Anti-inflammatory Role of Curcumin in LPS Treated A549 cells at Global Proteome level and on Mycobacterial infection.

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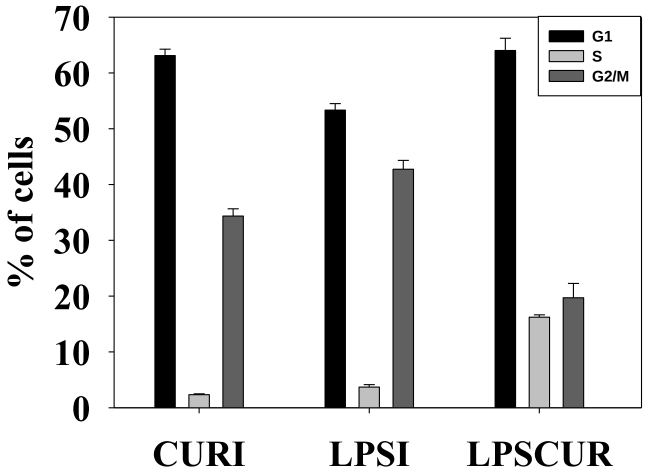

Figure S1: Effect of curcumin and/or LPS treatment on A549 cell viability A549 cells were treated with curcumin (10 µM) and/or LPS or 1 µg/ml for the indicated times and after fixation were stained with propidium iodide and Annexin V-FITC. The DNA contents were determined by flow cytometry to calculate percentage of cells present in each phase of the cell cycle (G1, S and G2/M) using Flowing analysis software.

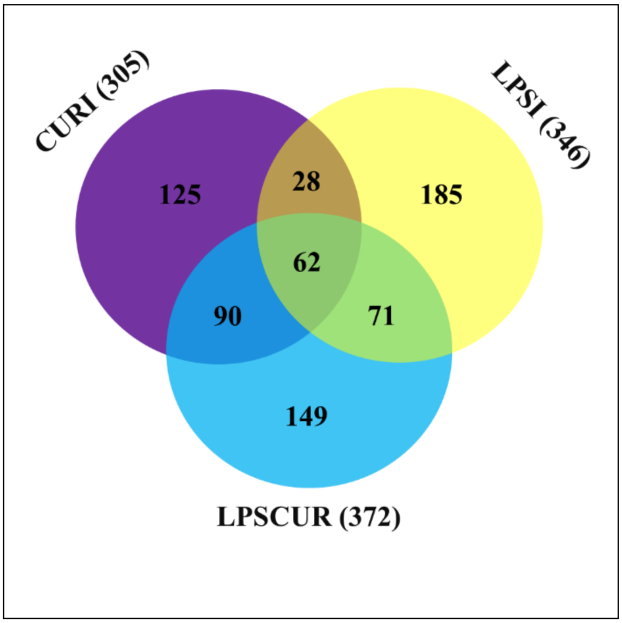

Figure S2: Total proteins identified in all the three experiments and their distribution betwee curcumin and/or LPS treated conditions. The proteins showing differential expressions ($\log_2$ fold change≥2) in these experiments were presented in the venn diagram and certain number of proteins are common in all three experiments.

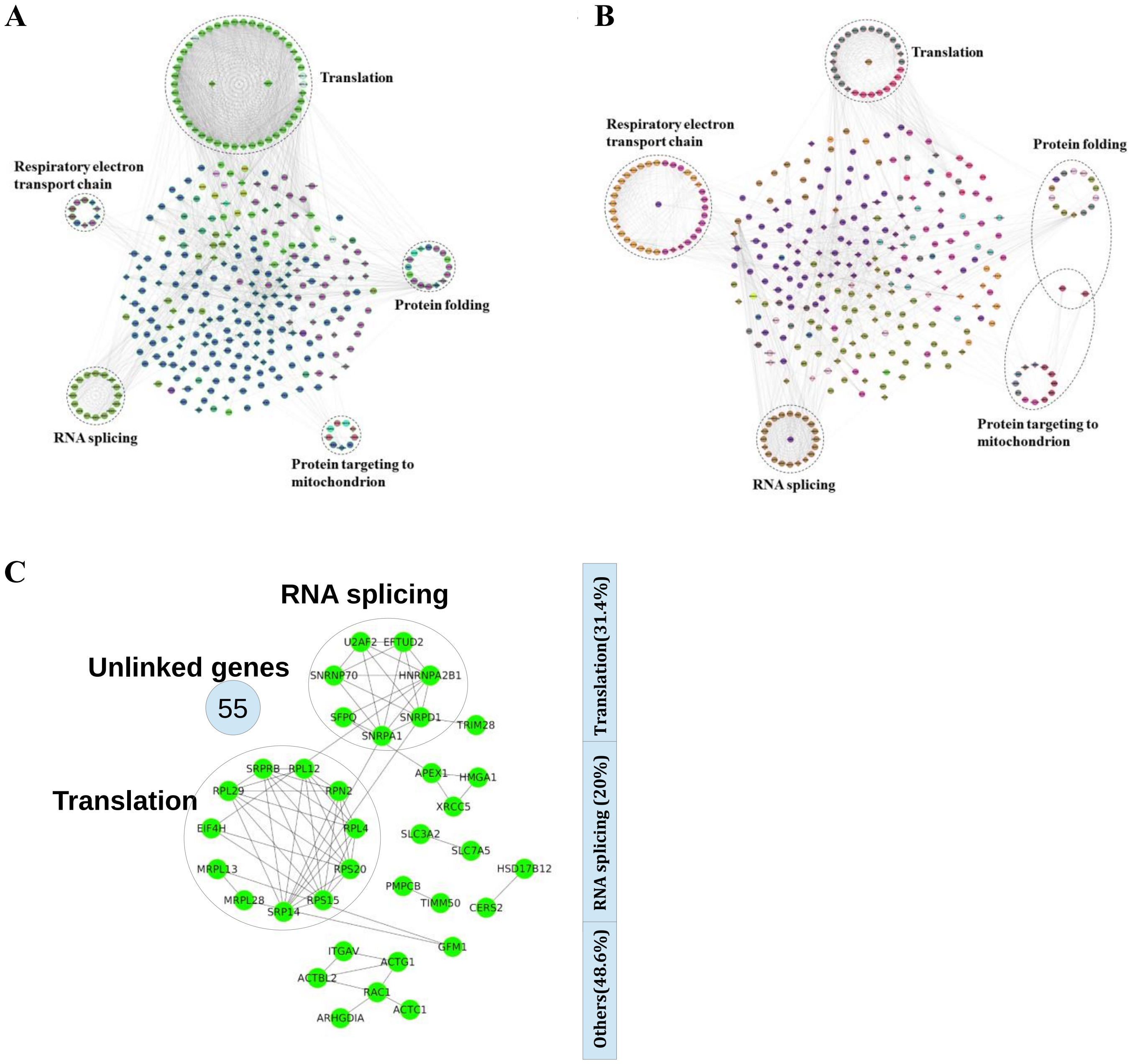

Figure S3: Treatment of the A549 cells with curcumin and LPS show altered biological activity. Subnetwork in (A) curcumin treated cells (out of 305 deregulated genes only 257 were mapped to the database with 75 linker genes) and (B) LPs treated cells (out of 346 deregulated genes only 265 were mapped to the database with 65 linker genes). Different colors shows different modules in which the interaction of the genes are highest based on the modularity. The circled maps of the subnetworks involves different biological processes. Linker genes are shown by diamond shaped nodes. (C) Reactome FI network of 90 common deregulated genes/proteins between curcumin and LPS treated experiments. The important biological processes like translation and RNA splicing accounts for 31.4% and 20% respectively. About 48.4% of genes which are not linked to other genes may be involved in some other biological processes.

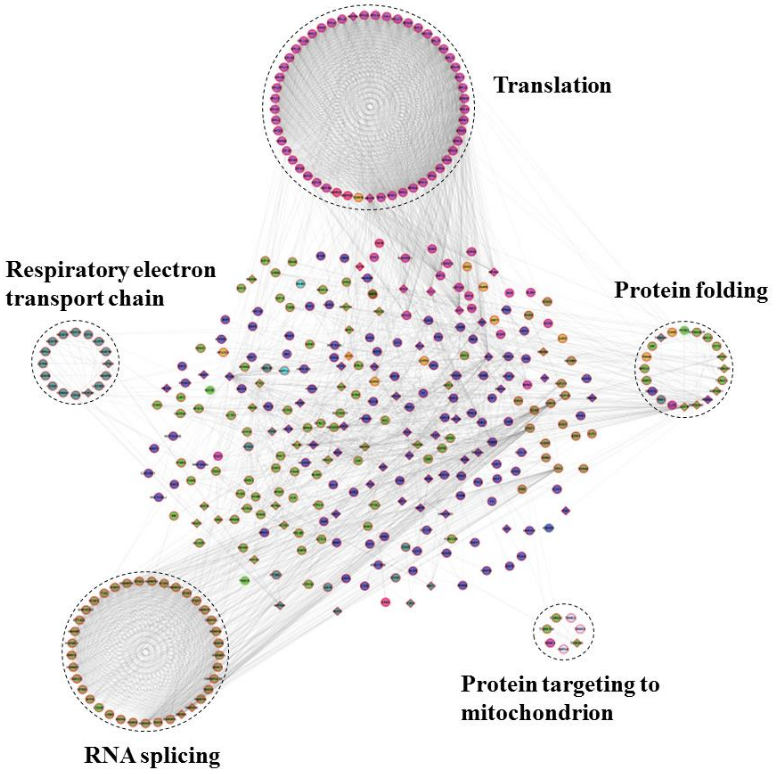

Figure S4: **Simultaneous treatment of A549 cells with curcumin and LPS and its effect on the biological pathways**. Subnetwork in LPSCUR (out of 372 deregulated genes only 317 were mapped to the database with 76 linker genes). Functional categorization and the distribution of LPSCUR differentially expressed proteins to extract the information of their known functions.

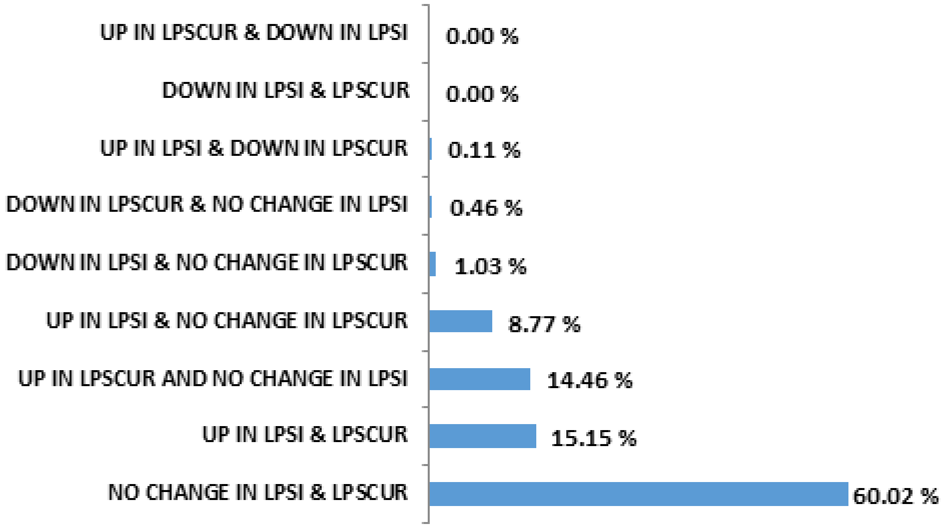

Figure S5: Percentage distribution of the deregulated proteins in LPS treated and both LPS and curcumin treated cells. A total of 878 proteins were common in these experiments. The proteins upregulated in LPS treated cells did not show change in both LPS and curcumin treated cells accounts for 8.77%. About 15.15% accounts for upregulation in both the experiments with 60% with no significant change in both experiments.

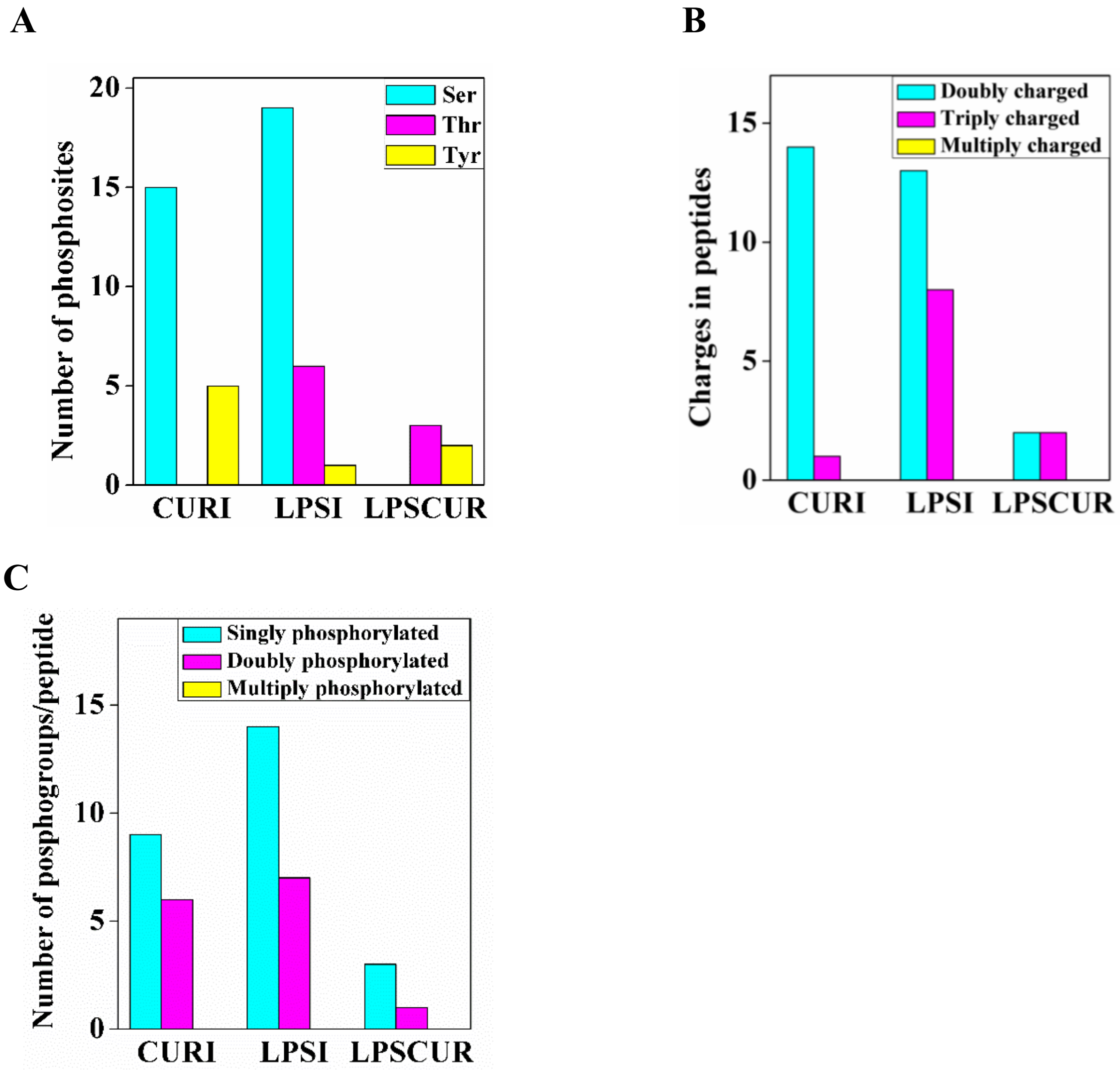

Figure S6: Alteration in phosphoproteins in curcumin and/or LPS treated cells. (A) Distribution of the phosphosite localization of class I identified phsphosites. (B) Distribution of the charges in peptides of phosphorylated proteins. (C) Distribution of no. of phosphogroups per peptide.

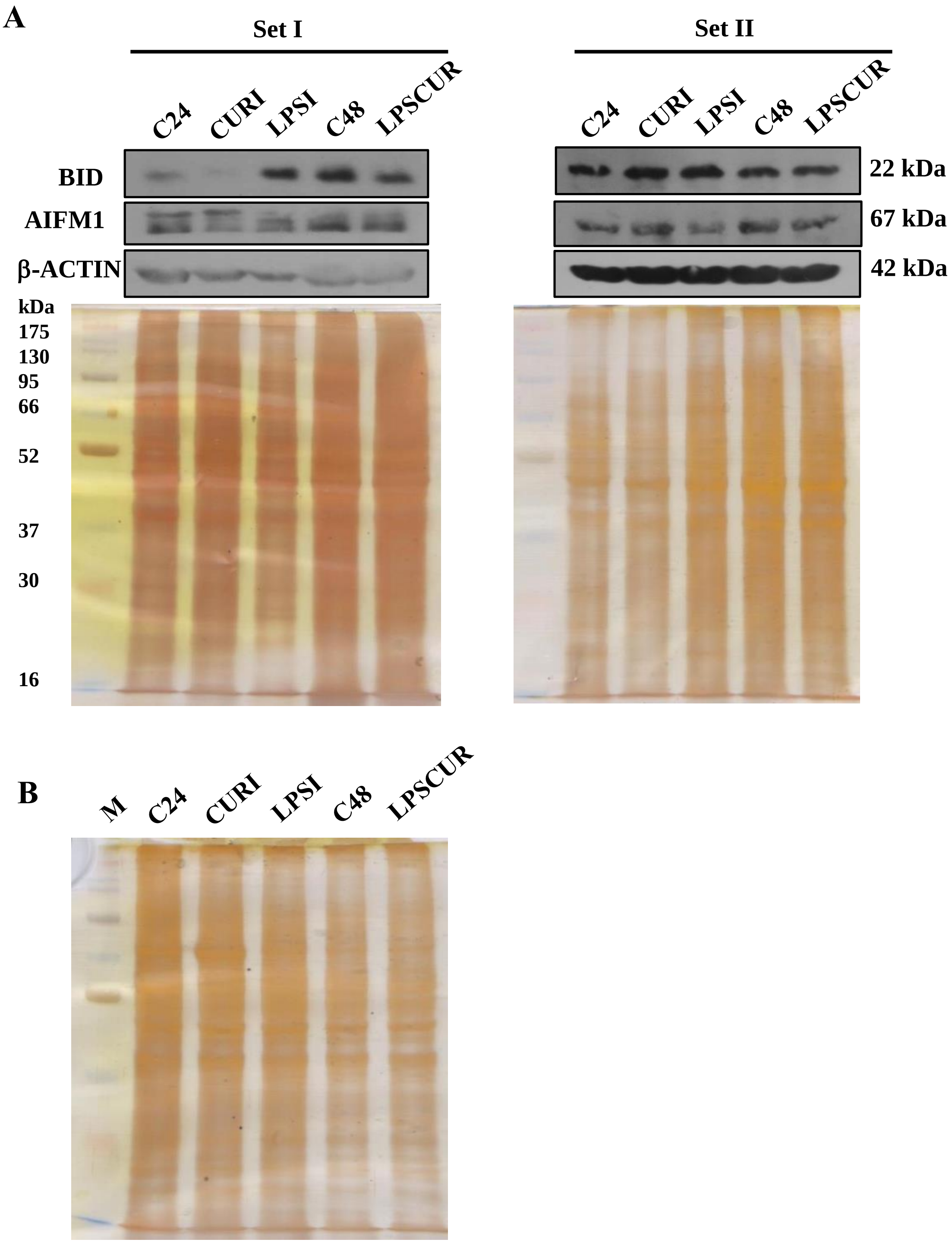

Figure S7: Western blot analysis of BID and AIFM1 proteins isolated from A549 cells treated with LPS and/or curcumin in independent sample sets. A549 cells were treated with curcumin (10 µM) or LPS (1 µg/ml) and both for 24 hours and 48 hours respectively showed BID and AIFM1 expression as analysed by Western blot. (A) Two independent sets (B) silver stained gel for Figure 6A . Silver staining gels are shown for loading control (6 µg). Proteins were transferred to membrane and the blot was cut into 3 parts for probing BID, AIFM1 and b-actin. Extracted intensities data presented Fig. 6A

REPLICATE A

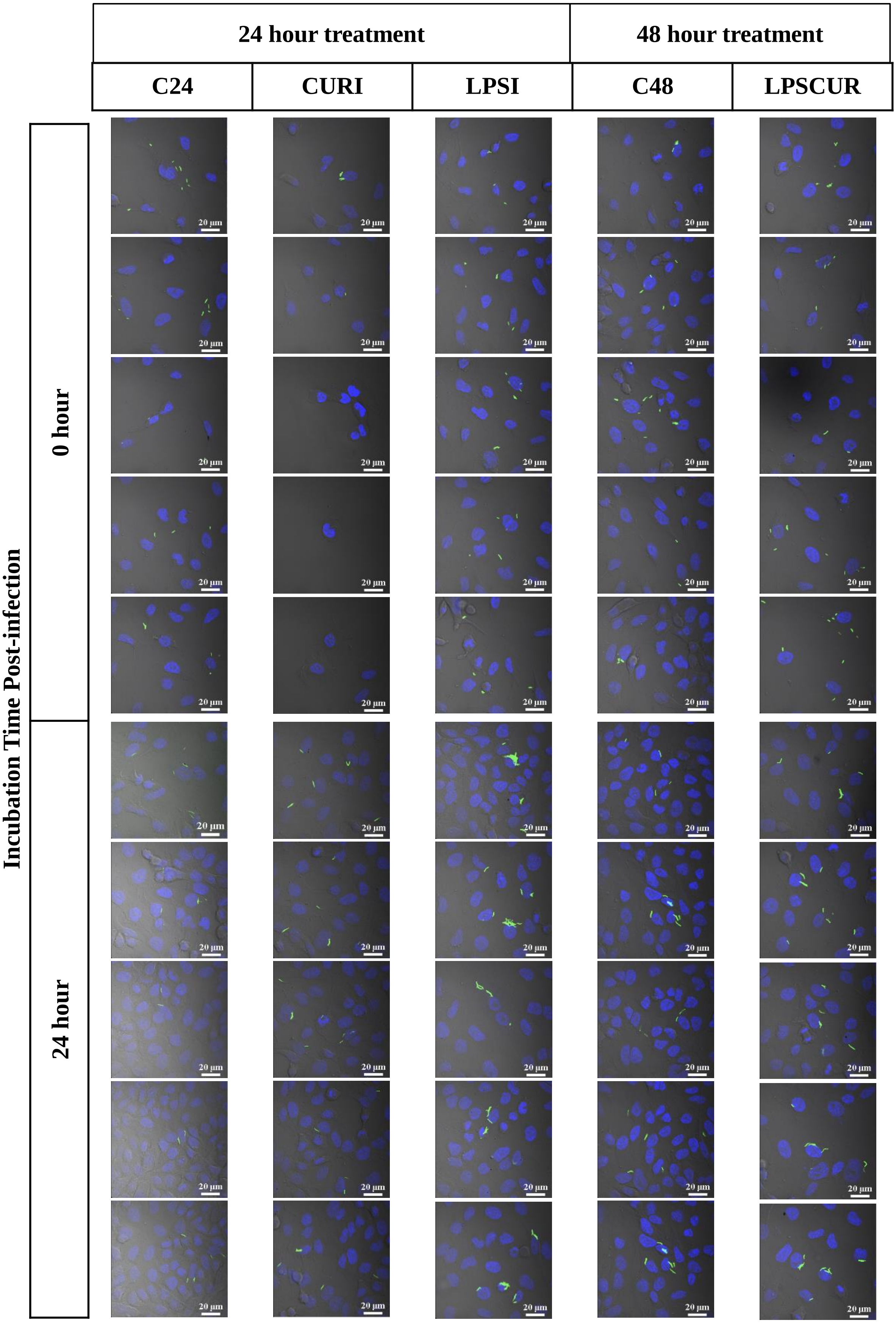

Figure S8A: Confocal images of H37Rv-GFP infected A549 cells (at multiplicity of infection 1:5) treated with Curcumin (CURI), Lipopolysaccharide (LPSI) or both (LPSCUR). Cells were incubated with DAPI (blue, 1 µg/ml) to stain nucleus. Scale : 20 µm

REPLICATE B

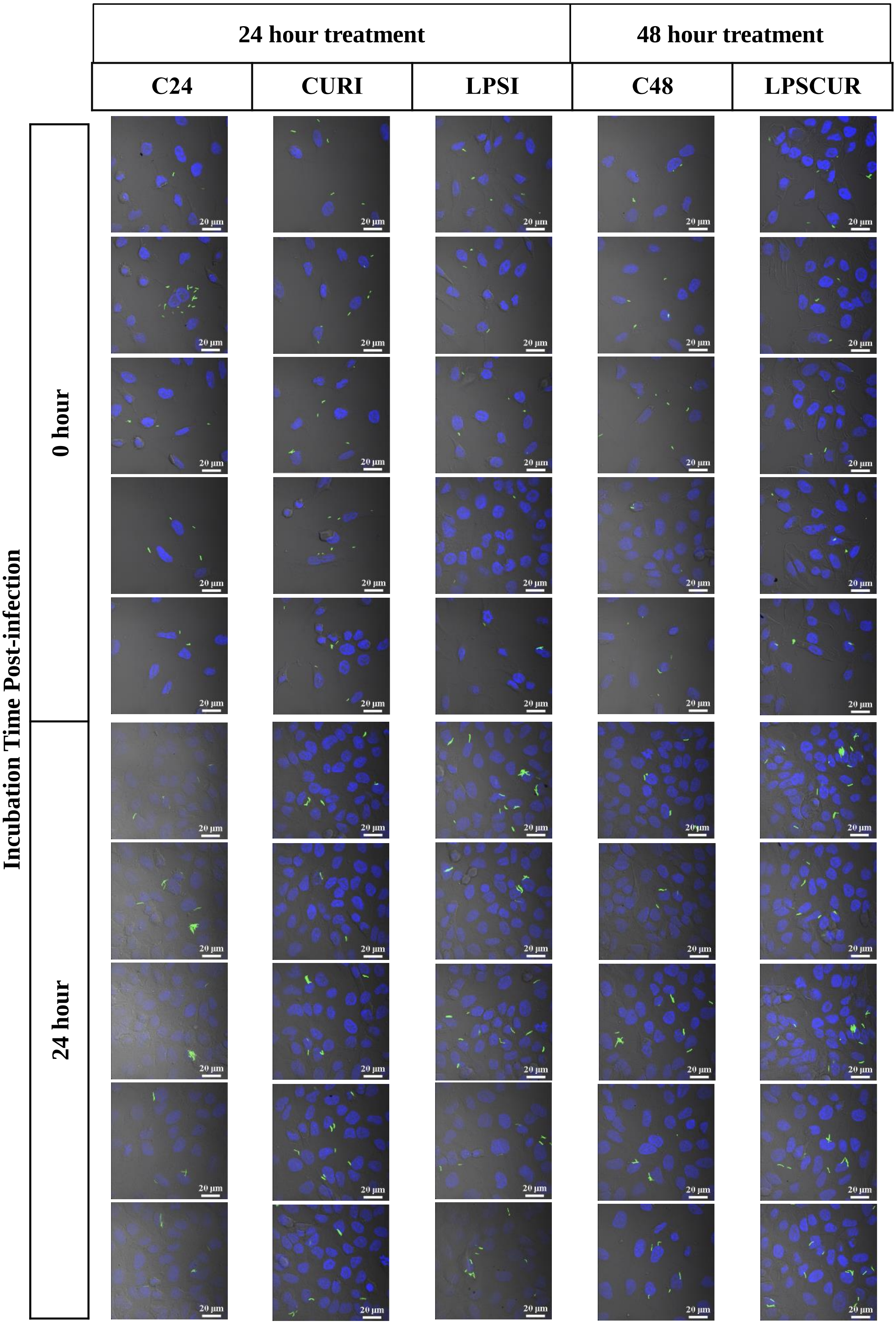

Figure S8B: Confocal images of H37Rv-GFP infected A549 cells (at multiplicity of infection 1:5) treated with Curcumin (CURI), Lipopolysaccharide (LPSI) or both (LPSCUR). Cells were incubated with DAPI (blue, 1 µg/ml) to stain nucleus. Scale : 20 µm

REPLICATE C

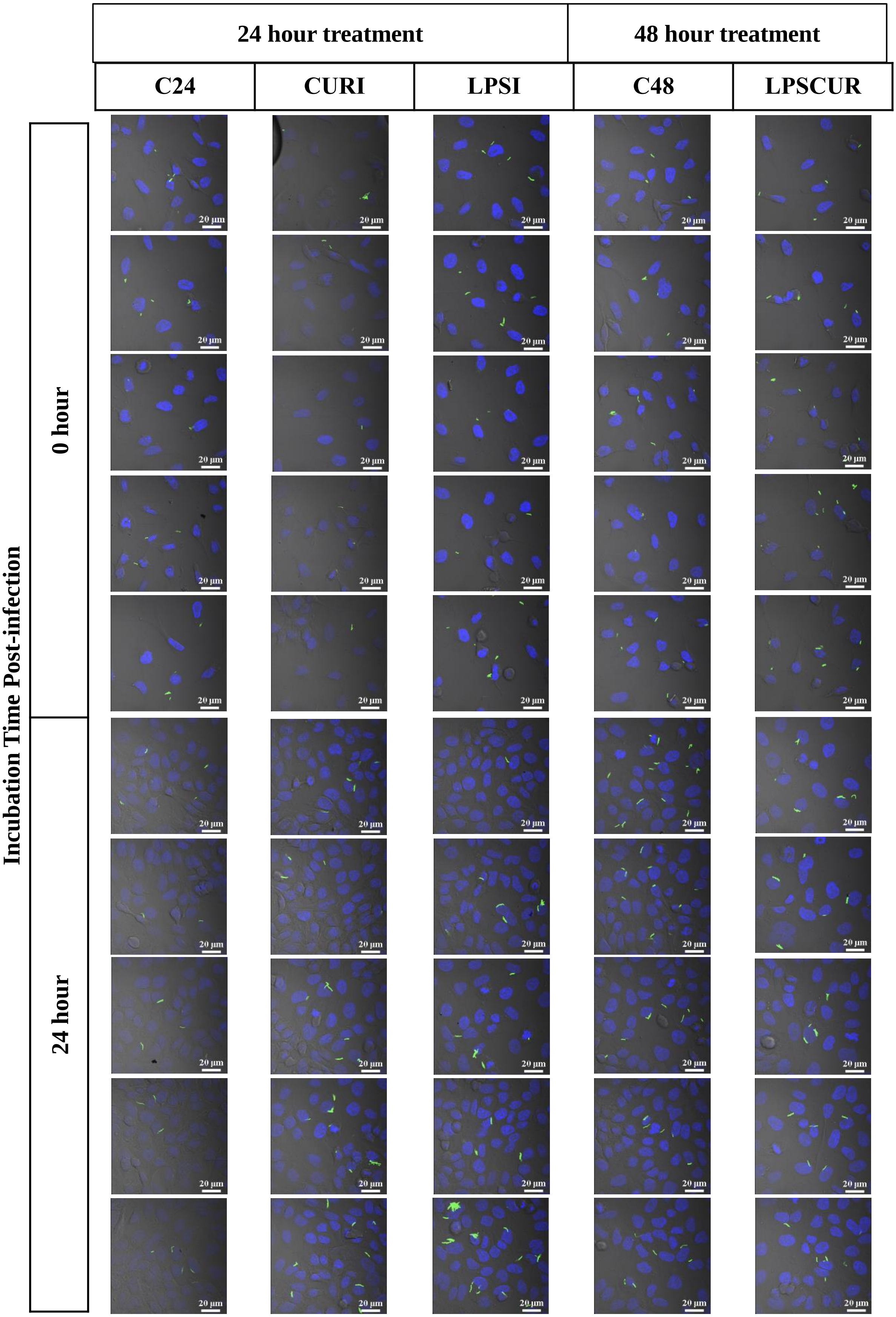

Figure S8C: Confocal images of H37Rv-GFP infected A549 cells (at multiplicity of infection 1:5) treated with Curcumin (CURI), Lipopolysaccharide (LPSI) or both (LPSCUR). Cells were incubated with DAPI (blue, 1 µg/ml) to stain nucleus. Scale : 20 µm

Table S1. List of all identified proteins from SILAC experiments in CURI, LPSI and LPSCUR

	Experiments							**Peptides**			**Sequence coverage (%)**		
S. No.	**CURI**	**LPSI**	**LPSCUR**	**protein ID**	**Protein names**	**Length**	**Gene**	**CURI**	**LPSI**	**LPSCUR**	**CURI**	**LPSI**	**LPSCUR**
1	-4.32	5.04	7.56	P81605	Dermcidin (EC 3.4.-.-) (Preproteolysin) [Cleaved into: Survival-promoting peptide; DCD-1]	110	DCD	2	5	2	25.5	35.5	12.7
2	-4.28	4.55	2.47	P35908	Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (CK-2e) (Epithelial keratin-2e) (Keratin-2 epidermis) (Keratin-2e) (K2e) (Type-II keratin Kb2)	639	KRT2	16	52	21	37.6	82.9	47.1
3	-4.23	0.81	1.23	K7ENV7	Isochorismatase domain-containing protein 2, mitochondrial (Fragment)	174	ISOC2	1	1	1	19	9.2	9.2
4	-3.92	0.00	0.00	J3KT51	Hematological and neurological-expressed 1 protein	104	HN1	1	0	0	24	0	0
5	-3.80	0.00	3.47	Q05639	Elongation factor 1-alpha 2 (EF-1-alpha-2) (Eukaryotic elongation factor 1 A-2) (eEF1A-2) (Statin-S1)	463	EEF1A2	8	4	8	21	8.4	21

6	-3.59	2.30	0.00	P17096	High mobility group protein HMG-I/HMG-Y (HMG-I(Y)) (High mobility group AT-hook protein 1) (High mobility group protein A1) (High mobility group protein R)	107	HMGA1	2	1	0	23.4	15	0
7	-3.46	0.00	3.47	A0A087WY55	Chromosome 6 open reading frame 55, isoform CRA_b (Vacuolar protein sorting-associated protein VTA1 homolog)	280	VTA1	1	0	1	5	0	5
8	-3.43	2.43	4.28	P08621	U1 small nuclear ribonucleoprotein 70 kDa (U1 snRNP 70 kDa) (U1-70K) (snRNP70)	437	SNRNP70	1	1	2	2.5	2.5	5.5
9	-3.39	0.00	3.13	H7C3S9	COP9 signalosome complex subunit 8 (Fragment)	83	COPS8	2	1	1	27.7	12	15.7
10	-3.36	2.68	0.00	P16402	Histone H1.3 (Histone H1c) (Histone H1s-2)	221	HIST1H1D	6	5	5	22.6	22.2	14.9
11	-3.35	1.69	1.71	Q6S8J3	POTE ankyrin domain family member E (ANKRD26-like family C member 1A) (Prostate, ovary, testis-expressed protein on chromosome 2) (POTE-2)	1075	POTEE	6	8	4	7.7	9.7	6.3
12	-3.29	0.00	0.00	P25325	3-mercaptopyruvate sulfurtransferase (MST) (EC 2.8.1.2)	297	MPST	1	0	0	9.1	0	0
13	-3.28	-0.46	0.42	Q99536	Synaptic vesicle membrane protein VAT-1 homolog (EC 1.-.-.-)	393	VAT1	1	1	2	3.8	3.6	7.4
14	-3.04	0.00	2.30	P05026	Sodium/potassium-transporting ATPase subunit beta-1 (Sodium/potassium-dependent ATPase subunit beta-1)	303	ATP1B1	1	0	1	4.7	0	8.3
15	-3.01	3.17	3.20	Q562R1	Beta-actin-like protein 2 (Kappa-actin)	376	ACTBL2	4	4	4	14.1	14.1	14.1
16	-2.83	0.64	0.00	H3BQZ9	Adenine phosphoribosyltransferase	153	APRT	2	1	0	17	8.5	0

17	-2.83	2.97	2.95	Q9NS69	Mitochondrial import receptor subunit TOM22 homolog (hTom22) (1C9-2) (Translocase of outer membrane 22 kDa subunit homolog)	142	TOMM22	3	3	3	43.7	39.4	43.7
18	-2.81	0.00	1.54	P43243	Matrin-3	847	MATR3	1	0	2	1.7	0	3.8
19	-2.71	0.57	0.00	J3QL05	Serine/arginine-rich-splicing factor 2 (Fragment)	130	SRSF2	1	1	0	12.3	6.2	0
20	-2.71	0.00	1.36	Q53FA7	Quinone oxidoreductase PIG3 (EC 1.-.-.-) (Tumor protein p53-inducible protein 3) (p53-induced gene 3 protein)	332	TP53I3	3	0	1	16.6	0	4.2
21	-2.57	2.20	2.37	Q16543	Hsp90 co-chaperone Cdc37 (Hsp90 chaperone protein kinase-targeting subunit) (p50Cdc37) [Cleaved into: Hsp90 co-chaperone Cdc37, N-terminally processed]	378	CDC37	1	1	1	5.6	5.6	5.6
22	-2.55	0.00	0.00	H7C2I4	Zinc phosphodiesterase ELAC protein 2 (Fragment)	286	ELAC2	1	0	0	7.3	0	0
23	-2.54	0.00	0.00	Q9Y584	Mitochondrial import inner membrane translocase subunit Tim22 (Testis-expressed sequence 4)	194	TIMM22	1	0	0	7.7	0	0
24	-2.49	2.03	2.04	P47914	60S ribosomal protein L29 (Cell surface heparin-binding protein HIP)	159	RPL29	2	1	2	14.5	9.4	14.5
25	-2.46	0.00	1.65	P00374	Dihydrofolate reductase (EC 1.5.1.3)	187	DHFR	1	0	1	11.9	0	11.9
26	-2.46	0.00	2.02	Q00796	Sorbitol dehydrogenase (EC 1.1.1.14) (L-iditol 2-dehydrogenase)	357	SORD	2	0	1	35	0	20
27	-2.46	1.75	0.00	Q9NRF9	DNA polymerase epsilon subunit 3 (EC 2.7.7.7) (Arsenic-transactivated protein) (AsTP) (Chromatin accessibility complex 17 kDa protein) (CHRAC-17) (HuCHRAC17) (DNA polymerase II subunit 3) (DNA polymerase epsilon subunit p17)	147	POLE3	1	1	0	10.9	10.9	0

28	-2.44	1.94	1.97	K7EM56	40S ribosomal protein S15	112	RPS15	4	1	3	52.7	10.7	28.6
29	-2.43	0.97	2.02	Q16531	DNA damage-binding protein 1 (DDB p127 subunit) (DNA damage-binding protein a) (DDBa) (Damage-specific DNA-binding protein 1) (HBV X-associated protein 1) (XAP-1) (UV-damaged DNA-binding factor) (UV-damaged DNA-binding protein 1) (UV-DDB 1) (XPE-binding factor) (XPE-BF) (Xeroderma pigmentosum group E-complementing protein) (XPCe)	1140	DDB1	1	2	2	0.9	2	3
30	-2.41	0.84	1.28	P24666	Low molecular weight phosphotyrosine protein phosphatase (LMW-PTP) (LMW-PTPase) (EC 3.1.3.48) (Adipocyte acid phosphatase) (Low molecular weight cytosolic acid phosphatase) (EC 3.1.3.2) (Red cell acid phosphatase 1)	158	ACP1	1	4	1	11.4	41.8	8.2
31	-2.40	-0.04	1.58	Q00839	Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (Scaffold attachment factor A) (SAF-A) (p120) (pp120)	825	HNRNPU	7	3	7	11.3	3.8	9.2
32	-2.38	0.00	2.20	Q8NBX0	Saccharopine dehydrogenase-like oxidoreductase (EC 1.-.-.-)	429	SCCPDH	1	0	1	3.3	0	3.3
33	-2.36	0.97	-0.18	P33991	DNA replication licensing factor MCM4 (EC 3.6.4.12) (CDC21 homolog) (P1-CDC21)	863	MCM4	2	3	1	4.5	5.7	1.5
34	-2.34	-0.07	0.86	Q9UMY4	Sorting nexin-12	172	SNX12	2	4	1	24.7	20.4	4.3
35	-2.34	1.21	2.03	J3KTF8	Rho GDP-dissociation inhibitor 1 (Fragment)	193	ARHGDIA	3	1	1	31.6	7.8	16.6
36	-2.28	0.00	0.47	Q6PUV4	Complexin-2 (Complexin II) (CPX II) (Synaphin-1)	134	CPLX2	1	0	1	8.2	0	4.5

37	-2.27	0.00	0.00	Q16537	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit epsilon isoform (PP2A B subunit isoform B'-epsilon) (PP2A B subunit isoform B56-epsilon) (PP2A B subunit isoform PR61-epsilon) (PP2A B subunit isoform R5-epsilon)	467	PPP2R5E	1	0	0	3.2	0	0
38	-2.25	0.93	2.29	E9PES6	High mobility group protein B3 (Fragment)	153	HMGB3	1	2	3	9.2	19	28.1
39	-2.24	1.20	1.13	P07954	Fumarate hydratase, mitochondrial (Fumarase) (EC 4.2.1.2)	510	FH	3	3	3	9.9	7.5	10.1
40	-2.22	0.00	1.97	C9IZ80	Basic leucine zipper and W2 domain-containing protein 1 (Fragment)	294	BZW1	1	0	2	8.8	0	12.9
41	-2.18	0.31	1.85	F8VSD4	Ubiquitin-conjugating enzyme E2 N	105	UBE2N	6	4	4	63.8	42.9	38.1
42	-2.17	1.52	1.57	P63000	Ras-related C3 botulinum toxin substrate 1 (Cell migration-inducing gene 5 protein) (Ras-like protein TC25) (p21-Rac1)	192	RAC1	4	2	3	25.5	13	19.8
43	-2.17	0.00	1.95	P40818	Ubiquitin carboxyl-terminal hydrolase 8 (EC 3.4.19.12) (Deubiquitinating enzyme 8) (Ubiquitin isopeptidase Y) (hUBPy) (Ubiquitin thioesterase 8) (Ubiquitin-specific-processing protease 8)	1118	USP8	1	0	1	1	0	1
44	-2.17	1.54	0.00	P08559	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial (EC 1.2.4.1) (PDHE1-A type I)	390	PDHA1	1	2	0	3.6	6.7	0
45	-2.14	-0.79	1.80	P60983	Glia maturation factor beta (GMF-beta)	142	GMFB	1	1	1	16.2	6.3	16.2

46	-2.14	0.00	0.44	O60762	Dolichol-phosphate mannosyltransferase subunit 1 (EC 2.4.1.83) (Dolichol-phosphate mannose synthase subunit 1) (DPM synthase subunit 1) (Dolichyl-phosphate beta-D-mannosyltransferase subunit 1) (Mannose-P-dolichol synthase subunit 1) (MPD synthase subunit 1)	260	DPM1	2	0	1	8.8	0	4.2
47	-2.13	0.00	0.00	H7C2Y1	E3 ubiquitin-protein ligase TRIP12 (Fragment)	187	TRIP12	1	0	0	5.9	0	0
48	-2.11	0.29	0.00	B1AH58	Intraflagellar transport protein 27 homolog (Fragment)	116	IFT27	1	1	0	18.1	6.9	0
49	-2.10	1.34	0.00	A2IDC6	39S ribosomal protein L28, mitochondrial (Fragment)	240	MRPL28	1	1	0	5	2.9	0
50	-2.09	1.20	1.28	Q9Y320	Thioredoxin-related transmembrane protein 2 (Cell proliferation-inducing gene 26 protein) (Thioredoxin domain-containing protein 14)	296	TMX2	1	2	1	5.8	10.5	4.7
51	-2.09	0.00	0.00	Q9NX08	COMM domain-containing protein 8	183	COMMD8	1	0	0	6.6	0	0
52	-2.07	0.00	0.00	C9J306	2-hydroxyacyl-CoA lyase 1 (Fragment)	244	HACL1	1	0	0	4.1	0	0
53	-2.07	0.00	0.98	D6R9A6	High mobility group protein B2 (Fragment)	134	HMGB2	2	0	2	23.1	0	17.2
54	-2.05	0.00	0.56	Q9UHX1	Poly(U)-binding-splicing factor PUF60 (60 kDa poly(U)-binding-splicing factor) (FUSE-binding protein-interacting repressor) (FBP-interacting repressor) (Ro-binding protein 1) (RoBP1) (Siah-binding protein 1) (Siah-BP1)	559	PUF60	2	0	2	8.6	0	6.8
55	-2.04	0.32	0.70	P18669	Phosphoglycerate mutase 1 (EC 3.1.3.13) (EC 5.4.2.11) (EC 5.4.2.4) (BPG-dependent PGAM 1) (Phosphoglycerate mutase isozyme B) (PGAM-B)	254	PGAM1	10	5	6	50	31.1	34.6

56	-2.02	0.00	0.00	C9JQQ5	Atlastin-2 (Fragment)	175	ATL2	1	0	0	8.6	0	0
57	-2.02	0.00	0.00	Q9UN86	Ras GTPase-activating protein-binding protein 2 (G3BP-2) (GAP SH3 domain-binding protein 2)	482	G3BP2	1	0	0	3.8	0	0
58	-2.00	0.00	2.05	P53618	Coatomer subunit beta (Beta-coat protein) (Beta-COP)	953	COPB1	4	0	5	9.2	0	9.8
59	-1.98	1.80	0.00	C9JAZ1	Metaxin-2 (Fragment)	229	MTX2	1	2	0	9.6	16.6	0
60	-1.97	1.93	1.12	Q15056	Eukaryotic translation initiation factor 4H (eIF-4H) (Williams-Beuren syndrome chromosomal region 1 protein)	248	EIF4H	1	2	3	9.2	21.9	28.1
61	-1.97	0.00	2.14	A0A087 WZX2	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6	97	NDUFB6	1	0	1	18.6	0	18.6
62	-1.96	1.73	2.17	B3KUB4	Carbonic anhydrase 12 (Carbonic anhydrase XII, isoform CRA_d) (cDNA FLJ39526 fis, clone PUAEN2003018, highly similar to CARBONIC ANHYDRASE XII (EC 4.2.1.1))	283	CA12	4	2	3	23.3	9.5	13.4
63	-1.96	0.00	0.00	P52907	F-actin-capping protein subunit alpha-1 (CapZ alpha-1)	286	CAPZA1	1	0	0	5.2	0	0
64	-1.95	1.99	1.94	Q14764	Major vault protein (MVP) (Lung resistance-related protein)	893	MVP	3	1	3	4.3	1.8	4.8
65	-1.94	1.16	1.47	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	353	HNRNPA2B 1	4	5	6	19.3	16.7	14.7
66	-1.92	0.00	1.79	A0A087 WTP3	Far upstream element-binding protein 2	711	KHSRP	2	0	1	6	0	1.5
67	-1.91	0.00	1.45	O00625	Pirin (EC 1.13.11.24) (Probable quercetin 2,3-dioxygenase PIR) (Probable quercetinase)	290	PIR	2	0	4	11	0	18.3
68	-1.90	1.18	1.83	O75439	Mitochondrial-processing peptidase subunit beta (EC 3.4.24.64) (Beta-MPP) (P-52)	489	PMPCB	1	1	1	2.2	2.2	2.2

69	-1.90	0.00	0.47	P49915	GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2) (GMP synthetase) (Glutamine amidotransferase)	693	GMPS	2	0	3	3.9	0	5.7
70	-1.90	0.78	1.08	P52895	Aldo-keto reductase family 1 member C2 (EC 1.-.-.-) (3-alpha-HSD3) (Chlordecone reductase homolog HAKRD) (Dihydrodiol dehydrogenase 2) (DD-2) (DD2) (Dihydrodiol dehydrogenase/bile acid-binding protein) (DD/BABP) (Trans-1,2-dihydrobenzene-1,2-diol dehydrogenase) (EC 1.3.1.20) (Type III 3-alpha-hydroxysteroid dehydrogenase) (EC 1.1.1.357)	323	AKR1C2	8	10	10	39.6	49.2	49.2
71	-1.89	0.00	2.47	P11498	Pyruvate carboxylase, mitochondrial (EC 6.4.1.1) (Pyruvic carboxylase) (PCB)	1178	PC	2	0	1	2.2	0	1.1
72	-1.88	0.00	0.00	C9JYQ9	60S ribosomal protein L22-like 1	121	RPL22L1	1	0	0	19.8	0	0
73	-1.88	0.00	1.25	O00159	Unconventional myosin-Ic (Myosin I beta) (MMI-beta) (MMIb)	1063	MYO1C	1	0	2	1.8	0	2.9
74	-1.87	0.23	0.39	Q01105	Protein SET (HLA-DR-associated protein II) (Inhibitor of granzyme A-activated DNase) (IGAAD) (PHAPII) (Phosphatase 2A inhibitor I2PP2A) (I-2PP2A) (Template-activating factor I) (TAF-I)	290	SET	2	5	2	7.9	30.2	7.9
75	-1.87	1.28	1.97	Q9BSJ8	Extended synaptotagmin-1 (E-Syt1) (Membrane-bound C2 domain-containing protein)	1104	ESYT1	2	4	1	2.9	4.9	1.4

76	-1.87	0.56	1.34	P30041	Peroxiredoxin-6 (EC 1.11.1.15) (1-Cys peroxiredoxin) (1-Cys PRX) (24 kDa protein) (Acidic calcium-independent phospholipase A2) (aiPLA2) (EC 3.1.1.-) (Antioxidant protein 2) (Liver 2D page spot 40) (Non-selenium glutathione peroxidase) (NSGPx) (EC 1.11.1.9) (Red blood cells page spot 12)	224	PRDX6	8	9	9	41.5	51.3	33.9
77	-1.86	0.70	2.05	P62861	40S ribosomal protein S30	59	FAU	1	1	1	16.9	16.9	16.9
78	-1.86	1.77	1.64	Q14696	LDLR chaperone MESD (Mesoderm development candidate 2) (Mesoderm development protein) (Renal carcinoma antigen NY-REN-61)	234	MESDC2	1	2	1	4.3	9	4.7
79	-1.85	0.00	0.00	H0YN84	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit gamma isoform (Fragment)	89	PPP2R5C	1	0	0	12.4	0	0
80	-1.85	0.00	2.33	O76031	ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	633	CLPX	1	0	1	2.1	0	2.1
81	-1.85	0.00	0.00	O60884	DnaJ homolog subfamily A member 2 (Cell cycle progression restoration gene 3 protein) (Dnj3) (Dj3) (HIRA-interacting protein 4) (Renal carcinoma antigen NY-REN-14)	412	DNAJA2	1	0	0	3.6	0	0
82	-1.82	1.97	1.71	P51970	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8 (Complex I-19kD) (CI-19kD) (Complex I-PGIV) (CI-PGIV) (NADH-ubiquinone oxidoreductase 19 kDa subunit)	172	NDUFA8	2	3	1	22.7	27.3	10.5
83	-1.82	0.72	1.11	Q8TEX9	Importin-4 (Imp4) (Importin-4b) (Imp4b) (Ran-binding protein 4) (RanBP4)	1081	IPO4	4	3	2	5.5	3.1	2
84	-1.80	1.89	1.70	Q5SZE2	Ceramide synthase 2 (Fragment)	128	CERS2	1	1	1	12.5	12.5	12.5

85	-1.80	1.34	2.08	J3KNF8	Cytochrome b5 type B (Cytochrome b5 type B (Outer mitochondrial membrane), isoform CRA_a)	150	CYB5B	2	4	2	35.3	53.3	35.3
86	-1.79	1.30	2.00	P07099	Epoxide hydrolase 1 (EC 3.3.2.9) (Epoxide hydratase) (Microsomal epoxide hydrolase)	455	EPHX1	6	5	9	24	14.7	35.2
87	-1.79	1.96	2.08	P10606	Cytochrome c oxidase subunit 5B, mitochondrial (Cytochrome c oxidase polypeptide Vb)	129	COX5B	2	4	2	18.6	24.8	17.8
88	-1.79	0.00	1.13	F5GZ49	Glycolipid transfer protein (Glycolipid transfer protein isoform 1)	67	GLTP	1	0	1	22.4	0	22.4
89	-1.76	0.00	1.32	Q9Y2V2	Calcium-regulated heat stable protein 1 (Calcium-regulated heat-stable protein of 24 kDa) (CRHSP-24)	147	CARHSP1	2	0	2	35.4	0	35.4
90	-1.76	-0.05	1.04	P62899	60S ribosomal protein L31	125	RPL31	3	4	1	24.8	31.2	6.4
91	-1.75	0.00	2.30	Q5VWN6	Protein FAM208B	2430	FAM208B	1	0	1	0.4	0	0.4
92	-1.75	3.47	1.29	K7ESE8	Bleomycin hydrolase (Fragment)	231	BLMH	1	1	1	4.8	4.8	4.8
93	-1.74	1.12	1.35	Q9Y3E5	Peptidyl-tRNA hydrolase 2, mitochondrial (PTH 2) (EC 3.1.1.29) (Bcl-2 inhibitor of transcription 1)	179	PTRH2	3	5	2	31.8	44.7	21.2
94	-1.73	1.73	0.00	Q8N766	ER membrane protein complex subunit 1	993	EMC1	1	2	0	1.6	3.1	0
95	-1.72	2.20	1.71	P62314	Small nuclear ribonucleoprotein Sm D1 (Sm-D1) (Sm-D autoantigen) (snRNP core protein D1)	119	SNRPD1	2	2	2	26.1	26.1	26.1
96	-1.70	2.07	1.64	Q09666	Neuroblast differentiation-associated protein AHNAK (Desmoyokin)	5890	AHNAK	7	22	17	4.2	15.3	10.6

97	-1.68	0.75	1.12	P35268	60S ribosomal protein L22 (EBER-associated protein) (EAP) (Epstein-Barr virus small RNA-associated protein) (Heparin-binding protein HBp15)	128	RPL22	1	1	1	20.3	8.6	8.6
98	-1.68	0.13	1.48	E1CEI4	Glutamate--cysteine ligase catalytic subunit (Glutamate-cysteine ligase delta4 alternative splicing variant)	599	GCLC	1	1	2	1.5	1.5	4.5
99	-1.68	0.00	1.27	Q15233	Non-POU domain-containing octamer-binding protein (NonO protein) (54 kDa nuclear RNA- and DNA-binding protein) (55 kDa nuclear protein) (DNA-binding p52/p100 complex, 52 kDa subunit) (NMT55) (p54(nrb)) (p54nrb)	471	NONO	2	0	3	7.9	0	11.5
100	-1.68	6.59	0.69	P21399	Cytoplasmic aconitate hydratase (Aconitase) (EC 4.2.1.3) (Citrate hydro-lyase) (Ferritin repressor protein) (Iron regulatory protein 1) (IRP1) (Iron-responsive element-binding protein 1) (IRE-BP 1)	889	ACO1	2	1	2	4.3	0.9	3.7
101	-1.67	0.44	1.96	E9PLL6	60S ribosomal protein L27a	108	RPL27A	2	2	1	23.1	18.5	11.1
102	-1.67	0.00	2.52	Q6PI78	Transmembrane protein 65	240	TMEM65	1	0	1	4.6	0	4.6
103	-1.66	1.65	0.00	Q9Y2B0	Protein canopy homolog 2 (MIR-interacting saposin-like protein) (Putative secreted protein Zsig9) (Transmembrane protein 4)	182	CNPY2	1	4	0	8.8	31.3	0
104	-1.66	0.00	0.00	B1ANR0	Polyadenylate-binding protein (PABP)	615	PABPC4	4	2	4	8.5	4.4	8.8
105	-1.65	0.00	0.43	P08243	Asparagine synthetase [glutamine-hydrolyzing] (EC 6.3.5.4) (Cell cycle control protein TS11) (Glutamine-dependent asparagine synthetase)	561	ASNS	2	0	1	4.6	0	2
106	-1.64	-0.54	0.75	A0A087WSW9	Thioredoxin reductase 1, cytoplasmic	548	TXNRD1	9	1	10	23.2	1.8	19.3

107	-1.64	0.17	1.57	P61353	60S ribosomal protein L27	136	RPL27	1	1	2	6.6	6.6	22.1
108	-1.63	0.00	0.83	E9PNF3	L-aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase (Fragment)	160	AASDHPPT	2	0	1	17.5	0	10.6
109	-1.61	0.00	0.32	D6RD69	GTP-binding protein SAR1b (Fragment)	170	SAR1B	3	2	4	27.6	11.2	34.1
110	-1.61	1.06	2.06	Q99880	Histone H2B type 1-L (Histone H2B.c) (H2B/c)	126	HIST1H2BL	2	4	3	15.1	23.8	27
111	-1.61	0.92	2.62	Q5T7C4	High mobility group protein B1	158	HMGB1	5	5	2	32.9	34.8	14.6
112	-1.58	0.76	0.00	E9PGT1	Translin	223	TSN	1	1	0	7.2	7.2	0
113	-1.58	0.77	1.63	Q08257	Quinone oxidoreductase (EC 1.6.5.5) (NADPH:quinone reductase) (Zeta-crystallin)	329	CRYZ	4	5	3	21.7	24.1	17.3
114	-1.57	1.09	1.12	P68032	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin)	377	ACTC1	7	10	7	22.3	30.5	22.3
115	-1.55	1.94	0.00	Q9BYN0	Sulfiredoxin-1 (EC 1.8.98.2)	137	SRXN1	1	2	0	10.2	14.6	0
116	-1.54	0.13	1.69	M0R3D6	60S ribosomal protein L18a (Fragment)	141	RPL18A	2	4	1	13.5	29.1	7.1
117	-1.54	0.56	0.70	P11586	C-1-tetrahydrofolate synthase, cytoplasmic (C1-THF synthase) [Cleaved into: C-1-tetrahydrofolate synthase, cytoplasmic, N-terminally processed] [Includes: Methylenetetrahydrofolate dehydrogenase (EC 1.5.1.5); Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9); Formyltetrahydrofolate synthetase (EC 6.3.4.3)]	935	MTHFD1	5	4	6	7.4	6.8	10.9
118	-1.54	0.00	1.57	J3QSB5	60S ribosomal protein L36	94	RPL36	1	1	1	9.6	9.6	9.6
119	-1.53	0.00	0.00	Q9NUQ9	Protein FAM49B (L1)	324	FAM49B	1	0	0	10.7	0	0
120	-1.53	0.00	1.85	F5H6T1	ARP2 actin-related protein 2 homolog (Yeast), isoform CRA_d (Actin-related protein 2)	339	ACTR2	2	0	2	8	0	9.4
121	-1.53	0.00	2.15	P62277	40S ribosomal protein S13	151	RPS13	4	1	3	27.8	7.3	25.2

122	-1.53	0.00	0.00	F8WBT4	Ribulose-phosphate 3-epimerase	60	RPE	1	0	0	31.7	0	0
123	-1.52	2.22	1.06	Q9UJZ1	Stomatin-like protein 2, mitochondrial (SLP-2) (EPB72-like protein 2) (Paraprotein target 7) (Paratarg-7)	356	STOML2	2	3	6	10.3	15.4	39.5
124	-1.51	0.00	0.00	B0QZK9	Heterochromatin protein 1-binding protein 3 (Fragment)	75	HP1BP3	1	0	0	20	0	0
125	-1.50	0.48	0.30	Q9NTK5	Obg-like ATPase 1 (DNA damage-regulated overexpressed in cancer 45) (DOC45) (GTP-binding protein 9)	396	OLA1	4	1	5	12.9	3.8	14.6
126	-1.50	0.38	2.18	P62854	40S ribosomal protein S26	115	RPS26	1	1	1	13	13	13
127	-1.49	0.51	1.87	P62081	40S ribosomal protein S7	194	RPS7	6	6	7	34.5	30.4	45.9
128	-1.49	0.46	0.09	Q15691	Microtubule-associated protein RP/EB family member 1 (APC-binding protein EB1) (End-binding protein 1) (EB1)	268	MAPRE1	3	7	2	15.7	27.2	11.2
129	-1.49	0.00	1.15	H0YL99	28S ribosomal protein S11, mitochondrial	118	MRPS11	2	0	1	22	0	9.3
130	-1.48	0.95	1.09	P23396	40S ribosomal protein S3 (EC 4.2.99.18)	243	RPS3	9	10	8	45.3	47.7	30
131	-1.47	0.00	0.00	Q9UIM3	FK506-binding protein-like (WAF-1/CIP1 stabilizing protein 39) (WISp39)	349	FKBPL	1	0	0	2.3	0	0
132	-1.47	0.00	0.00	O00764	Pyridoxal kinase (EC 2.7.1.35) (Pyridoxine kinase)	312	PDXK	1	0	0	8.8	0	0
133	-1.47	1.71	2.32	Q9H061	Transmembrane protein 126A	195	TMEM126A	1	1	1	10.3	4.6	10.3
134	-1.47	0.76	0.90	P62263	40S ribosomal protein S14	151	RPS14	5	2	2	30.5	13.9	7.9
135	-1.47	0.92	0.67	O96008	Mitochondrial import receptor subunit TOM40 homolog (Protein Haymaker) (Translocase of outer membrane 40 kDa subunit homolog) (p38.5)	361	TOMM40	3	3	2	11.9	7.2	4.7
136	-1.46	0.00	0.00	P58557	Putative ribonuclease	167	YBEY	1	0	0	9.6	0	0

137	-1.46	0.00	1.19	P09972	Fructose-bisphosphate aldolase C (EC 4.1.2.13) (Brain-type aldolase)	364	ALDOC	1	1	1	6.3	1.9	6.3
138	-1.46	1.23	0.00	E5RJI7	39S ribosomal protein L13, mitochondrial (Fragment)	147	MRPL13	1	1	0	10.2	10.2	0
139	-1.45	1.08	1.73	Q9Y295	Developmentally-regulated GTP-binding protein 1 (DRG-1) (Neural precursor cell expressed developmentally down-regulated protein 3) (NEDD-3)	367	DRG1	1	2	2	3	6.8	6.8
140	-1.45	0.71	0.40	Q9HC38	Glyoxalase domain-containing protein 4	313	GLOD4	4	2	4	13.8	8.1	13.1
141	-1.45	-0.09	0.39	Q9UKK9	ADP-sugar pyrophosphatase (EC 3.6.1.13) (8-oxo-dGDP phosphatase) (EC 3.6.1.58) (Nucleoside diphosphate-linked moiety X motif 5) (Nudix motif 5) (YSA1H)	219	NUDT5	4	3	5	26.5	16.4	26
142	-1.44	0.67	1.06	H0Y2V1	Microtubule-associated protein (Fragment)	463	MAP4	1	1	1	3.7	3.7	3.7
143	-1.44	1.58	0.84	P04844	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 (EC 2.4.99.18) (Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit) (RIBIIR) (Ribophorin II) (RPN-II) (Ribophorin-2)	631	RPN2	3	6	4	8.3	19	13.2
144	-1.44	0.92	1.68	M0R3H0	40S ribosomal protein S16	100	RPS16	2	3	2	18	29	18
145	-1.44	1.01	1.76	K7ENG2	Splicing factor U2AF 65 kDa subunit	307	U2AF2	3	1	2	8.5	5.2	9.1

146	-1.43	0.79	1.11	P23141	Liver carboxylesterase 1 (Acyl-coenzyme A:cholesterol acyltransferase) (ACAT) (Brain carboxylesterase hBr1) (Carboxylesterase 1) (CE-1) (hCE-1) (EC 3.1.1.1) (Cocaine carboxylesterase) (Egasyn) (HMSE) (Methylumbelliferyl-acetate deacetylase 1) (EC 3.1.1.56) (Monocyte/macrophage serine esterase) (Retinyl ester hydrolase) (REH) (Serine esterase 1) (Triacylglycerol hydrolase) (TGH)	567	CES1	5	5	3	13.6	13.8	7.8
147	-1.43	0.00	0.00	Q9NR09	Baculoviral IAP repeat-containing protein 6 (EC 6.3.2.-) (BIR repeat-containing ubiquitin-conjugating enzyme) (BRUCE) (Ubiquitin-conjugating BIR domain enzyme apollon) (APOLLON)	4857	BIRC6	1	0	0	0.2	0	0
148	-1.43	0.00	0.92	P29144	Tripeptidyl-peptidase 2 (TPP-2) (EC 3.4.14.10) (Tripeptidyl aminopeptidase) (Tripeptidyl-peptidase II) (TPP-II)	1249	TPP2	2	0	1	2.2	0	0.8
149	-1.43	0.63	0.59	Q99832	T-complex protein 1 subunit eta (TCP-1-eta) (CCT-eta) (HIV-1 Nef-interacting protein)	543	CCT7	10	4	10	20.1	10.9	22.5
150	-1.43	0.00	1.03	H0YKU1	Tropomodulin-3 (Fragment)	187	TMOD3	1	0	1	7.5	0	7.5
151	-1.42	1.13	1.83	P30050	60S ribosomal protein L12	165	RPL12	3	4	3	24.2	35.8	26.1
152	-1.42	0.00	0.00	F8VUA7	Oxysterol-binding protein (Fragment)	694	OSBPL8	1	0	0	1.6	0	0
153	-1.42	-0.60	0.59	P00491	Purine nucleoside phosphorylase (PNP) (EC 2.4.2.1) (Inosine phosphorylase) (Inosine-guanosine phosphorylase)	289	PNP	2	2	6	8.7	7.3	29.8
154	-1.42	1.07	1.05	Q9Y5M8	Signal recognition particle receptor subunit beta (SR-beta) (Protein APMCF1)	271	SRPRB	1	3	1	7	17	5.9

155	-1.41	0.05	0.39	Q14566	DNA replication licensing factor MCM6 (EC 3.6.4.12) (p105MCM)	821	MCM6	5	1	3	10.6	2.1	4.9
156	-1.41	0.89	0.99	J3QRD1	Fatty aldehyde dehydrogenase	393	ALDH3A2	7	4	6	23.7	13.2	20.4
157	-1.40	0.48	1.23	Q02878	60S ribosomal protein L6 (Neoplasm-related protein C140) (Tax-responsive enhancer element-binding protein 107) (TaxREB107)	288	RPL6	4	2	4	16.3	8.7	14.2
158	-1.40	1.01	1.45	P41250	Glycine--tRNA ligase (EC 6.1.1.14) (Diadenosine tetraphosphate synthetase) (AP-4-A synthetase) (Glycyl-tRNA synthetase) (GlyRS)	739	GARS	5	1	5	9.3	1.5	11
159	-1.39	0.65	1.52	H0YEN5	40S ribosomal protein S2 (Fragment)	195	RPS2	4	5	5	24.1	28.2	26.7
160	-1.39	0.61	1.25	Q5JP53	Tubulin beta chain	426	TUBB	6	10	9	20.9	34.3	27.2
161	-1.39	0.63	0.61	P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform (Medium tumor antigen-associated 61 kDa protein) (PP2A subunit A isoform PR65-alpha) (PP2A subunit A isoform R1-alpha)	589	PPP2R1A	4	2	2	9.7	5.3	5.1
162	-1.39	1.20	0.90	B4DJV2	Citrate synthase	453	CS	5	2	5	9.7	4.4	9.5
163	-1.38	-0.02	0.78	P11413	Glucose-6-phosphate 1-dehydrogenase (G6PD) (EC 1.1.1.49)	515	G6PD	11	6	12	27	12.4	34.6
164	-1.38	1.21	2.04	Q9HDC9	Adipocyte plasma membrane-associated protein (Protein BSCv)	416	APMAP	3	4	2	14.2	19.7	11.4
165	-1.38	-0.24	0.90	P46781	40S ribosomal protein S9	194	RPS9	3	3	3	15.5	11.9	11.9
166	-1.38	0.00	0.00	H7C286	N-acetyl-D-glucosamine kinase	196	NAGK	1	0	0	8.7	0	0

167	-1.37	0.54	1.78	Q9NZI8	Insulin-like growth factor 2 mRNA-binding protein 1 (IGF2 mRNA-binding protein 1) (IMP-1) (IMP1) (Coding region determinant-binding protein) (CRD-BP) (IGF-II mRNA-binding protein 1) (VICKZ family member 1) (Zipcode-binding protein 1) (ZBP-1)	577	IGF2BP1	1	1	1	2.4	2.4	2.4
168	-1.37	0.74	1.39	P62913	60S ribosomal protein L11 (CLL-associated antigen KW-12)	178	RPL11	4	3	4	18.1	16.9	18.1
169	-1.36	1.53	2.42	P68036	Ubiquitin-conjugating enzyme E2 L3 (EC 6.3.2.19) (L-UBC) (UbcH7) (Ubiquitin carrier protein L3) (Ubiquitin-conjugating enzyme E2-F1) (Ubiquitin-protein ligase L3)	154	UBE2L3	1	2	2	7.4	19.7	19.7
170	-1.36	1.38	1.53	Q99714	3-hydroxyacyl-CoA dehydrogenase type-2 (EC 1.1.1.35) (17-beta-hydroxysteroid dehydrogenase 10) (17-beta-HSD 10) (EC 1.1.1.51) (3-hydroxy-2-methylbutyryl-CoA dehydrogenase) (EC 1.1.1.178) (3-hydroxyacyl-CoA dehydrogenase type II) (Endoplasmic reticulum-associated amyloid beta-peptide-binding protein) (Mitochondrial ribonuclease P protein 2) (Mitochondrial RNase P protein 2) (Short chain dehydrogenase/reductase family 5C member 1) (Short-chain type dehydrogenase/reductase XH98G2) (Type II HADH)	261	HSD17B10	5	7	9	33.7	51.3	51.7
171	-1.36	2.04	1.27	F8WAU4	Elongation factor G, mitochondrial	453	GFM1	1	1	1	2.4	2.4	2.4
172	-1.36	0.00	0.00	Q6PIU2	Neutral cholesterol ester hydrolase 1 (NCEH) (EC 3.1.1.-) (Arylacetamide deacetylase-like 1)	408	NCEH1	1	0	0	5.8	0	0

173	-1.35	-0.56	0.00	Q9H8S9	MOB kinase activator 1A (Mob1 alpha) (Mob1A) (Mob1 homolog 1B) (Mps one binder kinase activator-like 1B)	216	MOB1A	1	1	1	5.1	5.6	5.1
174	-1.35	1.74	1.34	Q15084	Protein disulfide-isomerase A6 (EC 5.3.4.1) (Endoplasmic reticulum protein 5) (ER protein 5) (ERp5) (Protein disulfide isomerase P5) (Thioredoxin domain-containing protein 7)	440	PDIA6	6	6	7	21.5	20.4	25.4
175	-1.35	1.20	0.46	Q53GQ0	Very-long-chain 3-oxoacyl-CoA reductase (EC 1.1.1.330) (17-beta-hydroxysteroid dehydrogenase 12) (17-beta-HSD 12) (3-ketoacyl-CoA reductase) (KAR) (Estradiol 17-beta-dehydrogenase 12) (EC 1.1.1.62) (Short chain dehydrogenase/reductase family 12C member 1)	312	HSD17B12	2	5	2	9.3	17	9.6
176	-1.34	0.42	1.69	H0YA96	Heterogeneous nuclear ribonucleoprotein D0 (Fragment)	210	HNRNPD	3	3	3	15.2	12.4	15.2
177	-1.33	0.00	-0.08	G3V158	2-deoxyribose-5-phosphate aldolase homolog (C. elegans), isoform CRA_a (Deoxyribose-phosphate aldolase)	230	DERA	1	0	1	6.5	0	5.2
178	-1.33	0.23	0.83	P62750	60S ribosomal protein L23a	156	RPL23A	4	4	4	20.5	19.2	18.6
179	-1.33	0.63	1.11	Q58FF8	Putative heat shock protein HSP 90-beta 2 (Heat shock protein 90-beta b) (Heat shock protein 90Bb)	381	HSP90AB2P	8	4	8	19.7	11.3	19.7
180	-1.32	0.07	0.61	P62937	Peptidyl-prolyl cis-trans isomerase A (PPIase A) (EC 5.2.1.8) (Cyclophilin A) (Cyclosporin A-binding protein) (Rotamase A) [Cleaved into: Peptidyl-prolyl cis-trans isomerase A, N-terminally processed]	165	PPIA	9	9	7	43	38.8	33.9

181	-1.32	0.31	1.12	P54136	Arginine--tRNA ligase, cytoplasmic (EC 6.1.1.19) (Arginyl-tRNA synthetase) (ArgRS)	660	RARS	5	4	4	10.4	8	8.2
182	-1.32	-0.05	0.76	Q07020	60S ribosomal protein L18	188	RPL18	2	2	1	13.2	15.1	6.9
183	-1.32	2.41	0.00	K9J7I2	Uncharacterized protein	107		1	2	0	17.8	19.6	0
184	-1.32	1.21	0.00	C9J6B1	Ras-related protein Ral-B (Fragment)	167	RALB	1	1	0	9.6	9.6	0
185	-1.32	1.59	1.74	O75947	ATP synthase subunit d, mitochondrial (ATPase subunit d)	161	ATP5H	2	7	4	19.3	41	32.3
186	-1.31	0.00	0.00	P55957	BH3-interacting domain death agonist (p22 BID) (BID) [Cleaved into: BH3-interacting domain death agonist p15 (p15 BID); BH3-interacting domain death agonist p13 (p13 BID); BH3-interacting domain death agonist p11 (p11 BID)]	195	BID	1	1	0	15.2	15.2	0
187	-1.31	1.42	1.30	Q15029	116 kDa U5 small nuclear ribonucleoprotein component (Elongation factor Tu GTP-binding domain-containing protein 2) (SNU114 homolog) (hSNU114) (U5 snRNP-specific protein, 116 kDa) (U5-116 kDa)	972	EFTUD2	3	3	5	4.3	3.9	7.3
188	-1.30	-0.30	0.81	P00390	Glutathione reductase, mitochondrial (GR) (GRase) (EC 1.8.1.7)	522	GSR	6	1	8	20.7	2.3	21.9
189	-1.30	1.52	1.90	Q9NR30	Nucleolar RNA helicase 2 (EC 3.6.4.13) (DEAD box protein 21) (Gu-alpha) (Nucleolar RNA helicase Gu) (Nucleolar RNA helicase II) (RH II/Gu)	783	DDX21	3	1	4	4.6	1.5	6.2
190	-1.30	0.03	-0.97	P47897	Glutamine--tRNA ligase (EC 6.1.1.18) (Glutaminyl-tRNA synthetase) (GlnRS)	775	QARS	5	1	1	7.7	2.1	2.1
191	-1.30	0.65	0.52	P49368	T-complex protein 1 subunit gamma (TCP-1-gamma) (CCT-gamma) (hTRiC5)	545	CCT3	9	3	5	17.6	6.2	8.4

192	-1.30	2.06	1.36	P23246	Splicing factor, proline- and glutamine-rich (100 kDa DNA-pairing protein) (hPOMp100) (DNA-binding p52/p100 complex, 100 kDa subunit) (Polypyrimidine tract-binding protein-associated-splicing factor) (PSF) (PTB-associated-splicing factor)	707	SFPQ	1	4	2	2.4	9.6	5.1
193	-1.29	0.84	1.29	Q9HB71	Calcyclin-binding protein (CacyBP) (hCacyBP) (S100A6-binding protein) (Siah-interacting protein)	228	CACYBP	6	3	6	40.4	17.1	36
194	-1.29	-0.36	-0.11	Q7Z6Z7	E3 ubiquitin-protein ligase HUWE1 (EC 6.3.2.-) (ARF-binding protein 1) (ARF-BP1) (HECT, UBA and WWE domain-containing protein 1) (Homologous to E6AP carboxyl terminus homologous protein 9) (HectH9) (Large structure of UREB1) (LASU1) (Mcl-1 ubiquitin ligase E3) (Mule) (Upstream regulatory element-binding protein 1) (URE-B1) (URE-binding protein 1)	4374	HUWE1	2	1	1	0.8	0.3	0.3
195	-1.29	-0.29	0.94	Q99497	Protein deglycase DJ-1 (DJ-1) (EC 3.1.2.-) (EC 3.5.1.-) (Oncogene DJ1) (Parkinson disease protein 7)	189	PARK7	10	6	9	68.8	36	50.8
196	-1.29	1.34	0.87	M0R3D4	Prenylated Rab acceptor protein 1 (Rab acceptor 1 (Prenylated), isoform CRA_a)	151	RABAC1	1	1	1	9.9	9.9	9.9
197	-1.29	0.00	2.91	P35637	RNA-binding protein FUS (75 kDa DNA-pairing protein) (Oncogene FUS) (Oncogene TLS) (POMp75) (Translocated in liposarcoma protein)	526	FUS	2	0	1	5.3	0	3

198	-1.29	0.00	0.62	P20042	Eukaryotic translation initiation factor 2 subunit 2 (Eukaryotic translation initiation factor 2 subunit beta) (eIF-2-beta)	333	EIF2S2	1	0	1	4.5	0	4.5
199	-1.29	0.24	0.77	P41567	Eukaryotic translation initiation factor 1 (eIF1) (A121) (Protein translation factor SUI1 homolog) (Sui1iso1)	113	EIF1	1	4	1	15	53.1	14.2
200	-1.29	0.90	0.79	Q9UQ80	Proliferation-associated protein 2G4 (Cell cycle protein p38-2G4 homolog) (hG4-1) (ErbB3-binding protein 1)	394	PA2G4	4	6	5	11.9	21.6	16.2
201	-1.29	0.03	0.91	Q04828	Aldo-keto reductase family 1 member C1 (EC 1.1.1.-) (20-alpha-hydroxysteroid dehydrogenase) (20-alpha-HSD) (EC 1.1.1.149) (Chlordecone reductase homolog HAKRC) (Dihydrodiol dehydrogenase 1/2) (DD1/DD2) (High-affinity hepatic bile acid-binding protein) (HBAB) (Indanol dehydrogenase) (EC 1.1.1.112) (Trans-1,2-dihydrobenzene-1,2-diol dehydrogenase) (EC 1.3.1.20)	323	AKR1C1	8	9	10	39.6	43.3	49.2
202	-1.29	0.00	0.00	A2A2U4	Ribosyldihydronicotinamide dehydrogenase [quinone] (Fragment)	63	NQO2	1	0	0	17.5	0	0
203	-1.28	1.13	0.00	Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein (PAI1 RNA-binding protein 1) (PAI-RBP1) (SERPINE1 mRNA-binding protein 1)	408	SERBP1	1	1	0	4.1	2.3	0
204	-1.27	0.41	0.91	P56537	Eukaryotic translation initiation factor 6 (eIF-6) (B(2)GCN homolog) (B4 integrin interactor) (CAB) (p27(BBP))	245	EIF6	4	5	5	31.4	33.5	30.6

205	-1.27	-0.12	0.97	Q9ULC4	Malignant T-cell-amplified sequence 1 (MCT-1) (Multiple copies T-cell malignancies)	181	MCTS1	2	2	1	19.9	14.9	9.4
206	-1.25	0.00	0.00	A8MXH2	Nucleosome assembly protein 1-like 4 (Fragment)	156	NAP1L4	1	0	0	11.5	0	0
207	-1.23	0.00	1.78	E9PR16	Nuclear pore complex protein Nup160 (Fragment)	1123	NUP160	1	0	1	1.1	0	1.1
208	-1.23	0.44	1.58	P41252	Isoleucine--tRNA ligase, cytoplasmic (EC 6.1.1.5) (Isoleucyl-tRNA synthetase) (IRS) (IleRS)	1262	IARS	1	5	1	1	4.8	1
209	-1.22	0.47	1.05	Q96Q11	CCA tRNA nucleotidyltransferase 1, mitochondrial (EC 2.7.7.72) (Mitochondrial tRNA nucleotidyl transferase, CCA-adding) (mt CCA-adding enzyme) (mt tRNA CCA-diphosphorylase) (mt tRNA CCA-pyrophosphorylase) (mt tRNA adenylyltransferase)	434	TRNT1	1	1	1	2.4	2.4	2.4
210	-1.21	1.21	1.47	P60866	40S ribosomal protein S20	119	RPS20	2	2	1	22.7	19.3	12.6
211	-1.21	-0.03	0.04	Q9NQR4	Omega-amidase NIT2 (EC 3.5.1.3) (Nitrilase homolog 2)	276	NIT2	4	4	2	19.9	23.9	10.1
212	-1.21	0.17	0.00	Q13283	Ras GTPase-activating protein-binding protein 1 (G3BP-1) (EC 3.6.4.12) (EC 3.6.4.13) (ATP-dependent DNA helicase VIII) (hDH VIII) (GAP SH3 domain-binding protein 1)	466	G3BP1	2	1	0	7.1	3.6	0
213	-1.21	-0.17	0.00	Q14691	DNA replication complex GINS protein PSF1 (GINS complex subunit 1)	196	GINS1	1	1	0	7.7	7.1	0

214	-1.21	1.45	2.14	P07858	Cathepsin B (EC 3.4.22.1) (APP secretase) (APPS) (Cathepsin B1) [Cleaved into: Cathepsin B light chain; Cathepsin B heavy chain]	339	CTSB	2	5	2	10.3	20.6	8.3
215	-1.21	0.60	1.13	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4 (PPIase FKBP4) (EC 5.2.1.8) (51 kDa FK506-binding protein) (FKBP51) (52 kDa FK506-binding protein) (52 kDa FKBP) (FKBP-52) (59 kDa immunophilin) (p59) (FK506-binding protein 4) (FKBP-4) (FKBP59) (HSP-binding immunophilin) (HBI) (Immunophilin FKBP52) (Rotamase) [Cleaved into: Peptidyl-prolyl cis-trans isomerase FKBP4, N-terminally processed]	459	FKBP4	2	2	6	6.1	5.7	20
216	-1.20	0.20	0.78	P09211	Glutathione S-transferase P (EC 2.5.1.18) (GST class-pi) (GSTP1-1)	210	GSTP1	1	4	1	4.8	26.7	4.8
217	-1.20	0.13	0.00	A6NDF3	Protein PBDC1	232	PBDC1	1	2	0	6.5	11.2	0
218	-1.19	1.12	0.00	P00387	NADH-cytochrome b5 reductase 3 (B5R) (Cytochrome b5 reductase) (EC 1.6.2.2) (Diaphorase-1) [Cleaved into: NADH-cytochrome b5 reductase 3 membrane-bound form; NADH-cytochrome b5 reductase 3 soluble form]	301	CYB5R3	2	2	0	8.6	8.3	0
219	-1.19	0.43	0.93	P09960	Leukotriene A-4 hydrolase (LTA-4 hydrolase) (EC 3.3.2.6) (Leukotriene A(4) hydrolase)	611	LTA4H	5	1	3	9.7	1.9	5.6
220	-1.18	0.98	1.18	H0YHC3	Nucleosome assembly protein 1-like 1 (Fragment)	198	NAP1L1	3	2	4	20.7	14.1	29.3
221	-1.18	0.20	1.24	D3YTB1	60S ribosomal protein L32 (Fragment)	133	RPL32	6	2	5	30.1	20.3	36.8
222	-1.18	0.96	1.37	P62318	Small nuclear ribonucleoprotein Sm D3 (Sm-D3) (snRNP core protein D3)	126	SNRPD3	2	2	2	13.3	13.3	13.3

223	-1.17	1.15	0.98	P08195	4F2 cell-surface antigen heavy chain (4F2hc) (4F2 heavy chain antigen) (Lymphocyte activation antigen 4F2 large subunit) (Solute carrier family 3 member 2) (CD antigen CD98)	630	SLC3A2	13	14	12	32.4	31.2	27.1
224	-1.17	1.11	1.09	P13010	X-ray repair cross-complementing protein 5 (EC 3.6.4.-) (86 kDa subunit of Ku antigen) (ATP-dependent DNA helicase 2 subunit 2) (ATP-dependent DNA helicase II 80 kDa subunit) (CTC box-binding factor 85 kDa subunit) (CTC85) (CTCBF) (DNA repair protein XRCC5) (Ku80) (Ku86) (Lupus Ku autoantigen protein p86) (Nuclear factor IV) (Thyroid-lupus autoantigen) (TLAA) (X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining))	732	XRCC5	8	7	9	14.6	12.2	13.5
225	-1.17	1.14	2.25	Q15758	Neutral amino acid transporter B(0) (ATB(0)) (Baboon M7 virus receptor) (RD114/simian type D retrovirus receptor) (Sodium-dependent neutral amino acid transporter type 2) (Solute carrier family 1 member 5)	541	SLC1A5	2	1	3	4.3	2.4	7.9
226	-1.16	1.34	1.32	P63261	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	375	ACTG1	13	18	12	51.2	67.2	47.5
227	-1.16	1.75	1.74	P36578	60S ribosomal protein L4 (60S ribosomal protein L1)	427	RPL4	6	1	7	16.6	3.7	21.1
228	-1.15	0.00	0.00	Q2TAA2	Isoamyl acetate-hydrolyzing esterase 1 homolog (EC 3.1.-.-)	248	IAH1	1	0	0	12.6	0	0

229	-1.15	-0.13	0.28	P06744	Glucose-6-phosphate isomerase (GPI) (EC 5.3.1.9) (Autocrine motility factor) (AMF) (Neuroleukin) (NLK) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) (Sperm antigen 36) (SA-36)	558	GPI	7	5	4	15.9	11.5	8.4
230	-1.15	0.00	0.00	Q13618	Cullin-3 (CUL-3)	768	CUL3	1	0	1	1.3	0	1.5
231	-1.15	0.00	0.00	C9J255	Mannose-1-phosphate guanyltransferase alpha (Fragment)	179	GMPPA	1	0	0	5.6	0	0
232	-1.15	0.00	0.96	C9IZG3	Ubiquitin fusion degradation protein 1 homolog (Fragment)	190	UFD1L	2	0	1	12.1	0	5.3
233	-1.15	0.09	0.41	Q14847	LIM and SH3 domain protein 1 (LASP-1) (Metastatic lymph node gene 50 protein) (MLN 50)	261	LASP1	1	5	1	5	19.9	3.4
234	-1.14	-0.16	-0.30	A2A2D0	Stathmin (Fragment)	85	STMN1	3	3	1	42.4	35.3	10.6
235	-1.14	0.58	1.04	P05388	60S acidic ribosomal protein P0 (60S ribosomal protein L10E)	317	RPLP0	10	8	11	45.4	32.8	47.3
236	-1.14	-0.29	1.15	Q5W0S5	UV excision repair protein RAD23 homolog B (Fragment)	146	RAD23B	1	2	1	7.5	13	7.5
237	-1.14	1.75	0.00	Q01650	Large neutral amino acids transporter small subunit 1 (4F2 light chain) (4F2 LC) (4F2LC) (CD98 light chain) (Integral membrane protein E16) (L-type amino acid transporter 1) (hLAT1) (Solute carrier family 7 member 5) (y+ system cationic amino acid transporter)	507	SLC7A5	1	3	1	3.6	7.1	1.8
238	-1.14	0.00	0.98	A6NJA2	Ubiquitin carboxyl-terminal hydrolase (EC 3.4.19.12)	448	USP14	2	0	1	5.4	0	2.5
239	-1.14	0.00	1.06	C9JVE2	DCN1-like protein (Defective in cullin neddylation protein 1-like protein)	244	DCUN1D1	2	0	1	12.3	0	5.3

240	-1.14	0.00	0.00	P23381	Tryptophan--tRNA ligase, cytoplasmic (EC 6.1.1.2) (Interferon-induced protein 53) (IFP53) (Tryptophanyl-tRNA synthetase) (TrpRS) (hWRS) [Cleaved into: T1-TrpRS; T2-TrpRS]	471	WARS	2	0	0	8.3	0	0
241	-1.13	0.00	0.81	A0A087 WW66	26S proteasome non-ATPase regulatory subunit 1	953	PSMD1	5	0	5	8	0	7
242	-1.13	0.94	1.65	P19338	Nucleolin (Protein C23)	710	NCL	12	10	10	18.5	17.2	16.8
243	-1.13	0.76	1.35	Q15365	Poly(rC)-binding protein 1 (Alpha-CP1) (Heterogeneous nuclear ribonucleoprotein E1) (hnRNP E1) (Nucleic acid-binding protein SUB2.3)	356	PCBP1	1	3	2	7	10.7	9.3
244	-1.12	1.72	1.74	Q3ZCQ8	Mitochondrial import inner membrane translocase subunit TIM50	353	TIMM50	3	3	3	12.2	12.2	12.2
245	-1.12	0.53	0.94	P31939	Bifunctional purine biosynthesis protein PURH [Includes: Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3) (5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase) (AICAR transformylase); IMP cyclohydrolase (EC 3.5.4.10) (ATIC) (IMP synthase) (Inosinicase)]	592	ATIC	13	4	10	27	10.5	21.3
246	-1.12	2.27	1.57	A0A0A0 MTN9	NADPH:adrenodoxin oxidoreductase, mitochondrial (EC 1.18.1.6)	439	FDXR	1	2	5	3.2	5.7	16.9
247	-1.12	0.00	0.00	D6R918	OCIA domain-containing protein 1 (Fragment)	73	OCIAD1	1	0	0	24.7	0	0
248	-1.12	1.01	1.07	P17812	CTP synthase 1 (EC 6.3.4.2) (CTP synthetase 1) (UTP--ammonia ligase 1)	591	CTPS1	2	1	2	3.4	2.7	5.1
249	-1.12	1.42	1.13	J3QS48	Mannose-P-dolichol utilization defect 1 protein	101	MPDU1	2	2	2	23.8	23.8	23.8

250	-1.11	0.99	1.05	Q9H3N1	Thioredoxin-related transmembrane protein 1 (Thioredoxin domain-containing protein 1) (Transmembrane Trx-related protein)	280	TMX1	2	6	3	8.2	20.7	11.4
251	-1.11	-0.06	0.79	P46778	60S ribosomal protein L21	160	RPL21	2	2	1	16.2	13.8	9.4
252	-1.11	-0.25	0.24	O60493	Sorting nexin-3 (Protein SDP3)	162	SNX3	3	3	2	16	10.5	10.5
253	-1.10	0.00	0.00	P61966	AP-1 complex subunit sigma-1A (Adaptor protein complex AP-1 subunit sigma-1A) (Adaptor-related protein complex 1 subunit sigma-1A) (Clathrin assembly protein complex 1 sigma-1A small chain) (Clathrin coat assembly protein AP19) (Golgi adaptor HA1/AP1 adaptin sigma-1A subunit) (HA1 19 kDa subunit) (Sigma 1a subunit of AP-1 clathrin) (Sigma-adaptin 1A) (Sigma1A-adaptin)	158	AP1S1	1	0	0	10.1	0	0
254	-1.10	1.64	0.99	Q9NYL4	Peptidyl-prolyl cis-trans isomerase FKBP11 (PPIase FKBP11) (EC 5.2.1.8) (19 kDa FK506-binding protein) (19 kDa FKBP) (FKBP-19) (FK506-binding protein 11) (FKBP-11) (Rotamase)	201	FKBP11	1	2	1	7.5	14.4	6.8
255	-1.10	-0.20	0.14	H0YJG7	Activator of 90 kDa heat shock protein ATPase homolog 1 (Fragment)	216	AHSA1	2	1	1	15.3	5.1	5.1
256	-1.10	0.73	1.41	H0Y8E6	DNA replication licensing factor MCM2 (Fragment)	836	MCM2	4	3	1	6.1	4.4	1.4
257	-1.09	0.58	1.21	P55145	Mesencephalic astrocyte-derived neurotrophic factor (Arginine-rich protein) (Protein ARMET)	182	MANF	2	4	3	18.7	19.8	24.7

258	-1.09	0.46	0.79	Q14204	Cytoplasmic dynein 1 heavy chain 1 (Cytoplasmic dynein heavy chain 1) (Dynein heavy chain, cytosolic)	4646	DYNC1H1	6	30	29	2.3	8.3	8.1
259	-1.09	1.66	1.18	P05023	Sodium/potassium-transporting ATPase subunit alpha-1 (Na(+)/K(+) ATPase alpha-1 subunit) (EC 3.6.3.9) (Sodium pump subunit alpha-1)	1023	ATP1A1	4	4	6	6	5.2	7.4
260	-1.09	0.00	0.70	P04075	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Lung cancer antigen NY-LU-1) (Muscle-type aldolase)	364	ALDOA	7	9	7	28.8	30.5	31.3
261	-1.08	0.00	0.00	P55263	Adenosine kinase (AK) (EC 2.7.1.20) (Adenosine 5'-phosphotransferase)	362	ADK	1	0	0	4.9	0	0
262	-1.08	0.00	1.09	I3L4U9	Nuclear protein localization protein 4 homolog	135	NPLOC4	1	0	1	13.3	0	13.3
263	-1.08	0.00	3.58	Q96AE4	Far upstream element-binding protein 1 (FBP) (FUSE-binding protein 1) (DNA helicase V) (hDH V)	644	FUBP1	1	0	1	1.9	0	4
264	-1.08	1.74	1.78	H0YLR3	U2 small nuclear ribonucleoprotein A' (Fragment)	89	SNRPA1	1	1	1	12.4	13.5	13.5
265	-1.08	0.75	0.71	Q9Y277	Voltage-dependent anion-selective channel protein 3 (VDAC-3) (hVDAC3) (Outer mitochondrial membrane protein porin 3)	283	VDAC3	3	4	3	8.8	16.3	17
266	-1.07	1.27	0.00	H0YLA2	Signal recognition particle 14 kDa protein	115	SRP14	1	1	0	11.3	11.3	0
267	-1.07	0.39	0.76	P07900	Heat shock protein HSP 90-alpha (Heat shock 86 kDa) (HSP 86) (HSP86) (Lipopolysaccharide-associated protein 2) (LAP-2) (LPS-associated protein 2) (Renal carcinoma antigen NY-REN-38)	732	HSP90AA1	29	14	25	37.3	24.2	32.1

268	-1.06	0.51	0.92	P48507	Glutamate--cysteine ligase regulatory subunit (GCS light chain) (Gamma-ECS regulatory subunit) (Gamma-glutamylcysteine synthetase regulatory subunit) (Glutamate--cysteine ligase modifier subunit)	274	GCLM	3	2	1	15.3	10.6	5.8
269	-1.06	0.79	-0.13	O15498	Synaptobrevin homolog YKT6 (EC 2.3.1.-)	198	YKT6	1	2	1	10.4	18.3	5.5
270	-1.06	0.79	0.84	Q8NFH3	Nucleoporin Nup43 (Nup107-160 subcomplex subunit Nup43) (p42)	380	NUP43	1	1	1	3.7	3.7	3.7
271	-1.06	0.00	1.20	O75607	Nucleoplasmin-3	178	NPM3	1	0	1	8.4	0	8.4
272	-1.06	1.66	0.81	Q5JRX3	Presequence protease, mitochondrial (hPreP) (EC 3.4.24.-) (Pitrilysin metalloproteinase 1) (Metalloprotease 1) (hMP1)	1037	PITRM1	1	2	1	1.4	3.8	1.4
273	-1.06	0.40	0.53	P20290	Transcription factor BTF3 (Nascent polypeptide-associated complex subunit beta) (NAC-beta) (RNA polymerase B transcription factor 3)	206	BTF3	4	3	4	30.2	29	38.3
274	-1.06	0.57	0.83	P28072	Proteasome subunit beta type-6 (EC 3.4.25.1) (Macropain delta chain) (Multicatalytic endopeptidase complex delta chain) (Proteasome delta chain) (Proteasome subunit Y)	239	PSMB6	1	1	1	4.2	4.2	4.2
275	-1.05	0.62	0.82	P46777	60S ribosomal protein L5	297	RPL5	3	1	6	13.1	4.7	22.6
276	-1.05	0.11	1.16	P62701	40S ribosomal protein S4, X isoform (SCR10) (Single copy abundant mRNA protein)	263	RPS4X	6	3	5	20.9	9.5	19
277	-1.05	0.00	1.05	O00487	26S proteasome non-ATPase regulatory subunit 14 (EC 3.4.19.-) (26S proteasome regulatory subunit RPN11) (26S proteasome-associated PAD1 homolog 1)	310	PSMD14	1	0	1	4.2	0	4.2

278	-1.04	1.41	0.86	P37235	Hippocalcin-like protein 1 (Calcium-binding protein BDR-1) (HLP2) (Visinin-like protein 3) (VILIP-3)	193	HPCAL1	1	3	1	6.2	19.2	6.2
279	-1.04	0.86	1.15	P22695	Cytochrome b-c1 complex subunit 2, mitochondrial (Complex III subunit 2) (Core protein II) (Ubiquinol-cytochrome-c reductase complex core protein 2)	453	UQCRC2	8	4	5	29.1	12.6	17.9
280	-1.04	-0.11	1.74	Q92499	ATP-dependent RNA helicase DDX1 (EC 3.6.4.13) (DEAD box protein 1) (DEAD box protein retinoblastoma) (DBP-RB)	740	DDX1	1	1	1	2.9	2.9	2.9
281	-1.04	0.14	0.97	K7EK18	Septin-9 (Fragment)	195	sept9	2	1	1	14.4	5.1	5.1
282	-1.04	0.00	-0.19	Q9NRX4	14 kDa phosphohistidine phosphatase (EC 3.1.3.-) (Phosphohistidine phosphatase 1) (Protein janus-A homolog)	125	PHPT1	2	0	1	32.8	0	16
283	-1.03	0.40	0.90	P22314	Ubiquitin-like modifier-activating enzyme 1 (Protein A1S9) (Ubiquitin-activating enzyme E1)	1058	UBA1	9	12	8	12.9	17.3	10.6
284	-1.03	1.04	1.55	P06756	Integrin alpha-V (Vitronectin receptor subunit alpha) (CD antigen CD51) [Cleaved into: Integrin alpha-V heavy chain; Integrin alpha-V light chain]	1048	ITGAV	3	4	3	3.4	5.9	5.6
285	-1.02	0.92	1.25	F8WAS3	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	70	NDUFA5	1	4	1	14.3	51.4	14.3
286	-1.02	-0.07	0.88	A0A087WYR0	Signal recognition particle 19 kDa protein	120	SRP19	2	2	2	20	22.5	20
287	-1.02	0.24	0.32	P62979	Ubiquitin-40S ribosomal protein S27a (Ubiquitin carboxyl extension protein 80) [Cleaved into: Ubiquitin; 40S ribosomal protein S27a]	156	RPS27A	1	3	2	10.3	24.4	11.5

288	-1.02	2.43	1.46	Q13263	Transcription intermediary factor 1-beta (TIF1-beta) (E3 SUMO-protein ligase TRIM28) (EC 6.3.2.-) (KRAB-associated protein 1) (KAP-1) (KRAB-interacting protein 1) (KRIP-1) (Nuclear corepressor KAP-1) (RING finger protein 96) (Tripartite motif-containing protein 28)	835	TRIM28	5	3	2	10.4	8.2	3.3
289	-1.02	0.30	0.55	P50395	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2)	445	GDI2	5	5	6	13	16	16.6
290	-1.02	1.26	0.00	P26885	Peptidyl-prolyl cis-trans isomerase FKBP2 (PPIase FKBP2) (EC 5.2.1.8) (13 kDa FK506-binding protein) (13 kDa FKBP) (FKBP-13) (FK506-binding protein 2) (FKBP-2) (Immunophilin FKBP13) (Rotamase)	142	FKBP2	1	3	0	10.6	33.8	0
291	-1.02	1.22	1.25	P27695	DNA-(apurinic or apyrimidinic site) lyase (EC 3.1.-.-) (EC 4.2.99.18) (APEX nuclease) (APEN) (Apurinic-apyrimidinic endonuclease 1) (AP endonuclease 1) (APE-1) (REF-1) (Redox factor-1) [Cleaved into: DNA-(apurinic or apyrimidinic site) lyase, mitochondrial]	318	APEX1	1	2	3	5.7	12.3	16.7
292	-1.02	0.37	0.89	K7EJR3	26S proteasome non-ATPase regulatory subunit 8 (Fragment)	250	PSMD8	1	2	3	3.2	6.8	13.2
293	-1.02	0.50	1.40	B8ZZJ0	Small ubiquitin-related modifier 1	58	SUMO1	1	1	1	20.7	20.7	20.7
294	-1.01	0.21	0.00	P62633	Cellular nucleic acid-binding protein (CNBP) (Zinc finger protein 9)	177	CNBP	1	3	0	8.8	23.5	0

295	-1.01	0.70	0.48	P50990	T-complex protein 1 subunit theta (TCP-1-theta) (CCT-theta) (Renal carcinoma antigen NY-REN-15)	548	CCT8	11	4	14	23.9	10.8	30.5
296	-1.01	0.00	0.00	C9JYM0	Ribonuclease P protein subunit p20 (Fragment)	137	POP7	1	0	0	10.9	0	0
297	-1.01	0.83	1.12	E9PKD5	26S protease regulatory subunit 6A (Fragment)	311	PSMC3	3	2	5	14.5	9.6	24.4
298	-1.01	0.27	0.89	Q13151	Heterogeneous nuclear ribonucleoprotein A0 (hnRNP A0)	305	HNRNPA0	1	2	1	4.9	2.6	4.9
299	-1.01	0.00	0.00	H7C531	26S proteasome non-ATPase regulatory subunit 6 (Fragment)	138	PSMD6	1	0	0	10.9	0	0
300	-1.00	0.54	0.72	P61923	Coatomer subunit zeta-1 (Zeta-1-coat protein) (Zeta-1 COP)	177	COPZ1	3	4	2	29.9	30.5	16.9
301	-1.00	0.48	1.83	Q16555	Dihydropyrimidinase-related protein 2 (DRP-2) (Collapsin response mediator protein 2) (CRMP-2) (N2A3) (Unc-33-like phosphoprotein 2) (ULIP-2)	572	DPYSL2	4	2	8	9.5	4.5	23.9
302	-1.00	0.00	0.59	O75822	Eukaryotic translation initiation factor 3 subunit J (eIF3j) (Eukaryotic translation initiation factor 3 subunit 1) (eIF-3-alpha) (eIF3 p35)	258	EIF3J	1	0	2	6.2	0	14.8
303	-1.00	-0.21	0.37	P60174	Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Triose-phosphate isomerase)	286	TPI1	12	14	11	66.3	69.1	57
304	-1.00	1.01	1.04	P07339	Cathepsin D (EC 3.4.23.5) [Cleaved into: Cathepsin D light chain; Cathepsin D heavy chain]	412	CTSD	2	9	2	5.1	23.8	6.8
305	-1.00	0.50	0.00	A0A087WVZ9	DNA-directed RNA polymerases I, II, and III subunit RPABC1	184	POLR2E	2	2	0	16.8	16.8	0

306	-1.00	-0.10	0.79	P06733	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	434	ENO1	28	15	24	71	41.9	55.3
307	-0.99	0.13	1.39	P05455	Lupus La protein (La autoantigen) (La ribonucleoprotein) (Sjoegren syndrome type B antigen) (SS-B)	408	SSB	6	4	5	20.1	12.3	18.6
308	-0.99	0.75	1.09	A0A087WXM6	60S ribosomal protein L17 (Fragment)	169	RPL17	6	4	3	30.8	29.6	16
309	-0.99	1.49	1.06	P24752	Acetyl-CoA acetyltransferase, mitochondrial (EC 2.3.1.9) (Acetoacetyl-CoA thiolase) (T2)	427	ACAT1	3	2	2	8	8.7	6.3
310	-0.99	1.01	0.99	B4DLN1	Uncharacterized protein (cDNA FLJ60124, highly similar to Mitochondrial dicarboxylate carrier)	442		3	6	3	5.2	14.5	5.2
311	-0.99	0.18	0.82	D6R9P3	Heterogeneous nuclear ribonucleoprotein A/B	280	HNRNPAB	2	1	1	7.9	2.9	2.9
312	-0.99	0.45	0.36	P78371	T-complex protein 1 subunit beta (TCP-1-beta) (CCT-beta)	535	CCT2	12	5	13	27.7	14	29.5
313	-0.99	0.53	1.46	P61158	Actin-related protein 3 (Actin-like protein 3)	418	ACTR3	2	2	5	4.3	5.7	19.9
314	-0.98	0.13	0.48	P35270	Sepiapterin reductase (SPR) (EC 1.1.1.153)	261	SPR	6	2	3	32.2	13	13.8
315	-0.98	0.20	0.59	H0Y3P2	Eukaryotic translation initiation factor 4 gamma 2	869	EIF4G2	1	1	1	1.2	1.2	1.2
316	-0.98	0.12	-3.49	O60925	Prefoldin subunit 1	122	PFDN1	1	2	1	8.2	16.4	10.7
317	-0.98	0.12	1.12	Q01518	Adenylyl cyclase-associated protein 1 (CAP 1)	475	CAP1	4	5	4	14.1	14.1	12

318	-0.98	2.02	0.49	P08574	Cytochrome c1, heme protein, mitochondrial (Complex III subunit 4) (Complex III subunit IV) (Cytochrome b-c1 complex subunit 4) (Ubiquinol-cytochrome-c reductase complex cytochrome c1 subunit) (Cytochrome c-1)	325	CYC1	2	1	2	8.9	7.4	11.4
319	-0.98	0.86	0.96	F8W8A6	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial (Fragment)	128	HIBCH	1	1	1	9.4	9.4	9.4
320	-0.98	0.04	0.35	P14618	Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	531	PKM	23	14	20	52.5	31.1	49.7
321	-0.98	-0.12	0.21	P16152	Carbonyl reductase [NADPH] 1 (EC 1.1.1.184) (15-hydroxyprostaglandin dehydrogenase [NADP(+)]) (EC 1.1.1.197) (NADPH-dependent carbonyl reductase 1) (Prostaglandin 9-ketoreductase) (Prostaglandin-E(2) 9-reductase) (EC 1.1.1.189) (Short chain dehydrogenase/reductase family 21C member 1)	277	CBR1	4	6	5	21.7	26	22.7
322	-0.98	1.00	0.79	P11021	78 kDa glucose-regulated protein (GRP-78) (Endoplasmic reticulum lumenal Ca(2+)-binding protein grp78) (Heat shock 70 kDa protein 5) (Immunoglobulin heavy chain-binding protein) (BiP)	654	HSPA5	17	12	12	32.4	28.1	22.5
323	-0.98	1.01	0.59	Q9HAV7	GrpE protein homolog 1, mitochondrial (HMGE) (Mt-GrpE#1)	217	GRPEL1	3	5	3	18.9	27.2	18.9

324	-0.98	1.37	1.31	P00367	Glutamate dehydrogenase 1, mitochondrial (GDH 1) (EC 1.4.1.3)	558	GLUD1	1	3	5	2.8	8.9	14.1
325	-0.98	0.21	0.49	E7EQR4	Ezrin	586	EZR	12	8	10	19.1	17.1	20.1
326	-0.97	0.00	0.00	Q96CS3	FAS-associated factor 2 (Protein ETEA) (UBX domain-containing protein 3B) (UBX domain-containing protein 8)	445	FAF2	1	0	0	4	0	0
327	-0.97	0.00	0.00	P68402	Platelet-activating factor acetylhydrolase IB subunit beta (EC 3.1.1.47) (PAF acetylhydrolase 30 kDa subunit) (PAF-AH 30 kDa subunit) (PAF-AH subunit beta) (PAFAH subunit beta)	229	PAFAH1B2	1	0	0	3.9	0	0
328	-0.97	0.33	2.03	P51858	Hepatoma-derived growth factor (HDGF) (High mobility group protein 1-like 2) (HMG-1L2)	240	HDGF	1	2	3	4.2	11.2	20
329	-0.97	0.00	0.00	Q96RS6	NudC domain-containing protein 1 (Chronic myelogenous leukemia tumor antigen 66) (Tumor antigen CML66)	583	NUDCD1	1	0	0	2.9	0	0
330	-0.96	1.09	1.28	E7ENZ3	T-complex protein 1 subunit epsilon	486	CCT5	8	4	7	21.2	14	20.2
331	-0.96	1.15	1.02	P04843	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 (EC 2.4.99.18) (Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit) (Ribophorin I) (RPN-I) (Ribophorin-1)	607	RPN1	7	4	5	16.8	9.2	13.2
332	-0.96	1.22	1.52	P84095	Rho-related GTP-binding protein RhoG	191	RHOG	2	4	1	13.1	29.8	7.3
333	-0.96	1.19	0.91	P38117	Electron transfer flavoprotein subunit beta (Beta-ETF)	255	ETFB	4	8	7	18	34.1	26.7
334	-0.95	0.51	0.70	P13489	Ribonuclease inhibitor (Placental ribonuclease inhibitor) (Placental RNase inhibitor)	461	RNH1	1	1	2	2.4	3	4.3

					(Ribonuclease/angiogenin inhibitor 1) (RAI)								
335	-0.94	1.30	1.27	Q9P035	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 3 (EC 4.2.1.134) (3-hydroxyacyl-CoA dehydratase 3) (HACD3) (Butyrate-induced protein 1) (B-ind1) (hB-ind1) (Protein-tyrosine phosphatase-like A domain-containing protein 1)	362	HACD3	2	4	1	8.8	15.5	5.8
336	-0.94	0.60	0.24	C9J3L8	Translocon-associated protein subunit alpha	265	SSR1	1	2	2	4.2	7.2	7.2
337	-0.94	0.41	0.54	Q13185	Chromobox protein homolog 3 (HECH) (Heterochromatin protein 1 homolog gamma) (HP1 gamma) (Modifier 2 protein)	183	CBX3	3	1	3	16.4	7.7	16.4
338	-0.94	0.69	0.00	Q8NCW5	NAD(P)H-hydrate epimerase (EC 5.1.99.6) (Apolipoprotein A-I-binding protein) (AI-BP) (NAD(P)HX epimerase) (YjeF N-terminal domain-containing protein 1) (YjeF_N1)	288	APOA1BP	1	2	0	5.9	16.2	0
339	-0.94	0.39	1.37	P26641	Elongation factor 1-gamma (EF-1-gamma) (eEF-1B gamma)	437	EEF1G	7	9	8	18.3	27.5	17.2
340	-0.94	0.99	1.42	P42765	3-ketoacyl-CoA thiolase, mitochondrial (EC 2.3.1.16) (Acetyl-CoA acyltransferase) (Beta-ketothiolase) (Mitochondrial 3-oxoacyl-CoA thiolase) (T1)	397	ACAA2	1	1	1	2.8	2.8	2.8
341	-0.94	0.62	1.16	Q9NSD9	Phenylalanine--tRNA ligase beta subunit (EC 6.1.1.20) (Phenylalanyl-tRNA synthetase beta subunit) (PheRS)	589	FARSB	3	4	4	5.1	7	7
342	-0.93	0.18	0.60	P37802	Transgelin-2 (Epididymis tissue protein Li 7e) (SM22-alpha homolog)	199	TAGLN2	6	11	7	32.7	63.3	37.2

343	-0.93	0.05	1.10	Q5T8U3	60S ribosomal protein L7a (Ribosomal protein L7a) (Fragment)	191	RPL7A	6	3	4	31.4	17.3	17.8
344	-0.93	0.79	0.54	Q00610	Clathrin heavy chain 1 (Clathrin heavy chain on chromosome 17) (CLH-17)	1675	CLTC	18	23	22	15.9	21.6	19.3
345	-0.92	1.71	1.80	Q9BSD7	Cancer-related nucleoside-triphosphatase (NTPase) (EC 3.6.1.15) (Nucleoside triphosphate phosphohydrolase)	190	NTPCR	2	3	3	15.8	27.9	23.7
346	-0.92	0.00	1.72	B0QYA5	Eukaryotic translation initiation factor 3 subunit D (Fragment)	269	EIF3D	2	0	1	9.7	0	4.5
347	-0.92	-0.17	1.00	P62269	40S ribosomal protein S18 (Ke-3) (Ke3)	152	RPS18	4	4	4	19.1	19.7	19.1
348	-0.92	0.00	0.47	K7EML9	Thioredoxin-like protein 1 (Fragment)	138	TXNL1	2	0	1	18.8	0	10.9
349	-0.92	0.00	0.00	Q96JB2	Conserved oligomeric Golgi complex subunit 3 (COG complex subunit 3) (Component of oligomeric Golgi complex 3) (Vesicle-docking protein SEC34 homolog) (p94)	828	COG3	1	0	0	3.4	0	0
350	-0.92	0.45	0.80	Q92598	Heat shock protein 105 kDa (Antigen NY-CO-25) (Heat shock 110 kDa protein)	858	HSPH1	7	6	9	12.8	9.5	15.2
351	-0.92	0.72	0.09	P51148	Ras-related protein Rab-5C (L1880) (RAB5L)	216	RAB5C	5	4	2	28.2	23.6	11.6
352	-0.92	0.00	0.00	Q9Y3C6	Peptidyl-prolyl cis-trans isomerase-like 1 (PPIase) (EC 5.2.1.8) (Rotamase PPIL1)	166	PPIL1	1	0	0	10.2	0	0
353	-0.91	4.52	0.00	Q9BQ61	Uncharacterized protein C19orf43	176	C19orf43	1	1	0	7.4	13.6	0
354	-0.91	0.00	0.00	F5GXQ0	BRO1 domain-containing protein BROX	338	BROX	1	0	0	5.6	0	0
355	-0.91	0.30	0.94	A0A087WTT1	Polyadenylate-binding protein (PABP)	522	PABPC1	7	5	10	17.4	12.6	24.1
356	-0.91	0.00	0.92	Q6NZI2	Polymerase I and transcript release factor (Cavin-1)	390	PTRF	1	0	1	5	0	5

357	-0.90	0.00	0.20	P54577	Tyrosine--tRNA ligase, cytoplasmic (EC 6.1.1.1) (Tyrosyl-tRNA synthetase) (TyrRS) [Cleaved into: Tyrosine--tRNA ligase, cytoplasmic, N-terminally processed]	528	YARS	1	0	1	2.3	0	2.3
358	-0.90	1.01	0.54	Q15021	Condensin complex subunit 1 (Chromosome condensation-related SMC-associated protein 1) (Chromosome-associated protein D2) (hCAP-D2) (Non-SMC condensin I complex subunit D2) (XCAP-D2 homolog)	1401	NCAPD2	3	2	1	2.4	1.6	0.9
359	-0.90	0.00	0.90	Q01085	Nucleolysin TIAR (TIA-1-related protein)	375	TIAL1	1	0	1	3.5	0	8.3
360	-0.90	0.73	0.28	F8W1R7	Myosin light polypeptide 6	145	MYL6	2	2	4	17.2	17.2	34.5
361	-0.89	1.15	1.24	P06576	ATP synthase subunit beta, mitochondrial (EC 3.6.3.14)	529	ATP5B	10	12	9	25.5	29.7	22.5
362	-0.89	0.10	1.12	P62266	40S ribosomal protein S23	143	RPS23	2	3	2	15.4	21	15.4
363	-0.89	0.54	0.99	P30837	Aldehyde dehydrogenase X, mitochondrial (EC 1.2.1.3) (Aldehyde dehydrogenase 5) (Aldehyde dehydrogenase family 1 member B1)	517	ALDH1B1	5	2	3	12.4	4.4	6.2
364	-0.89	0.00	1.09	Q5T5U7	Selenide, water dikinase 1 (Fragment)	91	SEPHS1	1	0	1	11	0	11
365	-0.89	0.99	1.04	P13804	Electron transfer flavoprotein subunit alpha, mitochondrial (Alpha-ETF)	333	ETFA	7	8	6	31.2	36.9	22.2
366	-0.89	0.00	0.66	F2Z3P2	Uridine 5'-monophosphate synthase	57	UMPS	1	0	1	29.8	0	29.8
367	-0.89	-0.15	0.20	P09382	Galectin-1 (Gal-1) (14 kDa laminin-binding protein) (HLBP14) (14 kDa lectin) (Beta-galactoside-binding lectin L-14-I) (Galaptin) (HBL) (HPL) (Lactose-binding lectin 1) (Lectin galactoside-binding soluble 1) (Putative MAPK-activating protein PM12) (S-Lac lectin 1)	135	LGALS1	5	6	4	48.1	57	34.8

368	-0.88	0.00	0.00	J3QRD6	60S ribosome subunit biogenesis protein NIP7 homolog (Fragment)	70	NIP7	1	0	0	20	0	0
369	-0.88	0.73	1.06	A0A0A0MSS8	Aldo-keto reductase family 1 member C3	323	AKR1C3	7	6	7	33.4	22.9	26
370	-0.88	0.70	-0.67	I3L4X2	Multidrug resistance-associated protein 1 (Fragment)	1440	ABCC1	2	6	3	2	5.8	2.6
371	-0.88	0.00	0.87	P54886	Delta-1-pyrroline-5-carboxylate synthase (P5CS) (Aldehyde dehydrogenase family 18 member A1) [Includes: Glutamate 5-kinase (GK) (EC 2.7.2.11) (Gamma-glutamyl kinase); Gamma-glutamyl phosphate reductase (GPR) (EC 1.2.1.41) (Glutamate-5-semialdehyde dehydrogenase) (Glutamyl-gamma-semialdehyde dehydrogenase)]	795	ALDH18A1	2	0	3	3.2	0	5.2
372	-0.88	1.16	0.97	P42704	Leucine-rich PPR motif-containing protein, mitochondrial (130 kDa leucine-rich protein) (LRP 130) (GP130)	1394	LRPPRC	36	31	35	32.4	27.9	31.3
373	-0.88	0.93	0.98	O43809	Cleavage and polyadenylation specificity factor subunit 5 (Cleavage and polyadenylation specificity factor 25 kDa subunit) (CFIm25) (CPSF 25 kDa subunit) (Nucleoside diphosphate-linked moiety X motif 21) (Nudix motif 21) (Pre-mRNA cleavage factor Im 25 kDa subunit)	227	NUDT21	5	4	4	24.2	30	18.9
374	-0.87	1.70	0.00	P11441	Ubiquitin-like protein 4A (Ubiquitin-like protein GDX)	157	UBL4A	1	1	0	6.4	9.6	0
375	-0.87	0.00	1.40	P51991	Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3)	378	HNRNPA3	2	0	3	7.9	0	10.7
376	-0.87	0.40	1.94	P62805	Histone H4	103	HIST1H4A	3	3	3	22.3	28.2	22.3

377	-0.87	-0.07	1.19	P62847	40S ribosomal protein S24	133	RPS24	4	2	2	30	20.8	20.8
378	-0.87	1.37	0.91	P10809	60 kDa heat shock protein, mitochondrial (60 kDa chaperonin) (Chaperonin 60) (CPN60) (Heat shock protein 60) (HSP-60) (Hsp60) (HuCHA60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein)	573	HSPD1	25	20	26	45.4	41.7	39.1
379	-0.87	0.69	0.52	P50991	T-complex protein 1 subunit delta (TCP-1-delta) (CCT-delta) (Stimulator of TAR RNA-binding)	539	CCT4	8	6	5	20.6	14.3	11.2
380	-0.87	0.63	0.87	P46821	Microtubule-associated protein 1B (MAP-1B) [Cleaved into: MAP1B heavy chain; MAP1 light chain LC1]	2468	MAP1B	4	5	3	2.2	2.8	1.7
381	-0.87	0.00	0.81	P38919	Eukaryotic initiation factor 4A-III (eIF-4A-III) (eIF4A-III) (EC 3.6.4.13) (ATP-dependent RNA helicase DDX48) (ATP-dependent RNA helicase eIF4A-3) (DEAD box protein 48) (Eukaryotic initiation factor 4A-like NUK-34) (Eukaryotic translation initiation factor 4A isoform 3) (Nuclear matrix protein 265) (NMP 265) (hNMP 265) [Cleaved into: Eukaryotic initiation factor 4A-III, N-terminally processed]	411	EIF4A3	2	2	1	5.6	5.8	2.2
382	-0.86	1.69	0.73	F8W1A4	Adenylate kinase 2, mitochondrial (AK 2) (EC 2.7.4.3) (ATP-AMP transphosphorylase 2) (ATP:AMP phosphotransferase) (Adenylate monophosphate kinase)	232	AK2	6	6	5	37.9	39.2	30.2

383	-0.86	0.55	0.58	P12956	X-ray repair cross-complementing protein 6 (EC 3.6.4.-) (EC 4.2.99.-) (5'-deoxyribose-5-phosphate lyase Ku70) (5'-dRP lyase Ku70) (70 kDa subunit of Ku antigen) (ATP-dependent DNA helicase 2 subunit 1) (ATP-dependent DNA helicase II 70 kDa subunit) (CTC box-binding factor 75 kDa subunit) (CTC75) (CTCBF) (DNA repair protein XRCC6) (Lupus Ku autoantigen protein p70) (Ku70) (Thyroid-lupus autoantigen) (TLAA) (X-ray repair complementing defective repair in Chinese hamster cells 6)	609	XRCC6	13	9	10	30.4	17.2	19.9
384	-0.86	0.66	0.00	Q5VVW2	GTPase-activating Rap/Ran-GAP domain-like protein 3	1013	GARNL3	1	1	0	2.6	2.6	0
385	-0.86	0.67	0.62	P55072	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	806	VCP	12	15	17	19.7	26.3	27.3
386	-0.86	0.00	0.00	D6RDJ3	DNA-directed RNA polymerases I and III subunit RPAC1 (Fragment)	124	POLR1C	1	0	0	10.5	0	0
387	-0.86	1.00	1.23	P13073	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial (Cytochrome c oxidase polypeptide IV) (Cytochrome c oxidase subunit IV isoform 1) (COX IV-1)	169	COX4I1	3	5	2	13.6	30.2	12.4

388	-0.86	-0.11	0.63	P30086	Phosphatidylethanolamine-binding protein 1 (PEBP-1) (HCNPpp) (Neuropolypeptide h3) (Prostatic-binding protein) (Raf kinase inhibitor protein) (RKIP) [Cleaved into: Hippocampal cholinergic neurostimulating peptide (HCNP)]	187	PEBP1	2	4	2	8.6	24.6	8.6
389	-0.85	1.12	1.08	O75489	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-30kD) (CI-30kD) (NADH-ubiquinone oxidoreductase 30 kDa subunit)	264	NDUFS3	1	5	1	6.4	26.1	4.9
390	-0.85	0.00	1.35	Q9Y4Z0	U6 snRNA-associated Sm-like protein LSm4 (Glycine-rich protein) (GRP)	139	LSM4	1	0	3	5.8	0	21.6
391	-0.85	0.06	1.08	P62280	40S ribosomal protein S11	158	RPS11	4	6	3	17.1	35.4	19
392	-0.85	0.00	0.00	Q8N1F7	Nuclear pore complex protein Nup93 (93 kDa nucleoporin) (Nucleoporin Nup93)	819	NUP93	2	0	0	3.3	0	0
393	-0.84	0.76	0.60	P61978	Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (Transformation up-regulated nuclear protein) (TUNP)	463	HNRNPK	8	10	7	21.6	32.5	24.8
394	-0.84	0.00	1.23	A0A087X1S2	Nuclease-sensitive element-binding protein 1	314	YBX1	1	0	3	4.8	0	16.2
395	-0.84	0.36	0.03	O00303	Eukaryotic translation initiation factor 3 subunit F (eIF3f) (Deubiquitinating enzyme eIF3f) (EC 3.4.19.12) (Eukaryotic translation initiation factor 3 subunit 5) (eIF-3-epsilon) (eIF3 p47)	357	EIF3F	4	1	3	13.7	3.1	11.8
396	-0.83	-0.41	0.73	P42766	60S ribosomal protein L35	123	RPL35	1	2	1	8.1	15.4	8.1

397	-0.83	0.93	0.80	P39656	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit (DDOST 48 kDa subunit) (Oligosaccharyl transferase 48 kDa subunit) (EC 2.4.99.18)	456	DDOST	2	2	2	5	4.6	4.1
398	-0.83	1.18	0.02	C9JFR7	Cytochrome c (Fragment)	101	CYCS	1	3	2	14.9	22.8	21.8
399	-0.83	0.53	1.19	P62829	60S ribosomal protein L23 (60S ribosomal protein L17)	140	RPL23	4	3	2	37.9	27.1	20
400	-0.83	-0.57	1.25	Q15435	Protein phosphatase 1 regulatory subunit 7 (Protein phosphatase 1 regulatory subunit 22)	360	PPP1R7	1	1	1	8.1	8.1	8.1
401	-0.83	0.39	0.33	Q92841	Probable ATP-dependent RNA helicase DDX17 (EC 3.6.4.13) (DEAD box protein 17) (DEAD box protein p72) (RNA-dependent helicase p72)	729	DDX17	4	1	3	6.6	2	4.6
402	-0.83	0.18	1.46	E7EPB3	60S ribosomal protein L14	124	RPL14	2	2	2	17.7	17.7	17.7
403	-0.83	0.00	0.00	O00203	AP-3 complex subunit beta-1 (Adaptor protein complex AP-3 subunit beta-1) (Adaptor-related protein complex 3 subunit beta-1) (Beta-3A-adaptin) (Clathrin assembly protein complex 3 beta-1 large chain)	1094	AP3B1	1	0	0	1.1	0	0
404	-0.82	0.57	1.26	Q7L014	Probable ATP-dependent RNA helicase DDX46 (EC 3.6.4.13) (DEAD box protein 46) (PRP5 homolog)	1031	DDX46	2	2	2	2.2	1.8	2
405	-0.82	0.00	0.28	F5H7R9	Parathymosin (Fragment)	57	PTMS	1	0	1	19.3	0	19.3
406	-0.82	0.00	1.23	P41091	Eukaryotic translation initiation factor 2 subunit 3 (Eukaryotic translation initiation factor 2 subunit gamma X) (eIF-2-gamma X) (eIF-2gX)	472	EIF2S3	1	0	3	3.4	0	9.3
407	-0.82	1.09	0.94	Q5QP23	RNA-binding protein 39 (Fragment)	231	RBM39	1	1	1	6.5	6.5	6.5
408	-0.82	-0.39	0.34	Q9Y281	Cofilin-2 (Cofilin, muscle isoform)	166	CFL2	4	4	5	34.3	36.1	32.5

409	-0.82	1.00	0.00	Q9UMS0	NFU1 iron-sulfur cluster scaffold homolog, mitochondrial (HIRA-interacting protein 5)	254	NFU1	1	3	0	4.3	17	0
410	-0.82	0.85	0.69	P45880	Voltage-dependent anion-selective channel protein 2 (VDAC-2) (hVDAC2) (Outer mitochondrial membrane protein porin 2)	294	VDAC2	3	5	6	17.3	20.5	30.4
411	-0.81	0.00	0.00	G3V4D9	Nuclear export mediator factor NEMF (Fragment)	178	NEMF	1	0	0	5.6	0	0
412	-0.81	1.66	0.00	A0A087 WTZ2	Ran-binding protein 17	518	RANBP17	1	2	0	2.1	3.9	0
413	-0.81	0.78	0.67	Q9UIJ7	GTP:AMP phosphotransferase AK3, mitochondrial (EC 2.7.4.10) (Adenylate kinase 3) (AK 3) (Adenylate kinase 3 alpha-like 1)	227	AK3	2	5	3	11	26	14.5
414	-0.81	-0.09	0.06	P13797	Plastin-3 (T-plastin)	630	PLS3	9	5	6	17.6	11.4	9.5
415	-0.81	0.57	0.41	P11142	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LPS-associated protein 1)	646	HSPA8	18	15	15	34.8	31.6	28.3
416	-0.80	1.10	0.57	F5GY37	Prohibitin-2	267	PHB2	3	5	2	11.2	22.8	7.1
417	-0.80	0.87	0.57	Q60FE5	Filamin A (Filamin-A)	2620	FLNA	25	26	28	13.5	14.2	14.8
418	-0.80	0.03	0.55	A0A0A0 MTR7	E3 ubiquitin-protein ligase RNF213	5207	RNF213	2	1	4	0.5	0.3	0.9
419	-0.80	0.48	0.13	E7EQ69	N-alpha-acetyltransferase 50	168	NAA50	5	3	6	28.6	19.6	28.6
420	-0.80	0.30	0.62	Q92616	Translational activator GCN1 (HsGCN1) (GCN1-like protein 1)	2671	GCN1L1	8	9	17	4.3	4.3	8.8
421	-0.80	-0.05	0.64	O00571	ATP-dependent RNA helicase DDX3X (EC 3.6.4.13) (DEAD box protein 3, X-chromosomal) (DEAD box, X isoform) (Helicase-like protein 2) (HLP2)	662	DDX3X	6	2	4	11	4.5	7.1

422	-0.79	1.29	0.93	O95292	Vesicle-associated membrane protein-associated protein B/C (VAMP-B/VAMP-C) (VAMP-associated protein B/C) (VAP-B/VAP-C)	243	VAPB	3	3	4	16.9	16	22.6
423	-0.79	-0.66	0.64	Q9NR33	DNA polymerase epsilon subunit 4 (EC 2.7.7.7) (DNA polymerase II subunit 4) (DNA polymerase epsilon subunit p12)	117	POLE4	1	1	1	9.4	9.4	9.4
424	-0.79	-0.27	0.00	P17931	Galectin-3 (Gal-3) (35 kDa lectin) (Carbohydrate-binding protein 35) (CBP 35) (Galactose-specific lectin 3) (Galactoside-binding protein) (GALBP) (IgE-binding protein) (L-31) (Laminin-binding protein) (Lectin L-29) (Mac-2 antigen)	250	LGALS3	2	1	0	8.8	4.4	0
425	-0.79	0.00	0.00	M0R253	Deoxyhypusine synthase	132	DHPS	1	0	0	9.1	0	0
426	-0.79	0.00	0.81	Q15404	Ras suppressor protein 1 (RSP-1) (Rsu-1)	277	RSU1	2	0	3	8	0	16.1
427	-0.79	1.54	1.47	B4DY09	Interleukin enhancer-binding factor 2 (cDNA FLJ51660, highly similar to Interleukin enhancer-binding factor 2)	352	ILF2	1	1	2	5.7	4.5	8.5
428	-0.79	0.08	0.78	P61970	Nuclear transport factor 2 (NTF-2) (Placental protein 15) (PP15)	127	NUTF2	1	2	1	6.3	11.8	12.6
429	-0.78	1.28	0.31	P05387	60S acidic ribosomal protein P2 (Renal carcinoma antigen NY-REN-44)	115	RPLP2	2	4	1	39.1	62.6	10.4
430	-0.78	0.00	0.39	F8WEG8	Interferon-inducible double-stranded RNA-dependent protein kinase activator A	95	PRKRA	1	0	1	10.5	0	10.5
431	-0.78	0.00	0.78	Q12765	Secernin-1	414	SCRN1	1	0	1	3.8	0	3.8
432	-0.78	0.00	0.00	Q96S52	GPI transamidase component PIG-S (Phosphatidylinositol-glycan biosynthesis class S protein)	555	PIGS	1	0	0	2	0	0

433	-0.78	0.68	0.52	P08107	Heat shock 70 kDa protein 1A/1B (Heat shock 70 kDa protein 1/2) (HSP70-1/HSP70-2) (HSP70.1/HSP70.2)	641	HSPA1A	11	11	8	21.1	25.3	13.7
434	-0.78	0.00	0.81	B4DQI4	Alpha/beta hydrolase domain-containing protein 14B (cDNA FLJ52723, highly similar to Abhydrolase domain-containing protein 14B)	188	ABHD14B	1	0	1	6.9	0	6.9
435	-0.78	0.00	0.11	H0YF12	Tyrosine-protein phosphatase non-receptor type 11 (Fragment)	108	PTPN11	1	0	1	13	0	13
436	-0.77	-0.02	0.36	P42224	Signal transducer and activator of transcription 1-alpha/beta (Transcription factor ISGF-3 components p91/p84)	750	STAT1	3	1	2	6.2	1.7	3.5
437	-0.77	0.00	0.00	Q08J23	tRNA (cytosine(34)-C(5))-methyltransferase (EC 2.1.1.203) (Myc-induced SUN domain-containing protein) (Misu) (NOL1/NOP2/Sun domain family member 2) (Substrate of AIM1/Aurora kinase B) (tRNA (cytosine-5-)-methyltransferase) (tRNA methyltransferase 4 homolog) (hTrm4)	767	NSUN2	1	0	0	2.1	0	0
438	-0.77	0.15	0.27	P60228	Eukaryotic translation initiation factor 3 subunit E (eIF3e) (Eukaryotic translation initiation factor 3 subunit 6) (Viral integration site protein INT-6 homolog) (eIF-3 p48)	445	EIF3E	5	2	3	11.7	4.7	6.3
439	-0.77	0.00	0.85	A0A087WUT6	Eukaryotic translation initiation factor 5B	1220	EIF5B	1	0	1	0.7	0	0.9
440	-0.77	0.00	0.00	X6RDA4	Paraspeckle component 1 (Fragment)	248	PSPC1	1	0	0	4.4	0	0

441	-0.77	1.22	1.19	O75369	Filamin-B (FLN-B) (ABP-278) (ABP-280 homolog) (Actin-binding-like protein) (Beta-filamin) (Filamin homolog 1) (Fh1) (Filamin-3) (Thyroid autoantigen) (Truncated actin-binding protein) (Truncated ABP)	2602	FLNB	19	43	34	11.3	23.1	19.4
442	-0.76	0.48	0.84	P34932	Heat shock 70 kDa protein 4 (HSP70RY) (Heat shock 70-related protein APG-2)	840	HSPA4	10	10	10	15.6	15.4	15.4
443	-0.76	0.08	0.74	O76003	Glutaredoxin-3 (PKC-interacting cousin of thioredoxin) (PICOT) (PKC-theta-interacting protein) (PKCq-interacting protein) (Thioredoxin-like protein 2)	335	GLRX3	6	2	5	20.6	6.6	17.6
444	-0.76	-0.17	0.92	P61758	Prefoldin subunit 3 (HIBBJ46) (Von Hippel-Lindau-binding protein 1) (VBP-1) (VHL-binding protein 1)	197	VBP1	4	3	4	23.9	18.8	23.9
445	-0.76	0.05	0.89	O43242	26S proteasome non-ATPase regulatory subunit 3 (26S proteasome regulatory subunit RPN3) (26S proteasome regulatory subunit S3) (Proteasome subunit p58)	534	PSMD3	2	1	3	6.7	3.4	10.7
446	-0.76	0.57	-3.51	P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial (HIBADH) (EC 1.1.1.31)	336	HIBADH	2	4	2	8	14.6	8.9
447	-0.76	1.22	0.14	O75323	Protein NipSnap homolog 2 (NipSnap2) (Glioblastoma-amplified sequence)	286	GBAS	1	2	2	5.6	8.7	8
448	-0.76	0.47	1.01	H0Y3Y4	Septin-7 (Fragment)	373	sept7	1	1	2	2.4	2.4	7
449	-0.76	0.00	0.00	Q6P1M0	Long-chain fatty acid transport protein 4 (FATP-4) (Fatty acid transport protein 4) (EC 6.2.1.-) (Solute carrier family 27 member 4)	643	SLC27A4	1	0	0	1.7	0	0

450	-0.75	0.00	0.00	Q12904	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 (Multisynthase complex auxiliary component p43) [Cleaved into: Endothelial monocyte-activating polypeptide 2 (EMAP-2) (Endothelial monocyte-activating polypeptide II) (EMAP-II) (Small inducible cytokine subfamily E member 1)]	312	AIMP1	1	0	0	5.8	0	0
451	-0.75	0.00	0.68	P50995	Annexin A11 (56 kDa autoantigen) (Annexin XI) (Annexin-11) (Calcyclin-associated annexin 50) (CAP-50)	505	ANXA11	1	0	2	2.3	0	5.5
452	-0.75	1.45	-0.07	P21964	Catechol O-methyltransferase (EC 2.1.1.6)	271	COMT	1	2	1	7.2	17.2	7.2
453	-0.75	-0.35	-0.10	Q01469	Fatty acid-binding protein, epidermal (Epidermal-type fatty acid-binding protein) (E-FABP) (Fatty acid-binding protein 5) (Psoriasis-associated fatty acid-binding protein homolog) (PA-FABP)	135	FABP5	1	4	1	8.1	31.1	8.1
454	-0.75	1.18	1.26	Q9H7Z7	Prostaglandin E synthase 2 (Membrane-associated prostaglandin E synthase-2) (mPGE synthase-2) (Microsomal prostaglandin E synthase 2) (mPGES-2) (Prostaglandin-H(2) E-isomerase) (EC 5.3.99.3) [Cleaved into: Prostaglandin E synthase 2 truncated form]	377	PTGES2	3	2	5	11.1	10.9	24.1
455	-0.75	0.31	0.83	P55010	Eukaryotic translation initiation factor 5 (eIF-5)	431	EIF5	2	1	3	5.6	2.1	8.6
456	-0.75	0.00	2.51	X1WI28	60S ribosomal protein L10 (Fragment)	200	RPL10	1	0	3	6.5	0	21
457	-0.75	0.73	2.36	P10412	Histone H1.4 (Histone H1b) (Histone H1s-4)	219	HIST1H1E	5	5	5	15.5	22.4	15.1

458	-0.74	0.97	1.11	P62316	Small nuclear ribonucleoprotein Sm D2 (Sm-D2) (snRNP core protein D2)	118	SNRPD2	4	4	4	28.8	36.4	28.8
459	-0.74	1.45	0.95	Q9P0L0	Vesicle-associated membrane protein-associated protein A (VAMP-A) (VAMP-associated protein A) (VAP-A) (33 kDa VAMP-associated protein) (VAP-33)	249	VAPA	2	4	2	5.6	17.7	5.6
460	-0.74	0.00	1.32	O95831	Apoptosis-inducing factor 1, mitochondrial (EC 1.1.1.-) (Programmed cell death protein 8)	613	AIFM1	1	0	1	2.6	0	2.6
461	-0.74	-0.28	0.24	Q99471	Prefoldin subunit 5 (C-Myc-binding protein Mm-1) (Myc modulator 1)	154	PFDN5	3	3	2	31.2	21.4	21.4
462	-0.74	3.08	1.04	P53597	Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial (EC 6.2.1.4) (EC 6.2.1.5) (Succinyl-CoA synthetase subunit alpha) (SCS-alpha)	346	SUCLG1	1	1	1	2.9	4.6	2.9
463	-0.74	1.61	3.10	Q99878	Histone H2A type 1-J (Histone H2A/e)	128	HIST1H2AJ	1	3	2	8.6	27.3	23.4
464	-0.73	0.59	0.53	Q9HAV4	Exportin-5 (Exp5) (Ran-binding protein 21)	1204	XPO5	2	2	2	2.1	2.1	2.1
465	-0.73	0.61	0.46	P23919	Thymidylate kinase (EC 2.7.4.9) (dTMP kinase)	212	DTYMK	2	4	2	9.4	26.9	9.4
466	-0.72	-0.04	0.61	P07195	L-lactate dehydrogenase B chain (LDH-B) (EC 1.1.1.27) (LDH heart subunit) (LDH-H) (Renal carcinoma antigen NY-REN-46)	334	LDHB	13	13	12	40.7	40.7	39.5
467	-0.72	1.47	1.25	E5RJU9	Protein LYRIC	526	MTDH	1	2	1	2.3	6.1	2.3
468	-0.72	0.38	0.74	O75396	Vesicle-trafficking protein SEC22b (ER-Golgi SNARE of 24 kDa) (ERS-24) (ERS24) (SEC22 vesicle-trafficking protein homolog B) (SEC22 vesicle-trafficking protein-like 1)	215	SEC22B	2	3	2	13.5	18.1	13.5

469	-0.72	1.05	1.37	O75533	Splicing factor 3B subunit 1 (Pre-mRNA-splicing factor SF3b 155 kDa subunit) (SF3b155) (Spliceosome-associated protein 155) (SAP 155)	1304	SF3B1	4	5	5	3.9	5.1	5.7
470	-0.71	0.27	0.81	Q06830	Peroxiredoxin-1 (EC 1.11.1.15) (Natural killer cell-enhancing factor A) (NKEF-A) (Proliferation-associated gene protein) (PAG) (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2)	199	PRDX1	10	12	11	55.3	68.8	51.3
471	-0.71	-0.21	0.06	O94903	Proline synthase co-transcribed bacterial homolog protein	275	PROSC	3	1	1	17.5	4.7	4.7
472	-0.70	0.61	0.76	O60506	Heterogeneous nuclear ribonucleoprotein Q (hnRNP Q) (Glycine- and tyrosine-rich RNA-binding protein) (GRY-RBP) (NS1-associated protein 1) (Synaptotagmin-binding, cytoplasmic RNA-interacting protein)	623	SYNCRIP	5	2	6	13.1	6.5	13.9
473	-0.70	0.00	-0.01	E9PHI6	Cytoplasmic dynein 1 light intermediate chain 1	407	DYNC1LI1	1	0	1	4.7	0	4.7
474	-0.70	0.00	0.87	Q9NZN4	EH domain-containing protein 2 (PAST homolog 2)	543	EHD2	1	0	2	2.8	0	5
475	-0.70	1.27	1.55	Q15393	Splicing factor 3B subunit 3 (Pre-mRNA-splicing factor SF3b 130 kDa subunit) (SF3b130) (STAF130) (Spliceosome-associated protein 130) (SAP 130)	1217	SF3B3	2	3	3	1.7	3.5	4.1
476	-0.70	0.66	-0.13	P61006	Ras-related protein Rab-8A (Oncogene c-mel)	207	RAB8A	3	4	3	14.5	21.3	14.5
477	-0.70	-0.76	0.16	Q14116	Interleukin-18 (IL-18) (Iboctadekin) (Interferon gamma-inducing factor) (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma)	193	IL18	2	2	2	13.2	9.5	10.1
478	-0.70	0.85	0.58	P61026	Ras-related protein Rab-10	200	RAB10	2	7	3	9.5	32	17

479	-0.70	1.11	0.91	P40926	Malate dehydrogenase, mitochondrial (EC 1.1.1.37)	338	MDH2	4	15	8	15.4	56.5	25.7
480	-0.69	0.76	0.36	Q8TED1	Probable glutathione peroxidase 8 (GPx-8) (GSHPx-8) (EC 1.11.1.9)	209	GPX8	1	2	2	5.3	10	10
481	-0.69	-0.08	0.71	P49773	Histidine triad nucleotide-binding protein 1 (EC 3.-.-.-) (Adenosine 5'-monophosphoramidase) (Protein kinase C inhibitor 1) (Protein kinase C-interacting protein 1) (PKCI-1)	126	HINT1	2	4	2	35.7	31	35.7
482	-0.69	-0.48	-0.23	P22102	Trifunctional purine biosynthetic protein adenosine-3 [Includes: Phosphoribosylamine--glycine ligase (EC 6.3.4.13) (Glycinamide ribonucleotide synthetase) (GARS) (Phosphoribosylglycinamide synthetase); Phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1) (AIR synthase) (AIRS) (Phosphoribosyl-aminoimidazole synthetase); Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2) (5'-phosphoribosylglycinamide transformylase) (GAR transformylase) (GART)]	1010	GART	3	1	1	4.6	1.3	1.3
483	-0.69	-0.04	0.76	P62826	GTP-binding nuclear protein Ran (Androgen receptor-associated protein 24) (GTPase Ran) (Ras-like protein TC4) (Ras-related nuclear protein)	216	RAN	8	7	6	38.4	38.9	27.3
484	-0.69	0.00	0.85	Q5T4S7	E3 ubiquitin-protein ligase UBR4 (EC 6.3.2.-) (600 kDa retinoblastoma protein-associated factor) (N-recognin-4) (Retinoblastoma-associated factor of 600 kDa)	5183	UBR4	1	0	2	0.2	0	0.4

					(RBAF600) (p600) (Zinc finger UBR1-type protein 1)								
485	-0.69	-0.04	0.93	O14980	Exportin-1 (Exp1) (Chromosome region maintenance 1 protein homolog)	1071	XPO1	10	7	7	11.4	8.3	8.3
486	-0.68	0.00	1.37	P62195	26S protease regulatory subunit 8 (26S proteasome AAA-ATPase subunit RPT6) (Proteasome 26S subunit ATPase 5) (Proteasome subunit p45) (Thyroid hormone receptor-interacting protein 1) (TRIP1) (p45/SUG)	406	PSMC5	4	0	6	15.8	0	22.1
487	-0.68	0.33	0.40	O14818	Proteasome subunit alpha type-7 (EC 3.4.25.1) (Proteasome subunit RC6-1) (Proteasome subunit XAPC7)	248	PSMA7	6	8	5	32.7	40.3	23.4
488	-0.68	1.03	0.40	P61106	Ras-related protein Rab-14	215	RAB14	6	9	5	39.1	58.1	23.7
489	-0.68	0.29	1.03	P20618	Proteasome subunit beta type-1 (EC 3.4.25.1) (Macropain subunit C5) (Multicatalytic endopeptidase complex subunit C5) (Proteasome component C5) (Proteasome gamma chain)	241	PSMB1	3	7	4	20.3	35.7	26.6
490	-0.67	0.35	0.46	O15145	Actin-related protein 2/3 complex subunit 3 (Arp2/3 complex 21 kDa subunit) (p21-ARC)	178	ARPC3	3	3	1	16.3	20.8	7.3
491	-0.67	0.00	0.30	E9PI86	Nuclear autoantigenic sperm protein (Fragment)	256	NASP	2	0	1	13.7	0	4.7

492	-0.67	0.00	0.00	Q9NR28	Diablo homolog, mitochondrial (Direct IAP-binding protein with low pI) (Second mitochondria-derived activator of caspase) (Smac)	239	DIABLO	2	0	0	12.4	0	0
493	-0.67	0.00	0.84	B7ZBQ0	Serine/threonine-protein phosphatase 2A activator (EC 5.2.1.8) (Phosphotyrosyl phosphatase activator)	61	PPP2R4	1	0	1	13.1	0	13.1
494	-0.67	0.10	0.11	O14737	Programmed cell death protein 5 (TF-1 cell apoptosis-related protein 19) (Protein TFAR19)	125	PDCD5	3	2	3	18.4	17.6	18.4
495	-0.66	0.12	0.58	P33316	Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial (dUTPase) (EC 3.6.1.23) (dUTP pyrophosphatase)	252	DUT	2	2	2	18.9	15.9	17.7
496	-0.66	0.18	0.60	P13639	Elongation factor 2 (EF-2)	858	EEF2	15	20	24	21.9	33.4	34.5
497	-0.66	0.64	0.47	P0CW22	40S ribosomal protein S17-like	135	RPS17L	4	5	1	51.9	39.3	7.4
498	-0.65	0.06	0.75	P62851	40S ribosomal protein S25	125	RPS25	3	3	2	24	16	16
499	-0.65	-0.32	0.37	H0YH58	Oligoribonuclease, mitochondrial (Fragment)	111	REXO2	1	1	1	9	9	9
500	-0.65	0.62	0.00	A0A0A0MSK5	Torsin-1A-interacting protein 1	462	TOR1AIP1	1	1	0	2.6	2.8	0
501	-0.65	0.75	1.08	P04792	Heat shock protein beta-1 (HspB1) (28 kDa heat shock protein) (Estrogen-regulated 24 kDa protein) (Heat shock 27 kDa protein) (HSP 27) (Stress-responsive protein 27) (SRP27)	205	HSPB1	4	10	5	21.5	69.8	24.9
502	-0.65	-0.76	0.70	P00352	Retinal dehydrogenase 1 (RALDH 1) (RalDH1) (EC 1.2.1.36) (ALDH-E1) (ALHDII) (Aldehyde dehydrogenase family 1 member A1) (Aldehyde dehydrogenase, cytosolic)	501	ALDH1A1	24	21	22	58.7	47.5	53.5

503	-0.64	0.00	1.10	Q6NUK1	Calcium-binding mitochondrial carrier protein SCaMC-1 (Mitochondrial ATP-Mg/Pi carrier protein 1) (Mitochondrial Ca(2+)-dependent solute carrier protein 1) (Small calcium-binding mitochondrial carrier protein 1) (Solute carrier family 25 member 24)	477	SLC25A24	1	0	1	3.5	0	3.5
504	-0.64	-0.25	0.60	Q13200	26S proteasome non-ATPase regulatory subunit 2 (26S proteasome regulatory subunit RPN1) (26S proteasome regulatory subunit S2) (26S proteasome subunit p97) (Protein 55.11) (Tumor necrosis factor type 1 receptor-associated protein 2)	908	PSMD2	5	1	4	8.5	1.2	7.1
505	-0.64	1.02	1.48	G3V576	Heterogeneous nuclear ribonucleoproteins C1/C2	231	HNRNPC	4	5	5	15.2	22.9	19.5
506	-0.64	1.04	1.05	Q7KZF4	Staphylococcal nuclease domain-containing protein 1 (100 kDa coactivator) (EBNA2 coactivator p100) (Tudor domain-containing protein 11) (p100 co-activator)	910	SND1	6	3	7	9.7	5.5	12.7
507	-0.64	0.00	0.00	Q12974	Protein tyrosine phosphatase type IVA 2 (EC 3.1.3.48) (HU-PP-1) (OV-1) (PTP(CAAXII)) (Protein-tyrosine phosphatase 4a2) (Protein-tyrosine phosphatase of regenerating liver 2) (PRL-2)	167	PTP4A2	1	0	0	11	0	0
508	-0.64	1.26	0.63	Q9NZM1	Myoferlin (Fer-1-like protein 3)	2061	MYOF	11	22	14	5.7	13.3	8.9
509	-0.63	0.51	0.03	Q13509	Tubulin beta-3 chain (Tubulin beta-4 chain) (Tubulin beta-III)	450	TUBB3	4	5	7	11.8	14.4	17.1
510	-0.63	-0.23	0.21	P31947	14-3-3 protein sigma (Epithelial cell marker protein 1) (Stratifin)	248	SFN	6	8	8	27	36.7	36.7

511	-0.63	0.55	0.22	C9J9K3	40S ribosomal protein SA (Fragment)	263	RPSA	9	7	5	36.5	38.8	23.2
512	-0.63	0.12	0.37	P68371	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	445	TUBB4B	8	11	9	26.7	36.2	26.5
513	-0.62	0.75	0.83	P01111	GTPase NRas (Transforming protein N-Ras)	189	NRAS	3	1	2	20.1	6.3	12.2
514	-0.62	0.90	0.71	J3QR09	Ribosomal protein L19	193	RPL19	2	1	2	8.8	8.8	8.8
515	-0.62	0.00	0.17	O00429	Dynamin-1-like protein (EC 3.6.5.5) (Dnm1p/Vps1p-like protein) (DVLP) (Dynamin family member proline-rich carboxyl-terminal domain less) (Dymple) (Dynamin-like protein) (Dynamin-like protein 4) (Dynamin-like protein IV) (HdynIV) (Dynamin-related protein 1)	736	DNM1L	2	0	1	2.9	0	1.6
516	-0.62	0.72	0.31	P07355	Annexin A2 (Annexin II) (Annexin-2) (Calpactin I heavy chain) (Calpactin-1 heavy chain) (Chromobindin-8) (Lipocortin II) (Placental anticoagulant protein IV) (PAP-IV) (Protein I) (p36)	339	ANXA2	17	17	11	51	52.8	29.5
517	-0.62	0.26	0.34	P04406	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (EC 1.2.1.12) (Peptidyl-cysteine S-nitrosylase GAPDH) (EC 2.6.99.-)	335	GAPDH	8	9	8	31.9	46	28.7
518	-0.62	1.25	1.21	H7C2U6	Protein NipSnap homolog 1 (Fragment)	221	NIPSNAP1	2	1	2	10.9	6.3	10.9
519	-0.62	0.35	0.40	F8VZJ2	Nascent polypeptide-associated complex subunit alpha	136	NACA	3	3	2	30.1	30.9	20.6
520	-0.61	0.18	0.69	P08238	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	724	HSP90AB1	28	14	29	35.8	21.3	35.6
521	-0.61	2.78	0.63	A0A087 WTV6	Pyrroline-5-carboxylate reductase 2	246	PYCR2	2	1	1	13.4	7.3	6.1

522	-0.61	0.37	0.64	P31948	Stress-induced-phosphoprotein 1 (STI1) (Hsc70/Hsp90-organizing protein) (Hop) (Renal carcinoma antigen NY-REN-11) (Transformation-sensitive protein IEF SSP 3521)	543	STIP1	11	5	15	20.3	11.2	30.9
523	-0.61	0.58	-0.03	P26639	Threonine--tRNA ligase, cytoplasmic (EC 6.1.1.3) (Threonyl-tRNA synthetase) (ThrRS)	723	TARS	3	1	2	4	1.4	2.6
524	-0.61	-1.22	0.29	Q9Y617	Phosphoserine aminotransferase (EC 2.6.1.52) (Phosphohydroxythreonine aminotransferase) (PSAT)	370	PSAT1	7	1	6	19.7	2.7	16.8
525	-0.61	0.00	0.59	P68366	Tubulin alpha-4A chain (Alpha-tubulin 1) (Testis-specific alpha-tubulin) (Tubulin H2-alpha) (Tubulin alpha-1 chain)	448	TUBA4A	8	8	11	25.4	26.6	37.9
526	-0.61	0.47	0.87	P53396	ATP-citrate synthase (EC 2.3.3.8) (ATP-citrate (pro-S-)-lyase) (ACL) (Citrate cleavage enzyme)	1101	ACLY	9	12	10	11.2	14.8	14.2
527	-0.60	-0.50	-0.02	P60981	Destrin (Actin-depolymerizing factor) (ADF)	165	DSTN	6	6	3	34.5	41.9	14.9
528	-0.60	0.03	0.71	O60218	Aldo-keto reductase family 1 member B10 (EC 1.1.1.-) (ARL-1) (Aldose reductase-like) (Aldose reductase-related protein) (ARP) (hARP) (Small intestine reductase) (SI reductase)	316	AKR1B10	15	16	13	50.9	64.6	49.1
529	-0.59	0.29	0.84	A0A024QZP7	Cell division cycle 2, G1 to S and G2 to M, isoform CRA_a (Cyclin-dependent kinase 1)	297	CDC2	1	2	3	4	7.7	11.8
530	-0.59	0.02	-0.14	O75223	Gamma-glutamylcyclotransferase (EC 2.3.2.4) (Cytochrome c-releasing factor 21)	188	GGCT	2	3	1	14.4	17	5.3
531	-0.59	2.57	1.07	M0QXS5	Heterogeneous nuclear ribonucleoprotein L (Fragment)	530	HNRNPL	2	2	2	4.9	4	9.6

532	-0.59	-0.53	0.12	P43490	Nicotinamide phosphoribosyltransferase (NAmPRTase) (Nampt) (EC 2.4.2.12) (Pre-B-cell colony-enhancing factor 1) (Pre-B cell-enhancing factor) (Visfatin)	491	NAMPT	10	6	10	28.9	16.9	25.1
533	-0.59	0.60	0.72	Q9Y266	Nuclear migration protein nudC (Nuclear distribution protein C homolog)	331	NUDC	4	2	2	13.9	6.9	7.9
534	-0.58	0.88	1.99	Q08211	ATP-dependent RNA helicase A (RHA) (EC 3.6.4.13) (DEAH box protein 9) (Leukophysin) (LKP) (Nuclear DNA helicase II) (NDH II)	1270	DHX9	5	3	7	4.4	2.8	7.2
535	-0.58	1.13	1.17	P05556	Integrin beta-1 (Fibronectin receptor subunit beta) (Glycoprotein IIa) (GPIIA) (VLA-4 subunit beta) (CD antigen CD29)	798	ITGB1	6	9	6	11	14.2	9.5
536	-0.58	1.25	0.88	P30048	Thioredoxin-dependent peroxide reductase, mitochondrial (EC 1.11.1.15) (Antioxidant protein 1) (AOP-1) (HBC189) (Peroxiredoxin III) (Prx-III) (Peroxiredoxin-3) (Protein MER5 homolog)	256	PRDX3	7	7	6	34	43.3	21
537	-0.58	0.00	0.49	P14735	Insulin-degrading enzyme (EC 3.4.24.56) (Abeta-degrading protease) (Insulin protease) (Insulinase) (Insulysin)	1019	IDE	3	0	3	3.5	0	3.5
538	-0.58	1.02	0.60	P48047	ATP synthase subunit O, mitochondrial (Oligomycin sensitivity conferral protein) (OSCP)	213	ATP5O	5	7	5	25.8	39	33.3
539	-0.58	0.03	0.36	B8ZZQ6	Prothymosin alpha	107	PTMA	1	1	1	13.1	13.1	13.1
540	-0.58	1.77	0.28	P09601	Heme oxygenase 1 (HO-1) (EC 1.14.99.3)	288	HMOX1	4	6	2	15.3	26	4.5

541	-0.58	0.01	1.10	P62906	60S ribosomal protein L10a (CSA-19) (Neural precursor cell expressed developmentally down-regulated protein 6) (NEDD-6)	217	RPL10A	9	5	8	36.9	23.5	36.9
542	-0.57	0.00	1.00	P04181	Ornithine aminotransferase, mitochondrial (EC 2.6.1.13) (Ornithine delta-aminotransferase) (Ornithine--oxo-acid aminotransferase) [Cleaved into: Ornithine aminotransferase, hepatic form; Ornithine aminotransferase, renal form]	439	OAT	3	0	3	11.6	0	11.6
543	-0.57	0.21	1.18	P52272	Heterogeneous nuclear ribonucleoprotein M (hnRNP M)	730	HNRNPM	3	1	5	6.2	2.3	11
544	-0.57	1.02	0.53	Q13162	Peroxiredoxin-4 (EC 1.11.1.15) (Antioxidant enzyme AOE372) (AOE37-2) (Peroxiredoxin IV) (Prx-IV) (Thioredoxin peroxidase AO372) (Thioredoxin-dependent peroxide reductase A0372)	271	PRDX4	5	7	4	23.6	35.4	15.9
545	-0.57	0.81	0.00	P02792	Ferritin light chain (Ferritin L subunit)	175	FTL	1	1	0	8.6	8.6	0
546	-0.57	0.76	0.69	P30101	Protein disulfide-isomerase A3 (EC 5.3.4.1) (58 kDa glucose-regulated protein) (58 kDa microsomal protein) (p58) (Disulfide isomerase ER-60) (Endoplasmic reticulum resident protein 57) (ER protein 57) (ERp57) (Endoplasmic reticulum resident protein 60) (ER protein 60) (ERp60)	505	PDIA3	10	9	10	22.8	18.4	26.7
547	-0.57	0.54	0.20	K7ERF1	Eukaryotic translation initiation factor 3 subunit K (eIF3k) (Eukaryotic translation initiation factor 3 subunit 12) (eIF-3 p25)	192	EIF3K	2	2	1	14.6	13	7.3

548	-0.57	0.25	0.86	Q02218	2-oxoglutarate dehydrogenase, mitochondrial (EC 1.2.4.2) (2-oxoglutarate dehydrogenase complex component E1) (OGDC-E1) (Alpha-ketoglutarate dehydrogenase)	1023	OGDH	2	2	2	2.1	2.5	2.1
549	-0.56	0.49	0.65	Q5VTE0	Putative elongation factor 1-alpha-like 3 (EF-1-alpha-like 3) (Eukaryotic elongation factor 1 A-like 3) (eEF1A-like 3) (Eukaryotic translation elongation factor 1 alpha-1 pseudogene 5)	462	EEF1A1P5	11	9	13	30.5	29.7	33.3
550	-0.56	-0.10	0.56	P27348	14-3-3 protein theta (14-3-3 protein T-cell) (14-3-3 protein tau) (Protein HS1)	245	YWHAQ	6	9	7	31.8	36.7	29
551	-0.56	1.28	0.97	P35998	26S protease regulatory subunit 7 (26S proteasome AAA-ATPase subunit RPT1) (Proteasome 26S subunit ATPase 2) (Protein MSS1)	433	PSMC2	4	2	4	11.3	6.9	12.5
552	-0.56	0.00	0.71	O43837	Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial (EC 1.1.1.41) (Isocitric dehydrogenase subunit beta) (NAD(+)-specific ICDH subunit beta)	385	IDH3B	3	0	3	9.9	0	9.9
553	-0.56	-0.04	0.23	P31689	DnaJ homolog subfamily A member 1 (DnaJ protein homolog 2) (HSDJ) (Heat shock 40 kDa protein 4) (Heat shock protein J2) (HSJ-2) (Human DnaJ protein 2) (hDj-2)	397	DNAJA1	3	1	3	10	3.9	10
554	-0.56	-0.29	0.97	Q9UBQ7	Glyoxylate reductase/hydroxypyruvate reductase (EC 1.1.1.79) (EC 1.1.1.81)	328	GRHPR	3	1	5	18	3	24.1
555	-0.56	1.59	0.86	P61604	10 kDa heat shock protein, mitochondrial (Hsp10) (10 kDa chaperonin) (Chaperonin 10) (CPN10) (Early-pregnancy factor) (EPF)	102	HSPE1	1	7	4	13.7	57.8	35.3

556	-0.55	1.44	1.14	E9PKG1	Protein arginine N-methyltransferase 1	325	PRMT1	1	2	2	3.7	8.3	8.3
557	-0.55	0.15	0.52	P26038	Moesin (Membrane-organizing extension spike protein)	577	MSN	10	5	9	15.3	8.7	13.5
558	-0.55	0.00	1.09	Q6PI48	Aspartate--tRNA ligase, mitochondrial (EC 6.1.1.12) (Aspartyl-tRNA synthetase) (AspRS)	645	DARS2	1	0	1	1.9	0	1.1
559	-0.55	0.43	0.52	P23284	Peptidyl-prolyl cis-trans isomerase B (PPIase B) (EC 5.2.1.8) (CYP-S1) (Cyclophilin B) (Rotamase B) (S-cyclophilin) (SCYLP)	216	PPIB	6	10	6	21.3	48.1	22.2
560	-0.55	0.91	0.93	O14880	Microsomal glutathione S-transferase 3 (Microsomal GST-3) (EC 2.5.1.18) (Microsomal GST-III)	152	MGST3	1	1	1	9.2	9.2	9.9
561	-0.54	1.63	0.88	E9PPQ5	Cysteine and histidine-rich domain-containing protein 1	184	CHORDC1	2	1	3	12.5	7.6	25
562	-0.54	0.00	2.38	J3KQV6	COP9 signalosome complex subunit 7b	54	COPS7B	1	0	1	35.2	0	35.2
563	-0.54	-0.25	-0.11	P13693	Translationally-controlled tumor protein (TCTP) (Fortilin) (Histamine-releasing factor) (HRF) (p23)	172	TPT1	4	4	2	30.2	30.2	15.7
564	-0.54	0.00	0.97	O00116	Alkyldihydroxyacetonephosphate synthase, peroxisomal (Alkyl-DHAP synthase) (EC 2.5.1.26) (Aging-associated gene 5 protein) (Alkylglycerone-phosphate synthase)	658	AGPS	2	0	3	4	0	6.5
565	-0.54	0.81	0.49	Q05193	Dynamin-1 (EC 3.6.5.5)	864	DNM1	2	1	2	2.1	0.8	2.5

566	-0.54	0.32	0.54	Q06323	Proteasome activator complex subunit 1 (11S regulator complex subunit alpha) (REG-alpha) (Activator of multicatalytic protease subunit 1) (Interferon gamma up-regulated I-5111 protein) (IGUP I-5111) (Proteasome activator 28 subunit alpha) (PA28a) (PA28alpha)	249	PSME1	7	6	9	32.5	24.5	36.5
567	-0.54	0.00	1.10	Q9H814	Phosphorylated adapter RNA export protein (RNA U small nuclear RNA export adapter protein)	394	PHAX	1	0	1	2.8	0	2.8
568	-0.53	-0.16	0.44	Q9Y237	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 (EC 5.2.1.8) (Parvulin-14) (Par14) (hPar14) (Parvulin-17) (Par17) (hPar17) (Peptidyl-prolyl cis-trans isomerase Pin4) (PPIase Pin4) (Peptidyl-prolyl cis/trans isomerase EPVH) (hEPVH) (Rotamase Pin4)	131	PIN4	1	1	2	9.2	9.2	17.6
569	-0.53	0.18	0.64	C9J2Q4	Septin-2 (Fragment)	184	sept2	2	2	2	10.9	10.9	10.9
570	-0.53	1.87	1.19	Q07021	Complement component 1 Q subcomponent-binding protein, mitochondrial (ASF/SF2-associated protein p32) (Glycoprotein gC1qBP) (C1qBP) (Hyaluronan-binding protein 1) (Mitochondrial matrix protein p32) (gC1q-R protein) (p33)	282	C1QBP	1	2	3	3.9	11	24.1
571	-0.53	0.22	1.19	P55884	Eukaryotic translation initiation factor 3 subunit B (eIF3b) (Eukaryotic translation initiation factor 3 subunit 9) (Prt1 homolog) (hPrt1) (eIF-3-eta) (eIF3 p110) (eIF3 p116)	814	EIF3B	3	3	3	4.4	4.2	4.4

572	-0.53	1.54	1.06	P52597	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein F, N-terminally processed]	415	HNRNPF	2	1	2	6.5	4.1	7.2
573	-0.53	0.00	0.00	A0A087X1D8	Farnesyl pyrophosphate synthase (Fragment)	174	FDPS	2	0	0	17.8	0	0
574	-0.53	0.02	0.05	O00410	Importin-5 (Imp5) (Importin subunit beta-3) (Karyopherin beta-3) (Ran-binding protein 5) (RanBP5)	1097	IPO5	6	5	4	8.4	6.8	5.8
575	-0.53	1.13	0.45	Q92973	Transportin-1 (Importin beta-2) (Karyopherin beta-2) (M9 region interaction protein) (MIP)	898	TNPO1	6	3	6	8	3.6	6.9
576	-0.52	0.95	0.42	P38646	Stress-70 protein, mitochondrial (75 kDa glucose-regulated protein) (GRP-75) (Heat shock 70 kDa protein 9) (Mortalin) (MOT) (Peptide-binding protein 74) (PBP74)	679	HSPA9	11	6	14	22.7	12.4	27.4
577	-0.52	0.22	0.71	D6RAN4	60S ribosomal protein L9 (Fragment)	181	RPL9	4	3	6	19.9	23.8	45.3
578	-0.52	0.00	0.74	P25205	DNA replication licensing factor MCM3 (EC 3.6.4.12) (DNA polymerase alpha holoenzyme-associated protein P1) (P1-MCM3) (RLF subunit beta) (p102)	808	MCM3	3	0	3	4.5	0	4.2
579	-0.52	0.00	0.47	Q9Y3E7	Charged multivesicular body protein 3 (Chromatin-modifying protein 3) (Neuroendocrine differentiation factor) (Vacuolar protein sorting-associated protein 24) (hVps24)	222	CHMP3	1	0	1	7.7	0	7.7

580	-0.52	0.36	0.58	O00299	Chloride intracellular channel protein 1 (Chloride channel ABP) (Nuclear chloride ion channel 27) (NCC27) (Regulatory nuclear chloride ion channel protein) (hRNCC)	241	CLIC1	3	6	5	13.7	28.6	26.1
581	-0.52	1.15	1.73	P27824	Calnexin (IP90) (Major histocompatibility complex class I antigen-binding protein p88) (p90)	592	CANX	4	5	4	9.6	11.8	8.3
582	-0.52	1.68	1.81	P26599	Polypyrimidine tract-binding protein 1 (PTB) (57 kDa RNA-binding protein PPTB-1) (Heterogeneous nuclear ribonucleoprotein I) (hnRNP I)	531	PTBP1	3	2	4	6.2	6.6	11.9
583	-0.52	0.00	0.69	H7C235	Sphingomyelin phosphodiesterase 4 (Fragment)	211	SMPD4	1	0	1	4.3	0	4.3
584	-0.52	0.00	0.02	C9J363	Programmed cell death 10, isoform CRA_b (Programmed cell death protein 10)	149	PDCD10	1	0	1	8.7	0	8.7
585	-0.51	0.00	0.45	M0QX85	Nitric oxide synthase-interacting protein (Fragment)	96	NOSIP	1	0	1	11.5	0	11.5
586	-0.51	0.33	0.94	Q9Y6C9	Mitochondrial carrier homolog 2 (Met-induced mitochondrial protein)	303	MTCH2	5	4	4	27.1	21.1	18.5
587	-0.51	1.05	0.42	Q9Y6N5	Sulfide:quinone oxidoreductase, mitochondrial (SQOR) (EC 1.8.5.-)	450	SQRDL	4	3	3	9.1	7.3	7.1
588	-0.51	0.69	0.37	Q01082	Spectrin beta chain, non-erythrocytic 1 (Beta-II spectrin) (Fodrin beta chain) (Spectrin, non-erythroid beta chain 1)	2364	SPTBN1	11	17	10	6.6	9.8	6.2
589	-0.51	-0.26	1.14	C9JXB8	60S ribosomal protein L24	121	RPL24	3	4	2	25.6	32.2	17.4
590	-0.50	0.53	0.64	P17987	T-complex protein 1 subunit alpha (TCP-1-alpha) (CCT-alpha)	556	TCP1	5	3	6	11.5	5.8	13.1

591	-0.50	0.98	0.99	P07602	Prosaposin (Proactivator polypeptide) [Cleaved into: Saposin-A (Protein A); Saposin-B-Val; Saposin-B (Cerebroside sulfate activator) (CSAct) (Dispersin) (Sphingolipid activator protein 1) (SAP-1) (Sulfatide/GM1 activator); Saposin-C (A1 activator) (Co-beta-glucosidase) (Glucosylceramidase activator) (Sphingolipid activator protein 2) (SAP-2); Saposin-D (Component C) (Protein C)]	524	PSAP	1	6	2	2.5	12.6	5.3
592	-0.50	0.27	0.31	Q92688	Acidic leucine-rich nuclear phosphoprotein 32 family member B (Acidic protein rich in leucines) (Putative HLA-DR-associated protein I-2) (PHAPI2) (Silver-stainable protein SSP29)	251	ANP32B	4	5	3	22.6	22.6	16.4
593	-0.50	0.09	-0.05	P16435	NADPH--cytochrome P450 reductase (CPR) (P450R) (EC 1.6.2.4)	677	POR	4	1	2	8.4	1.3	3.4
594	-0.50	0.15	0.76	Q86VP6	Cullin-associated NEDD8-dissociated protein 1 (Cullin-associated and neddylation-dissociated protein 1) (TBP-interacting protein of 120 kDa A) (TBP-interacting protein 120A) (p120 CAND1)	1230	CAND1	9	10	13	9.6	11.1	14.2
595	-0.50	0.00	0.94	G5EA06	28S ribosomal protein S27, mitochondrial (Mitochondrial ribosomal protein S27, isoform CRA_b)	358	MRPS27	2	0	1	7.5	0	3.4
596	-0.50	0.00	0.08	J3KTI3	NAD kinase (Fragment)	74	NADK	1	0	1	13.5	0	13.5
597	-0.50	0.21	1.49	O00151	PDZ and LIM domain protein 1 (C-terminal LIM domain protein 1) (Elfin) (LIM domain protein CLP-36)	329	PDLIM1	2	1	3	8.8	3	17

598	-0.50	0.70	0.47	P62877	E3 ubiquitin-protein ligase RBX1 (EC 6.3.2.-) (Protein ZYP) (RING finger protein 75) (RING-box protein 1) (Rbx1) (Regulator of cullins 1) [Cleaved into: E3 ubiquitin-protein ligase RBX1, N-terminally processed]	108	RBX1	1	1	1	17.6	16.7	16.7
599	-0.49	-0.27	0.62	I3L3P7	40S ribosomal protein S15a	100	RPS15A	4	2	3	26	15	19
600	-0.49	-0.26	0.45	P00338	L-lactate dehydrogenase A chain (LDH-A) (EC 1.1.1.27) (Cell proliferation-inducing gene 19 protein) (LDH muscle subunit) (LDH-M) (Renal carcinoma antigen NY-REN-59)	332	LDHA	8	15	8	21.1	46.4	20.2
601	-0.49	0.00	0.50	P30419	Glycylpeptide N-tetradecanoyltransferase 1 (EC 2.3.1.97) (Myristoyl-CoA:protein N-myristoyltransferase 1) (NMT 1) (Type I N-myristoyltransferase) (Peptide N-myristoyltransferase 1)	496	NMT1	2	0	2	6.5	0	6.5
602	-0.49	0.88	0.64	Q96AG4	Leucine-rich repeat-containing protein 59 (Ribosome-binding protein p34) (p34)	307	LRRC59	4	5	6	17.6	21.5	25.1
603	-0.49	0.01	0.43	M0QZ52	Calmodulin (Calmodulin 3 (Phosphorylase kinase, delta), isoform CRA_d)	83	CALM3	4	2	3	62.7	20.5	62.7
604	-0.49	0.00	-0.63	P51452	Dual specificity protein phosphatase 3 (EC 3.1.3.16) (EC 3.1.3.48) (Dual specificity protein phosphatase VHR) (Vaccinia H1-related phosphatase) (VHR)	185	DUSP3	2	1	1	14.1	7.6	6.5
605	-0.48	0.00	0.00	Q96F63	Coiled-coil domain-containing protein 97	343	CCDC97	1	0	0	3.2	0	0
606	-0.48	0.35	0.12	P07737	Profilin-1 (Epididymis tissue protein Li 184a) (Profilin I)	140	PFN1	8	7	6	48.6	61.4	37.1

607	-0.48	-0.07	0.64	P49207	60S ribosomal protein L34	117	RPL34	1	2	1	6.8	14.5	6.8
608	-0.48	-0.71	0.00	Q00535	Cyclin-dependent-like kinase 5 (EC 2.7.11.1) (Cell division protein kinase 5) (Serine/threonine-protein kinase PSSALRE) (Tau protein kinase II catalytic subunit) (TPKII catalytic subunit)	292	CDK5	1	1	0	3.1	3.1	0
609	-0.47	0.44	0.98	P49721	Proteasome subunit beta type-2 (EC 3.4.25.1) (Macropain subunit C7-I) (Multicatalytic endopeptidase complex subunit C7-I) (Proteasome component C7-I)	201	PSMB2	2	6	5	14.4	28.4	28.9
610	-0.47	-0.17	0.28	P43487	Ran-specific GTPase-activating protein (Ran-binding protein 1) (RanBP1)	201	RANBP1	1	2	1	5.5	10	5.5
611	-0.47	0.36	0.49	P40227	T-complex protein 1 subunit zeta (TCP-1-zeta) (Acute morphine dependence-related protein 2) (CCT-zeta-1) (HTR3) (Tcp20)	531	CCT6A	9	3	8	24.5	10	24.1
612	-0.47	0.21	0.75	P49914	5-formyltetrahydrofolate cyclo-ligase (EC 6.3.3.2) (5,10-methenyl-tetrahydrofolate synthetase) (MTHFS) (Methenyl-THF synthetase)	203	MTHFS	1	2	2	4.4	10.3	10.3
613	-0.47	0.72	1.08	Q15366	Poly(rC)-binding protein 2 (Alpha-CP2) (Heterogeneous nuclear ribonucleoprotein E2) (hnRNP E2)	365	PCBP2	1	5	3	3.9	18.8	13.6
614	-0.47	0.73	0.61	Q14152	Eukaryotic translation initiation factor 3 subunit A (eIF3a) (Eukaryotic translation initiation factor 3 subunit 10) (eIF-3-theta) (eIF3 p167) (eIF3 p180) (eIF3 p185)	1382	EIF3A	8	8	8	6	6.7	6.4
615	-0.46	0.00	0.75	E7ESP4	Integrin alpha-2	942	ITGA2	1	0	1	1.4	0	1.1

616	-0.46	0.05	0.36	P22234	Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole-succinocarboxamide synthase (EC 6.3.2.6) (SAICAR synthetase); Phosphoribosylaminoimidazole carboxylase (EC 4.1.1.21) (AIR carboxylase) (AIRC)]	425	PAICS	6	6	5	15.5	15.5	12.5
617	-0.46	0.11	0.36	P12004	Proliferating cell nuclear antigen (PCNA) (Cyclin)	261	PCNA	9	5	8	51.3	25.7	36
618	-0.46	-0.26	0.73	P22392	Nucleoside diphosphate kinase B (NDK B) (NDP kinase B) (EC 2.7.4.6) (C-myc purine-binding transcription factor PUF) (Histidine protein kinase NDKB) (EC 2.7.13.3) (nm23-H2)	152	NME2	5	10	6	28.8	55.4	34.5
619	-0.46	-0.35	1.44	O15067	Phosphoribosylformylglycinamidine synthase (FGAM synthase) (FGAMS) (EC 6.3.5.3) (Formylglycinamide ribonucleotide amidotransferase) (FGAR amidotransferase) (FGAR-AT) (Formylglycinamide ribotide amidotransferase)	1338	PFAS	2	1	3	2.2	0.7	3.2
620	-0.46	1.26	0.00	Q5T4L4	40S ribosomal protein S27	66	RPS27	1	2	0	19.7	36.4	0
621	-0.46	0.47	0.72	Q01813	ATP-dependent 6-phosphofructokinase, platelet type (ATP-PFK) (PFK-P) (EC 2.7.1.11) (6-phosphofructokinase type C) (Phosphofructo-1-kinase isozyme C) (PFK-C) (Phosphohexokinase)	784	PFKP	4	4	4	5.5	4.3	5.5
622	-0.46	-0.69	0.06	P10599	Thioredoxin (Trx) (ATL-derived factor) (ADF) (Surface-associated sulphydryl protein) (SASP)	105	TXN	5	6	3	42.9	51.4	32.4

623	-0.46	0.87	0.57	P32322	Pyrroline-5-carboxylate reductase 1, mitochondrial (P5C reductase 1) (P5CR 1) (EC 1.5.1.2)	319	PYCR1	1	1	2	3.4	3.4	7.2
624	-0.45	0.00	0.00	H0YLC0	Tumor necrosis factor alpha-induced protein 2 (Fragment)	347	TNFAIP2	1	0	0	3.2	0	0
625	-0.45	-0.32	0.38	Q99598	Translin-associated protein X (Translin-associated factor X)	290	TSNAX	1	1	2	3.4	6.9	10.3
626	-0.45	0.92	0.28	F5H7F6	Microsomal glutathione S-transferase 1 (Fragment)	77	MGST1	1	1	1	18.2	16.9	16.9
627	-0.45	-0.43	0.03	D6RFZ2	TBC1 domain family member 8B	419	TBC1D8B	1	1	1	2.6	2.6	2.6
628	-0.45	0.68	1.74	P49327	Fatty acid synthase (EC 2.3.1.85) [Includes: [Acyl-carrier-protein] S-acetyltransferase (EC 2.3.1.38); [Acyl-carrier-protein] S-malonyltransferase (EC 2.3.1.39); 3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41); 3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100); 3-hydroxyacyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.59); Enoyl-[acyl-carrier-protein] reductase (EC 1.3.1.39); Oleoyl-[acyl-carrier-protein] hydrolase (EC 3.1.2.14)]	2511	FASN	10	17	20	5.5	10.4	11.6
629	-0.45	0.19	0.18	O95373	Importin-7 (Imp7) (Ran-binding protein 7) (RanBP7)	1038	IPO7	6	5	5	6.9	6.3	6.4
630	-0.45	0.00	-0.56	D6RA82	Annexin	284	ANXA3	3	0	3	14.4	0	12.3
631	-0.45	0.48	0.71	K9J957	Proteasome activator complex subunit 3 (REG gamma-3 variant)	231	PSME3	4	3	4	20.8	15.2	15.6

632	-0.45	1.04	0.52	Q8NBS9	Thioredoxin domain-containing protein 5 (Endoplasmic reticulum resident protein 46) (ER protein 46) (ERp46) (Thioredoxin-like protein p46)	432	TXNDC5	3	2	4	9	5.9	11.7
633	-0.44	0.00	1.36	Q9Y224	UPF0568 protein C14orf166 (CLE7 homolog) (CLE)	244	C14orf166	2	0	3	10.2	0	16.8
634	-0.44	-0.30	0.36	P49588	Alanine--tRNA ligase, cytoplasmic (EC 6.1.1.7) (Alanyl-tRNA synthetase) (AlaRS) (Renal carcinoma antigen NY-REN-42)	968	AARS	7	4	7	8	4.3	8
635	-0.44	0.85	0.75	Q12931	Heat shock protein 75 kDa, mitochondrial (HSP 75) (TNFR-associated protein 1) (Tumor necrosis factor type 1 receptor-associated protein) (TRAP-1)	704	TRAP1	4	3	3	9.4	6.1	5.7
636	-0.44	1.14	0.72	P13667	Protein disulfide-isomerase A4 (EC 5.3.4.1) (Endoplasmic reticulum resident protein 70) (ER protein 70) (ERp70) (Endoplasmic reticulum resident protein 72) (ER protein 72) (ERp-72) (ERp72)	645	PDIA4	7	7	11	14.9	13.5	23.4
637	-0.44	-0.52	0.56	P52209	6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	483	PGD	9	10	13	25.5	23.6	33.6
638	-0.44	-0.02	0.25	B8ZZU8	Transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B), isoform CRA_b (Transcription elongation factor B polypeptide 2)	113	TCEB2	2	2	2	16.8	17.7	16.8

639	-0.44	0.00	0.43	Q2TAY7	WD40 repeat-containing protein SMU1 (Smu-1 suppressor of mec-8 and unc-52 protein homolog) [Cleaved into: WD40 repeat-containing protein SMU1, N-terminally processed]	513	SMU1	1	0	1	1.9	0	1.9
640	-0.44	0.00	0.05	Q7L2H7	Eukaryotic translation initiation factor 3 subunit M (eIF3m) (Fetal lung protein B5) (hFL-B5) (PCI domain-containing protein 1)	374	EIF3M	3	0	3	12	0	9.1
641	-0.44	-0.72	0.00	Q9BRG1	Vacuolar protein-sorting-associated protein 25 (hVps25) (Dermal papilla-derived protein 9) (ELL-associated protein of 20 kDa) (ESCRT-II complex subunit VPS25)	176	VPS25	1	2	0	5.7	10.2	0
642	-0.43	0.35	0.39	Q14974	Importin subunit beta-1 (Importin-90) (Karyopherin subunit beta-1) (Nuclear factor p97) (Pore targeting complex 97 kDa subunit) (PTAC97)	876	KPNB1	12	6	9	20	9.2	13.4
643	-0.43	0.25	0.50	P29401	Transketolase (TK) (EC 2.2.1.1)	623	TKT	20	13	14	40.6	31	23.1
644	-0.43	-0.05	0.39	I3L397	Eukaryotic translation initiation factor 5A (eIF-5A) (Fragment)	146	EIF5A	7	5	8	34.9	37	37.7
645	-0.43	-0.26	0.68	Q04760	Lactoylglutathione lyase (EC 4.4.1.5) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (Methylglyoxalase) (S-D-lactoylglutathione methylglyoxal lyase)	184	GLO1	3	4	4	19.5	26	29
646	-0.42	1.22	-0.22	H3BN98	Uncharacterized protein (Fragment)	237		3	2	2	11	8	8
647	-0.42	0.00	0.16	P46109	Crk-like protein	303	CRKL	1	0	1	4	0	4
648	-0.42	0.00	0.29	A6NDG6	Phosphoglycolate phosphatase (PGP) (PGPase) (EC 3.1.3.18) (EC 3.1.3.48)	321	PGP	2	0	1	9	0	4.7

649	-0.42	0.42	1.36	O75643	U5 small nuclear ribonucleoprotein 200 kDa helicase (EC 3.6.4.13) (Activating signal cointegrator 1 complex subunit 3-like 1) (BRR2 homolog) (U5 snRNP-specific 200 kDa protein) (U5-200KD)	2136	SNRNP200	1	3	3	0.5	1.7	1.9
650	-0.42	0.49	0.14	F8W914	Reticulon	345	RTN4	5	5	4	18.8	18.8	15.1
651	-0.42	0.00	0.00	H7C131	3-ketoacyl-CoA thiolase, peroxisomal (Fragment)	290	ACAA1	1	0	0	4.5	0	0
652	-0.42	-0.27	0.40	P00492	Hypoxanthine-guanine phosphoribosyltransferase (HGPRT) (HGPRTase) (EC 2.4.2.8)	218	HPRT1	5	8	6	25.7	43.1	32.1
653	-0.42	1.42	1.12	P55084	Trifunctional enzyme subunit beta, mitochondrial (TP-beta) [Includes: 3-ketoacyl-CoA thiolase (EC 2.3.1.16) (Acetyl-CoA acyltransferase) (Beta-ketothiolase)]	474	HADHB	2	1	5	4.2	1.7	12
654	-0.42	-0.07	0.54	P23526	Adenosylhomocysteinase (AdoHcyase) (EC 3.3.1.1) (S-adenosyl-L-homocysteine hydrolase)	432	AHCY	4	4	6	12	12	19.7
655	-0.42	0.56	0.61	H0YAM7	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment)	247	GNB2L1	3	7	3	25.5	43.7	25.5
656	-0.41	0.50	0.89	P09651	Heterogeneous nuclear ribonucleoprotein A1 (hnRNP A1) (Helix-destabilizing protein) (Single-strand RNA-binding protein) (hnRNP core protein A1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein A1, N-terminally processed]	372	HNRNPA1	2	6	3	14.2	29.6	13.9
657	-0.41	0.38	0.51	P47813	Eukaryotic translation initiation factor 1A, X-chromosomal (eIF-1A X isoform) (Eukaryotic translation initiation factor 4C) (eIF-4C)	144	EIF1AX	3	4	5	26.4	25	33.3

658	-0.41	0.00	0.52	Q92600	Cell differentiation protein RCD1 homolog (Rcd-1) (CCR4-NOT transcription complex subunit 9)	299	RQCD1	1	1	2	3.5	4.7	8.1
659	-0.41	-0.20	0.29	H0YKT8	Proteasome subunit beta type (EC 3.4.25.1) (Fragment)	181	PSMA4	4	3	3	30.9	14.9	18.8
660	-0.40	-0.48	0.19	P55327	Tumor protein D52 (Protein N8)	224	TPD52	2	3	2	15.8	20.7	15.8
661	-0.40	-0.07	0.59	P37837	Transaldolase (EC 2.2.1.2)	337	TALDO1	6	8	5	16.9	26.1	11.6
662	-0.40	0.76	1.25	O15355	Protein phosphatase 1G (EC 3.1.3.16) (Protein phosphatase 1C) (Protein phosphatase 2C isoform gamma) (PP2C-gamma) (Protein phosphatase magnesium-dependent 1 gamma)	546	PPM1G	1	1	3	2.2	2.2	6.6
663	-0.40	0.37	1.67	P18124	60S ribosomal protein L7	248	RPL7	3	4	4	15.7	19.8	16.5
664	-0.40	-0.36	-0.81	Q13501	Sequestosome-1 (EBI3-associated protein of 60 kDa) (EBIAP) (p60) (Phosphotyrosine-independent ligand for the Lck SH2 domain of 62 kDa) (Ubiquitin-binding protein p62)	440	SQSTM1	2	1	1	4.8	1.4	3.4
665	-0.39	1.11	0.00	G3V5X4	Nesprin-2	6818	SYNE2	1	3	1	0.1	0.4	0.1
666	-0.39	0.00	0.51	Q9Y305	Acyl-coenzyme A thioesterase 9, mitochondrial (Acyl-CoA thioesterase 9) (EC 3.1.2.-) (Acyl-CoA thioester hydrolase 9)	439	ACOT9	2	0	3	5.8	0	7.1
667	-0.39	0.62	0.45	E9PJK1	Tetraspanin	165	CD81	3	2	3	35.8	23.6	35.8
668	-0.39	0.14	0.60	O15144	Actin-related protein 2/3 complex subunit 2 (Arp2/3 complex 34 kDa subunit) (p34-ARC)	300	ARPC2	3	3	4	9.3	8.7	12.3
669	-0.38	0.94	1.09	Q9NSE4	Isoleucine--tRNA ligase, mitochondrial (EC 6.1.1.5) (Isoleucyl-tRNA synthetase) (IleRS)	1012	IARS2	6	6	10	6.9	6.9	12.2
670	-0.38	1.06	1.14	P31327	Carbamoyl-phosphate synthase [ammonia], mitochondrial (EC 6.3.4.16) (Carbamoyl-phosphate synthetase I) (CPSase I)	1500	CPS1	2	5	4	1.7	4.1	3.3

671	-0.38	1.13	0.65	O95881	Thioredoxin domain-containing protein 12 (EC 1.8.4.2) (Endoplasmic reticulum resident protein 18) (ER protein 18) (ERp18) (Endoplasmic reticulum resident protein 19) (ER protein 19) (ERp19) (Thioredoxin-like protein p19) (hTLP19)	172	TXNDC12	2	3	3	13.4	22.1	22.1
672	-0.38	-0.29	0.62	H0YN26	Acidic leucine-rich nuclear phosphoprotein 32 family member A	177	ANP32A	3	3	3	18.6	18.6	11.9
673	-0.38	-0.43	0.29	P15531	Nucleoside diphosphate kinase A (NDK A) (NDP kinase A) (EC 2.7.4.6) (Granzyme A-activated DNase) (GAAD) (Metastasis inhibition factor nm23) (NM23-H1) (Tumor metastatic process-associated protein)	152	NME1	5	6	5	36.8	42.8	36.8
674	-0.38	0.07	0.31	A0A087WZB3	Proline and serine-rich protein 3	324	PROSER3	1	1	1	2.8	2.8	2.8
675	-0.38	2.00	1.11	Q07955	Serine/arginine-rich splicing factor 1 (Alternative-splicing factor 1) (ASF-1) (Splicing factor, arginine/serine-rich 1) (pre-mRNA-splicing factor SF2, P33 subunit)	248	SRSF1	1	1	2	4	5.6	8.5
676	-0.37	0.09	0.08	P29692	Elongation factor 1-delta (EF-1-delta) (Antigen NY-CO-4)	281	EEF1D	4	6	3	20.3	30.2	11.7
677	-0.37	0.33	0.91	I3L1L3	Myb-binding protein 1A (Fragment)	1252	MYBBP1A	3	4	4	2.7	3.7	3.7
678	-0.37	-0.21	-0.12	Q96A49	Synapse-associated protein 1	352	SYAP1	1	1	1	4.3	4.3	4.3
679	-0.37	0.20	0.63	P11216	Glycogen phosphorylase, brain form (EC 2.4.1.1)	843	PYGB	3	3	6	3.1	3.1	8.4
680	-0.37	0.25	1.33	P55060	Exportin-2 (Exp2) (Cellular apoptosis susceptibility protein) (Chromosome segregation 1-like protein) (Importin-alpha re-exporter)	971	CSE1L	10	7	9	11.5	11.1	11.3

681	-0.37	-0.75	0.56	D6RE83	Ubiquitin carboxyl-terminal hydrolase (EC 3.4.19.12)	207	UCHL1	5	6	6	34.3	36.7	41.5
682	-0.37	-0.45	0.98	F8WBS5	60S ribosomal protein L35a	55	RPL35A	1	1	1	16.4	16.4	16.4
683	-0.36	-0.06	0.35	Q9BTT0	Acidic leucine-rich nuclear phosphoprotein 32 family member E (LANP-like protein) (LANP-L)	268	ANP32E	2	4	2	15	20.9	15
684	-0.36	1.07	0.60	Q9GZT3	SRA stem-loop-interacting RNA-binding protein, mitochondrial	109	SLIRP	1	4	2	13.1	48.6	24.3
685	-0.36	1.65	0.69	P35232	Prohibitin	272	PHB	3	7	2	9.9	37.9	6.6
686	-0.36	0.63	0.47	Q13813	Spectrin alpha chain, non-erythrocytic 1 (Alpha-II spectrin) (Fodrin alpha chain) (Spectrin, non-erythroid alpha subunit)	2472	SPTAN1	21	29	21	13.5	15.7	12.7
687	-0.36	-0.25	0.37	Q15185	Prostaglandin E synthase 3 (EC 5.3.99.3) (Cytosolic prostaglandin E2 synthase) (cPGES) (Hsp90 co-chaperone) (Progesterone receptor complex p23) (Telomerase-binding protein p23)	160	PTGES3	3	4	4	24.6	36.9	30.8
688	-0.36	0.51	0.54	Q9Y265	RuvB-like 1 (EC 3.6.4.12) (49 kDa TATA box-binding protein-interacting protein) (49 kDa TBP-interacting protein) (54 kDa erythrocyte cytosolic protein) (ECP-54) (INO80 complex subunit H) (Nuclear matrix protein 238) (NMP 238) (Pontin 52) (TIP49a) (TIP60-associated protein 54-alpha) (TAP54-alpha)	456	RUVBL1	6	5	8	17.3	16	23
689	-0.36	0.00	0.21	Q15526	Surfeit locus protein 1	300	SURF1	1	0	1	5.6	0	5.6
690	-0.36	1.91	0.00	Q6P1J9	Parafibromin (Cell division cycle protein 73 homolog) (Hyperparathyroidism 2 protein)	531	CDC73	2	1	0	5.6	3.8	0

691	-0.36	0.21	0.20	P25786	Proteasome subunit alpha type-1 (EC 3.4.25.1) (30 kDa prosomal protein) (PROS-30) (Macropain subunit C2) (Multicatalytic endopeptidase complex subunit C2) (Proteasome component C2) (Proteasome nu chain)	263	PSMA1	4	6	5	17.9	26.2	20.2
692	-0.35	0.15	0.66	O94925	Glutaminase kidney isoform, mitochondrial (GLS) (EC 3.5.1.2) (K-glutaminase) (L-glutamine amidohydrolase)	669	GLS	3	1	4	6.2	1.7	10.5
693	-0.35	-0.36	0.48	B1AK87	Capping protein (Actin filament) muscle Z-line, beta, isoform CRA_a (F-actin-capping protein subunit beta)	260	CAPZB	1	1	1	3.8	3.8	3.8
694	-0.35	-0.54	-0.12	C9JD53	Isopentenyl-diphosphate Delta-isomerase 1 (Fragment)	120	IDI1	1	1	1	10	10	10
695	-0.35	0.71	0.43	P50454	Serpin H1 (47 kDa heat shock protein) (Arsenic-transactivated protein 3) (AsTP3) (Cell proliferation-inducing gene 14 protein) (Collagen-binding protein) (Colligin) (Rheumatoid arthritis-related antigen RA-A47)	418	SERPINH1	4	7	4	12.7	27.3	12.2
696	-0.35	0.50	1.34	P52758	Ribonuclease UK114 (EC 3.1.-.-) (14.5 kDa translational inhibitor protein) (p14.5) (Heat-responsive protein 12) (UK114 antigen homolog)	137	HRSP12	1	3	1	7.3	27	7.3
697	-0.35	0.23	0.54	P49755	Transmembrane emp24 domain-containing protein 10 (21 kDa transmembrane-trafficking protein) (S31III125) (S31I125) (Tmp-21-I) (Transmembrane protein Tmp21) (p23) (p24 family protein delta-1) (p24delta1) (p24delta)	219	TMED10	3	4	3	17.8	21	17.8

698	-0.35	-0.11	0.63	P26447	Protein S100-A4 (Calvasculin) (Metastasin) (Placental calcium-binding protein) (Protein Mts1) (S100 calcium-binding protein A4)	101	S100A4	2	5	2	18.8	33.7	18.8
699	-0.35	0.00	1.34	Q9UJS0	Calcium-binding mitochondrial carrier protein Aralar2 (Citrin) (Mitochondrial aspartate glutamate carrier 2) (Solute carrier family 25 member 13)	675	SLC25A13	1	0	1	1.8	0	3.3
700	-0.35	0.80	-0.31	P05783	Keratin, type I cytoskeletal 18 (Cell proliferation-inducing gene 46 protein) (Cytokeratin-18) (CK-18) (Keratin-18) (K18)	430	KRT18	6	7	5	24.7	21.4	20.5
701	-0.35	0.88	-0.08	D6R967	Inorganic pyrophosphatase 2, mitochondrial (Fragment)	191	PPA2	3	1	1	17.3	6.8	5.8
702	-0.34	-0.56	0.09	H0YI98	Dynactin subunit 2 (Fragment)	268	DCTN2	1	1	1	3.4	3.4	3.4
703	-0.34	0.80	0.40	P24539	ATP synthase F(0) complex subunit B1, mitochondrial (ATP synthase proton-transporting mitochondrial F(0) complex subunit B1) (ATP synthase subunit b) (ATPase subunit b)	256	ATP5F1	5	6	4	21.5	27	15.6
704	-0.34	0.54	0.24	Q9NP72	Ras-related protein Rab-18	206	RAB18	4	4	2	22.8	22.8	10.2
705	-0.34	-0.03	-0.04	K7EM62	GPI ethanolamine phosphate transferase 1 (Fragment)	257	PIGN	1	1	1	6.2	6.2	6.2
706	-0.34	0.00	0.36	O43172	U4/U6 small nuclear ribonucleoprotein Prp4 (PRP4 homolog) (hPrp4) (U4/U6 snRNP 60 kDa protein) (WD splicing factor Prp4)	522	PRPF4	1	0	1	2.5	0	2.5
707	-0.33	0.27	0.65	P51572	B-cell receptor-associated protein 31 (BCR-associated protein 31) (Bap31) (6C6-AG tumor-associated antigen) (Protein CDM) (p28)	246	BCAP31	6	5	4	26.8	22.4	18.7

708	-0.33	-0.31	0.68	P35241	Radixin	583	RDX	12	5	8	19.2	8.2	11.8
709	-0.33	0.00	0.29	P42166	Lamina-associated polypeptide 2, isoform alpha (Thymopoietin isoform alpha) (TP alpha) (Thymopoietin-related peptide isoform alpha) (TPRP isoform alpha) [Cleaved into: Thymopoietin (TP) (Splenin); Thymopentin (TP5)]	694	TMPO	1	0	2	2.9	0	5.2
710	-0.33	0.13	0.23	Q9Y3A6	Transmembrane emp24 domain-containing protein 5 (p24 family protein gamma-2) (p24gamma2) (p28)	229	TMED5	1	2	1	5.2	10	5.2
711	-0.33	0.89	1.13	P25787	Proteasome subunit alpha type-2 (EC 3.4.25.1) (Macropain subunit C3) (Multicatalytic endopeptidase complex subunit C3) (Proteasome component C3)	234	PSMA2	4	8	8	27.4	50	47.4
712	-0.33	1.72	1.33	P40939	Trifunctional enzyme subunit alpha, mitochondrial (78 kDa gastrin-binding protein) (TP-alpha) [Includes: Long-chain enoyl-CoA hydratase (EC 4.2.1.17); Long chain 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.211)]	763	HADHA	8	3	9	15.6	5.8	15.5
713	-0.32	0.32	0.84	P46940	Ras GTPase-activating-like protein IQGAP1 (p195)	1657	IQGAP1	10	16	12	7.8	13.5	10.9
714	-0.31	0.69	0.00	Q86SX6	Glutaredoxin-related protein 5, mitochondrial (Monothiol glutaredoxin-5)	157	GLRX5	1	2	0	7	15.9	0
715	-0.31	0.00	0.00	F8WDI0	Ubiquitin-like-conjugating enzyme ATG3	74	ATG3	1	0	1	12.2	0	12.2

716	-0.31	0.15	0.90	Q9Y3B4	Splicing factor 3B subunit 6 (Pre-mRNA branch site protein p14) (SF3b 14 kDa subunit) (SF3B14a) (Spliceosome-associated protein, 14-kDa) (Splicing factor 3b, subunit 6, 14kDa)	125	SF3B6	3	2	2	25.6	20.8	20.8
717	-0.31	0.39	0.41	Q15417	Calponin-3 (Calponin, acidic isoform)	329	CNN3	2	1	2	7.8	3.9	7.8
718	-0.31	1.47	1.53	Q8IWJ2	GRIP and coiled-coil domain-containing protein 2 (185 kDa Golgi coiled-coil protein) (GCC185) (CLL-associated antigen KW-11) (CTCL tumor antigen se1-1) (Ran-binding protein 2-like 4) (RanBP2L4) (Renal carcinoma antigen NY-REN-53)	1684	GCC2	1	2	1	0.5	1.1	0.5
719	-0.31	0.00	0.16	O43933	Peroxisome biogenesis factor 1 (Peroxin-1) (Peroxisome biogenesis disorder protein 1)	1283	PEX1	1	0	1	0.9	0	0.9
720	-0.31	0.00	0.07	P41227	N-alpha-acetyltransferase 10 (EC 2.3.1.-) (EC 2.3.1.88) (N-terminal acetyltransferase complex ARD1 subunit homolog A) (NatA catalytic subunit Naa10)	235	NAA10	2	0	2	6.4	0	6.4
721	-0.31	0.00	0.96	Q9P287	BRCA2 and CDKN1A-interacting protein (P21- and CDK-associated protein 1) (Protein TOK-1)	314	BCCIP	1	0	2	2.7	0	8.2
722	-0.31	0.00	0.41	P43686	26S protease regulatory subunit 6B (26S proteasome AAA-ATPase subunit RPT3) (MB67-interacting protein) (MIP224) (Proteasome 26S subunit ATPase 4) (Tat-binding protein 7) (TBP-7)	418	PSMC4	4	0	6	14.5	0	17.3
723	-0.30	-0.01	0.43	P60842	Eukaryotic initiation factor 4A-I (eIF-4A-I) (eIF4A-I) (EC 3.6.4.13) (ATP-dependent RNA helicase eIF4A-1)	406	EIF4A1	7	8	9	21.2	20.2	21.4

724	-0.30	0.00	0.90	D6RD67	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial (Fragment)	286	MCCC2	1	0	1	4.2	0	4.2
725	-0.30	0.12	0.02	F8WBH7	Proteasome assembly chaperone 1	63	PSMG1	1	1	1	15.9	15.9	15.9
726	-0.30	0.43	0.70	Q9NPJ3	Acyl-coenzyme A thioesterase 13 (Acyl-CoA thioesterase 13) (EC 3.1.2.-) (Thioesterase superfamily member 2) [Cleaved into: Acyl-coenzyme A thioesterase 13, N-terminally processed]	140	ACOT13	4	3	4	45.3	29.9	45.3
727	-0.30	0.00	0.55	E7EMC6	Annexin	330	ANXA6	2	0	1	7.9	0	3.3
728	-0.30	0.58	0.36	P62820	Ras-related protein Rab-1A (YPT1-related protein)	205	RAB1A	4	8	5	22.9	42.4	36.6
729	-0.29	-0.15	0.35	P28066	Proteasome subunit alpha type-5 (EC 3.4.25.1) (Macropain zeta chain) (Multicatalytic endopeptidase complex zeta chain) (Proteasome zeta chain)	241	PSMA5	5	5	6	30.7	27	33.6
730	-0.29	0.59	0.11	P40925	Malate dehydrogenase, cytoplasmic (EC 1.1.1.37) (Cytosolic malate dehydrogenase) (Diiodophenylpyruvate reductase) (EC 1.1.1.96)	334	MDH1	6	2	3	19.5	5.7	10.5
731	-0.29	0.01	0.53	Q9Y490	Talin-1	2541	TLN1	22	14	19	13.2	9.1	11.6
732	-0.29	0.02	0.85	P00558	Phosphoglycerate kinase 1 (EC 2.7.2.3) (Cell migration-inducing gene 10 protein) (Primer recognition protein 2) (PRP 2)	417	PGK1	15	12	19	37.2	33.1	49.4
733	-0.29	0.11	0.00	F5GWX2	Heme-binding protein 1	133	HEBP1	2	1	0	15.8	12.8	0

734	-0.29	0.04	0.36	P63010	AP-2 complex subunit beta (AP105B) (Adaptor protein complex AP-2 subunit beta) (Adaptor-related protein complex 2 subunit beta) (Beta-2-adaptin) (Beta-adaptin) (Clathrin assembly protein complex 2 beta large chain) (Plasma membrane adaptor HA2/AP2 adaptin beta subunit)	937	AP2B1	5	2	3	7.7	3.6	4.4
735	-0.29	0.23	0.20	P06753	Tropomyosin alpha-3 chain (Gamma-tropomyosin) (Tropomyosin-3) (Tropomyosin-5) (hTM5)	285	TPM3	6	5	7	25.4	20.6	27
736	-0.29	0.34	0.71	P61224	Ras-related protein Rap-1b (GTP-binding protein smg p21B)	184	RAP1B	2	3	2	15.8	20.6	15.8
737	-0.28	0.00	1.76	P17844	Probable ATP-dependent RNA helicase DDX5 (EC 3.6.4.13) (DEAD box protein 5) (RNA helicase p68)	614	DDX5	2	0	1	3.4	0	2.6
738	-0.28	1.67	0.37	Q9H9B4	Sideroflexin-1 (Tricarboxylate carrier protein) (TCC)	322	SFXN1	3	3	1	14.9	13.7	4.7
739	-0.28	-0.30	0.04	P63104	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1)	245	YWHAZ	11	11	11	40.8	48.2	38.4
740	-0.28	0.14	0.68	O60701	UDP-glucose 6-dehydrogenase (UDP-Glc dehydrogenase) (UDP-GlcDH) (UDPGDH) (EC 1.1.1.22)	494	UGDH	10	12	14	27.7	34.6	31
741	-0.28	-0.49	-0.24	Q9BRA2	Thioredoxin domain-containing protein 17 (14 kDa thioredoxin-related protein) (TRP14) (Protein 42-9-9) (Thioredoxin-like protein 5)	123	TXNDC17	2	2	2	15.4	15.4	15.4
742	-0.28	0.69	0.41	Q99613	Eukaryotic translation initiation factor 3 subunit C (eIF3c) (Eukaryotic translation initiation factor 3 subunit 8) (eIF3 p110)	913	EIF3C	2	2	1	2.3	2.2	1.2

743	-0.28	-0.31	0.35	B1ALC0	Actin-related protein 2/3 complex subunit 5	135	ARPC5	1	1	1	9.6	9.6	9.6
744	-0.28	-0.35	0.53	Q96KP4	Cytosolic non-specific dipeptidase (EC 3.4.13.18) (CNDP dipeptidase 2) (Glutamate carboxypeptidase-like protein 1) (Peptidase A)	475	CNDP2	3	1	5	11	2	18.9
745	-0.27	0.00	0.00	Q9NY33	Dipeptidyl peptidase 3 (EC 3.4.14.4) (Dipeptidyl aminopeptidase III) (Dipeptidyl arylamidase III) (Dipeptidyl peptidase III) (DPP III) (Enkephalinase B)	737	DPP3	1	0	0	1.4	0	0
746	-0.27	-0.73	0.09	A0A0A0MR52	Eukaryotic translation initiation factor 4 gamma 1	1395	EIF4G1	2	2	1	1.5	1.5	0.8
747	-0.27	0.00	-0.34	B4DIH5	COP9 signalosome complex subunit 2 (cDNA FLJ52928, highly similar to COP9 signalosome complex subunit 2)	379	COPS2	1	0	1	2.6	0	2.6
748	-0.27	0.33	0.21	P46779	60S ribosomal protein L28	137	RPL28	2	5	4	13.9	29.9	22.6
749	-0.27	0.46	0.69	P78527	DNA-dependent protein kinase catalytic subunit (DNA-PK catalytic subunit) (DNA-PKcs) (EC 2.7.11.1) (DNPK1) (p460)	4128	PRKDC	19	35	30	6.3	9.8	9
750	-0.27	-0.34	0.25	P62258	14-3-3 protein epsilon (14-3-3E)	255	YWHAE	11	9	13	35.3	33.3	44.7
751	-0.27	0.92	0.76	P25705	ATP synthase subunit alpha, mitochondrial	553	ATP5A1	9	6	12	18.5	14.7	28
752	-0.26	0.32	0.15	A6NNI4	Tetraspanin	159	CD9	1	1	1	6.3	6.3	6.3
753	-0.26	0.71	0.37	P21796	Voltage-dependent anion-selective channel protein 1 (VDAC-1) (hVDAC1) (Outer mitochondrial membrane protein porin 1) (Plasmalemmal porin) (Porin 31HL) (Porin 31HM)	283	VDAC1	6	9	8	25.8	33.6	34.3

754	-0.26	0.00	1.05	P30085	UMP-CMP kinase (EC 2.7.4.14) (Deoxycytidylate kinase) (CK) (dCMP kinase) (Nucleoside-diphosphate kinase) (EC 2.7.4.6) (Uridine monophosphate/cytidine monophosphate kinase) (UMP/CMP kinase) (UMP/CMPK)	196	CMPK1	1	3	2	8.7	18.9	14.8
755	-0.26	0.21	-0.23	P60953	Cell division control protein 42 homolog (G25K GTP-binding protein)	191	CDC42	4	5	2	27.7	32.5	11
756	-0.26	-0.18	0.34	P28074	Proteasome subunit beta type-5 (EC 3.4.25.1) (Macropain epsilon chain) (Multicatalytic endopeptidase complex epsilon chain) (Proteasome chain 6) (Proteasome epsilon chain) (Proteasome subunit MB1) (Proteasome subunit X)	263	PSMB5	4	3	3	13.7	13.3	13.3
757	-0.25	0.00	-0.42	F8VS02	Alpha-aminoadipic semialdehyde dehydrogenase	475	ALDH7A1	3	0	2	8.8	0	5.9
758	-0.25	1.12	0.49	P27105	Erythrocyte band 7 integral membrane protein (Protein 7.2b) (Stomatin)	288	STOM	2	3	2	9	16.7	9
759	-0.25	0.00	0.00	Q9NX02	NACHT, LRR and PYD domains-containing protein 2 (Nucleotide-binding site protein 1) (PYRIN domain and NACHT domain-containing protein 1) (PYRIN-containing APAF1-like protein 2)	1062	NLRP2	1	0	0	1	0	0

760	-0.25	0.99	0.00	Q99643	Succinate dehydrogenase cytochrome b560 subunit, mitochondrial (Integral membrane protein CII-3) (QPs-1) (QPs1) (Succinate dehydrogenase complex subunit C) (Succinate-ubiquinone oxidoreductase cytochrome B large subunit) (CYBL)	169	SDHC	1	1	0	11.2	11.2	0
761	-0.25	-0.59	-0.23	P18206	Vinculin (Metavinculin) (MV)	1134	VCL	9	11	12	11.7	12.8	13.9
762	-0.25	0.04	0.44	E9PLK3	Puromycin-sensitive aminopeptidase	915	NPEPPS	6	4	7	7.8	4.7	8.9
763	-0.25	1.08	0.61	Q14697	Neutral alpha-glucosidase AB (EC 3.2.1.84) (Alpha-glucosidase 2) (Glucosidase II subunit alpha)	944	GANAB	4	9	11	5.7	12.3	12.4
764	-0.24	-0.48	0.60	P54652	Heat shock-related 70 kDa protein 2 (Heat shock 70 kDa protein 2)	639	HSPA2	5	6	5	8.8	10.3	9.5
765	-0.24	0.50	-0.09	P35579	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIA)	1960	MYH9	15	10	16	9.3	6.9	9.9
766	-0.24	-0.68	-0.10	P08758	Annexin A5 (Anchorin CII) (Annexin V) (Annexin-5) (Calphobindin I) (CBP-I) (Endonexin II) (Lipocortin V) (Placental anticoagulant protein 4) (PP4) (Placental anticoagulant protein I) (PAP-I) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)	320	ANXA5	7	7	5	24.1	25	15.6
767	-0.24	0.00	1.03	Q12874	Splicing factor 3A subunit 3 (SF3a60) (Spliceosome-associated protein 61) (SAP 61)	501	SF3A3	3	0	2	6.2	0	4.4

768	-0.24	-0.57	0.53	P15121	Aldose reductase (AR) (EC 1.1.1.21) (Aldehyde reductase) (Aldo-keto reductase family 1 member B1)	316	AKR1B1	10	12	10	38.3	49.7	47.8
769	-0.24	1.22	0.98	Q12797	Aspartyl/asparaginyl beta-hydroxylase (EC 1.14.11.16) (Aspartate beta-hydroxylase) (ASP beta-hydroxylase) (Peptide-aspartate beta-dioxygenase)	758	ASPH	3	5	4	4.7	10.2	11.9
770	-0.24	0.30	0.55	P63092	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short (Adenylate cyclase-stimulating G alpha protein)	394	GNAS	3	2	2	7.9	5.3	5.3
771	-0.24	0.00	0.00	P61086	Ubiquitin-conjugating enzyme E2 K (EC 6.3.2.19) (Huntingtin-interacting protein 2) (HIP-2) (Ubiquitin carrier protein) (Ubiquitin-conjugating enzyme E2-25 kDa) (Ubiquitin-conjugating enzyme E2(25K)) (Ubiquitin-conjugating enzyme E2-25K) (Ubiquitin-protein ligase)	200	UBE2K	3	0	0	26.5	0	0
772	-0.24	0.01	0.20	P31946	14-3-3 protein beta/alpha (Protein 1054) (Protein kinase C inhibitor protein 1) (KCIP-1) [Cleaved into: 14-3-3 protein beta/alpha, N-terminally processed]	246	YWHAB	6	8	8	30.7	43.9	38.9
773	-0.24	0.00	0.00	Q96K76	Ubiquitin carboxyl-terminal hydrolase 47 (EC 3.4.19.12) (Deubiquitinating enzyme 47) (Ubiquitin thioesterase 47) (Ubiquitin-specific-processing protease 47)	1375	USP47	1	0	0	0.7	0	0

774	-0.24	-0.25	0.00	P30043	Flavin reductase (NADPH) (FR) (EC 1.5.1.30) (Biliverdin reductase B) (BVR-B) (EC 1.3.1.24) (Biliverdin-IX beta-reductase) (Green heme-binding protein) (GHBP) (NADPH-dependent diaphorase) (NADPH-flavin reductase) (FLR)	206	BLVRB	2	3	0	11.7	22.8	0
775	-0.24	-0.52	1.17	Q8J015	60S ribosomal protein L13a (Ribosomal protein L13a) (Ribosomal protein L13a, isoform CRA_b)	142	RPL13a	3	2	4	14.8	7	20.4
776	-0.24	0.00	0.63	Q15006	ER membrane protein complex subunit 2 (Tetratricopeptide repeat protein 35) (TPR repeat protein 35)	297	EMC2	1	0	1	6.4	0	6.4
777	-0.24	1.32	0.00	E9PH64	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9	168	NDUFB9	1	3	0	8.3	22	0
778	-0.23	0.00	1.40	Q92820	Gamma-glutamyl hydrolase (EC 3.4.19.9) (Conjugase) (GH) (Gamma-Glu-X carboxypeptidase)	318	GGH	1	0	2	4.1	0	7.2
779	-0.23	-0.22	0.20	O00231	26S proteasome non-ATPase regulatory subunit 11 (26S proteasome regulatory subunit RPN6) (26S proteasome regulatory subunit S9) (26S proteasome regulatory subunit p44.5)	422	PSMD11	7	5	7	20.4	14	20.1
780	-0.23	-0.02	0.89	E5RI99	60S ribosomal protein L30 (Fragment)	114	RPL30	4	3	4	32.5	35.1	32.5
781	-0.23	0.84	0.64	P52701	DNA mismatch repair protein Msh6 (hMSH6) (G/T mismatch-binding protein) (GTBP) (GTMBP) (MutS-alpha 160 kDa subunit) (p160)	1360	MSH6	2	3	2	2.4	3.4	2.4
782	-0.23	-0.04	-0.02	M0R0F0	40S ribosomal protein S5 (Fragment)	200	RPS5	1	2	1	7.5	12	7.5
783	-0.23	0.00	0.00	E9PDQ8	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	379	SUCLG2	1	0	0	4	0	0

784	-0.23	0.00	0.11	P11766	Alcohol dehydrogenase class-3 (EC 1.1.1.1) (Alcohol dehydrogenase 5) (Alcohol dehydrogenase class chi chain) (Alcohol dehydrogenase class-III) (Glutathione-dependent formaldehyde dehydrogenase) (FALDH) (FDH) (GSH-FDH) (EC 1.1.1.-) (S-(hydroxymethyl)glutathione dehydrogenase) (EC 1.1.1.284)	374	ADH5	4	0	3	11.5	0	9.9
785	-0.23	0.33	0.66	Q9Y230	RuvB-like 2 (EC 3.6.4.12) (48 kDa TATA box-binding protein-interacting protein) (48 kDa TBP-interacting protein) (51 kDa erythrocyte cytosolic protein) (ECP-51) (INO80 complex subunit J) (Repressing pontin 52) (Reptin 52) (TIP49b) (TIP60-associated protein 54-beta) (TAP54-beta)	463	RUVBL2	6	4	8	15.8	10.2	22.9
786	-0.23	-0.05	-0.60	K7EL96	Perilipin-3 (Fragment)	172	PLIN3	2	2	3	15.7	18	24.4
787	-0.22	-0.78	0.62	Q16719	Kynureninase (EC 3.7.1.3) (L-kynurenine hydrolase)	465	KYNU	7	8	12	20.6	21.5	37
788	-0.22	-0.09	-0.24	P31949	Protein S100-A11 (Calgizzarin) (Metastatic lymph node gene 70 protein) (MLN 70) (Protein S100-C) (S100 calcium-binding protein A11) [Cleaved into: Protein S100-A11, N-terminally processed]	105	S100A11	1	3	3	15.2	34.3	34.3
789	-0.22	-0.33	0.70	P48163	NADP-dependent malic enzyme (NADP-ME) (EC 1.1.1.40) (Malic enzyme 1)	572	ME1	1	1	1	3.6	4.2	3.6
790	-0.22	-0.72	-0.26	Q14019	Coactosin-like protein	142	COTL1	4	3	4	15.5	19.7	15.5

791	-0.22	0.00	0.62	Q92905	COP9 signalosome complex subunit 5 (SGN5) (Signalosome subunit 5) (EC 3.4.-.-) (Jun activation domain-binding protein 1)	334	COPS5	1	0	1	4.5	0	4.5
792	-0.21	-0.15	0.19	G3V295	Proteasome subunit alpha type (EC 3.4.25.1)	203	PSMA6	2	7	4	10.3	36.9	21.7
793	-0.21	0.61	0.47	E9PEX6	Dihydrolipoyl dehydrogenase (EC 1.8.1.4)	486	DLD	3	2	5	8.8	5.1	11.7
794	-0.21	0.39	0.00	P19525	Interferon-induced, double-stranded RNA-activated protein kinase (EC 2.7.11.1) (Eukaryotic translation initiation factor 2-alpha kinase 2) (eIF-2A protein kinase 2) (Interferon-inducible RNA-dependent protein kinase) (P1/eIF-2A protein kinase) (Protein kinase RNA-activated) (PKR) (Protein kinase R) (Tyrosine-protein kinase EIF2AK2) (EC 2.7.10.2) (p68 kinase)	551	EIF2AK2	1	1	0	2.4	2.4	0
795	-0.21	0.36	0.64	P28070	Proteasome subunit beta type-4 (EC 3.4.25.1) (26 kDa prosomal protein) (HsBPROS26) (PROS-26) (Macropain beta chain) (Multicatalytic endopeptidase complex beta chain) (Proteasome beta chain) (Proteasome chain 3) (HsN3)	264	PSMB4	3	4	2	20.8	25.4	15.9
796	-0.21	-0.14	1.26	P09012	U1 small nuclear ribonucleoprotein A (U1 snRNP A) (U1-A) (U1A)	282	SNRPA	1	4	2	2.8	15.6	9.6
797	-0.21	0.27	1.29	P61586	Transforming protein RhoA (Rho cDNA clone 12) (h12)	193	RHOA	5	5	5	35.2	24.4	24.4

798	-0.21	0.23	0.28	P25788	Proteasome subunit alpha type-3 (EC 3.4.25.1) (Macropain subunit C8) (Multicatalytic endopeptidase complex subunit C8) (Proteasome component C8)	255	PSMA3	3	2	3	8.5	8.1	8.5
799	-0.21	1.04	0.46	P12236	ADP/ATP translocase 3 (ADP,ATP carrier protein 3) (ADP,ATP carrier protein, isoform T2) (ANT 2) (Adenine nucleotide translocator 3) (ANT 3) (Solute carrier family 25 member 6) [Cleaved into: ADP/ATP translocase 3, N-terminally processed]	298	SLC25A6	8	8	8	27.2	29.5	26.2
800	-0.20	0.00	0.17	O95202	LETM1 and EF-hand domain-containing protein 1, mitochondrial (Leucine zipper-EF-hand-containing transmembrane protein 1)	739	LETM1	2	0	2	2.7	0	2.7
801	-0.20	-0.43	0.13	P23528	Cofilin-1 (18 kDa phosphoprotein) (p18) (Cofilin, non-muscle isoform)	166	CFL1	12	10	13	57.2	63.9	57.2
802	-0.20	0.00	-0.02	P21283	V-type proton ATPase subunit C 1 (V-ATPase subunit C 1) (Vacuolar proton pump subunit C 1)	382	ATP6V1C1	1	0	1	4.2	0	4.2
803	-0.20	-0.29	0.86	P33176	Kinesin-1 heavy chain (Conventional kinesin heavy chain) (Ubiquitous kinesin heavy chain) (UKHC)	963	KIF5B	2	2	1	2.4	2.5	1
804	-0.20	-0.31	0.11	R4GMY8	Transcription elongation factor B polypeptide 1	65	TCEB1	1	2	1	18.5	33.8	18.5
805	-0.20	-0.29	0.24	H7C3I1	Hsc70-interacting protein (Fragment)	146	ST13	1	2	3	6.8	18.5	25.3
806	-0.20	0.00	0.24	O14828	Secretory carrier-associated membrane protein 3 (Secretory carrier membrane protein 3)	347	SCAMP3	1	0	1	6.2	0	6.2
807	-0.20	0.44	0.15	P20340	Ras-related protein Rab-6A (Rab-6)	208	RAB6A	4	3	4	23.6	17.8	22.6

808	-0.20	-0.41	0.10	Q8WUM4	Programmed cell death 6-interacting protein (PDCD6-interacting protein) (ALG-2-interacting protein 1) (ALG-2-interacting protein X) (Hp95)	868	PDCD6IP	5	3	6	5.8	5.2	6.9
809	-0.20	0.00	-0.12	P35237	Serpin B6 (Cytoplasmic antiproteinase) (CAP) (Peptidase inhibitor 6) (PI-6) (Placental thrombin inhibitor)	376	SERPINB6	3	0	2	12.5	0	8.5
810	-0.19	0.74	0.23	P07814	Bifunctional glutamate/proline--tRNA ligase (Bifunctional aminoacyl-tRNA synthetase) (Cell proliferation-inducing gene 32 protein) (Glutamatyl-prolyl-tRNA synthetase) [Includes: Glutamate--tRNA ligase (EC 6.1.1.17) (Glutamyl-tRNA synthetase) (GluRS); Proline--tRNA ligase (EC 6.1.1.15) (Prolyl-tRNA synthetase)]	1512	EPRS	5	4	4	4.4	3.6	3.3
811	-0.19	0.33	0.37	Q9P2J5	Leucine--tRNA ligase, cytoplasmic (EC 6.1.1.4) (Leucyl-tRNA synthetase) (LeuRS)	1176	LARS	5	9	6	5.1	9.6	6
812	-0.19	0.00	-0.31	Q7Z406	Myosin-14 (Myosin heavy chain 14) (Myosin heavy chain, non-muscle IIc) (Non-muscle myosin heavy chain IIc) (NMHC II-C)	1995	MYH14	2	2	2	1.1	1.3	1.1
813	-0.19	-0.13	1.09	Q13347	Eukaryotic translation initiation factor 3 subunit I (eIF3i) (Eukaryotic translation initiation factor 3 subunit 2) (TGF-beta receptor-interacting protein 1) (TRIP-1) (eIF-3-beta) (eIF3 p36)	325	EIF3I	1	1	4	3.4	2.8	21.5
814	-0.19	-0.39	0.16	Q02809	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 (EC 1.14.11.4) (Lysyl hydroxylase 1) (LH1)	727	PLOD1	1	1	1	2.1	2.1	2.1

815	-0.19	0.00	1.22	B4DT28	Heterogeneous nuclear ribonucleoprotein R (Heterogeneous nuclear ribonucleoprotein R, isoform CRA_a) (cDNA FLJ54544, highly similar to Heterogeneous nuclear ribonucleoprotein R)	494	HNRNPR	2	1	3	4.9	2.6	7.1
816	-0.18	-0.50	-0.48	Q5VYK3	Proteasome-associated protein ECM29 homolog (Ecm29)	1845	ECM29	2	1	1	1.4	0.7	0.7
817	-0.18	0.00	0.11	Q58FF6	Putative heat shock protein HSP 90-beta 4	505	HSP90AB4P	5	1	5	7.7	2.4	7.7
818	-0.18	-0.21	0.33	Q5TA02	Glutathione S-transferase omega-1 (Fragment)	200	GSTO1	2	4	4	11	20	20.5
819	-0.18	0.27	0.31	P39019	40S ribosomal protein S19	145	RPS19	3	6	3	18.6	34.5	18.6
820	-0.18	0.00	0.04	C9J0K5	Cytoplasmic protein NCK1 (Fragment)	75	NCK1	1	0	1	12	0	12
821	-0.17	-0.72	-0.01	Q15819	Ubiquitin-conjugating enzyme E2 variant 2 (DDVit 1) (Enterocyte differentiation-associated factor 1) (EDAF-1) (Enterocyte differentiation-promoting factor 1) (EDPF-1) (MMS2 homolog) (Vitamin D3-inducible protein)	145	UBE2V2	2	2	1	11.7	11.7	6.9
822	-0.17	-0.90	0.72	O43143	Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 (EC 3.6.4.13) (ATP-dependent RNA helicase #46) (DEAH box protein 15)	795	DHX15	2	1	2	2.9	1.5	2.9
823	-0.17	-0.10	0.32	Q9Y5S9	RNA-binding protein 8A (Binder of OVCA1-1) (BOV-1) (RNA-binding motif protein 8A) (RNA-binding protein Y14) (Ribonucleoprotein RBM8A)	174	RBM8A	1	2	1	6.4	11	6.4

824	-0.17	-0.07	0.33	Q13838	Spliceosome RNA helicase DDX39B (EC 3.6.4.13) (56 kDa U2AF65-associated protein) (ATP-dependent RNA helicase p47) (DEAD box protein UAP56) (HLA-B-associated transcript 1 protein)	428	DDX39B	3	2	5	8.2	5.1	16.6
825	-0.17	0.89	0.38	E9PLD0	Ras-related protein Rab-1B	169	RAB1B	3	5	5	20.7	30.8	37.9
826	-0.17	0.00	-0.06	C9JIJ1	RAC-beta serine/threonine-protein kinase (Fragment)	119	AKT2	1	0	1	8.4	0	8.4
827	-0.17	2.06	0.37	O95573	Long-chain-fatty-acid--CoA ligase 3 (EC 6.2.1.3) (Long-chain acyl-CoA synthetase 3) (LACS 3)	720	ACSL3	2	2	2	3.5	4.6	3.5
828	-0.17	0.01	0.07	A0A0A6YYA0	Protein TMED7-TICAM2	188	TMED7-TICAM2	1	1	2	10.1	6.4	16.5
829	-0.16	-0.63	-1.88	B1AJY5	26S proteasome non-ATPase regulatory subunit 10	185	PSMD10	2	1	3	10.8	4.3	21.1
830	-0.16	0.26	0.86	Q01081	Splicing factor U2AF 35 kDa subunit (U2 auxiliary factor 35 kDa subunit) (U2 small nuclear RNA auxiliary factor 1) (U2 snRNP auxiliary factor small subunit)	240	U2AF1	2	2	2	5.8	10.4	5.8
831	-0.16	0.42	0.23	Q9Y6M7	Sodium bicarbonate cotransporter 3 (Electroneutral Na/HCO(3) cotransporter) (Sodium bicarbonate cotransporter 2) (Sodium bicarbonate cotransporter 2b) (Bicarbonate transporter) (Solute carrier family 4 member 7)	1214	SLC4A7	3	2	1	4.8	3.5	2.1

832	-0.16	0.74	0.66	P16615	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 (SERCA2) (SR Ca(2+)-ATPase 2) (EC 3.6.3.8) (Calcium pump 2) (Calcium-transporting ATPase sarcoplasmic reticulum type, slow twitch skeletal muscle isoform) (Endoplasmic reticulum class 1/2 Ca(2+) ATPase)	1042	ATP2A2	8	10	12	10.9	13.2	17.7
833	-0.16	-0.29	-0.46	P61956	Small ubiquitin-related modifier 2 (SUMO-2) (HSMT3) (SMT3 homolog 2) (SUMO-3) (Sentrin-2) (Ubiquitin-like protein SMT3B) (Smt3B)	95	SUMO2	1	2	2	16.9	31	31
834	-0.15	-0.04	0.43	Q9UBT2	SUMO-activating enzyme subunit 2 (EC 6.3.2.-) (Anthracycline-associated resistance ARX) (Ubiquitin-like 1-activating enzyme E1B) (Ubiquitin-like modifier-activating enzyme 2)	640	UBA2	3	1	1	7	2.3	2.3
835	-0.15	0.31	0.61	Q15181	Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-hydrolase) (PPase)	289	PPA1	1	1	3	3.5	3.1	11.8
836	-0.15	2.08	0.44	H0YDT8	ER membrane protein complex subunit 7 (Fragment)	192	EMC7	1	1	2	6.8	8.3	10.9
837	-0.15	0.00	0.00	F8WCQ2	Phosphatidylinositide phosphatase SAC1	71	SACM1L	1	0	0	12.7	0	0
838	-0.15	-0.41	0.29	Q86Y56	Dynein assembly factor 5, axonemal (HEAT repeat-containing protein 2)	855	DNAAF5	1	1	1	4.7	4.7	4.7
839	-0.15	0.46	0.01	P30049	ATP synthase subunit delta, mitochondrial (F-ATPase delta subunit)	168	ATP5D	1	1	1	5.4	5.4	5.4
840	-0.15	0.00	0.00	Q9UBK9	Protein UXT (Androgen receptor trapped clone 27 protein) (ART-27) (Ubiquitously expressed transcript protein)	157	UXT	1	0	0	8.3	0	0

841	-0.15	2.44	0.00	Q96HC4	PDZ and LIM domain protein 5 (Enigma homolog) (Enigma-like PDZ and LIM domains protein)	596	PDLIM5	1	1	0	1.9	2.9	0
842	-0.15	0.00	-0.08	Q92621	Nuclear pore complex protein Nup205 (205 kDa nucleoporin) (Nucleoporin Nup205)	2012	NUP205	1	0	2	0.6	0	1.2
843	-0.14	0.00	0.33	Q16878	Cysteine dioxygenase type 1 (EC 1.13.11.20) (Cysteine dioxygenase type I) (CDO) (CDO-I)	200	CDO1	1	0	1	4	0	4
844	-0.14	0.00	2.49	O94826	Mitochondrial import receptor subunit TOM70 (Mitochondrial precursor proteins import receptor) (Translocase of outer membrane 70 kDa subunit)	608	TOMM70A	1	0	2	1.5	0	7.6
845	-0.14	-0.14	0.13	P61981	14-3-3 protein gamma (Protein kinase C inhibitor protein 1) (KCIP-1) [Cleaved into: 14-3-3 protein gamma, N-terminally processed]	247	YWHAG	6	8	7	33.2	47	37.2
846	-0.14	0.27	0.61	O43707	Alpha-actinin-4 (Non-muscle alpha-actinin 4)	911	ACTN4	18	28	22	24.3	38.5	30.7
847	-0.14	-0.10	0.19	P62333	26S protease regulatory subunit 10B (26S proteasome AAA-ATPase subunit RPT4) (Proteasome 26S subunit ATPase 6) (Proteasome subunit p42)	389	PSMC6	4	3	5	11.8	9.5	14.9
848	-0.14	1.04	-0.24	P00167	Cytochrome b5 (Microsomal cytochrome b5 type A) (MCB5)	134	CYB5A	1	3	1	9.2	36.7	9.2
849	-0.14	1.07	0.64	Q8N5K1	CDGSH iron-sulfur domain-containing protein 2 (Endoplasmic reticulum intermembrane small protein) (MitoNEET-related 1 protein) (Miner1) (Nutrient-deprivation autophagy factor-1) (NAF-1)	135	CISD2	3	7	3	21.5	47.4	21.5
850	-0.14	0.37	0.31	E9PF10	Nuclear pore complex protein Nup155	1327	NUP155	1	1	1	0.8	0.8	0.8

851	-0.14	-0.59	0.61	Q08752	Peptidyl-prolyl cis-trans isomerase D (PPIase D) (EC 5.2.1.8) (40 kDa peptidyl-prolyl cis-trans isomerase) (Cyclophilin-40) (CYP-40) (Cyclophilin-related protein) (Rotamase D)	370	PPID	2	1	1	4.6	2.4	2.2
852	-0.14	0.00	0.26	H0Y4Q3	Ran GTPase-activating protein 1 (Fragment)	253	RANGAP1	2	0	2	11.1	0	11.1
853	-0.14	-0.05	-0.12	A8MU58	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	242	AIMP2	2	1	2	8.7	3.7	8.7
854	-0.13	1.31	-0.18	P47985	Cytochrome b-c1 complex subunit Rieske, mitochondrial (EC 1.10.2.2) (Complex III subunit 5) (Cytochrome b-c1 complex subunit 5) (Rieske iron-sulfur protein) (RISP) (Ubiquinol-cytochrome c reductase iron-sulfur subunit) [Cleaved into: Cytochrome b-c1 complex subunit 11 (Complex III subunit IX) (Ubiquinol-cytochrome c reductase 8 kDa protein)]	274	UQCRFS1	2	3	1	10.9	15.3	7.7
855	-0.13	1.40	0.23	Q9P0I2	ER membrane protein complex subunit 3 (Transmembrane protein 111)	261	EMC3	1	1	1	3.4	5	3.4
856	-0.13	0.11	0.42	P53621	Coatomer subunit alpha (Alpha-coat protein) (Alpha-COP) (HEP-COP) (HEPCOP) [Cleaved into: Xenin (Xenopsin-related peptide); Proxenin]	1224	COPA	4	3	4	4.3	3.2	4
857	-0.13	0.00	0.07	B4E1C5	Histidine--tRNA ligase, cytoplasmic (cDNA FLJ58562, highly similar to Histidyl-tRNA synthetase (EC 6.1.1.21))	395	HARS	1	0	2	3.3	0	6.3
858	-0.13	0.00	-0.09	P63096	Guanine nucleotide-binding protein G(i) subunit alpha-1 (Adenylate cyclase-inhibiting G alpha protein)	354	GNAI1	2	1	2	6.8	3.1	6.8

859	-0.13	0.04	0.53	Q14914	Prostaglandin reductase 1 (PRG-1) (EC 1.3.1.-) (15-oxoprostaglandin 13-reductase) (EC 1.3.1.48) (NADP-dependent leukotriene B4 12-hydroxydehydrogenase) (EC 1.3.1.74)	329	PTGR1	5	5	5	22.2	26.1	21.3
860	-0.13	0.00	0.15	Q5MIZ7	Serine/threonine-protein phosphatase 4 regulatory subunit 3B (SMEK homolog 2)	849	SMEK2	1	0	1	1.6	0	1.6
861	-0.12	0.46	-0.44	Q9NX63	MICOS complex subunit MIC19 (Coiled-coil-helix-coiled-coil-helix domain-containing protein 3)	227	CHCHD3	2	2	3	11.5	11.5	11.9
862	-0.12	0.00	0.67	H0YA83	Beta-hexosaminidase subunit beta (Fragment)	170	HEXB	1	0	1	5.9	0	5.9
863	-0.12	1.26	0.70	Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1 (UGT1) (hUGT1) (EC 2.4.1.-) (UDP--Glc:glycoprotein glucosyltransferase) (UDP-glucose ceramide glucosyltransferase-like 1)	1555	UGGT1	1	3	3	0.8	3.4	2.9
864	-0.12	0.36	0.93	Q9UKD2	mRNA turnover protein 4 homolog (Ribosome assembly factor MRTO4)	239	MRTO4	1	1	1	5.4	5.4	5.4
865	-0.12	0.27	0.11	P61019	Ras-related protein Rab-2A	212	RAB2A	4	5	5	20.8	25.5	28.3
866	-0.12	0.00	-0.01	Q8N0U8	Vitamin K epoxide reductase complex subunit 1-like protein 1 (VKORC1-like protein 1) (EC 1.17.4.4)	176	VKORC1L1	1	0	1	6.2	0	6.2
867	-0.12	-0.49	0.38	O00232	26S proteasome non-ATPase regulatory subunit 12 (26S proteasome regulatory subunit RPN5) (26S proteasome regulatory subunit p55)	456	PSMD12	2	1	2	5	2.2	5
868	-0.12	0.35	0.22	P51149	Ras-related protein Rab-7a	207	RAB7A	5	8	6	29	47.8	34.8

869	-0.12	0.59	1.31	K7EJE8	Lon protease homolog, mitochondrial (EC 3.4.21.-) (Lon protease-like protein) (Mitochondrial ATP-dependent protease Lon) (Serine protease 15)	829	LONP1	1	3	3	1.3	4.2	4.5
870	-0.11	0.94	0.44	P02786	Transferrin receptor protein 1 (TR) (TfR) (TfR1) (Trfr) (T9) (p90) (CD antigen CD71) [Cleaved into: Transferrin receptor protein 1, serum form (sTfR)]	760	TFRC	5	5	9	7.6	8.4	14.5
871	-0.11	0.00	0.22	Q9H0A8	COMM domain-containing protein 4	199	COMMD4	1	0	1	13.3	0	13.3
872	-0.11	-0.44	-0.15	P21291	Cysteine and glycine-rich protein 1 (Cysteine-rich protein 1) (CRP) (CRP1) (Epididymis luminal protein 141) (HEL-141)	193	CSRP1	6	8	7	50.3	55.4	59.1
873	-0.11	-0.52	0.40	P04083	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	346	ANXA1	11	17	12	32.7	55.5	30.3
874	-0.11	0.00	0.00	K7EP09	Bifunctional coenzyme A synthase (Fragment)	90	COASY	1	0	0	11.1	0	0
875	-0.11	0.49	0.77	C9JQ41	Coiled-coil domain-containing protein 58	130	CCDC58	1	1	2	6.9	8.5	20
876	-0.11	0.62	0.32	I3L1P8	Mitochondrial 2-oxoglutarate/malate carrier protein (Fragment)	296	SLC25A11	3	1	1	14.5	3.7	5.4
877	-0.11	1.23	0.23	F8VVM2	Phosphate carrier protein, mitochondrial	324	SLC25A3	2	4	2	5.9	17.9	5.9
878	-0.11	0.07	0.09	M0QZS6	SUMO-activating enzyme subunit 1	265	SAE1	3	1	2	12.1	4.9	7.9
879	-0.11	0.75	1.02	P49720	Proteasome subunit beta type-3 (EC 3.4.25.1) (Proteasome chain 13) (Proteasome component C10-II) (Proteasome theta chain)	205	PSMB3	5	4	6	25.4	25.4	33.2

880	-0.11	0.00	0.09	Q9Y262	Eukaryotic translation initiation factor 3 subunit L (eIF3l) (Eukaryotic translation initiation factor 3 subunit 6-interacting protein) (Eukaryotic translation initiation factor 3 subunit E-interacting protein)	564	EIF3L	1	0	1	1.6	0	1.6
881	-0.10	0.61	-0.23	P04632	Calpain small subunit 1 (CSS1) (Calcium-activated neutral proteinase small subunit) (CANP small subunit) (Calcium-dependent protease small subunit) (CDPS) (Calcium-dependent protease small subunit 1) (Calpain regulatory subunit)	268	CAPNS1	3	3	2	10.8	14.9	6
882	-0.10	-0.06	0.28	J3KTJ1	Myosin regulatory light chain 12A (Fragment)	114	MYL12A	1	1	1	15.8	15.8	15.8
883	-0.10	-0.33	0.10	P56192	Methionine--tRNA ligase, cytoplasmic (EC 6.1.1.10) (Methionyl-tRNA synthetase) (MetRS)	900	MARS	3	1	2	4.1	1.2	2.6
884	-0.10	1.04	0.28	P00505	Aspartate aminotransferase, mitochondrial (mAspAT) (EC 2.6.1.1) (EC 2.6.1.7) (Fatty acid-binding protein) (FABP-1) (Glutamate oxaloacetate transaminase 2) (Kynurenine aminotransferase 4) (Kynurenine aminotransferase IV) (Kynurenine--oxoglutarate transaminase 4) (Kynurenine--oxoglutarate transaminase IV) (Plasma membrane-associated fatty acid-binding protein) (FABPpm) (Transaminase A)	430	GOT2	4	7	8	13	16.5	21.4

885	-0.10	0.67	0.35	P30040	Endoplasmic reticulum resident protein 29 (ERp29) (Endoplasmic reticulum resident protein 28) (ERp28) (Endoplasmic reticulum resident protein 31) (ERp31)	261	ERP29	2	5	3	7.7	25.3	21.8
886	-0.09	0.07	0.22	P46108	Adapter molecule crk (Proto-oncogene c-Crk) (p38)	304	CRK	2	1	2	9.5	5.6	9.5
887	-0.09	0.82	0.76	P14625	Endoplasmin (94 kDa glucose-regulated protein) (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	803	HSP90B1	14	14	18	16.9	20.7	23.8
888	-0.09	0.54	0.53	P30044	Peroxiredoxin-5, mitochondrial (EC 1.11.1.15) (Alu corepressor 1) (Antioxidant enzyme B166) (AOEB166) (Liver tissue 2D-page spot 71B) (PLP) (Peroxiredoxin V) (Prx-V) (Peroxisomal antioxidant enzyme) (TPx type VI) (Thioredoxin peroxidase PMP20) (Thioredoxin reductase)	214	PRDX5	5	7	6	37	62.3	48.8
889	-0.09	0.86	0.64	H7C0V0	Uncharacterized protein C2orf47, mitochondrial (Fragment)	225	C2orf47	1	1	1	4.4	4.4	4.4
890	-0.09	0.00	0.00	H0YLW7	SAFB-like transcription modulator	62	SLTM	1	0	0	30.6	0	0
891	-0.09	0.14	0.09	Q9H488	GDP-fucose protein O-fucosyltransferase 1 (EC 2.4.1.221) (Peptide-O-fucosyltransferase 1) (O-FucT-1)	388	POFUT1	1	1	1	5.2	5.2	5.2
892	-0.09	0.65	-0.40	O43674	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial (Complex I-SGDH) (CI-SGDH) (NADH-ubiquinone oxidoreductase SGDH subunit)	189	NDUFB5	1	1	1	5.8	4.2	5.8
893	-0.09	0.30	0.63	A6PVX3	26S proteasome non-ATPase regulatory subunit 4 (Fragment)	203	PSMD4	1	1	3	7.4	7.4	19.7

894	-0.09	0.41	0.18	P07237	Protein disulfide-isomerase (PDI) (EC 5.3.4.1) (Cellular thyroid hormone-binding protein) (Prolyl 4-hydroxylase subunit beta) (p55)	508	P4HB	15	13	17	26	33.1	30.9
895	-0.08	0.00	0.09	H3BP42	Apoptosis-associated speck-like protein-containing a CARD (Fragment)	125	PYCARD	1	0	1	13.6	0	13.6
896	-0.08	0.00	0.21	O15143	Actin-related protein 2/3 complex subunit 1B (Arp2/3 complex 41 kDa subunit) (p41-ARC)	372	ARPC1B	2	0	2	8.3	0	8.3
897	-0.08	0.00	0.22	Q9UHN6	Transmembrane protein 2	1383	TMEM2	1	0	1	0.9	0	0.9
898	-0.08	0.00	0.22	A0A087WXS7	ATPase ASNA1 (EC 3.6.-.-) (Arsenical pump-driving ATPase) (Arsenite-stimulated ATPase)	331	ASNA1	1	0	1	4.8	0	4.8
899	-0.08	-0.49	0.13	Q9UNM6	26S proteasome non-ATPase regulatory subunit 13 (26S proteasome regulatory subunit RPN9) (26S proteasome regulatory subunit S11) (26S proteasome regulatory subunit p40.5)	376	PSMD13	3	1	5	9	2.4	15.7
900	-0.08	-0.17	-0.06	Q9UBQ0	Vacuolar protein sorting-associated protein 29 (hVPS29) (PEP11 homolog) (Vesicle protein sorting 29)	182	VPS29	1	3	1	7.1	19.2	7.1
901	-0.08	-0.16	-0.26	R4GMT0	Alpha-centractin	332	ACTR1A	1	2	1	4.8	7.2	4.8
902	-0.08	0.00	0.15	O75083	WD repeat-containing protein 1 (Actin-interacting protein 1) (AIP1) (NORI-1)	606	WDR1	1	0	2	2.3	0	5
903	-0.08	0.00	0.00	M0R0Q7	DNA ligase (EC 6.5.1.1)	800	LIG1	1	0	1	1.8	0	1.5
904	-0.08	0.00	0.25	Q96FX7	tRNA (adenine(58)-N(1))-methyltransferase catalytic subunit TRMT61A (EC 2.1.1.220) (tRNA(m1A58)-methyltransferase subunit TRMT61A) (tRNA(m1A58)MTase subunit TRMT61A)	289	TRMT61A	1	0	1	3.5	0	3.5

905	-0.08	-0.25	-0.11	Q9P000	COMM domain-containing protein 9	198	COMMD9	1	1	1	10.3	10.3	10.3
906	-0.08	0.00	0.00	E9PNC7	Dr1-associated corepressor (Fragment)	155	DRAP1	1	0	0	7.1	0	0
907	-0.07	-0.07	0.37	Q9NR31	GTP-binding protein SAR1a (COPII-associated small GTPase)	198	SAR1A	2	4	5	9.6	25.8	32.8
908	-0.07	0.00	0.18	M0R208	ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92)	190	CLPP	1	0	1	7.9	0	7.9
909	-0.07	-0.01	0.50	Q00688	Peptidyl-prolyl cis-trans isomerase FKBP3 (PPIase FKBP3) (EC 5.2.1.8) (25 kDa FK506-binding protein) (25 kDa FKBP) (FKBP-25) (FK506-binding protein 3) (FKBP-3) (Immunophilin FKBP25) (Rapamycin-selective 25 kDa immunophilin) (Rotamase)	224	FKBP3	2	6	3	14.7	28.1	18.3
910	-0.07	0.00	0.00	Q96P11	Probable 28S rRNA (cytosine-C(5))-methyltransferase (EC 2.1.1.-) (NOL1-related protein) (NOL1R) (NOL1/NOP2/Sun domain family member 5) (Williams-Beuren syndrome chromosomal region 20A protein)	429	NSUN5	1	0	0	2.3	0	0
911	-0.07	-0.08	0.18	P84077	ADP-ribosylation factor 1	181	ARF1	3	4	3	19.9	33.1	19.9
912	-0.07	-0.32	-0.09	P61020	Ras-related protein Rab-5B	215	RAB5B	3	2	2	20.1	13.2	14.4
913	-0.07	0.51	0.08	Q07812	Apoptosis regulator BAX (Bcl-2-like protein 4) (Bcl2-L-4)	192	BAX	1	1	1	6.1	7.3	6.1
914	-0.06	0.26	0.31	Q04917	14-3-3 protein eta (Protein AS1)	246	YWHAH	3	5	3	12.2	26.8	13.4

915	-0.06	0.00	0.46	O96007	Molybdopterin synthase catalytic subunit (EC 2.8.1.12) (MOCO1-B) (Molybdenum cofactor synthesis protein 2 large subunit) (Molybdenum cofactor synthesis protein 2B) (MOCS2B) (Molybdopterin-synthase large subunit) (MPT synthase large subunit)	188	MOCS2	1	0	1	8	0	8
916	-0.06	0.00	0.97	P82673	28S ribosomal protein S35, mitochondrial (MRP-S35) (S35mt) (28S ribosomal protein S28, mitochondrial) (MRP-S28) (S28mt)	323	MRPS35	1	0	1	3.1	0	3.1
917	-0.06	-0.27	0.61	Q9Y678	Coatomer subunit gamma-1 (Gamma-1-coat protein) (Gamma-1-COP)	874	COPG1	4	2	4	6.8	3.3	6.8
918	-0.06	0.24	-0.20	Q9H4M9	EH domain-containing protein 1 (PAST homolog 1) (hPAST1) (Testilin)	534	EHD1	1	1	2	1.7	2.2	6
919	-0.06	-0.38	0.00	G5E9R3	60S ribosomal protein L37a (Ribosomal protein L37a, isoform CRA_b)	58	RPL37A	1	2	0	15.5	29.3	0
920	-0.05	-0.01	0.28	Q9NYP7	Elongation of very long chain fatty acids protein 5 (EC 2.3.1.199) (3-keto acyl-CoA synthase ELOVL5) (ELOVL fatty acid elongase 5) (ELOVL FA elongase 5) (Fatty acid elongase 1) (hELO1) (Very-long-chain 3-oxoacyl-CoA synthase 5)	299	ELOVL5	1	1	1	14.8	14.8	14.8
921	-0.05	0.00	0.30	A0A0A0MSP6	Serrate RNA effector molecule homolog (Fragment)	148	SRRT	1	0	1	8.8	0	8.8
922	-0.05	0.00	0.10	P25398	40S ribosomal protein S12	132	RPS12	6	7	4	63.6	50	42.4
923	-0.05	-0.34	-0.16	E9PQH6	Rho-related GTP-binding protein RhoC (Fragment)	169	RHOC	3	5	5	18.9	27.8	27.8
924	-0.05	0.07	0.13	P46783	40S ribosomal protein S10	165	RPS10	4	4	2	24.2	24.2	9.7

925	-0.05	0.05	0.53	P42126	Enoyl-CoA delta isomerase 1, mitochondrial (EC 5.3.3.8) (3,2-trans-enoyl-CoA isomerase) (Delta(3),Delta(2)-enoyl-CoA isomerase) (D3,D2-enoyl-CoA isomerase) (Dodecenoyl-CoA isomerase)	302	ECI1	2	2	2	9.3	10.6	9.3
926	-0.05	0.39	-0.06	P35606	Coatomer subunit beta' (Beta'-coat protein) (Beta'-COP) (p102)	906	COPB2	2	5	2	2.7	7.2	2.7
927	-0.05	0.93	0.15	P27797	Calreticulin (CRP55) (Calregulin) (Endoplasmic reticulum resident protein 60) (ERp60) (HACBP) (grp60)	417	CALR	7	5	7	15.1	21.3	14.4
928	-0.04	0.00	0.19	A0FGR8	Extended synaptotagmin-2 (E-Syt2) (Chr2Syt)	921	ESYT2	1	0	1	3.7	0	3.7
929	-0.04	-0.09	0.24	H0YJS4	Eukaryotic translation initiation factor 2 subunit 1 (Fragment)	252	EIF2S1	1	1	1	6	6	6
930	-0.04	-0.13	0.30	Q09161	Nuclear cap-binding protein subunit 1 (80 kDa nuclear cap-binding protein) (CBP80) (NCBP 80 kDa subunit)	790	NCBP1	1	1	1	1.4	1.4	1.4
931	-0.04	1.80	0.98	P36957	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial (EC 2.3.1.61) (2-oxoglutarate dehydrogenase complex component E2) (OGDC-E2) (Dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex) (E2K)	453	DLST	1	2	3	2	6	7.9
932	-0.03	-0.49	0.12	Q9BTW9	Tubulin-specific chaperone D (Beta-tubulin cofactor D) (tfcD) (SSD-1) (Tubulin-folding cofactor D)	1192	TBCD	2	2	1	2.6	2.6	1.3
933	-0.03	0.08	0.11	M0R0Y2	Alpha-soluble NSF attachment protein	256	NAPA	3	3	5	19.9	15.6	32.4

934	-0.03	0.12	0.29	P50213	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial (EC 1.1.1.41) (Isocitric dehydrogenase subunit alpha) (NAD(+)-specific ICDH subunit alpha)	366	IDH3A	1	4	1	2.7	13.9	6.3
935	-0.03	0.00	0.86	Q9UIQ6	Leucyl-cystinyl aminopeptidase (Cystinyl aminopeptidase) (EC 3.4.11.3) (Insulin-regulated membrane aminopeptidase) (Insulin-responsive aminopeptidase) (IRAP) (Oxytocinase) (OTase) (Placental leucine aminopeptidase) (P-LAP) [Cleaved into: Leucyl-cystinyl aminopeptidase, pregnancy serum form]	1025	LNPEP	1	0	1	1.5	0	1.5
936	-0.03	0.00	0.00	E9PLB0	RNA-binding protein 4B	143	RBM4B	1	0	0	8.4	0	0
937	-0.03	0.00	0.00	Q9H173	Nucleotide exchange factor SIL1 (BiP-associated protein) (BAP)	461	SIL1	1	0	0	2.6	0	0
938	-0.03	0.00	1.02	Q9UBB4	Ataxin-10 (Brain protein E46 homolog) (Spinocerebellar ataxia type 10 protein)	475	ATXN10	1	0	3	2.4	0	10.2
939	-0.03	0.37	0.24	C9JIS1	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 (Fragment)	232	GNB2	1	1	1	4.3	4.7	4.3
940	-0.03	0.00	0.36	Q16401	26S proteasome non-ATPase regulatory subunit 5 (26S protease subunit S5 basic) (26S proteasome subunit S5B)	504	PSMD5	2	0	1	6.7	0	4.1
941	-0.02	0.06	0.62	P36542	ATP synthase subunit gamma, mitochondrial (F-ATPase gamma subunit)	298	ATP5C1	2	3	2	7.7	11.4	7.7
942	-0.02	0.27	0.35	Q86UP2	Kinectin (CG-1 antigen) (Kinesin receptor)	1357	KTN1	10	15	11	9.8	14.2	10.2
943	-0.02	-0.71	0.16	P36405	ADP-ribosylation factor-like protein 3	182	ARL3	1	2	1	6	12.6	6
944	-0.02	0.04	0.26	K7ENK9	Vesicle-associated membrane protein 2	68	VAMP2	1	1	1	25	25	25

945	-0.02	0.00	1.05	P11177	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial (PDHE1-B) (EC 1.2.4.1)	359	PDHB	1	0	2	4.7	0	7.9
946	-0.02	0.37	0.33	Q04837	Single-stranded DNA-binding protein, mitochondrial (Mt-SSB) (MtSSB) (PWP1-interacting protein 17)	148	SSBP1	3	3	4	28.4	27.7	33.8
947	-0.02	-0.29	0.07	P15559	NAD(P)H dehydrogenase [quinone] 1 (EC 1.6.5.2) (Azoreductase) (DT-diaphorase) (DTD) (Menadione reductase) (NAD(P)H:quinone oxidoreductase 1) (Phylloquinone reductase) (Quinone reductase 1) (QR1)	274	NQO1	8	10	7	25.8	32.1	22.5
948	-0.01	-0.36	-0.07	Q96EK6	Glucosamine 6-phosphate N-acetyltransferase (EC 2.3.1.4) (Phosphoglucosamine acetylase) (Phosphoglucosamine transacetylase)	184	GNPNAT1	2	2	2	15.8	13.6	15.8
949	-0.01	1.37	1.36	O00264	Membrane-associated progesterone receptor component 1 (mPR)	195	PGRMC1	2	4	2	9.2	22.6	12.3
950	-0.01	-0.08	0.11	P51665	26S proteasome non-ATPase regulatory subunit 7 (26S proteasome regulatory subunit RPN8) (26S proteasome regulatory subunit S12) (Mov34 protein homolog) (Proteasome subunit p40)	324	PSMD7	2	2	2	6.5	5.9	6.5
951	-0.01	0.00	0.16	J9JIC5	Protein Njmu-R1	396	C17orf75	1	0	1	2.8	0	2.8
952	-0.01	0.00	0.15	Q9P032	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 4 (Hormone-regulated proliferation-associated protein of 20 kDa)	175	NDUFAF4	1	0	1	8	0	8
953	-0.01	0.48	0.51	Q96E11	Ribosome-recycling factor, mitochondrial (RRF) (Ribosome-releasing factor, mitochondrial)	262	MRRF	1	1	3	5.7	4.3	17.1

954	-0.01	1.03	0.69	P49411	Elongation factor Tu, mitochondrial (EF-Tu) (P43)	452	TUFM	7	8	8	21.2	26.3	25
955	-0.01	0.00	0.32	P06730	Eukaryotic translation initiation factor 4E (eIF-4E) (eIF4E) (eIF-4F 25 kDa subunit) (mRNA cap-binding protein)	217	EIF4E	1	0	1	6.5	0	6.5
956	0.00	0.40	0.44	P10619	Lysosomal protective protein (EC 3.4.16.5) (Carboxypeptidase C) (Carboxypeptidase L) (Cathepsin A) (Protective protein cathepsin A) (PPCA) (Protective protein for beta-galactosidase) [Cleaved into: Lysosomal protective protein 32 kDa chain; Lysosomal protective protein 20 kDa chain]	480	CTSA	1	3	1	2.4	8	2.4
957	0.00	0.43	0.51	Q71U36	Tubulin alpha-1A chain (Alpha-tubulin 3) (Tubulin B-alpha-1) (Tubulin alpha-3 chain)	451	TUBA1A	10	10	12	34.9	35.1	43
958	0.00	0.00	1.06	Q9BQE3	Tubulin alpha-1C chain (Alpha-tubulin 6) (Tubulin alpha-6 chain)	449	TUBA1C	10	11	12	32.3	35.6	39.9
959	0.00	0.00	0.23	V9GYG0	ADP/ATP translocase 1	208	SLC25A4	3	3	3	15.9	15.9	16.8
960	0.00	0.90	0.00	Q9Y6H1	Coiled-coil-helix-coiled-coil-helix domain-containing protein 2 (Aging-associated gene 10 protein) (HCV NS2 trans-regulated protein) (NS2TP)	151	CHCHD2	1	1	0	15.9	8.6	0
961	0.00	0.09	0.00	Q71UM5	40S ribosomal protein S27-like	84	RPS27L	1	2	0	15.5	28.6	0
962	0.00	-0.41	0.00	C9J1Z8	ADP-ribosylation factor 5 (Fragment)	150	ARF5	2	3	2	14	27.3	14
963	0.00	1.46	0.00	Q15388	Mitochondrial import receptor subunit TOM20 homolog (Mitochondrial 20 kDa outer membrane protein) (Outer mitochondrial membrane receptor Tom20)	145	TOMM20	1	2	0	9	17.2	0

964	0.00	3.39	0.00	P12273	Prolactin-inducible protein (Gross cystic disease fluid protein 15) (GCDFP-15) (Prolactin-induced protein) (Secretory actin-binding protein) (SABP) (gp17)	146	PIP	1	5	1	8.2	33.6	8.2
965	0.00	0.42	0.00	A0A087X1K9	Acyl-protein thioesterase 1	166	LYPLA1	1	4	0	7.8	27.7	0
966	0.00	0.00	1.47	K7ESM5	Tubulin beta-6 chain (Fragment)	338	TUBB6	2	4	5	7.7	11.5	18.3
967	0.00	2.32	0.00	C9J1E7	AP-1 complex subunit beta-1 (Fragment)	578	AP1B1	3	2	2	6.9	6.2	5
968	0.00	1.20	0.00	Q6P1L8	39S ribosomal protein L14, mitochondrial (L14mt) (MRP-L14) (39S ribosomal protein L32, mitochondrial) (L32mt) (MRP-L32)	145	MRPL14	1	2	0	6.2	15.9	0
969	0.00	0.06	1.05	Q5JR95	40S ribosomal protein S8	188	RPS8	1	2	1	5.9	13.3	6.9
970	0.00	-0.70	0.00	E5RGX5	Stathmin	168	STMN2	1	2	1	5.4	11.3	5.4
971	0.00	1.29	0.00	P00403	Cytochrome c oxidase subunit 2 (Cytochrome c oxidase polypeptide II)	227	MT-CO2	1	3	1	4.4	20.3	4.4
972	0.00	1.68	1.63	O15173	Membrane-associated progesterone receptor component 2 (Progesterone membrane-binding protein) (Steroid receptor protein DG6)	223	PGRMC2	1	2	3	4	12.6	18.8
973	0.00	0.78	0.00	P08579	U2 small nuclear ribonucleoprotein B'' (U2 snRNP B'')	225	SNRPB2	1	4	1	3.6	16	3.6
974	0.00	-0.47	0.38	A0A087WZK9	Eukaryotic translation initiation factor 3 subunit H (eIF3h) (Eukaryotic translation initiation factor 3 subunit 3) (eIF-3 gamma) (eIF3 p40 subunit)	349	EIF3H	1	1	3	3.4	2.6	12
975	0.00	0.44	0.24	E9PCY7	Heterogeneous nuclear ribonucleoprotein H	429	HNRNPH1	1	3	1	2.3	11.7	4

976	0.00	0.66	1.64	P06748	Nucleophosmin (NPM) (Nucleolar phosphoprotein B23) (Nucleolar protein NO38) (Numatrin)	294	NPM1	0	6	5	0	26.4	18.9
977	0.00	0.97	0.89	P26006	Integrin alpha-3 (CD49 antigen-like family member C) (FRP-2) (Galactoprotein B3) (GAPB3) (VLA-3 subunit alpha) (CD antigen CD49c) [Cleaved into: Integrin alpha-3 heavy chain; Integrin alpha-3 light chain]	1051	ITGA3	0	4	3	0	4.8	3.8
978	0.00	0.60	0.98	P61081	NEDD8-conjugating enzyme Ubc12 (EC 6.3.2.-) (NEDD8 carrier protein) (NEDD8 protein ligase) (Ubiquitin-conjugating enzyme E2 M)	183	UBE2M	0	3	3	0	16.9	19.7
979	0.00	0.40	0.66	P31153	S-adenosylmethionine synthase isoform type-2 (AdoMet synthase 2) (EC 2.5.1.6) (Methionine adenosyltransferase 2) (MAT 2) (Methionine adenosyltransferase II) (MAT-II)	395	MAT2A	0	1	3	0	3.8	8.1
980	0.00	0.00	2.43	E9PC52	Histone-binding protein RBBP7	416	RBBP7	0	0	3	0	0	13.2
981	0.00	0.00	0.84	P14868	Aspartate--tRNA ligase, cytoplasmic (EC 6.1.1.12) (Aspartyl-tRNA synthetase) (AspRS) (Cell proliferation-inducing gene 40 protein)	501	DARS	0	0	3	0	0	7
982	0.00	0.65	1.84	Q71UI9	Histone H2A.V (H2A.F/Z)	128	H2AFV	0	4	2	0	31.2	18.8
983	0.00	-0.47	1.75	A0A096LPI6	Uncharacterized protein	238		0	3	2	0	14.7	13.4
984	0.00	-0.55	0.21	H3BPH4	Phosphomannomutase (EC 5.4.2.8) (Fragment)	142	PMM2	0	2	2	0	16.2	14.1
985	0.00	0.93	0.48	A0A087WX29	TAR DNA-binding protein 43 (Fragment)	243	TARDBP	0	1	2	0	4.9	12.3
986	0.00	2.15	2.68	A0A087WZZ5	Splicing factor 3B subunit 2	871	SF3B2	0	1	2	0	1.6	3.1
987	0.00	0.83	1.84	A0A0A0MSJ0	ATP-dependent RNA helicase DDX42	708	DDX42	0	1	2	0	1.6	5.8

988	0.00	0.50	-0.31	P11717	Cation-independent mannose-6-phosphate receptor (CI Man-6-P receptor) (CI-MPR) (M6PR) (300 kDa mannose 6-phosphate receptor) (MPR 300) (Insulin-like growth factor 2 receptor) (Insulin-like growth factor II receptor) (IGF-II receptor) (M6P/IGF2 receptor) (M6P/IGF2R) (CD antigen CD222)	2491	IGF2R	0	1	2	0	0.4	0.8
989	0.00	0.80	1.02	P23634	Plasma membrane calcium-transporting ATPase 4 (PMCA4) (EC 3.6.3.8) (Matrix-remodeling-associated protein 1) (Plasma membrane calcium ATPase isoform 4) (Plasma membrane calcium pump isoform 4)	1241	ATP2B4	0	1	2	0	1.6	3.1
990	0.00	0.17	0.63	P30740	Leukocyte elastase inhibitor (LEI) (Monocyte/neutrophil elastase inhibitor) (EI) (M/NEI) (Peptidase inhibitor 2) (PI-2) (Serpin B1)	379	SERPINB1	0	1	2	0	3.7	6.6
991	0.00	0.85	0.49	Q6P587	Acylpyruvase FAHD1, mitochondrial (EC 3.7.1.5) (Fumarylacetoacetate hydrolase domain-containing protein 1) (Oxaloacetate decarboxylase) (OAA decarboxylase) (EC 4.1.1.3) (YisK-like protein)	224	FAHD1	0	1	2	0	7.1	13.4
992	0.00	0.00	1.08	A0A024R4E5	High density lipoprotein binding protein (Vigilin), isoform CRA_a (Vigilin)	1268	HDLBP	0	0	2	0	0	2.1
993	0.00	0.00	2.02	A0A087WZU1	Protein-tyrosine-phosphatase (EC 3.1.3.48)	2299	PTPRQ	0	0	2	0	0	1.5
994	0.00	0.00	-0.05	E7EQL5	Cytoplasmic dynein 1 intermediate chain 2 (Fragment)	305	DYNC1I2	0	0	2	0	0	9.2
995	0.00	0.00	0.65	F8VR84	UPF0160 protein MYG1, mitochondrial	213	C12orf10	0	0	2	0	0	12.2

996	0.00	0.00	1.06	H7C3C5	Polyribonucleotide nucleotidyltransferase 1, mitochondrial (Fragment)	139	PNPT1	0	0	2	0	0	20.1
997	0.00	0.00	1.17	O95782	AP-2 complex subunit alpha-1 (100 kDa coated vesicle protein A) (Adaptor protein complex AP-2 subunit alpha-1) (Adaptor-related protein complex 2 subunit alpha-1) (Alpha-adaptin A) (Alpha1-adaptin) (Clathrin assembly protein complex 2 alpha-A large chain) (Plasma membrane adaptor HA2/AP2 adaptin alpha A subunit)	977	AP2A1	0	0	2	0	0	2.2
998	0.00	0.00	0.35	P07384	Calpain-1 catalytic subunit (EC 3.4.22.52) (Calcium-activated neutral proteinase 1) (CANP 1) (Calpain mu-type) (Calpain-1 large subunit) (Cell proliferation-inducing gene 30 protein) (Micromolar-calpain) (muCANP)	714	CAPN1	0	0	2	0	0	2.8
999	0.00	0.00	0.14	P12270	Nucleoprotein TPR (Megator) (NPC-associated intranuclear protein) (Translocated promoter region protein)	2363	TPR	0	0	2	0	0	2.9
1000	0.00	0.00	1.29	P45974	Ubiquitin carboxyl-terminal hydrolase 5 (EC 3.4.19.12) (Deubiquitinating enzyme 5) (Isopeptidase T) (Ubiquitin thioesterase 5) (Ubiquitin-specific-processing protease 5)	858	USP5	0	0	2	0	0	3.2
1001	0.00	0.00	1.72	P46063	ATP-dependent DNA helicase Q1 (EC 3.6.4.12) (DNA helicase, RecQ-like type 1) (RecQ1) (DNA-dependent ATPase Q1) (RecQ protein-like 1)	649	RECQL	0	0	2	0	0	4.2

1002	0.00	0.00	0.92	P67775	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform (PP2A-alpha) (EC 3.1.3.16) (Replication protein C) (RP-C)	309	PPP2CA	0	0	2	0	0	11.4
1003	0.00	0.00	-1.61	Q02818	Nucleobindin-1 (CALNUC)	461	NUCB1	0	0	2	0	0	5
1004	0.00	0.00	0.98	Q5T3Q7	HEAT repeat-containing protein 1	2063	HEATR1	0	0	2	0	0	1.2
1005	0.00	0.00	1.23	Q8TEM1	Nuclear pore membrane glycoprotein 210 (Nuclear pore protein gp210) (Nuclear envelope pore membrane protein POM 210) (POM210) (Nucleoporin Nup210) (Pore membrane protein of 210 kDa)	1887	NUP210	0	0	2	0	0	1.4
1006	0.00	0.00	1.42	Q99426	Tubulin-folding cofactor B (Cytoskeleton-associated protein 1) (Cytoskeleton-associated protein CKAPI) (Tubulin-specific chaperone B)	244	TBCB	0	0	2	0	0	22.3
1007	0.00	0.00	-0.28	Q9BTV4	Transmembrane protein 43 (Protein LUMA)	400	TMEM43	0	0	2	0	0	6.2
1008	0.00	0.00	1.39	Q9NR45	Sialic acid synthase (N-acetylneuraminate synthase) (EC 2.5.1.56) (N-acetylneuraminate-9-phosphate synthase) (EC 2.5.1.57) (N-acetylneuraminic acid phosphate synthase) (N-acetylneuraminic acid synthase)	359	NANS	0	0	2	0	0	6.7
1009	0.00	4.31	3.06	P06702	Protein S100-A9 (Calgranulin-B) (Calprotectin L1H subunit) (Leukocyte L1 complex heavy chain) (Migration inhibitory factor-related protein 14) (MRP-14) (p14) (S100 calcium-binding protein A9)	114	S100A9	0	5	1	0	44.7	13.2

1010	0.00	1.09	1.01	F5GXX5	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1 (Oligosaccharyl transferase subunit DAD1) (EC 2.4.99.18)	85	DAD1	0	4	1	0	47.1	14.1
1011	0.00	1.09	0.66	H7C1U8	Apolipoprotein O (Fragment)	178	APOO	0	4	1	0	30.9	8.4
1012	0.00	1.08	0.15	O00483	Cytochrome c oxidase subunit NDUFA4 (Complex I-MLRQ) (CI-MLRQ) (NADH-ubiquinone oxidoreductase MLRQ subunit)	81	NDUFA4	0	4	1	0	46.9	12.3
1013	0.00	0.11	0.69	P00568	Adenylate kinase isoenzyme 1 (AK 1) (EC 2.7.4.3) (EC 2.7.4.6) (ATP-AMP transphosphorylase 1) (ATP:AMP phosphotransferase) (Adenylate monophosphate kinase) (Myokinase)	194	AK1	0	4	1	0	30.9	6.7
1014	0.00	3.75	0.00	P05109	Protein S100-A8 (Calgranulin-A) (Calprotectin L1L subunit) (Cystic fibrosis antigen) (CFAG) (Leukocyte L1 complex light chain) (Migration inhibitory factor-related protein 8) (MRP-8) (p8) (S100 calcium-binding protein A8) (Urinary stone protein band A) [Cleaved into: Protein S100-A8, N-terminally processed]	93	S100A8	0	4	1	0	39.8	11.8
1015	0.00	1.17	1.65	P63279	SUMO-conjugating enzyme UBC9 (EC 6.3.2.-) (SUMO-protein ligase) (Ubiquitin carrier protein 9) (Ubiquitin carrier protein I) (Ubiquitin-conjugating enzyme E2 I) (Ubiquitin-protein ligase I) (p18)	158	UBE2I	0	4	1	0	34.2	7.6
1016	0.00	1.30	0.37	Q8IVF2	Protein AHNAK2	5795	AHNAK2	0	4	1	0	2.1	2.4
1017	0.00	1.13	1.06	B9A067	MICOS complex subunit MIC60	711	IMMT	0	3	1	0	6.3	1.8
1018	0.00	0.58	-0.22	E9PN17	ATP synthase subunit g, mitochondrial	76	ATP5L	0	3	1	0	43.4	14.5

1019	0.00	-0.28	2.29	P00441	Superoxide dismutase [Cu-Zn] (EC 1.15.1.1) (Superoxide dismutase 1) (hSod1)	154	SOD1	0	3	1	0	21.4	21.4
1020	0.00	1.13	1.07	P24534	Elongation factor 1-beta (EF-1-beta)	225	EEF1B2	0	3	1	0	26.7	4
1021	0.00	0.79	0.32	P49458	Signal recognition particle 9 kDa protein (SRP9)	86	SRP9	0	3	1	0	34.9	12.8
1022	0.00	-0.23	0.61	Q99584	Protein S100-A13 (S100 calcium-binding protein A13)	98	S100A13	0	3	1	0	33.7	12.2
1023	0.00	-0.53	-0.13	Q9Y3F4	Serine-threonine kinase receptor-associated protein (MAP activator with WD repeats) (UNR-interacting protein) (WD-40 repeat protein PT-WD)	350	STRAP	0	3	1	0	9.7	5.1
1024	0.00	1.28	1.22	Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13	95	TIMM13	0	3	1	0	44.2	11.6
1025	0.00	-0.30	-0.41	C9J0K6	Sorcin	155	SRI	0	2	1	0	14.2	7.7
1026	0.00	-0.21	0.55	D6RCD0	Estradiol 17-beta-dehydrogenase 11	256	HSD17B11	0	2	1	0	10.2	3.9
1027	0.00	0.35	1.78	E9PKZ0	60S ribosomal protein L8 (Fragment)	205	RPL8	0	2	1	0	11.2	7.8
1028	0.00	1.51	2.78	E9PQR7	Vacuolar protein sorting-associated protein 28 homolog (Fragment)	161	VPS28	0	2	1	0	21.7	15.5
1029	0.00	0.17	0.93	F2Z2K0	NSFL1 cofactor p47	274	NSFL1C	0	2	1	0	9.9	4
1030	0.00	1.98	1.58	H0YLY7	Calcineurin B homologous protein 1 (Fragment)	91	CHP1	0	2	1	0	30.8	17.6
1031	0.00	1.19	0.91	H0YNK8	ER membrane protein complex subunit 4	102	EMC4	0	2	1	0	25.5	15.7
1032	0.00	2.70	2.16	J3QQY2	Transmembrane and coiled-coil domain-containing protein 1 (Transmembrane and coiled-coil domains 1, isoform CRA_c)	104	TMCO1	0	2	1	0	27.9	14.4
1033	0.00	2.10	1.33	O14925	Mitochondrial import inner membrane translocase subunit Tim23	209	TIMM23	0	2	1	0	12	8.1

1034	0.00	0.91	0.91	O43181	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial (Complex I-18 kDa) (CI-18 kDa) (Complex I-AQDQ) (CI-AQDQ) (NADH-ubiquinone oxidoreductase 18 kDa subunit)	175	NDUFS4	0	2	1	0	14.3	8.6
1035	0.00	-0.53	-0.16	O43399	Tumor protein D54 (hD54) (Tumor protein D52-like 2)	206	TPD52L2	0	2	1	0	12.9	6.1
1036	0.00	-0.93	1.31	O75368	SH3 domain-binding glutamic acid-rich-like protein	114	SH3BGRL	0	2	1	0	21.9	15.8
1037	0.00	1.53	0.32	P20674	Cytochrome c oxidase subunit 5A, mitochondrial (Cytochrome c oxidase polypeptide Va)	150	COX5A	0	2	1	0	15.3	12.7
1038	0.00	1.31	1.33	P56134	ATP synthase subunit f, mitochondrial	94	ATP5J2	0	2	1	0	49	14.3
1039	0.00	0.32	0.37	P61009	Signal peptidase complex subunit 3 (EC 3.4.-.-) (Microsomal signal peptidase 22/23 kDa subunit) (SPC22/23) (SPase 22/23 kDa subunit)	180	SPCS3	0	2	1	0	12.8	6.1
1040	0.00	-0.60	0.19	P62993	Growth factor receptor-bound protein 2 (Adapter protein GRB2) (Protein Ash) (SH2/SH3 adapter GRB2)	217	GRB2	0	2	1	0	9.7	3.4
1041	0.00	1.04	1.61	P84090	Enhancer of rudimentary homolog	104	ERH	0	2	1	0	21.2	10.6
1042	0.00	0.90	0.88	Q03135	Caveolin-1	178	CAV1	0	2	1	0	10.7	7.9
1043	0.00	0.83	1.36	Q16629	Serine/arginine-rich splicing factor 7 (Splicing factor 9G8) (Splicing factor, arginine/serine-rich 7)	238	SRSF7	0	2	1	0	19.7	9.1
1044	0.00	0.19	0.76	Q5JWB9	Transmembrane protein 230 (Fragment)	74	TMEM230	0	2	1	0	33.8	18.9

1045	0.00	0.17	1.10	Q5VTU3	Dynein light chain Tctex-type 1 (Dynein, light chain, Tctex-type 1, isoform CRA_a)	92	DYNLT1	0	2	1	0	37	17.4
1046	0.00	1.36	-1.05	Q9C002	Normal mucosa of esophagus-specific gene 1 protein (Protein FOAP-11)	83	NMES1	0	2	1	0	27.7	9.6
1047	0.00	1.19	-0.05	Q9NVJ2	ADP-ribosylation factor-like protein 8B (ADP-ribosylation factor-like protein 10C) (Novel small G protein indispensable for equal chromosome segregation 1)	186	ARL8B	0	2	1	0	21.5	8.6
1048	0.00	0.67	0.84	Q9Y248	DNA replication complex GINS protein PSF2 (GINS complex subunit 2)	185	GINS2	0	2	1	0	14.1	7
1049	0.00	-0.10	0.03	A0A087WU14	Secretory carrier-associated membrane protein 1 (Fragment)	206	SCAMP1	0	1	1	0	11.2	11.2
1050	0.00	3.16	4.57	C9JHF5	Mitochondrial fission factor (Fragment)	138	MFF	0	1	1	0	13	19.6
1051	0.00	1.28	0.47	E7EU96	Casein kinase II subunit alpha	385	CSNK2A1	0	1	1	0	3.9	3.9
1052	0.00	0.00	1.38	E7EW33	Cytoplasmic FMR1-interacting protein 2	1057	CYFIP2	0	1	1	0	0.9	1
1053	0.00	0.87	0.96	F5GYK7	Glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)	379	GPD2	0	1	1	0	2.4	4.2
1054	0.00	0.39	0.36	F5H6P7	Protein mago nashi homolog 2	102	MAGOHB	0	1	1	0	10.8	10.8
1055	0.00	1.67	2.60	G3V1U5	Golgi transport 1 homolog B (S. cerevisiae), isoform CRA_c (Vesicle transport protein GOT1B)	74	GOLT1B	0	1	1	0	18.9	20.3
1056	0.00	1.11	2.91	G3V2V8	Epididymal secretory protein E1 (Fragment)	122	NPC2	0	1	1	0	7.4	18.9
1057	0.00	0.71	1.30	G3V4F2	Acyl-coenzyme A thioesterase 1	395	ACOT1	0	1	1	0	2.8	2.8
1058	0.00	9.25	0.84	H0YE25	Parkinson disease 7 domain-containing protein 1 (Fragment)	144	PDDC1	0	1	1	0	6.2	6.9
1059	0.00	1.35	1.73	H7BZ81	All-trans-retinol 13,14-reductase (Fragment)	320	RETSAT	0	1	1	0	3.8	5.6

1060	0.00	1.12	1.15	H7C3P7	Ras-related protein Ral-A (Fragment)	164	RALA	0	1	1	0	9.1	9.1
1061	0.00	2.54	0.07	J3KT68	Transmembrane protein 97	92	TMEM97	0	1	1	0	16.3	8.7
1062	0.00	1.46	1.62	J3QLR8	28S ribosomal protein S23, mitochondrial	152	MRPS23	0	1	1	0	6.6	6.6
1063	0.00	1.39	1.87	K7EM02	Katanin p60 ATPase-containing subunit A-like 2 (Fragment)	128	KATNAL2	0	1	1	0	9.4	9.4
1064	0.00	1.19	1.17	K7ENI6	Uncharacterized protein	41		0	1	1	0	68.3	68.3
1065	0.00	0.51	1.33	M0QY80	Persulfide dioxygenase ETHE1, mitochondrial	95	ETHE1	0	1	1	0	14.7	14.7
1066	0.00	0.31	-0.20	O14672	Disintegrin and metalloproteinase domain-containing protein 10 (ADAM 10) (EC 3.4.24.81) (CDw156) (Kuzbanian protein homolog) (Mammalian disintegrin-metalloprotease) (CD antigen CD156c)	748	ADAM10	0	1	1	0	1.6	1.6
1067	0.00	0.85	-0.69	O14975	Very long-chain acyl-CoA synthetase (VLACS) (VLCS) (EC 6.2.1.-) (Fatty acid transport protein 2) (FATP-2) (Fatty-acid-coenzyme A ligase, very long-chain 1) (Long-chain-fatty-acid--CoA ligase) (EC 6.2.1.3) (Solute carrier family 27 member 2) (THCA-CoA ligase) (Very long-chain-fatty-acid-CoA ligase)	620	SLC27A2	0	1	1	0	3.5	1.9

1068	0.00	0.68	1.37	O75915	PRA1 family protein 3 (ADP-ribosylation factor-like protein 6-interacting protein 5) (ARL-6-interacting protein 5) (Aip-5) (Cytoskeleton-related vitamin A-responsive protein) (Dermal papilla-derived protein 11) (GTRAP3-18) (Glutamate transporter EAAC1-interacting protein) (JM5) (Prenylated Rab acceptor protein 2) (Protein JWa) (Putative MAPK-activating protein PM27)	188	ARL6IP5	0	1	1	0	10.1	10.1
1069	0.00	0.82	0.75	P01034	Cystatin-C (Cystatin-3) (Gamma-trace) (Neuroendocrine basic polypeptide) (Post-gamma-globulin)	146	CST3	0	1	1	0	7.5	7.5
1070	0.00	-0.97	0.31	P11908	Ribose-phosphate pyrophosphokinase 2 (EC 2.7.6.1) (PPRibP) (Phosphoribosyl pyrophosphate synthase II) (PRS-II)	318	PRPS2	0	1	1	0	3.1	3.1
1071	0.00	1.98	1.09	P14174	Macrophage migration inhibitory factor (MIF) (EC 5.3.2.1) (Glycosylation-inhibiting factor) (GIF) (L-dopachrome isomerase) (L-dopachrome tautomerase) (EC 5.3.3.12) (Phenylpyruvate tautomerase)	115	MIF	0	1	1	0	7.8	9.6
1072	0.00	2.17	2.22	P14678	Small nuclear ribonucleoprotein-associated proteins B and B' (snRNP-B) (Sm protein B/B') (Sm-B/B') (SmB/B')	240	SNRPB	0	1	1	0	6.1	6.1
1073	0.00	0.55	2.01	P15927	Replication protein A 32 kDa subunit (RP-A p32) (Replication factor A protein 2) (RF-A protein 2) (Replication protein A 34 kDa subunit) (RP-A p34)	270	RPA2	0	1	1	0	3	5.2

1074	0.00	2.09	2.25	P17152	Transmembrane protein 11, mitochondrial (Protein PM1) (Protein PMI)	192	TMEM11	0	1	1	0	8.3	8.3
1075	0.00	1.26	0.33	P17568	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7 (Cell adhesion protein SQM1) (Complex I-B18) (CI-B18) (NADH-ubiquinone oxidoreductase B18 subunit)	137	NDUFB7	0	1	1	0	7.3	7.3
1076	0.00	-0.18	1.27	P35754	Glutaredoxin-1 (Thioltransferase-1) (TTase-1)	106	GLRX	0	1	1	0	10.4	10.4
1077	0.00	-0.11	0.60	P52434	DNA-directed RNA polymerases I, II, and III subunit RPABC3 (RNA polymerases I, II, and III subunit ABC3) (DNA-directed RNA polymerase II subunit H) (DNA-directed RNA polymerases I, II, and III 17.1 kDa polypeptide) (RPB17) (RPB8 homolog) (hRPB8)	150	POLR2H	0	1	1	0	7.4	9.8
1078	0.00	2.34	1.27	P60903	Protein S100-A10 (Calpactin I light chain) (Calpactin-1 light chain) (Cellular ligand of annexin II) (S100 calcium-binding protein A10) (p10 protein) (p11)	97	S100A10	0	1	1	0	17.5	17.5
1079	0.00	-0.57	-0.15	P61011	Signal recognition particle 54 kDa protein (SRP54)	504	SRP54	0	1	1	0	2.4	2.4
1080	0.00	0.30	0.36	P62273	40S ribosomal protein S29	56	RPS29	0	1	1	0	19.6	14.3
1081	0.00	2.39	0.89	P78347	General transcription factor II-I (GTFII-I) (TFII-I) (Bruton tyrosine kinase-associated protein 135) (BAP-135) (BTK-associated protein 135) (SRF-Phox1-interacting protein) (SPIN) (Williams-Beuren syndrome chromosomal region 6 protein)	998	GTF2I	0	1	1	0	0.9	1.3
1082	0.00	6.44	2.92	Q15058	Kinesin-like protein KIF14	1648	KIF14	0	1	1	0	0.7	0.7

1083	0.00	1.00	2.57	Q15149	Plectin (PCN) (PLTN) (Hemidesmosomal protein 1) (HD1) (Plectin-1)	4684	PLEC	0	1	1	0	0.3	0.3
1084	0.00	0.03	3.59	Q6P2Q9	Pre-mRNA-processing-splicing factor 8 (220 kDa U5 snRNP-specific protein) (PRP8 homolog) (Splicing factor Prp8) (p220)	2335	PRPF8	0	1	1	0	0.3	1.1
1085	0.00	1.89	1.54	Q8N6L1	Keratinocyte-associated protein 2 (KCP-2)	136	KRTCAP2	0	1	1	0	12.5	12.5
1086	0.00	0.42	1.32	Q93009	Ubiquitin carboxyl-terminal hydrolase 7 (EC 3.4.19.12) (Deubiquitinating enzyme 7) (Herpesvirus-associated ubiquitin-specific protease) (Ubiquitin thioesterase 7) (Ubiquitin-specific-processing protease 7)	1102	USP7	0	1	1	0	1.2	1.1
1087	0.00	0.29	1.00	Q96TA1	Niban-like protein 1 (Meg-3) (Melanoma invasion by ERK) (MINERVA) (Protein FAM129B)	746	FAM129B	0	1	1	0	1.8	1.8
1088	0.00	-0.31	1.90	Q99436	Proteasome subunit beta type-7 (EC 3.4.25.1) (Macropain chain Z) (Multicatalytic endopeptidase complex chain Z) (Proteasome subunit Z)	277	PSMB7	0	1	1	0	3.2	4.7
1089	0.00	0.00	1.24	Q9NPA8	Transcription and mRNA export factor ENY2 (Enhancer of yellow 2 transcription factor homolog)	101	ENY2	0	1	1	0	9.4	17.7
1090	0.00	2.65	2.47	Q9UBI6	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12	72	GNG12	0	1	1	0	22.2	25
1091	0.00	-0.20	0.30	Q9UHV9	Prefoldin subunit 2	154	PFDN2	0	1	1	0	7.8	7.8
1092	0.00	1.26	0.97	S4R3B5	Protein transport protein Sec61 subunit beta	42	SEC61B	0	1	1	0	23.8	23.8
1093	0.00	-0.58	-0.37	U3KQT1	S-formylglutathione hydrolase (Fragment)	120	ESD	0	1	1	0	7.5	7.5

1094	0.00	0.00	0.12	A0A087WTA2	Protein SYNJ2BP-COX16	40	SYNJ2BP-COX16	0	0	1	0	0	35
1095	0.00	0.00	2.48	C9JUG7	F-actin-capping protein subunit alpha-2	146	CAPZA2	0	0	1	0	0	12.3
1096	0.00	0.00	1.64	D6RDY6	Signal recognition particle subunit SRP72 (Fragment)	357	SRP72	0	0	1	0	0	5.3
1097	0.00	0.00	1.03	D6RGI3	Septin 11, isoform CRA_b (Septin-11)	425	sept11	0	0	1	0	0	3.1
1098	0.00	0.00	-0.22	D6RH17	Alcohol dehydrogenase 6 (Fragment)	257	ADH6	0	0	1	0	0	3.9
1099	0.00	0.00	1.14	D6RHZ5	Protein transport protein Sec31A	877	SEC31A	0	0	1	0	0	1.5
1100	0.00	0.00	-0.15	E5RIX8	Tubulin-specific chaperone A	79	TBCA	0	0	1	0	0	12.7
1101	0.00	0.00	2.51	E7EMM4	Acid ceramidase	370	ASAH1	0	0	1	0	0	4.6
1102	0.00	0.00	2.39	F5GX77	Multifunctional methyltransferase subunit TRM112-like protein	106	TRMT112	0	0	1	0	0	12.3
1103	0.00	0.00	0.60	F8VVL1	Density-regulated protein	160	DENR	0	0	1	0	0	5
1104	0.00	0.00	0.43	F8VVW8	3'(2'),5'-bisphosphate nucleotidase 1 (Fragment)	130	BPNT1	0	0	1	0	0	8.5
1105	0.00	0.00	0.54	F8WJN3	Cleavage and polyadenylation-specificity factor subunit 6	478	CPSF6	0	0	1	0	0	2.9
1106	0.00	0.00	0.38	H0Y9Q1	Cytosol aminopeptidase (Fragment)	208	LAP3	0	0	1	0	0	8.7
1107	0.00	0.00	1.20	H0YDS0	Ubiquilin-1 (Fragment)	157	UBQLN1	0	0	1	0	0	10.2
1108	0.00	0.00	3.28	H0YE46	RNA-binding protein 25 (Fragment)	73	RBM25	0	0	1	0	0	20.5
1109	0.00	0.00	4.86	H0YFA4	Cysteine-rich protein 2 (Fragment)	192	CRIP2	0	0	1	0	0	16.7
1110	0.00	0.00	1.27	I3L252	Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing) (Fragment)	219	DAK	0	0	1	0	0	5.5
1111	0.00	0.00	0.96	J3QLD9	Flotillin-2 (HCG1998851, isoform CRA_h)	428	FLOT2	0	0	1	0	0	4.4
1112	0.00	0.00	1.63	K7EMV3	Histone H3	92	H3F3B	0	0	1	0	0	7.6
1113	0.00	0.00	1.23	K7EP16	Eukaryotic translation initiation factor 3 subunit G (Fragment)	118	EIF3G	0	0	1	0	0	13.6

1114	0.00	0.00	1.70	O00170	AH receptor-interacting protein (AIP) (Aryl-hydrocarbon receptor-interacting protein) (HBV X-associated protein 2) (XAP-2) (Immunophilin homolog ARA9)	330	AIP	0	0	1	0	0	4.2
1115	0.00	0.00	0.77	O43852	Calumenin (Crocalbin) (IEF SSP 9302)	315	CALU	0	0	1	0	0	8.4
1116	0.00	0.00	3.17	O43896	Kinesin-like protein KIF1C	1103	KIF1C	0	0	1	0	0	0.8
1117	0.00	0.00	1.24	O60869	Endothelial differentiation-related factor 1 (EDF-1) (Multiprotein-bridging factor 1) (MBF1)	148	EDF1	0	0	1	0	0	10.1
1118	0.00	0.00	0.95	O75436	Vacuolar protein sorting-associated protein 26A (Vesicle protein sorting 26A) (hVPS26)	327	VPS26A	0	0	1	0	0	5.5
1119	0.00	0.00	4.01	O75937	DnaJ homolog subfamily C member 8 (Splicing protein spf31)	253	DNAJC8	0	0	1	0	0	11.5
1120	0.00	0.00	1.76	P12074	Cytochrome c oxidase subunit 6A1, mitochondrial (Cytochrome c oxidase polypeptide VIa-liver) (Cytochrome c oxidase subunit VIA-liver) (COX VIa-L)	109	COX6A1	0	0	1	0	0	16.5
1121	0.00	0.00	2.35	P13995	Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial [Includes: NAD-dependent methylenetetrahydrofolate dehydrogenase (EC 1.5.1.15); Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9)]	350	MTHFD2	0	0	1	0	0	9.3
1122	0.00	0.00	1.94	P17174	Aspartate aminotransferase, cytoplasmic (cAspAT) (EC 2.6.1.1) (EC 2.6.1.3) (Cysteine aminotransferase, cytoplasmic) (Cysteine transaminase, cytoplasmic) (cCAT) (Glutamate oxaloacetate transaminase 1) (Transaminase A)	413	GOT1	0	0	1	0	0	3.6

1123	0.00	0.00	2.22	P18084	Integrin beta-5	799	ITGB5	0	0	1	0	0	2.5
1124	0.00	0.00	-0.01	P20073	Annexin A7 (Annexin VII) (Annexin-7) (Synexin)	488	ANXA7	0	0	1	0	0	1.9
1125	0.00	0.00	0.79	P25685	DnaJ homolog subfamily B member 1 (DnaJ protein homolog 1) (Heat shock 40 kDa protein 1) (HSP40) (Heat shock protein 40) (Human DnaJ protein 1) (hDj-1)	340	DNAJB1	0	0	1	0	0	2.9
1126	0.00	0.00	2.33	P26196	Probable ATP-dependent RNA helicase DDX6 (EC 3.6.4.13) (ATP-dependent RNA helicase p54) (DEAD box protein 6) (Oncogene RCK)	483	DDX6	0	0	1	0	0	3.5
1127	0.00	0.00	1.07	P39023	60S ribosomal protein L3 (HIV-1 TAR RNA-binding protein B) (TARBP-B)	403	RPL3	0	0	1	0	0	2
1128	0.00	0.00	0.54	P39748	Flap endonuclease 1 (FEN-1) (EC 3.1.-.-) (DNase IV) (Flap structure-specific endonuclease 1) (Maturation factor 1) (MF1) (hFEN-1)	380	FEN1	0	0	1	0	0	4.2
1129	0.00	0.00	1.53	Q13045	Protein flightless-1 homolog	1269	FLII	0	0	1	0	0	0.8
1130	0.00	0.00	0.51	Q13085	Acetyl-CoA carboxylase 1 (ACC1) (EC 6.4.1.2) (ACC-alpha) [Includes: Biotin carboxylase (EC 6.3.4.14)]	2346	ACACA	0	0	1	0	0	0.5
1131	0.00	0.00	0.36	Q14320	Protein FAM50A (Protein HXC-26) (Protein XAP-5)	339	FAM50A	0	0	1	0	0	4.7
1132	0.00	0.00	-0.10	Q5QPP3	UDP-glucose 4-epimerase (Fragment)	227	GALE	0	0	1	0	0	6.2
1133	0.00	0.00	0.18	Q7KZ85	Transcription elongation factor SPT6 (hSPT6) (Histone chaperone suppressor of Ty6) (Tat-cotransactivator 2 protein) (Tat-CT2 protein)	1726	SUPT6H	0	0	1	0	0	1.5

1134	0.00	0.00	1.28	Q8WVM8	Sec1 family domain-containing protein 1 (SLY1 homolog) (Sly1p) (Syntaxin-binding protein 1-like 2)	642	SCFD1	0	0	1	0	0	2.5
1135	0.00	0.00	-0.14	Q8WZ42	Titin (EC 2.7.11.1) (Connectin) (Rhabdomyosarcoma antigen MU-RMS-40.14)	34350	TTN	0	0	1	0	0	0
1136	0.00	0.00	1.88	Q92887	Canalicular multispecific organic anion transporter 1 (ATP-binding cassette sub-family C member 2) (Canalicular multidrug resistance protein) (Multidrug resistance-associated protein 2)	1545	ABCC2	0	0	1	0	0	1
1137	0.00	0.00	0.76	Q93008	Probable ubiquitin carboxyl-terminal hydrolase FAF-X (EC 3.4.19.12) (Deubiquitinating enzyme FAF-X) (Fat facets in mammals) (hFAM) (Fat facets protein-related, X-linked) (Ubiquitin thioesterase FAF-X) (Ubiquitin-specific protease 9, X chromosome) (Ubiquitin-specific-processing protease FAF-X)	2570	USP9X	0	0	1	0	0	0.5
1138	0.00	0.00	1.59	Q96BS2	Calcineurin B homologous protein 3 (Tescalcin) (TSC)	214	TESC	0	0	1	0	0	8
1139	0.00	0.00	2.18	Q96GC9	Vacuole membrane protein 1 (Transmembrane protein 49)	406	VMP1	0	0	1	0	0	14
1140	0.00	0.00	0.54	Q96HE7	ERO1-like protein alpha (ERO1-L) (ERO1-L-alpha) (EC 1.8.4.-) (Endoplasmic oxidoreductin-1-like protein) (Oxidoreductin-1-L-alpha)	468	ERO1L	0	0	1	0	0	3
1141	0.00	0.00	2.13	Q96K17	Transcription factor BTF3 homolog 4 (Basic transcription factor 3-like 4)	158	BTF3L4	0	0	1	0	0	26

1142	0.00	0.00	0.60	Q9BSH4	Translational activator of cytochrome c oxidase 1 (Coiled-coil domain-containing protein 44) (Translational activator of mitochondrially-encoded cytochrome c oxidase I)	297	TACO1	0	0	1	0	0	6.1
1143	0.00	0.00	0.99	Q9BZX2	Uridine-cytidine kinase 2 (UCK 2) (EC 2.7.1.48) (Cytidine monophosphokinase 2) (Testis-specific protein TSA903) (Uridine monophosphokinase 2)	261	UCK2	0	0	1	0	0	6.9
1144	0.00	0.00	0.28	Q9H0U6	39S ribosomal protein L18, mitochondrial (L18mt) (MRP-L18)	180	MRPL18	0	0	1	0	0	5
1145	0.00	0.00	0.24	Q9Y512	Sorting and assembly machinery component 50 homolog (Transformation-related gene 3 protein) (TRG-3)	469	SAMM50	0	0	1	0	0	3.2
1146	0.00	0.00	-0.11	R4GN98	Protein S100 (S100 calcium-binding protein) (Fragment)	85	S100A6	0	0	1	0	0	8.2
1147	0.00	0.00	1.29	V9H019	DNA mismatch repair protein Msh2 (MSH2 protein)	810	MSH2	0	0	1	0	0	1.4
1148	0.00	4.06	0.00	P15924	Desmoplakin (DP) (250/210 kDa paraneoplastic pemphigus antigen)	2871	DSP	0	35	0	0	13.1	0
1149	0.00	4.04	0.00	Q02413	Desmoglein-1 (Cadherin family member 4) (Desmosomal glycoprotein 1) (DG1) (DGI) (Pemphigus foliaceus antigen)	1049	DSG1	0	12	0	0	16.2	0
1150	0.00	3.40	0.00	P31944	Caspase-14 (CASP-14) (EC 3.4.22.-) [Cleaved into: Caspase-14 subunit p17, mature form; Caspase-14 subunit p10, mature form; Caspase-14 subunit p20, intermediate form; Caspase-14 subunit p8, intermediate form]	242	CASP14	0	5	0	0	17.8	0
1151	0.00	4.93	0.00	Q96P63	Serpin B12	405	SERPINB12	0	5	0	0	12.3	0

1152	0.00	0.39	0.00	P09669	Cytochrome c oxidase subunit 6C (Cytochrome c oxidase polypeptide VIc)	75	COX6C	0	4	0	0	30.7	0
1153	0.00	4.10	0.00	Q08554	Desmocollin-1 (Cadherin family member 1) (Desmosomal glycoprotein 2/3) (DG2/DG3)	894	DSC1	0	4	0	0	6.2	0
1154	0.00	4.03	0.00	Q5T749	Keratinocyte proline-rich protein (hKPRP)	579	KPRP	0	4	0	0	5	0
1155	0.00	0.13	0.00	Q96FQ6	Protein S100-A16 (Aging-associated gene 13 protein) (Protein S100-F) (S100 calcium-binding protein A16)	103	S100A16	0	4	0	0	51.5	0
1156	0.00	1.16	0.00	K7ESP4	Dephospho-CoA kinase domain-containing protein (Fragment)	209	DCAKD	0	3	0	0	16.7	0
1157	0.00	1.27	0.00	O95168	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4 (Complex I-B15) (CI-B15) (NADH-ubiquinone oxidoreductase B15 subunit)	129	NDUFB4	0	3	0	0	21.7	0
1158	0.00	4.07	0.00	P04040	Catalase (EC 1.11.1.6)	527	CAT	0	3	0	0	7	0
1159	0.00	4.53	0.00	P05089	Arginase-1 (EC 3.5.3.1) (Liver-type arginase) (Type I arginase)	322	ARG1	0	3	0	0	9.6	0
1160	0.00	-0.09	0.00	Q6GMV3	Putative peptidyl-tRNA hydrolase PTRHD1 (EC 3.1.1.29) (Peptidyl-tRNA hydrolase domain-containing protein 1)	140	PTRHD1	0	3	0	0	21.4	0
1161	0.00	0.69	0.00	Q7RTV0	PHD finger-like domain-containing protein 5A (PHD finger-like domain protein 5A) (Splicing factor 3B-associated 14 kDa protein) (SF3b14b)	110	PHF5A	0	3	0	0	28.2	0

1162	0.00	0.87	0.00	Q9Y2R0	Cytochrome c oxidase assembly factor 3 homolog, mitochondrial (Coiled-coil domain-containing protein 56) (Mitochondrial translation regulation assembly intermediate of cytochrome c oxidase protein of 12 kDa)	106	COA3	0	3	0	0	29.2	0
1163	0.00	0.98	0.00	C9JQD4	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) (Fragment)	144	PPIH	0	2	0	0	13.2	0
1164	0.00	0.20	0.00	D6RAW0	Ubiquitin-conjugating enzyme E2 D3 (Fragment)	72	UBE2D3	0	2	0	0	23.6	0
1165	0.00	0.27	0.00	E7EQV9	Ribosomal protein L15 (Fragment)	174	RPL15	0	2	0	0	14.9	0
1166	0.00	0.15	0.00	E7ERH2	S-phase kinase-associated protein 1 (Fragment)	142	SKP1	0	2	0	0	14.8	0
1167	0.00	1.63	0.00	E9PPW7	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial (Fragment)	184	NDUFS8	0	2	0	0	16.3	0
1168	0.00	0.75	0.00	F5H702	39S ribosomal protein L48, mitochondrial	113	MRPL48	0	2	0	0	21.2	0
1169	0.00	0.43	0.00	H7C0A3	Protein ARPC4-TTLL3 (Fragment)	167	ARPC4-TTLL3	0	2	0	0	11.4	0
1170	0.00	0.76	0.00	H7C585	Frataxin, mitochondrial (Fragment)	108	FXN	0	2	0	0	22.2	0
1171	0.00	1.05	0.00	J3QL56	Protein SCO1 homolog, mitochondrial	270	SCO1	0	2	0	0	10.4	0
1172	0.00	0.49	0.00	O14907	Tax1-binding protein 3 (Glutaminase-interacting protein 3) (Tax interaction protein 1) (TIP-1) (Tax-interacting protein 1)	124	TAX1BP3	0	2	0	0	25	0
1173	0.00	1.19	0.00	O14949	Cytochrome b-c1 complex subunit 8 (Complex III subunit 8) (Complex III subunit VIII) (Ubiquinol-cytochrome c reductase complex 9.5 kDa protein) (Ubiquinol-cytochrome c reductase complex ubiquinone-binding protein QP-C)	82	UQCRQ	0	2	0	0	25.6	0

1174	0.00	1.27	0.00	O43678	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2 (Complex I-B8) (CI-B8) (NADH-ubiquinone oxidoreductase B8 subunit)	99	NDUFA2	0	2	0	0	30.3	0
1175	0.00	1.04	0.00	O60830	Mitochondrial import inner membrane translocase subunit Tim17-B	172	TIMM17B	0	2	0	0	21.5	0
1176	0.00	0.53	0.00	O75340	Programmed cell death protein 6 (Apoptosis-linked gene 2 protein) (Probable calcium-binding protein ALG-2)	191	PDCD6	0	2	0	0	21.2	0
1177	0.00	1.25	0.00	O95182	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7 (Complex I-B14.5a) (CI-B14.5a) (NADH-ubiquinone oxidoreductase subunit B14.5a)	113	NDUFA7	0	2	0	0	23	0
1178	0.00	5.02	0.00	P01040	Cystatin-A (Cystatin-AS) (Stefin-A) [Cleaved into: Cystatin-A, N-terminally processed]	98	CSTA	0	2	0	0	30.6	0
1179	0.00	2.08	0.00	P10253	Lysosomal alpha-glucosidase (EC 3.2.1.20) (Acid maltase) (Aglucosidase alfa) [Cleaved into: 76 kDa lysosomal alpha-glucosidase; 70 kDa lysosomal alpha-glucosidase]	952	GAA	0	2	0	0	4.5	0
1180	0.00	1.09	0.00	P14927	Cytochrome b-c1 complex subunit 7 (Complex III subunit 7) (Complex III subunit VII) (QP-C) (Ubiquinol-cytochrome c reductase complex 14 kDa protein)	111	UQCRB	0	2	0	0	21.6	0
1181	0.00	1.07	0.00	P21912	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial (EC 1.3.5.1) (Iron-sulfur subunit of complex II) (Ip)	280	SDHB	0	2	0	0	7.5	0
1182	0.00	0.68	0.00	P26373	60S ribosomal protein L13 (Breast basic conserved protein 1)	211	RPL13	0	2	0	0	14	0

1183	0.00	1.75	0.00	P29508	Serpin B3 (Protein T4-A) (Squamous cell carcinoma antigen 1) (SCCA-1)	390	SERPINB3	0	2	0	0	5.9	0
1184	0.00	0.58	0.00	P53999	Activated RNA polymerase II transcriptional coactivator p15 (Positive cofactor 4) (PC4) (SUB1 homolog) (p14)	127	SUB1	0	2	0	0	11	0
1185	0.00	0.10	0.00	P55769	NHP2-like protein 1 (High mobility group-like nuclear protein 2 homolog 1) (OTK27) (SNU13 homolog) (hSNU13) (U4/U6.U5 tri-snRNP 15.5 kDa protein) [Cleaved into: NHP2-like protein 1, N-terminally processed]	128	NHP2L1	0	2	0	0	18	0
1186	0.00	1.11	0.00	P61769	Beta-2-microglobulin [Cleaved into: Beta-2-microglobulin form pI 5.3]	119	B2M	0	2	0	0	26.9	0
1187	0.00	1.04	0.00	P62304	Small nuclear ribonucleoprotein E (snRNP-E) (Sm protein E) (Sm-E) (SmE)	92	SNRPE	0	2	0	0	25	0
1188	0.00	-0.13	0.00	P63167	Dynein light chain 1, cytoplasmic (8 kDa dynein light chain) (DLC8) (Dynein light chain LC8-type 1) (Protein inhibitor of neuronal nitric oxide synthase) (PIN)	89	DYNLL1	0	2	0	0	20.2	0
1189	0.00	0.81	0.00	P63173	60S ribosomal protein L38	70	RPL38	0	2	0	0	28.6	0
1190	0.00	1.73	0.00	P82664	28S ribosomal protein S10, mitochondrial (MRP-S10) (S10mt)	201	MRPS10	0	2	0	0	14.4	0
1191	0.00	0.74	0.00	P82979	SAP domain-containing ribonucleoprotein (Cytokine-induced protein of 29 kDa) (Nuclear protein Hcc-1) (Proliferation-associated cytokine-inducible protein CIP29)	210	SARNP	0	2	0	0	9	0
1192	0.00	-0.07	0.00	Q13247	Serine/arginine-rich splicing factor 6 (Pre-mRNA-splicing factor SRP55) (Splicing factor, arginine/serine-rich 6)	344	SRSF6	0	2	0	0	6.3	0

1193	0.00	1.99	0.00	Q15125	3-beta-hydroxysteroid-Delta(8),Delta(7)-isomerase (EC 5.3.3.5) (Cholestenol Delta-isomerase) (Delta(8)-Delta(7) sterol isomerase) (D8-D7 sterol isomerase) (Emopamil-binding protein)	230	EBP	0	2	0	0	12.2	0
1194	0.00	0.06	0.00	Q3ZAQ7	Vacuolar ATPase assembly integral membrane protein VMA21 (Myopathy with excessive autophagy protein)	101	VMA21	0	2	0	0	21.8	0
1195	0.00	1.30	0.00	Q6P1X6	UPF0598 protein C8orf82	216	C8orf82	0	2	0	0	13.5	0
1196	0.00	1.37	0.00	Q7Z7K0	COX assembly mitochondrial protein homolog (Cmc1p)	106	CMC1	0	2	0	0	18.9	0
1197	0.00	0.17	0.00	Q8N983	39S ribosomal protein L43, mitochondrial (L43mt) (MRP-L43) (Mitochondrial ribosomal protein bMRP36a)	215	MRPL43	0	2	0	0	12.6	0
1198	0.00	0.92	0.00	Q8NI27	THO complex subunit 2 (Tho2) (hTREX120)	1593	THOC2	0	2	0	0	1.4	0
1199	0.00	0.21	0.00	Q8WVC2	40S ribosomal protein S21	81	RPS21	0	2	0	0	35.8	0
1200	0.00	1.77	0.00	Q9HB66	Alternative protein MKKS (McKusick-Kaufman syndrome, isoform CRA_a) (McKusick-Kaufman/Bardet-Biedl syndromes putative chaperonin) (PNAS-117)	63	MKKS	0	2	0	0	41.3	0
1201	0.00	0.69	0.00	Q9NP97	Dynein light chain roadblock-type 1 (Bithoraxoid-like protein) (BLP) (Dynein light chain 2A, cytoplasmic) (Dynein-associated protein Km23) (Roadblock domain-containing protein 1)	96	DYNLRB1	0	2	0	0	25	0

1202	0.00	0.86	0.00	Q9Y333	U6 snRNA-associated Sm-like protein LSm2 (Protein G7b) (Small nuclear ribonuclear protein D homolog) (snRNP core Sm-like protein Sm-x5)	95	LSM2	0	2	0	0	31.6	0
1203	0.00	1.06	0.00	Q9Y3B7	39S ribosomal protein L11, mitochondrial (L11mt) (MRP-L11)	192	MRPL11	0	2	0	0	17.5	0
1204	0.00	0.83	0.00	Q9Y3D6	Mitochondrial fission 1 protein (FIS1 homolog) (hFis1) (Tetratricopeptide repeat protein 11) (TPR repeat protein 11)	152	FIS1	0	2	0	0	15.8	0
1205	0.00	0.35	0.00	Q9Y5J7	Mitochondrial import inner membrane translocase subunit Tim9	89	TIMM9	0	2	0	0	29.2	0
1206	0.00	2.12	0.00	A0A087WUD3	Oligosaccharyltransferase complex subunit OSTC	83	OSTC	0	1	0	0	14.5	0
1207	0.00	2.31	0.00	A0A087WVT9	Nucleoside diphosphate kinase (EC 2.7.4.6)	153	NME4	0	1	0	0	7.8	0
1208	0.00	0.22	0.00	A0A087WY88	Protein jagunal homolog 1	181	JAGN1	0	1	0	0	6.6	0
1209	0.00	6.49	0.00	A0A087WYF5	Salivary acidic proline-rich phosphoprotein 1/2 (Fragment)	140	PRH1	0	1	0	0	12.1	0
1210	0.00	-0.20	0.00	B5MC59	Replication protein A 14 kDa subunit (Replication protein A3, 14kDa, isoform CRA_a)	82	RPA3	0	1	0	0	14.6	0
1211	0.00	1.43	0.00	B8ZZV5	39S ribosomal protein L30, mitochondrial	101	MRPL30	0	1	0	0	10.9	0
1212	0.00	0.32	0.00	C9IZG4	Protein CutA	135	CUTA	0	1	0	0	13.3	0
1213	0.00	1.97	0.00	C9JAW5	HIG1 domain family member 1A, mitochondrial	83	HIGD1A	0	1	0	0	21.7	0
1214	0.00	2.68	0.00	C9JEV0	Zinc-alpha-2-glycoprotein	227	AZGP1	0	1	0	0	5.3	0
1215	0.00	0.99	0.00	C9JKQ2	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3 (Fragment)	65	NDUFB3	0	1	0	0	16.9	0

1216	0.00	0.18	0.00	C9JL85	Myotrophin	52	MTPN	0	1	0	0	32.7	0
1217	0.00	0.90	0.00	C9JY28	LYR motif-containing protein 4	70	LYRM4	0	1	0	0	20	0
1218	0.00	0.38	0.00	C9JYN0	Synaptophysin-like protein 1	224	SYPL1	0	1	0	0	4.9	0
1219	0.00	5.73	0.00	D3DRR9	Chromosome 10 open reading frame 47, isoform CRA_b (Proline and serine-rich protein 2)	239	C10orf47	0	1	0	0	5.4	0
1220	0.00	1.32	0.00	D6R9Z7	Cytochrome c oxidase subunit 7C, mitochondrial	56	COX7C	0	1	0	0	16.1	0
1221	0.00	1.32	0.00	E5RGY0	Derlin-1	151	DERL1	0	1	0	0	7.3	0
1222	0.00	2.21	0.00	E7EWF7	Uncharacterized protein (Fragment)	191		0	1	0	0	13.1	0
1223	0.00	2.20	0.00	E9PKY5	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) (Fragment)	213	PPIE	0	1	0	0	4.2	0
1224	0.00	-0.04	0.00	E9PNW4	CD59 glycoprotein	108	CD59	0	1	0	0	7.4	0
1225	0.00	-0.58	0.00	E9PPQ4	Ferritin (Fragment)	58	FTH1	0	1	0	0	12.1	0
1226	0.00	1.45	0.00	F5H169	26S proteasome non-ATPase regulatory subunit 9	128	PSMD9	0	1	0	0	9.4	0
1227	0.00	-0.11	0.00	F5H1S8	Malectin (Fragment)	146	MLEC	0	1	0	0	8.2	0
1228	0.00	1.60	0.00	F6WST4	ORM1-like protein 1 (Fragment)	108	ORMDL1	0	1	0	0	13.9	0
1229	0.00	0.17	0.00	F8VSA6	NEDD8	50	NEDD8	0	1	0	0	22	0
1230	0.00	2.57	0.00	F8VV32	Lysozyme (EC 3.2.1.17)	104	LYZ	0	1	0	0	11.5	0
1231	0.00	0.85	0.00	F8WEX5	Sulfatase-modifying factor 2	165	SUMF2	0	1	0	0	6.1	0
1232	0.00	4.84	0.00	G8JLG2	Corneodesmosin	529	CDSN	0	1	0	0	3.4	0
1233	0.00	-0.45	0.00	G8JLQ3	Biogenesis of lysosome-related organelles complex 1 subunit 1	75	BLOC1S1	0	1	0	0	14.7	0
1234	0.00	0.69	0.00	H0Y993	Protein DEK (Fragment)	156	DEK	0	1	0	0	8.3	0
1235	0.00	1.42	0.00	H0YDP7	39S ribosomal protein L49, mitochondrial (Fragment)	127	MRPL49	0	1	0	0	11	0

1236	0.00	-0.02	0.00	H0YER1	Remodeling and spacing factor 1 (Fragment)	702	RSF1	0	1	0	0	1.7	0
1237	0.00	1.58	0.00	H0YF90	Cation-dependent mannose-6-phosphate receptor (Fragment)	148	M6PR	0	1	0	0	18.2	0
1238	0.00	0.82	0.00	H3BSA6	dCTP pyrophosphatase 1	71	DCTPP1	0	1	0	0	14.1	0
1239	0.00	-0.12	0.00	H7BY91	60S ribosomal protein L36a	70	RPL36A	0	1	0	0	14.3	0
1240	0.00	1.56	0.00	J3KS15	Peptidyl-tRNA hydrolase ICT1, mitochondrial (Fragment)	192	ICT1	0	1	0	0	7.3	0
1241	0.00	0.74	0.00	J3KTI5	Receptor tyrosine-protein kinase erbB-2 (Fragment)	251	ERBB2	0	1	0	0	4.8	0
1242	0.00	-9.65	0.00	J3KTP2	WD repeat-containing protein WRAP73 (Fragment)	200	WRAP73	0	1	0	0	4.5	0
1243	0.00	-0.19	0.00	J3QR72	Bromodomain-containing protein 2	162	BRD2	0	1	0	0	8	0
1244	0.00	-0.97	0.00	K4DIB9	Cysteine-rich protein 1 (Fragment)	46	CRIP1	0	1	0	0	19.6	0
1245	0.00	-0.04	0.00	K7EM09	Transmembrane protein 205 (Fragment)	120	TMEM205	0	1	0	0	10.8	0
1246	0.00	-0.07	0.00	K7ENF1	Peroxisomal acyl-coenzyme A oxidase 1 (Fragment)	132	ACOX1	0	1	0	0	10.6	0
1247	0.00	1.70	0.00	K7EQ77	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11	120	NDUFA11	0	1	0	0	19.2	0
1248	0.00	2.27	0.00	K7EQQ1	Cleft lip and palate transmembrane protein 1 (Fragment)	171	CLPTM1	0	1	0	0	8.8	0
1249	0.00	0.81	0.00	L0R6Q1	Alternative protein SLC35A4 (Probable UDP-sugar transporter protein SLC35A4)	103	SLC35A4	0	1	0	0	7.8	0
1250	0.00	0.29	0.00	M0QXH0	Thioredoxin, mitochondrial	64	TXN2	0	1	0	0	23.4	0
1251	0.00	-2.71	0.00	M0R050	Exosome complex component RRP46	197	EXOSC5	0	1	0	0	6.1	0

1252	0.00	0.52	0.00	M0R203	Heterogeneous nuclear ribonucleoprotein U-like protein 1 (Fragment)	81	HNRNPUL1	0	1	0	0	13.6	0
1253	0.00	0.08	0.00	O15155	BET1 homolog (hBET1) (Golgi vesicular membrane-trafficking protein p18)	118	BET1	0	1	0	0	13.3	0
1254	0.00	1.39	0.00	O43402	ER membrane protein complex subunit 8 (Neighbor of COX4) (Protein FAM158B)	210	EMC8	0	1	0	0	5.7	0
1255	0.00	-0.58	0.00	O43598	2'-deoxynucleoside 5'-phosphate N-hydrolase 1 (EC 3.2.2.-) (c-Myc-responsive protein RCL)	174	DNPH1	0	1	0	0	11.5	0
1256	0.00	-0.30	0.00	O60763	General vesicular transport factor p115 (Protein USO1 homolog) (Transcytosis-associated protein) (TAP) (Vesicle-docking protein)	962	USO1	0	1	0	0	1.2	0
1257	0.00	1.42	0.00	O60783	28S ribosomal protein S14, mitochondrial (MRP-S14) (S14mt)	128	MRPS14	0	1	0	0	11.7	0
1258	0.00	1.02	0.00	O75380	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial (Complex I-13kD-A) (CI-13kD-A) (NADH-ubiquinone oxidoreductase 13 kDa-A subunit)	124	NDUFS6	0	1	0	0	12.1	0
1259	0.00	-0.23	0.00	O75531	Barrier-to-autointegration factor (Breakpoint cluster region protein 1) [Cleaved into: Barrier-to-autointegration factor, N-terminally processed]	89	BANF1	0	1	0	0	13.5	0
1260	0.00	0.75	0.00	O75934	Pre-mRNA-splicing factor SPF27 (Breast carcinoma-amplified sequence 2) (DNA amplified in mammary carcinoma 1 protein) (Spliceosome-associated protein SPF 27)	225	BCAS2	0	1	0	0	5.8	0

1261	0.00	1.57	0.00	O95298	NADH dehydrogenase [ubiquinone] 1 subunit C2 (Complex I-B14.5b) (CI-B14.5b) (Human lung cancer oncogene 1 protein) (HLC-1) (NADH-ubiquinone oxidoreductase subunit B14.5b)	119	NDUFC2	0	1	0	0	12.5	0
1262	0.00	0.50	0.00	O95969	Secretoglobin family 1D member 2 (Lipophilin-B)	90	SCGB1D2	0	1	0	0	10	0
1263	0.00	0.41	0.00	P00846	ATP synthase subunit a (F-ATPase protein 6)	226	MT-ATP6	0	1	0	0	4.4	0
1264	0.00	2.42	0.00	P03928	ATP synthase protein 8 (A6L) (F-ATPase subunit 8)	68	MT-ATP8	0	1	0	0	13.2	0
1265	0.00	1.75	0.00	P05386	60S acidic ribosomal protein P1	114	RPLP1	0	1	0	0	14	0
1266	0.00	0.31	0.00	P07311	Acylphosphatase-1 (EC 3.6.1.7) (Acylphosphatase, erythrocyte isozyme) (Acylphosphatase, organ-common type isozyme) (Acylphosphate phosphohydrolase 1)	99	ACYP1	0	1	0	0	13.1	0
1267	0.00	1.10	0.00	P09234	U1 small nuclear ribonucleoprotein C (U1 snRNP C) (U1-C) (U1C)	159	SNRPC	0	1	0	0	11.3	0
1268	0.00	1.70	0.00	P10301	Ras-related protein R-Ras (p23)	218	RRAS	0	1	0	0	5	0
1269	0.00	7.51	0.00	P11532	Dystrophin	3685	DMD	0	1	0	0	0.5	0
1270	0.00	1.11	0.00	P14406	Cytochrome c oxidase subunit 7A2, mitochondrial (Cytochrome c oxidase subunit VIIa-liver/heart) (Cytochrome c oxidase subunit VIIa-L) (Cytochrome c oxidase subunit VIIaL)	83	COX7A2	0	1	0	0	15.7	0
1271	0.00	1.26	0.00	P14854	Cytochrome c oxidase subunit 6B1 (Cytochrome c oxidase subunit VIb isoform 1) (COX VIb-1)	86	COX6B1	0	1	0	0	20.9	0

1272	0.00	-0.09	0.00	P25815	Protein S100-P (Migration-inducing gene 9 protein) (MIG9) (Protein S100-E) (S100 calcium-binding protein P)	95	S100P	0	1	0	0	13.7	0
1273	0.00	0.70	0.00	P28288	ATP-binding cassette sub-family D member 3 (70 kDa peroxisomal membrane protein) (PMP70)	659	ABCD3	0	1	0	0	2.2	0
1274	0.00	0.13	0.00	P36543	V-type proton ATPase subunit E 1 (V-ATPase subunit E 1) (V-ATPase 31 kDa subunit) (p31) (Vacuolar proton pump subunit E 1)	226	ATP6V1E1	0	1	0	0	5.1	0
1275	0.00	4.09	0.00	P47929	Galectin-7 (Gal-7) (HKL-14) (PI7) (p53-induced gene 1 protein)	136	LGALS7	0	1	0	0	8.1	0
1276	0.00	0.79	0.00	P51151	Ras-related protein Rab-9A	201	RAB9A	0	1	0	0	7	0
1277	0.00	0.43	0.00	P56385	ATP synthase subunit e, mitochondrial (ATPase subunit e)	69	ATP5I	0	1	0	0	14.5	0
1278	0.00	-0.15	0.00	P61254	60S ribosomal protein L26	145	RPL26	0	1	0	0	5.5	0
1279	0.00	0.43	0.00	P61457	Pterin-4-alpha-carbinolamine dehydratase (PHS) (EC 4.2.1.96) (4-alpha-hydroxy-tetrahydropterin dehydratase) (Dimerization cofactor of hepatocyte nuclear factor 1-alpha) (DCoH) (Dimerization cofactor of HNF1) (Phenylalanine hydroxylase-stimulating protein) (Pterin carbinolamine dehydratase) (PCD)	104	PCBD1	0	1	0	0	12.5	0
1280	0.00	2.05	0.00	P62306	Small nuclear ribonucleoprotein F (snRNP-F) (Sm protein F) (Sm-F) (SmF)	86	SNRPF	0	1	0	0	8.1	0
1281	0.00	0.05	0.00	P62312	U6 snRNA-associated Sm-like protein LSm6	80	LSM6	0	1	0	0	13.8	0
1282	0.00	0.40	0.00	P63218	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-5	68	GNG5	0	1	0	0	13.2	0

1283	0.00	2.08	0.00	P80723	Brain acid soluble protein 1 (22 kDa neuronal tissue-enriched acidic protein) (Neuronal axonal membrane protein NAP-22)	227	BASP1	0	1	0	0	6.2	0
1284	0.00	4.91	0.00	Q08188	Protein-glutamine gamma-glutamyltransferase E (EC 2.3.2.13) (Transglutaminase E) (TG(E)) (TGE) (TGase E) (Transglutaminase-3) (TGase-3) [Cleaved into: Protein-glutamine gamma-glutamyltransferase E 50 kDa catalytic chain; Protein-glutamine gamma-glutamyltransferase E 27 kDa non-catalytic chain]	693	TGM3	0	1	0	0	1.3	0
1285	0.00	5.57	0.00	Q12873	Chromodomain-helicase-DNA-binding protein 3 (CHD-3) (EC 3.6.4.12) (ATP-dependent helicase CHD3) (Mi-2 autoantigen 240 kDa protein) (Mi2-alpha) (Zinc finger helicase) (hZFH)	2000	CHD3	0	1	0	0	0.5	0
1286	0.00	0.01	0.00	Q14061	Cytochrome c oxidase copper chaperone	63	COX17	0	1	0	0	25.4	0
1287	0.00	1.22	0.00	Q16864	V-type proton ATPase subunit F (V-ATPase subunit F) (V-ATPase 14 kDa subunit) (Vacuolar proton pump subunit F)	119	ATP6V1F	0	1	0	0	16	0
1288	0.00	0.51	0.00	Q5HYK3	2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial (EC 2.1.1.201) (Ubiquinone biosynthesis methyltransferase COQ5)	327	COQ5	0	1	0	0	4.1	0
1289	0.00	1.02	0.00	Q5JTJ3	Cytochrome c oxidase assembly factor 6 homolog	125	COA6	0	1	0	0	17.7	0
1290	0.00	0.64	0.00	Q5QPM9	Proteasome inhibitor PI31 subunit (Fragment)	183	PSMF1	0	1	0	0	9.3	0

1291	0.00	1.51	0.00	Q5RI15	Cytochrome c oxidase protein 20 homolog	118	COX20	0	1	0	0	11.9	0
1292	0.00	1.91	0.00	Q5RKV6	Exosome complex component MTR3 (Exosome component 6) (mRNA transport regulator 3 homolog) (hMtr3) (p11)	272	EXOSC6	0	1	0	0	5.9	0
1293	0.00	-1.33	0.00	Q5SXM8	DNL-type zinc finger protein (Hsp70-escort protein 1) (HEP1) (mtHsp70-escort protein)	178	DNLZ	0	1	0	0	5.1	0
1294	0.00	0.34	0.00	Q5T123	SH3 domain-binding glutamic acid-rich-like protein 3	88	SH3BGRL3	0	1	0	0	17	0
1295	0.00	0.38	0.00	Q5TGZ0	MICOS complex subunit MIC10 (Mitochondrial inner membrane organizing system protein 1)	78	MINOS1	0	1	0	0	33.3	0
1296	0.00	5.34	0.00	Q5VTQ0	Tetratricopeptide repeat protein 39B (TPR repeat protein 39B)	682	TTC39B	0	1	0	0	6	0
1297	0.00	0.56	0.00	Q5VU10	Ribonuclease P protein subunit p30 (Fragment)	212	RPP30	0	1	0	0	4.7	0
1298	0.00	6.60	0.00	Q5VXJ5	Synaptonemal complex protein 1 (Fragment)	792	SYCP1	0	1	0	0	1.6	0
1299	0.00	0.62	0.00	Q6IAK0	SELT protein (Selenoprotein T) (cDNA FLJ90525 fis, clone NT2RP4001001, highly similar to Selenoprotein T)	137	SELT	0	1	0	0	9.5	0
1300	0.00	3.80	0.00	Q6UWP8	Suprabasin	590	SBSN	0	1	0	0	9.2	0
1301	0.00	0.27	0.00	Q7Z5G4	acety	137	GOLGA7	0	1	0	0	8.2	0
1302	0.00	-0.15	0.00	Q7Z7H5	Transmembrane emp24 domain-containing protein 4 (Endoplasmic reticulum stress-response protein 25) (ERS25) (GMP25iso) (Putative NF-kappa-B-activating protein 156) (p24 family protein alpha-3) (p24alpha3)	227	TMED4	0	1	0	0	5.9	0

1303	0.00	2.08	0.00	Q7Z7H8	39S ribosomal protein L10, mitochondrial (L10mt) (MRP-L10) (39S ribosomal protein L8, mitochondrial) (L8mt) (MRP-L8)	261	MRPL10	0	1	0	0	7.3	0
1304	0.00	0.81	0.00	Q86YN1	Dolichyldiphosphatase 1 (EC 3.6.1.43) (Dolichyl pyrophosphate phosphatase 1)	238	DOLPP1	0	1	0	0	5.5	0
1305	0.00	1.46	0.00	Q8N4V1	Membrane magnesium transporter 1 (ER membrane protein complex subunit 5) (Transmembrane protein 32)	131	MMGT1	0	1	0	0	18.3	0
1306	0.00	-0.32	0.00	Q8WVF3	RAB28 protein (Ras-related protein Rab-28)	95	RAB28	0	1	0	0	11.6	0
1307	0.00	1.53	0.00	Q8WW12	PEST proteolytic signal-containing nuclear protein (PCNP) (PEST-containing nuclear protein)	178	PCNP	0	1	0	0	11.5	0
1308	0.00	3.57	0.00	Q8WY22	BRI3-binding protein (I3-binding protein) (Cervical cancer 1 proto-oncogene-binding protein KG19) (HCCRBP-1)	251	BRI3BP	0	1	0	0	6.8	0
1309	0.00	-0.98	0.00	Q969X5	Endoplasmic reticulum-Golgi intermediate compartment protein 1 (ER-Golgi intermediate compartment 32 kDa protein) (ERGIC-32)	290	ERGIC1	0	1	0	0	5.1	0
1310	0.00	1.22	0.00	Q96DA6	Mitochondrial import inner membrane translocase subunit TIM14 (DnaJ homolog subfamily C member 19)	116	DNAJC19	0	1	0	0	15.4	0
1311	0.00	0.55	0.00	Q96EL3	39S ribosomal protein L53, mitochondrial (L53mt) (MRP-L53)	112	MRPL53	0	1	0	0	8.9	0
1312	0.00	1.01	0.00	Q96EX1	Small integral membrane protein 12	92	SMIM12	0	1	0	0	9.8	0
1313	0.00	1.63	0.00	Q96IX5	Up-regulated during skeletal muscle growth protein 5 (Diabetes-associated protein in insulin-sensitive tissues) (HCV F-transactivated protein 2)	58	USMG5	0	1	0	0	25.9	0

1314	0.00	1.11	0.00	Q96PD2	Discoidin, CUB and LCCL domain-containing protein 2 (CUB, LCCL and coagulation factor V/VIII-homology domains protein 1) (Endothelial and smooth muscle cell-derived neuropilin-like protein)	775	DCBLD2	0	1	0	0	1.3	0
1315	0.00	5.08	0.00	Q99595	Mitochondrial import inner membrane translocase subunit Tim17-A (Inner membrane preprotein translocase Tim17a)	171	TIMM17A	0	1	0	0	19.3	0
1316	0.00	0.31	0.00	Q9BQC6	Ribosomal protein 63, mitochondrial (hMRP63) (Mitochondrial ribosomal protein 63) (Mitochondrial ribosomal protein L57)	102	MRPL57	0	1	0	0	12.7	0
1317	0.00	-0.29	0.00	Q9BRF8	Serine/threonine-protein phosphatase CPPED1 (EC 3.1.3.16) (Calcineurin-like phosphoesterase domain-containing protein 1) (Complete S-transactivated protein 1)	314	CPPED1	0	1	0	0	9	0
1318	0.00	0.45	0.00	Q9BWJ5	Splicing factor 3B subunit 5 (SF3b5) (Pre-mRNA-splicing factor SF3b 10 kDa subunit)	86	SF3B5	0	1	0	0	12.8	0
1319	0.00	3.54	0.00	Q9BXW7	Cat eye syndrome critical region protein 5	423	CECR5	0	1	0	0	3.6	0
1320	0.00	0.55	0.00	Q9BZG1	Ras-related protein Rab-34 (Ras-related protein Rab-39) (Ras-related protein Rah)	259	RAB34	0	1	0	0	5.9	0
1321	0.00	-0.16	0.00	Q9H3Z4	DnaJ homolog subfamily C member 5 (Cysteine string protein) (CSP)	198	DNAJC5	0	1	0	0	8.4	0
1322	0.00	6.18	0.00	Q9H7L9	Sin3 histone deacetylase corepressor complex component SDS3 (45 kDa Sin3-associated polypeptide) (Suppressor of defective silencing 3 protein homolog)	328	SUDS3	0	1	0	0	5.8	0

1323	0.00	1.60	0.00	Q9HD45	Transmembrane 9 superfamily member 3 (EP70-P-iso) (SM-11044-binding protein)	589	TM9SF3	0	1	0	0	1.9	0
1324	0.00	0.70	0.00	Q9NQ50	39S ribosomal protein L40, mitochondrial (L40mt) (MRP-L40) (Nuclear localization signal-containing protein deleted in velocardiofacial syndrome) (Up-regulated in metastasis)	206	MRPL40	0	1	0	0	4.4	0
1325	0.00	1.13	0.00	Q9NTX5	Ethylmalonyl-CoA decarboxylase (EC 4.1.1.94) (Enoyl-CoA hydratase domain-containing protein 1) (Methylmalonyl-CoA decarboxylase) (MMCD) (EC 4.1.1.41)	307	ECHDC1	0	1	0	0	4.9	0
1326	0.00	-0.11	0.00	Q9NVS9	Pyridoxine-5'-phosphate oxidase (EC 1.4.3.5) (Pyridoxamine-phosphate oxidase)	261	PNPO	0	1	0	0	6.9	0
1327	0.00	0.02	0.00	Q9NW13	RNA-binding protein 28 (RNA-binding motif protein 28)	759	RBM28	0	1	0	0	1.5	0
1328	0.00	0.55	0.00	Q9NZL9	Methionine adenosyltransferase 2 subunit beta (Methionine adenosyltransferase II beta) (MAT II beta) (Putative dTDP-4-keto-6-deoxy-D-glucose 4-reductase)	334	MAT2B	0	1	0	0	3.3	0
1329	0.00	-1.44	0.00	Q9P1F3	Costars family protein ABRACL (ABRA C-terminal-like protein)	81	ABRACL	0	1	0	0	16	0
1330	0.00	0.50	0.00	Q9UDW1	Cytochrome b-c1 complex subunit 9 (Complex III subunit 9) (Complex III subunit X) (Cytochrome c1 non-heme 7 kDa protein) (Ubiquinol-cytochrome c reductase complex 7.2 kDa protein)	63	UQCR10	0	1	0	0	27	0

1331	0.00	0.78	0.00	Q9UHA4	Ragulator complex protein LAMTOR3 (Late endosomal/lysosomal adaptor and MAPK and MTOR activator 3) (MEK-binding partner 1) (Mp1) (Mitogen-activated protein kinase kinase 1-interacting protein 1) (Mitogen-activated protein kinase scaffold protein 1)	124	LAMTOR3	0	1	0	0	13.7	0
1332	0.00	7.17	0.00	Q9UKX3	Myosin-13 (Myosin heavy chain 13) (Myosin heavy chain, skeletal muscle, extraocular) (MyHC-EO) (Myosin heavy chain, skeletal muscle, laryngeal) (MyHC-IIL) (Superfast myosin)	1938	MYH13	0	1	0	0	0.8	0
1333	0.00	1.24	0.00	Q9Y5U9	Immediate early response 3-interacting protein 1	82	IER3IP1	0	1	0	0	24.4	0
1334	0.00	1.16	0.00	R4GN18	Membrane cofactor protein (Fragment)	78	CD46	0	1	0	0	16.7	0
1335	0.00	1.61	0.00	R4GN83	Basigin (Fragment)	52	BSG	0	1	0	0	26.9	0
1336	0.00	0.91	0.00	R4GN99	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	145	PPIF	0	1	0	0	6.2	0
1337	0.00	1.15	0.00	R4GNH9	Exosome complex component CSL4	139	EXOSC1	0	1	0	0	11.5	0
1338	0.00	2.84	0.00	S4R3I5	NADH dehydrogenase (Ubiquinone) 1 alpha subcomplex, 3, 9kDa, isoform CRA_b (NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3)	41	NDUFA3	0	1	0	0	26.8	0
1339	0.00	-0.76	0.00	S4R402	Nucleolar and coiled-body phosphoprotein 1	46	NOLC1	0	1	0	0	21.7	0
1340	0.00	-0.06	0.06	O95670	V-type proton ATPase subunit G 2 (V-ATPase subunit G 2) (V-ATPase 13 kDa subunit 2) (Vacuolar proton pump subunit G 2)	118	ATP6V1G2	1	1	1	19.2	19.2	19.2
1341	0.00	0.03	0.36	Q3BDU5	Prelamin-A/C (Rhabdomyosarcoma antigen MU-RMS-40.12)	487	LMNA	5	3	6	11.7	7.2	14

1342	0.00	-0.89	-0.30	H0YM70	Proteasome activator complex subunit 2	228	PSME2	4	3	4	28.9	19.3	28.1
1343	0.01	-0.47	0.65	P30046	D-dopachrome decarboxylase (EC 4.1.1.84) (D-dopachrome tautomerase) (Phenylpyruvate tautomerase II)	118	DDT	1	4	2	10.2	35.6	21.2
1344	0.01	0.00	0.00	O00267	Transcription elongation factor SPT5 (hSPT5) (DRB sensitivity-inducing factor 160 kDa subunit) (DSIF p160) (DRB sensitivity-inducing factor large subunit) (DSIF large subunit) (Tat-cotransactivator 1 protein) (Tat-CT1 protein)	1087	SUPT5H	1	0	0	1.4	0	0
1345	0.01	0.95	0.88	P19404	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial (EC 1.6.5.3) (EC 1.6.99.3) (NADH-ubiquinone oxidoreductase 24 kDa subunit)	249	NDUFV2	1	2	2	4	9.2	9.2
1346	0.01	0.22	0.66	M0QZR9	ELAV-like protein 1	153	ELAVL1	1	1	1	8.5	8.5	8.5
1347	0.02	0.90	0.13	P30084	Enoyl-CoA hydratase, mitochondrial (EC 4.2.1.17) (Enoyl-CoA hydratase 1) (Short-chain enoyl-CoA hydratase) (SCEH)	290	ECHS1	1	5	2	6.2	27.6	9.3
1348	0.03	0.16	-0.03	Q00765	Receptor expression-enhancing protein 5 (Polyposis locus protein 1) (Protein TB2)	189	REEP5	4	5	4	16.4	21.2	16.4
1349	0.03	0.25	1.21	Q8N257	Histone H2B type 3-B (H2B type 12)	126	HIST3H2BB	2	3	3	15.1	23.8	27
1350	0.03	-0.46	0.10	Q3ZCM7	Tubulin beta-8 chain	444	TUBB8	5	6	5	16	16.4	13.1
1351	0.03	0.79	0.10	Q07065	Cytoskeleton-associated protein 4 (63-kDa cytoskeleton-linking membrane protein) (Climp-63) (p63)	602	CKAP4	6	2	8	11.8	4.3	15.9

1352	0.04	0.63	1.04	P53007	Tricarboxylate transport protein, mitochondrial (Citrate transport protein) (CTP) (Solute carrier family 25 member 1) (Tricarboxylate carrier protein)	311	SLC25A1	2	2	2	7.7	7.4	7.7
1353	0.04	1.07	0.24	Q5JPE7	Nodal modulator 2 (pM5 protein 2)	1267	NOMO2	1	3	1	0.8	3.2	0.8
1354	0.04	0.36	0.41	Q6Y1H2	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 2 (EC 4.2.1.134) (3-hydroxyacyl-CoA dehydratase 2) (HACD2) (Protein-tyrosine phosphatase-like member B)	254	HACD2	1	1	1	3.9	3.5	3.9
1355	0.05	-0.17	0.24	H0YD18	Nucleobindin-2 (Fragment)	73	NUCB2	1	1	1	12.3	12.3	12.3
1356	0.05	0.00	0.54	P51610	Host cell factor 1 (HCF) (HCF-1) (C1 factor) (CFF) (VCAF) (VP16 accessory protein) [Cleaved into: HCF N-terminal chain 1; HCF N-terminal chain 2; HCF N-terminal chain 3; HCF N-terminal chain 4; HCF N-terminal chain 5; HCF N-terminal chain 6; HCF C-terminal chain 1; HCF C-terminal chain 2; HCF C-terminal chain 3; HCF C-terminal chain 4; HCF C-terminal chain 5; HCF C-terminal chain 6]	2035	HCFC1	1	0	1	0.8	0	0.8
1357	0.05	0.25	0.88	P62191	26S protease regulatory subunit 4 (P26s4) (26S proteasome AAA-ATPase subunit RPT2) (Proteasome 26S subunit ATPase 1)	440	PSMC1	1	1	3	2.5	5.7	10.9
1358	0.06	0.00	0.86	A6NKB8	Aminopeptidase B	611	RNPEP	1	0	1	1.6	0	2
1359	0.06	0.50	0.65	P05091	Aldehyde dehydrogenase, mitochondrial (EC 1.2.1.3) (ALDH class 2) (ALDH-E2) (ALDHI)	517	ALDH2	7	7	8	16.2	16.8	19.1
1360	0.07	0.00	0.65	P60891	Ribose-phosphate pyrophosphokinase 1 (EC 2.7.6.1) (PPRibP) (Phosphoribosyl pyrophosphate synthase I) (PRS-I)	318	PRPS1	1	0	2	4.1	0	7.2

1361	0.07	0.10	1.13	Q15005	Signal peptidase complex subunit 2 (EC 3.4.-.-) (Microsomal signal peptidase 25 kDa subunit) (SPase 25 kDa subunit)	226	SPCS2	3	2	1	13.3	8	8.4
1362	0.08	0.40	0.52	C9J0J7	Profilin-2	91	PFN2	1	2	1	8.8	29.7	8.8
1363	0.08	0.35	0.23	P05141	ADP/ATP translocase 2 (ADP,ATP carrier protein 2) (ADP,ATP carrier protein, fibroblast isoform) (Adenine nucleotide translocator 2) (ANT 2) (Solute carrier family 25 member 5) [Cleaved into: ADP/ATP translocase 2, N-terminally processed]	298	SLC25A5	7	7	8	21.8	24.2	24.5
1364	0.08	0.00	-0.16	D6REM1	Golgi phosphoprotein 3	93	GOLPH3	1	0	1	14	0	14
1365	0.08	0.39	0.49	P34897	Serine hydroxymethyltransferase, mitochondrial (SHMT) (EC 2.1.2.1) (Glycine hydroxymethyltransferase) (Serine methylase)	504	SHMT2	3	1	8	8.1	2.3	21.7
1366	0.09	0.00	0.28	Q9Y3I0	tRNA-splicing ligase RtcB homolog (EC 6.5.1.3)	505	RTCB	1	0	1	3.2	0	3.2
1367	0.10	0.67	0.52	A0A087X054	Hypoxia up-regulated protein 1	937	HYOU1	7	8	6	8	12.8	8.5
1368	0.10	-0.09	0.33	P38606	V-type proton ATPase catalytic subunit A (V-ATPase subunit A) (EC 3.6.3.14) (V-ATPase 69 kDa subunit) (Vacuolar ATPase isoform VA68) (Vacuolar proton pump subunit alpha)	617	ATP6V1A	1	1	2	3.1	3.1	3.4
1369	0.10	0.00	0.00	Q15813	Tubulin-specific chaperone E (Tubulin-folding cofactor E)	527	TBCE	1	0	0	2.1	0	0
1370	0.10	-0.03	0.44	J3QT77	Serum paraoxonase/arylesterase 2	342	PON2	1	1	3	5.6	3.5	12.3
1371	0.10	0.03	0.44	P12814	Alpha-actinin-1 (Alpha-actinin cytoskeletal isoform) (F-actin cross-linking protein) (Non-muscle alpha-actinin-1)	892	ACTN1	13	20	13	20	27	20.3

1372	0.10	-0.30	0.18	O43324	Eukaryotic translation elongation factor 1 epsilon-1 (Aminoacyl tRNA synthetase complex-interacting multifunctional protein 3) (Elongation factor p18) (Multisynthase complex auxiliary component p18)	174	EEF1E1	2	2	2	12.1	12.6	12.1
1373	0.11	-0.60	0.30	Q9NQ88	Fructose-2,6-bisphosphatase TIGAR (EC 3.1.3.46) (TP53-induced glycolysis and apoptosis regulator)	270	TIGAR	2	2	1	8.9	8.9	4.8
1374	0.11	0.00	0.83	Q12792	Twinfilin-1 (Protein A6) (Protein tyrosine kinase 9)	350	TWF1	1	0	2	2.8	0	10.3
1375	0.11	-0.88	0.37	Q9BY32	Inosine triphosphate pyrophosphatase (ITPase) (Inosine triphosphatase) (EC 3.6.1.19) (Non-canonical purine NTP pyrophosphatase) (Non-standard purine NTP pyrophosphatase) (Nucleoside-triphosphate diphosphatase) (Nucleoside-triphosphate pyrophosphatase) (NTPase) (Putative oncogene protein hlc14-06-p)	194	ITPA	5	3	3	24.2	16	19.1
1376	0.11	1.04	-0.03	H0YD13	CD44 antigen	206	CD44	2	4	3	9.2	22.3	17
1377	0.12	0.00	0.25	Q15046	Lysine--tRNA ligase (EC 6.1.1.6) (Lysyl-tRNA synthetase) (LysRS)	597	KARS	4	0	3	6.5	0	4.2
1378	0.13	-0.95	0.07	P30838	Aldehyde dehydrogenase, dimeric NADP-preferring (EC 1.2.1.5) (ALDHIII) (Aldehyde dehydrogenase 3) (Aldehyde dehydrogenase family 3 member A1)	453	ALDH3A1	10	8	13	21.4	21.4	30
1379	0.13	0.36	-0.22	Q9UL25	Ras-related protein Rab-21	225	RAB21	2	2	1	12.4	12.4	7.6

1380	0.13	0.00	0.15	Q14232	Translation initiation factor eIF-2B subunit alpha (eIF-2B GDP-GTP exchange factor subunit alpha)	305	EIF2B1	2	0	2	6.6	0	8.2
1381	0.14	-1.36	-0.14	P15428	15-hydroxyprostaglandin dehydrogenase [NAD(+)] (15-PGDH) (EC 1.1.1.141) (Prostaglandin dehydrogenase 1) (Short chain dehydrogenase/reductase family 36C member 1)	266	HPGD	3	3	3	14.3	13.2	13.2
1382	0.14	-0.07	0.28	P20700	Lamin-B1	586	LMNB1	2	4	3	3.9	9.9	6
1383	0.14	0.00	0.00	P49589	Cysteine--tRNA ligase, cytoplasmic (EC 6.1.1.16) (Cysteinyl-tRNA synthetase) (CysRS)	748	CARS	1	0	1	1.4	0	1.4
1384	0.15	0.00	0.06	P62873	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 (Transducin beta chain 1)	340	GNB1	2	1	2	6.6	3.3	6.6
1385	0.15	-0.34	0.09	O14579	Coatomer subunit epsilon (Epsilon-coat protein) (Epsilon-COP)	308	COPE	1	1	1	5.4	5.4	5.4
1386	0.16	1.44	0.25	P51571	Translocon-associated protein subunit delta (TRAP-delta) (Signal sequence receptor subunit delta) (SSR-delta)	173	SSR4	1	2	1	7.5	16.8	7.5
1387	0.16	0.83	0.68	P62140	Serine/threonine-protein phosphatase PP1-beta catalytic subunit (PP-1B) (PPP1CD) (EC 3.1.3.16) (EC 3.1.3.53)	327	PPP1CB	1	2	3	4	9.5	13.8
1388	0.17	0.04	0.93	Q9BVK6	Transmembrane emp24 domain-containing protein 9 (GMP25) (Glycoprotein 25L2) (p24 family protein alpha-2) (p24alpha2) (p25)	235	TMED9	1	4	3	4.7	12.8	14.9
1389	0.17	-0.28	0.00	P36404	ADP-ribosylation factor-like protein 2	184	ARL2	1	2	0	6.5	12	0

1390	0.18	0.97	0.52	B4DEZ3	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13 (cDNA FLJ57958, highly similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 13 (EC 1.6.5.3))	120	NDUFA13	1	2	1	9.2	20.8	9.2
1391	0.18	0.00	-0.34	H7C4M9	Ubiquitin-conjugating enzyme E2 H (Fragment)	62	UBE2H	1	0	1	24.2	0	24.2
1392	0.18	-0.45	-0.11	P18085	ADP-ribosylation factor 4	180	ARF4	3	3	3	17.2	22.8	17.2
1393	0.19	0.45	0.81	P56556	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6 (Complex I-B14) (CI-B14) (LYR motif-containing protein 6) (NADH-ubiquinone oxidoreductase B14 subunit)	154	NDUFA6	2	1	2	15.6	5.2	15.6
1394	0.19	-1.06	-0.17	P04080	Cystatin-B (CPI-B) (Liver thiol proteinase inhibitor) (Stefin-B)	98	CSTB	2	1	2	21.4	12.2	21.4
1395	0.19	1.53	1.08	Q9NZ45	CDGSH iron-sulfur domain-containing protein 1 (MitoNEET)	108	CISD1	1	1	2	12	13.9	25.9
1396	0.20	0.51	0.33	F5H6I7	Atlastin-3	523	ATL3	1	1	3	3.4	3.4	7.5
1397	0.20	0.00	0.58	Q07973	1,25-dihydroxyvitamin D(3) 24-hydroxylase, mitochondrial (24-OHase) (Vitamin D(3) 24-hydroxylase) (EC 1.14.13.126) (Cytochrome P450 24A1) (Cytochrome P450-CC24)	514	CYP24A1	1	0	1	3.8	0	3.8
1398	0.20	-0.17	0.00	P29317	Ephrin type-A receptor 2 (EC 2.7.10.1) (Epithelial cell kinase) (Tyrosine-protein kinase receptor ECK)	976	EPHA2	1	3	0	1	3.6	0
1399	0.20	1.05	1.02	Q9BX68	Histidine triad nucleotide-binding protein 2, mitochondrial (HINT-2) (EC 3.-.-.-) (HINT-3) (HIT-17kDa) (PKCI-1-related HIT protein)	163	HINT2	1	4	2	12.3	41.7	21.5

1400	0.21	-0.29	0.17	P48444	Coatomer subunit delta (Archain) (Delta-coat protein) (Delta-COP)	511	ARCN1	2	2	2	4.1	4.3	4.1
1401	0.21	-0.40	-0.05	P36406	E3 ubiquitin-protein ligase TRIM23 (EC 6.3.2.-) (ADP-ribosylation factor domain-containing protein 1) (GTP-binding protein ARD-1) (RING finger protein 46) (Tripartite motif-containing protein 23)	574	TRIM23	1	1	1	1.8	1.8	1.8
1402	0.21	-0.67	-1.21	Q01995	Transgelin (22 kDa actin-binding protein) (Protein WS3-10) (Smooth muscle protein 22-alpha) (SM22-alpha)	201	TAGLN	1	2	1	6	9.5	6
1403	0.22	0.00	-0.06	I3L1U8	Active breakpoint cluster region-related protein (Fragment)	165	ABR	1	0	1	6.1	0	6.1
1404	0.22	0.30	0.81	O00469	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2 (EC 1.14.11.4) (Lysyl hydroxylase 2) (LH2)	737	PLOD2	2	1	3	2.6	1.4	4.9
1405	0.22	-0.71	0.07	P12931	Proto-oncogene tyrosine-protein kinase Src (EC 2.7.10.2) (Proto-oncogene c-Src) (pp60c-src) (p60-Src)	536	SRC	2	1	2	5.2	2.8	5.2
1406	0.23	0.52	0.53	B0YJC4	Vimentin (Vimentin variant 3)	431	VIM	3	2	2	8.6	3.9	5.6
1407	0.23	0.16	0.18	Q15907	Ras-related protein Rab-11B (GTP-binding protein YPT3)	218	RAB11B	5	5	4	34.6	34.6	29.6
1408	0.23	0.76	0.30	Q8NE86	Calcium uniporter protein, mitochondrial (Coiled-coil domain-containing protein 109A)	351	MCU	1	4	2	5.3	18.5	9.6
1409	0.23	0.00	-0.11	Q8NBU5	ATPase family AAA domain-containing protein 1 (EC 3.6.1.3) (Thorase)	361	ATAD1	1	0	1	3.8	0	3.8
1410	0.23	0.00	0.10	A0A087X1I3	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	519	SDHA	1	0	1	2.5	0	2.5

1411	0.23	0.00	1.43	P55265	Double-stranded RNA-specific adenosine deaminase (DRADA) (EC 3.5.4.37) (136 kDa double-stranded RNA-binding protein) (p136) (Interferon-inducible protein 4) (IFI-4) (K88DSRBP)	1226	ADAR	1	0	1	1.1	0	1.1
1412	0.24	1.34	0.47	Q6KC79	Nipped-B-like protein (Delangin) (SCC2 homolog)	2804	NIPBL	1	1	1	0.4	0.5	0.4
1413	0.24	0.03	0.61	P49748	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial (VLCAD) (EC 1.3.8.9)	655	ACADVL	2	2	7	3.2	3.5	15.3
1414	0.24	1.06	0.40	Q16762	Thiosulfate sulfurtransferase (EC 2.8.1.1) (Rhodanese)	297	TST	1	3	1	4	14.5	4
1415	0.24	1.08	1.08	C9JT21	Elongation factor Ts (Fragment)	168	TSFM	1	2	2	8.3	18.5	18.5
1416	0.24	0.01	0.76	Q96QK1	Vacuolar protein sorting-associated protein 35 (hVPS35) (Maternal-embryonic 3) (Vesicle protein sorting 35)	796	VPS35	2	1	1	3.5	1.8	1.8
1417	0.24	0.00	0.85	Q96BP3	Peptidylprolyl isomerase domain and WD repeat-containing protein 1 (EC 5.2.1.8) (Spliceosome-associated cyclophilin)	646	PPWD1	1	0	1	2.4	0	2.4
1418	0.24	0.23	0.09	Q9BRX8	Redox-regulatory protein FAM213A (Peroxiredoxin-like 2 activated in M-CSF stimulated monocytes) (Protein PAMM)	229	FAM213A	3	3	4	13.8	17.4	20.6
1419	0.26	-0.97	0.01	C9JP16	Cartilage-associated protein	358	CRTAP	1	1	1	3.1	3.1	3.1
1420	0.26	-0.08	0.20	P51809	Vesicle-associated membrane protein 7 (VAMP-7) (Synaptobrevin-like protein 1) (Tetanus-insensitive VAMP) (Ti-VAMP)	220	VAMP7	1	1	1	5	6.7	5
1421	0.26	0.00	0.01	P67936	Tropomyosin alpha-4 chain (TM30p1) (Tropomyosin-4)	248	TPM4	3	2	6	14.5	10.9	31

1422	0.26	-0.49	-0.04	Q16851	UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) (UDP-glucose pyrophosphorylase) (UDPGP) (UGPase)	508	UGP2	2	1	2	7.6	3.6	6.4
1423	0.26	0.07	0.33	P31930	Cytochrome b-c1 complex subunit 1, mitochondrial (Complex III subunit 1) (Core protein I) (Ubiquinol-cytochrome-c reductase complex core protein 1)	480	UQCRC1	1	3	2	2.5	6.2	6.7
1424	0.27	0.50	0.53	Q15363	Transmembrane emp24 domain-containing protein 2 (Membrane protein p24A) (p24) (p24 family protein beta-1) (p24beta1)	201	TMED2	2	2	4	19.9	14.4	26.4
1425	0.27	0.12	0.36	Q53H82	Beta-lactamase-like protein 2 (EC 3.-.-.-)	288	LACTB2	1	4	3	2.8	16.7	12.2
1426	0.27	-0.50	-0.69	P49902	Cytosolic purine 5'-nucleotidase (EC 3.1.3.5) (Cytosolic 5'-nucleotidase II)	561	NT5C2	1	1	2	3.2	2.4	5.6
1427	0.28	0.64	0.43	P26640	Valine--tRNA ligase (EC 6.1.1.9) (Protein G7a) (Valyl-tRNA synthetase) (ValRS)	1264	VARS	1	2	1	0.9	2.5	0.9
1428	0.28	0.61	0.16	D6RAA6	Transmembrane protein 33 (Fragment)	222	TMEM33	1	1	2	4.5	4.5	9.9
1429	0.28	-0.74	0.14	Q06210	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 (EC 2.6.1.16) (D-fructose-6-phosphate amidotransferase 1) (Glutamine:fructose-6-phosphate amidotransferase 1) (GFAT 1) (GFAT1) (Hexosephosphate aminotransferase 1)	699	GFPT1	1	1	2	2.1	2.1	4.1
1430	0.28	0.00	0.33	P53004	Biliverdin reductase A (BVR A) (EC 1.3.1.24) (Biliverdin-IX alpha-reductase)	296	BLVRA	3	0	2	11.5	0	6.8
1431	0.30	0.01	0.45	P62330	ADP-ribosylation factor 6	175	ARF6	1	1	2	6.3	6.3	18.3

1432	0.30	0.36	0.19	Q9BUP3	Oxidoreductase HTATIP2 (EC 1.1.1.-) (30 kDa HIV-1 TAT-interacting protein) (HIV-1 TAT-interactive protein 2)	242	HTATIP2	1	3	4	4.1	12.4	16.1
1433	0.31	0.30	1.56	D6RAT0	40S ribosomal protein S3a	227	RPS3A	4	4	6	20.3	18.9	23.3
1434	0.31	0.00	0.39	P46977	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A (Oligosaccharyl transferase subunit STT3A) (STT3-A) (EC 2.4.99.18) (B5) (Integral membrane protein 1) (Transmembrane protein TMC)	705	STT3A	1	0	1	1.3	0	1.3
1435	0.31	0.54	0.00	E5RJZ1	Cytochrome c oxidase subunit 7A-related protein, mitochondrial	79	COX7A2L	1	2	0	16.5	26.6	0
1436	0.32	0.59	0.87	Q9UM22	Mammalian ependymin-related protein 1 (MERP-1) (Upregulated in colorectal cancer gene 1 protein)	224	EPDR1	1	1	1	5.5	5.5	5.5
1437	0.34	0.86	1.26	B4DJ81	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial (cDNA FLJ60586, highly similar to NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial (EC 1.6.5.3))	611	NDUFS1	1	1	2	2.6	2.6	4.3
1438	0.34	0.48	0.05	F5GX19	Ragulator complex protein LAMTOR1	142	LAMTOR1	1	3	1	9.2	26.1	9.2
1439	0.34	0.00	1.08	M0R261	6-phosphogluconolactonase (Fragment)	216	PGLS	1	0	3	5.1	0	25
1440	0.35	-0.04	0.08	Q9NUJ1	Mycophenolic acid acyl-glucuronide esterase, mitochondrial (EC 3.1.1.93) (Alpha/beta hydrolase domain-containing protein 10) (Abhydrolase domain-containing protein 10)	306	ABHD10	1	2	2	8.3	14.1	12.7

1441	0.35	0.00	1.04	Q12906	Interleukin enhancer-binding factor 3 (Double-stranded RNA-binding protein 76) (DRBP76) (M-phase phosphoprotein 4) (MPP4) (Nuclear factor associated with dsRNA) (NFAR) (Nuclear factor of activated T-cells 90 kDa) (NF-AT-90) (Translational control protein 80) (TCP80)	894	ILF3	2	0	2	2.8	0	2.8
1442	0.35	0.16	0.27	Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial (EC 5.3.3.-)	328	ECH1	1	3	1	3.4	12.8	3.4
1443	0.35	0.00	0.36	E7ER27	Peroxisomal multifunctional enzyme type 2	500	HSD17B4	1	0	1	2.8	0	2.8
1444	0.36	0.00	0.00	P10155	60 kDa SS-A/Ro ribonucleoprotein (60 kDa Ro protein) (60 kDa ribonucleoprotein Ro) (RoRNP) (Ro 60 kDa autoantigen) (Sjoegren syndrome antigen A2) (Sjoegren syndrome type A antigen) (SS-A) (TROVE domain family member 2)	538	TROVE2	1	0	0	2	0	0
1445	0.36	0.29	0.13	Q969H8	Myeloid-derived growth factor (MYDGF) (Interleukin-25) (IL-25) (Stromal cell-derived growth factor SF20)	173	MYDGF	1	2	1	5.2	13.9	5.2
1446	0.37	-1.26	0.40	B0QZ43	Erlin-1 (Fragment)	275	ERLIN1	1	2	1	4.4	8.7	4.4
1447	0.37	-0.48	-0.19	P14550	Alcohol dehydrogenase [NADP(+)] (EC 1.1.1.2) (Aldehyde reductase) (Aldo-keto reductase family 1 member A1)	325	AKR1A1	2	2	2	7.4	6.8	7.4
1448	0.37	0.00	0.32	Q16658	Fascin (55 kDa actin-bundling protein) (Singed-like protein) (p55)	493	FSCN1	1	0	2	2	0	5.3

1449	0.37	0.27	0.45	O75874	Isocitrate dehydrogenase [NADP] cytoplasmic (IDH) (EC 1.1.1.42) (Cytosolic NADP-isocitrate dehydrogenase) (IDP) (NADP(+)-specific ICDH) (Oxalosuccinate decarboxylase)	414	IDH1	5	3	5	13	8.2	14.7
1450	0.38	0.46	0.49	F8W7Q4	Protein FAM162A	144	FAM162A	1	2	2	7.6	15.3	19.4
1451	0.40	-0.20	0.44	F5GYN4	Ubiquitin thioesterase OTUB1	241	OTUB1	3	3	5	14.5	17.4	27.4
1452	0.41	0.00	1.21	P07305	Histone H1.0 (Histone H1') (Histone H1(0)) [Cleaved into: Histone H1.0, N-terminally processed]	194	H1F0	1	0	1	7.3	0	7.3
1453	0.41	0.00	1.07	Q16795	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial (Complex I-39kD) (CI-39kD) (NADH-ubiquinone oxidoreductase 39 kDa subunit)	377	NDUFA9	1	0	2	2.7	0	8
1454	0.41	0.00	-0.02	H0Y6T7	Nicastrin (Fragment)	275	NCSTN	2	0	1	7.3	0	4.4
1455	0.42	0.00	0.37	G3V2G6	Retinol dehydrogenase 11 (Fragment)	178	RDH11	1	1	1	7.3	7.3	7.3
1456	0.42	1.99	1.98	P52292	Importin subunit alpha-1 (Karyopherin subunit alpha-2) (RAG cohort protein 1) (SRP1-alpha)	529	KPNA2	3	2	2	7	7	5.5
1457	0.42	0.00	0.00	Q6SZW1	Sterile alpha and TIR motif-containing protein 1 (Sterile alpha and Armadillo repeat protein) (Sterile alpha motif domain-containing protein 2) (MyD88-5) (SAM domain-containing protein 2) (Tir-1 homolog)	724	SARM1	1	0	0	1.6	0	0
1458	0.43	0.70	1.27	Q16698	2,4-dienoyl-CoA reductase, mitochondrial (EC 1.3.1.34) (2,4-dienoyl-CoA reductase [NADPH]) (4-enoyl-CoA reductase [NADPH]) (Short chain dehydrogenase/reductase family 18C member 1)	335	DECR1	1	4	2	4	17.8	10.7

1459	0.43	0.18	-0.23	Q56VL3	OCIA domain-containing protein 2 (Ovarian carcinoma immunoreactive antigen-like protein)	154	OCIAD2	1	3	1	8.4	21.4	8.4
1460	0.44	0.16	0.49	O95994	Anterior gradient protein 2 homolog (AG-2) (hAG-2) (HPC8) (Secreted cement gland protein XAG-2 homolog)	175	AGR2	4	4	3	26.3	36	33.1
1461	0.44	1.96	0.43	Q9UI09	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12 (13 kDa differentiation-associated protein) (Complex I-B17.2) (CI-B17.2) (CIB17.2) (NADH-ubiquinone oxidoreductase subunit B17.2)	145	NDUFA12	1	1	1	5.5	11.7	5.5
1462	0.44	0.09	-0.09	Q16836	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial (HCDH) (EC 1.1.1.35) (Medium and short-chain L-3-hydroxyacyl-coenzyme A dehydrogenase) (Short-chain 3-hydroxyacyl-CoA dehydrogenase)	314	HADH	1	1	1	3.2	3.2	3.2
1463	0.44	-0.16	0.06	P40616	ADP-ribosylation factor-like protein 1	181	ARL1	1	2	1	5.5	12.2	5.5
1464	0.46	0.00	-0.57	B4DHN5	Syntenin-1 (cDNA FLJ55055, moderately similar to Syntenin-1)	239	SDCBP	1	0	2	4.6	0	8.8
1465	0.48	0.23	0.08	P23434	Glycine cleavage system H protein, mitochondrial (Lipoic acid-containing protein)	173	GCSH	1	2	1	8.1	13.9	8.1
1466	0.50	0.54	0.79	H3BPJ9	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	161	NDUFB10	1	2	2	6.2	14.9	14.3
1467	0.51	0.11	-0.02	P18564	Integrin beta-6	788	ITGB6	1	1	1	1.3	1.3	1.3

1468	0.52	-0.60	0.01	P21980	Protein-glutamine gamma-glutamyltransferase 2 (EC 2.3.2.13) (Tissue transglutaminase) (Transglutaminase C) (TG(C)) (TGC) (TGase C) (Transglutaminase H) (TGase H) (Transglutaminase-2) (TGase-2)	687	TGM2	6	2	4	9.5	3.8	7.1
1469	0.53	0.00	-0.46	P48735	Isocitrate dehydrogenase [NADP], mitochondrial (IDH) (EC 1.1.1.42) (ICD-M) (IDP) (NADP(+)-specific ICDH) (Oxalosuccinate decarboxylase)	452	IDH2	2	1	1	5	2.8	2.8
1470	0.54	0.52	0.77	E9PFN5	Glutathione S-transferase kappa 1	190	GSTK1	1	4	4	7.4	26.8	25.8
1471	0.55	0.00	0.44	A0A024R7W5	YTH domain family, member 3, isoform CRA_a (YTH domain-containing family protein 3)	534	YTHDF3	1	0	1	2.6	0	2.6
1472	0.55	0.00	-0.18	D6RG15	Twinfilin-2	254	TWF2	2	0	2	9.8	0	9.8
1473	0.55	0.00	-0.30	Q9UNH7	Sorting nexin-6 (TRAF4-associated factor 2) [Cleaved into: Sorting nexin-6, N-terminally processed]	406	SNX6	1	0	1	3.8	0	3.8
1474	0.58	0.40	0.26	P14314	Glucosidase 2 subunit beta (80K-H protein) (Glucosidase II subunit beta) (Protein kinase C substrate 60.1 kDa protein heavy chain) (PKCSH)	528	PRKCSH	2	2	3	4.2	4.4	6.3
1475	0.59	0.25	-0.11	P22307	Non-specific lipid-transfer protein (NSL-TP) (EC 2.3.1.176) (Propanoyl-CoA C-acyltransferase) (SCP-chi) (SCPX) (Sterol carrier protein 2) (SCP-2) (Sterol carrier protein X) (SCP-X)	547	SCP2	1	6	2	13.6	30	16.4

1476	0.61	0.26	-0.05	Q9BW60	Elongation of very long chain fatty acids protein 1 (EC 2.3.1.199) (3-keto acyl-CoA synthase ELOVL1) (ELOVL fatty acid elongase 1) (ELOVL FA elongase 1) (Very-long-chain 3-oxoacyl-CoA synthase 1)	279	ELOVL1	1	1	1	5.2	5.2	5.2
1477	0.61	0.00	-0.23	O43175	D-3-phosphoglycerate dehydrogenase (3-PGDH) (EC 1.1.1.95)	533	PHGDH	1	0	2	2.4	0	4.7
1478	0.62	-0.22	0.12	Q6YN16	Hydroxysteroid dehydrogenase-like protein 2 (EC 1.-.-.-) (Short chain dehydrogenase/reductase family 13C member 1)	418	HSDL2	2	1	2	9.6	5.2	9.6
1479	0.64	3.22	2.05	P14923	Junction plakoglobin (Catenin gamma) (Desmoplakin III) (Desmoplakin-3)	745	JUP	1	10	1	1.3	15.8	1.6
1480	0.64	-0.62	-0.47	G3XAM7	Catenin (Cadherin-associated protein), alpha 1, 102kDa, isoform CRA_a (Catenin alpha-1)	841	CTNNA1	4	3	4	6.3	4.9	6.3
1481	0.66	-1.33	-0.10	P40261	Nicotinamide N-methyltransferase (EC 2.1.1.1)	264	NNMT	3	3	4	17.4	17.4	17
1482	0.69	-1.30	-0.31	M0R0M3	Gamma-glutamylaminecyclotransferase (Fragment)	26	GGACT	1	1	1	38.5	38.5	38.5
1483	0.72	0.00	0.48	H0YM76	WD repeat-containing protein 61	48	WDR61	1	0	1	33.3	0	33.3
1484	0.73	0.31	-0.19	P19367	Hexokinase-1 (EC 2.7.1.1) (Brain form hexokinase) (Hexokinase type I) (HK I)	917	HK1	2	2	2	2.5	2.5	2.5
1485	0.75	-1.17	-0.78	O00194	Ras-related protein Rab-27B (C25KG)	218	RAB27B	2	2	2	10.1	10.1	10.1
1486	0.80	0.33	0.07	G3XAL9	Solute carrier family 12 (Sodium/potassium/chloride transporters), member 2, isoform CRA_a (Solute carrier family 12 member 2)	1150	SLC12A2	1	2	1	1.9	3	1.9

1487	0.90	-0.83	-0.47	F5H3C5	Superoxide dismutase [Mn], mitochondrial (Fragment)	111	SOD2	6	5	6	47.7	45.9	47.7
1488	0.94	0.00	0.00	F8WAU7	Vesicle-trafficking protein SEC22a	71	SEC22A	1	0	0	14.1	0	0
1489	0.99	0.00	-0.78	Q2TB90	Putative hexokinase HKDC1 (EC 2.7.1.1) (Hexokinase domain-containing protein 1)	917	HKDC1	1	1	2	1.1	1	2.1
1490	1.01	-1.43	-0.89	Q6P452	Annexin	299	ANXA4	5	10	4	18.7	30.1	17.1
1491	1.13	-1.82	-0.21	Q9BS40	Latexin (Endogenous carboxypeptidase inhibitor) (ECI) (Protein MUM) (Tissue carboxypeptidase inhibitor) (TCI)	222	LXN	1	1	1	4.1	4.1	4.1
1492	1.39	0.00	-0.22	O14684	Prostaglandin E synthase (EC 5.3.99.3) (Microsomal glutathione S-transferase 1-like 1) (MGST1-L1) (Microsomal prostaglandin E synthase 1) (MPGES-1) (p53-induced gene 12 protein)	152	PTGES	1	0	1	6.6	0	6.6

Table S2A. List of all identified phosphoproteins from SILAC experiments in CURI

S. No.	log2 CURI	Amino acid	Number of Phospho (STY)	Protein	Protein names	Gene names	Charge	Localization prob	PEP	Score	Delta score	Score for localization	Mass error [ppm]	Position	Positions within proteins	Sequence window
1	-0.19	S	1	E7ENN3	Nesprin-1	SYNE1	2	0.90	0.01	63.18	63.18	63.18	-0.92	1916	1916;1896;1903;1896	SGILRQLRQTVEATNSMNKNESDLIEKDLND
2	6.28	S	2	O75691	Small subunit processome component 20 homolog	UTP20	2	1	0.01	72.32	22.13	72.32	1.02	241	241	QLLFEMCKGVRNMFHSCTGQAVKLILRKLGP
3	5.10	S	2	Q5VY30	Retinol-binding protein 4;Plasma retinol-binding protein(1-182);Plasma retinol-binding protein(1-181);Plasma retinol-binding protein(1-179);Plasma retinol-binding protein(1-176)	RBP4	2	1	0.01	69.43	23.32	69.43	-0.14	194	194;196	RQYRLIVHNGYCDGRSERNLL__________
4	-2.02	S	1	P35558	Phosphoenolpyruvate carboxykinase, cytosolic [GTP]	PCK1	2	0.97	0.01	91.31	9.68	91.31	-0.97	286	286	TNPEGEKKYLAAAFPSACGKTNLAMMNPSLP
5	-1.15	S	1	P51858-2	Hepatoma-derived growth factor	HDGF	2	1	0.003	103.04	67.36	103.04	-0.83	158	158;165;181	EKGALKRRAGDLLEDSPKRPKEAENPEGEEK
6	-0.64	S	1	Q5JR89	Kinesin-like protein KIF2C	KIF2C	2	0.99	0.008	72.2	27.58	72.2	-1.01	273	273;241;228;282	PLNKQELAKKEIDVISIPSKCLLLVHEPKL_
7	8.87	S	2	Q7L513-15			2	1	0.02	75.10	26.55	74.40	-1.20	6	6;6;6;6;6;6;6	__________MLKKISVGVAGDLNTVTMKLG
8	-3.95	S	1	Q8N0V4	Leucine-rich repeat LGI family member 2	LGI2	2	1	0.01	81.27	10.87	81.27	-0.005	461	461	MRWNSKQFVEIQALPSRGAMTLQPFSFKDNH
9	-1.71	S	2	Q8NB66	Protein unc-13 homolog C	UNC13C	2	1	0.002	104.35	10.26	104.35	-0.90	1534	1534	LTSITFFRMKVLELQSPPKASMVVKDCVRAC
10	-1.71	S	2	Q8NB66	Protein unc-13 homolog C	UNC13C	2	1	0.002	104.3	10.26	104.35	-0.90	1539	1539	FFRMKVLELQSPPKASMVVKDCVRACLDSTY
11	0.06	Y	1	C9JEV4	Tectonin beta-propeller repeat-containing protein 1	TECPR1	2	0.99	0.01	72.81	72.81	72.81	-0.91	24	24;24;24;24;24;24	VDLFGRVYTLSTAGQYWEMCKDSQLEFKRVS
12	0.05	Y	1	D6REQ7	Protein ZGRF1	ZGRF1	2	0.84	0.01	78.50	41.51	78.50	-0.92	10	10;10;10;10;10;10;10;10	______MESQEFIVLYTHQKMKKSKVWQDGI
13	8.11	Y	1	G3V500	Echinoderm microtubule-associated protein-like 1	EML1	3	1	0.004	93.10	49.26	93.10	-0.42	155	155;173;174;186;205	SESKPKEPVFSAEEGYVKMFLRGRPVTMYMP
14	5.10	Y	2	Q5VY30	Retinol-binding protein 4;Plasma retinol-binding protein(1-182);Plasma retinol-binding protein(1-181);Plasma retinol-binding protein(1-179);Plasma retinol-binding protein(1-176)	RBP4	2	1	0.01	69.43	23.32	69.43	-0.14	189	189;191	ELCLARQYRLIVHNGYCDGRSERNLL_____
15	0.09	Y	0	Q5VWW1-3	Complement C1q-like protein 3	C1QL3	2	1	0.007	76.67	76.67	76.67	-2.2	98	98;116;140	PKIAFYAGLKRQHEGYEVLKFDDVVTNLGNH

Table S2B. List of all identified phosphoproteins from SILAC experiments in LPSI

S. No.	log2 LPSI	Amino acid	Number of Phospho (STY)	Protein	Protein names	Gene names	Charge	Localization prob	PEP	Score	Delta score	Score for localization	Mass error [ppm]	Position	Positions within proteins	Sequence window
1	0.86	S	1	A0A0A0MRP6	Probable global transcription activator SNF2L1	SMARCA1	2	0.99	0.02	68.66	14.90	68.66	1.17	420	420;420;420;420	KSLPPKKEIKIYLGLSKMQREWYTKILMKDI
2	-0.90	S	1	C9J8H5	Zinc finger matrin-type protein 3	ZMAT3	3	1.00	0.03	53.26	53.26	53.26	-0.44	44	44;44;44	GTLQLPPQKPFGQEASLPLAGEEELSKGGEQ
3	8.00	S	1	C9JZY6	Ubiquitin-conjugating enzyme E2 H	UBE2H	2	1.00	0.01	66.06	39.27	66.06	1.45	2	2;2;2	______________MSSPSPGKRRMDTDVVK
4	-8.63	S	2	D6RFK7		THAP6	3	1.00	0.02	67.42	63.31	67.42	-0.25	50	50	PNIKLKPGVIPSIFDSPYHLQKHRKRKQEQE
5	-8.63	S	2	D6RFK7		THAP6	3	1.00	0.02	67.42	63.31	67.42	-0.25	46	46	DRSAPNIKLKPGVIPSIFDSPYHLQKHRKRK
6	4.28	S	1	E5RJ66	Leucine-rich repeat-containing protein 69	LRRC69	2	1.00	0.03	65.57	16.51	65.57	-0.27	31	31;31;31;31	TKIITLNGKKMTKMPSALGKLPGLKTLVLQN
7	0.78	T		E7EPV1	Speedy protein A	SPDYA	2	1.00	0.01	96.33	35.30	96.33	-1.44	104	104;104;104	MDCCCKIADKYLLAMTFVYFKRAKFTISEHT
8	5.86	S	1	E9PMS6	LIM domain only protein 7	LMO7	2	1.00	0.00	118.24	40.58	92.94	-0.17	1053	1053;1176;1176;1409;1446;1127;1176;1461;1461;1461	NMTSSQRRSKKEQVPSGAELERQQILQEMRK
9	5.19	S	1	F5H0J3		NDUFA9	3	1.00	0.01	81.81	16.63	81.81	-0.98	9	9	_______MDQKAEVASQVEVVIFLKKKNQFR
10	-9.75	Y	1	G3V500	Echinoderm microtubule-associated protein-like 1	EML1	3	1.00	0.01	85.99	57.36	77.73	-1.09	155	155;173;174;186;205	SESKPKEPVFSAEEGYVKMFLRGRPVTMYMP
11	6.01	S	1	P28329-3	Choline O-acetyltransferase	CHAT	3	0.85	0.01	91.59	56.49	81.53	0.96	77	77;113;195	QQKLLERQEKTANWVSEYWLNDMYLNNRLAL
12	0.35	T	2	Q05193-5	Dynamin-1	DNM1	2	1.00	0.01	96.05	96.05	96.05	-0.31	461	461;461;461;461	LQQYPRLREEMERIVTTHIREREGRTKEQVM
13	0.35	T	2	Q05193-5	Dynamin-1	DNM1	2	1.00	0.01	96.05	96.05	96.05	-0.31	462	462;462;462;462	QQYPRLREEMERIVTTHIREREGRTKEQVML
14	0.18	S	1	Q5JR89	Kinesin-like protein KIF2C	KIF2C	2	1.00	0.01	67.39	30.97	67.39	-0.32	273	273;241;228;282	PLNKQELAKKEIDVISIPSKCLLLVHEPKL_
15	0.41	S		Q5T1R4-2	Transcription factor HIVEP3	HIVEP3	2	0.91	0.02	68.26	31.22	68.26	0.89	2254	2254;2255	ERGRWSPTESSSASVSPVAKVSKFTLSSELE
16	6.50	S	1	Q7L311	Armadillo repeat-containing X-linked protein 2	ARMCX2	3	1.00	0.02	58.48	28.44	58.48	-0.99	533	533	SQGGGKIKVEILKILSNFAENPDMLKKLLST
17	-2.34	S	1	Q8ND07	Basal body-orientation factor 1	CCDC176	3	1.00	0.02	82.59	34.65	82.59	-1.46	37	37	IKTDESVVDRAKANASLWEARLEVTELSRIK
18	6.59	S	2	Q8NDT2-2	Putative RNA-binding protein 15B	RBM15B	2	1.00	0.00	112.30	74.75	112.30	-0.43	301	301;628	ERSRTKGSGQQSERGSDRTPERSRKENHSSE
19	6.59	T	2	Q8NDT2-2	Putative RNA-binding protein 15B	RBM15B	2	1.00	0.00	112.30	74.75	112.30	-0.43	304	304;631	RTKGSGQQSERGSDRTPERSRKENHSSEGTK
20	2.51	S	1	Q96JS4		hucep-3	2	0.87	0.03	65.24	23.05	65.24	0.75	93	93	GKGMGLWGRGGMGFRSICTIRKVLRSFFLEG
21	9.57	S	2	Q9BXJ3	Complement C1q tumor necrosis factor-related protein 4	C1QTNF4	2	1.00	0.02	63.18	63.18	63.18	0.39	244	244	YFFSFTLGKLPRKTLSVKLMKNRDEVQAMIY

Table S2C. List of all identified phosphoproteins from SILAC experiments in LPSCUR

S. No.	log2 LPSCUR	Amino acid	Number of Phospho (STY)	Protein	Protein names	Gene names	Charge	Localization prob	PEP	Score	Delta score	Score for localization	Mass error [ppm]	Position	Positions within proteins	Sequence window
1	7.70	Y	1	G3V500	Echinoderm microtubule-associated protein-like 1	EML1	3	1.00	0.01	70.45	18.92	70.45	-0.94	155	155;173;174;186;205	SESKPKEPVFSAEEGYVKMFLRGRPVTMYMP
2	3.39	T	1	A6NHA9	Olfactory receptor 4C46	OR4C46	3	1.00	0.00	98.18	49.58	98.18	-3.77	16	16	MENRNNMTEFVLLGLTENPKMQKIIFVVFFV
3	2.52	T	2	O75691	Small subunit processome component 20 homolog	UTP20	2	1.00	0.00	92.94	36.37	92.94	0.92	243	243	LFEMCKGVRNMFHSCTGQAVKLILRKLGPVT
4	-0.94	Y	1	Q658L1-2	Protein FAM154B	FAM154B	2	1.00	0.01	79.20	27.13	79.20	-3.97	140	140;155	RSTAPFNGITSHRLDYIPHQLELKFERPKEV

Table S3. Number of phosphosites, charges in peptides and number of phosphogroups per peptide identified in CURI, LPSI and LPSCUR experiments.

Table S3A. Number of phosphosites

Experiments	Serine (S)	Threonine (T)	Tyrosine (Y)
CURI	15	0	5
LPSI	19	6	1
LPSCUR	0	3	2

Table S3B. Charges in peptides

Experiments	Doubly charge	Triply charge	Multiply charge
CURI	14	1	0
LPSI	13	8	0
LPSCUR	2	2	0

Table S3C. phosphogroups per peptide

Experiments	Singly phosphorylated	Doubly phosphorylated	Multiply phosphorylated
CURI	9	6	0
LPSI	14	7	0
LPSCUR	3	1	0