMTIITKPGEEKVQCDLIVTVLDVKELTGNMERDCLQGVTGQGGIASCYTG
WLLIGSQFSGCSHKERLTPQKKTKKKKKEEEEDKEEEEDKEEEDKEEDEEEEDEDEDKEEDEDEEEEEEEEDEDEEDEEDEE
DEEGDEEGDKEGDEGDEDDEDDKDDKDEEDEDEEDEEDEDEEDEEDEDEEEEEEEEEEEEEEDEEEDEEDEEEDEEDEEDE
EEEEEEEEEEEEEEEEEEEEEEEEEEDEKEEEEDEDEEEEEDDDDDDDDDDDDDDDDDDDDDDDPGWIMVVAVNSFP
```

240 - 259:	EEEEEEEEEEEEEEEEEEEE
241 - 260:	EEEEEEEEEEEEEEEEEEEE
242 - 261:	EEEEEEEEEEEEEEEEEEEE
243 - 262:	EEEEEEEEEEEEEEEEEEEE
244 - 263:	EEEEEEEEEEEEEEEEEEEE
245 - 264:	EEEEEEEEEEEEEEEEEEEE
246 - 265:	EEEEEEEEEEEEEEEEEEEE

A0A3M0KCD7 **A0A3M0KCD7_HIRRU** (92 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MELVEGLEHEPDEEWLKELAKNGVEEEEEEEEEEEEEEEEEEEEEEEEEEETPPKILHPALIYLHTKTQNYKFLPCDKLN
YYFKSLLLLIHL
```

25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE

A0A3M0KE31 **A0A3M0KE31_HIRRU** (77 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MKKKKEKKEKRRREGEERREEKEKEKEKEKEKEKEKEKEKEKEKEKEKEEEEEEEEEEEEEEEEEEEEEERRYVAAEA
```

49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE

A0A3M0KFN9 **A0A3M0KFN9_HIRRU** (215 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MSSPGAHEGEGEGEGEGEGEEEKEKEKEKEKEKEKEKEKEKEKEKEKEKEKEKEKEEEEEEEEEEEEEEEEEEEEKEKEKEK
EKEKEKEKEKEKKEKEKEKEEEKEKEKEKEKEKEKEKEKEEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEERRRRGEGGGGGG
GGGGGGGEEEEEEEEEEEEEEEEEEEEEEEKQALRVSKVSSPDLLCSVQQKVAFD
```

123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE

169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE

A0A3M0KFW3 **A0A3M0KFW3_HIRRU** (161 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MMEMIALNVCGSSKKPSNYNRKKKKKKKKKKKKKKKKKKKKEEEEEEEEEEEEEEEEEEEEEEEEEREKKRRREEEEEERR
RERRRRKKKKGRRRRRRRRREEEEEEEGGGRIFYNDDDDDDDYIEYFYLRMPKFFCDRANFSFLPGREGLSSGSFVLRGK
G
```

42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE

A0A3M0KHK2 **A0A3M0KHK2_HIRRU** (102 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MAFHLHCPYLGVVSCTCARQFPYWRAPGNNFGVRNSFCVKNLRLPAAVGYEPADRRFGLACQLLAQCMAEESEEEEEEEE
EEEEEEEEEEEEEEEEEEETK
```

73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE

A0A3M0KHR7 **A0A3M0KHR7_HIRRU** (461 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MSTGGSVDLAMPGVLLICNGNSALAWNFPDWIWRSYGSALSAWGGVGSWETKPCSPWEGIEKRFGTEIYHFLPVHVFART
SALGLDSKVVKREILFDVSIRERRQDWWEGIVTCGNTTQGIRKRTDRVHFFEEKCGFNPNGDMKELPCPEELEDFGPLPL
FISLSFAMLQKLFGEGKHKVWKPCTMYLLDQNYNSGCLFKTEGPTLAISIRNSNGSEEIFSKKLKADFYIKPSPPENVTF
FWEEDTVAVSCNQPKRNARCLRLELQYKSKFDREWQEWLDKNDHVVFQTKLEYEEPESITEAESQQEDGKNCEKPGPLEE
ITFPAAAENNDGKATEIACLIPVPNKDVQCSALLQKVSAFIFIAVEAEERIKEVLQKLKTESQPWETPANLFLYIKKKKK
KKKKKKKKKKKKKKKKKKKKKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVM
```

423 - 442:	EEEEEEEEEEEEEEEEEEEE
424 - 443:	EEEEEEEEEEEEEEEEEEEE
425 - 444:	EEEEEEEEEEEEEEEEEEEE
426 - 445:	EEEEEEEEEEEEEEEEEEEE
427 - 446:	EEEEEEEEEEEEEEEEEEEE
428 - 447:	EEEEEEEEEEEEEEEEEEEE
429 - 448:	EEEEEEEEEEEEEEEEEEEE
430 - 449:	EEEEEEEEEEEEEEEEEEEE
431 - 450:	EEEEEEEEEEEEEEEEEEEE
432 - 451:	EEEEEEEEEEEEEEEEEEEE
433 - 452:	EEEEEEEEEEEEEEEEEEEE
434 - 453:	EEEEEEEEEEEEEEEEEEEE
435 - 454:	EEEEEEEEEEEEEEEEEEEE
436 - 455:	EEEEEEEEEEEEEEEEEEEE
437 - 456:	EEEEEEEEEEEEEEEEEEEE
438 - 457:	EEEEEEEEEEEEEEEEEEEE
439 - 458:	EEEEEEEEEEEEEEEEEEEE

440 - 459:	EEEEEEEEEEEEEEEEEEEE

A0A3M0KHS5 **A0A3M0KHS5_HIRRU** (209 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MISVGSLETPGAWTWKEEEEEEEEEEEEEEEEEEEEELWGRIIQHERMRVYNATVGKATAGFWYALEKQGMQKTSAHRAPF
SKDTLVNIISLRSCSGPAGCCSAVKGKPCIRGEHIRGGLVTIQLGGGIWARAQQAQPWVSGWMWAKARYTNLCSPQPAPG
HTNVPTVRLCLAWVKLAQFCLNENWFGNQFWKAEPPSVQTDEEEENQCP
```

17 - 36:	EEEEEEEEEEEEEEEEEEEE

A0A3M0KJK2 **A0A3M0KJK2_HIRRU** (76 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MTARGGGGGGGGGGGGGRGRGRGKEEEEEEEEEEEEEEEEEEEEEEEEEEDIWTDGVCLPMSSLHVNDPCFPGYG
```

26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE

A0A3M0KKN1 **A0A3M0KKN1_HIRRU** (134 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MRKKQTVTNMEKEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEKKKKEEERKKKKKEKRKKRKKKEKRRNPPP
PLQKEKKKKKKKKKPKKKRKEKEKEKKKKKKKKKKKRKKKKKEKEKERKMRKKE
```

15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE

A0A3M0KNX5 **A0A3M0KNX5_HIRRU** (107 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MRFLLPSMEKVYGKSIAGGGRSGRSGRRRRIKRKKKKKKKKKKKKKKKKKKKKKKEKEKKKKKKKEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEREEEEEEEEEEI
```

64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE

69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE

A0A3M0KNZ1 **A0A3M0KNZ1_HIRRU** (113 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MLDKAAALGHFTCGKPYGCVGLSLCTVLGRFACGTPYGHAGSSRHGNRKIKEFISWMKEEEEEVVVEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEKKWAHADHFKTLI
```

67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE

A0A3M0KQ23 **A0A3M0KQ23_HIRRU** (69 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MFSVQTWGRGGGRKEKKKKKKEKEKEKEKEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEERESCI
```

34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE

A0A3M0KRS9 **A0A3M0KRS9_HIRRU** (196 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MYIRHIKEEKSIEEEEEEEEEEEEEEEEEEEEEEEEEESKTCVGDNAVTMQYVLYYLFVMINKGYSSVSTVHHYGLAKEF
QPKTKASSHTPPVWSLTLSLLTLVSSCCLSARLHSPFLSLERRSVSHKFNLCNKRVNIVPGACRRHDDFRQAVAKVVTVV
DSGHARAVPGSRGLAWPALQQRQGLVWPGPARPTLE
```

13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE

15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE

A0A3M0KSV5 **A0A3M0KSV5_HIRRU** (77 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MKKKKKKKKEEEKKKEEEEEEEEEEEEKKKKKKKKKKKKKKKKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEIPSAFS
```

43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE

A0A3M0KSZ6 **A0A3M0KSZ6_HIRRU** (167 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MQFNKDKCKVLHLGKHNPGVKYRLGSTHLESSSVERVLGVLVDNKFHMNDQSLSGAKRANRASLAEIKYHNLTRFYSTDG
SIDEYMQEECLHFTGNGEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
SFLLLNI
```

102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE

129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE

A0A3M0KU00 **A0A3M0KU00_HIRRU** (132 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MDLQKSLRSPRLVGLRGRERDKIPKATGVLITEEEEEEEEEEEEEEEEEEEEEEEEEEKEKEKEKEKEKEKEKEKEKEKEK
EKEKEKKMTVTVGQEEGQKTPTPSIFQKTKSIEGFTVQFLPPFIRHSDTDLT
```

33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE

A0A3M0KVB2 **A0A3M0KVB2_HIRRU** (230 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MLSSPPWDPGTGLTGMVQSAWGGLDWTSGTISSPAQEGPGAVGKSPEEDQDDQRDGAALLCGKSGKIGIVQPGEEKASRE
LSDTECEAQSCTLGSTEYENMKAKTEGIKISEEEEERRERRERGEERRKRKREEEEEEEEEEEEEEEEEEEEEEERKRK
RKRKVFFAAGQKCIPLTPGSTLSVTETSLTCQFFSGAKVCAENPKYLGGPESCSFHRELCVNELTLLGWV
```

133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE

A0A3M0KVT2 **A0A3M0KVT2_HIRRU** (271 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MDASPFVIQNIPLALPLSHRTPQWFGRNMPNIASAKGETKAEVNSSLTTWSVTMRLSALQNQWSLKIHLSSLLQTLRLLT
GCSVFHVPLEQTLHTVVSDMPGFHHLKGCAESQFWSWFFPQKSSSKEPGEKESGNQDNRKKKKKKKEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEDEEEEEEEEEDEEDEEDQQQQQQYQAVVIINSR
KLSPWCLFPHTICSHSVLPSWSSSSGVRPSC
```

147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE

158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE
180 - 199:	EEEEEEEEEEEEEEEEEEEE
181 - 200:	EEEEEEEEEEEEEEEEEEEE
182 - 201:	EEEEEEEEEEEEEEEEEEEE
183 - 202:	EEEEEEEEEEEEEEEEEEEE
184 - 203:	EEEEEEEEEEEEEEEEEEEE
185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE

A0A3M0KX93 **A0A3M0KX93_HIRRU** (365 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MDEGMESFISKFADDTKLGTCVDLLEGQRTLQKDLEQLDRWAESNRMRFSKSKCRVLHFGHNNPLQRYRLGSVWLDSAQE
ERDLGVLVPAAEHEPAVCPGGQEGQWHPGLDQEWLSGMNLPSPVISSKNWLRLHFTSDSNHRRKGFNAQFQVKKAIELKS
RGVKMLPSKDSNHKNSVLTQGGDAIASDTCPDPGIPENGKRNSVDSIEEEEEEEEEEEEEEEEEEEEEEEEEEEEAEAA
AESISCFPTLQKLLKILKNVANSVSEAVMNAFSCFFLFSPFVILQKRQQGQMDPYGERRKFALSPLRKKGRELKVRQRKG
SKEGDGSLQPMQRFINFSAEYGESDLRDRKNSQKLEGIVQSALQL
```

208 - 227:	EEEEEEEEEEEEEEEEEEEE
209 - 228:	EEEEEEEEEEEEEEEEEEEE
210 - 229:	EEEEEEEEEEEEEEEEEEEE
211 - 230:	EEEEEEEEEEEEEEEEEEEE
212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE

A0A3M0KY13 **A0A3M0KY13_HIRRU** (539 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MGKMKARRKKARRNQSLRTQRLMGSEEKEKEETKRREYSSEDEDDYERRRKKEEKGKKSKDKKKKKGDKSKKGKIDDNFL
EMYEQELRDYHSDSSNATEDEYNKKKACNVDPFTQLERTTQNQEEVYEVVTVTGDVRGAGTDANVFVTLFGEHGITPKTH
LTSKSSTAFERSKTDVFRVKTNNVGQIKKIRIEHDNTGLNAGWFLDRVIVTDMNRPHLRFYFPCNNWLSKEDGDGLYVRD
LVGSLNPMDVPKINKYVVRVFTGEVSGSGTDADVFINIFGEKGDTGVRKLDNDKDNFEKGAEDKFTLDAPNLGKLRKINI
GHNNKGGSAGWFLAKVIIEDIGNKCVYQFPVGRWFALDEDDGKIQRDILVGGTEATGIVYNVAVVTGDIRGAGTNSKIHV
ILHGSKGLKNSGKIFLEGGEFERARTDLFNVEIAALLSPLSRVTIGHDNCGVSSGWFCEKVVVYCPFTGIEQTFPCGKWL
DEDEGDGLIERELYEMVSLRQKRLKKEEEEEEEEEEEEEEEEEEEEEEEEKKKKKKKKT
```

507 - 526:	EEEEEEEEEEEEEEEEEEEE
508 - 527:	EEEEEEEEEEEEEEEEEEEE
509 - 528:	EEEEEEEEEEEEEEEEEEEE
510 - 529:	EEEEEEEEEEEEEEEEEEEE
511 - 530:	EEEEEEEEEEEEEEEEEEEE

A0A3M0KYC8 **A0A3M0KYC8_HIRRU** (113 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MRRSDCSAIQKVSNNARFEGGQNPKAGPQLSKTVHNQLITVFLAHNKCKKLLVSCMETIWMEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEELSIWTHPRQCLLFMQCTLGL
```

62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE

A0A3M0KZW3 **A0A3M0KZW3_HIRRU** (96 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MPEAGRLDFDVSHSQTAEAAVVTLRDSQTQKSPFFSFTKEVTASEGKKKKKKEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEERMSKDGFKA
```

53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE

A0A3M0L0H2 **A0A3M0L0H2_HIRRU** (1136 aa)
KRAP_IP3R_bind domain-containing protein. *Hirundo rustica rustica*

```
MEQPPAAEEWQGATQKRKAWAKSRDSWQASEAEDFSAAALARGEEEEEEEEEEEEEEEEEEEEEEEDVGGGELPLAAGAG
MLVRNGGSFEDDLSLGAEANHLRSDTQTETCNGVLAKDRRLQFHQKGRSMNSTGSGKSSATVSSVSELLELYEEDPEEVL
YNLGFGRDEPDIASKIPARFFNSSSFARGIDIKVFLNAQIQRMEVENPSFALTSRFRQIEVLTTVANAFSSLYSQVSGTP
LQKIGSMNSVSSSKEASSPPPLNRSNTASRLIKTLSKLNLCVTQQADGSSSSNQLLRTASQHSDSSGFAEDSTDCSPFNQ
LQVQESLQGMGSSADSCDSETTVTSHSEEQKTPIAKELPCFDKFEEEEEDDDEEDYDDDEEDIISQVERRKVGGSSESRR
SEDRKISDCETEQNQGQESKSSHLSETVQGEVSSKEEDISSEQRESDLLEEGNVFEFPQYHTHHILKSMQSLEGGGSSTS
SVDRVQVALKRAEMRIISSPDTKARCTLLKSKDLLRKQRLWFAESGYPLRRSQSLPTALLNPVKVVSSVNVQLTPGKETL
CSPPSFTYKYTQEEEEDKRAASEKDRSEDEAASSHPVCKSTLFIAPSSSKKEVPQAGPSRLSEELSPTRVQSCPLHTPAM
SQSTCSLHSLPTEWQDRPLCEHMRTLSTHSVPSISSSSFGAMLSPFSCPFFPRHGVPHRPLAMNPPSTVEMQLRRVLHDI
RNSLQNLSQYPVMRGQDLSAATGYTTQRSSILPLYENTFQELQVVRRNLNLFRTQMMDLELTMLRQQTTVYQHMTEEERF
EADQLQSLRKSVRMELQELEMQLEERLLALEDQLRSLHMSSPYRPQAHIGMYGSRSADNLSCPSPLNVIEPVSELIREQS
FLKSELGLGLGELGLETLPAEGTESIFSHGNSDSSSVCSGHTGRKAKSQSKKLYRASVALTPAAPVRAGTGQPVESPEEL
EDSKPEVEHKLEKVPLMPSVDEIHKAVEQEELQQVIREIKESIVGEIRREIALTCQMSPGNSSRGEEAVPECAEENSLTH
LVTVMFDKLKREKDMSSSQNKASSPWIRKRRPTPASLVIMNEHMPPEKDEKRTNISQAESQSASPKQRKQSVFTPPALKG
SCEKENNRNCGLGIRP
```

44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE

A0A3M0L191 **A0A3M0L191_HIRRU** (94 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MYTYQPSIIFEYFSKRTGEKEGEEEEEEEEGEGQQEGEGEGEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEERRRLD
DSSSVHSVFLCLSA
```

50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE

A0A3M0L2M3 **A0A3M0L2M3_HIRRU** (1097 aa)
Integrase (EC 2.7.7.49) (Reverse transcriptase). *Hirundo rustica rustica*

```
MSSITENGDVTAGKPNEEKTYKKTASSAIKGAIQLGIGYTVGNLTSKPDRDVLMQDFYVVESVFLPSLVKIYNNWRFTCG
LKPQKVPQKLEEPLGEHMAEESHTVHAAVGEAIILHYVDDVLMCAPNDDLLSHALDLTIDSLVAAGFKLQEEKIQRMLPW
KYLGLEIGKRTIVPQKLVVRNNIKTLADVQQLCGSLNWVMHIRSHTDLPGFIADGNRRADALAVPVEMAPLPDIFGQAKI
SHQLFHQNAPGLVRQFHLTREQARAIVAMCPSCQQHALPALSAGASPRGLKSCEVWQTDVTHIMSFGRQGYVHVSAYICS
GAVYASAHTGEKSSDAMKHLIQAFSFLGIPKSIKTDNGPTYTSKEFRSFLQQWGAEHKTGIPYSPTGQAIVERTHQNLKR
VLSQQHQSLKLETPQIQLSKALLTLNFLNCTFENLNPAVVCHFRENCQLQLKAKPPVMVKDPATRETKGPHDLITWGCGY
ACVSTPPGPNEGSNLTPAHHYPDFRFKTYAPLAFRYFRELFGIKPDDYLYSICSEPLIELSNPGASGSLFFVTSGDEFII
KTVQHKEAEFLQKLLPGYYMNLNQNPRTLLPKFYGLYCVQSGGINIRIVVMNNVLPRALKMHFTYDLKGSTYKRRASRKE
REKSSPTFKDLDFLQDMHEGLYFDSETHSALMKTLQRDCRVLESFKIMDYSLLLGIHILNSNMKEKGECSQSASDTKRHG
GQKVLYSTAMESIQGPGKSGDSVARETANTMGGIPAKSYKGEKLLLFMGIIDILQSYRLMKKLEHSWKALVYDGDTVSVH
RPSFYADRFLKFMNTRVFKKAQVLKPSPSKKRCNSITALKAASQEIVSAVSQEWKDQKHGILAEGQSYASLDEEVLGSHH
RPDLVPSTPSLFEAASLATTLSSSSLNANEHCQRDPPTLYSSSKGLPSSSTFTLGDSAIYLTSEQSTLEMENDNASVLDV
YLWHTLAGRATFQRQEQAQRLGHKNCVKFNQEKCRVLHLGTQNQESSQTRTHELWNSLAKRSPGVSVDNTQTPEEEEEEE
EERRRRRKKKKKKKKKKKKKKKKKKKKEEEEEEEEEEEEEEEEEEEEEEEEEELCSR
```

1067 - 1086:	EEEEEEEEEEEEEEEEEEEE
1068 - 1087:	EEEEEEEEEEEEEEEEEEEE
1069 - 1088:	EEEEEEEEEEEEEEEEEEEE
1070 - 1089:	EEEEEEEEEEEEEEEEEEEE
1071 - 1090:	EEEEEEEEEEEEEEEEEEEE
1072 - 1091:	EEEEEEEEEEEEEEEEEEEE
1073 - 1092:	EEEEEEEEEEEEEEEEEEEE
1074 - 1093:	EEEEEEEEEEEEEEEEEEEE

A0A3M0L2V5 **A0A3M0L2V5_HIRRU** (993 aa)
Bone sialoprotein 2 (Bone sialoprotein II) (Cell-binding sialoprotein) (Integrin-binding sialoprotein). *Hirundo rustica rustica*

```
MRSVLVFVCLVGMACAFSVKSWLRRPKLDDSEENAVFKSRHRHYLYRYIYAYPPQRRYQGSDSSEEEGDGSEEEEGGGKG
CQGILKGIRQRTASKGEDSENEDSDENEEEEEEEEVDENENGVNGTSTNTTEGIGPHGNGTAVAEEGTGEAEEEEEEEEE
EEEEEEEEEEEEEEEAEATTIASTTNEEGLTQATTMDDGAPTDATTDATTAGELWEYDVTARDHGRGDEGTTEAGYEEQDE
YARGDSYRAYEDEYGYYKGHGYDVYGQDYYYSQFHRRCLGELLGTVWDSTGYVSLCHLLGPQWILLKGCNAKHGFYIFKY
VYSFSTRRNQTQIKKEEADHQSIIPGHRLDEDNARREPPEAGTAPEHGANSSTEVIEYGIVLKPQNRSTPGISRDGPSPR
```

```
PGTGTRARGSGGGSGPTASSSEGSGDLDLVLEVDGGAPILPQGERPSEVAVGNRSSARSEDKDDGAPRVVPAEGATTAGR
SRAPTTRGAGDVGSREATVSGQGQEGVKHGTGTGGIASSSVTEKMEDVQVDAAGVDEYAYVPDSGSVTITRGSLDGTDRA
TGFTQVSPDKDDEVNIFIGRANIHVGEQESTQAGATVGSEDDGIPSVGTSSPLPRPDITAARSGGEDDSIPARRQPERLA
TTARPSRGDRVTSGLRDGRLTGEDEEGATTIGVDRRLVTPAPWRVTSGDITIPTVAGIRRKDDDEVRGEGQRSKGKPDHV
AATTPSQWGDVEAAVTVPAEGAGIRPATTEGGRITPSVTASGRKAGTGTVPGRGGSGEVGTATSRPPRVEARPGTGVKVR
PGGAGPDKAPRTDKAPSPSGKPGSWASSGAQTSAGGHDGDAGGTSHATKAGASPAPQAGQDAGSVAAGKGREPGRGAGSG
TAAPGAGGGRLPGHHGRRLGAGAPGTIATLGRSRQLDQVKRADELHVRERAFYSLGGAGGGPHGPYPGLGSADSSQSSEG
DRGSHSESGQTGLQPSGWGSPGYPQGRWIQGPL
```

152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE

A0A3M0L2Y2 **A0A3M0L2Y2_HIRRU** (96 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MQLLHQAHYPNVFVPMSQQKEEEEEEEEEEEEEEEEEEEEEEEKKKKKKKKKKKKRHHPKSSISLSSISILKTQNYNFHPV
TNYTIYFESLLLVIHL
```

21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE

A0A3M0L401 **A0A3M0L401_HIRRU** (704 aa)
Integrin beta. *Hirundo rustica rustica*

```
MEEQPKIAVGLSTGATPSVSTQILKQNQGRETLYSLPTAVPAEPLLCKFADGGQKKRQNQNKYIQNGRAWHREGEAGMTL
TYDPTTAALQNGFYPSPYSITANRMITQTSITPYIASPVSTYQYMPATTAMQGAYIPQYTHVQTAAVPVELNKLTSFDSF
TAIQRDIWRTEGMKNFTDSSGIHGRCDTPENLLSKGCQLNLIEFPISEVEIHRNDPLTASSQRNSSDVTQISPQKLTLRL
RPGHEETIQIKVRQTEDYPIDLYYLMDLSASMDDDLNTIKELGSTLSKEMSKLTSNFRLGFGSFVEKPVSPFIKTTAAEI
NNPCRSVPYECLPTFGYKNVLPLTNDAEKFNEIVKGQRISANIDTPEGGFDAIMQAAVCKEKIGWRNDSLHLLVFVSDAD
SHFGMDSKLAGIVIPNDGNCHLDHNNEYSMSTVLEYPTIGQLIDKLVQNNVLLIFAVTNEQVHIYENYAKLIPGATVGRL
QKDSGNILQLIIAAYQELRSEVELEILGETEGLNLSFTAICNNGTFFPHQKKCSHVKVGDTAMVIVTVGNASATVDGLVN
TVIAQLIPAPALLRMGRCAVGEVNASAGHVLAPIQGLRAKYVKDALSAVIPAVPDDYSEDKSISCSLQGENECITTFLLA
VDEQGRTIIHGIEQKVDLTKTKTKEEEEEEEEEEEEEEEEEEEEEEEEEEVSYRRHSSLTSP
```

665 - 684:	EEEEEEEEEEEEEEEEEEEE
666 - 685:	EEEEEEEEEEEEEEEEEEEE
667 - 686:	EEEEEEEEEEEEEEEEEEEE
668 - 687:	EEEEEEEEEEEEEEEEEEEE
669 - 688:	EEEEEEEEEEEEEEEEEEEE
670 - 689:	EEEEEEEEEEEEEEEEEEEE
671 - 690:	EEEEEEEEEEEEEEEEEEEE
672 - 691:	EEEEEEEEEEEEEEEEEEEE
673 - 692:	EEEEEEEEEEEEEEEEEEEE

A0A3M0LBD0 **A0A3M0LBD0_HIRRU** (75 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MLGDSPALSRAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGGHVSRGLSPCPGIPSLLEGPARLSSPGPGPCP
```

12 - 31:	EEEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEEE
14 - 33:	EEEEEEEEEEEEEEEEEEEE
15 - 34:	EEEEEEEEEEEEEEEEEEEE
16 - 35:	EEEEEEEEEEEEEEEEEEEE
17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE
22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE

A0A3M0LDU7 **A0A3M0LDU7_HIRRU** (69 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MGILGWKLLRFDGKMKEEEEEEEEEEEEEEKKKKKKKKKKKKKKEEEEEEEEEEEEEEEEEEEEEEEED
```

45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE

A0A3M0LFT2 **A0A3M0LFT2_HIRRU** (201 aa)
Uncharacterized protein. *Hirundo rustica rustica*

```
MEGIGIGIGILLGPELALGKGLGAAGRVWGEAGEGPGSADSAREEEEDEEDEEEEDDEEDEQDEEDEDGKEKDELDEEDE
DEDEDNNDEEDDEDEEGEEDEDEEDEDEEDEEDEDEEDEEDEDEEDEEAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEGSILENPLEAHEDREGRKIPGCSRLEWRGGAGRGQ
```

130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE

A0A3M0LNG9 **A0A3M0LNG9_HIRRU** (479 aa)
Reverse transcriptase domain-containing protein. *Hirundo rustica rustica*

```
MICKLESQGVVSKARSPFNSPIWPVRKSSGEWRLTVDYRALNEVTPPRSAAVPDMLELQYELESKAAKWYATIDIANAFF
SIPLAAECRAQFAFTWKGVQYTWNRLPQGWKHSPTICHGLIQAALEKGEAPEHLQYIDDIIVWGNTAGEAFEKGEKIIQI
LLKAGFAIKRSKVKGPAQEIQFLGVKWQDGCRQIPTEVINKITTMSPPTNKKETQAFLGSIGFWRMLIPDYSQFVSPLYL
VTRKKNDFHWGPEQQQAFVQIKQEIAHAVALGPVRTGPDVKNVLYSAAGNNGLSWSLWQKVPGETRGRPLGFWSRSYRGS
EANYIPTEKEILATYEGVQAASEVIGTGTQLLLAPRLLVLGWMFKGKVPSTHHATDTTWSKWIALITQRAHIGNPNCPEI
LEIITNWPEGETFGLSEEEEEEEEEEEEEEEEEEEEEEVTCAEEAPPYNELPETERQYALFTDGSCQIVGANLKWKAAV
```

417 - 436:	EEEEEEEEEEEEEEEEEEEE
418 - 437:	EEEEEEEEEEEEEEEEEEEE
419 - 438:	EEEEEEEEEEEEEEEEEEEE

A0A3M6UF38 **A0A3M6UF38_POCDA** (2306 aa)
Poly [ADP-ribose] polymerase (PARP) (EC 2.4.2.-). *Pocillopora damicornis (Cauliflower coral) (Millepora damicornis)*

```
MPFSKKSQDNEYAQLSFEDDNSIQEKKRNPFSPQKNTELESCVRRKSFTDVFEPGKEVQANSVKVLRTTSCDRISGTQEI
SLSFDVVPEQVQLALEKSPVLLPSPPKRDVSDAATKILYNYAGQIVSNDDVIVTLPVKTEESVDVSNFDSVRSIDAYKID
GGSVKGDSPSIGHQSVTKAGNNGHSDTRNSVDIGGVSMTCTDNIDRSGQVVSSTGGNKNVGSTEACKNGENCKSGIELNE
TNSPAMDESATVNLKLAGSHHAFASDTCDRKNIGNVDFREVQKCADSCLDNTGNITAVKNNTHASLETNDDRNDGDAVPF
ALVESVSIGSFAHTRGLEKDESGTENVRNAICVSADNEITPVIDRNTIGDNDFEGDFIITGLSARAIGQVSGKDANSSPK
SSSNSNSHRGGEFHSSAETGIESIVPTDGKLRSGKYSSNTFEYDGSGGREIVHEGTICAKFNDVQSSRALNVEVDHENMR
NVHPALEKCDCYGSGDVCYSLEEGVKDEYGIDDSYADFCFEDYAKHTSRTDEIPEDTDDDDTYADFCYKDYSKRNSKTDE
TQEGGDDNDGCADLYFEDYAKQNSKAAKIQEEKEEDIEEEEGDEDEEEWSWFDSCTRKRDNFADEELGGEGRADEKGEKK
DKEDQQDDNDGDDGGKDNGDEMEHEQEKIRGKDYGIDDHDYISVNYVVEDDMEDEEDNEGEEAEYEEEEGEEEEEEEEEE
EEEEEEEEEEEQEEEEEDDEEEEDEEEDEEEKETEEEEEYDDDDSDDYEEVQKELEKKGEEKKYVEEDDFTNWWYDGDEV
YDDLYDYESELVCGQDIKGYESNTSHLRNSIIYSSHHVESNVHSSVSLTKPSWQVYDERSENLKRELFIDARARHEESFS
ESQFIPGDPDDASLPHLLSSDSEAYHTDAFLVKGLNTRTTKDALLNFFEVISGGQVKEITSLNEGTTLVTMEFPIKDIAK
```

```
MKEKCGGRTLDGSKIIITPASPCTSVIVSGLSLDTSHDFVKLYFESPRSGGGPVDTVHFTEKRGQAVVVFNNAKDMERVL
ARQTERPHVLDGQDLIVTVFHGLFPNLDQEDIVGHVDSSPPRDRSEQYIATKQPIQTAKQTLCLAVNPDVMEFIHNSLHF
NDLQDLLEKRRCDLDWKAGGKHALIQCNGDPEGNCCPSLCVDEVQAFLEKFVQWHVPIEEEIWNSLDSGSLANVCDFIGD
DPPLVKISEGNSGFYLRMVSLRSDKESHEEIFQEALSHIYQLERKQNYRTENIPNVPKERIQLLKKTNFEDKLEEEFEDL
IVRIDDESDEILFKGPTDEVTDAITRYCMLNAEVTDKKLQFPPYILQVLNTDTALQAIKDEMAENEADAVFVLEEDESTS
RVVAAKVTGISSEQAEKAYNLIKRFTAEAVLKIEDQDLVLTTTPEWNQACDEIEKDGTVAIRRDETGRTWLGGLSRDVEF
SIKKLQLFIKKRAVKISRKNFLCPSKQIKRYLREHCKSDFIAIQTKYDITILDGQAGDKFIISGRDDGLNPASHMLDRLI
EGFVTKKLELRQAGLGKFFSDGKADNLVEKIEKDLKCVICIEKTMAKIRTESLASKTALFESDSTESEDDEVTEDNSALS
LVKQSSASFYVTTQGHSISWRAGDIVKEQADIVVASQGACARSIRRAAGPRMRLVTPNPGEIEVSPGFQLPCTHVIHTYC
AEWNGGNGETALGSIVRKSLRKSDELSANSIAFPVIGTGNLLFPKRKASRIMLDEVVSFCDNNPHSSVKDVRFVIFDQDQ
NLITAFQQEMSSLQLRCGSVAKSGNTVEAQTWWKKIEVVEGNLTEQRVDAIVNIIGKDMDLSRAGALSKAVARAAGGRVV
RECMDLGPQPGGSVVMTSGGNLPVSNIIHLVPRSSDKQHLKACLEKCLYLAHSKGLHSIAIPAIGTGAYQMTASDSALLT
FQALGNVGVVCSSFSRIKIVIFVKEMLKTFVKEHKRIEEAFRKKSPNVTVGLRGDQFQLHFRDSTGKGSLSGEKIKISRK
VVGTSDAGGISLPNHWEAMPKEANGNEITVHTVKLQSQSSEFQGVVQMFTKTMNSVTVKRVERIQNPLLYQAYQLRKQKM
DKDNGGNNELQLFHGTAYNNVKKINSQGFNRNFSGLAHGTRLEMLLSPCGSPPRELITVDTCTLRVSWLEGIVKEIHMPI
KGEMFDLSSISSKILHKEFCSLTSVDWKEVYLLAFNVTLDTKFRVFEYKLLNCIILQLIIFLNSRFLIRHFVTSERLINS
PPSILLFFCKTTDVFWKEILSWPAINKNVIVFHSLMFCLVNLTLKTLLLLAKFHISSAGVRIFRSF
```

711 - 730:	EEEEEEEEEEEEEEEEEEEE
712 - 731:	EEEEEEEEEEEEEEEEEEEE

A0A3M6V1S9 **A0A3M6V1S9_POCDA** (337 aa)
Uncharacterized protein. *Pocillopora damicornis (Cauliflower coral) (Millepora damicornis)*

```
MPNERGKKLLLETTVVFLVHKSGAGDNVHHHMYIVFLSRYCTKMYPIALMLLCPLSSVCPEAWIPHVLVSSCGPPVPNPI
LESTSRQLFWLLAKIPILALEALLFQNALSGSRLNPSLLQEPCTPISDFHVSRPNEVGRYCPSAISEYRESAFVLMRMNL
SSWLIFIPRQILEKEVFHYSDMKIRNIYICKINNNKEKNSGDEEEEEEEEKEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEDEEDEEKEEEEEEEEEEEEEEGGRRRRYRKMNDYKTNEDPFTIITDTVWFHETKQFTQFSVLNTMNSNQMVS
QALTFNSISGVEYQMAA
```

212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEEE
219 - 238:	EEEEEEEEEEEEEEEEEEEE
220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEEE
225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE

A0A3M6VSR6 **A0A3M6VSR6_9STRA** (2435 aa)
DUF3677 domain-containing protein. *Peronospora effusa*

```
MKRGRVATRGSTRHALRRKNVVVDEDDEEEGEDMRQEEEEEEEETKKTPPLKLTRAQTRKQEEEAKKNRKNGRKKRKEER
EEEDDEDDEEMEEDEEEEEEEEEEEEEEEEEEEEEEADVEERHRGTRERGSNKPQLRGTQRPLRKKQRCKIIVSEDEEEEEE
QEEQEEQEEQEEEEKEEEEEEEEEEEEEEEEEEEEDDDEMAKKETPQKRKMQMRNGEKMAMLGRKTRAKIAAASGSKHPTKI
VRRQIQKKAEESTESEGQEEQSQEESAKSESKEEDKLGSEPSSAATTPSSSPAKRKGLSINTLVNDADEEEDHVEQADVS
MTLAPASALNAGTKNATEVPDQHFREVLSKATSAPKLMERFKHPAMLKYLLRLLRSKHYIGMKDSSEHGTTTSLVPGHLP
GPAEYIHLSLPVLVTNLLVQIMKDLDEWPIDSVKVFLDDSLYSRVWVDHELSQLFVQNVKTVLEMESGGQQFAQPLVRQR
FQGVTVMQEMRELITTHIRSRLVELEKERSGSVGGAPGAGGNYAVRNMIMTLAECASIPQVRLFGAENLEAWLQNPSVKG
PAKELLNKIVSLCKSTSSIDTATVDLLLKLKLKSTMFQLKVEAITHIVCNHPVYLKRALSMFIAQERPNNMSRDVDNMKM
LQHIFRASRSTSASSILGSSDDLFYRRPIEHQGTLASRELARVFREMASISDVTPVLKTIVRKILKQLTFEQVDIKALCV
GILDNDGHWDALAGDARVLDYMGLVTGVVWLILLMRGAAVKSLQIQQSNAANRQSTGSATLASSGLKHGGTQAISRRGAN
PPLPLSRANRLGPLKAKQSLSKSSLSSSHAAVGSGFSVPSSQGRSGNNGSNGGGSVVSEESKTVKISVWAKDELQQALAF
VQREAILCCRDVLTHFGLNGDSPFEKTLYEGIVKKLLFLDIPPDVQPTEHDRTCFQATQEDIPVHPDSLELLTSLYNSCR
AIDRMEALRTLETVVFRGAEAHMHRETLWRHHADELTSYTQNGGVLGIEVNGSQFVQHLLKLALWQGGGDKQEQEFCHSS
RFWICCSILLVVGCFNPNTVGAFLWEEFPTLRGLMQMVITERYTFPAISTPDPLLLGKHGATFPDLIQGNIQLRDYEQQL
LQLNQADLSVTGDPLMLFDASGLARQPPPAILDHLRTLDRKFKLGMRLRQSRKKDFLMEMVAGSDAKNELQNANPAGAAA
SSAWWIADLVCEDFNTMQYLPHECLCQLLLLALRQSNPNNHADLQGQVSLNQPALIQITPRLLKKLRDYLADDSSSSSNV
VLFYLECLNSRELVTRRVASRILYLLTAPGSVDDVSVEIREVVVTFGPESNLSFLWLYELEKFSCYSSIRNKIFRCLENL
LELEASIPSLGTCMKALHDFSKNGSDISPSMNSSENMKQDGDNNPQKITVEQSLLLAGAYGRLLAGRDMVATVLLKDYDI
YAITLEVIWRAIETQLEIAPQLKATLGISFSDCKVFYVTDGTNAIREIKLPLTIIHGAIRVLCSPHAHNELSTFDSNGTA
TCLAKLTQSLFPKPTANTAILSSTGLIATKDPRLYPDHLLIKLAAAASTTTSHLCGTAIRAITTDTLWNLLEQSALSEQC
LEMALRSILETTKKDESKAIASLLAAMKTSDISVAARAVLMQISAYDAMDSLTPDVVEKLKLLREWLQDQCGAKGSMLTD
EDDEEAHLLSEGFTTFKIKASEPSATPHMFTFYAEGMEEVPKVEPTQQPIPERPKTDMTIFQDTYFIPTHHLHSKKDVAA
```

```
SDDSVSLLTGLMKELKRSSSSGSLPAIIAPENFVLATSQALRRSCPTSEDTITHSAADTWSLLMALLHFARSSCSSEAAA
TQLAKALLEVVGHLPTCPSVSHRKECIGFVRRVLDNLSETFTSSYSASVSFIQYLSQASTTEGLYELEDPSVMPDVFAVL
QSVVQFIDRNFAWWKMHGITLRLNAMALHSLVVLVKEVEVLQRLQVNHTGNVYRTCATGLLTSIAHDQGDVSRMLNLLDP
IMTADPHLGYISGIISIHADVKRDLVGALYFQNPTLVAGLLGELNPDWESFVNFDASVDQQHDLIIQDRGLLSQVDDILH
DLTKDGSGVMERFRELTRSHPMLVLLRFPRQLMQHFGTVSLSQLYLKATFFQNILGAMQIMRPYMRHQQSVMKPFCQFLF
EILRVIVDHNAVEFRRLVSHTWEFFYDALEADFDLASDLIFSEPRIVLLESIVNMYESHPETVAFGEVLAQRHNESSLHA
TLESIRTERSKHQSAASQQHQIEQLLTLIESQDSMLASGGKPLPEHTNMTTITQGLQAIDIVCAKTDQGAAAVALLRRCT
APVASLLVTEKVTKAVMATLCQTLLNLMRYDSICVDDVMHYYVQCLRSVRPGLKEAAVNTVLEFLVFADARQRRQILQHL
FNDPSETAKNKLGVYLKSAAFRTTLLVASKKLTQT
```

95 - 114:	EEEEEEEEEEEEEEEEEEEE

A0A3M7DQN7 **A0A3M7DQN7_HORWE** (515 aa)
Uncharacterized protein (Fragment). *Hortaea werneckii*

```
MSTLTPDPDPSPNPQPDNSNTWAFPGPSSRFHTRERIRPRREVKSTYTPIAPNLSTAQRAHHKRAQSAQVVPLAKRSQGE
ESAGPPSPPASESARRSPYLARYSSWTGGESPSLLRGRRRRTSLAMSSAGGMMTPARRSGGEWDKRLQDSPFSDYFTDDA
RSVDTSAGKSSRHSGVDGGAGAWLSEEGQDLLARLGRLQMRVRRAEEGEQEWVRKVVERKVREVERELEDWDRRPGSAEL
EDSGFIDEEGEETGGGSEGVEGLGLHGVSECPEREEVEQEDVSSQKVDSESDLQLSEARQILENVTKAQEELRKRHTELR
LLNDQHLEQLETNETEIETLRSDNEGLRSDLGFDHSELLFLKLQMKAIEVEVEDLDKPASQSQKLATHNQHGEKNIRREQ
ILQEMDQWRNDWQDVNGRLKRRLSRYGVLSADKRDHSLEKELQVRGEDLGDWQLETIRERSGGKVASLTIRRVEGAESAA
NGVVEIQAELGKAEEEEEEEEEEEEEEEEEEEEEE
```

494 - 513:	EEEEEEEEEEEEEEEEEEEE
495 - 514:	EEEEEEEEEEEEEEEEEEEE
496 - 515:	EEEEEEEEEEEEEEEEEEEE

A0A3M7G795 **A0A3M7G795_HORWE** (589 aa)
Aminoacylproline aminopeptidase (EC 3.4.11.9) (Prolidase). *Hortaea werneckii*

```
MESNQAHPSHLSIRLHVDGPVNKYPAKAHARRVADALAGSSSFDISGDLIVVTAAQSRPWPDSDMPAPFRQARYFYYLTG
CNEPGCCVVYDIKHDRLTLWLPPIDQSRVVWTGRGSTVEEALDKYDIDEARYLTKSSSPLGRCLDHDEVVYIHDEHNVLP
ATIPRSLRRPVLQNRLKQAMDACRVIKDAHEIDLIRRANQISSDAHVAVFKSLHGFTNEAQVEATYMAHCIASHAKEQAY
APIAGSGPNGATLHYGANTADFDGAETLVLDAGCEVSCYASDVTRTVPINPSQPGTWPSPEAKQIYALVEEVQEACIAQM
RPGKAFIEIVTLSRRMTLEGLLKLGILKGDVDEIEKWGTVAGFFPHGLGHHVGLDVHDVSPVPHPPAIPRAAISPVGHRK
EDGSGEQDGLEEEEEEEEEEEEEEEEEEEEEEEEEDDDDDDDNEWEPTEEEREAETAAHQQLDEYLKHAVQYPIPPSCL
PSWSFHTSPLCFLPEYESSARRAYESLLRPGMVVTIEPGIYFNRSLLEQVFLSDPYHSRFIDQDALDRYWKVGGVRIEDD
ILITGDGYENLTPAPKGREMLEVIRKGAL
```

411 - 430:	EEEEEEEEEEEEEEEEEEEE
412 - 431:	EEEEEEEEEEEEEEEEEEEE
413 - 432:	EEEEEEEEEEEEEEEEEEEE
414 - 433:	EEEEEEEEEEEEEEEEEEEE
415 - 434:	EEEEEEEEEEEEEEEEEEEE
416 - 435:	EEEEEEEEEEEEEEEEEEEE
417 - 436:	EEEEEEEEEEEEEEEEEEEE

A0A3M7GNX4 **A0A3M7GNX4_HORWE** (599 aa)
Aminoacylproline aminopeptidase (EC 3.4.11.9) (Prolidase). *Hortaea werneckii*

```
MKLLDSLPPTIPPEVPHLPKAHPSHLSIRLHVDGPVNKYPAKAHARRVADALAGSSSFDISGDLIVVTAAQSRPWPDSDM
PAPFRQARYFYYLTGCNEPGCCVVYDIKHDRLTLWLPPIDQSRVVWTGRGSTVEEALDKYDIDEARYLTKSSSPLGRCLD
HDEVVYIHDEHNVLPATIPRSLRRPVLQNRLKQAMDACRVIKDAHEIDLIRRANQISSDAHVAVFKSLHGFTNEAQVEAT
YMAHCIASHAKEQAYAPIAGSGPNGATLHYGANTADFDGAETLVLDAGCEVSCYASDVTRTVPINPSQPGTWPSPEAKQI
YALVEEVQEACIAQMRPGKAFIEIVTLSRRMTLEGLLKLGILKGDVDEIEKWGTVAGFFPHGLGHHVGLDVHDVSPVPHP
PAIPRAAISPVGHRKEDGSGEQDGLEEEEEEEEEEEEEEEEEEEEEEEDDDDDDNEWEPTEEEREAETAAHQQLDEYLKHA
VQYPIPPSCLPSWSFHTSPLCFLPEYESSARRAYESLLRPGMVVTIEPGIYFNRSLLEQVFLSDPYHSRFIDQDALDRYW
KVGGVRIEDDILITGDGYENLTPAPKGREMLEVIRKGAL
```

426 - 445:	EEEEEEEEEEEEEEEEEEEE
427 - 446:	EEEEEEEEEEEEEEEEEEEE
428 - 447:	EEEEEEEEEEEEEEEEEEEE

A0A3M7K765 **A0A3M7K765_ASPFL** (1429 aa)
Telo_bind domain-containing protein. *Aspergillus flavus*

```
MDANEQFPTSEPLRASRIPIAQLSPSLEHFSESSIHASVTLLWPYSSSTKSLSLLLAEPDFRLRHSNGQVKAVFHGHIAE
SVAQSHIGIGDSVYLSLNGARLSDNVTAPGTPGRSVAWDMHFDDRVFLEIWRSLNHLSTVKVDPPTPSPNDTTDAPPATP
IAKGYDRSDRNLLIDGLSSWQSPAFLGRSRTALGGLADSVLDHFAEEDGFVPGKGRKRPRFSMRSSEWRVIDEPESPGER
GEVPDWTHIFDEDWGSEPEPGPDGLSETEERPPDATKIKNTGIDSEEVSLTVPASEADVAMENASLASSRTSPERHIAQT
ADGIRLPPHGISGIAEFSRKRGVLNCSAHLPIETPRLHPIPSPGLPVPSPLITMSNSPQGYFTPAAATAHSHTSQIPTTL
SREVTDLENEIPGAQPDTSQTPECKETVITSGTEDRAIGVPEFTSESNSTKITLKATSQPHTMANTGLEGLLPDEDSKAA
AEPAQVHQFTPHISEKDTERLDGHLGDTDQLRSPNRVGNEFELDETCIEAQMKAESEKDKGETHQEQEVVKEDNLEDNGH
TFTRTSKSLVPGDTRASGVAKVVEYGTDGSGEEDTEALERSGHYHDLATQSETYTPETDREHPTGVAHEGENKWERKESE
GESEEELEEEEEPEEEQAQGIKETDREGDADNEEMERDDLEAEWDDEEGWYEEEEEEEEEEEEEEEEEEEEEEKEEEEDE
```

EQEEGEEAEDMYEDEYGDGAESEIVSDQMSIDTPTQPPAMKNVHPEVIVLDSDSEDEATPASQAYPMTTSRDEASTQEIE
SSEPEISASEEGSLRSRRSDNSESSEDEEDENWSDENSEDEQLLDETGGEMMEDERGRANGEQQRAGHAVDELSDNGSTR
GEQVDEDSVDAHEEYQADNEVMKEQPETKRGQVSVSQPMDIRDAGSDTDEPTPQHYQLGHTIRAPFHDSEQRNLDYHACT
MASAQDPHSDSRTTLHEFETVIDPELQNIGLAEEQANKDVEEEHRSDYIYAEPRPEVPAKIPEVVQDIDQGLFLDGTSSS
QASHDSREAVSEKSPQLQHLIPMDTQLAEVDQPSVDFTTTGILPTSEHVQRKTTVQSQGQMPPAIQIGTIAPAERHLNVA
EDVEHEARLVPPQREGEHELEEFSADGDVGTPASFSGDPAQADELYSDDESVGDLDEVHLIGIDRHYPGLHSQLSYLAPL
ATLVDHYNALVDTISVVSEVQPVFRAASGKKDFILTLQLTDQSMAGTTLYAQIFRPSKVALPSVEEGNAVLLRNFRVKSF
NRSIMLISLDTSAWAVFKGLDDKALTHDPPIEYGSEEEACATDLRQWYQETGMAMVADNQLQASINRESREGTPTSSAAL
SDSGSIESTLRDARGESSFSSRGSRRGKKSHRRITIHELRDGRRYTEVGSPSGKESIHELRDGTVYANL

692 - 711:	EEEEEEEEEEEEEEEEEEEE
693 - 712:	EEEEEEEEEEEEEEEEEEEE
694 - 713:	EEEEEEEEEEEEEEEEEEEE

A0A3M7LXK3 **A0A3M7LXK3_9PLEO** (509 aa)
Thioredoxin-like fold. *Pyrenophora seminiperda CCB06*

MPMAELSVYDNDPTIYLFTSLTAGSSHIITATSRIETILRANKIPFKGVDTATDELAKKLFQRRASGKKLPLIVKEGYVL
GGITEIEEWNEYDEIREALGVTSAFTPFPAKPGPPPMASAPPSSSITAGAAAKKENVVAPSLETNLALRQLGAEAAKKAA
SLKPTPSNIKTTNPLLSEKTNTPTSATSGILSPKSVPLPATPAVTNLKSLVKEAPSGILSPKSVPLPDTPTVAALKSPTK
EALKSPTKETQSGILSPKSVPLPQTPTVATPATPTTAKDTKPATAKPDSKPTTTKGTKATDAKAKDTKAKDVKAKDVKAK
DTKAKALSTSASASKDTKSKTTTRKPTTGLFGLGKSAAKPKAKSTSVKETRSKDVQAKDVKTSKPAAKSGIPKPTATKKT
TKAPVGGAKKAAISAGAVGAVGAAAAIAAKEKKEESLEEEEEDDDDDEDDDDEEEEEEEESDEEEEEEEEEEEEEEEEE
EEEEEEEKEEKTQVQPSKDATKAGVSVKD

463 - 482:	EEEEEEEEEEEEEEEEEEEE
464 - 483:	EEEEEEEEEEEEEEEEEEEE
465 - 484:	EEEEEEEEEEEEEEEEEEEE
466 - 485:	EEEEEEEEEEEEEEEEEEEE
467 - 486:	EEEEEEEEEEEEEEEEEEEE
468 - 487:	EEEEEEEEEEEEEEEEEEEE

A0A3M7ME12 **A0A3M7ME12_9PLEO** (791 aa)
RING-type domain-containing protein. *Pyrenophora seminiperda CCB06*

MAFPLASRLMPALKDGKVAKFPASRDVRDATEVAGASHSRAAACTLNTQLSLVLPVCDRPMDSSFDLPDSTDWIGTTLPS
FEPLEAALRCEICKEFYNNPVITSCHHTFCSICIRRCIAADGKCPSCMTVCSSDKLAPNIAIREVVTRFQEARPKAMELA
RADKVETIAGSKKKKRKLDDTDMEDDDNGRHTRSRTTRSRGQRNGGAVVVVDSEDDGDEDFIPDGMVKCPMCNRAMKEEL
VYNHLDVCKGLDASQGRNTRTKNSTTFPAALQRRQKDASPPPTRLSQFNYAMLKEGAMRKKLQEAGIPSWGTKDLMKRRH
IEWLNIHNSNCDAEENLRKSKKQLLRELDEWEKTQGGKADAKESKIMKKDFDGQGYAKSNKSEFDELIARARQKRDTPKA
DGDSSTRQSTPTGAEVQGYHHTGPPNGTELSLEQNPWNHGSSNTPPLPSTHPYEYNESAPDSIRIRAKVAEANLTFSPKA
PTLASETSIENAQGYDPSIDGIRNPLGTPSRKLPMFAPPEDPVLDVLLKAMSQRSPTSFEEGPSLDSGIAMDTNSQHKHQ
EHAAALASSSPISPASKKRRSNNSMLRAASKSALPPSRVSHRSPSPPSSHANSSLPYFHAFPSIHDRRQVIDRVLETPPR
RKTPRTLLDSEVLHAQQPYSLSDSIVSSVPSLRIASALPVTRVTHADVVQSRVTVTVTQGVAPVSRIVATQPVGSPVPLS
SSSTRYAQQGEEEEEEEEEEEEEEEEEEEEEEEYRSLAELVRKREKKRASIKGRLERMVEKLASFCCKKE

731 - 750:	EEEEEEEEEEEEEEEEEEEE
732 - 751:	EEEEEEEEEEEEEEEEEEEE
733 - 752:	EEEEEEEEEEEEEEEEEEEE
734 - 753:	EEEEEEEEEEEEEEEEEEEE
735 - 754:	EEEEEEEEEEEEEEEEEEEE

A0A3M7NAB4 **A0A3M7NAB4_9EURO** (1467 aa)
Uncharacterized protein (Fragment). *Chaetothyriales sp. CBS 132003*

MPAPYIATPRATDASYLSSGLERLGEMSPEKSFVNPPQGRDLISQMKSIRQNGLSQKTPRNASRDPLRLLPNGNQGKSEF
TPLMKSGVKNNMAKRLSARKTGGIETPAYLRNGYLEGRTPALPRLDDNSHLQNENTSSSAGNANDYTPMPNTISSSARST
PLAQLPRQDAGGVVDDGNVMTLREQENIINKIEKENFGLKMKIIFLESAMSKRGAEFNQAALKENTDLKVNRVTMQRELH
KLKKNIAQAERDAETYRLQLEEYRERIRRKQVDGTVLVELENLRSEVKAKEKEMARFEEKQHSRASEKEAELQRFRDEIE
DLQAEIREKDRQIDNRDDELDQMKLNASKDSNASAELEDELETIKQQVEALKQDLERSRQQEAGARKEREEAIDERRRAE
ENLEELQDEMANKSFTTRGLSRQLEEKSNKLEDELEELSARHSETQRELEMKVQSEKRLQERVRELEREGASDSRNLQQQ
LDIAQQQRDTFERKLTNMTRQVENAEEELQIKIGEKDLLQTRHDALTTESAQLQADLTKAQKSIHELELALDVERQRSAQ
QDSLLRTQHQHELERLNEQIDSLHRDINSKENEHAADIEEFEAKRKSLESAVSRAEERASGLQRTVDKLQDAQGTLSGRE
MALQEAVDSEKQRHQQEEKILSRQIEELNDDLAAKRLAAESNRTELNNAKEELRISIREQAALKEKVAELEEEIEVLQAD
IEQEHELVEQFQKKSNENADSQVLKLKREKQDLQEHLANAQMELQNVRRELQAAETDREELEGKLLKAHKSADETFHVDS
EKRELSRAKQKLEKEVERLKSERDNLQASNDALEEEVNHEVERATAEENRLNNELDRIRKHQSGTESRERELRAAKNKVE
RLEIRVKELEDMLDNQSRALGSPAGDLSGLQNDLDDARRKEAVAIKKESELKAANRDLKIKVNDLERELHAARLNQLKSR
SPSASPSNQKELAQLRQELVEARAKIKELKLQLSKSGDSQTGVGDHSIHLSMRDNEVKEMKRQLIRIREERKAANDKADA
VESELEILQSRYENILEKLSSGKHSADEVRRKEIKGLIKEITWLKAKCRREERLRKDIAFSKKYLEQGEAMRVQCNQIDL
RILREMGVQIDKSKYQARLKPIQKFRAGVFAVIAAIRMSEMEEQWRDVKKLGDELQSLRTRQPIGKARLHFQYIVVLPEI
GANVADDRGQHRRSTDPKIYSWTYPNKSVFVVEKSTENVFYKVKRFFGECPTVVIYNGFARSLHDAKDPLSTITKDDVER
EMNANTNSALIAAQQAVNGWKETPQSPYKTFIYTGNKLPFMSRPFAPIFGMGKSAAAHLIWDLSSQMDAKARGQLYWTLT
ENPEQGSFYYTYVKDKGYVDFQDLYGEEEEEEEEEEEEEEEEEEEEEEWYELNIEDVEDVSVEYGVHAVPTFMLFKDGD
MLPEDKITGAGDAQRKVREMIEKNLKA

1387 - 1406:	EEEEEEEEEEEEEEEEEEEE

1388 - 1407:	EEEEEEEEEEEEEEEEEEEE
1389 - 1408:	EEEEEEEEEEEEEEEEEEEE
1390 - 1409:	EEEEEEEEEEEEEEEEEEEE

A0A3M7P2Q2 **A0A3M7P2Q2_BRAPC** (25 aa)
Uncharacterized protein (Fragment). *Brachionus plicatilis (Marine rotifer) (Brachionus muelleri)*

```
EEEEEEEEEEEEEEEEEEEEEEEEE
```

1 - 20:	EEEEEEEEEEEEEEEEEEEE
2 - 21:	EEEEEEEEEEEEEEEEEEEE
3 - 22:	EEEEEEEEEEEEEEEEEEEE
4 - 23:	EEEEEEEEEEEEEEEEEEEE
5 - 24:	EEEEEEEEEEEEEEEEEEEE
6 - 25:	EEEEEEEEEEEEEEEEEEEE

A0A3M7R1J7 **A0A3M7R1J7_BRAPC** (517 aa)
Transposable element Tcb2 transposase. *Brachionus plicatilis (Marine rotifer) (Brachionus muelleri)*

```
MTRHNKTIRQQIQTSTPVTRRQLKLKQQEELEKLKEDESGHNKALKAEEAKAESQVEEEEEEEEEEEEEEEEEEEEEDKN
AKNAKNEKYEKNECEADNCTETIRKLPKQNDTQNESIACCDNEPLVLTQAQQNGTEQIIVQREEIQEIMADMNISKSIKE
KLDVKMSFEHDGQTEMDDGGGEDSSEESEIEPHDLQLSLVANEENAENENVSDVVSSQLCKIQKKADHEKLRRRLPVSIK
ELIDYHSSNGKSIKEIVSRINMVCKPEEKVSYGYVQKYLYRKKLEATTAKKARYYRKKYGFVYRRMRRKPVLTENHRQSR
IQWCQAHVEDKFDQDIFIGKTSLKPFLASLNQLKGQPPDPSQPRQQTTLHLWGAISRKGASPLQIFDGSLTTAMYLEILL
ENVVPFIAENFPNGHRFHQDNNPKHSAKLSQEFLESTGINWVKSPPRSHDLNPIELVWTDLIQNVSKRLPKTLGQVVIAV
KDYWKTLTPQKCSEFIDKLCSIVPRVLEKNGEWVSLS
```

57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE

A0A3M9VU65 **A0A3M9VU65_9EURY** (341 aa)
Uncharacterized protein. *Natronomonas sp. CBA1133*

```
MTDDTLTTLSRRRLLAGLATIGGSMSAAGVGTWSLFSDDEQRNISVKAGTVSLSVDEGADPVITIDGVAPGAGGTERVTL
RNTGTLDAGLALCVSDVSHPNGGASSGTDADAVADVDFNGCGTAEVEFEDESADPVQATIEYGDGETSKRTVSPGGEMRL
LKKSGGKNGYIASVSIGGTTYENDACKHASETDNGNGQRQGSSDRAEEKGSKNNKSKNTEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEQRADDDSDSGSLAEVLTVEIGLDADDGGREVLFGPRKLAELTDGGGERCTAAAARLASGATTELFVDWDVD
DDAEELAGQTVELDIEVNLQA
```

220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE
222 - 241:	EEEEEEEEEEEEEEEEEEEE
223 - 242:	EEEEEEEEEEEEEEEEEEEE
224 - 243:	EEEEEEEEEEEEEEEEEEEE
225 - 244:	EEEEEEEEEEEEEEEEEEEE
226 - 245:	EEEEEEEEEEEEEEEEEEEE
227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE

A0A3N0XMD5 **A0A3N0XMD5_ANAGA** (1206 aa)
Peptidylprolyl isomerase (EC 5.2.1.8). *Anabarilius grahami (Kanglang fish) (Barilius grahami)*

```
MAGQQDNDYKWREIRGAKLASLFGLDQAASKGNESFQYTAPKQPRKNAANSGAPTQKPASTQNPPAVLFATAVHAYRYIN
GQYAKQGKLGAAVLGNHTTKEYKILLYVSQQKQVTAARIHRGFILTVQPSNYCTFYDDQRQNWSLMFESEKAATDFSKEV
CLAKVNCGGPVDSVLTQDLLLGEGQAVENGDSLEVAYSGWLLQNHTIGQMFDSNLNKDKLLRLKLGAGKVIKGWEEGMLN
MRKGGRRLMVIPPGLAYGSQGVPNRVPPDSILVFEAEIRRVKFAKDGSSSDSAAPSPAPSVESLGPSELNQALSSVPQPS
KPSEPPLRAKSNSLSEQLSNPDATKAKLISRMARMGQPMLPFIAGPASSPSQPDSSDSELEARLCFITDPSVSRLKERSS
APSPQPVHMTSAPPPSVQGAALLPVSLATANPQPMMPGVIHAFQPVSQMYPTQTVPYQGSSDVTSFLMTEARQHNTEIRL
AVGKVGDKLDHLSSKIDDLQKQGSVSLGLSNMSMETAMIMHNIQRIIQESECLKKEVFEKSSRIEEQNRKISELINQNQR
YVEQSNLMMEQRNDSLKNSSEQNQTRILQAEQDKVRLTEELASSTARVSELQLELSAQQQKAAALLAKLNSALQDGQQHS
TQITALEAQTLELKETAERVQGQYKMEKQKRKELELKLNNMEEELQDMKTEKDSLERTLSERKRKWQAERQRCDEELEEV
RRAGQQEMDSLRSQLRKARTSTDHAAAEQLSQLQADLEQEWQVKCDQALAAAREQKRRETTELTEHRDALQLKLTQLQEK
FNALKQSRDSEEQRLLQQQDQGEELQSLREKCRALEQRAALLKQQEETHVSEQQQTDTAEEVKRVMNGVFQSLRGEFDLN
ETYSGSAVLRVLVNTIKSVTLQLLTKTERSSPEHSEKEEDEEEDDEERESDARHTQAHMNGQREEEEPTDTDPEDGLPQV
EEDATPAEEEEEETEEIKSEQEVVEERNKEKVVEEKEVEVNVSTEHNVQDQDSETTHEEEAESDVTPTQEVTAKLPDDIS
PQEVKVVDEGVPGPVDKAESTLTLGGPPKNPPPPPAALHEDSSATPAQINSSSERVEEENGKEPFFQSPVSHAPAPPPAT
TPAAAPAAADEEEEELEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

ECEILC

1137 - 1156:	EEEEEEEEEEEEEEEEEEEE
1138 - 1157:	EEEEEEEEEEEEEEEEEEEE
1139 - 1158:	EEEEEEEEEEEEEEEEEEEE
1140 - 1159:	EEEEEEEEEEEEEEEEEEEE
1141 - 1160:	EEEEEEEEEEEEEEEEEEEE
1142 - 1161:	EEEEEEEEEEEEEEEEEEEE
1143 - 1162:	EEEEEEEEEEEEEEEEEEEE
1144 - 1163:	EEEEEEEEEEEEEEEEEEEE
1145 - 1164:	EEEEEEEEEEEEEEEEEEEE
1146 - 1165:	EEEEEEEEEEEEEEEEEEEE
1147 - 1166:	EEEEEEEEEEEEEEEEEEEE
1148 - 1167:	EEEEEEEEEEEEEEEEEEEE
1149 - 1168:	EEEEEEEEEEEEEEEEEEEE
1150 - 1169:	EEEEEEEEEEEEEEEEEEEE
1151 - 1170:	EEEEEEEEEEEEEEEEEEEE
1152 - 1171:	EEEEEEEEEEEEEEEEEEEE
1153 - 1172:	EEEEEEEEEEEEEEEEEEEE
1154 - 1173:	EEEEEEEEEEEEEEEEEEEE
1155 - 1174:	EEEEEEEEEEEEEEEEEEEE
1156 - 1175:	EEEEEEEEEEEEEEEEEEEE
1157 - 1176:	EEEEEEEEEEEEEEEEEEEE
1158 - 1177:	EEEEEEEEEEEEEEEEEEEE
1159 - 1178:	EEEEEEEEEEEEEEEEEEEE
1160 - 1179:	EEEEEEEEEEEEEEEEEEEE
1161 - 1180:	EEEEEEEEEEEEEEEEEEEE
1162 - 1181:	EEEEEEEEEEEEEEEEEEEE
1163 - 1182:	EEEEEEEEEEEEEEEEEEEE
1164 - 1183:	EEEEEEEEEEEEEEEEEEEE
1165 - 1184:	EEEEEEEEEEEEEEEEEEEE
1166 - 1185:	EEEEEEEEEEEEEEEEEEEE
1167 - 1186:	EEEEEEEEEEEEEEEEEEEE
1168 - 1187:	EEEEEEEEEEEEEEEEEEEE
1169 - 1188:	EEEEEEEEEEEEEEEEEEEE
1170 - 1189:	EEEEEEEEEEEEEEEEEEEE
1171 - 1190:	EEEEEEEEEEEEEEEEEEEE
1172 - 1191:	EEEEEEEEEEEEEEEEEEEE
1173 - 1192:	EEEEEEEEEEEEEEEEEEEE
1174 - 1193:	EEEEEEEEEEEEEEEEEEEE
1175 - 1194:	EEEEEEEEEEEEEEEEEEEE
1176 - 1195:	EEEEEEEEEEEEEEEEEEEE
1177 - 1196:	EEEEEEEEEEEEEEEEEEEE
1178 - 1197:	EEEEEEEEEEEEEEEEEEEE
1179 - 1198:	EEEEEEEEEEEEEEEEEEEE
1180 - 1199:	EEEEEEEEEEEEEEEEEEEE
1181 - 1200:	EEEEEEEEEEEEEEEEEEEE
1182 - 1201:	EEEEEEEEEEEEEEEEEEEE

A0A3N2PQ12 **A0A3N2PQ12_9PEZI** (152 aa)
Non-heme 11 kDa protein of cytochrome bc1 complex. *Sodiomyces alkalinus F11*

MGIWDLVTDLAEAALPWSTVEAEAPAAEEKTEETTEETSTKAEEPEQASAEAEAEEEPAVEEAEEEEEEEEEEEEEEEE
EEETVDPKETLEEECKQSKVCAEPKHHFDDCVERVTAAESEGGPKEDCVEEFFHLAHCATTCAAPKLWSQLK

64 - 83:	EEEEEEEEEEEEEEEEEEEE

A0A3N2PQJ3 **A0A3N2PQJ3_9PEZI** (393 aa)
G-patch domain-containing protein. *Sodiomyces alkalinus F11*

```
MNPPDSTTRNQNETEDDQDDQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDYMSMSFADEPDPVAKQPLTSLQRRQQEK
RLAEARARPKSKAQLAEEEEAARQASLSRSLLEGPQAQKSKGFAMMARMGFKPGSTLGAAGSRGVTEPLRVVVKEDRGGI
GMESEKRRKLREAFGEDEEARKRQKPGEDPIAYRDRMAREREAVRVEGLVAAAQRVAEGMAADAEAEVETGVEAAAKGED
VAPKGAEKSGSKDERNGKNPKPKRRHIPSRPLKSVNVLWRGLVRRREEAERNARLRRDMEQSLSRLPTYEDSDEDEDDKR
ALGRDAKTVYVFAEDLDEEDPELEEFEALDAHEKLRRLVVFLREEFCYCFWCKTRYPDAQMEDCPGLTEEDHD
```

22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE

A0A3N2PY99 **A0A3N2PY99_9PEZI** (182 aa)
Uncharacterized protein. *Sodiomyces alkalinus F11*

```
MSYAKFLEEGWRNWDVRTNEHSVITYIHVCVKVSNGIRTVRGPRPRQTDWRLGSVGFAFISRRSAHAQAQHPGNLHEASL
CLCINTSISEGRKEGGKEEEEEEEEEEEEEEEEEEEEKTKTEDHDNDENECEPQLTNALRAGLGLDEVAAVRAASGTHRH
ANPHLAELCNSAPPPPYFGKLV
```

98 - 117:	EEEEEEEEEEEEEEEEEEEE

A0A3N4JRC5 **A0A3N4JRC5_9PEZI** (110 aa)
Uncharacterized protein. *Choiromyces venosus 120613-1*

```
MNETEIAAAIESLLDAIKGKGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEQGRDWRQEREEREEREEEVNRMADDN
CGEREEELGEERISEERDMREKEVREEFGA
```

22 - 41:	EEEEEEEEEEEEEEEEEEEE
23 - 42:	EEEEEEEEEEEEEEEEEEEE
24 - 43:	EEEEEEEEEEEEEEEEEEEE
25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE
27 - 46:	EEEEEEEEEEEEEEEEEEEE
28 - 47:	EEEEEEEEEEEEEEEEEEEE
29 - 48:	EEEEEEEEEEEEEEEEEEEE
30 - 49:	EEEEEEEEEEEEEEEEEEEE
31 - 50:	EEEEEEEEEEEEEEEEEEEE
32 - 51:	EEEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEEE

A0A3N4JZY5 **A0A3N4JZY5_9PEZI** (192 aa)
Uncharacterized protein. *Choiromyces venosus 120613-1*

```
MTLAQSQLGDLFKLYKLKPRERIQRILRYRMAKSKTEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEGETTEWEGGVKELALTRTQHEIRIMTGMEHYRAQTNPHISTFGVICCTRSRAANEVNMIYEHSTIALV
CYVLIVDLSFWRLTVLSLASMIHSPIAPSPVC
```

37 - 56:	EEEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEEE

39 - 58:	EEEEEEEEEEEEEEEEEEEE
40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE
42 - 61:	EEEEEEEEEEEEEEEEEEEE
43 - 62:	EEEEEEEEEEEEEEEEEEEE
44 - 63:	EEEEEEEEEEEEEEEEEEEE
45 - 64:	EEEEEEEEEEEEEEEEEEEE
46 - 65:	EEEEEEEEEEEEEEEEEEEE
47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE

A0A3N4KMM6 **A0A3N4KMM6_9PEZI** (267 aa)
Uncharacterized protein. *Morchella conica CCBAS932*

```
MYLDKNLLYHASNIGRPRGNWWIVRARGPQADKCLLESSRHPSYRTDITCRGATARPWMCPLAVVYWYQWLQRNLGFYWE
LVLSQVPTALMGLQYARPTRIEGTATRTQWSGLGAEDVRGPGLFEARNRRMTLRHQILLNPSTMMSIARQLLRYRENTHD
SSSTSDGKKDEQRPTTRGYLGVVPEHIINGLHLMPMMAWAARSVNLTRGLATKCGQGPRGFRRDLTFTMRIPALADKLEI
KGGEGEEEEEEEEEEEEEEEEEEEEE
```

246 - 265:	EEEEEEEEEEEEEEEEEEEE
247 - 266:	EEEEEEEEEEEEEEEEEEEE
248 - 267:	EEEEEEEEEEEEEEEEEEEE

A0A3N4KPC7 **A0A3N4KPC7_9PEZI** (1888 aa)
Vacuolar import and degradation protein 21. *Morchella conica CCBAS932*

```
MVEKITIENLRKDALNAVCDERKSIIISRKRKLQELYAVCRHVERSKEFPNADIMAAWGTVEDYGAANMEDAEKRFLEEN
DIEKGRLFKESTLPQHSSYLPEPGGLPKATPTRGLSHPSVSPGTSTPPKSTAQTSIHLPSTAVKQPKARPESTNSPELPV
EKRQRRDPNDESVRHEPSVELPALNGNRTDGDSTMEEESAQPLDQDHPHRASSSKPSPAVDDSRSEPLAPIFNLGGVPVI
QETTTKVPDEKEEALGVRPPPIPKALTERSGEDVTMQDTAPSDKPLTASAETIQDLEKLKEVSPLQKSTETEVLSSQESS
VVPATPPIRPIAKVFEHREEARLPAHPSQLQQLPPHAPLVVLTGQHNRPYPIAFASPEKEGSAHPEVSSPTSSVDGGDGF
GTPGNAALSSATSPDASHMALESQSSGTDKKDTREVVTENGGDRIASVSSSQAEEDEKAGVVVEKEPECCSDRPDAVLPS
VSMAEEVVGTEVDTEPTLPTIPPREIPVEERGLQEQENKEISSLPNAHCEDGVEDQQATNPLTQEAPVVPVKDKEPTTPI
TSKPMESIVAVSLAGQQSPDPSAQLRLEHQLANGEPIVPSTVTTHKVASFNNEIKAAPELVMSHAHDEEDDEDQVQLVGS
REPEPVSVRRKAPAEPPAQPKEEIVEALEETVKEVLSTQEKEVPIHIPSPEPEVQAPIEVKQKTPEPVEVRVETEIKEDK
EGEEGEEVEEEEEEEEEEEEEEEEEEEEEEGGDVEMGEAEHNDPEAISVPYQPSPEPEPEGDDELDDEPLKRDEIPEEDE
```

```
RMEIAEEKAPEMPLDPSPIPATTEGSNASAAESAEKPDFVQSTPVTDANAMDINLPTPDATRASVPASTKSVSPPRPKPS
KTIGRNKQREKSRAKLHKVVISSAHYAAAAAEAEAQRLREDQENQGMIVVARRRDQAAAARGRSAQFPPGSKTDVLTRYG
IADPPPTDGDKKKNLEMFDVLYTVKSAHTSAKELISRANKTVSTSNHQVHYFESQAARILEMIQKNQDMGISSLRQIARA
REPKRRKCHWDYLIEEAKWLREDFREERKWKIAVAKQVADWCVEWHEIGEDKQELVVDKRKWGVVPKGARDEKKKIASGG
DVEMGGAGSFSELNQPTPELVVGGATPDDEGSEDYFPNGIEQSGGVGWGIPDFFGYLQDPPPAALFALSPDETIFGVAPT
KAAEDMLGQLPLFAPPKPPNVESRRFEHVDEEWMTPIIPVTKYCTGKLTLKQEEEGPPRKKSRYEYDENYELFADDSDED
DITSGGPYGQHGKREKDKTRKPVPLPPEQTDVALFNPGSKALLSRIHNAHLFRPPSDLPPQAFFESRLPSLWTSAEDDML
KQLARDYHHNWALVSTCMQLEGTWHSGSERRSPWECFERWIGLEPVSPDFMKSPYYKPVQQRLDIAARVGGIYVANPGSV
GGNNPNGITKRRGTVPVKVEKRRVTKYFNIFEAMRKLAKKRETSISKQQSGRAAQMAAMRKAQDPASTTSTQRTPAFFSN
LKYDREQKQLEHKALYAAQLQMQQAGRNPQGQPLPAQAGRLHPAQQQALANGVPVPGQRVPQAAMPNGLPAGVRAQPGVI
PNGSVPVGMNGIPMGARVHPQTQMRAPMTAEQIAQLRTLHLKQQQQQAAAQGQSYSQAGMQGFPAGAVGSRDPAAVKAMI
QQAQQAALGGQRPANAANGQAGSPRMQNQQPLNPQQQQAPAGRGQFQLTAAEMTALVQHQHPHLPPSEIAKATQQHLANY
HHQMRQTMTVSANGNGQGIPNMASSPPTSQLIARAQQQQAARAAAANTGPMIGANGPVGPGANVASRSATPQQQRSTSVQ
SPMSVQQSPRLGQAMLAGQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ
```

729 - 748:	EEEEEEEEEEEEEEEEEEEE
730 - 749:	EEEEEEEEEEEEEEEEEEEE
731 - 750:	EEEEEEEEEEEEEEEEEEEE

A0A3N4LBL3 **A0A3N4LBL3_9PEZI** (249 aa)
SAP domain-containing protein. *Terfezia boudieri ATCC MYA-4762*

```
MLDPSTLKVADLKAQLKKRGLAVGGLKKELIERLRKALDAENANAGEEEEEEEEEEEEEEEEEEEEEKKKKEEEKEEEKE
PGEEEWHKKVDKVEHRGNEVGQTNGTPEDDAGTDSIIEAHTGIVDAKNAPLTPPERQPGDEIQKTAQPPLEAIDPEQDTV
KEALEEQQEIKHVSVQDETKASQLPVEEVPEPEPMEIDTDEEKPEKVPGPMETDIPEEKPAKVPDTDTTTEVNLTVVPDN
DKAEDVQTR
```

47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE

A0A3N4LGN8 **A0A3N4LGN8_9PEZI** (519 aa)
EAF domain-containing protein. *Terfezia boudieri ATCC MYA-4762*

```
MPPTFVAGAPRKMIDPLKPGKFSVKIGDSLKDPSSGKKRLTSLKYNHKPSPALSNGRKSNLKSENGGTRNEVTLDIAPVC
HLPRGTLQATETNIVPMQNDAAEPTVTFSGAQGSAKKTECVLIYDPATGAFTLEKLLSTFTLNLTSAGANLHPALSLPKY
NPGQSDDSGASDDGSSDGDATKADKENPFDYRNFINNKFEVPASSSQLRDRKQRPEKLHEELSDPNASGEDEGVDNEGLI
IEDNPVISTPAPLQQTLPARPRATPSAAAPKPRTKPAPKIPATIRKSSANGAISLFSTAKKGAVPTEEIDLAPFHPQPSN
KRPRDEVSSSESDADNESGESDDEENEFAGSGELIVEGEDADDGRDNRSRSTTAGLGSSWVGGNRGGPVSLATAAQGDSG
TRINSDENEEMELVAQSPILYNEPISVSGRQGHMLDEDEESSDEDAPDRQQAQSAPTPNRGNGDEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEFDLAGMLEEALDEGEEEESESEEE
```

465 - 484:	EEEEEEEEEEEEEEEEEEEE
466 - 485:	EEEEEEEEEEEEEEEEEEEE
467 - 486:	EEEEEEEEEEEEEEEEEEEE
468 - 487:	EEEEEEEEEEEEEEEEEEEE
469 - 488:	EEEEEEEEEEEEEEEEEEEE
470 - 489:	EEEEEEEEEEEEEEEEEEEE
471 - 490:	EEEEEEEEEEEEEEEEEEEE
472 - 491:	EEEEEEEEEEEEEEEEEEEE
473 - 492:	EEEEEEEEEEEEEEEEEEEE
474 - 493:	EEEEEEEEEEEEEEEEEEEE
475 - 494:	EEEEEEEEEEEEEEEEEEEE
476 - 495:	EEEEEEEEEEEEEEEEEEEE

A0A3N4LK93 **A0A3N4LK93_9PEZI** (829 aa)
SAP domain-containing protein. *Terfezia boudieri ATCC MYA-4762*

```
MLDPSTLKVADLKAQLKKRGLAVGGLKKELIERLRKALDAENANAGEEEEEEEEEEEEEEEEEEEEEKKKKEEEKEEEKE
PGEEEWHKKVDKVEHRGNEVGQTNGTPEDDAGTDSIIEAHTGIVDAKNAPLTPPERQPGDEIQKTAQPPLEAIDPEQDTV
KEALEEQQEIKHVSVQDETKASQLPVEEVPEPEPMEIDTDEEKPEKVPGPMETDIPEEKPAKVPDTDTTTEVNLTVVPDN
DKAEDVQADDNKELEPTKEEPSSPPTLVQQDAITTTATTATTAAPATTAAPATTAAPATTTATTNTVVTLEITSQADLPP
PGPTQEEDTMDTSLDFTVDLRKRKRRSPSPAPHATPLSEEKGSPEGPSPKKSRQETIYKRADIRFKSLVEPTAPSIVDPT
STSIDTTTAAEPQADEDSDSEIYSTPALHPATPALYIRDLMRPLKPQILRSHLIALATKQPADQQHMSEDVIRTFYINPL
KTHAFVVFESTLFATRARAGLNGRKFPINERGRKPLWVDFVPKEVVGQWIGEEEDGAGVVGAVGARGGRGMVRWNVVYEE
TKDGVMRVWHEEADGGGANGRGTISVTSAGPMRVLAPNANRDDPPPPASSARRASPSSPRHHRHNRSPPPTMPRADRERL
SRAHGHPSATNESSGGGSGGGNARNFQTIDQLFRSTAAKPKLYYLPVLEEIAQRRLSEEREREKLVREGEIRDARERPGA
PNWGGSGKRKGGGRDTMSAVGGPIGKSGGLPARGGRRGDYYVPGALADGDRDRERERERERGEKERGGRDREEREGSMYSG
GRRERDWDRDEDKNGGRRDRDRSRSREWR
```

47 - 66:	EEEEEEEEEEEEEEEEEEEE
48 - 67:	EEEEEEEEEEEEEEEEEEEE

A0A3N4LMI5 **A0A3N4LMI5_9PEZI** (861 aa)
Uncharacterized protein. *Terfezia boudieri ATCC MYA-4762*

```
MSGQGQPNPYFFSPEFTQQLLHQERKERGSSPADYRGWRKWSLARDGMEARLHRGKPSKTRMGRAAVQDGRVQKRASTML
EVQGRLLAKAAEYAASPVLPAGVEREGVGAAETEEEEEEEGEEEEEEEEEEEEEEEEEEEEEEEEGEEEEEGEEEEEEEWEG
DEKLEVTAQLQRESGVEPLFENERQFQYAPEIAMDAEVDEEGILHGRPSKRRKRTVTINTVPEVTEIEDTEDIKDIGPSP
PYLDYYSLEGSPDVELEDIYDMSEDYRGKFERPMEPVEKPFFPTLPRPKTEIAKQAEVIEVWEALVEKRKALEPYDTDLV
KHTENRLQAHLAELERLIVVEPSLPQYSTTRIATLKECLTRYVNADEIVNVKAVIKAFENKVLGNYMDQWTIFYNGKIVD
RINSYRELLWSVRNPLYKEIYGPNGSIWIEPPTNDLGKACAMIESPQFVSGAHWYVKQNICLPWYHEKYALELDFLLDSG
ATDPLVDDKDLLDLGLIKTDCPHVTNRGVSTASGKISVDFYPLFIQHLDPQNHDVQGNKLPLYPFMDTIIGTTVGHVERL
SGLDIYRFCYVASEPSTGSCSYHPQFKKLEICRNIAPGGSMTPRAWFTRTWDNRTQRFTVSSKMCSLTGRQPRLLNPDGD
RWVRGAKGYPYQYGREDRSPYRVGYIPGHKVHPPTPDAIRDDRKYYWSRGLAYRDNRPFVAPRVHTTDKLHYPRDQYYDY
RIREGGTLVLRPTPRPLNPWQFKIPQQYYRQPTGLLTNPPLNPPGVMYWDRKFPVVANRLNLDPGIVPKKWGLHFQHRKG
DNYWEMRNAHLAGLGQGCQATDASTSTYSGPVMSKEKLKRPKYFGEEEEQKEGEEEKEKGG
```

122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE

A0A3N4LPX4 **A0A3N4LPX4_9PEZI** (652 aa)
Uncharacterized protein. *Terfezia boudieri ATCC MYA-4762*

```
MNNIMDHRRGSAPQGSFRVPWNAQENLAPRAHSVSYPSQVLFRQASMCHPNLGFIVHPDNVNSGPEFCDSCSRVLPQIVP
MINGSTPLINPGPMADVNPLYTYSVNVILPSPPRHAPVPGFSFDHDKIQALASSLEDLLRQHRQGTERLNPPAFESREEL
PVQETTAWGWEDEEEEVYTFPSRGDQDTASSSDPSRDPSIRNLLNDPIEHIDPTQLSSDTEDAIMHDQGEDLQIEEQLGD
SIFLQGQEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEGEEEEEEEEGDEWEEGEERGEAEGESDGMNKDAQSVVGGQEDIEDTIENLSQIGLDTPVPQPVAADLRPIKPGLPEF
WDTAKSVTAPSSGNKIWISSCFFVGLGVNSVGRYEYTQMILPRRSGERVQHVATTTCDKCGTVVMYGRYNSPEVVPEHPR
VSVYILRLEAELVKPYRRGIQFVDSWPDIDLIIHNDLFQITEYYVEDHSTPHWVIQHSNSWDAVKKAIMGGMTWAQHWYP
LKLREHLNCLVVYIQALRYLLMCKILMATESVEFGGLRWEMPRPEFHRGSIAEEFRCWAGLQLVVFKSISGGYGNFLDFS
PDANDGSGGFGY
```

250 - 269:	EEEEEEEEEEEEEEEEEEEE
251 - 270:	EEEEEEEEEEEEEEEEEEEE
252 - 271:	EEEEEEEEEEEEEEEEEEEE
253 - 272:	EEEEEEEEEEEEEEEEEEEE
254 - 273:	EEEEEEEEEEEEEEEEEEEE
255 - 274:	EEEEEEEEEEEEEEEEEEEE
256 - 275:	EEEEEEEEEEEEEEEEEEEE
257 - 276:	EEEEEEEEEEEEEEEEEEEE
258 - 277:	EEEEEEEEEEEEEEEEEEEE
259 - 278:	EEEEEEEEEEEEEEEEEEEE
260 - 279:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE
262 - 281:	EEEEEEEEEEEEEEEEEEEE
263 - 282:	EEEEEEEEEEEEEEEEEEEE
264 - 283:	EEEEEEEEEEEEEEEEEEEE
265 - 284:	EEEEEEEEEEEEEEEEEEEE
266 - 285:	EEEEEEEEEEEEEEEEEEEE
267 - 286:	EEEEEEEEEEEEEEEEEEEE
268 - 287:	EEEEEEEEEEEEEEEEEEEE
269 - 288:	EEEEEEEEEEEEEEEEEEEE
270 - 289:	EEEEEEEEEEEEEEEEEEEE
271 - 290:	EEEEEEEEEEEEEEEEEEEE

A0A3N4LQU6 **A0A3N4LQU6_9PEZI** (843 aa)
Het-C-domain-containing protein. *Terfezia boudieri ATCC MYA-4762*

```
MGSMVSLGLLAVLCWFAVPVQAFGAGNIASFSVAEGTQWRHGDIEDVLLTLTMAASCHSKKFDALHVKRVYFGNWLRDYS
QAIDVGSLKSVDKHTIRMLLWVLSFMTFGYATGEFEVTEERLGCYRPEEHIDNPKGYPSDAQAYDERLRGPVNETLELAI
DPETGMKNYIANERVGIMTSANLIRRMIGRSIELGRSYARTGIKKEKYEALRLLGTGLHCLEDFVAHSNYIELVLRELGE
VAIFPHCGTATQQWIQGKPIFPLTTGTFGGVDLLHSVLGEASDKIVQSEIQQLENSIIASEQAAEQDGGEGSVIQGLLNM
LPAGLFSGGGGDNDPDVGSGTTNTADLGGHALNLEARAKKKKQTGDDDTGVDLATSLYAIMEFHDTITRAINRAIESIPG
LAALVEKLSESVSIFVFSLLAPYLMPIIKQAKGKLKVASSEVITEAKQEQHNIFYDPHSSNPTHSMLSKDHFTNRLNEPA
GMVAQEILRFCVPLIMQAWDDESIDIGSLLNNIIAIFHHPALRTHPYGPHPAREAMFEVIRHWWQDGKSEEERNMLRHAL
SAPGIQAGLNHKEGHDTGSGCAGHAPITKLATTHKNTTHKNRSVGPEGMLEKSFSGGAGGLLGAFGGVAAAGAFEGFFGG
KKKDKQPMTADYRYHEAIPGGYVAGGEATTTYYGGEGGGYQTQSQGYHYQELRQEYHGGEMRYGGEGYVKESHKEKKKDK
KDKKKKLDKKAIAAGLGLVALGAGAGAYALEYEADQAAEGFASGGGDNLENEDDEGDGYYVEEEEEEEEEEEEEEEEEE
EEEEEEEEEQEEEEEQEEQEEQEEEEEGEEEEEEGCEECEDSN
```

782 - 801:	EEEEEEEEEEEEEEEEEEEE
783 - 802:	EEEEEEEEEEEEEEEEEEEE
784 - 803:	EEEEEEEEEEEEEEEEEEEE
785 - 804:	EEEEEEEEEEEEEEEEEEEE
786 - 805:	EEEEEEEEEEEEEEEEEEEE
787 - 806:	EEEEEEEEEEEEEEEEEEEE
788 - 807:	EEEEEEEEEEEEEEEEEEEE
789 - 808:	EEEEEEEEEEEEEEEEEEEE
790 - 809:	EEEEEEEEEEEEEEEEEEEE

A0A3N4M3N8 **A0A3N4M3N8_9PEZI** (515 aa)
DNA ligase/mRNA capping enzyme. *Terfezia boudieri ATCC MYA-4762*

```
MPPTPKILLKDNETRTVTFTMKRSADNYYCTCRSWIISARSISGRSCDHLKELLGEEYEVWRLDVTRLKGKKRKAVEAED
EDNDATGKDGKKEKEDDAAKKDTAAKGKGKVKVDAVELKGKQVATMAARKKAKLSEDEVEEKEDDGDEEAEEEAEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEPASKRSRTTTTRPVRAVATAATS
KPADLSQYTSKPLLAHKYEPGSAISTRGWFASEKLDGVRAIWTGTKFISREGNPFYAPAWFTKRLPTDVVLDGELFTKRG
GFQDCVSIVRTQDAPKRWKFKVSYQVFDVPSMGHLPFEKRLAFLKNLIEVKLKIKWINLVKHFPVRDDAHIQEVLDEVTS
EGGEGLMLREPGSVYIHGRSRTLLKVKKFFDADAIVRGYNQGSGKNSNVVGALLCEMLDPKTNKPNGTMFKVGSGLTDAQ
RAKPPKIGAVIIFKYQELSKSGTPRFPTYAGERAD
```

155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE
180 - 199:	EEEEEEEEEEEEEEEEEEEE
181 - 200:	EEEEEEEEEEEEEEEEEEEE
182 - 201:	EEEEEEEEEEEEEEEEEEEE
183 - 202:	EEEEEEEEEEEEEEEEEEEE
184 - 203:	EEEEEEEEEEEEEEEEEEEE
185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE

190 - 209:	EEEEEEEEEEEEEEEEEEEE
191 - 210:	EEEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE
194 - 213:	EEEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEEE
196 - 215:	EEEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEEE

A0A3N6PPP1 **A0A3N6PPP1_BRACR** (389 aa)
BHLH domain-containing protein. *Brassica cretica (Mustard)*

```
MELVCENGQILAKSRKTNNNGYFQNQRRQSILDLYETEYDESFKKNIKNLEETQVVPVSGEQTNNKKRTTKPSKNELERA
LLTGNKRFESSTLNDDSLKGLKNVEVIKAPPDEQSEAVGRSTKLYFTPSSMLSRRTSRDLSISLKKRKCGDNEEEEEEEE
EEEEEEEEEEEEEEEETTYLSNSSDDESDDAKTRVPARTRKTMAKRKRSTEVHRLSERKRRHEISKKMRALQDLLPNCYK
DDKVSLLDEAIKYMRTLQLQVQMMSMGNGLIQPSVMLPMGNYSPMGLGMHMGAAATTPSLPQFMPMDVQGTGFLGINNAS
SQMLSAFLNHPTGLIPNSPIFSPLESCSQQLVTPSCFPETQTTSFSQFPMSGSTTNFEDAMQFRESSGY
```

153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE

A0A3P4KLA2 **A0A3P4KLA2_GULGU** (628 aa)
YTH domain-containing protein. *Gulo gulo (Wolverine) (Gluton)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESADIKRQKPSVHSRQLISKPLSSSASN
NKRIVSTKGKSVAEYKNEEYQRSERSKRLEADRKIRLSSSASREPYKSQPEKTCLRKRDPERRTKSPTPDDSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEEE
EEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGS
SASESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSARSV
ILIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDG
QEIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYAPEF
HQRPGYLKDPRYQEVDSFTNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMVCILFLQII
```

229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE

A0A3P5XQF0 **A0A3P5XQF0_9BACL** (217 aa)
Uncharacterized protein. *Filibacter tadaridae*

```
MKNERGLTLVELLAVLAIVGVIMALLGSVLINGIKASNRTTTRQQLQQEANYITEVVRNEYLGQGSGSFTIYSDDVNQTL
KIESKIISEGYIYKLCYEGENEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEQDEEDCEEADDDEE
DCEEEEDEEDCEEADDDCEDECDDSITVNRKENSKFYLKVLKGDLFYIVETTLSKLH
```

102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE

114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE
116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
119 - 138:	EEEEEEEEEEEEEEEEEEEE
120 - 139:	EEEEEEEEEEEEEEEEEEEE
121 - 140:	EEEEEEEEEEEEEEEEEEEE
122 - 141:	EEEEEEEEEEEEEEEEEEEE
123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE

A0A3P5YY39 **A0A3P5YY39_BRACM** (727 aa)
Protein kinase domain-containing protein. *Brassica campestris (Field mustard)*

```
MPELRRGVRRVRVPDAVAPNQQPKDKNQRKSNGKAVAVGVAERPRTRLAARRLKEEDKKVTLKENLKDSDIEKKKGKEVV
VEEEEEEEEEEEEEEEEEEEEEEEKEVMAIGNDSGGSNKAAAQEEEGNTAPFPERVQVGGSPLYKVERKLGKGGFGQVFV
GRRISGGNDRSAGASILEVALKFEHRSSKGCNYGPPHEWQVYNTLGGSHGVPRVHFKGRQGDYYIMVLDASLLFSPFCFS
RAVMDILGPSLWDIWNTSGQAMSSEMVACIAVESLSILEKMHAKGYVHGDVKPENFLLGQPSTSQEKKLFLVDLGLATKW
REGGGSGQHVEYDQRPDMFRGTVRYASAHAHLGRTASRRDDLESLAYTLIFLHRGRLPWQGYQGDNKSFLVCKKKMATSP
DMLCCFCPAPFKQFLEIVVNMKFDEEPNYGKLVSLFQELLGENPAIRPINTEGAQKIIFQVGQKRGRLSIGEEEEDAPRK
KVRLGVPATQWISIYNARQPMKQRYHYNVADSRLAQHIERGIADGLLISCVSSCSNLWALIMDAGTGFTNQVYELSPVFL
HKEWIMEQWEKNYYISSIAGATNGSSLVVMSKGTQYSQQSYKVSDSFPFKWINKKWREGFHVTSMATAGSRWGVVMSRNS
GYSEQVVELDFLYPSEGVHRRWDGGYRITSTAATTDQAALILSIPRRRLADETQETLRTSQFPSTHVKEKWGKNLYLASL
SYGRTVS
```

82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE

A0A3P6AGZ5 **A0A3P6AGZ5_BRAOL** (336 aa)
Chromo domain-containing protein. *Brassica oleracea (Wild cabbage)*

```
MTDTPLDSSTQNMEGAGVKNDAGEADTAVETVGGSGDEGGRGETIPGKIGDDRRTEDVEEKEEEEEEEEEEEEEEEEEEE
EEGKEDGPKVAEEFYEVEAIRHKRVHKGEVQYLIKWKGWPETDNTWEPLENLQSLSASIDAFEKRLKKADKKRKSQYGGS
NSQSKKKKQQKRLTSTSHDASERTDPTLNELKGQVTNSDGSGSSQEGEAAIGSEGDNARTNDLLKGKRKEKSGVRGVKRR
KPSIVKKYMIPDETTTSNNQTTTATDQNETPNLDIVRIIKPVEVITSITNNVQDSLVTFSVQRADGEEVTVDNKFLRAHN
HHLLLDFYEQHITYKS
```

62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE

A0A3P6B0I1 **A0A3P6B0I1_BRAOL** (115 aa)
Uncharacterized protein. *Brassica oleracea (Wild cabbage)*

```
MRVGTVRLEERNYLGLGEEKMVLYGVCYLLGLLRWLLRGEEEEEEEEEEEEEEEEEEEEEEDEMATEMATEISGRRRRKRA
DMGGNDGLASETPTQQQVFVLDTSSWCESRRWPRE
```

40 - 59:	EEEEEEEEEEEEEEEEEEEE
41 - 60:	EEEEEEEEEEEEEEEEEEEE

A0A3P6BEC4 **A0A3P6BEC4_BRACM** (710 aa)
RING-type domain-containing protein. *Brassica campestris (Field mustard)*

```
MASSQVEIPSPSPSQRFGFIHRDRNQTPIVYKKAPNHHQPVSDENSQNLVDSWIQTLNKKKENNNARSTEKPIALEKSDE
SNRNGASSLVQIWEARLLNRSTSPSHNQSPVNSSRSDSGVSVQESPSIEESEAEISDVEIESRSHGGSVSDSCRVADLIR
RLSKEAKVISGGGLSTIRTPRPCVSSWSSSEKSSFPMVTPRIRGRQAFTDLLMHMERDRHRELDSLLERNAVSRFTQRGR
LQSMLRLRNLKRCQAVQEQNRSNSKSTGLNRIGSGGGSSVLHLRERFRADVDKRKDHHFMNKKTVEETEVTSDNKTMKNG
GLTLEAFFKERLSLPNPNLEKATLRKGEETVNGAVGSKTNCLQLQETIEVEEVCCNDDDSDKKEEEKTSPSACVDQETQP
QSVVPESIEVDQCLEQQETSYLNGWEDEEEYEEDEQSYYYGETNNDWLHEISRPRSYWEELRKTRYLEVMNTRSEKEDIR
RLLERGPVTDFLQSGLRDQIDRLMMSRVQTHSNKHSEKWELQHEEEEEEHRNENVEETEEEEEEEEEEEEEEEEEEEEP
FTEEGEEQDDGDDSSSSPIFASSPAGSWSCQDTEVTSTPVLSVHNPPSPEMELISEMRTQIQQLQQEMSLLRDSVKTCLD
TNASLVHRENPMKRKCCVCDEAQVEAVLYRCGHMCTCLKCANELHWSGGKCPICRAQIMDVVRVFFDRRN
```

539 - 558:	EEEEEEEEEEEEEEEEEEE
540 - 559:	EEEEEEEEEEEEEEEEEEE

A0A3P6DUP9 **A0A3P6DUP9_BRAOL** (108 aa)
Uncharacterized protein. *Brassica oleracea (Wild cabbage)*

```
MCGNLVASFVNQEPGEINIEEDRYNVRGEVQEEEEEEEEEEEEEEEEEEEEEEEEEEEKTREIRTLNFFPVRENQEKTDW
FAEKKKANANRMCYNYRYYYEFMPLKKN
```

32 - 51:	EEEEEEEEEEEEEEEEEEE
33 - 52:	EEEEEEEEEEEEEEEEEEE
34 - 53:	EEEEEEEEEEEEEEEEEEE
35 - 54:	EEEEEEEEEEEEEEEEEEE
36 - 55:	EEEEEEEEEEEEEEEEEEE
37 - 56:	EEEEEEEEEEEEEEEEEEE
38 - 57:	EEEEEEEEEEEEEEEEEEE
39 - 58:	EEEEEEEEEEEEEEEEEEE

A0A3P6E472 **A0A3P6E472_BRAOL** (801 aa)
Uncharacterized protein. *Brassica oleracea (Wild cabbage)*

```
MEFLGPLDSDSDYAFRLQMEEALAASLATRSRAPQHPPSPPVVARCGFAVVEENASTPRGNSETVRRGNTGGGEGSSRGK
GKTHETVASERRDDRNPNSIKVGNFQNASGRPSPGVTVGPAQSVAVGEGSSKVSGVKGSFRGDLMYRLYFKGLVSEETGT
GKGKGKGKGKVSDVAAGFGVAICDQRDTLLFESKGQLVGRGANRQGAEIQALTRGLTEAWKLGIKHVSIFCDSFPIFQFV
KGSWTPKQKKIAMLMDDLQRIRQQFSFTQAVLVAGNQVKYAYKLARESIVSQATPHENPRQAKLAARKEECLICFNDIDP
ERMFSIGKCTHRFCFQCVKQHVEVKLLHGMIPNCPHDKCNSEMVIDACGKLLTPKLGEMWKQRIKENAIPVTERVYCPYL
RCSALMSKTKISESAKSLQSAYPASGVRRCVECRGLFCVDCKVPWHGKLSCTEYKKLHPNPPADDVKLKSLANNKMWRQC
GKCQHMIELSQGCNHITCRCGHEFCYNCGGGWNKKTGTCAKQCPTWDEAYIMRQDPAPARVYVLPNNYFDDYDEDEYEDY
EADEDFEYEDYDADEDFEEEEEEVEVEVEEEVEEEEDEDEDEDEDEEEEEEEEEEEEEEEEEEEEDIFGRFSSEKFVETL
GLKRECTVTERVWKLLTPTIFDACGKLLTPKLGEMWKQRIKENAIPVTERVYCPYVRCSALMSKTKISESAKSLQSAYPA
SGVRRCVECRGLFCVDCKVPWHGKLSCTEYKKLHPNPPADDVKLKSLANNKMWRQCGKCQHMIELTQGRNHITCRYLSLT
L
```

606 - 625:	EEEEEEEEEEEEEEEEEEE

A0A3P6F770 **A0A3P6F770_BRAOL** (588 aa)
Uncharacterized protein. *Brassica oleracea (Wild cabbage)*

```
MALLSSCWLIIESIVIQDGFLKWSYMRLYMHPLVLFLCQLLLWLSVFLLWLVPYFQASYSSFLSFLVTFSKLFNSFLRVI
MSRREVTYNVASRQENKNTLVNLELSRRIHNPVPSFSFSFKHQVDSQLKVLLVLQEGKILEDEDFCSQLDQEDGAVHFLD
AKESEEEEDTIDFVDVVNVENNLEFEHQTMPMDQDEEEEEEEEEEEEEEEEEEEEEEEEDIVTSNVGNYLSSLEASDDINS
LNSDGDQPSPFSISSLDSVLQESIVIENPTHRDEDDDTNEVCNTYCQRMRWYDILSRDRTYGLSVMMNQEKASTLSLWGI
TAEKRLKQSIEKDLELVYVAQSCLSWEALQHQYLIVRDRMKASDSKGGSYEDNISKEFQKFQVLLERFLEDERCEGKRVL
RFVQRRFEHMSFFQVPRLSGYKRKGPQEGGRESNEKQVLKAIERCITVFYDFVKADTNRPLVWERLKISFVNSPLMEVED
PRDIMLFLNLKNLLQKKEQSLKEAQGNKKKTWFKKKNKSPYMKEDEIEKDENSMLLTFLKIELKLVSRVLQMSLVSSSHL
KWCEDKLNNIDFNGGKFSRTSSPILFPS
```

196 - 215:	EEEEEEEEEEEEEEEEEEE
197 - 216:	EEEEEEEEEEEEEEEEEEE
198 - 217:	EEEEEEEEEEEEEEEEEEE
199 - 218:	EEEEEEEEEEEEEEEEEEE

A0A3P6FYX7 **A0A3P6FYX7_BRAOL** (650 aa)
RING-type E3 ubiquitin transferase (EC 2.3.2.27). *Brassica oleracea (Wild cabbage)*

```
MDRGEIQLPCDADDVCMRCKSKIPSEECLTCSTCVTPWHVSCLRSPPATLASTQSWECPDCSGDVDPAPAPASGLNPSNS
SLVAAIRAIEADASLNEAQKAKKRQQLVSGKAVEEEEKEEQQSDDFLVSLRKNVSCSICLHLPERPVTTPCGHNFCLKCF
QKWVAGKRKPTCGTCRASIPKKMKDNPRINSVLVSAIRLAMVSKSTTVSTAKTYQFIRNVDRPEKAFTTERAKKTGKANA
CSGRIYVTVPSDHFGPILAGNDPDRNQGVLVGESWEDRQECRQWGAHFPHVAGIGGQSSYGAQSVALSGGYKDDEDHGEW
FLYTGSGGRDLTGNKRTNKDQAFDQQFTKSNAALRISCKMGYPVRVVRSHKEKRSAYAPAEKSVRYDGVYRIEKCWRKVG
IQGKRVCRYLFVRVDNEPAPWTSDEHGDRPRPLPSIPELKKATDMFVRTESPSWDFDESDGRWKWMKSPPASRKAIAALD
PAARKAMKGGGNKRDKFLKEFGCQICRKVMSSPVTTPCAHNFCKECLTGKFAGITQVRQRSRGGRTLRAQKNVMKCPCCP
NDISDFLQNPQVNRELMDVIEEVKKKKELEERQDEGNSENSAEGENTGSEEEEEEEEEEEEEEEEEEEEEESDVHVSEDE
PAAKKIKLSA
```

610 - 629:	EEEEEEEEEEEEEEEEEEE
611 - 630:	EEEEEEEEEEEEEEEEEEE
612 - 631:	EEEEEEEEEEEEEEEEEEE

A0A3P6H1T7 **A0A3P6H1T7_BRAOL** (92 aa)

Uncharacterized protein. *Brassica oleracea (Wild cabbage)*

```
MGQLTKLETVSKQSTIIAEFVRSEAETAVAETNGDDDDDDDDDYDDDYERMSVVGTCWTYMQGVEDLDGSEEEEEEEEEE
EEEEEEEEEEEE
```

71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE

A0A3P7DQK8 **A0A3P7DQK8_WUCBA** (536 aa)
Uncharacterized protein (Fragment). *Wuchereria bancrofti*

```
MKKTETIIEPDKMMIENEMDDEQLEEEEEEEEEEEEEEEEEEEEEEKRENEKEEEEKAKEEEEKAENKQNMINRKPPLLLV
TQPSTQNSPNHLTTEFTFDGNINFDIMRNDDDDSDDNASDGDDDDDNDDDDDNDGNAIILNAQKDNVENDVSISETIELQ
PDAGKTERKLRGDLYPVSLSKRRKRFISPIPFYENDFNEEFIVEAPTRNNDNRGRVSEIMAVPAPILTTSVSYDDMDDWD
STQEESVESLSDYEDIDDFNSEERYSRNRSRLENDDYRPTSSGFGIYFSPISSPINDYDDIQYQDNIDVGFTLKLVEKAA
LKETNEDESSSEYYDDSEYNLRYDLQYEGEELCRSDENDDDNDDVDVDDNDDDSEYTDDEEELDDVTSEDSCITENISTE
PLESAIDSVSSISIPLLTPTSMQEDDDIEIDEIFDQSVKKINKDEAMEQIAEGATEIAIRKVTPQHVIPAEENVEIIETN
ELKIQMPEQINVIVEEDKNEKEINQIEVVPTYVWPTIENYPIDSARSFIERKPCTD
```

25 - 44:	EEEEEEEEEEEEEEEEEEEE
26 - 45:	EEEEEEEEEEEEEEEEEEEE

A0A3P7L7A8 **A0A3P7L7A8_STRVU** (425 aa)
Uncharacterized protein. *Strongylus vulgaris (Blood worm)*

```
MGEEDYREEESRPRKRWTLEQLKSGNTFLSMQAATNKFDSQSGMTAPGMPRWNIVRDKQLGYIEPDRRSENVLRVQCGTN
QYASQKGETPIGASRFQVPKVSYKKDWETILDKEGEKIIPKQAGDYGLXXXXPIGASRFQVPKVSYKKDWETILDKEGEK
IIPKQAGDYGLATQSGEVSMGAHRNQVANVRGRLPHDRRTHGVLVFQNGTNIFASQTGMTAPPGVGAVRQATQRIEGLDM
TEDQQRRGTEFTPWYSGQNKFATQAGSGGFLKVRDVLPHSVGGKEIDEDLKQKSEGIVPLQSGTNKLASQRGMTGFGTPR
NTMLRSGWKKEWIEEYELALKEWEETKPPGSASSADPFGHYKKKFEERESSRQSEIDSQSVKAGEQAEEDKEAAAEEEEE
EEEEEEEEEEEEEEEEEEEEEEEE
```

396 - 415:	EEEEEEEEEEEEEEEEEEEE
397 - 416:	EEEEEEEEEEEEEEEEEEEE
398 - 417:	EEEEEEEEEEEEEEEEEEEE
399 - 418:	EEEEEEEEEEEEEEEEEEEE
400 - 419:	EEEEEEEEEEEEEEEEEEEE
401 - 420:	EEEEEEEEEEEEEEEEEEEE
402 - 421:	EEEEEEEEEEEEEEEEEEEE
403 - 422:	EEEEEEEEEEEEEEEEEEEE
404 - 423:	EEEEEEEEEEEEEEEEEEEE
405 - 424:	EEEEEEEEEEEEEEEEEEEE
406 - 425:	EEEEEEEEEEEEEEEEEEEE

A0A3P7PQ44 **A0A3P7PQ44_CYLGO** (305 aa)
Uncharacterized protein. *Cylicostephanus goldi (Nematode worm)*

```
MFCEYNAEQISMHPKKVPKVSYKKEWETILDKEGEKIIPKQSGDYGLATQAGEVSMGAHRNQVANVRGRTNIFASQTGMT
APPGIGAVRQATQRIEGLDMTEDQQRRGTEFTPWYSGQNKFATQAGSGGFLKVRDVLPHTVGGKEIDEDLKQKSEGIVPL
QSGTNKLASQRGMTGFGTPRNTMLRSGWKKEWQEIYRIEEYELALKEWEESKPPGSASSADPFGHYKKKFEERESSRQSE
VDTQSKAAEEEKEEEKEELEEEEEKEVEVEVGEEEEKPVEEEEEEEEEEEEEEEEEEEEEEEEEE
```

280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE

A0A3P7TBV2 **A0A3P7TBV2_HELPZ** (667 aa)
Uncharacterized protein. *Heligmosomoides polygyrus (Parasitic roundworm)*

```
MDQQVKHSSKHDRKNDESTIKPTSQATGWSEDDEKLRKTIPCDCGIPSTSSAELAEWVVQRTHEHEKRFVEREEEEKEEE
EEEEEEEEEEEEEEEEEQEEEEEEEEEEEEEEEEQEEDKEEEEEEEEEEEKEEREEKEQEEEEEEKEEEEEEEEEEEE
QEEEEEEEEEEEEEEEEEEEEEEEEQEEEEEEEEEEEEEEEEQEEDKEEEEEEEKEEKEEKEQEEEEEEEEEKEEEEE
```

```
EEEEEEEEGEEEEQEEEEEEEEEEEEEEEEEEEEEEEEQEEEEEEEEEEEEEEEEEQEEDKEEEEEEEEEEEKEEREEKE
QEEEEEEKEEEEEEEEEEEEQEEEEEEEEEEEEEEEEEEEEEEEEEQEEEEEEEEEEEEEEEEEQEEDKEEEEEEEKEEK
EEKEQEEEEEEEEEEKEEEEEEEEEEEEEEEEGEEEEQEEEEEEEEEEEEEEEEEEEEEEEEEEQEEEEGEEEEEEEEEEEEEG
EEEEEQEEEEEEGEEEEEEEAEEEEEEEEEGEEEEEQEEEEEEGEEEEEEEAEEEEEEEEEEEEKEEERKKKRRRKKKER
KKKRRKKKKRKKKGRKKKKFKMMMIMMMRGGAEEDSLSLMMMMMMIIIIIILFFFFFSPLLFCETSGVRAVNASVAKRSR
KNMGNKSGMKWTSTMPPLWGKPRWLTI
```

78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE
255 - 274:	EEEEEEEEEEEEEEEEEEEE
256 - 275:	EEEEEEEEEEEEEEEEEEEE
257 - 276:	EEEEEEEEEEEEEEEEEEEE
258 - 277:	EEEEEEEEEEEEEEEEEEEE
259 - 278:	EEEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEEE
344 - 363:	EEEEEEEEEEEEEEEEEEEE
345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
435 - 454:	EEEEEEEEEEEEEEEEEEEE
436 - 455:	EEEEEEEEEEEEEEEEEEEE
437 - 456:	EEEEEEEEEEEEEEEEEEEE
438 - 457:	EEEEEEEEEEEEEEEEEEEE
439 - 458:	EEEEEEEEEEEEEEEEEEEE
440 - 459:	EEEEEEEEEEEEEEEEEEEE

A0A3P8AF24 **A0A3P8AF24_HELPZ** (67 aa)
Uncharacterized protein. *Heligmosomoides polygyrus (Parasitic roundworm)*

```
MRTPPRSGTNADEEEGEEEEEEEEEEEEEEEEEEEEEEEEEDMITHVFYRFVLSRYNSTPLFFALYNA
```

17 - 36:	EEEEEEEEEEEEEEEEEEEE
18 - 37:	EEEEEEEEEEEEEEEEEEEE
19 - 38:	EEEEEEEEEEEEEEEEEEEE
20 - 39:	EEEEEEEEEEEEEEEEEEEE
21 - 40:	EEEEEEEEEEEEEEEEEEEE

A0A3P8HC56 **A0A3P8HC56_9TREM** (484 aa)
CW-type domain-containing protein. *Echinostoma caproni*

```
MRQIRRLRTTAAELRNLVTVRQNAVARKQKSIRDPKTLTFYFGVNVMNRACDGMFVYNCSRLIKMYQRIGPQQDSSMMCR
GVVGIVDVPYMVLEPTHNKQDFADAKEYRQLMRAMADHLMQYWDDLGIDKEAEDLVRFWKSFGYLSARWRDPPSGEDKYA
RRRCCSVSICVQCDKCLKWRVLPFSQSLVGRDVPDTWQCRDNPDHKHKRCEDPEEDLSPPMGVLKRKIKTKEQRQAELEK
QIRKKQLELIQDPDDENDARSGGNTRSSRSLTGSFAKPAVQVSSPRKRPPAVSPGSTLPTKRPTHPVTPPSRAMTVAEKK
RQITNSNGCASTQKRTGLPLPTTNQRQPPSGGLVPKVQREAPAKNRRVVVMDEEEEEEEEEEEEEEEEEEEEEEKVEKMAR
KNASRAKPSDKTKPTKAPPSTAVETTSEPKTLVSHLGIFPSNYDMHATRHEITIVQTNFGYLRGFAIGTEYKYYMSGLIY
LHPS
```

373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE

A0A3P8IKA7 **A0A3P8IKA7_HELPZ** (37 aa)
Uncharacterized protein. *Heligmosomoides polygyrus (Parasitic roundworm)*

```
MRLRGTKRTGEEEEEEEEEEEEEEEEEEEEEEEYVSCH
```

11 - 30:	EEEEEEEEEEEEEEEEEEE
12 - 31:	EEEEEEEEEEEEEEEEEEE
13 - 32:	EEEEEEEEEEEEEEEEEEE

A0A3P8JCD8 **A0A3P8JCD8_9TREM** (38 aa)
Uncharacterized protein. *Schistosoma curassoni*

```
MSQISEEEEEEEEEEEEEEEEEEEEEEEEEEKNTPFPNQ
```

6 - 25:	EEEEEEEEEEEEEEEEEEE
7 - 26:	EEEEEEEEEEEEEEEEEEE
8 - 27:	EEEEEEEEEEEEEEEEEEE
9 - 28:	EEEEEEEEEEEEEEEEEEE
10 - 29:	EEEEEEEEEEEEEEEEEEE
11 - 30:	EEEEEEEEEEEEEEEEEEE

A0A3P8PE56 **A0A3P8PE56_ASTCA** (1794 aa)
Bromodomain and WD repeat domain containing 3. *Astatotilapia calliptera (Eastern happy) (Chromis callipterus)*

```
MAREQCSQIEAELYYLIARFLQSGPCKKAAKILIEELEEYELVPQRWSWDGKKYKRNFQDWVVLNQHIPADYLLRICQRI
GPLIEKEIPPCVPGVQTLLGLGRQSLLRTSKSCSHKVCSGSAVAALHRGRPPEPPVSNGSSPNVVSIMGARQATGTGRFG
QVLPSSSYQHMKIHKRILGHLSSVYCVAFDRTGRRIFTGSDDCLVKIWATDDGRLLATLRGHSAEICDMAVNHENSLIAS
ASCDKVIRVWCLRTCAPITVLQAHAASITSIQFCPAARGTTRYLASTGADGMVCFWKWHSLTMKFNDHPVKFMERSRPGV
QVSTSSFSSGGMFMATGGTDHMIRVYYLGAESPMKVSEMDAHTDKVVVVQFSNNSDSLRFVSGSRDGTVKIWHYQQQEWK
STTLDMAARLPGSTAATGDDKAKLVVTMVAWDRTDSTIITAVSNYLLKVWSTSTGQLLHILSGHDDEVFVLEAHPFDSRI
MLSAGHDGNIYIWDLTKGVKIRNFFNMIEGQGHGAIFDCKFSADGQHFACTDSHGHLLIFGFGCSRPYEKIPDQMFFHTD
YRPLIRDSNNYVLDEQTQQAPHLMPPPFLVDVDGNPHPSHYQRLVPGRENCKEEQLIPQMGYMANNDGELVEQVLGQQTA
ENGESPLDNLIRQLQNEQDERQNAEQEAEGEEAGEGAEAVPSSPVVAPRRSGQVDGVWQMQHNALPSQVATERDLLAWSR
RVVVNEVLQGIFRVSEECRQAKGDIECSLYYAERKKKPVTCAPKSDLLSSRLRSLRPTKKTHKRHAYQTRSAQIRRPGTR
SRNPSNRRTSNSQMDSESDGEQAEEQVEQTDASSDGDARWQSESSSSDSSSEYSDWTADAGINLQPPKRPTRRPVQPPDY
SSSEEEGDNEAKEARTREKEKRKKKSKETKQKPTSSLGGLDAEEWLPPSWIMETVPRCSPFVPQMGDELIYFKQGHQAYV
RAVRRAKAYSINPQKQPWNRLNLRDQESVKVVGIKYEVGPPTLCCLKVAFLDPVSGKMTNESFSLKYHDMPDVIDFLVLQ
QFYNEAKEHNWQPGMRFRSIIDDAWWFGSVEDQEPLQPEYPDSLFQCYAVKWDNGEREKMSPWDMEPIPEEAALPEQVGD
GVEVAEEELKALLYEPQEGEWGAHTRDEECERVIHGIDQLLTLDVAKAFALPVNLQDYPLYCTVVAYPTDLSSIRTRLEN
RFYRRISALMWEVRYIEHNARTFNEPQSPIVAAAKVVTDVLLHYIGDQSCIDVLDLYRKLKSEVSSEAEVDLDVDSDTPG
TSTGHRGGTANSKKRGVVLDPKAWRGQCRELLRRMTASTNSEPFRQPVDLFEYPDYRDIIDTPMDLGTVSETLAVGNYEN
PMEFSKDIRLIFSNSKAYTPNKKSQIYTMTLSLSAFFEKHIISIISDYKSAIQNERRARQHLTYRNRLHNGGSSPPNSPS
HSSKGKHKSGKASKPKKSQTSTKNRSQRSHKAQQSGNVAEEEDVQPSSPTSGTSVRSRNQGPHRVTRSQATPVKKSGHQN
NLHLSNGSRQRHLRETSQSDDEEEASGSNSSSLESSSTSSSSSSSSSSSSSSSDSDNSSDSEVEKYVEGGGDHDYSKAP
CLSVRLSAKGKVAASEKRRHKGGEDTEAQGPKRARLQLEVEEQQDEEEEEAEEDEEEEEEEEEEEEEKEQQQQVDLKHE
EEEEEEEEEEEEEEEEEEEEEEEPEDEDDNNSEVQTRAAAAPAAASSQRGSQCKSRRVNTRNQGRRTVRYGDDSEDDGH
GSKDDPLNLGMSRSGRVRRMTEKARVSHLMGWSH
```

1680 - 1699:	EEEEEEEEEEEEEEEEEEE
1681 - 1700:	EEEEEEEEEEEEEEEEEEE
1682 - 1701:	EEEEEEEEEEEEEEEEEEE
1683 - 1702:	EEEEEEEEEEEEEEEEEEE
1684 - 1703:	EEEEEEEEEEEEEEEEEEE
1685 - 1704:	EEEEEEEEEEEEEEEEEEE

A0A3P8PUH7 **A0A3P8PUH7_ASTCA** (914 aa)
B-cell lymphoma/leukemia 11A-like. *Astatotilapia calliptera (Eastern happy) (Chromis callipterus)*

```
MSRRKQGKPQHLSKRDFSPEPLSTAVVSSEELSERCSENSEESGSLNGHHPGSNVGRLARLGHDAHPSLEQDLLTCGQCQ
ATFPLADILLFIEHKRKRCHGPPCLTVGRGLDKPPSPSPGLALTPSPAMGSLRSRRLEVGVQATLADEDDDRFSSPRGIC
PKQEPLPGKEEPTTYTCTTCKQSYGSAWFLLQHAQNTHGFRIYLESEHGSPLTPRMGGPSSLGGGADCPSQPPLHGLHLP
PDASPFNLLRIPGSGSGGRDSVGAGGGIGTGAVGGGHHQRFPPTPPLFSPPPRNHLDPHHLSPEELALAAHHPSAFDRVL
RLNPPLPLDPPPTMDFSRRLRELAGNTSGSTPPLSPSRPSPMQRLLQPFQTGGGSGGTGGAGGSKPPYLATPPPLPGSMQ
SPVGSQTTPTTPLPSAGATPSSTTQLKSKCCEFCGKAFKFQSNLIVHRRSHTGEKPYKCHLCDHACTQASKLKRHMKTHM
HKSSSPNTGKSEDGLSTASSPEPGTSEHVGSASNALKSVVAKLKSENDRMLRENGEEEEEEEEEEEEEEEEEEEEEEEE
GEEEEEQNGERVARRNNNSYHFGLNLETARQHENNGSIGSRLGGVADEGSIPRSLPEVMQGMGLAASMQHFSEALNAHKR
NAMAQENHLHHHLNRDHHHNREICDGDSVLETDRGEEGSVSTVNGRGASPNESASVGLSKKLLLGSPSPLSPFSKRIKLE
KEFDLPTSTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRFSTPPGELDGGMSGRSGTGSG
GSTPHLGGPGRPSSKDGRRSDTCEFCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQSSKLTRHMKTHGQVGKDVYK
CEICQMPFSVYSTLEKHMKKWHSDRPLSTEIKSE
```

536 - 555:	EEEEEEEEEEEEEEEEEEE
537 - 556:	EEEEEEEEEEEEEEEEEEE

538 - 557:	EEEEEEEEEEEEEEEEEEEE
539 - 558:	EEEEEEEEEEEEEEEEEEEE
540 - 559:	EEEEEEEEEEEEEEEEEEEE
541 - 560:	EEEEEEEEEEEEEEEEEEEE

A0A3P8PUZ7 **A0A3P8PUZ7_ASTCA** (928 aa)
B-cell lymphoma/leukemia 11A-like. *Astatotilapia calliptera (Eastern happy) (Chromis callipterus)*

```
MSRRKQGKPQHLSKRDFSPAEPLSTAVVSSEELSERCSENSEESGSLNGHHPGSNVGRLARLGHDAHPSLEQDLLTCGQC
QATFPLADILLFIEHKRKRCHGPPCLTVGRGLDKPPSPSPGLALTPSPAMGSLRSRRLEVGVQATLADEDDDRFSSPRGI
CPKQEPLPGKEEPTTYTCTTCKQSYGSAWFLLQHAQNTHGFRIYLESEHGSPLTPRMGGPSSLGGGADCPSQPPLHGLHL
PPDASPFNLLRIPGSGSGGRDSVGAGGGIGTGAVGGGHHQRFPPTPPLFSPPPRNHLDPHHLSPEELALAAHHPSAFDRV
LRLNPPLPLDPPPTMDFSRRLRELAGNTSGSTPPLSPSRPSPMQRLLQPFQTGGGSGGTGGAGGSKPPYLATPPPLPGSM
QSPVGSQTTPTTPLPSAGATPSSTTQLKSKCCEFCGKAFKFQSNLIVHRRSHTGEKPYKCHLCDHACTQASKLKRHMKTH
MHKSSSPNTGKSEDGLSTASSPEPGTSEHVGSASNALKSVVAKLKSENDRMLRENGEEEEEEEEEEEEEEEEEEEEEEE
EGEEEEEQNGERVARRNNNSYHFGLNLETARQHENNGSIGSRLGGVADEGSIPRSLPEVMQGMGLAASMQHFSEALNAHK
RNAMAQENHLHHHLNRDHHHNREICDGDSVLETDRGEEGSVSTVNGRGASPNESASVGLSKKLLLGSPSPLSPFSKRIKL
EKEFDLPTSTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRFSTPPGELDGGMSGRSGTGS
GGSTPHLGGPGRPSSKDGRRSDTCEFCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQSSKLTRHMKTHGQRLGGVQ
DSDHSIYEMIQKKDEKQTNKKQNKKKTNSVIFFFSVFCFALALHSSSG
```

537 - 556:	EEEEEEEEEEEEEEEEEEEE
538 - 557:	EEEEEEEEEEEEEEEEEEEE
539 - 558:	EEEEEEEEEEEEEEEEEEEE
540 - 559:	EEEEEEEEEEEEEEEEEEEE
541 - 560:	EEEEEEEEEEEEEEEEEEEE
542 - 561:	EEEEEEEEEEEEEEEEEEEE

A0A3P8PV38 **A0A3P8PV38_ASTCA** (852 aa)
B-cell lymphoma/leukemia 11A-like. *Astatotilapia calliptera (Eastern happy) (Chromis callipterus)*

```
MSRRKQGKPQHLSKRDFSLNGHHPGSNVGRLARLGHDAHPSLEQDLLTCGQCQATFPLADILLFIEHKRKRCHGPPCLTV
GRGLDKPPSPSPGLALTPSPAMGSLRSRRLEVGVQATLADEDDDRFSSPRGICPKQEPLPGKEEPTTYTCTTCKQSYGSA
WFLLQHAQNTHGFRIYLESEHGSPLTPRMGGPSSLGGGADCPSQPPLHGLHLPPDASPFNLLRIPGSGSGGRDSRFPPTP
PLFSPPPRNHLDPHHLSPEELALAAHHPSAFDRVLRLNPPLPLDPPPTMDFSRRLRELAGNTSGSTPPLSPSRPSPMQRL
LHKPPYLATPPPLPGSMQSPVGSQTTPTTPLPSAGATPSSTTQLKSKCCEFCGKAFKFQSNLIVHRRSHTGEKPYKCHLC
DHACTQASKLKRHMKTHMHKSSSPNTGKSEDGLSTASSPEPGTSEHVGSASNALKSVVAKLKSENDRMLRENGEEEEEEE
EEEEEEEEEEEEEEEEEEGEEEEEQNGERVARRNNNSYHFGLNLETARQHENNGSIGSRLGGVADEGSIPRSLPEVMQGM
GLAASMQHFSEALNAHKRNAMAQENHLHHHLNRDHHHNREICDGDSVLETDRGEEGSVSTVNGRGASPNESASVGLSKKL
LLGSPSPLSPFSKRIKLEKEFDLPTSTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRFST
PPGELDGGMSGRSGTGSGGSTPHLGGPGRPSSKDGRRSDTCEFCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQSS
KLTRHMKTHGQVGKDVYKCEICQMPFSVYSTLEKHMKKWHSDRPLSTEIKSE
```

474 - 493:	EEEEEEEEEEEEEEEEEEEE
475 - 494:	EEEEEEEEEEEEEEEEEEEE
476 - 495:	EEEEEEEEEEEEEEEEEEEE
477 - 496:	EEEEEEEEEEEEEEEEEEEE
478 - 497:	EEEEEEEEEEEEEEEEEEEE
479 - 498:	EEEEEEEEEEEEEEEEEEEE

A0A3P8R7R9 **A0A3P8R7R9_ASTCA** (836 aa)
B-cell lymphoma/leukemia 11B-like. *Astatotilapia calliptera (Eastern happy) (Chromis callipterus)*

```
MSRRKQVNPQHLSLTHRETIQEANHDSGAGSPSPELSTPSPRRRASGEHDLLTCGQCQTNFPLGDILVFIEHKRRLCRGP
IGGLGSFSKPGAAGGVMGLPISPRARSLELGRGAVPVEVGVQVTPGGEEDQARRLTPAKGICPKQERGEKDEPSSYICTT
CKQTFTSAWFLLQHAQHTHGIRIYLDNHPVNCSLTPRMALPPPPGADALPRSPLPTFLGDASNPFHLLRMAGPQLRDHPH
PPGYMETRLPATPPFVSPPPPPRPPRERLGPEEMGLLSQHPSAFERVMRMTPMEHPPMDFSRRLRELAGNTTNNGGPTPP
LSPNRVPPMHRLLSPTLFQPGSQLSPFLTYPPQPPTSQGGHGSSSPPDTQGQNQAPGKSKSCEFCGKIFKFQSNLIVHRR
SHTGERPYKCHLCDHACSQASKLKRHMKTHMHNKSGAITGSPEQGNRGEGGEGEEKNREGDARGMGMDNEEEEEEEEEEE
EEEEEEEEELQNGSRPDSNLSEDSQEFTQNRENGSRQSPSEKPPSGDRVNDSGGVGIMHPYNHLDNHLRLNPNKRSLERQ
PNGDGGEGVEGERERENEREPDRQREEQEDQRPVMNGRISVSEAECFPGLFQRRPTPITSPSPSNNKRIKIEKEQLEIPP
TIPLISPENVYSQLLAGYAASRHFIREPFLGFTDSRQSPFATSSEHSSSETGSLRFSTPPGELMEGGSASGRSGSSTPHL
LRGPGPGRPPSSKERRNDTCEFCGKVFKNCSNLTVHRRSHTGERPYKCDLCSYACAQSSKLTRHMKTHGQYGKEVYRCDI
CHMPFSVYSTLEKHMKKWHGEHLMASEVKLEQADRS
```

470 - 489:	EEEEEEEEEEEEEEEEEEEE

A0A3P8SFX1 **A0A3P8SFX1_AMPPE** (848 aa)
BAF chromatin remodeling complex subunit BCL11A a. *Amphiprion percula (Orange clownfish) (Lutjanus percula)*

```
MSRRKQGKPQHLSKRDFSRSTVGRLARLGHDAHPSLEQDLLTCGQCQATFPLADILLFIEHKRKRCHGPPCLAVGRGLDK
PPSPSPGLALTPSPALGSLRSRRPVEVGVQATLADEDDDRFSSHRGICPKQEPLPGKEEPTTYTCTTCKQSYGSAWFLLQ
HAQNTHGFRIYLESEHGSPLTPRMGGPSSLGGGADCPSQPPLHGLHLPPDASPFNLLRIPGSGSGGRDSRFPPTPPLFSP
```

```
PPRNHLDPHHLSPEELALAAHHPSAFDRVLRLNPPLPLDPPPTMDFSRRLRELAGNTSGSTPPLSPSRPSPMQRLLHKPP
YLATPPPLPGSMQSPVGSQTTPTTPLPSAGATPSSTTQMKSKCCEFCGKAFKFQSNLIVHRRSHTGEKPYKCHLCDHACT
QASKLKRHMKTHMHKSSSPNTGKSEDGLSTASSPEPGTSEHMGSASNALKSVVAKLKSENHRMLRENGEEEEEEEEEEEE
EEEEEEEEEEEEEEGEEEEEQNGERAARRNNNSYHFGLNLEAARQHENNGGIGSRLGGVADEASIPHSLPEVMQGMGLAA
SMQHFSEALHAHKRNAMAQENHLHHHLNRDHHHNRELCDGDSVLETDRVEEGSVSTVNGRGASPNESASVGLSKKLLLGS
PSPLSPFSKRIKLEKEFDLPTPTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRFSTPPGE
LDGGMSGRSGTGSGGSTPHLGGPGRPSSKDGRRSDTCEYCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQSSKLTR
HMKTHGQVGKDVYKCEICQMPFSVYSTLEKHMKKWHSDRPLSTEIKSE
```

469 - 488:	EEEEEEEEEEEEEEEEEEEE
470 - 489:	EEEEEEEEEEEEEEEEEEEE
471 - 490:	EEEEEEEEEEEEEEEEEEEE
472 - 491:	EEEEEEEEEEEEEEEEEEEE
473 - 492:	EEEEEEEEEEEEEEEEEEEE
474 - 493:	EEEEEEEEEEEEEEEEEEEE
475 - 494:	EEEEEEEEEEEEEEEEEEEE

A0A3P8TGX5 **A0A3P8TGX5_AMPPE** (837 aa)
lm:7142702. *Amphiprion percula (Orange clownfish) (Lutjanus percula)*

```
MSRRKQVNPQHFSLTHRETIQAEANHDSGAGSPSPEPSTPSPRRAGPGEHDLLTCGQCQTNFPLGDILVFIEHKRRLCRG
PSGRPGSFSKPGEAGGVMGIPISPRVRSLELGRGAIPVEVGIQVTPGGEEDEARRLTPAKGICPKQERGDKDEPSSYICT
TCKQTFNSAWFLLQHAQHTHGIRIYLDNHPANCSLTPRMALPPPPGVDALPRSPLPTFLGDTNNPFHLLRMAAPLLREHP
PPPGYMETRLPATPPFVSPPPPPRPPLERLGPEEMGLLSQHPSAFERVMRMTPMEPPSMDFSRRLRELAGNTTNNGGPTP
PLSPNRVPPMHRLLSPTLFQPGAKPPAFLTYAPQPPTSQGGHGSSSPPDSQGQSQTPGKSKSCEFCGKIFKFQSNLIVHR
RSHTGERPYKCHLCDHACSQASKLKRHMKTHMHNKSGAMSGSPEQGNRGEGGDGEDKTREGDAREMGMDNEEEEEEEEEE
EEEEEEEEEELRNGSRPDSNLSEDSQEFSQNRENGPRHSPEDKSLSGNRVSDSGGVGIMHPYNHLDNHLRLNPNKRSLER
QPNGDGGERGEVERQRDNERDQDRERDEQEDQRPVMNGRISVSEAESFPGLFQRRPTPITSPSPSNNKRIKIEKEQLEIP
PTIPLISPENVYSQLLAGYAASRHFIREPFLGFTDSRQSPFATSSEHSSSETGSLRFSTPPGELMEGGSASGRSGSSTPH
LLRGPGPGRPPSSKDRRNDTCEYCGKVFKNCSNLTVHRRSHTGERPYKCDLCSYACAQSSKLTRHMKTHGQFGKEVYRCD
ICHMPFSVYSTLEKHMKKWHGEHLMASEVKLEQADRG
```

471 - 490:	EEEEEEEEEEEEEEEEEEEE

A0A3P8TXP9 **A0A3P8TXP9_AMPPE** (813 aa)
BAF chromatin remodeling complex subunit BCL11A b. *Amphiprion percula (Orange clownfish) (Lutjanus percula)*

```
MSRRKQGKPQHLSKREFSPEPLAGVLPEEDSQDSPRLGVAHGEPLKGDQDLLTCGQCHSRFPLADILLFIEHKRRQCHGS
LCADKPLDRPPSSPLASPLSTSSSHSRTQHQHPRRVRQPVEVAVQVSPQDEDCLSAPLQGIIPKQENITDKDEPSSYTCT
TCKQPFTSAWFLLQHAQNTHGFRIYLESEPGSPLTPRVAAAPGMGGDCASSQPPLHAVHLADGSPYSLLRMPGSGSGRDS
ASTPREGRYPRTPPLFSPPPRHHLSPDDLALATHHPSAFDRVMRLNSVPLDPPQSMDFSRRLRELAGNATGGSPPLSPNR
PNPMQRLLQPFQPGSKPPFSATPPLSTSQSPSGSRSTPNPVSNAVQPGTPLKAKSCEFCGKTFKFQSNLIVHRRSHTGEK
PFKCHLCNHACTQASKLKRHMKTHCQSKSTVLNTKSDDGLSTASSPEPGTSELMGSATDALKSVVAKFKSENNGLMPENG
EEEEEDEEEEEEEEEEEEEEEEEEEEEEGEAEEEEIESKPGVDEEGRNDYRFSLRLEGARHHQNSEALYPHRRSLSREPG
DEDSAMESDRADDGSTTTINGLGSLPNDNLSRKLLGGGVSPGSLSPLSKRIKVEKDIDPPTPTIPNTENVYSQWLAGYAA
SRQLKDPFISFTGGDSRQSPFASSSEHSSENGSLRFSTPPGELDGERAASGRSGTGSGASTPHGGSGNGRPSSKDGRRSD
TCEFCGKVFKNCSNLTVHRRSHTGERPYKCELCSYACAQSSKLTRHMKTHGQMGKDVYKCEICHMPFSVYSTLEKHMKKW
HSDRPLANDIKTE
```

487 - 506:	EEEEEEEEEEEEEEEEEEEE
488 - 507:	EEEEEEEEEEEEEEEEEEEE
489 - 508:	EEEEEEEEEEEEEEEEEEEE

A0A3P8US53 **A0A3P8US53_CYNSE** (763 aa)
BAF chromatin remodeling complex subunit BCL11A a. *Cynoglossus semilaevis (Tongue sole)*

```
MSRRKQGKPQHLSKREFSKEEPTTYTCTTCKQSYGSAWFLLQHAQNTHGFRIYLESEHGSPLTPRMGGPSSLGGGADCPS
QPPLHGLHLPPDASPFNLLRIPGSGSGGRDSVGALGGIGAVPTTAPVHHQRFPPTPPLFSPPPRNHLEPHHLSPEELALA
AHHPSAFDRVLRLNPPMPLDPPPTMDFSRRLRELAGNASGSTPPLSPSRPSPMQRLLQPFQTGGGSGGSVGAGGSKPPYL
ATPPPLPGSLQSPVGSQTTPTTPLQSAEATPTSTTPLKSKCCEFCGKAFKFQSNLIVHRRSHTGEKPYKCHLCDHACSQA
SKLKRHMKTHMHKSSSPNASKSEDGLSTASSPEPGTSEHLGSASNALKSVVAKLKNENNRILRENGEGEEEEEEEEEEEE
EEEEEEEEEEVEEEEDPNGERQPRRNNSFHFGLNLETTRQHENNVGIGSRLGGLTDEGSLPRSLPEVMQGMGLAASMQHF
SEALNAHKRNAMAQENHLHHHLNREHHHNRNMCDGDSVLETDRGEEGSVSAVNGRGASPNESASVGLSKKLLLGSPSPLS
PFSKRIKLEKEFDLPTPTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFTSSSEHSSENGSLRFSTPPGELDGGI
SGRSGTGSGGSTPHLGGHGRPSSKDSRRCDTCEYCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQSSKLTRHMKTH
GQVGKDVYKCEVCQMPFSVYSTLEKHMKKWHSDRPLSTEIKSE
```

389 - 408:	EEEEEEEEEEEEEEEEEEEE
390 - 409:	EEEEEEEEEEEEEEEEEEEE
391 - 410:	EEEEEEEEEEEEEEEEEEEE

A0A3P8V328 **A0A3P8V328_CYNSE** (2010 aa)
Uncharacterized protein. *Cynoglossus semilaevis (Tongue sole)*

```
MAGERRSGNLLVQLGPKLQAYPEELIRQRRTHDGQTEYLIRWCVGGSNSSTSGETKQENILMWMSTEDVYANCPMLLGKR
```

KTDAHAGGAEEFPSDVTFDEVELSDMKEDVKNLVRRARKQMAKKSDYSISITHTIHVLSAYAGIGSLVGVFKETGALNLL
MELLCNKETQTRRSAGKMLRALASHDAGSRAYVLLSLSQQDGIEQHMDFDNRYTLLELFAETTSSEEHGISFEGIHLPQI
PGKLLFSLVKRYLCVTSLMDKLNTVGAESNSDRQDGSPCPSSASSTGTIHQAERLRLQREFDFTMAMANLISELVRVMGW
DRNRQSLDNPAYLMGEGGVVAEEQVEEAARPILRSIFQPRFCASPLTFPISAAASAPPAIPPKKKKTGDGFKTRSDFASR
SAYVEYVQENLKSGMTVRMLEDYEEVNAGDDGVFRYSNDGSPPVQVYWNSLSRTYWVHWHMVEILSNGAGSQSEKESQDK
PPGGLYSLPYLSEDLQTEPAVLNRAEWGEILFFTKEARAETAAGNTVYVSLSCSVLCACPCVLCFTPLCPLCVLRDKVLK
QLVDFLSSPSKEVVDSSLRLTHSLMMKFEWRVSFATEGGVKAVLSCMQEFASVPAIQQLGLAVRIISTSNRSGYSAFYPQ
VFQNRSLYFCVDMLLLMLNKFLDNYQEDLLPWHESIEPCLSSMTAFINDREVVQQFIRFLYRLASLNKDYAVVMCRLGAK
EALVKALDKHSTNLLLVGELRDVVSDCDKYASLYKKMTTSVLAGCIQMVLGQIEEHRRSHQPINIPFFDVFLKNLCQGSS
VELKEDKCWEKVEVSSNHHRANKLTDKNPKTYWESNGCTGSHFINIFMHKGVIIRQLAILVATEDSSYMPARVVVLGGDD
PTNITTELNTVNVVPSANRVVLLENMTRFWSIIQIRIKRCQQGGIDTRVHGFEVLGPKPTFWPVFKEQLCCRTYLFYSTK
SHTWCQEVMEDRTQLLQLFNKLNSALKHEQLFADRFLPDAEASEALGQTCWEALITPIVHSITLSESSASSPLSWLLSEY
LENTESSRRCKSRAAIFNSRVRRLTHLLVHVDTSRTDSEELKPPVKSSESETTSPFYTVKSSSSIAGIALCWQGVVKRQV
KKFLESSFSLPDFVEKYRILYLRLKNAMEELFGQQTAFVLALRHGFSAALLQLSILRAMHVSERFAQYIDQMIHLSGSGA
ASGSMETLEKLQQFLEPVLFLSGLELANTFEHFYRYYLGDRLLAQGNVQLENAVVALIGSCFPDRIPQQMLKNLSESAEL
QQEFHLYQLQRLDRRLQDQEPEEEEEEEEEEEEEEEEEEEEEEEEDEADVQALVLSPRYWAVSSNCFLDEPTKNFPTELC
SYLKQFTQFYTHSQYHFAHINQDQDHIHLLINTKSKKHERQQDARKCYTTLSCVTADVLSCIMHVISKGCVRRNEDNLHI
VEFVPEDPSTPQKGQAQFSFSHTDIRKNSNANEPHFEDGVLDTILFSMGRTMTPEEVRQLMQTTVQQVSGTLSLDVDQTE
HLLLHCKWNVDLLVQRYTDDPETLIVAAGLKSRNPPPPPSPASTCPVCLSPCNNNPFTGAEPVPLLSCMHYCCRLCWQKY
LTARIEQNLVMNCNCPITDCQAQPTSRFFLNILTDKDTIAKYESALLRVYVECCSNLTWCTNPQGCDQILCKENMGSMGT
CSKCCWSSCFSCNFPEAHYPASCSHMSQWMDDGGFYEGMTVEAQSKHLAKLISKRCPSCQAQIEKNEGCLHMTCAKCNHG
FCWRCLKPWKPTHKDYYNCSAMVSKAARQEKKFQDYNERCTFHHQAKDFAINLENKVSSINEALQMKSLTFVIDACKILA
QARKVLAYSCVYSYYNQETEKMDVMEQQTEALDLHTNALQILLEETLLQCTDLASCVRLLKPEHLNTGLELIRRIKERLL
AILQHSTQDFRVGYQSSSNQEPTGRGSDSGDSDNNNYAGEEGGDEAEEEDDEYDEEYVPEWHEDYDEDDIDEDDFFSDES
ENLEHYSPVL

1302 - 1321:	EEEEEEEEEEEEEEEEEEEE
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1305 - 1324:	EEEEEEEEEEEEEEEEEEEE
1306 - 1325:	EEEEEEEEEEEEEEEEEEEE

A0A3P8V417 **A0A3P8V417_CYNSE** (1020 aa)
CCAAT enhancer binding protein zeta. *Cynoglossus semilaevis (Tongue sole)*

MAAKNKQRKKTKSSLKQNFQSEEKEPEPEDSGAEQDEESEYSNGGGGGGGGGGGNLDEEELSLDEVLRLGGTQADYILL
AALEDNVELVDGGKKGAIDDLEEGELETFIKKLDFKAFAGQHVIPDEPDLDGAKEGKKTKTKTGASAADHEAGGQEEVGS
DRQEVTKQKAKKKTPEQGSAGKKARHNVNLFEFQPRHNLLLKPGGKWFDLEYSAEGSSSPQDPQLVSQYKTLAQQLLEAE
VALYKNKKVLQKGANSAWMKTVVSSGVLADRMAAMTVLIQDAPVHALEHVSSLVAMVKRKGSRRMGLMALDTLRELLLSD
LLPENRKLRTFAEHPFHQLEEKASGNRDARDRRLLIWYFEHQLKHHVAEFVEALDSVAHDTVAATKAKALATAHELLCNR
PEQEKALLGQVVNKLGDPEYKTAAKASYLLETLLHRHPNMKAVVCCEVERLVFRPNISAKAQYYAVCFLSQVLLSHEEAA
LAAKLINIYFSFFRACVKKKEVESKMLSVLLSGVNRAYPYAAAGDEKVKEQLDTLFRVVHLVKFNTAVQALMLLFQVMDS
QQTVSDRYYVALYRKLLDPGLSSSSRQSMFLNLLYKSLKVDIVLRRVKAFVKRLLQVSAEQSASFACGALFLVSEVMKVK
PGLKTLLQEDEEEEEEEEEEEEEEEEEEEEEEEQEVHKDEGNPQRSKVKPAASWVHHQNMEGVSKVYDPLHRNPLFCGAD
HSGLWELQRLTQHFHPSVSLFAKTLLQGGTILYSGDPLQDFTLIRFLDRFVFRNPKKAKGQQNTDSAVMRPKQKLSFKSL
PVNCEEFLSKDESQIPVEEIFFHRFFKKRQQEKQKLGLRDRVGDNESVEDVDDEEFEKILDSCEGDSYFTDLGDQDLDFA
GNVKSKKGKKGEEDSDVDDSDVDDLDDEEVSLGSMEDEDFGDELEEDGGMFMDPDADEGTEFGSLLDENAGSKFDNIGLN
AMANTDRAGVKQLKWEAQRDDWIHGRDVKTLRRKKTAFNRRRAVGGARMMGKRKVIKSTV

651 - 670:	EEEEEEEEEEEEEEEEEEEE
652 - 671:	EEEEEEEEEEEEEEEEEEEE
653 - 672:	EEEEEEEEEEEEEEEEEEEE
654 - 673:	EEEEEEEEEEEEEEEEEEEE

A0A3P8VNS6 **A0A3P8VNS6_CYNSE** (597 aa)
Si:ch211-203d1.3. *Cynoglossus semilaevis (Tongue sole)*

MALLTLHRNPSLSCVTPYEPRRGRLQKRESFALVKGAVLLLEGGEGEEHRGETSPTVTSPVKSSGASNMRHRHLQAMIEQ
LRPEDTIQLAVQLESLNPVRVRYLIVVSTLGRKHESVLLGMDFPNTDRCCTIGLVMPVWSDTQVYLDGDGGFSVTSAVDT
RIFKPISMQTMWSVLQSLHGCCERAVKAAVIPGSGLEWVEHYNKHIESDRFCLNEWEIMDDLASVRKDMAGLSSEDRFSK
EVLIKEHLRDIMRTEDLDNLTSKMVKTALETRIGFDVRLYKEYIDNEIMVTMAQMDKPSKIFDYLYLGSEWNAANFEELQ
KNNVGYILNVTREIDNFFPDSFSYMNIRVYDVESTDLLPYWTNTYKFINNARKSGQAVLVHCKMGISRSASTVIAYAMKQ
LRWPLDVALSYVRERRAIIHPNDGFMKQLQTYNGILNASEQRHSALWRRKSKDLRQKSLSKEEKGSQGEERNGKEEEEEE
DEGLYDDEEEEEEEEEEEEEEEEEEEEEEDEESPIEKDGEVTSHSDKTLKYCGAFVLRLFSNKQVFEDLDCRSDLPGSPRRS
PQQRRRSQGRRSLTHQNACVDVSPEPRCLLATDENKP

488 - 507:	EEEEEEEEEEEEEEEEEEEE

A0A3P8VVE9 **A0A3P8VVE9_CYNSE** (808 aa)
B-cell lymphoma/leukemia 11A-like. *Cynoglossus semilaevis (Tongue sole)*

MSRRKQGKPQHLSKREFSPEPLSGVLPEEDSQDSPRLGAVPDDPLKGDQDLLTCGQCHSRFPLADILLFIEHKRRQCHGS
LCADKPLDRPPSSPLASPLSTSSSHSRTTHQHPRRACHPVEVAIQVSPQDEDCLSTPLQGIIPKTEHITDKDEPSSYTCT
TCKQPFTSAWFLLQHAQNTHGFRIYLESEPGSPLTPRVATAPGMGGDCASSQPPLHAVHLAEGSPYSLLRMPGSGSGRDS
ASTPREGRYPRTPPLFSPPPRHHLSPDDLTLATHHPSAFDRVMRLNSVPLEIPPSMDFSRRLRELAGNATGSSPPLSPNR
PNPMQRLLQPFQPGSKPPFSATPPLSTSQSPSGSRSTPNTITNAVQPATPLKAKSCEFCGKTFKFQSNLIVHRRSHTGEK
PFKCHLCNHACTQASKLKRHMKTHSQNKSSAINAKSDDGLSTASSPEPGTSELIGSATDALKSVVAKYKSDNNHLRENGE
EEEDEEEEEEEEEEEEEEEEEEEEEEEEVENKPVVEEEDGRNDYRFSLRLEGARHHQNSDALHPRRRSSSQDPADDDSA
MESDRADDGTTTTINGLGPLSTESLSRKLLGGRVSPGSLSPLSKRIKVEKDIDPPTPTIPNTENVYSQWLAGYAASRQLK
DPFLSFTGGDSRQSPFASSSEHSSENGSLRFSTPPGELDGERAASGRSGTGSGASTPHGGNGNGRPNSKDSRRSDTCEYC
GKVFKNCSNLTVHRRSHTGERPYKCELCSYACAQSSKLTRHMKTHGQLGKDVYKCEICHMPFSVYSTLEKHMKKWHSDRP

LANEIKTE

485 - 504:	EEEEEEEEEEEEEEEEEEEE
486 - 505:	EEEEEEEEEEEEEEEEEEEE
487 - 506:	EEEEEEEEEEEEEEEEEEEE
488 - 507:	EEEEEEEEEEEEEEEEEEEE
489 - 508:	EEEEEEEEEEEEEEEEEEEE
490 - 509:	EEEEEEEEEEEEEEEEEEEE

A0A3P8WTS5 **A0A3P8WTS5_CYNSE** (1013 aa)
PH and SEC7 domain-containing protein 1-like. *Cynoglossus semilaevis (Tongue sole)*

MEEETLCSPPHPGLEESQSSTDQLHVNGEQQALISRRSEQESTPTRGAAAPTPEGTEKWEQMIWSARPVTGAGVPLHFAT
VLWDMPGVCGEEPPLLTERSLANELTFLNGTSPLFPPSKEDDEAQPLIDEEEEEEEEEEEERREEEHEELEPQQLDPNPE
SPANSPEPCDTATDVAEPTTQEKEESENHLVDGFEVTARRSSTPGPDLVELIAAVDEDQDFTDEDNGLVSFSLEETRVES
DLSGTSGSQDGSLDSDVTEEEEEEEEEEEEEEEEEEEEEEGEGEGEEEQPKRNQSDTAENQEAKTDVVGSPEALQTDGAG
LNPDLGQVPPSEEGQQSEIQEDTQILEPELRGATVLETENTEMHKDVDHGPGSERPEVVDTEEEGATDAEKAENSEGTLE
MSTSEQEEGGASPRSEPSDDQQLEVTRAPELIQEVVPHDPSLDREDSPLMDLAGDSESEQPGPELCEQLTESENSDESET
AEQLCADAEVTQPTPQADPDQVDPRGKVLDQSDQLTSPEVQPDVPYMNGAQVDRDMACSLAERLFKLDGIQRVDVVQYLD
KDNDYSRVVGEEYLKFFDFTGLTLDQALRSFLKVVVLIGESQERERVLEHFSCRFHHCNPDSFSSSEAALALTCALMLLN
TDLHGQHVGKSMSSSKFVSNLEGMNEGENFNKDLLKSLYNSIKNEPLQWAVDDEELRRSVLADESAGDDSDILLLSKDNP
FQVVSHDKNASVIKEGFLQRKLHADVDGKRTPWGKRGWKTFYGVLRGMVLYLQKNDYRREQQTTEDVLSVHHSLAERATD
YTKKPHVFRLQTADWRVFLFQASSKVEMNSWISRLNLVSALHSSPPFPAAVGSQRKFFRPILPASLSAHTLERQLQSYTG
MLESFRTDLSYLQQNCSEGKKVKAKELEELRVREEYLHYEICRYEIYTRVLEGWKKLEETGHNVLVSTELHLFDKEVCVE
SVGDEEDVEGGLKKSHSSPSLKLELAPPTIKVKRNISERRTYRRTIVPRNKDK

259 - 278:	EEEEEEEEEEEEEEEEEEEE
260 - 279:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE

A0A3P8WXB5 **A0A3P8WXB5_CYNSE** (549 aa)
Testis-specific Y-encoded-like protein 1. *Cynoglossus semilaevis (Tongue sole)*

MSEVTDCTQSADSASRKRCPPSLEKEEDNTVPIKSTKVSDESSDAGVTSESCKSGETTGSKKDSKDGKTGEKEKAAVHTD
HSSDSAGNTGSRHVNKFSVGGHNKTNTKEPRSSHSHVPSEATEASEKTRKAEEVLNPVLQSDSAAIAAAEALASLTGGDG
EASQETPCSSEKAKVKQGSKFRHRGSLQHSSKVGTVTQAAAADSSTSLHSTEREEPEDVADADEGDESMSATSSTPSSSF
PSDNEENDDGECAIVSVKMAPEMRQSVALLAQVQMRLESLEKRSARLHQRLDLKINRQRRPHLDQRSSITKTIPGFWVTA
LLNHPHLSAHIDETDEDALSYMTDLEVESFKNNKVGFRIRFHFRRNPYFQNNIIMKELHLGMGAPMSFSNPILWHRGQNL
TANSEPRKSSRRVYQTFFNWFSDHSSPGQDDVAQILKDDLYRDPLRYYLTPLWEPQENGSGSEEKAAGNGNGDECVVISD
SDDEEGEEGEDKPQSQSRDQEEEEEEEEEEEEEEEEEEEEKGDRGPSGDESPEEEDEGGEIVIDGKTAL

501 - 520:	EEEEEEEEEEEEEEEEEEEE

A0A3P8X0B2 **A0A3P8X0B2_CYNSE** (588 aa)
CREB3 regulatory factor-like. *Cynoglossus semilaevis (Tongue sole)*

MPQPGMNGMEPAFGEAYGGHRGLLSPYPLAMSPQGGRTEYDQGDLLMLGSPASPRKRPFELLSDLVDDGGFGEDLHPERW
DVSALDEMARYTKLGLGVAGELAGSEEAVLMGRWGRSHDEGAEEEMGEEKRSNSASVPSANHVVQDTAAGREDGHMSVAT
TTEQDQCVAGGLAEGGQDGGMSKEHTVEVYQVGQQEEEEEEVAAASLALEHCSEEHNYSLGQGGDLAPGPCVQTEENNED
AQREIQEREESPVHLDDEEQQDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEGTEETAVEAELSSSSESDCEAEAEPVTQPGERPSKRRCFWEYRRARETASKKKLGGDV
HWSLSWSSSTLPSTLYRREGKKGRRKARKTDASDLTPNPQKLHNIGEQLQKLNAAIDGMGPVNELPAVARARSRKEKNKL
ASRACRLKKKAQHEANKIKLWGLNQEYENLLGALLRIKEVIRRRVESSEDEDTDERGMTQRLEDILRESSGPLVAGRTKD
FVQRILAASAGGQNQRKEPLQEGDGTAG

263 - 282:	EEEEEEEEEEEEEEEEEEEE
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323 - 342:	EEEEEEEEEEEEEEEEEEEE

A0A3P8X2N3 **A0A3P8X2N3_CYNSE** (564 aa)
Testis-specific Y-encoded-like protein 1. *Cynoglossus semilaevis (Tongue sole)*

```
MSEVTDCTQSADSASRKRCPPSLEKEEDNTVPIKSTKVSDESSDAGVTSESCKSGETTGSKKDSKDGKTGEKEKAAVHTD
HSSDSAGNTGSRHVNKFSVGGHNKTNTKEPRSSHSHVPSEATEASEKTRKAEEVLNPVLQSDSAAIAAAEALASLTGGDG
EASQETPCSSEKAKVKQGSKFRHRGSLQHSSKVGTVTQAAAADSSTSLHSTEREEPEDVADADEGDESMSATSSTPSSSF
```

PSDNEENDDGECAIVSVKMAPEMRQSVALLAQVQMRLESLEKRSARLHQRLDLKINRQRRPHLDQRSSITKTIPGFWVTA
LLNHPHLSAHIDETDEDALSYMTDLEVESFKNNKVGFRIRFHFRRNPYFQNNIIMKELHLGMGAPMSFSNPILWHRGQNL
TANSEPRKSSRRVYQTFFNWFSDHSSPGQDDVAQILKDDLYRDPLRYYLTPLWEPQENGSGSEEKAAGNGNGDECVVISD
SDDEEGEEGEDKPQSQSRDQEEEEEEEEEEEEEEEEEEEKGDRGPSGDESPEEEDEGGEIVIDGSDDSDQEEEEEEEEE
EEEA

501 - 520:	EEEEEEEEEEEEEEEEEEE

A0A3P8X571 **A0A3P8X571_CYNSE** (572 aa)
CREB3 regulatory factor-like. *Cynoglossus semilaevis (Tongue sole)*

MPQPGMNGMEPAFGEAYGGHRGLLSPYPLAMSPQGGRTEYDQGDLLMLGSPASPRKRPFELLSDLVDDGGFGEDLHPERW
DVSALDEMARYTKLGLGVAGELAGSEEAVLMGRWGRSHDEGAEEEMGEEKRSNSASVPSANHVVQDTAAGREDGHMSVAT
TTEQDQCVAGGLAEGGQDGGMSKEHTVEVYQGGDLAPGPCVQTEENNEDAQREIQEREESPVHLDDEEQQDEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGTEETAVEA
ELSSSSESDCEAEAEPVTQPGERPSKRRCFWEYRRARETASKKKLGGDVHWSLSWSSSTLPSTLYRREGKKGRRKARKTD
ASDLTPNPQKLHNIGEQLQKLNAAIDGMGPVNELPAVARARSRKEKNKLASRACRLKKKAQHEANKIKLWGLNQEYENLL
GALLRIKEVIRRRVESSEDEDTDERGMTQRLEDILRESSGPLVAGRTKDFVQRILAASAGGQNQRKEPLQEGDGTAGACS
LEPQGPVSQLNQ

232 - 251:	EEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEE
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252 - 271:	EEEEEEEEEEEEEEEEEEE
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292 - 311:	EEEEEEEEEEEEEEEEEEEE

A0A3P8XAM9 **A0A3P8XAM9_ESOLU** (2157 aa)
Uncharacterized protein. *Esox lucius (Northern pike)*

```
MAGVGHVGICLLLVLGLALILSVDAKEANRRKKLKRQKREWILPPSRIKENVDYTQKEYIAKIRSDMDRNAKVLYSLKGE
GADRPPFHLFIVNPENGFVRIRGILDREKCPVYNLTGEAKYMNGTMAEADIPLQIHVIDVNDNPPYFDLHTGSIKESSEA
GTEIMQIIGKDDDQEGTINSKIHYKIISQEPAGSGSMFTIDANTGKLYTKDESLDRETVDSYTLIVQGTDLDGAAGGLSG
TGTVQVKVLDINDNVPTLEKEQYAGNVDENTVDVVVMRIKAEDKDLEHTDNWLAVFHITKGNEDGLFSIETDPATNEGIL
KLIKAVDFEEVQKLELGLLIENVAPFVAGNAVGMDVEVYAGEGGGPGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAEA
GAEAGVDVGVDVGVDVGVDTDAGAGPEVGGGAGLKPGPNVKPKPKPDPTGGKSYPVSIAVNNLPEGPAFKPKIKPVPVSE
DPKEMPKDGVIATYTATDKDTGKPAEDVRYAKVYDPDNWVTIDEKTAEIKLTKTPDRESKFLVNGTYFAKILCMTQDMPS
KTATGTIAIQVKDSNDNCPALTSNHESLCSDERKVSVTAFDEDAWPNGPPFNFTVVAKGTTGDWEVEHVNDKTVVLRSTK
MLWPGVYDIMVAVADKQGLSCPEPELITVEVCTCAEGEECSPRSVSMLQKSPSTNIGTPAIGLLILASCVLLLVPLMLLL
CQCRGDMGGGAFSDQFTDLPFDTKEHLISYHTEGKGEDKEVPLLSFPAAANVVTQLSRNTSNSLRQTSGVFREEMHTLSQ
EQRLGHMNLEMDCSYGLQSVGGYGASMGLGSGTMRSRYGTHSSRVDEDLYDIALPDDVLEKYYSERAASQYPPLHDGLLV
YDYEGQGSPAGSLGCGSLLGDDGDLQFLNDLGPKFKTLAGICTPKPPPEARVKQVVELVTQPKLPEIERESVVTSSHINV
TKSSVSDTTINQSSAGVSKVIQQLPATSPPNRIVTHFSNVSQSPPPTQTILLQQQPMFYSTIQPMMQPVMQPIQYVVSDG
SSTNNLQHLVVVNRPLGSGSLGGLVIQDNRVISETSTSPVSPGSPTSPTILGTGSPGSPGWIQGSLPMASFGGVPVAGQG
PNGNYVYVERQVNVLGDPQRVGVPGVPSQGSLPRGAFLVREAAPPQGVVGSAAWGMGGVDGGLYGVLPGQTFTEVRQNGV
GPAEARIIGFGPGGVRVGNVGAGSFGMGPGGEGQIFMGSQGIPMWVPQSPPGYVTGHLMHEGAGPIAESVESMAVADVES
KVLFEGHSEPGDSLEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEMDDEKEEEEKQIAEKAVSEDQLSDEDESMVEQASSGE
AFMFTSEMTGLVEFTSAEEEIIDLLDTDQPTEKTIIDLVDTDQIVEEDSEQIPQEEVVSKWQEVELTVLPVPDSQQEEGI
TEKVMVESAELLNQMTVDYVTNSQEECITEEEVMSMLQLDQFTLDRHSDKQEEEAEAPGEVFLESELLRPGYSVLHGQET
SPEDNLVSEEEEREVEGEVEGDLGRAVEEDVEVEGEMEGEEEREVEGDLGRAVEEDVEGEMEGEEEREVEGDLGRAVEED
VEVEGEMEEKEEREVEGEVEGDLGRAVEEEVGVEGEMEEEEEREVEGEVEEEEEREVEGDLEVEGEMEEEEEREVEGELE
VEGEMEEEEEREVEGDLEVEGEMEEEEEREVEGELEVEGEMEEEEEREVDGEVEGEEQEAIETMVEGEMEGDMEGEIEEE
VEGEKEEEVEGEMEGEVEGESERELEEEEQEAIETNVGGEMEDMESEVEKEMKGEVESSEEPEENTSVVQSETLEESAPD
REDTEVVVETETEGWSEALDSENNIHGQVPTAVTPYVEATGEVKLSAEKMTESLVTSQIADEEETEDSENVADEVEYGGS
VAVERVKKVEASSTTKSVGQAESEKEVPLLVSTDWVAETQRLHSSSLYEFESSPQLVESSSYVVQTESLGYEQEQGSDLP
YLGDRSVFQNLEDVNNLSVASEEEESHLVTEVSSKGKVATESACTTQAEGESGSQCQVQAEGTGEITNKATIEVVSQDLG
KALTGELDICGATGQIAAGHGQAVFEVAGETEDEATQASGELEQVPKSFASSLRRKLRKGSKKEPTPKSPRLKCKQQ
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1295 - 1314:	EEEEEEEEEEEEEEEEEEEE
1296 - 1315:	EEEEEEEEEEEEEEEEEEEE
1297 - 1316:	EEEEEEEEEEEEEEEEEEEE
1298 - 1317:	EEEEEEEEEEEEEEEEEEEE
1299 - 1318:	EEEEEEEEEEEEEEEEEEEE
1300 - 1319:	EEEEEEEEEEEEEEEEEEEE
1301 - 1320:	EEEEEEEEEEEEEEEEEEEE
1302 - 1321:	EEEEEEEEEEEEEEEEEEEE
1303 - 1322:	EEEEEEEEEEEEEEEEEEEE
1304 - 1323:	EEEEEEEEEEEEEEEEEEEE

A0A3P8XAN3 **A0A3P8XAN3_ESOLU** (2128 aa)

Uncharacterized protein. *Esox lucius (Northern pike)*

```
MSRVSLPAAALLLFALTVLVSVAVVGAGGSAGLKRHKREWIIPPQKLTENQDYTKKDYIARIRSDTDDGNGNVQYFLKGV
GASQYPFNLFVVNPDNGYVRVTGLLDREAIAQYNLSGIAMYKDGREAEKDIDLRIQVVDENDNPPVFDHMEPANVYELSP
PDTVVTKVVATDADEPGNRNSMIAYSLVDQKPPGDMFYIQKDGTLRVKQSTLDREIYDSYVLTVKGTDLDGSPMGNTGIG
TIKVNLLDVNDNPPTLEKDVYEGSIEENTENVEVMRFKAEDKDLVNTPNWVAQYAIVKGNEAGYFTIETDPNTNEGVLML
RKAVDYEDVKDLELGVVVTNQAPPYDGFGSGGGSGGGGGGGGGGGGGGGGGGGGGGGGGGSSGGSSGGSSGGSSGGSS
GGSSGGSWSISYPGKPLKTYPVKIAVKNQPEGPRFEPKVKAIPISEGADFKINKVIASYPAIDGDTRLPAENVRYARGFD
PGNWLIIDEVTGDIKLSQKPDRESPFLVNGTYYAKVLCITQDMPSKTATGTVAIQVEDFNDHCPKLTSDLQTTCTTANAV
TVTAVDEDAFPNGAPFRFLIIPEGTKGVWAVEHLNDTSAILRSHNDLWPGLYEIAVEVRDQQGLACPDLQKVKVEVCTCV
DNQKTCMGRAAGSMGSTLGPAAIGLLVLGLLMLLLVPLLLLFCNCGGAGGLPGGFTEMPFDTKAHLISYHTEGQGENTEV
PLINPPGQVSSAVMGQASMVGAGFGIADGQLVNSSSEFGRGFDTLDSCIDVGYGGGMMGQQSKEHWSTYDSREGGGDYEG
MALPDRILEDYYSQKSRADHHVQKDSLLVYNYEGQGSPAGSLGCGSLLGDDGDLQFLNDLGPKFKTLAEVCRGERFQTEV
AAPPPRPAVYTPKTDSRVMTSVVSNVVSAAPPQAPALSPVPAHVPAPVPAPAPAKAPAKVPPKVTHVEKTVVKGSAHSDH
SATVRQDRVVEGQGQTILLQQQPMFYSTMQPMMQPMMQPMMQPIQYVVSDGSSTNNLQHLVVVNRPLGSGSLGGLVIQDN
RVISETSTSPVSPGSPTSPTILGTGSPGSPGWIQGSLPMASFGGVPVAGQGPNGNYVYVERQVNVLGDPQRVGVPGVPSQ
GSLPRGAFLVREAAPPQGVVGSAAWGMGGVDGGLYGVLPGQTFTEVRQNGVGPAEARIIGFGPGGVRVGNVGAGSFGMGP
GGEGQIFMGSQGIPMWVPQSPPGYVTGHLMHEGAGPIAESVESMAVADVESKVLFEGHSEPGDSLEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEMDDEKEEEEKQIAEKAVSEDQLSDEDESMVEQASSGEAFMFTSEMTGLVEFTSAEEEIIDLLDTDQ
PTEKTIIDLVDTDQIVEEDSEQIPQEEVVSKWQEVELTVLPVPDSQQEEGITEKVMVESAELLNQMTVDYVTNSQEECIT
EEEVMSMLQLDQFTLDRHSDKQEEEAEAPGEVFLESELLRPGYSVLHGQETSPEDNLVSEEEEREVEGEVEGDLGRAVEE
DVEVEGEMEGEEEREVEGDLGRAVEEDVEGEMEGEEEREVEGDLGRAVEEDVEVEGEMEEKEEREVEGEVEGDLGRAVEE
EVGVEGEMEEEEEREVEGEVEEEEEREVEGDLEVEGEMEEEEEREVEGELEVEGEMEEEEEREVEGDLEVEGEMEEEEER
EVEGELEVEGEMEEEEEREVDGEVEGEEQEAIETMVEGEMEGDMEGEIEEEVEGEKEEEVEGEMEGEVEGESERELEEEE
QEAIETNVGGEMEDMESEVEKEMKGEVESSEEPEENTSVVQSETLEESAPDREDTEVVVETETEGWSEALDSENNIHGQV
PTAVTPYVEATGEVKLSAEKMTESLVTSQIADEEETEDSENVADEVEYGGSVAVERVKKVEASSTTKSVGQAESEKEVPL
LVSTDWVAETQRLHSSSLYEFESSPQLVESSSYVVQTESLGYEQEQGSDLPYLGDRSVFQNLEDVNNLSVASEEEESHLV
TEVSSKGKVATESACTTQAEGESGSQCQVQAEGTGEITNKATIEVVSQDLGKALTGELDICGATGQIAAGHGQAVFEVAG
ETEDEATQASGELEQVPKSFASSLRRKLRKGSKKEPTPKSPRLKCKQQ
```

1266 - 1285:	EEEEEEEEEEEEEEEEEEEE
1267 - 1286:	EEEEEEEEEEEEEEEEEEEE
1268 - 1287:	EEEEEEEEEEEEEEEEEEEE
1269 - 1288:	EEEEEEEEEEEEEEEEEEEE
1270 - 1289:	EEEEEEEEEEEEEEEEEEEE
1271 - 1290:	EEEEEEEEEEEEEEEEEEEE
1272 - 1291:	EEEEEEEEEEEEEEEEEEEE
1273 - 1292:	EEEEEEEEEEEEEEEEEEEE
1274 - 1293:	EEEEEEEEEEEEEEEEEEEE
1275 - 1294:	EEEEEEEEEEEEEEEEEEEE

A0A3P8XC74 **A0A3P8XC74_ESOLU** (2122 aa)
Uncharacterized protein. *Esox lucius (Northern pike)*

```
MSRVSLPAAALLLFALTVLVSVAVVGAGGSAGLKRHKREWIIPPQKLTENQDYTKKDYIARIRSDTDDGNGNVQYFLKGV
GASQYPFNLFVVNPDNGYVRVTGLLDREAIAQYNLSGIAMYKDGREAEKDIDLRIQVVDENDNPPVFDHMEPANVYELSP
PDTVVTKVVATDADEPGNRNSMIAYSLVDQKPPGDMFYIQKDGTLRVKQSTLDREIYDSYVLTVKGTDLDGSPMGNTGIG
TIKVNLLDVNDNPPTLEKDVYEGSIEENTENVEVMRFKAEDKDLVNTPNWVAQYAIVKGNEAGYFTIETDPNTNEGVLML
RKAVDYEDVKDLELGVVVTNQAPPYDGFGSGGGSGGGGGGGGGGGGGGGGGGGGGGGGGGSSGGSSGGSSGGSSGGSS
GGSSGGSWSISYPGKPLKTYPVKIAVKNQPEGPRFEPKVKAIPISEGADFKINKVIASYPAIDGDTRLPAENVRYARGFD
PGNWLIIDEVTGDIKLSQKPDRESPFLVNGTYYAKVLCITQDMPSKTATGTIAIQVKDSNDNCPALTSNHESLCSDERKV
SVTAFDEDAWPNGPPFNFTVVAKGTTGDWEVEHVNDKTVVLRSTKMLWPGVYDIMVAVADKQGLSCPEPELITVEVCTCA
EGEECSPRSVSMLQKSPSTNIGTPAIGLLILASCVLLLVPLMLLLCQCRGDMGGGAFSDQFTDLPFDTKEHLISYHTEGK
GEDKEVPLLSFPAAANVVTQLSRNTSNSLRQTSGVFREEMHTLSQEQRLGHMNLEMDCSYGLQSVGGYGASMGLGSGTMR
SRYGTHSSRVDEDLYDIALPDDVLEKYYSERAASQYPPLHDGLLVYDYEGQGSPAGSLGCGSLLGDDGDLQFLNDLGPKF
KTLAGICTPKPPPEARVKQVVELVTQPKLPEIERESVVTSSHINVTKSSVSDTTINQSSAGVSKVIQQLPATSPPNRIVT
HFSNVSQSPPPTQTILLQQQPMFYSTIQPMMQPVMQPIQYVVSDGSSTNNLQHLVVVNRPLGSGSLGGLVIQDNRVISET
STSPVSPGSPTSPTILGTGSPGSPGWIQGSLPMASFGGVPVAGQGPNGNYVYVERQVNVLGDPQRVGVPGVPSQGSLPRG
AFLVREAAPPQGVVGSAAWGMGGVDGGLYGVLPGQTFTEVRQNGVGPAEARIIGFGPGGVRVGNVGAGSFGMGPGGEGQI
FMGSQGIPMWVPQSPPGYVTGHLMHEGAGPIAESVESMAVADVESKVLFEGHSEPGDSLEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEMDDEKEEEEKQIAEKAVSEDQLSDEDESMVEQASSGEAFMFTSEMTGLVEFTSAEEEIIDLLDTDQPTEKTI
IDLVDTDQIVEEDSEQIPQEEVVSKWQEVELTVLPVPDSQQEEGITEKVMVESAELLNQMTVDYVTNSQEECITEEEVMS
MLQLDQFTLDRHSDKQEEEAEAPGEVFLESELLRPGYSVLHGQETSPEDNLVSEEEEREVEGEVEGDLGRAVEEDVEVEG
EMEGEEEREVEGDLGRAVEEDVEGEMEGEEEREVEGDLGRAVEEDVEVEGEMEEKEEREVEGEVEGDLGRAVEEEVGVEG
EMEEEEEREVEGEVEEEEEREVEGDLEVEGEMEEEEEREVEGELEVEGEMEEEEEREVEGDLEVEGEMEEEEEREVEGEL
EVEGEMEEEEEREVDGEVEGEEQEAIETMVEGEMEGDMEGEIEEEVEGEKEEEVEGEMEGEVEGESERELEEEEQEAIET
NVGGEMEDMESEVEKEMKGEVESSEEPEENTSVVQSETLEESAPDREDTEVVVETETEGWSEALDSENNIHGQVPTAVTP
YVEATGEVKLSAEKMTESLVTSQIADEEETEDSENVADEVEYGGSVAVERVKKVEASSTTKSVGQAESEKEVPLLVSTDW
VAETQRLHSSSLYEFESSPQLVESSSYVVQTESLGYEQEQGSDLPYLGDRSVFQNLEDVNNLSVASEEEESHLVTEVSSK
GKVATESACTTQAEGESGSQCQVQAEGTGEITNKATIEVVSQDLGKALTGELDICGATGQIAAGHGQAVFEVAGETEDEA
TQASGELEQVPKSFASSLRRKLRKGSKKEPTPKSPRLKCKQQ
```

1260 - 1279:	EEEEEEEEEEEEEEEEEEEE
1261 - 1280:	EEEEEEEEEEEEEEEEEEEE
1262 - 1281:	EEEEEEEEEEEEEEEEEEEE
1263 - 1282:	EEEEEEEEEEEEEEEEEEEE
1264 - 1283:	EEEEEEEEEEEEEEEEEEEE
1265 - 1284:	EEEEEEEEEEEEEEEEEEEE
1266 - 1285:	EEEEEEEEEEEEEEEEEEEE

1267 - 1286:	EEEEEEEEEEEEEEEEEEEE
1268 - 1287:	EEEEEEEEEEEEEEEEEEEE
1269 - 1288:	EEEEEEEEEEEEEEEEEEEE

A0A3P8Y256 **A0A3P8Y256_ESOLU** (435 aa)
Exosome complex component RRP45 (Exosome component 9). *Esox lucius (Northern pike)*

```
MRDTPLSNCERDFILKAIEEKRRLDGRQTYDYRNIKISFGTDYGCCFVDLGKTRVMAQVSCELITPKENRPNDGIMFFNI
ELSPMASPAFETGRQSELMVKLNRQLERCLRNSKCIDTESLCVVSGEKVWQIRVDVHLLNHDGNLMDATSIAAITALCHF
RRPDVGIQGEDVTVYSTEERDPIPLSIYHMPISVSFSFFQQGTYLLVDPCDREERVMDGLLMIAMNKHREICSIQSSGGI
MLLKDQVLRCSKIASVKVSEITELINRALENDKKVRKAGGRCGFAESMPQERITALKTHVSPLEMTDVEEKANEIVLRAE
APPQTVPSPVLPGPGTGQVGEGLQSSWGLEEEEEEEEEEEEEEEEEEEQQHKAEEEVTCVAEEKRGVDVVLISDSDSEE
EEVVILNQKTLTKNATSSNQQMAVDSKLKRQRERQ
```

350 - 369:	EEEEEEEEEEEEEEEEEEEE

A0A3P8YBA6 **A0A3P8YBA6_ESOLU** (1608 aa)
Myosin light chain kinase. *Esox lucius (Northern pike)*

```
WLYFTCYYIGHPEPQVTWSRNGKTIQASSHFSMFEKSGIHFLEIREVCVEDAGTYICSVANSAGKATAMAELNVQGRTPQ
PQRLVIQPSAALYCTSIRAHYSTWVIGCHLGPLLYMGNWESRETTGTKGPAWKANASSPKPPVTSAKPPAKLPEEAPRKP
WVASPKAASTNPLQHQLRGQGAAHAGPEPHSRAPDRDSRDTVKGPRGPSSDPPKESRRQARESRSDRATVTAGAPPRFDS
VPQSQDAMEGTGVTFKCQVSGSPMPVLSWFKDGLPLRPRAGLSFQQDGNIHILTVDNVQKRDSGTYECTMTTSTGKMSST
WNLSVKNKPVPDARSSFENGLAQLTVCGALPEDEGLYTCVAENSHGRAVCTAGVLVKAKKSAKRSDPQHASDTKKQSKPS
APVFFRGLKDLKVMDGSQVIMTVEVTGNPHPEVVWLHNGKEIQESEDFHFEQKGNQYSLFIQEVFPEDTGKYTCEVWNEV
GVVRTEASLTVQEPQDGVQPWFITKPKSITAFLGQNILLSCAIAGDPFPQWTWKKQGQVISTGLDYEILQKEDVVSLLIR
QVRTQHAGDYEISLRNKVGDCSCVATLLVSEGAPCQRVGGVDGTVRGRGAAGSSHTQKEPEDSEEPSAARGLLKRRVETK
EHCEDQIRLLEAEQRDFRTVLGRKVTTKSVSEEDLKEIMAEQMDFRGQLKGVKPKTLSIDERKVSSPAQVDFRAVLGKKG
GAGVTPPKPGAASTEKAEPADFKSVLANKKKQTILEKNGESPASGPAAATPKALGPSPDKKDKEKNAVNCVDGGIIDKKS
NNIGKEPCFSQKLSDVSVVDGARLRLQCQVTSDPPATITWTLDGKVIKPSKFIKISNDGKYCSLTIDKALPEDEGQYKCR
AENSAGKAECSCMVLVDGKLFPGTSSGAPLPWVPHGPAGRPSLSPGEARIKKPNTKTPPKQAMPPQIVQFPDDMKILAGE
KVEILCKFGGAQPINCTWLKFRKPVQGDLTIVTTETSSKLTIADSQQEHCGCYTLELRNSYGLRQAALNLTIVDKPDPPA
RVPAASDIRRSTLTLSWYGPTYDGGSAVQSYNLEIWNSVDKEWKELASCNSTSYNVQNLLGQRQYKFRVRAVNIYGVGEP
SAESEAVTMLEEDVEDKEPDYRDVIVRTDVKVKDLYDVEERLGTGKFGQVFKLLEKATKKTWAGKFIKAYSAKEKENVRQ
EIMIMNSLHHPKLVQCVDAFEGKSDIVMVLEMISGGELFERIIDEDFELTEREVIKYMLQIVDGVHYIHKQGIVHLDLKP
ENIMCVNKTGSTIKLIDFGLARRLESSGTLKVLFGTPEFVAPEVINYEAISYPTDMWSIGVICYILVSGLSPFMGDNDNE
TLSNVTSATWDFEDDAFDEISDHAKDFITKLLKKDMKARLTCAQCYEHPWLKQDTGKMEAKKLSKERMKKYILRRKWQKT
GHAVRAIGRLSSMAMLAGVSAKKGSPTEEDNQFLECLEYEEKTQVKPTFSSVIKDVEVVEGSAARFDCKIEGYPDPEVVW
YKDDQPIKETRHFQIDYDEDGNCSLVISEVNGDDDAKYTVKAVNSLGEATCTAELLVEVMAGEEEEEEEEEEEEEEEEEE
EEEEEEEE
```

1583 - 1602:	EEEEEEEEEEEEEEEEEEEE
1584 - 1603:	EEEEEEEEEEEEEEEEEEEE
1585 - 1604:	EEEEEEEEEEEEEEEEEEEE
1586 - 1605:	EEEEEEEEEEEEEEEEEEEE
1587 - 1606:	EEEEEEEEEEEEEEEEEEEE
1588 - 1607:	EEEEEEEEEEEEEEEEEEEE
1589 - 1608:	EEEEEEEEEEEEEEEEEEEE

A0A3P9A330 **A0A3P9A330_ESOLU** (1735 aa)
Myosin light chain kinase. *Esox lucius (Northern pike)*

```
MILRYILFRYDPLKFFYHPQVRGHPEPQVTWSRNGKTVIAGERIVMEQSSRGTFSLVVRGVQDSDAGLYTCDAVNDAGSR
QVTVEITVEGTPQQPLVLGRFGVPAVESRPSIWGESPPKFVTKPSRVFARIGQSGKFSAKITGRPQPLVTWLKGDKEIQA
SSHFSMFEKSGIHFLEIREVCVEDAGTYICSVANSAGKATAMAELNVQGRTPQPQRLVIQPSAALYCTSIRAHYSTWVIG
CHLGPLLYMGNWVSFGPTTWANASSPKPPVTSAKPPAKLPEEAPRKPWVASPKAASTNPLQHQLRGQGAAHAGPEPHSRA
PDRDSRDTVKGPRGPSSDPPKESRRQARESRSDRATVTAGAPPRFDSVPQSQDAMEGTGVTFKCQVSGSPMPVLSWFKDG
LPLRPRAGLSFQQDGNIHILTVDNVQKRDSGTYECTMTTSTGKMSSTWNLSVKNKPVPDARSSFENGLAQLTVCGALPED
EGLYTCVAENSHGRAVCTAGVLVKAKKSAKRSDPQHASDTKKQSKPSAPVFFRGLKDLKVMDGSQVIMTVEVTGNPHPEV
VWLHNGKEIQESEDFHFEQKGNQYSLFIQEVFPEDTGKYTCEVWNEVGVVRTEASLTVQEPQDGVQPWFITKPKSITAFL
GQNILLSCAIAGDPFPQWTWKKQGQVISTGLDYEILQKEDVVSLLIRQVRTQHAGDYEISLRNKVGDCSCVATLLVSEGA
PCQRVGGVDGTVRGRGAAGSSHTQKEPEDSEEPSAARGLLKRRVETKEHCEDQIRLLEAEQRDFRTVLGRKVTTKSVSEE
DLKEIMAEQMDFRGQLKGVKPKTLSIDERKVSSPAQVDFRAVLGKKGGAGVTPPKPGAASTEKAEPADFKSVLANKKKQT
ILEKNGESPASGPAAATPKALGPSPDKKDKEKNAVNCVDGGIIDKKSNNIGKEPCFSQKLSDVSVVDGARLRLQCQVTSD
PPATITWTLDGKVIKPSKFIKISNDGKYCSLTIDKALPEDEGQYKCRAENSAGKAECSCMVLVDGKLFPGTSSGAPLPWV
PHGPAGRPSLSPGEARIKKPNTKTPPKQAMPPQIVQFPDDMKILAGEKVEILCKFGGAQPINCTWLKFRKPVQGDLTIVT
TETSSKLTIADSQQEHCGCYTLELRNSYGLRQAALNLTIVDKPDPPARVPAASDIRRSTLTLSWYGPTYDGGSAVQSYNL
EIWNSVDKEWKELASCNSTSYNVQNLLGQRQYKFRVRAVNIYGVGEPSAESEAVTMLEEDVEDKEPDYRDVIVRTDVKVK
DLYDVEERLGTGKFGQVFKLLEKATKKTWAGKFIKAYSAKEKENVRQEIMIMNSLHHPKLVQCVDAFEGKSDIVMVLEMI
SGGELFERIIDEDFELTEREVIKYMLQIVDGVHYIHKQGIVHLDLKPENIMCVNKTGSTIKLIDFGLARRLESSGTLKVL
FGTPEFVAPEVINYEAISYPTDMWSIGVICYILVSGLSPFMGDNDNETLSNVTSATWDFEDDAFDEISDHAKDFITKLLK
KDMKARLTCAQCYEHPWLKQDTGKMEAKKLSKERMKKYILRRKWQKTGHAVRAIGRLSSMAMLAGVSAKKGSPTEEDNQF
LECLEYEEKTQVKPTFSSVIKDVEVVEGSAARFDCKIEGYPDPEVVWYKDDQPIKETRHFQIDYDEDGNCSLVISEVNGD
DDAKYTVKAVNSLGEATCTAELLVEVMAGEEEEEEEEEEEEEEEEEEEEEEEEE
```

1710 - 1729:	EEEEEEEEEEEEEEEEEEEE
1711 - 1730:	EEEEEEEEEEEEEEEEEEEE
1712 - 1731:	EEEEEEEEEEEEEEEEEEEE

1713 - 1732:	EEEEEEEEEEEEEEEEEEEE
1714 - 1733:	EEEEEEEEEEEEEEEEEEEE
1715 - 1734:	EEEEEEEEEEEEEEEEEEEE
1716 - 1735:	EEEEEEEEEEEEEEEEEEEE

A0A3P9AJE3 **A0A3P9AJE3_ESOLU** (552 aa)
CREB3 regulatory factor. *Esox lucius (Northern pike)*

```
MPQPGMNGMEPAFGEAYGSRSCFLSHYPLAVSPLGGRTEYDQSVLLTLGSPATPRKRPFELLSDLVDDGGFGEELHTERW
DVSALDDITRYTKLGLGGELASAEDAVLMGRWGGTREEEEEEEEERRKRKAQALAQQTSHVTVTTVTHLHGNDVTMTPDP
CLGRAQRGRVDKEGLDVPIETELGAVKGDAPAGGRRIPTVEVYQVAEKEVATEASVARAEVVATVTDTSGILPRGSVLEH
NYSLTQGGDRPSSETETEEEEEGVGQIEKRGEEVLVVEEEEEEEEEEEEEEEEEEEEEDGAGDETTVEAELSSSSETECE
LEPDRGRGPGERPQKRRCFWEYRHAHARDSGRQKTCGEVRWSLSWSSSTLPSTLYRREGKKGRRKARKTDASDLTPNPVK
LTNIGEQLQKLNAAIGGMGPVNDLPVVARARSRKEKNKLASRACRLKKKAQHEANKIKLWGLNQEYDNLLGALLRIKEVI
RQRVESSGEEVDSDERGMTQRLEDILKESSGPLVAGRTKEFVQRILEGSGGAQAKAGARRMTPTPLVEETAA
```

278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE

A0A3P9BU50 **A0A3P9BU50_9CICH** (880 aa)
B-cell lymphoma/leukemia 11B. *Maylandia zebra (zebra mbuna)*

```
MRWKLFGGHPGSHRHLEKRYLASDHHSRANHDSGAGSPSPELSTPSPRRRASGEHDLLTCGQCQTNFPLGDILVFIEHKR
RLCRGPIGGLGSFSKPGAAGGVMGLPISPRARSLELGRGAVPVEVGVQVTPGGEEDQARRLTPAKGICPKQERGGKEIVS
LHLSSYPLSSSSSFPLPSLALFSPSKLLSCPALCCQAFLVSSLMVIFFLSWSTEKDEPSSYICTTCKQTFTSAWFLLQHA
QHTHGIRIYLDNHPVNCSLTPRMALPPPPGADALPRSPLPTFLGDASNPFHLLRMAGPQLRDHPHPPGYMETRLPATPPF
VSPPPPPRPPRERLGPEEMGLLSQHPSAFERVMRMTPMEHPPMDFSRRLRELAGNTTNNGGPTPPLSPNRVPPMHRLLSP
TLFQPGSQLSPFLTYPPQPPTSQGGHGSSSPPDTQGQNQAPGKSKSCEFCGKIFKFQSNLIVHRRSHTGERPYKCHLCDH
ACSQASKLKRHMKTHMHNKSGAITGSPEQGNRGEGGEGEEKNREGDARGMGMDNEEEEEEEEEEEEEEEEEEEEELQNGSR
PDSNLSEDSQEFTQNRENGSRQSPSEKPPSGDRVNDSGGVGIMHPYNHLDNHLRLNPNKRSLERQPNGDGGEGDQRPVMN
GRISVSEAECFPGLFQRRPTPITSPSPSNNKRIKIEKEQLEIPPTIPLISPENVYSQLLAGYAASRHFIREPFLGFTDSR
QSPFATSSEHSSSETGSLRFSTPPGELMEGGSASGRSGSSTPHLLRGPGPGRPPSSKERRNDTCEFCGKVFKNCSNLTVH
RRSHTGERPYKCDLCSYACAQSSKLTRHMKTHGQYGKEVYRCDICHMPFSVYSTLEKHMKKWHGEHLMASEVKLEQADRS
```

535 - 554:	EEEEEEEEEEEEEEEEEEEE

A0A3P9BUD5 **A0A3P9BUD5_9CICH** (837 aa)
B-cell lymphoma/leukemia 11B. *Maylandia zebra (zebra mbuna)*

```
MSRRKQVNPQHLSLTHRETIQAEANHDSGAGSPSPELSTPSPRRRASGEHDLLTCGQCQTNFPLGDILVFIEHKRRLCRG
PIGGLGSFSKPGAAGGVMGLPISPRARSLELGRGAVPVEVGVQVTPGGEEDQARRLTPAKGICPKQERGEKDEPSSYICT
TCKQTFTSAWFLLQHAQHTHGIRIYLDNHPVNCSLTPRMALPPPPGADALPRSPLPTFLGDASNPFHLLRMAGPQLRDHP
HPPGYMETRLPATPPFVSPPPPPRPPRERLGPEEMGLLSQHPSAFERVMRMTPMEHPPMDFSRRLRELAGNTTNNGGPTP
PLSPNRVPPMHRLLSPTLFQPGSQLSPFLTYPPQPPTSQGGHGSSSPPDTQGQNQAPGKSKSCEFCGKIFKFQSNLIVHR
RSHTGERPYKCHLCDHACSQASKLKRHMKTHMHNKSGAITGSPEQGNRGEGGEGEEKNREGDARGMGMDNEEEEEEEEEE
EEEEEEEEEELQNGSRPDSNLSEDSQEFTQNRENGSRQSPSEKPPSGDRVNDSGGVGIMHPYNHLDNHLRLNPNKRSLER
QPNGDGGEGVEGERERENEREPDRQREEQEDQRPVMNGRISVSEAECFPGLFQRRPTPITSPSPSNNKRIKIEKEQLEIP
PTIPLISPENVYSQLLAGYAASRHFIREPFLGFTDSRQSPFATSSEHSSSETGSLRFSTPPGELMEGGSASGRSGSSTPH
LLRGPGPGRPPSSKERRNDTCEFCGKVFKNCSNLTVHRRSHTGERPYKCDLCSYACAQSSKLTRHMKTHGQYGKEVYRCD
ICHMPFSVYSTLEKHMKKWHGEHLMASEVKLEQADRS
```

471 - 490:	EEEEEEEEEEEEEEEEEEEE

A0A3P9CPW7 **A0A3P9CPW7_9CICH** (914 aa)
B-cell lymphoma/leukemia 11A. *Maylandia zebra (zebra mbuna)*

```
MSRRKQGKPQHLSKRDFSPEPLSTAVVSSEELSERCSENSEESGSLNGHHPGSNVGRLARLGHDAHPSLEQDLLTCGQCQ
ATFPLADILLFIEHKRKRCHGPPCLTVGRGLDKPPSPSPGLALTPSPAMGSLRSRRLEVGVQATLADEDDDRFSSPRGIC
PKQEPLPGKEEPTTYTCTTCKQSYGSAWFLLQHAQNTHGFRIYLESEHGSPLTPRMGGPSSLGGGADCPSQPPLHGLHLP
PDASPFNLLRIPGSGSGGRDSVGAGGGIGTGAVGGGHHQRFPPTPPLFSPPPRNHLDPHHLSPEELALAAHHPSAFDRVL
RLNPPLPLDPPPTMDFSRRLRELAGNTSGSTPPLSPSRPSPMQRLLQPFQTGGGSGGTGGAGGSKPPYLATPPPLPGSMQ
SPVGSQTTPTTPLPSAGATPSSTTQLKSKCCEFCGKAFKFQSNLIVHRRSHTGEKPYKCHLCDHACTQASKLKRHMKTHM
HKSSSPNTGKSEDGLSTASSPEPGTSEHVGSASNALKSVVAKLKSENDRMLRENGEEEEEEEEEEEEEEEEEEEEEEEEE
GEEEEEQNGERVARRNNNSYHFGLNLETARQHENNGSIGSRLGGVADEGSIPRSLPEVMQGMGLAASMQHFSEALNAHKR
NAMAQENHLHHHLNRDHHHNREICDGDSVLETDRGEEGSVSTVNGRGASPNESASVGLSKKLLLGSPSPLSPFSKRIKLE
KEFDLPTSTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRFSTPPGELDGGMSGRSGTGSG
GSTPHLGGPGRPSSKDGRRSDTCEFCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQSSKLTRHMKTHGQVGKDVYK
CEICQMPFSVYSTLEKHMKKWHSDRPLSTEIKSE
```

536 - 555:	EEEEEEEEEEEEEEEEEEEE
537 - 556:	EEEEEEEEEEEEEEEEEEEE
538 - 557:	EEEEEEEEEEEEEEEEEEEE
539 - 558:	EEEEEEEEEEEEEEEEEEEE
540 - 559:	EEEEEEEEEEEEEEEEEEEE
541 - 560:	EEEEEEEEEEEEEEEEEEEE

A0A3P9CQQ2 **A0A3P9CQQ2_9CICH** (852 aa)
B-cell lymphoma/leukemia 11A. *Maylandia zebra (zebra mbuna)*

```
MSRRKQGKPQHLSKRDFSLNGHHPGSNVGRLARLGHDAHPSLEQDLLTCGQCQATFPLADILLFIEHKRKRCHGPPCLTV
GRGLDKPPSPSPGLALTPSPAMGSLRSRRLEVGVQATLADEDDDRFSSPRGICPKQEPLPGKEEPTTYTCTTCKQSYGSA
WFLLQHAQNTHGFRIYLESEHGSPLTPRMGGPSSLGGGADCPSQPPLHGLHLPPDASPFNLLRIPGSGSGGRDSRFPPTP
PLFSPPPRNHLDPHHLSPEELALAAHHPSAFDRVLRLNPPLPLDPPPTMDFSRRLRELAGNTSGSTPPLSPSRPSPMQRL
LHKPPYLATPPPLPGSMQSPVGSQTTPTTPLPSAGATPSSTTQLKSKCCEFCGKAFKFQSNLIVHRRSHTGEKPYKCHLC
DHACTQASKLKRHMKTHMHKSSSPNTGKSEDGLSTASSPEPGTSEHVGSASNALKSVVAKLKSENDRMLRENGEEEEEEE
EEEEEEEEEEEEEEEEEEGEEEEEQNGERVARRNNNSYHFGLNLETARQHENNGSIGSRLGGVADEGSIPRSLPEVMQGM
GLAASMQHFSEALNAHKRNAMAQENHLHHHLNRDHHHNREICDGDSVLETDRGEEGSVSTVNGRGASPNESASVGLSKKL
LLGSPSPLSPFSKRIKLEKEFDLPTSTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRFST
PPGELDGGMSGRSGTGSGGSTPHLGGPGRPSSKDGRRSDTCEFCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQSS
KLTRHMKTHGQVGKDVYKCEICQMPFSVYSTLEKHMKKWHSDRPLSTEIKSE
```

474 - 493:	EEEEEEEEEEEEEEEEEEEE
475 - 494:	EEEEEEEEEEEEEEEEEEEE
476 - 495:	EEEEEEEEEEEEEEEEEEEE
477 - 496:	EEEEEEEEEEEEEEEEEEEE
478 - 497:	EEEEEEEEEEEEEEEEEEEE
479 - 498:	EEEEEEEEEEEEEEEEEEEE

A0A3P9GZR2 **A0A3P9GZR2_ORYLA** (1054 aa)
MORC family CW-type zinc finger 2. *Oryzias latipes (Japanese rice fish) (Japanese killifish)*

```
MAYSSYSSLSRAQLTFEYLHTNSTTHEFLFGALAELVDNSRDANATRIDIYTEKTPELRGGFMLCFLDDGIGMDPNEATH
VIQFGKSSKRSPESTQIGQYGNGLKSGSMRIGKDFILFTKKDNALTCLFLSRTFHEEEGLDEVIVPLPSWDLKTKEPLTS
DPEKYAIETELIFKYSPFKNEQQLMQQFNKIESSSGTLVIVYNLKLMDSGEPELDIDTDHQDILMAGTPAEGVKPERRSF
RAYTAVLYIDPRMRIFIQGHKVRTKRLSCCLYKPRLYKYTSTRFKTRAEQEVKKADHLAKIAEEKAREAESKRIAMEARL
GEDISKDSRAILRKVQDSAMMLRREADMRKRNLEAKQKALKEPKDLNFIFGVNIEQRDLDGMFVYNCSRLIKMYEKTGPQ
LEGGMACGGVVGVVDVPYLVLEPTHNKQDFADAKEYRHLLKSMGEHLAQYWKDTNIAQKGIVKFWDEFGYLSASWSAPPS
SELRYKRRRAMEIPITIQCDKCLKWRTLPFQMDAVDKRYPDSWVCLMNPDSSQDRCDAPEQKQNLPCGILKKDKITAEDK
RKELEEKIKLQQEKLEALQKTSTIKSAADIKKLPLEVSMKPTESSSQSTRSSERSVTRPRSPPLPSVLKNAQSTPPTRTV
SQRPTRSPAPPAASTKVEPSRSRAAAKPPPPAAKPVPKAAAKPPPSRNLRASTKASTVKPATDGKRKRVIEREDSEEEEE
EEEEEEEEEEEEEEEDSDEESEEVQTKKSKMSTAISNRGKVVEKAPPAPKRGKMDEVKTLSQAEKKGVSTPARQQATTPS
SVLKSISYLQQGTKEKAPEKAQQKEPENDTKNAQKDKGLLVEVRVNNEWFTGKVIAVEVNKQGVRWKVKFDYVPRATPKD
RWVFKGSDEVRLMRPPSPISQTPDTQQETEKGPAPMEPDTTQPGTSREVTDSLVTMLRTMLRYFFPPAFRIPKDDVSSMT
AEELVAFPLKEYFQQYESGLQSLCNSYQSRADARAKAVEEKSKVTDLKLKEADEKLQKLRTNIVALLQKVQEDIDINTDD
ELDAYIEDLLTKGD
```

716 - 735:	EEEEEEEEEEEEEEEEEEEE

A0A3P9HP79 **A0A3P9HP79_ORYLA** (511 aa)
Uncharacterized protein. *Oryzias latipes (Japanese rice fish) (Japanese killifish)*

```
METPAVSFSAAVRAAAMHTSPVYSSRWRGAEERMLVPGKKEDREEDSEDEEREEDGEVCRKEAMKVLCNIIYNSPRAQER
ASTLRLLQGLWETLKQGIWSSVPPSGQFYKLRLLFILTALRPELRLQLQQERGVPVLTKALEQCLAVQWEGGSEVVIDNQ
APPISKKSSQDIIEILKTLFNIAHRFHKQEPDEEEAALCRHLAAVLRRCLLLSCDGEDTLEELQGHTVNILSALPLTCLD
VMVAVPVEGAAHKCEGVNMDCVHALLLFMDRRLNRSQKLKEKLTPVLNLLTESSRVHRETRHYLRQKILPPLREVGVRPE
QDGSLRGRLVRLMTHVDTDVKDCAAELLFVLCKENVGRFVKYTGYGNAAGLLAARGLLNGRRNSGDSQFASRYSSDSDSD
TEEYREARAKINLVTGCVEAEQPDPMEGMTEEEKEEEARRLISMINRMSRDQIIQPMGVTAEGRLAPLYGRMRGCTEEEE
EEEEEEEEEEEEEEEEILDLNAIMRKDKQSN
```

477 - 496:	EEEEEEEEEEEEEEEEEEEE

A0A3P9HR02 **A0A3P9HR02_ORYLA** (1248 aa)
MYT1 domain-containing protein. *Oryzias latipes (Japanese rice fish) (Japanese killifish)*

```
MEVDADDKRHRIRSKVPVDPALTELFSVYGCPLAKKRKSLDLEPLETSPKRSTLLDDMDNSTMEECYDTDGTEEMDDREE
EEEEGAMEGGGEVVEEEEDVGGYMDYNVEQMEHENEEGEDRGEEEDLEEEDVEVEQEEEEDSDEVRVEEAEEEEEEAIEE
VDYEDDEEEEEEEQNMGQEDNQLSPGDSTSEGGGGDGCSKLGPAMEKDDNNNDEYENYDELVAKSLLNLGKIAEDAANRA
MTESEMNSNSPNSAEDEGEEEEEEEEEEEEEEEEEEEEEEEEDEEEEEEESDLQRGDLSLDVESDVVRETVDSLKLLAQGHG
AVLSDSLDGQDFEGSARLGDQTNYSHNGGNGQMKTTNNGKIEGSDEEVCLSSLECLRNQCFDLARKLSETKSIDRNGPSQ
QNHYSCGDPSQQPQHHGYGDFHNSQDSRRTLDRNYSDMDNLMKLEEQLSPRSKAFSSCAQDERYHTSHRDFDEDTASITS
DRSEEVFDMTKGNLSLLEKAIALESERAKAMRDKLAAEAARRDGVRYAHEDHGPRHSYGVERKARLPDGMKKPFFHKDPS
RADKKESRCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRVPPEIVAMYENVLKCPTPGCTGRGHVNSNRNSHRSLSGCPIA
AAEKLAKAQEKHQSCDGPKSNQSSDRVLSTPRSNLAKELEKYSKTSFDYSAFDSTNNHHVYGKRAIAPKAHGQRDASPKG
HDAKRYCKNSSSASSTTSTYAPSSSNSSLSCIGGGGGGGGGGSSASSTCSKSSFDYSHDMEAAHMAATAILNLSTRCREM
PHGIGGKPQDLCSQSPGLDVDENGTLDLSMSKRLCGGGAGDAVLTPLEPMSPQRQAALLGSRCYGMGDAADCWDLPVDYT
KIKHIDEDEKETDDLDPFQDLLDDRSYTTDVNMPSPKPKYVQCKETKKDLITCPTPGCDGSGHLTSNFASHRSLSGCPLA
DKSIRSMLANNAQELKCPTPGCDGSGHITGNYASHRSLSGCPRARKSGIKIIHSKENKEDQEPIRCPVPGCDGQGHVTGK
YASHRSASGCPIAAKRQKDGYLNGIQFTWKSGKTEGMSCPTPGCDGSGHVSGSFLTHRSLSGCPRATSAMRKARLSGVEM
LTIKQQHASNVLDHEEEIKQLDEEIKDLSESNSQVEADMIKLRTQITTMESSLKSLEEENKKPLSHKEPLLRTSSCLQLH
QQESLSEQNFDAYVTTLTDMYTNQDQYQSVENKTLLENIKQAVQGIQV
```

259 - 278:	EEEEEEEEEEEEEEEEEEEE
260 - 279:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE

A0A3P9HR54 **A0A3P9HR54_ORYLA** (1251 aa)
MYT1 domain-containing protein. *Oryzias latipes (Japanese rice fish) (Japanese killifish)*

```
MQLMEVDADDKRHRIRSKVPVDPALTELFSVYGCPLAKKRKSLDLEPLETSPKRSTLLDDMDNSTMEECYDTDGTEEMDD
REEEEEEGAMEGGGEVVEEEEDVGGYMDYNVEQMEHENEEGEDRGEEEDLEEEDVEVEQEEEEDSDEVRVEEAEEEEEEA
IEEVDYEDDEEEEEEEQNMGQEDNQLSPGDSTSEGGGGDGCSKLGPAMEKDDNNNDEYENYDELVAKSLLNLGKIAEDAA
NRAMTESEMNSNSPNSAEDEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEESDLQRGDLSLDVESDVVRETVDSLKLLAQ
GHGAVLSDSLDGQDFEGSARLGDQTNYSHNGGNGQMKTTNNGKIEGSDEEVCLSSLECLRNQCFDLARKLSETKSIDRNG
PSQQNHYSCGDPSQQPQHHGYGDFHNSQDSRRTLDRNYSDMDNLMKLEEQLSPRSKAFSSCAQDERYHTSHRDFDEDTAS
ITSDRSEEVFDMTKGNLSLLEKAIALESERAKAMRDKLAAEAARRDGVRYAHEDHGPRHSYGVERKARLPDGMKKPFFHK
DPSRADKKESRCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRVPPEIVAMYENVLKCPTPGCTGRGHVNSNRNSHRSLSGC
PIAAAEKLAKAQEKHQSCDGPKSNQSSDRVLSTPRSNLAKELEKYSKTSFDYSAFDSTNNHHVYGKRAIAPKAHGQRDAS
PKGHDAKRYCKNSSSASSTTSTYAPSSSNSSLSCIGGGGGGGGGGSSASSTCSKSSFDYSHDMEAAHMAATAILNLSTRC
REMPHGIGGKPQDLCSQSPGLDVDENGTLDLSMSKRLCGGGAGDAVLTPLEPMSPQRQAALLGSRCYGMGDAADCWDLPV
DYTKIKHIDEDEKETDDLDPFQDLLDDRSYTTDVNMPSPKPKYVQCKETKKDLITCPTPGCDGSGHLTSNFASHRSLSGC
PLADKSIRSMLANNAQELKCPTPGCDGSGHITGNYASHRSLSGCPRARKSGIKIIHSKENKEDQEPIRCPVPGCDGQGHV
TGKYASHRSASGCPIAAKRQKDGYLNGIQFTWKSGKTEGMSCPTPGCDGSGHVSGSFLTHRSLSGCPRATSAMRKARLSG
VEMLTIKQQHASNVLDHEEEIKQLDEEIKDLSESNSQVEADMIKLRTQITTMESSLKSLEEENKKPLSHKEPLLRTSSCL
QLHQQESLSEQNFDAYVTTLTDMYTNQDQYQSVENKTLLENIKQAVQGIQV
```

262 - 281:	EEEEEEEEEEEEEEEEEEEE
263 - 282:	EEEEEEEEEEEEEEEEEEEE
264 - 283:	EEEEEEEEEEEEEEEEEEEE

A0A3P9IIQ4 **A0A3P9IIQ4_ORYLA** (819 aa)
Cyclin-dependent kinase 11B. *Oryzias latipes (Japanese rice fish) (Japanese killifish)*

```
MGDEKETWKVKTLDEILLEKRRRRELEEKSNPKRQKNCAPGLVPQANDRETKRDTPEEGELRDQRMEITIRNSPYAREDS
LEDRGEEDESLAIKPPQQVARKEKSHHRKEEKRKDKRRHRSHSAEGGGKHVRPKEKEKERESDRRKRQWEEDKARRDWER
QKRRDQARAHSRRESKFSSHRDRLEQLERQRERDRKIREQQKEQRERERRTEERRKEREGRRDVPSHHRMLLDEYSDKPP
KQSHRSRSPLPVPRDRPEPGEPRKSAVSKEDKPDLKDLLADLQDISDTERKTSTAESSMASGSGSEVEEDEEEEEEGASS
SQSGGEEEPEEEESVSGSGRSEQSPDISEEEQSVEDYDEEERENGNHIPAVPQSRFDHDSEESGEEEEEEEEEEEEEEEE
EEEEDDTGGEGDATPHSQTHSHSLTPEESYIPESPPVSPVELKKELPKYLPAVQGCRSVEEFQCLNRIEEGTYGVVYRAK
DKKTDEIVALKRLKMEKEKEGFPITSLREINTILKAQHPNIVTVREIVVGSNMDKIYIVMNYVEHDLKSLMETMKQPFLP
GEVKTLMIQLLRGVRHLHDNWILHRDLKTSNLLLSHKGILKIGDFGLAREYGSPLKPYTPIVVTLWYRSPELLLGAKEYS
TAVDMWSVGCIFGELLTQKPLFPGKSEIDQINKIFKDLGSPSDKIWPGYSELPAVKKMTFTEYPYNNLRKRFGALLSDQG
FDLMNTFLTYCPSKRILSDAALKHEYFRESPLPIDPSMFPTWPAKSEQQRVKRGTSPRPPEGGLAYSHLGDDDLKDTGFH
LTTSNQGVSAVGPGFSLKF
```

385 - 404:	EEEEEEEEEEEEEEEEEEEE

A0A3P9IIY2 **A0A3P9IIY2_ORYLA** (862 aa)
Cyclin-dependent kinase 11B. *Oryzias latipes (Japanese rice fish) (Japanese killifish)*

```
MPMNTYFTCSCDVVGCKSWMFLREELKTKTLSRLVSCVFLWADCGESTLMGDEKETWKVKTLDEILLEKRRRRELEEKSN
PKRQKNCAPGLVPQANDRETKRDTPEEGELRDQRMEITIRNSPYAREDSLEDRGEEDESLAIKPPQQVARKEKSHHRKEE
KRKDKRRHRSHSAEGGGKHVRPKEKEKERESDRRKRQWEEDKARRDWERQKRRDQARAHSRRERDRLEQLERQRERDRKI
REQQKEQRERERRTEERRKEREGRRDVPSHHRMLLDEYSDKPPKQSHRSRSPLPVPRDRPEPGEPRKSAVSKEDKPDLKD
LLADLQDISDTERKTSTAESSMASGSGSEVEEDEEEEEEGASSSQSGGEEEPEEEESVSGSGRSEQSPDISEEEQSVEDY
DEEERENGNHIPAVPQSRFDHDSEESGEEEEEEEEEEEEEEEEEEEEDDTGGEGDATPHSQTHSHSLTPEESYIPESPPV
SPVELKKELPKYLPAVQGCRSVEEFQCLNRIEEGTYGVVYRAKDKKTDEIVALKRLKMEKEKEGFPITSLREINTILKAQ
HPNIVTVREIVVGSNMDKIYIVMNYVEHDLKSLMETMKQPFLPGEVKTLMIQLLRGVRHLHDNWILHRDLKTSNLLLSHK
GILKIGDFGLAREYGSPLKPYTPIVVTLWYRSPELLLGAKEYSTAVDMWSVGCIFGELLTQKPLFPGKSEIDQINKIFKD
LGSPSDKIWPGYSELPAVKKMTFTEYPYNNLRKRFGALLSDQGFDLMNTFLTYCPSKRILSDAALKHEYFRESPLPIDPS
MFPTWPAKSEQQRVKRGTSPRPPEGGLAYSHLGDDDLKDTGFHLTTSNQGVSAVGPGFSLKF
```

428 - 447:	EEEEEEEEEEEEEEEEEEEE

A0A3P9IQJ3 **A0A3P9IQJ3_ORYLA** (598 aa)
Phosphatase and actin regulator. *Oryzias latipes (Japanese rice fish) (Japanese killifish)*

```
MTGRGGGGVFSGAWTDTSCCCEEDKPKKRRRALCLSRRKPRGQQPREAPAHNRKNTPLSTSIHCQLGKEIKHICTNCGRA
EQLDGERTDAAAEEVERLAAMRSDSLVPGTHTPPIRRRSKFANLGRLFKPWKWRKKKSEKFKQTSAVLERKMSTRQSREE
LIKKGLLKEVFDKDGAPSSLQEEMKMEKGRSPPLGAAPSFCDGGEQMDGATAAGGSPDVQMPSDATCQQDFCQAPPTKTS
ATCPSDSAESPLFRPPSVHKQPPALPPKPFNRLPNHFTDGAPIRLPCLSIKLSPPQPSKKLLISVPVGPMEPSPLAFQKC
PAPSSHAPVGGPSLQYRQLPLHPPSRIIEELNKTLALTMQRFESSMMHAGPAVMIECDDDDKENRPDEADYEDMPGMYNE
EREEEEEEEEEEEEEEEEEEEEDDDTLFSSTLAMKILRRDSLAIKLSNRPSKRELEEKNILPLQSDQERLESRQQTATKL
TRRLSQRPTAEELEQRNILKPRNDQEEQEEKREIKRHLSKKLSQRPTVEELREAKILIRFSDYVEVAEAQDYDRRADKPW
TRLTAADKAAIRKELNEFKSTEMEVHESSRHLTRFHRP
```

403 - 422:	EEEEEEEEEEEEEEEEEEEE

A0A3P9IQU3 **A0A3P9IQU3_ORYLA** (545 aa)
Phosphatase and actin regulator. *Oryzias latipes (Japanese rice fish) (Japanese killifish)*

```
MMAAAPEEEVDRRPIRRVRSKSDTPYINEARISLHLETAEEVERLAAMRSDSLVPGTHTPPIRRRSKFANLGRLFKPWKW
RKKKSEKFKQTSAVLERKMSTRQSREELIKKGLLKEVFDKDGAPSSLQEEMKMEKGRSPPLGAAPSFCDGGEQMDGATAA
GGSPDVQMPSDATCQQDFCQAPPTKTSATCPSDSAESPLFRPPSVHKQPPALPPKPFNRLPNHFTDGAPIRLPCLSIKLS
PPQPSKKLLISVPVGPMEPSPLAFQKCPAPSSHAPVGGPSLQYRQLPLHPPSRIIEELNKTLALTMQRFESSMMHAGPAV
MIECDDDDKENRPDEADYEDMPGMYNEEREEEEEEEEEEEEEEEEEEEEDDDTLFSSTLAMKILRRDSLAIKLSNRPSKR
ELEEKNILPLQSDQERLESRQQTATKLTRRLSQRPTAEELEQRNILKPRNDQEEQEEKREIKRHLSKKLSQRPTVEELRE
```

AKILIRFSDYVEVAEAQDYDRRADKPWTRLTAADKAAIRKELNEFKSTEMEVHESSRHLTRFHRP

350 - 369:	EEEEEEEEEEEEEEEEEEE

A0A3P9IQZ0 **A0A3P9IQZ0_ORYLA** (1014 aa)
MORC family CW-type zinc finger 2. *Oryzias latipes (Japanese rice fish) (Japanese killifish)*

MAYSSYSSLSRAQLTFEYLHTNSTTHEFLFGALAELVDNSRDANATRIDIYTEKTPELRGGFMLCFLDDGIGMDPNEATH
VIQFGKSSKRSPESTQIGQYGNGLKSGSMRIGKDFILFTKKDNALTCLFLSRTFHEEEGLDEVIVPLPSWDLKTKEPLTS
DPEKYAIETELIFKYSPFKNEQQLMQQFNKIESSSGTLVIVYNLKLMDSGEPELDIDTDHQDILMAGTPAEGVKPERRSF
RAYTAVLYIDPRMRIFIQGHKVRTKRLSCCLYKPRLYKYTSTRFKTRAEQEVKKADHLAKIAEEKAREAESKRIAMEARL
GEDISKDSRAILRKVQDSAMMLRREADMRKRNLEAKQKALKEPKDLNFIFGVNIEQRDLDGMFVYNCSRLIKMYEKTGPQ
LEGGMACGGVVGVVDVPYLVLEPTHNKQDFADAKEYRHLLKSMGEHLAQYWKDTNIAQKGIVKFWDEFGYLSASWSAPPS
SELRYKRRRAMEIPITIQCDKCLKWRTLPFQMDAVDKRYPDSWVCLMNPDSSQDRCDAPEQKQNLPCGILKKDKITAEDK
RKELEEKIKLQQEKLEALQKTSTIKSAADIKKLPLEVSMKPTESSSQSTRSSERSVTRPRSPPLPSVLKNAQSTPPTRTV
SQRPTRSPAPPAASTKVEPSRSRAAAKPPPPAAKPVPKAAAKPPPSRNLRASTKASTVKPATDGKRKRVIEREDSEEEEE
EEEEEEEEEEEEEEEDSDEESEEVQTKKSKMSTAISNRGKVVEKAPPAPKRGKMDEAPEKAQQKEPENDTKNAQKDKGLL
VEVRVNNEWFTGKVIAVEVNKQGVRWKVKFDYVPRATPKDRWVFKGSDEVRLMRPPSPISQTPDTQQETEKGPAPMEPDT
TQPGTSREVTDSLVTMLRTMLRYFFPPAFRIPKDDVSSMTAEELVAFPLKEYFQQYESGLQSLCNSYQSRADARAKAVEE
KSKVTDLKLKEADEKLQKLRTNIVALLQKVQEDIDINTDDELDAYIEDLLTKGD

716 - 735:	EEEEEEEEEEEEEEEEEEE

A0A3P9IR22 **A0A3P9IR22_ORYLA** (1020 aa)
MORC family CW-type zinc finger 2. *Oryzias latipes (Japanese rice fish) (Japanese killifish)*

MSTQGLFLQCLLFFVIRTEKTPELRGGFMLCFLDDGIGMDPNEATHVIQFGKSSKRSPESTQIGQYGNGLKSGSMRIGKD
FILFTKKDNALTCLFLSRTFHEEEGLDEVIVPLPSWDLKTKEPLTSDPEKYAIETELIFKYSPFKNEQQLMQQFNKIESS
SGTLVIVYNLKLMDSGEPELDIDTDHQDILMAGTPAEGVKPERRSFRAYTAVLYIDPRMRIFIQGHKVRTKRLSCCLYKP
RLYKYTSTRFKTRAEQEVKKADHLAKIAEEKAREAESKRIAMEARLGEDISKDSRAILRKVQDSAMMLRREADMRKRNLE
AKQKALKEPKDLNFIFGVNIEQRDLDGMFVYNCSRLIKMYEKTGPQLEGGMACGGVVGVVDVPYLVLEPTHNKQDFADAK
EYRHLLKSMGEHLAQYWKDTNIAQKGIVKFWDEFGYLSASWSAPPSSELRYKRRRAMEIPITIQCDKCLKWRTLPFQMDA
VDKRYPDSWVCLMNPDSSQDRCDAPEQKQNLPCGILKKDKITAEDKRKELEEKIKLQQEKLEALQKTSTIKSAADIKKLP
LEVSMKPTESSSQSTRSSERSVTRPRSPPLPSVLKNAQSTPPTRTVSQRPTRSPAPPAASTKVEPSRSRAAAKPPPPAAK
PVPKAAAKPPPSRNLRASTKASTVKPATDGKRKRVIEREDSEEEEEEEEEEEEEEEEEEEEDSDEESEEVQTKKSKMSTA
ISNRGKVVEKAPPAPKRGKMDEVKTLSQAEKKGVSTPARQQATTPSSVLKSISYLQQGTKEKAPEKAQQKEPENDTKNAQ
KDKGLLVEVRVNNEWFTGKVIAVEVNKQGVRWKVKFDYVPRATPKDRWVFKGSDEVRLMRPPSPISQTPDTQQETEKGPA
PMEPDTTQPGTSREVTDSLVTMLRTMLRYFFPPAFRIPKDDVSSMTAEELVAFPLKEYFQQYESGLQSLCNSYQSRADAR
AKAVEEKSKVTDLKLKEADEKLQKLRTNIVALLQKVQEDIDINTDDELDAYIEDLLTKGD

682 - 701:	EEEEEEEEEEEEEEEEEEE

A0A3P9J891 **A0A3P9J891_ORYLA** (1227 aa)
MYT1 domain-containing protein. *Oryzias latipes (Japanese rice fish) (Japanese killifish)*

MEVDADDKRHRIRSKVPVDPALTELFSVYGCPLAKKRKSLDLEPLETSPKRSTLLDDMDNSTMEECYDTDGTEEMDDREE
EEEEGAMEGGGEVVEEEEDVGGYMDYNVEQMEHENEEGEDRGEEEDLEEEDVEVEQEEEEDSDEVRVEEAEEEEEEAIEE
VDYEDDEEEEEEEQNMGQEDNQLSPGDSTSEGGGGDGCSKLGPAMEKDDNNNDEYENYDELVAKSLLNLGKIAEDAANRA
MTESEMNSNSPNSAEDEGEEEEEEEEEEEEEEEEEEEEEEEEDEEEEEEESDLQRGDLSLDVESDVVRETVDSLKLLAQGHG
AVLSDSLDGQDFEGSARLGDQTNYSHNGGNGQMKTTNNGKIEGSDEEVCLSSLECLRNQCFDLARKLSETKSIDRNGPSQ
QNHYSCGDPSQQPQHHGYGDFHNSQDSRRTLDRNYSDMDNLMKLEEQLSPRSKAFSSCAQDERYHTSHRDFDEDTASITS
DRSEEVFDMTKGNLSLLEKAIALESERAKAMRDKLAAEAARRDGVRYAHEDHGPRHSYGVERKARLPDGMKKPFFHKDPS
RADKKESRCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRVPPEIVAMYENVLKCPTPGCTGRGHVNSNRNSHRSLSGCPIA
AAEKLAKAQEKHQSCDGPKSNQSSDRVLSTPRSNLAKELEKYSKTSFDYSAFDSTNNHHVYGKRAIAPKAHGQRDASPKG
HDAKRYCKNSSSASSTTSTYAPSSSNSSLSCIGGGGGGGGGGSSASSTCSKSSFDYSHDMEAAHMAATAILNLSTRCREM
PHGIGGKPQDLCSQSPGLDVDENGTLDLSMSKRLCGGGAGDAVLTPLEPMSPQRQAALLGSRCYGMGDAADCWDLPVDYT
KIKHIDEDEKETDDLDPFQDLLDDRSYTTDVNMPSPKPKYVQCKETKKDLITLSGCPLADKSIRSMLANNAQELKCPTPG
CDGSGHITGNYASHRSLSGCPRARKSGIKIIHSKENKEDQEPIRCPVPGCDGQGHVTGKYASHRSASGCPIAAKRQKDGY
LNGIQFTWKSGKTEGMSCPTPGCDGSGHVSGSFLTHRSLSGCPRATSAMRKARLSGVEMLTIKQQHASNVLDHEEEIKQL
DEEIKDLSESNSQVEADMIKLRTQITTMESSLKSLEEENKKPLSHKEPLLRTSSCLQLHQQESLSEQNFDAYVTTLTDMY
TNQDQYQSVENKTLLENIKQAVQGIQV

259 - 278:	EEEEEEEEEEEEEEEEEEE
260 - 279:	EEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEE

A0A3P9K1N2 **A0A3P9K1N2_ORYLA** (593 aa)
Phosphatase and actin regulator. *Oryzias latipes (Japanese rice fish) (Japanese killifish)*

MTGREGGGVFSRAWTDTSCCCEEDKPKKRRRALCLSRRKPRGQQPREAPAHNRKNTPLSTSIHCQLGKEIKHICSNCRRA
EQLDAEEVERLAAMRSDSLVPGTHTPPIRRRSKFANLGRLFKPWKWRKKKSEKFKQTSAVLERKMSTRQSREELIKKGLL
KEVFDKDGAPSSLQEEMKMEKGRSLPLGAAPSDCDGGEQMDGATAAGGSSVVQMPSDATCQQDFCQAPPTKTSAVCPSDS
AESPLFRPPSVHKQPPALPPKPFNRLPNHFTDGAPIRLPCLSIKLSPPQPSKKLLISVPVGPMEPSPLAFQKCPAPSSHA
PVGGPSLQYRQLPLHPPSRIIEELNKTLALTMQRFESSMMHAGPAGMIECDDDDKENRPDEADYEDMPGMYNEEREEEEE
EEEEEEEEEEEEEEEEEDDDTLFSSTLAMKILRRDSLAIKLSNRPSKRELEEKNILPVQSDQERLESRQQTATKLTRRLS
QRPTAEELEQRNILKPRNDQEEQEEKREIKRHLSKKLSQRPTVEELREAKILIRFSDYVEVAEAQDYDRRADKPWTRLTA
ADKAAIRKELNEFKSTEMEVHESSRHLTRFHRP

396 - 415:	EEEEEEEEEEEEEEEEEEE

397 - 416:	EEEEEEEEEEEEEEEEEEEE
398 - 417:	EEEEEEEEEEEEEEEEEEEE

A0A3P9K2H7 **A0A3P9K2H7_ORYLA** (547 aa)
Phosphatase and actin regulator. *Oryzias latipes (Japanese rice fish) (Japanese killifish)*

```
MMAAAPEEEVDRRPIRRVRSKSDTPYINEARISLHLETAEEVERLAAMRSDSLVPGTHTPPIRRRSKFANLGRLFKPWKW
RKKKSEKFKQTSAVLERKMSTRQSREELIKKGLLKEVFDKDGAPSSLQEEMKMEKGRSLPLGAAPSDCDGGEQMDGATAA
GGSSVVQMPSDATCQQDFCQAPPTKTSAVCPSDSAESPLFRPPSVHKQPPALPPKPFNRLPNHFTDGAPIRLPCLSIKLS
PPQPSKKLLISVPVGPMEPSPLAFQKCPAPSSHAPVGGPSLQYRQLPLHPPSRIIEELNKTLALTMQRFESSMMHAGPAG
MIECDDDDKENRPDEADYEDMPGMYNEEREEEEEEEEEEEEEEEEEEEEEEEEDDDTLFSSTLAMKILRRDSLAIKLSNRPS
KRELEEKNILPVQSDQERLESRQQTATKLTRRLSQRPTAEELEQRNILKPRNDQEEQEEKREIKRHLSKKLSQRPTVEEL
REAKILIRFSDYVEVAEAQDYDRRADKPWTRLTAADKAAIRKELNEFKSTEMEVHESSRHLTRFHRP
```

350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE

A0A3P9KYF9 **A0A3P9KYF9_ORYLA** (1257 aa)
Myelin transcription factor 1 like. *Oryzias latipes (Japanese rice fish) (Japanese killifish)*

```
MEVDADDKRHRTRSKVPVDPALTELFSVYGCPLAKKRKSLDLEPLETSTKRSTLLDDMDNSTMEECYDTDGTEEMDDREE
EEEEGAMEGGGEVVEEEEDVGGYMDYNVEQMEHENEEGEERGEEEDIEEEDVEVEQEEEEDSDEVRVEEAEEEEEEAIEE
VDYEDDEEEEEEEQNMGQEDNQLSPGDSTSEGGGGDGCSKLGPAMEKDDNNNDEYENYDELVAKSLLNLGKIAEDAANRA
MTESEMNSNSPNSAEDEGEEEEEEEEEEEEEEEEEEEEEEEEEDEEEEEEEEEEESELQRGDLSLDVESDVVRETVDSLKLL
AQGHGAVLSDSLDGQDFEGSARPGDQTNYSHNGGNGQMKTTNNGKIEGSDEEVCLSSLECLRNQCFDLARKLSETKSIDR
NGPSQQNHYSCGDPSQQPQHHGYGDFHNSQDSRRTLDRNYSDMDNLMKLEEQLSPRSKAFSSCAQDERYHTSHRDFDEDT
ASITSDRSEEVFDMTKGNLSLLEKAIALESERAKAMRDKLAAEAARRDGVRYAHEDHGPRHGYGVERKARLPDGMKKPFF
HKDPSRADKKESRCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRVPPEIVAMYENVLKCPTPGCTGRGHVNSNRNSHRSLS
GCPIAAAEKLAKAQEKHQSCDGPKSNQSSDRVLSTPRSNLAKELEKYSKTSFDYSAFDSTNNHHVYGKRAIAPKAHGQRD
ASPKGHDAKRYCKNSSSASSTTSTYAPSSSNSSLSCIGGGGGGGGGGRGGGSSASSTCSKSSFDYSHDMEAAHMAATAIL
NLSTRCREMPHGIGGKPQDLCSQSPGLDVDENGTLDLSMSKRLCGGGAGDAVLTPLEPMSPQRQAALLGSRCYGMGDAAD
CWDLPVDYTKIKHIDEDEKETDDLDPFQDLLDDRSYTTDVNMPSPKPKYVQCKETKKDLITCPTPGCDGSGHLTSNFASH
RSLSGCPLADKSIRSMLANNAQELKCPTPGCDGSGHITGNYASHRSLSGCPRARKSGIKIIHSKENKEDQEPIRCPVPGC
DGQGHVTGKYASHRSASGCPIAAKRQKDGYLNGIQFTWKSGKTEGMSCPTPGCDGSGHVSGSFLTHRSLSGCPRATSAMR
KARLSGVEMLTIKQQHASNVLDHEEEIKQLDEEIKDLSESNSQVEADMIKLRTQITTMESSLKSLEEENKKPLSHKEPLL
RTSSCLQLHQQESLSEQNFDAYVTTLTDMYTNQDQYQSVENKTLLENIKQAVQGIQV
```

259 - 278:	EEEEEEEEEEEEEEEEEEEE
260 - 279:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE
262 - 281:	EEEEEEEEEEEEEEEEEEEE

A0A3P9KYJ9 **A0A3P9KYJ9_ORYLA** (1229 aa)
Myelin transcription factor 1 like. *Oryzias latipes (Japanese rice fish) (Japanese killifish)*

```
MEVDADDKRHRTRSKVPVDPALTELFSVYGCPLAKKRKSLDLEPLETSTKRSTLLDDMDNSTMEECYDTDGTEEMDDREE
EEEEGAMEGGGEVVEEEEDVGGYMDYNVEQMEHENEEGEERGEEEDIEEEDVEVEQEEEEDSDEVRVEEAEEEEEEAIEE
VDYEDDEEEEEEEQNMGQEDNQLSPGDSTSEGGGGDGCSKLGPAMEKDDNNNDEYENYDELVAKSLLNLGKIAEDAANRA
MTESEMNSNSPNSAEDEGEEEEEEEEEEEEEEEEEEEEEEEEEDEEEEEEEEEEESELQRGDLSLDVESDVVRETVDSLKLL
AQGHGAVLSDSLDGQDFEGSARPGDQTNYSHNGGNGQMKTTNNGKIEGSDEEVCLSSLECLRNQCFDLARKLSETKSIDR
NGPSQQNHYSCGDPSQQPQHHGYGDFHNSQDSRRTLDRNYSDMDNLMKLEEQLSPRSKAFSSCAQDERYHTSHRDFDEDT
ASITSDRSEEVFDMTKGNLSLLEKAIALESERAKAMRDKLAAEAARRDGVRYAHEDHGPRHGYGVERKARLPDGMKKPFF
HKDPSRADKKESRCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRVPPEIVAMYENVLKCPTPGCTGRGHVNSNRNSHRSLS
GCPIAAAEKLAKAQEKHQSCDGPKSNQSSDRVLSTPRSNLAKELEKYSKTSFDYSAFDSTNNHHVYGKRAIAPKAHGQRD
ASPKGHDAKRYCKNSSSASSTTSTYAPSSSNSSLSCIGGGGGGGGGGRGGGSSASSTCSKSSFDYSHDMEAAHMAATAIL
NLSTRCREMPHGIGGKPQDLCSQSPGLDVDENGTLDLSMSKRLCGGGAGDAVLTPLEPMSPQRQAALLGSRCYGMGDAAD
CWDLPVDYTKIKHIDEDEKETDDLDPFQDLLDDRSYTTDVNMPSPKPKYVQCKETKKDLITCPTPGCDGSGHLTSNFASH
RSLSGCPLADKSIRSMLANNAQELKCPTPGCDGSGHITGNYASHRRCPVPGCDGQGHVTGKYASHRSASGCPIAAKRQKD
GYLNGIQFTWKSGKTEGMSCPTPGCDGSGHVSGSFLTHRSLSGCPRATSAMRKARLSGVEMLTIKQQHASNVLDHEEEIK
QLDEEIKDLSESNSQVEADMIKLRTQITTMESSLKSLEEENKKPLSHKEPLLRTSSCLQLHQQESLSEQNFDAYVTTLTD
MYTNQDQYQSVENKTLLENIKQAVQGIQV
```

259 - 278:	EEEEEEEEEEEEEEEEEEEE
260 - 279:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE
262 - 281:	EEEEEEEEEEEEEEEEEEEE

A0A3P9LAE7 **A0A3P9LAE7_ORYLA** (1287 aa)
Protein phosphatase 1 regulatory subunit 9A-like B. *Oryzias latipes (Japanese rice fish) (Japanese killifish)*

```
MMRTDHKGRSASPHRITYKSDFHAIKCSFDTGNISHGSSAASHRTAAHPDKLFSTMSDSIISHTSTDSGGRGRIQSTRGT
KIRENIFLQMDNPHSRQDGAPVQSSGSTPLLLVPKPNSLSQTSPVFGCRRSIISSSSVLSSLTSTQEKVRGKKPSKSEDI
SDFDRAALAQKFSVTRSLFESKMMEVGDNGVQALKPVIRGSSGAADGKGEAEKKLLSEKMNHTEENCLEKPKPVNQLINT
LTLKPHVVKSVSKCSKSPGVHEPDEEPNKSASHHGECDETTTTQTEADGGKRATFNPFLTPDETLRAERVSIKNESSESD
ENEEEKLWNENKHWLKGEMNMSVSQGEGDKEVALVDEVFEDIIVDTTPELFGKEEDELIVSLEHPKELSEDGHDRKDMYQ
QVNEQREGEREEQSAKSIAQSEEESMAEGDDGKKNMETKLGESVQGLEEVILQGEKEEGEAREVSEQSQSLEAKETAELQ
```

```
EVLVSEMKNGIRKGGSDGTDGVGEEEDQMVISGIENKAFVDEQDTHLEVLEGESAEQGVSLQSEDDLEEEYEEIPGVPEL
DEREDEDTSDNVKRKVRFSTAPIKVYSTFSNEEYDRHNEDIDPVSASAEFELEKRVDRMDVFPVEIQKGEDGLGISIIGM
GVGADQGLEKLGIFVKTVTEGGATHKDGRIQVNDQIVEVDGRSLVGVSQLFAATVLKNTSGLVKFLIGREKEGVESEVAR
LINESLEMDKTKSKKRANRSSGDEDINDTTGVRSSVEEEEEEEEEEEEEEEEEEEEEEDVSLLSSLDNYQLCLKYQQLQA
KIHRQTAQLHCAKEKLRTWEEQQANWVSEKAELQQRVEEEEEKAEKLEKYWQEAQTLCRVVSQRLADAQNQTESLEVKYS
KAKRLVREYQSREEEMEKTLSDLRREMEDREKQHKETIERLQMQVGHLERIEPDPQIKNQSVESSATDWYVPLPNTGRLD
SSAHIARAQLAQKSKRHPPSRDKLRESFKKQEECVTKPEEDQSLPSSTTVQSSRTELSNANSFSILSPQPLTSSLSTPPI
FITDTEALSPCKSSSSKKSKSKFPDFSGLRKSLSRRTGEKTSRSANSRGSCGDLVDEPVEVSPSGSVSSVPSCLRLPWFG
ERGRDKAGERENIRERLRSVSSNSLPYLTTTGRRDQTLDDCPVPNNNNNQWQTRPVSEWNNQQVSLWLIAMNMDQYSAEF
SAKGLDGSQLLNLDSHKLKALGVSSQSDRSIIKKKLKDMKKREEKEQRKEEKKLKEEDEKLTGLREEERSVKSIGRRGQT
VRTESLL
```

757 - 776:	EEEEEEEEEEEEEEEEEEEE
758 - 777:	EEEEEEEEEEEEEEEEEEEE
759 - 778:	EEEEEEEEEEEEEEEEEEEE

A0A3P9LAG7 **A0A3P9LAG7_ORYLA** (1320 aa)
Protein phosphatase 1 regulatory subunit 9A-like B. *Oryzias latipes (Japanese rice fish) (Japanese killifish)*

```
MMRTDHKGRSASPHRITYKSDFHAIKCSFDTGNISHGSSAASHRTAAHPDKLFSTMSDSIISHTSTDSGGRGRIQSTRGT
KIRENIFLQMDNPHSRQDGAPVQSSGSTPLLLVPKPNSLSQTSPVFGCRRSIISSSSVLSSLTSTQEKVRGKKPSKSEDI
SDFDRAALAQKFSVTRSLFESKMMEVGDNGVQALKPVIRGSSGAADGKGEAEKKLLSEKMNHTEENCLEKPKPVNQLINT
LTLKPHVVKSVSKCSKSPGVHEPDEEPNKSASHHGECDETTTTQTEADGGKRATFNPFLTPDETLRAERVSIKNESSESD
ENEEEKLWNENKHWLKGEMNMSVSQGEGDKEVALVDEVFEDIIVDTTPELFGKEEDELIVSLEHPKELSEDGHDRKDMYQ
QVNEQREGEREEQSAKSIAQSEEESMAEGDDGKKNMETKLGESVQGLEEVILQGEKEEGEAREVSEQSQSLEAKETAELQ
EVLVSEMKNGIRKGGSDGTDGVGEEEDQMVISGIENKAFVDEQDTHLEVLEGESAEQGVSLQSEDDLEEEYEEIPGVPEL
DEREDEDTSDNVKRKVRFSTAPIKVYSTFSNEEYDRHNEDIDPVSASAEFELEKRVDRMDVFPVEIQKGEDGLGISIIGM
GVGADQGLEKLGIFVKTVTEGGATHKDGRIQVNDQIVEVDGRSLVGVSQLFAATVLKNTSGLVKFLIGREKEGVESEVAR
LINESLEMDKTKSKKRANRSSGDEDINDTTGVRSSVEEEEEEEEEEEEEEEEEEEEEEDVSLLSSLDNYQLCLKYQQLQA
KIHRQTAQLHCAKEKLRTWEEQQANWVSEKAELQQRVEEEEEKAEKLEKYWQEAQTLCRVVSQRLADAQNQTESLEVKYS
KAKRLVREYQSREEEMEKTLSDLRREMEDREKQHKETIERLQMQVGHLERIEPDPQIKNQSVESSATDWYVPLPNTGRLD
SSAHIARAQLAQKSKRHPPSRDKLRESFKKQEECVTKPEEDQSLPSSTTVQSSRTELSNANSFSILSPQPLTSSLSTPPI
FITDTEALSPCKSSSSKKSKSKFPDFSGLRKSLSRRTGEKTSRSANSRGSCGDLVDEPVEVSPSGSVSSVPSCLRLPWFG
ERGRDKAGERENIRERLRSVSSNSLPYLTTTGRRDQTIGSPVGSSSLVGHVSDYSFSGNSHTCTFSSSETLDDCPVPNNN
NNQWQTRPVSEWNNQQVSLWLIAMNMDQYSAEFSAKGLDGSQLLNLDSHKLKALGVSSQSDRSIIKKKLKDMKKREEKEQ
RKEEKKLKEEDEKLTGLREEERSVKSIGRRGQTVRTESLL
```

757 - 776:	EEEEEEEEEEEEEEEEEEEE
758 - 777:	EEEEEEEEEEEEEEEEEEEE
759 - 778:	EEEEEEEEEEEEEEEEEEEE

A0A3P9LW32 **A0A3P9LW32_ORYLA** (822 aa)
Cyclin-dependent kinase 11B. *Oryzias latipes (Japanese rice fish) (Japanese killifish)*

```
MGDEKETWKVKTLDEILLEKRRRRELEEKSNPKRQKNCAPGLVPQANDRETKRDTPEEGELRDQRMEITIRNSPYAREDS
LEDRGEEDESLAIKPPQQVARKEKSHHRKEEKRKDKRRHRSHSAEGGGKHVRPKEKEKERESDRRKRQWEEDKARRDWER
QKRRDQARAHSRRESKFSSHRDRLEQLERQRERDRKIREQQKEQRDIKERERRTEERRKEREGRRDVPSHHRMLLDEYSD
KPPKQSHRSRSPLPVPRDRPEPGEPRKSAVSKEDKPDLKDLLADLQDISDTERKTSTAESSMASGSGSEVEEDEEEEEEG
ASSSQSGGEEEPEEEESVSGSGRSEQSPDISEEEQSVEDYDEEERENGNHIPAVPQSRFDHDSEESGEEEEEEEEEEEEE
EEEEEEEDDTGGEGEATPHSQTHSRSLTPEESYIPESPPVSPVELKKELPKYLPAVQGCRSVEEFQCLNRIEEGTYGVVY
RAKDKKTDEIVALKRLKMEKEKEGFPITSLREINTILKAQHPNIVTVREIVVGSNMDKIYIVMNYVEHDLKSLMETMKQP
FLPGEVKTLMIQLLRGVRHLHDNWILHRDLKTSNLLLSHKGILKIGDFGLAREYGSPLKPYTPIVVTLWYRSPELLLGAK
EYSTAVDMWSVGCIFGELLTQKPLFPGKSEIDQINKIFKDLGSPSDKIWPGYSELPAVKKMTFTEYPYNNLRKRFGALLS
DQGFDLMNTFLTYCPSKRILSDAALKHEYFRESPLPIDPSMFPTWPAKSEQQRVKRGTSPRPPEGGLAYSHLGDDDLKDT
GFHLTTSNQGVSAVGPGFSLKF
```

388 - 407:	EEEEEEEEEEEEEEEEEEEE

A0A3P9LW56 **A0A3P9LW56_ORYLA** (816 aa)
Cyclin-dependent kinase 11B. *Oryzias latipes (Japanese rice fish) (Japanese killifish)*

```
MGDEKETWKVKTLDEILLEKRRRRELEEKSNPKRQKNCAPGLVPQANDRETKRDTPEEGELRDQRMEITIRNSPYAREDS
LEDRGEEDESLAIKPPQQVARKEKSHHRKEEKRKDKRRHRSHSAEGGGKHVRPKEKEKERESDRRKRQWEEDKARRDWER
QKRRDQARAHSRRERDRLEQLERQRERDRKIREQQKEQRDIKERERRTEERRKEREGRRDVPSHHRMLLDEYSDKPPKQS
HRSRSPLPVPRDRPEPGEPRKSAVSKEDKPDLKDLLADLQDISDTERKTSTAESSMASGSGSEVEEDEEEEEEGASSSQS
GGEEEPEEEESVSGSGRSEQSPDISEEEQSVEDYDEEERENGNHIPAVPQSRFDHDSEESGEEEEEEEEEEEEEEEEEE
EDDTGGEGEATPHSQTHSRSLTPEESYIPESPPVSPVELKKELPKYLPAVQGCRSVEEFQCLNRIEEGTYGVVYRAKDKK
TDEIVALKRLKMEKEKEGFPITSLREINTILKAQHPNIVTVREIVVGSNMDKIYIVMNYVEHDLKSLMETMKQPFLPGEV
KTLMIQLLRGVRHLHDNWILHRDLKTSNLLLSHKGILKIGDFGLAREYGSPLKPYTPIVVTLWYRSPELLLGAKEYSTAV
DMWSVGCIFGELLTQKPLFPGKSEIDQINKIFKDLGSPSDKIWPGYSELPAVKKMTFTEYPYNNLRKRFGALLSDQGFDL
MNTFLTYCPSKRILSDAALKHEYFRESPLPIDPSMFPTWPAKSEQQRVKRGTSPRPPEGGLAYSHLGDDDLKDTGFHLTT
SNQGVSAVGPGFSLKF
```

382 - 401:	EEEEEEEEEEEEEEEEEEEE

A0A3P9MAQ8 **A0A3P9MAQ8_ORYLA** (1236 aa)
Myelin transcription factor 1 like. *Oryzias latipes (Japanese rice fish) (Japanese killifish)*

```
MEVDADDKRHRTRSKVPVDPALTELFSVYGCPLAKKRKSLDLEPLETSTKRSTLLDDMDNSTMEECYDTDGTEEMDDREE
EEEEGAMEGGGEVVEEEEDVGGYMDYNVEQMEHENEEGEERGEEEDIEEEDVEVEQEEEEDSDEVRVEEAEEEEEEAIEE
```

```
VDYEDDEEEEEEEEQNMGQEDNQLSPGDSTSEGGGGDGCSKLGPAMEKDDNNNDEYENYDELVAKSLLNLGKIAEDAANRA
MTESEMNSNSPNSAEDEGEEEEEEEEEEEEEEEEEEEEEEEDEEEEEEEEEEESELQRGDLSLDVESDVVRETVDSLKLL
AQGHGAVLSDSLDGQDFEGSARPGDQTNYSHNGGNGQMKTTNNGKIEGSDEEVCLSSLECLRNQCFDLARKLSETKSIDR
NGPSQQNHYSCGDPSQQPQHHGYGDFHNSQDSRRTLDRNYSDMDNLMKLEEQLSPRSKAFSSCAQDERYHTSHRDFDEDT
ASITSDRSEEVFDMTKGNLSLLEKAIALESERAKAMRDKLAAEAARRDGVRYAHEDHGPRHGYGVERKARLPDGMKKPFF
HKDPSRADKKESRCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRVPPEIVAMYENVLKCPTPGCTGRGHVNSNRNSHRSLS
GCPIAAAEKLAKAQEKHQSCDGPKSNQSSDRVLSTPRSNLAKELEKYSKTSFDYSAFDSTNNHHVYGKRAIAPKAHGQRD
ASPKGHDAKRYCKNSSSASSTTSTYAPSSSNSSLSCIGGGGGGGGGGRGGGSSASSTCSKSSFDYSHDMEAAHMAATAIL
NLSTRCREMPHGIGGKPQDLCSQSPGLDVDENGTLDLSMSKRLCGGGAGDAVLTPLEPMSPQRQAALLGSRCYGMGDAAD
CWDLPVDYTKIKHIDEDEKETDDLDPFQDLLDDRSYTTDVNMPSPKPKYVQCKETKKDLITLSGCPLADKSIRSMLANNA
QELKCPTPGCDGSGHITGNYASHRSLSGCPRARKSGIKIIHSKENKEDQEPIRCPVPGCDGQGHVTGKYASHRSASGCPI
AAKRQKDGYLNGIQFTWKSGKTEGMSCPTPGCDGSGHVSGSFLTHRSLSGCPRATSAMRKARLSGVEMLTIKQQHASNVL
DHEEEIKQLDEEIKDLSESNSQVEADMIKLRTQITTMESSLKSLEEENKKPLSHKEPLLRTSSCLQLHQQESLSEQNFDA
YVTTLTDMYTNQDQYQSVENKTLLENIKQAVQGIQV
```

259 - 278:	EEEEEEEEEEEEEEEEEEEE
260 - 279:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE
262 - 281:	EEEEEEEEEEEEEEEEEEEE

A0A3P9MWK1 **A0A3P9MWK1_POERE** (597 aa)
Serine/threonine-protein kinase SRK2H-like. *Poecilia reticulata (Guppy) (Acanthophacelus reticulatus)*

```
MDSSRDLTSALDGPADPRGFSGRSDLSGLYHLGRTLGRGHFAVVKLGRHVNTGQLVAVKMIDKTKLDVMATSHLLQEVRC
MRLVQHPNVVRLYEVIDTPTTLYLVMELAEGGDLYDYILRHEGGVVEGTAKRHFAQIVRAVSYCHQLHVVHRDLKPENVV
FFPQQGAVKLTDFGFSNLFQPGMMLATSCGSLAYSAPEILLGEEYDAPAVDIWSLGVILYMLVCGVPPFQETNDSETLVM
ILDCRYSVPEHVSDGCRDLISRMLQKDPCRRASLDEIEAHQWLQGLDDALLSPEAPPHWVAGALSASSSSLCAPECGDLL
AMRTSTQQAFPGTWQPSLGFSLRPAPAEEPPVGKNVPALQQICEEEEEEEEEEEEEEEEEEEEEEREELRELEGEAEEDG
LEYVEEGEELGNTGEEKVEEMQRENEDSGCVISDQPVSHRDETLSQTSEVTLASEVTPSSPTFRVSCCQLNISNRKEGQD
EEMEPNNNTGKPPPLLPTPESCQSCISASSASLREKTEREEELNEKNESAAKSPAQNPQGSRDESVPRAEQGKRHSIRLR
DRLFQFPLCEKALAFNIPSQNKPKILPLAQYNCCHVL
```

364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE

A0A3P9NEF8 **A0A3P9NEF8_POERE** (531 aa)
Palm2 and akap2 fusion. *Poecilia reticulata (Guppy) (Acanthophacelus reticulatus)*

```
PTQNPWRAAEDATDASPRERAVKSVSFQESVSVITDRPANMELESQQIQHGCLRSPSNQGKSVVVKVETPDSEEICYLDQ
VLDAASETPTNGNPSLXEHKKPISINGTXSSVCVSDNRQSITVEEQRSSTFPHRESAVRTNGHVQGDESGHGAVKFELRA
FQEERRPAKLFTPGEEQQVRVTRRRPSEEVQELERERQELIKDQAVKKNPGIAQRWWNPPXEVPLEEQLDGDQLESLRKY
QERKQQKQNHPYPYVQPHMSGPPTMVTFDPDVTRKEDILEEQIDFSSARKQFLQGDAAKKSITPQLYSAKPFCKSGTRSS
PSISDFVAETGETRVTWSDEGLAEEFTCARAVMTILPEQDEGKXLSQPFHXEEFDSGLDELSVRSQDTTLFSLDNVSDSG
ASLPPTPLPLTPNLNLANHTPLNWKIEKVRPAPPVSPSPSEGALSDAGSEDSGGSRPKNLMQTLLEDYETHKVKRKEKME
DNSVLEATRMTRRKSNMALKWEAGIYANEEGEEEEEEEEEEEEEEEEEEE
```

512 - 531:	EEEEEEEEEEEEEEEEEEEE

A0A3P9NXV0 **A0A3P9NXV0_POERE** (914 aa)
BAF chromatin remodeling complex subunit BCL11A. *Poecilia reticulata (Guppy) (Acanthophacelus reticulatus)*

```
MSRRKQGKPQHLSKRDFSPAEPLSTAVVSSEELSERCSEHSEDSGSLNGHHPVPTAGRLARLGPDSHPSPEQDLLTCGQC
QATFPLADILLFIEHKRKRCHGPPCLAIGRGLDKPPSPSPGLALTPSPALNSLRGRRPVEVGVQATLADEDDERFSSPRG
ICPKQEPLPGKEEPTTYTCTTCKQSYGSAWFLLQHAQNSHGFRIYLESEHGSPLTPRMGGPSSLGGGADCPSQPPLHGLH
LPPDASPFNLLRIPGSGSGGRDSIGAGGAVGSGVPGGHHQRFPPTPPLFSPPPRNHLDPHHLSPEELALAAHHPSAFDRV
LRLNPPLPLDPPPTMDFSRRLRELAGNTSGSTPPLSPSRPSPMQRLLQPFQTGGTAGAGGAGGSKPPYLATPPPLQGSMQ
SPVGSQTTPPTPLPTAGPPSSSNTQLKSKCCEFCGKAFKFQSNLIVHRRSHTGEKPYKCHLCDHACTQASKLKRHMKTHM
HKSSSPNTGKSEDGLSIASSPEPGTSEHIGSASNALKSVVAKLKSENNRMLRENGEEEEEEEEEEEEEEEEEEEEEEEEE
EGEEEEVQNGERPPKRNNSYHFGLSLEAARQHENSSGIGSRLGGVADETSIPRSLPEVMQGMGLAASMQHFSEALNAHKR
NAMAQENHLHHHLSRDHHHSRNMCDGDSVLETERVEEGTVSAVNGRGASPNESSSIGLSKKLLLGSPSPLSPFSKRIKLE
KEFDLPTPTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRFSTPPGELDGGMSGRSGTGSG
GSTPHLGGPGRPSSKDGRRSDTCEYCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQSSKLTRHMKTHGQVGKDVYK
CEICQMPFSVYSTLEKHMKKWHSDRPLSTEIKSE
```

536 - 555:	EEEEEEEEEEEEEEEEEEEE
537 - 556:	EEEEEEEEEEEEEEEEEEEE
538 - 557:	EEEEEEEEEEEEEEEEEEEE
539 - 558:	EEEEEEEEEEEEEEEEEEEE
540 - 559:	EEEEEEEEEEEEEEEEEEEE
541 - 560:	EEEEEEEEEEEEEEEEEEEE
542 - 561:	EEEEEEEEEEEEEEEEEEEE

A0A3P9NXV7 **A0A3P9NXV7_POERE** (898 aa)

BAF chromatin remodeling complex subunit BCL11A. *Poecilia reticulata (Guppy) (Acanthophacelus reticulatus)*

```
MSRRKQGKPQHLSKRDFSPEPLSTAVVSSEELSERCSEHSEDSGSLNGHHPVPTAGRLARLGPDSHPSPEQDLLTCGQCQ
ATFPLADILLFIEHKRKRCHGPPCLAIGRGLDKPPSPSPGLALTPSPALNSLRGRRPVEVGVQATLADEDDERFSSPRGI
CPKQEPLPGKEEPTTYTCTTCKQSYGSAWFLLQHAQNSHGFRIYLESEHGSPLTPRMGGPSSLGGGADCPSQPPLHGLHL
PPDASPFNLLRIPGSGSGGRDSIGRFPPTPPLFSPPPRNHLDPHHLSPEELALAAHHPSAFDRVLRLNPPLPLDPPPTMD
FSRRLRELAGNTSGSTPPLSPSRPSPMQRLLQPFQTGGTAGAGGAGGSKPPYLATPPPLQGSMQSPVGSQTTPPTPLPTA
GPPSSSNTQLKSKCCEFCGKAFKFQSNLIVHRRSHTGEKPYKCHLCDHACTQASKLKRHMKTHMHKSSSPNTGKSEDGLS
IASSPEPGTSEHIGSASNALKSVVAKLKSENNRMLRENGEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEVQNGERPPKR
NNSYHFGLSLEAARQHENSSGIGSRLGGVADETSIPRSLPEVMQGMGLAASMQHFSEALNAHKRNAMAQENHLHHHLSRD
HHHSRNMCDGDSVLETERVEEGTVSAVNGRGASPNESSSIGLSKKLLLGSPSPLSPFSKRIKLEKEFDLPTPTIPNTENV
YSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRFSTPPGELDGGMSGRSGTGSGGSTPHLGGPGRPSSKD
GRRSDTCEYCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQSSKLTRHMKTHGQVGKDVYKCEICQMPFSVYSTLEK
HMKKWHSDRPLSTEIKSE
```

520 - 539:	EEEEEEEEEEEEEEEEEEEE
521 - 540:	EEEEEEEEEEEEEEEEEEEE
522 - 541:	EEEEEEEEEEEEEEEEEEEE
523 - 542:	EEEEEEEEEEEEEEEEEEEE
524 - 543:	EEEEEEEEEEEEEEEEEEEE
525 - 544:	EEEEEEEEEEEEEEEEEEEE
526 - 545:	EEEEEEEEEEEEEEEEEEEE

A0A3Q0CAE6 **A0A3Q0CAE6_MESAU** (1156 aa)
histone-lysine N-methyltransferase EHMT2 isoform X1. *Mesocricetus auratus (Golden hamster)*

```
MGALLLEKEPRGAAAERVHGPLGDTPHAEETLPKADPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDEPESLEGD
GGRALLGHATKSFPSSPSKGGACPSRAKMSVTGAGKSPPSVQSLAMRLLSMPGAQGAATAGPEPPPAAATTTGQEGQPKV
HRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHPLGKVTSDAAKRRKLNSGSLTEDFGSARGSGDMALEKGEPRPLEE
WETVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEDEEEDEESGNQSDRSGSSGRR
KAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDG
ELSGCNAAILKRETMRPSSRVALMVLCEAHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCP
HCGEDASEAQEVTIPRGDGGTPPAGTAAPAPLPLAQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPN
GSCLSAVGLPPGPGREALEKALVIQESERRKKLRFHPRQLYVSVKQGELQKVILMLLDNLDPNVQNDQQSKRTPLHAAAQ
KGFVEICHVLLQAGANINAVDKQQRTPLMEAVVHNRLEVARYMVQLGGCVYSKEEDGSTCLHHAAKMGNLEMVSLLLSTG
QVDVNAQDSGGWTPIIWAAEHKHIDVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTP
LHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAVRTEKIICRDVARGYENVP
IPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLI
FECNQACSCWRSCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDG
EVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEK
CKHSAEAIALEQSRLARLDPHPELLPELSALPPMNA
```

279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE

A0A3Q0CIK2 **A0A3Q0CIK2_MESAU** (2152 aa)
AT-rich interactive domain-containing protein 1B. *Mesocricetus auratus (Golden hamster)*

```
MAHSASAAGSNSAQSGGGSEAALKEGAGASAAAAALSSSSSAAAVAVAASSSSSSSAGPGSTMETGLLPNHKLKAVGEAP
AAPPHPQQHHHHAHHLHHHHHHHAHHLHHLHHHHALQQQLNQFQQPQQQPQPHPQQPPPPQQQHPTANNSLGGAGGGGGA
PQPGPDMEQPQHGGAKDSAAGSQAEPQGQPLLSKPGDEDDAPPKMGEPAGSRYEHPGLGAQQPPAPVAVPGGGGGGPAAV
SEFNNYYGSAAPASGGPGGRAGPCFDQHGGQQSPGMGMMHSASAAAAGAPSSMDPLQNSHEGYPNSQYNHYPGYSRPGAG
GGGGGGGGAAAGGQQAAAGMGLGKDLGAQYAAASPAWAAAQQRSHPAMSPGTPGPTMGRSQGSPMDPMVMKRPQLYGMGA
HPHSQPQQSSPYPGGSYGPPGAQRYPLSMQGRAPGTLGGMQYPQQQMPPQYGQQGVSGYCQQGQQPYYNQQPQQHLPPQA
QYLQPPAQQRYQPQQDMSQEGYGTRSQPPLAPGKSNHEDLNLIQQERPSSLPDLSGSIDDLPTGTEATLSSAVSASGSTS
SQGDQSNPAQSPFSPHASPHLSSIPGGPSPSPVGSPVGSNQSRSGPISPASIPGSQMPPQPPGSQSESSSHPALSQSPMP
QERGFMAGTQRNPQMSQYGPQQAGPSMSPHPSPGGQMHPGISNFQQSNSSGTYGPQMSQYGPQGNYSRTPTYSGVPSASY
SGPGPGMGINANNQMHGQGPTQPCGAMPLGRMASAGMQSRPFPGNMSSATPSSPGMSQQGGPGMGPPMPTVNRKAQEAAA
AVMQAAANSAQSRQGSFPGMNQGGLMASSSPYSQPMNNSSGLMNTQAQPYSMTPSMVNSSTASMGLADMMSPGESKLSVP
LKADGKEEGVSQPESKSKDSYSSQGISQPPTPGNLPVPSPMSPSSASISSFHGDESDSISSPGWPKTPSSPKSSSSSTTG
EKITKVYELGNEPERKLWVDRYLAFMEERGSPVSSLPAVGKKPLDLFRLYVCVKEIGGLAQVNKNKKWRELATNLNVGTS
SSAASSLKKQYIQYLFAFECKIERGEEPPPEVFSTGDAKKQPKLQPPSPANSGSLQGPQTPQSTGSNSMTEVPGDLKPPT
PASTPHGQMTPMQSGRSSTISVHDPFSDVGDSSYPKRNSMTPNAPYQQGMSMPDMMGRMPYEPNKDPFSGMRKVPGSNEP
FMTQGQMPNSSMQDMYNQSPSGAMSNLGMGQRQQFPYGASYDRRHEAYGQQYPGQGPPTGQPPYGGHQPGLYPQQPNYKR
HMDGMYGPPAKRHEGDMYNMQYGSQQQEVYNQYGSSYSGPDRRPLQGQYPYPYNRERMQGPGQMQPHGIPPQMMGGPMQP
SSSEGPQQNMWATRNEMPYPYQNRQGPGGPAQAPPYPGMNRTDDMMVPDQRINHESQWPSHVSQRQPYMSSSASMQPITR
PPQSSYQTPPSLPNHISRAPSPASFQRSLESRMSPSKSPFLPAMKMQKVMPTVPTAQVTGPPPQPPPIRREITFPPGSVE
ASQPVLKQRRKITSKDIVTPEAWRVMMSLKSGLLAESTWALDTINILLYDDSTVATFNLSQLSGFLELLVEYFRRCLIDI
FGILMEYEVGNPSQKALDHHAGKKDDSQSSGDDSGKEEEEEEEEEEEEEEEEEEEEEDSEKMEPEGKTSAAPDATTDPKET
PKQASKFDKLPIKIVKKNNLFVVDRSHKLGRAQEFNSGLLHWQLGGGDTTEHIQTHFESKMEIPPRRRPPPPLSSTGRKK
EQEGKGDSEEQPEKSIIATIDDVLSARPGALPEDANPGPQTDSSKFPFGIQQAKSHRNIRLLEDEPRSRDETPLCTIAHW
QDSLAKRCICVSNIVRSLSFVPGNDAEMSKHPGLVLILGKLILLHHEHPERKRAPQTYEKEEDEDKGVACSKDEWWWDCL
EVLRDNTLVTLANISGQLDLSAYTESICLPILDGLLHWMVCPSAEAQDPFPTVGPNSVLSPQRLVLETLCKLSIQDNNVD
LILATPPFSRQEKFYATLVRYVGDRKNPVCREMSMALLSNLAQGDALAARAIAVQKGSIGNLISFLEDGVTMAQYQQNQQ
SLMHMQPPPLEPPSVDMMCRAAKALLAMARVDENRSEFLLHEGRLLDISISAVLNSLVASVICDVLFQIGQL
```

1637 - 1656:	EEEEEEEEEEEEEEEEEEEE

A0A3Q0CU89 **A0A3Q0CU89_MESAU** (1309 aa)
tau-tubulin kinase 1 isoform X1. *Mesocricetus auratus (Golden hamster)*

```
MQCLAAALKDETNMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTRENVALKVESAQQPKQVLKMEVAV
LKKLQGKDHVCRFIGCGRNEKFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESIEAIHSVGFLHRDIKPSNF
AMGRLPSTYRKCYMLDFGLARQYTNTTGDVRPPRNVAGFRGTVRYASVNAHKNREMGRHDDLWSLFYMLVEFAVGQLPWR
KIKDKEQVGMIKEKYEHRMLLKHMPSEFHLFLDHIASLDYFTKPDYQLIMSVFENSMKERGIAENEAFDWEKAGTDTLLS
TSTSTPPQQNTRQTAAMFGVVNVTPVPGDLLRENTEDVLQGEHLSDQENAPPILPGRPPEGLGPSPHLVPHPGGPEAEVW
EETDVNRNKLRINIGKTPCVEEEQSRGVGVPSSPVRAPPDSPTTPVRSLRYRRVNSPESERLSTAADGRIELHERRSRMD
LPGSPSRQACSSQPAQMLSVDTGHADRQASGRMDVSASVEQEALSNAFRSVPLAEEEDFDSKEWVIIDKETELKDFPPGA
EPSTSGTTDEEPEELRPLPEEGEERRRLGTEPSVRPRGRGMQTLAEEDLRQGLPQPAPPLLSQADGRSETSQPPTPGSLS
HSPLHSGPRPRRRESDPTGPQRQVFSVAPPFEVNGLPRAVPLGLPYQDFKRDASDYGERARLLTRVRRVGFSHMLLTTAQ
VPLTPFQPQANGKEGEEEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEGEAGALGEVLGPRSLSSSEGSERSTERSQEGAPS
TLLADDQRDTRGRASMADGDLEPEEGSKTLVLVSPGDVKKSPVTAELAPDPDLGTLAALTPQHEQPQPTGSQLDVSEPGT
LSSVLKSEPKPSGPGTGLGAGLVAAGGAGAVTSSPFTKVERTFVHIAEKTHLNVMSSGGQASRPEGSGTGGELGLEMLSE
GGAAEERGPVPLENGMALSGLDGTETESCALSGPPGETPSEVVTDSLPNGPALADGPAPATPLEPVTKKGTAISPSRHAM
PGSRPRSRIPVLLSEEDTGSEPSGSLSAKERWSKRARPQQDLARLVMEKRQGRLLLRLASGASSSSSEEQRRASETLSGT
GSEEDTPASEPTAALPRKVGRAATTRSRIPRPIGVSASAEGQQLPGRPHGAASASDLAITSSRLQLQKPSGSTTTADLRP
KHSASRGPGPGRAQVSRSAAPRSPGLPASTARHPSGSPRSQSLSRKESSSPSHQARSGVPPPRGVLQARSQPEASPGAPK
KGPRGKQQQTQRAATKGRGAVSEGRPGTR
```

744 - 763:	EEEEEEEEEEEEEEEEEEEE
745 - 764:	EEEEEEEEEEEEEEEEEEEE
746 - 765:	EEEEEEEEEEEEEEEEEEEE
747 - 766:	EEEEEEEEEEEEEEEEEEEE

A0A3Q0CYZ1 **A0A3Q0CYZ1_MESAU** (1123 aa)
sodium/potassium/calcium exchanger 1 isoform X1. *Mesocricetus auratus (Golden hamster)*

```
MGKLIRIGTRERRLFRRPKRLHWSRLLFLLGMLIIGSTYQHLRRPQNSPSMWTKVSSQQPIKLAGRDLPSDEMTVVGSDP
PEASSEVDGEILAPQNTVIRDEATPSITMEDTPNPPRTTKITPTSPKNDYSPIAAGTERKKEKPPPTSSRASNHFISTSG
RERIKNYTPIPRGERRNSTPAHSREKGRKYTPSPAGAPSATTPITTEKDSKTMATYRLLETRPPERIVEETTAASFRRVV
PNTPTFLTREAETSLLTTPSLVEENTLGSPGREEQNSSTSLQGTVPQHTPATSEEQVTVRARMGSNPATVGASTAAWRIS
NLLSRTSAPTIRIASVTNREGAKRPSTAPVTSKVKAILTTQVHRCVVMEPVPAVPMTPSPSITNILFPGAPSPSPSASPP
GWPKLHAKAEYPPDLFSVEDRRQGWVALHIFGMMYVFVALAIVCDEYFVPALGVITDKLQISEDVAGATFMAAGGSAPEL
FTSLIGVFISHSNVGIGTIVGSAVFNILFVIGTCALFSREILNLTWWPLFRDVSFYILDLSMLIVFFLDSLIAWWESLLL
LLAYALYVFTMKWNKQIELWVKEQLSRRPVAKVMALGDLSKPSEGAIEENESQDNKKLKLPSVLTRGSSSASLHNSIIRS
TIYHLMLHSLDPLGEARPSKDKQESLNQEARAHPQTKAESSPDEEEPAQLPEVTVTPAPAPDVKGDQEEDPGCQEEVGEA
DRTGETQPGERETEAEGNEDEEGETEAEGKEAEQEEETEAEGKEDEQEGETEAGGKEDEHEGETXXXXXXXXXEGETEAE
GKEDEGETEAEGKGDEQEGETEAEGKGDEQEGETEAEGKEDELKRQGEIQADDTEVKDGDDETEANAENQCETTQGEKGA
DDEGGSDGGDSGEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEPLSLEWPESRQKQALYLFLLPIVFPLWLTVPDVRRQESRKF
FVITFLGSIIWIAMFSYLMVWWAHQVGETIGISEEIMGLTILAAGTSIPDLITSVIVARKGLGDMAVSSSVGSNIFDITV
GLPVPWLLFSLINTLQPVPVSSNGLFCAIVLLFLMLLFVIFSIASCKWRMNKILGFTMFLLYFVFLVISVMLEDRIIACP
VSV
```

897 - 916:	EEEEEEEEEEEEEEEEEEEE

A0A3Q0D354 **A0A3Q0D354_MESAU** (1009 aa)
zinc finger protein 592. *Mesocricetus auratus (Golden hamster)*

```
MGDMKTPDFDDLLAAFDIPDPTSLDAKEAIQTPSEENESPLKSSGMCMDESVSLSHSGSAPDVPAVSVIVKNTSRQESFE
AEKDHIAPSLLHNGFRGSDLPPDSHHCGKFDSTFINGDSARSFTSKLEPSKSEPLPTFNQFSPISSPEPEDPVKDNGFGI
KPKHSDSYFPPPPGCGAVGGPVLEALGKFPVPELHMFDHFCKKEPKPEPLPLESQQEHERGGPKVLEPPKDLDSSRFFGE
ALEFNSHSNNSIGEPKKLAPELSTCSSVPPRQRLKPAHSKLSSCVAALVALQAKRVASVTKEDQPGHTKDSSGPTKEGSK
SSPKMPKSPKSPRSPLEATRKSIKPSDSPRSICSDSSSKGSPSVAASSPPAIPKVRIKTIKTSSGEIKRTVTRILPDPDD
PSKSPVESPLGSTIAEAPSEVPGDEGAALPVEEHFSEAGINSGSPQGDRKGDESMVKASDSSSPCRISGPRAPKGAALNS
QASKKQQSTALQASTLAPASLLPKAVHLANLNLVPHSVAASVTAKSSAQRRSQPQVTQMTVPLVHQVKKASPLIVEVFNK
VLHSSNPVPLYAPNLSPPVDSRIHVPASGYCCLECGDAFALEKSLSQHYSRRSVHIEVLCTLCSKTLLFFNKCSLLRHAR
DHKSKGLVMQCSQLLVKPISADQMFVTAPVNSTAPATPAASSSPKPSSTSGNASPVIPALPLYPDPVRLIRYGTKCPECH
KQMRDYMVLAAHFQRTSEETEGLLSSHICEEYGEPEVSPPPYLCSCRYCTEDSPSFPRPSLLESHISLMHGIRNPDLSQT
SKIRHPGGHSPQVNHLKRPVSRVADAPGTSNGTTVPSTKRHKSLFQCAKCSFATDSEPEFQSHIPQHQVDSSTAQCLLCG
LCYTSASSLNRHLFIVHKVRDQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAKVVGVKVEATEPEACSAEEVAMETRENGL
EECAREPLVADLEPRRSLGLSLEEDSTQGPQNPPQASQDQNSHAVSPQV
```

903 - 922:	EEEEEEEEEEEEEEEEEEEE
904 - 923:	EEEEEEEEEEEEEEEEEEEE
905 - 924:	EEEEEEEEEEEEEEEEEEEE
906 - 925:	EEEEEEEEEEEEEEEEEEEE
907 - 926:	EEEEEEEEEEEEEEEEEEEE
908 - 927:	EEEEEEEEEEEEEEEEEEEE
909 - 928:	EEEEEEEEEEEEEEEEEEEE
910 - 929:	EEEEEEEEEEEEEEEEEEEE
911 - 930:	EEEEEEEEEEEEEEEEEEEE

A0A3Q0DJ41 **A0A3Q0DJ41_CARSF** (941 aa)
proline-, glutamic acid- and leucine-rich protein 1. *Carlito syrichta (Philippine tarsier) (Tarsius syrichta)*

```
MQGKLASFFLSRVDAVSPQLQQLACECYSRLPSLGAGFSQGLKHTESWEQEVHSLLDSLHSLLGALYEGAETAPVQSEGP
GVETLLSPSEDGEAHILLRLRQRFSGLARCLGLMLSSEFGAPVSVPVQEILDVICRTLSVSSKNISLLGDGPLRLLLLPS
VHLEALDLLSALILACGGRLLRFGVLISRLLPQVLNAWSIGRDSFSPGQEKPYSTIRTKVYAVLELWVKVCGASAGVLQG
GASGEALLTHLLSDISPPADALKLRSPRGSPDGGLQTGKPSAPKKLKLDVGEAMAPPSHRKGDTNANSDVCAAALRGLSR
```

```
TILMCGPVIKEETHRRLHDLVLPLVMGVQQGEALGSSPYNSSCCRRELYRLLLALLLAPSPRCPPPLACALQAFSLGQQE
DSLEVSSFCSEALVTCAALTHPRVPPLQSMGSTCPTPAPVPPPEAPSPFRAPPFHPPGPMPSVGPMPSAGPMPSAGPMSS
TGPMPSAGPMSSAGSMSSTGPVPSARPGPPATANHLGLSVPGLVSVPPRLLPGPENHRAGSNEDPVLAPSGTPPPTIPPD
ETFGGRVPRPAFVHYDKEEASDVEISLESDSDDSVVIVPEGLPPLPPPPPSGTTPPPTASAGPPAASPPVPAKEEPEELP
AAPGPLPPPPPPPPPVPGPVTLQPPQLVPEGTPGGGGPPALEEDLTVININSSDEEEEEEEEEEEEEEEEEEEEEDFEEE
EEDEEEYFEEEEEEEEEFEEEFEEEEGELEEEEEEEEEEEEEELEEVEELEFGSAGGEVEEGGPPPPTLPPALAPSESPK
VQPEPEPEPGLLLEVEEPGAEEEHGAETAPTLAPEILPSQGEAEGEGVSPAAGPPPQELVEEEPCSAPPTLLEEGTEGGD
DKVPPPPETSAEEEMEMETETEAEATALQEKEQDDTAAMLADFIDCPPDDEKPPPTTEPDS
```

695 - 714:	EEEEEEEEEEEEEEEEEEEE
696 - 715:	EEEEEEEEEEEEEEEEEEEE

A0A3Q0E4N5 **A0A3Q0E4N5_CARSF** (739 aa)
YTH domain-containing protein 1 isoform X1. *Carlito syrichta (Philippine tarsier) (Tarsius syrichta)*

```
MAADSREEKENYQDCSSWLFSDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQ
LISKPLSSSVSNNKRIVSTKGKSVTEYKNEEYQRSERNKRIDADRKIRLSSSASREPYKSQPEKTCLRKRDPERRAKSPT
PDGSERIGLEVDRRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDPEEDEEVDED
GEEEEEEEEEEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGIS
PIVFDRSGSSASESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLN
VAFRSARSVILIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEH
KPVKIGRDGQEIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKK
PRIDYPPEFHQRPGYLKDPRYQEVDRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAP
PPQAHPPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERE
RERLCDRDRDRGERGRYRR
```

242 - 261:	EEEEEEEEEEEEEEEEEEEE

A0A3Q0EA78 **A0A3Q0EA78_CARSF** (709 aa)
YTH domain-containing protein 1 isoform X3. *Carlito syrichta (Philippine tarsier) (Tarsius syrichta)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLISKPLSSSVSN
NKRIVSTKGKSVTEYKNEEYQRSERNKRIDADRKIRLSSSASREPYKSQPEKTCLRKRDPERRAKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEEDVEEDEEVEEDPEEDEEVDEDGEEEEEEEEEEE
EEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSSAS
ESYADQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNVAFRSARSVILIFSVRESGKFQGFARLSSE
SHHGGSPIHWVLPAGMSAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLLFPPDESI
DLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYPPEFHQRPGYLKDPRYQEVDRRFSG
VRRDVFLNGSYNDYVREFHNMGPPPPWQGMPPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHHPVPHEARYRDKRVHDYDM
RVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDRGERGRYRR
```

230 - 249:	EEEEEEEEEEEEEEEEEEEE

A0A3Q0ECE6 **A0A3Q0ECE6_CARSF** (585 aa)
ran GTPase-activating protein 1 isoform X1. *Carlito syrichta (Philippine tarsier) (Tarsius syrichta)*

```
MASEDIAKLAETLAKTQVAGGQLSFKGKSLKLNTAEDAKDVIKEIEDFDSLEALRLEGNTVGVEAAKVIAKALEKKSELK
RCHWSDMFTGRLRSEIPPALISLGEGLITAGAQLVELDLSDNAFGPDGVKGFEALLKSSACFTLHELKLNNCGMGIGGGK
ILAAALTECHRKSSAQGKPLTLKVFVAGRNRLENDGATALAEAFGIIGTLEEVHMPQNGINHPGITALAQAFAINPLLRV
INLNDNTFTEKGAVAMAETLKTLRQVEVINFGDCLVRSKGAVAIADAIRGGLPKLKELNLSFCEIKRDAALAVAEAMADK
AELEKLDLNGNTLGEEGCEQLQEMLDGFNMTKVLASLSDDEDEEEEEGEEEEEEGEEEEEEEEEEEEEEEEEEEEPQQRR
QGEESCTPSRKILDPNTREPAPVLSSPPPVDVSTFLAFPSPEKLLRLGPKSSVLIAQQTDTSDPEKVVSAFLKVSSVFKE
EATVRTAVQDAVDALMKKAFSSSSFNSNAFLTRLLVHMGLLKSEDKIKAIANLYGPLMALNHMVQQDYFPKSLAPLLLAF
MTKPNGALESCSFARHNLLQTLYKV
```

376 - 395:	EEEEEEEEEEEEEEEEEEEE

A0A3Q0IUW1 **A0A3Q0IUW1_DIACI** (218 aa)
LOW QUALITY PROTEIN: vicilin-like seed storage protein At2g18540. *Diaphorina citri (Asian citrus psyllid)*

```
MLAKRERRRQITERRKKEKRKGKEEGEREKRRNREMRKRLGKQKKSKKKERECGKRXENEXKRRKLSSXKEKKRKKEKQE
KMENRKNRTIKKXRGKRKKKTKEKKKKTKEEKEEKEKKEEKKKKKREEEEEEEEEEEEEEEEEEEEEEEKRRRRRRRRRKR
LXRREDKERGKRREVVDGMRKLKEXRKERKRKXKKTKKRRENKGKDKNKDVRGNRERK
```

127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE

A0A3Q0IXX9 **A0A3Q0IXX9_DIACI** (450 aa)
glutamic acid-rich protein-like. *Diaphorina citri (Asian citrus psyllid)*

```
MPKPLEGLNQNQIEKSTQKKKRDSTEALRKLEQKLKENENKRFEKEKKKEIKILEKEIKKEEKMRVKEEIERVKSESKSR
QAAKKLKLEASNGPVCKTEEEYEQLKNLYEQVKNKLERLEKDLKSKRKHSKPDDSDDVSDDTSFDSEPNKRVHEKNSRKR
QEKVSFNESLWKDKKIRKSGNNTQTKKNTRDSSSRNSSKARDTKKDKKNTRDSSSRNSSKAKDNRKSDKSAKKKTNTSRD
SSSRNTSKSRGDKRHDSPKKVKKIKTKKEKPKEDKLEEKKKPKKKQKKLKVNYALLPEEQSTAFNRSKREKSKRFCITIC
DSEINSRGEKPKEDKLEEKKKPKKKQKKLKKKKEEEEEEEEEEEEEEEEEEEEEEKKKEEEEEEEEEEKKKKKEEEEEE
EEEEEDCSSIEDFSKVRSSGDNEDIHRIQDAGREDYAEEETQMKGLLYMK
```

354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE

A0A3Q0R019 **A0A3Q0R019_AMPCI** (334 aa)
Transmembrane protein 79a. *Amphilophus citrinellus (Midas cichlid) (Cichlasoma citrinellum)*

```
HSRMADTNTSEEVSFSPAGSVAEPQTAGSKKLQESSSLEDKRELTEKTEEEEEEEEEEEEEEEEEEEEEEEEEGKVTVKC
LALLEPSTLPWSADKKSRPLTDQDDELDIDFPCLSVLTLVNNKHLLYSSSSDLCEHICSEKLRLVLSMVAAIILFPLLVW
GGYALIPFDSPPLESAPLRVLYTLRCAFFATIPIMLGVVVQGVARLRYSVLEPLYQSTLVNMEVVVHWHYVNESLGLFLF
YFLQLAVMATYISQELIKLVPLLTIIFVFGRLIYWLCLSLGSSVRGLGFGFSFFPILVMLGTNLYFVCSSMGQDGVFDVV
LPTTAPAPRLRWWG
```

49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE

A0A3Q0RQZ1 **A0A3Q0RQZ1_AMPCI** (853 aa)
BAF chromatin remodeling complex subunit BCL11A a. *Amphilophus citrinellus (Midas cichlid) (Cichlasoma citrinellum)*

```
MSRRKQGKPQHLSKRDFSLNGHHPGSNMGRLARLGHDAHPSLEQDLLTCGQCQATFPLADILLFIEHKRKRCHGPPCLTV
GRGLDKPPSPSPGLALTPSPAMGSLRSRRLEVGVQATLADEDDDRFSSPRGICPKQEPLPGKEEPTTYTCTTCKQSYGSA
WFLLQHAQNTHGFRIYLESEHGSPLTPRMGGPSSLGGGADCPSQPPLHGLHLPPDASPFNLLRIPGSGSGGRDSRFPPTP
PLFSPPPRNHLDPHHLSPEELALAAHHPSAFDRVLRLNPPLPLDPPPTMDFSRRLRELAGNTSGSTPPLSPSRPSPMQRA
GGGKPPYLATPPPLPGSMQSPVGSQTTPTTPLPSAGATPSSTTQMKSKCCEFCGKAFKFQSNLIVHRRSHTGEKPYKCHL
CDHACTQASKLKRHMKTHMHKSSSPNTGKSEDGLSTASSPEPGTSEHVGSASNALKSVVAKLKSENDRMLRENGEEEEEE
EEEEEEEEEEEEEEEEEEEGEEEEEQNGERAARRNNNSYHFGLNLEAARQHENNGSIGSRLGGVADEGSIPRSLPEVMQG
MGLAASMQHFSEALNAHKRNAMAQENHLHHHLSRDHHHNREICDGDSVLETDRGEEGSVSTVNGRGASPNESASVGLSKK
LLLGSPSPLSPFSKRIKLEKEFDLPTPTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRFS
TPPGELDGGMSGRSGTGSGGSTPHLGGPGRPSSKDGRRSDTCEFCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQS
SKLTRHMKTHGQVGKDVYKCEICQMPFSVYSTLEKHMKKWHSDRPLSTEIKSE
```

475 - 494:	EEEEEEEEEEEEEEEEEEEE
476 - 495:	EEEEEEEEEEEEEEEEEEEE
477 - 496:	EEEEEEEEEEEEEEEEEEEE
478 - 497:	EEEEEEEEEEEEEEEEEEEE
479 - 498:	EEEEEEEEEEEEEEEEEEEE
480 - 499:	EEEEEEEEEEEEEEEEEEEE

A0A3Q0S640 **A0A3Q0S640_AMPCI** (1689 aa)
Bromodomain and WD repeat domain containing 3. *Amphilophus citrinellus (Midas cichlid) (Cichlasoma citrinellum)*

```
MLFFFSELYYLIARFLQSGPCKKAAKLVPQRWSWDGKKYKRTFQDWVMLNQHIPADYLLHVCQRIGPLIEKEIPPSVPGV
QTLLGVGRQSLLRTTKSCSYKVCSGSAVAALHRGRPPEPPASNGHSFNVVSVMGARQATGTARFGQVLPSSTYQHMKIHK
RILGHLSSVYCVAFDRTGRRIFTGSDDCLVKIWATDDGRLLATLRGHSAEICDMAVNHENSLIASASCDKVIRVWCLRTC
APITVLQAHAASITSIQFCPAVRGTTRYLASTGADGMVCFWKWHSLTMKFNDQPVKFVERSRPGVQVSTSSFSSGGMFMA
TGSTDHMIRVYYLGADSPMKVSEMDAHTDKVVVVQFSNNSDSLRFVSGSRDGTVRIWHYQQQEWKSITLDMAARLPGSTA
TTGDDKAKLVVTMVAWDRTDSTVITAVSNYLLKVWSTCTGQLLHVLSGHDDEVFVLEAHPFDSRIMLSAGHDGNIYIWDL
TKGLKIRNFFNMIEGQGHGAIFDCKFSADGQYFACTDSHGHFSLIIRLGIPDQMFFHTDYRPLIRDSNNYVLDEQTQQAP
HLMPPPFLVDVDGNPHPPHYQRLVPGRENCKEEQLIPQMGYMANSDGELVEQVLGQQTAENGESLLDNLIRQLQNEQDER
QNAEQQAEEDEEVVPSSPVVAPRRSGQVDGVWQMQHNALRSQVATERDLLAWSRRVVVNEVPQGIFRVSEQCRKAKGDIE
CSLYNAERRKKPATCNDLLSSRLRSLRPTKKTQQRHAYQTRSAQIRRPGTRSRNPSTRRNSNTQMESDTDGEQAEEQGVQ
TDASSDGEARWQSESSSSDSSSEYSDWTADAGINLQPPKRPTRRPVQPPDYSSSEEDDRGKEAKEAKTREKEKRKKPKET
KQKPTSSLGGLDAEEWLPPSWIVEIIPHRSPFVPQMGDELIYFKQGHQAYVRAVRRAKAYSINPQKQPWNRLNLRDQESV
KVVGIKYEVGPPTLCCLKLAFLDPVSGKMTNESFSLKYHDMPDVIDFLVLQQFYNEAKEHNWQPGMRFRSIIDDAWWFGS
VEDQEPLQPEYPDSLFQCYAVKWDNGEREKMSPWDMEPIPEEAALPEQVGDGVEVAEEELKALLYKPQEGEWGAHTRDEE
CERVIHGINQLVTLDVAKAFATPVNLQDYPLYCTAVAYPTDLSTIRKRLENRFYRRISALMWEVRYIEHNARTFNEPQSP
IVAAAKVVTDVLLHYIGDQSCTDILDLYRKLKSEVSSEGEAEVRLLAIPNSKKRGVVLDAKAWRSQCRELLRRMIASRDS
QPFRQPIEFKVDDYRDIIDTPMDLGTVSETLIAGNYENPMEFAKDIRLIFSNSKAYTPNKKSQIYTMTLSLSAFFEKHII
SIISDYKSAIQNERRARQRLTYRSRLHNGGSSPPISPSSRYRATFINTLCYEIIFFIRAPQSVSALGCRNEPSPSCFSSG
HQNNLHLSNGSRQRHGQETLQSDDDEEASGSNSSSSESSSTSSSSSSSSSSDSENSSDSEMEKYVEGGGDHDYSKAPCLS
VRLSAKGKVAASGKRRHKGGEDMAQRSKRARVQLPVEEEEDDEEEEEEAEDEEEEEEEEEEEEEEEQQQQQQQVAVRHEE
EEEEEEEEEEEEEEEEEEEEEDQRGSQCKSRRVNTRNQGRRTVRYRDDSEDDGHGSKDDPLNLGMSRSGRVRRMTEKAR
```

VSHLMGWSH

1599 - 1618:	EEEEEEEEEEEEEEEEEEEE
1600 - 1619:	EEEEEEEEEEEEEEEEEEEE
1601 - 1620:	EEEEEEEEEEEEEEEEEEEE
1602 - 1621:	EEEEEEEEEEEEEEEEEEEE
1603 - 1622:	EEEEEEEEEEEEEEEEEEEE

A0A3Q0SM20 **A0A3Q0SM20_AMPCI** (303 aa)
Nucleolar protein interacting with the FHA domain of MKI67. *Amphilophus citrinellus (Midas cichlid) (Cichlasoma citrinellum)*

MSESGAEAAPAAAKELLALNPAQESEFRKKVQEVKKKKKSGQGNRLTPGVVYVGHLPRDLVEPQLKSYFGQFGKILRLRL
SRSKKTGNSKGYAFIEFDCDEVAKIVAETMNNYLMGERLIKCQVMPPEKVHEKLFVGSERAFKKPSYPAVTRYNKKRTEE
EIAKMTGKLLRKESKLRKRLAAYGIEYDFPGFAAQVPKKKSCSDTGNASSCTDDSTPVCTPSFLEKRKSTAADDADDEII
IKMPAVDKDEESSEEEDDDDDDDDEEEEEEEEEEEEEEEEEEEEDDEDDEESGEGSEEEAEA

265 - 284:	EEEEEEEEEEEEEEEEEEEE
266 - 285:	EEEEEEEEEEEEEEEEEEEE

A0A3Q1B650 **A0A3Q1B650_AMPOC** (528 aa)
BAF chromatin remodeling complex subunit BCL11A a. *Amphiprion ocellaris (Clown anemonefish)*

MQRLLQPFQTGGGSGGAGGVGASKPPYLATPPPLPGSMQSPVGSQTTPTTPLPSAGATPSSTTQMKSKCCEFCGKAFKFQ
SNLIVHRRSHTGEKPYKCHLCDHACTQASKLKRHMKTHMHKSSSPNTGKSEDGLSTASSPEPGTSEHMGSASNALKSVVA
KLKSENHRMLRENGEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEEQNGERAARRNNNSYHFGLNLEAARQHENNGGIGS
RLGGVADEASIPRSLPEVMQGMGLAASMQHFSEALHLCDGDSVLETDRVEEGSVSTVNGRGASPNESASVGLSKKLLLGS
PSPLSPFSKRIKLEKEFDLPTPTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRFSTPPGE
LDGGMSGRSGTGSGGSTPHLGGPGRPSSKDGRRSDTCEYCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQSSKLTR
HMKTHGQVGKDVYKCEICQMPFSVYSTLEKHMKKWHSDRPLSTEIKSE

175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE
180 - 199:	EEEEEEEEEEEEEEEEEEEE
181 - 200:	EEEEEEEEEEEEEEEEEEEE

A0A3Q1BBB1 **A0A3Q1BBB1_AMPOC** (807 aa)
BAF chromatin remodeling complex subunit BCL11A b. *Amphiprion ocellaris (Clown anemonefish)*

MSRRKQGKPQHLSKREFSPEPLAGVLPEEDSQDSPRLGVAQGEPLKGDQDLLTCGQCHSRFPLADILLFIEHKRRQCHGS
LCADKPLDRPPSSPLASVRQPVEVAVQVSPQDEDCLSAPLQGIIPKQENITGKHTGSLRWLPYTNVHGRLANGVSVKDQA
SGLYKDEPSSYTCTTCKQPFTSAWFLLQHAQNTHGFRIYLESEPGSPLTPRVAAAPGMGGDCASSQPPLHAVHLADGSPY
SLLRMPGSGSGRDSASTPREGRYPRTPPLFSPPPRHHLSPDDLALATHHPSAFDRVMRLNSVPLDPPQSMDFSRRLRELA
GNATGGSPPLSPNRPNPMQRLLQPFQPGSKPPFSATPPLSTSQSPSGSRSTPNPVSNAVQPGTPLKAKSCEFCGKTFKFQ
SNLIVHRRSHTGEKPFKCHLCNHACTQASKLKRHMKTHCQSKSTVLNTKSDDGLSTASSPEPGTSELMGSATDALKSVVA
KFKSENNGLMPENGEEEEEDEEEEEEEEEEEEEEEEEEEEEEEGEGEEEEIERARHHQNSEALYPHRRSLSREPGDEDSAM
ESDRADDGSTTTINGLGSLPNDNLSRKLLGGGVSPGSLSPLSKRIKVEKDIDPPTPTIPNTENVYSQWLAGYAASRQLKD
PFISFTGGDSRQSPFASSSEHSSENGSLRFSTPPGELDGERAASGRSGTGSGASTPHGGSGNGRPSSKDGRRSDTCEFCG
KVFKNCSNLTVHRRSHTGERPYKCELCSYACAQSSKLTRHMKTHGQMGKDVYKCEICHMPFSVYSTLEKHMKKWHSDRPL
ANDIKTE

501 - 520:	EEEEEEEEEEEEEEEEEEEE
502 - 521:	EEEEEEEEEEEEEEEEEEEE
503 - 522:	EEEEEEEEEEEEEEEEEEEE

A0A3Q1CJ92 **A0A3Q1CJ92_AMPOC** (837 aa)
B-cell lymphoma/leukemia 11B-like. *Amphiprion ocellaris (Clown anemonefish)*

MSRRKQVNPQHFSLTHRETIQAEANHDSGAGSPSPEPSTPSPRRAGPGEHDLLTCGQCQTNFPLGDILVFIEHKRRLCRG
PSGRPGSFSKPGEAGGVMGIPISPRVRSLELGRGAIPVEVGIQVTPGGEEDEARRLTPAKGICPKQERGDKDEPSSYICT
TCKQTFNSAWFLLQHAQHTHGIRIYLDNHPANCSLTPRMALPPPPGVDALPRSPLPTFLGDTNNPFHLLRMAAPLLREHP
PPPGYMETRLPATPPFVSPPPPPRPPLERLGPEEMGLLSQHPSAFERVMRMTPMEPPSMDFSRRLRELAGNTTNNGGPTP
PLSPNRVPPMHRLLSPTLFQPGAKPPAFLTYAPQPPTSQGGHGSSSPPDSQGQSQTPGKSKSCEFCGKIFKFQSNLIVHR
RSHTGERPYKCHLCDHACSQASKLKRHMKTHMHNKSGAMSGSPEQGNRGEGGDGEDKTREGDAREMGMDNEEEEEEEEEE
EEEEEEEEEELRNGSRPDSNLSEDSQEFSQNRENGPRHSPEDKSLSGNRVSDSGGVGIMHPYNHLDNHLRLNPNKRSLER
QPNGDGGERGEVERQRDNERDQDRERDEQEDQRPVMNGRISVSEAESFPGLFQRRPTPITSPSPSNNKRIKIEKEQLEIP
PTIPLISPENVYSQLLAGYAASRHFIREPFLGFTDSRQSPFATSSEHSSSETGSLRFSTPPGELMEGGSASGRSGSSTPH
LLRGPGPGRPPSSKDRRNDTCEYCGKVFKNCSNLTVHRRSHTGERPYKCDLCSYACAQSSKLTRHMKTHGQFGKEVYRCD
ICHMPFSVYSTLEKHMKKWHGEHLMASEVKLEQADRG

471 - 490:	EEEEEEEEEEEEEEEEEEEE

A0A3Q1FBA1 **A0A3Q1FBA1_9TELE** (801 aa)
B-cell lymphoma/leukemia 11A-like. *Acanthochromis polyacanthus (spiny chromis)*

```
MSRRKQGKPQHLSKREFSPEPLAGVLPEEDSQDSPRLGVAQGEPLKGDQDLLTCGQCHSRFPLADILLFIEHKRRQCHGS
LCADKPLDRPPSSPLASVRQPVEVAVQVSPQDEDCLSAPLQGIIPKQENITGTVLTTLHLPKALTPTPINTYEYWQRPAI
NKDEPSSYTCTTCKQPFTSAWFLLQHAQNTHGFRIYLESEPGSPLTPRVAAAPGMGGDCASSQPPLHAVHLADGSPYSLL
RMPGSGSGRDSASTPREGRYPRTPPLFSPPPRHHLSPDDLALATHHPSAFDRVMRLNSVPLDPPQSMDFSRRLRELAGNA
TGGSPPLSPNRPNPMQRLLQPFQPGSKPPFSATPPLSTSQSPSGSRSTPNPVSNAVQPGTPLKAKSCEFCGKTFKFQSNL
IVHRRSHTGEKPFKCHLCNHACTQASKLKRHMKTHCQSKSTVLNTKSDDGLSTASSPEPGTSELMGSATDALKSVVAKFK
SENNGLMPENGEEEEEDEEEEEEEEEEEEEEEEEEEEEEGEEEEIERARHHQNSEALYPHRRSLSREPGDEDSAMESDRAD
DGSTTTINGLGSLPNDNLSRKLLGGGVSPGSLSPLSKRIKVEKDIDPPTPTIPNTENVYSQWLAGYAASRQLKDPFISFT
GGDSRQSPFASSSEHSSENGSLRFSTPPGELDGERAASGRSGTGSGASTPHGGSGNGRPSSKDGRRSDTCEFCGKVFKNC
SNLTVHRRSHTGERPYKCELCSYACAQSSKLTRHMKTHGQMGKDVYKCEICHMPFSVYSTLEKHMKKWHSDRPLANDIKT
E
```

498 - 517:	EEEEEEEEEEEEEEEEEEEE
499 - 518:	EEEEEEEEEEEEEEEEEEEE

A0A3Q1FN99 **A0A3Q1FN99_9TELE** (837 aa)
B-cell lymphoma/leukemia 11B-like. *Acanthochromis polyacanthus (spiny chromis)*

```
MSRRKQVNPQHFSLTHRETVQAEANHDSRAGSPSPEPSTPSPRRAGPGEHDLLTCGQCQTNFPLGDILVFIEHKRRLCRG
PCGRPGSFSKPGEAGGVMGIPISPRVRSLELGRGAIPVEVGIQVTPGGEEDEARRLTPAKGICPKQERGEKDEPSSYICT
TCKQTFNSAWFLLQHAQHTHGIRIYLDNHPANCSLTPRMALPPPPGADALPRSPLPTFLGDTNNPFHLLRMAAPLLREHP
PPPGYMETRLPATPPFVSPPPPPRPPLERLGPEEMGLLSQHPSAFERVMRMTPMEPPSMDFSRRLRELAGNTTNNGGPTP
PLSPNRVPPMHRLLSPTLFQPGAKPPAFLTYAPQPPTSQGGHGSSSPPDSQGQSQTPGKSKSCEFCGKIFKFQSNLIVHR
RSHTGERPYKCHLCDHACSQASKLKRHMKTHMHNKSGTMSGSPEQGNRGEGGDGEDKTREGDAREMGMDNEEEEEEEEEE
EEEEEEEEEELRNGSRPDSNLSEDSQEFSQNRENGPRHSPEDKSLGGNRVSDSGGVGIMHPYNHLDNHLRLNPNKRSLER
QPNGDGGERGEVERQRDNERDQDRERDEQEDQRPVMNGRISVSEAESFPGLFQRRPTPITSPSPSNNKRIKIEKEQLEIP
PTIPLISPENVYSQLLAGYAASRHFIREPFLGFTDSRQSPFATSSEHSSSETGSLRFSTPPGELMEGGSASGRSGSSTPH
LLRGPGPGRPPSSKDRRNDTCEYCGKVFKNCSNLTVHRRSHTGERPYKCDLCSYACAQSSKLTRHMKTHGQFGKEVYRCD
ICHMPFSVYSTLEKHMKKWHGEHLMASEVKLEQADRG
```

471 - 490:	EEEEEEEEEEEEEEEEEEEE

A0A3Q1GJ48 **A0A3Q1GJ48_9TELE** (573 aa)
5'-nucleotidase, cytosolic II. *Acanthochromis polyacanthus (spiny chromis)*

```
MTTSWSDRLQNYADLPANMDGLAMKKYRREPYHRVFVNRSLAMEKIKCFGFDMDYTLAVYKSPEYESLGFELTVERLVSI
GYPQELLSFVYDPSFPTRGLVFDTMYGNLLKVDAYGNILVCVHGFNFLRGPEIRERYPNKFIQRDDTERFYILNTLFNLP
ETYLFACLVDFFSNCDRYTSCETGFKDGDLFMSYKSMFQDVRDAVDWVHFKGTLKEKTVENLEKYVVKDGKLPLLLSRMN
EVAKVFLATNSDYKYTDKIMTYLFDFPHGPKPGTSHRPWQSYFDLILVDARKPLFFGEGTVLRQVDTTTGRLKIGTYTGP
LQHGIVYSGGSSDIVCDLLGAKGKDIVYIGDHIFGDILKSKKRQGWRTFLVIPELAQELHVWTDKSSLFEELQGLDIFLA
ELYKHLDSSSNERPDISTIQRRVKKVTHDMDMCYGMMGSLFRSGSRQTLFASQVMRYADLYAASFINLLYYPFSYLFRAA
HVLMPHESTVEHTHVDIDTESPLATRNRTQCSDCKDLECKRNQLTRSFSEIKPPNLFPQTPQEITHCHDEDDDEEEEEEE
EEEEEEEEEEEEE
```

554 - 573:	EEEEEEEEEEEEEEEEEEEE

A0A3Q1GJX6 **A0A3Q1GJX6_9TELE** (810 aa)
B-cell lymphoma/leukemia 11A-like. *Acanthochromis polyacanthus (spiny chromis)*

```
MSRRKQGKPQHLSKREFSPEPLAGVLPEEDSQDSPRLGVAQGEPLKGDQDLLTCGQCHSRFPLADILLFIEHKRRQCHGS
LCADKPLDRPPSSPLASPLSTSSSHSRTQHQHPRRVRQPVEVAVQVSPQDEDCLSAPLQGIIPKQENITDKDEPSSYTCT
TCKQPFTSAWFLLQHAQNTHGFRIYLESEPGSPLTPRVAAAPGMGGDCASSQPPLHAVHLADGSPYSLLRMPGSGSGRDS
ASTPREGRYPRTPPLFSPPPRHHLSPDDLALATHHPSAFDRVMRLNSVPLDPPQSMDFSRRLRELAGNATGGSPPLSPNR
PNPMQRLLQPFQPGSKPPFSATPPLSTSQSPSGSRSTPNPVSNAVQPGTPLKAKSCEFCGKTFKFQSNLIVHRRSHTGEK
PFKCHLCNHACTQASKLKRHMKTHCQSKSTVLNTKSDDGLSTASSPEPGTSELMGSATDALKSVVAKFKSENNGLMPENG
EEEEEDEEEEEEEEEEEEEEEEEEEEEEEGEEEEIESKPGVDEEGRNDYRFSLRLEGARHHQNSEALYPHRRSLSREPGDED
SAMESDRADDGSTTTINGLGSLPNDNLSRKLLGGGVSPGSLSPLSKRIKVEKDIDPPTPTIPNTENVYSQWLAGYAASRQ
LKDPFISFTGGDSRQSPFASSSEHSSENGSLRFSTPPGELDGERAASGRSGTGSGASTPHGGSGNGRPSSKDGRRSDTCE
FCGKVFKNCSNLTVHRRSHTGERPYKCELCSYACAQSSKLTRHMKTHGQMGKDVYKCEICHMPFSVYSTLEKHMKKWHSD
RPLANDIKTE
```

487 - 506:	EEEEEEEEEEEEEEEEEEEE
488 - 507:	EEEEEEEEEEEEEEEEEEEE

A0A3Q1GRQ2 **A0A3Q1GRQ2_9TELE** (599 aa)
Cysteine/serine-rich nuclear protein 3-like. *Acanthochromis polyacanthus (spiny chromis)*

```
MSGILKRKLEEGPSPYLSLQGSDDDEVSCSDSGNSSDSLNHSVPSGLLDSSLQQQSKRLRGRNVHFESVTVYYFNRRQGF
TSVPTQGGSTLGMSPRHSGVKRFTLREFAMEQKRSHRNMLRDHLKEEKLNAIKLKLTKNGTVSSLEADTLTLDDISEDDL
DVDNTEVDDYFFLQPLTTRRRRALLRASGVRRIDVEEKHELRTLRISREECGCRCRGICDPETCACSLAGIKCQVDRMSF
PCGCTKEGCSNTTGRLEFNPVRVRTHFLHTIMKLELEKSREEQYQHQQPEQQLVTNGNGYHGDSTLVQQQQQQQQQPNLQ
FPLMSGTPHIPIMHLQNTGDTESHLDEEEEEEEEEEEEEEEEEEEEEEDDEEEDDEAYDEDGSSVCSGLSDCSTHSLETI
DPEEGEEDEEDEEDDEEEEDDEDEEDDWDCSLHGTSPPPYSVPLPSVLSYSSSTLMSLGGPFSNTPPMQHYQRDGSVSDT
PAFLTENVSVTPTLPTVESALGSEINTELNCQTEQQSARCCFSESPALQTSSHVDTRETNTAPAGGSDEQPRSTDLQNNP
```

DHHDSQTEASAERETAEKTVQEQPGLQTNGDQMTSAESV

347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE

A0A3Q1I3C0 **A0A3Q1I3C0_9TELE** (917 aa)
B-cell lymphoma/leukemia 11A-like. *Acanthochromis polyacanthus (spiny chromis)*

MSRRKQGKPQHLSKRDFSPEPLSTAVVSSEELSERCSEHSEESGSLNGHHPGSTVGRLARLGHDAHPSLEQDLLTCGQCQ
ATFPLADILLFIEHKRKRCHGPPCLAVGRGLDKPPSPSPGLALTPSPALGSLRSRRPVEVGVQATLADEDDDRFSSHRGI
CPKQEPLPGKEEPTTYTCTTCKQSYGSAWFLLQHAQNTHGFRIYLESEHGSPLTPRMGGPSSLGGGADCPSQPPLHGLHL
PPDASPFNLLRIPGSGSGGRDSVGAGGGVGAGGIAGGGHHQRFPPTPPLFSPPPRNHLDPHHLSPEELALAAHHPSAFDR
VLRLNPPLPLDPPPTMDFSRRLRELAGNTSGSTPPLSPSRPSPMQRLLQPFQTGGGSGGAGGAGGSKPPYLATPPPLPGS
MQSPVGSQTTPTTPLPSAGATPSSTTQMKSKCCEFCGKAFKFQSNLIVHRRSHTGEKPYKCHLCDHACTQASKLKRHMKT
HMHKSSSPNTGKSEDGLSTASSPEPGTSEHMGSASNALKSVVAKLKSENHRMLRENGEEEEEEEEEEEEEEEEEEEEEE
EEEAEEEEEQNGERAARRNNNSYHFGLNLEAARQHENNGGIGSRLGGVADEGSIPRSLPEVMQGMGLAASMQHFSEALHA
HKRNAMAQENHLHHHLNRDHHHNRELCDGDSVLETDRVEEGSVSTVNGRGASPNESASVGLSKKLLLGSPSPLSPFSKRI
KLEKEFDLPTPTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRFSTPPGELDGGMSGRSGT
GSGGSTPHLGGPGRPSSKDGRRSDTCEYCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQSSKLTRHMKTHGQVGKD
VYKCEICQMPFSVYSTLEKHMKKWHSDRPLSTEIKSE

538 - 557:	EEEEEEEEEEEEEEEEEEEE
539 - 558:	EEEEEEEEEEEEEEEEEEEE
540 - 559:	EEEEEEEEEEEEEEEEEEEE
541 - 560:	EEEEEEEEEEEEEEEEEEEE
542 - 561:	EEEEEEEEEEEEEEEEEEEE
543 - 562:	EEEEEEEEEEEEEEEEEEEE
544 - 563:	EEEEEEEEEEEEEEEEEEEE

A0A3Q1JA81 **A0A3Q1JA81_ANATE** (918 aa)
BAF chromatin remodeling complex subunit BCL11A a. *Anabas testudineus (Climbing perch) (Anthias testudineus)*

MSRRKQGKPQHLSKRDFSPAEPLSTAVISSEELSERCSDQSEESSSLNGHHPGSSVGRLARLGHDAHPSLEQDLLTCGQC
QATFPLADILLFIEHKRKRCHGPPCLAVGRGLDKPPSPSPGLALTPSPSLSSLRSRRPVEVGVQATLADDDDDRLSSPRG
ICPKQELLPGKEEPTTYTCTTCKQSYGSAWFLLQHAQNTHGFRIYLESDHGSPLTPRMGGPSSLGGGADCPSQPPLHGLH
LPPDASPFNLLRIPGSGSGGRDSVGAVGGIGTAGGAGGGHHQRFPPTPPLFSPPPRNHLDPHHLSPEELALAAHHPSAFD
RVLRLNPPLPLDPPPTMDFSRRLRELAGNTSGSTPPLSPSRPSPMQRLLQPFQTGGGTGGTGGAGGSKPPYLATPPPLPG
SMQSPVGSQTTPTTPLPSAGVTPSSTNPMKSKHCEFCGKAFKFQSNLIVHRRSHTGEKPYKCHLCDHACTQASKLKRHMK
THMHKSSSPNTGKSEDGLSTASSPEPGTSEHMGSASNALKSVVAKLKSENGRMLRENGEEEEEEEEEEEEEEEEEEEEE
EEEEGEEEEEQNGERAARRNNNSYHFGLNLEAGRQHENNGSIGSRLGAVADEGSIPRSLPEVMQGMGLAASMQHFSEALN
AHKRNAMAQENHLHHHLSRDHHHNRDMCDGGSVLETDRGEEGSVSTVNGRGASPNESASAGLSKKLLLGSPSPLSPFSKR
IKLEKEFDLPTPTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRFSTPPGELDGGMSGRSG
TGSGGSTPHLGGPGRPSSKDGRRSDTCEFCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQSSKLTRHMKTHGQVGK
DVYKCEICQMPFSVYSTLEKHMKKWHSDRPLSTEIKSE

539 - 558:	EEEEEEEEEEEEEEEEEEEE
540 - 559:	EEEEEEEEEEEEEEEEEEEE
541 - 560:	EEEEEEEEEEEEEEEEEEEE
542 - 561:	EEEEEEEEEEEEEEEEEEEE
543 - 562:	EEEEEEEEEEEEEEEEEEEE
544 - 563:	EEEEEEEEEEEEEEEEEEEE
545 - 564:	EEEEEEEEEEEEEEEEEEEE

A0A3Q1LL11 **A0A3Q1LL11_BOVIN** (1258 aa)
Protein kinase domain-containing protein. *Bos taurus (Bovine)*

MDLLTRENVALKVESAQQPKQVLKMEVAVLKKLQGKDHVCRFIGCGRNEKFNYVVMQLQGRNLADLRRSQPRGTFTLSTT
LRLGKQILESIEAIHSVGFLHRDIKPSNFAMGRLPSTYRKCYMLDFGLARQYTNTTGDVRPPRNVAGFRGTVRYASVNAH
KNREMGRHDDLWSLFYMLVEFAVGQLPWRKIKDKEQVGMIKEKYEHRMLLKHMPSEFHLFLDHIASLDYFTKPDYQLIMS
VFENSMKERGIAENEAFDWEKAGNDALLSTSTSTPPQQNTRQTAAMFGVVNVTPVPGDLLRENTEDVLQGEHLSDQENAP
PILPGRPPEGLGPSPHLVPHPGGPEAEVWEETDVNRNKLRINIGKTPAVVEEEQTRGVGVPSSPVRAPPDSPTTPVRSLR
YRRVNSPESERLSTADGRVELHDRRSRMDLPGSPSRQACSSQPAQMLSVDTGHADRQASGRMDVSASVEQEALSNAFRSV
PLAEEEDFDSKEWVIIDKETELKDFPPGAEPSTSGTTDEEPEELRPLPEEAEERRRPGPEPAVRPRGRGMHTLAEEDLRL
TPSQPPPPQLSQADGRSETSQPPTPGSPSHSPLHSGPRPRRRESDPTGPQRQVFSVAPPFEVNGLPRAVPLSLPYQDFKK
DLSDYRERARLLNRVRRVGFSHMLLTPPQVPLAPAQPQTNGKEEEEEEEEEEEEEEEEEEEEEEDEEEEDEEEEEEEEEA
VALGEVLGPHSGSSSEGSERSTDRSQEGAPSTLLADDQKESRGRASMADGDLEPEEGSKTLVLVSPGDMKKSPVTADLAP
DPDLGTMAVLTPQQERPQPTGSQLDVSEPGTLSSVLKSEPKPPGPGAGPGTGAVAMGAGGAAVTSSPFTKVERTFVHIAE
KTHLNVMSSGGQASRSEELSSGGELGLEVTSDGRVAEEGASAHLENGIALSGLESCVPSAPPGSGPLEVTADSLPNGPAL
ADGPAPVSLLEPGPEKLATISPSRHAVPGPRPRSRIPVLLSEEDTGSEPSGSLSAKERWGKRARPQQDLARLVMEKRQGR
LLLRLASGASSSSSEEQRRASETLSGTGSEEDTPASEPAVPKKAGRAAATRSRIPRPISVRMPTPATAQQPPDRPQGAAP
ASDTAITSRLQLQKPPGTAIAADLRPKQPSGRGPGPGRAPAGTRPPAPRSPGLPASSAHHPSASPRSRSLSRKESPSPSH
QARPGPAPPRGAPQARAQPEGTPSPLGGPKKGPRGKVQTQRAATKGRAGVAESRAGAR

683 - 702:	EEEEEEEEEEEEEEEEEEEE
684 - 703:	EEEEEEEEEEEEEEEEEEEE
685 - 704:	EEEEEEEEEEEEEEEEEEEE

A0A3Q1LSA6 **A0A3Q1LSA6_BOVIN** (1211 aa)
Euchromatic histone lysine methyltransferase 2. *Bos taurus (Bovine)*

```
MAAAAGAAAAAAAEGEAPAEMGALVLEKEPRGATERVHGSLGDTSRSEETLPKANPDSLETAGPSSPASVTVTVGDEGAD
TPVGATPLIGDEPENLEGDGDLHGGRILLGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGA
PAAGPEPPPATASPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEEL
ASTRSSGEVTLEKGDPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEE
EEEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGT
LSPNHAGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMV
LCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAG
TAAPAPPPLAQDAPGRADTSQPSARMRGQGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPPGPGREALEKALVIQ
ESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQR
TPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIE
VIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPEL
RNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCET
STMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVR
LQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNI
IPVRVFMLHQDLRFPRIAFFSSRDIRAGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELL
PELSSLPPVNP
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300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE

A0A3Q1LU60 **A0A3Q1LU60_BOVIN** (2054 aa)
Histone acetyltransferase (EC 2.3.1.48). *Bos taurus (Bovine)*

```
MVKLANPLYTEWILEAIQKIKKQKQRPSEERICHAVSTSHGLDKKTVSEQLELSVQDGSVLKVTNKGLASYKDPDNPGRF
SSVKPGTFPKSTKGSRGSCNDLRNVDWNKLLRRAIEGLEEPNGSSLKNIEKYLRSQSDLTSTTTNPAFQQRLRLGAKRAV
NNGRLLKDGPQYRVNYGGLDGKGAPKYPSAFPSSLPPVSLLPHEKDQPRADPIPICSFCLGTKESNREKKPEELLSCADC
GSSGHPSCLKFCPELTTNVKALRWQCIECKTCSACRIQGKNADNMLFCDSCDRGFHMECCDPPLSRMPKGMWICQVCRPK
KKGRKLLHEKAAQIKRRYAKPIGRPKNKLKQRLLSVTSDEGSMNAFTGRGSPGRGQKTKVCTTPSSGHAASGKDSSSRLA
VTDPTRPGATTKITTTSTYISASTLKVNKKTKGLIDGLTKFFTPSPDGRRSRGEIIDFSKHYRPRKKVSQKQPCTSHVLA
PGTTQKLKPPLSSLPPPTPISGQSPSSQKSSTSVSSTSPQSSSSQSSVPSFSSLTNNSQLKALFDGLSHIYTTQGQSRQK
GHPSYAPPKRMRRKTEFPLTAKSKAHFFGKRDVRSRFISHSSSSSWGMARGRIFKAIAHFKRTTFLKKHRMLGRLKYKVT
PQMGTPSPGKGSLTDGRIKPDQDDDTEIKISIKQESTDINVIGNKDTVTEEDLDVFKQAQELSWEKIECESGVEDCGRYP
SVIEFGKYEIQTWYSSPYPQEYARLPKLYLCEFCLKYMKSKNILLRHSKKCGWFHPPANEIYRRKDLSVFEVDGNMSKIY
CQNLCLLAKLFLDHKTLYYDVEPFLFYVLTKNDEKGCHLVGYFSKEKLCQQKYNVSCIMIMPQHQRQGFGRFLIDFSYLL
SRREGQAGSPEKPLSDLGRLSYLAYWKSVILEYLYHHHERHISIKAISRATGMCPHDIATTLQHLHMIDKRDGRFVIIRR
EKLILGHMEKLKTCSRTNELDPESLRWTPILISNAAVSEEEREAEKEAERLMEQASCWEKEEQEILSSRANSRQSPAKVQ
SKNKYLHSPESRPVAGERGQLMELSKESSEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEENIQSSPPRLTKPQSVAIKRKR
PFVLKKKRGRKRRRINSSVTTETISETTEVLNEPFDNSDEERPMPQLEPTCEIEVEEDGRKPVLRKAFQHQPGKKRQTEE
EEGKDNHCFKNTDPCRNNMDDGANNLKEASRDNPEPLKCKQWPKGTKRGLSKWRPNKERKTGFKLNLYTPPETPMEPDDQ
VTVEEQKETPADKSSPSSTRIEEGVKEAVEPLLPQDENGREETCAPVSPNKSPAGKPEDDVIKPEEEEEEEEEEEEEGNV
EKDPSGAKSQEKEEPEVCMDKEDPVRLDDHEEEEEEEEEPSHNEGHDADDEDDSHMESAEVEKEEHPREAFKEVLENQEA
FLDLSVQPSHSNPEVLMDCGVDLPASCNSEPKELAGATETAPESDEEPPGEQAQKQDQKNSEEVDSEFKEGNTATLEIDS
ETVQAVQSLTQENSEQDDTFQDCAETQEACRSLQNYTHADQSPQISATLDDCQQSDHSSPVSSVHSHPGQSVRSVSSPSV
PALENSYAQISPDQSAISVPSLQNMETSPMMDVPSVSDHSQQVVDSGFSDLGSIESTTENYENPSSYDSTMGGSICGNGS
SQNSCSYSNLTSSSLTQSSCAVTQQMSNISGSCSMLQQSSISSPPTCSVKSPQGCVVERPPSSSQQLAQCSMAANFTPPM
QLAEIPETGNANLGLYERMGQSDFGAGHYPQPSATFSLAKLQQLTNTLIDHSLPYSHSAAVTSYANSASLSTPLSNTGLV
QLSQSPHSVPGGPQAQATMTPPPNLTPPPMNLPPPLLQRNMAASNIGISHSQRLQTQIASKGHVSMRTKSASLSPAAATH
QSQIYGRSQTVAMQGPARTLTMQRGMNMSVNLMPSPAYNVNSVNMNMNTLNAMNGYSMSQPMMNSGYHSNHGYMNQTPQY
PMQMQMGMMGTQPYAQQPMQTPPHSNMMYTAPGHHGYMNTGMSKQSLNGSYMRR
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1070 - 1089:	EEEEEEEEEEEEEEEEEEEE
1071 - 1090:	EEEEEEEEEEEEEEEEEEEE
1072 - 1091:	EEEEEEEEEEEEEEEEEEEE
1073 - 1092:	EEEEEEEEEEEEEEEEEEEE
1074 - 1093:	EEEEEEEEEEEEEEEEEEEE
1075 - 1094:	EEEEEEEEEEEEEEEEEEEE
1076 - 1095:	EEEEEEEEEEEEEEEEEEEE
1077 - 1096:	EEEEEEEEEEEEEEEEEEEE
1078 - 1097:	EEEEEEEEEEEEEEEEEEEE
1079 - 1098:	EEEEEEEEEEEEEEEEEEEE
1080 - 1099:	EEEEEEEEEEEEEEEEEEEE

A0A3Q1LW37 **A0A3Q1LW37_BOVIN** (1699 aa)

Histone acetyltransferase (EC 2.3.1.48). *Bos taurus (Bovine)*

```
MVKLANPLYTEWILEAIQKIKKQKQRPSEERICHAVSTSHGLDKKTVSEQLELSVQDGSVLKVTNKGLASYKDPDNPGRF
SSVKPGTFPKSTKGSRGSCNDLRNVDWNKLLRRAIEGLEEPNGSSLKNIEKYLRSQSDLTSTTTNPAFQQRLRLGAKRAV
NNGRLLKDGPQYRVNYGGLDGKGAPKYPSAFPSSLPPVSLLPHEKDQPRADPIPICSFCLGTKESNREKKPEELLSCADC
GSSGHPSCLKFCPELTTNVKALRWQCIECKTCSACRIQGKNADNMLFCDSCDRGFHMECCDPPLSRMPKDTEIKISIKQE
STDINVIGNKDTVTEEDLDVFKQAQELSWEKIECESGVEDCGRYPSVIEFGKYEIQTWYSSPYPQEYARLPKLYLCEFCL
KYMKSKNILLRHSKKCGWFHPPANEIYRRKDLSVFEVDGNMSKIYCQNLCLLAKLFLDHKTLYYDVEPFLFYVLTKNDEK
GCHLVGYFSKEKLCQQKYNVSCIMIMPQHQRQGFGRFLIDFSYLLSRREGQAGSPEKPLSDLGRLSYLAYWKSVILEYLY
HHHERHISIKAISRATGMCPHDIATTLQHLHMIDKRDGRFVIIRREKLILGHMEKLKTCSRTNELDPESLRWTPILISNA
AVSEEEREAEKEAERLMEQASCWEKEEQEILSSRANSRQSPAKVQSKNKYLHSPESRPVAGERGQLMELSKESSEEEEEE
EEEEEEEEEEEEEEEEEEEEEEENIQSSPPRLTKPQSVAIKRKRPFVLKKKRGRKRRRINSSVTTETISETTEVLNEPF
DNSDEERPMPQLEPTCEIEVEEDGRKPVLRKAFQHQPGKKRQTEEEEGKDNHCFKNTDPCRNNMDDGANNLKEASRDNPE
PLKCKQWPKGTKRGLSKWRPNKERKTGFKLNLYTPPETPMEPDDQVTVEEQKETPADKSSPSSTRIEEGVKEAVEPLLPQ
DENGREETCAPVSPNKSPAGKPEDDVIKPEEEEEEEEEEEEEGNVEKDPSGAKSQEKEEPEVCMDKEDPVRLDDHEEEEE
EEEEPSHNEGHDADDEDDSHMESAEVEKEEHPREAFKEVLENQEAFLDLSVQPSHSNPEVLMDCGVDLPASCNSEPKELA
GATETAPESDEEPPGEQAQKQDQKNSEEVDSEFKEGNTATLEIDSETVQAVQSLTQENSEQDDTFQDCAETQEACRSLQN
YTHADQSPQISATLDDCQQSDHSSPVSSVHSHPGQSVRSVSSPSVPALENSYAQISPDQSAISVPSLQNMETSPMMDVPS
VSDHSQQVVDSGFSDLGSIESTTENYENPSSYDSTMGGSICGNGSSQNSCSYSNLTSSSLTQSSCAVTQQMSNISGSCSM
LQQSSISSPPTCSVKSPQGCVVERPPSSSQQLAQCSMAANFTPPMQLAEIPETGNANLGLYERMGQSDFGAGHYPQPSAT
FSLAKLQQLTNTLIDHSLPYSHSAAVTSYANSASLSTPLSNTGLVQLSQSPHSVPGGPQAQATMTPPPNLTPPPMNLPPP
LLQRNMAASNIGISHSQRLQTQIASKGHVSMRTKSASLSPAAATHQSQIYGRSQTVAMQGPARTLTMQRGMNMSVNLMPS
PAYNVNSVNMNMNTLNAMNGYSMSQPMMNSGYHSNHGYMNQTPQYPMQMQMGMMGTQPYAQQPMQTPPHSNMMYTAPGHH
GYMNTGMSKQSLNGSYMRR
```

715 - 734:	EEEEEEEEEEEEEEEEEEEE
716 - 735:	EEEEEEEEEEEEEEEEEEEE
717 - 736:	EEEEEEEEEEEEEEEEEEEE
718 - 737:	EEEEEEEEEEEEEEEEEEEE
719 - 738:	EEEEEEEEEEEEEEEEEEEE
720 - 739:	EEEEEEEEEEEEEEEEEEEE
721 - 740:	EEEEEEEEEEEEEEEEEEEE
722 - 741:	EEEEEEEEEEEEEEEEEEEE
723 - 742:	EEEEEEEEEEEEEEEEEEEE
724 - 743:	EEEEEEEEEEEEEEEEEEEE
725 - 744:	EEEEEEEEEEEEEEEEEEEE

A0A3Q1M4W7 **A0A3Q1M4W7_BOVIN** (1224 aa)
Euchromatic histone lysine methyltransferase 2. *Bos taurus (Bovine)*

```
MRARGRGRAAPPGSRGRGRGGAHRGRGRPRSLLSLPRAQASWAPQLPTGLTSPPIPCVPSQGEAPAEMGALVLEKEPRGA
TERVHGSLGDTSRSEETLPKANPDSLETAGPSSPASVTVTVGDEGADTPVGATPLIGDEPENLEGDGDLHGGRILLGHAT
KSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAPAAGPEPPPATASPEGQPKVHRARKTMSKPGNG
QPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSGGGLSEELASTRSSGEVTLEKGDPGSLEEWETVVGDDFSLY
YDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAKKKWRKDSPW
VKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKR
ETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEV
TIPRGDGVTPPAGTAAPAPPPLAQDAPGRADTSQPSARMRGQGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPPG
PGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQ
AGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGW
TPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDC
VLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPC
PEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRN
CKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGN
ISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRAGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQ
SRLARLDPHPELLPELSSLPPVNP
```

347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
349 - 368:	EEEEEEEEEEEEEEEEEEEE
350 - 369:	EEEEEEEEEEEEEEEEEEEE
351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE

A0A3Q1M9F1 **A0A3Q1M9F1_BOVIN** (2940 aa)
WD repeat domain 87. *Bos taurus (Bovine)*

```
MPFPLLLPILDSFHLILSQAVVWMKSKTEDMVEKRMFSMTDRLPPIQSMVHTGSFHILVVYCGDLLLRLFGDHLRSFKSL
GVVPCRFNITCLCYDPGMKMLLSGILGAVVTWTIERSGRGLQIAHMVALPGDEFIHDIMLNGPNGSLIAMCENVVRVLER
QGHGLLAEVKKFSSTISGSSITCCFTCSEQGFLYAGNKTGEIQVWNLNWGHSLHTFKAHFSSVICIRSQPEAHTLLTAGR
EGIIKEWNLTSGNLLRRLELGEELYRLQFIDGTTFFCQTTHSFSLRSLPFFYSLFNVCGSAPQQVRRVRCGSNWFRILCT
TEDGLLRFVSPLTGNLLVITWPFSILDQATDWAYDPNKEELFVATGSPDVLVFDTTRSPCMAKYLLCTSPDSQDLVQCLA
YGHFHLGRGLEGLMFSGYQSGVIRVLSQHSCARIETYIHFGSVLALSTLPGGLSGSRENSLLCSYGMDDYIHLSEAVLEG
VRVKLRILASILCSCQLTHLILLPKSVGAITQTNCLRLWKFHDFLSSGSQDGSTFIETLPLHQCTIISFDVCLSLSLFVT
GGSDGSVRIWNFHGRLIAMLDSSLHFGPLCFANDRGDLLVTFNQSLYLVSCLKLLPPTLLVRLSLMGLTDEVLEVPKPFI
PSFFFSFETMFVPKYIYPGHGKQQLVGLESLVNHRAIAFDHNVPHVIEEDEQGSPVLLSSFKHDSGYMEVDVSQVKKPPY
FHYVLPPQLQLTTWDELNPYQILRCYFGHRRKWLLAPDCYIPNSVIRARLWPEGSPIYLQCSLHSPVRELEWDKSQQFFF
WHSRARAISDAEQYIHEKEDEDFLLTRASKDITYTVLTDAANRSWLGKKMSEIAINSLIETILSIIIHATPLKYQCCIGA
```

```
LGQIFASYQVSPPLRSETAHRLLDDTTNSNPLIRELAWEGLKRLGMITHLFAVPLAQGLMDKDDRVRNKTLSLMAETGVH
SRTSLLNLVQNRETFREMQQEMVGDETLDRLLGLRAPDLQILHTQVSQRLNEDLTLYQGDEKPTFTLDVSGASELTALSK
ETDTVPEEPEAAFKHSKGPRRSRPVVRKHTRKFLRSLKKLKETVTEPGPLQDEGDQSEAAPTEMEEARSSASSILKVAKD
DEQESLEVDASKDHVALTMKMLRKTRDKRGRKSVSQKTMKRRKRKVTDTEITHEGFPHTEKTDSIMRPMQVTGRGASGAP
GLRSRDSSMWRDDLCRLMTLRISGSQTKMLEALNNELVTTAQEMLADRQPSWELFQEICPLLKKDSEELLEDLDWDVAWP
EEKPVFIHGSAIREDMMIRDMEEETRETQKRKTEKDIQDLRETHVSPKKGKKKKVLFAEPDLSKGKRISKKEEKKSSKPS
KQRKAVQQEIKVDKKEKKIAKEERGMSQEVEVVDKLKEKVVEQEKKPLKDEIKLSWQEWKKSWDQWKNAFGETRISWDEW
KKTWESQRHQEEEQVPEEEEKLLPDAEEGQVRRDKTKRTWDEWSQIWEKMSARAREKMLVTQEEVTLEEELPQEQEEEAE
ATAAEEEALMTEEQRQIHQEYKQAQVERKRAQAERRRAQEERKLAQEEEKLAQEEKRLAQEERKMVQEYEKLAEKDRKMV
QMERKLIQNEEKLAQIEEMLSQDAEKLAQQRKRLAKKLEKLARAEENIAKKGGKLAEVKKIMMQKLDKLAQKELDLAWQE
KELAQELEDLTWEEEELALKEEELNQEEEELINEGDRLDQEEMTLASQEEKLDAEEKAVIQEEELLVQEKRRLAQDKQNL
SEKKEGLDQKREQLMENKHNLAQEEELLIQEEKELAQDKVKLPGEEEKLTEKREQLMEKKQKLAQEEELLIQEEKKLAQN
METLPVKEAKIAQKAEKFIKNKQKLAWEKTKLVQNMEELPKAKEILAWRQKNLAQEKEKLAQEKVKLAQRRETLIRLQES
LIQSRKKSVPEKEVYDMYKNRLVQIEKKLMEEKEKLFQKKEKLATVEEKLTQLEKSLAEKQHKVAHDKMKLALGKRAVFQ
ELNQLRGDWSITREEKALDMEMKILTWEKETLAEQKEILFKEETQETSKEKRLPKDELEVIKRKLSLEEKILLYEERILA
TEQTDMAKEKLEFTRGERVYAQEQRKLARLLRKLTEESKGISKEPLKVSSKVLKTLQGLIKEERKLTQEEIEMTKLKRLF
VLKERELNKVQNELDAKEWDFSEEQPEITIDEKKLAKRQRRLAKEIRRLIKREKNITEQESILARQQRDVIQETDEEETT
EEEEAKSFLKHKSRKREKLKTADTQQEELLSQEDEVKSVKSEEISSEEMECLLDEIEQESLSEEEEEEEEEEEEEEEEEE
EEEEMEEEEVKEKKMVEKELGKEEEEGKERKKKRKKKKKKKVLEKEEKEEGKEEVVEEESTSDEEMEHLSEKEEREDRSL
FEEEVDKKKAIFKREKIYKLLEGKKHLRGREEFLSIEKRIPDIKSSAVKLESPPKQLISVVLGSKEKISEPLLTKQISWE
DKAIALGKPGVFPGAGFIDKQELLKKYKPMPLHVLDIVLEAQEPDLETPYLSHILRKTIEAQKLQGKPLGAKWQWILQRH
PSLKKQSEVQLPLSKILPEEIYTDISVSDVEWIHHVLEKMEAGEQLSRDSFHRLCQLLKDLTAKENLEWMHLAKLEAIVY
HHKQIMESRGTHISKPSKEPLGPKYLKVIPPIKGREKESWLKRLAVSTPKSLLATKGIPDPKAINWHLLGEPYRSARAKQ
IATSLRGMEMRYYDSATRDIFTGALDPVEKQTLALMFQKDFLAFKDKSRFARLPKLEKKARPISKVKEEVPLWETFVALY
HVLRMLQERYARDSAAWMEQFNRLMELYQLKSPRIQKLMQDLLLREKPQFQEVTYKDALRAAELAPGERLFYHLLCGGSQ
AHKGPLAFQEVVPLPRQNNVQTMLPMGIAQYGILELAWKSLPEADLHLTNELPYVAAPTL
```

2303 - 2322:	EEEEEEEEEEEEEEEEEEEE
2304 - 2323:	EEEEEEEEEEEEEEEEEEEE
2305 - 2324:	EEEEEEEEEEEEEEEEEEEE

A0A3Q1MDY9 **A0A3Q1MDY9_BOVIN** (687 aa)
YTH domain containing 1. *Bos taurus (Bovine)*

```
ESLDSRQVNLHGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESADTKRQKPSVHSRQLISKPLSSSVN
NNKRMVSTKGKSVTEYKNEEYQRSERNKRLEADRKIRLSSSASREPYKSQPDKTCLRKRDPERRVKSPTPDDSERIGLEV
DRRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEE
EEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVTFTDGSVRSGSGTDGSDEKKKERKRARGISPIIFDRSGSS
ASESYAVLISGMFSGVWSTLPVNEKKLNVAFRSARSVILIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMSAKMLG
GVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSR
GRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYAPEFHQRPGYLKDPRYQEVDRRFSGVRRDVFLNGSYNDYVREFHNMG
PPPPWQGMTPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRE
RDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDRGERGRYRR
```

230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE

A0A3Q1MQW5 **A0A3Q1MQW5_BOVIN** (1138 aa)
Euchromatic histone lysine methyltransferase 2. *Bos taurus (Bovine)*

```
MAAAAGAAAAAAAEGEAPAEMGALVLEKEPRGATERGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLS
MPGAQGAPAAGPEPPPATASPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSLGKVTSDVAKRRKLNSG
GGLSEELASTRSSGEVTLEKGDPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEE
EEEEEEEEEEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSL
ELPSEGTLSPNHAGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPS
SRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGD
GVTPPAGTAAPAPPPLAQDAPGRADTSQPSARMRGQGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPPGPGREAL
EKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANIN
AVDKQQRTPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWA
AEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLS
RGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKY
ISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVV
QSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFIN
HLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRAGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARL
DPHPELLPELSSLPPVNP
```

227 - 246:	EEEEEEEEEEEEEEEEEEEE
228 - 247:	EEEEEEEEEEEEEEEEEEEE
229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE

A0A3Q2CR51 **A0A3Q2CR51_CYPVA** (605 aa)
Extracellular matrix protein 2-like. *Cyprinodon variegatus (Sheepshead minnow)*

```
MQIPRIWIVIIFVVGTIFSGESKEVDELNAMLEINSDAPEKEMATSHPWRIESGENRLDPHVIDSGAEVQPQLELGEKTD
QREAVPQKLEVGRGRRSTWGRRRHAATVETTAYRIAGLSQPLKGWRQSMKGEMETSLLMATLKELHAEKKRLMDNGKTQE
EGQEEEEEEEDSDEEEEEEDSDEEEEEEEEEEEEEEEEEEEEVEEEATEPPTNQTQFNMTELPDECQAADREISCRGVGM
```

```
IHLPVFQSLDVTKLDMGENNISILAPESFFGLPNLDTLDLSQNQLDDESFSQNPLLNLTVLRKLNLDSNQITRIPTLPPS
LEELNISNNKLTVLTDQCLEGLKNLLKLELRMNTLYEASVSPTAFRPLQKLLDLQLDNNLFRSIPLGLPSSLQVLRMSEN
LIEEVTGGPLRDCIHLRVIDLRHNYIHDQSFTGDPWTRLRSLEDLDLSHNRLTSVPTNLPRFLRRLILQHNNIRHIPAFV
FRHMHASLQSLHLSHNELSTEDIERHSFVGTYRSMKELLLDNNRLQDVPRCIRQFKNLQVLRLENNQIRQVRQWAVCHPH
NSGSTLTSVHLEYNLLEERAIPPKAFFCVTDTQGVVLYPQHGKPS
```

183 - 202:	EEEEEEEEEEEEEEEEEEEE

A0A3Q2D726 **A0A3Q2D726_CYPVA** (912 aa)
BAF chromatin remodeling complex subunit BCL11A. *Cyprinodon variegatus (Sheepshead minnow)*

```
MSRRKQGKPQHLSKRDFSPAEPLSTAVVSSEELSERCSEHSEDSGILNGHHPAPLVGRLARLGPDSHSSPEQDLLTCGQC
QATFPLADILLFIEHKRKRCHGPPCLTIGRGLDKPPSPSPGLALTPSPALNTLRGRRPVEVGVQATLADEDDDRFSSPRG
ICPKQEPLPGKEEPTTYTCTTCKQSYGSAWFLLQHAQNSHGFRIYLESEHGSPLTPRMGGPSSLGGGADCPSQPPLHGLH
LPPDASPFNLLRIPGSGSGGRDSVGAGGAIGSGVPGGHHQRFPPTPPLFSPPPRNHLDPHHLSPEELALAAHHPSAFDRV
LRLNPPLPLEPPPTMDFSRRLRELAGNTSGSTPPLSPSRPSPMQRLLQPFQTGGNGGTGGTGGSKPPYLATPPPLQGSMQ
SPVGSQTTPPTPLPSAGPPSSSNTQLKSKCCEFCGKAFKFQSNLIVHRRSHTGEKPYKCHLCDHACTQASKLKRHMKTHM
HKSSSPNTGKSEDGLSIASSPEPGTSDHIGSASNALKSVVAKLKSENDRMIRENGEEEEEEEEEEEEEEEEEEEEEEEEG
EEEEVQNGERPPKRNNSYHFGLNLEASRQHENSSGIASRLAGVADEASIPRSLPEVMQGMGLAASMQHFSEALNAHKRNA
MLQENHLHHHLSRDHHHNRDLCDGDSVLETERVEEGTVSTVNGRGASPNESSSIGLSKKLLLGSPSPLSPFSKRIKLEKE
FDLPTPTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRFSTPPGELDGGMSGRSGTGSGGS
TPHLGGPGRPSSKDGRRSDTCEFCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQSSKLTRHMKTHGQVGKDVYKCE
ICQMPFSVYSTLEKHMKKWHSDRPLSTEIKSE
```

536 - 555:	EEEEEEEEEEEEEEEEEEEE
537 - 556:	EEEEEEEEEEEEEEEEEEEE
538 - 557:	EEEEEEEEEEEEEEEEEEEE
539 - 558:	EEEEEEEEEEEEEEEEEEEE
540 - 559:	EEEEEEEEEEEEEEEEEEEE

A0A3Q2H434 **A0A3Q2H434_HORSE** (1642 aa)
Histone acetyltransferase (EC 2.3.1.48). *Equus caballus (Horse)*

```
MVKLANPLYTEWILEAIQKIKKQKQRPSEERICHAVSTSHGLDKKTVSEQLELSVQDGSVLKVTNKGLASYKDPDNPGRF
SSVKPGTFPKSTKGSRGSCNDLRNVDWNKLLRRAIEGLEEPNGSSLKNIEKYLRSQSDLTGTTNNPAFQQRLRLGAKRAV
NNGRLLKDGPQYRVNYGSLDGKGAPKYPSAFPSSLPPVSLLPHEKDQPRADPIPICSFCLGTKESNREKKPEELLSCADC
GSSDTEIKISVKQESTDINVVGNKDTVTEEDLDVFKQAQELSWEKIECESGVEDCGRYPSVIEFGKYEIQTWYSSPYPQE
YARLPKLYLCEFCLKYMKSKNILLRHSKKCGWFHPPANEIYRRKDLSVFEVDGNMSKIYCQNLCLLAKLFLDHKTLYYDV
EPFLFYVLTKNDEKGCHLVGYFSKEKLCQQKYNVSCIMIMPQHQRQGFGRFLIDFSYLLSRREGQAGSPEKPLSDLGRLS
YLAYWKSVILEYLYHHHERHISIKAISRATGMCPHDIATTLQHLHMIDKRDGRFVIIRREKLILGHMEKLKTCSRTNELD
PESLRWTPILISNAAVSEEEREAEKEAERLMEQASCWEKEEQEILSSRANSRQSPAKVQSKNKYLHSPESRPVAGERGQL
MELSKESSEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEENIQSSPPRLTKPQSVAIKRKRPFVLKKKRGRKRRRINSSVT
TETISETTEVLNEPFDNSDEERPMPQLEPTCEIEVEEDGEKPPLRKAFQHQPGKKRQTGEEEGKDNRCFKNSDPCRNNMD
DDANNLKEGSRDNPEPLKCKQVWPKGTKHGLSKWRPNKERKTGFKLNLYTPPETPMEPDDQVTVEEQKETPEDKTSPTST
RIEEEVEEAVEPLLPRDENRREETCAPISPNKSPGEKPEDDLIKPEEEEEEEEEEEEEEEEEEEEGNVEKDPGGAKSQEK
EEPEVCMDKEDSVRLDDHEEEEEEDEEPSHNEGHDADDEDDSHMESAEAEKKEHPREAFKEVLENQEAFLDLSVQPSHSN
PEVLMDCGVDLAASCNSEPKELAGDTETAPESDEEPPEEQAQKQDQKNREEVDSEFKEGNTATMEIDSETVQAVQSLTQE
NSEQDDTFQDCAETQEACRSLQNYTHADQSPQIAATLDDCQQSDHSSPVSSVHSHPGQSVRSVNSPSVPALENSYAQISP
DQSAISVPSLQNMETSPMMDVPSVSDHSQQVVDSGFSDLGSIESTTENYENPSSYDSTMGGSICGNGSSQNSCSYSNLTS
SNLTQSSCAVTQQMSNISGSCSMLQQTSISSPPTCNVKSPQGCVVERPPSSSQQLAPCSMAANFTPPMQLAEIPETGNAN
IGLYERMGQSDFGAGHYPQPSATFSLAKLQQLTNTLIDHSLPYSHSAAVTSYANSASLSTPLSNTGLVQLSQSPHSVPGG
PQAQATMTPPPNLTPPPMNLPPPLLQRNMAASNIGISHSQRLQTQIASKGHVSMRTKSASLSPAAATHQSQIYGRSQTVA
MQGPARTLTMQRGMNMSVNLMPAPAYNVNSVNMNMNTLNAMNGYSMSQPMMNSGYHSNHGYMNQTPQYPMQMQMGMMGTQ
PYAQQPMQTPPHGNMMYTAPGHHGYMNTGMSKQSLNGSYMRR
```

649 - 668:	EEEEEEEEEEEEEEEEEEEE
650 - 669:	EEEEEEEEEEEEEEEEEEEE
651 - 670:	EEEEEEEEEEEEEEEEEEEE
652 - 671:	EEEEEEEEEEEEEEEEEEEE
653 - 672:	EEEEEEEEEEEEEEEEEEEE
654 - 673:	EEEEEEEEEEEEEEEEEEEE
655 - 674:	EEEEEEEEEEEEEEEEEEEE
656 - 675:	EEEEEEEEEEEEEEEEEEEE
657 - 676:	EEEEEEEEEEEEEEEEEEEE
658 - 677:	EEEEEEEEEEEEEEEEEEEE
659 - 678:	EEEEEEEEEEEEEEEEEEEE
660 - 679:	EEEEEEEEEEEEEEEEEEEE
926 - 945:	EEEEEEEEEEEEEEEEEEEE

A0A3Q2H775 **A0A3Q2H775_HORSE** (1826 aa)
Histone acetyltransferase (EC 2.3.1.48). *Equus caballus (Horse)*

```
MVKLANPLYTEWILEAIQKIKKQKQRPSEERICHAVSTSHGLDKKTVSEQLELSVQDGSVLKVTNKGLASYKDPDNPGRF
```

```
SSVKPGTFPKSTKGSRGSCNDLRNVDWNKLLRRAIEGLEEPNGSSLKNIEKYLRSQSDLTGTTNNPAFQQRLRLGAKRAV
NNGRLLKDGPQYRVNYGSLDGKGAPKYPSAFPSSLPPVSLLPHEKDQPRADPIPICSFCLGTKESNREKKPEELLSCADC
GSSGHPSCLKFCPELTTNVKALRWQCIECKTCSACRIQGKNADNMLFCDSCDRGFHMECCDPPLSRMPKGMWICQVCRPK
KKGRKLLHEKAAQIKRRYAKPIGRPKNKLKQRLLSVTSDEGSMNAFTGRGSPGRGQKTKVCTTPSSGHAASGKDSSSRLA
VTDPTRPGATTKITTTSTYISASTLKVNKKTKGLIDGLTKFFTPSPDGRRSRGEIIDFSKHYRPRKKVSQKQSCTSHVLA
TDTEIKISVKQESTDINVVGNKDTVTEEDLDVFKQAQELSWEKIECESGVEDCGRYPSVIEFGKYEIQTWYSSPYPQEYA
RLPKLYLCEFCLKYMKSKNILLRHSKKCGWFHPPANEIYRRKDLSVFEEKLCQQKYNVSCIMIMPQHQRQGFGRFLIDFS
YLLSRREGQAGSPEKPLSDLGRLSYLAYWKSVILEYLYHHHERHISIKAISRATGMCPHDIATTLQHLHMIDKRDGRFVI
IRREKLILGHMEKLKTCSRTNELDPESLRWTPILISNAAVSEEEREAEKEAERLMEQASCWEKEEQEILSSRANSRQSPA
KVQSKNKYLHSPESRPVAGERGQLMELSKESSEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEENIQSSPPRLTKPQSVAI
KRKRPFVLKKKRGRKRRRINSSVTTETISETTEVLNEPFDNSDEERPMPQLEPTCEIEVEEDGEKPPLRKAFQHQPGKKR
QTGEEEGKDNRCFKNSDPCRNNMDDDANNLKEGSRDNPEPLKCKQVWPKGTKHGLSKWRPNKERKTGFKLNLYTPPETPM
EPDDQVTVEEQKETPEDKTSPTSTRIEEEVEEAVEPLLPRDENRREETCAPISPNKSPGEKPEDDLIKPEEEEEEEEEEE
EEEEEEEEEEGNVEKDPGGAKSQEKEEPEVCMDKEDSVRLDDHEEEEEEDEEPSHNEGHDADDEDDSHMESAEAEKKEHPR
EAFKEVLENQEAFLDLSVQPSHSNPEVLMDCGVDLAASCNSEPKELAGDTETAPESDEEPPEEQAQKQDQKNREEVDSEF
KEGNTATMEIDSETVQAVQSLTQENSEQDDTFQDCAETQEACRSLQNYTHADQSPQIAATLDDCQQSDHSSPVSSVHSHP
GQSVRSVNSPSVPALENSYAQISPDQSAISVPSLQNMETSPMMDVPSVSDHSQQVVDSGFSDLGSIESTTENYENPSSYD
STMGGSICGNGSSQNSCSYSNLTSSNLTQSSCAVTQQMSNISGSCSMLQQTSISSPPTCNVKSPQGCVVERPPSSSQQLA
PCSMAANFTPPMQLAEIPETGNANIGLYERMGQSDFGAGHYPQPSATFSLAKLQQLTNTLIDHSLPYSHSAAVTSYANSA
SLSTPLSNTGLVQLSQSPHSVPGGPQAQATMTPPPNLTPPPMNLPPPLLQRNMAASNIGISHSQRLQTQIASKGHVSMRT
KSASLSPAAATHQSQIYGRSQTVAMQGPARTLTMQRGMNMSVNLMPAPAYNVNSVNMNMNTLNAMNGYSMSQPMMNSGYH
SNHGYMNQTPQYPMQMQMGMMGTQPYAQQPMQTPPHGNMMYTAPGHHGYMNTGMSKQSLNGSYMRR
```

833 - 852:	EEEEEEEEEEEEEEEEEEEE
834 - 853:	EEEEEEEEEEEEEEEEEEEE
835 - 854:	EEEEEEEEEEEEEEEEEEEE
836 - 855:	EEEEEEEEEEEEEEEEEEEE
837 - 856:	EEEEEEEEEEEEEEEEEEEE
838 - 857:	EEEEEEEEEEEEEEEEEEEE
839 - 858:	EEEEEEEEEEEEEEEEEEEE
840 - 859:	EEEEEEEEEEEEEEEEEEEE
841 - 860:	EEEEEEEEEEEEEEEEEEEE
842 - 861:	EEEEEEEEEEEEEEEEEEEE
843 - 862:	EEEEEEEEEEEEEEEEEEEE
844 - 863:	EEEEEEEEEEEEEEEEEEEE
1110 - 1129:	EEEEEEEEEEEEEEEEEEEE

A0A3Q2HMV2 **A0A3Q2HMV2_HORSE** (773 aa)
YTH domain containing 1. *Equus caballus (Horse)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLLSKPLSSSVSN
NKRIVSTKGKSVTEYKNEDYQRSERSKRLEADRKIRLSSSASREPYKSQPEKTCLRKRDPERRAKSPTPDASERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEE
EEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSVICLDDFHCSFDLRIIVGRQDHK
LKSSGNYMYKKDEKSLENSHDEKKKERKRARGISPIVFDRSGSSASESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQD
ARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSARSVILIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGM
NAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMH
SQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYAPEFHQRPGYLKDPRYQEVDRRFSGVRRDVFLNGSYNDYVR
EFHNMGPPPPWQGMAPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGR
RSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDRGERGRYRR
```

229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE

A0A3Q2HTP9 **A0A3Q2HTP9_HORSE** (746 aa)
YTH domain containing 1. *Equus caballus (Horse)*

```
MLNDNDFFLLLLIFLLSDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLLSK
PLSSSVSNNKRIVSTKGKSVTEYKNEDYQRSERSKRLEADRKIRLSSSASREPYKSQPEKTCLRKRDPERRAKSPTPDAS
ERIGLEVDRRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEE
EEEEEEEEEEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISP
IVFDRSGSSASESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNA
AFRSARSVILIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHK
PVKIGRDGQEIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKP
RIDYAPEFHQRPGYLKDPRYQEVDSFTNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMAPYPGMEQPPHHP
YYQHHAPPPQAHPPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDR
GRDRERERERLCDRDRDRGERGRYRR
```

237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE

239 - 258:	EEEEEEEEEEEEEEEEEEEE
240 - 259:	EEEEEEEEEEEEEEEEEEEE
241 - 260:	EEEEEEEEEEEEEEEEEEEE

A0A3Q2HUZ1 **A0A3Q2HUZ1_HORSE** (763 aa)
YTH domain containing 1. *Equus caballus (Horse)*

```
MLNDNDFFLLLLIFLLSDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLLSK
PLSSSVSNNKRIVSTKGKSVTEYKNEDYQRSERSKRLEADRKIRLSSSASREPYKSQPEKTCLRKRDPERRAKSPTPDAS
ERIGLEVDRRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEE
EEEEEEEEEEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSVICLDDFHCSFDLRI
IVGRQDHKLKSSGNYMYKKDEKSLENSHDEKKKERKRARGISPIVFDRSGSSASESYADQTSKLKYVLQDARFFLIKSNN
HENVSLAKAKGVWSTLPVNEKKLNAAFRSARSVILIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMNAKMLGGVFK
IDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPS
RREPVRDVGRRRPEDYDIHNSRKKPRIDYAPEFHQRPGYLKDPRYQEVDRRFSGVRRDVFLNGSYNDYVREFHNMGPPPP
WQGMAPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRE
RERDRPRDNRRDRERDRGRDRERERERLCDRDRDRGERGRYRR
```

237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE
239 - 258:	EEEEEEEEEEEEEEEEEEEE
240 - 259:	EEEEEEEEEEEEEEEEEEEE
241 - 260:	EEEEEEEEEEEEEEEEEEEE

A0A3Q2HX00 **A0A3Q2HX00_HORSE** (834 aa)
Disintegrin and metalloproteinase domain-containing protein 1a-like. *Equus caballus (Horse)*

```
MSVAASVRDSASFLSSLQKNQAVMYEASRVLQTWAPQMKGFRLALVPGPSRVRLGIMLVLALIFLPRLYCDLGAVYYSSY
ETVIPKSLTVNGREDPVEKASYMLLMQGQKQLLHLKVKRDYFVDNFPIFSYHNGILGQEMPVLAHDCHYEGYIEGVPGSF
VSVNTCSGLRGVLIKEGKSYGIEPVGASKKFEHVLYTMAREARISCSVTSKDSQVVSTSQQRGSRKPRSAQALSYLWSHT
KYVEMFVVVSNQRFQMSACLDGSNINETVQRVMGRHCPGQRLTRGINTEVVLAGMEIWTEGDLIEVPADLQVTLRNFNSW
RQDKLFHRVKHDVAHMILGHRPQEDTGQAFLNGACSTGFAAAVESFHHEDALLFAALMVHELGHNLGIQHDHSACVCKDT
HFCLMHENITKESGFSNCSSDDFYQFLLDHKGACLFNKPQHKGRVRRDAECGNGVVEEDEQCDCGSACDNHPCCNPACKL
KDNAQCSPGPCCNSSCLFAESGSTCRSAFDDCDLPEYCDGNSAECPTDSYKQDGTKCYGSHYCVQGQCRTPDEQCARVFG
HPSKSAPSDCYNLFNRKGTRFGNCGPPTLNNPEYVKCADDNLYCGKIICTNIRQLPPIKPLHTLIQVPFEDDFCWSMDAT
NGTADIPDDGDVFAGTLCSSGKVCMGHSCSPDTVLNYDCNPEEMCAGKGICNNLKHCHCNFGYAPPNCTTPGNGGSLDSG
PPGLPSAEEPQSQSTTSPPKGAGLLLDMMVLIFLILLLILLLMLIICGIYCCLGAKEEEKPAEEAAEKPPEEAAEKPPEA
EPKEAGSEAPSEEEEEEEEEEEEEEEEEEEESEP
```

812 - 831:	EEEEEEEEEEEEEEEEEEEE

A0A3Q2ICZ9 **A0A3Q2ICZ9_HORSE** (1316 aa)
Tau tubulin kinase 1. *Equus caballus (Horse)*

```
MQCLAAALKDETNMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTRENVALKVESAQQPKQVLKMEVAV
LKKLQGKDHVCRFIGCGRNEKFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESIEAIHSVGFLHRDIKPSNF
AMGRLPSTYRKCYMLDFGLARQYTNTTGDVRPPRNVAGFRGTVRYASVNAHKNREMGRHDDLWSLFYMLVEFAVGQLPWR
KIKDKEQVGMIKEKYEHRMLLKHMPSEFHLFLDHIASLDYFTKPDYQLIMSVFENSMKERGIAENEAFDWEKAGTDTLLS
TSTSTPPQQNTRQTAAMFGVVNVTPVPGDLLRENTEDVLQGEHLSDQENAPPILPGRPPEGLGPGPHLVPHPGGPEAEVW
EETDVNRNKLRINIGKTPCVVEEEQSRGVGVPSSPVRAPPDSPTTPVRSLRYRRVNSPESERLSTADGRVELHERRSRMD
LPGSPSRQACSSQPAQMLSVDTGHVDRQASGRMDVSASVEQEALSNAFRSVPLAEEEDFDSKEWVIIDKETELKDFPPGA
EPSTSGTTDEEPEELRPLPEEGEERRRPGAEPAVRPRGRGMQMLAEEDLRQTPSQPPPPQLSQADGRSETSQPPTPGSPS
HSPLHSGPRPRRRESDPTGPQRQVFSVAPPFEVNGLPRAVPLSLPYQDFKKDLSDYRERARLLNRVRRVGFSHVLLTAPQ
VPLTPVQPQANGKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVVALGEVLGPHSGSSSDGSERS
TDRSQEGAPSTLLADDQKESRGRASMADGDLEPEEGSKTLVLVSPGDMKKSPVTADLAPDPDLGTLAAFTPQHERPQPTG
SQLDVSEPGTLSSVLKSEPKPPGPGIGPGAGAVTTGAGGVAVTSSPFTKVERTFVHIAEKTHLNVMSSGGQASRPEELSA
GGELGLEVPSDGGAVEEGVFVPLENDIAQSGLESGALSGPPRDTSVEVATDSLPNGPTLAEGPAPASPLEPGPEKLATVS
PSRLAMPGPRPRSRIPVLLSEEDTGSEPSGSLSAKERWGKRARPQQDLARLVMEKRQGRLLLRLASGASSSSSEEQRRAS
ETLSGTGSEEDTPASEPTAPRKVGQAAATRSRIPRPISIRMPTPATAQQPPGRPHGAAPASDSAITSRLQLQKPPGSSVA
TDLRPKQPPGRGVGPGRAPAGLRPSAPRSPGLPASAPRHPSASPRSQSLSRRESSSPSHQARPGGPPPRGAPQARAQPDG
TPSPGGPKKGPRGKLQTQRSATKGRAGAAEGRAGAR
```

734 - 753:	EEEEEEEEEEEEEEEEEEEE
735 - 754:	EEEEEEEEEEEEEEEEEEEE
736 - 755:	EEEEEEEEEEEEEEEEEEEE
737 - 756:	EEEEEEEEEEEEEEEEEEEE
738 - 757:	EEEEEEEEEEEEEEEEEEEE
739 - 758:	EEEEEEEEEEEEEEEEEEEE
740 - 759:	EEEEEEEEEEEEEEEEEEEE
741 - 760:	EEEEEEEEEEEEEEEEEEEE
742 - 761:	EEEEEEEEEEEEEEEEEEEE
743 - 762:	EEEEEEEEEEEEEEEEEEEE
744 - 763:	EEEEEEEEEEEEEEEEEEEE

745 - 764:	EEEEEEEEEEEEEEEEEEEE
746 - 765:	EEEEEEEEEEEEEEEEEEEE
747 - 766:	EEEEEEEEEEEEEEEEEEEE
748 - 767:	EEEEEEEEEEEEEEEEEEEE
749 - 768:	EEEEEEEEEEEEEEEEEEEE
750 - 769:	EEEEEEEEEEEEEEEEEEEE
751 - 770:	EEEEEEEEEEEEEEEEEEEE
752 - 771:	EEEEEEEEEEEEEEEEEEEE
753 - 772:	EEEEEEEEEEEEEEEEEEEE
754 - 773:	EEEEEEEEEEEEEEEEEEEE
755 - 774:	EEEEEEEEEEEEEEEEEEEE
756 - 775:	EEEEEEEEEEEEEEEEEEEE
757 - 776:	EEEEEEEEEEEEEEEEEEEE
758 - 777:	EEEEEEEEEEEEEEEEEEEE
759 - 778:	EEEEEEEEEEEEEEEEEEEE

A0A3Q2L711 **A0A3Q2L711_HORSE** (541 aa)
YTH domain containing 1. *Equus caballus (Horse)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDTKRQKPSVHSRQLLSKPLSSSVSN
NKRIVSTKGKSVTEYKNEDYQRSERSKRLEADRKIRLSSSASREPYKSQPEKTCLRKRDPERRAKSPTPDASERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEE
EEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGS
SASESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSARSV
ILIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDG
QEIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRCVSG
```

229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE

A0A3Q2QAL5 **A0A3Q2QAL5_FUNHE** (873 aa)
B-cell lymphoma/leukemia 11B-like. *Fundulus heteroclitus (Killifish) (Mummichog)*

```
MSRRKQVNPQHLSLTHRETVQAEVNHDSGAQSPSPEQSTPSPRRMGQGEHDLLTCGQCQTNFPLGDILVFIEHKRRLCRG
PGGGPAAFSKPGEAGGIMGVPISPRTRSLELGRGSVPVEVGIQVTPGGEDDEQRRLTPAKGICPKQEKGALGARARRLCV
ASSCVWPSSVTVGSICKRRSETISDSKDKDEPSSYICTTCKQTFTSAWFLLQHAQHTHGIRIYLDNHLANCSLTPRMALP
PPPGADALPRSPLPTFLGDTNNPFHLLRMAAPLLREHPHPPGYMETRLPATPPFVSPPPPPRPPLERLGPEEMGLLSQHP
SAFERVMRMTPMEPPSMDFSRRLRELAGNTTNNGGPTPPLSPNRVPPMHRLLSPTLFQPGAKPPTFLTYAPQPPASQGGH
GSSSPPDAQGQNQAPGKSKSCEFCGKIFKFQSNLIVHRRSHTGERPYKCHLCDHACSQASKLKRHMKTHMHNKSGNMTGS
PEQGSRGEEGEGEGKNREGDARVMEMENEEEEEEEEEEEEEEEEEEEELRNGSRPDSNLSEDSQEFSQNRENGPRQSPEE
KSMSGDRVNDNGGVGIMHPYNHLDNHLRLNPNKRNLERQPNGDSGERNDTERENDREPDREREEQEDIRPLMNGRISVSE
AESFPGLFQRRPTPITSPSPSNNKRIKIEKEHLDMPPTIPLISPENVYSQLLAGYAASRHFIREPFLGFTDSRQSPFATS
SDHSSSETGSLRYSTPPGELIEGGSASGRSGSSTPHLLRGPGPGRPPSSKEKRNDTCEYCGKVFKNCSNLTVHRRSHTGE
RPYKCDLCSYACAQSSKLTRHMKTHGQFGKEVYRCDICHMPFSVYSTLEKHMKKWHGEHLMASEVKLEQADRG
```

509 - 528:	EEEEEEEEEEEEEEEEEEEE

A0A3Q2ULF9 **A0A3Q2ULF9_FUNHE** (863 aa)
B-cell lymphoma/leukemia 11A-like. *Fundulus heteroclitus (Killifish) (Mummichog)*

```
MSRRKQGKPQHLSKRDFSPPGAGRPARLGPDSHPSSEQDLLTCGQCQATFPLADILLFIEHKRKRCHGPPCLTIGRGLDK
PPSPSPGLALTPSPALNSLRGRRPVEVGVQATLADEDDERFSTPRGICPKQEPLPGKEEPTTYTCTTCKQSYGSAWFLLQ
HAQNSHGFRIYLESEHGSPLTPRMGGRSSLGGGADCPSQPPLHGLHLPPDASPFNLLRIPGSGSGGRDSRFPPTPPLFSP
PPRNHLDPHHLSPEELALAAHHPSAFDRVLRLNPPLPLDPPPTMDFSRRLRELAGNTSGSTPPLSPSRPSPMQRLLQPFQ
TGGNGGAGGAGGSKPPYLATPPPLQGSMQSPVGSQTTPPAPLPAAGPASSSSTQLKSKCCEFCGKAFKFQSNLIVHRRSH
TGEKPYKCHLCDHACTQASKLKRHMKTHMHKSSSPNTGKSEDGLSLASSPEPGTSEHLGSASNALKSVVAKLKSENDRML
RENGEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEVQNGERPPKRNNRYHFGLNLEAARQHENSSSIGSRLGGVADEVSI
PRSLPEVMQGMGLAASMQHFSEALNAHKRNAMAQENHLHHHLSRDHHHSRDMCDGDSVLETERVEEGTVSTVNGRGVSPN
ESSSIGLSKKLLLGSPSPLSPFSKRIKLEKEFDLPTPTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEH
SSENGSLRFSTPPGELDGGMSGRSGTGSGGSTPHLGGPGRPSSKDGRRSDTCEFCGKVFKNCSNLTVHRRSHTGERPYKC
ELCNYACAQSSKLTRHMKTHGQVGKDVYKCEICQMPFSVYSTLEKHMKKWHSDRPLSTEIKSE
```

485 - 504:	EEEEEEEEEEEEEEEEEEEE
486 - 505:	EEEEEEEEEEEEEEEEEEEE
487 - 506:	EEEEEEEEEEEEEEEEEEEE

488 - 507:	EEEEEEEEEEEEEEEEEEEE
489 - 508:	EEEEEEEEEEEEEEEEEEEE
490 - 509:	EEEEEEEEEEEEEEEEEEEE
491 - 510:	EEEEEEEEEEEEEEEEEEEE

A0A3Q2VQD8 **A0A3Q2VQD8_HAPBU** (837 aa)
B-cell lymphoma/leukemia 11B-like. *Haplochromis burtoni (Burton's mouthbrooder) (Chromis burtoni)*

```
MSRRKQVNPQHLSLTHRETIQAEANHDSGAGSPSPELSTPSPRRRASGEHDLLTCGQCQTNFPLGDILVFIEHKRRLCRG
PIGGLGSFSKPGAAGGVMGLPISPRARSLELGRGAVPVEVGVQVTPGGEEDQARRLTPAKGICPKQERGEKDEPSSYICT
TCKQTFTSAWFLLQHAQHTHGIRIYLDNHPVNCSLTPRMALPPPPGADALPRSPLPTFLGDASNPFHLLRMAGPQLRDHP
HPPGYMETRLPATPPFVSPPPPPRPPRERLGPEEMGLLSQHPSAFERVMRMTPMEPPPMDFSRRLRELAGNTTNNGGPTP
PLSPNRVPPMHRLLSPTLFQPGSQLSPFLTYPPQPPTSQGGHGSSSPPDTQGQNQAPGKSKSCEFCGKIFKFQSNLIVHR
RSHTGERPYKCHLCDHACSQASKLKRHMKTHMHHNKSGAITGSPEQGNRGEGGEGEEKNREGDARGMGMDNEEEEEEEEE
EEEEEEEEEELQNGSRPDSNLSEDSQEFTQNRENGSRQSPSEKPPSGDRVNDSGGVGIMHPYNHLDNHLRLNPNKRSLER
QPNGDGGEGVEGERERENEREPDRQREEQEDQRPVMNGRISVSEAECFPGLFQRRPTPITSPSPSNNKRIKIEKEQLEIP
PTIPLISPENVYSQLLAGYAASRHFIREPFLGFTDSRQSPFATSSEHSSSETGSLRFSTPPGELMEGGSASGRSGSSTPH
LLRGPGPGRPPSSKERRNDTCEFCGKVFKNCSNLTVHRRSHTGERPYKCDLCSYACAQSSKLTRHMKTHGQYGKEVYRCD
ICHMPFSVYSTLEKHMKKWHGEHLMASEVKLEQADRS
```

471 - 490:	EEEEEEEEEEEEEEEEEEEE

A0A3Q2WB21 **A0A3Q2WB21_HAPBU** (850 aa)
BAF chromatin remodeling complex subunit BCL11A. *Haplochromis burtoni (Burton's mouthbrooder) (Chromis burtoni)*

```
MSRRKQGKPQHLSKRDFSRHHPGSNVGRLARLGHDAHPSLEQDLLTCGQCQATFPLADILLFIEHKRKRCHGPPCLTVGR
GLDKPPSPSPGLALTPSPAMGSLRSRRLEVGVQATLADEDDDRFSSPRGICPKQEPLPGKEEPTTYTCTTCKQSYGSAWF
LLQHAQNTHGFRIYLESEHGSPLTPRMGGPSSLGGGADCPSQPPLHGLHLPPDASPFNLLRIPGSGSGGRDSRFPPTPPL
FSPPPRNHLDPHHLSPEELALAAHHPSAFDRVLRLNPPLPLDPPPTMDFSRRLRELAGNTSGSTPPLSPSRPSPMQRLLH
KPPYLATPPPLPGSMQSPVGSQTTPTTPLPSAGATPSSTTQLKSKCCEFCGKAFKFQSNLIVHRRSHTGEKPYKCHLCDH
ACTQASKLKRHMKTHMHKSSSPNTGKSEDGLSTASSPEPGTSEHVGSASNALKSVVAKLKSENDRMLRENGEEEEEEEEE
EEEEEEEEEEEEEEEEEGEEEEEQNGERVARRNNNSYHFGLNLETARQHENNGSIGSRLGGVADEGSIPRSLPEVMQGMGL
AASMQHFSEALNAHKRNAMAQENHLHHHLNRDHHHNREICDGDSVLETDRGEEGSVSTVNGRGASPNESASVGLSKKLLL
GSPSPLSPFSKRIKLEKEFDLPTSTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRFSTPP
GELDGGMSGRSGTGSGGSTPHLGGPGRPSSKDGRRSDTCEFCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQSSKL
TRHMKTHGQVGKDVYKCEICQMPFSVYSTLEKHMKKWHSDRPLSTEIKSE
```

472 - 491:	EEEEEEEEEEEEEEEEEEEE
473 - 492:	EEEEEEEEEEEEEEEEEEEE
474 - 493:	EEEEEEEEEEEEEEEEEEEE
475 - 494:	EEEEEEEEEEEEEEEEEEEE
476 - 495:	EEEEEEEEEEEEEEEEEEEE
477 - 496:	EEEEEEEEEEEEEEEEEEEE

A0A3Q2X331 **A0A3Q2X331_HAPBU** (812 aa)
B-cell lymphoma/leukemia 11A-like. *Haplochromis burtoni (Burton's mouthbrooder) (Chromis burtoni)*

```
MSRRKQGKPQHLSKREFSPEPLSGVLPEEDSQDSPSLGVAQGEPLKGDQDLLTCGQCHSRFPLADILLFIEHKRRQCHGS
LCVDKPLDRPPSSPLASPLSTSSSHSRTQHQHQRRVRQPVEVAVQVSPQDEDCLSAPLQGIIPKQENMTDKDEPSSYTCT
TCKQPFTSAWFLLQHAQNTHGFRIYLESEPGSPLTPRVAAAPGMGGDCNSSQPPLHAVHLADGSPYSLLRMPGSGSGRDS
ASTPREGRYPRTPPLFSPPPRHHLSPDDLALATHHPSAFDRVMRLNSVPLEAPQTMDFSRRLRELAGNATGGSPPLSPNR
PNPMQRLLQPFQPGSKPPFSATPPLSTSQSPSGSRSTPNPVTNAVQSTTPLKAKSCEFCGKTFKFQSNLIVHRRSHTGEK
PFKCHLCNHACTQASKLKRHMKTHCQSKSSLLNAKSDDGLSTASSPEPGTSELMGSATDALKSVVAKFKSENNGLLPENG
EEEEEEEDDEEEEEEEEEEEEEEEEEEEEEGEEEEIERKPGVEEEGRNDYRFSLRLEGARHHQNSEALHPHRRSLSREPID
ENSAIESDRADDGTTTTINGLRPLSNDNMSRKLLGGGVSPGSLSPLSKRIKVEKDLDPPTPTIPNTENVYSQWLAGYAAS
RQLKDPFISFTGGDSRQSPFASSSEHSSENGSLRFSTPPGELDGERAASVRSGTGSGASTPHGVSGNGRPSSKDGRRSDT
CEYCGKVFKNCSNLTVHRRSHTGERPYKCELCSYACAQSSKLTRHMKTHGQMGKDVYKCEICHMPFSVYSTLEKHMKKWH
SDRPLANDIKTE
```

490 - 509:	EEEEEEEEEEEEEEEEEEEE

A0A3Q2X4B0 **A0A3Q2X4B0_HAPBU** (809 aa)
B-cell lymphoma/leukemia 11A-like. *Haplochromis burtoni (Burton's mouthbrooder) (Chromis burtoni)*

```
MHSSRVSKCGDVSRLAEPLSGVLPEEDSQDSPSLGVAQGEPLKGDQDLLTCGQCHSRFPLADILLFIEHKRRQCHGSLCV
DKPLDRPPSSPLASPLSTSSSHSRTQHQHQRRVRQPVEVAVQVSPQDEDCLSAPLQGIIPKQENMTDKDEPSSYTCTTCK
QPFTSAWFLLQHAQNTHGFRIYLESEPGSPLTPRVAAAPGMGGDCNSSQPPLHAVHLADGSPYSLLRMPGSGSGRDSAST
PREGRYPRTPPLFSPPPRHHLSPDDLALATHHPSAFDRVMRLNSVPLEAPQTMDFSRRLRELAGNATGGSPPLSPNRPNP
MQRLLQPFQPGSKPPFSATPPLSTSQSPSGSRSTPNPVTNAVQSTTPLKAKSCEFCGKTFKFQSNLIVHRRSHTGEKPFK
CHLCNHACTQASKLKRHMKTHCQSKSSLLNAKSDDGLSTASSPEPGTSELMGSATDALKSVVAKFKSENNGLLPENGEEE
EEEEDDEEEEEEEEEEEEEEEEEEEEEGEEEEIERKPGVEEEGRNDYRFSLRLEGARHHQNSEALHPHRRSLSREPIDENS
AIESDRADDGTTTTINGLRPLSNDNMSRKLLGGGVSPGSLSPLSKRIKVEKDLDPPTPTIPNTENVYSQWLAGYAASRQL
KDPFISFTGGDSRQSPFASSSEHSSENGSLRFSTPPGELDGERAASVRSGTGSGASTPHGVSGNGRPSSKDGRRSDTCEY
CGKVFKNCSNLTVHRRSHTGERPYKCELCSYACAQSSKLTRHMKTHGQMGKDVYKCEICHMPFSVYSTLEKHMKKWHSDR
PLANDIKTE
```

487 - 506:	EEEEEEEEEEEEEEEEEEEE

A0A3Q2XM71 **A0A3Q2XM71_HIPCM** (867 aa)
BAF chromatin remodeling complex subunit BCL11A. *Hippocampus comes (Tiger tail seahorse)*

```
MSRRKQGKPQHLSKRDFSRSTLGRLSRLGHEPHHSPEQDLLTCGQCQATFPLADILLFIEHKRKRCHGPPCLTVGRGLDK
PPSPSPGLALTPSPALSSLRSRRPVEVGIQATLADDDDERFSSPRGICPKQELLPGKEEPTTYTCTTCKQSYGSAWFLLQ
HAQNSHGFRIYLESEHGSPLTPRMGGPSSMGGGADCPSHPPLHGLHLPPDASPFNLLRIPGSGSGGRDSVGAGSTLGVPG
GLHHQRFPPTPPIFSPPPRNHLDPHHLSPEELALAAHHPSAFDRVLRLNPPLPMEPPPTMDFSRRLRELAGNTSGSTPPL
SPSRPGPMQRLLQPFQTSGNKTPYLATPPPLPGSMQSPVGSQTTPPTPLPSAGATPSSNTPMKSKCCEFCGKAFKFQSNL
IVHRRSHTGEKPYKCHLCDHACTQASKLKRHMKTHMHKSSSPNTGKSEDGLSTASSPEPGTSEHMGSASNALKSVVAKLK
CENNRMLRENGEEEEEEEEEEEEEEEEEEEEEEEEAEEEEAQNGERAARRNNSYHFGLNLEATRQHENNGGIGTRLGGMTD
EGSIPRSLPEVMQGMGLAASMQHFSEALNAHKRNAIAQENHLHHHLNRGHPQNREMCDSNSVQETNRGEEGSLSTVNGRG
ASPNESASACLSKKLLLGSPSPLSPFSKRIKLEKEFDLPTPTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFAS
SSEHSSENGSLRFSTPPGELDGGMSGRSGTGSGGSTPHLGGPGRPSSKDGRRSDTCEYCGKVFKNCSNLTVHRRSHTGER
PYKCELCNYACAQSSKLTRHMKTHGQVGKDVYKCEICQMPFSVYSTLEKHMKKWHSDRPLSTEIKSE
```

492 - 511:	EEEEEEEEEEEEEEEEEEEE
493 - 512:	EEEEEEEEEEEEEEEEEEEE
494 - 513:	EEEEEEEEEEEEEEEEEEEE
495 - 514:	EEEEEEEEEEEEEEEEEEEE

A0A3Q2YQE1 **A0A3Q2YQE1_HIPCM** (911 aa)
BAF chromatin remodeling complex subunit BCL11A. *Hippocampus comes (Tiger tail seahorse)*

```
MSRRKQGKPQHLSKRDFSPDPLSTAVVVSSEELSERCSEHSEGSSSLNGHRPGSTLGRLSRLGHEPHHSPEQDLLTCGQC
QATFPLADILLFIEHKRKRCHGPPCLTVGRGLDKPPSPSPGLALTPSPALSSLRSRRPVEVGIQATLADDDDERFSSPRG
ICPKQELLPGKEEPTTYTCTTCKQSYGSAWFLLQHAQNSHGFRIYLESEHGSPLTPRMGGPSSMGGGADCPSHPPLHGLH
LPPDASPFNLLRIPGSGSGGRDSVGAGSTLGVPGGLHHQRFPPTPPIFSPPPRNHLDPHHLSPEELALAAHHPSAFDRVL
RLNPPLPMEPPPTMDFSRRLRELAGNTSGSTPPLSPSRPGPMQRLLQPFQTSVGSIGTGGGGGNKTPYLATPPPLPGSMQ
SPVGSQTTPPTPLPSAGATPSSNTPMKSKCCEFCGKAFKFQSNLIVHRRSHTGEKPYKCHLCDHACTQASKLKRHMKTHM
HKSSSPNTGKSEDGLSTASSPEPGTSEHMGSASNALKSVVAKLKCENNRMLRENGEEEEEEEEEEEEEEEEEEEEEEEAE
EEEAQNGERAARRNNSYHFGLNLEATRQHENNGGIGTRLGGMTDEGSIPRSLPEVMQGMGLAASMQHFSEALNAHKRNAI
AQENHLHHHLNRGHPQNREMCDSNSVQETNRGEEGSLSTVNGRGASPNESASACLSKKLLLGSPSPLSPFSKRIKLEKEF
DLPTPTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRFSTPPGELDGGMSGRSGTGSGGST
PHLGGPGRPSSKDGRRSDTCEYCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQSSKLTRHMKTHGQVGKDVYKCEI
CQMPFSVYSTLEKHMKKWHSDRPLSTEIKSE
```

536 - 555:	EEEEEEEEEEEEEEEEEEEE
537 - 556:	EEEEEEEEEEEEEEEEEEEE
538 - 557:	EEEEEEEEEEEEEEEEEEEE
539 - 558:	EEEEEEEEEEEEEEEEEEEE

A0A3Q3A5B0 **A0A3Q3A5B0_KRYMA** (817 aa)
Cyclin-dependent kinase 11B-like. *Kryptolebias marmoratus (Mangrove killifish) (Rivulus marmoratus)*

```
MLMGDEKETWKVKTLDEILLEKKRRRELEEKTDIKRQKNFSQGLVSQANDREAKRDTPEEGELRDQRMEITIRNSPYTRE
DSTEDRGEEDESLAIKPPQQVARKDKSHHRKEEKRKDKRRHRSHSAEGAGGKHVRAKDKERESDRRKRLWEEDNARRNWE
RQKRREEARAHSRRERDRLEQLERQRERDRKLREQQKEQRDFKDWERRADDRHKERGTRREMPSHHRMLPDEYDDKQKQS
HHSRSPNRVPRDRSEHSEPQKIATTKEDRPDIKDLLADLQDISDTERKTSTAESSIASGSGSEEEGDDDEGEEGSSSQSE
GEEEEEEEGESVSGSGHSEQSAEDVSEEEQSEEEEERENGNHIPAVPESRFDHDSEESGEDMEEEEEEEEEEEEEEEEEE
EEEEEGGEDEPTPHSQTHSRSPTPEENYIPESPPVSPVELKKELPKYLPALQGCRSVEEFQCLNRIEEGTYGVVYRAKDK
KTDEIVALKRLKMEKEKEGFPITSLREINTILKAQHPNIVTVREIVVGSNMDKIYIVMNYVEHDLKSLMETMKQPFLPGE
VKTLMIQLLRGVRHLHDNWILHRDLKTSNLLLSHKGILKIGDFGLAREYGSPLKPYTPVVVTLWYRSPELLLGAKEYSTA
VDMWSVGCIFGELLTQKPLFPGKSEIDQINKIFKDLGSANEKIWPGYSELPAVKKMSFTEYPYNNLRKRFGALLSDQGFD
LMNKFLTYCPSKRISADDALKHEYFRETPLPIDPSMFPTWPAKSEQQRVKRGTSPRPPEGGLGYRNLGDDDLKDTGFHLT
TSNQGASAVGPGFSLKF
```

383 - 402:	EEEEEEEEEEEEEEEEEEEE
384 - 403:	EEEEEEEEEEEEEEEEEEEE
385 - 404:	EEEEEEEEEEEEEEEEEEEE
386 - 405:	EEEEEEEEEEEEEEEEEEEE

A0A3Q3ASH1 **A0A3Q3ASH1_KRYMA** (1966 aa)
Protein Wiz-like. *Kryptolebias marmoratus (Mangrove killifish) (Rivulus marmoratus)*

```
MSGNGTWEPAGGGRPERRQDSQPVAAAELRRTARQRLKPSAFPSSLSWDSDSEKEALDAEELENLSNPHGLAAHSPGSPS
TGLRSGGEDELELDREEPQPFRADAPESARAGEPDARELGRKESADGGCWSDPEPSLSKVKEGCRMEEEGDGGEGDTTRP
KGKDGKEPERDVYTFPGDSDPESPPPAPWAHCTFIQRCRKKRALLRPFSGIGVSRRSSPDKLGAQRADGTEASPPSPEGG
DFEDGVAAVEAAPGEDAEDEDGGQESGADIFTCVECSIYFKKQIHLQEHMAEHCQGGAGAGRRSGKGGRLQCAECGWTLP
SRLALTEHRRKHQESRLKILEEIEKLNEPEKPKDGPTPDCGAARNPFSNPGEKSLPGLDKSPPLSPALVAAADADPAVID
LDATPVNSDRSPAQARAASGPRRRFICTECNFSTKTSQALANHSKTHNRKPPVNMAAASLACGHCAFLTTSRARLKEHLT
VVHSEQLSVGTRRPPRSNHRAPVSNEGPPEHDAAREDTTAPGGGRSSAGGRTSTDLSAFDPEADNDRLPGSEEEDHTGEF
NPSRQEADSHVGGKLRSGAQHNTDDSPRRRNATLPSPAKQGARNKGKEEAKKDRKVFFLRRRSNRISAASTQTDSDDDDG
GGVGERAPCFLPEGVLDEVETDDDDAEALRSVERKCPYCPDRFHNGIGLANHVRGHLNRVGVSYNVRHFISPEEVNAIEK
KYSYQKKKKKVANFDPDTFSVMHCEFCSAGFDTRAGLSSHARAHLRDFGITNWDVTISPIHILRELFSSRPDLAIPTAPP
RSCESSEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGDLEEEENDFEEGGIIKVKLEGETGDRSLDASDPGVLPSARRQ
```

```
RLKRSDGGGDEEEAAEEEEEEEDLRFASLDGLSSSPRRSSSLSPPEDGDTKVRGLKCEVCNSQFGSKRGLSIHARAHLRQ
LGITVAENSGPSIEILHKLVKERGQDGKLNPSLLKLPSAKNPSLSAPLKDEELEDMDVDEKPLALSIMAKAAKPGPPPSA
SPTPTPSPCASPAPSHSGSPSSVVKKAPISSLLPVSSPLRSPEHKAGGIKSLTSNLSAASTISTAKPLWAPQENDAPLNL
TLEADSDKDLVCQLCGAWFETRKGLSSHARAHLRHFGVECSEPKGSPIRLLNEFMDTDDFKHKASAMELDSPAEPQGAAA
AATLSSSKQPRLTLSSSSSSPLIYKVTTAGGGSTSKASSASSVPGPPAKRLKTSSMQVFRLSSGELMAVPHSEPPKEIGC
EYCGEYFENRKGLSSHARSHLRQMGITEWSVNGSPIDTLREVITRRGLPCALPLKPLKTPPPSSPIPPRSPLSASSSPSG
SLLGRLPFAFARPSSPPQVAASKSSSAPLSSLSSLTLKPKPEPVQVEVTKPGVVGRSGGFPAESLSSNWGGSDNGFPLNL
AMTNEVEPTRDIRCEFCGEYFENRKGLSSHARSHLRQMGITEWTVNGSPIDTLREVMKKRGRGGSSHLSQGVKKESTHRA
GSPSWESASGTGGSEGLGASGYQSAKFHKSPLNLAQSGSRFQKQGLGSVGLSAPQPAGKFFRMSPLGKRPLSEEAQAVEM
AQSPPNRLKTFSSLPHDFSFKRKPSPDKHAHQDPSCELCGFYFENRKALASHARAHLRQFGVTEWSVNGSPIETLSAWIR
SRPQKVLEMHRNYMQGSRTTLKKKAHSSSSSSSPWSSSLAVSLARSQNHRVSHSSSEAAEDESGAGGLQAAPLRPGHSSP
GSSRLSGSLPLQAQVARSELNVRLPRGFERRPLKHPSCPEGAERDSGTPKPPRTGTIPSLVPKPPSYPLVKLVGKFYTLK
CRFCEVEFHGPLSVQEDWIRHLQQHILKMNYNKSAAPKAAVAAPAAAAATAEPPTSADDQAPAPPPASTPTSRATSTPSR
STAPSSRSPSPPADCAPSITATETVQIPEEQPAIVPTPIPVPTRIV
```

807 - 826:	EEEEEEEEEEEEEEEEEEEE
808 - 827:	EEEEEEEEEEEEEEEEEEEE
809 - 828:	EEEEEEEEEEEEEEEEEEEE
810 - 829:	EEEEEEEEEEEEEEEEEEEE
811 - 830:	EEEEEEEEEEEEEEEEEEEE
812 - 831:	EEEEEEEEEEEEEEEEEEEE
813 - 832:	EEEEEEEEEEEEEEEEEEEE
814 - 833:	EEEEEEEEEEEEEEEEEEEE
815 - 834:	EEEEEEEEEEEEEEEEEEEE
816 - 835:	EEEEEEEEEEEEEEEEEEEE
817 - 836:	EEEEEEEEEEEEEEEEEEEE
818 - 837:	EEEEEEEEEEEEEEEEEEEE

A0A3Q3B5S0 **A0A3Q3B5S0_KRYMA** (838 aa)
B cell CLL/lymphoma 11A. *Kryptolebias marmoratus (Mangrove killifish) (Rivulus marmoratus)*

```
MHLYHYKADPLPPPLIVRTTGLCLCGSDVLCVSSRKKSELSERCSEHSEESGSLNGHHPGSTRGRLARLGHDAHPSVEQD
LLTCGQCQATFPLADILLFIEHKRKRCHGPPCFAVGRGLDKPPSPSPGLALTPSPALGALRGRRPVEVGVQATLADEDER
FSSPRGICPKQEPLPGKEEPTTYTCTTCKQSYGSAWFLLQHAQNTHGFRIYLESEHGSPLTPRMGGPSSLGGGADCPSQP
PLHGLHLPPDASPFNLLRIPGSGSGGRDSVGAGGVIGASGPVAGGHHQRFPPTPPLFSPPPRNHLDPHHLSPEELALAAH
HPSAFDRVLRLNPPLPLEPPPTMDFSRRLRELAGNTSGSTPPLSPSRPSPMQRLLQPFQTGGNGSTTPTTPLPSAGATPS
STTQLKSKCCEFCGKAFKFQSNLIVHRRSHTGEKPYKCHLCDHACTQASKLKRHMKTHMHKSSSPNTGKSEDGLSLASSP
EPGTSDHIGSASNALKSVVAKLKSENNRMLRENGEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEASIPRSLPEVMQGMG
LAASMQHFSENHLHHHLNRDHHHSREMCDGDSVLETDRGEESSVLVVNGRGASPNESASVGLSKKLLLGSPSPLSPFSKR
IKLEKEFDLPTPTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRFSTPPGELDGGMSGRSG
TGSGGSTPHLGGPGRPSSKDGRRSDTCEYCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQSSKLTRHMKTHGQVGK
DVYKCEICQMPFSVYSTLEKHMKKWHSDRPLSTEIKSE
```

515 - 534:	EEEEEEEEEEEEEEEEEEEE
516 - 535:	EEEEEEEEEEEEEEEEEEEE
517 - 536:	EEEEEEEEEEEEEEEEEEEE
518 - 537:	EEEEEEEEEEEEEEEEEEEE
519 - 538:	EEEEEEEEEEEEEEEEEEEE
520 - 539:	EEEEEEEEEEEEEEEEEEEE
521 - 540:	EEEEEEEEEEEEEEEEEEEE

A0A3Q3CI02 **A0A3Q3CI02_HAPBU** (915 aa)
BAF chromatin remodeling complex subunit BCL11A. *Haplochromis burtoni (Burton's mouthbrooder) (Chromis burtoni)*

```
MSRRKQGKPQHLSKRDFSPAEPLSTAVVSSEELSERCSENSEESGSLKGHHPGSNVGRLARLGHDAHPSLEQDLLTCGQC
QATFPLADILLFIEHKRKRCHGPPCLTVGRGLDKPPSPSPGLALTPSPAMGSLRSRRLEVGVQATLADEDDDRFSSPRGI
CPKQEPLPGKEEPTTYTCTTCKQSYGSAWFLLQHAQNTHGFRIYLESEHGSPLTPRMGGPSSLGGGADCPSQPPLHGLHL
PPDASPFNLLRIPGSGSGGRDSVGAGGGIGTGAVGGGHHQRFPPTPPLFSPPPRNHLDPHHLSPEELALAAHHPSAFDRV
LRLNPPLPLDPPPTMDFSRRLRELAGNTSGSTPPLSPSRPSPMQRLLQPFQTGGGSGGTGGAGGSKPPYLATPPPLPGSM
QSPVGSQTTPTTPLPSAGATPSSTTQLKSKCCEFCGKAFKFQSNLIVHRRSHTGEKPYKCHLCDHACTQASKLKRHMKTH
MHKSSSPNTGKSEDGLSTASSPEPGTSEHVGSASNALKSVVAKLKSENDRMLRENGEEEEEEEEEEEEEEEEEEEEEEEE
EGEEEEEQNGERVARRNNNSYHFGLNLETARQHENNGSIGSRLGGVADEGSIPRSLPEVMQGMGLAASMQHFSEALNAHK
RNAMAQENHLHHHLNRDHHHNREICDGDSVLETDRGEEGSVSTVNGRGASPNESASVGLSKKLLLGSPSPLSPFSKRIKL
EKEFDLPTSTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRFSTPPGELDGGMSGRSGTGS
GGSTPHLGGPGRPSSKDGRRSDTCEFCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQSSKLTRHMKTHGQVGKDVY
KCEICQMPFSVYSTLEKHMKKWHSDRPLSTEIKSE
```

537 - 556:	EEEEEEEEEEEEEEEEEEEE
538 - 557:	EEEEEEEEEEEEEEEEEEEE
539 - 558:	EEEEEEEEEEEEEEEEEEEE
540 - 559:	EEEEEEEEEEEEEEEEEEEE

541 - 560:	EEEEEEEEEEEEEEEEEEEE
542 - 561:	EEEEEEEEEEEEEEEEEEEE

A0A3Q3DZ28 **A0A3Q3DZ28_9LABR** (798 aa)
PH and SEC7 domain-containing protein 1-like. *Labrus bergylta (ballan wrasse)*

```
MRAEAEAADEGEADSTFGSNCSARANSSFSPAEVSPKPGTGGGKEEEEEEEEEEEEEEEEEEEEGVVSWATVRMLGDRQR
QRATKEEDEVFSLLLKGTLDGSSNSHGGLKSPISLGSPRRPSECNLDSFSRHFESIMESHRAKGTSYSSLDSVDLLTSGS
TSVFTFDLPTLTPEIQSQICDSAKQIIELSFAPLAHPELYGPSERSRSSFTLSASGPGLRGGSKDDSGPPVRSKSEKETW
RRSILKEGFRKASSVPSLNSNLRERPVNNLPELLYPQADVAERLALGGSDDALANGTKPDLQAAKRLAKRLYNLEGFRKS
DVARHLSKNNEFSQMVAEEYLSNFNFKGLTIDQALRTFLRKFALMGETQERERVLAQFSRRYRQCNPESVTTEDSVHTLT
CAVMLLNTDLHGNNIGKRMSCSQFITNLEGLNDGKDFPKDLLKTLYSSIKNEKLQWTIDEEELRKSMSELTDVRTDSASH
TMKRLGTGGNPLVGVAQQADGELYKNGFLIRKVHADPDGKRTPRGKRGWKSFYAMLKGMVLYLQKDEYRAERELTEEDVK
NAVSIHHSLAMRAADYSKRPNVFYLRTADWRVFLFQAPNPEQMQSWITRINVVAAMFSAPPFPAAIGSQKRFSRPLLPGS
NTKLTQEEQVKSHENRFRAVSSELADLTASTPDRKVKGRELEEHKLRQEYLEFEKTRYGTYAMLLRAKLSSGDEDLSAFE
SRLFDDGGLQRAHSSPTLPQDVANKEKTRGTKTSKSLKVTSTSSKSSGSTKEASKKNGGENNQQFEVQKQSSKQEAAP
```

45 - 64:	EEEEEEEEEEEEEEEEEEEE

A0A3Q3EA95 **A0A3Q3EA95_9LABR** (1094 aa)
ZP domain-containing protein. *Labrus bergylta (ballan wrasse)*

```
MSLVACILWTLFSGSLGGPVPVTHEVQTYHHLPMFLDAPEPVVAQELFLPVPHKRPVPAGITSLLLPVKRPQQSVQGTGT
RAVEVFCGGDGIRVDRFQVRSWTNPYLFSLGTCRVTKVTPRFLYFHYKLTECGGESQIVGGQLVYSFTLSYTPPPPQGFA
IRVMALTLPLHCHYNRFHYSYKVGFRPQVQPKTFLKSTRSKLSFSLTVCNEHWEPVPEGQEFVLGELVYFIAQSGVLLAG
ESLYVDSCYATSTKDPDSQLRVDIITNYGCMTDSRREGSSSYFLSAGGAVLKFSVDALLFRAVSQVLYLHCSMSVSLTTS
HVSKSCNYNTAAGRWEELEASPSVCSCCDSTCTDGQDVIKNTVSSQGWFVEQNVEQKPRMRASSLQAEEEEEEEEEEEEE
EEEAEEKEEEEEEEEEEEEEEEAEEKEEEEEEEEEEAEEKEEEEEEEEAEEKEEGEEEEEEEAEEEAEEKEEEEEEEEEEEEA
EEKEEEEEEEAEEKEEEEEEEAEEEEEEEEEEEEEEEQKRKRKQKRRRRKKGSRRGGGGGGGRRRRRGSRRGGGGRRRGSRRG
GGGRRRGSRRGEGGRRRGSRGEEEEEEEEEEEEEEEEEGAEEEEEEEEEEEEEEEEEEAEEEEEEEEEEEAEEGEEEGAEEE
EEEEEEEEEEEAEEEEEEEEEEEAEEGRRRRRRRGGGGGRRRRGGGGRRRRRGGGRGRRRGGGGGRRRGGRGRRRRRGGGRR
GRRRGSRRGGGRRRRGSRRGEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEDYEDLPPETDINSNEGKAVSEKMPELDERKERRNSSAVSHQGERETEEKVKQEDNQMK
QLGMMKAGNESVSGALNSSEFIEKSSINVQRDYSGKKTFSATRDKESSPAGNVSTAAALCPKGDHMNCSSADDGVESYPS
GSTNAAVGADLPSKDRAPSDLGRSGSVWDSSVRASPLGSGLETRLEPDSHPAGFSGLIRRLLVFESGLKDDEALHHLGQF
TEAAEPHKEEFPGRAHSLSSGLVGSEQQDNPDHSSVVTVTESSESSSMFDRKWA
```

745 - 764:	EEEEEEEEEEEEEEEEEEEE
746 - 765:	EEEEEEEEEEEEEEEEEEEE
747 - 766:	EEEEEEEEEEEEEEEEEEEE
748 - 767:	EEEEEEEEEEEEEEEEEEEE
749 - 768:	EEEEEEEEEEEEEEEEEEEE
750 - 769:	EEEEEEEEEEEEEEEEEEEE
751 - 770:	EEEEEEEEEEEEEEEEEEEE
752 - 771:	EEEEEEEEEEEEEEEEEEEE
753 - 772:	EEEEEEEEEEEEEEEEEEEE
754 - 773:	EEEEEEEEEEEEEEEEEEEE
755 - 774:	EEEEEEEEEEEEEEEEEEEE
756 - 775:	EEEEEEEEEEEEEEEEEEEE
757 - 776:	EEEEEEEEEEEEEEEEEEEE
758 - 777:	EEEEEEEEEEEEEEEEEEEE
759 - 778:	EEEEEEEEEEEEEEEEEEEE
760 - 779:	EEEEEEEEEEEEEEEEEEEE
761 - 780:	EEEEEEEEEEEEEEEEEEEE
762 - 781:	EEEEEEEEEEEEEEEEEEEE
763 - 782:	EEEEEEEEEEEEEEEEEEEE
764 - 783:	EEEEEEEEEEEEEEEEEEEE
765 - 784:	EEEEEEEEEEEEEEEEEEEE
766 - 785:	EEEEEEEEEEEEEEEEEEEE
767 - 786:	EEEEEEEEEEEEEEEEEEEE
768 - 787:	EEEEEEEEEEEEEEEEEEEE
769 - 788:	EEEEEEEEEEEEEEEEEEEE
770 - 789:	EEEEEEEEEEEEEEEEEEEE
771 - 790:	EEEEEEEEEEEEEEEEEEEE
772 - 791:	EEEEEEEEEEEEEEEEEEEE

773 - 792:	EEEEEEEEEEEEEEEEEEEE
774 - 793:	EEEEEEEEEEEEEEEEEEEE
775 - 794:	EEEEEEEEEEEEEEEEEEEE
776 - 795:	EEEEEEEEEEEEEEEEEEEE
777 - 796:	EEEEEEEEEEEEEEEEEEEE
778 - 797:	EEEEEEEEEEEEEEEEEEEE
779 - 798:	EEEEEEEEEEEEEEEEEEEE
780 - 799:	EEEEEEEEEEEEEEEEEEEE
781 - 800:	EEEEEEEEEEEEEEEEEEEE
782 - 801:	EEEEEEEEEEEEEEEEEEEE
783 - 802:	EEEEEEEEEEEEEEEEEEEE
784 - 803:	EEEEEEEEEEEEEEEEEEEE
785 - 804:	EEEEEEEEEEEEEEEEEEEE
786 - 805:	EEEEEEEEEEEEEEEEEEEE
787 - 806:	EEEEEEEEEEEEEEEEEEEE
788 - 807:	EEEEEEEEEEEEEEEEEEEE
789 - 808:	EEEEEEEEEEEEEEEEEEEE
790 - 809:	EEEEEEEEEEEEEEEEEEEE
791 - 810:	EEEEEEEEEEEEEEEEEEEE
792 - 811:	EEEEEEEEEEEEEEEEEEEE
793 - 812:	EEEEEEEEEEEEEEEEEEEE
794 - 813:	EEEEEEEEEEEEEEEEEEEE
795 - 814:	EEEEEEEEEEEEEEEEEEEE
796 - 815:	EEEEEEEEEEEEEEEEEEEE
797 - 816:	EEEEEEEEEEEEEEEEEEEE
798 - 817:	EEEEEEEEEEEEEEEEEEEE
799 - 818:	EEEEEEEEEEEEEEEEEEEE
800 - 819:	EEEEEEEEEEEEEEEEEEEE
801 - 820:	EEEEEEEEEEEEEEEEEEEE
802 - 821:	EEEEEEEEEEEEEEEEEEEE
803 - 822:	EEEEEEEEEEEEEEEEEEEE

A0A3Q3ELW6 **A0A3Q3ELW6_9LABR** (782 aa)
Im:7142702. *Labrus bergylta (ballan wrasse)*

```
MSDKGLLTAEANHDSGAGSSSPQLSTPSPQRLGPGEHDLLTCGQCQTNFPLGDILVFIEHKRRLCRGPGSRPGTFLKPGE
SGGVAGIEISPRIRTLELGRGSIPVEVGIQVTPGGEEHEERRMTPARGICPKQERGDKDEPSSYICTTCKQTFTSAWFLL
QHAQHTHGIRIYLDNHLVNCSLTPRMALPPPPCTDALPRSPLPTFLGDTNNPFHLLRMAAPLLREHPPATPRPPLERLGP
EEMGLLSQHPSAFERVMRMAPMDPPSMDFSRRLRELAGNTTNNGGPTPPLSPNRVPPMHRLLSPTLFQPGAKPPTFLTFA
PQPPTSQGGHGSSTPPDPQGQNQTPGKSKSCEFCGKIFKFQSNLIVHRRSHTGERPYKCHLCDHACSQASKLKRHMKTHM
HNKSGSMSGSPEQGNRGEGEGEEKSRDGDSRGMIIDNEEEEEEEEEEEEEEEEEEEEELRNGCRTDSNLSEDLQEFGQNRE
NGTRQSPEGKPLSGDRGSDSAGMGIMHPYNHLDNHLRLNPNKRSLERQPNGDGGDEHRPLMNGRMSVSEADSFPGLFQRR
PTPITSQSPSNNKRIKIEKEQLELPPTIPLISPENVYSQLLAGYAASRHFIREPFLGFTDSRQSPFATSSEHSSSETGSL
RFSTPPGELMEGGSASGRSGSSTPHLMRGPGPGRPPSSKDRRNDTCEYCGKVFKNCSNLTVHRRSHTGERPYKCDLCSYA
CAQSSKLTRHMKTHGQFGKEVYRCDICHMPFSVYSTLEKHMKKWHGEHLMASEVKLEQADRG
```

438 - 457:	EEEEEEEEEEEEEEEEEEEE

A0A3Q3EUQ1 **A0A3Q3EUQ1_9LABR** (976 aa)
Uncharacterized protein. *Labrus bergylta (ballan wrasse)*

```
RRLQVVREVGGATGGGATSQDGDTPTFPPAHLQQARLSHLQEEVLVLLVLFIIYYIYLNKFTEREEEEEEEEEEEEEEEE
EEGGGGGGGGGRGGRGGGGGRRGGGGGGGGGRGGRGGGGGRRGGGGGGGGGGGGGGGRRGGRGGGGGGRGGRGGGEEEE
EEEEEEEEEEEEEEEEEKKRRRRRRRRRRRRRKRRRKKRRKRRRRKRRRRRKKRRKRRRRRRRGRRGGGGGRRGGGRRGG
GGGGGGRRGGGGRRGGGRGGGGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEGGGGGGGGGGGGGRRGGRGGGGGGRGGRGGGGGRRGGGGGGGGRGGRGGGGGRRG
GGGGGGGGGGGRGGGRRGGRGGGGRGGGGGRRGGRGGGGGGRGGRGGGGRRGGGRRGGGGGGGGRRGGGGRRGGGRGGGG
RGGGGGRGGGGGRRGGGRRGGGGGGGGRRGGGRRGGGRGGGGRGGGGGRGGGGRRGGGRRGGGGGGGGRRGGGGGR
GGGGGGGRGGGGGRRGGGGGGGGRRGGGGGRGGGGGGGRRGGGGGRGGRGGGGGGGRRGGGGGGRRGGGRRGGGRGG
GGGGRGGRGRGRGGRGGGGGRGGGGGRGGRGGGRGGGGGGGRGGGRGGRRGGGRRGRGGRGGRGGRGGRGGKGGRGGRG
GRGGRRGKGGRGGRGERGGRGGRGGGGGRRGRGGRRGGGRGGRGGRRGGGGRGGEEEEEEEEEEEEEEEDSVIKSENSSLI
SVMFLKSIFIILSFYE
```

157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
263 - 282:	EEEEEEEEEEEEEEEEEEEE
264 - 283:	EEEEEEEEEEEEEEEEEEEE
265 - 284:	EEEEEEEEEEEEEEEEEEEE
266 - 285:	EEEEEEEEEEEEEEEEEEEE
267 - 286:	EEEEEEEEEEEEEEEEEEEE
268 - 287:	EEEEEEEEEEEEEEEEEEEE
269 - 288:	EEEEEEEEEEEEEEEEEEEE
270 - 289:	EEEEEEEEEEEEEEEEEEEE
271 - 290:	EEEEEEEEEEEEEEEEEEEE
272 - 291:	EEEEEEEEEEEEEEEEEEEE
273 - 292:	EEEEEEEEEEEEEEEEEEEE
274 - 293:	EEEEEEEEEEEEEEEEEEEE
275 - 294:	EEEEEEEEEEEEEEEEEEEE
276 - 295:	EEEEEEEEEEEEEEEEEEEE
277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE
307 - 326:	EEEEEEEEEEEEEEEEEEEE
308 - 327:	EEEEEEEEEEEEEEEEEEEE
309 - 328:	EEEEEEEEEEEEEEEEEEEE
310 - 329:	EEEEEEEEEEEEEEEEEEEE
311 - 330:	EEEEEEEEEEEEEEEEEEEE
312 - 331:	EEEEEEEEEEEEEEEEEEEE
313 - 332:	EEEEEEEEEEEEEEEEEEEE
314 - 333:	EEEEEEEEEEEEEEEEEEEE
315 - 334:	EEEEEEEEEEEEEEEEEEEE
316 - 335:	EEEEEEEEEEEEEEEEEEEE
317 - 336:	EEEEEEEEEEEEEEEEEEEE
318 - 337:	EEEEEEEEEEEEEEEEEEEE
319 - 338:	EEEEEEEEEEEEEEEEEEEE
320 - 339:	EEEEEEEEEEEEEEEEEEEE
321 - 340:	EEEEEEEEEEEEEEEEEEEE
322 - 341:	EEEEEEEEEEEEEEEEEEEE
323 - 342:	EEEEEEEEEEEEEEEEEEEE
324 - 343:	EEEEEEEEEEEEEEEEEEEE
325 - 344:	EEEEEEEEEEEEEEEEEEEE
326 - 345:	EEEEEEEEEEEEEEEEEEEE
327 - 346:	EEEEEEEEEEEEEEEEEEEE
328 - 347:	EEEEEEEEEEEEEEEEEEEE
329 - 348:	EEEEEEEEEEEEEEEEEEEE
330 - 349:	EEEEEEEEEEEEEEEEEEEE
331 - 350:	EEEEEEEEEEEEEEEEEEEE
332 - 351:	EEEEEEEEEEEEEEEEEEEE

333 - 352:	EEEEEEEEEEEEEEEEEEEE
334 - 353:	EEEEEEEEEEEEEEEEEEEE
335 - 354:	EEEEEEEEEEEEEEEEEEEE
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337 - 356:	EEEEEEEEEEEEEEEEEEEE
338 - 357:	EEEEEEEEEEEEEEEEEEEE
339 - 358:	EEEEEEEEEEEEEEEEEEEE
340 - 359:	EEEEEEEEEEEEEEEEEEEE
341 - 360:	EEEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEEE
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374 - 393:	EEEEEEEEEEEEEEEEEEEE
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377 - 396:	EEEEEEEEEEEEEEEEEEEE
378 - 397:	EEEEEEEEEEEEEEEEEEEE
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381 - 400:	EEEEEEEEEEEEEEEEEEEE
382 - 401:	EEEEEEEEEEEEEEEEEEEE
383 - 402:	EEEEEEEEEEEEEEEEEEEE
384 - 403:	EEEEEEEEEEEEEEEEEEEE

385 - 404:	EEEEEEEEEEEEEEEEEEEE
386 - 405:	EEEEEEEEEEEEEEEEEEEE
387 - 406:	EEEEEEEEEEEEEEEEEEEE
388 - 407:	EEEEEEEEEEEEEEEEEEEE
389 - 408:	EEEEEEEEEEEEEEEEEEEE
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408 - 427:	EEEEEEEEEEEEEEEEEEEE
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437 - 456:	EEEEEEEEEEEEEEEEEEEE
438 - 457:	EEEEEEEEEEEEEEEEEEEE
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442 - 461:	EEEEEEEEEEEEEEEEEEEE
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445 - 464:	EEEEEEEEEEEEEEEEEEEE
446 - 465:	EEEEEEEEEEEEEEEEEEEE
447 - 466:	EEEEEEEEEEEEEEEEEEEE
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454 - 473:	EEEEEEEEEEEEEEEEEEEE
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457 - 476:	EEEEEEEEEEEEEEEEEEEE
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462 - 481:	EEEEEEEEEEEEEEEEEEEE
463 - 482:	EEEEEEEEEEEEEEEEEEEE

464 - 483:	EEEEEEEEEEEEEEEEEEEE
465 - 484:	EEEEEEEEEEEEEEEEEEEE
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471 - 490:	EEEEEEEEEEEEEEEEEEEE
472 - 491:	EEEEEEEEEEEEEEEEEEEE
473 - 492:	EEEEEEEEEEEEEEEEEEEE
474 - 493:	EEEEEEEEEEEEEEEEEEEE
475 - 494:	EEEEEEEEEEEEEEEEEEEE
476 - 495:	EEEEEEEEEEEEEEEEEEEE
477 - 496:	EEEEEEEEEEEEEEEEEEEE
478 - 497:	EEEEEEEEEEEEEEEEEEEE
479 - 498:	EEEEEEEEEEEEEEEEEEEE
480 - 499:	EEEEEEEEEEEEEEEEEEEE
481 - 500:	EEEEEEEEEEEEEEEEEEEE
482 - 501:	EEEEEEEEEEEEEEEEEEEE
483 - 502:	EEEEEEEEEEEEEEEEEEEE
484 - 503:	EEEEEEEEEEEEEEEEEEEE
485 - 504:	EEEEEEEEEEEEEEEEEEEE

A0A3Q3EZI8 **A0A3Q3EZI8_9LABR** (574 aa)
Cytosolic purine 5'-nucleotidase. *Labrus bergylta (ballan wrasse)*

```
MTTSWSDRLQNYADLPANMDGLSMKKYRREAYHRVFVNRSLAMEKIKCFGFDMDYTLAVYKSPEYESLGFELTVERLVYI
GYPQELLSFVYDPSFPTRGLVFDTMYGNLLKVDAYGNILVCVHGFNFLRGPEIRERYPNKFIQRDDTERFYILNTLFNLP
ETYLFACLVDFFSNCDRYTSCETGFKNGDLFMSYKSMFQDIRDAVDWVHFKGTLKEKTVENLEKYVVRDGKLPLLLSRMN
EVAKVFLATNSDYKYTDKIMTYLFDFPHGPKPGTSHRPWKSYFDLILVDARKPLFFGEGTVLRQVDTTTGRLKIGTYTGP
LQHGIVYSGGSSDIVCDLLGAKGKDIVYIGDHIFGDILKSKKRQGWRTFLVIPELAQELHVWTDKSSSLALSVSLSSLLR
HLDSSSNERPDISTIQRRVKKVTHDMDMCYGMMGSLFRSGSRQTLFASQVMRYADLYAASFINLLYYPFSYLFRAAHVLM
PHESTVEHAHVDIDIESPLATRNRSQCSNCKDLDCKRNQLTRSFSEIKPPNLFPQTPQEITHCHDEDDDEEEEEEEEEE
EEEEEEEEEEEEE
```

550 - 569:	EEEEEEEEEEEEEEEEEEEE
551 - 570:	EEEEEEEEEEEEEEEEEEEE
552 - 571:	EEEEEEEEEEEEEEEEEEEE
553 - 572:	EEEEEEEEEEEEEEEEEEEE
554 - 573:	EEEEEEEEEEEEEEEEEEEE
555 - 574:	EEEEEEEEEEEEEEEEEEEE

A0A3Q3F4I8 **A0A3Q3F4I8_9LABR** (811 aa)
B-cell lymphoma/leukemia 11A-like. *Labrus bergylta (ballan wrasse)*

```
MSRRKQGKPQHLSKREFSPEPLSGILPEEDFQDSTRLGVDEGEPLKGDQDLLTCGQCHSRFPLADILLFIEHKRRQCHGS
LCTDKPLDRPPSSPLASPLSTSSSHSQTHHQHPRRVYHPVEVAIQVSPQDEDCLSAPLQGIIPKQENITDKVEPNSFTCT
TCKQPFTSAWFLLQHAQNTHGFRIYLESEPGSPLTPRVAAAPGMGGDCASSQPPLHAVHLAEGSPYSLLRMPGSGSGRDT
ASTPREGRYPRTPPLFSPPPRHHLSPDDLALATHHPSAFDRVMRLNSVPLEAPPMDFSRRLRELAGNATGASPPLSPNRP
SPMQRLLQPFQPGSKPPFSATPPLSSSQSPSGARSTPNPVSNAAQPGTPLKAKSCEFCGKTFKFQSNLIVHRRSHTGEKP
FKCHLCNHACTQASKLKRHMKTHCQSKSSSLNAKSDDGLSTASSPEPGTSDLMGSATDALKSVVAKFKSENNGLITENGE
EDEEEEEEEEEEEEEEEEEEEEEEEEEGEEEEMESKPGVKEGNGRNDYHFSLRLEGAHHHQNSDALRPRRRSLSRDRGDE
DSALESDRADDGTVTTVNGTGPLSSDSLSRKLLGGRVSPGSLSPLSKRIKVEKDLDPPTPTIPNTENVYSQWLAGYAASR
QLKDPFISFTGGDSRQSPFASSSEHSSENGSLRYSTPPGELDGERAASGRSGTGSGASTPHGGSGNGRPSSKDGRRSDTC
EYCGKVFKNCSNLTVHRRSHTGERPYKCELCSYACAQSSKLTRHMKTHGQMGKDVYKCEICHMPFSVYSTLEKHMKKWHS
DRPLSADIKTE
```

483 - 502:	EEEEEEEEEEEEEEEEEEEE
484 - 503:	EEEEEEEEEEEEEEEEEEEE
485 - 504:	EEEEEEEEEEEEEEEEEEEE
486 - 505:	EEEEEEEEEEEEEEEEEEEE
487 - 506:	EEEEEEEEEEEEEEEEEEEE
488 - 507:	EEEEEEEEEEEEEEEEEEEE

A0A3Q3F9F9 **A0A3Q3F9F9_9LABR** (890 aa)
Zinc finger ZZ-type containing 3. *Labrus bergylta (ballan wrasse)*

```
MAASRSSRVTRSSVGLNGLDENFCGRTLRNRSIAQPEETSVSPLPRARSPKKKQDTKQQESKQDAKQDSKQDAKHSRKRG
VSCLEKDISPENCDRGKGARDICTQIKRAKRCSRSGDSQGHEEDPVLLKTESPVSVLEPCKDSSCEEFPSQNSANTSPVS
PVLSKEEVELTGGQAEDGHVECDGAAQPPNAHKASNGLKDNKAEESCTLTEEPSANPSSANNCLSLLNGSQTGAPSSPDP
TVPCSEDLPASSAPNLEAVSEESVPELIVAEEHEVEEVEVDVVGNPLCLAHEEQVMETENNTNGRPLTPVPINNNSNSGE
TTPPLATTPSPTEPECTPSISSTPPSFTELYEHRYTLRTSPRRAASGGKASSSKLSSPPRDNGPLREEGEVVVGLEEDCP
MVEEPAPSEFIGPSIEELVCVDPGDRTGGEEVGLVESKEAGKSKALTKSQAAEEEEEEEEEEEEEEEEEEEEPDVYYFES
DHLALKHNKDYQRLLQTIGVLEAQRTQAILDLETLARQQREALADPISFVEQLQKQVSLGLPCPQRVVQLPDVAWEQYTS
GLGDFEREFCDKKRKTRRLQLIFDQGLPDRPKSPVEAKKEGESSTMYTSLPMSDAPENSGIYGNMIRGRICHPNKSDTFN
QLWTVEEQKKLEQLLVKFPPEEVESRRWQKIADELGNRTAKQVASRVQKYFIKLTKAGIPVPGRTPNLCMYTKKASSKRQ
HHLNKHLYRPSTFLTSYEPPVYMDDDDERAAYFSSMQDPSADDSDEEGIPLELRNLPEYKELLELKRLKKQTLHEIHEDK
ASVRHVGYKCDVCGMDPIQGVRWHCQDCPQDNSVDFCSNCSDCLFKTETHKPNHHLEPVHQPDTFLDRDYCLPQSTGYNY
LDPNYFPANR
```

453 - 472:	EEEEEEEEEEEEEEEEEEEE

A0A3Q3FLN8 **A0A3Q3FLN8_9LABR** (272 aa)
Uncharacterized protein. *Labrus bergylta (ballan wrasse)*

```
FIIGHINLANEPKPHRSKTAKRAAGDMYSPSIDLEYDFQRDYYDRMYSYQARVPPLPPPPLSRAVVPSKRPRVSLSGGGS
RRTKTSFSSSKNSQRTSRNVKSDDLQAIKRELTQIKHKVDYLLESLERMEKDHGKKSEEEEEGEEEEEEKEEEEEEEEEE
EEEEEEEEEEEERRRRREEEEEGEEEEEEEDGGEEEGEERKRRGGGRARGRRRMRGGGEREEEEEEEGEGEQEGRRKRRRR
RRRKRRRRRRMRGRGGGGGRGGGGKRGGGGGR
```

151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE

A0A3Q3FP62 **A0A3Q3FP62_KRYMA** (1923 aa)
Protein Wiz-like. *Kryptolebias marmoratus (Mangrove killifish) (Rivulus marmoratus)*

```
MSGNGTWEPAGGGRPERRQDSQPVAAAELRRTARQRLKPSAFPSSLSWDSDSEKEALDAEELENLSNPHGLAAHSPGSPS
TGLRSGGEDELELDREEPQPFRADAPESARAGEPDARELGRKESADGGCWSDPEPSLSKVKEGCRMEEEGDGGEGDTTRP
KGKDGKEPERDVYTFPGDSDPESPPPAPWAHCTFIQRCRKKRALLRPFSGIGVSRRSSPDKLGAQRADGTEASPPSPEGG
DFEDGVAAVEAAPGEDAEDEDGGQESGADIFTCVECSIYFKKQIHLQEHMAEHCQGGAGAGRRSGKGGRLQCAECGWTLP
SRLALTEHRRKHQESRLKILEEIEKLNEPEKPKDGPTPDCGAARNPFSNPGEKSLPGLDKSPPLSPALVAAADADPAVID
LDATPVNSDRSPAQARAASGPRRRFICTECNFSTKTSQALANHSKTHNRKPPVNMAAASLACGHCAFLTTSRARLKEHLT
VVHSEQLSVGTRRPPRSNHRAPVSNEGPPEHDAAREDTTAPGGGRSSAGGRTSTDLSAFDPEADNDRLPGSEEEDHTGEF
NPSRQEADSHVGGKLRSGAQHNTDDSPRRRNATLPSPAKQGARNKGKEEAKKDRKVFFLRRRSNRISAASTQTDSDDDDG
GGVGERAPCFLPEGVLDEVETDDDDAEALRSVERKCPYCPDRFHNGIGLANHVRGHLNRVGVSYNVRHFISPEEVNAIEK
KYSYQKKKKKVANFDPDTFSVMHCEFCSAGFDTRAGLSSHARAHLRDFGITNWDVTISPIHILRELFSSRPDLAIPTAPP
RSCESSEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEGDLEEEENDFEEGGIIKVKLEGETGDRSLDASDPGVLPSARRQ
RLKRSDGGVRGLKCEVCNSQFGSKRGLSIHARAHLRQLGITVAENSGPSIEILHKLVKERGQDGKLNPSLLKLPSAKNPS
LSAPLKDEELEDMDVDEKPLALSIMAKAAKPGPPPSASPTPTPSPCASPAPSHSGSPSSVVKKAPISSLLPVSSPLRSPE
HKAGGIKSLTSNLSAASTISTAKPLWAPQENDAPLNLTLEADSDKDLVCQLCGAWFETRKGLSSHARAHLRHFGVECSEP
KGSPIRLLNEFMDTDDFKHKASAMELDSPAEPQGAAAAATLSSSKQPRLTLSSSSSSPLIYKVTTAGGGSTSKASSASSV
PGPPAKRLKTSSMQVFRLSSGELMAVPHSEPPKEIGCEYCGEYFENRKGLSSHARSHLRQMGITEWSVNGSPIDTLREVI
TRRGLPCALPLKPLKTPPPSSPIPPRSPLSASSSPSGSLLGRLPFAFARPSSPPQVAASKSSSAPLSSLSSLTLKPKPEP
VQVEVTKPGVVGRSGGFPAESLSSNWGGSDNGFPLNLAMTNEVEPTRDIRCEFCGEYFENRKGLSSHARSHLRQMGITEW
TVNGSPIDTLREVMKKRGRGGSSHLSQGVKKESTHRAGSPSWESASGTGGSEGLGASGYQSAKFHKSPLNLAQSGSRFQK
QGLGSVGLSAPQPAGKFFRMSPLGKRPLSEEAQAVEMAQSPPNRLKTFSSLPHDFSFKRKPSPDKHAHQDPSCELCGFYF
ENRKALASHARAHLRQFGVTEWSVNGSPIETLSAWIRSRPQKVLEMHRNYMQGSRTTLKKKAHSSSSSSSPWSSSLAVSL
ARSQNHRVSHSSSEAAEDESGAGGLQAAPLRPGHSSPGSSRLSGSLPLQAQVARSELNVRLPRGFERRPLKHPSCPEGAE
RDSGTPKPPRTGTIPSLVPKPPSYPLVKLVGKFYTLKCRFCEVEFHGPLSVQEDWIRHLQQHILKMNYNKSAAPKAAVAA
PAAAAATAEPPTSADDQAPAPPPASTPTSRATSTPSRSTAPSSRSPSPPADCAPSITATETVQIPEEQPAIVPTPIPVPT
RIV
```

807 - 826:	EEEEEEEEEEEEEEEEEEEE
808 - 827:	EEEEEEEEEEEEEEEEEEEE
809 - 828:	EEEEEEEEEEEEEEEEEEEE
810 - 829:	EEEEEEEEEEEEEEEEEEEE
811 - 830:	EEEEEEEEEEEEEEEEEEEE
812 - 831:	EEEEEEEEEEEEEEEEEEEE
813 - 832:	EEEEEEEEEEEEEEEEEEEE
814 - 833:	EEEEEEEEEEEEEEEEEEEE
815 - 834:	EEEEEEEEEEEEEEEEEEEE
816 - 835:	EEEEEEEEEEEEEEEEEEEE
817 - 836:	EEEEEEEEEEEEEEEEEEEE
818 - 837:	EEEEEEEEEEEEEEEEEEEE

A0A3Q3GA11 **A0A3Q3GA11_KRYMA** (1132 aa)
Nucleolar protein 8. *Kryptolebias marmoratus (Mangrove killifish) (Rivulus marmoratus)*

```
MREIHGSTIVTLKHREHGAMRRRLYVGGLSHTVTQKDLKDRFGKFGEVEEVELRTRRDEGGVPYKTFGYININISDADLK
KCLTVLNKSKWKGGTLQIEAAKESFLHRLAQERQEAAEQHLHQSAAEDQTQKLLDSLSKAGVENFTMKAAVPGSEVPGHK
```

```
DWVVSKFGRVLPVLQLRCQKGTKARTAKYDPSKYCHNIRRLDRTTADGSTPVTQLTWELQGGDDDISKKRRGEFPPFEPS
RPKKNRTDAGNICSVLSRNRSERTIGSDHHTEVHRLTNGSQLPSNHRAAQWKGRRFSDSDSDEEVRRLVAAQQNSHDALQ
QEVEDNNLEVVGIDYLVKSGQQDDRGEDEYDSADTDELFASRNKPSAQTIERCSNNKKTKKDVLLPCSKPSSSHRPAVLP
PTQRSSSEEEEGESSSSSLDSGYEAMFSNVTHLEISLADLQKLAETTAPRILSSGASSPAERPAPKKGTTPEEILASILG
EDSSEDEEQQKKKKRKRKGATMTPLPAFMGTKSLMDTSGRDEGQREEEEGGGREADKQKLNSESEKEEEVKNVASSKAAK
TVLHQVLLNPQTGSSSGRDEEEEEDEEEEEDEEEEEDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEEEEDEEEEEL
QVSPAPHGEEEEEDEEEEELQVSPAPHGEEEEEKEEEEQAPSRVALGAEEEEELQRKANMRRLAALQQRQEEAEEHRKLI
RGALANLDAPAPSAGKHIVFGSDEEEEEDEEQQEAVSKTSQSEEEGGGAAANQKEVQLKPSGPRLFADSEDDEGGDEEDG
GRFDIRPEFEGRAGQKLMALQSRFGTDERFRMDSRFMEDEEEEEEEEQQTEVKESLMEDDEALQEEKKKTLSILQSVLGS
SRQTGSKTTSKAKRFRDMSALHYDPSREEHAAFETKPDETKKDSKSARRKKREEAQKLPEVSKEIYYNVSGDLKTVFGPT
KDDGSEGQNPNWDQLEEEEGGGEEEEERLLSAGLSSENNESSGFKFSFFGDDVETGSGEMTEYQAETIQAPKVSWHQDPR
YHDSSSEEEEEEEEEPRSVAAKTSEKETPSNPDFFFFSDDSRLEEGPSLFCRPSQLEEQREQWEEGRSTLRQEYRKKHR
DARRKLRGARKS
```

598 - 617:	EEEEEEEEEEEEEEEEEEEE
599 - 618:	EEEEEEEEEEEEEEEEEEEE
600 - 619:	EEEEEEEEEEEEEEEEEEEE
601 - 620:	EEEEEEEEEEEEEEEEEEEE
602 - 621:	EEEEEEEEEEEEEEEEEEEE
603 - 622:	EEEEEEEEEEEEEEEEEEEE
604 - 623:	EEEEEEEEEEEEEEEEEEEE
605 - 624:	EEEEEEEEEEEEEEEEEEEE
606 - 625:	EEEEEEEEEEEEEEEEEEEE
607 - 626:	EEEEEEEEEEEEEEEEEEEE
608 - 627:	EEEEEEEEEEEEEEEEEEEE

A0A3Q3GJK8 **A0A3Q3GJK8_9LABR** (631 aa)
Uncharacterized protein. *Labrus bergylta (ballan wrasse)*

```
MVPSSLDVQSSSGDSTPLLTQSEEEEEEEEEEEEEEEEEEEEKEEEEEQEEEEEEEEEEEEEEEKEEEEEKRKRKRKRRKR
RRRRRKRRRKRKRRRRKRKRRRKRKRRRKRKRRRKRKRRRKRRRRKRKRRRKRKRRRKRRRKRRRKSRRKRKRKRKRKRKRRRKRRRR
GRGRGRGRGGGGRGGGRGRGGRGGGGRGRGGGRGRGGGGRGGGRGGRGGRGRGGGGGRGGERGGGRAGGRGRGRGRGREG
GRGGEEEEEEEEQEEEEEDEEEEEEEEEEEEEEEEEEERRKRKRRRKRRRRGRGGGRAGGRGRGRGGGRGRGGREGGRGGE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEKEEEEEKRKRRRKRRKRKRKRKRRKRRKRRRRGRGGGGRGRGGRGRGGGGRGGGGRGGGRGGRGRGRGGGRGGGGRGGG
RGGGGRGGGRGGGRGRGGRGRGRGGGRGGGGGGGGRGRGGRGRGRGGGGGGGGGRGRGGGRGGGGRGGGGGGGRGGGRR
GGGGGGGGRGRGRGGGRGGGRGGGGGRGGGGRGGGGGGGGRGRGRGGGRGGGGRGGGRGEFNRQQTALETF
```

320 - 339:	EEEEEEEEEEEEEEEEEEEE
321 - 340:	EEEEEEEEEEEEEEEEEEEE
322 - 341:	EEEEEEEEEEEEEEEEEEEE
323 - 342:	EEEEEEEEEEEEEEEEEEEE
324 - 343:	EEEEEEEEEEEEEEEEEEEE
325 - 344:	EEEEEEEEEEEEEEEEEEEE
326 - 345:	EEEEEEEEEEEEEEEEEEEE
327 - 346:	EEEEEEEEEEEEEEEEEEEE
328 - 347:	EEEEEEEEEEEEEEEEEEEE
329 - 348:	EEEEEEEEEEEEEEEEEEEE
330 - 349:	EEEEEEEEEEEEEEEEEEEE
331 - 350:	EEEEEEEEEEEEEEEEEEEE
332 - 351:	EEEEEEEEEEEEEEEEEEEE
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334 - 353:	EEEEEEEEEEEEEEEEEEEE
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341 - 360:	EEEEEEEEEEEEEEEEEEEE
342 - 361:	EEEEEEEEEEEEEEEEEEEE
343 - 362:	EEEEEEEEEEEEEEEEEEEE
344 - 363:	EEEEEEEEEEEEEEEEEEEE

345 - 364:	EEEEEEEEEEEEEEEEEEEE
346 - 365:	EEEEEEEEEEEEEEEEEEEE
347 - 366:	EEEEEEEEEEEEEEEEEEEE
348 - 367:	EEEEEEEEEEEEEEEEEEEE
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351 - 370:	EEEEEEEEEEEEEEEEEEEE
352 - 371:	EEEEEEEEEEEEEEEEEEEE
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357 - 376:	EEEEEEEEEEEEEEEEEEEE
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360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE

A0A3Q3GKK5 **A0A3Q3GKK5_9LABR** (1355 aa)
Nuclear receptor binding SET domain protein 3. *Labrus bergylta (ballan wrasse)*

```
MDFSFSFMQGIMGNTIQQPPQLIDSANIRQEGTCDTGSDPGEDGGPSYDAALDEFSYPSSAPEDMSQVSNGYPPGLGMYE
PQAKFSMYSQFPNGSANGYGAIRSYAEHGLLTPSSQPSHAPSITPGGVLKKTSSPEIKLKIIKTYQNGKELFESALCGDL
LQELQVMHYQPRHERKKEKRKKSARLQLQVQEQNLDQSQPQTGTTEQTEDIHIQPQPTETTPVPKVHHPSVIQETGFCKE
FVIGDLVWSKVGTYPWWPCMVSSDPQMKVHTRINTRGHREYHVQFFGSVAERAWIHEKRIVVYQGKKQFDDLQAETLRKT
SNPVEKSKLLKPIPQRERSQWEVGVGHAEDAFVMTKQERIDNYTFIYVDPEPAEAPPSKKPNIRAEKRNRRSSEDNAHSQ
ASNEDQNQKGDQLKTCSPKQNSGGEARTRQDSPPPVRAWKTAAARKLLPLSITMKRLNVEITKCDWPLLQKKAATSPKKD
KEEEEEEEEEEEEEEEEEEEEEEEKEEEQVEQEARQPDLGYWASEISDACKPLKKRSRASTDVEMASSQYRDTSDSDSRG
LNDPQGLFGKSLDSPAAADADASDTQSVDSGLSRKDSSTGKRDTVCQICETYGDGLVVCEGECSRQFHLDCLGLSSLPEG
RYVCLECRNGNHPCFSCKTSGREVTRCSVSGCGCFYHEDCVQKLPGTTSSQGGGFCCPQHSCSTCCLERDLQRASKGRLM
RCIRCPVAYHTGDGCVAAGSVALTHHIMICSNHGSTKKNGLLSSPVNVGWCFLCARGLLVQDLTDTILSSYAYKSHYLLT
ESNRAELKLPMIPSPSSATKKNVGKGGKLLCCDSCPASFHPECLEIEMPEGAWSCSDCRAGKKPHYKQIVWVKLGNYRWW
PAEICNPRLVPSNIQSLRHDVGDFPVFFFGSHDYYWINQGRVFPYVENDKNFVTGQININKTFKKALEEAARRFQELKAQ
RESREALEQERNSRKPPPYKFIKSNKPVGKVQVHIADLSEISRCNCRPTDDHPCSLHSQCLNRMLQYECHPQVCPAGDNC
ENQCFSKRLYAETEVVKTDGRGWGLRTNQALRKGDFVTEYVGEVIDSEECQQRIKRAHENHLTNFYMLTLTKDRVIDAGP
KGNSSRFMNHSCSPNCETQKWTVNGDVRIGLFALCDIEADTELTFNYNLHCVGNRRASCNCGSDNCSGFLGVQPTSAVVM
EKEEKARNAKLKPKKRKLRLEGKHTHEYFCFWCGEGGELVMCDRKDCPKAYHLLCLNLTKPPYGRWECPWHDCSVCGSPA
SSLCDFCPRSFCQDHETGALTSSSLEGRPCCSSHNPADPLGSECGPEPGSTQRRRSALSPVRVKEEPEQVMPDTE
```

482 - 501:	EEEEEEEEEEEEEEEEEEEE
483 - 502:	EEEEEEEEEEEEEEEEEEEE
484 - 503:	EEEEEEEEEEEEEEEEEEEE
485 - 504:	EEEEEEEEEEEEEEEEEEEE

A0A3Q3GMQ8 **A0A3Q3GMQ8_9LABR** (917 aa)
B-cell lymphoma/leukemia 11A-like. *Labrus bergylta (ballan wrasse)*

```
MSRRKQGKPQHLSKRDFSPEPLSTAVISSEELSERCSEHSEESGSFNGHHPGSTVGRLARLGHDPSHPSLEQDLLTCGQC
QSTFPLADILLFIEHKRKRCHGPPCLTVGRGLDKPPSPSPGLALTPSPALGSRRGRRPVEVGVQATLAEDDEDRFSMPRG
IFPKLEPLPGKEEPTTYTCTTCKQPYGSAWFLLQHAQNTHGFRIYLDSEHGSPLTPRMGGPSSMGGGADCPSQPPLHGLH
LPPDASPFNLLRIPGSVSGGRDSVGVGGGIGGGGHGGGHHQRFPPTPPLFSPPPRNHLDPHHLSPEELALAAHHPSAFDR
VLRLNPPLPLDPPPTMDFSRRLRELAGNTSGSSPPLSPSRPSPMQRLLQPFQTGGGNGSIGGAGGGKPPYLATPPPLPGP
MQSPVGSQTTPTTPLPSAGATPSSTNPLKSKCCEFCGKAFKFQSNLIVHRRSHTGEKPYKCHLCDHACTQASKLKRHMKT
HMHKSSSPNTGKSEDGLSTASSPEPGTSEHLGSASNALKSVVAKLKSENNRRLRENGEEEEEEEEEEEEEEEEEEEEEE
EEEVEEEEPHNGERAARRNNNSYHFGLNLDAARQHENNGGLGSRLGGVAEEGSIPRSLPEVMQGMGLAASMQHFSEALSA
HKRNAMAQENHLHHHLNRDHHHNRDMCDGNSVLETDRGEECSVSTVNGRGASPNESASVGLSKKLLLGSPSPLSPFTKRI
KLEKEFDLPTPTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRFSTPPGELDGGMSGRSGT
GSGGSTPHLGGHGRPTSKDGRRSDTCEYCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQSSKLTRHMKTHGQVGKD
VFKCEICQMPFSVYSTLEKHMKKWHSDRPLSTEIKSE
```

538 - 557:	EEEEEEEEEEEEEEEEEEEE
539 - 558:	EEEEEEEEEEEEEEEEEEEE
540 - 559:	EEEEEEEEEEEEEEEEEEEE
541 - 560:	EEEEEEEEEEEEEEEEEEEE
542 - 561:	EEEEEEEEEEEEEEEEEEEE
543 - 562:	EEEEEEEEEEEEEEEEEEEE
544 - 563:	EEEEEEEEEEEEEEEEEEEE

A0A3Q3GQC2 **A0A3Q3GQC2_9LABR** (858 aa)
B-cell lymphoma/leukemia 11A-like. *Labrus bergylta (ballan wrasse)*

```
MSRRKQGKPQHLSKRDFSRSTVGRLARLGHDPSHPSLEQDLLTCGQCQSTFPLADILLFIEHKRKRCHGPPCLTVGRGLD
KPPSPSPGLALTPSPALGSRRGRRPVEVGVQATLAEDDEDRFSMPRGIFPKLEPLPGKEEPTTYTCTTCKQPYGSAWFLL
QHAQNTHGFRIYLDSEHGSPLTPRMGGPSSMGGGADCPSQPPLHGLHLPPDASPFNLLRIPGSVSGGRDSVGRFPPTPPL
FSPPPRNHLDPHHLSPEELALAAHHPSAFDRVLRLNPPLPLDPPPTMDFSRRLRELAGNTSGSSPPLSPSRPSPMQRLLH
IGGAGGGKPPYLATPPPLPGPMQSPVGSQTTPTTPLPSAGATPSSTNPLKSKCCEFCGKAFKFQSNLIVHRRSHTGEKPY
KCHLCDHACTQASKLKRHMKTHMHKSSSPNTGKSEDGLSTASSPEPGTSEHLGSASNALKSVVAKLKSENNRRLRENGEE
EEEEEEEEEEEEEEEEEEEEEEEEVEEEEPHNGERAARRNNNSYHFGLNLDAARQHENNGGLGSRLGGVAEEGSIPRSLP
EVMQGMGLAASMQHFSEALSAHKRNAMAQENHLHHHLNRDHHHNRDMCDGNSVLETDRGEECSVSTVNGRGASPNESASV
GLSKKLLLGSPSPLSPFTKRIKLEKEFDLPTPTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENG
SLRFSTPPGELDGGMSGRSGTGSGGSTPHLGGHGRPTSKDGRRSDTCEYCGKVFKNCSNLTVHRRSHTGERPYKCELCNY
ACAQSSKLTRHMKTHGQVGKDVFKCEICQMPFSVYSTLEKHMKKWHSDRPLSTEIKSE
```

479 - 498:	EEEEEEEEEEEEEEEEEEEE
480 - 499:	EEEEEEEEEEEEEEEEEEEE
481 - 500:	EEEEEEEEEEEEEEEEEEEE
482 - 501:	EEEEEEEEEEEEEEEEEEEE
483 - 502:	EEEEEEEEEEEEEEEEEEEE
484 - 503:	EEEEEEEEEEEEEEEEEEEE
485 - 504:	EEEEEEEEEEEEEEEEEEEE

A0A3Q3GW10 **A0A3Q3GW10_9LABR** (1655 aa)
[Histone H3]-trimethyl-L-lysine(9) demethylase (EC 1.14.11.66). *Labrus bergylta (ballan wrasse)*

```
MAGAEVFTPANPTCKIMTFRPTMEEFQNFNQYLVYMESQGAHRAGLAKVIPPKGWKPRRTYDDIDDLMIDAPIQQMVAGQ
SGLFTQYNIQKKPLSVQEFRRLANSDMYCTPRYLNYEDLERKYWKNLTFVSPIYGADVSGSLYDEDVEEWNIGHLNSILD
VIEEDCGVSIQGVNTPYLYFGMWKTTFSWHTEDMDLYSINYLHFGEPKSWYAIPPEHGKRLERLATGFFPNSFKSCEAFL
RHKMTLISPSILKKYGIPFDKITQEAGEFMVTFPYGYHAGFNHGFNCAESTNFATVRWIDYGKVATQCTCSRDMVKISME
PFVKRFQPDRYPNWMLGKDSTPIDHTHPTPGSTPELQSWLQSRRKTKPANKGSHSRMRSKRLRTTEEPVGLDGSSALNST
KRKGLGGPLGPKVRRSASGATCREEEKEKKKEAESKHNQNHNYFQLPGPCRQMCVVKVNRVESNGLGFSTKGPSDNSPCS
TFTSAASTVKNDPNAKTDTHIDPPHLSGSGVPSRTPEGLRPWPEAAQIHPGNNEPRCCSPEPQDLSTLQGCSIRVPPREA
NRLSSPSHTTSSSAEPEMSLCPPDCEAQAPSSSCREDTLSLMPNTDSYMATGSEKNTNNAANAEKMDTVAEPKCIKPHSN
AEALYNVKTEPVEGKGHTSCGPFMDLEKSNTEENLFPPLLQRNAVDMPQLTPEPADKLGICPLPPPVLTQEMPSLTPAND
GLRDVPKSRRCRDHVAPVLQRETPTGSPSSHGERETDPMTAKKEPLAVKLANNWHSDSPYNCTGAAVSVSEGNMAHLTTN
ATHRITSGGVHEMLITAGIAAERAHTELENVTAGQTEASPRQLVQSASSQTEQQYSLAELANKDNSKDPVQRGGASSLSR
AGSLLSGSSNNNPPAPSPAVCTQSDSHSASQHNTTYPPSLCATQNSYLEPKPFSSSIWKNFNSQSPAVLIQSLNPDLPSD
FTHDTLPYTMWTEPQCKEVTDLDDAHQGLRESESLEEEAGPLTWAQLEPTSLVSVGALEPMGICGDYELHRGEAEGSEAL
SLCRELERQRDAEESLHSDTSVSPLGVAGGEQDGVSDMEEGGSDGDEMEQQSIAKGESSSDSSDEEEEEEEEEEEEEEEE
EEEEEEEEDNTTNFKCDELGLEPGEYPALSVKRTSKSWRHPLRKPTARAVPTAVKQQVASDDEPTEATLAEEEEEEQEIE
AWAKPLIYLWQNRKSCFTAEREYNAHSATMEPFCAVCTLFMPYYQVEDKAEDNSSIAAEDCATPSSPVEGPTRPCRSLRR
TKPLVPEICFSFREQNCPPTPTNPLLQEDGTSPLLYCQGCCLQVHASCYGVAADDVGEQWSCDRCTEGSFTAECCLCNLR
GGALKKTQNDKWAHIMCAVALPEARFSDEAKRAPIDTSRIPMQRYKLRCIYCRKRCGGKRQAGACIQCSCGRCPTSFHVT
CAHAAGVTMEPDDWPYVVSITCHRHQSRSSSAKQRACQASIALGQTVISKHKNLRYYSSKVTQITSQTFYEVMFDDGSFS
NDTYPEDIVSRDCVNLGPPEVGEAVQVKWPDGLFYGAKYLGSNVSYMYQVEFEDGSQVLAKRDDVYTLDEDLPKKVKRRL
STASSMRFQDAFFTTQGERKRQRTPNSRFQNDYVALPGLRTTAKSTWEQRSHKGK
```

1105 - 1124:	EEEEEEEEEEEEEEEEEEEE
1106 - 1125:	EEEEEEEEEEEEEEEEEEEE
1107 - 1126:	EEEEEEEEEEEEEEEEEEEE
1108 - 1127:	EEEEEEEEEEEEEEEEEEEE
1109 - 1128:	EEEEEEEEEEEEEEEEEEEE

A0A3Q3H334 **A0A3Q3H334_9LABR** (1615 aa)
[Histone H3]-trimethyl-L-lysine(9) demethylase (EC 1.14.11.66). *Labrus bergylta (ballan wrasse)*

```
MAGAEVFTPANPTCKIMTFRPTMEEFQNFNQYLVYMESQGAHRAGLAKVIPPKGWKPRRTYDDIDDLMIDAPIQQMVAGQ
SGLFTQYNIQKKPLSVQEFRRLANSDMYCTPRYLNYEDLERKYWKNLTFVSPIYGADVSGSLYDEDVEEWNIGHLNSILD
VIEEDCGVSIQGVNTPYLYFGMWKTTFSWHTEDMDLYSINYLHFGEPKSWYAIPPEHGKRLERLATGFFPNSFKSCEAFL
RHKMTLISPSILKKYGIPFDKITQEAGEFMVTFPYGYHAGFNHGFNCAESTNFATVRWIDYGKVATQCTCSRDMVKISME
PFVKRFQPDRYPNWMLGKDSTPIDHTHPTPGSTPELQSWLQSRRKTKPANKGSHSRMRSKRLRTTEEPVGLDGSSALNST
KRKGLGGPLGPKVRRSASGATCREEEKEKKKEAESKHNQNHNYFQLPGPCRQMCVVKVNRVESNGLGFSTKGPSDNSPCS
TFTSAASTVKNDPNAKTDTHIDPPHLSGSGVPSRTPEGLRPWPEAAQIHPGNNEPRCCSPEPQDLSTLQGCSIRVPPREA
NRLSSPSHTTSSSAEPEMSLCPPDCEAQAPSSSCREDTLSLMPNTDSYMATGSEKNTNNAANAEKMDTVAEPKCIKPHSN
AEALYNVKTEPVEGKGHTSCGPFMDLEKSNTEENLFPPLLQRNAVDMPQLTPEPADKLGICPLPPPVLTQEMPSLTPAND
GLRDVPKSRRCRDHVAPVLQRETPTGSPSSHGERETDPMTAKKEPLAVKLANNWHSDSPYNCTGAAVSVSEGNMAHLTTN
```

```
ATHRITSGGVHEMLITAGIAAERAHTELENVTAGQTEASPRQLVQSASSQTEQQYSLAELANKDNSKDPVQRGGASSLSR
AGSLLSGSSNNNPPAPSPAVCTQSDSHSASQHNTTYPPSLCATQNSYLEPKPFSSSIWKNFNSQSPAVLIQSLNPDLPSD
FTHDTLPYTMWTEPQCKEVTDLDDAHQGLRESESLEEEAGPLTWAQLEPTSLVSVGALEPMGICGDYELHRGEAEGSEAL
SLCRELERQRDAEESLHSDTSVSPLGVAGGEQDGVSDMEEGGSDGDEMEQQSIAKGESSSDSSDEEEEEEEEEEEEEEEE
EEEEEEEEDNTTNFKCDELGLEPGEYPALSVKRTSKSWRHPLRKPTARAVPTAVKQQVASDDEPTEATLAEEEEEEQEIE
AWAKPLIYLWQNRKSCFTAEREYNAHSATMEPFCAVCTLFMPYYQVEDKAEDNSSIAAEDCATPSSPVEGPTRPCRSLRR
TKPLVPEICFSFREQNCPPTPTNPLLQEDGTSPLLYCQGCCLQVHASCYGVAADDVGEQWSCDRCTEGSFTAECCLCNLR
GGALKKTQNDKWAHIMCAVALPEARFSDEAKRAPIDTSRIPMQRYKLRCIYCRKRCGGKRQAGACIQCSCGRCPTSFHVT
CAHAAGVTMEPDDWPYVVSITCHRHQSRSSSAKQRACQASIALGQTVISKHKNLRYYSSKVTQITSQTFYEVMFDDGSFS
NDTYPEDIVVEFEDGSQVLAKRDDVYTLDEDLPKKVKRRLSTASSMRFQDAFFTTQGERKRQRTPNSRFQNDYVALPGLR
TTAKSTWEQRSHKGK
```

1105 - 1124:	EEEEEEEEEEEEEEEEEEEE
1106 - 1125:	EEEEEEEEEEEEEEEEEEEE
1107 - 1126:	EEEEEEEEEEEEEEEEEEEE
1108 - 1127:	EEEEEEEEEEEEEEEEEEEE
1109 - 1128:	EEEEEEEEEEEEEEEEEEEE

A0A3Q3H3V4 **A0A3Q3H3V4_9LABR** (1624 aa)
[Histone H3]-trimethyl-L-lysine(9) demethylase (EC 1.14.11.66). *Labrus bergylta (ballan wrasse)*

```
MAGAEVFTPANPTCKIMTFRPTMEEFQNFNQYLVYMESQGAHRAGLAKVIPPKGWKPRRTYDDIDDLMIDAPIQQMVAGQ
SGLFTQYNIQKKPLSVQEFRRLANSDMYCTPRYLNYEDLERKYWKNLTFVSPIYGADVSGSLYDEDVEEWNIGHLNSILD
VIEEDCGVSIQGVNTPYLYFGMWKTTFSWHTEDMDLYSINYLHFGEPKSWYAIPPEHGKRLERLATGFFPNSFKSCEAFL
RHKMTLISPSILKKYGIPFDKITQEAGEFMVTFPYGYHAGFNHGFNCAESTNFATVRWIDYGKVATQCTCSRDMVKISME
PFVKRFQPDRYPNWMLGKDSTPIDHTHPTPGSTPELQSWLQSRRKTKPANKGSHSRMRSKRLRTTEEPVGLDGSSALNST
KRKGLGGPLGPKVRRSASGATCREEEKEKKKEAESKHNQNHNYFQLPGPCRQMCVVKVNRVESNGLGFSTKGPSDNSPCS
TFTSAASTVKNDPNAKTDTHIDPPHLSGSGVPSRTPEGLRPWPEAAQIHPGNNEPRCCSPEPQDLSTLQGCSIRVPPREA
NRLSSPSHTTSSSAEPEMSLCPPDCEAQAPSSSCREDTLSLMPNTDSYMATGSEKNTNNAANAEKMDTVAEPKCIKPHSN
AEALYNVKTEPVEGKGHTSCGPFMDLEKSNTEENLFPPLLQRNAVDMPQLTPEPADKLGICPLPPPVLTQEMPSLTPAND
GLRDVPKSRRCRDHVAPVLQRETPTGSPSSHGERETDPMTAKKEPLAVKLANNWHSDSPYNCTGAAVSVSEGNMAHLTTN
ATHRITSGGVHEMLITAGIAAERAHTELENVTAGQTEASPRQLVQSASSQTEQQYSLAELANKDNSKDPVQRGGASSLSR
AGSLLSGSSNNNPPAPSPAVCTQSDSHSASQHNTTYPPSLCATQNSYLEPKPFSSSIWKNFNSQSPAVLIQSLNPDLPSD
FTHDTLPYTMWTEPQCKEVTDLDDAHQGLRESESLEEEAGPLTWAQLEPTSLVSVGALEPMGICGDYELHRGEAEGSEAL
SLCRELERQRDAEESLHSDTSVSPLGVAGGEQDGVSDMEEGGSDGDEMEQQSIAKGESSSDSSDEEEEEEEEEEEEEEEE
EEEEEEEEDNTTNFKCDELGLEPGEYPALSVKRTSKSWRHPLRKPTARAVPTAVKQQVASDDEPTEATLAEEEEEEQEIE
AWAKPLIYLWQNRKSCFTAEREYNAHSATMEPFCAVCTLFMPYYQVEDKAEDNSSIAAEDCATPSSPVEGPTRPCRSLRR
TKPLVPEICFSFREQNCPPTPTNPLLQEDGTSPLLYCQGCCLQVHASCYGVAADDVGEQWSCDRCTEGSFTAECCLCNLR
GGALKKTQNDKWAHIMCAVALPEARFSDEAKRAPIDTSRIPMQRYKLRCIYCRKRCGGKRQAGACIQCSCGRCPTSFHVT
CAHAAGVTMEPDDWPYVVSITCHRHQSRSSSAKQRACQASIALGQTVISKHKNLRYYSSKVTQITSQTFYEVMFDDGSFS
NDTYPEDIVSRDCVNLGPPEVGEAVQVKWPDGLFYGAKYLGSNVSYMYQSTASSMRFQDAFFTTQGERKRQRTPNSRFQN
DYVALPGLRTTAKSTWEQRSHKGK
```

1105 - 1124:	EEEEEEEEEEEEEEEEEEEE
1106 - 1125:	EEEEEEEEEEEEEEEEEEEE
1107 - 1126:	EEEEEEEEEEEEEEEEEEEE
1108 - 1127:	EEEEEEEEEEEEEEEEEEEE
1109 - 1128:	EEEEEEEEEEEEEEEEEEEE

A0A3Q3H400 **A0A3Q3H400_9LABR** (402 aa)
Autophagy_act_C domain-containing protein. *Labrus bergylta (ballan wrasse)*

```
MKPSPHAVTTQRLYNNLRLVFPDSPTRASAFLMVVNKVGQALEPSTPIRRNEAVLLSIIRTHPKKKKKRRRRRRKRRRKK
RRRKRRKRKRRRKRRKRRRKRRRRKRRRRRKRRRKRRKRRRRRRRKKRRRKRRKRKRRRKRRKRRRKRRRKGGGGGRGG
GRGGRGGGGGGGRGGGRGGGGRGGRGGGRRGGGRGGRGGGRGGRGGGRGGGGGRGGGRGGRGGGGGGGRRGGG
RGGRGRGGGRGGRGGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEKRRRRRKRRRKRRKRRRRKRRRKRRRRKRKRRRKRRRRKRRRKRRKRRRRKRRRKRRKRRRRKRKRRR
SL
```

256 - 275:	EEEEEEEEEEEEEEEEEEEE
257 - 276:	EEEEEEEEEEEEEEEEEEEE
258 - 277:	EEEEEEEEEEEEEEEEEEEE
259 - 278:	EEEEEEEEEEEEEEEEEEEE
260 - 279:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE
262 - 281:	EEEEEEEEEEEEEEEEEEEE
263 - 282:	EEEEEEEEEEEEEEEEEEEE
264 - 283:	EEEEEEEEEEEEEEEEEEEE
265 - 284:	EEEEEEEEEEEEEEEEEEEE
266 - 285:	EEEEEEEEEEEEEEEEEEEE
267 - 286:	EEEEEEEEEEEEEEEEEEEE
268 - 287:	EEEEEEEEEEEEEEEEEEEE

269 - 288:	EEEEEEEEEEEEEEEEEEEE
270 - 289:	EEEEEEEEEEEEEEEEEEEE
271 - 290:	EEEEEEEEEEEEEEEEEEEE
272 - 291:	EEEEEEEEEEEEEEEEEEEE
273 - 292:	EEEEEEEEEEEEEEEEEEEE
274 - 293:	EEEEEEEEEEEEEEEEEEEE
275 - 294:	EEEEEEEEEEEEEEEEEEEE
276 - 295:	EEEEEEEEEEEEEEEEEEEE
277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE
287 - 306:	EEEEEEEEEEEEEEEEEEEE
288 - 307:	EEEEEEEEEEEEEEEEEEEE
289 - 308:	EEEEEEEEEEEEEEEEEEEE
290 - 309:	EEEEEEEEEEEEEEEEEEEE
291 - 310:	EEEEEEEEEEEEEEEEEEEE
292 - 311:	EEEEEEEEEEEEEEEEEEEE
293 - 312:	EEEEEEEEEEEEEEEEEEEE
294 - 313:	EEEEEEEEEEEEEEEEEEEE
295 - 314:	EEEEEEEEEEEEEEEEEEEE
296 - 315:	EEEEEEEEEEEEEEEEEEEE
297 - 316:	EEEEEEEEEEEEEEEEEEEE
298 - 317:	EEEEEEEEEEEEEEEEEEEE
299 - 318:	EEEEEEEEEEEEEEEEEEEE
300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE
306 - 325:	EEEEEEEEEEEEEEEEEEEE
307 - 326:	EEEEEEEEEEEEEEEEEEEE
308 - 327:	EEEEEEEEEEEEEEEEEEEE
309 - 328:	EEEEEEEEEEEEEEEEEEEE
310 - 329:	EEEEEEEEEEEEEEEEEEEE
311 - 330:	EEEEEEEEEEEEEEEEEEEE
312 - 331:	EEEEEEEEEEEEEEEEEEEE
313 - 332:	EEEEEEEEEEEEEEEEEEEE

A0A3Q3JKM4 **A0A3Q3JKM4_MONAL** (2565 aa)
Histone-lysine N-methyltransferase, H3 lysine-36 and H4 lysine-20 specific-like. *Monopterus albus (Swamp eel)*

```
MSSPYAGPGRETHQSSCPLTPGCDISTHSCSSRHHDHKISLSMSAAASSLKHASIYGFAPRVHSSSSSSSYSPLRRLQHL
TSMVSQPDLVLPVREPERSWEWGTHKKERGKAMERESWADCTSRDYSGSHNTSREESVGNSSAGQKQPEGRTGCRDVPAA
NHSDHVTEAKKSESCFSDPPSPAFSLDSNSPFTNGFLHFESSLFEDDDNNEMRETTSPIGDLQDKHERAGSVLQSTPADL
NSDTKDATLLSAKVITRSQSSGQRRRYWYCSDDEWESDAELLLFGDSPSRHSVNSLKKKSLPPVKFLEHEVIWAKFGRRP
WWPCEVIIDPVQGTYHRMKEPSDRPCRLYHVRTFGEPVEFIWVEEKSTHAFHGGFEFEQLLLLRRRGKQRDHNYKYTIAK
RFQDSWKSSVAEAESVLPERPKMVSSISSSLDDAFHDSSTSERENKACPTLSSSTSPVCTLPETLHVTNGSISSPVTTPP
KQSTLRKSSGKKKQRKLLKGVSSKHSKNMLRNSPDPSDRDNGECPYSDLDSIPKILCPKALERQPKLVQTQPSAMVVKEV
KKQPEIQSGLWFSKSGKDRRPKTTSPMPDRTLFSKVPCKKKNSSVFCKRMLSSSGGPSDQSGFLDKHKTLAETNLPPEES
GHFKCKNTLVANRPFGTSGSLADPSGLPDKEKSLASTETTVPSDKCQHSKCRQTPNNTTDTIIGMPSGQFGSSDVKKALE
```

```
PSTKVTFDDQPRLLESVKSISRTKHSDVVAKKKVHVIERISNQAEAKESNNAALSGVNARTTDQLGRLEKQTSLVSKCRL
PFVKLIRKDIKGKKFKSSNSSDQPSRTKKEKTPDNNLTKMSSKQSHWVDSKANVSTAQANSSVSLKVSVKKLKASDGSGV
LRLSSESSPEETVMTTDLTSVSVDSTHLSGSPVLNVSPSNVTCPSSNQLDRSESKKTPTTNGTSMTYDELVSSEKKNTTA
TNTAYNTNRASHRQRNALSRNVSKGLLSEKSKKVLYKLKQVPDDMNQVLREQPAHLPASSRLMTRALKAMQEAEQKKREK
AGKETEQKGLLNSFRKAEDTVCHSACSSTWNPEAKLGSCTKRKSLKSHYNDIVEYDQDTFSSCSTPSLVFSDSVDFEADV
KSEDEDLSISSTPPMDFIPLTSRVKAKKDNHSSDICSSYSPPSPFSFMNAFKNVKEVSFQSLASEANGKPISFKPDTNYK
FSTFLMMLKDLHDTREREGAPLELEIGPPCAHVKEEPLVMPGEVKPAGQDQRIEYVNNLNSSPEKNMITHKEDSTSRMWK
RPYNRRGTSTRLKKKASRKVPCRSARSGPGFPGLESLPEVATLPTVDSSSRVDCSSKVQSLLGTQASSWERQNGGLEEMV
QEEEEDEEGWSRVNENLRNMVPLEQRGCNTTLFLGQPNGLVADCTETKTSLMHNTGGCDEAPAAHKRIRKPSKRLIEWTQ
EYDQIFSTRKKTKKPLQPSGKATQPITSMSEPLGSDKNTHDHLSMNLLPEIQTPPPEEIAATVPSELQISSSENTPPQDA
QVLSIDTLTPPPEAEPLLSESLAKDNENAPLLEKKRKRKPTQKILEYCLEAEASTGPRKKVKTVKNNSNLAPQSDSGPPS
LKSKSKQLSALTSAPTTPEVSTCTTTPSIQPNPAPSTPAATTPAPAPPEPDQVETASADVDAPQLEDSKDTAESEGDQSC
LDHSFSSINNDLALCDDPLLPSRKIIGDRGGPASMKENICQVCEKTGELLLCEGQCCGAFHLPCISLAQAPRGKFVCPEC
KSGIHTCFVCKKRSEDVRRCMIPVCGKFYHGECIANYAPTAPVNRGFRCSIHVCLTCFITNPNSSSISKGRLVRCVRCPV
AYHATDLCMAAGSVVLSNNSIVCPNHFTPRRGVKNHEHVNVSWCFVCTEGGSLLCCESCPAAFHCECLNIEMPKGSWYCN
DCKAGKKPRYKDILWVKVGRYRWWPAEVSHPKTIPENIQRMRHDVGEFPVHFFGSNDYLWTYQARVFPYMDVDANSREKM
GKGVDATYKKALEEAAVRFRELQAEKELRQLQEDRKNDRKPPPYKHIKVNRPIGKVQIFTADLSEIPRCNCKAKDESPCG
MDSECINRMLLYECHPQVCPAGERCLNQAFTKRQYSQVEIFRTLSRGWGLRCVHDIKKGQFVSEYVGEVIDEEECRSRIR
HAQENDICNFYMLTLDKDRIIDAGPKGNEARFMNHSCQPNCETQKWTVSGDTRVGLFALVDITAGTELTFNYNLECLGNG
KTVCKCGAPNCSGFLGVRPKNNPPSDDKGRKLKRRGHGKKKKKVVVTKEREDECFSCGDGGQMVSCKRPGCPKVYHADCL
NLTKRPAGRWECPWHQCDICGKEAASFCEMCPSSYCCQHRDGLLFISKLDGKLSCSEHDPCGPEPLEPGEIREYTPDPRA
LTSGLGMAIIPSATSNTTTSLNPTTRRVQEMSAGAGMCAAESFPAFSIPVPITIPVTAPAVSSPPGNSDAPSSPQVFDLP
HYSPISSYEEERDVLEDEEGEEELLEEVEEELAEEGEMGRQKSDPHEEDEEEEIEEVGLEYLEIKEEEEEEEEEEEEEEE
EEEEE
```

2546 - 2565:	EEEEEEEEEEEEEEEEEEE

A0A3Q3L8A3 **A0A3Q3L8A3_9TELE** (369 aa)
MYCN proto-oncogene, bHLH transcription factor. *Mastacembelus armatus (zig-zag eel)*

```
MPAITSKNSDLEFDSLQPCFYPDEDDFYFCGPDSAPPGEDIWKKFELLPTPPLSPSRAALPGEPAIASPEVDPLGFGLGD
PLDWASELLLLPEDDIWGASDDVDLFGSALDTNPNNIIIQDCMWSGFSAREKLERAVTEKLGKAISTATAGGRNVCVKAP
EVVSRSSVSECVDPTVVFPFPVNKKNGNRDSSGTVNTSTTHESAPSDSEEDDDEEEEEEEEEEEEEEEEEEEEEEEEIDV
VTLILKRSSVHQQQHNYAAPSTISSSSSSSSTSYSSPRGSDSEDSERRRNHNILERQRRNDLRSSFLTLRDHVPELAHNE
KAAKVLILKKATEYVSSLETEEMRLQQEKDRLHARRQQLMRRLDQARTR
```

214 - 233:	EEEEEEEEEEEEEEEEEEE
215 - 234:	EEEEEEEEEEEEEEEEEEE
216 - 235:	EEEEEEEEEEEEEEEEEEE
217 - 236:	EEEEEEEEEEEEEEEEEEE
218 - 237:	EEEEEEEEEEEEEEEEEEE

A0A3Q3LI94 **A0A3Q3LI94_9LABR** (663 aa)
Im:7142702. *Labrus bergylta (ballan wrasse)*

```
NLQNPAANPFHLTFHLRHKDEPSSYICTTCKQTFTSAWFLLQHAQHTHGIRIYLDNHLVNCSLTPRMALPPPPCTDALPR
SPLPTFLGDTNNPFHLLRMAAPLLREHPPATPRPPLERLGPEEMGLLSQHPSAFERVMRMAPMDPPSMDFSRRLRELAGN
TTNNGGPTPPLSPNRVPPMHRLLSPTLFQPGAKPPTFLTFAPQPPTSQGGHGSSTPPDPQGQNQTPGKSKSCEFCGKIFK
FQSNLIVHRRSHTGERPYKCHLCDHACSQASKLKRHMKTHMHNKSGSMSGSPEQGNRGEGEGEEKSRDGDSRGMIIDNEE
EEEEEEEEEEEEEEEEEELRNGCRTDSNLSEDLQEFGQNRENGTRQSPEGKPLSGDRGSDSAGMGIMHPYNHLDNHLRLN
PNKRSLERQPNGDGGDEHRPLMNGRMSVSEADSFPGLFQRRPTPITSQSPSNNKRIKIEKEQLELPPTIPLISPENVYSQ
LLAGYAASRHFIREPFLGFTDSRQSPFATSSEHSSSETGSLRFSTPPGELMEGGSASGRSGSSTPHLMRGPGPGRPPSSK
DRRNDTCEYCGKVFKNCSNLTVHRRSHTGERPYKCDLCSYACAQSSKLTRHMKTHGQFGKEVYRCDICHMPFSVYSTLEK
HMKKWHGEHLMASEVKLEQADRG
```

319 - 338:	EEEEEEEEEEEEEEEEEEE

A0A3Q3LP00 **A0A3Q3LP00_9TELE** (916 aa)
BAF chromatin remodeling complex subunit BCL11A a. *Mastacembelus armatus (zig-zag eel)*

```
MSRRKQGKPQHLSKRDFSPEPLSTAVVTSEELSERCLEHSEESSNLNGHHPGSTVGRLGRLGHDAHPSLEQDLLTCGQCQ
ATFPLADILLFIEHKRKRCHGLPCLSVGRGLDKPPSPSPGLALTPSPNLGSLRSRRPVEVGVQATLADDDDDRFSSPRGI
CPKQELLPGKEEPTTYTCTTCKQSYGSAWFLLQHAQNTHGFRIYLESEHGSPLTPRMGGPSSLGGGADCPSQPPLHGLHL
PPDASPFNLLRIPGSGSGGRDSVGAGGGIGAAGTAGGGHHQRFPPTPPLFSPPPRNHLDPHHLSPEELALAAHHPSAFDR
VLRLNPPLPLDPPPTMDFSRRLRELAGNTSGSTPPLSPSRPSPMQRLLQPFQTGGGSGGTGGAGSSKPPYLATPPPLPGS
MQSPVGSQTTPTTPLPSSGATTSSTTPMKSKCCEFCGKAFKFQSNLIVHRRSHTGEKPYKCHLCDHACTQASKLKRHMKT
HMHKSSSPNTGKSEDGLSTASSPEPGTSEHMGSASNALKSVVAKLKSENNRMLRENGEEEEEEEEEEEEEEEEEEEEEE
EEEGEEEEEQNGERAARRNNSYHFGLNLDAARQHENNGSIGSRLGAVADEGSIPRSLPEVMQGMGLAASMQHFSEALNAH
KRNAMAQENHLHHHLNRDHHHNREMCDGGSVLETDRGEEGSVSTVNGRGASPNESASVGLSKKLLLGSPSPLSPFSKRIK
LEKEFDLPTPTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRFSTPPGELDGGMSGRSGTG
SGGSTPHLGGPGRPSSKDGRRSDTCEYCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQSSKLTRHMKTHGQVGKDV
YKCEICQMPFSVYSTLEKHMKKWHSDRPLSTEIKSE
```

538 - 557:	EEEEEEEEEEEEEEEEEEE
539 - 558:	EEEEEEEEEEEEEEEEEEE
540 - 559:	EEEEEEEEEEEEEEEEEEE
541 - 560:	EEEEEEEEEEEEEEEEEEE
542 - 561:	EEEEEEEEEEEEEEEEEEE

543 - 562:	EEEEEEEEEEEEEEEEEEEE
544 - 563:	EEEEEEEEEEEEEEEEEEEE

A0A3Q3NRP4 **A0A3Q3NRP4_9LABR** (1598 aa)
[Histone H3]-trimethyl-L-lysine(9) demethylase (EC 1.14.11.66). *Labrus bergylta (ballan wrasse)*

```
MAGAEVFTPANPTCKIMTFRPTMEEFQNFNQYLVYMESQGAHRAGLAKVIPPKGWKPRRTYDDIDDLMIDAPIQQMVAGQ
SGLFTQYNIQKKPLSVQEFRRLANSDMYCTPRYLNYEDLERKYWKNLTFVSPIYGADVSGSLYDEDVEEWNIGHLNSILD
VIEEDCGVSIQGVNTPYLYFGMWKTTFSWHTEDMDLYSINYLHFGEPKSWYAIPPEHGKRLERLATGFFPNSFKSCEAFL
RHKMTLISPSILKKYGIPFDKITQEAGEFMVTFPYGYHAGFNHGFNCAESTNFATVRWIDYGKVATQCTCSRDMVKISME
PFVKRFQPDRYPNWMLGKDSTPIDHTHPTPGSTPELQSWLQSRRKTKPANKGSHSRMRSKRLRTTEEPVGLDGSSALNST
KRKGLGGPLGPKVRRSASGATCREEEKEKKKEAESKHNQNHNYFQLPGPCRQMCVVKVNRVESNGLGFSTKGPSDNSPCS
TFTSAASTVKNDPNAKTDTHIDPPHLSGSGVPSRTPEGLRPWPEAAQIHPGNNEPRCCSPEPQDLSTLQGCSIRVPPREA
NRLSSPSHTTSSSAEPEMSLCPPDCEAQAPSSSCREDTLSLMPNTDSYMATGSEKNTNNAANAEKMDTVAEPKCIKPHSN
AEALYNVKTEPVEGKGHTSCGPFMDLEKSNTEENLFPPLLQRNAVDMPQLTPEPADKLGICPLPPPVLTQEMPSLTPAND
GLRDVPKSRRCRDHVAPVLQRETPTGSPSSHGERETDPMTAKKEPLAVKLANNWHSDSPYNCTGAAVSVSEGNMAHLTTN
ATHRITSGGVHEMLITAGIAAERAHTELENVTAGQTEASPRQLVQSASSQTEQQYSLAELANKDNSKDPVQRGGASSLSR
AGSLLSGSSNNNPPAPSPAVCTQSDSHSASQHNTTYPPSLCATQNSYLEPKPFSSSIWKNFNSQSPAVLIQSLNPDLPSD
FTHDTLPYTMWTEPQCKEVTDLDDAHQGLRESESLEEEAGPLTWAQLEPTSLVSVGALEPMGICGDYELHRGEAEGSEAL
SLCRELERQRDAEESLHSDTSVSPLGVAGGEQDGVSDMEEGGSDGDEMEQQSIAKGESSSDSSDEEEEEEEEEEEEEEEE
EEEEEEEEDNTTNFKCDELGLEPGEYPALSVKRTSKSWRHPLRKPTARAVPTAVKQQVASDDEPTEATLAEEEEEEQEIE
AWAKPLIYLWQNRKSCFTAEREYNAHSATMEPFCAVCTLFMPYYQVEDKAEDNSSIAAEDCATPSSPVEGPTRPCRSLRR
TKPLVPEICFSFREQNCPPTPTNPLLQEDGTSPLLYCQGCCLQVHASCYGVAADDVGEQWSCDRCTEGSFTAECCLCNLR
GGALKKTQNDKWAHIMCAVALPEARFSDEAKRAPIDTSRIPMQRYKLRCIYCRKRCGGKRQAGACIQCSCGRCPTSFHVT
CAHAAGVTMEPDDWPYVVSITCHRHQSRSSSASRDCVNLGPPEVGEAVQVKWPDGLFYGAKYLGSNVSYMYQVEFEDGSQ
VLAKRDDVYTLDEDLPKKVKRRLSTASSMRFQDAFFTTQGERKRQRTPNSRFQNDYVALPGLRTTAKSTWEQRSHKGK
```

1105 - 1124:	EEEEEEEEEEEEEEEEEEEE
1106 - 1125:	EEEEEEEEEEEEEEEEEEEE
1107 - 1126:	EEEEEEEEEEEEEEEEEEEE
1108 - 1127:	EEEEEEEEEEEEEEEEEEEE
1109 - 1128:	EEEEEEEEEEEEEEEEEEEE

A0A3Q3R6E6 **A0A3Q3R6E6_MONAL** (921 aa)
B-cell lymphoma/leukemia 11A-like. *Monopterus albus (Swamp eel)*

```
MSRRKQGKPQHLSKRDFSPEPLSTAVVSSEVLSERCLEHSEDSGNLNGHHLGSTVGRLARLARLGHDAHPSLEQDLLTCG
QCQATFPLADILLFIEHKRKRCHGPPCLAVGRGLDKPPSPSPGLALTPSPSLASLRSRRPVEVGVQATLADEDDDRLTSP
RGICPKQEPLPGKEEPTTYTCTTCKQSYGSAWFLLQHAQNTHGFRIYLESEHGSPLTPRMGGPSSLGGGADCSSQPPLHG
LHLPPDASPFNLLRIPGSGSGGRDSAGAGGTVGATGTAGGAHHQRFPPTPPLFSPPPRNHLDPHHLSPEELALAAHHPSA
FDRVLRLNPPLPLDPPPTMDFSRRLRELAGNTSGSTPPLSPSRPSPMQRLLQPFQTGGGSGGTGVVGGNKPPYLATPPPL
PGSMQSPVGSQTTPTTPLPSSGVTPSSTTPMKSKCCEFCGKAFKFQSNLIVHRRSHTGEKPYKCHLCDHACTQASKLKRH
MKTHMHKSSSPNTGKSEDGLSTASSPEPGTSEHMASASNALKSVVAKLKSETDRMLRENGEEEEEEEEEEEEEEEEEEEE
EEEEEEEEREEEEEQNGLRTARRNNSYHFGLNLEPARQHENNGSIGSRLEAVTDEGSIPCSLPEVMQGMGLAATMQHFSD
ALNAHKRNAMVQENHLHHHLNRDHHHNHEMCDGGSVLETDRGEEGSVSTVNGRGASPNESASVGLSKKLLLGSPSPLSPF
SKRIKLEKEFDLPTPTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRFSTPPGELDGGMSG
RSGTGSGGSTPHLGGPGRPGSKDGRRSDTCEFCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQSSKLTRHMKTHGQ
VGKDVYKCEICQMPFSVYSTLEKHMKKWHSDRPLSTEIKSE
```

541 - 560:	EEEEEEEEEEEEEEEEEEEE
542 - 561:	EEEEEEEEEEEEEEEEEEEE
543 - 562:	EEEEEEEEEEEEEEEEEEEE
544 - 563:	EEEEEEEEEEEEEEEEEEEE
545 - 564:	EEEEEEEEEEEEEEEEEEEE
546 - 565:	EEEEEEEEEEEEEEEEEEEE
547 - 566:	EEEEEEEEEEEEEEEEEEEE
548 - 567:	EEEEEEEEEEEEEEEEEEEE
549 - 568:	EEEEEEEEEEEEEEEEEEEE

A0A3Q3R6F3 **A0A3Q3R6F3_MONAL** (851 aa)
B-cell lymphoma/leukemia 11A-like. *Monopterus albus (Swamp eel)*

```
MSRRKQGKPQHLSKRDFSRSTVGRLARLARLGHDAHPSLEQDLLTCGQCQATFPLADILLFIEHKRKRCHGPPCLAVGRG
LDKPPSPSPGLALTPSPSLASLRSRRPVEVGVQATLADEDDDRLTSPRGICPKQEPLPGKEEPTTYTCTTCKQSYGSAWF
LLQHAQNTHGFRIYLESEHGSPLTPRMGGPSSLGGGADCSSQPPLHGLHLPPDASPFNLLRIPGSGSGGRDSRFPPTPPL
FSPPPRNHLDPHHLSPEELALAAHHPSAFDRVLRLNPPLPLDPPPTMDFSRRLRELAGNTSGSTPPLSPSRPSPMQRGNK
PPYLATPPPLPGSMQSPVGSQTTPTTPLPSSGVTPSSTTPMKSKCCEFCGKAFKFQSNLIVHRRSHTGEKPYKCHLCDHA
CTQASKLKRHMKTHMHKSSSPNTGKSEDGLSTASSPEPGTSEHMASASNALKSVVAKLKSETDRMLRENGEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEREEEEEQNGLRTARRNNSYHFGLNLEPARQHENNGSIGSRLEAVTDEGSIPCSLPEVMQGMG
LAATMQHFSDALNAHKRNAMVQENHLHHHLNRDHHHNHEMCDGGSVLETDRGEEGSVSTVNGRGASPNESASVGLSKKLL
LGSPSPLSPFSKRIKLEKEFDLPTPTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRFSTP
PGELDGGMSGRSGTGSGGSTPHLGGPGRPGSKDGRRSDTCEFCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQSSK
LTRHMKTHGQVGKDVYKCEICQMPFSVYSTLEKHMKKWHSDRPLSTEIKSE
```

471 - 490:	EEEEEEEEEEEEEEEEEEEE

472 - 491:	EEEEEEEEEEEEEEEEEEEE
473 - 492:	EEEEEEEEEEEEEEEEEEEE
474 - 493:	EEEEEEEEEEEEEEEEEEEE
475 - 494:	EEEEEEEEEEEEEEEEEEEE
476 - 495:	EEEEEEEEEEEEEEEEEEEE
477 - 496:	EEEEEEEEEEEEEEEEEEEE
478 - 497:	EEEEEEEEEEEEEEEEEEEE
479 - 498:	EEEEEEEEEEEEEEEEEEEE

A0A3Q3W640 **A0A3Q3W640_MOLML** (848 aa)
BAF chromatin remodeling complex subunit BCL11A a. *Mola mola (Ocean sunfish) (Tetraodon mola)*

```
MSRRKQGKPQHLSKRDFSPGRSARLGHDAHPSLEQDLLTCGQCQTTFPLADILLFIEHKRKRCHGPPCLAVGRGLDKPPS
PSPGLALTPSPALGSLRARRPVEVGVQATLADDDNDRFSSPRGNCPKQEPLPGKEEPATYTCTTCKQSYGSAWFLLQHAQ
NIHGFRIYLESEHGSPLTPRMGGPSSLGGGADCPSQPPLHGLHLPPDASPFNLLRIPGSGSGGRDSRFPPTPPLFSPPPR
NHLDPHHLSPEELALAAHHPSAFDRVLRLNPPLPLDPPPTMDFSRRLRELAGNTSGSTPPLSPSRPSPMQRLLQPAKPPY
LATPPPLPGSMQSPVGSQTTPTTPLASAGATPSSTTPSKTKCCEFCGKAFKFQSNLIVHRRSHTGEKPYKCHLCDHACTQ
ASKLKRHMKTHMHKSSSPNTGKSEDGLSTASSPEPGTSEHMGSASNALKSVVAKLKSENDRMLRENGEEEEEEEEEEEEE
EEEEEEEEEEEEGEEEEEQNGERPARRNNNNNNNSYHFGLSLEATRQHENNGGIGSRLGADEGSIPRSLPEVMQGMGLAA
SMQHFSEALNAHKRNAMAQENHLHHHLNRDHHHSREMCDGNSVLETDRIEEGSVSTVNGRGASPNESASVGLSKKLLLGS
PSPLSPFSKRIKLEKEFDLPTPTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRFSTPPGE
LDGGLSGRSGTGSGGSTPHLGGPGRPSSKDGRRSDTCEFCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQSSKLTR
HMKTHGQIGKDVYKCEICQMPFSVYSTLEKHMKKWHSDRPLSTEIKSE
```

468 - 487:	EEEEEEEEEEEEEEEEEEEE
469 - 488:	EEEEEEEEEEEEEEEEEEEE
470 - 489:	EEEEEEEEEEEEEEEEEEEE
471 - 490:	EEEEEEEEEEEEEEEEEEEE
472 - 491:	EEEEEEEEEEEEEEEEEEEE
473 - 492:	EEEEEEEEEEEEEEEEEEEE

A0A3Q3WCD9 **A0A3Q3WCD9_MOLML** (738 aa)
BAF chromatin remodeling complex subunit BCL11A b. *Mola mola (Ocean sunfish) (Tetraodon mola)*

```
MSRRKQGKPQHLSKRDFSPEPLSGVLPEDDSQDSPRLGAGQGEPLKGDPDLLTCGQCHSRFPLADILLFIEHKRRQCHGS
LCTDKPLDRPPSSPLASVYHPVEVAVQVSPQDEDSLSAPLQGIIPKQENITVLHISLFYDDCSLHFSIFFLSVSLFLSDK
DEPSSYTCTTCKQPFTSAWFLLQHAQNTHGFRIYLESEPGSPLTPRVAAAPGMGGDCASSQPPLHAVHLADGSPYSLLRM
PGSGSGRDSASTPREGRYPRTPPLFSPPPRHHLSPDDLALATHHPSAFDRVMRLNSVPLEAPPSMDFSRRLRELAGNATG
ASPPLSPNRPNPMQRLLPPFQPGSKPPFSATPPLSTSQSPSGSRSTPNVISNAGQPGTPLKAKSCEFCGKTFKFQSNLIV
HRRSHTGEKPFKCQLCNHACTQASKLKRHMKTHCQNKSLVPNAKSDDGLSTTSSPEPGTSDLMGSATDALKSVVAKFKSE
NNGLISENGEEEEEEEEEEEEEEEEEEEEEEEEEEEDGEEEELESARHHQNSEALHPHRRSSSREPGDDDLAMESDRADDG
TTTINGLGPLSTDSLSRKLLGGRLSPGSLSPLSKRIKVEKDLDPPTPTIPNTENVYSQWLAGYAASRQLKDPFISFTGGD
SRQSPFASSSEHSSENGSLRFSTPPGELDGERVTSGRSGTGSGASTPHGNGRPSSKDGRRSDTCEFCGKVFKNCILASVS
FFFFFRLGPEPVSRFEEG
```

490 - 509:	EEEEEEEEEEEEEEEEEEEE
491 - 510:	EEEEEEEEEEEEEEEEEEEE
492 - 511:	EEEEEEEEEEEEEEEEEEEE
493 - 512:	EEEEEEEEEEEEEEEEEEEE
494 - 513:	EEEEEEEEEEEEEEEEEEEE
495 - 514:	EEEEEEEEEEEEEEEEEEEE
496 - 515:	EEEEEEEEEEEEEEEEEEEE

A0A3Q4HCW4 **A0A3Q4HCW4_NEOBR** (1667 aa)
Bromodomain and WD repeat-containing protein 3-like. *Neolamprologus brichardi (Fairy cichlid) (Lamprologus brichardi)*

```
RFLLSGPCKKAAKLVPQRWSWDGKKYKRNFQDWVVLNQHIPADYLLRICQRIGPLIEKEIPPSVPGVQTLLGLGRQSLLR
TSKSCSHKVCSGSAVAALHRGRPPEPPVSNGSSPNVVSIMGARQATGTGRFGQVLPSSSYQHMKIHKRILGHLSSVYCVA
FDRTGRRIFTGSDDCLVKIWATDDGRLLATLRGHSAEICDMAVNHENSLIASASCDKVIRVWCLRTCAPITVLQAHAASI
TSIQFCPAARGTTRYLASTGADGMVCFWKWHSLTMKFNDQPVKFMERSRPGVQVSTSSFSSGGMFMATGGTDHMIRVYYL
GAESPMKVSEMDAHTDKVVVVQFSNNSDSLRFVSGSRDGTVKIWHYQQQEWKSTTLDMAARLPGSTAATGDDKAKLVVTM
VAWDRTDSTVITAVSNYLLKVWSTSTGQLLHILSGHDDEVFVLEAHPFDSRIMLSAGHDGNIYIWDLTKGVKIRNFFNMI
EGQGHGAIFDCKFSADGQHFACTDSHGHLLIFGFGCSRPYEKIPDQMFFHTDYRPLIRDSNNYVLDEQTQQAPHLMPPPF
LVDVDGNPHPPHYQRLVPGRENCKEEQLIPQMGYMANNDGELVEQVLGQQTAENGESPLDNLIRQLQNEQDERQNAEREA
EGEEGAVPSSPVVAPRRSGQVDGVWQMQHNALPSQVATERDLLAWSRRVVVNEVLQGIFRVSEECRQAKGDIECSLYNAE
RKKKPVTCSDLLSSRLRSLRPTKKTNKRHAYQTRSAQIRRPGTRRRNPSNRRTSNSQMDSESDGEAEEQAEHTDASSDGD
ARWQSESSSSDSSSEYSDWTADAGINLQPPKRPTRRPVQPPDYSSSEEEEGDNEAKEARTREKEKRKKKSKETKQKPTSS
LGGLDAEEWLPPSWIMETVPRRSPFVPQMGDELIYFKQGHQAYVRAVRRAKAYSINPQKQPWNRLNLRDQESVKVVGIKY
EVGPPTLCCLKVAFLDPVSGKMTNESFSLKYHDMPDVIDFLVLQQFYNEAKEHNWQPGMRFRSIIDDAWWFGSVEDQEPL
QPEYPDSLFQCYAVKWDNGEREKMSPWDMEPIPEEAALPEQVGDGVEVAEEELKALLYEPQEGEWGAHTRDEECERVIHG
IDQLLTLDVAKAFALPVNLQDYPLYCTVVAYPTDLSSIRTRLENRFYRRISALMWEVRYIEHNARTFNEPQSPIVAAAKV
VTDVLLHYIGDQSCIDVLDLYRKLKSEVSSEAEVGFDLDVDSDTPGTSTGHRKRGVVLDPKAWRGQCRELLRRMTASTNS
EPFRQPVDLFEYPDYRDIIDTPMDLGTVSETLAVGNYENPMEFAKDIRLIFSNSKAYTPNKKSQIYTMTLSLSAFFEKHI
```

```
ISIISDYKSAIQNERRARQHLTYRNRLHNGGSSPPNSPSHRYTATFTNLDEEDVQPSSPTSGTSVRSRNQGPHRVTRSQA
TPVKKSGIASRSNSSSLESSSTSSSSSSSSSSSSSSSSDSDNSSDSEVEKYVEGGGDHDYSKAPCLSVRLSAKGKVAASG
KRRHKGGEDTEAQGPKRARLQLEVEEQEDDEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEPEDEDDNNSEVQTRAAAAPAAAS
SQRGSQCKSRRVNTRNQGRRTVRYGDDSEDDGHGSKDDPLNLGMSRSGRVRRMTEKARVSHLMGWSH
```

1551 - 1570:	EEEEEEEEEEEEEEEEEEEE
1552 - 1571:	EEEEEEEEEEEEEEEEEEEE
1553 - 1572:	EEEEEEEEEEEEEEEEEEEE
1554 - 1573:	EEEEEEEEEEEEEEEEEEEE
1555 - 1574:	EEEEEEEEEEEEEEEEEEEE
1556 - 1575:	EEEEEEEEEEEEEEEEEEEE
1557 - 1576:	EEEEEEEEEEEEEEEEEEEE
1558 - 1577:	EEEEEEEEEEEEEEEEEEEE

A0A3Q4HGE4 **A0A3Q4HGE4_NEOBR** (637 aa)
Protein ycf2-like. *Neolamprologus brichardi (Fairy cichlid) (Lamprologus brichardi)*

```
MTAKHRKAKNNHKHEDNIFKNEVMETEVRPGGNNYTLLLVLFLIFVIGGATGVWFCFQQYQTLTYLTDNLMGIQMKIGKL
QSSQEEMRQSGNKQHISDNVEARLNALEESYSLAQKQVGMALATAEQLKTSDLPAQVLSLHTEMKTRLAEMQQATVSLEQ
LSQLQTMLKGKSEEFEDVKMKVEVLATLTGELAQKVDILTGSLEEAESKLEEKVVEIATVSAALDRQAAVMLRLKEQLDA
YQTQLKASVVEMTTVRELFEHEQSQRLHQARVQELNVSVAETKPETKPLEKTEGETVPTTEEEAETKEEEEAAGSEEKEE
ETLVETEKRVETVETEKEALGSEEKVENVETDKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEALGTEKVE
DIDTEEETPIAAGEEEVAAPAESEEEETLPTADEKVTSTQEEEEAESDEPEELNTQDTAPVEKEESATEETVPTQQAEAV
EEDDAKQEKSVTVSEEEKGHTTLTEEEGHNAEEQMPEEENRKGDEEEAPEREKGEDDSTVQDESLKARDEDETVLEKEES
EDDEREKSEEHVPSGEEEQLWKAVLEAEQPDVEEEVSEAEDEQQETADEEENHGAEDPQEADEEEEFLEFDALPEDK
```

354 - 373:	EEEEEEEEEEEEEEEEEEEE
355 - 374:	EEEEEEEEEEEEEEEEEEEE
356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE
363 - 382:	EEEEEEEEEEEEEEEEEEEE
364 - 383:	EEEEEEEEEEEEEEEEEEEE
365 - 384:	EEEEEEEEEEEEEEEEEEEE
366 - 385:	EEEEEEEEEEEEEEEEEEEE
367 - 386:	EEEEEEEEEEEEEEEEEEEE
368 - 387:	EEEEEEEEEEEEEEEEEEEE
369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE

A0A3Q4HN71 **A0A3Q4HN71_NEOBR** (865 aa)
Im:7142702. *Neolamprologus brichardi (Fairy cichlid) (Lamprologus brichardi)*

```
MRWKLFGGRPGSHRHLEKRYLASDHHSRLSTPSPRRRASGEHDLLTCGQCQTNFPLGDILVFIEHKRRLCRGPIGRLGSF
SKPGAAGGVMGLPISPRARSLELGRGAIPVEVGVQVTPGGEEDQARRLTPAKGICPKQERGGKEIVAPAHIEEPHTPGPC
SMYMCTYIRTASDDVLVSSLMVIFFLSWSTEKDEPSSYICTTCKQTFTSAWFLLQHAQHTHGIRIYLDNHPVNCSLTPRM
ALPPPPGADALPRSPLPTFLGDANNPFHLLRMAAPQLRDHPHPPGYMETRLPATPPFVSPPPPPRPPRERLGPEEMGLLS
QHPSAFERVMRMTPMEPPPMDFSRRLRELAGNTTNNGGPTPPLSPNRVPPMHRLLSPTLFQPGSQLPPFLTYPPQPPTSQ
GGHGSSSPPDTQGQNQAPGKSKSCEFCGKIFKFQSNLIVHRRSHTGERPYKCHLCDHACSQASKLKRHMKTHMHNKSGAI
TGSPEQGNRGEGGEGEEKNREGDARGMGMDNEEEEEEEEEEEEEEEEEEEEELQNGSRPDSNLSEDSQEFTQNRENGSRQS
PSEKPPSGDRVNDSGGVGIILNPNKRSLERQPNGDGGEGVEGERENEREPDRQREEQEDQRPVMNGRISVSEAECFPGLF
QRRPTPITSPSPSNNKRIKIEKEQLEIPPTIPLISPENVYSQLLAGYAASRHFIREPFLGFTDSRQSPFATSSEHSSSET
GSLRFSTPPGELMEGGSASGRSGSSTPHLLRGPGPGRPPSSKERRNDTCEFCGKVFKNCSNLTVHRRSHTGERPYKCDLC
SYACAQSSKLTRHMKTHGQYGKEVYRCDICHMPFSVYSTLEKHMKKWHGEHLMASEVKLEQADRS
```

512 - 531:	EEEEEEEEEEEEEEEEEEEE

A0A3Q4HRV6 **A0A3Q4HRV6_NEOBR** (792 aa)

lm:7142702. *Neolamprologus brichardi (Fairy cichlid) (Lamprologus brichardi)*

```
LSLAIAAEKKGERASGEHDLLTCGQCQTNFPLGDILVFIEHKRRLCRGPIGRLGSFSKPGAAGGVMGLPISPRARSLELG
RGAIPVEVGVQVTPGGEEDQARRLTPAKGICPKQERGEKDEPSSYICTTCKQTFTSAWFLLQHAQHTHGIRIYLDNHPVN
CSLTPRMALPPPPGADALPRSPLPTFLGDANNPFHLLRMAAPQLRDHPHPPGYMETRLPATPPFVSPPPPPRPPRERLGP
EEMGLLSQHPSAFERVMRMTPMEPPPMDFSRRLRELAGNTTNNGGPTPPLSPNRVPPMHRLLSPTLFQPGSQLPPFLTYP
PQPPTSQGGHGSSSPPDTQGQNQAPGKSKSCEFCGKIFKFQSNLIVHRRSHTGERPYKCHLCDHACSQASKLKRHMKTHM
HNKSGAITGSPEQGNRGEGGEGEEKNREGDARGMGMDNEEEEEEEEEEEEEEEEEEEEEELQNGSRPDSNLSEDSQEFTQNR
ENGSRQSPSEKPPSGDRVNDSGGVGIILNPNKRSLERQPNGDGGEGVEGERENEREPDRQREEQEDQRPVMNGRISVSEA
ECFPGLFQRRPTPITSPSPSNNKRIKIEKEQLEIPPTIPLISPENVYSQLLAGYAASRHFIREPFLGFTDSRQSPFATSS
EHSSSETGSLRFSTPPGELMEGGSASGRSGSSTPHLLRGPGPGRPPSSKERRNDTCEFCGKVFKNCSNLTVHRRSHTGER
PYKCDLCSYACAQSSKLTRHMKTHGQYGKEVYRCDICHMPFSVYSTLEKHMKKWHGEHLMASEVKLEQADRS
```

439 - 458:	EEEEEEEEEEEEEEEEEEEE

A0A3Q4I444 **A0A3Q4I444_NEOBR** (816 aa)
lm:7142702. *Neolamprologus brichardi (Fairy cichlid) (Lamprologus brichardi)*

```
MRWKLFGGRPGSHRHLEKRYLASDHHSRLSTPSPRRRASGEHDLLTCGQCQTNFPLGDILVFIEHKRRLCRGPIGRLGSF
SKPGAAGGVMGLPISPRARSLELGRGAIPVEVGVQVTPGGEEDQARRLTPAKGICPKQERGEKDEPSSYICTTCKQTFTS
AWFLLQHAQHTHGIRIYLDNHPVNCSLTPRMALPPPPGADALPRSPLPTFLGDANNPFHLLRMAAPQLRDHPHPPGYMET
RLPATPPFVSPPPPPRPPRERLGPEEMGLLSQHPSAFERVMRMTPMEPPPMDFSRRLRELAGNTTNNGGPTPPLSPNRVP
PMHRLLSPTLFQPGSQLPPFLTYPPQPPTSQGGHGSSSPPDTQGQNQAPGKSKSCEFCGKIFKFQSNLIVHRRSHTGERP
YKCHLCDHACSQASKLKRHMKTHMHNKSGAITGSPEQGNRGEGGEGEEKNREGDARGMGMDNEEEEEEEEEEEEEEEEEE
EELQNGSRPDSNLSEDSQEFTQNRENGSRQSPSEKPPSGDRVNDSGGVGIILNPNKRSLERQPNGDGGEGVEGERENERE
PDRQREEQEDQRPVMNGRISVSEAECFPGLFQRRPTPITSPSPSNNKRIKIEKEQLEIPPTIPLISPENVYSQLLAGYAA
SRHFIREPFLGFTDSRQSPFATSSEHSSSETGSLRFSTPPGELMEGGSASGRSGSSTPHLLRGPGPGRPPSSKERRNDTC
EFCGKVFKNCSNLTVHRRSHTGERPYKCDLCSYACAQSSKLTRHMKTHGQYGKEVYRCDICHMPFSVYSTLEKHMKKWHG
EHLMASEVKLEQADRS
```

463 - 482:	EEEEEEEEEEEEEEEEEEEE

A0A3Q4MR11 **A0A3Q4MR11_NEOBR** (852 aa)
B-cell lymphoma/leukemia 11A-like. *Neolamprologus brichardi (Fairy cichlid) (Lamprologus brichardi)*

```
MSRRKQGKPQHLSKRDFSLNGHHPGSNVGRLARLGHDAHPSLEQDLLTCGQCQATFPLADILLFIEHKRKRCHGPPCLTV
GRGLDKPPSPSPGLALTPSPAMGSLRSRRLEVGVQATLADEDDDRFSSPRGICPKQEPLPGKEEPTTYTCTTCKQSYGSA
WFLLQHAQNTHGFRIYLESEHGSPLTPRMGGPSSLGGGADCPSQPPLHGLHLPPDASPFNLLRIPGSGSGGRDSRFPPTP
PLFSPPPRNHLDPHHLSPEELALAAHHPSAFDRVLRLNPPLPLDPPPTMDFSRRLRELAGNTSGSTPPLSPSRPSPMQRL
LHKPPYLATPPPLPGSMQSPVGSQTTPTTPLPSTGATPSSTTQLKSKCCEFCGKAFKFQSNLIVHRRSHTGEKPYKCHLC
DHACTQASKLKRHMKTHMHKSSSPNTGKSEDGLSTASSPEPGTSEHVGSASNALKSVVAKLKSENDRMLRENGEEEEEEE
EEEEEEEEEEEEEEEEEEGEEEEEQNGERVARRNNNSYHFGLNLETARQHENNGSIGSRLGGVADEGSIPRSLPEVMQGM
GLAASMQHFSEALNAHKRNAMAQENHLHHHLNRDHHHNREICDGDSVLETDRGEEGSVSTVNGRGASPNESASVGLSKKL
LLGSPSPLSPFSKRIKLEKEFDLPTSTIPNTENVYSQWLAGYAASRQLKDPFLNFGDSRQSPFASSSEHSSENGSLRFST
PPGELDGGMSGRSGTGSGGSTPHLGGPGRPSSKDGRRSDTCEFCGKVFKNCSNLTVHRRSHTGERPYKCELCNYACAQSS
KLTRHMKTHGQVGKDVYKCEICQMPFSVYSTLEKHMKKWHSDRPLSTEIKSE
```

474 - 493:	EEEEEEEEEEEEEEEEEEEE
475 - 494:	EEEEEEEEEEEEEEEEEEEE
476 - 495:	EEEEEEEEEEEEEEEEEEEE
477 - 496:	EEEEEEEEEEEEEEEEEEEE
478 - 497:	EEEEEEEEEEEEEEEEEEEE
479 - 498:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7HD19 **A0A3Q7HD19_SOLLC** (136 aa)
Uncharacterized protein. *Solanum lycopersicum (Tomato) (Lycopersicon esculentum)*

```
MGLRKSNTDAYMPMLISIGPCQKRNHELCSMEKYKLLYLPRFLQRKEGLDVESCISSLEKKKDETLQCYDDNLNTDIVDI
SLEMLLLDGCFVVESIREYYATDEEEEEEEEEEEEEEEEEEEEEEEDDNNNIINLE
```

104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7I509 **A0A3Q7I509_SOLLC** (221 aa)
Uncharacterized protein. *Solanum lycopersicum (Tomato) (Lycopersicon esculentum)*

```
MQNPYYVIEKKLLIYPHYQSITITAISRIIFFYYSCMIIIISSLQQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEDFPSINFIRTRTSLSSLGGIRSTITSGRLFFTLEICNRPFSRTISRSNLGRPFSFIL
NKSGGKFLTVGEGELVHFVFDLDLDLRSSNSSELQFDFSLKLSNPRVSVIVCNEMLSRGLL
```

47 - 66:	EEEEEEEEEEEEEEEEEEEE

48 - 67:	EEEEEEEEEEEEEEEEEEEE
49 - 68:	EEEEEEEEEEEEEEEEEEEE
50 - 69:	EEEEEEEEEEEEEEEEEEEE
51 - 70:	EEEEEEEEEEEEEEEEEEEE
52 - 71:	EEEEEEEEEEEEEEEEEEEE
53 - 72:	EEEEEEEEEEEEEEEEEEEE
54 - 73:	EEEEEEEEEEEEEEEEEEEE
55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE
64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7MEI6 **A0A3Q7MEI6_CALUR** (1333 aa)
splicing factor, arginine/serine-rich 19 isoform X1. *Callorhinus ursinus (Northern fur seal)*

```
MEEEDESRGKTEESGEDRGDGPPDRDPTLSPSAFILRAIQQAVGSSLQGDLPNDKDGSRCHGLRWRRCRSPRSEPRSQES
GGTDTATVLDMAADSFLTGLVSVLDPPDTWVPSHLDLRPGESEDMLELVAEVRIGDRDPIPLPVPSLLPRLRAWRTGKTV
SPQPHSSRPSCARHLLTLGTGDGGPAPPPAPSSASSSPSPSPSSSSPSPPPPPPPPAPPAPPAPRFDIYDPFHPTDEAYS
PPPAPEQKYDPFEPTGSNPSSSAGTPSPEEEEEEEEEEEEEEEEEEEEEEEGLSQSISRISETLAGIYDDNSLSQDFPGD
ESPRPDPQPPQPTPAPGTPPQVDSTRVDGATRRRVFVVGTEAEACREGKVSVEVVTAGGAAIPPTLLPPGDSEIEEGEIV
QPEEEPRVAVSLFRAAGGGGGGGGGRAARPPPAVAAPPAAQPPPPPPAARAPEGDDFLSLHAESDGEGALQVDLGEPAP
APPAADTRWGGLDLRRKILTQRRERYRQRSPSPAVAAAAAAAAAAAAAAAAAAAAAPAGPPTRKKSRRERKRSGGEAKEAA
SSSSGAPSAPPAPASPWDSKKHRSRDRKPGSHASASARRRSRSRSARRRSRSADRRRGGSRRSRSREKRRRRRRSASPPP
ATSSSSSSRRERHRGKHRDGGGSKKKKKRSRSRGEKRSGDSEKAPVPTQPPSGSSSLGGERDSRRRGAVPPSIQDLTDHD
LFAIKRTITVGRPDKSDPRGPSPAPASSPKREVLYDSEGLSAEERGGKSSEKDRRRSGAASSSSSSREKGSRRKALDGGD
RDRDRDRDRDRSSKKARPPKESAPSSGPPPKPPVSSGSGSSSSSCSSSSRKVKLQSKVAVLIREGVSSTTPAKEAASAGL
GSIGVKFSRDRESRSPFLKPDERAPAEVAKAAPGSTKPKKTKVKAKAGAKKAKGTKGKTKPSKTRKKIRGGGSGGGGGGP
VTLKKSKADSCSQAAGAKGVEETSWSGEERAAKAPSTPPPKAAPPPPALTPDSQTVDSSCKTPEVSFLPEEATEEAGVRG
GAEEEEEEEEEEEEEEEEEEQQPATTTATSTAAAAPSTAPSAGSTAGDSGAEDGPATRVSQLPTLPPPMPWNLPAGVDCT
TSGVLALTALLFKMEEANLASRAKAQELIQATNQILSHRKPPSSLGVTPTPVPTSLGLPPGPSSYLLPGSLPLGGCGSTP
PTPTGLAAASDKREGSSSSEGRGDTDKYLKKLHTQERAVEEVKLAIKPYYQKKDITKEEYKDILRKAVHKICHSKSGEIN
PVKVSNLVRAYVQRYRYFRKHGRKPGDPPGPPRPPKEPGPPDKGGPGLPLPPL
```

269 - 288:	EEEEEEEEEEEEEEEEEEEE
270 - 289:	EEEEEEEEEEEEEEEEEEEE

271 - 290:	EEEEEEEEEEEEEEEEEEEE
272 - 291:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7MEP7 **A0A3Q7MEP7_CALUR** (1243 aa)
splicing factor, arginine/serine-rich 19 isoform X2. *Callorhinus ursinus (Northern fur seal)*

```
MAADSFLTGLVSVLDPPDTWVPSHLDLRPGESEDMLELVAEVRIGDRDPIPLPVPSLLPRLRAWRTGKTVSPQPHSSRPS
CARHLLTLGTGDGGPAPPPAPSSASSSPSPSPSSSSPSPPPPPPPPAPPAPPAPRFDIYDPFHPTDEAYSPPPAPEQKYD
PFEPTGSNPSSSAGTPSPEEEEEEEEEEEEEEEEEEEEEEEGLSQSISRISETLAGIYDDNSLSQDFPGDESPRPDPQPP
QPTPAPGTPPQVDSTRVDGATRRRVFVVGTEAEACREGKVSVEVVTAGGAAIPPTLLPPGDSEIEEGEIVQPEEEPRVAV
SLFRAAGGGGGGGGGGRAARPPPAVAAPPAAQPPPPPPAARAPEGDDFLSLHAESDGEGALQVDLGEPAPAPPAADTRWG
GLDLRRKILTQRRERYRQRSPSPAVAAAAAAAAAAAAAAAAAAAAPAGPPTRKKSRRERKRSGGEAKEAASSSSGAPSAP
PAPASPWDSKKHRSRDRKPGSHASASARRRSRSRSARRRSRSADRRRGGSRRSRSREKRRRRRRSASPPPATSSSSSSRR
ERHRGKHRDGGGSKKKKKRSRSRGEKRSGDSEKAPVPTQPPSGSSSLGGERDSRRRGAVPPSIQDLTDHDLFAIKRTITV
GRPDKSDPRGPSPAPASSPKREVLYDSEGLSAEERGGKSSEKDRRRSGAASSSSSSREKGSRRKALDGGDRDRDRDRDRD
RSSKKARPPKESAPSSGPPPKPPVSSGSGSSSSSCSSSSRKVKLQSKVAVLIREGVSSTTPAKEAASAGLGSIGVKFSRD
RESRSPFLKPDERAPAEVAKAAPGSTKPKKTKVKAKAGAKKAKGTKGKTKPSKTRKKIRGGGSGGGGGGPVTLKKSKADS
CSQAAGAKGVEETSWSGEERAAKAPSTPPPKAAPPPPALTPDSQTVDSSCKTPEVSFLPEEATEEAGVRGGAEEEEEEEE
EEEEEEEEEEQQPATTTATSTAAAAPSTAPSAGSTAGDSGAEDGPATRVSQLPTLPPPMPWNLPAGVDCTTSGVLALTAL
LFKMEEANLASRAKAQELIQATNQILSHRKPPSSLGVTPTPVPTSLGLPPGPSSYLLPGSLPLGGCGSTPPTPTGLAAAS
DKREGSSSSEGRGDTDKYLKKLHTQERAVEEVKLAIKPYYQKKDITKEEYKDILRKAVHKICHSKSGEINPVKVSNLVRA
YVQRYRYFRKHGRKPGDPPGPPRPPKEPGPPDKGGPGLPLPPL
```

179 - 198:	EEEEEEEEEEEEEEEEEEEE
180 - 199:	EEEEEEEEEEEEEEEEEEEE
181 - 200:	EEEEEEEEEEEEEEEEEEEE
182 - 201:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7N3Y1 **A0A3Q7N3Y1_CALUR** (829 aa)
C-Jun-amino-terminal kinase-interacting protein 2. *Callorhinus ursinus (Northern fur seal)*

```
MADRAEMFSLSTFHSLSPPGCRPPQDISLEEFDDEDLSEITDDCGLGLSYDSDHCEKDSLSLGRSEQPHPICSFQDDFQE
FEMIDDNEEEEEEEEEEEEEEEEEEEEEEEGEGEGKEGGGPGSEAPAPEALIPSPSLEEPHKNRPTTLHLTTLGAQDSLNN
NGGFAPAPPASWQETVLCSPPQEPLRESPASLQPTDASPCGAQSPVRQGCDCEGNPPAAGPPAPCGASPSSDPGIEADLG
SRSSGGRGGRRSSQELSSPGSDSEDAGGARLGRMISSISETELELSSDGGSSSSGRSSHLTNSIEEASSPASEPEPEPET
PCEPPRRPAFLPVGPDDTNSEYESGSESEPDLSEDADSPWLLSNLVSRMISEGSSPIRCPGQCLSPASRPSGEPASPAGG
TTEAPEAAAGPGGVELVDMETLCGPPPPAPSAPRPGPAQPGPCLFLSNPTRDTITPLWAAPGRSARPARACSAACSEEDD
EDEDEDDAGDKGGPPGGGGVRPAAPLDASLVYDAVKYTLVVDEHTQLELVSLRRCAGLGEDSSEDSGGEASEEETAATLL
GGGQGPEDASPDSPDLTFSKKFLNVFVNSTSRSSSTESFGLFSCLVNGEEKEQTHRAVFRFIPRHPDELELDVDDPVLVE
AEEDDFWFRGFNMRTGERGVFPAFYAHAVPGPAKDLLGSKRSPCWVERFDVQFLGSVEVPCHQGNGILCAAMQKIATARK
LTVHLRPPASCDLEISLRGVKLSLSGGPEFQHCSHFFQMKNISFCGCHPRNSCYFGFITKHPLLSRFACHVFVSQESMRP
VAQSVGRAFLEYYQEHLEYACPTEDIYLE
```

88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7NAA8 **A0A3Q7NAA8_CALUR** (740 aa)
phospholipid phosphatase-related protein type 3. *Callorhinus ursinus (Northern fur seal)*

```
MIATKEKNKTPKDSMTLLPCFYFVELPIVASSVVSLYFLELTDLFKPAKVGFQCYDRTLSMPYVETNEELIPLLMLLSLA
FAAPAASIMVGEGMLYCLQSRLWGRGGGPGGAEGSINAGGCSFNSFLRRTVRFVGVHVFGLCATALVTDVIQLATGYHAP
FFLTVCKPNYTLLGTSCEANPYITQDICSGHDAHAILSARKTFPSQHATLSAFAAVYVSMYFNSVISDTTKLLKPVLVFA
FAIAAGVCGLTQITQYRSHPVDVYAGFLIGAGIAAYLACHAVGNFQAPTAEKPTALAPAKDALRALTQRGHDSVYQQNKS
VSTDELGPPGRLEGVPRPVAREKTSLGSLKRASVDVDLLAPRSPMGKENMVTFSHTLPRVSTPSLDDPARRHMTIHVPLD
ASRSKQLISEWKQKSLEGRGLGLPDEASPGHLRAPAEPMAEEEEEEEEEEEEEEEEEEEEGEEGGPAPPSLYPTVQARPG
LGPRVILPPRAGPQPLVHIPEEGAQAAAGLSPKSSAAVRAKWLMMAEKSGVAAAAAAAAAAASAQPRVANPPRLLQVIAM
SKAPGGPGPKVAETASSSSASSDSSQYRSPSDRDSASIVTIDAHAPHHPVVHLSAGNGPWEWKTAGGAAKGVEGEGGYEL
GDLARGFRGGPKPPGVSPGSSISDVDQEEPRFGAVATVNLATGEGLPPLSVTDGTLGPASRESTLRRKASGLVLGEREAA
GEAEAEAYYRKMQAARRFKD
```

441 - 460:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7NCN1 **A0A3Q7NCN1_CALUR** (1211 aa)
histone-lysine N-methyltransferase EHMT2. *Callorhinus ursinus (Northern fur seal)*

```
MAAAAGAAAAAAAAEGEAPAEMGALVLEKEPRGATERVHGSLGDTPRSEETLPKASPDSLEPAGPSSPASVTVTVGDEGAD
TPVGATPLIGDEPENLEGDGDLHGGRILLGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGA
ATAGPEPPVATPSPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDVHSMGKMTSEVAKRRKLNVGGGLSEEL
GSTRGSGEVTVEKGDPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEE
EEEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGT
LSPNHAGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMV
LCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAG
TAAPAPPPLAQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPPGPGREALEKALVIQ
ESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQR
TPLMEAVVNNHLEVARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIE
VIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPEL
RNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAVRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCET
STMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVR
LQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNI
```

```
IPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELL
PELSSLPPVNP
```

300 - 319:	EEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEE

A0A3Q7NCZ6 **A0A3Q7NCZ6_CALUR** (752 aa)
Daxx (Death domain-associated protein 6). *Callorhinus ursinus (Northern fur seal)*

```
MATANSIIVLDDDDEDEAAAQPGPSHPPPNPASPRAEAPGSSQPHGAGGSSSSGGKKCYKLENEKLFEEFLDLCKTQTAD
HPEVVPFLYNRQQRAHSVFLASAEFCNILSRVLSRARSRPAKLYVYINELCTVLKAHSAKKKLNLAPAATASSEPSGNNP
PTDPSSDPTNAKTTASEAPRTRGSRRQIQRLEQLLALYVAEIRRLQEKELDLSELDDPDSTYLQEARLKRKLIRLFGRLC
ELKDCSSLTGRVIEQRIPYRGTRYPEVNRRIERLINKPGPDTFPDYGDVLRAVEKAAARHSLGLPRQQLQLMAQDAFRDV
GIRLQERRHLDLIYNFGCHLTDDYRPGIDPALSDPALARRLRENRSLAMSRLDEVISKYAMMQDKSEEGERQKRRARLPR
ATSSHTADPPKASLDSGEGPSGMASQECPTPSKPETDDEEDEESDEEEEEEEEEEEEEEEEEEEEEATDSEEEEDLEQMQE
GQGADEEEEEEEEEEEEEEAGQDGDRSPMSPSRMSTENNLEPSKGISRSGGEQQNKGLMVSPSSLSEEPLAPSSVDAESN
GEHLEELPLEEESPVSQLFELEIEALPLDTTPSPEERDISSSRKQSEDPLTTVLENGAAMVTSTSFNGGVSPHTWGDSCP
PCKKSRKEKQTGTGPLGNSYVERQRAVHEKNGKKIPTLSSPPSPLTSMAPVADSSTRVDSPSHGLVTSSLCSPSPARLSQ
TPHSLPSRPGTYKMSVATQCDPEEIIVLSDSD
```

446 - 465:	EEEEEEEEEEEEEEEEEEE

A0A3Q7NCZ8 **A0A3Q7NCZ8_CALUR** (686 aa)
death domain-associated protein 6 isoform X3. *Callorhinus ursinus (Northern fur seal)*

```
MATANSIIVLDDDDEDEAAAQPGPSHPPPNPASPRAEAPGSSQPHGAGGSSSSGGKKCYKLENEKLFEEAHSAKKKLNLA
PAATASSEPSGNNPPTDPSSDPTNAKTTASEAPRTRGSRRQIQRLEQLLALYVAEIRRLQEKELDLSELDDPDSTYLQEA
RLKRKLIRLFGRLCELKDCSSLTGRVIEQRIPYRGTRYPEVNRRIERLINKPGPDTFPDYGDVLRAVEKAAARHSLGLPR
QQLQLMAQDAFRDVGIRLQERRHLDLIYNFGCHLTDDYRPGIDPALSDPALARRLRENRSLAMSRLDEVISKYAMMQDKS
EEGERQKRRARLPRATSSHTADPPKASLDSGEGPSGMASQECPTPSKPETDDEEDEESDEEEEEEEEEEEEEEEEEEEEA
TDSEEEEDLEQMQEGQGADEEEEEEEEEEEEEEAGQDGDRSPMSPSRMSTENNLEPSKGISRSGGEQQNKGLMVSPSSLS
EEPLAPSSVDAESNGEHLEELPLEEESPVSQLFELEIEALPLDTTPSPEERDISSSRKQSEDPLTTVLENGAAMVTSTSF
NGGVSPHTWGDSCPPCKKSRKEKQTGTGPLGNSYVERQRAVHEKNGKKIPTLSSPPSPLTSMAPVADSSTRVDSPSHGLV
TSSLCSPSPARLSQTPHSLPSRPGTYKMSVATQCDPEEIIVLSDSD
```

380 - 399:	EEEEEEEEEEEEEEEEEEE

A0A3Q7NDV1 **A0A3Q7NDV1_CALUR** (732 aa)
Daxx (Death domain-associated protein 6). *Callorhinus ursinus (Northern fur seal)*

```
MATANSIIVLDDDDEDEAAAQPGPSHPPPNPASPRAEAPGSSQPHGAGGSSSSGGKKCYKLENEKLFEEFLDLCKTQTAD
HPEVVPFLYNRQQRAHSVFLASAEFCNILSRVLSRARSRPAKLYVYINELCTVLKAHSAKKKLNLAPAATASSEPSGNNP
PTDPSSDPTNAKTTASEAPRTRGSRRQIQRLEQLLALYVAEIRRLQEKELDLSELDDPDSTYLQEARLKRKLIRLFGRLC
ELKDCSSLTGRVIEQRIPYRGTRYPEVNRRIERLINKPGPDTFPDYGDVLRAVEKAAARHSLGLPRQQLQLMAQDAFRDV
GIRLQERRHLDLIYNFGCHLTDDYRPGIDPALSDPALARRLRENRSLAMSRLDEVISKYAMMQDKSEEGERQKRRARLPR
ATSSHTADPPKASLDSGEGPSGMASQECPTPSKPETDDEEDEESDEEEEEEEEEEEEEEEEEEEEEATDSEEEEDLEQMQE
GQDGDRSPMSPSRMSTENNLEPSKGISRSGGEQQNKGLMVSPSSLSEEPLAPSSVDAESNGEHLEELPLEEESPVSQLFE
LEIEALPLDTTPSPEERDISSSRKQSEDPLTTVLENGAAMVTSTSFNGGVSPHTWGDSCPPCKKSRKEKQTGTGPLGNSY
VERQRAVHEKNGKKIPTLSSPPSPLTSMAPVADSSTRVDSPSHGLVTSSLCSPSPARLSQTPHSLPSRPGTYKMSVATQC
DPEEIIVLSDSD
```

446 - 465:	EEEEEEEEEEEEEEEEEEE

A0A3Q7NQW9 **A0A3Q7NQW9_CALUR** (1107 aa)
myelin transcription factor 1. *Callorhinus ursinus (Northern fur seal)*

```
MSLENEDKRARTRSKALRVPPEPTGADLSCPTPGCTGSGHIRGKYSRHRSLQSCPLAKKRKLEGAQAEHLASTRKSHPLK
LALDEGYSVDTDGSEDAEVKDASVSDESEGTLEDEAEMSGQEEIHRPEPAEGRAPAKSHFGPKPIGSSAGPAKGSYSSYQ
EIIATSLLNLGQIAVETLVGEDLGQVATPGPGVVHLVQEEAEEGATSDEGERDAFLPLEDAEGVAGVARERSQELCPQAV
EGVASEESRKMKVALGEEEEEEEEEEEEEEEEEEEEEEDEEEEEEEEEEEEEVAAPEVICQEDAPLAPTQKAPELRHPASP
SPKPEYSVIVEVHSDDGRDEDARSQKSAVTDESEMYDMMTRGNLGLLEQAIALKAEQVQAVCEPGCPPTEQGQLGPGEPG
KAVRPLDAARKNFCSKDPSRAEKREIKCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRIPPEILAMHENVLKCPTPGCTGQ
GHVNSNRNTHRSLSGCPIAAAEKLAKSHEKQQPQTGDPSKNSSNSDRILRPMCFVKQLEVPPYGSYRPSVAPATPRANLA
KELEKFSKVTFDYASFDAQVFGKRMLAPKIQTSETSPKAFKCFDYAHDAEAAHMAATAILNLSTRCWEMPENLSTKPQDL
PSKAGDIEVDENGTLDLSMHKHRKRESAFPSSSSPGVKSPEASQRQSSTSAPSSSMTSPQSSQASRQDEWDRPLDYTKPS
RQREEEPEESEPAAHSFASSEADDQEVSEESFEERKYPGEVTLTNFKMKFLSKDIKKELLTCPTPGCDGSGHITGNYASH
RSLSGCPLADKSLRNLMAAHSADLKCPTPGCDGSGHITGNYASHRSLSGCPRAKKSGARVTPTKDDKEDPELMKCPVPGC
VGLGHISGKYASHRSASGCPLAARRQKEGSLNGSPFSWKSLKNEGPTCPTPGCDGSGHANGSFLTHRSLSGCPRATFAGK
KGKVSGDEVLSAKFKTSDVLENDEEIKQLNQEIRDLNESNSEMEAAMVQLQSQISSMEKSLKNIEEENKLIEEQNEALFL
ELSGLSQALIQSLANIRLPHMEPICEQNFDAYVSTLTDMYSNQECYQNPENKDLLESIKRAVRGIQV
```

257 - 276:	EEEEEEEEEEEEEEEEEEE

258 - 277:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7QL77 **A0A3Q7QL77_CALUR** (730 aa)
YTH domain-containing protein 1 isoform X2. *Callorhinus ursinus (Northern fur seal)*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDIKRQKPSVHSRQLISKPLSSSASN
NKRIVSTKGKSVAEYKNEEYQRSERSKRLEADRKIRLSSSASREPYKSQPEKTCLRKRDPERRTKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEEE
EEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGS
SASESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSARSV
ILIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDG
QEIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYAPEF
HQRPGYLKDPRYQEVDRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMAPYPGMEQPPHHPYYQHHAPPPQAHPPYS
GHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDR
DRGERGRYRR
```

229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7QVY1 **A0A3Q7QVY1_CALUR** (1325 aa)
tau-tubulin kinase 1. *Callorhinus ursinus (Northern fur seal)*

```
MQCLAAALKDETNMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTRENVALKVESAQQPKQVLKMEVAV
LKKLQGKSHVCRFIGCGRNEKFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESIEAIHSVGFLHRDIKPSNF
AMGRLPSTYRKCYMLDFGLARQYTNTTGDVRPPRNVAGFRGTVRYASVNAHKNREMGRHDDLWSLFYMLVEFAVGQLPWR
KIKDKEQVGMIKEKYEHRMLLKHMPSEFHLFLDHIASLDYFTKPDYQLIMSVFENSMKERGIAENEAFDWEKAGTDALLS
TSTSTPPQQNTRQTAAMFGVVNVTPVPGDLLRENTEDVLQGEHLSDQENAPPILPGRPPEGLGPSPHLAPHPGGPEAEVW
EETDVNRNKLRINIGKTPCVVEEEQNRGVGVPSSPVRAPPDSPTTPVRSLRYRRVNSPESERLSTVDGRVELHERRSRMD
LPGSPSRQACSSQPAQMLSVDTGHPDRQASGRMDVSASVEQEALSNAFRSVPLAEEEDFDSKEWVIIDKETELKDFPPGA
EPSTSGTTDEEPEELRPLPEEGEERRRPGAEPSVRPRGRGMQTLAEEDPRQTPFQPLPPPLSQAEGRSETSQPPTPGSPS
HSPLHSGPRPRRRESDPTGPQRQVFSVAPPFEVNGLPRAVPLSLPYQDFKKDLSDYRERARLLNRVRRVGFSHMLLTTPQ
VPLATVQPQANGKEEEEEEEEEEEEEEEEEEEEEEDEEEEEEEEEEEEEEGEEEGEGEEEEGEEGEEAVALGEVLGPRSSSS
SDGSERSTDRSQEGAPSTLLADDQKESRGRASMADGDLEPEEGSKTLVLVSPGDMKKSPVTADLAPDPDLGTLAALTPQQ
ERPQPTGSQLDVSEPGTLSSVLKSEPKPPGPGTGQGAGAVTTGAGGVAVTSSPFTKVERTFVHIAEKTHLNVMSSGGQAS
RPEELGAGGELGLEAPSDGRAVEEGDSVPLENGIAQAGLESCAPTGPPGDTPLEVATDSLLNGPALANGPAPASPLEPGP
EKLATISPSRHAMAGPRPRSRIPVLLSEEDTGSEPSGSLSARERWGKRARPQQDLARLVMEKRQGRLLLRLASGASSSSS
EEQRRASETLSGTGSEEDTPASEPAAPRKVGRAAATRSRIPRPISIRMPTPAAAQQQSTGRPHGAAPASDTAITSRLQLQ
KPPGSAVTADLRPKQPPGRGPGPGRAPAGTRPPAPRSPGSSASAAPRHPNASPRSQSLSRKESSSPSHQARPAGPPPRGA
PQARAQPDGTPSPGGPKKGPRGKLQTQRAATKGRAGVAEGRAGAR
```

734 - 753:	EEEEEEEEEEEEEEEEEEEE
735 - 754:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7RM60 **A0A3Q7RM60_VULVU** (1267 aa)
histone-lysine N-methyltransferase EHMT2. *Vulpes vulpes (Red fox)*

```
MRGLPRGRGLMRARGRGRAAPQGSRGRGRGGPHRGRGRPRSLLSLPRAQASWAPQLPSGLTSPPIPCVPCQGEAPAEMGA
LVLEKEPRGASERVHGSLGDTPRGEETLPKASPDSLEPAGPSSPASVTVTVGDEGADTPLGATPLIGDEPENLEGDGDLH
GGRILLGHATKSFPSSPSKGGACPSRAKMSMTGAAKSPPSVQSLAMRLLSMPGAQGAAAGPEPPAATPSPEGQPKVHRAR
KTMSKPGNGQPPVPEKRPPEVQHFRMSDDLHSLGKMTSDVAKRRKLNSGGGLSEELGSARGSGEVTMEKGDPGSLEEWET
VVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKAK
KKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGISNDTSSLETERGFEEL
PLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTA
GTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLAQDAPGRADTSQPSA
RMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPPGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGEL
QKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANINAVDKQQRTPLMEAVVNNHLEVARYMVQRGGC
VYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLH
WASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQL
NRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSS
NCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTF
ICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRD
IRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPDLLPELSALPPVNP
```

356 - 375:	EEEEEEEEEEEEEEEEEEEE
357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7RQS6 **A0A3Q7RQS6_CALUR** (738 aa)
YTH domain-containing protein 1 isoform X1. *Callorhinus ursinus (Northern fur seal)*

MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDIKRQKPSVHSRQLISKPLSSSASN
NKRIVSTKGKSVAEYKNEEYQRSERSKRLEADRKIRLSSSASREPYKSQPEKTCLRKRDPERRTKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEEE
EEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGS
SASESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSARSV
ILIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDG
QEIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYAPEF
HQRPGYLKDPRYQEVDSFTNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMAPYPGMEQPPHHPYYQHHAPP
PQAHPPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERER
ERLCDRDRDRGERGRYRR

229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE
233 - 252:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7RVD8 **A0A3Q7RVD8_CALUR** (3703 aa)
zinc finger homeobox protein 3 isoform X1. *Callorhinus ursinus (Northern fur seal)*

MEGCDSPVVSGKDNGCGIPQHQQWTELNSTHLPDKPSSMEQSTSENHGPLDSLRAPFNERLVEGAAPAGPAAEPAGKEVS
CDECSASFASLQTYMEHHCPGARPPLPLREESGSDTSEEGDEESDVENLAGEIVYQPDGSAYIVESLSQLTQSGGTCGSG
GGPLPPLFLNSLPGAGGRQGDPSCAAPVYPQIINTFHIASSFGKWFEGPDQAFPNTSALTGLSPVLHSFRVFDVRHKSNK
DYLNSDGSAKSSCVSKDVPNNVDLSKFDGFVLYGKRKPILMCFLCKLSFGYVRSFVTHAVHDHRMTLSEDERKILSNKNI
SAIIQGIGKDKEPLVSFLEPKNKNFQHPLVSTANLIGPGHSFYGQFSGIRMEGEEALPAGSAAGPEQPQAGILTPSTLLN
LGGLTSSVLKTPITSVPLGPLASSPTRASEGKDSGVAAGEKQDVGDPDCLSEKAEPAEEEAEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEGCKGLFPSELDDDLEDRPREESGAAAGSSKKDLALSNQSISNSPLMPNVLQTLSRGAASTGSNSASS
FVVFDGADRRNRLSFNSEGVRASVAEGGRRLDFADESANKDNATAPEPNESTEGDDGGFVPHHQHAGSLCELGAGECPSG
SGVECPKCDTVLGSSRSLGGHMTMMHSRNSCKTLKCPKCNWHYKYQQTLEAHMKEKHPEPGGSCVYCKSGQPHPRLARGE
SYTCGYKPFRCEVCNYSTTTKGNLSIHMQSDKHLNNMQNLQNGGGEQVFSHSAGAAAAAAAAAAAAAANIGSSCGAPSPTK
PKTKPTWRCEVCDYETNVARNLRIHMTSEKHMHNMMLLQQNMTQIQHNRHLGLGSLPSPAEAELYQYYLAQNMNLPNLKM
DNTASDAQFVMSGFQLDPTGPMAAMTPALVGGEIPLDMRLGGGQLVSEELMNLGESFIQTNDPSLKLFQCAVCNKFTTDN
LDMLGLHMNVERSLPEDEWKAVMGDSYQCKLCRYNTQLKANFQLHCKTDKHVQKYQLVAHIKEGGKANEWRLKCVAIGNP
VHLKCNACDYYTNSLEKLRLHTVNSRHEASLKLYKHLQQHESGVEGESCSYHCVLCNYSTKAKLNLLQHVRSMKHQRSES
LRKLQRLQKGLPEEDEDLGQIFTIRRCPSTEPEEAIEDVEGPSDAAADPEELAKDQESGGEKDQSKWTASSSQAEKELTD
SPATSKRISFTGSSESPLSSKRPKTSEETKPEQMYQCPYCKYSNADVNRLRVHAMTQHSVQPMLRCPLCQDMLNNKIHLQ
LHLTHLHSVAPDCVEKLIMTVTTPEMVMPSSMFLPAAVPDRDGNSTLEEAGKQPETSEDLGKNILPSVSTEHSGDLKPSS
ADPGSVREDSGFLCWKKGCNQVFKTSATLQTHFNEVHAKRPQLPVSDRHVYKYRCNQCSLAFKTIEKLQLHSQYHVIRAA
TMCCLCQRSFRTFQALKKHLETSHLELSEADIQQLYGGLLANGDLLAMGDPTLAEDHTIIVEEDKEEESDLEDKQSPTGS
DSGSVQEDSGSEPKRALPFRKGPNFTMEKFLDPSRPYKCTVCKESFTQKNILLVHYNSVSHLHKLKRALQESATGQPEPT
SSPDNKPFKCNTCNVAYSQSSTLEIHMRSVLHQTKARAAKLEAASGSSNGTGNSSSVSLSSSTPSPVSTSASNTFTTTNP
NSAGITPSSNLLSQVPPESVGMPALGNPIGANITSPSEPKEANRKKLADMIASRQQQQQQQQQQQQQAQTLAQAQAQVQA
HLQQELQQQAALIQSQLFNPALLPHFPMTTETLLQLQQQQHLLFPFYIPSAEFQLNPDVSLPVTSGALTLTGTGPGLLDD
LKAQVQIPTQSHQQILHQQQQSQLSLSQTHSALLQPSQHSEKKNKLVIKEKEKEKESQRERDSVEVGEGNPGPKESLPDA
LKAKEKKELAPAASSEPSMLPPRIASDARGNATKALLENFGFELVIQYNENKQKVQKKNGKTEQGENLEKLECDSCGKLF
SNILILKSHQEHVHQNYFPFKQLERFAKQYREQYDKLYPLRPQTPEPPPPPPPPPPPPPLPAAPPQPASTPAIPASAPPI
TSPTIAPTQPSMPLTQLSMPMELPIFSPLMMQTMPLQTLPAQLPPQLGPVEPLPADLAQLYQHQLNPSLLQQQNKRPRTR
ITDDQLRVLRQYFDINNSPSEEQIKEMADKSGLPQKVIKHWFRNTLFKERQRNKDSPYNFSNPPITSLEELKIDSRPPSP
EPQKQEYWGSKRSSRTRFTDYQLRVLQDFFDANAYPKDDEFEQLSNLLNLPTRVIVVWFQNARQKARKNYENQGEGKDGE
RRELTNDRYIRTSNLNYQCKKCSLVFQRIFDLIKHQKKLCYKDEDEEGQDDSQNEDSMDAMEILTPTSSSCSTPMPSQAY
SAPAPSANTASSAFLQLTAEPDELATFSSKTEASDEKPKQAEPPSAQPNQTQEKQGQPKAELQQQDQPEQKTNAAQQKLP
QLTSPTSLPQPPPQAPPPQCPLPQSSPSPSQLSHLPLKPLHTSTPQQLANLPPQLIPYQCDQCKLAFPSFEHWQEHQQLH
FLSAQNQFIHPQFLDRSLDMPFMLFDPSNPLLASQLLSGAIPQIPASSATSPSTPTSTMNTLKRKLEEKASASPGENDSG
TGGEEPQRDKRLRTTITPEQLEILYQKYLLDSNPTRKMLDHIAHEVGLKKRVVQVWFQNTRARERKGQFRAVGPAQAHRR
CPFCRALFKAKTALEAHIRSRHWHEAKRAGYNLTLSAMLLDCDGGLQMKGDIFDGASFSHLPPSSSDGQGVPLSPVSKTM
DLSPRTLLSPSSIKVEGIEDFESPSMSSVNLNFDQTKLDNDDCSSVNTAITDTTTGDEGNADNDSATGIATETKSSSAPN
EGLTKAAMMAMSEYEDRLSSGLVSPAPSFYSKEYDNEGTVDYSETSSLADPCSPSPGASGSAGKSGDSGDRPGQKRFRTQ
MTNLQLKVLKSCFNDYRTPTMLECEVLGNDIGLPKRVVQVWFQNARAKEKKSKLSMAKHFGINQTSYEGPKTECTLCGIK
YSARLSVRDHIFSQQHISKVKDTIGSQLDKEKEYFDPATVRQLMAQQELDRIKKANEVLGLAAQQQGMFDNAPLQALNLP
TAYPALQGIPPVLLPGLNSPSLPGFTPSNTALTSPKPNLMGLPSTTVPSPGLPTSGLPNKPSSASLSSPTPAQATMALAP
QQPPQPQQQPQVQPPPPAAQPPPAPQLPPQQQQQQRKDKDSEKVKEKEKAHKGKGEPLPVPKKEKGEAPTAATATISAPL
PTMEYAVDPAQLQALQAALTSDPTALLTSQFLPYFVPGFSPYYAPQIPGALQSGYLQPMYGMEGLFPYSPALSQALMGLS
PGSLLQQYQQYQQSLQEAIQQQQQRQLQQQQQKVQQQPKASQTPVPQGAASPDKDPAKESPKPEEQKNAPREVSPLLPKP
PEEPEAESKSADSLYDPFIVPKVQYKLVCRKCQAGFGDEEAARSHLKSLCFFGQSVVNLQEMVLHVPTGGGGSGGGGGGG
GSGGGSYHCLACESALCGEEALSQHLESALHKHRTITRAARNAKEHPSLLPHSACFPDPSTASTSQSAAHSNDSPPPPSA
AAPSSSSASPHASRKSWPQVVSRASAAKPPSFPPLSSSSTVTSSSCSTSGVQPSMPTDDYSEESDTDLSQKSDGPASPVE
GPKDPSCPKDSGLTSVGTDTFRL

462 - 481:	EEEEEEEEEEEEEEEEEEEE
463 - 482:	EEEEEEEEEEEEEEEEEEEE
464 - 483:	EEEEEEEEEEEEEEEEEEEE
465 - 484:	EEEEEEEEEEEEEEEEEEEE
466 - 485:	EEEEEEEEEEEEEEEEEEEE
467 - 486:	EEEEEEEEEEEEEEEEEEEE
468 - 487:	EEEEEEEEEEEEEEEEEEEE
469 - 488:	EEEEEEEEEEEEEEEEEEEE
470 - 489:	EEEEEEEEEEEEEEEEEEEE
471 - 490:	EEEEEEEEEEEEEEEEEEEE
472 - 491:	EEEEEEEEEEEEEEEEEEEE
473 - 492:	EEEEEEEEEEEEEEEEEEEE

474 - 493:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7SF51 **A0A3Q7SF51_VULVU** (742 aa)
YTH domain-containing protein 1 isoform X2. *Vulpes vulpes (Red fox)*

```
MSCALKYRLPRPTDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDIKRQKPSVHSRQLISKPLSS
SVSNNKRIVSTKGKSVGEYKNEEYQRSERSKRLEADRKIRLSSSASREPYKSQPEKTCLRKRDPERRTKSPTPDGSERIG
LEVDRRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEE
EEEEEEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFD
RSGSSASESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRS
ARSVILIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKI
GRDGQEIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDY
APEFHQRPGYLKDPRYQEVDSFTNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMAPYPGMEQPPHHPYYQH
HAPPPQAHPPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDR
ERERERLCDRDRDRGERGRYRR
```

233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7SF53 **A0A3Q7SF53_VULVU** (716 aa)
YTH domain-containing protein 1 isoform X6. *Vulpes vulpes (Red fox)*

```
MSCALKYRLPRPTDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDIKRQKPSVHSRQLISKPLSS
SVSNNKRIVSTKGKSVGEYKNEEYQRSERSKRLEADRKIRLSSSASREPYKSQPEKTCLRKRDPERRTKSPTPDGSERIG
LEVDRRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEE
EEEEEEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFD
RSGSSASESYADQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSARSVILIFSVRESGKFQG
FARLSSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLL
FPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYAPEFHQRPGYLKDPRYQE
VDRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMAPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHHPVPHEARYRDK
RVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDRGERGRYRR
```

233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7SRF3 **A0A3Q7SRF3_VULVU** (743 aa)
YTH domain-containing protein 1 isoform X1. *Vulpes vulpes (Red fox)*

```
MSCALKYRLPRPTDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDIKRQKPSVHSRQLISKPLSS
SVSNNKRIVSTKGKSVGEYKNEEYQRSERSKRLEADRKIRLSSSASREPYKSQPEKTCLRKRDPERRTKSPTPDGSEVRI
GLEVDRRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEEEEE
EEEEEEEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVF
DRSGSSASESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFR
SARSVILIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVK
IGRDGQEIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRID
YAPEFHQRPGYLKDPRYQEVDSFTNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMAPYPGMEQPPHHPYYQ
HHAPPPQAHPPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRD
RERERERLCDRDRDRGERGRYRR
```

234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7SU56 **A0A3Q7SU56_VULVU** (734 aa)
YTH domain-containing protein 1 isoform X4. *Vulpes vulpes (Red fox)*

```
MSCALKYRLPRPTDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDIKRQKPSVHSRQLISKPLSS
SVSNNKRIVSTKGKSVGEYKNEEYQRSERSKRLEADRKIRLSSSASREPYKSQPEKTCLRKRDPERRTKSPTPDGSERIG
LEVDRRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEE
EEEEEEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFD
RSGSSASESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRS
ARSVILIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKI
GRDGQEIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDY
APEFHQRPGYLKDPRYQEVDRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMAPYPGMEQPPHHPYYQHHAPPPQAH
PPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLC
DRDRDRGERGRYRR
```

233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7SX08 **A0A3Q7SX08_VULVU** (1291 aa)
tau-tubulin kinase 1. *Vulpes vulpes (Red fox)*

```
MQCLAAALKDETNMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTRENVALKVESAQQPKQVLKMEVAV
LKKLQGKSHVCRFIGCGRNEKFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESIEAIHSVGFLHRDIKPSNF
AMGRLPSTYRKCYMLDFGLARQYTNTTGDVRPPRNVAGFRGTVRYASVNAHKNREMGRHDDLWSLFYMLVEFAVGQLPWR
KIKDKEQVGMIKEKYEHRMLLKHMPSEFHLFLDHIASLDYFTKPDYQLIMSVFENSMKERGIAENEAFDWEKAGTDALLS
TSTSTPPQQNTRQTAAMFGVVNVTPVPGDLLRENTEDVLQGEHLSDQENAPPILPGRPPEGLGPGPHLVPHPGGPEAEVW
EETDVNRNKLRINISKTPCVVEEEQSRGVGVPSSPVRAPPDSPTTPVRSLRYRRVNSPESERLSTADGRVELHERRSRMD
LPGSPSRQACSSQPAQMLSVDTGHPDRQASGRMDVSASVEQEALSNAFRSVPLAEEEDFDSKEWVIIDKETELKDFPPGA
EPSTSGTTDEEPEELRPLPEEGEERRRPGAEAAVRPRGRGMQTLAEEDPRLTPFQPLPPQLSQAEGRSEMSQPPTPGSPS
HSPLHSGPRPRRRESDPTGPQRQVFSVAPPFEVNGLPRAVPLSLPYQDFKKDLSDYRERARLLNRVRRVGFSHVLLTTPQ
VPLAPVQPQANGKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAVALGEVLGPRSGSSSDG
SERSTDRSQEGAPSTLLADDQKESRGRASMADGDLEPEEGSKTLVLVSPGDMKKSPVTADLAPDPDLGTLAALTPQQERP
QPTGSQLDVSEPGTLSSVLKSEPKPPGPGTGPGAGAVTTGAGGVAVTSSPFTKVERTFVHIAEKTHLNVMSSGGQASRPE
ELGAGGELGLEAPSDGKAVEEGASMPLENGIAPSGLESCALSAPPGDTPSEVATDSLPNGPALANGPAPASPLEPGPEKL
VTISPSRHAMPGSRPRSRIPVLLSEEDTGSEPSGSLSAKERWGKRARPQQDLARLVMEKRQGRLLLRLASGASSSSSEEQ
RRASETLSGTGSEEDTPASEPAAPRKAGRAATTRSRIPRPISIRMPTPAAAQQSPGRPHGAAPASDTAITSRLQLQKPPG
SAATADLRPKHLTRLTRTTRGPSFPPAPARTRASTCRAPCRPGPRGTRRRGGRARLLVLRPLSVTPALPLPLFGDLCLHH
LRRLSLLPAFF
```

734 - 753:	EEEEEEEEEEEEEEEEEEEE
735 - 754:	EEEEEEEEEEEEEEEEEEEE
736 - 755:	EEEEEEEEEEEEEEEEEEEE
737 - 756:	EEEEEEEEEEEEEEEEEEEE
738 - 757:	EEEEEEEEEEEEEEEEEEEE
739 - 758:	EEEEEEEEEEEEEEEEEEEE
740 - 759:	EEEEEEEEEEEEEEEEEEEE
741 - 760:	EEEEEEEEEEEEEEEEEEEE
742 - 761:	EEEEEEEEEEEEEEEEEEEE
743 - 762:	EEEEEEEEEEEEEEEEEEEE
744 - 763:	EEEEEEEEEEEEEEEEEEEE
745 - 764:	EEEEEEEEEEEEEEEEEEEE
746 - 765:	EEEEEEEEEEEEEEEEEEEE
747 - 766:	EEEEEEEEEEEEEEEEEEEE
748 - 767:	EEEEEEEEEEEEEEEEEEEE
749 - 768:	EEEEEEEEEEEEEEEEEEEE
750 - 769:	EEEEEEEEEEEEEEEEEEEE
751 - 770:	EEEEEEEEEEEEEEEEEEEE
752 - 771:	EEEEEEEEEEEEEEEEEEEE
753 - 772:	EEEEEEEEEEEEEEEEEEEE
754 - 773:	EEEEEEEEEEEEEEEEEEEE
755 - 774:	EEEEEEEEEEEEEEEEEEEE
756 - 775:	EEEEEEEEEEEEEEEEEEEE
757 - 776:	EEEEEEEEEEEEEEEEEEEE
758 - 777:	EEEEEEEEEEEEEEEEEEEE
759 - 778:	EEEEEEEEEEEEEEEEEEEE

760 - 779:	EEEEEEEEEEEEEEEEEEEE
761 - 780:	EEEEEEEEEEEEEEEEEEEE
762 - 781:	EEEEEEEEEEEEEEEEEEEE
763 - 782:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7SYZ5 **A0A3Q7SYZ5_VULVU** (1329 aa)
LOW QUALITY PROTEIN: splicing factor, arginine/serine-rich 19. *Vulpes vulpes (Red fox)*

```
MEEEDESRGKTEESGEDRGDGPPDRDPTLSPSAFILRAIQQAVGSSLQGDLPNDKDGSRCHGLRWRRCRSPRSEPRSQES
GGTDTATVLDMAADSFLAGLVSVLDPPDTWVPSHLDLRPGESEDMLELVAEVRIGDRDPIPLPVPSLLPRLRAWRTGKTV
SPQPHSSRPSCARHLLTLGTGDGGPAPPPAPSSASSSPSPSPSSSSPSPPPPPPPPPPPAPPAPPAPRFDIYDPFHPTDE
AYSPPPAPEQKYDPFEPTGSNPSSSAGTPSPEEEEEEEEEEEEEEEEEEEEEEEGLSQSISRISETLAGIYDDNSLSQDF
PGDESPRPDPQPPQSAPAPGTPPQVDSTRVDGATRRRVFVVGTEAEACREGKVSVEVVTAGGAAIPPALPPPGDSEIEEG
EIVQPEEEPRVAVSLFRASGRAARPPPAASAPPAAQPPPPPPAPRAPEGDDFLSLHAESDGEGALQVDLGEPAPAPPAAD
TRWGGLDLRRKILTQRRERYRQRSPSPAAASTAAATTAAAAPAGPPTRKKSRRERKRSGGEAKEAASSSSGGPPPPPAPX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXRGGSRRSRSREKRRRRRRSASPPPATSSSSSSRR
ERHRGKHRDGGGGGGKKKKKRSRSRGEKRSGDSEKGPAPTQPPSGSGSGSLGADRDSRRRGAVPPSIQDLTDHDLFAIKR
TITVGRPDKSDPRGPSPAPASSPKREVLYDSEGLSTEERGGKSSEKDRRRSGAASSSSSSREKGSRRKALDGGDRDRDRD
RDRDRDRSSKKARPPKESAPSSGPPPKPPVSSGSGSSSSSCSSSSRKVKLQSKVAVLIREGVSSTTPAKEAASAGLGSIG
VKFSRDRESRSPFLKPDERAPAEVAKAAPGSTKPKKTKVKAKAGAKKAKGTKGKTKPSKTRKKIRSGGSGGSSGGPVTLK
KSKADSCSQAAGAKGVEETSWSGEERAAKAPSTPPPKAAPPPPALTPDSQTVDSSCKTPEVSFLPEEATEEAGVRGGAEE
EEEEEEEEEEEEEEEEQQPATTTATSTAAAAPSTAPSAGSTAGDSGAEDGPATRVSQLPTLPPPMPWNLPAGVDCTTSGV
LALTALLFKMEEANLASRAKAQELIQATNQILSHRKPPSSLGVTPAPVPTSLGLPPGPSSYLLPGSLPLGGCGSTPPTPT
GLAAASDKREGSSSSEGRGDTDKYLKKLHTQERAVEEVKLAIKPYYQKKDITKEEYKDILRKAVHKICHSKSGEINPVKV
SNLVRAYVQRYRYFRKHGRKPGDPPGPPRPPKEPGPPDKGGPGLPLPPL
```

272 - 291:	EEEEEEEEEEEEEEEEEEEE
273 - 292:	EEEEEEEEEEEEEEEEEEEE
274 - 293:	EEEEEEEEEEEEEEEEEEEE
275 - 294:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7T1M9 **A0A3Q7T1M9_VULVU** (1122 aa)
myelin transcription factor 1 isoform X2. *Vulpes vulpes (Red fox)*

```
MSLDNEDKRARTRSKAVRVPPEPTGADLSCPTPGCTGSGHIRGKYSRHRSLQSCPLAKKRKLEGAQAEHLVSKRKSHPLK
LALDEGYSVDTDGSEDAEVKDASVSDESEGTLEEDEAEMSGQEEIHRPEPAEGRSPVKSHFASKPIGSSAGPAKGSYSSY
QEIIATSLLNLGQIAVETLVGEDLGQGAKPGPAVVHLLQEEAEEEATSDEGEKDVFIRPDDTEDVVEVSRECSQEPGPQS
VEGVAREESSKMKVALGNEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEEEEEEEEEEEEEEVPAPDVICQEDAPHAPTQ
KAPELRHPASPSPKPEYSVIVEVRSDDGKDEDSRSQKSAVTDESEMYDMMTRGNLGLLEQAIALKAEQVQAVCEPGCPPT
EQGQLGPGEPGKVARPLDASRKNYCSKDPSRAEKREIKCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRIPPEILAMHENV
LKCPTPGCTGQGHVNSNRNTHRSLSGCPIAAAEKLAKSHEKQQPQTGDPSKNSSNSDRILRPMCFVKQLEVPPYGSYRPS
VAPATPRANLAKELEKFSKVTFDYASFDAQVFGKRMLAPKIQTSETSPKAFKCFDYAHDAEAAHMAATAILNLSTRCWEM
PENLSTKPQDLPSKAADIEVDENGTLDLSMHKHRKRESAFPSSSSSSSSPGVKSPEASQRQSSTSAPSSSMTSPQSSQAS
RQDEWDRPLDYTKPSRQREEEPEESEPAAHSFASSEADDQEVSEESFEERKYPGEVTLTNFKMKFLSKDIKKELLTCPTP
GCDGSGHITGNYASHRSLSGCPLADKSLRNLMAAHSADLKCPTPGCDGSGHITGNYASHRSLSGCPRAKKSGARVTPTKD
DKEDPELMKCPVPGCVGLGHISGKYASHRSASGCPLAARRQKEGSLNGSPFSWKSLKNEGPTCPTPGCDGSGHANGSFLT
HRSLSGCPRATFAGKKGKVSGDEVLSTKFKTSDVLENDEEIKQLNQEIRDLNESNSEMEAAMVQLQSQISSMEKSLKNIE
EENKLIEEQNEALFLELSGLSQALIQSLANIRLPHMEPICEQNFDAYVSTLTDMYSNQECYQNPENKDLLESIKRAVRGI
QV
```

259 - 278:	EEEEEEEEEEEEEEEEEEEE
260 - 279:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE
262 - 281:	EEEEEEEEEEEEEEEEEEEE
263 - 282:	EEEEEEEEEEEEEEEEEEEE
264 - 283:	EEEEEEEEEEEEEEEEEEEE
265 - 284:	EEEEEEEEEEEEEEEEEEEE
266 - 285:	EEEEEEEEEEEEEEEEEEEE
267 - 286:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7TD38 **A0A3Q7TD38_VULVU** (725 aa)
YTH domain-containing protein 1 isoform X5. *Vulpes vulpes (Red fox)*

```
MSCALKYRLPRPTDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDIKRQKPSVHSRQLISKPLSS
SVSNNKRIVSTKGKSVGEYKNEEYQRSERSKRLEADRKIRLSSSASREPYKSQPEKTCLRKRDPERRTKSPTPDGSEVRI
GLEVDRRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEEEEE
EEEEEEEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVF
DRSGSSASESYADQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSARSVILIFSVRESGKFQ
GFARLSSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCL
LFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYAPEFHQRPGYLKDPRYQ
EVDSFTNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMAPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHHPV
PHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDRGER
GRYRR
```

234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7TKA9 **A0A3Q7TKA9_VULVU** (2754 aa)
Piezo-type mechanosensitive ion channel component. *Vulpes vulpes (Red fox)*

```
MASEVVCGLIFRLLLPICLAVACAFRYNGLSFVYLIYLLLIPLFSEPTKATMQGHTGRLLKSLCFTSLSFLLLHIIFHIT
LASLEAQHRIGPGYNCSTWEKTFRQIGFESLKGADAGNGIRVFVPDIGMFIASLTIWLVCRNIVQKPVTEETAQYNSEFE
NEELAGGEKLDPEEALIYEEDLDEGDGVEGEVEESTKLKMFRRLASVASKLKEFIGNMITTAGKVVVTILLGSSGMMLPS
LTSSVYFFVFLGLCTWWSWCRTFDPLLFSCLCVLLAIFTAGHLIGLYLYQFQFFQEAVPPNDYYARLFGIKSVIHTDCSS
TWKIIANPDLSWYHHANPIVLLVMYYTLATLIRIWLQEPLVQDDRTKEEDRALACSPIQITAERRRSLWYATHYPTDERK
LLSMTQDDYKPSDGLLVTVNGNPVDYHTIHPSLPVENGPAKADLYSTPQYRWEPSEDSSEKKEEEEDEKEEFEEERSHEE
KRSVKVHAMVSVFQFIMKQSYICALIAMMAWSITYHSWLTFVLLIWSCTLWMIRNRRKYAMISSPFMVVYGNLLLILQYI
WSFELPEIKKVPGFLEKKEPGELASKILFTITFWLLLRQHLTEQKALQEKEALLSEVKIGSQENEEKDDEQDIQMEGEAE
EKEEDEPKEEKQERRKEEEMEEDDDQDIMKVLGNLVVAMFIKYWIYVCGGMFFFVSFEGKIVMYKIIYMVLFLFCVALYQ
VHYEWWRRILKYFWMSVVIYTMLVLIFIYTYQFENFPGLWQNMTGLKKEKLEDLGLKQFTVAELFTRIFIPTSFLLVCIL
HLHYFHDRFLELTDLKSIPSKEDSAIYRLAHPEGSLPDLAMMNLTASLDKPDLKKLAEPREDKPEGYPEKAEKAELGKDS
AEEEEEEEEEEEEEEEEEEEEETSDLRNKWHLVIDRLTVLFLKFLEYFHKLQVFMWWILELHIIKIVSSYIIWVSVKEVS
LFNYVFLISWAFALPYAKLRRLASSVCTVWTCVIIVCKMLYQLQTIKPENFSVNCSLPNENQTNIPINQLNKSQLYSAPI
DPTEWVGLRKSSPLLVYLRNNLLMLAILAFEVTIYRHQEYYRGRNNLTAPVSKTIFHDITRLHLDDGLINCAKYFINYFF
YKFGLETCFLMSVNVIGQRMDFYAMIHACWLIAVLYRRRRKAIAEIWPKYCCFLACIITFQYFICIGIPPAPCRDYPWRF
KGASFNDNIIKWLYFPDFIVRPNPVFLVYDFMLLLCASLQRQIFEDENKAAVRIMAGDNVEICMNLDAASFSQHNPVPDF
IHCRSYLDMSKVIIFSYLFWFVLTIIFITGTTRISIFCMGYLVACFYFLLFGGDLLLKPIKSILRYWDWLIAYNVFVITM
KNILSIGACGYIEKLVQNSCWLIQAFSLACTVKGYKMPDDDSSCKLPSGEAGIIWDSICFAFLLLQRRVFMSYYFLHVVA
DIKASQILASRGAELFQATIVKAVKARIEEEKKSMDQLKRQMDRIKARQQKYKKGKERMLSLTQESGEGQDIQKLSEEDD
EREADKQKAKGKKKQWWRPWVDHASMVRSGDYYLFETDSEEEEEEELKKEDEEPPRRSAFQFVYQAWITDPKTALRQRRK
EKKKSAKEEQKRRRKGSGEGPVEWEDREDEPIKKKSDGPDNIIKRIFNILKFTWVLFLATVDSFTTWLNSISREHIDIST
VLRIERCMLTREIKKGNVPTRESIHMYYQNHIMNLSRESGLDTINDRPGAASGAQTAHRMDSLDSHDSISSEPTQCTMLY
SRQGTTETIAEVEAEQDDEAVAADVDQGGEATGNVGPEEASEGSEASEVGLTPDAELPQYPTEDGDVEAPPSYSKAVSFE
RLSFGSRDDSAGQSHMAVSPDDSRSDRLESSILPPLTHELTASELLLNKMFHDDELEESEKFYVGQPRFLLLFYAMYNTL
VARSEMVCYFVIILNHMVSASMITLVLPILIFLWAMLSVPRPSRRFWMMAIVYTEVAIVVKYFFQFGFFPWNKNVELNKD
KPYHPPNIIGVEKKEGYVLYDLIQLLALFFHRSILKCHGLWDEDDITDSGTDKEESDDELSLSRGRRASSDSLKSINLAA
SAESVHVSFPEQSTAIRRKRSGSSSQISPRSSFSSNRSKRGSTSTRNSSQKGSSVLSIKQKSKRELYMEKLQEHLIKAKA
FTIKKTLQIYVPIRQFFYDLIHPDYSAVTDVYVLMFLADTVDFVIIVFGFWAFGKHSAAADITSSLSEDQVPGPFLVMVL
IQFGTMVVDRALYLRKTVLGKVIFQVILVFGIHFWMFFILPGVTERKFSQNLVAQLWYFVKCVYFGLSAYQIRCGYPTRV
LGNFLTKSYNYVNLFLFQGFRLVPFLTELRAVMDWVWTDTTLSLSSWICVEDIYAHIFILKCWRESEKRYPQPRGQKKKK
VVKYGMGGMIIVLLICIVWFPLLFMSLIKSVAGVINQPLDVSVTITLGGYQPIFTMSAQQSQLKVMDQTRFNKFMKAFSR
DTGAMQFLENYEKEDITVAELEGNSNSLWTISPPSKQKMIHELMDPNSSFSVVFSWSIQRNMSLGAKAEIATDKLSFLLK
NNTRKNIAKMIAGNNTESSRTPVTIEKIYPYYVKAPSDSNSKPIKQLLSENNFMNITITLSRDNTTKTNSEWWVLNLTGN
RIYNQHAQALELVVFNDKVSPPSLGFLAGYGIMGLYASVVLVIGKFVREFFSGISHSIMFEELPNVDRILKLCTDIFLVR
ETGELELEEDLYAKLIFLYRSPETMIKWTREKTN
```

882 - 901:	EEEEEEEEEEEEEEEEEEEE
883 - 902:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7TVK6 **A0A3Q7TVK6_VULVU** (735 aa)
YTH domain-containing protein 1 isoform X3. *Vulpes vulpes (Red fox)*

```
MSCALKYRLPRPTDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDIKRQKPSVHSRQLISKPLSS
SVSNNKRIVSTKGKSVGEYKNEEYQRSERSKRLEADRKIRLSSSASREPYKSQPEKTCLRKRDPERRTKSPTPDGSEVRI
GLEVDRRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEEEEE
EEEEEEEEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVF
DRSGSSASESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFR
SARSVILIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVK
IGRDGQEIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRID
YAPEFHQRPGYLKDPRYQEVDRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMAPYPGMEQPPHHPYYQHHAPPPQA
HPPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERL
CDRDRDRGERGRYRR
```

234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7TZ75 **A0A3Q7TZ75_VULVU** (382 aa)
phospholipid phosphatase-related protein type 3. *Vulpes vulpes (Red fox)*

```
MIATKEKSKAPRDSMTLLPCFYFVELPIVASSVVSLYFLELTDLFKPAKVGFQCYDRTLSMPYVETNEELIPLLMLLSLA
FAAPAASVGRGAAGCHAVGNFQAPSAEKPVAPAPAKDALRALTQRGHDSVYQQNKSVSTDELGPPGRLEGVPRPVAREKS
SLGSLKRASVDADLLAPRSPMGKENMVTFSHTLPRVSTPSLDDPARRHMTIHVPLDASRSKQLISEWKQKSLEGRGLGLP
DEASPGHLRAPAEPMAEEEEEEEEEEEEEEEEEEEEEEEEGEEGGPAPPSLYPTVQARPGLGPRVILPPRAGPQPLVHIPE
EGVQAAAGLSPKSSAAVRAKWLMMAEKSGAAVAAARVIHAGGPPPPAPASAAARGPCHSSGF
```

257 - 276:	EEEEEEEEEEEEEEEEEEEE

258 - 277:	EEEEEEEEEEEEEEEEEEEE
259 - 278:	EEEEEEEEEEEEEEEEEEEE
260 - 279:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7TZM1 **A0A3Q7TZM1_VULVU** (1083 aa)
myelin transcription factor 1 isoform X4. *Vulpes vulpes (Red fox)*

```
MRISGLARAPRPSECPQSPQVPTSAAPPQGAPAQDTFGASTPGTADESEGTLEEDEAEMSGQEEIHRPEPAEGRSPVKSH
FASKPIGSSAGPAKGSYSSYQEIIATSLLNLGQIAVETLVGEDLGQGAKPGPAVVHLLQEEAEEEATSDEGEKDVFIRPD
DTEDVVEVSRECSQEPGPQSVEGVAREESSKMKVALGNEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEEEEEEEEEEE
EEVPAPDVICQEDAPHAPTQKAPELRHPASPSPKPEYSVIVEVRSDDGKDEDSRSQKSAVTDESEMYDMMTRGNLGLLEQ
AIALKAEQVQAVCEPGCPPTEQGQLGPGEPGKVARPLDASRKNYCSKDPSRAEKREIKCPTPGCDGTGHVTGLYPHHRSL
SGCPHKDRIPPEILAMHENVLKCPTPGCTGQGHVNSNRNTHRSLSGCPIAAAEKLAKSHEKQQPQTGDPSKNSSNSDRIL
RPMCFVKQLEVPPYGSYRPSVAPATPRANLAKELEKFSKVTFDYASFDAQVFGKRMLAPKIQTSETSPKAFKSKPFPKAS
SPRHSPCTSSSSAGFDYAHDAEAAHMAATAILNLSTRCWEMPENLSTKPQDLPSKAADIEVDENGTLDLSMHKHRKRESA
FPSSSSSSSSPGVKSPEASQRQSSTSAPSSSMTSPQSSQASRQDEWDRPLDYTKPSRQREEEPEESEPAAHSFASSEADD
QEVSEESFEERKYPGEVTLTNFKMKFLSKDIKKELLTCPTPGCDGSGHITGNYASHRSLSGCPLADKSLRNLMAAHSADL
KCPTPGCDGSGHITGNYASHRSLSGCPRAKKSGARVTPTKDDKEDPELMKCPVPGCVGLGHISGKYASHRSASGCPLAAR
RQKEGSLNGSPFSWKSLKNEGPTCPTPGCDGSGHANGSFLTHRSLSGCPRATFAGKKGKVSGDEVLSTKFKTSDVLENDE
EIKQLNQEIRDLNESNSEMEAAMVQLQSQISSMEKSLKNIEEENKLIEEQNEALFLELSGLSQALIQSLANIRLPHMEPI
CEQNFDAYVSTLTDMYSNQECYQNPENKDLLESIKRAVRGIQV
```

199 - 218:	EEEEEEEEEEEEEEEEEEEE
200 - 219:	EEEEEEEEEEEEEEEEEEEE
201 - 220:	EEEEEEEEEEEEEEEEEEEE
202 - 221:	EEEEEEEEEEEEEEEEEEEE
203 - 222:	EEEEEEEEEEEEEEEEEEEE
204 - 223:	EEEEEEEEEEEEEEEEEEEE
205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE
207 - 226:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7TZR2 **A0A3Q7TZR2_VULVU** (2067 aa)
Histone acetyltransferase (EC 2.3.1.48). *Vulpes vulpes (Red fox)*

```
MVKLANPLYTEWILEAIQKIKKQKQRPSEERICHAVSTSHGLDKKTVSEQLELSVQDGSVLKVTNKGLASYKDPDNPGRF
SSVKPGTFPKSTKGSRGSCNDLRNVDWNKLLRRAIEGLEEPNGSSLKNIEKYLRSQSDLTSTTNNPAFQQRLRLGAKRAV
NNGRLLKDGPQYRVNYGSLDGKGAPKYPSAFPSSLPPVSLLPHEKDQPRADPIPICSFCLGTKESNREKKPEELLSCADC
GSSGHPSCLKFCPELTTNVKALRWQCIECKTCSACRIQGKNADNMLFCDSCDRGFHMECCDPPLSRMPKGMWICQVCRPK
KKGRKLLHEKAAQIKRRYAKPIGRPKNKLKQRLLSVTSDEGSMNAFTGRGSPGRGQKTKVCTTPSSGHAASGKDSSSRLA
VTDPTRPGATTKITTTSTYISASTLKVNKKTKGLIDGLTKFFTPSPDGRRSRGEIIDFSKHYRPRKKVSQKQSCTSHVLA
TGTTQKLKPPPSSLPPPTPISGQSPSSQKSSTSTSSTSPQSSSSQSSVPSFSSLTKNSQLKALFDGLSHIYTTQGQSRKK
GHPSYAPPKRMRRKTELSSTAKSRAHFFGKRDIRSRFIAHSSSSSWGMARGRIFKAIAHFKRTTFLKKHRMLGRLKYKVT
PQMGTPSPGKGSLTDGRIKPDQDDDTEIKISIKQESTDINVIGNKDTVTEEDLDVFKQAQELSWEKIECESGVEDCGRYP
SVIEFGKYEIQTWYSSPYPQEYARLPKLYLCEFCLKYMKSKNILLRHSKKCGWFHPPANEIYRRRDLSVFEVDGNMSKIY
CQNLCLLAKLFLDHKTLYYDVEPFLFYVLTKNDEKGCHLVGYFSKEKLCQQKYNVSCIMIMPQHQRQGFGRFLIDFSYLL
SRREGQAGSPEKPLSDLGRLSYLAYWKSVILEYLYHHQERHISIKAISRATGMCPHDIATTLQHLHMIDKRDGRFVIIRR
EKLILGHMEKLKTCSRTNELDPESLRWTPILISNAAVSEEEREAEKEAERLMEQASCWEKEEQEILSSRANSRQSPAKVQ
SKNKYLHSPESRPVAGERGQLMELSKESSEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEENIQSSPPRLTKPQSVAIKRKR
PFVLKKKRGRKRRRINSSVTTETISETTEVLNEPFDNSDEERPMPHLEPTCEIEVEEDGGKPVLRKAFQHQPGKKKQTEE
EEEKDNHCFKNADPCRNNMDDDTDTLKEGSRDNPEPLKCKQVWPKGTKRGLSKWRPNKERKTGFKLNLYTPPETPMEPDD
QITVEEQKETPEDKSSPTPTRIEEEEVKEAMEPLLPQDENRRDETCAPISPNKSPGEKTEDDAIKPEEEEEEEEEEDDEEE
EEEEEEEEEEEENVAKDPGGAKSQEKEEPEVCLGKEDPVALDDHEEEEEEDEEPSHNEGHDADDEDDSHMEGVQAEKEDRP
REAFKEVLENQEAFLDLSVQPSHSNSEVLMDCGVDLAAACNGEPKELAGGTDAAPESDEESPEEQAPKQDQKSSEGVDSE
FKERNTATMEIDSETVQAVQSLTQENSEQDDTFQDCTETQEACRSLQNYTHADQSPQIATTLDDCQQSDHSSPVSSVHSH
PGQSVRSVNSPSVPALENSYAQISPDQSAISVPSLQNMETSPMMDVPSVSDHSQQVVDSGFSDLGSIESTTENYENPSSY
DSTMGGSICGNGSSQNSCSYSNLTSSNLTQSSCAVTQQMSNISGSCSMLQQTSISSPPTCSVKSPQGCVVERPPSSSQQL
AQCSMAANFTPPMQLPEIPETGNANIGLYERMGQSDFGAGHYPQPSATFSLAKLQQLTNTLIDHSLPYSHSAAVTSYANS
ASLSTPLSNTGLVQLSQSPHSVPGGPQAQATMTPPPNLTPPPMNLPPPLLQRNMAASNIGISHSQRLQTQIASKGHVSMR
TKSASLSPAAATHQSQIYGRSQTVAMQGPARTLTMQRGMNMSVNLMPAPAYNVNSVNMNMNTLNAMNGYSMSQPMMNSGY
HSNHGYMNQTPQYPMQMQMGMMGTQPYAQQPMQTPPHGNMMYTAPGHHGYMNTGMSKQSLNGSYMRR
```

1070 - 1089:	EEEEEEEEEEEEEEEEEEEE
1071 - 1090:	EEEEEEEEEEEEEEEEEEEE
1072 - 1091:	EEEEEEEEEEEEEEEEEEEE
1073 - 1092:	EEEEEEEEEEEEEEEEEEEE
1074 - 1093:	EEEEEEEEEEEEEEEEEEEE
1075 - 1094:	EEEEEEEEEEEEEEEEEEEE
1076 - 1095:	EEEEEEEEEEEEEEEEEEEE
1077 - 1096:	EEEEEEEEEEEEEEEEEEEE
1078 - 1097:	EEEEEEEEEEEEEEEEEEEE
1079 - 1098:	EEEEEEEEEEEEEEEEEEEE
1080 - 1099:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7U481 **A0A3Q7U481_URSAR** (829 aa)
C-Jun-amino-terminal kinase-interacting protein 2. *Ursus arctos horribilis*

```
MADRAEMFSLSTFHSLSPPGCRPPQDISLEEFDDEDLSEITDDCGLGLSYDSDHCEKDSLSLGRSEQPHPICSFQDDFQE
FEMIDDNEEEEEEEEEEEEEEEEEEEEEEEGEGEGKEGGGSGSEVPAPEALIPSPSLEESHKNRPTTLHLTTLGAQDSLNN
NGGFAPAPPASWQETVLCSPPQEPLRESPASLQPTDTSPCGAQSPVRPGCDCEGNRPASGPPAPCGASPSSDPGIEADLG
SHSSGGRGGRRSSQELSSPGSDSEDAGGARLGRMISSISETELELSSDGGSSSSGRSSHLTNSIEEASSPASEPEPEPEA
PCEPPRRPAFLPVGPDDTNSEYESGSESEPDLSEDADSPWLLSNLVSRMISEGSSPIRCPGQCLSPASRPSGEPASPVGG
AAEAPEAAAGPGGVELVDMETLCGPPPPAPSAPRPGPAQPGPCLFLSNPTRDTITPLWAAAGRSARPGRACSAACSEEDD
EDEEEEDADDKAGPPGGRGVGPAAPLDASLVYDAVKYTLVVDEHTQLELVSLRRCAGLGDDSSEDSGGEASEEETAATLL
GGGQGPEDASPDSPDLTFSKKFLNVFVNSTSRSSSTESFGLFSCLVNGEEKEQTHRAVFRFIPRHPDELELDVDDPVLVE
AEEDDFWFRGFNMRTGERGVFPAFYAHAVPGPAKDLLGSKRSPCWVERFDVQFLGSVEVPCHQGNGILCAAMQKIATARK
LTVHLRPPASCDLEISLRGVKLSLSGGPEFQHCSHFFQMKNISFCGCHPRNSCYFGFITKHPLLSRFACHVFVSQESMRP
VAQSVGRAFLEYYQEHLEYACPTEDIYLE
```

88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7UBG4 **A0A3Q7UBG4_URSAR** (1314 aa)
splicing factor, arginine/serine-rich 19. *Ursus arctos horribilis*

```
MEEEDESRGKTEESGEDRGDGPPDRDPTLSPSAFILRAIQQAVGSSLQGDLPNDKDGSRCHGLRWRRCRSPRSEPRSQES
GGTDTATVLDMAADSFLAGLVSVLDPPDTWVPSHLDLRPGESEDMLELVAEVRIGDRDPIPLPVPSLLPRLRAWRTGKTV
SPQPHSSRPSCARHLLTLGTGDGGPAPPPAPSSASSSPSPSPSSSSPSPPPPPPPPAPPAPPAPRFDIYDPFHPTDEAYS
PPPAPEQKYDPFEPTGSNPSSSAGTPSPEEEEEEEEEEEEEEEEEEEEEEEGLSQSISRISETLAGIYDDNSLSQDFPGD
ESPRPDPQPPQPTPAPGTPPQVDSTRVDGATRRRVFVVGTEAEACREGKVSVEVVTAGGAAIPPTLLPPGDSEIEEGEIV
QPEEEPRVAVSLFRASGGRAARPAPAAAAPPAAQPPPPPPAPRAPEGDDFLSLHAESDGESALQVDLGEPAPAPPAADTR
WGGLDLRRKILTQRRERYRQRSPSPATAAAASAAPAGPPTRKKSRRERKRSGGEAKEAASSSSGAPPAPPAPASPWDSKK
HRSRDRKPGSHASSSARRRSRSRSARRRSRSTDRRRGGSRRSRSREKRRRRRRSASPPPATSSSSSSRRERHRGKHRDGG
GSKKKKKRSRSRGEKRSGDSEKAPVPTQPPSGSSSLGGERDSRRRGAVPPSIQDLTDHDLFAIKRTITVGRPDKSDPRGP
SPAPASSPKREVLYDSEGLSAEERGGKSSEKDRRRSGAASSSSSSREKGSRRKALDGGDRDRDRDRDRDRDRSSKKARPP
KESAPSSGPPPKPPVSSGSGSSSSSCSSSSRKVKLQSKVAVLIREGVSSTTPAKEAASAGLGSIGVKFSRDRESRSPFLK
PDERAPAEVAKAAPGSTKPKKTKVKAKAGAKKAKGTKGKTKPSKTRKKIRSGGSSGGSGGPVTLKKSKADSCSQAAGAKG
VEETSWSGEERAAKAPSTPPPKAAPPPPALTPDSQTVDSSCKTPEVSFLPEEAAEEAGVRGGAEEEEEEEEEEEEEEEEE
EQQPATTTATSTAAAAPSAAPSAGSTAGDSGAEDGPATRVSQLPTLPPPMPWNLPAGVDCTTSGVLALTALLFKMEEANL
ASRAKAQELIQATNQILSHRKPPSSLGVTPAPVPTSLGLPPGPSSYLLPGSLPLGGCGSTPPTPTGLAAASDKREGSSSS
EGRGDTDKYLKKLHTQERAVEEVKLAIKPYYQKKDITKEEYKDILRKAVHKICHSKSGEINPVKVSNLVRAYVQRYRYFR
KHGRKPGDPPGPPRPPKEPGPPDKGGPGLPLPPL
```

269 - 288:	EEEEEEEEEEEEEEEEEEEE
270 - 289:	EEEEEEEEEEEEEEEEEEEE
271 - 290:	EEEEEEEEEEEEEEEEEEEE
272 - 291:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7UC47 **A0A3Q7UC47_VULVU** (1143 aa)
myelin transcription factor 1 isoform X1. *Vulpes vulpes (Red fox)*

```
MSLDNEDKRARTRSKAVRVPPEPTGADLSCPTPGCTGSGHIRGKYSRHRSLQSCPLAKKRKLEGAQAEHLVSKRKSHPLK
LALDEGYSVDTDGSEDAEVKDASVSDESEGTLEEDEAEMSGQEEIHRPEPAEGRSPVKSHFASKPIGSSAGPAKGSYSSY
QEIIATSLLNLGQIAVETLVGEDLGQGAKPGPAVVHLLQEEAEEEATSDEGEKDVFIRPDDTEDVVEVSRECSQEPGPQS
VEGVAREESSKMKVALGNEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEEEEEEEEEEEEEEEVPAPDVICQEDAPHAPTQ
KAPELRHPASPSPKPEYSVIVEVRSDDGKDEDSRSQKSAVTDESEMYDMMTRGNLGLLEQAIALKAEQVQAVCEPGCPPT
EQGQLGPGEPGKVARPLDASRKNYCSKDPSRAEKREIKCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRIPPEILAMHENV
LKCPTPGCTGQGHVNSNRNTHRSLSGCPIAAAEKLAKSHEKQQPQTGDPSKNSSNSDRILRPMCFVKQLEVPPYGSYRPS
VAPATPRANLAKELEKFSKVTFDYASFDAQVFGKRMLAPKIQTSETSPKAFKSKPFPKASSPRHSPCTSSSSAGFDYAHD
AEAAHMAATAILNLSTRCWEMPENLSTKPQDLPSKAADIEVDENGTLDLSMHKHRKRESAFPSSSSSSSSPGVKSPEASQ
RQSSTSAPSSSMTSPQSSQASRQDEWDRPLDYTKPSRQREEEPEESEPAAHSFASSEADDQEVSEESFEERKYPGEVTLT
NFKMKFLSKDIKKELLTCPTPGCDGSGHITGNYASHRSLSGCPLADKSLRNLMAAHSADLKCPTPGCDGSGHITGNYASH
RSLSGCPRAKKSGARVTPTKDDKEDPELMKCPVPGCVGLGHISGKYASHRSASGCPLAARRQKEGSLNGSPFSWKSLKNE
GPTCPTPGCDGSGHANGSFLTHRSLSGCPRATFAGKKGKVSGDEVLSTKFKTSDVLENDEEIKQLNQEIRDLNESNSEME
AAMVQLQSQISSMEKSLKNIEEENKLIEEQNEALFLELSGLSQALIQSLANIRLPHMEPICEQNFDAYVSTLTDMYSNQE
CYQNPENKDLLESIKRAVRGIQV
```

259 - 278:	EEEEEEEEEEEEEEEEEEEE
260 - 279:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE
262 - 281:	EEEEEEEEEEEEEEEEEEEE
263 - 282:	EEEEEEEEEEEEEEEEEEEE
264 - 283:	EEEEEEEEEEEEEEEEEEEE
265 - 284:	EEEEEEEEEEEEEEEEEEEE
266 - 285:	EEEEEEEEEEEEEEEEEEEE
267 - 286:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7UDA2 **A0A3Q7UDA2_URSAR** (2904 aa)

WD repeat-containing protein 87. *Ursus arctos horribilis*

```
MSSARLIPLWKDFKYLVNDIIHKSKQTSEDPKNDVVVLSDQSQILFRESRHPQNMPLICYYFSDANFFASLSWVTSAKEI
QAVVWMKSKTEDMVEKRTFSMTERLPPIQSMVHTGSFHILVAYCGDLILRLFGDHFRSFKPLGIVPCRFNINCLCYDPEM
KMLLSGILGAVVTWIIERSGKGLQVAHMVPMSGDELVQDIRLNGPNGSLLALCETVARVLERQGHGQLGEVQRFTSTTSG
SFITCCFTCFDQGFLYAGNKTGEIQVWSLVRGNSLHSFKAHFSSVICIRSRPEAHTLLTAGKEGLIKEWNLTLGNLLRRL
ELGEELYKLEFIDNITFFCQTTHTFSLRRLPCFYSLFNVCGSAPQQLRRVHCGENRFRILCSTEDGLLRFVSPLTGDLLV
LTWPFAILDQAVDWAYDPEKEELFVATGNAEVLVFDTTRCPCPAKYLLCTSPDSQDWVQCLAYGHFHLGRGLQGLVFSGH
QSGVIRVLSQNYCARIEKFMHFGAILALSTLPGGVFGSRENSLLCSYGMDDYVHLSEAVLEGKKVHLKPLASILSSCHLK
HLILLPTSVGAITETNCLRLWKFHDFLSSESQEGSTFIETLPLHQCPITSFDVCWSLSLFVTGGIDGSVRVWNFHGRLVA
MLDSSLHFGPLCFANDRGDLLVTFNHSLYLVSCLKLLHPTLLARLSFMSMTDEVLEAPKPFTPSFFFSFETIFVPKYIYL
GKGQQELVGLEKLVNKRAIAFDHTVPHVIEEDEQGSPTLLSAFRCGFLHKEETDGMEVSKPPHYMFPPQLQLTTWDGLNP
YQLLRCYFGHGRKWLLAPDCYIPNSVIRARLWPEGSPIYLQCNLHSPVWEMEWDKSEQFFFWHSREKALSDAGEYSQERE
DADFIEMRLSKDITYSVLTDSANRSWLGKKMSEIAINSLVETILNIMIHASPLKYQCCIGALGQIFASYEVSSSLRSETA
HRLLDDTTNSNPLIRELAWEGLKRLGMITHLFAMPLAQGLMDKDQRVRSKALSLMADTGIHSKSSLLNLIQHRETFREMQ
QEMIGEESLDHLLGMRATDLQVLHTQVEQRLNENLTLSEGQEKPAFSLEVSRVSEHVSLSKQPDVIPEETEAATKSGKGQ
RRGRAAVKKHTRKLWRAFKKIKEAGKEPGPLEGESDQREAAPVLVEDTATHSRMSSTISVLKISKDGEQHPPEKDTSKDH
FALTLKMLRKIHDRKGKKRTVQKPQKRHKKKTKDAEVTTEESLPAVKKEPVVKQLKAKGRGAAGAPGRKTIPEEGSSWRD
DLCRLMTLRISGSQTKMSEALNMELVTMAQEVLADQQPSWELFQEICPLLEKKSEVLLEDLQWDIAWPEERPIFIHERAI
REDMMVRREDEIPEVQEQVQKEAEDTPYLQETQVIPKKGKKKKIIFLGPSSLTKGKRISKKEEKNSFKKPFKQERKEVQQ
EIKVDKKETVSKGERDVSQEIEEVAKPEEEEVVKQEERPIMDERKLSWQEWKKSWDEWKQAQDETKISWDEWKNAWDKRH
LEEEEKQQTDERKPLPEEEKLDVDKLRWDEWLDVWEKIEARSREEHKDEEELTLEGEELSQEWGEEEQEEVMSEEQRQIQ
KEYNQAWIERKRAQAERKRAQEERKLAQEEEKLAQEERKLAQEERKLAREYGKLAQRDRTMVQAERNFVHNEEKLAQRED
KLSQEAEKLAQKRKKLAKQFEELAREEEKTAKKGGKLAEVKKILAQKMEKLTQKEQDLALQEKELAQELEELMWEEEELV
RKEEELNQELKDLAEEEEGLVQEEKTLAWQEQKLIKEEKTLALEEELLIQEEKKLAQDKEKLPGEEENLAQKRKKLMENK
LKLAQEKEKLAQDKEKLTKNKNILAWREKSLAQEKENLLQEKVKLAQRKENFLQVKQNLAQNKNKLVQAKEKLDMYKKKL
AQVEKKLMEEKEKLSQKKEKLDEAEKKLTQLEESLAQKQHNLAQDKMELATEKRAVFQELKMLRGEWDSAKEEKALGTEM
KKLAQEKIRLAEEKQILSAGETEETLKQIRLTKNELELIKRKLSLEEKILRYEDRVLATEQRDIAKGKLEFTRGGRVFAQ
EERKLAKVVRKLIKEKEGTSRAQSKVSSKVLKALRDLTKKEMKLTQEEIEMTKMKRNFFVKERRLSKEQNKLDAKEWDFS
EEEPEVTKDEKKLAKKQRKLAKEMKRMMKKEKKITEEESRLARQQREVIQEEKEEGLTKDEEVIPLLEQRSRKREEKGRK
ELKTVDTPWEKLPSQKESRDSLSEEMESLLDEIEQESLSEEEEEEEEEEEEEEEEEEEEEEEERKEEEEKEEEEKEEEEE
EEEGEEEEGSEEEEEESISEEESESLREEESESLSEKEEGESSLKKEADKKKEILKKEKLFKSQEERQKDRRGREIIPSI
GKRIPDIKDSAIQLKILKAPSRKVIPIALGRQEKIPVPVSMKQVPWEEKARAPEASRILPESRFMDRQGELLKKYKPKPL
QLLDTVLESPERDLKTPYLPHILRKTMEAHNLQGEPLEPKWQWILKHHPALMRKTKVPVPQIWAKEIGAQVGLSDIEWIH
HVLERMEAGEQLSRDSFHRLCQLLKDLTSKGNLEWLHLAQLEAIVYHHKQVLESQSTHISKPSKEPMGPKYLKVIPPIKG
KESWLKPFAVPIPKSPLGTKGIPTPKGVNWHLLEEPYRSAWAEQISTALKEMEVQHFHPATGDIFIGAHASVEKQTLALM
FQKDFWDFKDKGRFPRLPKLEKKAQAISKKKEEVPLWETFVALYYVLRMLQQRYAKDSAAWMEQFHQLMDLYQLKSPRIQ
KLLQELLLREEPQSQEITYEEALKAMELVPGERLFCHLFCGGSQNPKGPLEFREVVSLPGQNNVRTMSPMGIAQYGILEL
AWKSLPQADIHLTKEMPHIIAPAP
```

2280 - 2299:	EEEEEEEEEEEEEEEEEEEE
2281 - 2300:	EEEEEEEEEEEEEEEEEEEE
2282 - 2301:	EEEEEEEEEEEEEEEEEEEE
2283 - 2302:	EEEEEEEEEEEEEEEEEEEE
2284 - 2303:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7UDM6 **A0A3Q7UDM6_URSAR** (1211 aa)
histone-lysine N-methyltransferase EHMT2 isoform X3. *Ursus arctos horribilis*

```
MAAAAGAAAAAAAEGEAPAEMGALVLEKEPRGATERVHGSLGDTPRSEETLPKASPDSLEPAGPSSPASVTVTVGDEGAD
TPVGATPLIGDEPETLEGDGDLHGGRILLGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGA
ATAGPEPPVATPSPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDMHSLGKMTSEVAKRRKMNTGGGLSEEL
GSTRGSGEVTVEKGDPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEE
EEEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGT
LSPNHAGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMV
LCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAG
TAAPAPPPLAQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPPGPGREALEKALVIQ
ESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANLNAVDKQQR
TPLMEAVVNNHLELARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIE
VIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPEL
RNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCET
STMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVR
LQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNI
IPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELL
PELSSLPPVNP
```

300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7UQB0 **A0A3Q7UQB0_URSAR** (1268 aa)
histone-lysine N-methyltransferase EHMT2 isoform X1. *Ursus arctos horribilis*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWAPQLPTGLTSPPVPCVPCQGEAPAEMGA
LVLEKEPRGATERVHGSLGDTPRSEETLPKASPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDEPETLEGDGDLH
GGRILLGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAATAGPEPPVATPSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDMHSLGKMTSEVAKRRKMNTGGGLSEELGSTRGSGEVTVEKGDPGSLEEWE
TVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKA
KKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEE
LPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCT
AGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLAQDAPGRADTSQPS
```

```
ARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPPGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGE
LQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANLNAVDKQQRTPLMEAVVNNHLELARYMVQRGG
CVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICL
HWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQ
LNRKLRLGVGNRAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSS
SNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGT
FICEYVGELISDAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSR
DIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELSSLPPVNP
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7UQB5 **A0A3Q7UQB5_URSAR** (1029 aa)
histone-lysine N-methyltransferase EHMT2 isoform X5. *Ursus arctos horribilis*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWAPQLPTGLTSPPVPCVPCQGEAPAEMGA
LVLEKEPRGATERVHGSLGDTPRSEETLPKASPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDEPETLEGDGDLH
GGRILLGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAATAGPEPPVATPSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDMHSLGKMTSEVAKRRKMNTGGGLSEELGSTRGSGEVTVEKGDPGSLEEWE
TVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKA
KKKWRKDSPWVKPSRKRRKREPPRAKEPRGVNGVGSSGPSEYMEVPLGSLELPSEGTLSPNHAGVSNDTSSLETERGFEE
LPLCSCRMEAPKIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCT
AGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLAQDAPGRADTSQPS
ARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGGCLSAVGLPPGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGE
LQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANLNAVDKQQRTPLMEAVVNNHLELARYMVQRGG
CVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICL
HWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQ
LNRKLRLGVGNRAIRTEKIICRAPSPMSLLSGMWLGAMRMCLFPVSTAWMGSPALRITSTSRRTARHPP
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7URE0 **A0A3Q7URE0_URSAR** (1319 aa)
pleckstrin homology domain-containing family G member 3-like isoform X2. *Ursus arctos horribilis*

```
MPVSASLRRDGSQERPVSLTSTTSSSGSSRDSRGAMEEPSGPEAAAENGAGSLRGRHPPNGSTGSGGWLSGRGPLSPFGG
RATAAPVHKLSYLGRVVREIVETERMYVQDLRSIVEDYLLKIIDTPGLLTPEQVSALFGNIENIYALNSQLLRDLDSCNS
DPVAVASCFVERSQEFDIYTQYCNNYPNSVAALTECMRDKQQAKFFRDRQALLQHSLPLGSYLLKPVQRILKYHLLLQEI
AKHFDEEEDGFEVVEDAIDTMTCVAWYINDMKRRHEHAVRLQEVQSLLINWKGPDLTIYGELVLEGTFRVHRVRNERTFF
LFDKALLVTKKRGDHFVYKGHIPCSSLMLIESTRDSLCFTVTHYKHSKQQYNIQAKTVEEKRSWTHHIKRLILENHHTTI
PQKAKEAILEMDSYYPSRYRCSPERLKKAWSSQDEVSAHARQGRRQSEPARHLLRQPTEKARAAGMKHAGSAGALLDFGR
SPRTQGVQPEAEGAAREEEEEEEEEEEEEEEEEEEEEVVEEEEEEQAFQVSLEDLAGHEGSEKGARLDPPGSEEEEEEEE
EESLAVAEQEKGRRESEGPKSRRRSSGRSPTSTEKRVSLESASSLPDVEPDPEPEMEQEVFAAVEVPGIEEVPSDTESPE
ALETQLDAHQELLGLDPPGDMVDFVVAESTEDLKALSSEEEEEEEEEDMATQEAESLLPPSVLDQASVIAERFVGSFSRR
SSLAPEDGTAGGFGSPRLMSRSSSVLSLEGSEKGPARPGSTADALSSQLPPEVDSAAGVAADSGPSVNGTEPPSPGCPAE
PDRSSCKKKESTLSTRDRLLLDRIKSYYENAEHHDAGFSIRRRESLSYIPKGLVRNSVSRFNSLPRPDPEPVAPLGRKRQ
VGSRPPSWALFDLSGPGQASAGEPAPITDAEFRPSSEIVKIWDGMESPGESSRKGPCQGQANGFDLHEPLFILEEHELGA
ITEESATASPESASPTERPSPAHLARELKELVKELSSGVQGELVTPLHPRIVQLSHMMDGHVSERVKNKVYQLARQYSLR
IKSKSVTARPPLQWGKAAPIVPCLQEEAGAPSGGKGTRKPVLSLLHYEQTVAQEHSPPKPGSPRHLSFSPTAANPRTTSP
GVRPSSRSPLSPFDSETFNWPDVRELCSKYASHDEAFQAEGSRPRGPPVNRSRSAPENMVEPPLAGRVGRCCSVGSGRGR
AGPEASQPQPLGRLPQSRLVGEEALYVTADLTLENNRRVIVMEKGPLPCPAAGLEEGSGQGPSSPAAVVGQGLDFQESGI
SRSPEYWPKEEAPRDPADPSQQGRVRNLREKFQALNSIG
```

497 - 516:	EEEEEEEEEEEEEEEEEEEE
498 - 517:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7UU27 **A0A3Q7UU27_VULVU** (1120 aa)
myelin transcription factor 1 isoform X3. *Vulpes vulpes (Red fox)*

```
MSLDNEDKRARTRSKAVRVPPEPTGADLSCPTPGCTGSGHIRGKYSRHRSLQSCPLAKKRKLEGAQAEHLVSKRKSHPLK
LALDEGYSVDTDGSEDAEVKDASVSDESEGTLEEDEAEMSGQEEIHRPEPAEGRSPVKSHFASKPIGSSAGPAKGSYSSY
QEIIATSLLNLGQIAVETLVGEDLGQGAKPGPAVVHLLQEEAEEEATSDEGEKDVFIRPDDTEDVVEVSRECSQEPGPQS
VEGVAREESSKMKVALGNEEEEEEEEEEEEEEEEEEEEEEEEEEEEEDEEEEEEEEEEEEEEEVPAPDVICQEDAPHAPTQ
KAPELRHPASPSPKPEYSVIVEVRSDDGKDEDSRSQKSAVTDESEMYDMMTRGNLGLLEQAIALKAEQVQAVCEPGCPPT
EQGQLGPGEPGKVARPLDASRKNYCSKDPSRAEKREIKCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRIPPEILAMHENV
LKCPTPGCTGQGHVNSNRNTHRSLSGCPIAAAEKLAKSHEKQQPQTGDPSKNSSNSDRILRPMCFVKQLEVPPYGSYRPS
VAPATPRANLAKELEKFSKVTFDYASFDAQVFGKRMLAPKIQTSETSPKAFKSKPFPKASSPRHSPCTSSSSAGFDYAHD
AEAAHMAATAILNLSTRCWEMPENLSTKPQDLPSKAADIEVDENGTLDLSMHKHRKRESAFPSSSSSSSSPGVKSPEASQ
RQSSTSAPSSSMTSPQSSQASRQDEWDRPLDYTKPSRQREEEPEESEPAAHSFASSEADDQEVSEESFEERKYPGEVTLT
NFKMKFLSKDIKKELLTCPTPGCDGSGHITGNYASHRRCPTPGCDGSGHITGNYASHRSLSGCPRAKKSGARVTPTKDDK
```

```
EDPELMKCPVPGCVGLGHISGKYASHRSASGCPLAARRQKEGSLNGSPFSWKSLKNEGPTCPTPGCDGSGHANGSFLTHR
SLSGCPRATFAGKKGKVSGDEVLSTKFKTSDVLENDEEIKQLNQEIRDLNESNSEMEAAMVQLQSQISSMEKSLKNIEEE
NKLIEEQNEALFLELSGLSQALIQSLANIRLPHMEPICEQNFDAYVSTLTDMYSNQECYQNPENKDLLESIKRAVRGIQV
```

259 - 278:	EEEEEEEEEEEEEEEEEEEE
260 - 279:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE
262 - 281:	EEEEEEEEEEEEEEEEEEEE
263 - 282:	EEEEEEEEEEEEEEEEEEEE
264 - 283:	EEEEEEEEEEEEEEEEEEEE
265 - 284:	EEEEEEEEEEEEEEEEEEEE
266 - 285:	EEEEEEEEEEEEEEEEEEEE
267 - 286:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7V0N4 **A0A3Q7V0N4_URSAR** (1318 aa)
pleckstrin homology domain-containing family G member 3-like isoform X2. *Ursus arctos horribilis*

```
MPVSASLRRDGSQERPVSLTSTTSSSGSSRDSRGAMEEPSGPEAAAENGAGSLRGRHPPNGSTGSGGWLSGRGPLSPFGG
RATAAPVHKLSYLGRVVREIVETERMYVQDLRSIVEDYLLKIIDTPGLLTPEQVSALFGNIENIYALNSQLLRDLDSCNS
DPVAVASCFVERSQEFDIYTQYCNNYPNSVAALTECMRDKQQAKFFRDRQALLQHSLPLGSYLLKPVQRILKYHLLLQEI
AKHFDEEEDGFEVVEDAIDTMTCVAWYINDMKRRHEHAVRLQEVQSLLINWKGPDLTIYGELVLEGTFRVHRVRNERTFF
LFDKALLVTKKRGDHFVYKGHIPCSSLMLIESTRDSLCFTVTHYKHSKQQYNIQAKTVEEKRSWTHHIKRLILENHHTTI
PQKAKEAILEMDSYYPSRYRCSPERLKKAWSSQDEVSAHARQGRRQSEPARHLLRQPTEKARAAGMKHAGSAGALLDFGR
SPRTQGVQPEAEGAAREEEEEEEEEEEEEEEEEEEEEEVVEEEEEEQAFQVSLEDLAGHEGSEKGARLDPPGSEEEEEEEE
ESLAVAEQEKGRRESEGPKSRRRSSGRSPTSTEKRVSLESASSLPDVEPDPEPEMEQEVFAAVEVPGIEEVPSDTESPEA
LETQLDAHQELLGLDPPGDMVDFVVAESTEDLKALSSEEEEEEEEEDMATQEAESLLPPSVLDQASVIAERFVGSFSRRS
SLAPEDGTAGGFGSPRLMSRSSSVLSLEGSEKGPARPGSTADALSSQLPPEVDSAAGVAAESGPSVNGTEPPSPGCPAEP
DRSSCKKKESTLSTRDRLLLDRIKSYYENAEHHDAGFSIRRRESLSYIPKGLVRNSVSRFNSLPRPDPEPVAPLGRKRQV
GSRPPSWALFDLSGPGQASAGEPAPITDAEFRPSSEIVKIWDGMESPGESSRKGPCQGQANGFDLHEPLFILEEHELGAI
TEESATASPESASPTERPSPAHLARELKELVKELSSGVQGELVTPLHPRIVQLSHMMDGHVSERVKNKVYQLARQYSLRI
KSKSVTARPPLQWGKAAPIVPCLQEEAGAPSGGKGTRKPVLSLLHYEQTVAQEHSPPKPGSPRHLSFSPTAANPRTTSPG
VRPSSRSPLSPFDSETFNWPDVRELCSKYASHDEAFQAEGSRPRGPPVNRSRSAPENMVEPPLAGRVGRCCSVGSGRGRA
GPEASQPQPLGRLPQSRLVGEEALYVTADLTLENNRRVIVMEKGPLPCPAAGLEEGSGQGPSSPAAMVGQGLDFQESGIS
RSPEYWPKEEAPRDPADPSQQGRVRNLREKFQALNSIG
```

497 - 516:	EEEEEEEEEEEEEEEEEEEE
498 - 517:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7V5Y5 **A0A3Q7V5Y5_URSAR** (1234 aa)
histone-lysine N-methyltransferase EHMT2 isoform X2. *Ursus arctos horribilis*

```
MRGLPRGRGLMRARGRGRAAPPGSRGRGRGGPHRGRGRPRSLLSLPRAQASWAPQLPTGLTSPPVPCVPCQGEAPAEMGA
LVLEKEPRGATERVHGSLGDTPRSEETLPKASPDSLEPAGPSSPASVTVTVGDEGADTPVGATPLIGDEPETLEGDGDLH
GGRILLGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAATAGPEPPVATPSPEGQPKVHRA
RKTMSKPGNGQPPVPEKRPPEVQHFRMSDDMHSLGKMTSEVAKRRKMNTGGGLSEELGSTRGSGEVTVEKGDPGSLEEWE
TVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEEEEEEEDEESGNQSDRSGSSGRRKA
KKKWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAPKIDRISERAGHKCMATESVDGEL
SGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDFRVAHRFHKACVSQLNGMVFCPHC
GEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLAQDAPGRADTSQPSARMRGHGEPRRPPCDPLADTIDSSGPSLTLPNGG
CLSAVGLPPGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDNLDPNFQSDQQSKRTPLHAAAQKG
SVEICHVLLQAGANLNAVDKQQRTPLMEAVVNNHLELARYMVQRGGCVYSKEEDGSTCLHHAAKIGNLEMVSLLLSTGQV
DVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAIAEVLLNARCDLHAVNYHGDTPLH
IAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGNRAIRTEKIICRDVARGYENVPIP
CVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIRCWYDKDGRLLQEFNKIEPPLIFE
CNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELISDAEADVREDDSYLFDLDNKDGEV
YCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFDYGDRFWDIKSKYFTCQCGSEKCK
HSAEAIALEQSRLARLDPHPELLPELSSLPPVNP
```

357 - 376:	EEEEEEEEEEEEEEEEEEEE
358 - 377:	EEEEEEEEEEEEEEEEEEEE
359 - 378:	EEEEEEEEEEEEEEEEEEEE
360 - 379:	EEEEEEEEEEEEEEEEEEEE
361 - 380:	EEEEEEEEEEEEEEEEEEEE
362 - 381:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7VIG6 **A0A3Q7VIG6_URSAR** (1349 aa)
pleckstrin homology domain-containing family G member 3-like isoform X1. *Ursus arctos horribilis*

```
MPVSASLRRDGSQERPVSLTSTTSSSGSSRDSRGAMEEPSGPEAAAENGAGSLRGRHPPNGSTGSGGWLSGRGPLSPFGG
RATAAPVHKLSYLGRVVREIVETERMYVQDLRSIVEDYLLKIIDTPGLLTPEQVSALFGNIENIYALNSQLLRDLDSCNS
DPVAVASCFVERSQEFDIYTQYCNNYPNSVAALTECMRDKQQAKFFRDRQALLQHSLPLGSYLLKPVQRILKYHLLLQEI
AKHFDEEEDGFEVVEDAIDTMTCVAWYINDMKRRHEHAVRLQEVQSLLINWKGPDLTIYGELVLEGTFRVHRVRNERTFF
LFDKALLVTKKRGDHFVYKGHIPCSSLMLIESTRDSLCFTVTHYKHSKQQYNIQAKTVEEKRSWTHHIKRLILENHHTTI
PQKAKEAILEMDSYYPSRYRCSPERLKKAWSSQDEVSAHARQGRRQSEPGQRSFIRATLPSRQRGFMEPGLNGRRKSEPA
RHLLRQPTEKARAAGMKHAGSAGALLDFGRSPRTQGVQPEAEGAAREEEEEEEEEEEEEEEEEEEEEVVEEEEEEQAFQV
```

```
SLEDLAGHEGSEKGARLDPPGSEEEEEEEEEESLAVAEQEKGRRESEGPKSRRRSSGRSPTSTEKRVSLESASSLPDVEP
DPEPEMEQEVFAAVEVPGIEEVPSDTESPEALETQLDAHQELLGLDPPGDMVDFVVAESTEDLKALSSEEEEEEEEEDMA
TQEAESLLPPSVLDQASVIAERFVGSFSRRSSLAPEDGTAGGFGSPRLMSRSSSVLSLEGSEKGPARPGSTADALSSQLP
PEVDSAAGVAADSGPSVNGTEPPSPGCPAEPDRSSCKKKESTLSTRDRLLLDRIKSYYENAEHHDAGFSIRRRESLSYIP
KGLVRNSVSRFNSLPRPDPEPVAPLGRKRQVGSRPPSWALFDLSGPGQASAGEPAPITDAEFRPSSEIVKIWDGMESPGE
SSRKGPCQGQANGFDLHEPLFILEEHELGAITEESATASPESASPTERPSPAHLARELKELVKELSSGVQGELVTPLHPR
IVQLSHMMDGHVSERVKNKVYQLARQYSLRIKSKSVTARPPLQWGKAAPIVPCLQEEAGAPSGGKGTRKPVLSLLHYEQT
VAQEHSPPKPGSPRHLSFSPTAANPRTTSPGVRPSSRSPLSPFDSETFNWPDVRELCSKYASHDEAFQAEGSRPRGPPVN
RSRSAPENMVEPPLAGRVGRCCSVGSGRGRAGPEASQPQPLGRLPQSRLVGEEALYVTADLTLENNRRVIVMEKGPLPCP
AAGLEEGSGQGPSSPAAVVGQGLDFQESGISRSPEYWPKEEAPRDPADPSQQGRVRNLREKFQALNSIG
```

527 - 546:	EEEEEEEEEEEEEEEEEEEE
528 - 547:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7VK31 **A0A3Q7VK31_URSAR** (1177 aa)
histone-lysine N-methyltransferase EHMT2 isoform X4. *Ursus arctos horribilis*

```
MAAAAGAAAAAAAAEGEAPAEMGALVLEKEPRGATERVHGSLGDTPRSEETLPKASPDSLEPAGPSSPASVTVTVGDEGAD
TPVGATPLIGDEPETLEGDGDLHGGRILLGHATKSFPSSPSKGGACPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGA
ATAGPEPPVATPSPEGQPKVHRARKTMSKPGNGQPPVPEKRPPEVQHFRMSDDMHSLGKMTSEVAKRRKMNTGGGLSEEL
GSTRGSGEVTVEKGDPGSLEEWETVVGDDFSLYYDSYSVDERVDSDSKSEVEALAEQLSEEEEEEEEEEEEEEEEEEEE
EEEEDEESGNQSDRSGSSGRRKAKKKWRKDSPWVKPSRKRRKREPPRAKEPRGVSNDTSSLETERGFEELPLCSCRMEAP
KIDRISERAGHKCMATESVDGELSGCNAAILKRETMRPSSRVALMVLCETHRARMVKHHCCPGCGYFCTAGTFLECHPDF
RVAHRFHKACVSQLNGMVFCPHCGEDASEAQEVTIPRGDGVTPPAGTAAPAPPPLAQDAPGRADTSQPSARMRGHGEPRR
PPCDPLADTIDSSGPSLTLPNGGCLSAVGLPPGPGREALEKALVIQESERRKKLRFHPRQLYLSVKQGELQKVILMLLDN
LDPNFQSDQQSKRTPLHAAAQKGSVEICHVLLQAGANLNAVDKQQRTPLMEAVVNNHLELARYMVQRGGCVYSKEEDGST
CLHHAAKIGNLEMVSLLLSTGQVDVNAQDSGGWTPIIWAAEHKHIEVIRMLLTRGADVTLTDNEENICLHWASFTGSAAI
AEVLLNARCDLHAVNYHGDTPLHIAARESYHDCVLLFLSRGANPELRNKEGDTAWDLTPERSDVWFALQLNRKLRLGVGN
RAIRTEKIICRDVARGYENVPIPCVNGVDGEPCPEDYKYISENCETSTMNIDRNITHLQHCTCVDDCSSSNCLCGQLSIR
CWYDKDGRLLQEFNKIEPPLIFECNQACSCWRNCKNRVVQSGIKVRLQLYRTAKMGWGVRALQTIPQGTFICEYVGELIS
DAEADVREDDSYLFDLDNKDGEVYCIDARYYGNISRFINHLCDPNIIPVRVFMLHQDLRFPRIAFFSSRDIRTGEELGFD
YGDRFWDIKSKYFTCQCGSEKCKHSAEAIALEQSRLARLDPHPELLPELSSLPPVNP
```

300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
302 - 321:	EEEEEEEEEEEEEEEEEEEE
303 - 322:	EEEEEEEEEEEEEEEEEEEE
304 - 323:	EEEEEEEEEEEEEEEEEEEE
305 - 324:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7VQ30 **A0A3Q7VQ30_URSAR** (1323 aa)
tau-tubulin kinase 1. *Ursus arctos horribilis*

```
MQCLAAALKDETNMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTRENVALKVESAQQPKQVLKMEVAV
LKKLQGKSHVCRFIGCGRNEKFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESIEAIHSVGFLHRDIKPSNF
AMGRLPSTYRKCYMLDFGLARQYTNTTGDVRPPRNVAGFRGTVRYASVNAHKNREMGRHDDLWSLFYMLVEFAVGQLPWR
KIKDKEQVGMIKEKYEHRMLLKHMPSEFHLFLDHIAGLDYFTKPDYQLIMSVFENSMKERGIAENEAFDWEKAGNDALLS
TSTSTPPQQNTRQTAAMFGVVNVTPVPGDLLRENTEDVLQGEHLSDQENAPPILPGRPPEGLGPSPHLAPHPGGPEAEVW
EETDVNRNKLRINIGKTPCVVEEEQSRAVGVPSSPVRAPPDSPTTPVRSLRYRRVNSPESERLSTADGRVELHERRSRMD
LPGSPSRQACSSQPAQMLSVDTGHPDRQASGRMDVSASVEQEALSNAFRSVPLAEEEDFDSKEWVIIDKETELKDFPPGA
EPSTSGTTDEEPEELRPLPEEGEERRRPGAEPTVRPRGRGMQTLAEEDPRQTPFQPLPPQPSQAEGRSETSQPPTPGSPS
HSTLHSGPRPRRRESDPTGPQRQVFSVAPPFEVNGLPRAVPLSLPYQDFKKDLSDYRERARLLNRVRRVGFSHMLLTTPQ
VPLAPVQPQANGKEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEAVALGEVLGPRSGSSS
DGSERSTDRSQEGAPSTLLADDQKESRGRASMADGDLEPEEGSKTLVLVSPGDMKKSPVTADLAPDPDLGTLAALTPQQE
RPQPTGSQLDVSEPGTLSSVLKSEPKPPGPGPGPGAGAVTTGAGGVAVTSSPFTKVERTFVHIAEKTHLNVMSSGGQASR
PEELGAGGELGLEAPSDGRAVEEGASVPLENGIAQAGLESRALSGPSGDTPLEVATDSLPNGPALANGPAPASPLEPSPE
KLATISPSRHAMAGPRPRSRIPVLLSEEDTGSEPSGSLSAKERWGKRARPQQDLARLVMEKRQGRLLLRLASGASSSSSE
EQRPASETLSGTGSEEDAPASEPTAPRKAGRAAASRSRIPRPISIRMATPAAAQQQSTGRPHGAPAPDTAITSRLQLQKP
PVSAVAADLRPKQPPGRGPGPGRAAACTRPPAPRSPGPSAAAAPRHPSASPRSQSLSRKESSSPSHQARPAGPPPRGAPQ
ARAQPDGTPSPGGPKKGPRGKLQTQRAATKGRAGVAEGRAGAR
```

734 - 753:	EEEEEEEEEEEEEEEEEEEE
735 - 754:	EEEEEEEEEEEEEEEEEEEE
736 - 755:	EEEEEEEEEEEEEEEEEEEE
737 - 756:	EEEEEEEEEEEEEEEEEEEE
738 - 757:	EEEEEEEEEEEEEEEEEEEE
739 - 758:	EEEEEEEEEEEEEEEEEEEE
740 - 759:	EEEEEEEEEEEEEEEEEEEE
741 - 760:	EEEEEEEEEEEEEEEEEEEE
742 - 761:	EEEEEEEEEEEEEEEEEEEE
743 - 762:	EEEEEEEEEEEEEEEEEEEE
744 - 763:	EEEEEEEEEEEEEEEEEEEE
745 - 764:	EEEEEEEEEEEEEEEEEEEE

746 - 765:	EEEEEEEEEEEEEEEEEEEE
747 - 766:	EEEEEEEEEEEEEEEEEEEE
748 - 767:	EEEEEEEEEEEEEEEEEEEE
749 - 768:	EEEEEEEEEEEEEEEEEEEE
750 - 769:	EEEEEEEEEEEEEEEEEEEE
751 - 770:	EEEEEEEEEEEEEEEEEEEE
752 - 771:	EEEEEEEEEEEEEEEEEEEE
753 - 772:	EEEEEEEEEEEEEEEEEEEE
754 - 773:	EEEEEEEEEEEEEEEEEEEE
755 - 774:	EEEEEEEEEEEEEEEEEEEE
756 - 775:	EEEEEEEEEEEEEEEEEEEE
757 - 776:	EEEEEEEEEEEEEEEEEEEE
758 - 777:	EEEEEEEEEEEEEEEEEEEE
759 - 778:	EEEEEEEEEEEEEEEEEEEE
760 - 779:	EEEEEEEEEEEEEEEEEEEE
761 - 780:	EEEEEEEEEEEEEEEEEEEE
762 - 781:	EEEEEEEEEEEEEEEEEEEE
763 - 782:	EEEEEEEEEEEEEEEEEEEE
764 - 783:	EEEEEEEEEEEEEEEEEEEE
765 - 784:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7VUI3 **A0A3Q7VUI3_URSAR** (737 aa)
YTH domain-containing protein 1 isoform X1. *Ursus arctos horribilis*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDIKRQKPSVHSRQLISKPLSSSVSN
NKRIVSTKGKSVAEYKNEEYQRSERTKRLEADRKIRLSSSASREPYKSQPEKTCLRKRDPERRTKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEE
EEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSS
ASESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSARSVI
LIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQ
EIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYAPEFH
QRPGYLKDPRYQEVDSFTNLIPNRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMAPYPGMEQPPHHPYYQHHAPPP
QAHPPYSGHHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERE
RLCDRDRDRGERGRYRR
```

229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7VXJ7 **A0A3Q7VXJ7_URSAR** (1348 aa)
pleckstrin homology domain-containing family G member 3-like isoform X1. *Ursus arctos horribilis*

```
MPVSASLRRDGSQERPVSLTSTTSSSGSSRDSRGAMEEPSGPEAAAENGAGSLRGRHPPNGSTGSGGWLSGRGPLSPFGG
RATAAPVHKLSYLGRVVREIVETERMYVQDLRSIVEDYLLKIIDTPGLLTPEQVSALFGNIENIYALNSQLLRDLDSCNS
DPVAVASCFVERSQEFDIYTQYCNNYPNSVAALTECMRDKQQAKFFRDRQALLQHSLPLGSYLLKPVQRILKYHLLLQEI
AKHFDEEEDGFEVVEDAIDTMTCVAWYINDMKRRHEHAVRLQEVQSLLINWKGPDLTIYGELVLEGTFRVHRVRNERTFF
LFDKALLVTKKRGDHFVYKGHIPCSSLMLIESTRDSLCFTVTHYKHSKQQYNIQAKTVEEKRSWTHHIKRLILENHHTTI
PQKAKEAILEMDSYYPSRYRCSPERLKKAWSSQDEVSAHARQGRRQSEPGQRSFIRATLPSRQRGFMEPGLNGRRKSEPA
RHLLRQPTEKARAAGMKHAGSAGALLDFGRSPRTQGVQPEAEGAAREEEEEEEEEEEEEEEEEEEEEVVEEEEEEQAFQV
SLEDLAGHEGSEKGARLDPPGSEEEEEEEEESLAVAEQEKGRRESEGPKSRRRSSGRSPTSTEKRVSLESASSLPDVEPD
PEPEMEQEVFAAVEVPGIEEVPSDTESPEALETQLDAHQELLGLDPPGDMVDFVVAESTEDLKALSSEEEEEEEEEDMAT
QEAESLLPPSVLDQASVIAERFVGSFSRRSSLAPEDGTAGGFGSPRLMSRSSSVLSLEGSEKGPARPGSTADALSSQLPP
EVDSAAGVAAESGPSVNGTEPPSPGCPAEPDRSSCKKKESTLSTRDRLLLDRIKSYYENAEHHDAGFSIRRRESLSYIPK
GLVRNSVSRFNSLPRPDPEPVAPLGRKRQVGSRPPSWALFDLSGPGQASAGEPAPITDAEFRPSSEIVKIWDGMESPGES
SRKGPCQGQANGFDLHEPLFILEEHELGAITEESATASPESASPTERPSPAHLARELKELVKELSSGVQGELVTPLHPRI
VQLSHMMDGHVSERVKNKVYQLARQYSLRIKSKSVTARPPLQWGKAAPIVPCLQEEAGAPSGGKGTRKPVLSLLHYEQTV
AQEHSPPKPGSPRHLSFSPTAANPRTTSPGVRPSSRSPLSPFDSETFNWPDVRELCSKYASHDEAFQAEGSRPRGPPVNR
SRSAPENMVEPPLAGRVGRCCSVGSGRGRAGPEASQPQPLGRLPQSRLVGEEALYVTADLTLENNRRVIVMEKGPLPCPA
AGLEEGSGQGPSSPAAMVGQGLDFQESGISRSPEYWPKEEAPRDPADPSQQGRVRNLREKFQALNSIG
```

527 - 546:	EEEEEEEEEEEEEEEEEEEE
528 - 547:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7W0Y8 **A0A3Q7W0Y8_URSAR** (1125 aa)
myelin transcription factor 1. *Ursus arctos horribilis*

```
MSLENEDKRARTRSKALRVPPEPTGADLSCPTPGCTGSGHIRGKYSRHRSLQSCPLAKKRKLEGAQAEHLASTRKSHPLK
```

```
LALDEGYSVDTDGSEDAEVKDASVSDESEGTLEEDEAEMSGQEGIHRPEPAEGRSPVKSHFGSKPIGSSAGPAKGNYSSY
QEIIATSLLNLGQIAVETLVGEDLGQVAKPGPGVVHLVQEEAEEGATSDEGEKDVFLRPDGTEEVVGGTKEHSQELCPQS
VEGVASEESSKMKIALGNEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVAAPDVLCQEDA
PLAPTQKAPELRHPASPSPKPEYSVIVEVRSDDGKDEDSRSQKSAVTDESEMYDMMTRGNLGLLEQAIALKAGQVQAVCE
PGCPPTEQGPCEPGKAVRPLDAARKNYCSKDPSRAEKREIKCPTPGCDGTGHVTGLYPHHRSLSGCPHKDRIPPEILAMH
ENVLKCPTPGCTGQGHVNSNRNTHRSLSGCPIAAAEKLAKSHEKQQPQTGDPSKNSSNSDRILRPMCFVKQLEVPPYGSY
RPSVAPATPRANLAKELEKFSKVTFDYASFDAQVFGKRMLAPKIQTSETSPKAFKCFDYAHDAEAAHMAATAILNLSTRC
WEMPENLSTKPQDLPSKAADIEVDENGTLDLSMHKHRKRESAFPSSSSSSSSPGVKSPEASQRQSSTSAPSSSMTSPQSS
QASRQDEWDRPVDYTKPSRQREEEPEESEPAAHSFASSEADDQEVSEESFEERKYPGEVTLTNFKMKFLSKDIKKELLTC
PTPGCDGSGHITGNYASHRSLSGCPLADKSLRNLMAAHSADLKCPTPGCDGSGHITGNYASHRSLSGCPRAKKSGARVTP
TKDDKEDPELMKCPVPGCVGLGHISGKYASHRSASGCPLAARRQKEGSLNGSPFSWKSLKNEGPTCPTPGCDGSGHANGS
FLTHRSLSGCPRATFAGKKGKVSGDEVLSTKFKTSDVLENDEEIKQLNQEIHDLNESNSEMEAAMVQLQSQISSMEKSLK
NIEEENKLIEEQNEALFLELSGLSQALIQSLANIRLPHMEPICEQNFDAYVSTLTDMYSNQECYQNPENKDLLESIKRAV
RGIQV
```

259 - 278:	EEEEEEEEEEEEEEEEEEEE
260 - 279:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE
262 - 281:	EEEEEEEEEEEEEEEEEEEE
263 - 282:	EEEEEEEEEEEEEEEEEEEE
264 - 283:	EEEEEEEEEEEEEEEEEEEE
265 - 284:	EEEEEEEEEEEEEEEEEEEE
266 - 285:	EEEEEEEEEEEEEEEEEEEE
267 - 286:	EEEEEEEEEEEEEEEEEEEE
268 - 287:	EEEEEEEEEEEEEEEEEEEE
269 - 288:	EEEEEEEEEEEEEEEEEEEE
270 - 289:	EEEEEEEEEEEEEEEEEEEE
271 - 290:	EEEEEEEEEEEEEEEEEEEE
272 - 291:	EEEEEEEEEEEEEEEEEEEE
273 - 292:	EEEEEEEEEEEEEEEEEEEE
274 - 293:	EEEEEEEEEEEEEEEEEEEE
275 - 294:	EEEEEEEEEEEEEEEEEEEE
276 - 295:	EEEEEEEEEEEEEEEEEEEE
277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
280 - 299:	EEEEEEEEEEEEEEEEEEEE
281 - 300:	EEEEEEEEEEEEEEEEEEEE
282 - 301:	EEEEEEEEEEEEEEEEEEEE
283 - 302:	EEEEEEEEEEEEEEEEEEEE
284 - 303:	EEEEEEEEEEEEEEEEEEEE
285 - 304:	EEEEEEEEEEEEEEEEEEEE
286 - 305:	EEEEEEEEEEEEEEEEEEEE
287 - 306:	EEEEEEEEEEEEEEEEEEEE
288 - 307:	EEEEEEEEEEEEEEEEEEEE
289 - 308:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7W4X8 **A0A3Q7W4X8_URSAR** (424 aa)
Peptidylprolyl isomerase (EC 5.2.1.8). *Ursus arctos horribilis*

```
MASCAEPSASGPEPTAPPPAGVPPLEDFEVLDGVEDAEGEEEEEEEEEEEEEEEEEEEEDLSELPPLEDVGQPPLEEAEQ
PGALAREFLAAMAPEPEPAPAPDEWLDILGNGLLRKKTLVPGPPGSSRPAKGQVVTVQLQTSLENGTRVQEEPELVFTLG
DCDVIQALDLSVPLMDVGETAMVTADSKYCYGPQGRSPYIPPHAALCLEVTLKTAVDGPDLEMLTGQERVALANRKRECG
NAHYQRADFVLAANSYDLAIKAITSSAKVDMTFEEEEQLLQLKVKCLNNLAASQLKLDHYRAALRSCSLVLEHQPDNIKA
LFRKGKVLAQQGEYSEAIPILRAALKLEPSNKTIHAELSKLVKKHAAQRSTETALYRKMLGNPSRLPAKCPGKGAWSIPW
KWLFGATAVALGGVALSVVIAARN
```

40 - 59:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7W5S8 **A0A3Q7W5S8_URSAR** (1782 aa)
Histone acetyltransferase (EC 2.3.1.48). *Ursus arctos horribilis*

```
MVKLANPLYTEWILEAIQKIKKQKQRPSEERICHAVSTSHGLDKKTVSEQLELSVQDGSVLKVTNKGLASYKDPDNPGRF
SSVKPGTFPKSTKGSRGSCNDLRNVDWNKLLRRAIEGLEEPNGSSLKNIEKYLRSQSDLTSTTNNPAFQQRLRLGAKRAV
NNGRLLKDGPQYRVNYGSLDGKGAPKYPSAFPSSLPPVSLLPHEKDQPRADPIPICSFCLGTKESNREKKPEELLSCADC
```

```
GSSGHPSCLKFCPELTTNVKALRWQCIECKTCSACRIQGKNADNMLFCDSCDRGFHMECCDPPLSRMPKGMWICQVCRPK
KKGRKLLHEKAAQIKRRYAKPIGRPKNKLKQRLLSVTSDEGSMNAFTGRGSPDTEIKISIKQESTDINVIGNKDTVTEED
LDVFKQAQELSWEKIECESGVEDCGRYPSVIEFGKYEIQTWYSSPYPQEYARLPKLYLCEFCLKYMKSKNILLRHSKKCG
WFHPPANEIYRRKDLSVFEVDGNMSKIYCQNLCLLAKLFLDHKTLYYDVEPFLFYVLTKNDEKGCHLVGYFSKEKLCQQK
YNVSCIMIMPQHQRQGFGRFLIDFSYLLSRREGQAGSPEKPLSDLGRLSYLAYWKSVILEYLYHHQERHISIKAISRATG
MCPHDIATTLQHLHMIDKRDGRFVIIRREKLILGHMEKLKTCSRTNELDPESLRWTPILISNAAVSEEEREAEKEAERLM
EQASCWEKEEQEILSSRANSRQSPAKVQSKNKYLHSPESRPVAGERGQLMELSKDSSEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEENIQSSPPRLTKPQSVAIKRKRPFVLKKKRGRKRRRINSSVTTETISETTEVLNEPFDNSDEERPMPH
LEPTCEIEVEEDGGKPVLRKVFQHQPGKKRQTEEDEEKDNHCFKNADPCRNNMDDDTDNLKDSSRDNPEPLKCKQVWPKG
TKRGLSKWRPNKERKTGFKLNLYTPPETPMEPDDQITVEEQKETPEDKTSPTPTRIEEEVKETVEPLLPRDENRRDETCA
PVSPNKSPGEKPDDLIKPEEEEEEEEEEEDDEEEEEEEEEEEEEEEENVDKDPGGAKSQEKEEPEVCMDKEEPVPLDEHEE
EEEEDEEPSHNEGHDADDEDDSHMECTEAEKEERPREAFKEVLENQEAFLDLSVQPSHSNSEVLMDCGVDLAAACNSEPK
ELAGDTDAAPESDEESPEEQAQKQDQKSSEEVDAGFKERNTATLEIDSETVQAVQSLTQENSEQDDTFQDCTETQEACRS
LQNYTHADQSPQIAATLDDCQQSDHSSPVSSVHSHPGQSVRSVNSPSVPALENSYAQISPDQSAISVPSLQNMETSPMMD
VPSVSDHSQQVVDSGFSDLGSIESTTENYENPSSYDSTMGGSICGNGSSQNSCSYSNLTSSNLTQSSCAVTQQMSNMSGS
CSMLQQTSISSPPTCGVKSPQGCVVERPPSSSQQLAQCSMAANFTPPMQLAEIPETGNANLGLYERMGQSDFGAGHYPQP
SATFSLAKLQQLTNTLIDHSLPYSHSAAVTSYANSASLSTPLSNTGLVQLSQSPHSVPGGPQAQATMTPPPNLTPPPMNL
PPPLLQRNMAASNIGISHSQRLQTQIASKGHVSMRTKSASLSPAAATHQSQIYGRSQTVAMQGPARTLTMQRGMNMSVNL
MPAPAYNVNSVNMNMNTLNAMNGYSMSQPMMNSGYHSNHGYMNQTPQYPMQMQMGMMGTQPYAQQPMQTPPHGNMMYTAP
GHHGYMNTGMSKQSLNGSYMRR
```

778 - 797:	EEEEEEEEEEEEEEEEEEEE
779 - 798:	EEEEEEEEEEEEEEEEEEEE
780 - 799:	EEEEEEEEEEEEEEEEEEEE
781 - 800:	EEEEEEEEEEEEEEEEEEEE
782 - 801:	EEEEEEEEEEEEEEEEEEEE
783 - 802:	EEEEEEEEEEEEEEEEEEEE
784 - 803:	EEEEEEEEEEEEEEEEEEEE
785 - 804:	EEEEEEEEEEEEEEEEEEEE
786 - 805:	EEEEEEEEEEEEEEEEEEEE
787 - 806:	EEEEEEEEEEEEEEEEEEEE
788 - 807:	EEEEEEEEEEEEEEEEEEEE
789 - 808:	EEEEEEEEEEEEEEEEEEEE
790 - 809:	EEEEEEEEEEEEEEEEEEEE
791 - 810:	EEEEEEEEEEEEEEEEEEEE
792 - 811:	EEEEEEEEEEEEEEEEEEEE
793 - 812:	EEEEEEEEEEEEEEEEEEEE
794 - 813:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7WQ60 **A0A3Q7WQ60_URSAR** (425 aa)
Peptidylprolyl isomerase (EC 5.2.1.8). *Ursus arctos horribilis*

```
MASCAEPSASGPEPTAPPPAGVPPLEDFEVLDGVEDAEGEEEEEEEEEEEEEEEEEEEEDLSELPPLEDVGQPPLEEAEQ
PGALAREFLAAMAPEPEPAPAPDEWLDILGNGLLRKKTLVPGPPGSSRPAKGQVVTVQLQTSLENGTRVQEEPELVFTLG
DCDVIQALDLSVPLMDVGETAMVTADSKYCYGPQGSRSPYIPPHAALCLEVTLKTAVDGPDLEMLTGQERVALANRKREC
GNAHYQRADFVLAANSYDLAIKAITSSAKVDMTFEEEEQLLQLKVKCLNNLAASQLKLDHYRAALRSCSLVLEHQPDNIK
ALFRKGKVLAQQGEYSEAIPILRAALKLEPSNKTIHAELSKLVKKHAAQRSTETALYRKMLGNPSRLPAKCPGKGAWSIP
WKWLFGATAVALGGVALSVVIAARN
```

40 - 59:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7WST5 **A0A3Q7WST5_URSAR** (711 aa)
YTH domain-containing protein 1 isoform X3. *Ursus arctos horribilis*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDIKRQKPSVHSRQLISKPLSSSVSN
NKRIVSTKGKSVAEYKNEEYQRSERTKRLEADRKIRLSSSASREPYKSQPEKTCLRKRDPERRTKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEEE
EEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSS
ASESYADQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSARSVILIFSVRESGKFQGFARLS
SESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQEIELECGTQLCLLFPPDE
SIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYAPEFHQRPGYLKDPRYQEVDRRF
SGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMAPYPGMEQPPHHPYYQHHAPPPQAHPPYSGHHPVPHEARYRDKRVHDY
DMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRDRGERGRYRR
```

229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7X0Z8 **A0A3Q7X0Z8_URSAR** (1891 aa)
Histone acetyltransferase (EC 2.3.1.48). *Ursus arctos horribilis*

MVKLANPLYTEWILEAIQKIKKQKQRPSEERICHAVSTSHGLDKKTVSEQLELSVQDGSVLKVTNKGLASYKDPDNPGRF
SSVKPGTFPKSTKGSRGSCNDLRNVDWNKLLRRAIEGLEEPNGSSLKNIEKYLRSQSDLTSTTNNPAFQQRLRLGAKRAV
NNGRLLKDGPQYRVNYGSLDGKGAPKYPSAFPSSLPPVSLLPHEKDQPRADPIPICSFCLGTKESNREKKPEELLSCADC
GSSGHPSCLKFCPELTTNVKALRWQCIECKTCSACRIQGKNADNMLFCDSCDRGFHMECCDPPLSRMPKGMWICQVCRPK
KKGRKLLHEKAAQIKRRYAKPIGRPKNKLKQRLLSVTSDEGSMNAFTGRGSPGRGQKTKVCTTPSSGHAASGKDSSSRLA
VTDPTRPGATTKITTTSTYISASTLKVNKKTKGLIDGLTKFFTPSPDGRRSRGEIIDFSKHYRPRKKVSQKQSCTSHVLA
TDTEIKISIKQESTDINVIGNKDTVTEEDLDVFKQAQELSWEKIECESGVEDCGRYPSVIEFGKYEIQTWYSSPYPQEYA
RLPKLYLCEFCLKYMKSKNILLRHSKKCGWFHPPANEIYRRKDLSVFEVDGNMSKIYCQNLCLLAKLFLDHKTLYYDVEP
FLFYVLTKNDEKGCHLVGYFSKEKLCQQKYNVSCIMIMPQHQRQGFGRFLIDFSYLLSRREGQAGSPEKPLSDLGRLSYL
AYWKSVILEYLYHHQERHISIKAISRATGMCPHDIATTLQHLHMIDKRDGRFVIIRREKLILGHMEKLKTCSRTNELDPE
SLRWTPILISNAAVSEEEREAEKEAERLMEQASCWEKEEQEILSSRANSRQSPAKVQSKNKYLHSPESRPVAGERGQLME
LSKDSSEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEENIQSSPPRLTKPQSVAIKRKRPFVLKKKRGRKRRRINS
SVTTETISETTEVLNEPFDNSDEERPMPHLEPTCEIEVEEDGGKPVLRKVFQHQPGKKRQTEEDEEKDNHCFKNADPCRN
NMDDDTDNLKDSSRDNPEPLKCKQVWPKGTKRGLSKWRPNKERKTGFKLNLYTPPETPMEPDDQITVEEQKETPEDKTSP
TPTRIEEEVKETVEPLLPRDENRRDETCAPVSPNKSPGEKPDDLIKPEEEEEEEEEEEDDEEEEEEEEEEEEEEENVDKD
PGGAKSQEKEEPEVCMDKEEPVPLDEHEEEEEEDEEPSHNEGHDADDEDDSHMECTEAEKEERPREAFKEVLENQEAFLD
LSVQPSHSNSEVLMDCGVDLAAACNSEPKELAGDTDAAPESDEESPEEQAQKQDQKSSEEVDAGFKERNTATLEIDSETV
QAVQSLTQENSEQDDTFQDCTETQEACRSLQNYTHADQSPQIAATLDDCQQSDHSSPVSSVHSHPGQSVRSVNSPSVPAL
ENSYAQISPDQSAISVPSLQNMETSPMMDVPSVSDHSQQVVDSGFSDLGSIESTTENYENPSSYDSTMGGSICGNGSSQN
SCSYSNLTSSNLTQSSCAVTQQMSNMSGSCSMLQQTSISSPPTCGVKSPQGCVVERPPSSSQQLAQCSMAANFTPPMQLA
EIPETGNANLGLYERMGQSDFGAGHYPQPSATFSLAKLQQLTNTLIDHSLPYSHSAAVTSYANSASLSTPLSNTGLVQLS
QSPHSVPGGPQAQATMTPPPNLTPPPMNLPPPLLQRNMAASNIGISHSQRLQTQIASKGHVSMRTKSASLSPAAATHQSQ
IYGRSQTVAMQGPARTLTMQRGMNMSVNLMPAPAYNVNSVNMNMNTLNAMNGYSMSQPMMNSGYHSNHGYMNQTPQYPMQ
MQMGMMGTQPYAQQPMQTPPHGNMMYTAPGHHGYMNTGMSKQSLNGSYMRR

887 - 906:	EEEEEEEEEEEEEEEEEEEE
888 - 907:	EEEEEEEEEEEEEEEEEEEE
889 - 908:	EEEEEEEEEEEEEEEEEEEE
890 - 909:	EEEEEEEEEEEEEEEEEEEE
891 - 910:	EEEEEEEEEEEEEEEEEEEE
892 - 911:	EEEEEEEEEEEEEEEEEEEE
893 - 912:	EEEEEEEEEEEEEEEEEEEE
894 - 913:	EEEEEEEEEEEEEEEEEEEE
895 - 914:	EEEEEEEEEEEEEEEEEEEE
896 - 915:	EEEEEEEEEEEEEEEEEEEE
897 - 916:	EEEEEEEEEEEEEEEEEEEE
898 - 917:	EEEEEEEEEEEEEEEEEEEE
899 - 918:	EEEEEEEEEEEEEEEEEEEE
900 - 919:	EEEEEEEEEEEEEEEEEEEE
901 - 920:	EEEEEEEEEEEEEEEEEEEE
902 - 921:	EEEEEEEEEEEEEEEEEEEE
903 - 922:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7XCN1 **A0A3Q7XCN1_URSAR** (2074 aa)
Histone acetyltransferase (EC 2.3.1.48). *Ursus arctos horribilis*

MVKLANPLYTEWILEAIQKIKKQKQRPSEERICHAVSTSHGLDKKTVSEQLELSVQDGSVLKVTNKGLASYKDPDNPGRF
SSVKPGTFPKSTKGSRGSCNDLRNVDWNKLLRRAIEGLEEPNGSSLKNIEKYLRSQSDLTSTTNNPAFQQRLRLGAKRAV
NNGRLLKDGPQYRVNYGSLDGKGAPKYPSAFPSSLPPVSLLPHEKDQPRADPIPICSFCLGTKESNREKKPEELLSCADC
GSSGHPSCLKFCPELTTNVKALRWQCIECKTCSACRIQGKNADNMLFCDSCDRGFHMECCDPPLSRMPKGMWICQVCRPK
KKGRKLLHEKAAQIKRRYAKPIGRPKNKLKQRLLSVTSDEGSMNAFTGRGSPGRGQKTKVCTTPSSGHAASGKDSSSRLA
VTDPTRPGATTKITTTSTYISASTLKVNKKTKGLIDGLTKFFTPSPDGRRSRGEIIDFSKHYRPRKKVSQKQSCTSHVLA
TGTTQKLKPPPSSLPPPTPISGQSPSSQKSSTSTSSTSPQSSSSQSSVPSFSSLTKNSQLKALFDGLSHIYTTQGQSRKK
GHPSYAPPKRMRRKTELSSTAKSKAHFFGKRDIRSRFIAHSSSSSWGMARGRIFKAIAHFKRTTFLKKHRMLGRLKYKVT
PQMGTPSPGKGSLTDGRIKPDQDDDTEIKISIKQESTDINVIGNKDTVTEEDLDVFKQAQELSWEKIECESGVEDCGRYP
SVIEFGKYEIQTWYSSPYPQEYARLPKLYLCEFCLKYMKSKNILLRHSKKCGWFHPPANEIYRRKDLSVFEVDGNMSKIY
CQNLCLLAKLFLDHKTLYYDVEPFLFYVLTKNDEKGCHLVGYFSKEKLCQQKYNVSCIMIMPQHQRQGFGRFLIDFSYLL
SRREGQAGSPEKPLSDLGRLSYLAYWKSVILEYLYHHQERHISIKAISRATGMCPHDIATTLQHLHMIDKRDGRFVIIRR
EKLILGHMEKLKTCSRTNELDPESLRWTPILISNAAVSEEEREAEKEAERLMEQASCWEKEEQEILSSRANSRQSPAKVQ
SKNKYLHSPESRPVAGERGQLMELSKDSSEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEENIQSSPPRLTKPQSV
AIKRKRPFVLKKKRGRKRRRINSSVTTETISETTEVLNEPFDNSDEERPMPHLEPTCEIEVEEDGGKPVLRKVFQHQPGK
KRQTEEDEEKDNHCFKNADPCRNNMDDDTDNLKDSSRDNPEPLKCKQVWPKGTKRGLSKWRPNKERKTGFKLNLYTPPET
PMEPDDQITVEEQKETPEDKTSPTPTRIEEEVKETVEPLLPRDENRRDETCAPVSPNKSPGEKPDDLIKPEEEEEEEEEE
EDDEEEEEEEEEEEEEEEENVDKDPGGAKSQEKEEPEVCMDKEEPVPLDEHEEEEEEDEEPSHNEGHDADDEDDSHMECTE
AEKEERPREAFKEVLENQEAFLDLSVQPSHSNSEVLMDCGVDLAAACNSEPKELAGDTDAAPESDEESPEEQAQKQDQKS
SEEVDAGFKERNTATLEIDSETVQAVQSLTQENSEQDDTFQDCTETQEACRSLQNYTHADQSPQIAATLDDCQQSDHSSP
VSSVHSHPGQSVRSVNSPSVPALENSYAQISPDQSAISVPSLQNMETSPMMDVPSVSDHSQQVVDSGFSDLGSIESTTEN
YENPSSYDSTMGGSICGNGSSQNSCSYSNLTSSNLTQSSCAVTQQMSNMSGSCSMLQQTSISSPPTCGVKSPQGCVVERP
PSSSQQLAQCSMAANFTPPMQLAEIPETGNANLGLYERMGQSDFGAGHYPQPSATFSLAKLQQLTNTLIDHSLPYSHSAA
VTSYANSASLSTPLSNTGLVQLSQSPHSVPGGPQAQATMTPPPNLTPPPMNLPPPLLQRNMAASNIGISHSQRLQTQIAS
KGHVSMRTKSASLSPAAATHQSQIYGRSQTVAMQGPARTLTMQRGMNMSVNLMPAPAYNVNSVNMNMNTLNAMNGYSMSQ
PMMNSGYHSNHGYMNQTPQYPMQMQMGMMGTQPYAQQPMQTPPHGNMMYTAPGHHGYMNTGMSKQSLNGSYMRR

1070 - 1089:	EEEEEEEEEEEEEEEEEEEE
1071 - 1090:	EEEEEEEEEEEEEEEEEEEE
1072 - 1091:	EEEEEEEEEEEEEEEEEEEE
1073 - 1092:	EEEEEEEEEEEEEEEEEEEE

1074 - 1093:	EEEEEEEEEEEEEEEEEEEE
1075 - 1094:	EEEEEEEEEEEEEEEEEEEE
1076 - 1095:	EEEEEEEEEEEEEEEEEEEE
1077 - 1096:	EEEEEEEEEEEEEEEEEEEE
1078 - 1097:	EEEEEEEEEEEEEEEEEEEE
1079 - 1098:	EEEEEEEEEEEEEEEEEEEE
1080 - 1099:	EEEEEEEEEEEEEEEEEEEE
1081 - 1100:	EEEEEEEEEEEEEEEEEEEE
1082 - 1101:	EEEEEEEEEEEEEEEEEEEE
1083 - 1102:	EEEEEEEEEEEEEEEEEEEE
1084 - 1103:	EEEEEEEEEEEEEEEEEEEE
1085 - 1104:	EEEEEEEEEEEEEEEEEEEE
1086 - 1105:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7XDW4 **A0A3Q7XDW4_URSAR** (1062 aa)
pleckstrin homology domain-containing family G member 5 isoform X3. *Ursus arctos horribilis*

```
MDDQSLAEEKGLRCQNPDCVDKGRAAKVCHHADCQQRHHRGPLNLCEACDSKFHSAMHYDGHVRFDLPPQGSVLARNVST
RSCPPRTSPAVDLEEEEESSMDGKGDRKSTGLKLSKKARRRHTDDPSKECFTLKFDLNVDIETEIVPAMKKKSLGEVLLP
VFERKGIALGKVDIYLDQSNTPLSLTFEAYRFGGHYLRVKAKPGDEGKVEQGVKDSKSLSLPILRPARAGTPSLERVDPQ
SRRESLDVLAPGRRRKNMSEFLGDTSIPGQEAPTPSSCSLPSGSSGGSDSWKNRAASRFSGFFSSGPSASTFGREVDKME
QLEGKLHAYGLFGLPRLPRRLRFDHDSWEEEGDEEEEEDDSCLWLEDSWRELIDGHEKLTRRQCHQQEAVWELLHTEASY
IKKLRVITNLFLCCLLNLQESGLLCEVEAERLFSNIPEIARLHRRLWASVMAPVLEKARRTRALLQPGDFLRGFKMFGSL
FKPYVRYCMEEEGCMEYMRGLLRDNDLFRAYVTWAEKHQQCQRLKLSDMLAKPHQRLTKYPLLLKSVLRKTDEPRAKEAV
VTMIDSVERFIHHVNACMRQRQERQRLAAVVSRIDAYEVVEGSNDEVDKLLKEFLHLDLTAPIPGASPEETRQLLLEGSL
RMKEGKDSKMDVYCFLFTDLLLVTKAVKKAERTKVIRPPLLVDKIVCRELRDPGSFLLIYLNEFHSAVGAYTFQASGQAL
CRGWVDAIYNAQNQLQQLRAQEHPGSQQHLQSLEEEEEEEEEEEEEEEEEEEEEEGGESSTSAASSPTVLRKSSNSLNS
QHCASDGSTETLAMVVVEPGETLSSPEFEGGPFGSQSDETSLSTTASSVTPTSELLPLGPVDGRSCSMDSAYGTLSPTSL
QDFMAPAPMAEPVPRPPELPQAPSPPPSPRLRRRTPVQLLPRPPHLLKSKSEASLLQLLSGATACGPPPAPSRSLSELCL
AVTVPGTSTQVSPQEAGPSWVRRGTPSPGRGPEPSELEGRTSCPAGEPERPARRSKELPLGASPRVQPEPPPGISAQHRK
LTLAQLYRIRTTLLLNSTLTAS
```

754 - 773:	EEEEEEEEEEEEEEEEEEEE
755 - 774:	EEEEEEEEEEEEEEEEEEEE
756 - 775:	EEEEEEEEEEEEEEEEEEEE
757 - 776:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7XG98 **A0A3Q7XG98_URSAR** (1129 aa)
Modulator of non-genomic activity of estrogen receptor (Proline-, glutamic acid- and leucine-rich protein 1). *Ursus arctos horribilis*

```
MAAAVLSGPSAGSAAGVPGGTGGLSAVGSGPRLRLLLLESVSGLLQPRAGSAVAPVHPPVRSAPHLPGLMCLLRLHGTVG
GAQNLSAVGALVGLSNARLGSIKTRFEGLCLLSLLVGESPTEMFQQHCVSWLRSIQQVLQSQDPPPTMELAVAVLRDLLR
YAAQLPTLFRDISMNHLPGLLTSLLGLRPECELSALEGMKACMTYFPRACGSLKGKLASFFLSRVDALSPQLQQLACECY
SRLPSLGAGFSQGLKHTESWEQELHSLLASLHSLLGALYEGAETAPVQYEGPGVEVLLTPSEDGDAHVLLRLRQRFCGLA
RCLGLMLSSEFGAPVSVPVQEILDVICRTLSISAKNISLLGDGPLRLLLLPSIHLDALDLLSALILACGGRLLRFGALIS
RLLPQVLNAWNFGRDTLSPGQERPYSTVRTKVYAVLELWVQVCGASAGVLQGGASGEALLSHLLSDISPPADALKLRSPR
GSPDGGLQAGKPSAPKKLKLDMGEAMAPPSHRKGDSNANSDVCAAALRGLSRTVLMCGPLIKEETHRRLHDLVLPLVMGV
QQGEVLGSSPYTSSRCRRELYRLLLALLLAPSPRCPPPLACALQAFSLGQREDSLEVSSFCSEALVTCAALTHPRVPPLQ
SMGPACPTPAPVPPPEAPSPFRAPPFHTAGPMPSVGPMPSVGPMSSAGPMPSAGPMPPTRPGPPATANHLGLSVPGLVSV
PPRLLPGPENHRAGSNEDPVLAPSGTPPPAIPPDETFGGRVPRPAFVHYDKEEASDVEISLESDSDDSVVIVPEGLPPLP
PPPPSGTTPPPVAPAGPPTASPPVPAKEEPEELPAAPGPLPPPPPPPVPGPVALPPPQLVPEGTPGSGGPPALEEDLTVI
NINSSDEEEEEEEEEEEEEEEEEEEEEEDFEEEEEDEEEYFEEEEEEEEEFEEEFEEEEGELEEEEDEDEEEEEELEELEE
VEFGPAGGPAEEGGPPPASPAPALPPAQSPKVQPEPEGEPGLLLEVEEPGAEEEAGAEAAPTLAPEVLPSQGEGPRDTGS
PPAGPPPQELMEEEPLAPPTLLEEGTESGGDKVPPPAETAVAEDVETELETATAALQEKEQDDTAAMLADFIDCPPDDEK
PPPAPEPES
```

887 - 906:	EEEEEEEEEEEEEEEEEEEE
888 - 907:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7XM54 **A0A3Q7XM54_URSAR** (1071 aa)
pleckstrin homology domain-containing family G member 5 isoform X1. *Ursus arctos horribilis*

```
MGTGPGVSGRRAASRPGPGQPCRAGGRALDGEGQVCHHADCQQRHHRGPLNLCEACDSKFHSAMHYDGHVRFDLPPQGSV
LARNVSTRSCPPRTSPAVDLEEEEESSMDGKGDRKSTGLKLSKKARRRHTDDPSKECFTLKFDLNVDIETEIVPAMKKKS
LGEVLLPVFERKGIALGKVDIYLDQSNTPLSLTFEAYRFGGHYLRVKAKPGDEGKVEQGVKDSKSLSLPILRPARAGTPS
LERVDPQSRRESLDVLAPGRRRKNMSEFLGDTSIPGQEAPTPSSCSLPSGSSGGSDSWKNRAASRFSGFFSSGPSASTFG
REVDKMEQLEGKLHAYGLFGLPRLPRRLRFDHDSWEEEGDEEEEEDDSCLWLEDSWRELIDGHEKLTRRQCHQQEAVWEL
LHTEASYIKKLRVITNLFLCCLLNLQESGLLCEVEAERLFSNIPEIARLHRRLWASVMAPVLEKARRTRALLQPGDFLRG
FKMFGSLFKPYVRYCMEEEGCMEYMRGLLRDNDLFRAYVTWAEKHQQCQRLKLSDMLAKPHQRLTKYPLLLKSVLRKTDE
PRAKEAVVTMIDSVERFIHHVNACMRQRQERQRLAAVVSRIDAYEVVEGSNDEVDKLLKEFLHLDLTAPIPGASPEETRQ
LLLEGSLRMKEGKDSKMDVYCFLFTDLLLVTKAVKKAERTKVIRPPLLVDKIVCRELRDPGSFLLIYLNEFHSAVGAYTF
QASGQALCRGWVDAIYNAQNQLQQLRAQEHPGSQQHLQSLEEEEEEEEEEEEEEEEEEEEEEGGESSTSAASSPTVLRK
SSNSLNSQHCASDGSTETLAMVVVEPGETLSSPEFEGGPFGSQSDETSLSTTASSVTPTSELLPLGPVDGRSCSMDSAYG
```

```
TLSPTSLQDFMAPAPMAEPVPRPPELPQAPSPPPSPRLRRRTPVQLLPRPPHLLKSKSEASLLQLLSGATACGPPPAPSR
SLSELCLAVTVPGTSTQVSPQEAGPSWVRRGTPSPGRGPEPSELEGRTSCPAGEPERPARRSKELPLGASPRVQPEPPPG
ISAQHRKLTLAQLYRIRTTLLLNSTLTASEV
```

761 - 780:	EEEEEEEEEEEEEEEEEEEE
762 - 781:	EEEEEEEEEEEEEEEEEEEE
763 - 782:	EEEEEEEEEEEEEEEEEEEE
764 - 783:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7XPJ2 **A0A3Q7XPJ2_URSAR** (729 aa)
YTH domain-containing protein 1 isoform X2. *Ursus arctos horribilis*

```
MAADSREEKDGELNVLDDILTEVPEQDDELYNPESEQDKNEKKGSKRKSDRMESTDIKRQKPSVHSRQLISKPLSSSVSN
NKRIVSTKGKSVAEYKNEEYQRSERTKRLEADRKIRLSSSASREPYKSQPEKTCLRKRDPERRTKSPTPDGSERIGLEVD
RRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQGNNTENEEEGVEDVEEDEEVEEDAEEDEEVDEDGEEEEEEEEEEEE
EEEEEEEEEEEYEQDERDQKEEGNDYDTRSEASDSDSESVSFTDGSVRSGSGTDGSDEKKKERKRARGISPIVFDRSGSS
ASESYAGSEKKHEKLSSSVRAVRKDQTSKLKYVLQDARFFLIKSNNHENVSLAKAKGVWSTLPVNEKKLNAAFRSARSVI
LIFSVRESGKFQGFARLSSESHHGGSPIHWVLPAGMNAKMLGGVFKIDWICRRELPFTKSAHLTNPWNEHKPVKIGRDGQ
EIELECGTQLCLLFPPDESIDLYQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIHNSRKKPRIDYAPEFH
QRPGYLKDPRYQEVDRRFSGVRRDVFLNGSYNDYVREFHNMGPPPPWQGMAPYPGMEQPPHHPYYQHHAPPPQAHPPYSG
HHPVPHEARYRDKRVHDYDMRVDDFLRRTQAVVSGRRSRPRERDRERERDRPRDNRRDRERDRGRDRERERERLCDRDRD
RGERGRYRR
```

229 - 248:	EEEEEEEEEEEEEEEEEEEE
230 - 249:	EEEEEEEEEEEEEEEEEEEE
231 - 250:	EEEEEEEEEEEEEEEEEEEE
232 - 251:	EEEEEEEEEEEEEEEEEEEE

A0A3Q7Y4N7 **A0A3Q7Y4N7_URSAR** (1069 aa)
pleckstrin homology domain-containing family G member 5 isoform X2. *Ursus arctos horribilis*

```
MGTGPGVSGRRAASRPGPGQPCRAGGRALDGEGQVCHHADCQQRHHRGPLNLCEACDSKFHSAMHYDGHVRFDLPPQGSV
LARNVSTRSCPPRTSPAVDLEEEEESSMDGKGDRKSTGLKLSKKARRRHTDDPSKECFTLKFDLNVDIETEIVPAMKKKS
LGEVLLPVFERKGIALGKVDIYLDQSNTPLSLTFEAYRFGGHYLRVKAKPGDEGKVEQGVKDSKSLSLPILRPARAGTPS
LERVDPQSRRESLDVLAPGRRRKNMSEFLGDTSIPGQEAPTPSSCSLPSGSSGGSDSWKNRAASRFSGFFSSGPSASTFG
REVDKMEQLEGKLHAYGLFGLPRLPRRLRFDHDSWEEEGDEEEEEDDSCLWLEDSWRELIDGHEKLTRRQCHQQEAVWEL
LHTEASYIKKLRVITNLFLCCLLNLQESGLLCEVEAERLFSNIPEIARLHRRLWASVMAPVLEKARRTRALLQPGDFLRG
FKMFGSLFKPYVRYCMEEEGCMEYMRGLLRDNDLFRAYVTWAEKHQQCQRLKLSDMLAKPHQRLTKYPLLLKSVLRKTDE
PRAKEAVVTMIDSVERFIHHVNACMRQRQERQRLAAVVSRIDAYEVVEGSNDEVDKLLKEFLHLDLTAPIPGASPEETRQ
LLLEGSLRMKEGKDSKMDVYCFLFTDLLLVTKAVKKAERTKVIRPPLLVDKIVCRELRDPGSFLLIYLNEFHSAVGAYTF
QASGQALCRGWVDAIYNAQNQLQQLRAQEHPGSQQHLQSLEEEEEEEEEEEEEEEEEEEEEEEGGESSTSAASSPTVLRK
SSNSLNSQHCASDGSTETLAMVVVEPGETLSSPEFEGGPFGSQSDETSLSTTASSVTPTSELLPLGPVDGRSCSMDSAYG
TLSPTSLQDFMAPAPMAEPVPRPPELPQAPSPPPSPRLRRRTPVQLLPRPPHLLKSKSEASLLQLLSGATACGPPPAPSR
SLSELCLAVTVPGTSTQVSPQEAGPSWVRRGTPSPGRGPEPSELEGRTSCPAGEPERPARRSKELPLGASPRVQPEPPPG
ISAQHRKLTLAQLYRIRTTLLLNSTLTAS
```

761 - 780:	EEEEEEEEEEEEEEEEEEEE
762 - 781:	EEEEEEEEEEEEEEEEEEEE
763 - 782:	EEEEEEEEEEEEEEEEEEEE
764 - 783:	EEEEEEEEEEEEEEEEEEEE

A0A3R7CAA6 **A0A3R7CAA6_CLOSI** (170 aa)
Uncharacterized protein. *Clonorchis sinensis (Chinese liver fluke)*

```
MAVLNAIHFEAKRPAYSLQLLTKGKMGQWLGREFTDRKVRGSNPTFASRLPLSRLGQPGGILALEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEVTTNGPRDKFRPSVKLPLKLSIRLKNTSET
QKEDATRQAT
```

65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE

76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE

A0A3R7FEZ9 **A0A3R7FEZ9_CLOSI** (419 aa)
Uncharacterized protein. *Clonorchis sinensis (Chinese liver fluke)*

```
MARNMKMTDLTPGVLVKSQTVQRSQPEHQSHLALDLKDECASSVTEGGGKKEYVEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEERRRQR
```

55 - 74:	EEEEEEEEEEEEEEEEEEEE
56 - 75:	EEEEEEEEEEEEEEEEEEEE
57 - 76:	EEEEEEEEEEEEEEEEEEEE
58 - 77:	EEEEEEEEEEEEEEEEEEEE
59 - 78:	EEEEEEEEEEEEEEEEEEEE
60 - 79:	EEEEEEEEEEEEEEEEEEEE
61 - 80:	EEEEEEEEEEEEEEEEEEEE
62 - 81:	EEEEEEEEEEEEEEEEEEEE
63 - 82:	EEEEEEEEEEEEEEEEEEEE

64 - 83:	EEEEEEEEEEEEEEEEEEEE
65 - 84:	EEEEEEEEEEEEEEEEEEEE
66 - 85:	EEEEEEEEEEEEEEEEEEEE
67 - 86:	EEEEEEEEEEEEEEEEEEEE
68 - 87:	EEEEEEEEEEEEEEEEEEEE
69 - 88:	EEEEEEEEEEEEEEEEEEEE
70 - 89:	EEEEEEEEEEEEEEEEEEEE
71 - 90:	EEEEEEEEEEEEEEEEEEEE
72 - 91:	EEEEEEEEEEEEEEEEEEEE
73 - 92:	EEEEEEEEEEEEEEEEEEEE
74 - 93:	EEEEEEEEEEEEEEEEEEEE
75 - 94:	EEEEEEEEEEEEEEEEEEEE
76 - 95:	EEEEEEEEEEEEEEEEEEEE
77 - 96:	EEEEEEEEEEEEEEEEEEEE
78 - 97:	EEEEEEEEEEEEEEEEEEEE
79 - 98:	EEEEEEEEEEEEEEEEEEEE
80 - 99:	EEEEEEEEEEEEEEEEEEEE
81 - 100:	EEEEEEEEEEEEEEEEEEEE
82 - 101:	EEEEEEEEEEEEEEEEEEEE
83 - 102:	EEEEEEEEEEEEEEEEEEEE
84 - 103:	EEEEEEEEEEEEEEEEEEEE
85 - 104:	EEEEEEEEEEEEEEEEEEEE
86 - 105:	EEEEEEEEEEEEEEEEEEEE
87 - 106:	EEEEEEEEEEEEEEEEEEEE
88 - 107:	EEEEEEEEEEEEEEEEEEEE
89 - 108:	EEEEEEEEEEEEEEEEEEEE
90 - 109:	EEEEEEEEEEEEEEEEEEEE
91 - 110:	EEEEEEEEEEEEEEEEEEEE
92 - 111:	EEEEEEEEEEEEEEEEEEEE
93 - 112:	EEEEEEEEEEEEEEEEEEEE
94 - 113:	EEEEEEEEEEEEEEEEEEEE
95 - 114:	EEEEEEEEEEEEEEEEEEEE
96 - 115:	EEEEEEEEEEEEEEEEEEEE
97 - 116:	EEEEEEEEEEEEEEEEEEEE
98 - 117:	EEEEEEEEEEEEEEEEEEEE
99 - 118:	EEEEEEEEEEEEEEEEEEEE
100 - 119:	EEEEEEEEEEEEEEEEEEEE
101 - 120:	EEEEEEEEEEEEEEEEEEEE
102 - 121:	EEEEEEEEEEEEEEEEEEEE
103 - 122:	EEEEEEEEEEEEEEEEEEEE
104 - 123:	EEEEEEEEEEEEEEEEEEEE
105 - 124:	EEEEEEEEEEEEEEEEEEEE
106 - 125:	EEEEEEEEEEEEEEEEEEEE
107 - 126:	EEEEEEEEEEEEEEEEEEEE
108 - 127:	EEEEEEEEEEEEEEEEEEEE
109 - 128:	EEEEEEEEEEEEEEEEEEEE
110 - 129:	EEEEEEEEEEEEEEEEEEEE
111 - 130:	EEEEEEEEEEEEEEEEEEEE
112 - 131:	EEEEEEEEEEEEEEEEEEEE
113 - 132:	EEEEEEEEEEEEEEEEEEEE
114 - 133:	EEEEEEEEEEEEEEEEEEEE
115 - 134:	EEEEEEEEEEEEEEEEEEEE

116 - 135:	EEEEEEEEEEEEEEEEEEEE
117 - 136:	EEEEEEEEEEEEEEEEEEEE
118 - 137:	EEEEEEEEEEEEEEEEEEEE
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120 - 139:	EEEEEEEEEEEEEEEEEEEE
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123 - 142:	EEEEEEEEEEEEEEEEEEEE
124 - 143:	EEEEEEEEEEEEEEEEEEEE
125 - 144:	EEEEEEEEEEEEEEEEEEEE
126 - 145:	EEEEEEEEEEEEEEEEEEEE
127 - 146:	EEEEEEEEEEEEEEEEEEEE
128 - 147:	EEEEEEEEEEEEEEEEEEEE
129 - 148:	EEEEEEEEEEEEEEEEEEEE
130 - 149:	EEEEEEEEEEEEEEEEEEEE
131 - 150:	EEEEEEEEEEEEEEEEEEEE
132 - 151:	EEEEEEEEEEEEEEEEEEEE
133 - 152:	EEEEEEEEEEEEEEEEEEEE
134 - 153:	EEEEEEEEEEEEEEEEEEEE
135 - 154:	EEEEEEEEEEEEEEEEEEEE
136 - 155:	EEEEEEEEEEEEEEEEEEEE
137 - 156:	EEEEEEEEEEEEEEEEEEEE
138 - 157:	EEEEEEEEEEEEEEEEEEEE
139 - 158:	EEEEEEEEEEEEEEEEEEEE
140 - 159:	EEEEEEEEEEEEEEEEEEEE
141 - 160:	EEEEEEEEEEEEEEEEEEEE
142 - 161:	EEEEEEEEEEEEEEEEEEEE
143 - 162:	EEEEEEEEEEEEEEEEEEEE
144 - 163:	EEEEEEEEEEEEEEEEEEEE
145 - 164:	EEEEEEEEEEEEEEEEEEEE
146 - 165:	EEEEEEEEEEEEEEEEEEEE
147 - 166:	EEEEEEEEEEEEEEEEEEEE
148 - 167:	EEEEEEEEEEEEEEEEEEEE
149 - 168:	EEEEEEEEEEEEEEEEEEEE
150 - 169:	EEEEEEEEEEEEEEEEEEEE
151 - 170:	EEEEEEEEEEEEEEEEEEEE
152 - 171:	EEEEEEEEEEEEEEEEEEEE
153 - 172:	EEEEEEEEEEEEEEEEEEEE
154 - 173:	EEEEEEEEEEEEEEEEEEEE
155 - 174:	EEEEEEEEEEEEEEEEEEEE
156 - 175:	EEEEEEEEEEEEEEEEEEEE
157 - 176:	EEEEEEEEEEEEEEEEEEEE
158 - 177:	EEEEEEEEEEEEEEEEEEEE
159 - 178:	EEEEEEEEEEEEEEEEEEEE
160 - 179:	EEEEEEEEEEEEEEEEEEEE
161 - 180:	EEEEEEEEEEEEEEEEEEEE
162 - 181:	EEEEEEEEEEEEEEEEEEEE
163 - 182:	EEEEEEEEEEEEEEEEEEEE
164 - 183:	EEEEEEEEEEEEEEEEEEEE
165 - 184:	EEEEEEEEEEEEEEEEEEEE
166 - 185:	EEEEEEEEEEEEEEEEEEEE
167 - 186:	EEEEEEEEEEEEEEEEEEEE

168 - 187:	EEEEEEEEEEEEEEEEEEEE
169 - 188:	EEEEEEEEEEEEEEEEEEEE
170 - 189:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE
173 - 192:	EEEEEEEEEEEEEEEEEEEE
174 - 193:	EEEEEEEEEEEEEEEEEEEE
175 - 194:	EEEEEEEEEEEEEEEEEEEE
176 - 195:	EEEEEEEEEEEEEEEEEEEE
177 - 196:	EEEEEEEEEEEEEEEEEEEE
178 - 197:	EEEEEEEEEEEEEEEEEEEE
179 - 198:	EEEEEEEEEEEEEEEEEEEE
180 - 199:	EEEEEEEEEEEEEEEEEEEE
181 - 200:	EEEEEEEEEEEEEEEEEEEE
182 - 201:	EEEEEEEEEEEEEEEEEEEE
183 - 202:	EEEEEEEEEEEEEEEEEEEE
184 - 203:	EEEEEEEEEEEEEEEEEEEE
185 - 204:	EEEEEEEEEEEEEEEEEEEE
186 - 205:	EEEEEEEEEEEEEEEEEEEE
187 - 206:	EEEEEEEEEEEEEEEEEEEE
188 - 207:	EEEEEEEEEEEEEEEEEEEE
189 - 208:	EEEEEEEEEEEEEEEEEEEE
190 - 209:	EEEEEEEEEEEEEEEEEEEE
191 - 210:	EEEEEEEEEEEEEEEEEEEE
192 - 211:	EEEEEEEEEEEEEEEEEEEE
193 - 212:	EEEEEEEEEEEEEEEEEEEE
194 - 213:	EEEEEEEEEEEEEEEEEEEE
195 - 214:	EEEEEEEEEEEEEEEEEEEE
196 - 215:	EEEEEEEEEEEEEEEEEEEE
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205 - 224:	EEEEEEEEEEEEEEEEEEEE
206 - 225:	EEEEEEEEEEEEEEEEEEEE
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212 - 231:	EEEEEEEEEEEEEEEEEEEE
213 - 232:	EEEEEEEEEEEEEEEEEEEE
214 - 233:	EEEEEEEEEEEEEEEEEEEE
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220 - 239:	EEEEEEEEEEEEEEEEEEEE
221 - 240:	EEEEEEEEEEEEEEEEEEEE
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227 - 246:	EEEEEEEEEEEEEEEEEEEE
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233 - 252:	EEEEEEEEEEEEEEEEEEEE
234 - 253:	EEEEEEEEEEEEEEEEEEEE
235 - 254:	EEEEEEEEEEEEEEEEEEEE
236 - 255:	EEEEEEEEEEEEEEEEEEEE
237 - 256:	EEEEEEEEEEEEEEEEEEEE
238 - 257:	EEEEEEEEEEEEEEEEEEEE
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254 - 273:	EEEEEEEEEEEEEEEEEEEE
255 - 274:	EEEEEEEEEEEEEEEEEEEE
256 - 275:	EEEEEEEEEEEEEEEEEEEE
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272 - 291:	EEEEEEEEEEEEEEEEEEEE
273 - 292:	EEEEEEEEEEEEEEEEEEEE
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278 - 297:	EEEEEEEEEEEEEEEEEEEE
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282 - 301:	EEEEEEEEEEEEEEEEEEEE
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284 - 303:	EEEEEEEEEEEEEEEEEEEE
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322 - 341:	EEEEEEEEEEEEEEEEEEEE
323 - 342:	EEEEEEEEEEEEEEEEEEEE

324 - 343:	EEEEEEEEEEEEEEEEEEEE
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369 - 388:	EEEEEEEEEEEEEEEEEEEE
370 - 389:	EEEEEEEEEEEEEEEEEEEE
371 - 390:	EEEEEEEEEEEEEEEEEEEE
372 - 391:	EEEEEEEEEEEEEEEEEEEE
373 - 392:	EEEEEEEEEEEEEEEEEEEE
374 - 393:	EEEEEEEEEEEEEEEEEEEE
375 - 394:	EEEEEEEEEEEEEEEEEEEE

376 - 395:	EEEEEEEEEEEEEEEEEEEE
377 - 396:	EEEEEEEEEEEEEEEEEEEE
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382 - 401:	EEEEEEEEEEEEEEEEEEEE
383 - 402:	EEEEEEEEEEEEEEEEEEEE
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390 - 409:	EEEEEEEEEEEEEEEEEEEE
391 - 410:	EEEEEEEEEEEEEEEEEEEE
392 - 411:	EEEEEEEEEEEEEEEEEEEE
393 - 412:	EEEEEEEEEEEEEEEEEEEE
394 - 413:	EEEEEEEEEEEEEEEEEEEE
395 - 414:	EEEEEEEEEEEEEEEEEEEE

A0A3R7LUE7 **A0A3R7LUE7_PENVA** (379 aa)
Uncharacterized protein. *Penaeus vannamei (Whiteleg shrimp) (Litopenaeus vannamei)*

```
MAFSLPGLKKLRRQRTMEEVKEVKDPLEAMPSSSDEEEDIDTMRDDLQATKSQLAEEIKQRKKIERENKILKIDIESLQA
EVKKLKRQLKEAGAVEPKPLKSSEAEEIVPKLEKSMSKLRMREDDLDFTELDTLETEINNLKREVDFHKKQAEDYLTRYD
EVTQKLIVSENSADEWELRGNYYEKKYKALQKEHNIELPDIDTIGTQTDPVDFVEAPPSSPVGDDDDDDDDDDAAFPVPS
KSGSRRSFASSVHRMESFKEEDEEDEEEEEEDEEEEEEEEEEEEEEEEEEEEEAEEEGEEVDEETAAERRAENAQKKKDR
DLKLLQDRTKKHELSMNAMKKDNYVLKAQVERCEEMFDVEKRRHKRLNEELHIMLSELS
```

273 - 292:	EEEEEEEEEEEEEEEEEEEE
274 - 293:	EEEEEEEEEEEEEEEEEEEE

A0A3R7N8X4 **A0A3R7N8X4_9TRYP** (1052 aa)
Retrotransposon hot spot (RHS) protein. *Trypanosoma conorhini*

```
MPPKRTRARAAESSATDVPRGQRHARSEADSGDSTAPPAQRRRVERAQQRPTWTLTSTVEDVLLGGVGPIPDIKLNDFLR
DKLSGRGVVEANENLSMNAFALRPERYVTDPELREDILSLPEYQLLEDARRLRADARRLMEHDVGNIQRWRVFEQKEIVF
PVTRSTLNAALDAAEANESATRIQAVDSLPVPDGFYDSVLNAQCSHVLEFHEGEGSHRRVRMEVNAGQPPTQLWDYRRKG
RTLLPVEDAEQFIAPRPRLMILTSEKGWPYSLRRGRGITDCYINREVQRVWRIVQGDLEGAFGPRRPELPDLRRRLLIGT
PGIGKSMAAGSCLLYGLLHYDDTKLQVVVYCFGAGLAFVFDKEVQTVSKHTGELNISNLIEYLDCRGKKGYIIFEVDKKG
QGPDGFPTPKSWGFILLSSPNEANFKEWAKQADAIPIVMNCPDENDVKAMCAWETRAKSAQVQKKRWKVINKRMDYVGPI
PRGILDDDNYATHRPLTKRALRLIKASTADDYIPIGEGEMVPANDASSKLVKAVRICRAGENETFANLPVCLGLGHQILS
RLTAIRKQNDIVYQLLCCRDLFLPEFLEKYGVHAFTDRGFVNSIKGRIKELKPPTRRAGRPCVLQSHPETHPEVSVVLAR
LEYKPPKIDVEYGVLYIPKSREFPLIDGFFFVDTPRKTMVGLQATVRGEHHTTASKVKLFKKRMAKYFNDWEDFATGLSW
EIIYVQHRERDRIKTWQECRNSPNAGDNEDATQRRGAEEEEAEEEEEGEEEEEEEEEEEEEEEEEEEEEGEEEEEQEEEE
QEEEEEEEEEEQEEEEQEEEGEEEEEEEEEEAVEEEEAERTMRCWKEKVYQYQVAISAEDIGNTNNARSRRRPARRGNTDT
TTQSRRRPARRGNTDTTTQSRRRPARRGNTDTTTQSRRRPARQGNTDTTTQSRRRPARQGNTDTTTQSRRRPARQGNTDT
TTQSRRRPARRGNTDTTXXXXXXXXXNTDTTTQSRRRPARQGNTDTTTQSRRRPARQGNTDTTTQSRRRPARRGNTDTTT
QSRRRSARQGNE
```

769 - 788:	EEEEEEEEEEEEEEEEEEEE
770 - 789:	EEEEEEEEEEEEEEEEEEEE

A0A3R7SM39 **A0A3R7SM39_PENVA** (1282 aa)
Putative microtubule-associated protein futsch. *Penaeus vannamei (Whiteleg shrimp) (Litopenaeus vannamei)*

```
MADPPPPAAPQVRGEGALSPLSGSYLLIVVAEPKTDQHKDVILNRISKGFLSWDEEKAHVDIHKELTTIAELNLEGEEQK
GGERLIQYATENLVAEVLIHPQVNTLQQCLKNLLSSFTKHRHIIHAGYAFAGSGSWMLQDGTFSVADLIAAFSEYEVQRV
LHAYENCITIDIHCAPEGHWSTSYLAKESFSKLCRVTVNPDDKIETTPGISTFVQYLSQFLLSTPIEELLEPSDIVGNIR
FSRPTLYVFPGGQGDSALFGVNGFNMLVDGGYNYKACFWDFTRHLDRLDAVLVTRLNSSNLMDTITRILFPGSTPQHKIF
EGLERLKNLEYLKHTTCSAKSIKAAIEERKGITIESLAAIDEAKVSEAKVTTKEITETVTGVSVTKEAISAVTDSIETVT
KKDLVDAAERREITTQAVEVTTAVTDLKSRIETTGISEIKDIHEIEPLDVKEASLVSAESGVVTGEERESSLEIETLKEI
KPKEKPKEKKIKETGTPEKPKRYRKPKVESRIDTGDRRPRPEDRAARVERKKLVDDKNRAAKAAEAARKELKPSPKPTTA
PRTVARKAPPVGKAPKAKKIEKPPAPKTEGPIKRVITGAAVKAGVVAAAVSGVAVVEAAADREDVDEIVAPMKETDNLMI
APDQDEEDRISDIANIPGVQEIKLDEDTLQIIDKQQLEEEEKDSLILHEEGVVEHVEKEDIIEEVEEHVEEEAEKEIEEI
EEEEEEEEEEEEEEEEEEEEEEEEEEEVEEREAAVEEKEVGERIREKEVGEEEEEGPEDEEKVSITEKEDEAEKEKKEDK
IAEEAKEIEDIAKLDEKHEAEDIYEKIETEDRDVYATLPSSAKLTEYKEKYEEKPIRGLFTGFAMPSAEPQEAPQKAPSP
KPKEEVTVPTSLPEAIFKPTAPPVHPREIIKTPDEVDDLPIHEEVESIEHDIYEEDIEMEKPAEQELEAGSPLLEVKGEL
QIKEEVIAEKHEREIIKEKKLPEKEFEVEEEDEISREEKVSKSIEDFEAKYAEFKATAVSEVIQRGEVIAETKEIKKKVD
```

KVELLKDIAQTLEERDEKTVIKEKVSSPEVSEEIEMPVVKDKKPVKAVTPYEELDFDKIPEKERRVEDEKDIDELEFEKE
ILEAKKVSPEDTLLKEKVITEEIQEEKEKTKKEEVKMEEIVAKDKLEEKITTEVTKKEEVVAKDKLEEITKEEEVTKKEE
VVTKDELEEKITKEEEIKKEEVVTKDKLEEKITKEEEIKEEVVTKDKLEEKITKEEEIKKEEVVTKDKLEEKITKEEELR
RR

721 - 740:	EEEEEEEEEEEEEEEEEEEE
722 - 741:	EEEEEEEEEEEEEEEEEEEE
723 - 742:	EEEEEEEEEEEEEEEEEEEE
724 - 743:	EEEEEEEEEEEEEEEEEEEE
725 - 744:	EEEEEEEEEEEEEEEEEEEE
726 - 745:	EEEEEEEEEEEEEEEEEEEE
727 - 746:	EEEEEEEEEEEEEEEEEEEE
728 - 747:	EEEEEEEEEEEEEEEEEEEE

A0A3R7YWW6 **A0A3R7YWW6_TOXGO** (318 aa)
Brix domain-containing protein (Fragment). *Toxoplasma gondii CAST*

MGAAGGEARKAPHGAKAKKLSAADSGVSTLCEDAKESGKGIVGSEPEKKDRRALKKTKRFDKQKPAAVTSPFAAPSPAPL
AQTIEKRDVQKRTESSAGRNRGGAALEKNRANNASKRSPQKIKEEEEEEEEVEEDEEKEEEEEEEEEEEEEEEEEEEEKE
EEEEEEEVEEEDEEEDEVMSSRPRNSSVGTTGGEGEGKDAEGRDAEGVSPAPADPYLLAEADYLRREKRWVNRQRVLVLG
SRGVTHLQRHLMEDFKRLLPHHKAESKWERKQTMKDISELAQLRACNNVLYFESRKRDLLLHVSKIPHGPTLIFRVLN

139 - 158:	EEEEEEEEEEEEEEEEEEEE

A0A3R7Z5U1 **A0A3R7Z5U1_TOXGO** (989 aa)
Uncharacterized protein. *Toxoplasma gondii CAST*

MRGRRPSQQRKKAASLGASSLLSSLPSSLPSSLFSRGDSVGRRLGKRRGIEEEGGKRKRARGGRSARHNFPEVDQQGGSD
LDELPSSEADPREAQQDGEGSFGHEQELAETLKKSKRAVLERKRRRHEERRQKKQIHRKQQQLWKLERQKALLERQLDMQ
KAAISGIRVNQGTGSGVRTPCGPEADSEDEEEDVSPRREKKTPSSLSSSLSSSLSSLDVRGSVLSALSAKDKKHTASGEV
LLLSGVSSRSTEEQRKAEERRLALDAAGRQLDAELAFLESKLGIGKDSSKAGEKKKKKLAQELLDDGFDEDLQTLLDDIL
GGKAENRKRKTKTDYDHDEGEMEGEETQEGAHEELGRVEAEEDEEDEEEEDDEEDEEDDEEENEEEEEDEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEKEEEEEEEEDEGDEEDEEEGEDLKLKTEHYSTCASASAGKYLPPHLRNRAQRDLS
NEAEFDGDNPGRNSTRQHGAAPASEASDKANFVASKLPLSCLEKARQTATDAGRGLTQRLRGSLNRVSEGNVEVILQQIS
QEVKAALTQVLSGALPVPATSPALTPRDVRGLRREQEMSFFQEVNCIIVRLLMQSMVESKFSTASLVATQTALCCGLSCL
LDASLCSQLLAALGEAFRKFFPLALAQADRRTETGEPVGLYVRHTLMALCFLFDFNVVQPAVFLGLLQRLSGKVATTKEK
GGAKNGERNEPLVEFQVECLLMVLRLGGGKLRNDNPVLFKEAWNFLMTRVKGGEGEREVQVHSGREERPFEEQTREEQRA
RLARVSTSFSGALRQRQEGEQPATTGRLHYLARELEELKNNKGNTIHLASKASQEAMRRWLQTSPLLAQSPLRQCAGEGK
SVLVGVSSWQEVEDGVVSVSPSSHRPPVSPHKSVRVEEEKQSCLGDTGSEKALLDLAAKLRSANIQRLLFSIHLPSENRI
LCSPPCLESHFHMALCASFRTPLSSFIFV

390 - 409:	EEEEEEEEEEEEEEEEEEEE
391 - 410:	EEEEEEEEEEEEEEEEEEEE
392 - 411:	EEEEEEEEEEEEEEEEEEEE
393 - 412:	EEEEEEEEEEEEEEEEEEEE
394 - 413:	EEEEEEEEEEEEEEEEEEEE
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396 - 415:	EEEEEEEEEEEEEEEEEEEE
397 - 416:	EEEEEEEEEEEEEEEEEEEE
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401 - 420:	EEEEEEEEEEEEEEEEEEEE
402 - 421:	EEEEEEEEEEEEEEEEEEEE
403 - 422:	EEEEEEEEEEEEEEEEEEEE
404 - 423:	EEEEEEEEEEEEEEEEEEEE
405 - 424:	EEEEEEEEEEEEEEEEEEEE
406 - 425:	EEEEEEEEEEEEEEEEEEEE

A0A3R8AM13 **A0A3R8AM13_TOXGO** (807 aa)
WD domain, G-beta repeat-containing protein. *Toxoplasma gondii CAST*

MFIYDETYNVCFYELPVFAFACLSFHLLVRCLSCPFPFLILFQRVCHFAVRCPVVLSAVSFSRLLGAQRCLGRLAGCLAC
GDWQMPGASPSRPPWRRNQRCGFPAERMVRKSPELFAREHAVLVQYPTAGQGMLSATVARPLSLCWISPSLKLRPSPLFK
KSMREGVLAASGRKEKKESSDLSVPLCACDCRGINASTPHALLFAAASSGDHAVKVWKAEISPSFLSGKVRGDDEPGASG
KKKKTADTGHPQILVTSLASVVAHRKEINDVKISPNDALLCTVSQDKTGKLFSFPSLVYVGELRGHSRSIFACAFPKREK
IVATASADSTVKLWNVDTCACIKTFQSTVGGGVLALGFLSRDTQLVTGTSEGFLQLWNCRTAECVGSLPSVHEENKASIW

```
CLDVCGPAMVTGGSGGQLCLWEDVTNLVRHKAELAQQRETQQLAALKLLAAEGRGDEVFSLLLRLRRRAGMREFLENQCG
KILLQAFQRGLELQRRIALYSGQPLARSGSDQDASASTFGRLSAFLESLEEERVAAREDEDDRRGGQESKAELGASKKRK
GEKKVKGEETEAGARGRPDAPLRSAWLRDLNGDLSLPQLLKKMKKKDVATLLEFAAAWNTNSHTSWLAQGLVRLLLEARG
EDIFEGAEKAGRNVSDVENMISSFCAYTARHDRRLTALIEKTFLLDLLQGCESGDTRDLGDRWSGETRREPHREKTLDPR
DATTFTRLCLYGDESEQTEMSQGKKTKNEPKRDSDERSTQEEEEEGEGEEEEEEEEEEEEEEEEEEEEEEEEAEEEEAE
EEEEADA
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769 - 788:	EEEEEEEEEEEEEEEEEEEE
770 - 789:	EEEEEEEEEEEEEEEEEEEE
771 - 790:	EEEEEEEEEEEEEEEEEEEE
772 - 791:	EEEEEEEEEEEEEEEEEEEE
773 - 792:	EEEEEEEEEEEEEEEEEEEE
774 - 793:	EEEEEEEEEEEEEEEEEEEE

A0A3R8CLE4 **A0A3R8CLE4_9STRA** (2420 aa)
DUF3677 domain-containing protein. *Peronospora effusa*

```
MKRGRVATRGSTRHALRRKNVVVDEDDEEEGEDMRQEEEEEEEETKKTPPLKLTRAQTRKQEEEAKKNRKNGRKKRKEER
EEEDDEDDEEMEEDEEEEEEEEEEEEEEEEEEEEEEADVEERHRGTRERGSNKPQLRGTQRPLRKKQRCKIIVSEDEEEEEE
QEEQEEQEEQEEEEEEEEEEEEEEEEEEEEEEDDDEMAKKETPQKRKMHMRNGEKMAMLGRKTRAKIAAASGSKHPTKIVR
RQIQKKAEESTESEGQEEQSQEESAKSESKEEDKLGSEPSSAATTPSSSPAKRKGLSINTLVNDADEEEDHVEQADVSMT
LAPASALNAGTKNATEVPDQHFREVLSKATSAPKLMERFKHPAMLKYLLRLLRSKHYIGMKDSSEHGTTTSLVPGHLPGP
AEYIHLSLPVLVTNLLVQIMKDLDEWPIDSVKVFLDDSLYSRVWVDHELSQLFVQNVKTVLEMESGGQQFAQPLVRQRFQ
GVTVMQEMRELITTHIRSRLVELEKERSGSVGGAPGAGGNYAVRNMIMTLAECASIPQVRLFGAENLEAWLQNPSVKGPA
KELLNKIVSLCKSTSSIDTATVDLLLKLKLKSTMFQLKVEAITHIVCNHPVYLKRALSMFIAQERPNNMSRDVDNMKMLQ
HIFRASRSTSASSILGSSDDLFYRRPIEHQGTLASRELARVFREMASISDVTPVLKTIVRKILKQLTFEQVDIKALCVGI
LDNDGHWDALAGDARVLDYMGLVTGVVWLILLMRGAAVKSLQIQQSNAANRQSTGSATLASSGLKHGGTQAISRRGANPP
LPLSRANRLGPLKAKQSLSKSSLSSSHAAVGSGFSVPSSQGRSGNNGSNGGGSVVSEESKTVKISVWAKDELQQALAFVQ
REAILCCRDVLTHFGLNGDSPFEKTLYEGIVKKLLFLDIPPDVQPTEHDRTCFQATQEDIPVHPDSLELLTSLYNSCRAI
DRMEALRTLETVVFRGAEAHMHRETLWRHHADELTSYTQNGGVLGIEVNGSQFVQHLLKLALWQGGGDKQEQEFCHSSRF
WICCSILLVVGCFNPNTVGAFLWEEFPTLRGLMQMVITERYTFPAISTPDPLLLGKHGATFPDLIQGNIQLRDYEQQLLQ
LNQADLSVTGDPLMLFDASGLARQPPPAILDHLRTLDRKFKLGMRLRQSRKKDFLMEMVAGSDAKNELQNANPAGAAASS
AWWIADLVCEDFNTMQYLPHECLCQLLLLALRQSNPNNHADLQGQVSLNQPALIQITPRLLKKLRDYLADDSSSSSNVVL
FYLECLNSRELVTRRVASRILYLLTAPGSVDDVSVEIREVVVTFGPESNLSFLWLYELEKFSCYSSIRNKIFRCLENLLE
LEASIPSLGTCMKALHDFSKNGSDISPSMNSSENMKQDGDNNPQKITVEQSLLLAGAYGRLLAGRDMVATVLLKDYDIYA
ITLEVIWRAIETQLEIAPQLKATLGISFSDCKVFYVTDGTNAIREIKLPLTIIHGAIRQRNCYLFSKVMCVWRAEYPKPT
ANTAILSSTGLIATKDPRLYPDHLLIKLAAAASTTTSHLCGTAIRAITTDTLWNLLEQSALSEQCLEMALRSILETTKKD
ESKAIASLLAAMKTSDISVAARAVLMQISAYDAMDSLTPDVVEKLKLLREWLQDQCGAKGSMLTDEDDEEAHLLSEGFTT
FKIKASEPSATPHMFTFYAEGMEEVPKVEPTQQPIPERPKTDMTIFQDTYFIPTHHLHSKKDVAASDDSVSLLTGLMKEL
KRSSSSGSLPAIIAPENFVLATSQALRRSCPTSEDTITHSAADTWSLLMALLHFARSSCSSEAAATQLAKALLEVVGHLP
TCPSVSHRKECIGFVRRVLDNLSETFTSSYSASVSFIQYLSQASTTEGLYELEDPSVMPDVFAVLQSVVQFIDRNFAWWK
MHGITLRLNAMALHSLVVLVKEVEVLQRLQVNHTGNVYRTCATGLLTSIAHDQGDVSRMLNLLDPIMTADPHLGYISGII
SIHADVKRDLVGALYFQNPTLVAGLLGELNPDWESFVNFDASVDQQHDLIIQDRGLLSQVDDILHDLTKDGSGVMERFRE
LTRSHPMLVLLRFPRQLMQHFGTVSLSQLYLKATFFQNILGAMQIMRPYMRHQQSVMKPFCQFLFEILRVIVDHNAVEFR
RLVSHTWEFFYDALEADFDLASDLIFSEPRIVLLESIVNMYESHPETVAFGEVLAQRHNESSLHATLESIRTERSKHQSA
ASQQHQIEQLLTLIESQDSMLASGGKPLPEHTNMTTITQGLQAIDIVCAKTDQGAAAVALLRRCTAPVASLLVTEKVTKA
VMATLCQTLLNLMRYDSICVDDVMHYYVQCLRSVRPGLKEAAVNTVLEFLVFADARQRRQILQHLFNDPSETAKNKLGVY
LKSAAFRTTLLVASKKLTQT
```

95 - 114:	EEEEEEEEEEEEEEEEEEEE
171 - 190:	EEEEEEEEEEEEEEEEEEEE
172 - 191:	EEEEEEEEEEEEEEEEEEEE

A0A3R8GE19 **A0A3R8GE19_TOXGO** (3150 aa)
Ribonuclease type III Dicer (Fragment). *Toxoplasma gondii CAST*

```
SSSSLSSSSLSSSSLSSSSLSSSSSSLSSSSLSSSSSLSSSSLSSSSSLSSVTCLCRSPFVSFASSPEFSALRDALFAQV
HQLGEEEKAAHRGCLSLLLASRTSASASVACCGFSGGSATVLSPYDSQNVLPFQEQYAGGRGAAGVDDRAAARRREEATV
LRAVRAFGARTSAPLSETRAGRGEEDGRHSETGMCEEDEKEEESSRRRGDGERETLEERSWWTETPADAWEESGEGRSDG
DEVEDVEREQGPQGQQSTHPAEQNRGGDERRLGEERLARDEREEAGTLLQIEFEEETRGRTREEGSDRDPRRRGAERKTE
SKCEQETKSPHVAYCWWQAGARESGKRGHRVLKTCDAVLPLEEETYSDRDTRGQLQAWPYQYRVYRRATLENTVVALPTG
TGKTLVAAMVVHTWLANVFVADKLVIFLAPTTQLARQQHRAISTVLSLLRDPAGAEASRGRLAVRLPGVLEKERRTRGRV
ASRDDDDGERAYFRSVLRVDWSHPKYWAAFYSALSEYKAALLDLQRLPAAPPAAFDLRRFHTGRLLAPYRFVDSQRAALL
RESFAEPSSEEANVQAASLEDSEGERSGNREGEREEDENEQDVSEVEHQAVCWPRVFVMTPDKFRNLACRGLLRIDRIGL
LIFDEAHTVGRPLRSLGAYATILRVFLHLCQEEAKPRILGLTASPVPDGKLGFFDLESELKRAMRSLETIFQARIVKADT
ESAPGIRDWSQGQPDAQRQGEQQRGVMGVRLTAAGSREIREAVEEESERSAANEARGNARRGSGETRQDHLGGDKPLRTM
ETTEGDEETFTGCALKTVRYQLAPSPFYYDHELLILDRLTTPRVEAGRQQWRVAAWQPPPGTLRGSREPTGGVPAVSNGD
REQRKDRLPRREGTERGDPPTRSTSRKPNGTKERETEEEELEEKKAKEKEAKAKNGQVNRDGLEGKRSEGREDAVRWNGS
EVAAFRHFVEREARGRHTYFSLLLQEVLEICSTFFYVEVTRLKEEREANEERHHPHETTPAEEARQETMHRILKTDCGSP
CASHPSPSFSSFPSCSPPLSSSPAAPPLASSFSCSSASAAFSASALCSSAAPSRVPASLRSSFLAEVWGAADARLNVRVM
RRLWQHLAPLTKQRAQRNWENFRRHLLHVQSELGFWSVWRLKEKVEADLEAWQARLGAATEERSRAQTRRSRRDCEGAEC
EESEKEDETDNSGRGKESQKRVRFAGENQRTKAGRSEEGNRTRGDRDRIKSTLAEIPFWISFPFRRPLSSDLDLQHGSSL
SSSSLSSSSLSSLDPVGGQPVERLLRRLFFGFFFLFSKALSTACSHSSLQLTMQLCRSRDLAHVCLADVAALEGGVAGAE
RTGSLPQVLACSLFSDKLLRLDQVLRDSFGRAQAQAQTQTQRREGSVADDKRGSGPDKRAGRPGDEEERRTEDGGEATRS
GLRIKASSKGDRECSPSPKKSGVRTPVPSFSSSPSCVSPSALSSAPSSMSLSSRFPAASRSPASPDVAFGGVPKCGLVFC
RRRVDAWLVCEFLTARRLVFVDWICSSSLASQGASWLFGIGKASQGRSSCLDRLRAMHTVWGKLEKKTQKLNAQKHRPST
TPQSHSPSLASSLSSSLSSSLSSSASSSASSSASSSLSSSLSSSLSSSASSSASWGDGGKGVWRLMRRLGWGAPLQLLVS
TSVLEEGIDVPACNLVVQMDMPSSLVRFVQAKGRARKKPAEFVVLCPDSGPCGASWPDASLPFSSSFSSSSSFFPFSSSL
QPQTPDCTVSSPSLLLSLQSVSSLAVSSSSLSAPLSVSLRSRTGEAPTTPAFAAQGFSAAGGAACYLQAVSPSVNFELAR
LQLCEAKVAALAADVEATERFGLLGPFRCMRKVCSLDDLLLTHTGAMVHSSFAPALLREIVDACTAGKTDERIERGADER
GEEGRWAEDTEDEGREERERGNAELRTGREKALGTCCSNAPFSSSLSSSGMRRVSDLCEARRQRRPSALRLLSTQDGKWI
LSVPSLHGFRSSPLPPFSIEFSPTGSAPTRASAAAGVLAVRVLRRLVQEGVVDSFLRCRDRDSVEKDLRDEKERRRRENC
GGVGAVDLLWRELPACLLPPRSWRTASRASGDRHGDSEETLHTSAKTREEAARAEEAVSGSNEERRRSRDHKEGTTEEDA
GAQEVEENAEEGRKEEEGDQLKRLPSGTGKKDKTSTSNAKSETHREKTRTPAPPPGVTRLFLHRVWCTPLTAREAALERL
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EGDEDGLWWTGNRRQREACFEKREREGGDGKHDQCKENEKCRAEKEEEEEEEEEEEEEEEEEEEEEEEKKWSWQEEEKNR
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SNAWTELEADEEGEEGDEEGEEEGEEGEEEGEEEGEEDGEEEGDEEDVPGLMRVEVEKPEKTMFIDLPTEYVEKVLLRFT
HIHLFRLLQLSNFSPNGTCNSLLLTVLQFLSALPFRRFPFRTVPSSSSLSSSASASASASCLGGDGEPRSRFVSLPLPAC
ASASRLLPSHALSLFALPPSLFSLLSLLSLAAEEAEESTESTLHSQSPPSSPRSSSPRSSSPRSSSLSSSSPSTSAEQLK
RQMVEACSSLAKAGVVDLQRVMFPFFVLAPLSPLDAKSVDLDFIHRLASLRLFLRSGQRRSSGFLEAGACPPSLMLQHDR
RLLRGAVESLHCLPSLSAVARLFCPGNSARKLDYEGGRSLQKAERRSARKEQNEGDAAEENGAFNWPRSLLGTLPSSDRE
SESAKDTKEKRTPGSEKGERGEADGERREEDGEKGATKEDGLFSKEEQFFRRLQSYKGSIFSRGDDAANAWTTEEQKLLT
FFQQRNENALSVKEALREEGMEIFYHLRSRVFEPVALRMTHQFGRSFRFYRLQTIHRNLTPRNVVINSDAGFTLGTLCRV
YLSRFKQRLAEPHPDSQQGPQGNCFLVQGVKRRQEISWMPAILYQLEVQGKHCDLVRRLRQEMRPFLFTAEENISPPLVP
SEQCKRWKRPQQESQSAAEREKTRRSRKYV
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2366 - 2385:	EEEEEEEEEEEEEEEEEEEE
2367 - 2386:	EEEEEEEEEEEEEEEEEEEE
2368 - 2387:	EEEEEEEEEEEEEEEEEEEE
2369 - 2388:	EEEEEEEEEEEEEEEEEEEE

A0A3S0Z3P8 **A0A3S0Z3P8_ELYCH** (348 aa)
Uncharacterized protein (Fragment). *Elysia chlorotica (Eastern emerald elysia) (Sea slug)*

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KKKKKKKKKKKKKKKKKKKKKKKKKKKKQEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEEEEEEEEEEEEEEEEEEDDEEYFR
```

260 - 279:	EEEEEEEEEEEEEEEEEEEE
261 - 280:	EEEEEEEEEEEEEEEEEEEE
262 - 281:	EEEEEEEEEEEEEEEEEEEE
263 - 282:	EEEEEEEEEEEEEEEEEEEE
264 - 283:	EEEEEEEEEEEEEEEEEEEE
265 - 284:	EEEEEEEEEEEEEEEEEEEE
266 - 285:	EEEEEEEEEEEEEEEEEEEE
267 - 286:	EEEEEEEEEEEEEEEEEEEE
268 - 287:	EEEEEEEEEEEEEEEEEEEE
269 - 288:	EEEEEEEEEEEEEEEEEEEE
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271 - 290:	EEEEEEEEEEEEEEEEEEEE
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275 - 294:	EEEEEEEEEEEEEEEEEEEE
276 - 295:	EEEEEEEEEEEEEEEEEEEE
277 - 296:	EEEEEEEEEEEEEEEEEEEE
278 - 297:	EEEEEEEEEEEEEEEEEEEE
279 - 298:	EEEEEEEEEEEEEEEEEEEE
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282 - 301:	EEEEEEEEEEEEEEEEEEEE
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294 - 313:	EEEEEEEEEEEEEEEEEEEE

295 - 314:	EEEEEEEEEEEEEEEEEEEE
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300 - 319:	EEEEEEEEEEEEEEEEEEEE
301 - 320:	EEEEEEEEEEEEEEEEEEEE
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315 - 334:	EEEEEEEEEEEEEEEEEEEE
316 - 335:	EEEEEEEEEEEEEEEEEEEE
317 - 336:	EEEEEEEEEEEEEEEEEEEE
318 - 337:	EEEEEEEEEEEEEEEEEEEE
319 - 338:	EEEEEEEEEEEEEEEEEEEE
320 - 339:	EEEEEEEEEEEEEEEEEEEE
321 - 340:	EEEEEEEEEEEEEEEEEEEE
322 - 341:	EEEEEEEEEEEEEEEEEEEE

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