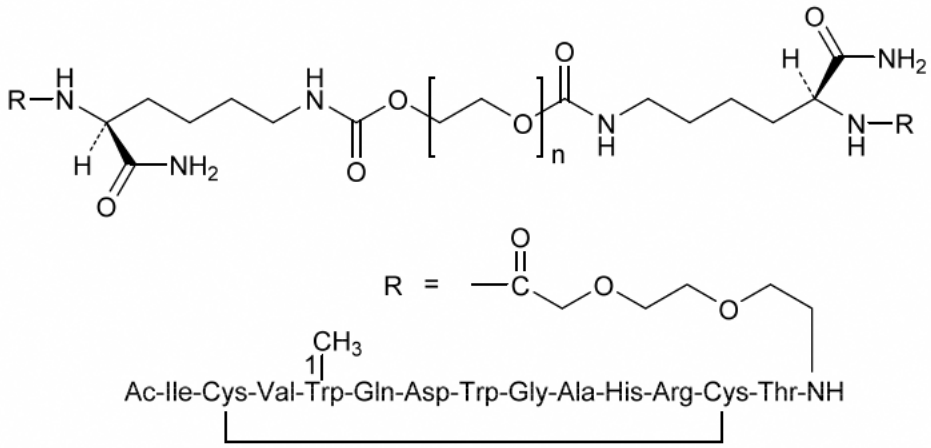
登録番号　303-3-B9

JAN（日本名）：ペグセタコプラン

JAN（英　名）：Pegcetacoplan



nは約800~1100である.

$C_{170}H_{248}N_{50}O_{47}S_4$（ペプチド部分）

ペグセタコプランはPEG化ペプチド（分子量：約43,500）であり，補体C3に結合する2本の同一の合成ペプチドが，C末端リシンアミドのε-アミノ基を介してポリエチレングリコール（分子量：約39,600）の両端にそれぞれ結合している．ペプチド部分は15個のアミノ酸残基からなる．化学名は以下の通りである．

O,*O*'-ビス[(S^2,S^{12}-シクロ{*N*-アセチル-L-イソロイシル-L-システイニル-L-バリル-1-メチル-L-トリプトフィル-L-グルタミニル-L-α-アスパルチル-L-トリプトフィルグリシル-L-アラニル-L-ヒスチジル-L-アルギニル-L-システイニル-L-スレオニル-2-[2-(2-アミノエトキシ)エトキシ]アセチル-L-リシンアミド})-$N^{6\,15}$-カルボニル]ポリエチレングリコール

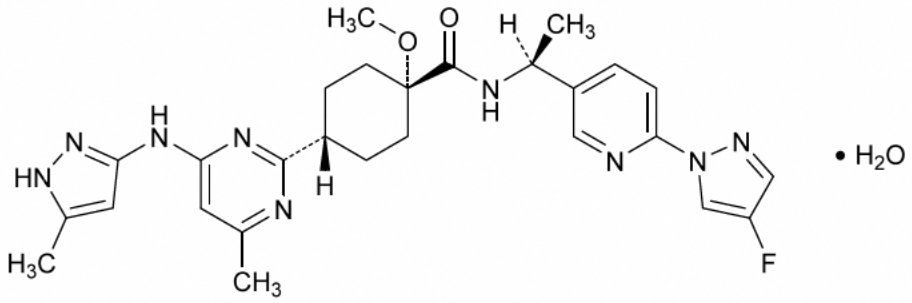
Pegcetacoplan is a PEGylated peptide (molecular weight: ca. 43,500) in which two identical synthetic peptides that bind to complement C3 are bound to each terminal of polyethylene glycol (molecular weight: ca. 39,600) via ε-amino group of C-terminal lysine amide. The peptide moiety consists of 15 amino acid residues. Chemical name is as follows:

O,*O*'-Bis[(S^2,S^{12}-cyclo{*N*-acetyl-L-isoleucyl-L-cysteinyl-L-valyl-1-methyl-L-tryptophyl-L-glutaminyl-L-α-aspartyl-L-tryptophylglycyl-L-alanyl-L-histidyl-L-arginyl-L-cysteinyl-L-threonyl-2-[2-(2-aminoethoxy)ethoxy]acetyl-L-lysinamide})-$N^{6\,15}$-carbonyl]polyethylene glycol

登録番号　303-3-B10

JAN（日本名）：プラルセチニブ水和物

JAN（英　名）：Pralsetinib Hydrate



$C_{27}H_{32}FN_9O_2 \cdot H_2O$

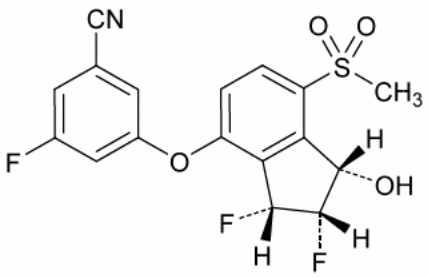
cis-*N*-{(1*S*)-1-[6-(4-フルオロ-1*H*-ピラゾール-1-イル)ピリジン-3-イル]エチル}-1-メトキシ-4-{4-メチル-6-[(5-メチル-1*H*-ピラゾール-3-イル)アミノ]ピリミジン-2-イル}シクロヘキサン-1-カルボキシアミド　一水和物

cis-*N*-{(1*S*)-1-[6-(4-Fluoro-1*H*-pyrazol-1-yl)pyridin-3-yl]ethyl}-1-methoxy-4-{4-methyl-6-[(5-methyl-1*H*-pyrazol-3-yl)amino]pyrimidin-2-yl}cyclohexane-1-carboxamide monohydrate

登録番号　303-3-B11

JAN（日本名）：ベルズチファン

JAN（英　名）：Belzutifan



$C_{17}H_{12}F_3NO_4S$

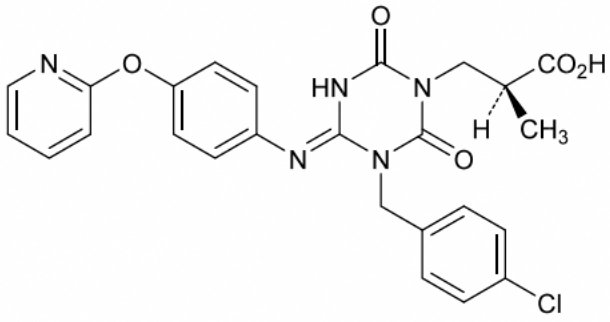
3-{[(1*S*,2*S*,3*R*)-2,3-ジフルオロ-1-ヒドロキシ-7-(メタンスルホニル)-2,3-ジヒドロ-1*H*-インデン-4-イル]オキシ}-5-フルオロベンゾニトリル

3-{[(1*S*,2*S*,3*R*)-2,3-Difluoro-1-hydroxy-7-(methanesulfonyl)-2,3-dihydro-1*H*-inden-4-yl]oxy}-5-fluorobenzonitrile

登録番号　303-4-B1

JAN（日本名）：シボピキサント

JAN（英　名）：Sivopixant



$C_{25}H_{22}ClN_5O_5$

(2*S*)-3-[(4*E*)-3-[(4-クロロフェニル)メチル]-2,6-ジオキソ-4-({4-[(ピリジン-2-イル)オキシ]フェニル}イミノ)-1,3,5-トリアジナン-1-イル]-2-メチルプロパン酸

(2*S*)-3-[(4*E*)-3-[(4-Chlorophenyl)methyl]-2,6-dioxo-4-({4-[(pyridin-2-yl)oxy]phenyl}imino)-1,3,5-triazinan-1-yl]-2-methylpropanoic acid

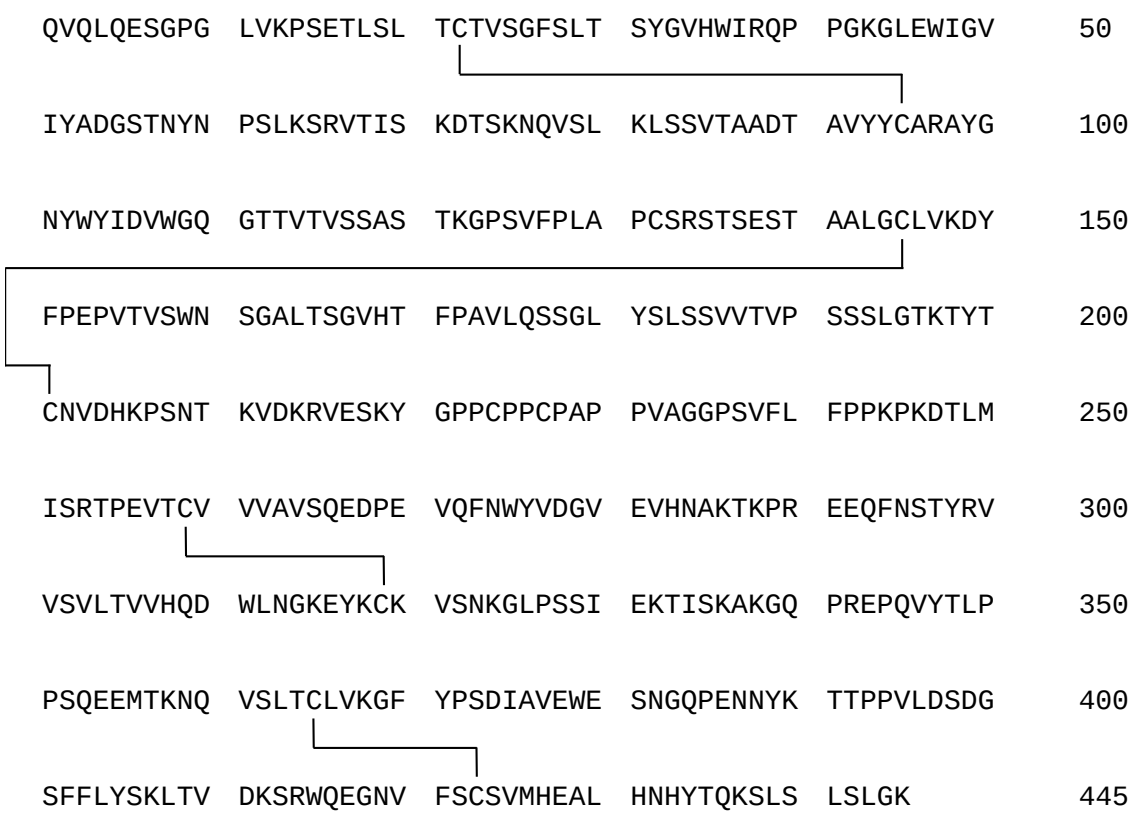
登録番号　303-4-B2

JAN（日本名）：チスレリズマブ（遺伝子組換え）

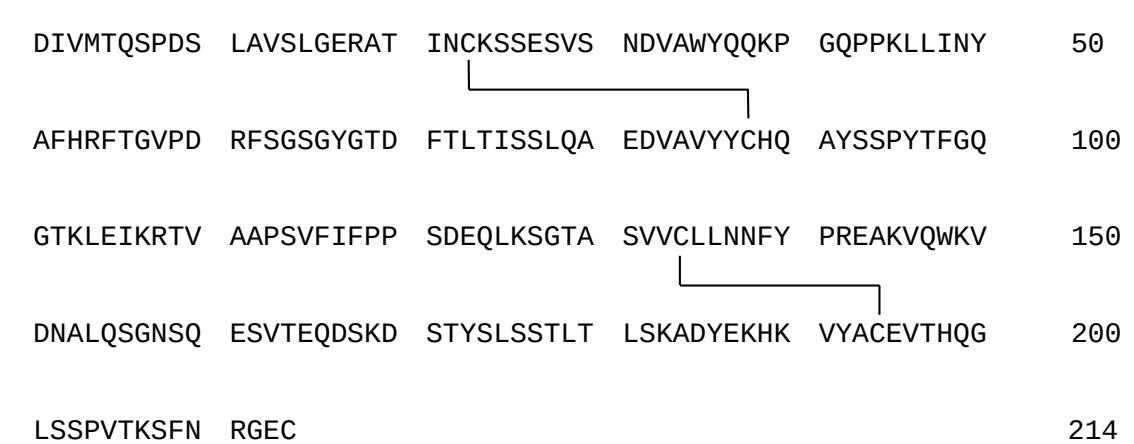
JAN（英　名）：Tislelizumab (Genetical Recombination)

アミノ酸配列及びジスルフィド結合

H 鎖



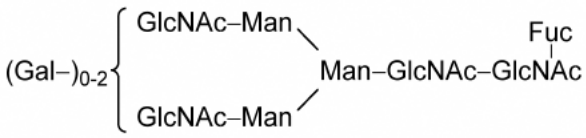
L 鎖



H 鎖 Q1：部分的ピログルタミン酸；H 鎖 N295：糖鎖結合；H 鎖 K445：部分的プロセシング

H 鎖 C132　L 鎖 C214，H 鎖 C224　H 鎖 C224，H 鎖 C227　H 鎖 C227：ジスルフィド結合

主な糖鎖の推定構造



$C_{6410}H_{9890}N_{1686}O_{2012}S_{40}$（タンパク質部分，4 本鎖）

H 鎖　$C_{2166}H_{3353}N_{567}O_{670}S_{14}$

L 鎖　$C_{1039}H_{1596}N_{276}O_{336}S_{6}$

チスレリズマブは，遺伝子組換え抗 PD-1 モノクローナル抗体であり，その相補性決定部はマウス抗体に由来し，その他はヒト IgG4 に由来する．H 鎖の 6 個のアミノ酸残基が置換（S226P，E231P，F232V，L233A，D263A，R407K）されている．チスレリズマブは，CHO 細胞により産生される．チスレリズマブは，445 個のアミノ酸残基からなる H 鎖（γ4 鎖）2 本及び 214 個のアミノ酸残基からなる L 鎖（κ 鎖）2 本で構成される糖タンパク質（分子量：約 147,000）である．

Tislelizumab is a recombinant anti-PD-1 monoclonal antibody, the complementarity-determining regions of which are derived from mouse antibody and other regions are derived from human IgG4. In the H-chain, the amino acid residues are substituted at 6 positions (S226P, E231P, F232V, L233A, D263A, R407K). Tislelizumab is produced in CHO cells. Tislelizumab is a glycoprotein (molecular weight: ca. 147,000) composed of 2 H-chains (γ4-chains) consisting of 445 amino acid residues each and 2 L-chains (κ-chains) consisting of 214 amino acid residues each.

※　JAN 以外の情報は、参考として掲載しました。

International Nonproprietary Names for Pharmaceutical Substances (INN)

RECOMMENDED International Nonproprietary Names: List 80

Notice is hereby given that, in accordance with paragraph 7 of the Procedure for the Selection of Recommended International Nonproprietary Names for Pharmaceutical Substances [*Off. Rec. Wld Health Org*., 1955, **60**, 3 (Resolution EB15.R7); 1969, **173**, 10 (Resolution EB43.R9); Resolution EB115.R4 (EB115/2005/REC/1)], the following names are selected as Recommended International Nonproprietary Names. The inclusion of a name in the lists of Recommended International Nonproprietary Names does not imply any recommendation of the use of the substance in medicine or pharmacy.
Lists of Proposed (1–117) and Recommended (1–78) International Nonproprietary Names can be found in *Cumulative List No. 17, 2017* (available in CD-ROM only).

Dénominations communes internationales des Substances pharmaceutiques (DCI)

Dénominations communes internationales RECOMMANDÉES: Liste 80

Il est notifié que, conformément aux dispositions du paragraphe 7 de la Procédure à suivre en vue du choix de Dénominations communes internationales recommandées pour les Substances pharmaceutiques [*Actes off. Org. mond. Santé*, 1955, **60**, 3 (résolution EB15.R7); 1969, **173**, 10 (résolution EB43.R9); résolution EB115.R4 (EB115/2005/REC/1)] les dénominations ci-dessous sont choisies par l'Organisation mondiale de la Santé en tant que dénominations communes internationales recommandées. L'inclusion d'une dénomination dans les listes de DCI recommandées n'implique aucune recommandation en vue de l'utilisation de la substance correspondante en médecine ou en pharmacie.
On trouvera d'autres listes de Dénominations communes internationales proposées (1–117) et recommandées (1–78) dans la *Liste récapitulative No. 17, 2017* (disponible sur CD-ROM seulement).

Denominaciones Comunes Internacionales para las Sustancias Farmacéuticas (DCI)

Denominaciones Comunes Internacionales RECOMENDADAS: Lista 80

De conformidad con lo que dispone el párrafo 7 del Procedimiento de Selección de Denominaciones Comunes Internacionales Recomendadas para las Sustancias Farmacéuticas [*Act. Of. Mund. Salud*, 1955, **60**, 3 (Resolución EB15.R7); 1969, **173**, 10 (Resolución EB43.R9); Résolution EB115.R4 (EB115/2005/REC/1) EB115.R4 (EB115/2005/REC/1)], se comunica por el presente anuncio que las denominaciones que a continuación se expresan han sido seleccionadas como Denominaciones Comunes Internacionales Recomendadas. La inclusión de una denominación en las listas de las Denominaciones Comunes Recomendadas no supone recomendación alguna en favor del empleo de la sustancia respectiva en medicina o en farmacia.
Las listas de Denominaciones Comunes Internacionales Propuestas (1–117) y Recomendadas (1–78) se encuentran reunidas en *Cumulative List No. 17, 2017* (dispon ble sólo en CD-ROM).

Latin, English, French, Spanish: *Recommended INN*	*Chemical name or description; Molecular formula; Graphic formula*
DCI Recommandée	*Nom chimique ou description; Formule brute; Formule développée*
DCI Recomendada	*Nombre químico o descripción; Fórmula molecular; Fórmula desarrollada*

abrezekimabum #

abrezekimab	immunoglobulin Fab G1-kappa, anti-[*Homo sapiens* IL13 (interleukin 13, IL-13)], neutralizing, humanized monoclonal antibody; VH-(CH1-hinge) gamma1 heavy chain (1-223) [humanized VH (*Homo sapiens* IGHV2-26*01 (80.8%) -(IGHD)-IGHJ4*01 (100%)) [8.7.14] (1-120) -*Homo sapiens* IGHG1*01, G1m17, K120 (217) (CH1 (121-218), hinge 1-5 (218-223)) (121-223)], (223-214')-disulfide with kappa light chain (1'-214') [humanized V-KAPPA (*Homo sapiens* IGKV1-39*01 (87.4%) -IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]
abrézékimab	immunoglobuline Fab G1-kappa, anti-[*Homo sapiens* IL13 (interleukine 13, IL-13)], neutralisant, anticorps monoclonal humanisé; VH-(CH1-charnière) chaîne lourde gamma1 (1-223) [VH humanisé (*Homo sapiens* IGHV2-26*01 (80.8%) -(IGHD)-IGHJ4*01 (100%)) [8.7.14] (1-120) -*Homo sapiens* IGHG1*01, G1m17, K120 (217) (CH1 (121-218), charnière 1-5 (218-223)) (121-223)], (223-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA humanisé (*Homo sapiens* IGKV1-39*01 (87.4%) -IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]
abrezekimab	inmunoglobulina Fab G1-kappa, anti-[*Homo sapiens* IL13 (interleukina 13, IL-13)], neutralizante, anticuerpo monoclonal humanizado; VH-(CH1-bisagra) cadena pesada gamma1 (1-223) [VH humanizado (*Homo sapiens* IGHV2-26*01 (80.8%) -(IGHD)-IGHJ4*01 (100%)) [8.7.14] (1-120) -*Homo sapiens* IGHG1*01, G1m17, K120 (217) (CH1 (121-218), bisagra 1-5 (218-223)) (121-223)], (223-214')-disulfuro con la cadena ligera kappa (1'-214') [V-KAPPA humanizado (*Homo sapiens* IGKV1-39*01 (87.4%) -IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]

Heavy chain / Chaîne lourde / Cadena pesada

```
QVTLKESGPV LVKPTETLTL TCTVSGFSLT NYHVQWIRQP PGKALEWLGV  50
MWSDGDTSFN SVLKSRLTIS RDTSKSQVVL TMTNMDPVDT ATYYCARDGT 100
IAAMDYFDYW GQGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKKVEP KSC                              223
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCLASEDIS NYLAWYQQKP GKAPKLLIYH  50
TSRLQDGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ GYRFPLTFGG 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

Intra-H (C23-C104) 22-95 147-203
Intra-L (C23-C104) 23'-88' 134'-194'
Inter-H-L (h 5-CL 126) 223-214'
No N-glycosylation sites / pas de site de N-glycosylation / ningún posición de N-glicosilación

adalimumabum beta #

adalimumab beta	immunoglobulin G1-kappa, anti-[*Homo sapiens* TNF (tumor necrosis factor (TNF) superfamily member 2, TNFSF2, TNF-alpha, TNFA)], human monoclonal ant body; gamma1 heavy chain (1-451) [*Homo sapiens* VH (IGHV3-9*01 (93.9%) -(IGHD) -IGHJ4*01 (92.9%)) [8.8.14] (1-121) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (218) (122-219), hinge (220-234), CH2 (235-344), CH3 D12 (360), L14 (362) (345-449), CHS (450-451)) (122-451)], (224-214')-disulfide with kappa light chain (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-27*01 (95.8%) -IGKJ1*01 (91.7%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (230-230":233-233")-bisdisulfide
adalimumab bêta	immunoglobuline G1-kappa, anti-[*Homo sapiens* TNF (facteur de nécrose tumorale membre 2 de la superfamille du TNF, TNFSF2, TNF-alpha, TNFA)], anticorps monoclonal humain; chaîne lourde gamma1 (1-451) [*Homo sapiens* VH (IGHV3-9*01 (93.9%) -(IGHD) -IGHJ4*01 (92.9%)) [8.8.14] (1-121) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (218) (122-219), charnière (220-234), CH2 (235-344), CH3 D12 (360), L14 (362) (345-449), CHS (450-451)) (122-451)], (224-214')-disulfure avec la chaîne légère kappa (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-27*01 (95.80%) -IGKJ1*01 (91.7%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (230-230":233-233")-bisdisulfure
adalimumab beta	inmunoglobulina G1-kappa, anti-[*Homo sapiens* TNF (factor de necrosis tumoral miembro 2 de la superfamilia del TNF, TNFSF2, TNF-afa, TNFA)], anticuerpo monoclonal humano; cadena pesada gamma1 (1-451) [*Homo sapiens* VH (IGHV3-9*01 (93.9%) -(IGHD) -IGHJ4*01 (92.9%)) [8.8.14] (1-121) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (218) (122-219), bisagra (220-234), CH2 (235-344), CH3 D12 (360), L14 (362) (345-449), CHS (450-451)) (122-451)], (224-214')-disulfuro con la cadena ligera kappa (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-27*01 (95.80%) -IGKJ1*01 (91.7%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (230-230":233-233")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGRSLRL SCAASGFTFD DYAMHWVRQA PGKGLEWVSA  50
ITWNSGHIDY ADSVEGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCAKVS 100
YLSTASSLDY WGQGTLVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200
TYICNVNHKP SNTKVDKKVE PKSCDKTHTC PPCPAPELLG GPSVFLFPPK 250
PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY 300
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP 350
QVYTLPPSRD ELTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP 400
VLDSDGSFFL YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG 450
K                                                       451
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCRASQGIR NYLAWYQQKP GKAPKLLIYA  50
ASTLQSGVPS RFSGSGSGTD FTLTISSLQP EDVATYYCQR YNRAPYTFGQ 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 148-204 265-325 371-429
22"-96" 148'-204' 265"-325" 371"-429"
Intra-L (C23-C104) 23'-88' 134'-194'
23"-88"' 134"'-194"'
Inter-H-L (h 5-CL 126) 224-214' 224"-214"'
Inter-H-H (h 11, h 14) 230-230' 233-233'
N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4
301, 301"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados
G0F predominant / prédominant / predominante, G2FS2 (0,10 ± 0,04 %), Man4 (0,00 ± 0,01%)

apadamtasum alfa #

apadamtase alfa — human metalloproteinase with thrombospondin motifs 13 (metalloproteinase ADAMTS13), produced in Chinese hamster ovary (CHO) cells, glycoform alfa

apadamtase alfa — métalloprotéinase avec thrombospondine motif 13 (métalloprotéinase ADAMTS13) humaine, produite par des cellules ovariennes de hamsters chinois (CHO), glycoforme alfa

apadamtasa alfa — metaloproteinasa con trombospondina-motif 13 (metaloproteinasa ADAMTS13) humana, producida por las células ováricas de hamsters chinos (CHO), glicoforma alfa

```
AAGGILHLEL LVAVGPDVFQ AHQEDTERYV LTNLNIGAEL LRDPSLGAQF 50
RVHLVKMVIL TEPEGAPNIT ANLTSSLLSV CGWSQTINPE DDTDPGHADL 100
VLYITRFDLE LPDGNRQVRG VTQLGGACSP TWSCLITEDT GFDLGVTIAH 150
EIGHSFGLEH DGAPGSGCGP SGHVMASDGA APRAGLAWSP CSRRQLLSLL 200
SAGRARCVWD PPRPQPGSAG HPPDAQPGLY YSANEQCRVA FGPKAVACTF 250
AREHLDMCQA LSCHTDPLDQ SSCSRLLVPL LDGTECGVEK WCSKGRCRSL 300
VELTPIAAVH GRWSSWGPRS PCSRSCGGGV VTRRRQCNNP RPAFGGRACV 350
GADLQAEMCN TQACEKTQLE FMSQQCARTD GQPLRSSPGG ASFYHWGAAV 400
PHSQGDALCR HMCRAIGESF IMKRGDSFLD GTRCMPSGPR EDGTLSLCVS 450
GSCRTFGCDG RMDSQQVWDR CQVCGGDNST CSPRKGSFTA GRAREYVTFL 500
TVTPNLTSVY IANHRPLFTH LAVRIGGRYV VAGKMSISPN TTYPSLLEDG 550
RVEYRVALTE DRLPRLEEIR IWGPLQEDAD IQVYRRYGEE YGNLTRPDIT 600
FTYFQPKPRQ AWVWAAVRGP CSVSCGAGLR WVNYSCLDQA RKELVETVQC 650
QGSQQPPAWP EACVLEPCPP YWAVGDFGPC SASCGGGLRE RPVRCVEAQG 700
SLLKTLPPAR CRAGAQQPAV ALETCNPQPC PARWEVSEPS SCTSAGGAGL 750
ALENETCVPG ADGLEAPVTE GPGSVDEKLP APEPCVGMSC PPGWGHLDAT 800
SAGEKAPSPW GSIRTGAQAA HVWTPAAGSC SVSCGRGLME LRFLCMDSAL 850
RVPVQEELCG LASKPGSRRE VCQAVPCPAR WQYKLAACSV SCGRGVVRRI 900
LYCARAHGED DGEEILLDTQ CQGLPRPEPQ EACSLEPCPP RWKVMSLGPC 950
SASCGLGTAR RSVACVQLDQ GQDVEVDEAA CAALVRPEAS VPCLIADCTY 1000
RWHVGTWMEC SVSCGDGIQR RRDTCLGPQA QAPVPADFCQ HLPKPVTVRG 1050
CWAGPCVGQG TPSLVPHEEA AAPGRTTATP AGASLEWSQA RGLLFSPAPQ 1100
PRRLLPGPQE NSVQSSACGR QHLEPTGTID MRGPGQADCA VAIGRPLGEV 1150
VTLRVLESSL NCSAGDMLLL WGRLTWRKMC RKLLDMTFSS KTNTLVVRQR 1200
CGRPGGGVLL RYGSQLAPET FYRECDMQLF GPWGEIVSPS LSPATSNAGG 1250
CRLFINVAPH ARIAIHALAT NMGAGTEGAN ASYILIRDTH SLRTTAFHGQ 1300
QVLYWESESS QAEMEFSEGF LKAQASLRGQ YWTLQSWVPE MQDPQSWKGK 1350
EGT                                                     1353
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
81-134 128-207 168-191 237-263 248-273 258-292
286-297 322-359 326-364 337-349 376-413 409-448
434-453 458-474 471-481

Glycosylation sites (N) / Sites de glycosylation (N) / Posiciones de glicosilación (N)
Asn-68 Asn-72 Asn-478 Asn-505 Asn-540 Asn-593
Asn-633 Asn-754 Asn-1161 Asn-1280

Glycosylation sites (O) / Sites de glycosylation (O) / Posiciones de glicosilación (O)
Ser-325 Ser-624 Ser-683 Ser-833 Ser-891 Ser-953 Ser-1013

apraglutidum

apraglutide — 5,7-*O*-didephosphono[Ala^{2}>Gly,Met^{10}>Ahx,Asn^{11}>D-Phe,Asn^{16}>Leu]human glucagon-like peptide 2 (1-33)-peptide 33-amide:
L-histidylglycyl-L-α-aspartylglycyl-L-seryl-L-phenylalanyl-L-seryl-L-α-aspartyl-L-α-glutamyl-L-2-aminohexanoyl-D-phenylalanyl-L-threonyl-L-isoleucyl-L-leucyl-L-α-aspartyl-L-leucyl-L-leucyl-L-alanyl-L-alanyl-L-arginyl-L-α-aspartyl-L-phenylalanyl-L-isoleucyl-L-asparaginyl-L-tryptophyl-L-leucyl-L-isoleucyl-L-glutaminyl-L-threonyl-L-lysyl-L-isoleucyl-L-threonyl-L-α-asparagine

apraglutide — 5,7-*O*-didephosphono[Ala^{2}>Gly,Met^{10}>Ahx,Asn^{11}>D-Phe,Asn^{16}>Leu]peptide semblable au glucagon 2 humain (1-33)-peptide 33-amide:
L-histidylglycyl-L-α-aspartylglycyl-L-séryl-L-phénylalanyl-L-séryl-L-α-aspartyl-L-α-glutamyl-L-2-aminohexanoyl-D-phénylalanyl-L-thréonyl-L-isoleucyl-L-leucyl-L-α-aspartyl-L-leucyl-L-leucyl-L-alanyl-L-alanyl-L-arginyl-L-α-aspartyl-L-phénylalanyl-L-isoleucyl-L-asparaginyl-L-tryptophyl-L-leucyl-L-isoleucyl-L-glutaminyl-L-thréonyl-L-lysyl-L-isoleucyl-L-thréonyl-L-α-asparagine

apraglutida — 5,7-*O*-didefosfono[Ala^{2}>Gly,Met^{10}>Ahx,Asn^{11}>D-Phe,Asn^{16}>Leu] péptido similar al glucagón humano 2-(1-33)-péptido 33-amida:
L-histidilglicil-L-α-aspartilglicil-L-seril-L-fenilalanil-L-seril-L-α-aspartil-L-α-glutamil-L-2-aminohexanoil-D-fenilalanil-L-treonil-L-isoleucil-L-leucil-L-α-aspartil-L-leucil-L-leucil-L-alanil-L-alanil-L-arginil-L-α-aspartil-L-fenilalanil-L-isoleucil-L-asparaginil-L-triptofil-L-leucil-L-isoleucil-L-glutaminil-L-treonil-L-lisil-L-isoleucil-L-threonil-L-α-asparagina

$C_{172}H_{263}N_{43}O_{52}$

H-His-Gly-Asp-Gly-Ser-Phe-Ser-Asp-Glu-Ahx-D-Phe-Thr-Ile-Leu-Asp-Leu-Leu-Ala-Arg-Ala-Asp-Phe-Ile-Asn-Trp-Leu-Ile-Gln-Thr-Lys-Ile-Thr-Asp-NH_2

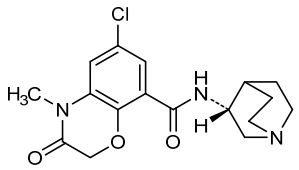
arazasetronum

arazasetron — *N*-[(3*R*)-1-azabicyclo[2.2.2]octan-3-yl]-6-chloro-4-methyl-3-oxo-3,4-dihydro-2*H*-1,4-benzoxazine-8-carboxamide

arazasétron — *N*-[(3*R*)-1-azabicyclo[2.2.2]octan-3-yl]-6-chloro-4-méthyl-3-oxo-3,4-dihydro-2*H*-1,4-benzoxazine-8-carboxamide

arazasetrón — *N*-[(3*R*)-1-azabiciclo[2.2.2]octan-3-il]-6-cloro-4-metil-3-oxo-3,4-dihidro-2*H*-1,4-benzoxazina-8-carboxamida

$C_{17}H_{20}ClN_3O_3$



belantamabum #

belantamab — immunoglobulin G1-kappa, anti-[*Homo sapiens* TNFRSF17 (TNF receptor superfamily member 17, tumor necrosis factor receptor superfamily, member 17, B cell maturation antigen, BCMA, BCM, TNFRSF13A, CD269)], humanized monoclonal antibody;

gamma1 heavy chain (1-451) [humanized VH (*Homo sapiens* IGHV1-69*06 (83.7%) -(IGHD)-IGHJ4*01 (85.7%)) [8.8.14] (1-121) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (218) (122-219), hinge (220-234), CH2 (235-344), CH3 D12 (360), L14 (362) (345-449), CHS (450-451)) (122-451)], (224-214')-disulfide with kappa light chain (1'-214') [humanized V-KAPPA (*Homo sapiens* IGKV1-33*01 (90.5%) -IGKJ2*02 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (230-230":233-233")-bisdisulfide

bélantamab

immunoglobuline G1-kappa, anti-[*Homo sapiens* TNFRSF17 (membre 17 de la superfamille des récepteurs du TNF, membre 17 de la superfamille des récepteur du facteur de nécrose tumorale, antigène de maturation de cellule B, BCMA, BCM, TNFRSF13A, CD269)], anticorps monoclonal humanisé; chaîne lourde gamma1 (1-451) [VH humanisé (*Homo sapiens* IGHV1-69*06 (83.7%) -(IGHD)-IGHJ4*01(85.7%)) [8.8.14] (1-121) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (218) (122-219), charnière (220-234), CH2 (235-344), CH3 D12 (360), L14 (362) (345-449), CHS (450-451)) (122-451)], (224-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA humanisé (*Homo sapiens* IGKV1-33*01 (90.5%) -IGKJ2*02 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (230-230":233-233")-bisdisulfure

belantamab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* TNFRSF17 (miembro 17 de la superfamilia de los receptores del TNF, miembro 17 de la superfamilia del receptor del factor de necrosis tumoral, antígeno de maduración de célula B, BCMA, BCM, TNFRSF13A, CD269)], anticuerpo monoclonal humanizado; cadena pesada gamma1 (1-451) [VH humanizado (*Homo sapiens* IGHV1-69*06 (83.7%) -(IGHD)-IGHJ4*01(85.7%)) [8.8.14] (1-121) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (218) (122-219), bisagra (220-234), CH2 (235-344), CH3 D12 (360), L14 (362) (345-449), CHS (450-451)) (122-451)], (224-214')-disulfuro con la cadena ligera kappa (1'-214') [V-KAPPA humanizado (*Homo sapiens* IGKV1-33*01 (90.5%) -IGKJ2*02 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (230-230":233-233")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGSSVKV SCKASGGTFS NYWMHWVRQA PGQGLEWMGA  50
TYRGHSDTYY NQKFKGRVTI TADKSTSTAY MELSSLRSED TAVYYCARGA 100
IYDGYDVLDN WGQGTLVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200
TYICNVNHKP SNTKVDKKVE PKSCDKTHTC PPCPAPELLG GPSVFLFPPK 250
PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY 300
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP 350
QVYTLPPSRD ELTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP 400
VLDSDGSFFL YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG 450
K                                                       451
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCSASQDIS NYLNWYQQKP GKAPKLLIYY  50
TSNLHSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YRKLPWTFGQ 100
GTKLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

Intra-H (C23-C104) 22-96 148-204 265-325 371-429
22"-96" 148"-204" 265"-325" 371"-429"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194'"
Inter-H-L (h 5-CL 126) 224-214' 224"-214'"
Inter-H-H (h 11, h 14) 230-230" 233-233"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
301, 301"
100% afucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes 100% afucosylés / glicanos de tipo CHO biantenarios complejos 100% afucosilados.
G0 > 75%.

C-terminal lysine clipping: H CHS K2: 451, 451" (clipping >90%).

belantamabum mafodotinum #

belantamab mafodotin

immunoglobulin G1-kappa, anti-[*Homo sapiens* TNFRSF17 (TNF receptor superfamily member 17, tumor necrosis factor receptor superfamily, member 17, B cell maturation antigen, BCMA, BCM, TNFRSF13A, CD269)], humanized monoclonal antibody conjugated to auristatin F;
gamma1 heavy chain (1-451) [humanized VH (*Homo sapiens* IGHV1-69*06 (83.7%) -(IGHD)-IGHJ4*01 (85.7%)) [8.8.14] (1-121) - *Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (218) (122-219), hinge (220-234), CH2 (235-344), CH3 D12 (360), L14 (362) (345-449), CHS (450-451)) (122-451)], (224-214')-disulfide with kappa light chain (1'-214') [humanized V-KAPPA (*Homo sapiens* IGKV1-33*01 (90.5%) -IGKJ2*02 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191)(108'-214')]; dimer (230-230":233-233")-bisdisulfide; conjugated, on an average of 4 cysteinyl, to monomethylauristatin F (MMAF), via a noncleavable maleimidocaproyl (mc) linker
For the *mafodotin* part, please refer to the document *"INN for pharmaceutical substances: Names for radicals, groups and others"**.

bélantamab mafodotine

immunoglobuline G1-kappa, anti-[*Homo sapiens* TNFRSF17 (membre 17 de la superfamille des récepteurs du TNF, membre 17 de la superfamille des récepteur du facteur de nécrose tumorale, antigène de maturation de cellule B, BCMA, BCM, TNFRSF13A, CD269)], anticorps monoclonal humanisé conjugué à l'auristatine F;
chaîne lourde gamma1 (1-451) [VH humanisé (*Homo sapiens* IGHV1-69*06 (83.7%) -(IGHD)-IGHJ4*01(85.7%)) [8.8.14] (1-121) - *Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (218) (122-219), charnière (220-234), CH2 (235-344), CH3 D12 (360), L14 (362) (345-449), CHS (450-451)) (122-451)], (224-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA humanisé (*Homo sapiens* IGKV1-33*01 (90.5%) -IGKJ2*02 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (230-230":233-233")-bisdisulfure; conjugué, sur 4 cystéinyl en moyenne, au monométhylauristatine F (MMAF), via un linker maléimidocaproyl (mc) non clivable
Pour la partie *mafodotine*, veuillez-vous référer au document *"INN for pharmaceutical substances: Names for radicals, groups and others"**.

belantamab mafodotina

inmunoglobulina G1-kappa, anti-[*Homo sapiens* TNFRSF17 (miembro 17 de la superfamilia de los receptores del TNF, miembro 17 de la superfamilia de los receptores del factor de necrosis tumoral, antígeno de maduración de célula B, BCMA, BCM, TNFRSF13A, CD269)], anticuerpo monoclonal humanizado conjugado con la auristatina F;
cadena pesada gamma1 (1-451) [VH humanizado (*Homo sapiens* IGHV1-69*06 (83.7%) -(IGHD)-IGHJ4*01(85.7%)) [8.8.14] (1-121) - *Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (218) (122-219), bisagra (220-234), CH2 (235-344), CH3 D12 (360), L14 (362) (345-449), CHS (450-451)) (122-451)], (224-214')-disulfuro con la cadena ligera kappa (1'-214') [V-KAPPA humanizado (*Homo sapiens* IGKV1-33*01 (90.5%) -IGKJ2*02 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (230-230":233-233")-bisdisulfuro; conjugado, en 4 cisteinil por término medio, con monometilauristatina F (MMAF), mediante un enlace maleimidocaproil (mc) no escindible
Para la fracción *mafodotina*, se pueden dirigir al documento "*INN for pharmaceutical substances: Names for radicals, groups and others*"*.

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGSSVKV SCKASGGTFS NYWMHWVRQA PGQGLEWMGA  50
TYRGHSDTYY NQKFKGRVTI TADKSTSTAY MELSSLRSED TAVYYCARGA 100
IYDGYDVLDN WGQGTLVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200
TYICNVNHKP SNTKVDKKVE PKSCDKTHTC PPCPAPELLG GPSVFLFPPK 250
PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY 300
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP 350
QVYTLPPSRD ELTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP 400
VLDSDGSFFL YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG 450
K                                                       451
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCSASQDIS NYLNWYQQKP GKAPKLLIYY  50
TSNLHSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YRKLPWTFGQ 100
GTKLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

Intra-H (C23-C104)	22-96	148-204	265-325	371-429
	22"-96"	148"-204"	265"-325"	371"-429"
Intra-L (C23-C104)	23'-88'	134'-194'		
	23'"-88'"	134'"-194'"		
Inter-H-L (h 5-CL 126)*	224-214'	224"-214'"		
Inter-H-H (h 11, h 14)*	230-230"	233-233"		

*Two or three of the inter-chain disulfide bridges are not present, an average of 4 cysteinyl being conjugated each via a thioether bond to a drug linker. *Deux ou trois des ponts disulfures inter-chaînes ne sont pas présents, 4 cystéinyl en moyenne étant chacun conjugué via une liaison thioéther à un linker-principe actif. *Faltan dos o tres puentes disulfuro inter-catenarios, una media de 4 cisteinil está conjugada a conectores de principio activo.

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
301, 301"
100% afucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes 100% afucosylés / glicanos de tipo CHO biantenarios complejos 100% afucosilados.
G0 > 75%.

C-terminal lysine clipping:
H CHS K2: 451, 451" (clipping >90%)

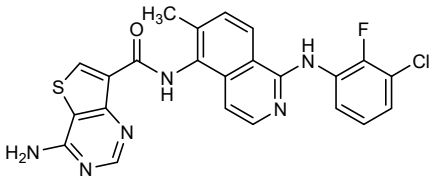
belvarafenibum

belvarafenib — 4-amino-*N*-[1-(3-chloro-2-fluoroanilino)-6-methylisoquinolin-5-yl]thieno[3,2-*d*]pyrimidine-7-carboxamide

belvarafénib — 4-amino-*N*-[1-(3-chloro-2-fluoroanilino)-6-méthylisoquinolin-5-yl]thiéno[3,2-*d*]pyrimidine-7-carboxamide

belvarafenib — 4-amino-*N*-[1-(3-cloro-2-fluoroanilino)-6-metilisoquinolin-5-il]tieno[3,2-*d*]pirimidina-7-carboxamida

$C_{23}H_{16}ClFN_6OS$



bersanlimabum #

bersanlimab — immunoglobulin G1-lambda, anti-[*Homo sapiens* ICAM1 (intercellular adhesion molecule 1, ICAM-1, CD54)], human monoclonal antibody;

gamma1 heavy chain (1-447) [*Homo sapiens* VH (IGHV3-33*01 (90.8%) -(IGHD) -IGHJ4*01 (100%)) [8.8.10] (1-117) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (214) (118-215), hinge (216-230), CH2 (231-340), CH3 D12 (356), L14 (358) (341-445), CHS (446-447)) (118-447)], (220-216')-disulfide with lambda light chain (1'-217') [*Homo sapiens* V-LAMBDA (IGKV1-40*01 (92.9%) -IGLJ3*02, 91.7%, V2>L (101)) [9.3.11] (1'-111') -*Homo sapiens* IGLC3*04 (112'-217')]; dimer (226-226":229-229")-bisdisulfide

bersanlimab

immunoglobuline G1-lambda, anti-[*Homo sapiens* ICAM1 (molécule 1 d'adhésion cellulaire, ICAM-1, CD54)], anticorps monoclonal humain;
chaîne lourde gamma1 (1-447) [*Homo sapiens* VH (IGHV3-33*01 (90.8%) -(IGHD) -IGHJ4*01 (100%)) [8.8.10] (1-117) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (214) (118-215), charnière (216-230), CH2 (231-340), CH3 D12 (356), L14 (358) (341-445), CHS (446-447)) (118-447)], (220-216')-disulfure avec la chaîne légère lambda (1'-217') [*Homo sapiens* V-LAMBDA (IGKV1-40*01 (92.9%) -IGLJ3*02, 91.7%, V2>L (101)) [9.3.11] (1'-111') -*Homo sapiens* IGLC3*04 (112'-217')]; dimère (226-226":229-229")-bisdisulfure

bersanlimab

inmunoglobulina G1-lambda, anti-[*Homo sapiens* ICAM1 (molécula 1 de adhesión celular, ICAM-1, CD54)], anticuerpo monoclonal humano;
cadena pesada gamma1 (1-447) [*Homo sapiens* VH (IGHV3-33*01 (90.8%) -(IGHD) -IGHJ4*01 (100%)) [8.8.10] (1-117) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (214) (118-215), bisagra (216-230), CH2 (231-340), CH3 D12 (356), L14 (358) (341-445), CHS (446-447)) (118-447)], (220-216')-disulfuro con la cadena ligera lambda (1'-217') [*Homo sapiens* V-LAMBDA (IGKV1-40*01 (92.9%) -IGLJ3*02, 91.7%, V2>L (101)) [9.3.11] (1'-111') -*Homo sapiens* IGLC3*04 (112'-217')]; dímero (226-226":229-229")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLLESGGG LVQPGGSLRL SCAASGFTFS NAWMSWVRQA PGKGLEWVAF  50
IWYDGSNKYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARYS 100
GWYFDYWGQG TLVTVSSAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF 150
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC 200
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT 250
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT 350
LPPSRDELTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS 400
DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPGK    447
```

Light chain / Chaîne légère / Cadena ligera

```
QSVLTQPPSA SGTPGQRVTI SCTGSSSNIG AGYDVHWYQQ LPGTAPKLLI  50
YDNNNRPSGV PDRFSGSKSG TSASLAISGL RSEDEADYYC QSYDSSLSAW 100
LFGGGTKLTV LGQPKAAPSV TLFPPSSEEL QANKATLVCL ISDFYPGAVT 150
VAWKADSSPV KAGVETTTPS KQSNNKYAAS SYLSLTPEQW KSHRSYSCQV 200
THEGSTVEKT VAPTECS                                     217
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

Intra-H (C23-C104)	22-96	144-200	261-321	367-425
	22"-96"	144"-200"	261"-321"	367"-425"
Intra-L (C23-C104)	22'-90'	139'-198'		
	22'"-90'"	139'"-198'"		
Inter-H-L (h 5-CL 126)	220-216'	220"-216'"		
Inter-H-H (h 11, h 14)	226-226"	229-229"		

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84 4:
297, 297"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados
G0F, G1F

bifikafuspum alfa #

bifikafusp alfa

immunoglobulin single-chain variable fragment anti-(human f bronectin ED-B domain) (1-236), with a GDGSSGGSGGAS linker (117-128) between the VH and VL regions, fused, via a $EF(S_4G)_3$ linker (237-253), to human interleukin-2 (IL2) (254-386), non-covalent dimer, produced in mouse hybridoma cells, glycoform alfa:
scFv-IL2 chain (1-386) [*Homo sapiens* VH (IGHV3-23*01 (94.9%) -(IGHD) -IGHJ4*01 (100%)) [8.8.9] (1-116) -12-mer linker (117-128) -*Homo sapiens* V-KAPPA (IGKV3-20*01 (94.8%) -IGKJ1*01 (100%)) [7.3.9] (129-236) -17-mer EF(SSSSG)3 linker (237-253) -*Homo sapiens* IL2 (Pr21-153) (254-386)]; noncovalent dimer

bifikafusp alfa

immunoglobuline à chaîne unique Fragment variable (scFv), anti-(domaine ED-B de la fibronectine humaine) (1-236), avec un linker GDGSSGGSGGAS (117-128) entre les régions VH et VL, fusionnée, via un linker $EF(S_4G)_3$ (237-253), à l'interleukine 2 (IL2) humaine (254-386), dimère non covalent, produit par des cellules hybridomes de souris, glycoforme alfa:
chaîne scFv-IL2 (1-386) [*Homo sapiens* VH (IGHV3-23*01 (94.9%) -(IGHD) -IGHJ4*01 (100%)) [8.8.9] (1-116) -12-mer linker(117-128) -*Homo sapiens* V-KAPPA (IGKV3-20*01 (94.80%) -IGKJ1*01 (100%)) [7.3.9] (129-236) -17-mer EF(SSSSG)3 linker (237-253) -*Homo sapiens* IL2 (Pr21-153) (254-386)]; dimère non-covalent

bifikafusp alfa

inmunoglobulina con una cadena única Fragmento variable (scFv), anti-(dominio ED-B de la fibronectina humana) (1-236), con un enlace GDGSSGGSGGAS (117-128) entre las regiones VH y VL, fusionada, a través de un enlace $EF(S_4G)_3$ (237-253), con la interleukina 2 (IL2) humana (254-386), dímero no covalente, producido por las células h bridomas de ratón, glicoforma alfa:
cadena scFv-IL2 (1-386) [*Homo sapiens* VH (IGHV3-23*01 (94.9%) -(IGHD) -IGHJ4*01 (100%)) [8.8.9] (1-116) -12-mer ligante (117-128) -*Homo sapiens* V-KAPPA (IGKV3-20*01 (94.80%) -IGKJ1*01 (100%)) [7.3.9] (129-236) -17-mer EF(SSSSG)3 ligante (237-253) -*Homo sapiens* IL2 (Pr21-153) (254-386)]; dímero no covalente

```
EVQLLESGGG LVQPGGSLRL SCAASGFTFS SFSMSWVRQA PGKGLEWVSS 50
ISGSSGTTYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPF 100
PYFDYWGQGT LVTVSSGDGS SGGSGGASEI VLTQSPGTLS LSPGERATLS 150
CRASQSVSSS FLAWYQQKPG QAPRLLIYYA SSRATGIPDR FSGSGSGTDF 200
TLTISRLEPE DFAVYYCQQT GRIPPTFGQG TKVEIKEFSS SSGSSSSGSS 250
SSGAPTSSST KKTQLQLEHL LLDLQMILNG INNYKNPKLT RMLTFKFYMP 300
KKATELKHLQ CLEEELKPLE EVLNLAQSKN FHLRPRDLIS NINVIVLELK 350
GSETTFMCEY ADETATIVEF LNRWITFCQS IISTLT                 386
```

Disulfide bridges location / Positions des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H : 22-96
Intra-L : 151-217
IL2 portion : 311-358

Glycosylation site (O) / Site de glycosylation (O) / Posición de glicosilación (O)
Thr-256

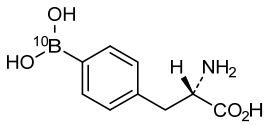
bizalimogenum ralaplasmidum #

bizalimogene ralaplasmid	a DNA plasmid encoding genes for human papilloma virus type 18 (HPV-18) E6 and E7 proteins whose expression is driven by the human cytomegalovirus (hCMV) promoter with the bovine growth hormone (bGH) 3'end gene and bGH gene polyA signal
bizalimogène ralaplasmide	ADN plasmidique contenant les gènes codant pour les protéines E6 et E7 du virus du papillome humain de type 18 (HPV-18), dont l'expression est dirigée par le promoteur du cytomégalovirus humain (hCMV) avec la région 3'-terminale du gène de l'hormone de croissance bovine (bGH) et le signal poly-A du gène de la bGH
bizalimogén ralaplásmido	un DNA plasmídico que contiene genes que codifican para las proteínas E6 y E7 del virus del papiloma humano tipo 18 (HPV-18), cuya expresión está dirigida por el promotor del citomegalovirus humano (hCMV) con la región 3' terminal del gen de la hormona de crecimiento bovina (bGH) y la señal poli A del gen de bGH

borofalanum (^{10}B)

borofalan (^{10}B)	4-[(^{10}B)borono]-L-phenylalanine
borofalan (^{10}B)	4-[(^{10}B)borono]-L-phénylalanine
borofalán (^{10}B)	4-[(^{10}B)borono]-L-fenilalanina

$C_9H_{12}{}^{10}BNO_4$



bulevirtidum

bulevirtide	*N*-tetradecanoylglycyl-L-threonyl-L-asparaginyl-L-leucyl-L-seryl-L-valyl-L-prolyl-L-asparaginyl-L-prolyl-L-leucylglycyl-L-phenylalanyl-L-phenylalanyl-L-prolyl-L-α-aspartyl-L-histidyl-L-glutaminyl-L-leucyl-L-α-aspartyl-L-prolyl-L-alanyl-L-phenylalanylglycyl-L-alanyl-L-asparaginyl-L-seryl-L-asparaginyl-L-asparaginyl-L-prolyl-L-α-aspartyl-L-tryptophyl-L-α-aspartyl-L-phenylalanyl-L-asparaginyl-L-prolyl-L-asparaginyl-L-lysyl-L-α-aspartyl-L-histidyl-L-tryptophyl-L-prolyl-L-α-glutamyl-L-alanyl-L-asparaginyl-L-lysyl-L-valylglycinamide
bulévirtide	*N*-tétradécanoylglycyl-L-thréonyl-L-asparaginyl-L-leucyl-L-séryl-L-valyl-L-prolyl-L-asparaginyl-L-prolyl-L-leucylglycyl-L-phénylalanyl-L-phénylalanyl-L-prolyl-L-α-aspartyl-L-histidyl-L-glutaminyl-L-leucyl-L-α-aspartyl-L-prolyl-L-alanyl-L-phénylalanylglycyl-L-alanyl-L-asparaginyl-L-séryl-L-asparaginyl-L-asparaginyl-L-prolyl-L-α-aspartyl-L-tryptophyl-L-α-aspartyl-L-phénylalanyl-L-asparaginyl-L-prolyl-L-asparaginyl-L-lysyl-L-α-aspartyl-L-histidyl-L-tryptophyl-L-prolyl-L-α-glutamyl-L-alanyl-L-asparaginyl-L-lysyl-L-valylglycinamide

bulevirtida

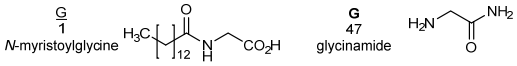
N-tetradecanoilglicil-L-treonil-L-asparaginil-L-leucil-L-seril-L-valil-L-prolil-L-asparaginil-L-prolil-L-leucilglicil-L-fenilalanil-L-fenilalanil-L-prolil-L-α-aspartil-L-histidil-L-glutaminil-L-leucil-L-α-aspartil-L-prolil-L-alanil-L-fenilalanilglicil-L-alanil-L-asparaginil-L-seril-L-asparaginil-L-asparaginil-L-prolil-L-α-aspartil-L-triptofil-L-α-aspartil-L-fenilalanil-L-asparaginil-L-prolil-L-asparaginil-L-lisil-L-α-aspartil-L-histidil-L-triptofil-L-prolil-L-α-glutamil-L-alanil-L-asparaginil-L-lisil-L-valilglicinamida

$C_{248}H_{355}N_{65}O_{72}$

Sequence / Séquence / Secuencia

GTNLSVPNPL GFFPDHQLDP AFGANSNNPD WDFNPNKDHW PEANKVG 47

Modified residues / Résidus modifiés / Restos modificados



cedazuridinum

cedazuridine

(4*R*)-1-(2-deoxy-2,2-difluoro-β-D-*erythro*-pentofuranosyl)-4-hydroxy-1,3-diazinan-2-one

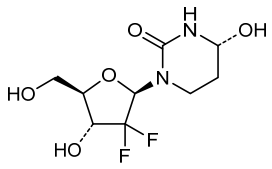
cédazuridine

(4*R*)-1-(2-désoxy-2,2-difluoro-β-D-*érythro*-pentofuranosyl)-4-hydroxy-1,3-diazinan-2-one

cedazuridina

(4*R*)-1-(2-desoxi-2,2-difluoro-β-D-e*ritro*-pentofuranosil)-4-hidroxi-1,3-diazinan-2-ona

$C_9H_{14}F_2N_2O_5$



cetrelimabum #

cetrelimab

immunoglobulin G4-kappa, anti-[*Homo sapiens* PDCD1 (programmed cell death 1, PD-1, PD1, CD279)], human monoclonal antibody;
gamma4 heavy chain (1-450) [*Homo sapiens* VH (IGHV1-69*01 (99.0%) -(IGHD) -IGHJ4*01 (92.9%)) [8.8.16] (1-123) -*Homo sapiens* IGHG4*01 (CH1 (124-221), hinge S10>P (231) (222-233), CH2 (234-343), CH3 (344-448), CHS (449-450)) (124-450)], (137-214')-disulfide with kappa light chain (1'-214') [*Homo sapiens* V-KAPPA (IGKV3-11*01 (96.8%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191)(108'-214')]; dimer (229-229'':232-232'')-bisdisulfide

cétrélimab

immunoglobuline G4-kappa, anti-[*Homo sapiens* PDCD1 (protéine 1 de mort cellulaire programmée, PD-1, PD1, CD279)], anticorps monoclonal humain;

	chaîne lourde gamma4 (1-450) [*Homo sapiens* VH (IGHV1-69*01 (99.0%) -(IGHD) -IGHJ4*01 (92.9%)) [8.8.16] (1-123) -*Homo sapiens* IGHG4*01 (CH1 (124-221), charnière S10>P (231) (222-233), CH2 (234-343), CH3 (344-448), CHS (449-450)) (124-450)], (137-214')-disulfure avec la chaîne légère kappa (1'-214') [*Homo sapiens* V-KAPPA (IGKV3-11*01 (96.8%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (229-229":232-232")-bisdisulfure
cetrelimab	inmunoglobulina G4-kappa, anti-[*Homo sapiens* PDCD1 (proteína 1 de muerte celular programada, PD-1, PD1, CD279)], anticuerpo monoclonal humanizado; cadena pesada gamma4 (1-450) [*Homo sapiens* VH (IGHV1-69*01 (99.0%) -(IGHD) -IGHJ4*01 (92.9%)) [8.8.16] (1-123) -*Homo sapiens* IGHG4*01 (CH1 (124-221), bisagra S10>P (231) (222-233), CH2 (234-343), CH3 (344-448), CHS (449-450)) (124-450)], (137-214')-disulfuro con la cadena ligera kappa (1'-214') [*Homo sapiens* V-KAPPA (IGKV3-11*01 (96.8%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (229-229":232-232")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGSSVKV SCKASGGTFS SYAISWVRQA PGQGLEWMGG  50
IIPIFDTANY AQKFQGRVTI TADESTSTAY MELSSLRSED TAVYYCARPG 100
LAAAYDTGSL DYWGQGTLVT VSSASTKGPS VFPLAPCSRS TSESTAALGC 150
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG 200
TKTYTCNVDH KPSNTKVDKR VESKYGPPCP PCPAPEFLGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS QEDPEVQFNW YVDGVEVHNA KTKPREEQFN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKG LPSSIEKTIS KAKGQPREPQ 350
VYTLPPSQEE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SRLTVDKSRW QEGNVFSCSV MHEALHNHYT QKSLSLSLGK 450
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Light chain / Chaîne légère / Cadena ligera

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EIVLTQSPAT LSLSPGERAT LSCRASQSVR SYLAWYQQKP GQAPRLLIYD  50
ASNRATGIPA RFSGSGSGTD FTLTISSLEP EDFAVYYCQQ RNYWPLTFGQ 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

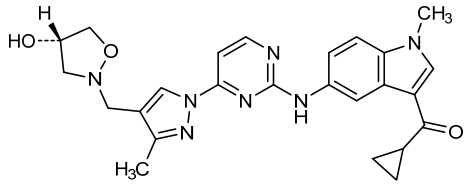
Intra-H (C23-C104)	22-96	150-206	264-324	370-428
	22"-96"	150"-206"	264"-324"	370"-428"
Intra-L (C23-C104)	23'-88'	134'-194'		
	23'"-88"'	134'"-194'"		
Inter-H-L (CH1 10-CL 126)	137-214'	137"-214'"		
Inter-H-H (h 8, h 11)	229-229"	232-232"		

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
300, 300"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

cevidoplenibum

cevidoplen b	(1^4*S*)-1^4-hydroxy-3^3,6^1-dimethyl-6^1*H*-5-aza-6(5,3)-indola-4(4,2)-pyrimidina-1(2)-[1,2]oxazolidina-3(4,1)-pyrazola-8(1)-cyclopropanaoctaphan-7-one
cévidoplén b	(1^4*S*)-1^4-hydroxy-3^3,6^1-diméthyl-6^1*H*-5-aza-6(5,3)-indola-4(4,2)-pyrimidina-1(2)-[1,2]oxazolidina-3(4,1)-pyrazola-8(1)-cyclopropanaoctaphan-7-one
cevidoplen b	(1^4*S*)-1^4-hidroxi-3^3,6^1-dimetil-6^1*H*-5-aza-6(5,3)-indola-4(4,2)-pirimidina-1(2)-[1,2]oxazolidina-3(4,1)-pirazola-8(1)-ciclopropanaoctafan-7-ona

$C_{25}H_{27}N_7O_3$



cibisatamabum #

cibisatamab

immunoglobulin G1-kappa/lambda with domain crossover, anti-[*Homo sapiens* CEACAM5 (carcinoembryonic antigen-related cell adhesion molecule 5, CEA, CD66e)] and anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], humanized monoclonal antibody, bispecific, trivalent;
gamma-kappa heavy chain anti-CEACAM5 and anti-CD3E (VH-CH1-VH-C-kappa-CH2-CH3) (1-694) [humanized VH anti-CEACAM5 (*Homo sapiens* IGHV1-18*01 (82.7%) -(IGHD) -IGHJ4*01 (92.3%)) [8.8.14] (1-121) -*Homo sapiens* IGHG1*01, G1m17 (CH1 K120 (218) (122-219), hinge 1-6 (220-225)) (122-225) -10-mer bis(tetraglycyl-seryl) linker (226-235) -humanized VH anti-CD3E (*Homo sapiens* IGHV3-23*03 (87.0%) -(IGHD) -IGHJ6*01 (90.9%)) [8.10.16] (236-360) -*Homo sapiens* IGKC*01, R1.4>S (361), Km3 A45.1 (406), V101 (444) (361-467) -*Homo sapiens* IGHG1*01, G1m1 (hinge 5-15 (467-477), CH2 [L1.3>A (481), L1.2>A (482), P114>G (576)] (478-587), CH3 D12 (603), L14 (605) [S10>C (601), T22>W (613)] (588-692), CHS (693-694)) (468-694)]; (224-215''')-disulfide with kappa light chain anti-CEACAM5 (1'''-215''') [humanized V-KAPPA (*Homo sapiens* IGKV1-16*01 (82.1%) -IGKJ2*02 (100%)) [6.3.10] (1'''-108''') -*Homo sapiens* IGKC*01 Km3 A45.1 (154), V101 (192) (109'''-215''')]; (467-214')-disulfide with lambda-gamma light chain anti-CD3E (1'-214') [V-LAMBDA (*Mus musculus* IGLV1*01 (81.2%) -IGLJ1*01 (100%)/*Homo sapiens* IGLV7-46*01 (80%) -IGLJ3*01 (100%)) [9.3.9] (1'-109') -2-mer biseryl linker (110'-111') -*Homo sapiens* IGHG1*01, G1m17 (CH1 K120 (208) (112'-209') -hinge 1-5 (210'-214'))]; gamma1 heavy chain anti-CEACAM5 (1''-451'') [humanized VH (*Homo sapiens* IGHV1-18*01 (82.7%) -(IGHD) -IGHJ4*01 (92.3%)) [8.8.14] (1''-121'') -*Homo sapiens* IGHG1*01, G1m17 (CH1 K120 (218) (122-219), hinge 1-15 (220-234), CH2 [L1.3>A (238), L1.2>A (239), P114>G (333)] (235-344), CH3 [Y5>C (353), T22>S (370), L24>A (372), Y86>V (411)] (345-449), CHS (450-451)) (122''-451'')]; (224''-215''')-disulfide with kappa light chain anti-CEACAM5 (1'''-215''') [humanized V-KAPPA (*Homo sapiens* IGKV1-16*01 (82.1%) -IGKJ2*02 (100%)) [6.3.10] (1'''-108''') -*Homo sapiens* IGKC*01 Km3 A45.1 (154), V101 (192) (109'''-215''')]; dimer (473-230'':476-233'':601-353'')-trisdisulfide

cibisatamab

immunoglobuline G1-kappa/lambda avec domaines échangés, anti-[*Homo sapiens* CEACAM5 (molécule d'adhésion cellulaire 5 apparentée à l'antigène carcinoembryonaire, CEA, CD66e)] et anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], anticorps monoclonal humanisé, bispécifique, trivalent;

	chaîne lourde gamma-kappa anti-CEACAM5 et anti-CD3E (VH-CH1-VH-C-kappa-CH2-CH3) (1-694) [VH anti-CEACAM5 humanisé (*Homo sapiens* IGHV1-18*01 (82.7%) -(IGHD) -IGHJ4*01 (92.3%)) [8.8.14] (1-121) -*Homo sapiens* IGHG1*01, G1m17 (CH1 K120 (218) (122-219), charnière 1-6 (220-225)) (122-225) -10-mer bis(tétraglycyl-séryl) linker (226-235) -VH anti-CD3E humanisé (*Homo sapiens* IGHV3-23*03 (87.0%) -(IGHD) -IGHJ6*01 (90.9%)) [8.10.16] (236-360) -*Homo sapiens* IGKC*01, R1.4>S (361), Km3 A45.1 (406), V101 (444) (361-467) -*Homo sapiens* IGHG1*01, G1m1 (charnière 5-15 (467-477), CH2 [L1.3>A (481), L1.2>A (482), P114>G (576)] (478-587), CH3 D12 (603), L14 (605) [S10>C (601), T22>W (613)] (588-692), CHS (693-694)) (468-694)]; (224-215'")-disulfure avec la chaîne légère kappa anti-CEACAM5 (1'"-215'") (V-KAPPA humanisé (*Homo sapiens* IGKV1-16*01 (82.1%) -IGKJ2*02 (100%)) [6.3.10] (1'"-108'") -*Homo sapiens* IGKC*01, Km3 A45.1 (154), V101 (192) (109'"-215'")]; (467-214')-disulfure avec la chaîne légère lambda-gamma anti-CD3E (1'-214') [V-LAMBDA (*Mus musculus* IGLV1*01 (81.2%) -IGLJ1*01 (100%)/*Homo sapiens* IGLV7-46*01 (80%) -IGLJ3*01 (100%)) [9.3.9] (1'-109') -2-mer biséryl linker (110'-111') -*Homo sapiens* IGHG1*01, G1m17 (CH1 K120 (208) (112'-209') -charnière 1-5 (210'-214'))]; chaîne lourde gamma1 anti-CEACAM5 (1''-451'') [VH humanisé (*Homo sapiens* IGHV1-18*01 (82.7%) -(IGHD) -IGHJ4*01 (92.3%)) [8.8.14] (1''-121'') -*Homo sapiens* IGHG1*01, G1m17 (CH1 K120 (218) (122-219), charnière 1-15 (220-234), CH2 [L1.3>A (238), L1.2>A (239), P114>G (333)] (235-344), CH3 [Y5>C (353), T22>S (370), L24>A (372), Y86>V (411)] (345-449), CHS (450-451)) (122''-451'')]; (224''-215''')-disulfure avec la chaîne légère kappa anti-CEACAM5 (1'''-215''') [V-KAPPA humanisé (*Homo sapiens* IGKV1-16*01 (82.1%) -IGKJ2*02 (100%)) [6.3.10] (1'''-108''') -*Homo sapiens* IGKC*01, Km3 A45.1 (154), V101 (192) (109'''-215''')]; dimère (473-230'':476-233'':601-353'')-trisdisulfure
cibisatamab	inmunoglobulina G1-kappa/lambda con dominios intercambiados, anti-[*Homo sapiens* CEACAM5 (molécula de adhesión celular 5 relacionada con el antígeno carcinoembrionario, CEA, CD66e)] y anti-[*Homo sapiens* CD3E (CD3 épsilon, Leu-4)], anticuerpo monoclonal humanizado, biespecífico, trivalente; cadena pesada gamma-kappa anti-CEACAM5 y anti-CD3E (VH-CH1-VH-C-kappa-CH2-CH3) (1-694) [VH anti-CEACAM5 humanizado (*Homo sapiens* IGHV1-18*01 (82.7%) -(IGHD) -IGHJ4*01 (92.3%)) [8.8.14] (1-121) -*Homo sapiens* IGHG1*01, G1m17 (CH1 K120 (218) (122-219), bisagra 1-6 (220-225)) (122-225) -10-mer bis(tetraglicil-seril) ligando (226-235) -VH anti-CD3E humanizado (*Homo sapiens* IGHV3-23*03 (87.0%) -(IGHD) -IGHJ6*01 (90.9%)) [8.10.16] (236-360) -*Homo sapiens* IGKC*01, R1.4>S (361), Km3 A45.1 (406), V101 (444) (361-467) -*Homo sapiens* IGHG1*01, G1m1 (bisagra 5-15 (467-477), CH2 [L1.3>A (481), L1.2>A (482), P114>G (576)] (478-587), CH3 D12 (603), L14 (605) [S10>C (601), T22>W (613)] (588-692), CHS (693-694)) (468-694)]; (224-215'")-disulfuro con la cadena ligera kappa anti-CEACAM5 (1'"-215'") (V-KAPPA humanizado (*Homo sapiens* IGKV1-16*01 (82.1%) -IGKJ2*02 (100%)) [6.3.10] (1'"-108'") -*Homo sapiens* IGKC*01, Km3 A45.1 (154), V101 (192) (109'"-215'")]; (467-214')-disulfuro con la cadena ligera lambda-gamma anti-CD3E (1'-214') [V-LAMBDA (*Mus musculus* IGLV1*01 (81.2%) -IGLJ1*01 (100%)/*Homo sapiens* IGLV7-46*01 (80%) -IGLJ3*01 (100%)) [9.3.9] (1'-109') -2-mer biseril ligando (110'-111') -*Homo sapiens* IGHG1*01, G1m17 (CH1 K120 (208) (112'-209') -bisagra 1-5 (210'-214'))]; cadena pesada gamma1 anti-CEACAM5 (1''-451'') [VH humanizado (*Homo sapiens* IGHV1-18*01 (82.7%) -(IGHD) -IGHJ4*01 (92.3%)) [8.8.14] (1''-121'') -*Homo sapiens* IGHG1*01, G1m17 (CH1 K120 (218) (122-219), bisagra 1-15 (220-234), CH2 [L1.3>A (238), L1.2>A (239), P114>G (333)] (235-344), CH3 [Y5>C (353), T22>S (370), L24>A (372), Y86>V (411)] (345-449), CHS (450-451)) (122''-451'')]; (224''-215''')-disulfuro con la cadena ligera kappa anti-CEACAM5 (1'''-215''') [V-KAPPA humanizado (*Homo sapiens* IGKV1-16*01 (82.1%) -IGKJ2*02 (100%)) [6.3.10] (1'''-108''') -*Homo sapiens* IGKC*01, Km3 A45.1 (154), V101 (192) (109'''-215''')]; dímero (473-230'':476-233'':601-353'')-trisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada anti-CEACAM5 and anti-CD3E

```
QVQLVQSGAE VKKPGASVKV SCKASGYTFT EFGMNWVRQA PGQGLEWMGW  50
INTKTGEATY VEEFKGRVTF TTDTSTSTAY MELRSLRSDD TAVYYCARWD 100
FAYYVEAMDY WGQGTTVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200
TYICNVNHKP SNTKVDKKVE PKSCDGGGGS GGGGSEVQLL ESGGGLVQPG 250
GSLRLSCAAS GFTFSTYAMN WVRQAPGKGL EWVSRIRSKY NNYATYYADS 300
VKGRFTISRD DSKNTLYLQM NSLRAEDTAV YYCVRHGNFG NSYVSWFAYW 350
GQGTLVTVSS ASVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ 400
WKVDNALQSG NSQESVTEQD SKDSTYSLSS TLTLSKADYE KHKVYACEVT 450
HQGLSSPVTK SFNRGECDKT HTCPPCPAPE AAGGPSVFLF PPKPKDTLMI 500
SRTPEVTCVV VDVSHEDPEV KFNWYVDGVE VHNAKTKPRE EQYNSTYRVV 550
SVLTVLHQDW LNGKEYKCKV SNKALGAPIE KTISKAKGQP REPQVYTLPP 600
CRDELTKNQV SLWCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS 650
FFLYSKLTVD KSRWQQGNVF SCSVMHEALH NHYTQKSLSL SPGK       694
```

Light chain / Chaîne légère / Cadena ligera anti-CD3E

```
QAVVTQEPSL TVSPGGTVTL TCGSSTGAVT TSNYANWVQE KPGQAFRGLI  50
GGTNKRAPGT PARFSGSLLG GKAALTLSGA QPEDEAEYYC ALWYSNLWVF 100
GGGTKLTVLS SASTKGPSVF PLAPSSKSTS GGTAALGCLV KDYFPEPVTV 150
SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ TYICNVNHKP 200
SNTKVDKKVE PKSC                                        214
```

Heavy chain / Chaîne lourde / Cadena pesada anti-CEACAM5

```
QVQLVQSGAE VKKPGASVKV SCKASGYTFT EFGMNWVRQA PGQGLEWMGW  50
INTKTGEATY VEEFKGRVTF TTDTSTSTAY MELRSLRSDD TAVYYCARWD 100
FAYYVEAMDY WGQGTTVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200
TYICNVNHKP SNTKVDKKVE PKSCDKTHTC PPCPAPEAAG GPSVFLFPPK 250
PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY 300
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALGAPIEKTI SKAKGQPREP 350
QVCTLPPSRD ELTKNQVSLS CAVKGFYPSD IAVEWESNGQ PENNYKTTPP 400
VLDSDGSFFL VSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG 450
K                                                      451
```

Light chain / Chaîne légère / Cadena ligera anti-CEACAM5

```
DIQMTQSPSS LSASVGDRVT ITCKASAAVG TYVAWYQQKP GKAPKLLIYS  50
ASYRKRGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCHQ YYTYPLFTFG 100
QGTKLEIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK 150
VDNALQSGNS QESVTEQDSK DSTYSLSSTL TLSKADYEKH KVYACEVTHQ 200
GLSSPVTKSF NRGEC                                       215
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

Intra-H (C23-C104)	22-96	148-204	257-333	387-447	508-568	614-672
	22"-96"	148"-204"	265"-325"	371"-429"		
Intra-L (C23-C104)	22'-90'	138'-194'				
	23'"-88'"	135'"-195'"				
Inter-H-L (h 5-CL 126)		224-215'"	467-214'	224"-215'"		
Inter-H-H (h 11, h 14, AA >C)	473-230"	476-233"	601-353"			

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
544, 301"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

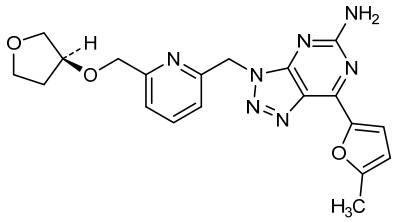
ciforadenantum

ciforadenant — (7^3S)-1^5-methyl-6-oxa-2(7,3)-[1,2,3]triazolo[4,5-*d*]pyrimidina-4(2,6)-pyridina-1(2)-furana-7(3)-oxolanaheptaphan-2^5-amine

ciforadénant — (7^3S)-1^5-méthyl-6-oxa-2(7,3)-[1,2,3]triazolo[4,5-*d*]pyrimidina-4(2,6)-pyridina-1(2)-furana-7(3)-oxolanaheptaphan-2^5-amine

ciforadenant — (7^3S)-1^5-metil-6-oxa-2(7,3)-[1,2,3]triazol[4,5-*d*]pirimidina-4(2,6)-piridina-1(2)-furana-7(3)-oxolanaheptafan-2^5-amina

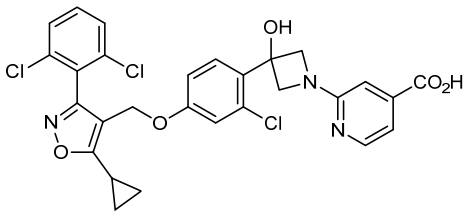
$C_{20}H_{21}N_7O_3$



cilofexorum

cilofexor	$3^2,7^2,7^6$-trichloro-6^5-cyclopropyl-2^3-hydroxy-4-oxa-1(2)-pyridina-6(4,3)-[1,2]oxazola-2(1,3)-azetidina-3(1,4),7(1)-dibenzenaheptaphane-1^4-carboxylic acid
cilofexor	acide $3^2,7^2,7^6$-trichloro-6^5-cyclopropyl-2^3-hydroxy-4-oxa-1(2)-pyridina-6(4,3)-[1,2]oxazola-2(1,3)-azétidina-3(1,4),7(1)-dibenzenaheptaphane-1^4-carboxylique
cilofexor	ácido $3^2,7^2,7^6$-tricloro-6^5-ciclopropil-2^3-hidroxi-4-oxa-1(2)-piridina-6(4,3)-[1,2]oxazola-2(1,3)-azetidina-3(1,4),7(1)-dibencenaheptafano-1^4-carboxílico

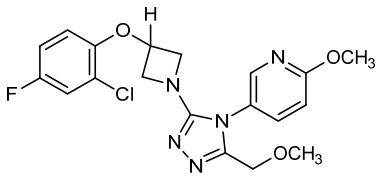
$C_{28}H_{22}Cl_3N_3O_5$



cligosibanum

cligosiban	5-{3-[3-(2-chloro-4-fluorophenoxy)azetidin-1-y]-5-(methoxymethyl)-4*H*-1,2,4-triazol-4-yl}-2-methoxypyridine
cligosiban	5-{3-[3-(2-chloro-4-fluorophénoxy)azétidin-1-y]-5-(méthoxyméthyl)-4*H*-1,2,4-triazol-4-yl}-2-méthoxypyridine
cligosibán	5-{3-[3-(2-cloro-4-fluorofenoxi)azetidin-1-il]-5-(metoximetil)-4*H*-1,2,4-triazol-4-il}-2-metoxipiridina

$C_{19}H_{19}ClFN_5O_3$



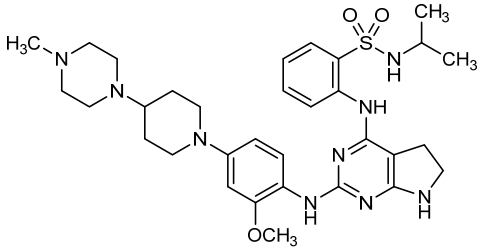
conteltinibum

conteltinib — 2-[(2-{2-methoxy-4-[4-(4-methylpiperazin-1-yl)piperidin-1-yl]anilino}-6,7-dihydro-5*H*-pyrrolo[2,3-*d*]pyrimidin-4-yl)amino]-*N*-(propan-2-yl)benzene-1-sulfonamide

conteltinib — 2-[(2-{2-méthoxy-4-[4-(4-méthylpipérazin-1-yl)pipéridin-1-yl]anilino}-6,7-dihydro-5*H*-pyrrolo[2,3-*d*]pyrimidin-4-yl)amino]-*N*-(propan-2-yl)benzène-1-sulfonamide

conteltinib — 2-[(2-{2-metoxi-4-[4-(4-metilpiperazin-1-il)piperidin-1-il]anilino}-6,7-dihidro-5*H*-pirrolo[2,3-*d*]pirimidin-4-il)amino]-*N*-(propan-2-il)benceno-1-sulfonamida

$C_{32}H_{45}N_9O_3S$



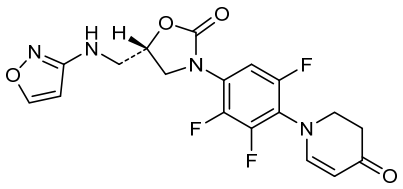
contezolidum

contezolid — 1-{2,3,6-trifluoro-4-[(5S)-5-{[(1,2-oxazol-3-yl)amino]methyl}-2-oxo-1,3-oxazolidin-3-yl]phenyl}-2,3-dihydropyridin-4(1*H*)-one

contézolid — 1-(2,3,6-trifluoro-4-{(5*S*)-5-[(1,2-oxazol-3-ylamino)méthyl]-2-oxo-1,3-oxazolidin-3-yl}phényl)-2,3-dihydropyridin-4(1*H*)-one

contezolid — 1-(2,3,6-trifluoro-4-{(5*S*)-5-[(1,2-oxazol-3-ilamino)metil]-2-oxo-1,3-oxazolidin-3-il}fenil)-2,3-dihidropiridin-4(1*H*)-ona

$C_{18}H_{15}F_3N_4O_4$



cusatuzumabum #

cusatuzumab — immunoglobulin G1-lambda, anti-[*Homo sapiens* CD70 (tumor necrosis factor superfamily member 7, TNFSF7, CD27LG, CD27L)], humanized monoclonal ant body;
gamma1 heavy chain (1-452) [humanized VH (*Homo sapiens* IGHV3-48*03 (90.8%) -(IGHD)-IGHJ5*01 (100%)) [8.8.15] (1-122) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (219) (123-220), hinge (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS (451-452)) (123-452)], (225-215')-disulfide with lambda light chain (1'-216') [humanized V-LAMBDA (*Homo sapiens* IGLV8-61*01 (78.1%) -IGLJ7*01 (100%)) [9.3.10] (1'-110') -*Homo sapiens* IGLC2*01 (111'-216')]; dimer (231-231":234-234")-bisdisulfide

cusatuzumab	immunoglobuline G1-lambda, anti-[*Homo sapiens* CD70 (membre 7 de la superfamille du facteur de nécrose tumorale (TNF), TNFSF7, CD27LG, CD27L)], anticorps monoclonal humanisé; chaîne lourde gamma1 (1-452) [VH humanisé (*Homo sapiens* IGHV3-48*03 (90.8%) -(IGHD)-IGHJ5*01 (100%)) [8.8.15] (1-122) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (219) (123-220), charnière (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS (451-452)) (123-452)], (225-215')-disulfure avec la chaîne légère lambda (1'-216') [V-LAMBDA humanisé (*Homo sapiens* IGLV8-61*01 (78.1%) -IGLJ7*01 (100%)) [9.3.10] (1'-110') -*Homo sapiens* IGLC2*01 (111'-216')]; dimère (231-231":234-234")-bisdisulfure
cusatuzumab	inmunoglobulina G1-lambda, anti-[*Homo sapiens* CD70 (miembro 7 de la superfamilia del factor de necrosis tumoral (TNF), TNFSF7, CD27LG, CD27L)], anticuerpo monoclonal humanizado; cadena pesada gamma1 (1-452) [VH humanizado (*Homo sapiens* IGHV3-48*03 (90.8%) -(IGHD)-IGHJ5*01 (100%)) [8.8.15] (1-122) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (219) (123-220), bisagra (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS (451-452)) (123-452)], (225-215')-disulfuro con la cadena ligera lambda (1'-216') [V-LAMBDA humanizado (*Homo sapiens* IGLV8-61*01 (78.1%) -IGLJ7*01 (100%)) [9.3.10] (1'-110') -*Homo sapiens* IGLC2*01 (111'-216')]; dímero (231-231":234-234")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAASGFTFS VYYMNWVRQA PGKGLEWVSD  50
INNEGGTTYY ADSVKGRFTI SRDNSKNSLY LQMNSLRAED TAVYYCARDA 100
GYSNHVPIFD SWGQGTLVTV SSASTKGPSV FPLAPSSKST SGGTAALGCL 150
VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ SSGLYSLSSV VTVPSSSLGT 200
QTYICNVNHK PSNTKVDKKV EPKSCDKTHT CPPCPAPELL GGPSVFLFPP 250
KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE 350
PQVYTLPPSR DELTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP 400
PVLDSDGSFF LYSKLTVDKS RWQQGNVFSC SVMHEALHNH YTQKSLSLSP 450
GK                                                      452
```

Light chain / Chaîne légère / Cadena ligera

```
QAVVTQEPSL TVSPGGTVTL TCGLKSGSVT SDNFPTWYQQ TPGQAPRLLI  50
YNTNTRHSGV PDRFSGSILG NKAALTITGA QADDEAEYFC ALFISNPSVE 100
FGGGTQLTVL GQPKAAPSVT LFPPSSEELQ ANKATLVCLI SDFYPGAVTV 150
AWKADSSPVK AGVETTTPSK QSNNKYAASS YLSLTPEQWK SHRSYSCQVT 200
HEGSTVEKTV APTECS                                       216
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

Intra-H (C23-C104)	22-96	149-205	266-326	372-430
	22"-96"	149"-205"	266"-326"	372"-430"
Intra-L (C23-C104)	22'-90'	138'-197'		
	22'"-90'"	138'"-197'"		
Inter-H-L (h 5-CL 126)	225-215'	225"-215'"		
Inter-H-H (h 11, h 14)	231-231"	234-234"		

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84 4:
302, 302"

Afucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes afucosylés / glicanos de tipo CHO biantenarios complejos afucosilados

dalcinonacogum alfa #

dalcinonacog alfa — human blood coagulation factor IX variant (R318Y, R338E, T343R), produced in Chinese hamster ovary (CHO) cells, glycoform alfa.

dalcinonacog alfa — variant (R318Y, R338E, T343R) du facteur de coagulation sanguine IX humain, produit par des cellules ovariennes de hamsters chinois (CHO), glycoforme alfa

dalcinonacog alfa — variante (R318Y, R338E, T343R) del factor de coagulación sanguínea IX humano, producido por las células ováricas de hamsters chinos (CHO), glicoforma alfa

```
YNSGKLEEFV QGNLERECME EKCSFEEARE VFENTERTTE FWKQYVDGDQ   50
CESNPCLNGG SCKDDINSYE CWCPFGFEGK NCELDVTCNI KNGRCEQFCK  100
NSADNKVVCS CTEGYRLAEN QKSCEPAVPF PCGRVSVSQT SKLTRAETVF  150
PDVDYVNSTE AETILDNITQ STQSFNDFTR VVGGEDAKPG QFPWQVVLNG  200
KVDAFCGGSI VNEKWIVTAA HCVETGVKIT VVAGEHNIEE TEHTEQKRNV  250
IRIIPHHNYN AAINKYNHDI ALLELDEPLV LNSYVTPICI ADKEYTNIFL  300
KFGSGYVSGW GRVFHKGYSA LVLQYLRVPL VDRATCLEST KFRIYNNMFC  350
AGFHEGGRDS CQGDSGGPHV TEVEGTSFLT GIISWGEECA MKGKYGIYTK  400
VSRYVNWIKE KTKLT                                        415
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Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
18-23 51-62 56-71 73-82 88-99 95-109
111-124 132-289 206-222 336-350 361-389
Glycosylation sites (N) / Sites de glycosylation (N) / Posiciones de glicosilación (N)
Asn-157 Asn-167
Glycosylation sites (O) / Sites de glycosylation (O) / Posiciones de glicosilación (O)
Ser-53 Ser-61 Thr-159 Thr-169 Thr-172 Thr-179
Non-conventional residues / Résidus non conventionnels / Restos no convencionales
Tyr-318 Glu-338 Arg-343

delolimogenum mupadenorepvecum #

delolimogene mupadenorepvec — a conditionally replicating adenovirus serotype 5/35 genetically engineered to express a trimerized membrane-bound CD40 ligand (TMZ-CD40L) and tumor necrosis factor superfamily member 9 (TNFSF9, 4-1BBL, CD137), under the control of a cytomegalovirus (CMV) promoter, and with deletions in E1A gene and E3 genes.

délolimogène mupadénorépvec — adénovirus de sérotype 5/35 dont la réplication est conditionnée, génétiquement modifié pour exprimer le ligand membranaire du récepteur CD40 (TMZ-CD40L) sous forme trimérique et le membre 9 de la superfamille du facteur de nécrose tumorale (TNFSF9, 4-1BBL, CD137), sous le contrôle d'un promoteur du cytomégalovirus (CMV) et avec des délétions sur le gène E1A et les gènes E3

delolimogén mupadenorepvec — un adenovirus de serotipo 5/35 con replicación condicionada, modificado genéticamente para expresar un ligando de membrana trimerizado de CD40 (TMZ-CD40L) y el miembro 9 de la superfamilia de factores de necrosis tumoral (TNFSF9, 4-1BBL, CD137), bajo el control de un promotor del citomegalovirus (CMV) y con deleciones en el gen E1A y en los genes E3

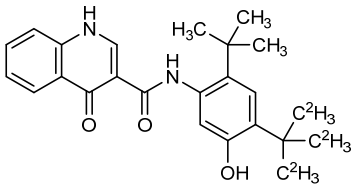
deutivacaftorum

deutivacaftor — *N*-{2-*tert*-butyl-5-hydroxy-4-[2-($^{2}H_{3}$)methyl(1,1,1,3,3,3-$^{2}H_{6}$)propan-2-y]phenyl}-4-oxo-1,4-dihydroquinoline-3-carboxamide

deutivacaftor — *N*-{2-*tert*-butyl-5-hydroxy-4-[2-($^2H_3$)méthyl(1,1,1,3,3,3-$^2H_6$)propan-2-y]phényl}-4-oxo-1,4-dihydroquinoline-3-carboxamide

deutivacaftor — *N*-{2-*tert*-butil-5-hidroxi-4-[2-($^2H_3$)metil(1,1,1,3,3,3-$^2H_6$)propan-2-il]fenil}-4-oxo-1,4-dihidroquinolina-3-carboxamida

$C_{24}H_{19}{}^2H_9N_2O_3$



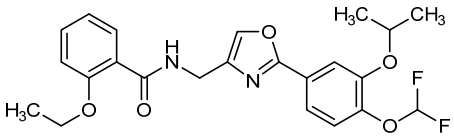
difamilastum

difamilast — *N*-({2-[4-(difluoromethoxy)-3-(propan-2-yloxy)pheny]-1,3-oxazol-4-yl}methyl)-2-ethoxybenzamide

difamilast — *N*-({2-[4-(difluorométhoxy)-3-(propan-2-yloxy)phény]-1,3-oxazol-4-yl}méthyl)-2-éthoxybenzamide

difamilast — *N*-({2-[4-(difluorometoxi)-3-(propan-2-iloxi)feni]-1,3-oxazol-4-il}metil)-2-etoxibenzamida

$C_{23}H_{24}F_2N_2O_5$



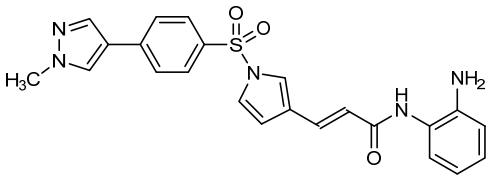
domatinostatum

domatinostat — (2*E*)-*N*-(2-aminophenyl)-3-(1-{[4-(1-methyl-1*H*-pyrazol-4-yl)phenyl]sulfonyl}-1*H*-pyrrol-3-yl)prop-2-enamide

domatinostat — (2*E*)-*N*-(2-aminophényl)-3-(1-{[4-(1-méthyl-1*H*-pyrazol-4-yl)phényl]sulfonyl}-1*H*-pyrrol-3-yl)prop-2-énamide

domatinostat — (2*E*)-*N*-(2-aminofenil)-3-(1-{[4-(1-metil-1*H*-pirazol-4-il)fenil]sulfonil}-1*H*-pirrol-3-il)prop-2-enamida

$C_{23}H_{21}N_5O_3S$



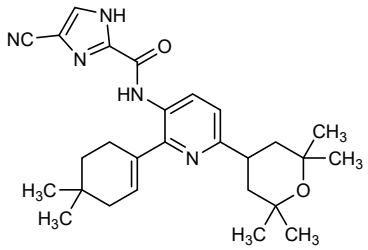
edicotinibum

edicotinib — 4-cyano-*N*-[2-(4,4-dimethylcyclohex-1-en-1-yl)-6-(2,2,6,6-tetramethyloxan-4-yl)pyridin-3-yl]-1*H*-imidazole-2-carboxamide

édicotinib — 4-cyano-*N*-[2-(4,4-diméthylcyclohex-1-én-1-yl)-6-(2,2,6,6-tétraméthyloxan-4-yl)pyridin-3-yl]-1*H*-imidazole-2-carboxamide

edicotinib — 4-ciano-*N*-[2-(4,4-dimetilciclohex-1-en-1-il)-6-(2,2,6,6-tetrametiloxan-4-il)piridin-3-i]-1*H*-imidazol-2-carboxamida

$C_{27}H_{35}N_5O_2$



efavaleukinum alfa #

efavaleukin alfa — immunoglobulin G1 γ1-chain C-terminal constant region fragment (Fc) (1-226 without C-terminal Lys, N77G,D136E,L138M variant)-G_4S linker (227-231)-human interleukin 2 (232-364, V322K,C356A variant) fusion protein, dimer disulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

éfavaleukine alfa — région constante C-terminale de la chaîne γ1 de l'immunoglobuline G1 humaine (fragment Fc) (1-226 sans la lysine C-terminale, variant N77G,D136E,L138M)-linker G_4S (227-231)-interleukine 2 humaine (232-364, variant V322K, C356A), protéine de fusion, dimère disulfure, produite par des cellules de hamsters chinois (CHO), glycoforme alfa

efavaleukina alfa — región constante C-terminal de la cadena γ1 de la inmunoglobulina G1 humana (fragmento Fc) (1-226 sin la lisina C-terminal, variante N77G,D136E,L138M)-ligante G_4S (227-231)-interleukina 2 humana (232-364, variante V322K, C356A), proteína de fusión, dímero disulfuro, producido por las células de hamsters chinos (CHO), glicoforma alfa

```
DKTHTCPPCP APELLGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED 50
PEVKFNWYVD GVEVHNAKTK PREEQYGSTY RVVSVLTVLH QDWLNGKEYK 100
CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSREEMTK NQVSLTCLVK 150
GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG 200
NVFSCSVMHE ALHNHYTQKS LSLSPGGGGG SAPTSSSTKK TQLQLEHLLL 250
DLQMILNGIN NYKNPKLTRM LTFKFYMPKK ATELKHLQCL EEELKPLEEV 300
LNLAQSKNFH LRPRDLISNI NKIVLELKGS ETTFMCEYAD ETATIVEFLN 350
RWITFAQSII STLT                                       364
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
intra-chain: 41-101 147-205 289-336
41'-101' 147'-205' 289'-336'
inter-chain: 6-6' 9-9'

Glycosylation site (O) / Site de glycosylation (O) / Posición de glicosilación (O)
Thr-234 Thr-234'

efineptakinum alfa

efineptakin alfa

Met-Gly-Met (1-3)-human interleukin 7 (4-155) fused to an antibody hybrid fragment (hyFc) consisting of human immunoglobulin D (IgD) hinge and N-terminal CH2 regions (156-193) and human immunoglobulin G4 (IgG4) C-terminal CH2 and complete CH3 regions (194-400), dimer disulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

éfineptakine alfa

Met-Gly-Met (1-3)-interleukine 7 humaine (4-155), fusionnée à un fragment Fc hybride d'anticorps (hyFc) consistant en la région charnière et le domaine CH2 N-terminal de l'immunoglobuline D (IgD) humaine (156-193), fusionné au domaine CH2 C-terminal et au domaine complet CH3 de l'immunoglobuline G4 (IgG4) humaine (194-400), dimère disulfure, produit par des cellules ovariennes de hamsters chinois (CHO), glycoforme alfa

efineptakina alfa

Met-Gly-Met (1-3)-interleukina 7 humana (4-155), fusionada con un fragmento Fc híbrido del anticuerpo (hyFc) consistente en la región bisagra y el dominio CH2 N-terminal de la inmunoglobulina D (IgD) humana (156-193), fusionada con el dominio CH2 C-terminal y con el dominio completo CH3 de la inmunoglobulina G4 (IgG4) humana (194-400), dímero disulfuro, producido por las células ováricas de hamsters chinos (CHO), glicoforma alfa

```
MGMDCDIEGK DGKQYESVLM VSIDQLLDSM KEIGSNCLNN EFNFFKRHIC 50
DANKEGMFLF RAARKLRQFL KMNSTGDFDL HLLKVSEGTT ILLNCTGQVK 100
GRKPAALGEA QPTKSLEENK SLKEQKKLND LCFLKRLLQE IKTCWNKILM 150
GTKEHRNTGR GGEEKKKEKE KEEQEERETK TPECPSHTQP LGVFLFPPKP 200
KDTLMISRTP EVTCVVVDVS QEDPEVQFNW YVDGVEVHNA KTKPREEQFN 250
STYRVVSVLT VLHQDWLNGK EYKCKVSNKG LPSSIEKTIS KAKGQPREPQ 300
VYTLPPSQEE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 350
LDSDGSFFLY SRLTVDKSRW QEGNVFSCSV MHEALHNHYT QKSLSLSLGK 400
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-chain: 5-95 37-132 50-144 214-274 320-378
5'-95' 37'-132' 50'-144' 214'-274' 320'-378'
Inter-chain: 184-184'

Glycosylation sites (N) / Sites de glycosylation (N) / Posiciones de glicosilación (N)
Asn-73 Asn-94 Asn-250
Glycosylation site (O) / Site de glycosylation (O) / Posición de glicosilación (O)
Thr-113

efinopegdutidum #

efinopegdutide

oxyntomodulin analogue, conjugated by a 10 kDa polyethylene glycol (PEG) linker (n ~ 225) to an Fc portion dimer of human immunoglobulin G4 (IgG4):
$N^{1.1}$-{3-[α-(3-{3-[(3*RS*)-3-({16,20-anhydro-[Ser^{2}>Aib,Ser^{16}>Glu,Arg^{17}>Lys,Gln^{20}>Lys,Asp^{21}>Glu,Lys^{30}> Cys]-oxyntomodulin
(1-30)-peptide 30-amide}-$S^{3.30}$-yl)-2,5-dioxopyrrolidin-1-yl]propanamido}propyl) poly(oxyethylene)-ω-yloxy]propyl}[immunoglobulin G4 heavy chain constant region C-terminal 221-peptide dimer disulfide], non-glycosylated, immunoglobulin fragment dimer produced in *Escherichia coli*

éfinopégdutide

analogue de l' oxyntomoduline, conjugué par un linker polyéthylène glycol (PEG) de 10 kDa (n ~ 225) à un dimère de fragment Fc d'immunoglobuline G4 (IgG4) humaine:
$N^{1.1}$-{3-[α-(3-{3-[(3*RS*)-3-({16,20-anhydro-[Ser^{2}>Aib,Ser^{16}>Glu,Arg^{17}>Lys,Gln^{20}>Lys,Asp^{21}>Glu,Lys^{30}> Cys]-oxyntomodulin

(1-30)-peptide 30-amide}-*S*$^{3.30}$-yl)-2,5-dioxopyrrolidin-1-yl]propanamido}propyl) poly(oxyéthylène)-ω-yloxy]propyl}[peptide de 221 acides aminés de la région constante C-terminale de la chaîne lourde G4 d'immunoglobuline, dimère disulfure], non-glycosylé, dimère du fragment d'immunoglobuline produit par *Escherichia coli*

efinopegdutida

análogo de la oxintomodulina, conjugado por un enlace polietileno glicol (PEG) de 10 kDa (n ~ 225) a un dímero del fragmento Fc de la inmunoglobulina G4 (IgG4) humana:
N$^{1.1}$-{3-[α-(3-{3-[(3*RS*)-3-({16,20-anhidro-[Ser^{2}>Aib,Ser^{16}>Glu,Arg^{17}>Lys,Gln^{20}>Lys,Asp^{21}>Glu,Lys^{30}> Cys]-oxintomodulin
(1-30)-péptido 30-amida}-*S*$^{3.30}$-il)-2,5-dioxopirrolidin-1-il]propanamido}propil)poli(oxietileno)-ω-iloxi]propil}[péptido de 221 aminoácidos de la región constante C-terminal de la cadena pesada G4 de la inmunoglobulina, dímero disulfuro], no glicosilado, dímero del fragmento de la inmunoglobulina producido por *Escherichia coli*

Conjugated peptide / peptide conjugué / péptido conjugado

HBQGTFTSDY SKYLDEKRAK EFVQWLMNTC-NH_2

Monomer / monomère / monómero IgG4 Fc

```
PSCPAPEFLG GPSVFLFPPK PKDTLMISRT PEVTCVVVDV SQEDPEVQFN 50
WYVDGVEVHN AKTKPREEQF NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK 100
GLPSSIEKTI SKAKGQPREP QVYTLPPSQE EMTKNQVSLT CLVKGFYPSD 150
IAVEWESNGQ PENNYKTTPP VLDSDGSFFL YSRLTVDKSR WQEGNVFSCS 200
VMHEALHNHY TQKSLSLSLG K                               221
```

Disulfide bridges location / Positions des ponts disulfure / Posiciones de los puentes disulfuro

Intra-chain: 35-95 141-199 35'-95' 141'-199'

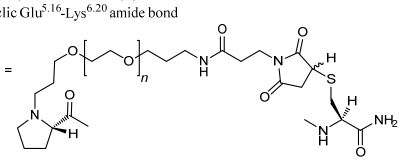
Inter-chain: 3-3'

Modified residues / résidus modifiés / restos modificados

B = 2-methylalanyl (2-aminoisobutyryl, Aib)

E...K = cyclic Glu$^{5.16}$-Lys$^{6.20}$ amide bond

C(-NH2) =



eftansomatropinum alfa #

eftansomatropin alfa

human somatotropin (1-191) fused to a hybrid Fc consisting of human immunoglobulin D (IgD) hinge region, fused to the IgD N-terminal CH2 region (192-229), fused to the immunoglobulin G4 (IgG4) C-terminal CH2 region, fused to the IgG4 CH3 region (230-436), disulfide dimer, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

eftansomatropine alfa

somatotropine humaine (1-191) fusionnée à un fragment Fc hybride consistant en la région charnière de l'immunoglobuline D (IgD) humaine, fusionnée au domaine CH2 N-terminal de l'IgD (192-229), fusionné au domaine CH2 C-terminal de l'immunoglobuline G4 (IgG4), fusionné au domaine CH3 de l'IgG4 (230-436), dimère disulfure, produit des cellules ovariennes de hamsters chinois (CHO), glycoforme alfa

eftansomatropina alfa

somatotropina humana (1-191) fusionada con un fragmento Fc híbrido consistente en la región bisagra de la inmunoglobulina D (IgD) humana, fusionada con el dominio CH2 N-terminal de la IgD (192-229), fusionada con el dominio CH2 C-terminal de la inmunoglobulina G4 (IgG4), fusionada con el dominio CH3 de la IgG4 (230-436), dímero disulfuro, producido en las células ováricas de hamsters chinos (CHO), glicoforma alfa

```
FPTIPLSRLF DNAMLRAHRL HQLAFDTYQE FEEAYIPKEQ KYSFLQNPQT 50
SLCFSESIPT PSNREETQQK SNLELLRISL LLIQSWLEPV QFLRSVFANS 100
LVYGASDSNV YDLLKDLEEG IQTLMGRLED GSPRTGQIFK QTYSKFDTNS 150
HNDDALLKNY GLLYCFRKDM DKVETFLRIV QCRSVEGSCG FRNTGRGGEE 200
KKKEKEKEEQ EERETKTPEC PSHTQPLGVF LFPPKPKDTL MISRTPEVTC 250
VVVDVSQEDP EVQFNWYVDG VEVHNAKTKP REEQFNSTYR VVSVLTVLHQ 300
DWLNGKEYKC KVSNKGLPSS IEKTISKAKG QPREPQVYTL PPSQEEMTKN 350
QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD GSFFLYSRLT 400
VDKSRWQEGN VFSCSVMHEA LHNHYTQKSL SLSLGK               436
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-chain : 53-165 182-189 250-310 356-414
53'-165' 182'-189' 250'-310' 356'-414'
Inter-chain : 220-220'

Glycosylation sites (O) / Sites de glycosylation (O) / Posiciones de glicosilación (O)
Ser-55 Ser-57 Thr-60 Ser-62 Thr-67

Glycosylation site (N) / Site de glycosylation (N) / Posición de glicosilación (N)
Asn-286

elismetrepum
elismetrep

4-[(4-cyclopropylisoquinolin-3-yl){[4-(trifluoromethoxy)phenyl]methyl}sulfamoy]benzoic acid

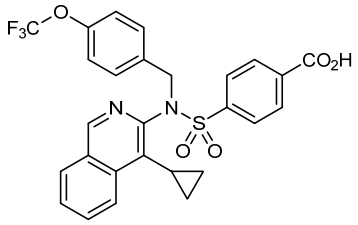
élismétrep

acide 4-[(4-cyclopropylisoquinoléin-3-yl){[4-(trifluorométhoxy)phényl]méthyl}sulfamoy]benzoïque

elismetrep

ácido 4-[(4-ciclopropilisoquinolein-3-il){[4-(trifluorometoxi)fenil]metil}sulfamoil]benzoico

$C_{27}H_{21}F_3N_2O_5S$



enapotamabum #
enapotamab

immunoglobulin G1-kappa, anti-[*Homo sapiens* AXL (AXL receptor tyrosine kinase, tyrosine-protein kinase receptor UFO)], *Homo sapiens* monoclonal antibody;
gamma1 heavy chain (1-445) [*Homo sapiens* VH (IGHV3-23*01 (95.9%) -(IGHD) -IGHJ3*02 (100%)) [8.8.9] (1-116) -*Homo sapiens* IGHG1*03, G1m3 nG1m1 (CH1 R120 (213) (117-214), hinge (215-229), CH2 (230-339), CH3 E12 (355), M14 (357) (340-444), CHS K>del (445)) (117-445)], (219-215')-disulfide with kappa light chain (1'-215') [*Homo sapiens* V-KAPPA (IGKV3-20*01 (100%) -IGKJ2*01 (100%)) [7.3.9] (1'-108') -*Homo sapiens* IGKC*01, Km3 A45.1 (154), V101 (192) (109'-215')]; dimer (225-225":228-228")-bisdisulfide

énapotamab

immunoglobuline G1-kappa, anti-[*Homo sapiens* AXL (récepteur tyrosine kinase AXL, récepteur tyrosine-protéine kinase UFO)], *Homo sapiens* anticorps monoclonal;
chaîne lourde gamma1 (1-445) [*Homo sapiens* VH (IGHV3-23*01 (95.90%) -(IGHD) -IGHJ3*02 (100%)) [8.8.9] (1-116) -*Homo sapiens* IGHG1*03, G1m3 nG1m1 (CH1 R120 (213) (117-214), charnière (215-229), CH2 (230-339), CH3 E12 (355), M14 (357) (340-444), CHS K>del (445)) (117-445)], (219-215')-disulfure avec la chaîne légère kappa (1'-215') [*Homo sapiens* V-KAPPA (IGKV3-20*01 (100%) -IGKJ2*01 (100%)) [7.3.9] (1'-108') -*Homo sapiens* IGKC*01, Km3 A45.1 (154), V101 (192) (109'-215')]; dimère (225-225'':228-228'')-bisdisulfure

enapotamab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* AXL (receptor tirosina kinasa AXL, receptor tirosina-proteína kinasa UFO)], *Homo sapiens* anticuerpo monoclonal;
cadena pesada gamma1 (1-445) [*Homo sapiens* VH (IGHV3-23*01 (95.90%) -(IGHD) -IGHJ3*02 (100%)) [8.8.9] (1-116) -*Homo sapiens* IGHG1*03, G1m3 nG1m1 (CH1 R120 (213) (117-214), bisagra (215-229), CH2 (230-339), CH3 E12 (355), M14 (357) (340-444), CHS K>del (445)) (117-445)], (219-215')-disulfuro con la cadena ligera kappa (1'-215') [*Homo sapiens* V-KAPPA (IGKV3-20*01 (100%) -IGKJ2*01 (100%)) [7.3.9] (1'-108') -*Homo sapiens* IGKC*01, Km3 A45.1 (154), V101 (192) (109'-215')]; dímero (225-225'':228-228'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLLESGGG LVQPGGSLRL SCAASGFTFS SYAMNWVRQA PGKGLEWVST  50
TSGSGASTYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKIW 100
IAFDIWGQGT MVTVSSASTK GPSVFPLAPS SKSTSGGTAA LGCLVKDYFP 150
EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVVTVPSS SLGTQTYICN 200
VNHKPSNTKV DKRVEPKSCD KTHTCPPCPA PELLGGPSVF LFPPKPKDTL 250
MISRTPEVTC VVVDVSHEDP EVKFNWYVDG VEVHNAKTKP REEQYNSTYR 300
VVSVLTVLHQ DWLNGKEYKC KVSNKALPAP IEKTISKAKG QPREPQVYTL 350
PPSREEMTKN QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD 400
GSFFLYSKLT VDKSRWQQGN VFSCSVMHEA LHNHYTQKSL SLSPG      445
```

Light chain / Chaîne légère / Cadena ligera

```
EIVLTQSPGT LSLSPGERAT LSCRASQSVS SSYLAWYQQK PGQAPRLLIY  50
GASSRATGIP DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QYGSSPYTFG 100
QGTKLEIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK 150
VDNALQSGNS QESVTEQDSK DSTYSLSSTL TLSKADYEKH KVYACEVTHQ 200
GLSSPVTKSF NRGEC                                       215
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

Intra-H (C23-C104)	22-96	143-199	260-320	366-424
	22"-96"	143"-199"	260"-320"	366"-424"
Intra-L (C23-C104)	23'-89'	135'-195'		
	23'"-89'"	135'"-195'"		
Inter-H-L (h 5-CL 126)	219-215'	219"-215'"		
Inter-H-H (h 11, h14)	225-225"	228-228"		

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
296, 296"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

enapotamabum vedotinum #
enapotamab vedotin

immunoglobulin G1-kappa, anti-[*Homo sapiens* AXL (AXL receptor tyrosine kinase, tyrosine-protein kinase receptor UFO)], *Homo sapiens* monoclonal antibody conjugated to auristatin E;

	gamma1 heavy chain (1-445) [*Homo sapiens* VH (IGHV3-23*01 (95.9%) -(IGHD) -IGHJ3*02 (100%)) [8.8.9] (1-116) -*Homo sapiens* IGHG1*03, G1m3 nG1m1 (CH1 R120 (213) (117-214), hinge (215-229), CH2 (230-339), CH3 E12 (355), M14 (357) (340-444), CHS K>del (445)) (117-445)], (219-215')-disulfide with kappa light chain (1'-215') [*Homo sapiens* V-KAPPA (IGKV3-20*01 (100%) -IGKJ2*01 (100%)) [7.3.9] (1'-108') -*Homo sapiens* IGKC*01, Km3 A45.1 (154), V101 (192) (109'-215')]; dimer (225-225":228-228")-bisdisulfide; conjugated, on an average of 4 cysteinyl, to monomethylauristatin E (MMAE), via a cleavable maleimidocaproyl-valyl-citrullinyl-p-aminobenzyloxycarbonyl (mc-val-cit-PABC) type linker For the *vedotin* part, please refer to the document *"INN for pharmaceutical substances: Names for radicals, groups and others"*.*
énapotamab védotine	immunoglobuline G1-kappa, anti-[*Homo sapiens* AXL (récepteur tyrosine kinase AXL, récepteur tyrosine-protéine kinase UFO)], *Homo sapiens* anticorps monoclonal conjugué à l'auristatine E; chaîne lourde gamma1 (1-445) [*Homo sapiens* VH (IGHV3-23*01 (95.90%) -(IGHD) -IGHJ3*02 (100%)) [8.8.9] (1-116) -*Homo sapiens* IGHG1*03, G1m3 nG1m1 (CH1 R120 (213) (117-214), charnière (215-229), CH2 (230-339), CH3 E12 (355), M14 (357) (340-444), CHS K>del (445)) (117-445)], (219-215')-disulfure avec la chaîne légère kappa (1'-215') [*Homo sapiens* V-KAPPA (IGKV3-20*01 (100%) -IGKJ2*01 (100%)) [7.3.9] (1'-108') -*Homo sapiens* IGKC*01, Km3 A45.1 (154), V101 (192) (109'-215')]; dimère (225-225":228-228")-bisdisulfure; conjugué sur 4 cystéinyl en moyenne, au monométhylauristatine E (MMAE), via un linker clivable de type maléimidocaproyl-valyl-citrullinyl-p-aminobenzyloxycarbonyl (mc-val-cit-PABC) Pour la partie *védotine*, veuillez-vous référer au document *"INN for pharmaceutical substances: Names for radicals, groups and others"*.*
enapotamab vedotina	inmunoglobulina G1-kappa, anti-[*Homo sapiens* AXL (receptor tirosina kinasa AXL, receptor tirosina-proteína kinasa UFO)], *Homo sapiens* anticuerpo monoclonal conjugado con la auristatina E; cadena pesada gamma1 (1-445) [*Homo sapiens* VH (IGHV3-23*01 (95.90%) -(IGHD) -IGHJ3*02 (100%)) [8.8.9] (1-116) -*Homo sapiens* IGHG1*03, G1m3 nG1m1 (CH1 R120 (213) (117-214), bisagra (215-229), CH2 (230-339), CH3 E12 (355), M14 (357) (340-444), CHS K>del (445)) (117-445)], (219-215')-disulfuro con la cadena ligera kappa (1'-215') [*Homo sapiens* V-KAPPA (IGKV3-20*01 (100%) -IGKJ2*01 (100%)) [7.3.9] (1'-108') -*Homo sapiens* IGKC*01, Km3 A45.1 (154), V101 (192) (109'-215')]; dímero (225-225":228-228")-bisdisulfuro; conjugado bajo una media de 4 cisteinil, con la monometilauristatina E (MMAE), a través de un enlace escind ble del tipo maliimidocaproil-valil-citrullinil-p-aminobenziloxicarbonil (mc-val-cit-PABC) Para la fracción *vedotina*, se pueden dirigir al documento *"INN for pharmaceutical substances: Names for radicals, groups and others"*.*

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLLESGGG LVQPGGSLRL SCAASGFTFS SYAMNWVRQA PGKGLEWVST  50
TSGSGASTYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKIW 100
IAFDIWGQGT MVTVSSASTK GPSVFPLAPS SKSTSGGTAA LGCLVKDYFP 150
EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVVTVPSS SLGTQTYICN 200
VNHKPSNTKV DKRVEPKSCD KTHTCPPCPA PELLGGPSVF LFPPKPKDTL 250
MISRTPEVTC VVVDVSHEDP EVKFNWYVDG VEVHNAKTKP REEQYNSTYR 300
VVSVLTVLHQ DWLNGKEYKC KVSNKALPAP IEKTISKAKG QPREPQVYTL 350
PPSREEMTKN QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD 400
GSFFLYSKLT VDKSRWQQGN VFSCSVMHEA LHNHYTQKSL SLSPG      445
```

Light chain / Chaîne légère / Cadena ligera

```
EIVLTQSPGT LSLSPGERAT LSCRASQSVS SSYLAWYQQK PGQAPRLLIY  50
GASSRATGIP DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QYGSSPYTFG 100
QGTKLEIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK 150
VDNALQSGNS QESVTEQDSK DSTYSLSSTL TLSKADYEKH KVYACEVTHQ 200
GLSSPVTKSF NRGEC                                       215
```

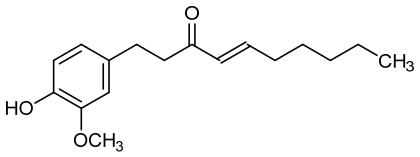
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 143-199 260-320 366-424
22"-96" 143"-199" 260"-320" 366"-424"
Intra-L (C23-C104) 23'-89' 135'-195'
23'"-89'" 135'"-195'"
Inter-H-L (h 5-CL 126) * 219-215' 219"-215"
Inter-H-H (h 11, h14) * 225-225" 228-228"
*Two or three of the inter-chain disulfide bridges are not present, an average of 4 cysteinyl being conjugated each via a thioether bond to a drug linker
*Deux ou trois des ponts disulfures inter-chaînes ne sont pas présents, 4 cystéinyl en moyenne étant chacun conjugué via une liaison thioéther à un linker-principe actif
*Faltan dos o tres puentes disulfuro inter-catenarios, una media de 4 cisteinil está conjugada a conectores de principio activo

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84 4:
296, 296"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

enexasogaolum

enexasogaol	(4*E*)-1-(4-hydroxy-3-methoxyphenyl)dec-4-en-3-one
énexasogaol	(4*E*)-1-(4-hydroxy-3-méthoxyphényl)déc-4-én-3-one
enexasogaol	(4*E*)-1-(4-hidroxi-3-metoxifenil)dec-4-en-3-ona

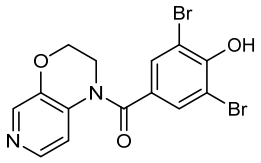
$C_{17}H_{24}O_3$



epaminuradum

epaminurad	(3,5-dibromo-4-hydroxyphenyl)(2,3-dihydro-4*H*-pyrido[4,3-*b*]-1,4-oxazin-4-yl)methanone
épaminurad	(3,5-dibromo-4-hydroxyphényl)(2,3-dihydro-4*H*-pyrido[4,3-*b*]-1,4-oxazin-4-yl)méthanone
epaminurad	(3,5-dibromo-4-hidroxifenil)(2,3-dihidro-4*H*-pirido[4,3-*b*]-1,4-oxazin-4-il)metanona

$C_{14}H_{10}Br_2N_2O_3$



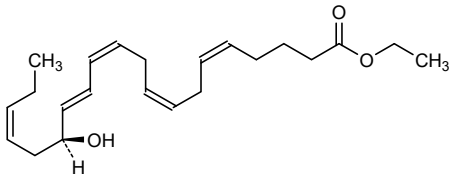
epeleutonum

epeleuton — ethyl (5*Z*,8*Z*,11*Z*,13*E*,15*S*,17*Z*)-15-hydroxyicosa-5,8,11,13,17-pentaenoate

épéleuton — (5*Z*,8*Z*,11*Z*,13*E*,15*S*,17*Z*)-15-hydroxyicosa-5,8,11,13,17-pentaénoate d'éthyle

epeleutón — (5*Z*,8*Z*,11*Z*,13*E*,15*S*,17*Z*)-15-hidroxiicosa-5,8,11,13,17-pentaenoato de etilo

$C_{22}H_{34}O_3$



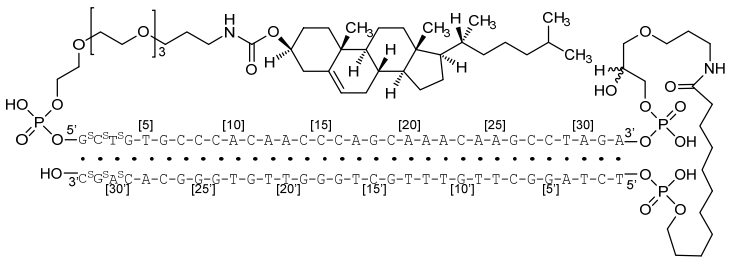
etidaligidum

etidaligide — *all-P-ambo*-5'-*O*-{(4*RS*)-1-[5'-*O*-{19-[(cholest-5-en-3β-yl)oxy]-1-hydroxy-1,19-dioxo-2,5,8,11,14-pentaoxa-18-aza-1λ^5-phosphanonadecan-1-yl}deoxy([1,2,3]tri-*P*-thio)(5'-GCTGTGCCCA CAACCCAGCA AACAAGCCTA GA-3')-3'-*O*-yl]-1,4,23-trihydroxy-1,11,23-trioxo-2,6,22-trioxa-10-aza-1λ^5,23λ^5-diphosphatricosan-23-yl}deoxy([29,30,31]tri-*P*-thio)(5'-TCTAGGCTTG TTTGCTGGGT TGTGGGCACA GC-3')

étidaligide — *tout-P-ambo*-5'-*O*-{(4*RS*)-1-[5'-*O*-{19-[(cholest-5-en-3β-yl)oxy]-1-hydroxy-1,19-dioxo-2,5,8,11,14-pentaoxa-18-aza-1λ^5-phosphanonadécan-1-yl}désoxy([1,2,3]tri-*P*-thio)(5'-GCTGTGCCCA CAACCCAGCA AACAAGCCTA GA-3')-3'-*O*-yl]-1,4,23-trihydroxy-1,11,23-trioxo-2,6,22-trioxa-10-aza-1λ^5,23λ^5-diphosphatricosan-23-yl}désoxy([29,30,31]tri-*P*-thio)(5'-TCTAGGCTTG TTTGCTGGGT TGTGGGCACA GC-3')

etidaligida — *todo-P-ambo*-5'-*O*-{(4*RS*)-1-[5'-*O*-{19-[(cholest-5-en-3β-yl)oxi]-1-hidroxi-1,19-dioxo-2,5,8,11,14-pentaoxa-18-aza-1λ^5-fosfanonadecan-1-yl}desoxi([1,2,3]tri-*P*-tio)(5'-GCTGTGCCCA CAACCCAGCA AACAAGCCTA GA-3')-3'-*O*-yl]-1,4,23-trihidroxi-1,11,23-trioxo-2,6,22-trioxa-10-aza-1λ^5,23λ^5-difosfatricosan-23-il}desoxi([29,30,31]tri-*P*-tio)(5'-TCTAGGCTTG TTTGCTGGGT TGTGGGCACA GC-3')

$C_{678}H_{885}N_{244}O_{392}P_{65}S_6$



etigilimabum #

etigilimab	immunoglobulin G1-kappa, anti-[*Homo sapiens* TIGIT (T-cell immunoreceptor with Ig domain and ITIM, V-set Ig member 9, VSIG9, V-set and transmembrane member 3, VSTM3)], humanized monoclonal antibody; gamma1 heavy chain (1-448) [*Homo sapiens* VH (IGHV4-59*01 (88.8%) -(IGHD)- IGHJ4*01 (92.9%)) [8.7.12] (1-118) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (215) (119-216), hinge (217-231), CH2 (232-341), CH3 E12 (357), M14 (359) (342-446), CHS (447-448)) (119-448)], (221-214')-disulfide with kappa light chain (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-33*01 (85.3%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*05, Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (227-227":230-230")-bisdisulfide
étigilimab	immunoglobuline G1-kappa, anti-[*Homo sapiens* TIGIT (immunorécepteur des lymphocytes T avec domaine Ig et ITIM, membre 9 de l'Ig V-set, VSIG9, membre 3 de l'Ig V-set et région transmembrane, VSTM3)], anticorps monoclonal humanisé; chaîne lourde gamma1 (1-448) [*Homo sapiens* VH (IGHV4-59*01 (88.8%) -(IGHD)- IGHJ4*01 (92.9%)) [8.7.12] (1-118) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (215) (119-216), charnière (217-231), CH2 (232-341), CH3 E12 (357), M14 (359) (342-446), CHS (447-448)) (119-448)], (221-214')-disulfure avec la chaîne légère kappa (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-33*01 (85.3%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*05, Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (227-227":230-230")-bisdisulfure
etigilimab	inmunoglobulina G1-kappa, anti-[*Homo sapiens* TIGIT (inmunoreceptor de los linfocitos T con dominio Ig e ITIM, miembro 9 de la Ig V-set, VSIG9, miembro 3 de la Ig V-set y región transmembrana, VSTM3)], anticuerpo monoclonal humanizado; cadena pesada gamma1 (1-448) [*Homo sapiens* VH (IGHV4-59*01 (88.8%) -(IGHD)- IGHJ4*01 (92.9%)) [8.7.12] (1-118) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (215) (119-216), bisagra (217-231), CH2 (232-341), CH3 E12 (357), M14 (359) (342-446), CHS (447-448)) (119-448)], (221-214')-disulfuro con la cadena ligera kappa (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-33*01 (85.3%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*05, Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (227-227":230-230")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLQESGPG LVKPSETLSL TCAVSGYSIT SDYAWNWIRQ PPGKGLEWIG  50
YISYSGSTSY NPSLRSRVTI SRDTSKNQFF LKLSSVTAAD TAVYYCARRQ 100
VGLGFAYWGQ GTLVTVSSAS TKGPSVFPLA PSSKSTSGGT AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTQTYI 200
CNVNHKPSNT KVDKRVEPKS CDKTHTCPPC PAPELLGGPS VFLFPPKPKD 250
TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNST 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY 350
TLPPSREEMT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD 400
SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPGK   448
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCKASQDVS TAVAWYQQKP GKAPKLLIYS 50
ASYRYTGVPS RFSGSGSGTD FTFTISSLQP EDIATYYCQQ HYSTPWTFGQ 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSNTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

Intra-H (C23-C104)	22-96	145-201	262-322	368-426
	22"-96"	145"-201"	262"-322"	368"-426"
Intra-L (C23-C104)	23'-88'	134'-194'		
	23'"-88'"	134'"-194'"		
Inter-H-L (h 5-CL 126)	221-214'	221"-214'"		
Inter-H-H (h 11, h 14)	227-227"	230-230"		

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
298, 298"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

faricimabum #

faricimab — immunoglobulin G1-kappa/lambda with domain crossover, anti-[*Homo sapiens* VEGFA (vascular endothelial growth factor A, VEGF-A, VEGF)] and anti-[*Homo sapiens* ANGPT2 (angiopoietin 2, Ang2)], humanized and *Homo sapiens* monoclonal antibody, bispecific; gamma1 heavy chain anti-VEGFA (1-453) [humanized VH (*Homo sapiens* IGHV3-30*02 (75.8%) -(IGHD) -IGHJ4*01 (93.3%)) [8.8.16] (1-123) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (220) (124-221), hinge 1-15 (222-236), CH2 [L1.3>A (240), L1.2>A (241), I15.2>A (259), H93>A (316), P114>G (335)](237-346), CH3D12 (362), L14 (364) [S10>C (360), T22>W (372), H115>A (441)](347-451), CHS (452-453)) (124-453)], (226-214')-disulfide with kappa light chain, anti-VEGFA (1'-214') [humanized V-KAPPA (*Homo sapiens* IGKV1-16*01 (87.4%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; gamma1-kappa heavy chain anti-ANGPT2 (1"-463") [*Homo sapiens* VH (IGHV1-2*02 (100%)-(IGHD)-IGHJ3*02 (100%)) [8.8.22] (1"-129") -*Homo sapiens* IGKC*01, Km3 A45.1 (175), V101 (213) [R1.4>A (130), T1.3>S (131)] (130"-236") -*Homo sapiens* IGHG1*01, G1m1 (hinge 6-15 (237-246), (CH2[L1.3>A (250), L1.2>A (251), I15.2>A (269), H93>A (326), P114>G (345)] (247-356), CH3 D12 (372), L14 (374) [Y5>C (365),T22>S (382), L24>A (384), Y86>V (423), H115>A (451)] (357-461), CHS (462-463)) (237"-463")], (236"-213'")-disulfide with lambda-gamma light chain anti-ANGPT2 (1'"-213'") [*Homo sapiens* V-LAMBDA (IGLV3-21*02 (100.00%) -IGLJ2*01 (100%)) [6.3.11] (1'"-108'") -2-mer linker biseryl (109'"-110'") -*Homo sapiens* IGHG1*01, G1m17(CH1 K120 (207) (111-208)-hinge 1-5 (209-213)) (111'"-213'")]; dimer (232-242":235-245":360-365")-trisdisulfide

faricimab — immunoglobuline G1-kappa/lambda avec domaines échangés, anti-[*Homo sapiens* VEGFA (facteur de croissance A de l'endothélium vasculaire, VEGF-A, VEGF)] et anti-[*Homo sapiens* ANGPT2 (angiopoiétine 2, Ang2)], anticorps monoclonal humanisé et *Homo sapiens*, bispécifique;

	chaîne lourde gamma1 anti-VEGFA (1-453) [VH humanisé (*Homo sapiens* IGHV3-30*02 (75.8%) -(IGHD) -IGHJ4*01 (93.3%)) [8.8.16] (1-123) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (220) (124-221), charnière 1-15 (222-236), CH2 [L1.3>A (240), L1.2>A (241), I15.2>A (259), H93>A (316), P114>G (335)](237-346), CH3D12 (362), L14 (364) [S10>C (360), T22>W (372), H115>A (441)](347-451), CHS (452-453)) (124-453)], (226-214')-disulfure avec la chaîne légère kappa, anti-VEGFA (1'-214') [V-KAPPA humanisé (*Homo sapiens* IGKV1-16*01 (87.4%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; chaîne lourde gamma1-kappa anti-ANGPT2 (1''-463'') [*Homo sapiens* VH (IGHV1-2*02 (100%) -(IGHD)-IGHJ3*02 (100%)) [8.8.22] (1''-129'') -*Homo sapiens* IGKC*01, Km3 A45.1 (175), V101 (213) [R1.4>A (130), T1.3>S (131)] (130''-236'') -*Homo sapiens* IGHG1*01, G1m1 (charnière 6-15 (237-246), (CH2 [L1.3>A (250), L1.2>A (251), I15.2>A (269), H93>A (326), P114>G (345)] (247-356), CH3 D12 (372), L14 (374) [Y5>C (365), T22>S (382), L24>A (384), Y86>V (423), H115>A (451)] (357-461), CHS (462-463)) (237''-463'')], (236''-213''')-disulfure avec la chaîne légère lambda-gamma anti-ANGPT2 (1'''-213''') [*Homo sapiens* V-LAMBDA (IGLV3-21*02 (100.00%) -IGLJ2*01 (100%)) [6.3.11] (1'''-108''') -2-mer linker biséryl (109'''-110''') -*Homo sapiens* IGHG1*01,G1m17 (CH1 K120 (207) (111-208)-charnière 1-5 (209-213)) (111'''-213''')]; dimère (232-242":235-245":360-365")-trisdisulfure
faricimab	inmunoglobulina G1-kappa/lambda con dominios intercambiados,anti-[*Homo sapiens* VEGFA (factor de crecimiento A del endotelio vascular, VEGF-A, VEGF)] y anti-[*Homo sapiens* ANGPT2 (angiopoyetina 2, Ang2)], anticuerpo monoclonal humanizado y *Homo sapiens*, biespecífico; cadena pesada gamma1 anti-VEGFA (1-453) [VH humanizado (*Homo sapiens* IGHV3-30*02 (75.8%) -(IGHD) -IGHJ4*01 (93.3%)) [8.8.16] (1-123) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (220) (124-221), bisagra 1-15 (222-236), CH2 [L1.3>A (240), L1.2>A (241), I15.2>A (259), H93>A (316), P114>G (335)](237-346), CH3D12 (362), L14 (364) [S10>C (360), T22>W (372), H115>A (441)](347-451), CHS (452-453)) (124-453)], (226-214')-disulfuro con la cadena ligera kappa,anti-VEGFA (1'-214') [V-KAPPA humanizado (*Homo sapiens* IGKV1-16*01 (87.4%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; cadena pesada gamma1-kappa anti-ANGPT2 (1''-463'') [*Homo sapiens* VH (IGHV1-2*02 (100%) -(IGHD)-IGHJ3*02 (100%)) [8.8.22] (1''-129'') -*Homo sapiens* IGKC*01, Km3 A45.1 (175), V101 (213) [R1.4>A (130), T1.3>S (131)] (130''-236'') -*Homo sapiens* IGHG1*01, G1m1 (bisagra 6-15 (237-246), (CH2 [L1.3>A (250), L1.2>A (251), I15.2>A (269), H93>A (326), P114>G (345)] (247-356), CH3 D12 (372), L14 (374) [Y5>C (365), T22>S (382), L24>A (384), Y86>V (423), H115>A (451)] (357-461), CHS (462-463)) (237''-463'')], (236''-213''')-disulfuro con la cadena ligera lambda-gamma anti-ANGPT2 (1'''-213''') [*Homo sapiens* V-LAMBDA (IGLV3-21*02 (100.00%) -IGLJ2*01 (100%)) [6.3.11] (1'''-108''') -2-mer ligando biseril (109'''-110''') -*Homo sapiens* IGHG1*01,G1m17 (CH1 K120 (207) (111-208)-bisagra 1-5 (209-213)) (111'''-213''')]; dímero (232-242":235-245":360-365")-trisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada anti-VEGFA

```
EVQLVESGGG LVQPGGSLRL SCAASGYDFT HYGMNWVRQA PGKGLEWVGW  50
INTYTGEPTY AADFKRRFTF SLDTSKSTAY LQMNSLRAED TAVYYCAKYP 100
YYYGTSHWYF DVWGQGTLVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC 150
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG 200
TQTYICNVNH KPSNTKVDKK VEPKSCDKTH TCPPCPAPEA AGGPSVFLFP 250
PKPKDTLMAS RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE 300
QYNSTYRVVS VLTVLAQDWL NGKEYKCKVS NKALGAPIEK TISKAKGQPR 350
EPQVYTLPPC RDELTKNQVS LWCLVKGFYP SDIAVEWESN GQPENNYKTT 400
PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN AYTQKSLSLS 450
PGK                                                     453
```

Light chain / Chaîne légère / Cadena ligera anti-VEGFA

```
DIQLTQSPSS LSASVGDRVT ITCSASQDIS NYLNWYQQKP GKAPKVLIYF  50
TSSLHSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YSTVPWTFGQ 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Heavy chain / Chaîne lourde / Cadena pesada anti-ANGPT2

```
QVQLVQSGAE VKKPGASVKV SCKASGYTFT GYYMHWVRQA PGQGLEWMGW  50
INPNSGGTNY AQKFQGRVTM TRDTSISTAY MELSRLRSDD TAVYYCARSP 100
NPYYYDSSGY YYPGAFDIWG QGTMVTVSSA SVAAPSVFIF PPSDEQLKSG 150
TASVVCLLNN FYPREAKVQW KVDNALQSGN SQESVTEQDS KDSTYSLSST 200
LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGECDKTH TCPPCPAPEA 250
AGGPSVFLFP PKPKDTLMAS RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV 300
HNAKTKPREE QYNSTYRVVS VLTVLAQDWL NGKEYKCKVS NKALGAPIEK 350
TISKAKGQPR EPQVCTLPPS RDELTKNQVS LSCAVKGFYP SDIAVEWESN 400
GQPENNYKTT PPVLDSDGSF FLVSKLTVDK SRWQQGNVFS CSVMHEALHN 450
AYTQKSLSLS PGK                                         463
```

Light chain / Chaîne légère / Cadena ligera anti-ANGPT2

```
SYVLTQPPSV SVAPGQTARI TCGGNNIGSK SVHWYQQKPG QAPVLVVYDD  50
SDRPSGIPER FSGSNSGNTA TLTISRVEAG DEADYYCQVW DSSSDHWVFG 100
GGTKLTVLSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS 150
WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT YICNVNHKPS 200
NTKVDKKVEP KSC                                         213
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 150-206 267-327 373-431
22"-96" 156"-216" 277"-337" 383"-441"
Intra-L (C23-C104) 23'-88' 134'-194'
22"'-87"' 137"'-193"'
Inter-H-L (h5-CL 126) 226-214' 236"-213"
Inter-H-H (h 11, h 14, AA >C) 232-242" 235-245" 360-365"
N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4 :
303, 313"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

fidanacogenum elaparvovecum #

fidanacogene elaparvovec	a non-replicating adeno-associated virus serotype 2 (AAV2) expressing the Padua variant (R338L) of human coagulation factor IX (F9, Factor IX, FIX), under the control of the liver-specific apolipoprotein E (Apo E) enhancer/alpha1-antitrypsin (hAAT) promoter (ApoE/hAAT), and all AAV genes encoding viral products deleted
fidanacogène élaparvovec	virus adéno-associé de sérotype 2 (AAV2) non-répliquant, exprimant le variant Padua (R338L) du facteur de coagulation IX humain (F9, Facteur IX, FIX), sous le contrôle de l'activateur de l'apolipoprotéine E (ApoE) spécifique du foie/promoteur de l'alpha1-antitrypsine (ApoE/hAAT) et tous les gènes de l'AAV codant pour des produits viraux ont été supprimés
fidanacogén elaparvovec	un virus adenoasociado de serotipo 2 (AAV2) no replicativo, que expresa la variante Padua (R338L) del factor de coagulación IX (F9, también conocido como Factor IX (FIX)), bajo el control del enhancer de la apolipoproteína E (Apo E) específica del hígado/promotor de la alfa1-antitripsina (hAAT) (ApoE/hAAT), y con todos los genes del AAV que codifican para productos del virus delecionados

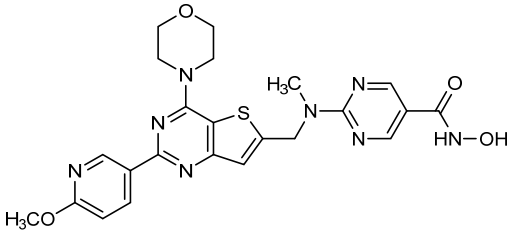
fimepinostatum

fimepinostat — *N*-hydroxy-2-[{[2-(6-methoxypyridin-3-yl)-4-(morpholin-4-yl)thieno[3,2-*d*]pyrimidin-6-yl]methyl}(methyl)amino]pyrimidine-5-carboxamide

fimépinostat — *N*-hydroxy-2-[{[2-(6-méthoxypyridin-3-yl)-4-(morpholin-4-yl)thiéno[3,2-*d*]pyrimidin-6-yl]méthyl}(méthyl)amino]pyrimidine-5-carboxamide

fimepinostat — *N*-hidroxi-2-[{[2-(6-metoxipiridin-3-il)-4-(morfolin-4-il)tieno[3,2-*d*]pirimidin-6-i]metil}(metil)amino]pirimidina-5-carboxamida

$C_{23}H_{24}N_8O_4S$



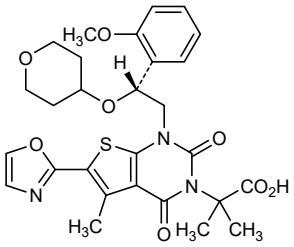
firsocostatum

firsocostat — 2-[1-{(2*R*)-2-(2-methoxyphenyl)-2-[(oxan-4-yl)oxy]ethyl}-5-methyl-6-(1,3-oxazol-2-yl)-2,4-dioxo-1,4-dihydrothieno[2,3-*d*]pyrimidin-3(2*H*)-yl]-2-methylpropanoic acid

firsocostat — acide 2-[1-{(2*R*)-2-(2-méthoxyphényl)-2-[(oxan-4-yl)oxy]éthyl}-5-méthyl-6-(1,3-oxazol-2-yl)-2,4-dioxo-1,4-dihydrothiéno[2,3-*d*]pyrimidin-3(2*H*)-yl]-2-méthylpropanoïque

firsocostat — ácido 2-[1-{(2*R*)-2-(2-metoxifenil)-2-[(oxan-4-il)oxi]etil}-5-metil-6-(1,3-oxazol-2-il)-2,4-dioxo-1,4-dihidrotieno[2,3-*d*]pirimidin-3(2*H*)-i]-2-metilpropanoico

$C_{28}H_{31}N_3O_8S$



flotetuzumabum #

flotetuzumab — immunoglobulin scFv_scFv, anti-[*Homo sapiens* IL3RA (interleukin 3 receptor subunit alpha, interleukin 3 receptor alpha (low affinity), CD123)] and anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)]; *Mus musculus* and humanized monoclonal antibody scFv_scFv, bispecific;

	scFv-lambda-heavy-E-coil (1-272) [V-LAMBDA anti-CD3E (*Mus musculus* IGLV1-01 (81.2%) -IGLJ1*01 (100%)/*Homo sapiens* IGLV7-46 (77.9%) -IGHJ3*02 (100%)) [9.3.9] (1-109) -9-mer tetraglycyl-seryl-tetraglycyl linker (110-118) -humanized VH anti-IL3RA (*Homo sapiens* IGHV1-46*01 (83.7%) -(IGHD) -IGHJ6*01 (90.9%)) [8.8.13] (119-238)-6-mer diglycyl-cysteinyl-triglycyl linker (239-244) -E-coil motif (245-272)], (241-249')-disulfide with scFv-kappa-heavy-K-coil (1'-280') [V-KAPPA anti-IL3RA (*Mus musculus* IGKV8-19*01 (91.1%) -IGKJ2*01 (91.7%)/*Homo sapiens* IGKV4-1*01 (88.1%) -IGKJ2*01 (100%)) [12.3.9] (1'-113') -8-mer triglycyl-seryl-tetraglycyl linker (114'-121') -VH anti-CD3E (*Mus musculus* IGHV10-1*02 (89.9%) -(IGHD) -IGHJ3*01 (93.9%)/*Homo sapiens* IGHV3-72*01 (87.0%) -(IGHD) -IGHJ6*01 (90.9%)) [8.10.16] (122'-246')] -6-mer diglycyl-cysteinyl-triglycyl linker (247'-252') -K-coil motif (253'-280')]
flotétuzumab	immunoglobuline scFv_scFv, anti-[*Homo sapiens* IL3RA (sous-unité alpha du récepteur de l'interleukine 3, récepteur alpha (faible affinité) de l'interleukine 3, CD123)] et anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)]; anticorps monoclonal scFv_scFv *Mus musculus* et humanisé, bispécifique; scFv-lambda-lourde-E-coil (1-272) [V-LAMBDA anti-CD3E (*Mus musculus* IGLV1-01 (81.2%) -IGLJ1*01 (100%)/*Homo sapiens* IGLV7-46 (77.9%) -IGHJ3*02 (100%)) [9.3.9] (1-109) -9-mer tétraglycyl-séryl-tétraglycyl linker (110-118) -VH anti-IL3RA humanisé (*Homo sapiens* IGHV1-46*01 (83.7%) -(IGHD) -IGHJ6*01 (90.9%)) [8.8.13] (119-238)-6-mer diglycyl-cystéinyl-triglycyl linker (239-243) -motif E-coil (245-272)], (241-249')-disulfure avec scFv-kappa-lourde-K-coil (1'-280') [V-KAPPA anti-IL3RA (*Mus musculus* IGKV8-19*01 (91.1%) -IGKJ2*01 (91.7%)/*Homo sapiens* IGKV4-1*01 (88.1%) -IGKJ2*01 (100%)) [12.3.9] (1'-113') -8-mer triglycyl-séryl-tétraglycyl linker (114'-121') -VH anti-CD3E (*Mus musculus* IGHV10-1*02 (89.9%) -(IGHD) -IGHJ3*01 (93.9%)/*Homo sapiens* IGHV3-72*01 (87.0%) -(IGHD) -IGHJ6*01 (90.9%)) [8.10.16] (122'-246')] -6-mer diglycyl-cystéinyl-triglycyl linker (247'-252')-motif K-coil (253'-280')]
flotetuzumab	inmunoglobulina scFv_scFv, anti-[*Homo sapiens* IL3RA (subunidad alfa del receptor de la interleukina 3, receptor alfa (baja afinidad) de la interleukina 3, CD123)]yt anti-[*Homo sapiens* CD3E (CD3 épsilon, Leu-4)]; *Mus musculus* y anticuerpo monoclonal humanizado scFv_scFv, biespecífico; scFv-lambda-pesada-E-coil (1-272) [V-LAMBDA anti-CD3E (*Mus musculus* IGLV1-01 (81.2%) -IGLJ1*01 (100%)/*Homo sapiens* IGLV7-46 (77.9%) -IGHJ3*02 (100%)) [9.3.9] (1-109) -9-mer tetraglicil-seril-tetraglicil ligando (110-118) -VH anti-IL3RA humanizado (*Homo sapiens* IGHV1-46*01 (83.7%) -(IGHD) -IGHJ6*01 (90.9%)) [8.8.13] (119-238)-6-mer diglicil-cisteinil-triglicil ligando (239-243) -motif E-coil (245-272)], (241-249')-disulfuro con scFv-kappa-pesada-K-coil (1'-280') [V-KAPPA anti-IL3RA (*Mus musculus* IGKV8-19*01 (91.1%) -IGKJ2*01 (91.7%)/*Homo sapiens* IGKV4-1*01 (88.1%) -IGKJ2*01 (100%)) [12.3.9] (1'-113') -8-mer triglicil-seril-tetraglicil ligando (114'-121') -VH anti-CD3E (*Mus musculus* IGHV10-1*02 (89.9%) -(IGHD) -IGHJ3*01 (93.9%)/*Homo sapiens* IGHV3-72*01 (87.0%) -(IGHD) -IGHJ6*01 (90.9%)) [8.10.16] (122'-246')] -6-mer diglicil-cisteinil-triglicil ligando (247'-252') -motif K-coil (253'-280')]

scFv-lambda-heavy-E-coil

```
QAVVTQEPSL TVSPGGTVTL TCRSSTGAVT TSNYANWVQQ KPGQAPRGLI  50
GGTNKRAPWT PARFSGSLLG GKAALTITGA QAEDEADYYC ALWYSNLWVF 100
GGGTKLTVLG GGGSGGGGEV QLVQSGAELK KPGASVKVSC KASGYTFTDY 150
YMKWVRQAPG QGLEWIGDII PSNGATFYNQ KFKGRVTITV DKSTSTAYME 200
LSSLRSEDTA VYYCARSHLL RASWFAYWGQ GTLVTVSSGG CGGGEVAALE 250
KEVAALEKEV AALEKEVAAL EK                              272
```

scFv-kappa-heavy-K-coil

```
DFVMTQSPDS LAVSLGERVT MSCKSSQSLL NSGNQKNYLT WYQQKPGQPP  50
KLLIYWASTR ESGVPDRFSG SGSGTDFTLT ISSLQAEDVA VYYCQNDYSY 100
PYTFGQGTKL EIKGGGSGGG GEVQLVESGG GLVQPGGSLR LSCAASGFTF 150
STYAMNWVRQ APGKGLEWVG RIRSKYNNYA TYYADSVKDR FTISRDDSKN 200
SLYLQMNSLK TEDTAVYYCV RHGNFGNSYV SWFAYWGQGT LVTVSSGGCG 250
GGKVAALKEK VAALKEKVAA LKEKVAALKE                      280
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-scFv (C23-C104) 22-90 140-214
23'-94' 143'-219'
Inter-chain (h 11, h 14) 241-249'

No N-glycosylation sites / pas de sites de N-glycosylation / ningún positión de N-glicosilación
N-terminal glutamine cyclization to Glp (5-oxoproline, pyroglutamic acid):
Q1>Glp (1)

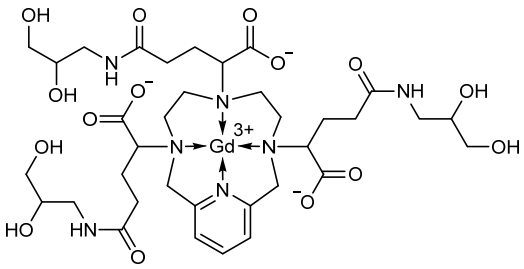
gadopiclenolum

gadopiclenol — *rac*-[(2*R*,2'Ξ,2''Ξ)-2,2',2''-(3,6,9-triaza-κ^3*N*^{3},*N*^{6},*N*^{9}-1(2,6)-pyridina-κ*N*^{1}-cyclodecaphane-3,6,9-triyl)tris(5-{[(2Ξ)-2,3-dihydroxypropyl]amino}-5-oxopentanoato-κ^3*O*^{1},*O*$^{1'}$,*O*$^{1''}$)(3−)]gadolinium

gadopiclénol — *rac*-[(2*R*,2'Ξ,2''Ξ)-2,2',2''-(3,6,9-triaza-κ^3*N*^{3},*N*^{6},*N*^{9}-1(2,6)-pyridina-κ*N*^{1}-cyclodécaphane-3,6,9-triyl)tris(5-{[(2Ξ)-2,3-dihydroxypropyl]amino}-5-oxopentanoato-κ^3*O*^{1},*O*$^{1'}$,*O*$^{1''}$)(3−)]gadolinium

gadopiclenol — *rac*-[(2*R*,2'Ξ,2''Ξ)-2,2',2''-(3,6,9-triaza-κ^3*N*^{3},*N*^{6},*N*^{9}-1(2,6)-piridina-κ*N*^{1}-ciclodecafano-3,6,9-triil)tris(5-{[(2Ξ)-2,3-dihidroxipropi]amino}-5-oxopentanoato-κ^3*O*^{1},*O*$^{1'}$,*O*$^{1''}$)(3−)]gadolinio

$C_{35}H_{54}GdN_7O_{15}$



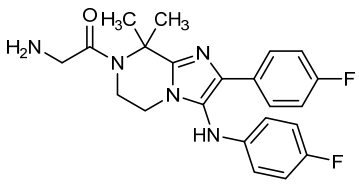
ganaplacidum

ganaplacide — 2-amino-1-[3-(4-fluoroanilino)-2-(4-fluorophenyl)-8,8-dimethyl-5,6-dihydroimidazo[1,2-*a*]pyrazin-7(8*H*)-yl]ethan-1-one

ganaplacide — 2-amino-1-[3-(4-fluoroanilino)-2-(4-fluorophényl)-8,8-diméthyl-5,6-dihydroimidazo[1,2-*a*]pyrazin-7(8*H*)-yl]éthan-1-one

ganaplacida — 2-amino-1-[3-(4-fluoroanilino)-2-(4-fluorofenil)-8,8-dimetil-5,6-dihidroimidazo[1,2-*a*]pirazin-7(8*H*)-i]etan-1-ona

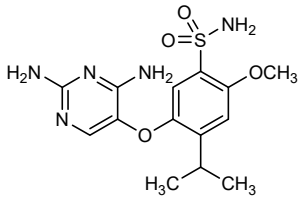
$C_{22}H_{23}F_2N_5O$



gefapixantum

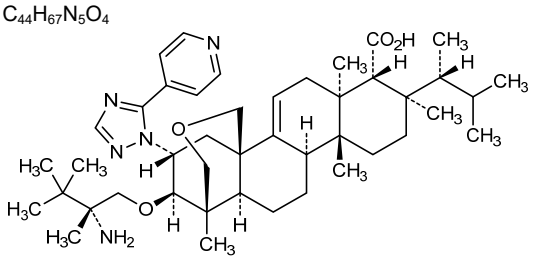
gefapixant	5-[(2,4-diaminopyrimidin-5-yl)oxy]-2-methoxy-4-(propan-2-yl)benzene-1-sulfonamide
géfapixant	5-[(2,4-diaminopyrimidin-5-yl)oxy]-2-méthoxy-4-(propan-2-yl)benzène-1-sulfonamide
gefapixant	5-[(2,4-diaminopirimidin-5-il)oxi]-2-metoxi-4-(propan-2-il)benceno-1-sulfonamida

$C_{14}H_{19}N_5O_4S$



ibrexafungerpum

ibrexafungerp	(1*S*,4a*R*,6a*S*,7*R*,8*R*,10a*R*,10b*R*,12a*R*,14*R*,15*R*)-15-[(2*R*)-2-amino-2,3,3-trimethylbutoxy]-1,6a,8,10a-tetrameth-yl-8-[(2*R*)-3-methylbutan-2-yl]-14-[5-(pyridin-4-yl)-1*H*-1,2,4-triazol-1-yl]-1,6,6a,7,8,9,10,10a,10b,11,12,12a-dodecahydro-2*H*,4*H*-1,4a-propanophenanthro[1,2-*c*]pyran-7-carboxylic acid
ibrexafungerp	acide (1*S*,4a*R*,6a*S*,7*R*,8*R*,10a*R*,10b*R*,12a*R*,14*R*,15*R*)-15-[(2*R*)-2-amino-2,3,3-triméthylbutoxy]-1,6a,8,10a-tétraméth-yl-8-[(2*R*)-3-méthylbutan-2-yl]-14-[5-(pyridin-4-yl)-1*H*-1,2,4-triazol-1-yl]-1,6,6a,7,8,9,10,10a,10b,11,12,12a-dodécahydro-2*H*,4*H*-1,4a-propanophénanthro[1,2-*c*]pyran-7-carboxylique
ibrexafungerp	ácido (1*S*,4a*R*,6a*S*,7*R*,8*R*,10a*R*,10b*R*,12a*R*,14*R*,15*R*)-15-[(2*R*)-2-amino-2,3,3-trimetilbutoxi]-1,6a,8,10a-tetramet-il-8-[(2*R*)-3-meti butan-2-il]-14-[5-(piridin-4-il)-1*H*-1,2,4-triazol-1-il]-1,6,6a,7,8,9,10,10a,10b,11,12,12a-dodecahidro-2*H*,4*H*-1,4a-propanofenantro[1,2-*c*]piran-7-carboxílico



imaprelimabum #

imaprelimab	immunoglobulin G1-kappa, anti-[*Homo sapiens* MCAM (melanoma cell adhesion molecule, gicerin, MUC18, CD146)], humanized monoclonal antibody; gamma1 heavy chain (1-448) [humanized VH (*Homo sapiens* IGHV2-26*01 (82.0%) -(IGHD)-IGHJ4*01 (93.3%)) [8.7.12] (1-118) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (215) (119-216), hinge (217-231), CH2 L1.3>A (235), L1.2>A (236) (232-341), CH3 E12 (357), M14 (359) (342-446), CHS (447-448)) (119-448)], (221-213')-disulfide with kappa light chain (1'-213') [humanized V-KAPPA (*Homo sapiens* IGKV1-12*01 (85.6%) -IGKJ2*01 (100%)) [6.3.8] (1'-106') -*Homo sapiens* IGKC*01, Km3 A45.1 (152), V101 (190) (107'-213')]; dimer (227-227":230-230")-bisdisulfide
imaprélimab	immunoglobuline G1-kappa, anti-[*Homo sapiens* MCAM (molécule d'adhésion de cellule de mélanome, gicérine, MUC18, CD146)], anticorps monoclonal humanisé; chaîne lourde gamma1 (1-448) [VH humanisé (*Homo sapiens* IGHV2-26*01 (82.0%) -(IGHD)-IGHJ4*01 (93.3%)) [8.7.12] (1-118) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (215) (119-216), charnière (217-231), CH2 L1.3>A (235), L1.2>A (236)(232-341), CH3 E12 (357), M14 (359) (342-446), CHS (447-448)) (119-448)], (221-213')-disulfure avec la chaîne légère kappa (1'-213') [V-KAPPA humanisé (*Homo sapiens* IGKV1-12*01 (85.6%) -IGKJ2*01 (100%)) [6.3.8] (1'-106') -*Homo sapiens* IGKC*01, Km3 A45.1 (152), V101 (190) (107'-213')]; dimère (227-227":230-230")-bisdisulfure
imaprelimab	inmunoglobulina G1-kappa, anti-[*Homo sapiens* MCAM (molécula de adhesión de célula de melanoma, gicerina, MUC18, CD146)], anticuerpo monoclonal humanizado; cadena pesada gamma1 (1-448) [VH humanizado (*Homo sapiens* IGHV2-26*01 (82.0%) -(IGHD)-IGHJ4*01 (93.3%)) [8.7.12] (1-118) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (215) (119-216), bisagra (217-231), CH2 L1.3>A (235), L1.2>A (236) (232-341), CH3 E12 (357), M14 (359) (342-446), CHS (447-448)) (119-448)], (221-213')-disulfuro con la cadena ligera kappa (1'-213') [V-KAPPA humanizado (*Homo sapiens* IGKV1-12*01 (85.6%) -IGKJ2*01 (100%)) [6.3.8] (1'-106') -*Homo sapiens* IGKC*01, Km3 A45.1 (152), V101 (190) (107'-213')]; dímero (227-227":230-230")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVTLKESGPV LVKPTETLTL TCTVSGFSLT SNAVSWVRQP PGKALEWIAA  50
ISSGGTTYYN SAFKSRLTIS RDTSKSQVVL TMTNMDPVDT ATYYCARRYG 100
YGWYFDFWGQ GTLVTVSSAS TKGPSVFPLA PSSKSTSGGT AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTQTYI 200
CNVNHKPSNT KVDKRVEPKS CDKTHTCPPC PAPEAAGGPS VFLFPPKPKD 250
TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNST 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY 350
TLPPSREEMT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD 400
SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPGK   448
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT INCKASQNIY NSLAWYQQKP GKAPKVLIFN  50
ANSLQTGIPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ FYSGYTFGQG 100
TKLEIKRTVA APSVFIFPPS DEQLKSGTAS VVCLLNNFYP REAKVQWKVD 150
NALQSGNSQE SVTEQDSKDS TYSLSSTLTL SKADYEKHKV YACEVTHQGL 200
SSPVTKSFNR GEC                                         213
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-95 145-201 262-322 368-426
22"-95" 145"-201" 262"-322" 368"-426"
Intra-L (C23-C104) 23'-88' 133'-193'
23'"-88'" 133'"-193'"
Inter-H-L (h 5-CL 126) 221-213' 221"-213'"
Inter-H-H (h 11, h 14) 227-227" 230-230"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
298, 298"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

iscalimabum #

iscalimab	immunoglobulin G1-kappa, anti-[*Homo sapiens* CD40 (tumor necrosis factor receptor superfamily member 5, TNFRSF5)], human monoclonal antibody; gamma1 heavy chain (1-450) [*Homo sapiens* VH (IGHV3-30*03 (93.9%) -(IGHD) -IGHJ4*01 (100%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (217) (121-218), hinge (219-233), CH2 N84.4>A (300) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-219')-disulfide with kappa light chain (1'-219') [*Homo sapiens* V-KAPPA (IGKV2-28*01 (95.0%) -IGKJ3*01 (91.7%, K12>R)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dimer (229-229":232-232")-bisdisulfide
iscalimab	immunoglobuline G1-kappa, anti-[*Homo sapiens* CD40 (membre 5 de la superfamille des récepteurs du TNF, TNFRSF5)], anticorps monoclonal humain; chaîne lourde gamma1 (1-450) [*Homo sapiens* VH (IGHV3-30*03 (93.9%) -(IGHD) -IGHJ4*01 (100%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*03 (CH1 (121-218), charnière (219-233), CH2 N84.4>A (300) (234-343), CH3 (344-448), CHS (449-450)) (121-450)], (223-219')-disulfure avec la chaîne légère kappa (1'-219') [*Homo sapiens* V-KAPPA (IGKV2-28*01 (95.0%) -IGKJ3*01 (91.7%, K12>R) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dimère (229-229":232-232")-bisdisulfure

iscalimab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CD40 (miembro 5 de la superfamilia de los receptores del TNF, TNFRSF5)], anticuerpo monoclonal humano;
cadena pesada gamma1 (1-450) [*Homo sapiens* VH (IGHV3-30*03 (93.9%) -(IGHD) -IGHJ4*01 (100%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*03 (CH1 (121-218), bisagra (219-233), CH2 N84.4>A (300) (234-343), CH3 (344-448), CHS (449-450)) (121-450)], (223-219')-disulfuro con la cadena ligera kappa (1'-219') [*Homo sapiens* V-KAPPA (IGKV2-28*01 (95.0%) -IGKJ3*01 (91.7%, K12>R) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dímero (229-229":232-232")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVESGGG VVQPGRSLRL SCAASGFTFS SYGMHWVRQA PGKGLEWVAV  50
ISYEESNRYH ADSVKGRFTI SRDNSKITLY LQMNSLRTED TAVYYCARDG 100
GIAAPGPDYW GQGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKRVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYA 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK 450
```

Light chain / Chaîne légère / Cadena ligera

```
DIVMTQSPLS LTVTPGEPAS ISCRSSQSLL YSNGYNYLDW YLQKPGQSPQ  50
VLISLGSNRA SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCMQARQTP 100
FTFGPGTKVD IRRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK 150
VQWKVDNALQ SGNSQESVTE QDSKDSTYSL SSTLTLSKAD YEKHKVYACE 200
VTHQGLSSPV TKSFNRGEC                                   219
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

```
Intra-H (C23-C104)  22-96     147-203    264-324    370-428
                    22"-96"   147"-203"  264"-324"  370"-428"
Intra-L (C23-C104)  23'-93'    139'-199'
                    23'"-93'"  139'"-199'"
Inter-H-L (h 5-CL 126)  223-219'  223"-219'"
Inter-H-H (h 11, h 14)  229-229"  232-232'
```

No N-glycosylation sites / pas de sites de N-glycosylation / ningún positión de N-glicosilación:
H CH2 N84 4>A (300, 300")

N-terminal glutamine cyclization to Glp (5-oxoproline, pyroglutamic acid):
H VH Q1>Glp (1, 1")

C-terminal lysine clipping:
H CHS K2: 450, 450"

lanraplenibum

lanraplenib

6-(6-aminopyrazin-2-yl)-*N*-{4-[4-(oxetan-3-yl)piperazin-1-yl]phenyl}imidazo[1,2-*a*]pyrazin-8-amine

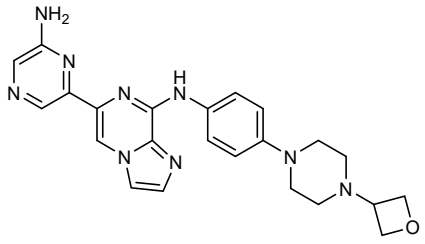
lanraplénib

6-(6-aminopyrazin-2-yl)-*N*-{4-[4-(oxétan-3-yl)pipérazin-1-yl]phényl}imidazo[1,2-*a*]pyrazin-8-amine

lanraplenib

6-(6-aminopirazin-2-il)-*N*-{4-[4-(oxetan-3-il)piperazin-1-il]fenil}imidazo[1,2-*a*]pirazin-8-amina

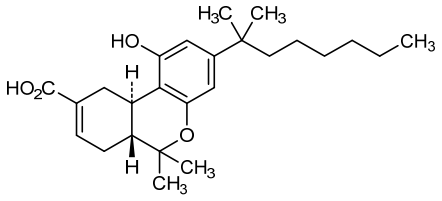
$C_{23}H_{25}N_9$



lenabasumum

lenabasum	(6a*R*,10a*R*)-1-hydroxy-6,6-dimethyl-3-(2-methyloctan-2-yl)-6a,7,10,10a-tetrahydro-6*H*-dibenzo[*b*,*d*]pyran-9-carboxylic acid
lénabasum	acide (6a*R*,10a*R*)-1-hydroxy-6,6-diméthyl-3-(2-méthyloctan-2-yl)-6a,7,10,10a-tétrahydro-6*H*-dibenzo[*b*,*d*]pyran-9-carboxylique
lenabasum	ácido (6a*R*,10a*R*)-1-hidroxi-6,6-dimetil-3-(2-metiloctan-2-il)-6a,7,10,10a-tetrahidro-6*H*-dibenzo[*b*,*d*]piran-9-carboxílico

$C_{25}H_{36}O_4$



lenvervimabum #

lenvervimab	immunoglobulin G1-kappa, anti-[Hepatitis B virus (HBV) surface antigen (HBsAg)], humanized monoclonal antibody; gamma1 heavy chain (1-459) [humanized VH (*Homo sapiens* IGHV3-21*01 (83.7%) -(IGHD) -IGHJ1*01 (90%), L12>T (124)) [8.8.22] (1-129) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (226) (130-227), hinge (228-242), CH2 (243-352), CH3 D12 (368), L14 (370) (353-457), CHS (458-459)) (130-459)], (232-214')-disulfide with kappa light chain (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-NL1*01 (87.4%) -IGKJ2*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (238-238":241-241")-bisdisulfide
lenvervimab	immunoglobuline G1-kappa, anti-[antigène de surface du virus de l'hépatite B (VHB) (AgsHB)], anticorps monoclonal humanisé; chaîne lourde gamma1 (1-459) [VH humanisé (*Homo sapiens* IGHV3-21*01 (83.7%) -(IGHD) -IGHJ1*01 (90%), L12>T (124)) [8.8.22] (1-129) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (226) (130-227), charnière (228-242), CH2 (243-352), CH3 D12 (368), L14 (370) (353-457), CHS (458-459)) (130-459)], (232-214')-disulfure avec la chaîne légère kappa (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-NL1*01 (87.4%) -IGKJ2*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (238-238":241-241")-bisdisulfure

lenvervimab

inmunoglobulina G1-kappa, anti-[antígeno de superficie del virus de la hepatitis B (VHB) (AgsHB)], anticuerpo monoclonal humanizado;
cadena pesada gamma1 (1-459) [VH humanizado (*Homo sapiens* IGHV3-21*01 (83.7%) -(IGHD) -IGHJ1*01 (90%), L12>T (124)) [8.8.22] (1-129) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (226) (130-227), bisagra (228-242), CH2 (243-352), CH3 D12 (368), L14 (370) (353-457), CHS (458-459)) (130-459)], (232-214')-disulfuro con la cadena ligera kappa (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-NL1*01 (87.4%) -IGKJ2*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (238-238":241-241")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVKPGGSLRL SCSASGFSLT KYKMTWVRQA PGKGLEWVSS  50
ISSTSRDIDY ADSVKGRFTI SRDNAKNSLF LQMSSLRVDD TAVYYCTRDG 100
WLWGWDVRSN YYYNALDVWG QGTTVTVSSA STKGPSVFPL APSSKSTSGG 150
TAALGCLVKD YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV 200
PSSSLGTQTY ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP CPAPELLGGP 250
SVFLFPPKPK DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK 300
TKPREEQYNS TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK 350
AKGQPREPQV YTLPPSRDEL TKNQVSLTCL VKGFYPSDIA VEWESNGQPE 400
NNYKTTPPVL DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ 450
KSLSLSPGK                                              459
```

Light chain / Chaîne légère / Cadena ligera

```
DIVVTQSPSS LSASVGDRVT ITCRASQGIY NSIAWYQQKP GKAPKLLLYS  50
TSTLLSGVPS RFSGSGSGTD YTLTITNLQP EDFATYYCQQ YFVTPETFGQ 100
GTKLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

Intra-H (C23-C104)	22-96	156-212	273-333	379-437
	22"-96"	156"-212"	273"-333"	379"-437"
Intra-L (C23-C104)	23'-88'	134'-194'		
	23'"-88'"	134'"-194'"		
Inter-H-L (h 5-CL 126)	232-214'	232"-214'"		
Inter-H-H (h 11, h 14)	238-238"	241-241"		

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84 4:
309, 309"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

leronlimabum #
leronlimab

immunoglobulin G4-kappa, anti-[*Homo sapiens* CCR5 (chemokine (C-C motif) receptor 5, CD195)], humanized monoclonal antibody;
gamma4 heavy chain (1-449) [humanized VH (*Homo sapiens* IGHV3-15*01 (72.40%) -(IGHD)-IGHJ4*01 (86.7%)) [7.8.16] (1-122) -*Homo sapiens* IGHG4*01 (CH1 (123-220), hinge (221-232), CH2 (233-342), CH3 (343-447), CHS (448-449)) (123-449)], (136-219')-disulfide with kappa light chain (1'-219') [humanized V-KAPPA (*Homo sapiens* IGKV2D-29*02 (87.0%) -IGKJ1*01 (100%)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dimer (228-228":231-231")-bisdisulfide

léronlimab

immunoglobuline G4-kappa, anti-[*Homo sapiens* CCR5 (récepteur 5 de la chimiokine (motif C-C), CD195)], anticorps monoclonal humanisé;

chaîne lourde gamma4 (1-449) [VH humanisé (*Homo sapiens* IGHV3-15*01 (72.40%) -(IGHD)- IGHJ4*01 (86.7%)) [7.8.16] (1-122) -*Homo sapiens* IGHG4*01 (CH1 (123-220), charnière (221-232), CH2 (233-342), CH3 (343-447), CHS (448-449)) (123-449)], (136-219')-disulfure avec la chaîne légère kappa (1'-219') [V-KAPPA humanisé (*Homo sapiens* IGKV2D-29*02 (87.0%) -IGKJ1*01 (100%)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dimère (228-228":231-231")-bisdisulfure

leronlimab

inmunoglobulina G4-kappa, anti-[*Homo sapiens* CCR5 (receptor 5 de la quimiocina (motif C-C), CD195)], anticuerpo monoclonal humanizado;
cadena pesada gamma4 (1-449) [VH humanizado (*Homo sapiens* IGHV3-15*01 (72.40%) -(IGHD)- IGHJ4*01 (86.7%)) [7.8.16] (1-122) -*Homo sapiens* IGHG4*01 (CH1 (123-220), bisagra (221-232), CH2 (233-342), CH3 (343-447), CHS (448-449)) (123-449)], (136-219')-disulfuro con la cadena ligera kappa (1'-219') [V-KAPPA humanizado (*Homo sapiens* IGKV2D-29*02 (87.0%) -IGKJ1*01 (100%)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dímero (228-228":231-231")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVKPGGSLRL SCAASGYTFS NYWIGWVRQA PGKGLEWIGD  50
IYPGGNYIRN NEKFKDKTTL SADTSKNTAY LQMNSLKTED TAVYYCGSSF 100
GSNYVFAWFT YWGQGTLVTV SSASTKGPSV FPLAPCSRST SESTAALGCL 150
VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ SSGLYSLSSV VTVPSSSLGT 200
KTYTCNVDHK PSNTKVDKRV ESKYGPPCPS CPAPEFLGGP SVFLFPPKPK 250
DTLMISRTPE VTCVVVDVSQ EDPEVQFNWY VDGVEVHNAK TKPREEQFNS 300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKGL PSSIEKTISK AKGQPREPQV 350
YTLPPSQEEM TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL 400
DSDGSFFLYS RLTVDKSRWQ EGNVFSCSVM HEALHNHYTQ KSLSLSLGK  449
```

Light chain / Chaîne légère / Cadena ligera

```
DIVMTQSPLS LPVTPGEPAS ISCRSSQRLL SSYGHTYLHW YLQKPGQSPQ  50
LLIYEVSNRF SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCSQSTHVP 100
LTFGQGTKVE IKRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK 150
VQWKVDNALQ SGNSQESVTE QDSKDSTYSL SSTLTLSKAD YEKHKVYACE 200
VTHQGLSSPV TKSFNRGEC                                   219
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

Intra-H (C23-C104)	22-96	149-205	263-323	369-427
	22"-96"	149"-205"	263"-323"	369"-427"
Intra-L (C23-C104)	23'-93'	139'-199'		
	23'"-93'"	139'"-199'"		
Inter-H-L (CH1 10-CL 126)	136-219'	136"-219'"		
Inter-H-H (h 8, h 11)	228-228'	231-231"		

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84 4:
299, 299"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

licogliflozinum

licogliflozin

(1*S*)-1,5-anhydro-1-*C*-{3-[(2,3-dihydro-1,4-benzodioxin-6-yl)methyl]-4-ethylphenyl}-D-glucitol

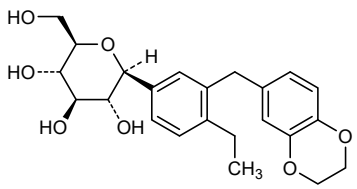
licogliflozine

(1*S*)-1,5-anhydro-1-*C*-{3-[(2,3-dihydro-1,4-benzodioxin-6-yl)méthyl]-4-éthylphényl}-D-glucitol

licogliflozina

(1*S*)-1,5-anhidro-1-*C*-{3-[(2,3-dihidro-1,4-benzodioxin-6-il)metil]-4-etilfenil}-D-glucitol

$C_{23}H_{28}O_7$



lifileucelum

lifileucel — human culture expanded activated autologous T cells for cell-based immunotherapy. The cell substance is a heterogeneous mixture consisting of CD4+ and CD8+ tumor-infiltrating lymphocytes (TIL), derived from isolated metastatic tumor biopsy of patients with metastatic melanoma, and cultured in the presence of feeder cells (irradiated allogeneic mononuclear cells from healthy donors) and human recombinant interleukin 2 (IL-2)/OKT3 anti-CD3 antibody (*muromonab-CD3 (59)(29)*) for T-cell activation.

lifileucel — lymphocytes T humains autologues, activés en culture d'expansion pour immunothérapie cellulaire. Les cellules sont un mélange hétérogène consistant en des lymphocytes T CD4+ et CD8+ infiltrant la tumeur (TIL), dérivés d'une biopsie isolée de la tumeur métastatique de patients avec un mélanome métastatique et mis en culture en présence de cellules nourricières (cellules mononucléaires allogéniques irradiées obtenues à partir de donneurs sains) et d'interleukine 2 (IL2) recombinante humaine/ anticorps OKT3 anti-CD3 (*muromonab-CD3 (59)(29)*) pour l'activation des lymphocytes T.

lifileucel — linfocitos T humanos autólogos activados y expandidos en cultivo para inmunoterapia celular. La substancia celular es una mezcla heterogénea consistente en linfocitos CD4+ y CD8+ infiltrantes de tumor, derivados de una biopsia aislada de tumor metastásico de pacientes con melanoma metastásico, y cultivados en presencia de células *feeder* (células mononucleares alogénicas irradiadas obtenidas de donantes sanos) e interleukina 2 recombinante humana (IL-2)/anticuerpo OKT3 anti-CD3 (*muromonab-CD3 (59)(29)*) para activación de linfocitos T.

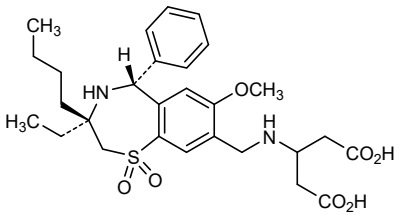
linerixibatum

linerixibat — 3-({[(3*R*,5*R*)-3-butyl-3-ethyl-7-methoxy-1,1-dioxo-5-phenyl-2,3,4,5-tetrahydro-1*H*-1λ^6,4-benzothiazepin-8-yl]methyl}amino)pentanedioic acid

linérixibat — acide 3-({[(3*R*,5*R*)-3-butyl-3-éthyl-7-méthoxy-1,1-dioxo-5-phényl-2,3,4,5-tétrahydro-1*H*-1λ^6,4-benzothiazépin-8-yl]méthyl}amino)pentanedioïque

linerixibat — ácido 3-({[(3*R*,5*R*)-3-butil-3-etil-7-metoxi-1,1-dioxo-5-fenil-2,3,4,5-tetrahidro-1*H*-1λ^6,4-benzotiazepin-8-il]metil}amino)pentanodioico

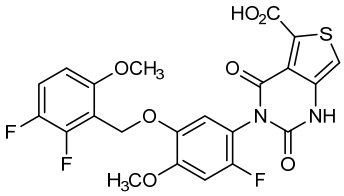
$C_{28}H_{38}N_2O_7S$



linzagolixum

linzagolix	3-{5-[(2,3-difluoro-6-methoxyphenyl)methoxy]-2-fluoro-4-methoxyphenyl}-2,4-dioxo-1,2,3,4-tetrahydrothieno[3,4-*d*]pyrimidine-5-carboxylic acid
linzagolix	acide 3-{5-[(2,3-difluoro-6-méthoxyphényl)méthoxy]-2-fluoro-4-méthoxyphényl}-2,4-dioxo-1,2,3,4-tétrahydrothiéno[3,4-*d*]pyrimidine-5-carboxylique
linzagolix	ácido 3-{5-[(2,3-difluoro-6-metoxifenil)metox]-2-fluoro-4-metoxifenil}-2,4-dioxo-1,2,3,4-tetrahidrotieno[3,4-*d*]pirimidina-5-carboxílico

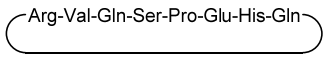
$C_{22}H_{15}F_3N_2O_7S$



livoletidum

livoletide	1,8-anhydro(L-arginyl-L-valyl-L-glutaminyl-L-seryl-L-prolyl-L-α-glutamyl-L-histidyl-L-glutaminyl)
livolétide	1,8-anhydro(L-arginyl-L-valyl-L-glutaminyl-L-séryl-L-prolyl-L-α-glutamyl-L-histidyl-L-glutaminyl)
livoletida	1,8-anhidro(L-arginil-L-valil-L-glutaminil-L-seril-L-prolil-L-α-glutamil-L-histidil-L-glutaminil)

$C_{40}H_{63}N_{15}O_{13}$

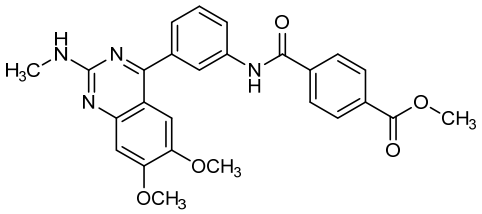


lotamilastum

lotamilast	methyl 4-({3-[6,7-dimethoxy-2-(methylamino)quinazolin-4-yl]phenyl}carbamoyl)benzoate
lotamilast	4-({3-[6,7-diméthoxy-2-(méthylamino)quinazolin-4-yl]phényl}carbamoyl)benzoate de méthyle

lotamilast	4-({3-[6,7-dimetoxi-2-(metilamino)quinazolin-4-il]fenil}carbamoil)benzoato de metilo

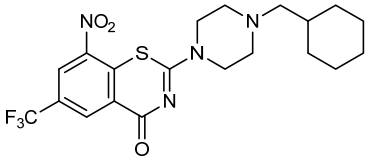
$C_{26}H_{24}N_4O_5$



macozinonum

macozinone	2-[4-(cyclohexylmethyl)piperazin-1-yl]-8-nitro-6-(trifluoromethyl)-4*H*-1,3-benzothiazin-4-one
macozinone	2-[4-(cyclohexylméthyl)pipérazin-1-yl]-8-nitro-6-(trifluorométhyl)-4*H*-1,3-benzothiazin-4-one
macozinona	2-[4-(ciclohexilmetil)piperazin-1-il]-8-nitro-6-(trifluorometil)-4*H*-1,3-benzotiazin-4-ona

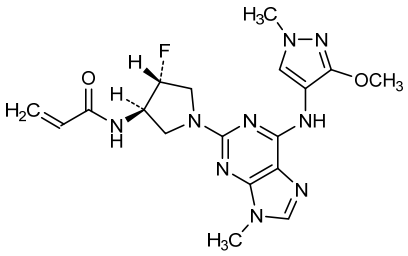
$C_{20}H_{23}F_3N_4O_3S$



mavelertinibum

mavelertinib	*N*-[(3*R*,4*R*)-4-fluoro-1-{6-[(3-methoxy-1-methyl-1*H*-pyrazol-4-yl)amino]-9-methyl-9*H*-purin-2-yl}pyrrolidin-3-y]prop-2-enamide
mavélertinib	*N*-[(3*R*,4*R*)-4-fluoro-1-{6-[(3-méthoxy-1-méthyl-1*H*-pyrazol-4-yl)amino]-9-méthyl-9*H*-purin-2-yl}pyrrolidin-3-y]prop-2-énamide
mavelertinib	*N*-[(3*R*,4*R*)-4-fluoro-1-{6-[(3-metoxi-1-metil-1*H*-pirazol-4-il)amino]-9-metil-9*H*-purin-2-il}pirrolidin-3-il]prop-2-enamida

$C_{18}H_{22}FN_9O_2$



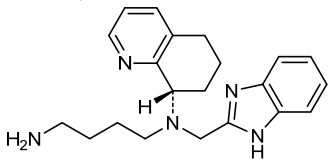
mavilimogenum ralaplasmidum #

mavilimogene ralaplasmid	a DNA plasmid encoding genes for human papilloma virus type 16 (HPV-16) E6 and E7 proteins whose expression is driven by the human cytomegalovirus (hCMV) promoter with the bovine growth hormone (bGH) 3'end gene and bGH gene polyA signal.
mavilimogène ralaplasmide	ADN plasmidique contenant les gènes codant pour les protéines E6 et E7 du virus du papillome humain de type 16 (HPV-16), dont l'expression est dirigée par le promoteur du cytomégalovirus humain (hCMV) avec la région 3'-terminale du gène de l'hormone de croissance bovine (bGH) et le signal poly-A du gène de la bGH
mavilimogén ralaplásmido	un DNA plasmídico que contiene genes que codifican para las proteínas E6 y E7 del virus del papiloma humano tipo 16 (HPV-16), cuya expresión está dirigida por el promotor del citomegalovirus humano (hCMV) con la región 3' terminal del gen de la hormona de crecimiento bovina (bGH) y la señal poli A del gen de bGH

mavorixaforum

mavorixafor	N^1-[(1*H*-benzimidazol-2-yl)methy]-N^1-[(8*S*)-5,6,7,8-tetrahydroquinolin-8-yl]butane-1,4-diamine
mavorixafor	N^1-[(1*H*-benzimidazol-2-yl)méthy]-N^1-[(8*S*)-5,6,7,8-tétrahydroquinoléin-8-y]butane-1,4-diamine
mavorixafor	N^1-[(1*H*-benzimidazol-2-il)metil]-N^1-[(8*S*)-5,6,7,8-tetrahidroquinolein-8-il]butano-1,4-diamina

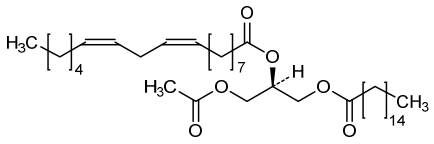
$C_{21}H_{27}N_5$



mosedipimodum

mosedipimod	*rac*-(2*R*)-propane-1,2,3-triyl 1-acetate 3-hexadecanoate 2-[(9*Z*,12*Z*)-octadeca-9,12-dienoate]
mosédipimod	1-acétate, 3-hexadécanoate et 2-[(9*Z*,12*Z*)-octadéca-9,12-diénoate]de *rac*-(2*R*)-propane-1,2,3-triyle
mosedipimod	1-acetato, 3-hexadecanoato y 2-[(9*Z*,12*Z*)-octadeca-9,12-dienoato]de *rac*-(2*R*)-propano-1,2,3-triilo

$C_{39}H_{70}O_6$



and enantiomer
et énantiomère
y enantiómero

nalotimagenum carmaleucelum #

nalotimagene carmaleucel	human culture expanded activated allogeneic T cells for adjunctive immunotherapy. Cells are derived from the haematopoietic stem cell (HSC) donor and are genetically modified *ex vivo* with a non-replicative SFCMM-3 gamma-retroviral vector derived from Moloney murine Leukemia Virus (Mo-MuLV), encoding for a truncated form of the human low affinity nerve growth factor receptor (ΔLNGFR) and the herpes simplex virus thymidine kinase (HSV-TK Mut2). Cells contain a suicide gene in case of graft versus host disease development.
nalotimagène carmaleucel	lymphocytes T humains allogéniques, activés, en culture d'expansion pour immunothérapie adjuvante. Les lymphocytes sont dérivés de cellules souches hématopoïétiques (CSH) d'un donneur et sont génétiquement modifiés *ex vivo* avec un vecteur rétroviral gamma SFCMM-3 non-répliquant dérivé du virus de la leucémie murine de Moloney (Mo-MuLV), codant pour une forme tronquée du récepteur du facteur de croissance nerveuse à faible affinité humain (ΔLNGFR) et la thymidine kinase du virus herpès simplex (HSV-TK Mut2). Les cellules contiennent un gène suicide en cas de développement de réaction du greffon contre l'hôte.
nalotimagén carmaleucel	linfocitos T humanos alogénicos activados y expandidos en cultivo para inmunoterapia adyuvante. Los linfocitos se derivan a partir del donante de las células madre hematopoyéticas (CMH) y se modifican genéticamente *ex vivo* con un vector retroviral gamma SFCMM-3 no replicativo derivado del virus de la leucemia murina de Moloney (Mo-MuLV), que codifica para una forma truncada del receptor para el factor de crecimiento nervioso de baja afinidad humano (ΔLNGFR) y de la timidina quinasa del virus del herpes simplex (HSV-TK Mut2). Las células contienen un gen suicida en caso de que se desarrolle la enfermdad de injerto contra huésped.

netakimabum #

netakimab	immunoglobulin G1-kappa, anti-[*Homo sapiens* IL17A (interleukin 17A, IL-17A)], chimeric and *Homo sapiens* monoclonal antibody; chimeric gamma1 heavy chain (1-455) [VH (*Lama glama* IGHV3S3*01 (80.2%) -(IGHD) -IGHJ3*01 (92.3%)/*Homo sapiens* IGHV3-23*04 -(IGHD) -IGHJ5*01 (92.9%)) [8.8.18] (1-124) -1-mer seryl linker (125) -*Homo sapiens* IGHG1*03, G1m3 (CH1 (126-223), hinge (224-238), CH2 [M15.1>Y (260), S16>T (262), T18>E (264)] (239-348), CH3 (349-453), CHS (454-455)) (126-455)], (228-215')-disulfide with *Homo sapiens* kappa light chain (1'-216') [*Homo sapiens* V-KAPPA (IGKV3-20*01 (96.9%) -IGKJ1*01 (100%)) [7.3.9] (1'-108') -*Homo sapiens* IGKC*01, Km3 A45.1 (154), V101 (192) (109'-215')]; dimer (234-234'':237-237'')-bisdisulfide

nétakimab

immunoglobuline G1-kappa, anti-[*Homo sapiens* IL17A (interleukine 17A, IL-17A)], anticorps monoclonal chimérique et *Homo sapiens*;
chaîne lourde gamma1 chimérique (1-455) [VH (*Lama glama* IGHV3S3*01 (80.2%) -(IGHD) -IGHJ3*01 (92.3%)/*Homo sapiens* IGHV3-23*04 -(IGHD) -IGHJ5*01 (92.9%)) [8.8.18] (1-124) -1-mer linker séryl (125) -*Homo sapiens* IGHG1*03, G1m3 (CH1 (126-223), charnière (224-238), CH2 [M15.1>Y (260), S16>T (262), T18>E (264)] (239-348), CH3 (349-453), CHS (454-455)) (126-455)], (228-215')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-216') [*Homo sapiens* V-KAPPA (IGKV3-20*01 (96.9%) -IGKJ1*01 (100%)) [7.3.9] (1'-108') -*Homo sapiens* IGKC*01, Km3 A45.1 (154), V101 (192) (109'-215')];
dimère (234-234":237-237")-bisdisulfure

netakimab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* IL17A (interleukina 17A, IL-17A)], anticuerpo monoclonal quimérico y *Homo sapiens*;
cadena pesada gamma1 quimérica (1-455) [VH (*Lama glama* IGHV3S3*01 (80.2%) -(IGHD) -IGHJ3*01 (92.3%)/*Homo sapiens* IGHV3-23*04 -(IGHD) -IGHJ5*01 (92.9%)) [8.8.18] (1-124) -1-mer ligando seril (125) -*Homo sapiens* IGHG1*03, G1m3 (CH1 (126-223), bisagra (224-238), CH2 [M15.1>Y (260), S16>T (262), T18>E (264)] (239-348), CH3 (349-453), CHS (454-455)) (126-455)], (228-215')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-216') [*Homo sapiens* V-KAPPA (IGKV3-20*01 (96.9%) -IGKJ1*01 (100%)) [7.3.9] (1'-108') -*Homo sapiens* IGKC*01, Km3 A45.1 (154), V101 (192) (109'-215')];
dímero (234-234":237-237")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGGG LVQAGGSLRL SCAASGGTFA TSPMGWLRQA PGKGTEFVAA  50
ISPSGGDRIY ADSVKGRFTI SRDNAGYFIY LQMNSLKPED TAVYYCAVRR 100
RFDGTSYYTG DYDSWGQGTL VTVSSASTKG PSVFPLAPSS KSTSGGTAAL 150
GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL SSVVTVPSSS 200
LGTQTYICNV NHKPSNTKVD KRVEPKSCDK THTCPPCPAP ELLGGPSVFL 250
FPPKPKDTLY ITREPEVTCV VVDVSHEDPE VKFNWYVDGV EVHNAKTKPR 300
EEQYNSTYRV VSVLTVLHQD WLNGKEYKCK VSNKALPAPI EKTISKAKGQ 350
PREPQVYTLP PSREEMTKNQ VSLTCLVKGF YPSDIAVEWE SNGQPENNYK 400
TTPPVLDSDG SFFLYSKLTV DKSRWQQGNV FSCSVMHEAL HNHYTQKSLS 450
LSPGK                                                   455
```

Light chain / Chaîne légère / Cadena ligera

```
EIVLTQSPGT LSLSPGERAT LSCRASQSVS SSYLAWYQQK PGQAPRLLIY  50
DASSRATGIP DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QYSYSPVTFG 100
QGTKVEIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK 150
VDNALQSGNS QESVTEQDSK DSTYSLSSTL TLSKADYEKH KVYACEVTHQ 200
GLSSPVTKSF NRGEC                                        215
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

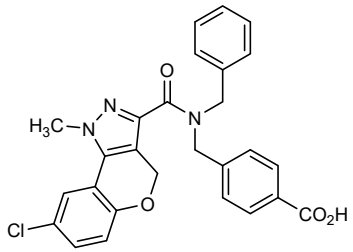
Intra-H (C23-C104)	22-96	152-208	269-329	375-433
	22"-96"	152"-208"	269"-329"	375"-433"
Intra-L (C23-C104)	23'-89'	135'-195'		
	23'"-89''	135'"-195'"		
Inter-H-L (h 5-CL 126)	228-215'	228"-215'"		
Inter-H-H (h 11, h 14)	234-234''	237-237"		

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84 4:
305, 305"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

nidufexorum

nidufexor	4-[(*N*-benzyl-8-chloro-1-methyl-1,4-dihydro[1]benzopyrano[4,3-*c*]pyrazole-3-carboxamido)methyl]benzoic acid
nidufexor	acide 4-[(*N*-benzyl-8-chloro-1-méthyl-1,4-dihydro[1]benzopyrano[4,3-*c*]pyrazole-3-carboxamido)méthyl]benzoïque
nidufexor	ácido 4-[(*N*-bencil-8-cloro-1-metil-1,4-dihidro[1]benzopirano[4,3-*c*]pirazol-3-carboxamido)meti]benzoico

$C_{27}H_{22}ClN_3O_4$



onfekafuspum alfa #

onfekafusp alfa	immunoglobulin single-chain variable fragment anti-(human f bronectin ED-B domain) (1-236), with a GDGSSGGSGGAS linker (117-128) between the VH and VL regions, fused, via a $EF(S_4G)_3$ linker (237-253), to human tumor necrosis factor (TNF) soluble form (254-410), non-covalent trimer, produced in Chinese hamster ovary (CHO) cells, glycoform alfa : scFv-TNF chain (1-410) [*Homo sapiens* VH (IGHV3-23*01 (94.9%)-(IGHD) -IGHJ4*01 (100%)) [8.8.9](1-116) -12-mer linker(117-128) -*Homo sapiens* V-KAPPA (IGKV3-20*01 (94.8%)-IGKJ1*01 (100%))[7.3.9] (129-236) -17-mer EF(SSSSG)3 linker (237-253)-*Homo sapiens* TNF (Pr77-233)(254-410)], non-covalent trimer
onfékafusp alfa	immunoglobuline à chaîne unique Fragment variable (scFv), anti-(domaine ED-B de la fibronectine humaine) (1-236), avec un linker GDGSSGGSGGAS (117-128) entre les régions VH et VL, fusionné, via un linker $EF(S_4G)_3$ (237-253), à la forme soluble du facteur de nécrose tumorale (TNF) humain (254-410), trimère non covalent, produit par des cellules ovariennes de hamsters chinois (CHO), glycoforme alfa: chaîne scFv-TNF (1-410) [*Homo sapiens* VH (IGHV3-23*01 (94.9%) -(IGHD) -IGHJ4*01 (100%))[8.8.9] (1-116) -12-mer linker (117-128) -*Homo sapiens* V-KAPPA (IGKV3-20*01 (94.8%) -IGKJ1*01 (100%))[7.3.9] (129-236) -17-mer EF(SSSSG)3 linker (237-253) -*Homo sapiens* TNF (Pr77-233) (254-410)], trimère non-covalent

onfekafusp alfa

inmunoglobulina con la cadena única Fragmento variable (scFv), anti-(dominio ED-B de la fibronectina humana) (1-236), con un ligando GDGSSGGSGGAS (117-128) entre las regiones VH y VL, fusionado, a través de un enlace $EF(S_4G)_3$ (237-253), con la forma soluble del factor de necrosis tumoral (TNF) humano (254-410), trímero no covalente, producido por las células ováricas de hamsters chinos (CHO), glicoforma alfa:
cadena scFv-TNF (1-410) [*Homo sapiens* VH (IGHV3-23*01 (94.9%) -(IGHD) -IGHJ4*01 (100%))[8.8.9] (1-116) -12-mer ligando (117-128) -*Homo sapiens* V-KAPPA (IGKV3-20*01 (94.8%) -IGKJ1*01 (100%))[7.3.9] (129-236) -17-mer EF(SSSSG)3 ligando (237-253) -*Homo sapiens* TNF (Pr77-233) (254-410)], trímero no covalente

Chain / Chaîne / Cadena scFv-TNF

```
EVQLLESGGG LVQPGGSLRL SCAASGFTFS SFSMSWVRQA PGKGLEWVSS 50
ISGSSGTTYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPF 100
PYFDYWGQGT LVTVSSGDGS SGGSGGASEI VLTQSPGTLS LSPGERATLS 150
CRASQSVSSS FLAWYQQKPG QAPRLLIYYA SSRATGIPDR FSGSGSGTDF 200
TLTISRLEPE DFAVYYCQQT GRIPPTFGQG TKVEIKEFSS SSGSSSSGSS 250
SSGVRSSSRT PSDKPVAHVV ANPQAEGQLQ WLNRRANALL ANGVELRDNQ 300
LVVPSEGLYL IYSQVLFKGQ GCPSTHVLLT HTISRIAVSY QTKVNLLSAI 350
KSPCQRETPE GAEAKPWYEP IYLGGVFQLE KGDRLSAEIN RPDYLDFAES 400
GQVYFGIIAL                                           410
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 151-217
Intra-TNF 322-354

Glycosylation site (O) / Site de glycosylation (O) / Posición de glicosilación (O)
Ser-257
CHO-type O-glycans / O-glycanes de type CHO / O-glicanos de tipo CHO

onvatilimabum #
onvatilimab

immunoglobulin G1-kappa, anti-[*Homo sapiens* VSIR (V-set immunoregulatory receptor, C10orf54, chromosome 10 orf54, B7H5, B7-H5, PDCD1 homolog, PD-1H, stress induced secreted protein 1, SISP1, V-domain Ig suppressor of T cell activation, VISTA)], human monoclonal antibody;
gamma1 heavy chain (1-450) [*Homo sapiens* VH (IGHV1-69*01 (100.00%) -(IGHD) -IGHJ4*01 (100%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (217) (121-218), hinge (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfide with kappa light chain (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-39*01 (92.6%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191)(223'-214')]; dimer (229-229'':232-232'')-bisdisulfide

onvatilimab

immunoglobuline G1-kappa, anti-[*Homo sapiens* VSIR (récepteur immunorégulateur du V-set, C10orf54, orf54 du chromosome 10, B7H5, B7-H5, homologue du PDCD1, PD-1H, protéine 1 secrétée induite par le stress, SISP1, suppresseur d'activation de cellule T du V-set Ig, VISTA)], anticorps monoclonal humain;

chaîne lourde gamma1 (1-450) [*Homo sapiens* VH (IGHV1-69*01 (100.00%) -(IGHD) -IGHJ4*01 (100%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (217) (121-218), charnière (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfure avec la chaîne légère kappa (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-39*01 (92.6%) - IGKJ1*01(100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191)(223'-214')]; dimère (229-229":232-232")-bisdisulfure

onvatilimab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* VSIR (receptor inmunoregulador del V-set, C10orf54, orf54 del cromosoma 10, B7H5, B7-H5, homólogo del PDCD1, PD-1H, proteína 1 secretada inducida por el estrés, SISP1, supresor de la activación de célula T del V-set Ig, VISTA)], anticuerpo monoclonal humano;
cadena pesada gamma1 (1-450) [*Homo sapiens* VH (IGHV1-69*01 (100.00%) -(IGHD) -IGHJ4*01 (100%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (217) (121-218), bisagra (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfuro con la cadena ligera kappa (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-39*01 (92.6%) - IGKJ1*01(100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (223'-214')]; dímero (229-229":232-232")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGSSVKV SCKASGGTFS SYAISWVRQA PGQGLEWMGG  50
IIPIFGTANY AQKFQGRVTI TADESTSTAY MELSSLRSED TAVYYCARSS 100
YGWSYEFDYW GQGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK 450
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCRASQSID TRLNWYQQKP GKAPKLLIYS  50
ASSLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ SAYNPITFGQ 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 147-203 264-324 370-428
22"-96" 147"-203" 264"-324" 370"-428"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194'"
Inter-H-L (h 5-CL 126) 223-214' 223"-214'"
Inter-H-H (h 11, h 14) 229-229" 232-232"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84 4:
300, 300"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

opigolixum
opigolix

(2*R*)-*N*-{5-[3-(2,5-difluorophenyl)-2-(1,3-dihydro-2*H*-benzimidazol-2-ylidene)-3-oxopropanoyl]-2-fluorobenzene-1-sulfonyl}-2-hydroxypropanimidamide

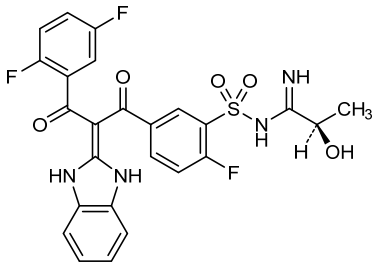
opigolix

(2*R*)-*N*-{5-[3-(2,5-difluorophényl)-2-(1,3-dihydro-2*H*-benzimidazol-2-ylidène)-3-oxopropanoyl]-2-fluorobenzène-1-sulfonyl}-2-hydroxypropanimidamide

opigolix

(2*R*)-*N*-{5-[3-(2,5-difluorofenil)-2-(1,3-dihidro-2*H*-benzimidazol-2-ilideno)-3-oxopropanoil]-2-fluorobenceno-1-sulfonil}-2-hidroxipropanimidamida

$C_{25}H_{19}F_3N_4O_5S$



opinerceptum #

opinercept

human tumor necrosis factor receptor-2 extracellular domain (1-235) fused to a fragment of immunoglobulin G1 consisting of the Fc portion and hinge region (236-467), dimer, produced in Chinese hamster ovary (CHO) cells, glycosylated

opinercept

domaine extracellulaire du récepteur 2 du facteur de nécrose tumorale humain (1-235) fusionné à un fragment d'immunoglobuline G1 constitué du fragment Fc et de la région charnière (236-467), dimère, produit par des cellules ovariennes de hamsters chinois (CHO), glycosylé

opinercept

dominio extracelular del receptor 2 del factor de necrosis tumoral humano (1-235) fusionado con un fragmento de inmunoglobulina G1 constituida por el fragmento Fc y la región bisagra (236-467), dímero, producido por las células ováricas de hamsters chinos (CHO), glicosilado

```
LPAQVAFTPY APEPGSTCRL REYYDQTAQM CCSKCSPGQH AKVFCTKTSD 50
TVCDSCEDST YTQLWNWVPE CLSCGSRCSS DQVETQACTR EQNRICTCRP 100
GWYCALSKQE GCRLCAPLRK CRPGFGVARP GTETSDVVCK PCAPGTFSNT 150
TSSTDICRPH QICNVVAIPG NASMDAVCTS TSPTRSMAPG AVHLPQPVST 200
RSQHTQPTPE PSTAPSTSFL LPMGPSPPAE GSTGDEPKSC DKTHTCPPCP 250
APELLGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD 300
GVEVHNAKTK PREEQYNSTY RVVSVLTVLH QDWLNGKEYK CKVSNKALPA 350
PIEKTISKAK GQPREPQVYT LPPSRDELTK NQVSLTCLVK GFYPSDIAVE 400
WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE 450
ALHNHYTQKS LSLSPGK                                    467
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
intra-chain: 18-31 32-45 35-53 56-71 74-88 78-96 98-104 112-121 115-139 142-157 163-178 281-341 387-445
inter-chain: 240-240' 246-246' 249-249'

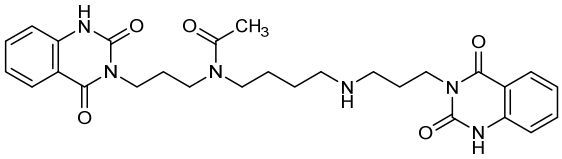
Glycosylation sites (N) / Sites de glycosylation (N) / Posiciones de glicosilación (N)
Asn-149 Asn-171 Asn-317

Glycosylation sites (O) / Sites de glycosylation (O) / Posiciones de glicosilación (O)
Thr-8 Thr-184 Ser-199 Thr-200 Ser-202 Thr-205 Thr-208 Ser-212 Thr-213 Ser-216 Thr-217 Ser-218 Ser-226 Ser-232 Thr-233 Thr-243

otaplimastatum

otaplimastat	*N*-[3-(2,4-dioxo-1,4-dihydroquinazolin-3(2*H*)-yl)propyl]-*N*-(4-{[3-(2,4-dioxo-1,4-dihydroquinazolin-3(2*H*)-yl)propyl]amino}butyl)acetamide
otaplimastat	*N*-[3-(2,4-dioxo-1,4-dihydroquinazolin-3(2*H*)-yl)propyl]-*N*-(4-{[3-(2,4-dioxo-1,4-dihydroquinazolin-3(2*H*)-yl)propyl]amino}butyl)acetamide
otaplimastat	*N*-[3-(2,4-dioxo-1,4-dihidroquinazolin-3(2*H*)-il)propil]-*N*-(4-{[3-(2,4-dioxo-1,4-dihidroquinazolin-3(2*H*)-il)propil]amino}butil)acetamida

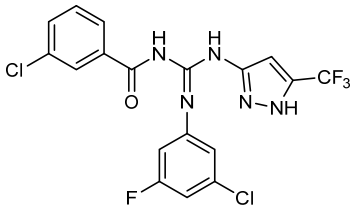
$C_{28}H_{34}N_6O_5$



parimifasorum

parimifasor	3-chloro-*N*-[(3-chloro-5-fluoroanilino){[5-(trifluoromethyl)-1*H*-pyrazol-3-yl]amino}methylidene]benzamide
parimifasor	3-chloro-*N*-[(3-chloro-5-fluoroanilino){[5-(trifluorométhyl)-1*H*-pyrazol-3-yl]amino}méthylidène]benzamide
parimifasor	3-cloro-*N*-[(3-cloro-5-fluoroanilino){[5-(trifluorometil)-1*H*-pirazol-3-il]amino}metilideno]benzamida

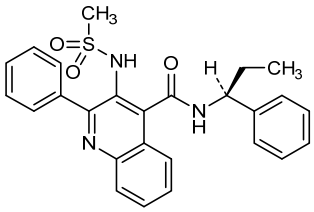
$C_{18}H_{11}Cl_2F_4N_5O$



pavinetantum

pavinetant	3-(methanesulfonamido)-2-phenyl-*N*-[(1*S*)-1-phenylpropy]quinoline-4-carboxamide
pavinétant	3-(méthanesulfonamido)-2-phényl-*N*-[(1*S*)-1-phénylpropy]quinoléine-4-carboxamide
pavinetant	3-(metanosulfonamido)-2-fenil-*N*-[(1*S*)-1-fenilpropil]quinoleína-4-carboxamida

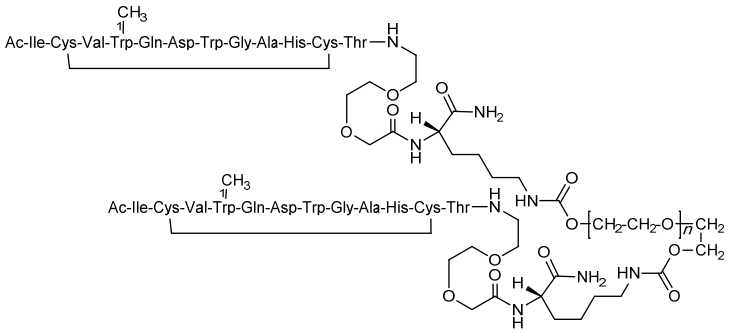
$C_{26}H_{25}N_3O_3S$



pegcetacoplanum

pegcetacoplan	*O*,*O*'-bis[(S^2,S^{12}-cyclo{*N*-acetyl-L-isoleucyl-L-cysteinyl-L-valyl-1-methyl-L-tryptophyl-L-glutaminyl-L-α-aspartyl-L-tryptophylglycyl-L-alanyl-L-histidyl-L-arginyl-L-cysteinyl-L-threonyl-2-[2-(2-aminoethoxy)ethoxy]acetyl-L-lysinamide})-$N^{6.15}$-carbony]polyethylene glycol (n = 800-1100)
pegcétacoplan	*O*,*O*'-bis[(S^2,S^{12}-cyclo{*N*-acétyl-L-isoleucyl-L-cystéinyl-L-valyl-1-méthyl-L-tryptophyl-L-glutaminyl-L-α-aspartyl-L-tryptophylglycyl-L-alanyl-L-histidyl-L-arginyl-L-cystéinyl-L-thréonyl-2-[2-(2-aminoéthoxy)éthoxy]acétyl-L-lysinamide})-$N^{6.15}$-carbony]polyéthylène glycol (n = 800-1100)
pegcetacoplán	*O*,*O*'-bis[(S^2,S^{12}-ciclo{*N*-acetil-L-isoleucil-L-cisteinil-L-valil-1-metil-L-triptofil-L-glutaminil-L-α-aspartil-L-triptofilglicil-L-alanil-L-histidil-L-arginil-L-cisteinil-L-treonil-2-[2-(2-aminoetoxi)etoxi]acetil-L-lisinamida})-$N^{6.15}$-carbonil]polietileno glicol (n = 800-1100)

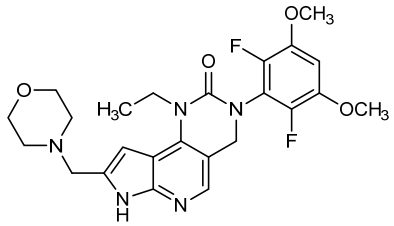
$C_{170}H_{248}N_{50}O_{47}S_4$



pemigatinibum

pemigatinib	3-(2,6-difluoro-3,5-dimethoxyphenyl)-1-ethyl-8-[(morpholin-4-yl)methyl]-1,3,4,7-tetrahydro-2*H*-pyrrolo[3',2':5,6]pyrido[4,3-*d*]pyrimidin-2-one
pémigatinib	3-(2,6-difluoro-3,5-diméthoxyphényl)-1-éthyl-8-[(morpholin-4-yl)méthyl]-1,3,4,7-tétrahydro-2*H*-pyrrolo[3',2':5,6]pyrido[4,3-*d*]pyrimidin-2-one
pemigatinib	3-(2,6-difluoro-3,5-dimetoxifenil)-1-etil-8-[(morfolin-4-il)metil]-1,3,4,7-tetrahidro-2*H*-pirrolo[3',2':5,6]pirido[4,3-*d*]pirimidin-2-ona

$C_{24}H_{27}F_2N_5O_4$



praconasum #

praconase — L-seryl (1)-[mono-ADP-ribosyltransferase C3 (exoenzyme C3, EC=2.4.2.-) of *Clostridium botulinum* D phage (2-212)] fusion protein with an artificial permeability-conferring C-terminal 19-peptide (213-231), produced in *Escherichia coli*

praconase — L-séryl (1)-[mono-ADP-ribosyltransférase C3 de phage de *Clostridium botulinum* de type D (exoenzyme C3, EC=2.4.2.-)], fusionnée par l'extrémité C-terminale à un peptide conférant une perméabilité artificielle (213-231), produite par *Escherichia coli*

praconasa — L-seril (1)-[mono-ADP-ribosiltransferasa C3 de phage de *Clostridium botulinum* de tipo D (exoenzima C3, EC=2.4.2.-) (2-212)], fusionada con la extremidad C-terminal a un péptido que confiere una permeabilidad artificial (213-231), producido por *Escherichia coli*

```
SAYSNTYQEF TNIDQAKAWG NAQYKKYGLS KSEKEAIVSY TKSASEINGK 50
LRQNKGVING FPSNLIKQVE LLDKSFNKMK TPENIMLFRG DDPAYLGTEF 100
QNTLLNSNGT INKTAFEKAK AKFLNKDRLE YGYISTSLMN VSQFAGRPII 150
TKFKVAKGSK AGYIDPISAF AGQLEMLLPR HSTYHIDDMR LSSDGKQIII 200
TATMMGTAIN PKEFVMNPAN AQGRHTPGTR L                     231
```

ravagalimabum #

ravagalimab — immunoglobulin G1-kappa, anti-[*Homo sapiens* CD40 (tumor necrosis factor super family member 5, TNFRSF5)], humanized monoclonal ant body;
gamma1 heavy chain (1-446) [humanized VH (*Homo sapiens* IGHV3-48*01 (89.8%) -(IGHD)-IGHJ6*01 (100%)) [8.8.9] (1-116) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (213) (117-214), hinge (215-229), CH2 L1.3>A (233), L1.2>A (234), T14>Q (249) (230-339), CH3 E12 (355), M14 (357), M107>L (427) (340-444), CHS (445-446)) (117-446)], (219-220')-disulfide with kappa light chain (1'-220') [humanized V-KAPPA (*Homo sapiens* IGKV4-1*01 (89.1%) -IGKJ2*01 (100%)) [12.3.9] (1'-113') -*Homo sapiens* IGKC*01, Km3 A45.1 (159), V101 (197) (114'-220')]; dimer (225-225":228-228")-bisdisulfide

ravagalimab — immunoglobuline G1-kappa, anti-[*Homo sapiens* CD40 (membre 5 de la superfamille des récepteurs du TNF, TNFRSF5)], anticorps monoclonal humanisé;

chaîne lourde gamma1 (1-446) [VH humanisé (*Homo sapiens* IGHV3-48*01 (89.8%) -(IGHD)-IGHJ6*01 (100%)) [8.8.9] (1-116) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (213) (117-214), charnière (215-229), CH2 L1.3>A (233), L1.2>A (234), T14>Q (249) (230-339), CH3 E12 (355), M14 (357), M107>L (427) (340-444), CHS (445-446)) (117-446)], (219-220')-disulfure avec la chaîne légère kappa (1'-220') [V-KAPPA humanisé (*Homo sapiens* IGKV4-1*01 (89.1%) -IGKJ2*01 (100%)) [12.3.9] (1'-113') -*Homo sapiens* IGKC*01, Km3 A45.1 (159), V101 (197) (114'-220')]; dimère (225-225":228-228")-bisdisulfure

ravagalimab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CD40 (miembro 5 de la superfamilia de los receptores del TNF, TNFRSF5)], anticuerpo monoclonal humanizado; cadena pesada gamma1 (1-446) [VH humanizado (*Homo sapiens* IGHV3-48*01 (89.8%) -(IGHD)-IGHJ6*01 (100%)) [8.8.9] (1-116) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (213) (117-214), bisagra (215-229), CH2 L1.3>A (233), L1.2>A (234), T14>Q (249) (230-339), CH3 E12 (355), M14 (357), M107>L (427) (340-444), CHS (445-446)) (117-446)], (219-220')-disulfuro con la cadena ligera kappa (1'-220') [V-KAPPA humanizado (*Homo sapiens* IGKV4-1*01 (89.1%) -IGKJ2*01 (100%)) [12.3.9] (1'-113') -*Homo sapiens* IGKC*01, Km3 A45.1 (159), V101 (197) (114'-220')]; dímero (225-225":228-228")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVKPGGSLRL SCAASGFTFS DYGMNWVRQA PGKGLEWIAY  50
ISSGRGNIYY ADTVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARSW 100
GYFDVWGQGT TVTVSSASTK GPSVFPLAPS SKSTSGGTAA LGCLVKDYFP 150
EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVVTVPSS SLGTQTYICN 200
VNHKPSNTKV DKKVEPKSCD KTHTCPPCPA PEAAGGPSVF LFPPKPKDQL 250
MISRTPEVTC VVVDVSHEDP EVKFNWYVDG VEVHNAKTKP REEQYNSTYR 300
VVSVLTVLHQ DWLNGKEYKC KVSNKALPAP IEKTISKAKG QPREPQVYTL 350
PPSREEMTKN QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD 400
GSFFLYSKLT VDKSRWQQGN VFSCSVLHEA LHNHYTQKSL SLSPGK     446
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Light chain / Chaîne légère / Cadena ligera

```
DIVMTQSPDS LAVSLGERAT INCKSSQSLL NRGNQKNYLT WFQQKPGQPP  50
KLLIYWASTR ESGVPDRFSG SGSGTDFTLT ISSLQAEDVA VYYCQNDYTY 100
PLTFGQGTKL EIKRTVAAPS VFIFPPSDEQ LKSGTASVVC LLNNFYPREA 150
KVQWKVDNAL QSGNSQESVT EQDSKDSTYS LSSTLTLSKA DYEKHKVYAC 200
EVTHQGLSSP VTKSFNRGEC                                  220
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

Intra-H (C23-C104)	22-96	143-199	260-320	366-424
	22"-96"	143"-199"	260"-320"	366"-424"
Intra-L (C23-C104)	23'-94'	140'-200'		
	23'"-94'"	140'"-200'"		
Inter-H-L (h 5-CL 126)	219-220'	219"-220'"		
Inter-H-H (h 11, h 14)	225-225"	228-228"		

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
296, 296"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

rebisufligenum etisparvovecum #
rebisufligene etisparvovec

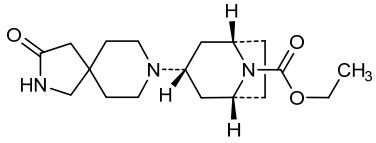
a non-replicating, recombinant, self-complementary adeno-associated virus serotype 9 (scAAV9) vector, expressing the human N-sulfoglucosamine sulfohydrolase (hSGSH) cDNA, under the control of a murine small nuclear RNA promoter U1a.

rébisufligène étisparvovec	vecteur viral adéno-associé de sérotype 9 non-répliquant, recombinant et autocomplémentaire (scAAV9), contenant l'ADN circulaire de la N-sulfoglucosamine sulfohydrolase humaine (hSGSH), sous le contrôle d'un promoteur U1a de petit ARN nucléaire murin.
rebisufligén etisparvovec	un vector de virus adeno-asociado serotipo 9 no-replicativo, recombinante, y auto-complementario, que expresa el cDNA de la N-sulfoglucosamina sulfohidrolasa humana, bajo el control de un promotor U1a de RNA nuclear pequeño murino.

revosimelinum

revosimeline	ethyl (1*R*,3*r*,5*S*)-3-(3-oxo-2,8-diazaspiro[4.5]decan-8-yl)-8-azabicyclo[3.2.1]octane-8-carboxylate
révosiméline	(1*R*,3*r*,5*S*)-3-(3-oxo-2,8-diazaspiro[4.5]décan-8-yl)-8-azabicyclo[3.2.1]octane-8-carboxylate d'éthyle
revosimelina	(1*R*,3*r*,5*S*)-3-(3-oxo-2,8-diazaspiro[4.5]decan-8-il)-8-azabiciclo[3.2.1]octano-8-carboxilato de etilo

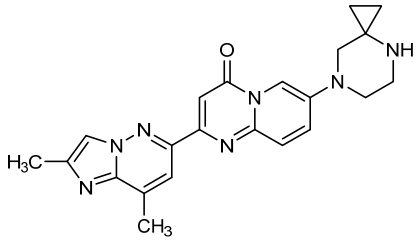
$C_{18}H_{29}N_3O_3$



risdiplamum

risdiplam	7-(4,7-diazaspiro[2.5]octan-7-yl)-2-(2,8-dimethylimidazo[1,2-*b*]pyridazin-6-yl)-4*H*-pyrido[1,2-*a*]pyrimidin-4-one
risdiplam	7-(4,7-diazaspiro[2.5]octan-7-yl)-2-(2,8-diméthylimidazo[1,2-*b*]pyridazin-6-yl)-4*H*-pyrido[1,2-*a*]pyrimidin-4-one
risdiplam	7-(4,7-diazaspiro[2.5]octan-7-il)-2-(2,8-dimetilimidazo[1,2-*b*]piridazin-6-il)-4*H*-pirido[1,2-*a*]pirimidin-4-ona

$C_{22}H_{23}N_7O$



roblitinibum

roblitinib	*N*-{5-cyano-4-[(2-methoxyethyl)amino]pyridin-2-yl}-7-formyl-6-[(4-methyl-2-oxopiperazin-1-yl)methyl]-3,4-dihydro-1,8-naphthyridine-1(2*H*)-carboxamide

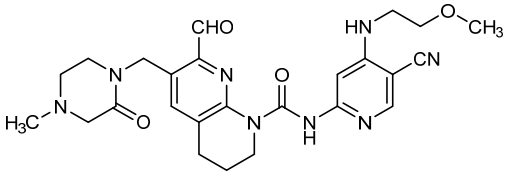
roblitinib

N-{5-cyano-4-[(2-méthoxyéthyl)amino]pyridin-2-yl}-7-formyl-6-[(4-méthyl-2-oxopipérazin-1-yl)méthyl]-3,4-dihydro-1,8-naphthyridine-1(2*H*)-carboxamide

roblitinib

N-{5-ciano-4-[(2-metoxietil)amino]piridin-2-il}-7-formil-6-[(4-metil-2-oxopiperazin-1-il)metil]-3,4-dihidro-1,8-naftiridina-1(2*H*)-carboxamida

$C_{25}H_{30}N_8O_4$



romilkimabum #

romilkimab

immunoglobulin G4-kappa, anti-[*Homo sapiens* IL13 (interleukin 13, IL-13)] and anti-[*Homo sapiens* IL4 (interleukin 4, IL-4)], chimeric and humanized monoclonal antibody, bispecific, tetravalent; gamma1 heavy chain (1-577) [VH anti-IL13 (*Mus musculus* IGHV2-6-7*01 (83.50%) -(IGHD) -IGHJ4*01 (93.8%)/*Homo sapiens* IGHV2-26*01 (59.6%) -(IGHD) -IGHJ1*01 (90.9%)) [8.7.12] (1-118) -10-mer linker bis(tetraglycyl-seryl) (119-128) -VH anti-IL4 (*Mus musculus* IGHV1S127*01 (81.6%) -(IGHD) -IGHJ1*01 (87.5%)/*Homo sapiens* IGHV1-46*01 (68.4%) -(IGHD) -IGHJ4*01 (86.7%)) [8.8.16] (129-251) -*Homo sapiens* IGHG4*01 (CH1 (252-349), hinge 1-12, S10>P (359) (350-361), CH2 L1.2>E (366) (362-471), CH3 (472-576), CHS K>del (577)) (252-577)]; (265-335')-disulfide with kappa light chain (1'-335') [V-KAPPA anti-IL13 (*Mus musculus* IGKV3-10*01 (92.90%) -IGKJ1*01 (100%)/*Homo sapiens*) IGKV4-1*01 (71.9%) -IGKJ4*01 (90.9%)) [10.3.9] (1'-111') -10-mer linker bis(tetraglycyl-seryl) (112'-121') -humanized V-KAPPA anti-IL4 (*Homo sapiens* IGKV1-12*01 (76.8%) -IGKJ2*02 (90.9%)) [6.3.9] (122'-228') -*Homo sapiens* IGKC*01, Km3 A45.1 (274), V101 (312) (229'-335')]; dimer (357-357":360-360")-bisdisulfide

romilkimab

immunoglobuline G4-kappa, anti-[*Homo sapiens* IL13 (interleukine 13, IL-13)] et anti-[*Homo sapiens* IL4 (interleukine 4, IL-4)], anticorps monoclonal chimérique et humanisé, bispécifique, tétravalent; chaîne lourde gamma1 (1-577) [VH anti-IL13 (*Mus musculus* IGHV2-6-7*01 (83.50%) -(IGHD) -IGHJ4*01) (93.8%)/*Homo sapiens* IGHV2-26*01 (59.6%) -(IGHD) -IGHJ1*01 (90.9%)) [8.7.12] (1-118) -10-mer linker bis(tétraglycyl-séryl) (119-128) -VH anti-IL4 (*Mus musculus* IGHV1S127*01 (81.6%) -(IGHD) -IGHJ1*01 (87.5%)/*Homo sapiens* IGHV1-46*01 (68.4%) -(IGHD) -IGHJ4*01 (86.7%)) [8.8.16] (129-251) -*Homo sapiens* IGHG4*01 (CH1 (252-349), charnière 1-12, S10>P (359) (350-361), CH2 L1.2>E (366) (362-471), CH3 (472-576), CHS K>del (577)) (129-577)]; (265-335')-disulfure avec la chaîne légère kappa (1'-335') [V-KAPPA anti-IL13 (*Mus musculus* IGKV3-10*01 (92.90%) -IGKJ1*01) (100%)/*Homo sapiens*) IGKV4-1*01 (71.9%) -IGKJ4*01 (90.9%)) [10.3.9] (1'-111') -10-mer linker bis(tétraglycyl-séryl) (112'-121') -V-KAPPA anti-IL4 humanisé (*Homo sapiens* IGKV1-12*01 (76.8%) -IGKJ2*02 (90.9%)) [6.3.9] (122'-228') -*Homo sapiens* IGKC*01,Km3 A45.1 (274), V101 (312) (229'-335')]; dimère (357-357":360-360")-bisdisulfure

romilkimab

inmunoglobulina G4-kappa, anti-[*Homo sapiens* IL13 (interleukina 13, IL-13)] y anti-[*Homo sapiens* IL4 (interleukina 4, IL-4)], anticuerpo monoclonal quimérico y humanizado, biespecífico, tetravalente;
cadena pesada gamma1 (1-577) [VH anti-IL13 (*Mus musculus* IGHV2-6-7*01 (83.50%) -(IGHD) -IGHJ4*01) (93.8%)/*Homo sapiens* IGHV2-26*01 (59.6%) -(IGHD) -IGHJ1*01 (90.9%)) [8.7.12] (1-118) -10-mer ligando bis(tetraglicil-seril) (119-128) -VH anti-IL4 (*Mus musculus* IGHV1S127*01 (81.6%) -(IGHD) -IGHJ1*01 (87.5%)/*Homo sapiens* IGHV1-46*01 (68.4%) -(IGHD) -IGHJ4*01 (86.7%)) [8.8.16] (129-251) -*Homo sapiens* IGHG4*01 (CH1 (252-349), bisagra 1-12, S10>P (359) (350-361), CH2 L1.2>E (366) (362-471), CH3 (472-576), CHS K>del (577)) (129-577)]; (265-335')-disulfuro con la cadena ligera kappa (1'-335') [V-KAPPA anti-IL13 (*Mus musculus* IGKV3-10*01 (92.90%) -IGKJ1*01) (100%)/*Homo sapiens*) IGKV4-1*01 (71.9%) -IGKJ4*01 (90.9%)) [10.3.9] (1'-111') -10-mer ligando bis(tetraglicil-seril) (112'-121') -V-KAPPA anti-IL4 humanizado (*Homo sapiens* IGKV1-12*01 (76.8%) -IGKJ2*02 (90.9%)) [6.3.9] (122'-228') -*Homo sapiens* IGKC*01,Km3 A45.1 (274), V101 (312) (229'-335')]; dímero (357-357":360-360")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLKESGPG LVAPGGSLSI TCTVSGFSLT DSSINWVRQP PGKGLEWLGM  50
IWGDGRIDYA DALKSRLSIS KDSSKSQVFL EMTSLRTDDT ATYYCARDGY 100
FPYAMDFWGQ GTSVTVSSGG GGSGGGGSQV QLQQSGPELV KPGASVKISC 150
KASGYSFTSY WIHWIKQRPG QGLEWIGMID PSDGETRLNQ RFQGRATLTV 200
DESTSTAYMQ LRSPTSEDSA VYYCTRLKEY GNYDSFYFDV WGAGTLVTVS 250
SASTKGPSVF PLAPCSRSTS ESTAALGCLV KDYFPEPVTV SWNSGALTSG 300
VHTFPAVLQS SGLYSLSSVV TVPSSSLGTK TYTCNVDHKP SNTKVDKRVE 350
SKYGPPCPPC PAPEFEGGPS VFLFPPKPKD TLMISRTPEV TCVVVDVSQE 400
DPEVQFNWYV DGVEVHNAKT KPREEQFNST YRVVSVLTVL HQDWLNGKEY 450
KCKVSNKGLP SSIEKTISKA KGQPREPQVY TLPPSQEEMT KNQVSLTCLV 500
KGFYPSDIAV EWESNGQPEN NYKTTPPVLD SDGSFFLYSR LTVDKSRWQE 550
GNVFSCSVMH EALHNHYTQK SLSLSLG                          577
```

Light chain / Chaîne légère / Cadena ligera

```
DIVLTQSPAS LAVSLGQRAT ISCRASESVD SYGQSYMHWY QQKAGQPPKL  50
LIYLASNLES GVPARFSGSG SRTDFTLTID PVQAEDAATY YCQQNAEDSR 100
TFGGGTKLEI KGGGGSGGGG SDIQMTQSPA SLSVSVGDTI TLTCHASQNI 150
DVWLSWFQQK PGNIPKLLIY KASNLHTGVP SRFSGSGSGT GFTLTISSLQ 200
PEDIATYYCQ QAHSYPFTFG GGTKLEIKRT VAAPSVFIFP PSDEQLKSGT 250
ASVVCLLNNF YPREAKVQWK VDNALQSGNS QESVTEQDSK DSTYSLSSTL 300
TLSKADYEKH KVYACEVTHQ GLSSPVTKSF NRGEC                 335
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

```
Intra-H (C23-C104)  22-95    150-224   278-334   392-452   498-556
                    22"-95"  150"-224"  278"-334"  392"-452"  498"-556"
Intra-L (C23-C104)  23'-92'   144'-209'    255'-315'
                   23'"-92'"  144'"-209'"  255'"-315'"
Inter-H-L (CH1 10-CL 126)  265-335'  265"-335'"
Inter-H-H (h 8, h 11)          357-357"  360-360"
```

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84 4:
428, 428"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

samrotamabum #

samrotamab

immunoglobulin G1-kappa, anti-[*Homo sapiens* LRRC15 (leucine-rich repeat-containing member 15, leucine-rich repeat member induced by beta-amyloid homolog, LIB)], humanized and chimeric monoclonal antibody;
gamma1 heavy chain (1-450) [humanized VH (*Homo sapiens* IGHV1-2*02 (77.6%) -(IGHD) -IGHJ5*01 (86.7%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*01 (CH1 (121-218), hinge (219-233), CH2 (234-343), CH3 (344-448), CHS (449-450)) (121-450)], (223-214')-disulfide with kappa light chain chimeric (1'-214') [*Mus musculus* V-KAPPA (IGKV10-96*01 (85.30%) -IGKJ1*01 (91.7%)/*Homo sapiens* IGKV1-39*01 (84.2%) -IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01,Km3 A45.1 (153), V101 (191)(108'-214')]; dimer (229-229":232-232")-bisdisulfide

samrotamab	immunoglobuline G1-kappa, anti-[*Homo sapiens* LRRC15 (membre 15 contenant des répétitions riches en leucine, membre des répétitions riches en leucine induit par l'homologue bêta-amyloïde, LIB)], anticorps monoclonal humanisé et chimérique; chaîne lourde gamma1 (1-450) [VH humanisé (*Homo sapiens* IGHV1-2*02 (77.60%) -(IGHD) -IGHJ5*01 (86.7%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*01 (CH1 (121-218), charnière (219-233), CH2 (234-343), CH3 (344-448), CHS (449-450)) (121-450)], (223-214')-disulfure avec la chaîne légère kappa chimérique (1'-214') [*Mus musculus* V-KAPPA (IGKV10-96*01 (85.30%) -IGKJ1*01 (91.7%)/*Homo sapiens* IGKV1-39*01 (84.2%) -IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191)(108'-214')]; dimère (229-229":232-232")-bisdisulfure
samrotamab	inmunoglobulina G1-kappa, anti-[*Homo sapiens* LRRC15 (miembro 15 que contiene las repeticiones ricas en leucina, miembro de las repeticiones ricas en leucina inducido por el homólogo beta-amiloide, LIB)], anticuerpo monoclonal humanizado y quimérico; cadena pesada gamma1 (1-450) [VH humanizado (*Homo sapiens* IGHV1-2*02 (77.60%) -(IGHD) -IGHJ5*01 (86.7%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*01 (CH1 (121-218), bisagra (219-233), CH2 (234-343), CH3 (344-448), CHS (449-450)) (121-450)], (223-214')-disulfuro con la cadena ligera kappa quimérica (1'-214') [*Mus musculus* V-KAPPA (IGKV10-96*01 (85.30%) -IGKJ1*01 (91.7%)/*Homo sapiens* IGKV1-39*01 (84.2%) -IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191)(108'-214')]; dímero (229-229":232-232")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVQSGAE VKKPGASVKV SCKASGYKFS SYWIEWVKQA PGQGLEWIGE  50
ILPGSDTTNY NEKFKDRATF TSDTSINTAY MELSRLRSDD TAVYYCARDR 100
GNYRAWFGYW GQGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK 450
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCRASQDIS NYLNWYQQKP GGAVKFLIYY  50
TSRLHSGVPS RFSGSGSGTD YTLTISSLQP EDFATYFCQQ GEALPWTFGG 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

Intra-H (C23-C104)	22-96	147-203	264-324	370-428
	22"-96"	147"-203"	264"-324"	370"-428"
Intra-L (C23-C104)	23'-88'	134'-194'		
	23'"-88'"	134'"-194'"		
Inter-H-L (h 5-CL 126)	223-214'	223"-214'"		
Inter-H-H (h 11, h 14)	229-229"	232-232"		

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
300, 300"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados
G0F, G1F

C-terminal lysine clipping:
H CHS K2: 450, 450"

samrotamabum vedotinum #

samrotamab vedotin

immunoglobulin G1-kappa, anti-[*Homo sapiens* LRRC15 (leucine-rich repeat-containing protein 15, leucine-rich repeat induced by beta-amyloid homolog, LIB)], humanized and chimeric monoclonal ant body conjugated to auristatin E;
gamma1 heavy chain (1-450) [humanized VH (*Homo sapiens* IGHV1-2*02 (77.6%) -(IGHD) -IGHJ5*01 (86.7%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*01 (CH1 (121-218), hinge (219-233), CH2 (234-343), CH3 (344-448), CHS (449-450)) (121-450)], (223-214')-disulfide with kappa light chain chimeric (1'-214') [*Mus musculus* V-KAPPA (IGKV10-96*01 (85.30%) -IGKJ1*01 (91.7%)/*Homo sapiens* IGKV1-39*01 (84.2%) -IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01,Km3 A45.1 (153), V101 (191)(108'-214')]; dimer (229-229'':232-232'')-bisdisulfide; conjugated, on an average of 2 cysteinyl, to monomethylauristatin E (MMAE), via a cleavable maleimidocaproyl-valyl-citrullinyl-p-aminobenzyloxycarbonyl (mc-val-cit-PABC) type linker
For the *vedotin* part, please refer to the document *"INN for pharmaceutical substances: Names for radicals, groups and others"*.*

samrotamab védotine

immunoglobuline G1-kappa, anti-[*Homo sapiens* LRRC15 (protéine 15 contenant des répétitions riches en leucine, répétition riche en leucine induite par l'homologue bêta-amyloïde, LIB)], anticorps monoclonal humanisé et chimérique conjugué à l'auristatine E;
chaîne lourde gamma1 (1-450) [VH humanisé (*Homo sapiens* IGHV1-2*02 (77.60%) -(IGHD) -IGHJ5*01 (86.7%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*01 (CH1 (121-218), charnière (219-233), CH2 (234-343), CH3 (344-448), CHS (449-450)) (121-450)], (223-214')-disulfure avec la chaîne légère kappa chimérique (1'-214') [*Mus musculus* V-KAPPA (IGKV10-96*01 (85.30%) -IGKJ1*01 (91.7%)/*Homo sapiens* IGKV1-39*01 (84.2%) -IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191)(108'-214')]; dimère (229-229'':232-232'')-bisdisulfure ; conjugué sur 2 cystéinyl en moyenne, au monométhylauristatine E (MMAE), via un linker clivable de type maléimidocaproyl-valyl-citrullinyl-p-aminobenzyloxycarbonyl (mc-val-cit-PABC)
Pour la partie *védotine*, veuillez-vous référer au document *"INN for pharmaceutical substances: Names for radicals, groups and others"*.*

samrotamab vedotina

inmunoglobulina G1-kappa, anti-[*Homo sapiens* LRRC15 (proteína 15 que contiene la repeticiones ricas en leucina, repetición rica en leucina inducida por el homólogo beta-amiloide, LIB)], anticuerpo monoclonal humanizado y quimérico conjugado con la auristatina E;
cadena pesada gamma1 (1-450) [VH humanizado (*Homo sapiens* IGHV1-2*02 (77.60%) -(IGHD) -IGHJ5*01 (86.7%9) [8.8.13] (1-120) -*Homo sapiens* IGHG1*01 (CH1 (121-218), bisagra (219-233), CH2 (234-343), CH3 (344-448), CHS (449-450)) (121-450)], (223-214')-disulfuro con la cadena ligera kappa quimérica (1'-214') [*Mus musculus* V-KAPPA (IGKV10-96*01 (85.30%) -IGKJ1*01 (91.7%)/*Homo sapiens* IGKV1-39*01 (84.2%) -IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191)(108'-214')]; dímero (229-229'':232-232'')-bisdisulfuro ;
conjugado bajo una media de 2 cisteinil, con la monometilauristatina E (MMAE), a través de un enlace escind ble del tipo maleimidocaproil-valil-citrullinil-p-aminobenciloxicarbonil (mc-val-cit-PABC)
Para la fracción *vedotina*, se pueden dirigir al documento "*INN for pharmaceutical substances: Names for radicals, groups and others*"*.

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVQSGAE VKKPGASVKV SCKASGYKFS SYWIEWVKQA PGQGLEWIGE  50
ILPGSDTTNY NEKFKDRATF TSDTSINTAY MELSRLRSDD TAVYYCARDR 100
GNYRAWFGYW GQGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK 450
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCRASQDIS NYLNWYQQKP GGAVKFLIYY  50
TSRLHSGVPS RFSGSGSGTD YTLTISSLQP EDFATYFCQQ GEALPWTFGG 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 147-203 264-324 370-428
22"-96" 147"-203" 264"-324" 370"-428"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194'"
Inter-H-L (h 5-CL 126) * 223-214' 223"-214'"
Inter-H-H (h 11, h 14) * 229-229" 232-232"
*One or two of the inter-chain disulfide bridges are not present, an average of 2 cysteinyl being conjugated each via a thioether bond to a drug linker
*Un ou deux des ponts disulfures inter-chaînes ne sont pas présents, 2 cystéinyl en moyenne étant chacun conjugué via une liaison thioéther à un linker-principe actif
*Faltan uno o dos puentes disulfuro inter-catenarios, una media de 2 cisteinil está conjugada a conectores de principio activo

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84 4:
300, 300"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados
G0F, G1F

C-terminal lysine clipping:
H CHS K2: 450, 450"

satoreotidum tetraxetanum

satoreotide tetraxetan

S^2,*S*^{7}-cyclo[4-chloro-*N*-{[4,7,10-tris(carboxymethyl)-1,4,7,10-tetraazacyclododecan-1-yl]acetyl}-L-phenylalanyl-D-cysteinyl-4-[(4*S*)-2,6-dioxo-1,3-diazinane-4-carboxamido]-L-phenylalanyl-4-(carbamoylamino)-D-phenylalanyl-L-lysyl-L-threonyl-L-cysteinyl-D-tyrosinamide]

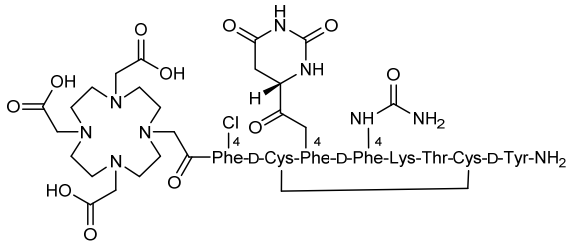
satoréotide tétraxétan

S^2,*S*^{7}-cyclo[4-chloro-*N*-{[4,7,10-tris(carboxyméthyl)-1,4,7,10-tétraazacyclododécan-1-yl]acétyl}-L-phénylalanyl-D-cystéinyl-4-[(4*S*)-2,6-dioxo-1,3-diazinane-4-carboxamido]-L-phénylalanyl-4-(carbamoylamino)-D-phénylalanyl-L-lysyl-L-thréonyl-L-cystéinyl-D-tyrosinamide]

satoreotida tetraxetán

S^2,*S*^{7}-ciclo[4-cloro-*N*-{[4,7,10-tris(carboximetil)-1,4,7,10-tetraazaciclododecan-1-il]acetil}-L-fenilalanil-D-cisteinil-4-[(4*S*)-2,6-dioxo-1,3-diazinane-4-carboxamido]-L-fenilalanil-4-(carbamoilamino)-D-fenilalanil-L-lisil-L-treonil-L-cisteinil-D-tirosinamida]

$C_{74}H_{98}ClN_{19}O_{21}S_2$



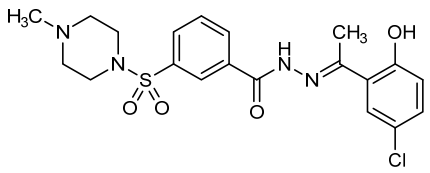
seclidemstatum

seclidemstat — *N′*-[(1*E*)-1-(5-chloro-2-hydroxyphenyl)ethylidene]-3-(4-methylpiperazine-1-sulfonyl)benzohydrazide

séclidemstat — *N′*-[(1*E*)-1-(5-chloro-2-hydroxyphényl)éthylidene]-3-(4-méthylpipérazine-1-sulfonyl)benzohydrazide

seclidemstat — *N′*-[(1*E*)-1-(5-cloro-2-hidroxifenil)etilideno]-3-(4-metilpiperazina-1-sulfonil)benzohidrazida

$C_{20}H_{23}ClN_4O_4S$



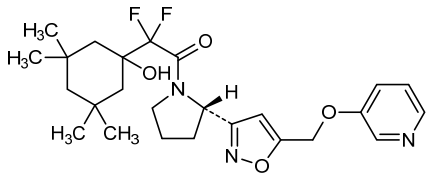
setafrastatum

setafrastat — (5^2*S*)-7,7-difluoro-8^1-hydroxy-8^3,8^3,8^5,8^5-tetramethyl-2-oxa-1(3)-pyridina-4(5,3)-[1,2]oxazola-5(2,1)-pyrrolidina-8(1)-cyclohexanaoctaphan-6-one

sétafrastat — (5^2*S*)-7,7-difluoro-8^1-hydroxy-8^3,8^3,8^5,8^5-tétraméthyl-2-oxa-1(3)-pyridina-4(5,3)-[1,2]oxazola-5(2,1)-pyrrolidina-8(1)-cyclohexanaoctaphan-6-one

setafrastat — (5^2*S*)-7,7-difluoro-8^1-hidroxi-8^3,8^3,8^5,8^5-tetrametil-2-oxa-1(3)-piridina-4(5,3)-[1,2]oxazola-5(2,1)-pirrolidina-8(1)-ciclohexanaoctafan-6-ona

$C_{25}H_{33}F_2N_3O_4$



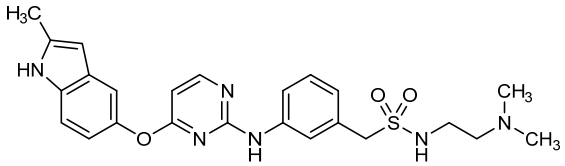
surufatinibum

surufatinib — *N*-[2-(dimethylamino)ethy]-1-[3-({4-[(2-methyl-1*H*-indol-5-yl)oxy]pyrimidin-2-yl}amino)pheny]methanesulfonamide

surufatinib — *N*-[2-(diméthylamino)éthy]-1-[3-({4-[(2-méthyl-1*H*-indol-5-yl)oxy]pyrimidin-2-yl}amino)phény]méthanesulfonamide

surufatinib — *N*-[2-(dimetilamino)etil]-1-[3-({4-[(2-metil-1*H*-indol-5-il)oxi]pirimidin-2-il}amino)fenil]metanosulfonamida

$C_{24}H_{28}N_6O_3S$



sutimlimabum #

sutimlimab — immunoglobulin G4-kappa, anti-[*Homo sapiens* C1S (complement C1s, complement component 1 subcomponent s)], humanized and chimeric monoclonal antibody;
gamma4 heavy chain (1-445) [humanized VH (*Homo sapiens* IGHV3-23*03 (89.8%) -(IGHD) -IGHJ4*01 (100%)) [8.8.11] (1-118) -*Homo sapiens* IGHG4*01 (CH1 (119-216), hinge S10>P (226) (217-228), CH2 L1.2>E (233) (229-338), CH3 (339-443), CHS (444-445)) (118-445)], (132-216')-disulfide with kappa light chain chimeric (1'-216') [V-KAPPA (*Mus musculus* IGKV4-74*01 (82.5%)/*Homo sapiens* IGKV3D-7*01 (78.1%) -*Homo sapiens* IGKJ2*01 (100%)) [7.3.10] (1'-109') -*Homo sapiens* IGKC*01, Km3 A45.1 (155), V101 (193) (110'-216')]; dimer (224-224'':227-227'')-bisdisulfide

sutimlimab — immunoglobuline G4-kappa, anti-[*Homo sapiens* C1S (composant C1s, composant du complément 1 sous-composant s)], anticorps monoclonal humanisé et chimérique;
chaîne lourde gamma4 (1-445) [VH humanisé (*Homo sapiens* IGHV3-23*03 (89.8%) -(IGHD) -IGHJ4*01 (100%)) [8.8.11] (1-118) -*Homo sapiens* IGHG4*01 (CH1 (119-216), charnière S10>P (226) (217-228), CH2 L1.2>E (233) (229-338), CH3 (339-443), CHS (444-445)) (118-445)], (132-216')-disulfure avec la chaîne légère kappa chimérique (1'-216') [V-KAPPA (*Mus musculus* IGKV4-74*01 (82.5%)/*Homo sapiens* IGKV3D-7*01 (78.1%) -*Homo sapiens* IGKJ2*01 (100%)) [7.3.10] (1'-109') -*Homo sapiens* IGKC*01, Km3 A45.1 (155), V101 (193) (110'-216')]; dimère (224-224'':227-227'')-bisdisulfure

sutimlimab — inmunoglobulina G4-kappa, anti-[*Homo sapiens* C1S (componente C1s, componente de complemento 1 subcomponente s)], anticuerpo monoclonal humanizado y quimérico;

cadena pesada gamma4 (1-445) [humanizado VH (*Homo sapiens* IGHV3-23*03 (89.8%) -(IGHD) -IGHJ4*01 (100%)) [8.8.11] (1-118) -*Homo sapiens* IGHG4*01 (CH1 (119-216), bisagra S10>P (226) (217-228), CH2 L1.2>E (233) (229-338), CH3 (339-443), CHS (444-445)) (118-445)], (132-216')-disulfuro con la cadena ligera kappa quimérica (1'-216') [V-KAPPA (*Mus musculus* IGKV4-74*01 (82.5%)/*Homo sapiens* IGKV3D-7*01 (78.1%) -*Homo sapiens* IGKJ2*01 (100%)) [7.3.10] (1'-109') -*Homo sapiens* IGKC*01, Km3 A45.1 (155), V101 (193) (110'-216')]; dímero (224-224":227-227")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVKPGGSLRL SCAASGFTFS NYAMSWVRQA PGKGLEWVAT  50
ISSGGSHTYY LDSVKGRFTI SRDNSKNTLY LQMNSLRAED TALYYCARLF 100
TGYAMDYWGQ GTLVTVSSAS TKGPSVFPLA PCSRSTSEST AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTKTYT 200
CNVDHKPSNT KVDKRVESKY GPPCPPCPAP EFEGGPSVFL FPPKPKDTLM 250
ISRTPEVTCV VVDVSQEDPE VQFNWYVDGV EVHNAKTKPR EEQFNSTYRV 300
VSVLTVLHQD WLNGKEYKCK VSNKGLPSSI EKTISKAKGQ PREPQVYTLP 350
PSQEEMTKNQ VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG 400
SFFLYSRLTV DKSRWQEGNV FSCSVMHEAL HNHYTQKSLS LSLGK      445
```

Light chain / Chaîne légère / Cadena ligera

```
QIVLTQSPAT LSLSPGERAT MSCTASSSVS SSYLHWYQQK PGKAPKLWIY  50
STSNLASGVP SRFSGSGSGT DYTLTISSLQ PEDFATYYCH QYYRLPPITF 100
GQGTKLEIKR TVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQW 150
KVDNALQSGN SQESVTEQDS KDSTYSLSST LTLSKADYEK HKVYACEVTH 200
QGLSSPVTKS FNRGEC                                      216
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

Intra-H (C23-C104)	22-96	145-201	259-319	365-423
	22"-96"	145"-201"	259"-319"	365"-423"
Intra-L (C23-C104)	23'-89'	136'-196'		
	23'"-89'"	136'"-196'"		
Inter-H-L (CH1 10-CL 126)	132-216'	132"-216'"		
Inter-H-H (h 8, h 11)	224-224"	227-227"		

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
295, 295"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

tagraxofuspum #

tagraxofusp — methionyl (1)-*Corynebacterium diphtheriae* toxin fragment (catalytic and transmembrane domains) (2-389, Q388R variant)-His390-Met391-human interleukin 3 (392-524, natural P399S variant) fusion protein, produced in *Escherichia coli*

tagraxofusp — méthionyl (1)-fragment de toxine de *Corynebacterium diphtheriae* (domaines catalytique et transmembranaire) (2-389, variant Q388R)-His390-Met391-interleukine 3 humaine (392-524, variant P399S naturel) protéine de fusion, produite par *Escherichia coli*

tagraxofusp — metionil (1)-fragmento de toxina de *Corynebacterium diphtheriae* (dominios catalíticos y transmembranarios) (2-389, variante Q388R)-His390-Met391-interleukina 3 humana (392-524, variante P399S natural) proteína de fusión, producida por *Escherichia coli*

```
MGADDVVDSS KSFVMENFSS YHGTKPGYVD SIQKGIQKPK SGTQGNYDDD 50
WKGFYSTDNK YDAAGYSVDN ENPLSGKAGG VVKVTYPGLT KVLALKVDNA 100
ETIKKELGLS LTEPLMEQVG TEEFIKRFGD GASRVVLSLP FAEGSSSVEY 150
INNWEQAKAL SVELEINFET RGKRGQDAMY EYMAQACAGN RVRRSVGSSL 200
SCINLDWDVI RDKTKTKIES LKEHGPIKNK MSESPNKTVS EEKAKQYLEE 250
FHQTALEHPE LSELKTVTGT NPVFAGANYA AWAVNVAQVI DSETADNLEK 300
TTAALSILPG IGSVMGIADG AVHHNTEEIV AQSIALSSLM VAQAIPLVGE 350
LVDIGFAAYN FVESIINLFQ VVHNSYNRPA YSPGHKTRPH MAPMTQTTSL 400
KTSWVNCSNM IDEIITHLKQ PPLPLLDFNN LNGEDQDILM ENNLRRPNLE 450
AFNRAVKSLQ NASAIESILK NLLPCLPLAT AAPTRHPIHI KDGDWNEFRR 500
KLTFYLKTLE NAQAQQTTLS LAIF                           524
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
187-202 407-475

tavokinogenum telseplasmidum #

tavokinogene telseplasmid	a DNA plasmid containing genes coding for the human interleukin 12 (IL-12) p35 and p40 subunits that are separated by an internal r bosomal entry site (IRES) and under the control of a single cytomegalovirus (CMV) promoter
tavokinogène telséplasmide	ADN plasmidique contenant les gènes codant pour les sous-unités p35 et p40 de l'interleukine 12 (IL-12) séparés par un site d'entrée interne du ribosome (IRES) et sous le contrôle d'un promoteur de cytomégalovirus (CMV) unique
tavokinogén telseplásmido	un DNA plasmídico que contiene genes que codifican para las subunidades p35 y p40 de la interleukina 12 (IL-12) que están separados por un sitio de entrada ribosómico interno (IRES) y bajo el control de un único promotor de citomegalovirus (CMV)

tavolimabum #

tavolimab	immunoglobulin G1-kappa, anti-[*Homo sapiens* TNFRSF4 (tumor necrosis factor receptor (TNFR) superfamily member 4, OX40, CD134)], humanized and chimeric monoclonal antibody; gamma1 heavy chain (1-451) [chimeric VH (*Mus musculus* IGHV3-8*02 -(IGHD)-*Homo sapiens* IGHJ4*01) [8.7.15] (1-121) -*Homo sapiens* IGHG1*03, G1m3 (CH1 (122-219), hinge (220-234), CH2 (235-344), CH3 (345-449), CHS (450-451)) (122-451)], (224-214')-disulfide with kappa light chain (1'-214') [humanized V-KAPPA (*Homo sapiens* IGKV1-39*01 (88.40%) -IGKJ1*01) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 (108'-214')]; dimer (230-230":233-233")-bisdisulfide
tavolimab	immunoglobuline G1-kappa, anti-[*Homo sapiens* TNFRSF4 (membre 4 de la superfamille des récepteurs du facteur de nécrose tumorale, OX40, CD134)], anticorps monoclonal humanisé et chimérique; chaîne lourde gamma1 (1-451) [VH chimérique (*Mus musculus* IGHV3-8*02 -(IGHD)-*Homo sapiens* IGHJ4*01) [8.7.15] (1-121) -*Homo sapiens* IGHG1*03, G1m3 (CH1 (122-219), charnière (220-234),CH2 (235-344), CH3 (345-449), CHS (450-451)) (122-451)], (224-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA humanisé (*Homo sapiens* IGKV1-39*01 (88.40%) -IGKJ1*01) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 (108'-214')]; dimère (230-230":233-233")-bisdisulfure

tavolimab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* TNFRSF4 (miembro 4 de la superfamilia de los receptores del factor de necrosis tumoral, OX40, CD134)], anticuerpo monoclonal humanizado y quimérico;
cadena pesada gamma1 (1-451) [VH quimérico (*Mus musculus* IGHV3-8*02 -(IGHD)-*Homo sapiens* IGHJ4*01) [8.7.15] (1-121) -*Homo sapiens* IGHG1*03, G1m3 (CH1 (122-219), bisagra (220-234),CH2 (235-344), CH3 (345-449), CHS (450-451)) (122-451)], (224-214')-disulfuro con la cadena ligera kappa (1'-214') [V-KAPPA humanizado (*Homo sapiens* IGKV1-39*01 (88.40%) -IGKJ1*01) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 (108'-214')];
dímero (230-230":233-233")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLQESGPG LVKPSQTLSL TCAVYGGSFS SGYWNWIRKH PGKGLEYIGY  50
ISYNGITYHN PSLKSRITIN RDTSKNQYSL QLNSVTPEDT AVYYCARYKY 100
DYDGGHAMDY WGQGTLVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200
TYICNVNHKP SNTKVDKRVE PKSCDKTHTC PPCPAPELLG GPSVFLFPPK 250
PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY 300
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP 350
QVYTLPPSRE EMTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP 400
VLDSDGSFFL YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG 450
K                                                       451
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCRASQDIS NYLNWYQQKP GKAPKLLIYY  50
TSKLHSGVPS RFSGSGSGTD YTLTISSLQP EDFATYYCQQ GSALPWTFGQ 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

Intra-H (C23-C104)	22-95	148-204	265-325	371-429
	22"-95"	148"-204"	265"-325"	371"-429"
Intra-L (C23-C104)	23'-88'	134'-194'		
	23'"-88'"	134'"-194'"		
Inter-H-L (h 5-CL 126)	224-214'	224"-214'"		
Inter-H-H (h 11, h 14)	230-230"	233-233"		

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84 4:
301, 301"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

tebentafuspum #
tebentafusp

soluble engineered human T cell receptor, dimer of alpha and beta chains, fused at the beta chain, via a linker (254-258), to a humanized immunoglobulin single-chain variable fragment anti-(human CD3), produced in *Escherichia coli*: IG-scFv-TR-BETA (1-500) [humanized V-KAPPA (*Homo sapiens* IGKV3-33*01 (87.2%) -IGKJ1*01 (100%)) [6.3.9] (1-107) -24-mer tetra(tetraglycyl-seryl)-triglycylseryl linker (108-131) -humanized VH (*Homo sapiens* IGHV3-66*01 (76.8%) -(IGHD) -IGHJ4*01 (93.3%)) [8.8.15] (132-253) -5-mer tetraglycyl-seryl linker(254-258) -*Homo sapiens* V-BETA (TRBV19*01 (95.7%) -(TRBD) -TRBJ2-7 (100%)) [5.6.11] (259-370) -*Homo sapiens* C-BETA (TRBC2*01 EX1 1.7-125, EX2 1 (97.7%) S79>C (427), C85.1>A (445), N97>D (459)) (371-500)], disulfide (427-157')with TR-ALPHA chain (1'-195') [*Homo sapiens* V-ALPHA (TRAV17*01 (98.9%) -TRAJ29*01 (100%)) [5.7.9](1'-109') -C-ALPHA (TRAC*01 EX1 1.3-119, N1.2>K (113), T84>C (157) (97.6%)) (110'-195')]

tébentafusp	récepteur des lymphocytes T humain modifié pour être soluble, dimère des chaînes alpha et bêta, fusionné sur la chaîne bêta, via un linker (254-258), au fragment de la chaîne unique variable de l'immunoglobuline humanisée anti-(CD3 humain), produit par *Escherichia coli:* IG-scFv-TR-BETA (1-500) [V-KAPPA humanisé (*Homo sapiens* IGKV3-33*01 (87.2%) -IGKJ1*01 (100%)) [6.3.9] (1-107) -24-mer tétra(tétraglycyl-séryl)-triglycylséryl linker (108-131) -VH humanisé (*Homo sapiens* IGHV3-66*01 (76.8%) -(IGHD) -IGHJ4*01 (93.3%)) [8.8.15] (132-253) -5-mer tétraglycyl-séryl linker (254-258) -*Homo sapiens* V-BETA (TRBV19*01 (95.7%) -(TRBD) -TRBJ2-7 (100%)) [5.6.11] (259-370) -*Homo sapiens* C-BETA (TRBC2*01 EX1 1.7-125, EX2 1 (97.7%) S79>C (427), C85.1>A (445), N97>D (459)) (371-500)], disulfide (427-157') avec la chaîne TR-ALPHA (1'-195') [*Homo sapiens* V-ALPHA (TRAV17*01 (98.9%) -TRAJ29*01 (100%)) [5.7.9](1'-109') -C-ALPHA (TRAC*01 EX1 1.3-119, N1.2>K (113), T84>C (157) (97.6%)) (110'-195')]
tebentafusp	receptor de linfocitos T humanos modificado por ser soluble, heterodímero de las cadenas alfa y beta, fusionados en la cadena beta, a través de un enlace (254-258), con el fragmento de la cadena única variable de la inmunoglobulina humanizada anti-(CD3 humano), producido por *Escherichia coli:* IG-scFv-TR-BETA (1-500) [V-KAPPA humanizado (*Homo sapiens* IGKV3-33*01 (87.2%) -IGKJ1*01 (100%)) [6.3.9] (1-107) -24-mer tetra(tetraglicil-seril)-triglicilseril ligando (108-131) -VH humanizado (*Homo sapiens* IGHV3-66*01 (76.8%) -(IGHD) -IGHJ4*01 (93.3%)) [8.8.15] (132-253) -5-mer tetraglicil-seril ligando (254-258) -*Homo sapiens* V-BETA (TRBV19*01 (95.7%) -(TRBD) -TRBJ2-7 (100%)) [5.6.11] (259-370) -*Homo sapiens* C-BETA (TRBC2*01 EX1 1.7-125, EX2 1 (97.7%) S79>C (427), C85.1>A (445), N97>D (459)) (371-500)], disulfuro (427-157') con la cadena TR-ALPHA (1'-195') [*Homo sapiens* V-ALPHA (TRAV17*01 (98.9%) -TRAJ29*01 (100%)) [5.7.9](1'-109') -C-ALPHA (TRAC*01 EX1 1.3-119, N1.2>K (113), T84>C (157) (97.6%)) (110'-195')]

TCR alpha chain / Chaîne alpha TCR / Cadena alfa TCR

```
AQQGEEDPQA LSIQEGENAT MNCSYKTSIN NLQWYRQNSG RGLVHLILIR 50
SNEREKHSGR LRVTLDTSKK SSSLLITASR AADTASYFCA TDGSTPMQFG 100
KGTRLSVIAN IQKPDPAVYQ LRDSKSSDKS VCLFTDFDSQ TNVSQSKDSD 150
VYITDKCVLD MRSMDFKSNS AVAWSNKSDF ACANAFNNSI IPEDT      195
```

Anti-CD3 scFv - TCR beta chain fusion / Anti-CD3 scFv - chaîne bêta TCR / Anti-CD3 scFv - cadena beta TCR

```
AIQMTQSPSS LSASVGDRVT ITCRASQDIR NYLNWYQQKP GKAPKLLIYY 50
TSRLESGVPS RFSGSGSGTD YTLTISSLQP EDFATYYCQQ GNTLPWTFGQ 100
GTKVEIKGGG GSGGGGSGGG GSGGGGSGGG SEVQLVESGG GLVQPGGSLR 150
LSCAASGYSF TGYTMNWVRQ APGKGLEWVA LINPYKGVST YNQKFKDRFT 200
ISVDKSKNTA YLQMNSLRAE DTAVYYCARS GYYGDSDWYF DVWGQGTLVT 250
VSSGGGGSDG GITQSPKYLF RKEGQNVTLS CEQNLNHDAM YWYRQDPGQG 300
LRLIYYSWAQ GDFQKGDIAE GYSVSREKKE SFPLTVTSAQ KNPTAFYLCA 350
SSWGAPYEQY FGPGTRLTVT EDLKNVFPPE VAVFEPSEAE ISHTQKATLV 400
CLATGFYPDH VELSWWVNGK EVHSGVCTDP QPLKEQPALN DSRYALSSRL 450
RVSATFWQDP RNHFRCQVQF YGLSENDEWT QDRAKPVTQI VSAEAWGRAD 500
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

Inter-chain: alpha chain C157 - beta chain C427

Intra-chain:

TCR alpha chain:	23-89	132-182		
scFv-TCR beta chain fusion:	23-88	153-227	281-349	401-466

α1-α195 = engineered T cell receptor (TCR) α chain fragment

β1-β107 = κ light chain fragment V-KAPPA (IGKV1-12 IGKJ1*01)
β108-β131 = artificial 24 aa peptide linker (G4S)4(G3S)
β132-β253 = heavy chain fragment VH (IGHV3-71 IGHJ2*01)
β254-β258 = artificial 5 aa peptide linker G4S
β259-β500 = engineered T cell receptor (TCR) β chain fragment

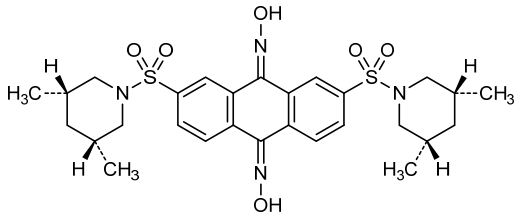
tegavivintum

tegavivint — {2,7-bis[(3*R*,5*S*)-3,5-dimethylpiperidine-1-sulfonyl]anthracene-9,10-diylidene}bis(hydroxylamine)

tégavivint — {2,7-bis[(3*R*,5*S*)-3,5-diméthylpipéridine-1-sulfonyl]anthracène-9,10-diylidène}bis(hydroxylamine)

tegavivint — {2,7-bis[(3*R*,5*S*)-3,5-dimetilpiperidina-1-sulfoni]antraceno-9,10-diilideno}bis(hidroxilamina)

$C_{28}H_{36}N_4O_6S_2$



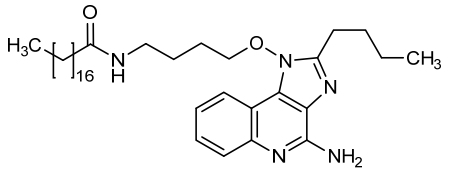
telratolimodum

telratolimod — *N*-{4-[(4-amino-2-butyl-1*H*-imidazo[4,5-*c*]quinolin-1-yl)oxy]butyl}octadecanamide

telratolimod — *N*-{4-[(4-amino-2-butyl-1*H*-imidazo[4,5-*c*]quinoléin-1-yl)oxy]butyl}octadécanamide

telratolimod — *N*-{4-[(4-amino-2-butil-1*H*-imidazo[4,5-*c*]quinolein-1-il)oxi]butil}octadecanamida

$C_{36}H_{59}N_5O_2$



tengonerminum #

tengonermin — human tumor necrosis factor (7-163) fused at the N-terminus to a peptide (1-6) ligand of the human CD13 antigen, trimer, produced in *Escherichia coli*; L-cysteinyl-L-asparaginylglycyl-L-arginyl-L-cysteinylglycyl (1-6, CNGRCG, ligand of the human CD13 antigen)-human tumor necrosis factor soluble form (7-163), non-covalent trimer, produced in *Escherichia coli*

tengonermine — facteur de nécrose tumorale humain (7-163), fusionné sur la partie N-terminale, à un peptide (1-6), se liant à l'antigène CD13 humain, trimère, produit dans *Escherichia coli*; L-cystéinyl-L-asparaginylglycyl-L-arginyl-L-cystéinylglycyl (1-6, CNGRCG, se liant à l'antigène CD13 humain)-forme soluble du facteur de nécrose tumorale humain (7-163), trimère non covalent, produit dans *Escherichia coli*

tengonermina

factor de necrosis tumoral humano (7-163), fusionado en el extremo N-terminal, a un péptido (1-6), unido al antígeno CD13 humano, trímero, producido en *Escherichia coli*; L-cisteinil-L-asparaginilglicil-L-arginil-L-cisteinilglicil (1-6, CNGRCG, unido al antígeno CD13 humano)-forma soluble del factor de necrosis tumoral humano (7-163), trímero no covalente, producido en *Escherichia coli*

```
CNGRCGVRSS SRTPSDKPVA HVVANPQAEG QLQWLNRRAN ALLANGVELR 50
DNQLVVPSEG LYLIYSQVLF KGQGCPSTHV LLTHTISRIA VSYQTKVNLL 100
SAIKSPCQRE TPEGAEAKPW YEPIYLGGVF QLEKGDRLSA EINRPDYLDF 150
AESGQVYFGI IAL                                       163
```

Disulfide bridges locations / Positions des ponts disulfure / Posiciones de los puentes disulfuro
Intra-chain: 1-5 75-107

tepilamidi fumaras
tepilamide fumarate

2-(diethylamino)-2-oxoethyl and methyl (2*E*)-but-2-enedioate

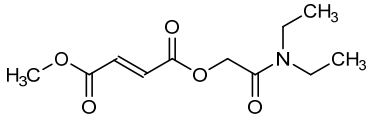
fumarate de tépilamide

(2*E*)-but-2-ènedioate de 2-(diéthylamino)-2-oxoéthyle et de méthyle

fumarato de tepilamida

(2*E*)-but-2-enedioato de 2-(dietilamino)-2-oxoetilo y de metilo

$C_{11}H_{17}NO_5$



tepoditamabum #
tepoditamab

immunoglobulin G1-kappa, anti-[*Homo sapiens* CLEC12A (C-type lectin domain family 12 member A, dendritic cell-associated lectin 2, DCAL-2, myeloid inhibitory C-type lectin-like receptor, MICL, CD371) and anti-[*Homo sapiens* CD3 epsilon (CD3E, Leu-4)], human monoclonal antibody, bispecific;
gamma1 heavy chain anti-CLEC12A (1-447) [*Homo sapiens* VH (IGHV1-46*01 (99.0%) -(IGHD) -IGHJ4*01 (93.3%)) [8.8.11] (1-118) -*Homo sapiens* IGHG1*03, G1m3 nG1m1 (CH1 R120 (215) (119-216), hinge (217-231), CH2 [L1.2>G (236), G1.1>R (237)] (232-341), CH3 E12 (357), M14 (359) [L7>D (352), L24>E (369)] (342-446), CHS K2>del (447)) (119-447)]; (221-214')-disulfide with kappa light chain (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-39*01 (100.00%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191)(108'-214')];
gamma1 heavy chain anti-CD3E (1''-447'') [*Homo sapiens* VH (IGHV3-33*01 (89.8%) -(IGHD) -IGHJ5*02 (100%)) [8.8.11] (1''-118'') -*Homo sapiens* IGHG1*03, G1m3 nG1m1 (CH1 R120 (215) (119-216), hinge (217-231), CH2 [L1.2>G (236), G1.1>R (237)] (232-341), CH3 [L7>K (352), T22>K (367)] (342-446), CHS K>del (447)) (119''-447'')], (221''-214''')-disulfide with kappa light chain (1'''-214''') [*Homo sapiens* V-KAPPA (IGKV1-39*01 (100%) -IGKJ1*01 (100%)) [6.3.9] (1'''-107''') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191)(108'''-214''')]; dimer (227-227'':230-230'')-bisdisulfide

tépoditamab	immunoglobuline G1-kappa, anti-[*Homo sapiens* CLEC12A (membre A de la famille 12 domaine lectine de type C, lectine 2 associée aux cellules dendritiques, DCAL-2, récepteur lectine-l ke de type C inhibiteur myéloïde, MICL, CD371) et anti-[*Homo sapiens* CD3 epsilon (CD3E, Leu-4)], anticorps monoclonal humain, bispécifique; chaîne lourde gamma1 anti-CLEC12A (1-447) [*Homo sapiens* VH (IGHV1-46*01 (99.0%) -(IGHD) -IGHJ4*01 (93.3%)) [8.8.11] (1-118) -*Homo sapiens* IGHG1*03, G1m3 nG1m1 (CH1 R120 (215) (119-216), charnière (217-231), CH2 [L1.2>G (236), G1.1>R (237)] (232-341), CH3 E12 (367), M14 (369) [L7>D (352), L24>E (369)] (342-446), CHS K2>del (447)) (119-447)]; (221-214')-disulfure avec la chaîne légère kappa (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-39*01 (100.00%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; chaîne lourde gamma1 anti-CD3E (1''-447'') [*Homo sapiens* VH (IGHV3-33*01 (89.8%) -(IGHD) -IGHJ5*02 (100%)) [8.8.11] (1''-118'') -*Homo sapiens* IGHG1*03, G1m3 nG1m1 (CH1 R120 (215) (119-216), charnière (217-231), CH2 [L1.2>G (236), G1.1>R (237)] (232-341), CH3 [L7>K (352), T22>K (367)] (342-446), CHS K>del (447)) (119''-447'')], (221''-214''')-disulfure avec la chaîne légère kappa (1'''-214''') [*Homo sapiens* V-KAPPA (IGKV1-39*01 (100%) -IGKJ1*01 (100%)) [6.3.9] (1'''-107''') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191)(108'''-214''')]; dimère (227-227''':230-230'')-bisdisulfure
tepoditamab	inmunoglobulina G1-kappa, anti-[*Homo sapiens* CLEC12A (miembro A de la familia 12 dominio lectina de tipo C, lectina 2 asociada con las células dendríticas, DCAL-2, semejante al receptor lectina de tipo C inhibidor mieloide, MICL, CD371) y anti-[*Homo sapiens* CD3 épsilon (CD3E, Leu-4)], anticuerpo monoclonal humano, biespecífico; cadena pesada gamma1 anti-CLEC12A (1-447) [*Homo sapiens* VH (IGHV1-46*01 (99.0%) -(IGHD) -IGHJ4*01 (93.3%)) [8.8.11] (1-118) -*Homo sapiens* IGHG1*03, G1m3 nG1m1 (CH1 R120 (215) (119-216), bisagra (217-231), CH2 [L1.2>G (236), G1.1>R (237)] (232-341), CH3 E12 (367), M14 (369) [L7>D (352), L24>E (369)] (342-446), CHS K2>del (447)) (119-447)]; (221-214')-disulfuro con la cadena ligera kappa (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-39*01 (100.00%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; gamma1 cadena pesada anti-CD3E (1''-447'') [*Homo sapiens* VH (IGHV3-33*01 (89.8%) -(IGHD) -IGHJ5*02 (100%)) [8.8.11] (1''-118'') -*Homo sapiens* IGHG1*03, G1m3 nG1m1 (CH1 R120 (215) (119-216), hinge (217-231), CH2 [L1.2>G (236), G1.1>R (237)] (232-341), CH3 [L7>K (352), T22>K (367)] (342-446), CHS K>del (447)) (119''-447'')], (221''-214''')-disulfuro con la cadena ligera kappa (1'''-214''') [*Homo sapiens* V-KAPPA (IGKV1-39*01 (100%) -IGKJ1*01 (100%)) [6.3.9] (1'''-107''') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191)(108'''-214''')]; dímero (227-227''':230-230'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada anti-CLEC12A

```
QVQLVQSGAE VKKPGASVKV SCKASGYTFT SYYMHWVRQA PGQGLEWMGI  50
INPSGGSTSY AQKFQGRVTM TRDTSTSTVY MELSSLRSED TAVYYCAKGT 100
TGDWFDYWGQ GTLVTVSSAS TKGPSVFPLA PSSKSTSGGT AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTQTYI 200
CNVNHKPSNT KVDKRVEPKS CDKTHTCPPC PAPELGRGPS VFLFPPKPKD 250
TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNST 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY 350
TDPPSREEMT KNQVSLTCEV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD 400
SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPG    447
```

Heavy chain / Chaîne lourde / Cadena pesada anti-CD3E

```
QVQLVQSGGG VVQPGRSLRL SCVASGFTFS SYGMHWVRQA PGKGLEWVAA  50
IWYNARKQDY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCTRGT 100
GYNWFDPWGQ GTLVTVSSAS TKGPSVFPLA PSSKSTSGGT AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTQTYI 200
CNVNHKPSNT KVDKRVEPKS CDKTHTCPPC PAPELGRGPS VFLFPPKPKD 250
TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNST 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY 350
TKPPSREEMT KNQVSLKCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD 400
SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPG    447
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCRASQSIS SYLNWYQQKP GKAPKLLIYA  50
ASSLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ SYSTPPTFGQ 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

Intra-H (C23-C104) 22-96 145-201 262-322 368-426
22"-96" 145"-201" 262"-322" 368"-426"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194'"
Inter-H-L (h 5-CL 126) 221-214' 221"-214'"
Inter-H-H (h 11, h 14) 227-227" 230-230"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación

H CH2 N84.4:
298, 298"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

timbetasinum #

timbetasin

human thymosin beta-4, N-terminal acetylated : 3,11,25,31,38-pentakis(de-*N*^{6}-acetyl)-1,22,30,33-tetrakis(de-*O*^{3}-phosphono)thymosin β4 (human): *N*-acetyl-L-seryl-L-α-aspartyl-L-lysyl-L-prolyl-L-α-aspartyl-L-methionyl-L-alanyl-L-α-glutamyl-L-isoleucyl-L-α-glutamyl-L-lysyl-L-phenylalanyl-L-α-aspartyl-L-lysyl-L-seryl-L-lysyl-L-leucyl-L-lysyl-L-lysyl-L-threonyl-L-α-glutamyl-L-threonyl-L-glutaminyl-L-α-glutamyl-L-lysyl-L-asparaginyl-L-prolyl-L-leucyl-L-prolyl-L-seryl-L-lysyl-L-α-glutamyl-L-threonyl-L-isoleucyl-L-α-glutamyl-L-glutaminyl-L-α-glutamyl-L-lysyl-L-glutaminyl-L-alanylglycyl-L-α-glutamyl-L-serine

timbétasine

thymosine beta-4 humaine, acétylée en son extrémité N-terminale : 3,11,25,31,38-pentakis(dé-*N*^{6}-acétyl)-1,22,30,33-tétrakis(dé-*O*^{3}-phosphono)thymosine β4 (humaine): *N*-acétyl-L-séryl-L-α-aspartyl-L-lysyl-L-prolyl-L-α-aspartyl-L-méthionyl-L-alanyl-L-α-glutamyl-L-isoleucyl-L-α-glutamyl-L-lysyl-L-phénylalanyl-L-α-aspartyl-L-lysyl-L-séryl-L-lysyl-L-leucyl-L-lysyl-L-lysyl-L-thréonyl-L-α-glutamyl-L-thréonyl-L-glutaminyl-L-α-glutamyl-L-lysyl-L-asparaginyl-L-prolyl-L-leucyl-L-prolyl-L-séryl-L-lysyl-L-α-glutamyl-L-thréonyl-L-isoleucyl-L-α-glutamyl-L-glutaminyl-L-α-glutamyl-L-lysyl-L-glutaminyl-L-alanylglycyl-L-α-glutamyl-L-sérine

timbetasina

timosina beta-4 humana, acetilada en su extremidad N-terminal :
3,11,25,31,38-pentakis(de-*N*^{6}-acetil)-1,22,30,33-tetrakis(de-*O*^{3}-fosfono)timosina β4 (humana):
N-acetil-L-seril-L-α-aspartil-L-lisil-L-prolil-L-α-aspartil-L-metionil-L-alanil-L-α-glutamil-L-isoleucil-L-α-glutamil-L-lisil-L-fenilalanil-L-α-aspartil-L-lisil-L-seril-L-lisil-L-leucil-L-lisil-L-lisil-L-treonil-L-α-glutamil-L-treonil-L-glutaminil-L-α-glutamil-L-lisil-L-asparaginil-L-prolil-L-leucil-L-prolil-L-seril-L-lisil-L-α-glutamil-L-treonil-L-isoleucil-L-α-glutamil-L-glutaminil-L-α-glutamil-L-lisil-L-glutaminil-L-alanilglicil-L-α-glutamil-L-serina

$C_{212}H_{350}N_{56}O_{78}S$

Sequence / Séquence / Secuencia
SDKPDMAEIE KFDKSKLKKT ETQEKNPLPS KETIEQEKQA GES 43

Modified residue / résidu modifié / resto modificado
Ser-1: *N*-acetyl-L-serine

tomivosertibum

tomivosertib

6'-[(6-aminopyrimidin-4-yl)amino]-8'-methyl-2'*H*-spiro[cyclohexane-1,3'-imidazo[1,5-*a*]pyridine]-1',5'-dione

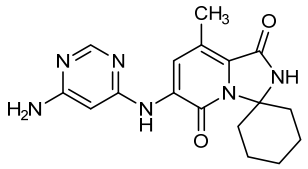
tomivosertib

6'-[(6-aminopyrimidin-4-yl)amino]-8'-méthyl-2'*H*-spiro[cyclohexane-1,3'-imidazo[1,5-*a*]pyridine]-1',5'-dione

tomivosertib

6'-[(6-aminopirimidin-4-il)amino]-8'-metil-2'*H*-spiro[ciclohexano-1,3'-imidazo[1,5-*a*]piridina]-1',5'-diona

$C_{17}H_{20}N_6O_2$



trastuzumabum beta #

trastuzumab beta

immunoglobulin G1-kappa, anti-[*Homo sapiens* ERBB2 (epidermal growth factor receptor 2, receptor tyrosine-protein kinase erbB-2, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], humanized monoclonal antibody; humanized gamma1 heavy chain (1-449) [humanized VH (*Homo sapiens* IGHV3-66*01 (81.6%) -(IGHD) -IGHJ4*01 (100%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (217) (121-218), hinge (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS K>del (449)) (121-449)], (223-214')-disulfide with humanized kappa light chain (1'-214') [humanized V-KAPPA (*Homo sapiens* IGKV1-39*01 (86.3%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (229-229":232-232")-bisdisulfide

trastuzumab bêta

immunoglobuline G1-kappa, anti-[*Homo sapiens* ERBB2 (récepteur 2 du facteur de croissance épidermique, récepteur tyrosine-protéine kinase erbB-2, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], anticorps monoclonal humanisé;
chaîne lourde gamma1 humanisée (1-449) [VH humanisé (*Homo sapiens* IGHV3-66*01 (81.6%) -(IGHD) -IGHJ4*01 (100%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (217) (121-218), charnière (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS K>del (449)) (121-449)], (223-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA humanisé (*Homo sapiens* IGKV1-39*01 (86.3%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (229-229":232-232")-bisdisulfure

trastuzumab beta

inmunoglobulina G1-kappa, anti-[*Homo sapiens* ERBB2 (receptor 2 del factor de crecimiento epidérmico, receptor tirosina-proteína kinasa erbB-2, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], anticuerpo monoclonal humanizado;
cadena pesada gamma1 humanizada (1-449) [VH humanizado (*Homo sapiens* IGHV3-66*01 (81.6%) -(IGHD) -IGHJ4*01 (100%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (217) (121-218), bisagra (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS K>del (449)) (121-449)], (223-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA humanizado (*Homo sapiens* IGKV1-39*01 (86.3%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (229-229":232-232")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAASGFNIK DTYIHWVRQA PGKGLEWVAR  50
IYPTNGYTRY ADSVKGRFTI SADTSKNTAY LQMNSLRAED TAVYYCSRWG 100
GDGFYAMDYW GQGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPG  449
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCRASQDVN TAVAWYQQKP GKAPKLLIYS  50
ASFLYSGVPS RFSGSRSGTD FTLTISSLQP EDFATYYCQQ HYTTPPTFGQ 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

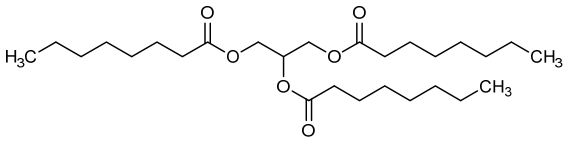
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 147-203 264-324 370-428
22"-96" 147"-203" 264"-324" 370"-428"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194'"
Inter-H-L (h 5-CL 126) 223-214' 223"-214'"
Inter-H-H (h 11, h 14) 229-229" 232-232"
N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
300, 300"

Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados
G0F predominant / prédominant / predominante, A1G0F (0.33 ± 0.05 %), A1G1F (0.35 ± 0.10 %)

tricaprilinum

tricaprilin	propane-1,2,3-triyl trioctanoate
tricapriline	trioctanoate de propane-1,2,3-triyle
tricaprilina	trioctanoato de propano-1,2,3-triilo

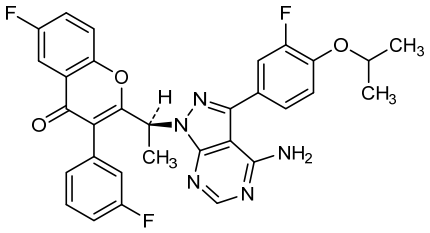
$C_{27}H_{50}O_6$



umbralisibum

umbralis b	2-[(1*S*)-1-{4-amino-3-[3-fluoro-4-(propan-2-yloxy)pheny]-1*H*-pyrazolo[3,4-*d*]pyrimidin-1-yl}ethyl]-6-fluoro-3-(3-fluorophenyl)-4*H*-1-benzopyran-4-one
umbralis b	2-[(1*S*)-1-{4-amino-3-[3-fluoro-4-(propan-2-yloxy)phény]-1*H*-pyrazolo[3,4-*d*]pyrimidin-1-yl}éthyl]-6-fluoro-3-(3-fluorophényl)-4*H*-1-benzopyran-4-one
umbralis b	2-[(1*S*)-1-{4-amino-3-[3-fluoro-4-(propan-2-iloxi)fenil]-1*H*-pirazolo[3,4-*d*]pirimidin-1-il}etil]-6-fluoro-3-(3-fluorofenil)-4*H*-1-benzopiran-4-ona

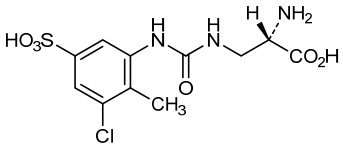
$C_{31}H_{24}F_3N_5O_3$



upacicalcetum

upacicalcet	(2*S*)-2-amino-3-{[(3-chloro-2-methyl-5-sulfophenyl)carbamoyl]amino}propanoic acid
upacicalcet	acide (2*S*)-2-amino-3-{[(3-chloro-2-méthyl-5-sulfophényl)carbamoyl]amino}propanoïque
upacicalcet	ácido (2*S*)-2-amino-3-{[(3-cloro-2-metil-5-sulfofenil)carbamoil]amino}propanoico

$C_{11}H_{14}ClN_3O_6S$



uproleselanum
uproleselan

(2*S*)-2-{2-acetamido-2-deoxy-1-*O*-[(1*R*,2*R*,3*S*,5*R*)-2-[(6-deoxy-α-L-galactopyranosyl)oxy]-3-ethyl-5-(38-oxo-2,5,8,11,14,17,20,23,26,29,32,35-dodecaoxa-39,42-diazatritetracontan-43-oyl)cyclohexyl]-β-D-galactopyranos-3-*O*-yl}-3-cyclohexylpropanoic acid

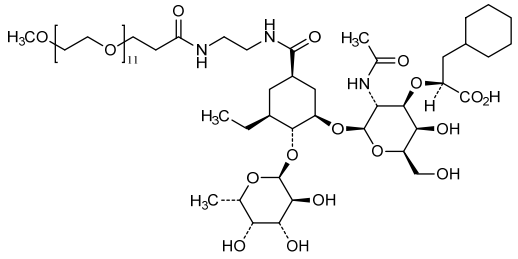
uprolésélan

acide (2*S*)-2-{2-acétamido-2-désoxy-1-*O*-[(1*R*,2*R*,3*S*,5*R*)-2-[(6-désoxy-α-L-galactopyranosyl)oxy]-3-éthyl-5-(38-oxo-2,5,8,11,14,17,20,23,26,29,32,35-dodécaoxa-39,42-diazatritétracontan-43-oyl)cyclohexyl]-β-D-galactopyranos-3-*O*-yl}-3-cyclohexylpropanoïque

uproleselán

ácido (2*S*)-2-{2-acetamido-2-desoxi-1-*O*-[(1*R*,2*R*,3*S*,5*R*)-2-[(6-desoxi-α-L-galactopiranosil)oxi]-3-etil-5-(38-oxo-2,5,8,11,14,17,20,23,26,29,32,35-dodecaoxa-39,42-diazatritetracontan-43-oil)ciclohexil]-β-D-galactopiranos-3-*O*-il}-3-ciclohexilpropanoico

$C_{60}H_{109}N_3O_{27}$



valanafuspum alfa #
valanafusp alfa

anti-(human insulin receptor) immunoglobulin G1 (chimeric human-*Mus musculus*) fused on both heavy chains (1-443, 1''-443'') to seryl-seryl (444-445, 444''-445'')-human α-L-iduronidase (IUDA) ((1-626) natural variant Gln6 (H452>Q)) (447-1072, 447''-1072''), produced in Chinese hamster ovary (CHO) cells, glycoform alfa:
gamma1 heavy chain fused to IDUA (1-1072) [*Mus musculus* VH (IGHV1S56*01 (91.8%) -(IGHD) -IGHJ3*01 (93.3%)) [8.8.6] (1-113) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (210) (114-211), hinge (212-226), CH2 (227-336), CH3 D12 (352), L14 (354) (337-441), CHS K2>S (443) (442-443)) (114-443) -2-mer diseryl linker (444-445) -*Homo sapiens* IDUA, catalytic glutamates E182 (601), E299 (718) (446-1072)], (216-214')-disulfide with kappa light chain (1'-214') [*Mus musculus* V-KAPPA (IGKV9-120*01 (94.7%) -IGKJ1*01 (91.7%), L9>M (104)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (222-222'':225-225'')-bisdisulfide

valanafusp alfa

immunoglobuline G1 (chimérique humaine-*Mus musculus*) anti-(récepteur à l'insuline humain), fusionnée sur les deux chaînes lourdes (1-443, 1"-443") à séryl-séryl (444-445, 444"-444")-α-L-iduronidase humaine (IDUA) (Gln6 variant naturel (H452Q)), produite dans des cellules ovariennes de hamsters chinois (CHO), glycoforme alfa:
chaîne lourde gamma1 fusionnée à l'IDUA (1-1072) [*Mus musculus* VH (IGHV1S56*01 (91.8%) -(IGHD) -IGHJ3*01 (93.3%)) [8.8.6] (1-113) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (210) (114-211), charnière (212-226), CH2 (227-336), CH3 D12 (352), L14 (354) (337-441), CHS K2>S (443) (442-443)) (114-443) -2-mer diséryl linker (444-445) -*Homo sapiens* IDUA, glutamates catalytiques E182 (601), E299 (718) (446-1072)], (216-214')-disulfure avec la chaîne légère kappa (1'-214') [*Mus musculus* V-KAPPA (IGKV9-120*01 (94.7%) -IGKJ1*01 (91.7%), L9>M (104)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3A45.1 (153), V101 (191) (108'-214')]; dimère (222-222":225-225")-bisdisulfure

valanafusp alfa

inmunoglobulina G1 (quimérica humana-*Mus musculus*) anti-(receptor de la insulina humana), fusionada con las diez cadenas pesadas (1-443, 1"-443") al seril-seril (444-445, 444"-444")-α-L-iduronidasa humana (IDUA) ((1-626) Gln6 variante natural (H452Q)), producida en las células ováricas de hamsters chinos (CHO), glicoforma alfa:
cadena pesada gamma1 fusionada con la IDUA (1-1072) [*Mus musculus* VH (IGHV1S56*01 (91.8%) -(IGHD) -IGHJ3*01 (93.3%)) [8.8.6] (1-113) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (210) (114-211), bisagra (212-226), CH2 (227-336), CH3 D12 (352), L14 (354) (337-441), CHS K2>S (443) (442-443)) (114-443) -2-mer ligante diseril (444-445) -*Homo sapiens* IDUA, glutamatos catalíticos E182 (601), E299 (718) (446-1072)], (216-214')-disulfuro con la cadena ligera kappa (1'-214') *[Mus musculus* V-KAPPA (IGKV9-120*01 (94.7%) -IGKJ1*01 (91.7%), L9>M (104)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3A45.1 (153), V101 (191) (108'-214')]; dímero (222-222":225-225")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLQQSGPE LVKPGALVKI SCKASGYTFT NYDIHWVKQR PGQGLEWIGW 50
IYPGDGSTKY NEKFKGKATL TADKSSSTAY MHLSSLTSEK SAVYFCAREW 100
AYWGQGTLVT VSAASTKGPS VFPLAPSSKS TSGGTAALGC LVKDYFPEPV 150
TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG TQTYICNVNH 200
KPSNTKVDKK VEPKSCDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS 250
RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYNSTYRVVS 300
VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR EPQVYTLPPS 350
RDELTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT PPVLDSDGSF 400
FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLS PGSSSEAPHL 450
VQVDAARALW PLRRFWRSTG FCPPLPHSQA DQYVLSWDQQ LNLAYVGAVP 500
HRGIKQVRTH WLLELVTTRG STGRGLSYNF THLDGYLDLL RENQLLPGFE 550
LMGSASGHFT DFEDKQQVFE WKDLVSSLAR RYIGRYGLAH VSKWNFETWN 600
EPDHHDFDNV SMTMQGFLNY YDACSEGLRA ASPALRLGGP GDSFHTPPRS 650
PLSWGLLRHC HDGTNFFTGE AGVRLDYISL HRKGARSSIS ILEQEKVVAQ 700
QIRQLFPKFA DTPIYNDEAD PLVGWSLPQP WRADVTYAAM VVKVIAQHQN 750
LLLANTTSAF PYALLSNDNA FLSYHPHPFA QRTLTARFQV NNTRPPHVQL 800
LRKPVLTAMG LLALLDEEQL WAEVSQAGTV LDSNHTVGVL ASAHRPQGPA 850
DAWRAAVLIY ASDDTRAHPN RSVAVTLRLR GVPPGPGLVY VTRYLDNGLC 900
SPDGEWRRLG RPVFPTAEQF RRMRAAEDPV AAAPRPLPAG GRLTLRPALR 950
LPSLLLVHVC ARPEKPPGQV TRLRALPLTQ GQLVLVWSDE HVGSKCLWTY 1000
EIQFSQDGKA YTPVSRKPST FNLFVFSPDT GAVSGSYRVR ALDYWARPGP 1050
FSDPVPYLEV PVPRGPPSPG NP                                1072
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASLGERVS LTCRASQDIG GNLYWLQQGP DGTIKRLIYA 50
TSSLDSGVPK RFSGSRSGSD YSLTISSLES EDFVDYYCLQ YSSSPWTFGG 100
GTKMEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

Intra-H (C23-C104) 22-96 140-196 257-317 363-421
22"-96" 140"-196" 257"-317" 363"-421"
Intra-H (IDUA) 472-624 660-900 960-996
472"-624" 660"-900" 960"-996"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194'"
Inter-H-L (h 5-CL 126) 216-214' 216"-214'"
Inter-H-H (h 11, h 14) 222-222" 225-225"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4: 293, 293"
IDUA: 529, 609, 755, 791, 834, 870, 529", 609", 755", 791", 834", 870"

Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

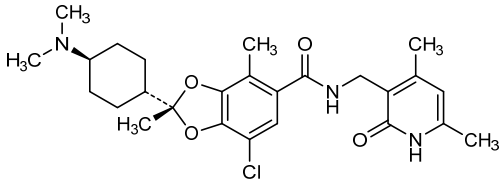
valemetostatum

valemetostat — (2*R*)-7-chloro-2-[*trans*-4-(dimethylamino)cyclohexyl]-*N*-[(4,6-dimethyl-2-oxo-1,2-dihydropyridin-3-yl)methyl]-2,4-dimethyl-1,3-benzodioxole-5-carboxamide

valémétostat — (2*R*)-7-chloro-2-[*trans*-4-(diméthylamino)cyclohexyl]-*N*-[(4,6-diméthyl-2-oxo-1,2-dihydropyridin-3-yl)méthyl]-2,4-diméthyl-1,3-benzodioxole-5-carboxamide

valemetostat — (2*R*)-7-cloro-2-[*trans*-4-(dimetilamino)ciclohexil]-*N*-[(4,6-dimetil-2-oxo-1,2-dihidropiridin-3-il)meti]-2,4-dimetil-1,3-benzodioxol-5-carboxamida

$C_{26}H_{34}ClN_3O_4$



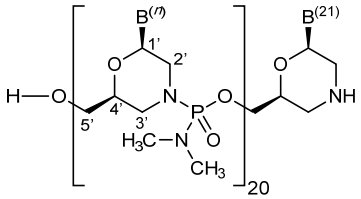
viltolarsenum

viltolarsen — *all-P-ambo*-[2',3'-azanediyl-*P*,2',3'-trideoxy-*P*-(dimethylamino)-2',3'-seco](2'-*N*→5')(CCTCCGGTTC TGAAGGTGTT C)

viltolarsen — *tout-P-ambo*-[2',3'-azanediyl-*P*,2',3'-tridésoxy-*P*-(diméthylamino)-2',3'-séco](2'-*N*→5')(CCTCCGGTTC TGAAGGTGTT C)

viltolarsén — *todo-P-ambo*-[2',3'-azanediil-*P*,2',3'-tridesoxi-*P*-(dimetilamino)-2',3'-seco](2'-*N*→5')(CCTCCGGTTC TGAAGGTGTT C)

$C_{244}H_{381}N_{113}O_{88}P_{20}$



CCTCCGGTTC TGAAGGTGTT C

vopratelimabum #

vopratelimab — immunoglobulin G1-kappa, anti-[*Homo sapiens* ICOS (inductible T-cell costimulatory, activation-induc ble lymphocyte immunomediatory molecule, AILIM, CD278)], humanized monoclonal ant body;

gamma1 heavy chain (1-447) [humanized VH (IGHV3-74*01 (88.8%) -(IGHD) -IGHJ5*01 (100%)) [8.8.10] (1-117) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (214) (118-215), hinge (216-230), CH2 (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-218')-disulfide with kappa light chain (1'-218') [humanized V-KAPPA (IGKV4-1*01 (84.2%) -IGKJ3*01 (100%)) [10.3.9] (1'-111') -*Homo sapiens* IGKC*01, Km3 A45.1 (157), V101 (195) (112'-218')]; dimer (226-226":229-229")-bisdisulfide

vopratélimab

immunoglobuline G1-kappa, anti-[*Homo sapiens* ICOS (costimulateur inductible du lymphocyte T, molécule immunomédiateur lymphocytaire inductible par activation, AILIM, CD278)], anticorps monoclonal humanisé; chaîne lourde gamma1 (1-447) [VH humanisé (IGHV3-74*01 (88.8%) -(IGHD) -IGHJ5*01 (100%)) [8.8.10] (1-117) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (214) (118-215), charnière (216-230), CH2 (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-218')-disulfure avec la chaîne légère kappa (1'-218') [V-KAPPA humanisé (IGKV4-1*01 (84.2%) -IGKJ3*01 (100%)) [10.3.9] (1'-111') -*Homo sapiens* IGKC*01, Km3 A45.1 (157), V101 (195) (112'-218')]; dimère (226-226":229-229")-bisdisulfure

vopratelimab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* ICOS (coestimulador induc ble del linfocito T, molécula inmunomediadora linfocitaria induc ble por activación, AILIM, CD278)], anticuerpo monoclonal humanizado; cadena pesada gamma1 (1-447) [VH humanizado (IGHV3-74*01 (88.8%) -(IGHD) -IGHJ5*01 (100%)) [8.8.10] (1-117) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (214) (118-215), bisagra (216-230), CH2 (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-218')-disulfuro con la cadena ligera kappa (1'-218') [V-KAPPA humanizado (IGKV4-1*01 (84.2%) -IGKJ3*01 (100%)) [10.3.9] (1'-111') -*Homo sapiens* IGKC*01, Km3 A45.1 (157), V101 (195) (112'-218')]; dímero (226-226":229-229")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAASGFTFS DYWMDWVRQA PGKGLVWVSN  50
IDEDGSITEY SPFVKGRFTI SRDNAKNTLY LQMNSLRAED TAVYYCTRWG 100
RFGFDSWGQG TLVTVSSAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF 150
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC 200
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT 250
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT 350
LPPSREEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS 400
DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPGK    447
```

Light chain / Chaîne légère / Cadena ligera

```
DIVMTQSPDS LAVSLGERAT INCKSSQSLL SGSFNYLTWY QQKPGQPPKL  50
LIFYASTRHT GVPDRFSGSG SGTDFTLTIS SLQAEDVAVY YCHHHYNAPP 100
TFGPGTKVDI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL NNFYPREAKV 150
QWKVDNALQS GNSQESVTEQ DSKDSTYSLS STLTLSKADY EKHKVYACEV 200
THQGLSSPVT KSFNRGEC                                    218
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

Intra-H (C23-C104) 22-96 144-200 261-321 367-425
22"-96" 144"-200" 261"-321" 367"-425"
Intra-L (C23-C104) 23'-92' 138'-198'
23"'-92"' 138"'-198"'
Inter-H-L (h 5-CL 126) 220-218' 220"-218"'
Inter-H-H (h 11, h 14) 226-226" 229-229"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
297, 297"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados
C-terminal lysine clipping: H CHS K2: 447, 447"

zilucoplanum

zilucoplan

N^2-acetyl-L-lysyl-L-valyl-L-α-glutamyl-L-arginyl-L-phenylalanyl-L-α-aspartyl-*N*-methyl-L-α-aspartyl-3-methyl-L-valyl-L-tyrosyl-3-(1*H*-pyrrolo[2,3-*b*]pyridin-3-yl)-L-alanyl-L-α-glutamyl-L-tyrosyl-L-prolyl-(2*S*)-2-cyclohexylglycyl-*N*^{6}-(3-{ω-[(*N*-hexadecanoyl-L-γ-glutamyl)amino]tetracosakis(oxyethylene)-α-yl}propanoyl)-L-lysine (6→1^6)-lactam

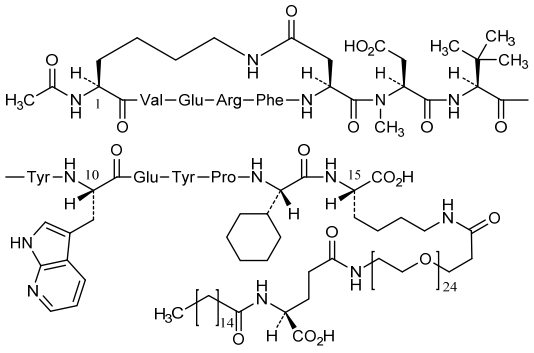
zilucoplan

N^2-acétyl-L-lysyl-L-valyl-L-α-glutamyl-L-arginyl-L-phénylalanyl-L-α-aspartyl-*N*-méthyl-L-α-aspartyl-3-méthyl-L-valyl-L-tyrosyl-3-(1*H*-pyrrolo[2,3-*b*]pyridin-3-yl)-L-alanyl-L-α-glutamyl-L-tyrosyl-L-prolyl-(2*S*)-2-cyclohexylglycyl-*N*^{6}-(3-{ω-[(*N*-hexadécanoyl-L-γ-glutamyl)amino]tétracosakis(oxyéthylène)-α-yl}propanoyl)-L-lysine (6→1^6)-lactam

zilucoplán

N^2-acetil-L-lisil-L-valil-L-α-glutamil-L-arginil-L-fenilalanil-L-α-aspartil-*N*-metil-L-α-aspartil-3-metil-L-valil-L-tirosil-3-(1*H*-pirrolo[2,3-*b*]piridin-3-il)-L-alanil-L-α-glutamil-L-tirosil-L-prolil-(2*S*)-2-ciclohexilglicil-*N*^{6}-(3-{ω-[(*N*-hexadecanoil-L-γ-glutamil)amino]tetracosakis(oxietileno)-α-yl}propanoil)-L-lisina (6→1^6)-lactam

$C_{172}H_{278}N_{24}O_{55}$



AMENDMENTS TO PREVIOUS LISTS
MODIFICATIONS APPORTÉES AUX LISTES ANTÉRIEURES
MODIFICACIONES A LAS LISTAS ANTERIORES

Recommended International Nonproprietary Names (Rec. INN): List 66
Dénominations communes internationales proposées (DCI Rec.): Liste 66
Denominaciones Comunes Internacionales Propuestas (DCI Rec.): Lista 66
(WHO Drug Information, Vol. 25, No. 3, 2011)

p. 327 **pracinostatum**

pracinostat	*replace the chemical name by the following one*
pracinostat	*sustitúyase el nombre químico por el siguiente*
	(2*E*)-3-{2-butyl-1-[2-(diethylamino)ethyl]-1*H*-benzimidazol-5-yl}-*N*-hydroxyprop-2-enamide
	(2*E*)-3-{2-butil-1-[2-(dietilamino)eti]-1*H*-benzimidazol-5-il}-*N*-hidroxiprop-2-enamida

Recommended International Nonproprietary Names (Rec. INN): List 70
Dénominations communes internationales proposées (DCI Rec.): Liste 70
Denominaciones Comunes Internacionales Propuestas (DCI Rec.): Lista 70
(WHO Drug Information, Vol. 27, No. 3, 2013)

p. 316 **turoctocogum alfa pegolum #**

turoctocog alfa pegol	*replace the description by the following one*
turoctocog alfa pégol	*remplacer la description par la suivante*
turoctocog alfa pegol	*sustitúyase la descripción por la siguiente*
	human coagulation factor VIII-(1-750)-(1638-1648)-peptide compound with human coagulation factor VIIIa light chain, glycosylated and pegylated;
	O$^{3.750}$-[α-methylpoly(oxyethylene) 5-(acetamido)-3,5-dideoxy-D-*glycero*-α-D-*galacto*-non-2-ulopyranosylonate-(2→4)-α-D-galactopyranosyl-(1→4)-2-(acetamido)-2-deoxy-α-D-galactopyranosy]-des-(751-1637)-human coagulation factor VIII-(1-1648)-peptide containing 92 kDa factor VIIIa heavy chain compound with human coagulation factor VIIIa light chain glycosylated (glycoform alfa produced in CHO cells)
	facteur VIII de coagulation humain-(1-750)-(1638-1648)-peptide associé à la chaîne légère du facteur VIIIa de coagulation humain glycosylés et pégylés;
	O$^{3.750}$-[5-(acétamido)-3,5-didésoxy-D-*glycéro*-α-D-*galacto*-non-2-ulopyranosylonate de α-méthylpoly(oxyéthylène)-(2→4)-α-D-galactopyranosyl-(1→4)-2-(acétamido)-2-déoxy-α-D-galactopyranosy]-dès-(751-1637)-facteur VIII de coagulation humain-(1-1648)-peptide contenant la chaîne lourde de 92 kDa du factor VIIIa associé à la chaîne légère du facteur VIIIa de coagulation humain glycosylés (glycoforme alfa produit par des cellules CHO)

factor VIII de coagulación humano-(1-750)-(1638-1648)-péptido asociado a la cadena ligera del factor VIIIa de coagulación humano glicosilados y pegilados;

O$^{3.750}$-[5-(acetamido)-3,5-didesoxi-D-*glicero*-β-D-*galacto*-non-2-ulopiranosilonato de α-metilpoli(oxietileno)-(2→4)-α-D-galactopiranosil-(1→4)-2-(acetamido)-2-desoxi-α-D-galactopiranosil]-des-(751-1637)-factor VIII de coagulación humano-(1-1648)-péptido que contiene la cadena pesada de 92 kDa del factor VIIIa asociado a la cadena ligera del factor VIIIa de coagulación humano glicosilados (glicoforma alfa producido por células CHO)

Recommended International Nonproprietary Names (Rec. INN): List 76
Dénominations communes internationales proposées (DCI Rec.): Liste 76
Denominaciones Comunes Internacionales Propuestas (DCI Rec.): Lista 76
(WHO Drug Information, Vol. 30, No. 3, 2016)

p. 525 **pibrentasvirum**

pibrentasvir	*replace the molecular formula by the following one*
pibrentasvir	*remplacer la formule moléculaire brute par la suivante*
pibrentasvir	*sustitúyase la fómula molecular por la siguiente*

$C_{57}H_{65}F_5N_{10}O_8$

Electronic structure available on Mednet: http://mednet.who.int/
Structure électronique disponible sur Mednet: http://mednet.who.int/
Estructura electrónica disponible en Mednet: http://mednet.who.int/
* http://www.who.int/medicines/services/inn/publication/en/

Procedure and Guiding Principles / Procédure et Directives / Procedimientos y principios generales

The text of the *Procedures for the Selection of Recommended International Nonproprietary Names for Pharmaceutical Substances* and *General Principles for Guidance in Devising International Nonproprietary Names for Pharmaceutical Substances* will be reproduced in proposed INN lists only.

Les textes de la *Procédure à suivre en vue du choix de dénominations communes internationales recommandées pour les substances pharmaceutiques* et des *Directives générales pour la formation de dénominations communes internationales applicables aux substances pharmaceutiques* seront publiés seulement dans les listes des DCI proposées.

El texto de los *Procedimientos de selección de denominaciones comunes internacionales recomendadas para las sustancias farmacéuticas* y de los *Principios generales de orientación para formar denominaciones comunes internacionales para sustancias farmacéuticas* aparece solamente en las listas de DCI propuestas.

International Nonproprietary Names for Pharmaceutical Substances (INN)

RECOMMENDED International Nonproprietary Names: List 81

Notice is hereby given that, in accordance with paragraph 7 of the Procedure for the Selection of Recommended International Nonproprietary Names for Pharmaceutical Substances [*Off. Rec. Wld Health Org.*, 1955, **60**, 3 (Resolution EB15.R7); 1969, **173**, 10 (Resolution EB43.R9); Resolution EB115.R4 (EB115/2005/REC/1)], the following names are selected as Recommended International Nonproprietary Names. The inclusion of a name in the lists of Recommended International Nonproprietary Names does not imply any recommendation of the use of the substance in medicine or pharmacy.
Lists of Proposed (1–117) and Recommended (1–78) International Nonproprietary Names can be found in *Cumulative List No. 17, 2017* (available in CD-ROM only).

Dénominations communes internationales des Substances pharmaceutiques (DCI)

Dénominations communes internationales RECOMMANDÉES: Liste 81

Il est notifié que, conformément aux dispositions du paragraphe 7 de la Procédure à suivre en vue du choix de Dénominations communes internationales recommandées pour les Substances pharmaceutiques [*Actes off. Org. mond. Santé*, 1955, **60**, 3 (résolution EB15.R7); 1969, **173**, 10 (résolution EB43.R9); résolution EB115.R4 (EB115/2005/REC/1)] les dénominations ci-dessous sont choisies par l'Organisation mondiale de la Santé en tant que dénominations communes internationales recommandées. L'inclusion d'une dénomination dans les listes de DCI recommandées n'implique aucune recommandation en vue de l'utilisation de la substance correspondante en médecine ou en pharmacie.
On trouvera d'autres listes de Dénominations communes internationales proposées (1–117) et recommandées (1–78) dans la *Liste récapitulative No. 17, 2017* (disponible sur CD-ROM seulement).

Denominaciones Comunes Internacionales para las Sustancias Farmacéuticas (DCI)

Denominaciones Comunes Internacionales RECOMENDADAS: Lista 81

De conformidad con lo que dispone el párrafo 7 del Procedimiento de Selección de Denominaciones Comunes Internacionales Recomendadas para las Sustancias Farmacéuticas [*Act. Of. Mund. Salud*, 1955, **60**, 3 (Resolución EB15.R7); 1969, **173**, 10 (Resolución EB43.R9); Résolution EB115.R4 (EB115/2005/REC/1) EB115.R4 (EB115/2005/REC/1)], se comunica por el presente anuncio que las denominaciones que a continuación se expresan han sido seleccionadas como Denominaciones Comunes Internacionales Recomendadas. La inclusión de una denominación en las listas de las Denominaciones Comunes Recomendadas no supone recomendación alguna en favor del empleo de la sustancia respectiva en medicina o en farmacia.
Las listas de Denominaciones Comunes Internacionales Propuestas (1–117) y Recomendadas (1–78) se encuentran reunidas en *Cumulative List No. 17, 2017* (disponible sólo en CD-ROM).

Latin, English, French, Spanish: *Recommended INN*	*Chemical name or description; Molecular formula; Graphic formula*
DCI Recommandée	*Nom chimique ou description; Formule brute; Formule développée*
DCI Recomendada	*Nombre químico o descripción; Fórmula molecular; Fórmula desarrollada*

abelacimabum #	
abelacimab	immunoglobulin G1-lambda, anti-[*Homo sapiens* F11 (coagulation factor XI, FXI, plasma thromboplastin antecedent, PTA)], *Homo sapiens* monoclonal antibody; gamma1 heavy chain (1-452) [*Homo sapiens* VH (IGHV3-23*01 (93.9%) -(IGHD) -IGHJ4*01 (100%)) [8.8.15] (1-122) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (219) (123-220), hinge (221-235), CH2 D27>A (270), P114>A (334) (236-345), CH3 E12 (361), M14 (363) (346-450), CHS (451-452)) (123-452)], (225-215')-disulfide with lambda light chain (1'-216') [*Homo sapiens* V-LAMBDA (IGLV1-44*01 (93.5%) -IGLJ2*01 (100%)) [8.3.11] (1'-110') -*Homo sapiens* IGLC2*01 (111'-216')]; dimer (231-231'':234-234'')-bisdisulfide
abélacimab	immunoglobuline G1-lambda, anti-[*Homo sapiens* F11 (facteur de coagulation XI, FXI, antécédent de la thromboplastine plasmatique, PTA)], *Homo sapiens* anticorps monoclonal; chaîne lourde gamma1 (1-452) [*Homo sapiens* VH (IGHV3-23*01 (93.9%) -(IGHD) -IGHJ4*01 (100%)) [8.8.15] (1-122) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (219) (123-220), charnière (221-235), CH2 D27>A (270), P114>A (334) (236-345), CH3 E12 (361), M14 (363) (346-450), CHS (451-452)) (123-452)], (225-215')-disulfure avec la chaîne légère lambda (1'-216') [*Homo sapiens* V-LAMBDA (IGLV1-44*01 (93.5%) -IGLJ2*01 (100%)) [8.3.11] (1'-110') -*Homo sapiens* IGLC2*01 (111'-216')]; dimère (231-231'':234-234'')-bisdisulfure
abelacimab	inmunoglobulina G1-lambda, anti-[*Homo sapiens* F11 (factor de coagulación XI, FXI, antecedente de la tromboplastina plasmática, PTA)], *Homo sapiens* anticuerpo monoclonal; cadena pesada gamma1 (1-452) [*Homo sapiens* VH (IGHV3-23*01 (93.9%) -(IGHD) -IGHJ4*01 (100%)) [8.8.15] (1-122) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (219) (123-220), bisagra (221-235), CH2 D27>A (270), P114>A (334) (236-345), CH3 E12 (361), M14 (363) (346-450), CHS (451-452)) (123-452)], (225-215')-disulfuro con la cadena ligera lambda (1'-216') [*Homo sapiens* V-LAMBDA (IGLV1-44*01 (93.5%) -IGLJ2*01 (100%)) [8.3.11] (1'-110') -*Homo sapiens* IGLC2*01 (111'-216')]; dímero (231-231'':234-234'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLLESGGG LVQPGGSLRL SCAASGFTFS TAAMSWVRQA PGKGLEWVSG  50
ISGSGSSTYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAREL 100
SYLYSGYYFD YWGQGTLVTV SSASTKGPSV FPLAPSSKST SGGTAALGCL 150
VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ SSGLYSLSSV VTVPSSSLGT 200
QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL GGPSVFLFPP 250
KPKDTLMISR TPEVTCVVVA VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALAAPIEKT ISKAKGQPRE 350
PQVYTLPPSR EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP 400
PVLDSDGSFF LYSKLTVDKS RWQQGNVFSC SVMHEALHNH YTQKSLSLSP 450
GK                                                      452
```

Light chain / Chaîne légère / Cadena ligera

```
QSVLTQPPSA SGTPGQRVTI SCSGSSSNIG SNDVSWYQQL PGTAPKLLIY  50
KNYNRPSGVP DRFSGSKSGT SASLAISGLQ SEDEADYYCS AWDQRQFDVV 100
FGGGTKLTVL GQPKAAPSVT LFPPSSEELQ ANKATLVCLI SDFYPGAVTV 150
AWKADSSPVK AGVETTTPSK QSNNKYAASS YLSLTPEQWK SHRSYSCQVT 200
HEGSTVEKTV APTECS                                      216
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 149-205 266-326 372-430
22"-96" 149"-205" 266"-326" 372"-430"
Intra-L (C23-C104) 22'-89' 138'-197'
22''-89"' 138"'-197"'
Inter-H-L (h 5-CL 126) 225-215' 225"-215"'
Inter-H-H (h 11, h 14) 231-231' 234-234"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4
302, 302"
fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

N-terminal glutamine cyclization to pyroglutamate (pE, 5-oxoproline)
H VH Q1 1, 1'
L VL Q1 1, 1'

C-terminal lysine clipping
H CHS K2 452, 452'

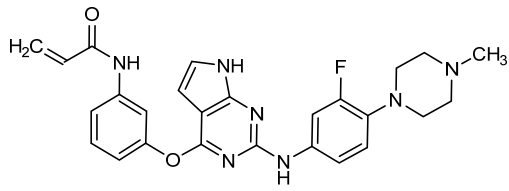
abivertinibum

abivertinib — *N*-[3-({2-[3-fluoro-4-(4-methylpiperazin-1-yl)anilino]-7*H*-pyrrolo[2,3-*d*]pyrimidin-4-yl}oxy)phenyl]prop-2-enamide

abivertinib — *N*-[3-({2-[3-fluoro-4-(4-méthylpipérazin-1-yl)anilino]-7*H*-pyrrolo[2,3-*d*]pyrimidin-4-yl}oxy)phényl]prop-2-énamide

abivertinib — *N*-[3-({2-[3-fluoro-4-(4-metilpiperazin-1-il)anilino]-7*H*-pirrolo[2,3-*d*]pirimidin-4-il}oxi)fenil]prop-2-enamida

$C_{26}H_{26}FN_7O_2$



adriforantum

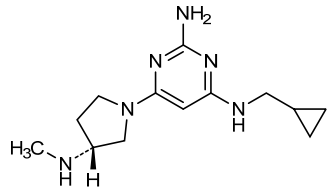
adriforant — N^4-(cyclopropylmethyl)-6-[(3*R*)-3-(methylamino)pyrrolidin-1-yl]pyrimidine-2,4-diamine

adriforant — N^4-(cyclopropylméthyl)-6-[(3*R*)-3-(méthylamino)pyrrolidin-1-yl]pyrimidine-2,4-diamine

adriforant

*N*⁴-(ciclopropilmetil)-6-[(3*R*)-3-(metilamino)pirrolidin-1-il]pirimidina-2,4-diamina

$C_{13}H_{22}N_6$



alteminostatum

alteminostat

N-[7-(hydroxyamino)-7-oxoheptyl]-4-methyl-*N*-[4-(1-methyl-1*H*-indazol-6-yl)phenyl]piperazine-1-carboxamide

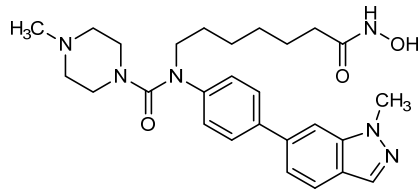
altéminostat

N-[7-(hydroxyamino)-7-oxoheptyl]-4-méthyl-*N*-[4-(1-méthyl-1*H*-indazol-6-yl)phényl]pipérazine-1-carboxamide

alteminostat

N-[7-(hidroxiamino)-7-oxoheptil]-4-metil-*N*-[4-(1-metil-1*H*-indazol-6-il)fenil]piperazina-1-carboxamida

$C_{27}H_{36}N_6O_3$



amelparibum

amelparib

10-ethoxy-8-[(morpholin-4-yl)methyl]-2,3,4,6-tetrahydrobenzo[*h*][1,6]naphthyridin-5(1*H*)-one

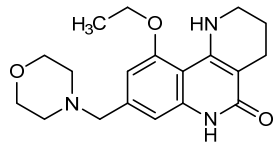
amelparib

10-éthoxy-8-[(morpholin-4-yl)méthyl]-2,3,4,6-tétrahydrobenzo[*h*][1,6]naphtyridin-5(1*H*)-one

amelparib

10-etoxi-8-[(morfolin-4-il)metil]-2,3,4,6-tetrahidrobenzo[*h*][1,6]naftiridin-5(1*H*)-ona

$C_{19}H_{25}N_3O_3$



amlivirsenum

amlivirsen

all-P-ambo-2'-*O*-(2-methoxyethyl)-*P*-thioguanylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-*P*-thioadenylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-*P*-thioguanylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-*P*-thioadenylyl-(3'→5')-2'-deoxy-*P*-thioguanylyl-(3'→5')-2'-deoxy-*P*-thioguanylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-deoxy-*P*-thioguanylyl-(3'→5')-2'-deoxy-*P*-thioadenylyl-(3'→5')-2'-deoxy-*P*-thioadenylyl-(3'→5')-2'-deoxy-*P*-thioguanylyl-(3'→5')-2'-deoxy-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-deoxy-*P*-thioguanylyl-(3'→5')-2'-deoxy-*P*-thioadenylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-*P*-thioadenylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-*P*-thioguanylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyl-*P*-thiouridylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-*P*-thioguanylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methylcytidine 5'-(1-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]-13,13-bis{[3-({6-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]hexyl}amino)-3-oxopropoxy]methyl}-8,15,19-trioxo-11-oxa-7,14,20-triazahexacosan-26-yl hydrogen phosphate)

amlivirsen

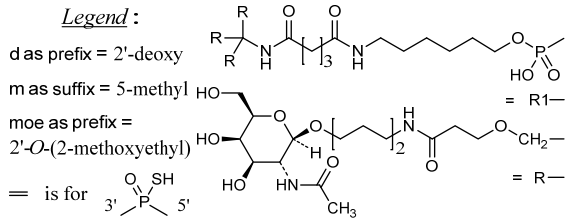
5'-(hydrogénophosphate de 1-[(2-acétamido-2-désoxy-β-D-galactopyranosyl)oxy]-13,13-bis{[3-({6-[(2-acétamido-2-désoxy-β-D-galactopyranosyl)oxy]hexyl}amino)-3-oxopropoxy]méthyl}-8,15,19-trioxo-11-oxa-7,14,20-triazahexacosan-26-yle) de *tout-P-ambo*-2'-*O*-(2-méthoxyéthyl)-*P*-thioguanylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-*P*-thioadénylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-*P*-thioguanylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-*P*-thioadénylyl-(3'→5')-2'-désoxy-*P*-thioguanylyl-(3'→5')-2'-désoxy-*P*-thioguanylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-désoxy-*P*-thioguanylyl-(3'→5')-2'-désoxy-*P*-thioadénylyl-(3'→5')-2'-désoxy-*P*-thioadénylyl-(3'→5')-2'-désoxy-*P*-thioguanylyl-(3'→5')-2'-désoxy-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-désoxy-*P*-thioguanylyl-(3'→5')-2'-désoxy-*P*-thioadénylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-*P*-thioadénylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-*P*-thioguanylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthyl-*P*-thiouridylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-*P*-thioguanylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthylcytidine

amlivirsén

5'-(hidrogenofosfato de 1-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]-13,13-bis{[3-({6-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]hexil}amino)-3-oxopropoxi]metil}-8,15,19-trioxo-11-oxa-7,14,20-triazahexacosan-26-ilo) de *todo-P-ambo*-2'-*O*-(2-metoxietil)-*P*-tioguanilil-(3'→5')-2'-*O*-(2-metoxietil)-5-metil-*P*-tiocitidilil-(3'→5')-2'-*O*-(2-metoxietil)-*P*-tioadenilil-(3'→5')-2'-*O*-(2-metoxietil)-*P*-tioguanilil-(3'→5')-2'-*O*-(2-metoxietil)-*P*-tioadenilil-(3'→5')-2'-desoxi-*P*-tioguanilil-(3'→5')-2'-desoxi-*P*-tioguanilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2'-desoxi-*P*-tioguanilil-(3'→5')-2'-desoxi-*P*-tioadenilil-(3'→5')-2'-desoxi-*P*-tioadenilil-(3'→5')-2'-desoxi-*P*-tioguanilil-(3'→5')-2'-desoxi-5-metil-*P*-tiocitidilil-(3'→5')-2'-desoxi-*P*-tioguanilil-(3'→5')-2'-desoxi-*P*-tioadenilil-(3'→5')-2'-*O*-(2-metoxietil)-*P*-tioadenilil-(3'→5')-2'-*O*-(2-metoxietil)-*P*-tioguanilil-(3'→5')-2'-*O*-(2-metoxietil)-5-metil-*P*-tiouridilil-(3'→5')-2'-*O*-(2-metoxietil)-*P*-tioguanilil-(3'→5')-2'-*O*-(2-metoxietil)-5-metilcitidina

$C_{296}H_{428}N_{96}O_{144}P_{20}S_{19}$

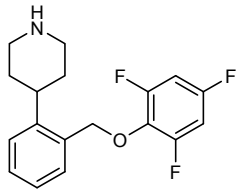
R1-moeG=moeCm=moeA=moeG=moeA=dG=dG=dT=dG=dA=dA=dG=dCm=dG=dA=moeA=moeG=moeUm=moeG=moeCm



ampreloxetinum

ampreloxetine	4-{2-[(2,4,6-trifluorophenoxy)methyl]phenyl}piperidine
ampréloxétine	4-{2-[(2,4,6-trifluorophénoxy)méthyl]phényl}pipéridine
ampreloxetina	4-{2-[(2,4,6-trifluorofenoxi)metil]fenil}piperidina

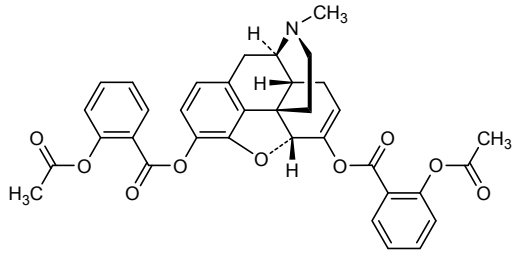
$C_{18}H_{18}F_3NO$



asalhydromorphonum

asalhydromorphone	17-methyl-4,5α-epoxy-6,7-didehydromorphinan-3,6-diyl bis[2-(acetyloxy)benzoate]
asalhydromorphone	bis[2-(acétyloxy)benzoate] de 17-méthyl-4,5α-époxy-6,7-didéshydromorphinane-3,6-diyle
asalhidromorfona	bis[2-(acetiloxi)benzoato] de 17-metil-4,5α-epoxi-6,7-dideshidromorfinano-3,6-diilo

$C_{35}H_{31}NO_9$



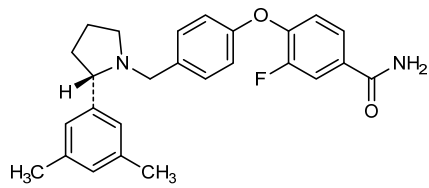
aticaprantum

aticaprant — 4-(4-{[(2*S*)-2-(3,5-dimethylphenyl)pyrrolidin-1-yl]methyl}phenoxy)-3-fluorobenzamide

aticaprant — 4-(4-{[(2*S*)-2-(3,5-diméthylphényl)pyrrolidin-1-yl]méthyl}phénoxy)-3-fluorobenzamide

aticaprant — 4-(4-{[(2*S*)-2-(3,5-dimetilfenil)pirrolidin-1-il]metil}fenoxi)-3-fluorobenzamida

$C_{26}H_{27}FN_2O_2$



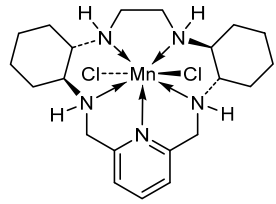
avasopasemum manganum

avasopasem manganese — (*PBPY*-7-11-2344'3')-dichlorido[(1^1*S*,1^2*S*,7^1*S*,7^2*S*)-2,6,8,11-tetraaza-4(2,6)-pyridina-1,7(1,2)-dicyclohexanacycloundecaphane-$\kappa^5N^2,N^{4'},N^6,N^8,N^{11}$]manganese

avasopasem manganèse — (*PBPY*-7-11-2344'3')-dichlorido[(1^1*S*,1^2*S*,7^1*S*,7^2*S*)-2,6,8,11-tetraaza-4(2,6)-pyridina-1,7(1,2)-dicyclohexanacycloundécaphane-$\kappa^5N^2,N^{4'},N^6,N^8,N^{11}$]manganese

avasopasem manganeso — (*PBPY*-7-11-2344'3')-diclorido[(1^1*S*,1^2*S*,7^1*S*,7^2*S*)-2,6,8,11-tetraaza-4(2,6)-piridina-1,7(1,2)-diciclohexanacicloundecafano-$\kappa^5N^2,N^{4'},N^6,N^8,N^{11}$]manganese

$C_{21}H_{35}Cl_2MnN_5$



avoplacelum

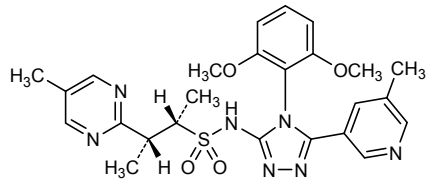
avoplacel — human culture expanded allogenic adherent mesenchymal-like stromal cells for cell-based therapy. Cells are of fetal origin and derived from isolated placentae of healthy donors following a cesarean section. Cells express cell surface markers CD29, CD73, and CD105 and exhibit immunomodulatory, and pro-angiogenic and muscle regeneration effects.

avoplacel	cellules stromales semblables au mésenchyme, humaines, allogéniques, adhérentes, en culture d'expansion, pour thérapie cellulaire. Les cellules sont d'origine fœtale et dérivent du placenta isolé de donneuses en bonne santé, à la suite d'une césarienne. Les cellules expriment les marqueurs de surface CD29, CD73 et CD105 et montrent des effets immunomodulateurs, pro-angiogéniques et de regénération musculaire.
avoplacel	células similares a mesenquimales, estromales, alogénicas, humanas, expandidas en cultivo para terapia celular. Las células son de origen fetal y derivadas de placentas aisladas de donantes sanas tras una cesárea. Las células expresan los marcadores de superficie CD29, CD73 y CD105, y poseen efectos inmunomoduladores, pro-angiogénicos y de regeneración muscular.

azelapragum

azelaprag	(2*S*,3*R*)-*N*-[4-(2,6-dimethoxyphenyl)-5-(5-methylpyridin-3-yl)-4*H*-1,2,4-triazol-3-yl]-3-(5-methylpyrimidin-2-yl)butane-2-sulfonamide
azélaprag	(2*S*,3*R*)-*N*-[4-(2,6-diméthoxyphényl)-5-(5-méthylpyridin-3-yl)-4*H*-1,2,4-triazol-3-yl]-3-(5-méthylpyrimidin-2-yl)butane-2-sulfonamide
azelaprag	(2*S*,3*R*)-*N*-[4-(2,6-dimetoxifenil)-5-(5-metilpiridin-3-il)-4*H*-1,2,4-triazol-3-il]-3-(5-metilpirimidin-2-il)butano-2-sulfonamida

$C_{25}H_{29}N_7O_4S$



bamadutidum

bamadutide	L-histidyl-D-seryl-L-glutaminylglycyl-L-threonyl-L-phenylalanyl-L-threonyl-L-seryl-L-α-aspartyl-L-leucyl-L-seryl-L-lysyl-L-glutaminyl-N^6-(*N*-hexadecanoyl-L-γ-glutamyl)-L-lysyl-L-α-glutamyl-L-seryl-L-lysyl-L-alanyl-L-alanyl-L-glutaminyl-L-α-aspartyl-L-phenylalanyl-L-isoleucyl-L-α-glutamyl-L-tryptophyl-L-leucyl-L-lysyl-L-alanylglycylglycyl-L-prolyl-L-seryl-L-serylglycyl-L-alanyl-L-prolyl-L-prolyl-L-prolyl-L-serinamide

bamadutide

L-histidyl-D-séryl-L-glutaminylglycyl-L-thréonyl-L-phénylalanyl-L-thréonyl-L-séryl-L-α-aspartyl-L-leucyl-L-séryl-L-lysyl-L-glutaminyl-N^6-(*N*-hexadécanoyl-L-γ-glutamyl)-L-lysyl-L-α-glutamyl-L-séryl-L-lysyl-L-alanyl-L-alanyl-L-glutaminyl-L-α-aspartyl-L-phénylalanyl-L-isoleucyl-L-α-glutamyl-L-tryptophyl-L-leucyl-L-lysyl-L-alanylglycylglycyl-L-prolyl-L-séryl-L-sérylglycyl-L-alanyl-L-prolyl-L-prolyl-L-prolyl-L-sérinamide

bamadutida

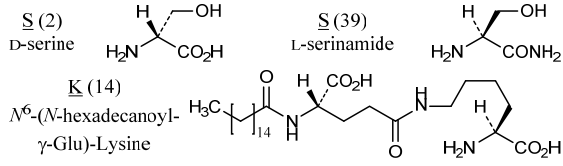
L-histidil-D-seril-L-glutaminilglicil-L-treonil-L-fenilalanil-L-treonil-L-seril-L-α-aspartil-L-leucil-L-seril-L-lisil-L-glutaminil-N^6-(*N*-hexadecanoil-L-γ-glutamil)-L-lisil-L-α-glutamil-L-seril-L-lisil-L-alanil-L-alanil-L-glutaminil-L-α-aspartil-L-fenilalanil-L-isoleucil-L-α-glutamil-L-triptofil-L-leucil-L-lisil-L-alanilglicilglicil-L-prolil-L-seril-L-serilglicil-L-alanil-L-prolil-L-prolil-L-prolil-L-serinamida

$C_{200}H_{313}N_{51}O_{63}$

Sequence / Séquence / Secuencia

HSQGTFTSDL SKQKESKAAQ DFIEWLKAGG PSSGAPPPS 39

Modified residues / Résidus modifiés / Restos modificados



bempegaldesleukinum #

bempegaldesleukin

human interleukin-2 variant (Ala[1] removed, C^{125}>S) produced in *Escherichia coli*, in which an average of 6 lysine residues are N^6 substituted with [(2,7-bis{[methylpoly(oxyethylene)]carbamoyl}-9*H*-fluoren-9-yl)methoxy]carbonyl

bempégaldesleukine

variant de l'interleukine 2 humaine (Ala1 supprimée, C^{125}>S), produit par *Escherichia coli,* dans lequel environ 6 lysines sont N^6 substituées par le radical [(2,7-bis{[méthylpoly(oxyéthylène)]carbamoyl}-9*H*-fluorén-9-yl)méthoxy]carbonyle

bempegaldesleukina

variante de la interleukina 2 humana (Ala1 suprimida, C^{125}>S), producida por *Escherichia coli,* en la que una media de 6 lisinas son N^6 sustituidas por el radical [(2,7-bis{[metilpoli(oxietileno)]carbamoil}-9*H*-fluoren-9-il)metoxi]carbonilo

$C_{690}H_{1113}N_{177}O_{203}S_6$ $(C_{19}H_{16}N_2O_4$ $[C_2H_4O]_{2n})_6$

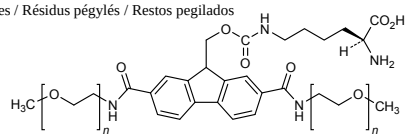
Sequence (132 residues) / Séquence (132 résidus) / Secuencia (132 restos)

```
 PTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA 50
TELKHLQCLE EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE 100
TTFMCEYADE TATIVEFLNR WITFSQSIIS TLT                   133
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
58-105

Pegylated residues / Résidus pégylés / Restos pegilados

#6 K
N^6-peg-Lys
n # 230



bevifimodum #

bevifimod	staphylococcal protein A (SpA), purified from *Staphylococcus aureus* strain A676 culture medium
bévifimod	protéine A staphylococcique (SpA), purifiée à partir de milieu de culture de la souche A676 de *Staphylococcus aureus*
bevifimod	proteína A estafilocócica (SpA), purificada a partir del medio de cultivo de la cepa A676 de *Staphylococcus aureus*

Sequence / Séquence / Secuencia

```
AQHDEAQQNA FYQVLNMPNL NADQRNGFIQ SLKDDPSQSA NVLGEAQKLN 50
DSQAPKADAQ QNNFNKDQQS AFYEILNMPN LNEAQRNGFI QSLKDDPSQS 100
TNVLGEAKKL NESQAPKADN NFNKEQQNAF YEILNMPNLN EEQRNGFIQS 150
LKDDPSQSAN LLSEAKKLNE SQAPKADNKF NKEQQNAFYE ILHLPNLNEE 200
QRNGFIQSLK DDPSQSANLL AEAKKLNDAQ APKADNKFNK EQQNAFYEIL 250
HLPNLTEEQR NGFIQSLKDD PSVSKEILAE AKKLNDAQAP KEEDNNKPGK 300
EDNNKPGKED NNKPGKEDNN KPGKEDGNKP GKEDNKKPGK EDGNKPGKED 350
NKKPGKEDGN KPGKEDGNKP GKEDGNGVHV VKPGDTVNDI AKANGTTADK 400
IAADNKLADK NMIKPGQEGS VAK                              423
```

bintrafuspum alfa #

bintrafusp alfa	immunoglobulin G1-lambda, anti-[human programmed cell death 1 ligand 1 (PD-L1, programmed death ligand 1, PDCD1 ligand 1, B7 homolog 1, B7-H1, CD274)], human monoclonal antibody, fused at the C-terminus of both heavy chains via a peptidyl linker (450-471), to a fragment of the mature human extracellular domain of human TGF-beta receptor type-2 (TGFR-2, TGFBR2, transforming growth factor-beta receptor type II)TGFβ type II receptor (472-607), dimer, produced in Chinese hamster ovary (CHO) cells, glycoform alfa; gamma1 heavy chain fused to TGFR-2 (1-607) [*Homo sapiens* VH (IGHV3-23*01 -(IGHD) -IGHJ4*01) [CDRKabatH1: SYIMM (31-35); CDRKabatH2: SIYPSGGITFYADTVKG (50-66); CDRKabatH3: IKLGTVTTVDY (99-109)] (1-120) -*Homo sapiens* IGHG1*03, (CH1 (121-218), hinge (219-233), CH2 (234-343), CH3 (344-448), CHS (449-449, K450del)) (121-449)], (223-215')-disulfide with lambda light chain (1'-216') [*Homo sapiens* V-LAMBDA (IGLV2-14*01 -IGLJ1*01) [CDRKabatL1: TGTSSDVGGYNYVS (23-36); CDRKabatL2: DVSNRPS (52-58); CDRKabatL3: SSYTSSSTRV (91-100)] (1'-110') -IGLC1*02 (111'-216')]; dimer (229-229'':232-232'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

bintrafusp alfa	immunoglobuline G1-lambda, anti-[ligand 1 de la protéine 1 de mort cellulaire programmée humain (PD-L1, ligand 1 de mort programmée, ligand 1 PDCD1, homologue 1 de B7, B7-H1, CD274)], anticorps monoclonal humain, fusionnée à l'extrémité C-terminale des deux chaînes lourdes via un linker peptidique (450-471), à un fragment du domaine extracellulaire du récepteur de type-2 du TGF-bêta humain (TGFR-2, TGFBR2, récepteur de type-2 du facteur de croissance transformant-bêta) (472-607), dimère, produit dans des cellules ovariennes de hamsters chinois (CHO), glycoforme alfa; chaîne lourde gamma1 fusionnée au TGFR-2 (1-607) [*Homo sapiens* VH (IGHV3-23*01 -(IGHD) -IGHJ4*01) [CDRKabatH1: SYIMM (31-35); CDRKabatH2: SIYPSGGITFYADTVKG (50-66); CDRKabatH3: IKLGTVTTVDY (99-109)] (1-120) -*Homo sapiens* IGHG1*03, (CH1 (121-218), charnière (219-233), CH2 (234-343), CH3 (344-448), CHS (449-449, K450del)) (121-449)], (223-215')-disulfure avec la chaîne légère lambda (1'-216') [*Homo sapiens* V-LAMBDA (IGLV2-14*01 -IGLJ1*01) [CDRKabatL1: TGTSSDVGGYNYVS (23-36); CDRKabatL2: DVSNRPS (52-58); CDRKabatL3: SSYTSSSTRV (91-100)] (1'-110') -IGLC1*02 (111'-216')]; dimère (229-229'':232-232'')-bisdisulfure, produit dans des cellules ovariennes de hamsters chinois (CHO), glycoforme alfa
bintrafusp alfa	inmunoglobulina G1-lambda, anti-[ligando 1 de la proteína 1 de muerte celular programada humana (PD-L1, ligando 1 de muerte programada, ligando 1 PDCD1, homólogo 1 de B7, B7-H1, CD274)], anticuerpo monoclonal humano, fusionado en el extremo C-terminal de las diez cadenas pesadas mediante un conector peptídico (451-471), a un fragmento del dominio mature human extracelular del receptor tipo-2 del TGF-beta humano (TGFR-2, TGFBR2, receptor tipo-2 del factor de crecimiento transformante-beta)TGFβ type II receptor (472-607), dímero, producido en las células ováricas de hamsters chinos (CHO), glicoforma alfa; cadena pesada gamma1 fusionada al TGFR-2 (1-607) [*Homo sapiens* VH (IGHV3-23*01 -(IGHD) -IGHJ4*01) [CDRKabatH1: SYIMM (31-35); CDRKabatH2: SIYPSGGITFYADTVKG (50-66); CDRKabatH3: IKLGTVTTVDY (99-109)] (1-120) -*Homo sapiens* IGHG1*03, (CH1 (121-218), bisagra (219-233), CH2 (234-343), CH3 (344-448), CHS (449-449, K450del)) (121-449)], (223-215')-disulfuro con la cadena ligera lambda (1'-216') [*Homo sapiens* V-LAMBDA (IGLV2-14*01 -IGLJ1*01) [CDRKabatL1: TGTSSDVGGYNYVS (23-36); CDRKabatL2: DVSNRPS (52-58); CDRKabatL3: SSYTSSSTRV (91-100)] (1'-110') -IGLC1*02 (111'-216')]; dímero (229-229'':232-232'')-bisdisulfuro, producido en las células ováricas de hamsters chinos (CHO), glicoforma alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLLESGGG LVQPGGSLRL SCAASGFTFS SYIMMWVRQA PGKGLEWVSS  50
IYPSGGITFY ADTVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARIK 100
LGTVTTVDYW GQGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKRVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGA 450
GGGGSGGGGS GGGGSGGGGS GIPPHVQKSV NNDMIVTDNN GAVKFPQLCK 500
FCDVRFSTCD NQKSCMSNCS ITSICEKPQE VCVAVWRKND ENITLETVCH 550
DPKLPYHDFI LEDAASPKCI MKEKKKPGET FFMCSCSSDE CNDNIIFSEE 600
YNTSNPD                                                 607
```

Light chain / Chaîne légère / Cadena ligera

```
QSALTQPASV SGSPGQSITI SCTGTSSDVG GYNYVSWYQQ HPGKAPKLMI  50
YDVSNRPSGV SNRFSGSKSG NTASLTISGL QAEDEADYYC SSYTSSSTRV 100
FGTGTKVTVL GQPKANPTVT LFPPSSEELQ ANKATLVCLI SDFYPGAVTV 150
AWKADGSPVK AGVETTKPSK QSNNKYAASS YLSLTPEQWK SHRSYSCQVT 200
HEGSTVEKTV APTECS                                       216
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

```
Intra-H    22-96    147-203    264-324    370-428
           22"-96"  147"-203"  264"-324"  370"-428"
Intra-H (TGFR-2)  499-532  502-519  509-515  525-549  569-584  586-591
                  499"-532" 502"-519" 509"-515" 525"-549" 569"-584' 586"-591"
Intra-L    22'-90'    138'-197'
           22'"-90'"  138'"-197'"
Inter-H-L  223-215'  223"-215"
Inter-H-H  229-229'  232-232"
```

Glycosylation sites (N) / Sites de glycosylation (N) / Posiciones de glicosilación (N)

```
H CH2  Asn-300
TGFR-2  Asn-518, Asn-542, Asn-602
```

birtamimabum #

birtamimab — immunoglobulin G1-kappa, anti-[*Homo sapiens* serum amyloid A (AA) and immunoglobulin amyloid light chain (AL)], monoclonal antibody;
gamma1 heavy chain (1-449) [VH (*Mus musculus* IGHV10-1*02 (89.8%)/*Homo sapiens* IGHV3-72*01 (84.0%) -(IGHD) -*Homo sapiens* IGHJ4*01 (92.9%)) [8.10.10] (1-119) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (216) (120-217), hinge (218-232), CH2 (233-342), CH3 E12 (358), M14 (360) (343-447), CHS (448-449)) (120-449)], (222-219')-disulfide with kappa light chain (1'-219') [V-KAPPA (*Mus musculus* IGKV1-110*01 (91.0%)/*Homo sapiens* IGKV2-30*02 (87.0%) -*Homo sapiens* IGKJ4*01 (91.7%)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01, Km3A45.1 (158), V101 (196)(113'-219')]; dimer (228-228'':231-231'')-bisdisulfide

birtamimab — immunoglobuline G1-kappa, anti-[*Homo sapiens* amyloïde A sérique (AA) et chaîne légère amyloïde (AL) d'immunoglobuline)], anticorps monoclonal;
chaîne lourde gamma1 (1-449) [VH (*Mus musculus* IGHV10-1*02 (89.8%)/*Homo sapiens* IGHV3-72*01 (84.0%) -(IGHD) -*Homo sapiens* IGHJ4*01 (92.9%)) [8.10.10] (1-119) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (216) (120-217), charnière (218-232), CH2 (233-342), CH3 E12 (358), M14 (360) (343-447), CHS (448-449)) (120-449)], (222-219') -disulfure avec la chaîne légère kappa (1'-219') [V-KAPPA (*Mus musculus* IGKV1-110*01 (91.0%)/*Homo sapiens* IGKV2-30*02 (87.0%) -*Homo sapiens* IGKJ4*01 (91.7%)) [11 3.9] (1'-112') -*Homo sapiens* IGKC*01, Km3A45.1 (158), V101 (196)(113'-219')]; dimère (228-228'':231-231'')-bisdisulfure

birtamimab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* amiloide A sérica (AA) y cadena ligera amiloide (AL) de inmunoglobulina)], anticuerpo monoclonal; cadena pesada gamma1 (1-449) [VH (*Mus musculus* IGHV10-1*02 (89.8%)/*Homo sapiens* IGHV3-72*01 (84.0%) -(IGHD) -*Homo sapiens* IGHJ4*01 (92.9%)) [8.10.10] (1-119) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (216) (120-217), bisagra (218-232), CH2 (233-342), CH3 E12 (358), M14 (360) (343-447), CHS (448-449)) (120-449)], (222-219') -disulfuro con la cadena ligera kappa (1'-219') [V-KAPPA (*Mus musculus* IGKV1-110*01 (91.0%)/*Homo sapiens* IGKV2-30*02 (87.0%) -*Homo sapiens* IGKJ4*01 (91.7%)) [11 3.9] (1'-112') -*Homo sapiens* IGKC*01, Km3A45.1 (158), V101 (196)(113'-219')]; dímero (228-228'':231-231'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAASGFTFN TYAMYWIRQA PGKGLEWVAR  50
IRSKSNNYAI YYADSVKDRF TISRDDSKNS LYLQMNSLKT EDTAVYYCAR 100
PYSDSFAYWG QGTLVTVSSA STKGPSVFPL APSSKSTSGG TAALGCLVKD 150
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY 200
ICNVNHKPSN TKVDKRVEPK SCDKTHTCPP CPAPELLGGP SVFLFPPKPK 250
DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS 300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV 350
YTLPPSREEM TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL 400
DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK  449
```

Light chain / Chaîne légère / Cadena ligera

```
DVVMTQSPLS LPVTPGEPAS ISCRSSQSLV HSTGNTYLHW YLQKPGQSPQ  50
LLIYKVSNRF SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCSQSTHVP 100
FTFGGGTKVE IKRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK 150
VQWKVDNALQ SGNSQESVTE QDSKDSTYSL SSTLTLSKAD YEKHKVYACE 200
VTHQGLSSPV TKSFNRGEC                                   219
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-98 146-202 263-323 369-427
22''-98'' 146''-202'' 263''-323'' 369''-427''
Intra-L (C23-C104) 23'-93' 139'-199'
23'''-93''' 139'''-199'''
Inter-H-L (h 5-CL 126) 222-219' 222''-219'''
Inter-H-H (h 11, h 14) 228-228'' 231-231''

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84 4:
299, 299''
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

brilaroxazinum

brilaroxazine

6-{4-[4-(2,3-dichlorophenyl)piperazin-1-yl]butoxy}-2*H*-1,4-benzoxazin-3(4*H*)-one

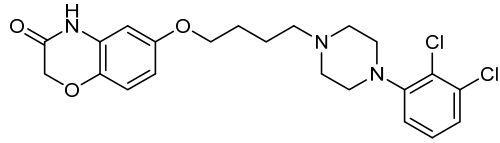
brilaroxazine

6-{4-[4-(2,3-dichlorophényl)pipérazin-1-yl]butoxy}-2*H*-1,4-benzoxazin-3(4*H*)-one

brilaroxazina

6-{4-[4-(2,3-diclorofenil)piperazin-1-il]butoxi}-2*H*-1,4-benzoxazin-3(4*H*)-ona

$C_{22}H_{25}Cl_2N_3O_3$



budigalimabum #

budigalimab	immunoglobulin G1-kappa, anti-[*Homo sapiens* PDCD1 (programmed cell death 1, PD-1, PD1, CD279)], monoclonal antibody; gamma1 heavy chain (1-448) [VH (*Homo sapiens* IGHV1-46*01 (76 5%) -(IGHD) -IGHJ6*03 (90.9%)) [8.8.11] (1-118) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (215) (119-216), hinge (217-231), CH2 L1 3>A (235), L1.2>A (236) (232-341), CH3 E12 (357), M14 (359) (342-446), CHS (447-448)) (119-448)], (221-219')-disulfide with kappa light chain (1'-219') [V-KAPPA (*Mus musculus* IGKV1-117*01 (89.0%)/*Homo sapiens* IGKV2-28*01 or IGKV2-29*02 (85.0%) -*Homo sapiens* IGKJ2*01 (100%)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dimer (227-227":230-230")-bisdisulfide
budigalimab	immunoglobuline G1-kappa, anti-[*Homo sapiens* PDCD1 (protéine 1 de mort cellulaire programmée, PD-1, PD1, CD279)], anticorps monoclonal; chaîne lourde gamma1 (1-448) [VH (*Homo sapiens* IGHV1-46*01 (76.5%) -(IGHD) -IGHJ6*03 (90.9%)) [8.8.11] (1-118) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (215) (119-216), charnière (217-231), CH2 L1.3>A (235), L1.2>A (236) (232-341), CH3 E12 (357), M14 (359) (342-446), CHS (447-448)) (119-448)], (221-219')-disulfure avec la chaîne légère kappa (1'-219') [V-KAPPA (*Mus musculus* IGKV1-117*01 (89.0%)/*Homo sapiens* IGKV2-28*01 or IGKV2-29*02 (85.0%) -*Homo sapiens* IGKJ2*01 (100%)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dimère (227-227":230-230")-bisdisulfure
budigalimab	inmunoglobulina G1-kappa, anti-[*Homo sapiens* PDCD1 (proteína 1 de muerte celular programada, PD-1, PD1, CD279)], anticuerpo monoclonal; cadena pesada gamma1 (1-448) [VH (*Homo sapiens* IGHV1-46*01 (76.5%) -(IGHD) -IGHJ6*03 (90.9%)) [8.8.11] (1-118) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (215) (119-216), bisagra (217-231), CH2 L1.3>A (235), L1.2>A (236) (232-341), CH3 E12 (357), M14 (359) (342-446), CHS (447-448)) (119-448)], (221-219')-disulfuro con la cadena ligera kappa (1'-219') [V-KAPPA (*Mus musculus* IGKV1-117*01 (89.0%)/*Homo sapiens* IGKV2-28*01 or IGKV2-29*02 (85.0%) -*Homo sapiens* IGKJ2*01 (100%)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dímero (227-227":230-230")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EIQLVQSGAE VKKPGSSVKV SCKASGYTFT HYGMNWVRQA PGQGLEWVGW  50
VNTYTGEPTY ADDFKGRLTF TLDTSTSTAY MELSSLRSED TAVYYCTREG 100
EGLGFGDWGQ GTTVTVSSAS TKGPSVFPLA PSSKSTSGGT AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTQTYI 200
CNVNHKPSNT KVDKKVEPKS CDKTHTCPPC PAPEAAGGPS VFLFPPKPKD 250
TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNST 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY 350
TLPPSREEMT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD 400
SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPGK   448
```

Light chain / Chaîne légère / Cadena ligera

```
DVVMTQSPLS LPVTPGEPAS ISCRSSQSIV HSHGDTYLEW YLQKPGQSPQ  50
LLIYKVSNRF SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCFQGSHIP 100
VTFGQGTKLE IKRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK 150
VQWKVDNALQ SGNSQESVTE QDSKDSTYSL SSTLTLSKAD YEKHKVYACE 200
VTHQGLSSPV TKSFNRGEC                                   219
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 145-201 262-322 368-426
22"-96" 145"-201" 262"-322" 368"-426"
Intra-L (C23-C104) 23'-93' 139'-199'
23'"-93"" 139'"-199'""
Inter-H-L (h 5-CL 126) 221-219' 221"-219'"
Inter-H-H (h 11, h 14) 227-227" 230-230'

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84 4:
298, 298"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

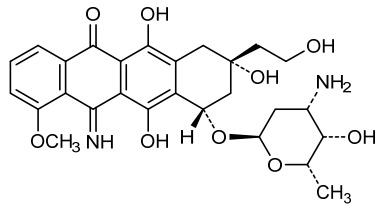
camsirubicinum

camsirubicin — (8*R*,10*S*)-10-[(3-amino-2,3,6-trideoxy-α-L-*lyxo*-hexopyranosyl)oxy]-6,8,11-trihydroxy-8-(2-hydroxyethyl)-12-imino-1-methoxy-7,9,10,12-tetrahydrotetracen-5(8*H*)-one

camsirubicine — (8*R*,10*S*)-10-[(3-amino-2,3,6-tridésoxy-α-L-*lyxo*-hexopyranosyl)oxy]-6,8,11-trihydroxy-8-(2-hydroxyéthyl)-12-imino-1-méthoxy-7,9,10,12-tétrahydrotétracén-5(8*H*)-one

camsirubicina — (8*R*,10*S*)-10-[(3-amino-2,3,6-tridesoxi-α-L-*lixo*-hexopiranosil)oxi]-6,8,11-trihidroxi-8-(2-hidroxietil)-12-imino-1-metoxi-7,9,10,12-tetrahidrotetracen-5(8*H*)-ona

$C_{27}H_{32}N_2O_9$



cemiplimabum #

cemiplimab — immunoglobulin G4-kappa, anti-[*Homo sapiens* PDCD1 (programmed cell death 1, PD-1, PD1, CD279)], *Homo sapiens* monoclonal antibody; gamma4 heavy chain (1-444) [*Homo sapiens* VH (IGHV3-23*01 (86.7%) -(IGHD) -IGHJ4*01 (100%)) [8.8.10] (1-117) -*Homo sapiens* IGHG4*01 (CH1 (118-215), hinge S10>P (225) (216-227), CH2 (228-337), CH3 (338-442), CHS (443-444)) (118-444)], (131-214')-disulfide with kappa light chain (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-39*01 (86.3%) -IGKJ3*01 (75.0%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (223-223'':226-226'')-bisdisulfide

cémiplimab

immunoglobuline G4-kappa, anti-[*Homo sapiens* PDCD1 (protéine 1 de mort cellulaire programmée, PD-1, PD1, CD279)], *Homo sapiens* anticorps monoclonal;
chaîne lourde gamma4 (1-444) [*Homo sapiens* VH (IGHV3-23*01 (86.7%) -(IGHD) -IGHJ4*01 (100%)) [8.8.10] (1-117) -*Homo sapiens* IGHG4*01 (CH1 (118-215), charnière S10>P (225) (216-227), CH2 (228-337), CH3 (338-442), CHS (443-444)) (118-444)], (131-214')-disulfure avec la chaîne légère kappa (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-39*01 (86.3%) -IGKJ3*01 (75.0%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')];
dimère (223-223'':226-226'')-bisdisulfure

cemiplimab

inmunoglobulina G4-kappa, anti-[*Homo sapiens* PDCD1 (proteína 1 de muerte celular programada, PD-1, PD1, CD279)], *Homo sapiens* anticuerpo monoclonal;
cadena pesada gamma4 (1-444) [*Homo sapiens* VH (IGHV3-23*01 (86.7%) -(IGHD) -IGHJ4*01 (100%)) [8.8.10] (1-117) -*Homo sapiens* IGHG4*01 (CH1 (118-215), bisagra S10>P (225) (216-227), CH2 (228-337), CH3 (338-442), CHS (443-444)) (118-444)], (131-214')-disulfuro con la cadena ligera kappa (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-39*01 (86.3%) -IGKJ3*01 (75.0%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')];
dímero (223-223'':226-226'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLLESGGV LVQPGGSLRL SCAASGFTFS NFGMTWVRQA PGKGLEWVSG  50
ISGGGRDTYF ADSVKGRFTI SRDNSKNTLY LQMNSLKGED TAVYYCVKWG 100
NIYFDYWGQG TLVTVSSAST KGPSVFPLAP CSRSTSESTA ALGCLVKDYF 150
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTKTYTC 200
NVDHKPSNTK VDKRVESKYG PPCPPCPAPE FLGGPSVFLF PPKPKDTLMI 250
SRTPEVTCVV VDVSQEDPEV QFNWYVDGVE VHNAKTKPRE EQFNSTYRVV 300
SVLTVLHQDW LNGKEYKCKV SNKGLPSSIE KTISKAKGQP REPQVYTLPP 350
SQEEMTKNQV SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS 400
FFLYSRLTVD KSRWQEGNVF SCSVMHEALH NHYTQKSLSL SLGK       444
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDSIT ITCRASLSIN TFLNWYQQKP GKAPNLLIYA  50
ASSLHGGVPS RFSGSGSGTD FTLTIRTLQP EDFATYYCQQ SSNTPFTFGP 100
GTVVDFRRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 144-200 258-318 364-422
22"-96" 144"-200" 258"-318" 364"-422"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194'"
Inter-H-L (CH1 10-CL 126) 131-214' 131"-214'"
Inter-H-H (h 8, h 11) 223-223" 226-226"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
294, 294"
C-terminal lysine clipping:
H CHS K2: 444, 444"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

cenupatidum

cenupatide

N^2-acetyl-L-arginyl-2-methylalanyl-L-arginyl-α-methyl-L-phenylalaninamide

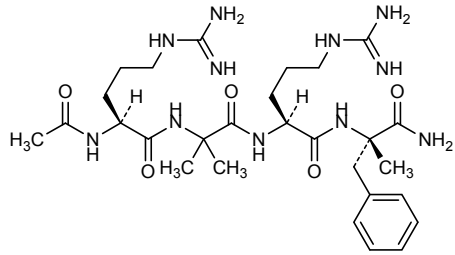
cénupatide

N^2-acétyl-L-arginyl-2-méthylalanyl-L-arginyl-α-méthyl-L-phénylalaninamide

cenupatida

N^2-acetil-L-arginil-2-metilalanil-L-arginil-α-metil-L-fenilalaninamida

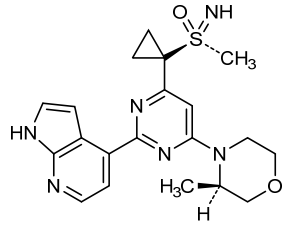
$C_{28}H_{47}N_{11}O_5$



ceralasertibum

ceralasertib	(*R*)-imino(methyl)(1-{6-[(3*R*)-3-methylmorpholin-4-yl]-2-(1*H*-pyrrolo[2,3-*b*]pyridin-4-yl)pyrimidin-4-yl}cyclopropyl)-λ^6-sulfanone
céralasertib	(*R*)-imino(méthyl)(1-{6-[(3*R*)-3-méthylmorpholin-4-yl]-2-(1*H*-pyrrolo[2,3-*b*]pyridin-4-yl)pyrimidin-4-yl}cyclopropyl)-λ^6-sulfanone
ceralasertib	(*R*)-imino(metil)(1-{6-[(3*R*)-3-metilmorfolin-4-il]-2-(1*H*-pirrolo[2,3-*b*]piridin-4-il)pirimidin-4-il}ciclopropil)-λ^6-sulfanona

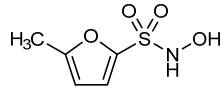
$C_{20}H_{24}N_6O_2S$



cimlanodum

cimlanod	*N*-hydroxy-5-methylfuran-2-sulfonamide
cimlanod	*N*-hydroxy-5-méthylfurane-2-sulfonamide
cimlanod	*N*-hidroxi-5-metilfurano-2-sulfonamida

$C_5H_7NO_4S$



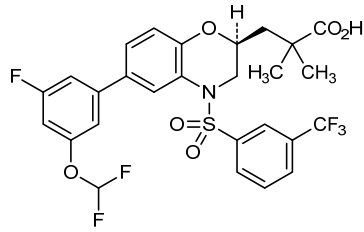
cintirorgonum

cintirorgon	3-{(2*S*)-6-[3-(difluoromethoxy)-5-fluorophenyl]-4-[3-(trifluoromethyl)benzene-1-sulfonyl]-3,4-dihydro-2*H*-1,4-benzoxazin-2-yl}-2,2-dimethylpropanoic acid
cintirorgon	acide 3-{(2*S*)-6-[3-(difluorométhoxy)-5-fluorophényl]-4-[3-(trifluorométhyl)ben-zène-1-sulfonyl]-3,4-dihydro-2*H*-1,4-benzoxazin-2-yl}-2,2-diméthylpropanoïque

cintirorgón

ácido 3-{(2*S*)-6-[3-(difluorometoxi)-5-fluorofenil]-4-[3-(trifluorometil)ben-ceno-1-sulfonil]-3,4-dihidro-2*H*-1,4-benzoxazin-2-il}-2,2-dimetilpropanoico

$C_{27}H_{23}F_6NO_6S$



coblopasvirum

coblopasvir

methyl {(2*S*)-1-[(2*S*)-2-(4-{4-[7-(2-[(2*S*)-1-{(2*S*)-2-[(methoxycarbonyl)amino]-3-methylbutanoyl}pyrrolidin-2-yl]-1*H*-imidazol-4-yl)-2*H*-1,3-benzodioxol-4-yl]phenyl}-1*H*-imidazol-2-yl)pyrrolidin-1-yl]-3-methyl-1-oxobutan-2-yl}carbamate

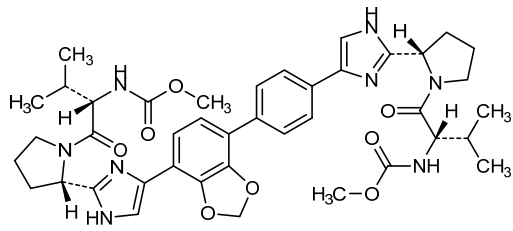
coblopasvir

{(2*S*)-1-[(2*S*)-2-(4-{4-[7-(2-[(2*S*)-1-{(2*S*)-2-[(méthoxycarbonyl)amino]-3-méthylbutanoyl}pyrrolidin-2-yl]-1*H*-imidazol-4-yl)-2*H*-1,3-benzodioxol-4-yl]phényl}-1*H*-imidazol-2-yl)pyrrolidin-1-yl]-3-méthyl-1-oxobutan-2-yl}carbamate de méthyle

coblopasvir

{(2*S*)-1-[(2*S*)-2-(4-{4-[7-(2-[(2*S*)-1-{(2*S*)-2-[(metoxicarbonil)amino]-3-metilbutanoil}pirrolidin-2-il]-1*H*-imidazol-4-il)-2*H*-1,3-benzodioxol-4-il]fenil}-1*H*-imidazol-2-il)pirrolidin-1-il]-3-metil-1-oxobutan-2-il}carbamato de metilo

$C_{41}H_{50}N_8O_8$



cotadutidum

cotadutide

L-histidyl-L-seryl-L-glutaminylglycyl-L-threonyl-L-phenylalanyl-L-threonyl-L-seryl-L-α-aspartyl-*N*^{6}-(*N*-hexadecanoyl-L-γ-glutamyl)-L-lysyl-L-seryl-L-α-glutamyl-L-tyrosyl-L-leucyl-L-α-aspartyl-L-seryl-L-α-glutamyl-L-arginyl-L-alanyl-L-arginyl-L-α-aspartyl-L-phenylalanyl-L-valyl-L-alanyl-L-tryptophyl-L-leucyl-L-α-glutamyl-L-alanylglycylglycine

cotadutide

L-histidyl-L-séryl-L-glutaminylglycyl-L-thréonyl-L-phénylalanyl-L-thréonyl-L-séryl-L-α-aspartyl-*N*^{6}-(*N*-hexadécanoyl-L-γ-glutamyl)-L-lysyl-L-séryl-L-α-glutamyl-L-tyrosyl-L-leucyl-L-α-aspartyl-L-séryl-L-α-glutamyl-L-arginyl-L-alanyl-L-arginyl-L-α-aspartyl-L-phénylalanyl-L-valyl-L-alanyl-L-tryptophyl-L-leucyl-L-α-glutamyl-L-alanylglycylglycine

cotadutida

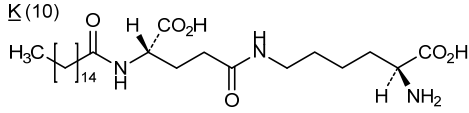
L-histidil-L-seril-L-glutaminilglicil-L-treonil-L-fenilalanil-L-treonil-L-seril-L-α-aspartil-*N*^{6}-(*N*-hexadecanoil-L-γ-glutamil)-L-lisil-L-seril-L-α-glutamil-L-tirosil-L-leucil-L-α-aspartil-L-seril-L-α-glutamil-L-arginil-L-alanil-L-arginil-L-α-aspartil-L-fenilalanil-L-valil-L-alanil-L-triptofil-L-leucil-L-α-glutamil-L-alanilglicilglicina

$C_{167}H_{252}N_{42}O_{55}$

Sequence / Séquence / Secuencia

HSQGTFTSDK SEYLDSERAR DFVAWLEAGG 30

Modified residue / Résidu modifié / Resto modificado



crovalimabum #

crovalimab

immunoglobulin G1-kappa, anti-[*Homo sapiens* C5 (complement 5)], monoclonal antibody;
gamma1 heavy chain (1-451) [VH (*Vicugna pacos* IGHV3S1*01 (70.4%)/*Homo sapiens* IGHV3-66*01 (69.4%) -(IGHD)-*Homo sapiens* IGHJ4*01 (100%)) [9.8.15] (1-123) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (220) (124-221), hinge (222-236), CH2 L1.2>R (241), G1.1>R (242), S3>K (245), A110>G (333), A115>S (336), P116>S (337) (237-346), CH3 E12 (362), M14 (364), M107>L (434), N114>A (440), Q118>R (444), S120>E (446) (347-451), CHS G1>del, K2>del) (124-451)], (226-217')-disulfide with kappa light chain (1'-217') [V-KAPPA (*Homo sapiens* IGKV1-13*02 or IGKV1D-13*01 (94.3%) -IGKJ4*01 (100%)) [6.3.12] (1'-110') -*Homo sapiens* IGKC*01, Km3 A45.1 (156), V101 (194) (111'-217')]; dimer (232-232":235-235")-bisdisulfide

crovalimab

immunoglobuline G1-kappa, anti-[*Homo sapiens* C5 (complément 5)], anticorps monoclonal;
chaîne lourde gamma1 (1-451) [VH (*Vicugna pacos* IGHV3S1*01 (70.4%)/*Homo sapiens* IGHV3-66*01 (69.4%) -(IGHD)-*Homo sapiens* IGHJ4*01 (100%)) [9.8.15] (1-123) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (220) (124-221), charnière (222-236), CH2 L1.2>R (241), G1.1>R (242), S3>K (245), A110>G (333), A115>S (336), P116>S (337) (237-346), CH3 E12 (362), M14 (364), M107>L (434), N114>A (440), Q118>R (444), S120>E (446) (347-451), CHS G1>del, K2>del) (124-451)], (226-217')-disulfure avec la chaîne légère kappa (1'-217') [V-KAPPA (*Homo sapiens* IGKV1-13*02 or IGKV1D-13*01 (94.3%) -IGKJ4*01 (100%)) [6.3.12] (1'-110') -*Homo sapiens* IGKC*01, Km3 A45.1 (156), V101 (194) (111'-217')]; dimère (232-232":235-235")-bisdisulfure

crovalimab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* C5 (complemento 5)], anticuerpo monoclonal; cadena pesada gamma1 (1-451) [VH (*Vicugna pacos* IGHV3S1*01 (70.4%)/*Homo sapiens* IGHV3-66*01 (69.4%) -(IGHD)-*Homo sapiens* IGHJ4*01 (100%)) [9.8.15] (1-123) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (220) (124-221), bisagra (222-236), CH2 L1.2>R (241), G1.1>R (242), S3>K (245), A110>G (333), A115>S (336), P116>S (337) (237-346), CH3 E12 (362), M14 (364), M107>L (434), N114>A (440), Q118>R (444), S120>E (446) (347-451), CHS G1>del, K2>del) (124-451)], (226-217')-disulfuro con la cadena ligera kappa (1'-217') [V-KAPPA (*Homo sapiens* IGKV1-13*02 or IGKV1D-13*01 (94.3%) -IGKJ4*01 (100%)) [6.3.12] (1'-110') -*Homo sapiens* IGKC*01, Km3 A45.1 (156), V101 (194) (111'-217')]; dímero (232-232":235-235")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVESGGG LVQPGRSLRL SCAASGFTVH SSYYMAWVRQ APGKGLEWVG  50
AIFTGSGAEY KAEWAKGRVT ISKDTSKNQV VLTMTNMDPV DTATYYCASD 100
AGYDYPTHAM HYWGQGTLVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC 150
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG 200
TQTYICNVNH KPSNTKVDKK VEPKSCDKTH TCPPCPAPEL RRGPKVFLFP 250
PKPKDTLMIS RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE 300
QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKGLPSSIEK TISKAKGQPR 350
EPQVYTLPPS REEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT 400
PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVLHEALHA HYTRKELSLS 450
P                                                       451
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCRASQGIS SSLAWYQQKP GKAPKLLIYG  50
ASETESGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQN TKVGSSYGNT 100
FGGGTKVEIK RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ 150
WKVDNALQSG NSQESVTEQD SKDSTYSLSS TLTLSKADYE KHKVYACEVT 200
HQGLSSPVTK SFNRGEC                                     217
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-97 150-206 267-327 373-431
22"-97" 150"-206" 267"-327" 373"-431"
Intra-L (C23-C104) 23'-88' 137'-197'
23'"-88'" 137'"-197'"
Inter-H-L (h 5-CL 126) 226-217' 226"-217'"
Inter-H-H (h 11, h 14) 232-232" 235-235"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84 4:
303, 303"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

danicopanum

danicopan

(2*S*,4*R*)-1-{[3-acetyl-5-(2-methylpyrimidin-5-yl)-1*H*-indazol-1-yl]acetyl}-*N*-(6-bromopyridin-2-yl)-4-fluoropyrrolidine-2-carboxamide

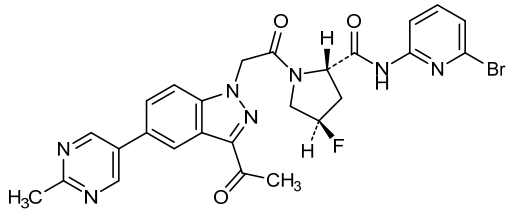
danicopan

(2*S*,4*R*)-1-{[3-acétyl-5-(2-méthylpyrimidin-5-yl)-1*H*-indazol-1-yl]acétyl}-*N*-(6-bromopyridin-2-yl)-4-fluoropyrrolidine-2-carboxamide

danicopán

(2*S*,4*R*)-1-{[3-acetil-5-(2-metilpirimidin-5-il)-1*H*-indazol-1-il]acetil}-*N*-(6-bromopiridin-2-il)-4-fluoropirrolidina-2-carboxamida

$C_{26}H_{23}BrFN_7O_3$



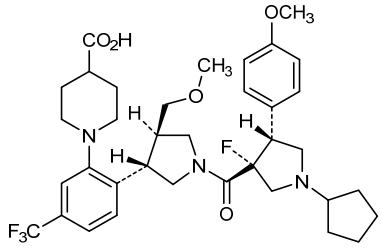
dersimelagonum

dersimelagon — 1-{2-[(3*S*,4*R*)-1-[(3*R*,4*R*)-1-cyclopentyl-3-fluoro-4-(4-methoxyphenyl)pyrrolidine-3-carbonyl]-4-(methoxymethyl)pyrrolidin-3-yl]-5-(trifluoromethyl)phenyl}piperidine-4-carboxylic acid

dersimélagon — acide 1-{2-[(3*S*,4*R*)-1-[(3*R*,4*R*)-1-cyclopentyl-3-fluoro-4-(4-méthoxyphényl)pyrrolidine-3-carbonyl]-4-(méthoxyméthyl)pyrrolidin-3-yl]-5-(trifluorométhyl)phényl}pipéridine-4-carboxylique

dersimelagón — ácido 1-{2-[(3*S*,4*R*)-1-[(3*R*,4*R*)-1-ciclopentil-3-fluoro-4-(4-metoxifenil)pirrolidina-3-carbonil]-4-(metoximetil)pirrolidin-3-il]-5-(trifluorometil)fenil}piperidina-4-carboxílico

$C_{36}H_{45}F_4N_3O_5$



dilanubicelum

dilanubicel — Allogeneic umbilical cord CD34$^+$ enriched blood cells. The drug substance consists of the total progeny generated from culture of enriched CD34$^+$ umbilical cord blood cells that have been cultured *ex vivo* in the presence of immobilised engineered Notch ligand Delta1$^{ext\text{-}IgG}$ (DXI) and recombinant cytokines. Cell phenotype distribution: CD3, CD7, CD14, CD15, CD16+CD56+ (both stained together), CD34, CD41, CD45RA, CD56, and CD90. Cells are intended to enhance reconstitution in hematopoietic stem cell transplantation patients with high risk of iatrogenic conditioning-related prolonged pancytopenia.

dilanubicel — cellules du sang de cordon ombilical, allogéniques, enrichies en CD34+. Le principe actif consiste en la totalité de la descendance générée par la culture des cellules de sang de cordon ombilical enrichies en CD34+ mises en culture *ex vivo* en présence de ligand Notch Delta1$^{ext\text{-}IgG}$ (DXI) immobile et de cytokines recombinantes. Distribution du phénotype cellulaire: CD3, CD7, CD14, CD15, CD16+CD56+ (les deux teintés ensemble), CD34, CD41, CD45RA, CD56, et CD90. Les cellules sont destinées à accroitre la récupération après une transplantation de cellules souches hématopoïétiques, des patients avec un fort risque de pancytopénie prolongée lié à la condition iatrogénique.

dilanubicel	Células de sangre de cordón umbilical, alogénicas, enriquecidas en CD34+. El principio activo consta del total de la progenie generada en el cultivo de células de sangre de cordón umbilical enriquecidas en CD34+ que se han cultivado *ex vivo* en presencia del ligando ingenierizado de Notch Delta1$^{ext\text{-}IgG}$ (DXI) inmovilizado y de citoquinas recombinantes. Distribución del fenotipo celular: CD3, CD7, CD14, CD15, CD16+CD56+ (ambos teñidos juntos), CD34, CD41, CD45RA, CD56 y CD90. Las células se pretenden usar para potenciar la reconstitución en pacientes sometidos a trasplante de células troncales hematopoyéticas con alto riesgo de pancitopenia prolongada, relacionada con el acondicionamiento iatrogénico.
dilpacimabum #	
dilpacimab	immunoglobulin G1-kappa, anti-[*Homo sapiens* DLL4 (delta-like 4)] and anti-[*Homo sapiens* VEGFA (vascular endothelial growth factor A,VEGF-A, VEGF)], dual-variable domain humanized monoclonal antibody, bispecific; dual-variable gamma1 heavy chain (1-577) [humanized VH anti-DLL4 (*Homo sapiens* IGHV3-48*01 (89.8%) -(IGHD)-IGHJ4*01 (92.9%)) [8.8.11] (1-118) -6-mer linker (119-124) -humanized VH anti-VEGFA (*Homo sapiens* IGHV3-23*03 or IGHV3-30*02 (76.8%) -(IGHD) -IGHJ4*01 (93.3%)) [8.8.16] (125-247) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (344) (248-345), hinge (346-360), CH2 L1 3>A (364), L1.2>A (365) (361-470), CH3 E12 (486), M14 (488) (471-575), CHS (576-577)) (248-577)], (350-334')-disulfide with dual-variable kappa light chain (1'-334') [humanized V-KAPPA anti-DLL4 (*Homo sapiens* IGKV1D-13*01 (88.3%) -IGKJ2*01 (100%)) [6.3.9] (1'-107') -13-mer linker (108-120) -humanized V-KAPPA anti-VEGFA (*Homo sapiens* IGKV1-16*01 (88.4%) -IGKJ1*01 (100%)) [6.3.9] (121-227) -*Homo sapiens* IGKC*01, Km3 A45.1 (273), V101 (311)(228'-334')]; dimer (356-356":359-359")-bisdisulfide
dilpacimab	immunoglobuline G1-kappa, anti-[*Homo sapiens* DLL4 (delta-like 4)] et anti-[*Homo sapiens* VEGFA (facteur de croissance A de l'endothélium vasculaire, VEGF-A, VEGF)], anticorps monoclonal humanisé double-variable domaine, bispécifique; chaîne lourde gamma1 avec double-variable (1-577) [VH humanisé anti-DLL4 (*Homo sapiens* IGHV3-48*01 (89.8%) -(IGHD)-IGHJ4*01 (92.9%)) [8.8.11] (1-118) -6-mer linker (119-124) -VH humanisé anti-VEGFA (*Homo sapiens* IGHV3-23*03 ou IGHV3-30*02 (76.8%) -(IGHD) -IGHJ4*01 (93.3%)) [8.8.16] (125-247) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (344) (248-345), charnière (346-360), CH2 L1 3>A (364), L1 2>A (365) (361-470), CH3 E12 (486), M14 (488) (471-575), CHS (576-577)) (248-577)], (350-334')-disulfure à la chaîne légère kappa avec double-variable (1'-334') [V-KAPPA humanisé anti-DLL4 (*Homo sapiens* IGKV1D-13*01 (88.3%) -IGKJ2*01 (100%)) [6.3.9] (1'-107') -13-mer linker (108-120) -V-KAPPA humanisé anti-VEGFA (*Homo sapiens* IGKV1-16*01 (88.4%) -IGKJ1*01 (100%)) [6.3.9] (121-227) -*Homo sapiens* IGKC*01, Km3 A45.1 (273), V101 (311) (228'-334')]; dimère (356-356":359-359")-bisdisulfure

dilpacimab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* DLL4 (delta-like 4)] y anti-[*Homo sapiens* VEGFA (factor de crecimiento A del endotelio vascular, VEGF-A, VEGF)], anticuerpo monoclonal humanizado doble-variable dominio, biespecífico;
cadena pesada gamma1 con doble-variable (1-577) [VH humanizado anti-DLL4 (*Homo sapiens* IGHV3-48*01 (89.8%) -(IGHD)-IGHJ4*01 (92.9%)) [8.8.11] (1-118) -6-mer espaciador (119-124) -VH humanizado anti-VEGFA (*Homo sapiens* IGHV3-23*03 orIGHV3-30*02 (76.8%) -(IGHD) -IGHJ4*01 (93.3%)) [8.8.16] (125-247) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (344) (248-345), bisagra (346-360), CH2 L1.3>A (364), L1.2>A (365) (361-470), CH3 E12 (486), M14 (488) (471-575), CHS (576-577)) (248-577)], (350-334')-disulfuro con la cadena ligera kappa con doble-variable (1'-334') [V-KAPPA humanizado anti-DLL4 (*Homo sapiens* IGKV1D-13*01 (88.3%) -IGKJ2*01 (100%)) [6 3.9] (1'-107') -13-mer espaciador (108-120) -V-KAPPA humanizado anti-VEGFA (*Homo sapiens* IGKV1-16*01 (88.4%) -IGKJ1*01 (100%)) [6.3.9] (121-227) -*Homo sapiens* IGKC*01, Km3 A45.1 (273), V101 (311) (228'-334')]; dímero (356-356":359-359")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAASGFTFS NFPMAWVRQA PGKGLEWVAT  50
ISSSDGTTYY RDSVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARGY 100
YNSPFAYWGQ GTLVTVSSAS TKGPEVQLVE SGGGLVQPGG SLRLSCAASG 150
YTFTNYGMNW VRQAPGKGLE WVGWINTYTG EPTYAADFKR RFTFSLDTSK 200
STAYLQMNSL RAEDTAVYYC AKYPHYYGSS HWYFDVWGQG TLVTVSSAST 250
KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF 300
PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC NVNHKPSNTK VDKKVEPKSC 350
DKTHTCPPCP APEAAGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED 400
PEVKFNWYVD GVEVHNAKTK PREEQYNSTY RVVSVLTVLH QDWLNGKEYK 450
CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSREEMTK NQVSLTCLVK 500
GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG 550
NVFSCSVMHE ALHNHYTQKS LSLSPGK                         577
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCRASEDIY SNLAWYQQKP GKAPKLLIYD  50
TNNLADGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YNNYPPTFGQ 100
GTKLEIKRTV AAPSVFIFPP DIQMTQSPSS LSASVGDRVT ITCSASQDIS 150
NYLNWYQQKP GKAPKVLIYF TSSLHSGVPS RFSGSGSGTD FTLTISSLQP 200
EDFATYYCQQ YSTVPWTFGQ GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA 250
SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSTLT 300
LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC                  334
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 146-220 274-330 391-451 497-555
22"-96" 146"-220" 274"-330" 391"-451" 497"-555"
Intra-L (C23-C104) 23'-88' 143'-208' 254'-314'
23'"-88'" 143'"-208'" 254'"-314'"
Inter-H-L (h 5-CL 126) 350-334' 350"-334'"
Inter-H-H (h 11, h 14) 356-356" 359-359"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84 4:
427, 427"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

dostarlimabum #
dostarlimab

immunoglobulin G4-kappa, anti-[*Homo sapiens* PDCD1 (programmed cell death 1, PD-1, PD1, CD279)], humanized monoclonal antibody;

gamma4 heavy chain (1-443) [humanized VH (*Homo sapiens* IGHV3-23*01 (93.8%) -(IGHD) -IGHJ4*01 (92.3%)) [8.8.9] (1-116) -*Homo sapiens* IGHG4*01 (CH1 (117-214), hinge S10>P (224) (215-226), CH2 (227-336), CH3 (337-441), CHS (442-443)) (117-443)], (130-214')-disulfide with kappa light chain (1'-214') [humanized V-KAPPA (*Homo sapiens* IGKV1-9*01 (85 3%) -IGKJ2*02 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (222-222'':225-225'')-bisdisulfide

dostarlimab

immunoglobuline G1-kappa, anti-[*Homo sapiens* PDCD1 (protéine 1 de mort cellulaire programmée, PD-1, PD1, CD279)], anticorps monoclonal humanisé;
chaîne lourde gamma4 (1-443) [VH humanisé (*Homo sapiens* IGHV3-23*01 (93.8%) -(IGHD) -IGHJ4*01 (92.3%)) [8.8.9] (1-116) -*Homo sapiens* IGHG4*01 (CH1 (117-214), charnière S10>P (224) (215-226), CH2 (227-336), CH3 (337-441), CHS (442-443)) (117-443)], (130-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA humanisé (*Homo sapiens* IGKV1-9*01 (85.3%) -IGKJ2*02 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (222-222'':225-225'')-bisdisulfure

dostarlimab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* PDCD1 (proteína 1 de muerte celular programada, PD-1, PD1, CD279)], anticuerpo monoclonal humanizado;
cadena pesada gamma4 (1-443) [VH humanizado (*Homo sapiens* IGHV3-23*01 (93.8%) -(IGHD) -IGHJ4*01 (92.3%)) [8.8.9] (1-116) -*Homo sapiens* IGHG4*01 (CH1 (117-214), bisagra S10>P (224) (215-226), CH2 (227-336), CH3 (337-441), CHS (442-443)) (117-443)], (130-214')-disulfuro con la cadena ligera kappa (1'-214') [V-KAPPA humanizado (*Homo sapiens* IGKV1-9*01 (85 3%) -IGKJ2*02 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (222-222'':225-225'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLLESGGG LVQPGGSLRL SCAASGFTFS SYDMSWVRQA PGKGLEWVST  50
ISGGGSYTYY QDSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCASPY 100
YAMDYWGQGT TVTVSSASTK GPSVFPLAPC SRSTSESTAA LGCLVKDYFP 150
EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVVTVPSS SLGTKTYTCN 200
VDHKPSNTKV DKRVESKYGP PCPPCPAPEF LGGPSVFLFP PKPKDTLMIS 250
RTPEVTCVVV DVSQEDPEVQ FNWYVDGVEV HNAKTKPREE QFNSTYRVVS 300
VLTVLHQDWL NGKEYKCKVS NKGLPSSIEK TISKAKGQPR EPQVYTLPPS 350
QEEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT PPVLDSDGSF 400
FLYSRLTVDK SRWQEGNVFS CSVMHEALHN HYTQKSLSLS LGK        443
```

Light chain / Chaîne légère / Cadena ligera

```
DIQLTQSPSF LSAYVGDRVT ITCKASQDVG TAVAWYQQKP GKAPKLLIYW  50
ASTLHTGVPS RFSGSGSGTE FTLTISSLQP EDFATYYCQH YSSYPWTFGQ 100
GTKLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

Intra-H (C23-C104)	22-96	143-199	257-317	363-421
	22"-96"	143"-199"	257"-317"	363"-421"
Intra-L (C23-C104)	23'-88'	134'-194'		
	23'"-88'"	134'"-194'"		
Inter-H-L (CH1 10-CL 126)	130-214'	130"-214'"		
Inter-H-H (h 8, h 11)	222-222"	225-225"		

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
293, 293"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados
C-terminal lysine clipping:
H CHS K2:
443, 443"

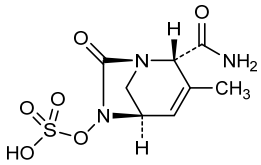
durlobactamum

durlobactam — (1*R*,2*S*,5*R*)-2-carbamoyl-3-methyl-7-oxo-1,6-diazabicyclo[3.2.1]oct-3-en-6-yl hydrogen sulfate

durlobactam — hydrogénosulfate de (1*R*,2*S*,5*R*)-2-carbamoyl-3-méthyl-7-oxo-1,6-diazabicyclo[3.2.1]oct-3-én-6-yle

durlobactam — hidrogenosulfato de (1*R*,2*S*,5*R*)-2-carbamoil-3-metil-7-oxo-1,6-diazabiciclo[3.2.1]oct-3-en-6-ile

$C_8H_{11}N_3O_6S$



eftozanerminum alfa #

eftozanermin alfa — Gln[1]-human single-chain tumor necrosis factor ligand superfamily member 10 (TNFSF10, tumor necrosis factor-related apoptosis-inducing ligand, TRAIL) receptor binding domain fragment, repeat of three identical chains (2-161, 171-330, 340-499) fused together via glycosylated linkers (162-170 connecting chain I to chain II and 331-339 connecting chain II to chain III), fused via linker (500-511) to an Fc fragment of human immunoglobulin G1 (512-740) [*Homo sapiens* IGHG1*03 (CH2 (524-633 (Asn[590]>Ser)), CH3 (634-738),CHS (739-740))], dimer, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

eftozanermine alfa — Gln[1]-chaîne unique du membre 10 de la superfamille des ligands du facteur de nécrose tumorale humain (TNFSF10, ligand inducteur d'apoptose apparenté au TNF, TRAIL) fragment du domaine se liant au récepteur, répétition de trois chaînes identiques, (2-161, 171-330, 340-499) fusionnées via des linkers glycosylés (162-170 liant la chaîne I à la chaîne II et 331-339 liant la chaîne II à la chaîne III), fusionné via un linker (500-511) au fragment Fc de l'immunoglobuline G1 humaine (512-740) [*Homo sapiens* IGHG1*03 (CH2 (524-633 (Asn[590]>Ser)), CH3 (634-738),CHS (739-740))], dimère, produit par des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

eftozanermina alfa — Gln[1]-cadena única del miembro 10 de la superfamilia de los ligandos del factor de necrosis tumoral humano (TNFSF10, ligando inductor de la apoptosis relacionado con el TNF, TRAIL) fragmento del dominio que se une al receptor, repetición de tres cadenas idénticas, (2-161, 171-330, 340-499) fusionadas mediante los conectores glicosilados (162-170 que une la cadena I a la cadena II y 331-339 que une la cadena II a la cadena III), fusionado mediante un enlace (500-511) al fragmento Fc de la inmunoglobulina G1 humana (512-740) [*Homo sapiens* IGHG1*03 (CH2 (524-633 (Asn[590]>Ser)), CH3 (634-738),CHS (739-740))], dímero, producido en las células ováricas de hamster chinos (CHO), glicoforma alfa

Monomer / monomère / monómero

```
QRVAAHITGT RGRSNTLSSP NSKNEKALGR KINSWESSRS GHSFLSNLHL  50
RNGELVIHEK GFYYIYSQTY FRFQEEIKEN TKNDKQMVQY IYKYTSYPDP 100
ILLMKSARNS CWSKDAEYGL YSIYQGGIFE LKENDRIFVS VTNEHLIDMD 150
HEASFFGAFL VGGSGSGNGS RVAAHITGTR GRSNTLSSPN SKNEKALGRK 200
INSWESSRSG HSFLSNLHLR NGELVIHEKG FYYIYSQTYF RFQEEIKENT 250
KNDKQMVQYI YKYTSYPDPI LLMKSARNSC WSKDAEYGLY SIYQGGIFEL 300
KENDRIFVSV TNEHLIDMDH EASFFGAFLV GGSGSGNGSR VAAHITGTRG 350
RSNTLSSPNS KNEKALGRKI NSWESSRSGH SFLSNLHLRN GELVIHEKGF 400
YYIYSQTYFR FQEEIKENTK NDKQMVQYIY KYTSYPDPIL LMKSARNSCW 450
SKDAEYGLYS IYQGGIFELK ENDRIFVSVT NEHLIDMDHE ASFFGAFLVG 500
GPGSSSSSSS GSCDKTHTCP PCPAPELLGG PSVFLFPPKP KDTLMISRTP 550
EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYS STYRVVSVLT 600
VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSREE 650
MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY 700
SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK           740
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

Intra-chain	111-280	554-614	660-718
	111-280'	554'-614'	660'-718'
Inter-chain	513-513'	519-519'	522-522'

Glycosylation sites (N) / Sites de glycosylation (N) / Posiciones de glicosilación (N)
Asn-168 Asn-337

eladocagenum exuparvovecum #

eladocagene exuparvovec	a recombinant non-replicating adeno-associated virus serotype 2 (AAV2) vector comprising a dopa decarboxylase (DDC, AADC) variant 2 cDNA transcript, which encodes human aromatic-L-amino-acid decarboxylase isoform 1, under the control of the cytomegalovirus (CMV) intermediate-early (IE) promoter and SV40 poly A transcription terminator.
éladocagène exuparvovec	vecteur viral adéno-associé de sérotype 2 (AAV2) non-répliquant recombinant contenant une transcription ADNc du variant 2 de la dopa décarboxylase (DDC, AADC) codant pour l'isoforme 1 de l'acide L-aminé aromatique décarboxylase humaine, sous le contrôle d'un promoteur intermédiaire précoce de cytomegalovirus (CMV) et une séquence poly-A de SV40 de terminaison de la transcription
eladocagén exuparvovec	Un vector de virus adenoasociado recombinante no replicativo de serotipo 2 (AAV2) que consta de un tránscrito cDNA de la variante 2 de la dopa descarboxilasa, que codifica para la isoforma 1 de la L-aminoácido aromático descarboxilasa humana, bajo el control del promotor intermedio temprano del citomegalovirus y un terminador de la transcripción poli A de SV40.

elopultidum

elopultide	L-isoleucyl-L-prolyl-L-seryl-L-seryl-L-prolyl-L-valyl-L-histidyl-L-leucyl-L-lysyl-L-arginyl-L-leucyl-L-lysyl-L-leucyl-L-leucyl-L-leucyl-L-leucyl-L-leucyl-L-leucyl-L-leucyl-L-leucyl-L-isoleucyl-L-leucyl-L-leucyl-L-leucyl-L-isoleucyl-L-leucylglycyl-L-alanyl-L-leucyl-L-leucyl-L-leucylglycyl-L-leucine
élopultide	L-isoleucyl-L-prolyl-L-séryl-L-séryl-L-prolyl-L-valyl-L-histidyl-L-leucyl-L-lysyl-L-arginyl-L-leucyl-L-lysyl-L-leucyl-L-leucyl-L-leucyl-L-leucyl-L-leucyl-L-leucyl-L-leucyl-L-leucyl-L-isoleucyl-L-leucyl-L-leucyl-L-leucyl-L-isoleucyl-L-leucylglycyl-L-alanyl-L-leucyl-L-leucyl-L-leucylglycyl-L-leucine

elopultida

L-isoleucil-L-prolil-L-seril-L-seril-L-prolil-L-valil-L-histidil-L-leucil-L-lisil-L-arginil-L-leucil-L-lisil-L-leucil-L-leucil-L-leucil-L-leucil-L-leucil-L-leucil-L-leucil-L-leucil-L-isoleucil-L-leucil-L-leucil-L-leucil-L-isoleucil-L-leucilglycil-L-alanil-L-leucil-L-leucil-L-leucilglicil-L-leucina

$C_{178}H_{320}N_{40}O_{36}$

IPSSPVHLKR LKLLLLLLLL ILLLILGALL LGL 33

eluforsenum

eluforsen

all-P-ambo-[1-33]tritriaconta-2'-*O*-methyl-[1-32]dotriaconta-*P*-thio-AUCAUAGGAA ACACCAAAGA UGAUAUUUUC UUU;
all-P-ambo-2'-*O*-methyl-*P*-thioadenylyl-(3'→5')-2'-*O*-methyl-*P*-thiouridylyl-(3'→5')-2'-*O*-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-methyl-*P*-thioadenylyl-(3'→5')-2'-*O*-methyl-*P*-thiouridylyl-(3'→5')-2'-*O*-methyl-*P*-thioadenylyl-(3'→5')-2'-*O*-methyl-*P*-thioguanylyl-(3'→5')-2'-*O*-methyl-*P*-thioguanylyl-(3'→5')-2'-*O*-methyl-*P*-thioadenylyl-(3'→5')-2'-*O*-methyl-*P*-thioadenylyl-(3'→5')-2'-*O*-methyl-*P*-thioadenylyl-(3'→5')-2'-*O*-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-methyl-*P*-thioadenylyl-(3'→5')-2'-*O*-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-methyl-*P*-thioadenylyl-(3'→5')-2'-*O*-methyl-*P*-thioadenylyl-(3'→5')-2'-*O*-methyl-*P*-thioguanylyl-(3'→5')-2'-*O*-methyl-*P*-thiouridylyl-(3'→5')-2'-*O*-methyl-*P*-thioguanylyl-(3'→5')-2'-*O*-methyl-*P*-thioadenylyl-(3'→5')-2'-*O*-methyl-*P*-thiouridylyl-(3'→5')-2'-*O*-methyl-*P*-thiouridylyl-(3'→5')-2'-*O*-methyl-*P*-thiouridylyl-(3'→5')-2'-*O*-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-methyl-*P*-thiouridylyl-(3'→5')-2'-*O*-methyluridine

éluforsen

tout-P-ambo-[1-33]tritriaconta-2'-*O*-méthyl-[1-32]dotriaconta-*P*-thio-AUCAUAGGAA ACACCAAAGA UGAUAUUUUC UUU;
tout-P-ambo-2'-*O*-méthyl-*P*-thioadénylyl-(3'→5')-2'-*O*-méthyl-*P*-thiouridylyl-(3'→5')-2'-*O*-méthyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-méthyl-*P*-thioadénylyl-(3'→5')-2'-*O*-méthyl-*P*-thiouridylyl-(3'→5')-2'-*O*-méthyl-*P*-thioadénylyl-(3'→5')-2'-*O*-méthyl-*P*-thioguanylyl-(3'→5')-2'-*O*-méthyl-*P*-thioguanylyl-(3'→5')-2'-*O*-méthyl-*P*-thioadénylyl-(3'→5')-2'-*O*-méthyl-*P*-thioadénylyl-(3'→5')-2'-*O*-méthyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-méthyl-*P*-thioadénylyl-(3'→5')-2'-*O*-méthyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-méthyl-*P*-thioadénylyl-(3'→5')-2'-*O*-méthyl-*P*-thioadénylyl-(3'→5')-2'-*O*-méthyl-*P*-thioguanylyl-(3'→5')-2'-*O*-méthyl-*P*-thiouridylyl-(3'→5')-2'-*O*-méthyl-*P*-thioguanylyl-(3'→5')-2'-*O*-méthyl-*P*-thioadénylyl-(3'→5')-2'-*O*-méthyl-*P*-thiouridylyl-(3'→5')-2'-*O*-méthyl-*P*-thioadénylyl-(3'→5')-2'-*O*-méthyl-*P*-thiouridylyl-(3'→5')-2'-*O*-méthyl-*P*-thiouridylyl-(3'→5')-2'-*O*-méthyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-méthyl-*P*-thiouridylyl-(3'→5')-2'-*O*-méthyluridine

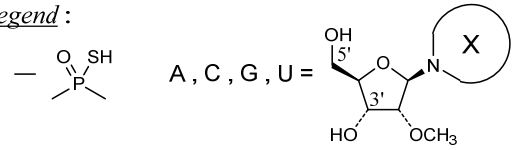
eluforsén

todo-P-ambo-[1-33]tritriaconta-2'-*O*-metil-[1-32]dotriaconta-*P*-tio-AUCAUAGGAA ACACCAAAGA UGAUAUUUUC UUU;
todo-P-ambo-2'-*O*-metil-*P*-tioadenilil-(3'→5')-2'-*O*-metil-*P*-tiouridilil-(3'→5')-2'-*O*-metil-*P*-tiocitidilil-(3'→5')-2'-*O*-metil-*P*-tioadenilil-(3'→5')-2'-*O*-metil-*P*-tiouridilil-(3'→5')-2'-*O*-metil-*P*-tioadenilil-(3'→5')-2'-*O*-metil-*P*-tioguanilil-(3'→5')-2'-*O*-metil-*P*-tioguanilil-(3'→5')-2'-*O*-metil-*P*-tioadenilil-(3'→5')-2'-*O*-metil-*P*-tioadenilil-(3'→5')-2'-*O*-metil-*P*-tiocitidilil-(3'→5')-2'-*O*-metil-*P*-tioadenilil-(3'→5')-2'-*O*-metil-*P*-tiocitidilil-(3'→5')-2'-*O*-metil-*P*-tioadenilil-(3'→5')-2'-*O*-metil-*P*-tioadenilil-(3'→5')-2'-*O*-metil-*P*-tioguanilil-(3'→5')-2'-*O*-metil-*P*-tiouridilil-(3'→5')-2'-*O*-metil-*P*-tioguanilil-(3'→5')-2'-*O*-metil-*P*-tioadenilil-(3'→5')-2'-*O*-metil-*P*-tiouridilil-(3'→5')-2'-*O*-metil-*P*-tiouridilil-(3'→5')-2'-*O*-metil-*P*-tiouridilil-(3'→5')-2'-*O*-metil-*P*-tiocitidilil-(3'→5')-2'-*O*-metil-*P*-tiouridilil-(3'→5')-2'-*O*-metiluridina

$C_{347}H_{452}N_{122}O_{195}P_{32}S_{32}$

(3'-5')(A-U-C-A-U-A-G-G-A-A-A-C-A-C-C-A-A-A-G-A-U-G-A-U-A-U-U-U-U-C-U-U-U)

Legend :



encequidarum

encequidar

N-[2-(2-{4-[2-(6,7-dimethoxy-3,4-dihydroisoquinolin-2(1*H*)-yl)ethyl]phenyl}-2*H*-tetrazol-5-yl)-4,5-dimethoxyphenyl]-4-oxo-4*H*-1-benzopyran-2-carboxamide

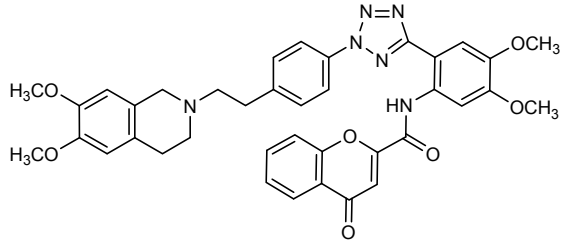
encéquidar

N-[2-(2-{4-[2-(6,7-diméthoxy-3,4-dihydroisoquinoléin-2(1*H*)-yl)éthyl]phényl}-2*H*-tétrazol-5-yl)-4,5-diméthoxyphényl]-4-oxo-4*H*-1-benzopyrane-2-carboxamide

encequidar

N-[2-(2-{4-[2-(6,7-dimetoxi-3,4-dihidroisoquinolein-2(1*H*)-il)etil]fenil}-2*H*-tetrazol-5-il)-4,5-dimetoxifenil]-4-oxo-4*H*-1-benzopirano-2-carboxamida

$C_{38}H_{36}N_6O_7$



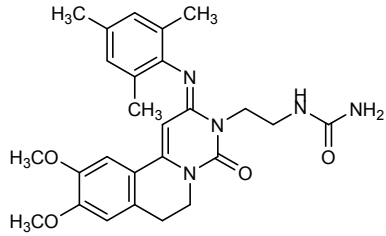
ensifentrinum

ensifentrine — *N*-(2-{(2*E*)-9,10-dimethoxy-4-oxo-2-[(2,4,6-trimethylphenyl)imino]-6,7-dihydro-2*H*-pyrimido[6,1-*a*]isoquinolin-3(4*H*)-yl}ethyl)urea

ensifentrine — *N*-(2-{(2*E*)-9,10-diméthoxy-4-oxo-2-[(2,4,6-triméthylphényl)imino]-6,7-dihydro-2*H*-pyrimido[6,1-*a*]isoquinoléin-3(4*H*)-yl}éthyl)urée

ensifentrina — *N*-(2-{(2*E*)-9,10-dimetoxi-4-oxo-2-[(2,4,6-trimetilfenil)imino]-6,7-dihidro-2*H*-pirimido[6,1-*a*]isoquinolein-3(4*H*)-il}etil)urea

$C_{26}H_{31}N_5O_4$



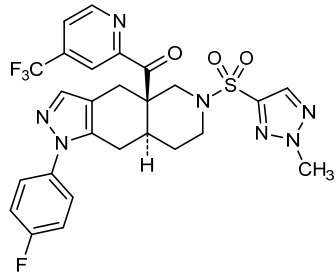
exicorilantum

exicorilant — [(4a*R*,8a*S*)-1-(4-fluorophenyl)-6-(2-methyl-2*H*-1,2,3-triazole-4-sulfonyl)-1,4,5,6,7,8,8a,9-octahydro-4a*H*-pyrazolo[3,4-*g*]isoquinolin-4a-yl][4-(trifluoromethyl)pyridin-2-yl]methanone

exicorilant — [(4a*R*,8a*S*)-1-(4-fluorophényl)-6-(2-méthyl-2*H*-1,2,3-triazole-4-sulfonyl)-1,4,5,6,7,8,8a,9-octahydro-4a*H*-pyrazolo[3,4-*g*]isoquinoléin-4a-yl][4-(trifluorométhyl)pyridin-2-yl]méthanone

exicorilant — [(4a*R*,8a*S*)-1-(4-fluorofenil)-6-(2-metil-2*H*-1,2,3-triazol-4-sulfonil)-1,4,5,6,7,8,8a,9-octahidro-4a*H*-pirazolo[3,4-*g*]isoquinolein-4a-il][4-(trifluorometil)piridin-2-il]metanona

$C_{26}H_{23}F_4N_7O_3S$



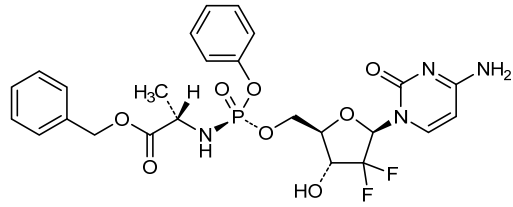
fosgemcitabinum palabenamidum

fosgemcitabine palabenamide — benzyl *N*-[(*P*$^{5'}$*S*)-2'-deoxy-2',2'-difluoro-*O*$^{5'}$-phenyl-5'-cytidylyl]-L-alaninate

fosgemcitabine palabénamide — *N*-[(*P*$^{5'}$*S*)-2'-désoxy-2',2'-difluoro-*O*$^{5'}$-phényl-5'-cytidylyl]-L-alaninate de benzyle

fosgemcitabina palabenamida — *N*-[(*P*$^{5'}$*S*)-2'-desoxi-2',2'-difluoro-*O*$^{5'}$-fenil-5'-citidilil]-L-alaninato de bencilo

$C_{25}H_{27}F_2N_4O_8P$



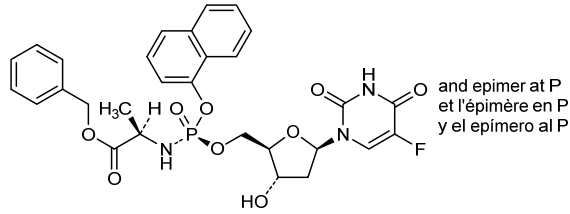
fosifloxuridinum nafalbenamidum

fosifloxuridine nafalbenamide — benzyl *N*-[*P*-*ambo*-2'-deoxy-5-fluoro-*O*$^{5'}$-(naphthalen-1-yl)-5'-uridylyl]-L-alaninate

fosifloxuridine nafalbénamide — *N*-[*P*-*ambo*-2'-désoxy-5-fluoro-*O*$^{5'}$-(naphtalén-1-yl)-5'-uridylyl]-L-alaninate de benzyle

fosifloxuridina nafalbenamida — *N*-[*P*-*ambo*-2'-desoxi-5-fluoro-*O*$^{5'}$-(naftalen-1-il)-5'-uridilil]-L-alaninato de bencilo

$C_{29}H_{29}FN_3O_9P$



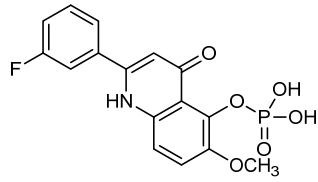
foslinanibum

foslinanib — 2-(3-fluorophenyl)-6-methoxy-4-oxo-1,4-dihydroquinolin-5-yl dihydrogen phosphate

foslinanib — dihydrogénophosphate de 2-(3-fluorophényl)-6-méthoxy-4-oxo-1,4-dihydroquinoléin-5-yle

foslinanib — dihidrogenofosfato de 2-(3-fluorofenil)-6-metoxi-4-oxo-1,4-dihidroquinolein-5-ilo

$C_{16}H_{13}FNO_6P$



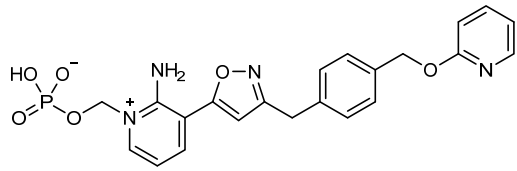
fosmanogepixum

fosmanogepix — [1^2-amino-6-oxa-1(3),7(2)-dipyridina-2(5,3)-[1,2]oxazola-4(1,4)-benzenaheptaphan-1^1-ium-1^1-yl]methyl hydrogen phosphate

fosmanogépix — hydrogénophosphate de [1^2-amino-6-oxa-1(3),7(2)-dipyridina-2(5,3)-[1,2]oxazola-4(1,4)-benzénaheptaphan-1^1-ium-1^1-yl]méthyle

fosmanogepix — hidrogenofosfato de [1^2-amino-6-oxa-1(3),7(2)-dipiridina-2(5,3)-[1,2]oxazola-4(1,4)-bencenaheptafan-1^1-ium-1^1-il]metilo

$C_{22}H_{21}N_4O_6P$



frovocimabum #

frovocimab — immunoglobulin G4-kappa, anti-[*Homo sapiens* PCSK9 (proprotein convertase subtilisin/kexin type 9, neural apoptosis-regulated convertase 1, NARC1, NARC-1, proprotein convertase 9, PC9) catalytic domain], humanized monoclonal antibody;
gamma4 heavy chain (1-451) [humanized VH (*Homo sapiens* IGHV3-21*01 (88.8%) -(IGHD)-IGHJ4*01 (100%)) [8.8.18] (1-125) -*Homo sapiens* IGHG4*01 (CH1 (126-223), hinge S10>P (233) (224-235), CH2 F1.3>A (239), L1.2>A (240) (236-345), CH3 (346-450), CHS K2>del (451)) (126-451)], (139-219')-disulfide with kappa light chain (1'-219') [humanized V-KAPPA (*Homo sapiens* IGKV2-28*01 (87.00%) -IGKJ1*01 (100%)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dimer (231-231":234-234")-bisdisulfide

frovocimab — immunoglobuline G4-kappa, anti-[*Homo sapiens* PCSK9 (proprotéine convertase subtilisine/kexine type 9, convertase 1 régulée par l'apoptose neuronale, NARC1, NARC-1, proprotéine convertase 9, PC9)], anticorps monoclonal humanisé;

chaîne lourde gamma4 (1-451) [VH humanisé (*Homo sapiens* IGHV3-21*01 (88.8%) -(IGHD)-IGHJ4*01 (100%)) [8.8.18] (1-125) -*Homo sapiens* IGHG4*01 (CH1 (126-223), charnière S10>P (233) (224-235), CH2 F1.3>A (239), L1 2>A (240) (236-345), CH3 (346-450), CHS K2>del (451)) (126-451)], (139-219')-disulfure avec la chaîne légère kappa (1'-219') [V-KAPPA humanisé (*Homo sapiens* IGKV2-28*01 (87.00%) -IGKJ1*01 (100%)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dimère (231-231":234-234")-bisdisulfure

frovocimab

inmunoglobulina G4-kappa, anti-[*Homo sapiens* PCSK9 (proproteína convertasa subtilisina/kexina tipo 9, convertasa 1 regulada por la apoptosa neuronal, NARC1, NARC-1, proproteína convertasa 9, PC9)], anticuerpo monoclonal humanizado;
cadena pesada gamma4 (1-451) [VH humanizado (*Homo sapiens* IGHV3-21*01 (88.8%) -(IGHD)-IGHJ4*01 (100%)) [8.8.18] (1-125) -*Homo sapiens* IGHG4*01 (CH1 (126-223), bisagra S10>P (233) (224-235), CH2 F1.3>A (239), L1.2>A (240) (236-345), CH3 (346-450), CHS K2>del (451)) (126-451)], (139-219')-disulfuro con la cadena ligera kappa (1'-219') [V-KAPPA humanizado (*Homo sapiens* IGKV2-28*01 (87.00%) -IGKJ1*01 (100%)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dímero (231-231":234-234")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVKPGGSLRL SCAASGFPFS KLGMVWVRQA PGKGLEWVST  50
ISSGGGYTYY PDSVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCAREG 100
ISFQGGTYTY VMDYWGQGTL VTVSSASTKG PSVFPLAPCS RSTSESTAAL 150
GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL SSVVTVPSSS 200
LGTKTYTCNV DHKPSNTKVD KRVESKYGPP CPPCPAPEAA GGPSVFLFPP 250
KPKDTLMISR TPEVTCVVVD VSQEDPEVQF NWYVDGVEVH NAKTKPREEQ 300
FNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KGLPSSIEKT ISKAKGQPRE 350
PQVYTLPPSQ EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP 400
PVLDSDGSFF LYSRLTVDKS RWQEGNVFSC SVMHEALHNH YTQKSLSLSL 450
G                                                       451
```

Light chain / Chaîne légère / Cadena ligera

```
DIVMTQSPLS LPVTPGEPAS ISCRSSKSLL HRNGITYSYW YLQKPGQSPQ  50
LLIYQLSNLA SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCYQNLELP 100
LTFGQGTKVE IKRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK 150
VQWKVDNALQ SGNSQESVTE QDSKDSTYSL SSTLTLSKAD YEKHKVYACE 200
VTHQGLSSPV TKSFNRGEC                                   219
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 152-208 266-326 372-430
22"-96" 152"-208" 266"-326" 372"-430"
Intra-L (C23-C104) 23'-93' 139'-199'
23'"-93'" 139'"-199'"
Inter-H-L (CH1 10-CL 126) 139-219' 139"-219'"
Inter-H-H (h 8, h 11) 231-231" 234-234"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84 4: 302, 302"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

futibatinibum

futibatinib

1-[(3*S*)-3-{4-amino-3-[(3,5-dimethoxyphenyl)ethynyl]-1*H*-pyrazolo[3,4-*d*]pyrimidin-1-yl}pyrrolidin-1-yl]prop-2-en-1-one

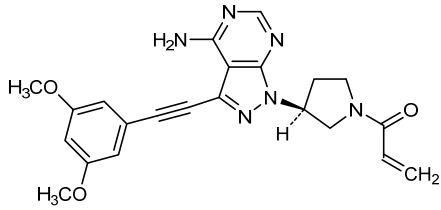
futibatinib

1-[(3*S*)-3-{4-amino-3-[(3,5-diméthoxyphényl)éthynyl]-1*H*-pyrazolo[3,4-*d*]pyrimidin-1-yl}pyrrolidin-1-yl]prop-2-én-1-one

futibatinib

1-[(3*S*)-3-{4-amino-3-[(3,5-dimetoxifenil)etinil]-1*H*-pirazolo[3,4-*d*]pirimidin-1-il}pirrolidin-1-il]prop-2-en-1-ona

$C_{22}H_{22}N_6O_3$



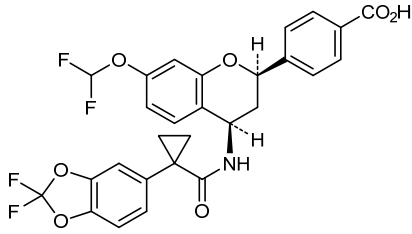
galicaftorum

galicaftor — 4-[(2*R*,4*R*)-4-[1-(2,2-difluoro-1,3-benzodioxol-5-yl)cyclopropane-1-carboxamido]-7-(difluoromethoxy)-3,4-dihydro-2*H*-1-benzopyran-2-yl]benzoic acid

galicaftor — acide 4-[(2*R*,4*R*)-4-[1-(2,2-difluoro-1,3-benzodioxol-5-yl)cyclopropane-1-carboxamido]-7-(difluorométhoxy)-3,4-dihydro-2*H*-1-benzopyran-2-yl]benzoïque

galicaftor — ácido 4-[(2*R*,4*R*)-4-[1-(2,2-difluoro-1,3-benzodioxol-5-il)ciclopropano-1-carboxamido]-7-(difluorometoxi)-3,4-dihidro-2*H*-1-benzopiran-2-il]benzoico

$C_{28}H_{21}F_4NO_7$



gancotamabum #

gancotamab — immunoglobulin scFv, anti-[*Homo sapiens* ERBB2 (epidermal growth factor receptor 2, receptor tyrosine-protein kinase erbB-2, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], *Homo sapiens* monoclonal antibody single chain;
scFv (1-251) [*Homo sapiens* VH (IGHV3-23*04 (94.9%) -(IGHD) -IGHJ4*01 (100%)) [8.8.12] (1-119) -15-mer tris(tetraglycyl-seryl) linker (120-134) -*Homo sapiens* V-LAMBDA (IGLV1-40*01(97.0%) -IGLJ3*02 (100%)) [9.3.11] (135-245) -6-mer bisglycyl-seryl-bisglycyl-cysteinyl (246-251)]

gancotamab — immunoglobuline scFv, anti-[*Homo sapiens* ERBB2 (récepteur 2 du facteur de croissance épidermique, récepteur tyrosine-protéine kinase erbB-2, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], *Homo sapiens* anticorps monoclonal à chaîne unique;
scFv (1-251) [*Homo sapiens* VH (IGHV3-23*04 (94.9%) -(IGHD) -IGHJ4*01 (100%)) [8.8.12] (1-119) -15-mer tris(tétraglycyl-séryl) linker (120-134) -*Homo sapiens* V-LAMBDA (IGLV1-40*01(97.0%) -IGLJ3*02 (100%)) [9.3.11] (135-245) -6-mer bisglycyl-séryl-bisglycyl-cystéinyl (246-251)]

gancotamab

inmunoglobulina scFv, anti-[*Homo sapiens* ERBB2 (receptor 2 del factor de crecimiento epidérmico, receptor tirosina-proteína kinasa erbB-2, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], *Homo sapiens* anticuerpo monoclonal con cadena única;
scFv (1-251) [*Homo sapiens* VH (IGHV3-23*04 (94.9%) -(IGHD) -IGHJ4*01 (100%)) [8.8.12] (1-119) -15-mer tris(tetraglicil-seril) conector (120-134) -*Homo sapiens* V-LAMBDA (IGLV1-40*01(97.0%) -IGLJ3*02 (100%)) [9.3.11] (135-245) -6-mer bisglicil-seril-bisglicil-cisteinil (246-251)]

```
QVQLVESGGG LVQPGGSLRL SCAASGFTFR SYAMSWVRQA PGKGLEWVSA  50
ISGRGDNTYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKMT 100
SNAFAFDYWG QGTLVTVSSG GGGSGGGGSG GGGSQSVLTQ PPSVSGAPGQ 150
RVTISCTGSS SNIGAGYGVH WYQQLPGTAP KLLIYGNTNR PSGVPDRFSG 200
FKSGTSASLA ITGLQAEDEA DYYCQSYDSS LSGWVFGGGT KLTVLGGSGG 250
C                                                       251
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-scFv (C23-C104) 22-96 156-224

golexanolonum

golexanolone

(17*E*)-3α-ethynyl-17-(hydroxyimino)-5α-androstan-3β-ol

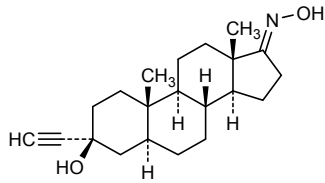
golexanolone

(17*E*)-3α-éthynyl-17-(hydroxyimino)-5α-androstan-3β-ol

golexanolona

(17*E*)-3α-etinil-17-(hidroxiimino)-5α-androstan-3β-ol

$C_{21}H_{31}NO_2$



gosuranemabum #

gosuranemab

immunoglobulin G4-kappa, anti-[*Homo sapiens* MAPT (microtubule-associated protein tau, tau)], monoclonal antibody;
gamma4 heavy chain (1-443)[VH (*Mus musculus* IGHV5-6*01 (85.6%)/*Homo sapiens* IGHV3-11*01 (84 5%) -(IGHD) -*Homo sapiens* IGHJ6*01 (92.9%)) [8.8.10] (1-117) -*Homo sapiens* IGHG4*01 (CH1 (118-215), hinge S10>P (225) (216-227), CH2 (228-337), CH3 (338-442), CHS K2>del (443)) (118-443)], (131-219')-disulfide with kappa light chain (1'-219') [V-KAPPA (*Mus musculus* IGKV1-117*01 (89.0%)/*Homo sapiens* IGKV2-30*02 (84.0%) -*Homo sapiens* IGKJ4*01 (100%)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dimer (223-223'':226-226'')-bisdisulfide

gosuranémab

immunoglobuline G4-kappa, anti-[*Homo sapiens* MAPT (protéine tau associée aux microtubules, tau)], anticorps monoclonal;
chaîne lourde gamma4 (1-443) [VH (*Mus musculus* IGHV5-6*01 (85.6%)/*Homo sapiens* IGHV3-11*01 (84.5%) -(IGHD) -*Homo sapiens* IGHJ6*01 (92.9%)) [8.8.10] (1-117) -*Homo sapiens* IGHG4*01 (CH1 (118-215), charnière S10>P (225) (216-227), CH2 (228-337), CH3 (338-442), CHS K2>del (443)) (118-443)], (131-219')-disulfure avec la chaîne légère kappa (1'-219') [V-KAPPA (*Mus musculus* IGKV1-117*01 (89.0%)/*Homo sapiens* IGKV2-30*02 (84.0%) -*Homo sapiens* IGKJ4*01 (100%)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dimère (223-223'':226-226'')-bisdisulfure

gosuranemab

inmunoglobulina G4-kappa, anti-[*Homo sapiens* MAPT (proteína tau asociada con microtúbulos, tau)], anticuerpo monoclonal;
cadena pesada gamma4 (1-443) [VH (*Mus musculus* IGHV5-6*01 (85.6%)/*Homo sapiens* IGHV3-11*01 (84.5%) -(IGHD) -*Homo sapiens* IGHJ6*01 (92.9%)) [8.8.10] (1-117) -*Homo sapiens* IGHG4*01 (CH1 (118-215), bisagra S10>P (225) (216-227), CH2 (228-337), CH3 (338-442), CHS K2>del (443)) (118-443)], (131-219')-disulfuro con la cadena ligera kappa (1'-219') [V-KAPPA (*Mus musculus* IGKV1-117*01 (89.0%)/*Homo sapiens* IGKV2-30*02 (84.0%) -*Homo sapiens* IGKJ4*01 (100%)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dímero (223-223'':226-226'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVHLVESGGA LVKPGGSLRL SCAASGFSFS KYGMSWVRQA PGKGLEWVAT  50
ISSSGSRTYY PDSVKGRFTI SRDNAKNTLY LQMNSLRAED TAMYYCSISW 100
DGAMDYWGQG TTVTVSSAST KGPSVFPLAP CSRSTSESTA ALGCLVKDYF 150
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTKTYTC 200
NVDHKPSNTK VDKRVESKYG PPCPPCPAPE FLGGPSVFLF PPKPKDTLMI 250
SRTPEVTCVV VDVSQEDPEV QFNWYVDGVE VHNAKTKPRE EQFNSTYRVV 300
SVLTVLHQDW LNGKEYKCKV SNKGLPSSIE KTISKAKGQP REPQVYTLPP 350
SQEEMTKNQV SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS 400
FFLYSRLTVD KSRWQEGNVF SCSVMHEALH NHYTQKSLSL SLG        443
```

Light chain / Chaîne légère / Cadena ligera

```
DVVMTQSPLS LPVTLGQPAS ISCKSSQSIV HSNGNTYLEW YLQKPGQSPQ  50
LLVYKVSNRF SGVPDRFSGS GSGTDFTLKI SRVEAEDVGT YYCFQGSLVP 100
WAFGGGTKVE IKRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK 150
VQWKVDNALQ SGNSQESVTE QDSKDSTYSL SSTLTLSKAD YEKHKVYACE 200
VTHQGLSSPV TKSFNRGEC                                   219
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 144-200 258-318 364-422
22"-96" 144"-200" 258"-318" 364"-422"
Intra-L (C23-C104) 23'-93' 139'-199'
23'"-93'" 139'"-199'"
Inter-H-L (CH1 10-CL 126) 131-219' 131"-219'"
Inter-H-H (h 8, h 11) 223-223' 226-226"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84 4:
294, 294"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

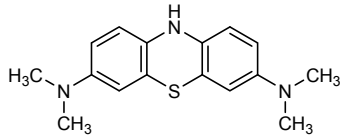
hydromethylthioninum

hydromethylthionine — N^3,N^3,N^7,N^7-tetramethyl-10*H*-phenothiazine-3,7-diamine

hydrométhylthionine — N^3,N^3,N^7,N^7-tétraméthyl-10*H*-phénothiazine-3,7-diamine

hidrometiltionina — N^3,N^3,N^7,N^7-tetrametil-10*H*-fenotiazina-3,7-diamina

$C_{16}H_{19}N_3S$



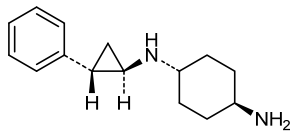
iadademstatum

iadademstat — *trans*-N^1-[(1*R*,2*S*)-2-phenylcyclopropyl]cyclohexane-1,4-diamine

iadademstat — *trans*-N^1-[(1*R*,2*S*)-2-phénylcyclopropyl]cyclohexane-1,4-diamine

iadademstat — *trans*-N^1-[(1*R*,2*S*)-2-fenilciclopropil]ciclohexano-1,4-diamina

$C_{15}H_{22}N_2$



idecabtagenum vicleucelum #

idecabtagene vicleucel — human culture expanded genetically modified autologous T cells for cell-based gene therapy. Cells are derived from isolated blood of the patient and are transduced with non-replicative self-inactivating (SIN) human immunodeficiency virus type 1 (HIV-1) based lentiviral vector (LVV) pseudotyped with the vesicular stomatitis virus glycoprotein G (VSV-G) envelope protein, and encoding the C11D5.3 anti-TNF receptor superfamily member 17 (TNFRSF17, BCMA) single chain variable fragment (scFv) CD8/4-1BB/CD3zeta chimeric antigen receptor (CAR) under the transcriptional control of the myeloproliferative sarcoma virus enhancer, negative control region deleted, dl587rev primer-binding site substituted (MND) promoter. Cells exhibit anti-tumoral activity in patients with multiple myeloma.

idécabtagène vicleucel — lymphocytes T humains, autologues, génétiquement modifiés, en culture d'expansion pour thérapie génique avec cellules. Les cellules sont dérivées du sang prélevé chez le patient et sont transduites avec un vecteur lentiviral basé sur le virus de l'immunodéficience humaine de type 1 (VIH-1) non-répliquant auto-inactivant, pseudotypé avec la

glycoprotéine G de l'enveloppe de du virus de la stomatite vésiculaire (VSV-G) et codant pour le récepteur de l'antigène chimérique (CAR) consistant en un fragment variable de la chaîne unique de l'anticoprs CD11D5.3 anti-membre 17 de la superfamille des récepteurs du TNF (TNFRSF17, BCMA)/CD8/4-1BB/CD3zêta sous le contrôle transcriptionnel d'un promoteur du virus du sarcome myéloprolifératif dont la région de contrôle négatif a été supprimée, et le site de liaison de l'amorce substitué par dl587rev (MND). Les cellules montrent une activité anti-tumorale chez de patients atteints de multiples myélomes.

idecabtagén vicleucel

Linfocitos T autólogos, modificados genéticamente, humanos, expandidos en cultivo para terapia génica con células. Las células se derivan de sangre aislada del paciente y se transducen con un vector lentiviral basado en el virus de la inmunodeficiencia humana tipo 1 (HIV-1) no replicativo y autoinactivante, seudotipado con la glicoproteina G de la envuelta del virus de la estomatitis vesicular (VSV-G), y que codifica para el receptor de antígeno quimérico (CAR) consistente en un fragmento variable de cadena sencilla (scFv) del anticuerpo CD11D5 3 anti-miembro 17 de la superfamilia de receptores de TNF (TNFRSF17, BCMA)/CD8/4-1BB/CD3zeta bajo el control transcripcional del enhancer del virus del sarcoma mieloproliferativo, y el promotor con la región de control negativo delecionada y el sitio de unión del cebador dl587rev sustituido (MND). Las células poseen actividad antitumoral en pacientes con mieloma múltiple.

ilginatinibum

ilginatinib

N^2-[(1*S*)-1-(4-fluorophenyl)ethyl]-4-(1-methyl-1*H*-pyrazol-4-yl)-*N*^{6}-(pyrazin-2-yl)pyridine-2,6-diamine

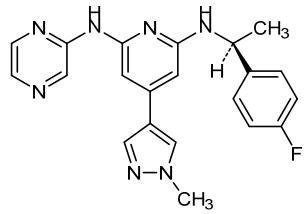
ilginatinib

N^2-[(1*S*)-1-(4-fluorophényl)éthyl]-4-(1-méthyl-1*H*-pyrazol-4-yl)-*N*^{6}-(pyrazin-2-yl)pyridine-2,6-diamine

ilginatinib

N^2-[(1*S*)-1-(4-fluorofenil)etil]-4-(1-metil-1*H*-pirazol-4-il)-*N*^{6}-(pirazin-2-il)piridina-2,6-diamina

$C_{21}H_{20}FN_7$



iodinum (^{131}I) apamistamabum #

iodine (^{131}I) apamistamab

immunoglobulin G1-kappa, anti-[*Homo sapiens* PTPRC (protein tyrosine phosphatase receptor type C, GP180, LCA, T200, CD45)], *Mus musculus* monoclonal antibody, conjugated on six tyrosyl, to iodine (^{131}I);
gamma1 heavy chain (1-444) [*Mus musculus* VH (IGHV4-1*02 (95.9%) -(IGHD) -IGHJ4*01 (100%)) [8.8.14] (1-121) -*Mus musculus* IGHG1*02 (CH1 Q100>E (199) (122-218), hinge (219-231), CH2 K81>Q (288), I84.3>F (294) (232-338), CH3 N27>D (369) (339-443), CHS (444-445)) (122-445)], (223-218')-disulfide with kappa light chain (1'-218') [*Mus musculus* V-KAPPA (IGKV3-12*01 (98.0%) -IGKJ4*01 (100%)) [10 3.9] (1'-111') -*Mus musculus* IGKC*01 (100%) (112'-218')]; dimer (225-225'':228-228'':230-230'')-trisdisulfide; conjugated on 6 tyrosyl (2 per H chain and 1 per L chain), to iodine (^{131}I)

iodine (^{131}I) apamistamab

immunoglobuline G1-kappa, anti-[*Homo sapiens* PTPRC (protéine tyrosine phosphatase de type récepteur C, GP180, LCA, T200, CD45)], *Mus musculus* anticorps monoclonal, conjugué sur 6 tyrosyl, à l'iode (^{131}I);
chaîne lourde gamma1 (1-444) [*Mus musculus* VH (IGHV4-1*02 (95.9%) -(IGHD) -IGHJ4*01 (100%)) [8.8.14] (1-121) -*Mus musculus* IGHG1*02 (CH1 Q100>E (199) (122-218), charnière (219-231), CH2 K81>Q (288), I84.3>F (294) (232-338), CH3 N27>D (369) (339-443), CHS (444-445)) (122-445)], (223-218')-disulfure avec la chaîne légère kappa (1'-218') [*Mus musculus* V-KAPPA (IGKV3-12*01 (98.0%) -IGKJ4*01 (100%)) [10.3.9] (1'-111') -*Mus musculus* IGKC*01 (100%) (112'-218')]; dimère (225-225'':228-228'':230-230'')-trisdisulfure; conjugué sur 6 tyrosyl (2 par chaîne H et 1 par chaîne L) à l'iode (^{131}I)

iodo (^{131}I) apamistamab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* PTPRC (proteína tirosina fosfatasa de tipo receptor C, GP180, LCA, T200, CD45)], *Mus musculus* anticuerpo monoclonal, conjugado con 6 restos tirosil, al iodo (^{131}I);
cadena pesada gamma1 (1-444) [*Mus musculus* VH (IGHV4-1*02 (95.9%) -(IGHD) -IGHJ4*01 (100%)) [8.8.14] (1-121) -*Mus musculus* IGHG1*02 (CH1 Q100>E (199) (122-218), bisagra (219-231), CH2 K81>Q (288), I84.3>F (294) (232-338), CH3 N27>D (369) (339-443), CHS (444-445)) (122-445)], (223-218')-disulfuro con la cadena ligera kappa (1'-218') [*Mus musculus* V-KAPPA (IGKV3-12*01 (98.0%) -IGKJ4*01 (100%)) [10 3.9] (1'-111') -*Mus musculus* IGKC*01 (100%) (112'-218')]; dímero (225-225'':228-228'':230-230'')-trisdisulfuro; conjugado con 6 restos tirosil (2 por cadena H y 1 por cadena L) al iodo (^{131}I)

Heavy chain / Chaîne lourde / Cadena pesada

```
EVKLLESGGG LVQPGGSLKL SCAASGFDFS RYWMSWVRQA PGKGLEWIGE  50
INPTSSTINF TPSLKDKVFI SRDNAKNTLY LQMSKVRSED TALYYCARGN 100
YYRYGDAMDY WGQGTSVTVS SAKTTPPSVY PLAPGSAAQT NSMVTLGCLV 150
KGYFPEPVTV TWNSGSLSSG VHTFPAVLQS DLYTLSSSVT VPSSTWPSET 200
VTCNVAHPAS STKVDKKIVP RDCGCKPCIC TVPEVSSVFI FPPKPKDVLT 250
ITLTPKVTCV VVDISKDDPE VQFSWFVDDV EVHTAQTQPR EEQFNSTFRS 300
VSELPIMHQD WLNGKEFKCR VNSAAFPAPI EKTISKTKGR PKAPQVYTIP 350
PPKEQMAKDK VSLTCMITDF FPEDITVEWQ WNGQPAENYK NTQPIMDTDG 400
SYFVYSKLNV QKSNWEAGNT FTCSVLHEGL HNHHTEKSLS HSPGK      445
```

Light chain / Chaîne légère / Cadena ligera

```
DIALTQSPAS LAVSLGQRAT ISCRASKSVS TSGYSYLHWY QQKPGQPPKL  50
LIYLASNLES GVPARFSGSG SGTDFTLNIH PVEEEDAATY YCQHSRELPF 100
TFGSGTKLEI KRADAAPTVS IFPPSSEQLT SGGASVVCFL NNFYPKDINV 150
KWKIDGSERQ NGVLNSWTDQ DSKDSTYSMS STLTLTKDEY ERHNSYTCEA 200
THKTSTSPIV KSFNRNEC                                    218
```

Post-translational modifications

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

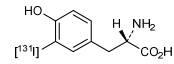
Intra-H (C23-C104) 22-96 148-203 259-319 365-423
22"-96" 148"-203" 259"-319" 365"-423"
Intra-L (C23-C104) 23'-92' 138'-198'
23'"-92'" 138'"-198'"
Inter-H-L (h 5-CL 126) 223-218' 223"-218'"
Inter-H-H (h7, h 10, h 12) 225-225" 228-228" 230-230"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación

H CH2 N84.4:
295, 295"
Mus musculus hybridoma-type glycans / glycanes de type hybridome de *Mus musculus* / glicanos de tipo híbridoma de *Mus musculus*

Iodination sites / Sites d'iodation / Posiciones de yodación

radiolabeled 3-[^{131}I]iodotyrosine
H VH Y109, Y110: 101 or 102, 101" or 102"
H CH3 Y85.2, Y86: 402 or 405, 402" or 405"
L V-KAPPA Y36, Y38, Y42: 334' or 36' or 40', 34'" or 36'" or 40'"



lenzumestrocelum

lenzumestrocel — human culture expanded autologous mesenchymal stromal cells for cell-based therapy. Cells are derived from isolated bone marrow of the patient. Cells express surface markers CD29, CD44, CD73, CD105 and CD49 and are intended to mediate immunomodulatory and neuroprotective effects

lenzumestrocel — cellules mésenchymales stromales humaines, autologues, expansées pour thérapie cellulaire. Les cellules sont dérivées de la moelle osseuse du patient. Les cellules expriment les marqueurs de surface CD29, CD44, CD73, CD105 et CD49, et sont destinées à avoir des effets immunomodulateurs et neuroprotecteurs.

lenzumestrocel — células mesenquimales estromales, autólogas, humanas, expandidas en cultivo para terapia celular. Las células derivan de médula ósea aislada del paciente. Las células expresan los marcadores de superficie CD29, CD44, CD73, CD105 y CD49, y se pretende que medien en efectos inmunomoduladores y neuroprotectores.

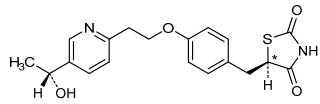
leriglitazonum

leriglitazone — *rac*-(5*R*)-5-{[4-(2-{5-[(1*RS*)-1-hydroxyethyl]pyridin-2-yl}ethoxy)phenyl]methyl}-1,3-thiazolidine-2,4-dione

lériglitazone — *rac*-(5*R*)-5-{[4-(2-{5-[(1*RS*)-1-hydroxyéthyl]pyridin-2-yl}éthoxy)phényl]méthyl}-1,3-thiazolidine-2,4-dione

leriglitazona — *rac*-(5*R*)-5-{[4-(2-{5-[(1*RS*)-1-hidroxietil]piridin-2-il}etoxi)fenil]metil}-1,3-tiazolidina-2,4-diona

$C_{19}H_{20}N_2O_4S$



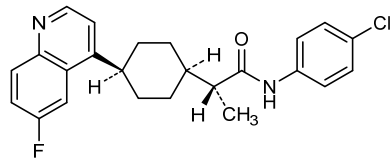
linrodostatum

linrodostat — (2*R*)-*N*-(4-chlorophenyl)-2-[*cis*-4-(6-fluoroquinolin-4-yl)cyclohexyl]propenamide

linrodostat — (2*R*)-*N*-(4-chlorophényl)-2-[*cis*-4-(6-fluoroquinoléin-4-yl)cyclohexyl]propenamide

linrodostat — (2*R*)-*N*-(4-clorofenil)-2-[*cis*-4-(6-fluoroquinolein-4-il)ciclohexil]propanamida

$C_{24}H_{24}ClFN_2O$



lisocabtagenum maraleucelum #

lisocabtagene maraleucel — human culture expanded genetically modified autologous T cells for cell-based gene therapy. CD4+ CD8+ T Cells are derived from isolated blood of the patient and are transduced with non-replicative self-inactivating (SIM) lentiviral vector encoding an FMC63 anti-CD19 single chain variable fragment (scFv) IgG4 hinge region/CD28/CD137 (4-1BB)/CD3zeta chimeric antigen receptor (CAR) and a truncated form of the human epidermal growth factor receptor (EGFRt) under the control of the elongation factor 1-alpha (EF1-alpha)/R region from the human T cell leukaemia virus 1 (HTLV-1 R) composite promoter. Cells exhibit anti-tumoral activity in patients with CD19-expressing B cell malignancies.

lisocabtagène maraleucel — lymphocytes T humains autologues en culture d'expansion et génétiquement modifiés pour thérapie génique avec cellules. Les lymphocytes T CD4+ et CD8+ sont dérivés du sang prélevé chez le patient et sont transduits avec un vecteur lentiviral non-répliquant et auto-inactivant codant pour un récepteur de l'antigène chimérique (CAR) consistant en un fragment variable de la chaîne unique (scFv) de l'anticorps FMC63 anti-CD-19, une région charnière de IgG4/CD28/CD137 (4-1BB)/CD3zêta et une forme tronquée du récepteur du facteur de croissance épidermique humain (EGFRt) sous le contrôle d'un promoteur composé du facteur d'élongation 1-alpha (EF1-alfa)/région R du virus T-lymphotrope humain (HTLV-1 R). Les cellules montrent une activité anti-tumorale chez les patients atteints de tumeurs malignes des lymphocytes B exprimant le CD-19.

lisocabtagén maraleucel

Linfocitos T autólogos, modificados genéticamente, humanos, expandidos en cultivo para terapia génica con células. Los linfocitos T CD4+ y CD8+ se derivan de sangre aislada del paciente y se transducen con un vector lentiviral no replicativo y autoinactivante que codifica para un receptor de antígeno quimérico (CAR) consistente en un fragmento variable de cadena sencilla (scFv) del anticuerpo FMC63 anti-CD19, una región bisagra de IgG4/CD28/CD137 (4-1BB)/CD3zeta y una forma truncada del receptor del factor de crecimiento epidérmico humano (EGFRt) bajo el control de un promotor compuesto del factor de elongación 1-alfa (EF1-alfa)/región R del virus de la leucemia humana de linfocitos T (HTLV-1 R). Las células poseen actividad anti-tumoral en pacientes con cánceres de linfocitos B que expresan CD19.

lorecivivintum

lorecivivint

N-(5-{3-[7-(3-fluorophenyl)-1*H*-imidazo[4,5-*c*]pyridin-2-yl]-1*H*-indazol-5-yl}pyridin-3-yl)-3-methylbutanamide

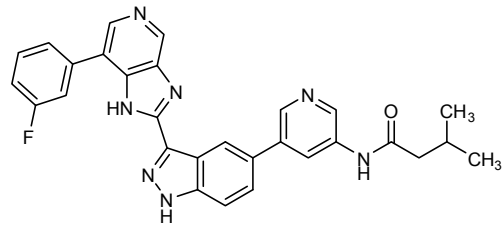
lorécivivint

N-(5-{3-[7-(3-fluorophényl)-1*H*-imidazo[4,5-*c*]pyridin-2-yl]-1*H*-indazol-5-yl}pyridin-3-yl)-3-méthylbutanamide

lorecivivint

N-(5-{3-[7-(3-fluorophényl)-1*H*-imidazo[4,5-*c*]pyridin-2-yl]-1*H*-indazol-5-yl}pyridin-3-yl)-3-méthylbutanamide

$C_{29}H_{24}FN_7O$



marstacimabum #

marstacimab

immunoglobulin G1-lambda, anti-[*Homo sapiens* TFPI (tissue factor pathway inhibitor, extrinsic pathway inhibitor, EPI, lipoprotein-associated coagulation inhibitor, LACI)], *Homo sapiens* monoclonal antibody; gamma1 heavy chain (1-449) [*Homo sapiens* VH (IGHV3-23*01 (100%) -(IGHD) -IGHJ3*02 (100%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (217) (121-218), hinge (219-233), CH2 L1.4>A (237), L1.3>A (238), G1>A (240) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS K2>del (449)) (121-449)], (223-217')-disulfide with lambda light chain (1'-218') [*Homo sapiens* V-LAMBDA (IGLV1-40*01 (100%) -IGLJ2*01 (100%)) [9 3.12] (1'-112') -*Homo sapiens* IGLC2*01 (113-218')]; dimer (229-229'':232-232'')-bisdisulfide

marstacimab

immunoglobuline G1-lambda, anti-[*Homo sapiens* TFPI (inhibiteur de la voie du facteur tissulaire, inhibiteur de la voie extrinsèque, EPI, inhibiteur de la coagulation associé aux lipoprotéines, LACI)], *Homo sapiens* anticorps monoclonal;
chaîne lourde gamma1 (1-449) [*Homo sapiens* VH (IGHV3-23*01 (100%) -(IGHD) -IGHJ3*02 (100%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (217) (121-218), charnière (219-233), CH2 L1.4>A (237), L1.3>A (238), G1>A (240) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS K2>del (449)) (121-449)], (223-217')-disulfure avec la chaîne légère lambda (1'-218') [*Homo sapiens* V-LAMBDA (IGLV1-40*01 (100%) -IGLJ2*01 (100%)) [9.3.12] (1'-112') -*Homo sapiens* IGLC2*01 (113-218')]; dimère (229-229'':232-232'')-bisdisulfure

marstacimab

inmunoglobulina G1-lambda, anti-[*Homo sapiens* TFPI (inhibidor de la vía del factor tisular, inhibidor de la vía extrínseca, EPI, inhibidor de la coagulación asociado a las lipoproteínas, LACI)], *Homo sapiens* anticuerpo monoclonal;
cadena pesada gamma1 (1-449) [*Homo sapiens* VH (IGHV3-23*01 (100%) -(IGHD) -IGHJ3*02 (100%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (217) (121-218), bisagra (219-233), CH2 L1.4>A (237), L1.3>A (238), G1>A (240) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS K2>del (449)) (121-449)], (223-217')-disulfuro con la cadena ligera lambda (1'-218') [*Homo sapiens* V-LAMBDA (IGLV1-40*01 (100%) -IGLJ2*01 (100%)) [9.3.12] (1'-112') -*Homo sapiens* IGLC2*01 (113-218')]; dímero (229-229'':232-232'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLLESGGG LVQPGGSLRL SCAASGFTFS SYAMSWVRQA PGKGLEWVSA  50
ISGSGGSTYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAILG 100
ATSLSAFDIW GQGTMVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPEAAGA PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPG  449
```

Light chain / Chaîne légère / Cadena ligera

```
QSVLTQPPSV SGAPGQRVTI SCTGSSSNIG AGYDVHWYQQ LPGTAPKLLI  50
YGNSNRPSGV PDRFSGSKSG TSASLAITGL QAEDEADYYC QSYDSSLSGS 100
GVFGGGTKLT VLGQPKAAPS VTLFPPSSEE LQANKATLVC LISDFYPGAV 150
TVAWKADSSP VKAGVETTTP SKQSNNKYAA SSYLSLTPEQ WKSHRSYSCQ 200
VTHEGSTVEK TVAPTECS                                    218
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 147-203 264-324 370-428
22"-96" 147"-203" 264"-324' 370"-428"
Intra-L (C23-C104) 22'-90' 140'-199'
22'"-90'" 140'"-199'"
Inter-H-L (h5-CL 126) 223-217' 223"-217'"
Inter-H-H (h11, h 14) 229-229" 232-232"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84 4:
300, 300"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

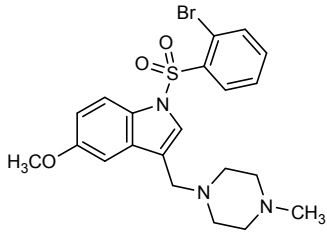
masupirdinum

masupirdine — 1-(2-bromobenzene-1-sulfonyl)-5-methoxy-3-[(4-methylpiperazin-1-yl)methyl]-1*H*-indole

masupirdine — 1-(2-bromobenzène-1-sulfonyl)-5-méthoxy-3-[(4-méthylpipérazin-1-yl)méthyl]-1*H*-indole

masupirdina — 1-(2-bromobenceno-1-sulfonil)-5-metoxi-3-[(4-metilpiperazin-1-il)metil]-1*H*-indol

$C_{21}H_{24}BrN_3O_3S$



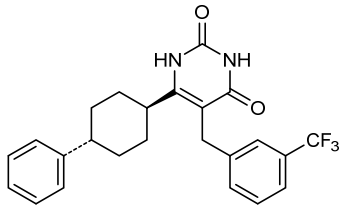
miricorilantum

miricorilant — 6-(*trans*-4-phenylcyclohexyl)-5-{[3-(trifluoromethyl)phenyl]methyl}pyrimidine-2,4(1*H*,3*H*)-dione

miricorilant — 6-(*trans*-4-phénylcyclohexyl)-5-{[3-(trifluorométhyl)phényl]méthyl}pyrimidine-2,4(1*H*,3*H*)-dione

miricorilant — 6-(*trans*-4-fenilciclohexil)-5-{[3-(trifluorometil)fenil]metil}pirimidina-2,4(1*H*,3*H*)-diona

$C_{24}H_{23}N_2O_2F_3$



mitazalimabum #

mitazalimab — immunoglobulin G1-lambda, anti-[*Homo sapiens* CD40 (tumor necrosis factor receptor superfamily member 5, TNFRSF5)], humanized monoclonal antibody;
gamma1 heavy chain (1-449) [humanized VH (IGHV3-48*01 (86.7%) -(IGHD) -IGHJ1*01 (100%)) [8.8.12] (1-119) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (216) (120-217), hinge (218-232), CH2 (233-342), CH3 D12 (358), L14 (360) (343-447), CHS (448-449)) (120-449)], (222-216')-disulfide with lambda light chain (1'-217') [humanized V-LAMBDA (*Homo sapiens* IGLV1-47*02 (90.9%) -IGLJ3*02 (100%)) [9.4.11] (1'-111') -*Homo sapiens* IGLC3*04 (112'-217')]; dimer (228-228'':231-231'')-bisdisulfide

mitazalimab

immunoglobuline G1-lambda, anti-[*Homo sapiens* CD40 (membre 5 de la superfamille des récepteurs du TNF, TNFRSF5)], anticorps monoclonal humanisé; chaîne lourde gamma1 (1-449) [VH humanisé (IGHV3-48*01 (86.7%) -(IGHD) -IGHJ1*01 (100%)) [8.8.12] (1-119) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (216) (120-217), charnière (218-232), CH2 (233-342), CH3 D12 (358), L14 (360) (343-447), CHS (448-449)) (120-449)], (222-216')-disulfure avec la chaîne légère lambda (1'-217') [V-LAMBDA humanisé (*Homo sapiens* IGLV1-47*02 (90.9%) -IGLJ3*02 (100%)) [9.4.11] (1'-111') -*Homo sapiens* IGLC3*04 (112'-217')]; dimère (228-228'':231-231'')-bisdisulfure

mitazalimab

inmunoglobulina G1-lambda, anti-[*Homo sapiens* CD40 (miembro 5 de la superfamilia de los receptores del TNF, TNFRSF5)], anticuerpo monoclonal humanizado; cadena pesada gamma1 (1-449) [VH humanizado (IGHV3-48*01 (86.7%) -(IGHD) -IGHJ1*01 (100%)) [8.8.12] (1-119) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (216) (120-217), bisagra (218-232), CH2 (233-342), CH3 D12 (358), L14 (360) (343-447), CHS (448-449)) (120-449)], (222-216')-disulfuro con la cadena ligera lambda (1'-217') [V-LAMBDA humanizado (*Homo sapiens* IGLV1-47*02 (90.9%) -IGLJ3*02 (100%)) [9.4.11] (1'-111') -*Homo sapiens* IGLC3*04 (112'-217')]; dímero (228-228'':231-231'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLLESGGG LVQPGGSLRL SCAASGFTFS TYGMHWVRQA PGKGLEWLSY  50
ISGGSSYIFY ADSVRGRFTI SRDNSENALY LQMNSLRAED TAVYYCARIL 100
RGGSGMDLWG QGTLVTVSSA STKGPSVFPL APSSKSTSGG TAALGCLVKD 150
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY 200
ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP CPAPELLGGP SVFLFPPKPK 250
DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS 300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV 350
YTLPPSRDEL TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL 400
DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK  449
```

Light chain / Chaîne légère / Cadena ligera

```
QSVLTQPPSA SGTPGQRVTI SCTGSSSNIG AGYNVYWYQQ LPGTAPKLLI  50
YGNINRPSGV PDRFSGSKSG TSASLAISGL RSEDEADYYC AAWDKSISGL 100
VFGGGTKLTV LGQPKAAPSV TLFPPSSEEL QANKATLVCL ISDFYPGAVT 150
VAWKADSSPV KAGVETTTPS KQSNNKYAAS SYLSLTPEQW KSHRSYSCQV 200
THEGSTVEKT VAPTECS                                     217
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 146-202 263-323 369-427
22"-96" 146"-202" 263"-323" 369"-427"
Intra-L (C23-C104) 22'-90' 139'-198'
22'"-90'" 139'"-198'"
Inter-H-L (h 5-CL 126) 222-216' 222"-216'"
Inter-H-H (h 11, h 14) 228-228" 231-231"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84 4:
299, 299"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

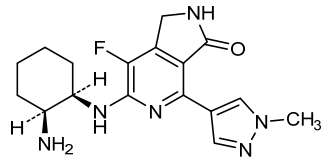
mivavotinibum

mivavotinib — 6-{[(1*R*,2*S*)-2-aminocyclohexyl]amino}-7-fluoro-4-(1-methyl-1*H*-pyrazol-4-yl)-1,2-dihydro-3*H*-pyrrolo[3,4-*c*]pyridin-3-one

mivavotinib — 6-{[(1*R*,2*S*)-2-aminocyclohexyl]amino}-7-fluoro-4-(1-méthyl-1*H*-pyrazol-4-yl)-1,2-dihydro-3*H*-pyrrolo[3,4-*c*]pyridin-3-one

mivavotinib — 6-{[(1*R*,2*S*)-2-aminociclohexil]amino}-7-fluoro-4-(1-metil-1*H*-pirazol-4-il)-1,2-dihidro-3*H*-pirrolo[3,4-*c*]piridin-3-ona

$C_{17}H_{21}FN_6O$



murlentamabum #

murlentamab — immunoglobulin G1-kappa, anti-[*Homo sapiens* AMHR2 (anti-Müllerian hormone (AMH) receptor type 2, Müllerian inhibiting substance type II receptor, MISRII, MISR2)], humanized monoclonal antibody;
gamma1 heavy chain (1-445) [humanized VH (*Homo sapiens* IGHV1-3*01 (90.8%) -(IGHD)-IGHJ4*01 (92.9%)) [8.8.8] (1-115) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (212) (116-213), hinge (214-228), CH2 (229-338), CH3 D12 (354), M14 (356) (339-443), CHS (444-445)) (116-445)], (218-213')-disulfide with kappa light chain (1'-213') [humanized V-KAPPA (*Homo sapiens* IGKV1-5*01 (86.2%) -IGKJ4*01 (100%)) [5.3.9] (1'-106') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191)(107'-213')]; dimer (224-224":227-227")-bisdisulfide

murlentamab — immunoglobuline G1-kappa, anti-[*Homo sapiens* AMHR2 (récepteur de type 2 de l'hormone anti-müllérienne, récepteur de type II de la substance inhibitrice müllérienne, MISRII, MISR2)], anticorps monoclonal humanisé;
chaîne lourde gamma1 (1-445) [VH humanisé (*Homo sapiens* IGHV1-3*01 (90.80%) -(IGHD)-IGHJ4*01 (92.9%)) [8.8.8] (1-115) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (212) (116-213), charnière (214-228), CH2 (229-338), CH3 D12 (354), M14 (356) (339-443), CHS (444-445)) (116-445)], (218-213')-disulfure avec la chaîne légère kappa (1'-213') [V-KAPPA humanisé (*Homo sapiens* IGKV1-5*01 (86.2%) -IGKJ4*01 (100%)) [5 3.9] (1'-106') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (107'-213')]; dimère (224-224":227-227")-bisdisulfure

murlentamab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* AMHR2 (receptor de tipo 2 de la hormona anti-mülleriana, receptor de tipo II de la sustancia inhibidora mülleriana, MISRII, MISR2)], anticuerpo monoclonal humanizado;
cadena pesada gamma1 (1-445) [VH humanizado (*Homo sapiens* IGHV1-3*01 (90.80%) -(IGHD)-IGHJ4*01 (92.9%)) [8.8.8] (1-115) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (212) (116-213), bisagra (214-228), CH2 (229-338), CH3 D12 (354), M14 (356) (339-443), CHS (444-445)) (116-445)], (218-213')-disulfuro con la cadena ligera kappa (1'-213') [V-KAPPA humanizado (*Homo sapiens* IGKV1-5*01 (86.2%) -IGKJ4*01 (100%)) [5 3.9] (1'-106') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (107'-213')]; dímero (224-224":227-227")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVRLVQSGAE VKKPGASVKV SCKASGYTFT SYHIHWVRQA PGQRLEWMGW  50
IYPGDDSTKY SQKFQGRVTI TRDTSASTAY MELSSLRSED TAVYYCTRGD 100
RFAYWGQGTL VTVSSASTKG PSVFPLAPSS KSTSGGTAAL GCLVKDYFPE 150
PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL SSVVTVPSSS LGTQTYICNV 200
NHKPSNTKVD KKVEPKSCDK THTCPPCPAP ELLGGPSVFL FPPKPKDTLM 250
ISRTPEVTCV VVDVSHEDPE VKFNWYVDGV EVHNAKTKPR EEQYNSTYRV 300
VSVLTVLHQD WLNGKEYKCK VSNKALPAPI EKTISKAKGQ PREPQVYTLP 350
PSRDELTKNQ VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG 400
SFFLYSKLTV DKSRWQQGNV FSCSVMHEAL HNHYTQKSLS LSPGK       445
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPST LSASVGDRVT ITCRASSSVR YIAWYQQKPG KAPKLLTYPT  50
SSLKSGVPSR FSGSGSGTEF TLTISSLQPD DFATYYCLQW SSYPWTFGGG 100
TKVEIKRTVA APSVFIFPPS DEQLKSGTAS VVCLLNNFYP REAKVQWKVD 150
NALQSGNSQE SVTEQDSKDS TYSLSSTLTL SKADYEKHKV YACEVTHQGL 200
SSPVTKSFNR GEC                                         213
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 142-198 259-319 365-423
22"-96" 142"-198" 259"-319" 365"-423"
Intra-L (C23-C104) 23'-87' 133'-193'
23'"-87'" 133'"-193'"
Inter-H-L (h 5-CL 126) 218-213' 218"-213'"
Inter-H-H (h 11, h 14) 224-224" 227-227'

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4 295, 295"
Low fucosylated complex bi-antennary rat myeloma YB2/0-type glycans / glycanes de type myélome de rat YB2/0 bi-antennaires complexes faiblement fucosylés / glicanos de tipo mieloma de rata YB2/0 biantenarios complejos bajo fucosilados

neluxicaponum

neluxicapone

4,5-dihydroxy-2-[(4-methylphenyl)methyl]benzene-1,3-dicarbonitrile

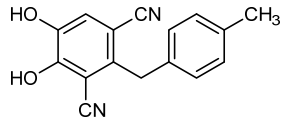
néluxicapone

4,5-dihydroxy-2-[(4-méthylphényl)méthyl]benzène-1,3-dicarbonitrile

neluxicapona

4,5-dihidroxi-2-[(4-metilfenil)metil]benzeno-1,3-dicarbonitrilo

$C_{16}H_{12}N_2O_2$



nerinetidum

nerinetide

L-tyrosylglycyl-L-arginyl-L-lysyl-L-lysyl-L-arginyl-L-arginyl-L-glutaminyl-L-arginyl-L-arginyl-L-arginyl-L-lysyl-L-leucyl-L-seryl-L-seryl-L-isoleucyl-L-α-glutamyl-L-seryl-L-α-aspartyl-L-valine

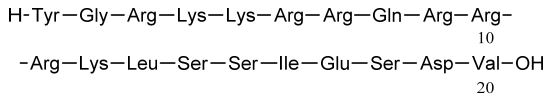
nérinétide

L-tyrosylglycyl-L-arginyl-L-lysyl-L-lysyl-L-arginyl-L-arginyl-L-glutaminyl-L-arginyl-L-arginyl-L-arginyl-L-lysyl-L-leucyl-L-séryl-L-séryl-L-isoleucyl-L-α-glutamyl-L-séryl-L-α-aspartyl-L-valine

nerinetida

L-tirosilglicil-L-arginil-L-lisil-L-lisil-L-arginil-L-arginil-L-glutaminil-L-arginil-L-arginil-L-arginil-L-lisil-L-leucil-L-seril-L-seril-L-isoleucil-L-α-glutamil-L-seril-L-α-aspartil-L-valina

$C_{105}H_{188}N_{42}O_{30}$



nevanimibum

nevanimibe

N-({1-[4-(dimethylamino)phenyl]cyclopentyl}methyl)-*N*'-[2,6-di(propan-2-yl)phenyl]urea

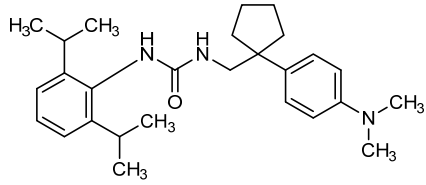
névanimibe

N-({1-[4-(diméthylamino)phényl]cyclopentyl}méthyl)-*N*'-[2,6-di(propan-2-yl)phényl]urée

nevanimiba

N-({1-[4-(dimetilamino)fenil]ciclopentil}metil)-*N*'-[2,6-di(propan-2-il)fenil]urea

$C_{27}H_{39}N_3O$



nirsevimabum #

nirsevimab

immunoglobulin G1-kappa, anti-[human respiratory virus (RSV) fusion glycoprotein F], monoclonal antibody; gamma1 heavy chain (1-456) [VH (*Homo sapiens* IGHV1-69*01 (82.5%) -(IGHD) -IGHJ4*01 (93.3%)) [8.8.19] (1-126) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (223) (127-224), hinge (225-239), CH2 M15.1>Y (261), S16>T (263), T18>E (265) (240-349), CH3 E12 (365), M14 (367) (350-454), CHS (455-456)) (127-456)], (229-214')-disulfide with kappa light chain (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (93.7%) -IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (235-235'':238-238'')-bisdisulfide

nirsévimab

immunoglobuline G1-kappa, anti-[glycoprotéine de fusion F du virus respiratoire syncytial (VRS) humain], anticorps monoclonal;
chaîne lourde gamma1 (1-456) [VH (*Homo sapiens* IGHV1-69*01 (82.5%) -(IGHD) -IGHJ4*01 (93.3%)) [8.8.19] (1-126) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (223) (127-224), charnière (225-239), CH2 M15.1>Y (261), S16>T (263), T18>E (265) (240-349), CH3 E12 (365), M14 (367) (350-454), CHS (455-456)) (127-456)], (229-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (93.7%) -IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (235-235'':238-238'')-bisdisulfure

nirsevimab

inmunoglobulina G1-kappa, anti-[glicoproteína de fusión F del virus respiratorio sincitial (VRS) humano], anticuerpo monoclonal;
cadena pesada gamma1 (1-456) [VH (*Homo sapiens* IGHV1-69*01 (82.5%) -(IGHD) -IGHJ4*01 (93.3%)) [8.8.19] (1-126) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (223) (127-224), bisagra (225-239), CH2 M15.1>Y (261), S16>T (263), T18>E (265) (240-349), CH3 E12 (365), M14 (367) (350-454), CHS (455-456)) (127-456)], (229-214')-disulfuro con la cadena ligera kappa (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (93.7%) -IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (235-235'':238-238'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGSSVMV SCQASGGLLE DYIINWVRQA PGQGPEWMGG  50
IIPVLGTVHY GPKFQGRVTI TADESTDTAY MELSSLRSED TAMYYCATET 100
ALVVSETYLP HYFDNWGQGT LVTVSSASTK GPSVFPLAPS SKSTSGGTAA 150
LGCLVKDYFP EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVVTVPSS 200
SLGTQTYICN VNHKPSNTKV DKRVEPKSCD KTHTCPPCPA PELLGGPSVF 250
LFPPKPKDTL YITREPEVTC VVVDVSHEDP EVKFNWYVDG VEVHNAKTKP 300
REEQYNSTYR VVSVLTVLHQ DWLNGKEYKC KVSNKALPAP IEKTISKAKG 350
QPREPQVYTL PPSREEMTKN QVSLTCLVKG FYPSDIAVEW ESNGQPENNY 400
KTTPPVLDSD GSFFLYSKLT VDKSRWQQGN VFSCSVMHEA LHNHYTQKSL 450
SLSPGK                                                 456
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSAAVGDRVT ITCQASQDIV NYLNWYQQKP GKAPKLLIYV  50
ASNLETGVPS RFSGSGSGTD FSLTISSLQP EDVATYYCQQ YDNLPLTFGG 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 153-209 270-330 376-434
22"-96" 153"-209" 270"-330" 376"-434"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194'"
Inter-H-L (h5-CL 126) 229-214' 229"-214'"
Inter-H-H (h 11, h 14) 235-235" 238-238'

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84 4:
306, 306"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

nomacopanum #

nomacopan — complement inhibitor from *Ornithodoros moubata* (soft tick or Argasid tick), produced in *Escherichia coli*

nomacopan — inhibiteur du complément de *Ornithodoros moubata* (tique molle ou Argasidé), produit dans *Escherichia coli*

nomacopán — inhibidor del complemento de *Ornithodoros moubata* (garrapata o Argásido), producido en *Escherichia coli*

$C_{720}H_{1107}N_{197}O_{244}S_{11}$

Sequence / Séquence / Secuencia

```
DSESDCTGSE PVDAFQAFSE GKEAYVLVRS TDPKARDCLK GEPAGEKQDN 50
TLPVMMTFKN GTDWASTDWT FTLDGAKVTA TLGNLTQNRE VVYDSQSHHC 100
HVDKVEKEVP DYEMWWMLDAG GLEVEVECCR QKLEELASGR NQMYPHLKDC 150
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
6-128 38-150 100-129

obexelimabum #

obexelimab — immunoglobulin G1-kappa, anti-[*Homo sapiens* CD19 (B lymphocyte surface antigen B4, Leu-12)], monoclonal antibody;
gamma1 heavy chain (1-451) [VH (*Mus musculus* IGHV1-14*01 (77.6%)/*Homo sapiens* IGHV1-3*01 (73.5%) -(IGHD)-*Homo sapiens* IGHJ4*01 (100%)) [8.8.14] (1-121) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (218) (122-219), hinge (220-234), CH2 S29>E (271), L113>F (332) (235-344), CH3 E12 (360), M14 (362) (345-449), CHS (450-451)) (122-451)], (224-219')-disulfide with kappa light chain (1'-219') [V-KAPPA (*Mus musculus* IGKV2-137*01 (75.0%)/*Homo sapiens* IGKV3D-11*03 (73.7%) -*Homo sapiens* IGKJ2*01 (90.9%)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dimer (230-230":233-233")-bisdisulfide

obéxélimab — immunoglobuline G1-kappa, anti-[*Homo sapiens* CD19 (antigène de surface B4 des lymphocytes B, Leu-12)], anticorps monoclonal;
chaîne lourde gamma1 (1-451) [VH (*Mus musculus* IGHV1-14*01 (77.6%)/*Homo sapiens* IGHV1-3*01 (73 5%) -(IGHD)-*Homo sapiens* IGHJ4*01 (100%)) [8.8.14] (1-121) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (218) (122-219), charnière (220-234), CH2 S29>E (271), L113>F (332) (235-344), CH3 E12 (360), M14 (362) (345-449), CHS (450-451)) (122-451)], (224-219')-disulfure avec la chaîne légère kappa (1'-219') [V-KAPPA (*Mus musculus* IGKV2-137*01 (75.0%)/*Homo sapiens* IGKV3D-11*03 (73.7%) -*Homo sapiens* IGKJ2*01 (90.9%)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dimère (230-230":233-233")-bisdisulfure

obexelimab — inmunoglobulina G1-kappa, anti-[*Homo sapiens* CD19 (antígeno de superficie B4 de los linfocitos B, Leu-12)], anticuerpo monoclonal;

cadena pesada gamma1 (1-451) [VH (*Mus musculus* IGHV1-14*01 (77.6%)/*Homo sapiens* IGHV1-3*01 (73.5%) -(IGHD)-*Homo sapiens* IGHJ4*01 (100%)) [8.8.14] (1-121) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (218) (122-219), bisagra (220-234), CH2 S29>E (271), L113>F (332) (235-344), CH3 E12 (360), M14 (362) (345-449), CHS (450-451)) (122-451)], (224-219')-disulfuro con la cadena ligera kappa (1'-219') [V-KAPPA (*Mus musculus* IGKV2-137*01 (75.0%)/*Homo sapiens* IGKV3D-11*03 (73.7%) -*Homo sapiens* IGKJ2*01 (90.9%)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dímero (230-230":233-233")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVKPGGSLKL SCAASGYTFT SYVMHWVRQA PGKGLEWIGY  50
INPYNDGTKY NEKFQGRVTI SSDKSISTAY MELSSLRSED TAMYYCARGT 100
YYYGTRVFDY WGQGTLVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200
TYICNVNHKP SNTKVDKKVE PKSCDKTHTC PPCPAPELLG GPSVFLFPPK 250
PKDTLMISRT PEVTCVVVDV EHEDPEVKFN WYVDGVEVHN AKTKPREEQY 300
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK AFPAPIEKTI SKAKGQPREP 350
QVYTLPPSRE EMTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP 400
VLDSDGSFFL YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG 450
K                                                       451
```

Light chain / Chaîne légère / Cadena ligera

```
DIVMTQSPAT LSLSPGERAT LSCRSSKSLQ NVNGNTYLYW FQQKPGQSPQ  50
LLIYRMSNLN SGVPDRFSGS GSGTEFTLTI SSLEPEDFAV YYCMQHLEYP 100
ITFGAGTKLE IKRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK 150
VQWKVDNALQ SGNSQESVTE QDSKDSTYSL SSTLTLSKAD YEKHKVYACE 200
VTHQGLSSPV TKSFNRGEC                                   219
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 148-204 265-325 371-429
22"-96" 148"-204" 265"-325" 371"-429"
Intra-L (C23-C104) 23'-93' 139'-199'
23'"-93'" 139'"-199'"
Inter-H-L (h 5-CL 126) 224-219' 224"-219'"
Inter-H-H (h 11, h 14) 230-230" 233-233"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
301, 301"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

odevixibatum

odevixibat

(2*S*)-2-[(2*R*)-2-(2-{[3,3-dibutyl-7-(methylsulfanyl)-1,1-dioxo-5-phenyl-2,3,4,5-tetrahydro-1*H*-1λ⁶,2,5-benzothiadiazepin-8-yl]oxy}acetamido)-2-(4-hydroxyphenyl)acetamido]butanoic acid

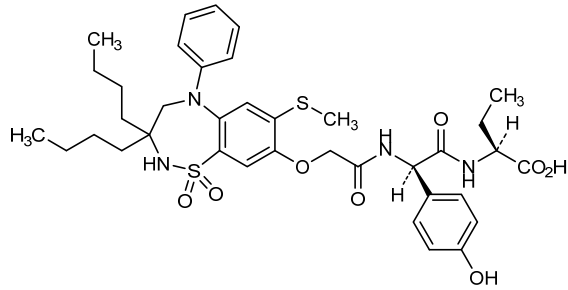
odévixibat

acide (2*S*)-2-[(2*R*)-2-(2-{[3,3-dibutyl-7-(méthylsulfanyl)-1,1-dioxo-5-phényl-2,3,4,5-tétrahyd-ro-1*H*-1λ⁶,2,5-benzothiadiazépin-8-yl]oxy}acétamido)-2-(4-hydroxyphényl)acétamido]butanoïque

odevixibat

ácido (2*S*)-2-[(2*R*)-2-(2-{[3,3-dibutil-7-(metilsulfanil)-1,1-dioxo-5-fenil-2,3,4,5-tetrahid-ro-1*H*-1λ⁶,2,5-benzotiadiazepin-8-il]oxi}acetamido)-2-(4-hidroxifenil)acetamido]butanoico

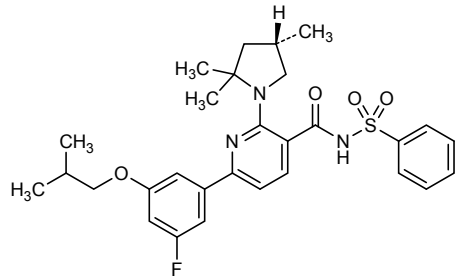
$C_{37}H_{48}N_4O_8S_2$



olacaftorum

olacaftor	*N*-(benzenesulfonyl)-6-[3-fluoro-5-(2-methylpropoxy)phenyl]-2-[(4*S*)-2,2,4-trimethylpyrrolidin-1-yl]pyridine-3-carboxamide
olacaftor	*N*-(benzènesulfonyl)-6-[3-fluoro-5-(2-méthylpropoxy)phényl]-2-[(4*S*)-2,2,4-triméthylpyrrolidin-1-yl]pyridine-3-carboxamide
olacaftor	*N*-(bencenosulfonil)-6-[3-fluoro-5-(2-metilpropoxi)fenil]-2-[(4*S*)-2,2,4-trimetilpirrolidin-1-il]piridina-3-carboxamida

$C_{29}H_{34}FN_3O_4S$



olenasufligenum relduparvovecum #

olenasufligene relduparvovec	A recombinant non-replicating adeno-associated virus serotype rh.10 (AAVrh.10) vector, comprised of a recombinant genome with the AAV2 Inverted Terminal Repeats (ITR) packaged into an AAVrh.10 capsid, expressing the human N-sulfoglucosamine sulfohydrolase (hSGSH) cDNA, under the control of the CMV immediate early enhancer/chicken β actin (CAG) promoter and a bovine hGH polyA transcription termination site.
olénasufligène relduparvovec	vecteur viraladéno-associé de sérotype rh.10 recombinant non-répliquant (AAVrh.10), comprenant un génome fait de séquences inverses terminales répétées (ITR) de AAV2 empaquetées dans une capside de AAVrh.10, exprimant l'ADNc de la N-sulfoglucosamine sulfohydrolase humaine (hSGSH), sous le contrôle du promoteur du CMV (cytomégalovirus) immédiat précoce / du promoteur de l'actine β du poulet et une séquence poly A de la hGH bovine comme terminaison de la transcription.

olenasufligén relduparvovec	Un vector de virus adenoasociado recombinante no replicativo de serotipo rh.10 (AAVrh.10), compuesto por un genoma recombinante con las Repeticiones Terminales Invertidas (ITR) empaquetadas en una cápside de AAVrh.10, expresando el cDNA de la N-sulfoglucosamina sulfohidrolasa humana, bajo el control del enhancer inmediato temprano del CMV/promotor de la b actina de pollo y un sitio poli A de la hGH bovina como terminación de la transcripción.
olinvacimabum #	
olinvacimab	immunoglobulin G1_V-lambda-C-kappa, anti-[*Homo sapiens* KDR (kinase insert domain receptor, vascular endothelial growth factor receptor 2, VEGFR2, VEGF-R2, FLK1, CD309)], monoclonal antibody; gamma1 heavy chain (1-462) [N-terminal 6-mer (1-6) -VH (*Homo sapiens* IGHV1-3*01 (84.7%) -(IGHD) -IGHJ4*01 (100%)) [8.8.14] (7-127) -5-mer linker (128-132) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (229) (133-230), hinge(231-245), CH2(246-355), CH3E12 (371), M14 (373) (356-460), CHS (461-462)) (133-462)], (235-227')-disulfide with V-lambda-C-kappa light chain (1'-227') [N-terminal 5-mer (1'-5') -V-LAMBDA (*Homo sapiens* IGLV3-21*01 (81.2%) -IGLJ1*01 (100%)) [6.3.10] (6'-112') -8-mer linker(113'-120') -*Homo sapiens* IGKC*01 T1.3>S (122), Km3 A45.1 (166), V101 (204) (121'-227')]; dimer (241-241'':244-244'')-bisdisulfide
olinvacimab	immunoglobuline G1_V-lambda-C-kappa, anti-[*Homo sapiens* KDR (récepteur à domaine insert kinase, récepteur 2 du facteur de croissance endothélial vasculaire, VEGFR2, VEGF-R2, FLK1, CD309)], anticorps monoclonal; chaîne lourde gamma1 (1-462) [6-mer N-terminal (1-6) -VH (*Homo sapiens* IGHV1-3*01 (84.7%) -(IGHD) -IGHJ4*01 (100%)) [8.8.14] (7-127) -5-mer linker (128-132) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (229) (133-230), charnière (231-245), CH2(246-355), CH3E12 (371), M14 (373) (356-460), CHS (461-462)) (133-462)], (235-227')-disulfure avec la chaîne légère V-lambda-C-kappa (1'-227') [5-mer N-terminal (1'-5') -V-LAMBDA (*Homo sapiens* IGLV3-21*01 (81.2%) -IGLJ1*01 (100%)) [6.3.10] (6'-112') -8-mer linker (113'-120') -*Homo sapiens* IGKC*01 T1.3>S (122), Km3 A45.1 (166), V101 (204) (121'-227')]; dimère (241-241'':244-244'')-bisdisulfure
olinvacimab	inmunoglobulina G1_V-lambda-C-kappa, anti-[*Homo sapiens* KDR (receptor con dominio inserto kinasa, receptor 2 del factor de crecimiento endotelial vascular, VEGFR2, VEGF-R2, FLK1, CD309)], anticuerpo monoclonal;

cadena pesada gamma1 (1-462) [6-mer N-terminal (1-6) -VH (*Homo sapiens* IGHV1-3*01 (84.7%) -(IGHD) - IGHJ4*01 (100%)) [8.8.14] (7-127) -5-mer ligante (128-132) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (229) (133-230), bisagra(231-245), CH2(246-355), CH3E12 (371), M14 (373) (356-460), CHS (461-462)) (133-462)], (235-227')-disulfuro con la cadena ligera V-lambda-C-kappa (1'-227') [5-mer N-terminal (1'-5') -V-LAMBDA (*Homo sapiens* IGLV3-21*01 (81.2%) -IGLJ1*01 (100%)) [6.3.10] (6'-112') -8-mer ligante (113'-120') - *Homo sapiens* IGKC*01 T1.3>S (122), Km3 A45.1 (166), V101 (204) (121'-227')]; dímero (241-241'':244-244'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
AQPAMAQMQL VQSGAEVKKP GASVKLSCKA SGYTFSSYWM HWVRQAPGQR  50
LEWMGEINPG NGHTNYNEKF KSRVTITVDK SASTAYMELS SLRSEDTAVY 100
YCAKIWGPSL TSPFDYWGQG TLVTVSSGLG GLASTKGPSV FPLAPSSKST 150
SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ SSGLYSLSSV 200
VTVPSSSLGT QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL 250
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH 300
NAKTKPREEQ YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT 350
ISKAKGQPRE PQVYTLPPSR EEMTKNQVSL TCLVKGFYPS DIAVEWESNG 400
QPENNYKTTP PVLDSDGSFF LYSKLTVDKS RWQQGNVFSC SVMHEALHNH 450
YTQKSLSLSP GK                                          462
```

Light chain / Chaîne légère / Cadena ligera

```
SGVGSNFMLT QPPSVSVSPG KTARITCRGD NLGDVNVHWY QQRPGQAPVL  50
VMYYDADRPS GIPERFSGSN SGNTATLTIS GVEAGDEADY YCQVWDRTSE 100
YVFGTGTKVT VLGGGASLVE RSVAAPSVFI FPPSDEQLKS GTASVVCLLN 150
NFYPREAKVQ WKVDNALQSG NSQESVTEQD SKDSTYSLSS TLTLSKADYE 200
KHKVYACEVT HQGLSSPVTK SFNRGEC                          227
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 28-102 159-215 276-336 382-440
28"-102" 159"-215" 276"-336" 382"-440"
Intra-L (C23-C104) 27'-92' 147'-207'
27'"-92'" 147'"-207'"
Inter-H-L (h 5-CL 126) 235-227' 235"-227'"
Inter-H-H (h 11, h 14) 241-241" 244-244"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
312, 312"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

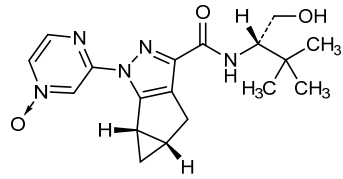
olorinabum

olorinab — 3-[(4a*S*,5a*S*)-3-{[(2*S*)-1-hydroxy-3,3-dimethylbutan-2-yl]carbamoyl}-4,4a,5,5a-tetrahydro-1*H*-cyclopropa[4,5]cyclopenta[1,2-*c*]pyrazol-1-yl]pyrazine 1-oxide

olorinab — 1-oxyde de 3-[(4a*S*,5a*S*)-3-{[(2*S*)-1-hydroxy-3,3-diméthylbutan-2-yl]carbamoyl}-4,4a,5,5a-tétrahydro-1*H*-cyclopropa[4,5]cyclopenta[1,2-*c*]pyrazol-1-yl]pyrazine

olorinab — 1-óxido de 3-[(4a*S*,5a*S*)-3-{[(2*S*)-1-hidroxi-3,3-dimetilbutan-2-il]carbamoil}-4,4a,5,5a-tetrahidro-1*H*-ciclopropa[4,5]ciclopenta[1,2-*c*]pirazol-1-il]pirazina

$C_{18}H_{23}N_5O_3$



omburtamabum #

omburtamab	immunoglobulin G1-kappa, anti-[*Homo sapiens* CD276 (B7H3, B7-H3, B7RP-2)], *Mus musculus* monoclonal antibody; gamma1 heavy chain (1-442) [*Mus musculus* VH (IGHV1-85*01 (88.8%) -(IGHD) -IGHJ3*01 (100%)) [8.8.11] (1-118) -*Mus musculus* IGHG1*02 (CH1 Q100>E (196) (119-215), hinge (216-228), CH2 K81>Q (285), I84.3>F (291) (229-335), CH3 N27>D (366) (336-440), CHS (441-442)) (119-442)], (220-214')-disulfide with kappa light chain (1'-214') [*Mus musculus* V-KAPPA (IGKV5-39*01 (100%) -IGKJ5*01 (100%)) [6.3.9] (1'-107') -*Mus musculus* IGKC*01 (100%) (108'-214')]; dimer (222-222'':225-225'':227-227'')-trisdisulfide
omburtamab	immunoglobuline G1-kappa, anti-[*Homo sapiens* CD276 (B7H3, B7-H3, B7RP-2)], *Mus musculus* anticorps monoclonal; chaîne lourde gamma1 (1-442) [*Mus musculus* VH (IGHV1-85*01 (88.8%) -(IGHD) -IGHJ3*01 (100%)) [8.8.11] (1-118) -*Mus musculus* IGHG1*02 (CH1 Q100>E (196) (119-215), charnière (216-228), CH2 K81>Q (285), I84.3>F (291) (229-335), CH3 N27>D (366) (336-440), CHS (441-442)) (119-442)], (220-214')-disulfure avec la chaîne légère kappa (1'-214') [*Mus musculus* V-KAPPA (IGKV5-39*01 (100%) -IGKJ5*01 (100%)) [6.3.9] (1'-107') -*Mus musculus* IGKC*01 (100%) (108'-214')]; dimère (222-222'':225-225'':227-227'')-trisdisulfure
omburtamab	inmunoglobulina G1-kappa, anti-[*Homo sapiens* CD276 (B7H3, B7-H3, B7RP-2)], *Mus musculus* anticuerpo monoclonal; cadena pesada gamma1 (1-442) [*Mus musculus* VH (IGHV1-85*01 (88.8%) -(IGHD) -IGHJ3*01 (100%)) [8.8.11] (1-118) -*Mus musculus* IGHG1*02 (CH1 Q100>E (196) (119-215), bisagra (216-228), CH2 K81>Q (285), I84.3>F (291) (229-335), CH3 N27>D (366) (336-440), CHS (441-442)) (119-442)], (220-214')-disulfuro con la cadena ligera kappa (1'-214') [*Mus musculus* V-KAPPA (IGKV5-39*01 (100%) -IGKJ5*01 (100%)) [6.3.9] (1'-107') -*Mus musculus* IGKC*01 (100%) (108'-214')]; dímero (222-222'':225-225'':227-227'')-trisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLQQSGAE LVKPGASVKL SCKASGYTFT NYDINWVRQR PEQGLEWIGW  50
IFPGDGSTQY NEKFKGKATL TTDTSSSTAY MQLSRLTSED SAVYFCARQT 100
TATWFAYWGQ GTLVTVSAAK TTPPSVYPLA PGSAAQTNSM VTLGCLVKGY 150
FPEPVTVTWN SGSLSSGVHT FPAVLQSDLY TLSSSVTVPS STWPSETVTC 200
NVAHPASSTK VDKKIVPRDC GCKPCICTVP EVSSVFIFPP KPKDVLTITL 250
TPKVTCVVVD ISKDDPEVQF SWFVDDVEVH TAQTQPREEQ FNSTFRSVSE 300
LPIMHQDWLN GKEFKCRVNS AAFPAPIEKT ISKTKGRPKA PQVYTIPPPK 350
EQMAKDKVSL TCMITDFFPE DITVEWQWNG QPAENYKNTQ PIMDTDGSYF 400
VYSKLNVQKS NWEAGNTFTC SVLHEGLHNH HTEKSLSHSP GK         442
```

Light chain / Chaîne légère / Cadena ligera

```
DIVMTQSPAT LSVTPGDRVS LSCRASQSIS DYLHWYQQKS HESPRLLIKY  50
ASQSISGIPS RFSGSGSGSD FTLSINSVEP EDVGVYYCQN GHSFPLTFGA 100
GTKLELKRAD AAPTVSIFPP SSEQLTSGGA SVVCFLNNFY PKDINVKWKI 150
DGSERQNGVL NSWTDQDSKD STYSMSSTLT LTKDEYERHN SYTCEATHKT 200
STSPIVKSFN RNEC                                        214
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

Intra-H (C23-C104) 22-96 145-200 256-316 362-420
22"-96" 145"-200" 256"-316" 362"-420"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194'"
Inter-H-L (h 5-CL 126) 220-214' 220"-214'"
Inter-H-H (h 7, h 10, h 12) 222-222" 225-225" 227-227"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación

H CH2 N84.4:
292, 292"
Mus musculus hybridoma-type glycans / glycanes de type hybridome de *Mus musculus* / glicanos de tipo hibridoma de *Mus musculus*

C-terminal lysine clipping:

H CHS K2:
442, 442"
(14.7% of H chain without the C-terminal lysine)

ontamalimabum #

ontamalimab	immunoglobulin G2-kappa, anti-[*Homo sapiens* MADCAM1 (mucosal vascular addressin cell adhesion molecule 1, mucosal addressin cell adhesion molecule-1, MAdCAM-1, MACAM1)], *Homo sapiens* monoclonal antibody; gamma2 heavy chain (1-450) [*Homo sapiens* VH (IGHV1-18*01 (93.9%) -(IGHD) -IGHJ6*01 (100%)) [8.8.17] (1-124) -*Homo sapiens* IGHG2*01, G2m.. (CH1 (125-222), hinge (223-234), CH2 V45.1 (285) (235-343), CH3 (344-448), CHS (449-450)) (125-450)], (138-219')-disulfide with kappa light chain (1'-219') [*Homo sapiens* V-KAPPA (IGKV2D-29*1 (96.0%) -IGKJ1*01 (100%)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dimer (226-226":227-227":230-230":233-233")-tetrakisdisulfide
ontamalimab	immunoglobuline G2-kappa, anti-[*Homo sapiens* MADCAM1 (molécule 1 d'adhésion cellulaire adressine de muqueuse vasculaire, molécule-1 d'adhésion cellulaire adressine de muqueuse, MAdCAM-1, MACAM1)], *Homo sapiens* anticorps monoclonal; chaîne lourde gamma2 (1-450) [*Homo sapiens* VH (IGHV1-18*01 (93.9%) -(IGHD) -IGHJ6*01 (100%)) [8.8.17] (1-124) -*Homo sapiens* IGHG2*01, G2m.. (CH1 (125-222), charnière (223-234), CH2 V45.1 (285) (235-343), CH3 (344-448), CHS (449-450)) (125-450)], (138-219')-disulfure avec la chaîne légère kappa (1'-219') [*Homo sapiens* V-KAPPA (IGKV2D-29*1 (96.0%) -IGKJ1*01 (100%)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dimère (226-226":227-227":230-230":233-233")-tétrakisdisulfure

ontamalimab

inmunoglobulina G2-kappa, anti-[*Homo sapiens* MADCAM1 (molécula 1 de adhesión celular adresina de mucosa vascular, molécula-1 de adhesión celular adresina de mucosa, MAdCAM-1, MACAM1)], *Homo sapiens* anticuerpo monoclonal;
cadena pesada gamma2 (1-450) [*Homo sapiens* VH (IGHV1-18*01 (93.9%) -(IGHD) -IGHJ6*01 (100%)) [8.8.17] (1-124) -*Homo sapiens* IGHG2*01, G2m.. (CH1 (125-222), bisagra (223-234), CH2 V45.1 (285) (235-343), CH3 (344-448), CHS (449-450)) (125-450)], (138-219')-disulfuro con la cadena ligera kappa (1'-219') [*Homo sapiens* V-KAPPA (IGKV2D-29*1 (96.0%) -IGKJ1*01 (100%)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dímero (226-226":227-227":230-230":233-233")-tetrakisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGASVKV SCKASGYTFT SYGINWVRQA PGQGLEWMGW  50
ISVYSGNTNY AQKVQGRVTM TADTSTSTAY MDLRSLRSDD TAVYYCAREG 100
SSSSGDYYYG MDVWGQGTTV TVSSASTKGP SVFPLAPCSR STSESTAALG 150
CLVKDYFPEP VTVSWNSGAL TSGVHTFPAV LQSSGLYSLS SVVTVPSSNF 200
GTQTYTCNVD HKPSNTKVDK TVERKCCVEC PPCPAPPVAG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS HEDPEVQFNW YVDGVEVHNA KTKPREEQFN 300
STFRVVSVLT VVHQDWLNGK EYKCKVSNKG LPAPIEKTIS KTKGQPREPQ 350
VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPM 400
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK 450
```

Light chain / Chaîne légère / Cadena ligera

```
DIVMTQTPLS LSVTPGQPAS ISCKSSQSLL HTDGTTYLYW YLQKPGQPPQ  50
LLIYEVSNRF SGVPDRFSGS GSGTDFTLKI SRVEAEDVGI YYCMQNIQLP 100
WTFGQGTKVE IKRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK 150
VQWKVDNALQ SGNSQESVTE QDSKDSTYSL SSTLTLSKAD YEKHKVYACE 200
VTHQGLSSPV TKSFNRGEC                                   219
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 151-207 264-324 370-428
22"-96" 151"-207" 264"-324" 370"-428"
Intra-L (C23-C104) 23'-93' 139'-199'
23'"-93'" 139'"-199'"
Inter-H-L (CH1 10-CL 126) 138-219' 138"-219'"
Inter-H-H (h 4, h 5, h 8, h 11) 226-226" 227-227" 230-230" 233-233"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
300, 300"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

orilanolimabum #
orilanolimab

immunoglobulin G4-kappa, anti-[*Homo sapiens* FCGRT (Fc fragment of IgG receptor and transporter, neonatal Fc receptor, FcRn, transmembrane alpha chain of the neonatal receptor)], monoclonal antibody;
gamma4 heavy chain (1-444) [VH (*Mus musculus* IGHV1-81*01 (92.9%)/*Homo sapiens* IGHV1-18*01 (77.6%) -(IGHD) -*Homo sapiens* IGHJ3*02 (83.3%)) [8.8.11] (1-118) -*Homo sapiens* IGHG4*01 (CH1 (119-216), hinge S10>P (226) (217-228), CH2 (229-338), CH3 (339-443), CHS K2>del (444)) (119-444)], (132-214')-disulfide with kappa light chain (1'-214') [V-KAPPA (*Mus musculus* IGKV13-85*01 (88.4%)/*Homo sapiens* IGKV1-NL1*01 (83.2%) -*Homo sapiens* IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191)(108'-214')]; dimer (224-224":227-227")-bisdisulfide

orilanolimab

immunoglobuline G4-kappa, anti-[*Homo sapiens* FCGRT (transporteur et récepteur du fragment Fc des IgG, récepteur Fc néonatal, FcRn, chaîne alpha transmembranaire du récepteur néonatal)], anticorps monoclonal;
chaîne lourde gamma4 (1-444) [VH (*Mus musculus* IGHV1-81*01 (92.9%)/*Homo sapiens* IGHV1-18*01 (77.6%) -(IGHD) -*Homo sapiens* IGHJ3*02 (83.3%)) [8.8.11] (1-118) -*Homo sapiens* IGHG4*01 (CH1 (119-216), charnière S10>P (226) (217-228), CH2 (229-338), CH3 (339-443), CHS K2>del (444)) (119-444)], (132-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA (*Mus musculus* IGKV13-85*01 (88.4%)/*Homo sapiens* IGKV1-NL1*01 (83.2%) -*Homo sapiens* IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191)(108'-214')]; dimère (224-224'':227-227'')-bisdisulfure

orilanolimab

inmunoglobulina G4-kappa, anti-[*Homo sapiens* FCGRT (transportador y receptor del fragmento Fc de las IgG, receptor Fc neonatal, FcRn, cadena alfa transmembranaria del receptor neonatal)], anticuerpo monoclonal;
cadena pesada gamma4 (1-444) [VH (*Mus musculus* IGHV1-81*01 (92.9%)/*Homo sapiens* IGHV1-18*01 (77.6%) -(IGHD) -*Homo sapiens* IGHJ3*02 (83.3%)) [8.8.11] (1-118) -*Homo sapiens* IGHG4*01 (CH1 (119-216), bisagra S10>P (226) (217-228), CH2 (229-338), CH3 (339-443), CHS K2>del (444)) (119-444)], (132-214')-disulfuro con la cadena ligera kappa (1'-214') [V-KAPPA (*Mus musculus* IGKV13-85*01 (88.4%)/*Homo sapiens* IGKV1-NL1*01 (83.2%) -*Homo sapiens* IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191)(108'-214')]; dímero (224-224'':227-227'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE LKKPGASVKL SCKASGYTFT SYGISWVKQA TGQGLEWIGE  50
IYPRSGNTYY NEKFKGRATL TADKSTSTAY MELRSLRSED SAVYFCARST 100
TVRPPGIWGT GTTVTVSSAS TKGPSVFPLA PCSRSTSEST AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTKTYT 200
CNVDHKPSNT KVDKRVESKY GPPCPPCPAP EFLGGPSVFL FPPKPKDTLM 250
ISRTPEVTCV VVDVSQEDPE VQFNWYVDGV EVHNAKTKPR EEQFNSTYRV 300
VSVLTVLHQD WLNGKEYKCK VSNKGLPSSI EKTISKAKGQ PREPQVYTLP 350
PSQEEMTKNQ VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG 400
SFFLYSRLTV DKSRWQEGNV FSCSVMHEAL HNHYTQKSLS LSLG       444
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCKASDHIN NWLAWYQQKP GQAPRLLISG  50
ATSLETGVPS RFSGSGTGKD YTLTISSLQP EDFATYYCQQ YWSTPYTFGG 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 145-201 259-319 365-423
22"-96" 145"-201" 259"-319" 365"-423"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194'"
Inter-H-L (CH1 10-CL 126) 132-214' 132"-214'"
Inter-H-H (h 8, h 11) 224-224" 227-227"
N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
295, 295"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

osocimabum #

osocimab — immunoglobulin G1-kappa, anti-[*Homo sapiens* F11 (coagulation factor XI, FXI, plasma thromboplastin antecedent, PTA) activated], *Homo sapiens* monoclonal antibody;
gamma1 heavy chain (1-449) [*Homo sapiens* VH (IGHV3-23*01 (90.8%) -(IGHD) -IGHJ6*01 (100%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (217) (121-218), hinge (219-233), CH2 (234-343), CH3 D12 (359), L14 (361) (344-448), CHS K2>del (449)) (120-449)], (223-214')-disulfide with kappa light chain (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-33*01 (96.8%) -IGKJ4*01 (91.7%)) [6 3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (229-229'':232-232'')-bisdisulfide

osocimab — immunoglobuline G1-kappa, anti-[*Homo sapiens* F11 (facteur de coagulation XI, FXI, antécédent de la thromboplastine plasmatique, PTA) activé], *Homo sapiens* anticorps monoclonal;
chaîne lourde gamma1 (1-449) [*Homo sapiens* VH (IGHV3-23*01 (90.8%) -(IGHD) -IGHJ6*01 (100%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (217) (121-218), charnière (219-233), CH2 (234-343), CH3 D12 (359), L14 (361) (344-448), CHS K2>del (449)) (120-449)], (223-214')-disulfure avec la chaîne légère kappa (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-33*01 (96.8%) -IGKJ4*01 (91.7%)) [6 3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (229-229'':232-232'')-bisdisulfure

osocimab — inmunoglobulina G1-kappa, anti-[*Homo sapiens* F11 (factor de coagulación XI, FXI, antecedente de la tromboplastina plasmática, PTA) activada], *Homo sapiens* anticuerpo monoclonal;
cadena pesada gamma1 (1-449) [*Homo sapiens* VH (IGHV3-23*01 (90.8%) -(IGHD) -IGHJ6*01 (100%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (217) (121-218), bisagra (219-233), CH2 (234-343), CH3 D12 (359), L14 (361) (344-448), CHS K2>del (449)) (120-449)], (223-214')-disulfuro con la cadena ligera kappa (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-33*01 (96.8%) -IGKJ4*01 (91.7%)) [6 3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (229-229'':232-232'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLLESGGG LVQPGGSLRL SCAASGFTFS QYGMDWVRQA PGKGLEWVSG  50
IGPSGGSTVY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCTRGG 100
PYYYYGMDVW GQGTTVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSRDE LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPG  449
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCQASQDIS NYLNWYQQKP GKAPKLLIYD  50
ASNLETGVPS RFSGSGSGTD FTFTISSLQP EDIATYYCQQ ADSFPVTFGG 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

Intra-H (C23-C104)	22-96	147-203	264-324	370-428
	22"-96"	147"-203"	264"-324"	370"-428"
Intra-L (C23-C104)	23'-88'	134'-194'		
	23'"-88"'	134'"-194"'		
Inter-H-L (h5-CL 126)	223-214'	223"-214"'		
Inter-H-H (h 11, h 14)	229-229"	232-232"		

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
300, 300"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

otilimabum #

otilimab — immunoglobulin G1-lambda, anti-[*Homo sapiens* CSF2 (colony stimulating factor 2 (granulocyte-macrophage), granulocyte-macrophage colony stimulating factor, GM-CSF)], *Homo sapiens* monoclonal antibody; gamma1 heavy chain (1-447) [*Homo sapiens* VH (IGHV3-NL1*01 (88.1%) -(IGHD) -IGHJ1*01 (100%)) [8.10.8] (1-117) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (214) (118-215), hinge (216-230), CH2 (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-209')-disulfide with lambda light chain (1'-210') -[*Homo sapiens* V-LAMBDA (IGLV3-1*01 (85.2%) -IGLJ3*02 (100%)) [6.1.9] (1'-104') -*Homo sapiens* IGLC2*01 (105'-210')]; dimer (226-226'':229-229'')-bisdisulfide

otilimab — immunoglobuline G1-lambda, anti-[*Homo sapiens* CSF2 (facteur 2 stimulant de colonies (granulocyte-macrophage), facteur stimulant des colonies de granulocytes et macrophages, GM-CSF)], *Homo sapiens* anticorps monoclonal; chaîne lourde gamma1 (1-447) [*Homo sapiens* VH (IGHV3-NL1*01 (88.1%) -(IGHD) -IGHJ1*01 (100%)) [8.10.8] (1-117) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (214) (118-215), charnière (216-230), CH2 (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-209')-disulfure avec la chaîne légère lambda (1'-210') -[*Homo sapiens* V-LAMBDA (IGLV3-1*01 (85.2%) -IGLJ3*02 (100%)) [6.1.9] (1'-104') -*Homo sapiens* IGLC2*01 (105'-210')]; dimère (226-226'':229-229'')-bisdisulfure

otilimab — inmunoglobulina G1-lambda, anti-[*Homo sapiens* CSF2 (factor 2 estimulante de colonias (granulocito-macrófago), factor estimulante de las colonias de granulocitos y macrófagos, GM-CSF)], *Homo sapiens* anticuerpo monoclonal; cadena pesada gamma1 (1-447) [*Homo sapiens* VH (IGHV3-NL1*01 (88.1%) -(IGHD) -IGHJ1*01 (100%)) [8.10.8] (1-117) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (214) (118-215), bisagra (216-230), CH2 (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-209')-disulfuro con la cadena ligera lambda (1'-210') -[*Homo sapiens* V-LAMBDA (IGLV3-1*01 (85.2%) -IGLJ3*02 (100%)) [6.1.9] (1'-104') -*Homo sapiens* IGLC2*01 (105'-210')]; dímero (226-226'':229-229'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVESGGG LVQPGGSLRL SCAASGFTFS SYWMNWVRQA PGKGLEWVSG  50
IENKYAGGAT YYAASVKGRF TISRDNSKNT LYLQMNSLRA EDTAVYYCAR 100
GFGTDFWGQG TLVTVSSAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF 150
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC 200
NVNHKPSNTK VDKRVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT 250
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT 350
LPPSREEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS 400
DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPGK    447
```

Light chain / Chaîne légère / Cadena ligera

```
DIELTQPPSV SVAPGQTARI SCSGDSIGKK YAYWYQQKPG QAPVLVIYKK  50
RPSGIPERFS GSNSGNTATL TISGTQAEDE ADYYCSAWGD KGMVFGGGTK 100
LTVLGQPKAA PSVTLFPPSS EELQANKATL VCLISDFYPG AVTVAWKADS 150
SPVKAGVETT TPSKQSNNKY AASSYLSLTP EQWKSHRSYS CQVTHEGSTV 200
EKTVAPTECS                                              210
```

Post-translational modifications

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

Intra-H (C23-C104) 22-98 144-200 261-321 367-425
22''-98'' 144''-200'' 261''-321' 367'-425''
Intra-L (C23-C104) 22'-85' 132'-191'
22''-85'' 132''-191'''
Inter-H-L (h5-CL 126) 220-209' 220''-209'''
Inter-H-H (h 11, h 14) 226-226'' 229-229''

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación

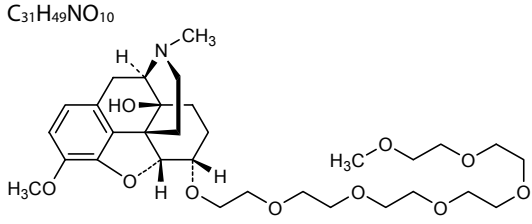
H CH2 N84.4
297, 297''
Fucosylated complex bi-antennary PER.C6-type glycans / glycanes de type PER.C6 bi-antennaires complexes fucosylés / glicanos de tipo PER.C6 biantenarios complejos fucosilados

oxycodegolum

oxycodegol — 4,5α-epoxy-6α-[(2,5,8,11,14,17-hexaoxanonadecan-19-yl)oxy]-3-methoxy-17-methylmorphinan-14-ol

oxycodégol — 4,5α-époxy-6α-[(2,5,8,11,14,17-hexaoxanonadécan-19-yl)oxy]-3-méthoxy-17-méthylmorphinan-14-ol

oxicodegol — 4,5α-epoxi-6α-[(2,5,8,11,14,17-hexaoxanonadecan-19-il)oxi]-3-metoxi-17-metilmorfinan-14-ol



prademagenum zamikeracelum #

prademagene zamikeracel — human culture expanded genetically modified autologous keratinocytes for cell-based gene therapy. Cells are isolated from skin of the patient, expanded and transduced with replication incompetent and non-self-inactivating Moloney murine leukemia virus (MMLV) derived retroviral vector encoding the functional collagen type VII alpha 1 chain (COL7A1) under the control of the mouse phosphoglycerol kinase-1 (mPGK-1) promoter.

pradémagène zamikéracel — kératinocytes humains, autologues, en culture d'expansion et génétiquement modifiés pour thérapie génique avec cellules. Les cellules sont isolées à partir de la peau du patient et sont expansées et transduites avec un vecteur rétroviral non-répliquant et auto-inactivant dérivé du virus de la leucémie murine de Moloney (MMLV) codant pour la chaîne fonctionnelle alpha 1 du collagène de type VII (COL7A1) sous le contrôle du promoteur de la phosphoglycérol kinase-1 murine (mPGK-1).

prademagén zamikeracel — queratinocitos autólogos, modificados genéticamente, humanos, expandidos en cultivo para terapia génica con células. Las células se aíslan de la piel del paciente, se expanden y transducen con un vector retroviral incompetente para replicación y no autoinactivante derivado del virus de la leucemia murina de Moloney (MMLV), que codifica para la cadena funcional alfa 1 del colágeno tipo VII (COL7A1) bajo el control del promotor de la fosfoglicerol cinasa-1 de ratón (mPGK-1).

prolgolimabum #

prolgolimab — immunoglobulin G1_V-lambda-C-kappa, anti-[*Homo sapiens* PDCD1 (programmed cell death 1, PD-1, PD1, CD279)], monoclonal antibody;

gamma1 heavy chain (1-459) [VH (*Vicugna pacos* IGHV3S1*01 (89.8%)/*Homo sapiens* IGHV3-23*04 or IGHV3-64*04 (85.7%) -(IGHD) -*Homo sapiens* IGHJ1*01 (100%)) [8.8.22] (1-129) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (226) (130-227), hinge (228-242), CH2 L1.3>A (246), L1.2>A (247) (243-352), CH3 E12 (368), M14 (370) (353-457), CHS (458-459)) (130-459)], (232-214')-disulfide with V-lambda-C-kappa light chain (1'-214') [V-LAMBDA (IGLV3-9*01 (100%) -IGLJ1*01 (90.9%)) [6 3.9] (1'-106') -1-mer glutaminyl linker (107') -*Homo sapiens* IGKC1*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (238-238'':241-241'')-bisdisulfide

prolgolimab

immunoglobuline G1_V-lambda-C-kappa, anti-[*Homo sapiens* PDCD1 (protéine 1 de mort cellulaire programmée, PD-1, PD1, CD279)], anticorps monoclonal; chaîne lourde gamma1 (1-459) [VH (*Vicugna pacos* IGHV3S1*01 (89.8%)/*Homo sapiens* IGHV3-23*04 or IGHV3-64*04 (85.7%) -(IGHD) -*Homo sapiens* IGHJ1*01 (100%)) [8.8.22] (1-129) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (226) (130-227), charnière (228-242), CH2 L1.3>A (246), L1.2>A (247) (243-352), CH3 E12 (368), M14 (370) (353-457), CHS (458-459)) (130-459)], (232-214')-disulfure avec la chaîne légère V-lambda-C-kappa (1'-214') [V-LAMBDA (IGLV3-9*01 (100%) -IGLJ1*01 (90.9%)) [6.3.9] (1'-106') -1-mer glutaminyl linker (107') -*Homo sapiens* IGKC1*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (238-238'':241-241'')-bisdisulfure

prolgolimab

inmunoglobulina G1_V-lambda-C-kappa, anti-[*Homo sapiens* PDCD1 (proteína 1 de muerrte celular programada, PD-1, PD1, CD279)], anticuerpo monoclonal; cadena pesada gamma1 (1-459) [VH (*Vicugna pacos* IGHV3S1*01 (89.8%)/*Homo sapiens* IGHV3-23*04 or IGHV3-64*04 (85.7%) -(IGHD) -*Homo sapiens* IGHJ1*01 (100%)) [8.8.22] (1-129) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (226) (130-227), bisagra (228-242), CH2 L1.3>A (246), L1.2>A (247) (243-352), CH3 E12 (368), M14 (370) (353-457), CHS (458-459)) (130-459)], (232-214')-disulfuro con la cadena ligera V-lambda-C-kappa (1'-214') [V-LAMBDA (IGLV3-9*01 (100%) -IGLJ1*01 (90.9%)) [6.3.9] (1'-106') -1-mer glutaminil linker (107') -*Homo sapiens* IGKC1*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (238-238'':241-241'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGGG LVQPGGSLRL SCAASGFTFS SYWMYWVRQV PGKGLEWVSA  50
IDTGGGRTYY ADSVKGRFAI SRVNAKNTMY LQMNSLRAED TAVYYCARDE 100
GGGTGWGVLK DWPYGLDAWG QGTLVTVSSA STKGPSVFPL APSSKSTSGG 150
TAALGCLVKD YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV 200
PSSSLGTQTY ICNVNHKPSN TKVDKRVEPK SCDKTHTCPP CPAPEAAGGP 250
SVFLFPPKPK DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK 300
TKPREEQYNS TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK 350
AKGQPREPQV YTLPPSREEM TKNQVSLTCL VKGFYPSDIA VEWESNGQPE 400
NNYKTTPPVL DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ 450
KSLSLSPGK                                              459
```

Light chain / Chaîne légère / Cadena ligera

```
QPVLTQPLSV SVALGQTARI TCGGNNIGSK NVHWYQQKPG QAPVLVIYRD  50
SNRPSGIPER FSGSNSGNTA TLTISRAQAG DEADYYCQVW DSSTAVFGTG 100
TKLTVLQRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 156-212 273-333 379-437
22''-96'' 156''-212'' 273''-333'' 379''-437''
Intra-L (C23-C104) 22'-87' 134'-194'
22'''-87''' 134'''-194'''
Inter-H-L (h 5-CL 126) 232-214' 232''-214'''
Inter-H-H (h 11, h 14) 238-238'' 241-241''

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84 4:
309, 309''
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

redipultidum

redipultide

L-cysteinyl-L-tryptophyl-L-leucyl-L-cysteinyl-L-arginyl-L-alanyl-L-leucyl-L-isoleucyl-L-lysyl-L-arginyl-L-isoleucyl-L-glutaminyl-L-alanyl-L-leucyl-L-isoleucyl-L-prolyl-L-lysylglycylglycyl-L-arginyl-L-leucyl-L-leucyl-L-prolyl-Lglutaminyl-L-leucyl-L-valyl-L-cysteinyl-L-arginyl-L-leucyl-L-valyl-L-leucyl-L-arginyl-L-cysteinyl-L-serine, cyclic (1-33:4-27)-bisdisulfide

rédipultide

bisdisulfure cyclique (1-33:4-27) de L-cystéinyl-L-tryptophyl-L-leucyl-L-cystéinyl-L-arginyl-L-alanyl-L-leucyl-L-isoleucyl-L-lysyl-L-arginyl-L-isoleucyl-L-glutaminyl-L-alanyl-L-leucyl-L-isoleucyl-L-prolyl-L-lysylglycylglycyl-L-arginyl-L-leucyl-L-leucyl-L-prolyl-Lglutaminyl-L-leucyl-L-valyl-L-cystéinyl-L-arginyl-L-leucyl-L-valyl-L-leucyl-L-arginyl-L-cystéinyl-L-sérine

redipultida

bisdisulfuro cíclico (1-33:4-27) de L-cisteinil-L-triptofil-L-leucil-L-cisteinil-L-arginil-L-alanil-L-leucil-L-isoleucil-L-lisil-L-arginil-L-isoleucil-L-glutaminil-L-alanil-L-leucil-L-isoleucil-L-prolil-L-lisilglicilglicil-L-arginil-L-leucil-L-leucil-L-prolil-Lglutaminil-L-leucil-L-valil-L-cisteinil-L-arginil-L-leucil-L-valil-L-leucil-L-arginil-L-cisteinil-L-serina

$C_{174}H_{302}N_{54}O_{38}S_4$

Sequence / Séquence / Secuencia
`CWLCRALIKR IQALIPKGGR LLPQLVCRLV LRCS` 34

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
1-33 4-27

relatlimabum #

relatlimab

immunoglobulin G4-kappa, anti-[*Homo sapiens* LAG3 (lymphocyte activating 3, lymphocyte-activation 3, CD223)], *Homo sapiens* monoclonal antibody;
gamma4 heavy chain (1-447) [*Homo sapiens* VH (IGHV4-34*01 (92.7%) -(IGHD) -IGHJ5*02 (100%)) [8.7.14] (1-120) -*Homo sapiens* IGHG4*01 (CH1 (121-218), hinge S10>P (228) (219-230), CH2 (231-340), CH3 (341-445), CHS (446-447)) (121-447)], (134-214')-disulfide with kappa light chain (1'-214') [*Homo sapiens* V-KAPPA (IGKV3-11*01 (98.9%) -IGKJ2*01 (90.9%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191)(108'-214')]; dimer (226-226'':229-229'')-bisdisulfide

rélatlimab

immunoglobuline G4-kappa, anti-[*Homo sapiens* LAG3 (activateur 3 des lymhocytes, lymphocyte-activation 3, CD223)], *Homo sapiens* anticorps monoclonal;
chaîne lourde gamma4 (1-447) [*Homo sapiens* VH (IGHV4-34*01 (92.7%) -(IGHD) -IGHJ5*02 (100%)) [8.7.14] (1-120) -*Homo sapiens* IGHG4*01 (CH1 (121-218), charnière S10>P (228) (219-230), CH2 (231-340), CH3 (341-445), CHS (446-447)) (121-447)], (134-214')-disulfure avec la chaîne légère kappa (1'-214') [*Homo sapiens* V-KAPPA (IGKV3-11*01 (98.9%) -IGKJ2*01 (90.9%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (226-226'':229-229'')-bisdisulfure

relatlimab

inmunoglobulina G4-kappa, anti-[*Homo sapiens* LAG3 (activador 3 de los linfocitos, linfocito-activación 3, CD223)], *Homo sapiens* anticuerpo monoclonal;
cadena pesada gamma4 (1-447) [*Homo sapiens* VH (IGHV4-34*01 (92.7%) -(IGHD) -IGHJ5*02 (100%)) [8.7.14] (1-120) -*Homo sapiens* IGHG4*01 (CH1 (121-218), bisagra S10>P (228) (219-230), CH2 (231-340), CH3 (341-445), CHS (446-447)) (121-447)], (134-214')-disulfuro con la cadena ligera kappa (1'-214') [*Homo sapiens* V-KAPPA (IGKV3-11*01 (98.9%) -IGKJ2*01 (90.9%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (226-226'':229-229'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLQQWGAG LLKPSETLSL TCAVYGGSFS DYYWNWIRQP PGKGLEWIGE  50
INHRGSTNSN PSLKSRVTLS LDTSKNQFSL KLRSVTAADT AVYYCAFGYS 100
DYEYNWFDPW GQGTLVTVSS ASTKGPSVFP LAPCSRSTSE STAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTKT 200
YTCNVDHKPS NTKVDKRVES KYGPPCPPCP APEFLGGPSV FLFPPKPKDT 250
LMISRTPEVT CVVVDVSQED PEVQFNWYVD GVEVHNAKTK PREEQFNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKGLPS SIEKTISKAK GQPREPQVYT 350
LPPSQEEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS 400
DGSFFLYSRL TVDKSRWQEG NVFSCSVMHE ALHNHYTQKS LSLSLGK    447
```

Light chain / Chaîne légère / Cadena ligera

```
EIVLTQSPAT LSLSPGERAT LSCRASQSIS SYLAWYQQKP GQAPRLLIYD  50
ASNRATGIPA RFSGSGSGTD FTLTISSLEP EDFAVYYCQQ RSNWPLTFGQ 100
GTNLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

Intra-H (C23-C104)	22-95	147-203	261-321	367-425
	22''-95''	147''-203'	261''-321''	367''-425''
Intra-L (C23-C104)	23'-88'	134'-194'		
	23'''-88'''	134'''-194'''		
Inter-H-L (CH1 10-CL 126)	134-214'	134''-214'''		
Inter-H-H (h 8, h 11)	226-226''	229-229''		

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84 4:
297, 297''
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

reldesemtivum

reldesemtiv

1-[2-({[*trans*-3-fluoro-1-(3-fluoropyridin-2-yl)cyclobutyl]methyl}amino)pyrimidin-5-yl]-1*H*-pyrrole-3-carboxamide

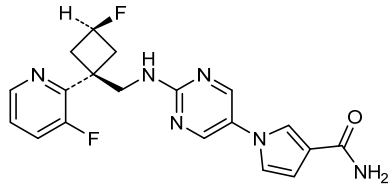
reldésemtiv

1-[2-({[*trans*-3-fluoro-1-(3-fluoropyridin-2-yl)cyclobutyl]méthyl}amino)pyrimidin-5-yl]-1*H*-pyrrole-3-carboxamide

reldesemtiv

1-[2-({[*trans*-3-fluoro-1-(3-fluoropiridin-2-il)ciclobutil]metil}amino)pirimidin-5-il]-1*H*-pirrol-3-carboxamida

$C_{19}H_{18}F_2N_6O$



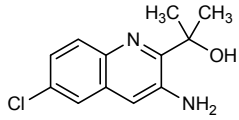
reproxalapum

reproxalap — 2-(3-amino-6-chloroquinolin-2-yl)propan-2-ol

réproxalap — 2-(3-amino-6-chloroquinoléin-2-yl)propan-2-ol

reproxalap — 2-(3-amino-6-cloroquinolein-2-il)propan-2-ol

$C_{12}H_{13}ClN_2O$



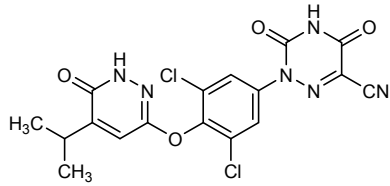
resmetiromum

resmetirom — 2-(3,5-dichloro-4-{[6-oxo-5-(propan-2-yl)-1,6-dihydropyridazin-3-yl]oxy}phenyl)-3,5-dioxo-2,3,4,5-tetrahydro-1,2,4-triazine-6-carbonitrile

resmétirom — 2-(3,5-dichloro-4-{[6-oxo-5-(propan-2-yl)-1,6-dihydropyridazin-3-yl]oxy}phényl)-3,5-dioxo-2,3,4,5-tétrahydro-1,2,4-triazine-6-carbonitrile

resmetirom — 2-(3,5-dicloro-4-{[6-oxo-5-(propan-2-il)-1,6-dihidropiridazin-3-il]oxi}fenil)-3,5-dioxo-2,3,4,5-tetrahidro-1,2,4-triazina-6-carbonitrilo

$C_{17}H_{12}Cl_2N_6O_4$



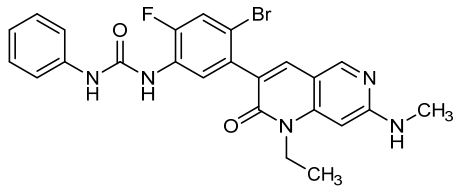
ripretinibum

ripretinib — *N*-{4-bromo-5-[1-ethyl-7-(methylamino)-2-oxo-1,2-dihydro-1,6-naphthyridin-3-yl]-2-fluorophenyl}-*N*′-phenylurea

riprétinib — *N*-{4-bromo-5-[1-éthyl-7-(méthylamino)-2-oxo-1,2-dihydro-1,6-naphtyridin-3-yl]-2-fluorophényl}-*N*′-phénylurée

ripretinib — *N*-{4-bromo-5-[1-etil-7-(metilamino)-2-oxo-1,2-dihidro-1,6-naftiridin-3-il]-2-fluorofenil}-*N*′-fenilurea

$C_{24}H_{21}BrFN_5O_2$



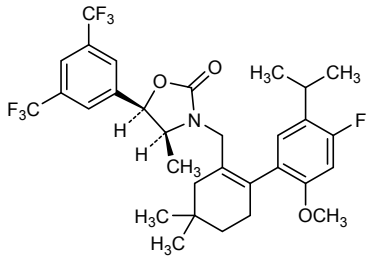
rocacetrapibum

rocacetrapib — (4*S*,5*R*)-5-[3,5-bis(trifluoromethyl)phenyl]-3-({2-[4-fluoro-2-methoxy-5-(propan-2-yl)phenyl]-5,5-dimethylcyclohex-1-en-1-yl}methyl)-4-methyl-1,3-oxazolidin-2-one

rocacétrapib — (4*S*,5*R*)-5-[3,5-bis(trifluorométhyl)phényl]-3-({2-[4-fluoro-2-méthoxy-5-(propan-2-yl)phényl]-5,5-diméthylcyclohex-1-én-1-yl}méthyl)-4-méthyl-1,3-oxazolidin-2-one

rocacetrapib — (4*S*,5*R*)-5-[3,5-bis(trifluorometil)fenil]-3-({2-[4-fluoro-2-metoxi-5-(propan-2-il)fenil]-5,5-dimetilciclohex-1-en-1-il}metil)-4-metil-1,3-oxazolidin-2-ona

$C_{31}H_{34}F_7NO_3$



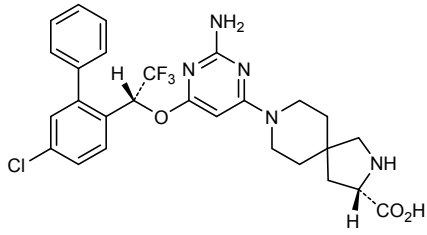
rodatristatum

rodatristat — (3*S*)-8-{2-amino-6-[(1*R*)-1-(5-chloro[1,1'-biphenyl]-2-yl)-2,2,2-trifluoroethoxy]pyrimidin-4-yl}-2,8-diazaspiro[4.5]decane-3-carboxylic acid

rodatristat — acide (3*S*)-8-{2-amino-6-[(1*R*)-1-(5-chloro[1,1'-biphényl]-2-yl)-2,2,2-trifluoroéthoxy]pyrimidin-4-yl}-2,8-diazaspiro[4.5]décane-3-carboxylique

rodatristat — ácido (3*S*)-8-{2-amino-6-[(1*R*)-1-(5-cloro[1,1'-bifenil]-2-il)-2,2,2-trifluoroetoxi]pirimidin-4-il}-2,8-diazaspiro[4.5]decano-3-carboxílico

$C_{27}H_{27}ClF_3N_5O_3$



rolinsatamabum #

rolinsatamab — immunoglobulin G1-kappa, anti-[*Homo sapiens* PRLR (prolactin receptor)], monoclonal antibody;

gamma1 heavy chain (1-450) [VH (*Mus musculus* IGHV1-69*02 (82.70%)/*Homo sapiens* IGHV1-46*01 (79.6%) -(IGHD)-*Homo sapiens* IGHJ6*01 (90.9%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (217) (121-218), hinge (219-233), CH2 S3>C (242) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfide with kappa light chain (1'-214') [V-KAPPA (*Mus musculus* IGKV6-13*01 (82.10%)/*Homo sapiens* IGKV1-12*01 (81.1%) -*Homo sapiens* IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (229-229":232-232")-bisdisulfide

rolinsatamab

immunoglobuline G1-kappa, anti-[*Homo sapiens* PRLR (récepteur de la prolactine)], anticorps monoclonal;
chaîne lourde gamma1 (1-450) [VH (*Mus musculus* IGHV1-69*02 (82.70%)/*Homo sapiens* IGHV1-46*01 (79.6%) -(IGHD)-*Homo sapiens* IGHJ6*01 (90.9%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (217) (121-218), charnière (219-233), CH2 S3>C (242) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA (*Mus musculus* IGKV6-13*01 (82.10%)/*Homo sapiens* IGKV1-12*01 (81.1%) -*Homo sapiens* IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (229-229":232-232")-bisdisulfure

rolinsatamab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* PRLR (receptor de la prolactina)], anticuerpo monoclonal;
cadena pesada gamma1 (1-450) [VH (*Mus musculus* IGHV1-69*02 (82.70%)/*Homo sapiens* IGHV1-46*01 (79.6%) -(IGHD)-*Homo sapiens* IGHJ6*01 (90.9%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (217) (121-218), bisagra (219-233), CH2 S3>C (242) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfuro con la cadena ligera kappa (1'-214') [V-KAPPA (*Mus musculus* IGKV6-13*01 (82.10%)/*Homo sapiens* IGKV1-12*01 (81.1%) -*Homo sapiens* IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (229-229":232-232")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVQSGAE VKKPGSSVKV SCKASGYTFT TYWMHWVRQA PGQGLEWIGE  50
IDPSDSYSNY NQKFKDRATL TVDKSTSTAY MELSSLRSED TAVYYCARNG 100
GLGPAWFSYW GQGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG PCVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK 450
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS VSASVGDRVT ITCKASQYVG TAVAWYQQKP GKSPKLLIYS  50
ASNRYTGVPS RFSDSGSGTD FTLTISSLQP EDFATYFCQQ YSSYPWTFGG 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 147-203 264-324 370-428
22"-96" 147"-203" 264"-324" 370"-428"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194'"
Inter-H-L (h 5-CL 126) 223-214' 223"-214'"
Inter-H-H (h 11, h 14) 229-229" 232-232"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
300, 300"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

rolinsatamabum talirinum #

rolinsatamab talirine	immunoglobulin G1-kappa, anti-[*Homo sapiens* PRLR (prolactin receptor)], monoclonal antibody, conjugated to the pyrrolobenzodiazepine (PDB) dimer SGD-1882; gamma1 heavy chain (1-450) [VH (*Mus musculus* IGHV1-69*02 (82.7%)/*Homo sapiens* IGHV1-46*01 (79.6%) -(IGHD)-*Homo sapiens* IGHJ6*01 (90.9%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (217) (121-218), hinge (219-233), CH2 S3>C (242) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfide with kappa light chain (1'-214') [V-KAPPA (*Mus musculus* IGKV6-13*01 (82.10%)/*Homo sapiens* IGKV1-12*01 (81.1%) -*Homo sapiens* IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (229-229":232-232")-bisdisulfide; conjugated, on two site-specific drug attachment engineered cysteines (C242, C242''), to a maximum of two pyrrolobenzodiazepine (PDB) dimers SGD-1882, each via a cleavable (valine-alanine dipeptide as cathepsin B cleavage site) maleimidocaproyl type linker
rolinsatamab talirine	immunoglobuline G1-kappa, anti-[*Homo sapiens* PRLR (récepteur de la prolactine)], anticorps monoclonal, conjugué à deux pyrrolobenzodiazépine (PDB) dimères SGD-1882; chaîne lourde gamma1 (1-450) [VH (*Mus musculus* IGHV1-69*02 (82.7%)/*Homo sapiens* IGHV1-46*01 (79.6%) -(IGHD)-*Homo sapiens* IGHJ6*01 (90.9%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (217) (121-218), charnière (219-233), CH2 S3>C (242) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA (*Mus musculus* IGKV6-13*01 (82.10%)/*Homo sapiens* IGKV1-12*01 (81.1%) -*Homo sapiens* IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (229-229":232-232")-bisdisulfure; conjugué, sur deux cystéines sites de fixation spécifique du linker-produit actif (C242, C242''), à un maximum de deux pyrrolobenzodiazépine (PDB) dimères SGD-1882, chacun via un linker clivable (dipeptide valine-alanine clivable par la cathepsine B) de type maléimidocaproyl
rolinsatamab talirina	inmunoglobulina G1-kappa, anti-[*Homo sapiens* PRLR (receptor de la prolactina)], anticuerpo monoclonal, conjugado con diez pirrolobenzodiazepinas (PDB) dímeros SGD-1882; cadena pesada gamma1 (1-450) [VH (*Mus musculus* IGHV1-69*02 (82.7%)/*Homo sapiens* IGHV1-46*01 (79.6%) -(IGHD)-*Homo sapiens* IGHJ6*01 (90.9%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (217) (121-218), bisagra (219-233), CH2 S3>C (242) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfuro con la cadena ligera kappa (1'-214') [V-KAPPA (*Mus musculus* IGKV6-13*01 (82.10%)/*Homo sapiens* IGKV1-12*01 (81.1%) -*Homo sapiens* IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (229-229":232-232")-bisdisulfuro; conjugado, en diez cisteinas sitios de fijación específicos del linker-producto activo (C242, C242''), con un máximo de diez dímeros de pirrolobenzodiazepina (PDB) SGD-1882, cada uno mediante un espaciador escindible (dipéptido valina-alanina escindible por la catepsina B) del tipo maleimidocaproil

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVQSGAE VKKPGSSVKV SCKASGYTFT TYWMHWVRQA PGQGLEWIGE  50
IDPSDSYSNY NQKFKDRATL TVDKSTSTAY MELSSLRSED TAVYYCARNG 100
GLGPAWFSYW GQGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG PCVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK 450
```

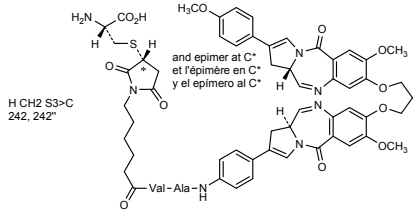
Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS VSASVGDRVT ITCKASQYVG TAVAWYQQKP GKSPKLLIYS  50
ASNRYTGVPS RFSDSGSGTD FTLTISSLQP EDFATYFCQQ YSSYPWTFGG 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                         214
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 147-203 264-324 370-428
22"-96" 147"-203" 264"-324" 370"-428"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194'"
Inter-H-L (h 5-CL 126) 223-214' 223"-214'"
Inter-H-H (h 11, h 14) 229-229" 232-232"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84 4:
300, 300"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

Modified residues / résidus modifiés / restos modificados



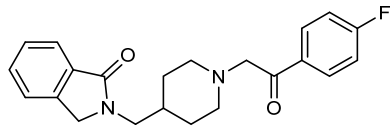
roluperidonum

roluperidone — 2-({1-[2-(4-fluorophenyl)-2-oxoethyl]piperidin-4-yl}methyl)-2,3-dihydro-1*H*-isoindol-1-one

rolupéridone — 2-({1-[2-(4-fluorophényl)-2-oxoéthyl]pipéridin-4-yl}méthyl)-2,3-dihydro-1*H*-isoindol-1-one

roluperidona — 2-({1-[2-(4-fluorofenil)-2-oxoetil]piperidin-4-il}metil)-2,3-dihidro-1*H*-isoindol-1-ona

$C_{22}H_{23}FN_2O_2$



rovafovirum etalafenamidum

rovafovir etalafenamide — ethyl (2*S*)-2-{[(*S*)-({[(2*R*,5*R*)-5-(6-amino-9*H*-purin-9-yl)-4-fluoro-2,5-dihydrofuran-2-yl]oxy}methyl)phenoxyphosphonoyl]amino}propanoate

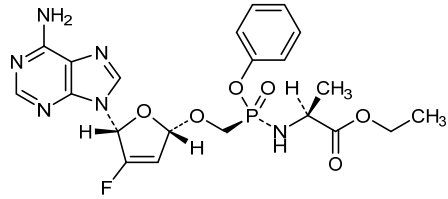
rovafovir étalafénamide

(2*S*)-2-{[(*S*)-({[(2*R*,5*R*)-5-(6-amino-9*H*-purin-9-yl)-4-fluoro-2,5-dihydrofuran-2-yl]oxy}méthyl)phénoxyphosphonoyl]amino}propanoate d'éthyle

rovafovir etalafenamida

(2*S*)-2-{[(*S*)-({[(2*R*,5*R*)-5-(6-amino-9*H*-purin-9-il)-4-fluoro-2,5-dihidrofuran-2-il]oxi}metil)fenoxifosfonoil]amino}propanoato de etilo

$C_{21}H_{24}FN_6O_6P$



ruxotemitidum

ruxotemitide

L-lysyl-L-lysyl-L-tryptophyl-L-tryptophyl-L-lysyl-L-lysyl-L-tryptophyl-β-phenyl-L-phenylalanyl- L-lysinamide

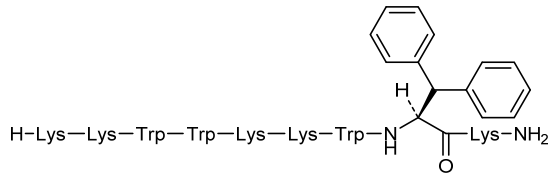
ruxotémitide

L-lysyl-L-lysyl-L-tryptophyl-L-tryptophyl-L-lysyl-L-lysyl-L-tryptophyl-β-phényl-L-phénylalanyl- L-lysinamide

ruxotemitida

L-lisil-L-lisil-L-triptopfil-L-triptopfil-L-lisil-L-lisil-L-triptopfil-β-fenil-L-fenilalanil- L-lisinamida

$C_{78}H_{106}N_{18}O_9$



selatogrelum

selatogrel

[(2*R*)-3-[4-(butoxycarbonyl)piperazin-1-yl]-2-{6-[(3*S*)-3-methoxypyrrolidin-1-yl]-2-phenylpyrimidine-4-carboxamido}-3-oxopropyl]phosphonic acid

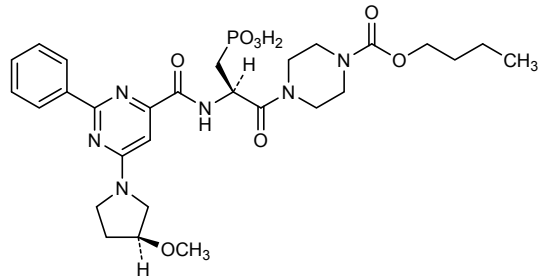
sélatogrel

acide [(2*R*)-3-[4-(butoxycarbonyl)pipérazin-1-yl]-2-{6-[(3*S*)-3-méthoxypyrrolidin-1-yl]-2-phénylpyrimidine-4-carboxamido}-3-oxopropyl]phosphonique

selatogrel

ácido [(2*R*)-3-[4-(butoxicarbonil)piperazin-1-il]-2-{6-[(3*S*)-3-metoxipirrolidin-1-il]-2-fenilpirimidina-4-carboxamida}-3-oxopropil]fosfónico

$C_{28}H_{39}N_6O_8P$



sintilimabum #

sintilimab	immunoglobulin G4-kappa, anti-[*Homo sapiens* PDCD1 (programmed cell death 1, PD-1, PD1, CD279)], *Homo sapiens* monoclonal antibody; gamma4 heavy chain (1-447) [*Homo sapiens* VH (IGHV1-69*01 (93.9%) -(IGHD) -IGHJ4*01 (100%)) [8.8.13] (1-120) -*Homo sapiens* IGHG4*01 (CH1 (121-218), hinge S10>P (228) (219-230), CH2 (231-340), CH3 (341-445), CHS (446-447)) (121-447)], (134-214')-disulfide with kappa light chain (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-12*01 (96.8%) -IGKJ4*01 (91.7%)) [6 3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (226-226'':229-229'')-bisdisulfide
sintilimab	immunoglobuline G4-kappa, anti-[*Homo sapiens* PDCD1 (protéine 1 de mort cellulaire programmée, PD-1, PD1, CD279)], *Homo sapiens* anticorps monoclonal; chaîne lourde gamma4 (1-447) [*Homo sapiens* VH (IGHV1-69*01 (93.9%) -(IGHD) -IGHJ4*01 (100%)) [8.8.13] (1-120) -*Homo sapiens* IGHG4*01 (CH1 (121-218), charnière S10>P (228) (219-230), CH2 (231-340), CH3 (341-445), CHS (446-447)) (121-447)], (134-214')-disulfure avec la chaîne légère kappa (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-12*01 (96.8%) -IGKJ4*01 (91.7%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (226-226'':229-229'')-bisdisulfure
sintilimab	inmunoglobulina G4-kappa, anti-[*Homo sapiens* PDCD1 (proteína 1 de muerte celular programada, PD-1, PD1, CD279)], *Homo sapiens* anticuerpo monoclonal; cadena pesada gamma4 (1-447) [*Homo sapiens* VH (IGHV1-69*01 (93.9%) -(IGHD) -IGHJ4*01 (100%)) [8.8.13] (1-120) -*Homo sapiens* IGHG4*01 (CH1 (121-218), bisagra S10>P (228) (219-230), CH2 (231-340), CH3 (341-445), CHS (446-447)) (121-447)], (134-214')-disulfuro con la cadena ligera kappa (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-12*01 (96.8%) -IGKJ4*01 (91.7%)) [6 3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (226-226'':229-229'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGSSVKV SCKASGGTFS SYAISWVRQA PGQGLEWMGL  50
IIPMFDTAGY AQKFQGRVAI TVDESTSTAY MELSSLRSED TAVYYCARAE 100
HSSTGTFDYW GQGTLVTVSS ASTKGPSVFP LAPCSRSTSE STAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTKT 200
YTCNVDHKPS NTKVDKRVES KYGPPCPPCP APEFLGGPSV FLFPPKPKDT 250
LMISRTPEVT CVVVDVSQED PEVQFNWYVD GVEVHNAKTK PREEQFNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKGLPS SIEKTISKAK GQPREPQVYT 350
LPPSQEEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS 400
DGSFFLYSRL TVDKSRWQEG NVFSCSVMHE ALHNHYTQKS LSLSLGK    447
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS VSASVGDRVT ITCRASQGIS SWLAWYQQKP GKAPKLLISA  50
ASSLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ ANHLPFTFGG 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 147-203 261-321 367-425
22"-96" 147"-203" 261"-321" 367"-425"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194'"
Inter-H-L (CH1 10-CL 126) 134-214' 134"-214'"
Inter-H-H (h 8, h 11) 226-226" 229-229"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4: 297, 297"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados
N-terminal glutamine cyclization to pyroglutamate (pE, 5-oxoproline)
H VH Q1:1, 1"
C-terminal lysine clipping
H CHS K2: 447, 447"

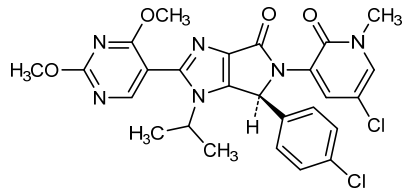
siremadlinum

siremadlin — (6*S*)-5-(5-chloro-1-methyl-2-oxo-1,2-dihydropyridin-3-yl)-6-(4-chlorophenyl)-2-(2,4-dimethoxypyrimidin-5-yl)-1-(propan-2-yl)-5,6-dihydropyrrolo[3,4-*d*]imidazol-4(1*H*)-one

sirémadline — (6*S*)-5-(5-chloro-1-méthyl-2-oxo-1,2-dihydropyridin-3-yl)-6-(4-chlorophényl)-2-(2,4-diméthoxypyrimidin-5-yl)-1-(propan-2-yl)-5,6-dihydropyrrolo[3,4-*d*]imidazol-4(1*H*)-one

siremadlina — (6*S*)-5-(5-cloro-1-metil-2-oxo-1,2-dihidropiridin-3-il)-6-(4-clorofenil)-2-(2,4-dimetoxipirimidin-5-il)-1-(propan-2-il)-5,6-dihidropirrolo[3,4-*d*]imidazol-4(1*H*)-ona

$C_{26}H_{24}Cl_2N_6O_4$



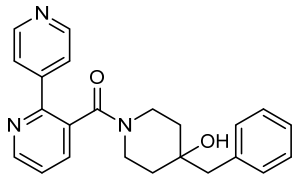
soticlestatum

soticlestat — (4-benzyl-4-hydroxypiperidin-1-yl)([2,4'-bipyridin]-3-yl)methanone

soticlestat — (4-benzyl-4-hydroxypipéridin-1-yl)([2,4'-bipyridin]-3-yl)méthanone

soticlestat — (4-bencil-4-hidroxipiperidin-1-il)([2,4'-bipiridin]-3-il)metanona

$C_{23}H_{23}N_3O_2$



spesolimabum #

spesolimab — immunoglobulin G1-kappa, anti-[*Homo sapiens* IL1RL2 (interleukin 1 receptor like 2, interleukin 36 receptor, IL1R-rp2, IL1RRP2)], humanized monoclonal antibody; gamma1 heavy chain humanized (1-449) [VH (*Homo sapiens* IGHV1-2*02 (81.20%) -(IGHD) -IGHJ4*01 (93.3%)) [8.8.12] (1-119) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (216) (120-217), hinge (218-232), CH2 L1.3>A (236), L1.2>A (237) (233-342), CH3 E12 (358), M14 (360) (343-447), CHS (448-449)) (120-449)], (222-215')-disulfide with kappa light chain humanized (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (79.2%)-*Homo sapiens* IGKJ2*01 (90.9%)) [7 3.9] (1'-108') -*Homo sapiens* IGKC*01, Km3 A45.1 (154), V101 (192)(109'-215')]; dimer (228-228'':231-231'')-bisdisulfide

spésolimab — immunoglobuline G1-kappa, anti-[*Homo sapiens* IL1RL2 (récepteur like 2 de l'interleukine 1, récepteur de l'interleukine 36, IL1R-rp2, IL1RRP2), anticorps monoclonal humanisé; chaîne lourde gamma1 humanisée (1-449) [VH (*Homo sapiens* IGHV1-2*02 (81.20%) -(IGHD) -IGHJ4*01 (93.3%)) [8.8.12] (1-119) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (216) (120-217), charnière (218-232), CH2 L1.3>A (236), L1.2>A (237) (233-342), CH3 E12 (358), M14 (360) (343-447), CHS (448-449)) (120-449)], (222-215')-disulfure avec la chaîne légère kappa humanisée (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (79.2%)-*Homo sapiens* IGKJ2*01 (90.9%)) [7 3.9] (1'-108') -*Homo sapiens* IGKC*01, Km3 A45.1 (154), V101 (192)(109'-215')]; dimère (228-228'':231-231'')-bisdisulfure

espesolimab — inmunoglobulina G1-kappa, anti-[*Homo sapiens* IL1RL2 (receptor like 2 de la interleukina 1, receptor de la interleukina 36, IL1R-rp2, IL1RRP2), anticuerpo monoclonal humanizado; cadena pesada gamma1 humanizada (1-449) [VH (*Homo sapiens* IGHV1-2*02 (81.20%) -(IGHD) -IGHJ4*01 (93.3%)) [8.8.12] (1-119) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (216) (120-217), bisagra (218-232), CH2 L1.3>A (236), L1.2>A (237) (233-342), CH3 E12 (358), M14 (360) (343-447), CHS (448-449)) (120-449)], (222-215')-disulfuro con la cadena ligera kappa humanizada (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (79.2%)-*Homo sapiens* IGKJ2*01 (90.9%)) [7.3.9] (1'-108') -*Homo sapiens* IGKC*01, Km3 A45.1 (154), V101 (192)(109'-215')]; dímero (228-228'':231-231'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGASVKV SCKASGYSFT SSWIHWVKQA PGQGLEWMGE  50
INPGNVRTNY NENFRNKVTM TVDTSISTAY MELSRLRSDD TAVYYCTVVF 100
YGEPYFPYWG QGTLVTVSSA STKGPSVFPL APSSKSTSGG TAALGCLVKD 150
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY 200
ICNVNHKPSN TKVDKRVEPK SCDKTHTCPP CPAPEAAGGP SVFLFPPKPK 250
DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS 300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV 350
YTLPPSREEM TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL 400
DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK  449
```

Light chain / Chaîne légère / Cadena ligera

```
QIVLTQSPGT LSLSPGERAT MTCTASSSVS SSYFHWYQQK PGQAPRLWIY  50
RTSRLASGVP DRFSGSGSGT DFTLTISRLE PEDAATYYCH QFHRSPLTFG 100
AGTKLEIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK 150
VDNALQSGNS QESVTEQDSK DSTYSLSSTL TLSKADYEKH KVYACEVTHQ 200
GLSSPVTKSF NRGEC                                       215
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 146-202 263-323 369-427
22"-96" 146"-202" 263"-323' 369"-427"
Intra-L (C23-C104) 23'-89' 135'-195'
23'"-89'" 135'"-195'"
Inter-H-L (h 5-CL 126) 222-215' 222"-215'"
Inter-H-H (h 11, h 14) 228-228" 231-231"
N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84 4:
299, 299"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

tabituximabum #

tabituximab — immunoglobulin G1-kappa, anti-[*Homo sapiens* FZD10 (frizzled class receptor 10, frizzled family receptor 10, Frizzled-10, CD350)], chimeric monoclonal antibody; gamma1 heavy chain chimeric (1-448) [*Mus musculus* VH (IGHV14-3*02 (99.0%) -(IGHD) -IGHJ3*01 (100%)) [8.8.11] (1-118) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (215) (119-216), hinge (217-231), CH2 (232-341), CH3 D12 (357), L14 (359) (342-446), CHS (447-448)) (119-448)], (221-214')-disulfide with kappa light chain chimeric (1'-214') [*Mus musculus* V-KAPPA (IGKV12-46*01 (98.9%) -IGKJ2*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (227-227'':230-230'')-bisdisulfide

tabituximab — immunoglobuline G1-kappa, anti-[*Homo sapiens* FZD10 (récepteur 10 de la classe frizzled, récepteur 10 de la famille frizzled, Frizzled-10, CD350)], anticorps monoclonal chimérique;
chaîne lourde gamma1 chimérique (1-448) [*Mus musculus* VH (IGHV14-3*02 (99.0%) -(IGHD) -IGHJ3*01 (100%)) [8.8.11] (1-118) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (215) (119-216), charnière (217-231), CH2 (232-341), CH3 D12 (357), L14 (359) (342-446), CHS (447-448)) (119-448)], (221-214')-disulfure avec la chaîne légère kappa chimérique (1'-214') [*Mus musculus* V-KAPPA (IGKV12-46*01 (98.9%) -IGKJ2*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (227-227'':230-230'')-bisdisulfure

tabituximab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* FZD10 (receptor 10 de la clase frizzled, receptor 10 de la familia frizzled, Frizzled-10, CD350)], anticuerpo monoclonal quimérico;
cadena pesada gamma1 quimérica (1-448) [*Mus musculus* VH (IGHV14-3*02 (99.0%) -(IGHD) -IGHJ3*01 (100%)) [8.8.11] (1-118) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (215) (119-216), bisagra (217-231), CH2 (232-341), CH3 D12 (357), L14 (359) (342-446), CHS (447-448)) (119-448)], (221-214')-disulfuro con la cadena ligera kappa quimérica (1'-214') [*Mus musculus* V-KAPPA (IGKV12-46*01 (98.9%) -IGKJ2*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (227-227'':230-230'')-bisdisulfuro

Heavy chain / chaîne lourde / cadena pesada

```
EVQLQQSGAE LVKPGASVKL SCTASGFNIN DTYMHWVKQR PEQGLEWIGR  50
IDPANGNTKY DPKFQGKATI TADTSSNTAY LQLSSLTSED TAVYYCARGA 100
RGSRFAYWGQ GTLVTVSAAS TKGPSVFPLA PSSKSTSGGT AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTQTYI 200
CNVNHKPSNT KVDKKVEPKS CDKTHTCPPC PAPELLGGPS VFLFPPKPKD 250
TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNST 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY 350
TLPPSRDELT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD 400
SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPGK   448
```

Light chain / chaîne légère / cadena ligera

```
DIQMTQSPAS LSVSVGETVT ITCRASENIY SNLAWYQQKQ GKSPQLLVYV  50
ATNLADGVPS RFSGSGSGTQ YSLKINSLQS EDFGSYYCQH FWGTPYTFGG 100
GTKLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Post-translational modifications
Disulfide bridges location / positions des ponts disulfure / posiciones de les puentos disulfuro
Intra-H (C23-C104) 22-96 145-201 262-322 368-426
22"-96" 145"-201" 262"-322" 368"-426"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194'"
Inter-H-L (h 5-CL 126) 221-214' 221"-214'"
Inter-H-H (h 11, h 14) 227-227" 230-230"
N-glycosylation sites / sites de N-glycosylation / posiciones de N-gicosilación
H VH N35:
30, 30"
H CH2 N84 4:
298, 298"
Fucosylated complex bi-antennary CHO-type glycans/ glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

tabituximabum barzuxetanum #

tabituximab barzuxetan

immunoglobulin G1-kappa, anti-[*Homo sapiens* FZD10 (frizzled class receptor 10, frizzled family receptor 10, Frizzled-10, CD350)], chimeric monoclonal antibody conjugated to *barzuxetan*, a DPTA chelator derivative; gamma1 heavy chain chimeric (1-448) [*Mus musculus* VH (IGHV14-3*02 (99.0%) -(IGHD) -IGHJ3*01 (100%)) [8.8.11] (1-118) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (215) (119-216), hinge (217-231), CH2 (232-341), CH3 D12 (357), L14 (359) (342-446), CHS (447-448)) (119-448)], (221-214')-disulfide with kappa light chain chimeric (1'-214') [*Mus musculus* V-KAPPA (IGKV12-46*01 (98.9%) -IGKJ2*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (227-227'':230-230'')-bisdisulfide; conjugated, on an average of 2 to 4 lysyl, to *barzuxetan*, *p*-SCN-Bn-CHX-A"-DPTA, a DPTA chelator derivative
For the *barzuxetan* part, please refer to the annex « *Names for radicals and groups* ».

tabituximab barzuxétan

immunoglobuline G1-kappa, anti-[*Homo sapiens* FZD10 (récepteur 10 de la classe frizzled, récepteur 10 de la famille frizzled, Frizzled-10, CD350)], anticorps monoclonal chimérique conjugué au *barzuxétan*, un dérivé du chélateur DPTA;
chaîne lourde gamma1 chimérique (1-448) [*Mus musculus* VH (IGHV14-3*02 (99.0%) -(IGHD) -IGHJ3*01 (100%)) [8.8.11] (1-118) - *Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (215) (119-216), charnière (217-231), CH2 (232-341), CH3 D12 (357), L14 (359) (342-446), CHS (447-448)) (119-448)], (221-214')-disulfure avec la chaîne légère kappa chimérique (1'-214') [*Mus musculus* V-KAPPA (IGKV12-46*01 (98.9%) -IGKJ2*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (227-227'':230-230'')-bisdisulfure; conjugué, sur une moyenne de 2 à 4 lysyl, au *barzuxétan*, *p*-SCN-Bn-CHX-A''-DPTA, un dérivé du chélateur DPTA
Pour la partie *barzuxétan*, veuillez-vous référer à l'annexe « *Noms pour radicaux et groupes».*

tabituximab barzuxetán

inmunoglobulina G1-kappa, anti-[*Homo sapiens* FZD10 (receptor 10 de la clase frizzled, receptor 10 de la familia frizzled, Frizzled-10, CD350)], anticuerpo monoclonal quimérico conjugado al *barzuxetán,* un derivado del DPTA;
cadena pesada gamma1 quimérica (1-448) [*Mus musculus* VH (IGHV14-3*02 (99.0%) -(IGHD) -IGHJ3*01 (100%)) [8.8.11] (1-118) - *Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (215) (119-216), bisagra (217-231), CH2 (232-341), CH3 D12 (357), L14 (359) (342-446), CHS (447-448)) (119-448)], (221-214')-disulfuro con la cadena ligera kappa quimérica (1'-214') [*Mus musculus* V-KAPPA (IGKV12-46*01 (98.9%) -IGKJ2*01 (100%)) [6 3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (227-227'':230-230'')-bisdisulfuro; conjugado,en 2 - 4 restos lisil, por término medio, al *barzuxetán*, p-SCN-Bn-CHX-A''-DPTA, un derivado de un agente quelante DPTA
Por la parte *barzuxetán*, por favor vaya al anexo *« Denominaciones para Radicales y Grupos »*.

Heavy chain / chaîne lourde / cadena pesada

```
EVQLQQSGAE LVKPGASVKL SCTASGFNIN DTYMHWVKQR PEQGLEWIGR  50
IDPANGNTKY DPKFQGKATI TADTSSNTAY LQLSSLTSED TAVYYCARGA 100
RGSRFAYWGQ GTLVTVSAAS TKGPSVFPLA PSSKSTSGGT AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTQTYI 200
CNVNHKPSNT KVDKKVEPKS CDKTHTCPPC PAPELLGGPS VFLFPPKPKD 250
TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNST 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY 350
TLPPSRDELT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD 400
SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPGK   448
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Light chain / chaîne légère / cadena ligera

```
DIQMTQSPAS LSVSVGETVT ITCRASENIY SNLAWYQQKQ GKSPQLLVYV  50
ATNLADGVPS RFSGSGSGTQ YSLKINSLQS EDFGSYYCQH FWGTPYTFGG 100
GTKLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Post-translational modifications
Disulfide bridges location / positions des ponts disulfure / posiciones de les puentos disulfuro
Intra-H (C23-C104) 22-96 145-201 262-322 368-426
22''-96'' 145''-201'' 262''-322'' 368''-426''
Intra-L (C23-C104) 23'-88' 134'-194'
23'''-88''' 134'''-194'''
Inter-H-L (h 5-CL 126) 221-214' 221''-214'''
Inter-H-H (h 11, h 14) 227-227'' 230-230''
conjugated, on an average of 2 to 4 lysyl, to *barzuxetan* / conjugué, sur une moyenne de 2 à 4 lysyl, au *barzuxétan* / conjugado en 2 - 4 restos lisil, por término medio, al *barzuxetán*
N-glycosylation sites / sites de N-glycosylation / posiciones de N-gicosilación
H VH N35:
30, 30''
H CH2 N84.4:
298, 298''
Fucosylated complex bi-antennary CHO-type glycans/ glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

tafasitamabum #

tafasitamab	immunoglobulin G1-G2-kappa, anti-[*Homo sapiens* CD19 (B lymphocyte surface antigen B4, Leu-12)], monoclonal antibody; gamma1-gamma2 heavy chain (1-451) [VH (*Mus musculus* IGHV1-14*01 (77.6%)/*Homo sapiens* IGHV1-3*01 (73.5%) -(IGHD) -*Homo sapiens* IGHJ4*01 (100%)) [8.8.14] (1-121) -*Homo sapiens* IGHG1*01 (CH1 G1m17, K120 (218) (122-219) -hinge (220-234) -CH2 1.6-1.1 (235-240)) (122-240) -*Homo sapiens* IGHG2*01 (CH2 1-125, S3>D (243), G2m.. V45.1 (286), G110>A (331), I117>E (336) (241-344) -CH3 nG1m1 E12 (360) M14 (362) (345-449) -CHS (450-451)) (241-451)], (224-219')-disulfide with kappa light chain (1'-219') [V-KAPPA *(Mus musculus* IGKV2-137*01 (75.0%)/*Homo sapiens* IGHV3D-11*03 (73.7%) -*Homo sapiens* IGKJ2*01 (90.9%)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dimer (230-230":233-233")-bisdisulfide
tafasitamab	immunoglobuline G1-G2-kappa, anti-[*Homo sapiens* CD19 (antigène de surface B4 des lymphocytes B, Leu-12)], anticorps monoclonal; chaîne lourde gamma1-gamma2 (1-451) [VH (*Mus musculus* IGHV1-14*01 (77.6%)/*Homo sapiens* IGHV1-3*01 (73.5%) -(IGHD) -*Homo sapiens* IGHJ4*01 (100%)) [8.8.14] (1-121) -*Homo sapiens* IGHG1*01 (CH1 G1m17, K120 (218) (122-219) -charnière (220-234) -CH2 1.6-1.1 (235-240)) (122-240) -*Homo sapiens* IGHG2*01 (CH2 1-125, S3>D (243), G2m.. V45.1 (286), G110>A (331), I117>E (336) (241-344) -CH3 nG1m1 E12 (360) M14 (362) (345-449) -CHS (450-451)) (241-451)], (224-219')-disulfure avec la chaîne légère kappa (1'-219') [V-KAPPA *(Mus musculus* IGKV2-137*01 (75.0%)/*Homo sapiens* IGHV3D-11*03 (73.7%) -*Homo sapiens* IGKJ2*01 (90.9%)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dimère (230-230":233-233")-bisdisulfure
tafasitamab	inmunoglobulina G1-G2-kappa, anti-[*Homo sapiens* CD19 (antígeno de superficie B4 de los linfocitos B, Leu-12)], anticuerpo monoclonal; cadena pesada gamma1-gamma2 (1-451) [VH (*Mus musculus* IGHV1-14*01 (77.6%)/*Homo sapiens* IGHV1-3*01 (73.5%) -(IGHD) -*Homo sapiens* IGHJ4*01 (100%)) [8.8.14] (1-121) -*Homo sapiens* IGHG1*01 (CH1 G1m17, K120 (218) (122-219) -bisagra(220-234) -CH2 1.6-1.1 (235-240)) (122-240) -*Homo sapiens* IGHG2*01 (CH2 1-125, S3>D (243), G2m.. V45.1 (286), G110>A (331), I117>E (336) (241-344) -CH3 nG1m1 E12 (360) M14 (362) (345-449) -CHS (450-451)) (241-451)], (224-219')-disulfuro con la cadena ligera kappa (1'-219') [V-KAPPA *(Mus musculus* IGKV2-137*01 (75.0%)/*Homo sapiens* IGHV3D-11*03 (73.7%) -*Homo sapiens* IGKJ2*01 (90.9%)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dímero (230-230":233-233")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVKPGGSLKL SCAASGYTFT SYVMHWVRQA PGKGLEWIGY  50
INPYNDGTKY NEKFQGRVTI SSDKSISTAY MELSSLRSED TAMYYCARGT 100
YYYGTRVFDY WGQGTLVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200
TYICNVNHKP SNTKVDKKVE PKSCDKTHTC PPCPAPELLG GPDVFLFPPK 250
PKDTLMISRT PEVTCVVVDV SHEDPEVQFN WYVDGVEVHN AKTKPREEQF 300
NSTFRVVSVL TVVHQDWLNG KEYKCKVSNK ALPAPEEKTI SKTKGQPREP 350
QVYTLPPSRE EMTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP 400
MLDSDGSFFL YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG 450
K                                                       451
```

Light chain / Chaîne légère / Cadena ligera

```
DIVMTQSPAT LSLSPGERAT LSCRSSKSLQ NVNGNTYLYW FQQKPGQSPQ  50
LLIYRMSNLN SGVPDRFSGS GSGTEFTLTI SSLEPEDFAV YYCMQHLEYP 100
ITFGAGTKLE IKRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK 150
VQWKVDNALQ SGNSQESVTE QDSKDSTYSL SSTLTLSKAD YEKHKVYACE 200
VTHQGLSSPV TKSFNRGEC                                    219
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 148-204 265-325 371-429
22"-96" 148"-204" 265"-325" 371"-429"
Intra-L (C23-C104) 23'-93' 139'-199'
23'"-93'" 139'"-199'"
Inter-H-L (h 5-CL 126) 224-219' 224"-219'"
Inter-H-H (h 11, h 14) 230-230" 233-233"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4: 301, 301"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.
C-terminal lysine clipping:
H CHS K2: 451, 451"

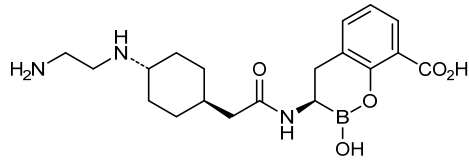
taniborbactamum

taniborbactam — (3*R*)-3-(2-{*trans*-4-[(2-aminoethyl)amino]cyclohexyl}acetamido)-2-hydroxy-3,4-dihydro-2*H*-1,2-benzoxaborinine-8-carboxylic acid

taniborbactam — acide (3*R*)-3-(2-{*trans*-4-[(2-aminoéthyl)amino]cyclohexyl}acétamido)-2-hydroxy-3,4-dihydro-2*H*-1,2-benzoxaborinine-8-carboxylique

taniborbactam — ácido (3*R*)-3-(2-{*trans*-4-[(2-aminoetil)amino]ciclohexil}acetamido)-2-hidroxi-3,4-dihidro-2*H*-1,2-benzoxaborinina-8-carboxílico

$C_{19}H_{28}BN_3O_5$

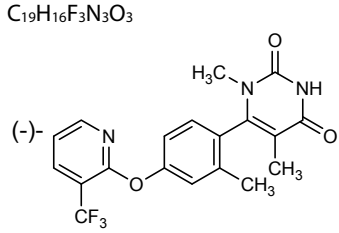


tavapadonum

tavapadon — (-)-(6*S*)-1,5-dimethyl-6-(2-methyl-4-{[3-(trifluoromethyl)pyridin-2-yl]oxy}phenyl)pyrimidine-2,4(1*H*,3*H*)-dione

tavapadon — (-)-(6*S*)-1,5-diméthyl-6-(2-méthyl-4-{[3-(trifluorométhyl)pyridin-2-yl]oxy}phényl)pyrimidine-2,4(1*H*,3*H*)-dione

tavapadón (-)-(6*S*)-1,5-dimetil-6-(2-metil-4-{[3-(trifluorometil)piridin-2-il]oxi}fenil)pirimidina-2,4(1*H*,3*H*)-diona

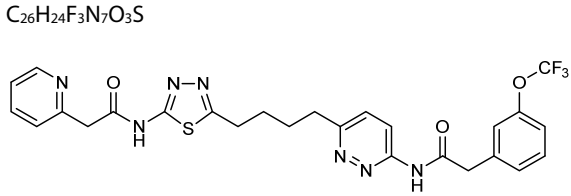


telaglenastatum

telaglenastat *N*-[6-(4-{5-[2-(pyridin-2-yl)acetamido]-1,3,4-thiadiazol-2-yl}butyl)pyridazin-3-yl]-2-[3-(trifluoromethoxy)phenyl]acetamide

télaglénastat *N*-[6-(4-{5-[2-(pyridin-2-yl)acétamido]-1,3,4-thiadiazol-2-yl}butyl)pyridazin-3-yl]-2-[3-(trifluorométhoxy)phényl]acetamide

telaglenastat *N*-[6-(4-{5-[2-(piridin-2-il)acetamido]-1,3,4-tiadiazol-2-il}butil)piridazin-3-il]-2-[3-(trifluorometoxi)fenil]acetamida



temelimabum #

temelimab immunoglobulin G4-kappa, anti-[*Homo sapiens* endogenous retrovirus (HERV) family W multiple sclerosis-associated retrovirus (MRSV) envelope protein], humanized monoclonal antibody; gamma4 heavy chain (1-443) [humanized VH (*Homo sapiens* IGHV1-46*01 (81.2%) -(IGHD)-IGHJ4*01 (92.9%)) [8.8.9] (1-116) -*Homo sapiens* IGHG4*01 (CH1 (117-214), hinge S10>P (224) (215-226), CH2 (227-336), CH3 (337-441), CHS (442-443)) (117-443)], (130-213')-disulfide with kappa light chain (1'-213') [humanized V-KAPPA (*Homo sapiens* IGKV1-39*01 (81.9%) -IGKJ4*01 (100%)) [5.3.9] (1'-106') -*Homo sapiens* IGKC*01, Km3 A45.1 (152), V101 (190) (107'-213')]; dimer (222-222":225-225")-bisdisulfide

témélimab immunoglobuline G4-kappa, anti-[protéine d'enveloppe du rétrovirus associé à la sclérose en plaques (MRSV) de la famille W des rétrovirus endogènes (HERV) d'*Homo sapiens*], anticorps monoclonal humanisé; chaîne lourde gamma4 (1-443) [VH humanisé (*Homo sapiens* IGHV1-46*01 (81.2%) -(IGHD)-IGHJ4*01 (92.9%)) [8.8.9] (1-116) -*Homo sapiens* IGHG4*01 (CH1 (117-214), charnière S10>P (224) (215-226), CH2 (227-336), CH3 (337-441), CHS (442-443)) (117-443)], (130-213')-disulfure avec la chaîne légère kappa (1'-213') [V-KAPPA humanisé (*Homo sapiens* IGKV1-39*01 (81.9%) -IGKJ4*01 (100%)) [5.3.9] (1'-106') -*Homo sapiens* IGKC*01, Km3 A45.1 (152), V101 (190) (107'-213')]; dimère (222-222":225-225")-bisdisulfure

temelimab

inmunoglobulina G4-kappa, anti-[proteína de la envoltura del retrovirus asociado a la esclerosis en placas (MRSV) de la familia W de los retrovirus endógenos (HERV) d'*Homo sapiens*], anticuerpo monoclonal humanizado;
cadena pesada gamma4 (1-443) [VH humanizado (*Homo sapiens* IGHV1-46*01 (81.2%) -(IGHD)-IGHJ4*01 (92.9%)) [8.8.9] (1-116) -*Homo sapiens* IGHG4*01 (CH1 (117-214), bisagra S10>P (224) (215-226), CH2 (227-336), CH3 (337-441), CHS (442-443)) (117-443)], (130-213')-disulfuro con la cadena ligera kappa (1'-213') [V-KAPPA humanizado (*Homo sapiens* IGKV1-39*01 (81.9%) -IGKJ4*01 (100%)) [5.3.9] (1'-106') -*Homo sapiens* IGKC*01, Km3 A45.1 (152), V101 (190) (107'-213')]; dímero (222-222":225-225")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGSSVKV SCKASGYTFT DYEMHWVRQA PGQGLEWIGA  50
VAPETGGTAY NQKFKGRATI TADKSTSTAY MELSSLRSED TAVYYCTSTV 100
VPFAYWGQGT LVTVSSASTK GPSVFPLAPC SRSTSESTAA LGCLVKDYFP 150
EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVVTVPSS SLGTKTYTCN 200
VDHKPSNTKV DKRVESKYGP PCPPCPAPEF LGGPSVFLFP PKPKDTLMIS 250
RTPEVTCVVV DVSQEDPEVQ FNWYVDGVEV HNAKTKPREE QFNSTYRVVS 300
VLTVLHQDWL NGKEYKCKVS NKGLPSSIEK TISKAKGQPR EPQVYTLPPS 350
QEEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT PPVLDSDGSF 400
FLYSRLTVDK SRWQEGNVFS CSVMHEALHN HYTQKSLSLS LGK        443
```

Light chain / Chaîne légère / Cadena ligera

```
QIQLTQSPSS LSASVGDRVT ITCSASSSVS YMYWYQQKPG KAPKAWIYRT  50
SNLASGVPSR FSGSGSGTDY TLTISSLQPE DFATYYCQQY QSLPLTFGGG 100
TKVEIKRTVA APSVFIFPPS DEQLKSGTAS VVCLLNNFYP REAKVQWKVD 150
NALQSGNSQE SVTEQDSKDS TYSLSSTLTL SKADYEKHKV YACEVTHQGL 200
SSPVTKSFNR GEC                                         213
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 143-199 257-317 363-421
22"-96" 143"-199" 257"-317' 363"-421"
Intra-L (C23-C104) 23'-87' 133'-193'
23'"-87'" 133'"-193'"
Inter-H-L (CH1 10-CL 126) 130-213' 130"-213'"
Inter-H-H (h 8, h 11) 222-222" 225-225"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84 4:
293, 293"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

teserpaturevum #

teserpaturev

A conditionally-replicating oncolytic Herpes simplex virus type 1 (HSV-1) strain F that has genetically engineered deletions within both copies of the γ34.5 gene and within the α47 gene, and further modified by insertion of an expressible beta-galactosidase (LacZ) gene in the ICP6 locus.

téserpaturev

souche F du virus Herpes simplex type 1 (HSV-1), oncolytique, dont la réplication est conditionnée, avec délétions par génie génétique dans les deux copies du gène γ34.5 et dans le gène α47 et avec des modifications par insertion du gène expressible de la bêta-galactosidase (LacZ) dans le locus ICP6

teserpaturev

Un virus Herpes simplex de tipo 1 (VHS-1) de la cepa F oncolítico, con replicación condicionada, que tiene deleciones introducidas por ingeniería genética en ambas copias del gen γ34 5 y en el gen α47, y con modificaciones adicionales mediante inserción de un gén expresable de beta-galactosidasa (LacZ) en el locus ICP6.

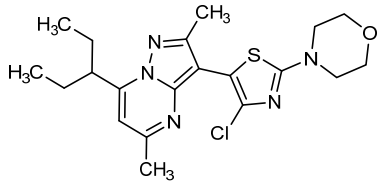
tildacerfontum

tildacerfont — 3-[4-chloro-2-(morpholin-4-yl)-1,3-thiazol-5-yl]-2,5-dimethyl-7-(pentan-3-yl)pyrazolo[1,5-*a*]pyrimidine

tildacerfont — 3-[4-chloro-2-(morpholin-4-yl)-1,3-thiazol-5-yl]-2,5-diméthyl-7-(pentan-3-yl)pyrazolo[1,5-*a*]pyrimidine

tildacerfont — 3-[4-cloro-2-(morfolin-4-il)-1,3-tiazol-5-il]-2,5-dimetil-7-(pentan-3-il)pirazolo[1,5-*a*]pirimidina

$C_{20}H_{26}ClN_5OS$



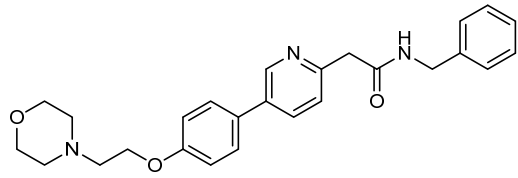
tirbanibulinum

tirbanibulin — *N*-benzyl-2-(5-{4-[2-(morpholin-4-yl)ethoxy]phenyl}pyridin-2-yl)acetamide

tirbanibuline — *N*-benzyl-2-(5-{4-[2-(morpholin-4-yl)éthoxy]phényl}pyridin-2-yl)acetamide

tirbanibulina — *N*-bencil-2-(5-{4-[2-(morfolin-4-il)etoxi]fenil}piridin-2-il)acetamida

$C_{26}H_{29}N_3O_3$



tirzepatidum

tirzepatide — L-tyrosyl-2-methylalanyl-L-α-glutamylglycyl-L-threonyl-L-phenylalanyl-L-threonyl-L-seryl-L-α-aspartyl-L-tyrosyl-L-seryl-L-isoleucyl-2-methylalanyl-L-leucyl-L-α-aspartyl-L-lysyl-L-isoleucyl-L-alanyl-L-glutaminyl-*N*^{6}-[(22*S*)-22,42-dicarboxy-10,19,24-trioxo-3,6,12,15-tetraoxa-9,18,23-triazadotetracontan-1-oyl]-L-lysyl-L-alanyl-L-phenylalanyl-L-valyl-L-glutaminyl-L-tryptophyl-L-leucyl-L-isoleucyl-L-alanylglycylglycyl-L-prolyl-L-seryl-L-serylglycyl-L-alanyl-L-prolyl-L-prolyl-L-prolyl-L-serinamide

tirzépatide — L-tyrosyl-2-méthylalanyl-L-α-glutamylglycyl-L-thréonyl-L-phénylalanyl-L-thréonyl-L-séryl-L-α-aspartyl-L-tyrosyl-L-séryl-L-isoleucyl-2-méthylalanyl-L-leucyl-L-α-aspartyl-L-lysyl-L-isoleucyl-L-alanyl-L-glutaminyl-*N*^{6}-[(22*S*)-22,42-dicarboxy-10,19,24-trioxo-3,6,12,15-tétraoxa-9,18,23-triazadotétracontan-1-oyl]-L-lysyl-L-alanyl-L-phénylalanyl-L-valyl-L-glutaminyl-L-tryptophyl-L-leucyl-L-isoleucyl-L-alanylglycylglycyl-L-prolyl-L-séryl-L-sérylglycyl-L-alanyl-L-prolyl-L-prolyl-L-prolyl-L-sérinamide

tirzepatida

L-tirosil-2-metilalanil-L-α-glutamilglicil-L-treonil-L-fenilalanil-L-treonil-L-seril-L-α-aspartil-L-tirosil-L-seril-L-isoleucil-2-metilalanil-L-leucil-L-α-aspartil-L-lisil-L-isoleucil-L-alanil-L-glutaminil-*N*^{6}-[(22*S*)-22,42-dicarboxi-10,19,24-trioxo-3,6,12,15-tetraoxa-9,18,23-triazadotetracontan-1-oil]-L-lisil-L-alanil-L-fenilalanil-L-valil-L-glutaminil-L-triptofil-L-leucil-L-isoleucil-L-alanilglicilglicil-L-prolil-L-seril-L-serilglicil-L-alanil-L-prolil-L-prolil-L-prolil-L-serinamida

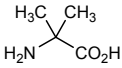
$C_{225}H_{348}N_{48}O_{68}$

Sequence / Séquence / Secuencia

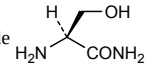
YXEGTFTSDY SIXLDKIAQK AFVQWLIAGG PSSGAPPPS 39

Modified residues / Résidus modifiés / Restos modificados

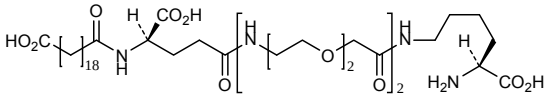
X (2 , 13) 2-methylalanine (Aib)



S (39) L-serinamide



K (20) *N*^{6}-{*N*-(hydrogen icosanedioyl)-γ-Glu-bis[iminobis(ethylenoxy)acetyl]}-Lysine



tofersenum

tofersen

all-P-ambo-2'-*O*-(2-methoxyethyl)-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-methoxyethyl)adenylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-*P*-thioguanylyl-(3'→5')-2'-*O*-(2-methoxyethyl)guanylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-*P*-thioadenylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-deoxy-*P*-thioadenylyl-(3'→5')-2'-deoxy-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-deoxy-*P*-thioadenylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-deoxy-5-methyl-*P*-thiocytidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-deoxy-*P*-thioadenylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methylcytidylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-*P*-thioadenylyl-(3'→5')-2'-*O*-(2-methoxyethyl)guanylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyluridine

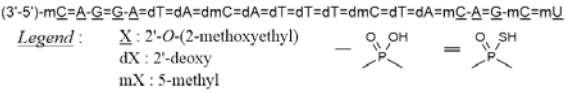
tofersen

tout-P-ambo-2'-*O*-(2-méthoxyéthyl)-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)adénylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-*P*-thioguanylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)guanylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-*P*-thioadénylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-désoxy-*P*-thioadénylyl-(3'→5')-2'-désoxy-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-désoxy-*P*-thioadénylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-désoxy-5-méthyl-*P*-thiocytidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-désoxy-*P*-thioadénylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthylcytidylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-*P*-thioadénylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)guanylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthyluridine

tofersén

todo-P-ambo-2'-*O*-(2-metoxietil)-5-metil-*P*-tiocitidilil-(3'→5')-2'-*O*-(2-metoxietil)adenilil-(3'→5')-2'-*O*-(2-metoxietil)-*P*-tioguanilil-(3'→5')-2'-*O*-(2-metoxietil)guanilil-(3'→5')-2'-*O*-(2-metoxietil)-*P*-tioadenilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2'-desoxi-*P*-tioadenilil-(3'→5')-2'-desoxi-5-metil-*P*-tiocitidilil-(3'→5')-2'-desoxi-*P*-tioadenilil-(3'→5')-*P*-tiotimidilil-(3'→5')-*P*-tiotimidilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2'-desoxi-5-metil-*P*-tiocitidilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2'-desoxi-*P*-tioadenilil-(3'→5')-2'-*O*-(2-metoxietil)-5-metilcitidilil-(3'→5')-2'-*O*-(2-metoxietil)-*P*-tioadenilil-(3'→5')-2'-*O*-(2-metoxietil)guanilil-(3'→5')-2'-*O*-(2-metoxietil)-5-metil-*P*-tiocitidilil-(3'→5')-2'-*O*-(2-metoxietil)-5-metiluridina

$C_{230}H_{317}N_{72}O_{123}P_{19}S_{15}$



toripalimabum #

toripalimab

immunoglobulin G4-kappa, anti-[*Homo sapiens* PDCD1 (programmed cell death 1, PD-1, PD1, CD279)], monoclonal antibody;
gamma4 heavy chain (1-452) [VH (*Homo sapiens* IGHV1-46*01 (80.6%) -(IGHD)-IGHJ3*01 (92.9%)) [8.8.18] (1-125) -*Homo sapiens* IGHG4*01 (CH1 (126-223), hinge S10>P (233) (224-235), CH2 (236-345), CH3 (346-450), CHS (451-452)) (126-452)], (139-219')-disulfide with kappa light chain (1'-219') [V-KAPPA (*Mus musculus* IGKV1-117*01 (93.0%)/*Homo sapiens* IGKV2-30*02 (88.0%) -*Homo sapiens* IGKJ2*01 (100%)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dimer (231-231":234-234")-bisdisulfide

toripalimab

immunoglobuline G4-kappa, anti-[*Homo sapiens* PDCD1 (protéine 1 de mort cellulaire programmée, PD-1, PD1, CD279)], anticorps monoclonal;
chaîne lourde gamma4 (1-452) [VH (*Homo sapiens* IGHV1-46*01 (80.6%) -(IGHD)-IGHJ3*01 (92.9%)) [8.8.18] (1-125) -*Homo sapiens* IGHG4*01 (CH1 (126-223), charnière S10>P (233) (224-235), CH2 (236-345), CH3 (346-450), CHS (451-452)) (126-452)], (139-219')-disulfure avec la chaîne légère kappa (1'-219') [V-KAPPA (*Mus musculus* IGKV1-117*01 (93.0%)/*Homo sapiens* IGKV2-30*02 (88.0%) -*Homo sapiens* IGKJ2*01 (100%)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dimère (231-231":234-234")-bisdisulfure

toripalimab

inmunoglobulina G4-kappa, anti-[*Homo sapiens* PDCD1 (proteína 1 de muerte celular programada, PD-1, PD1, CD279)], anticuerpo monoclonal;

cadena pesada gamma4 (1-452) [VH (*Homo sapiens* IGHV1-46*01 (80.6%) -(IGHD)-IGHJ3*01 (92.9%)) [8.8.18] (1-125) -*Homo sapiens* IGHG4*01 (CH1 (126-223), bisagra S10>P (233) (224-235), CH2 (236-345), CH3 (346-450), CHS (451-452)) (126-452)], (139-219')-disulfuro con la cadena ligera kappa (1'-219') [V-KAPPA (*Mus musculus* IGKV1-117*01 (93.0%)/*Homo sapiens* IGKV2-30*02 (88.0%) -*Homo sapiens* IGKJ2*01 (100%)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dímero (231-231":234-234")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

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QGQLVQSGAE VKKPGASVKV SCKASGYTFT DYEMHWVRQA PIHGLEWIGV  50
IESETGGTAY NQKFKGRVTI TADKSTSTAY MELSSLRSED TAVYYCAREG 100
ITTVATTYYW YFDVWGQGTT VTVSSASTKG PSVFPLAPCS RSTSESTAAL 150
GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL SSVVTVPSSS 200
LGTKTYTCNV DHKPSNTKVD KRVESKYGPP CPPCPAPEFL GGPSVFLFPP 250
KPKDTLMISR TPEVTCVVVD VSQEDPEVQF NWYVDGVEVH NAKTKPREEQ 300
FNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KGLPSSIEKT ISKAKGQPRE 350
PQVYTLPPSQ EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP 400
PVLDSDGSFF LYSRLTVDKS RWQEGNVFSC SVMHEALHNH YTQKSLSLSL 450
GK                                                      452
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Light chain / Chaîne légère / Cadena ligera

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DVVMTQSPLS LPVTLGQPAS ISCRSSQSIV HSNGNTYLEW YLQKPGQSPQ  50
LLIYKVSNRF SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCFQGSHVP 100
LTFGQGTKLE IKRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK 150
VQWKVDNALQ SGNSQESVTE QDSKDSTYSL SSTLTLSKAD YEKHKVYACE 200
VTHQGLSSPV TKSFNRGEC                                   219
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 152-208 266-326 372-430
22"-96" 152"-208" 266"-326" 372"-430"
Intra-L (C23-C104) 23'-93' 139'-199'
23'"-93'" 139'"-199'"
Inter-H-L (CH1 10-CL126) 139-219' 139"-219'"
Inter-H-H (h 8, h 11) 231-231" 234-234"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84 4:
302, 302"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

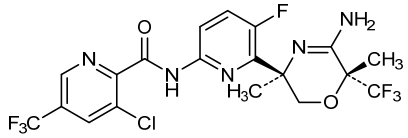
umibecestatum

umibecestat — *N*-{6-[(3*R*,6*R*)-5-amino-3,6-dimethyl-6-(trifluoromethyl)-3,6-dihydro-2*H*-1,4-oxazin-3-yl]-5-fluoropyridin-2-yl}-3-chloro-5-(trifluoromethyl)pyridine-2-carboxamide

umibécestat — *N*-{6-[(3*R*,6*R*)-5-amino-3,6-diméthyl-6-(trifluorométhyl)-3,6-dihydro-2*H*-1,4-oxazin-3-yl]-5-fluoropyridin-2-yl}-3-chloro-5-(trifluorométhyl)pyridine-2-carboxamide

umibecestat — *N*-{6-[(3*R*,6*R*)-5-amino-3,6-dimetil-6-(trifluorometil)-3,6-dihidro-2*H*-1,4-oxazin-3-il]-5-fluoropiridin-2-il}-3-cloro-5-(trifluorometil)piridina-2-carboxamida

$C_{19}H_{15}ClF_7N_5O_2$



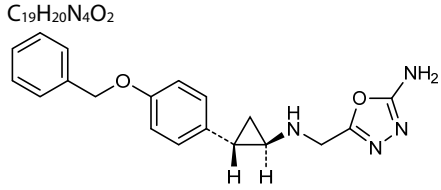
vafidemstatum

vafidemstat — (4[1]*R*,4[2]*S*)-6-oxa-3-aza-1(2)-[1,3,4]oxadiazola-5(1,4),8(1)-dibenzena-4(1,2)-cyclopropanaoctaphan-1[5]-amine

vafidemstat — (4[1]*R*,4[2]*S*)-6-oxa-3-aza-1(2)-[1,3,4]oxadiazola-5(1,4),8(1)-dibenzéna-4(1,2)-cyclopropanaoctaphan-1[5]-amine

vafidemstat — (4[1]*R*,4[2]*S*)-6-oxa-3-aza-1(2)-[1,3,4]oxadiazola-5(1,4),8(1)-dibencena-4(1,2)-ciclopropanaoctafan-1[5]-amina

$C_{19}H_{20}N_4O_2$



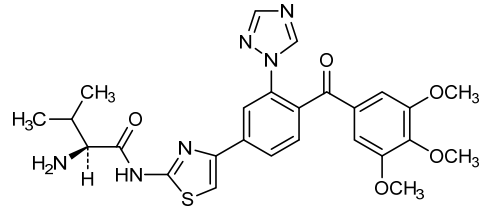
valecobulinum

valecobulin — (2*S*)-2-amino-3-methyl-*N*-{4-[3-(1*H*-1,2,4-triazol-1-yl)-4-(3,4,5-trimethoxybenzoyl)phenyl]-1,3-thiazol-2-yl}butanamide

valécobuline — (2*S*)-2-amino-3-méthyl-*N*-{4-[3-(1*H*-1,2,4-triazol-1-yl)-4-(3,4,5-triméthoxybenzoyl)phényl]-1,3-thiazol-2-yl}butanamide

valecobulina — (2*S*)-2-amino-3-metil-*N*-{4-[3-(1*H*-1,2,4-triazol-1-il)-4-(3,4,5-trimetoxibenzoil)fenil]-1,3-tiazol-2-il}butanamide

$C_{26}H_{28}N_6O_5S$



vutrisiranum

vutrisiran — {(2*S*,4*R*)-1-{1-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]-16,16-bis-({3-[(3-{5-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]pentanamido}propyl)amino]-3-oxopropoxy}methyl)-5,11,18-trioxo-14-oxa-6,10,17-triazanonacosan-29-oyl}-4-hydroxypyrrolidin-2-yl}methyl hydrogen *all-P-ambo*-2'-*O*-methyl-*P*-thiouridylyl-(3'→5')-2'-*O*-methyl-*P*-thioguanylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-deoxy-2'-fluorouridylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-deoxy-2'-fluorocytidylyl-(3'→5')-2'-deoxy-2'-fluoroadenylyl-(3'→5')-2'-deoxy-2'-fluorouridylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyl-3'-adenylate duplex

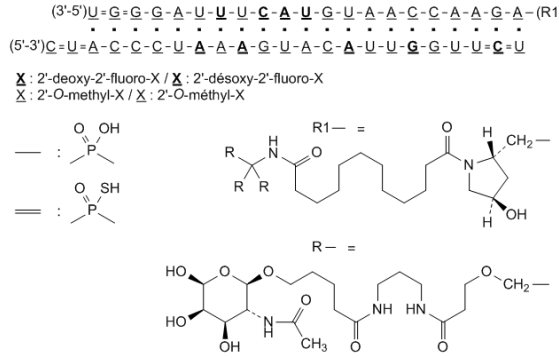
with *all-P-ambo*-2'-*O*-methyl-*P*-thiocytidylyl-(5'→3')-2'-*O*-methyl-*P*-thiouridylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-deoxy-2'-fluoroadenylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-deoxy-2'-fluoroadenylyl-(5'→3')-2'-*O*-methylguanylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-deoxy-2'-fluoroadenylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-deoxy-2'-fluoroguanylyl-(5'→3')-2'-*O*-methylguanylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-*O*-methyl-*P*-thiouridylyl-(5'→3')-2'-deoxy-2'-fluoro-*P*-thiocytidylyl-(5'→3')-2'-*O*-methyluridine

vutrisiran

hydrogéno-*tout-P-ambo*-2'-*O*-méthyl-*P*-thiouridylyl-(3'→5')-2'-*O*-méthyl-*P*-thioguanylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyladenylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-désoxy-2'-fluorouridylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-désoxy-2'-fluorocytidylyl-(3'→5')-2'-désoxy-2'-fluoroadénylyl-(3'→5')-2'-désoxy-2'-fluorouridylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthyladenylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyl-3'-adénylate de {(*2S,4R*)-1-{1-[(2-acétamido-2-désoxy-β-D-galactopyranosyl)oxy]-16,16-bis-({3-[(3-{5-[(2-acétamido-2-désoxy-β-D-galactopyranosyl)oxy]pentanamido}propyl)amino]-3-oxopropoxy}méthyl)-5,11,18-trioxo-14-oxa-6,10,17-triazanonacosan-29-oyl}-4-hydroxypyrrolidin-2-yl}méthyle duplex avec *tout-P-ambo*-2'-*O*-méthyl-*P*-thiocytidylyl-(5'→3')-2'-*O*-méthyl-*P*-thiouridylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-désoxy-2'-fluoroadénylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-désoxy-2'-fluoroadénylyl-(5'→3')-2'-*O*-méthylguanylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-désoxy-2'-fluoroadénylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-désoxy-2'-fluoroguanylyl-(5'→3')-2'-*O*-méthylguanylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-*O*-méthyl-*P*-thiouridylyl-(5'→3')-2'-désoxy-2'-fluoro-*P*-thiocytidylyl-(5'→3')-2'-*O*-méthyluridine

vutrisirán

hidrógeno-*todo-P-ambo*-2'-*O*-metil-*P*-tiouridilil-(3'→5')-2'-*O*-metil-*P*-tioguanilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-desoxi-2'-fluorouridilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-desoxi-2'-fluorocitidilil-(3'→5')-2'-desoxi-2'-fluoroadenilil-(3'→5')-2'-desoxi-2'-fluorouridilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metil-3'-adenilato de {(*2S,4R*)-1-{1-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]-16,16-bis-({3-[(3-{5-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]pentanamido}propil)amino]-3-oxopropoxi}metil)-5,11,18-trioxo-14-oxa-6,10,17-triazanonacosan-29-oil}-4-hidroxipirrolidin-2-il}metilo dúplex con *todo-P-ambo*-2'-*O*-metil-*P*-tiocitidilil-(5'→3')-2'-*O*-metil-*P*-tiouridilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-desoxi-2'-fluoroadenylyl-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-desoxi-2'-fluoroadenilil-(5'→3')-2'-*O*-metilguanilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-desoxi-2'-fluoroadenilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-desoxi-2'-fluoroguanilil-(5'→3')-2'-*O*-metilguanilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-*O*-metil-*P*-tiouridilil-(5'→3')-2'-desoxi-2'-fluoro-*P*-tiocitidilil-(5'→3')-2'-*O*-metiluridina



zampilimabum #

zampilimab	immunoglobulin G4-kappa, anti-[*Homo sapiens* TGM2 (transglutaminase 2, transglutaminase-2 (TG2), protein-glutamine-gamma-glutamyltransferase C polypeptide, TGC)], humanized and chimeric monoclonal antibody; gamma4 heavy chain (1-441) [humanized VH (*Homo sapiens* IGHV3-23*03 (89.8%) -(IGHD) -IGHJ4*01 (100%)) [8.8.7] (1-114) -*Homo sapiens* IGHG4*01 (CH1 (115-212), hinge S10>P (222) (213-224), CH2 (225-334), CH3 (335-439), CHS (440-441)) (115-441)], (128-214')-disulfide with kappa light chain chimeric (1'-214') [V-KAPPA (*Mus muculus* IGKV14-111*01 (82.1%)/*Homo sapiens* IGKV1-16*01 (78.9%) -*Homo sapiens* IGKJ1*01 (91.7%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (220-220":223-223")-bisdisulfide
zampilimab	immunoglobuline G4-kappa, anti-[*Homo sapiens* TGM2 (transglutaminase 2, transglutaminase-2, TG2, protéine-glutamine-gamma-glutamyltransférase polypeptide C, TGC)], anticorps monoclonal humanisé et chimérique; chaîne lourde gamma4 (1-441) [VH humanisé (*Homo sapiens* IGHV3-23*03 (89.8%) -(IGHD) -IGHJ4*01 (100%)) [8.8.7] (1-114) -*Homo sapiens* IGHG4*01 (CH1 (115-212), charnière S10>P (222) (213-224), CH2 (225-334), CH3 (335-439), CHS (440-441)) (115-441)], (128-214')-disulfure avec la chaîne légère kappa chimérique (1'-214') [V-KAPPA (*Mus muculus* IGKV14-111*01 (82.1%)/*Homo sapiens* IGKV1-16*01 (78.9%) -*Homo sapiens* IGKJ1*01 (91.7%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (220-220":223-223")-bisdisulfure
zampilimab	inmunoglobulina G4-kappa, anti-[*Homo sapiens* TGM2 (transglutaminasa 2, transglutaminasa-2, TG2, proteína-glutamina-gamma-glutamiltransferasa polipéptido C, TGC)], anticuerpo monoclonal humanizado y quimérico;

cadena pesada gamma4 (1-441) [VH humanizado (*Homo sapiens* IGHV3-23*03 (89.8%) -(IGHD) -IGHJ4*01 (100%)) [8.8.7] (1-114) -*Homo sapiens* IGHG4*01 (CH1 (115-212), bisagra S10>P (222) (213-224), CH2 (225-334), CH3 (335-439), CHS (440-441)) (115-441)], (128-214')-disulfuro con la cadena ligera kappa quimérica (1'-214') [V-KAPPA (*Mus musculus* IGKV14-111*01 (82.1%)/*Homo sapiens* IGKV1-16*01 (78.9%) -*Homo sapiens* IGKJ1*01 (91.7%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (220-220":223-223")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLLESGGG LVQPGGSLRL SCAASGFTLS THAMSWVRQA PGKGLEWVAT  50
ISSGGRSTYY PDSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYFCARLI 100
STYWGQGTLV TVSSASTKGP SVFPLAPCSR STSESTAALG CLVKDYFPEP 150
VTVSWNSGAL TSGVHTFPAV LQSSGLYSLS SVVTVPSSSL GTKTYTCNVD 200
HKPSNTKVDK RVESKYGPPC PPCPAPEFLG GPSVFLFPPK PKDTLMISRT 250
PEVTCVVVDV SQEDPEVQFN WYVDGVEVHN AKTKPREEQF NSTYRVVSVL 300
TVLHQDWLNG KEYKCKVSNK GLPSSIEKTI SKAKGQPREP QVYTLPPSQE 350
EMTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP VLDSDGSFFL 400
YSRLTVDKSR WQEGNVFSCS VMHEALHNHY TQKSLSLSLG K          441
```

Light chain / Chaîne légère / Cadena ligera

```
DITMTQSPSS LSASVGDRVT ITCKASQDIN SYLTWFQQKP GKAPKILIYL  50
VNRLVDGVPS RFSGSGSGQD YALTISSLQP EDFATYYCLQ YDDFPYTFGQ 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Post-translational modifications

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

Intra-H (C23-C104) 22-96 141-197 255-315 361-419
22"-96" 141"-197"' 255"-315" 361"-419"

Intra-L (C23-C104) 23'-88' 134'-194'
23"'-88"' 134"'-194"'

Inter-H-L (CH1 10-CL 126) 128-214' 128"-214"'

Inter-H-H (h 8, h 11) 220-220" 223-223"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación

H CH2 N84 4:
291, 291"

Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

Electronic structure available on Mednet: http://mednet.who.int/
Structure électronique disponible sur Mednet: http://mednet.who.int/
Estructura electrónica disponible en Mednet: http://mednet.who.int/
* http://www.who.int/medicines/services/inn/publication/en/

AMENDMENTS TO PREVIOUS LISTS
MODIFICATIONS APPORTÉES AUX LISTES ANTÉRIEURES
MODIFICACIONES A LAS LISTAS ANTERIORES

Recommended International Nonproprietary Names (Rec. INN): List 64
Dénominations communes internationales recommandées (DCI Rec.): Liste 64
Denominaciones Comunes internacionales recomendadas (DCI Rec.): Lista 64
(WHO Drug Information, Vol. 24, No. 3, 2010)

p. 286 **vonicogum alfa #**

vonicog alfa *replace the description and structure (corrected amino acids (A618 and H709) in bold) by the following ones, delete the molecular formula*

vonicog alfa *remplacer la description et structure (acides aminés corrigés (A618 et H709) en gras) par les suivantes, supprimer la formule moléculaire brute*

vonicog alfa *sustitúyase la descripción y la estructura (ácidos aminos corregidos (A618 y H709) en graso) por las siguientes, suprimáse la fórmula molecular*

[89-arginine]von Willebrand factor *Homo sapiens* (852Q>R variant), produced in Chinese hamster ovary (CHO) cells, glycoform alfa

[89-arginine]facteur de von Willebrand *Homo sapiens* (variant 852Q>R), produit par des cellules ovariennes de hamsters chinois (CHO), glycoforme alfa

[89-arginina]factor de von Willebrand *Homo sapiens* (variante 852Q>R), producido por las células ováricas de hamsters chinos (CHO), glicoforma alfa

```
SLSCRPPMVK LVCPADNLRA EGLECTKTCQ NYDLECMSMG CVSGCLCPPG   50
MVRHENRCVA LERCPCFHQG KEYAPGETVK IGCNTCVCRD RKWNCTDHVC  100
DATCSTIGMA HYLTFDGLKY LFPGECQYVL VQDYCGSNPG TFRILVGNKG  150
CSHPSVKCKK RVTILVEGGE IELFDGEVNV KRPMKDETHF EVVESGRYII  200
LLLGKALSVV WDRHLSISVV LKQTYQEKVC GLCGNFDGIQ NNDLTSSNLQ  250
VEEDPVDFGN SWKVSSQCAD TRKVPLDSSP ATCHNNIMKQ TMVDSSCRIL  300
TSDVFQDCNK LVDPEPYLDV CIYDTCSCES IGDCACFCDT IAAYAHVCAQ  350
HGKVVTWRTA TLCPQSCEER NLRENGYECE WRYNSCAPAC QVTCQHPEPL  400
ACPVQCVEGC HAHCPPGKIL DELLQTCVDP EDCPVCEVAG RRFASGKKVT  450
LNPSDPEHCQ ICHCDVVNLT CEACQEPGGL VVPPTDAPVS PTTLYVEDIS  500
EPPLHDFYCS RLLDLVFLLD GSSRLSEAEF EVLKAFVVDM MERLRISQKW  550
VRVAVVEYHD GSHAYIGLKD RKRPSELRRI ASQVKYAGSQ VASTSEVLKY  600
TLFQIFSKID RPEASRIALL LMASQEPQRM SRNFVRYVQG LKKKKVIVIP  650
VGIGPHANLK QIRLIEKQAP ENKAFVLSSV DELEQQRDEI VSYLCDLAPE  700
APPPTLPPHM AQVTVGPGLL GVSTLGPKRN SMVLDVAFVL EGSDKIGEAD  750
FNRSKEFMEE VIQRMDVGQD SIHVTVLQYS YMVTVEYPFS EAQSKGDILQ  800
RVREIRYQGG NRTNTGLALR YLSDHSFLVS QGDREQAPNL VYMVTGNPAS  850
DEIKRLPGDI QVVPIGVGPN ANVQELERIG WPNAPILIQD FETLPREAPD  900
LVLQRCCSGE GLQIPTLSPA PDCSQPLDVI LLLDGSSSFP ASYFDEMKSF  950
AKAFISKANI GPRLTQVSVL QYGSITTIDV PWNVVPEKAH LLSLVDVMQR 1000
EGGPSQIGDA LGFAVRYLTS EMHGARPGAS KAVVILVTDV SVDSVDAAAD 1050
AARSNRVTVF PIGIGDRYDA AQLRILAGPA GDSNVVKLQR IEDLPTMVTL 1100
GNSFLHKLCS GFVRICMDED GNEKRPGDVW TLPDQCHTVT CQPDGQTLLK 1150
SHRVNCDRGL RPSCPNSQSP VKVEETCGCR WTCPCVCTGS STRHIVTFDG 1200
QNFKLTGSCS YVLFQNKEQD LEVILHNGAC SPGARQGCMK SIEVKHSALS 1250
VELHSDMEVT VNGRLVSVPY VGGNMEVNVY GAIMHEVRFN HLGHIFTFTP 1300
QNNEFQLQLS PKTFASKTYG LCGICDENGA NDFMLRDGTV TTDWKTLVQE 1350
WTVQRPGQTC QPILEEQCLV PDSSHCQVLL LPLFAECHKV LAPATFYAIC 1400
QQDSCHQEQV CEVIASYAHL CRTNGVCVDW RTPDFCAMSC PPSLVYNHCE 1450
HGCPRHCDGN VSSCGDHPSE GCFCPPDKVM LEGSCVPEEA CTQCIGEDGV 1500
QHQFLEAWVP DHQPCQICTC LSGRKVNCTT QPCPTAKAPT CGLCEVARLR 1550
QNADQCCPEY ECVCDPVSCD LPPVPHCERG LQPTLTNPGE CRPNFTCACR 1600
KEECKRVSPP SCPPHRLPTL RKTQCCDEYE CACNCVNSTV SCPLGYLAST 1650
ATNDCGCTTT TCLPDKVCVH RSTIYPVGQF WEEGCDVCTC TDMEDAVMGL 1700
RVAQCSQKPC EDSCRSGFTY VLHEGECCGR CLPSACEVVT GSPRGDSQSS 1750
WKSVGSQWAS PENPCLINEC VRVKEEVFIQ QRNVSCPQLE VPVCPSGFQL 1800
SCKTSACCPS CRCERMEACM LNGTVIGPGK TVMIDVCTTC RCMVQVGVIS 1850
GFKLECRKTT CNPCPLGYKE ENNTGECCGR CLPTACTIQL RGGQIMTLKR 1900
DETLQDGCDT HFCKVNERGE YFWEKRVTGC PPFDEHKCLA EGGKIMKIPG 1950
TCCDTCEEPE CNDITARLQY VKVGSCKSEV EVDIHYCQGK CASKAMYSID 2000
INDVQDQCSC CSPTRTEPMQ VALHCTNGSV VYHEVLNAME CKCSPRKCSK 2050
```

Recommended International Nonproprietary Names (Rec. INN): List 72
Dénominations communes internationales recommandées (DCI Rec.): Liste 72
Denominaciones comunes internacionales recomendadas (DCI Rec.): Lista 72
(WHO Drug Information, Vol. 28, No. 3, 2014)

p. 381 **alpelisibum**

alpelisib	*replace the chemical name by the following one*
alpélisib	*remplacer le nom chimique par le suivant*
alpelisib	*sustitúyase el nombre químico por el siguiente*

(2*S*)-*N*^{1}-{4-methyl-5-[2-(1,1,1-trifluoro-2-methylpropan-2-yl)pyridin-4-yl]-1,3-thiazol-2-yl}pyrrolidine-1,2-dicarboxamide

(2*S*)-*N*^{1}-{4-méthyl-5-[2-(1,1,1-trifluoro-2-méthylpropan-2-yl)pyridin-4-yl]-1,3-thiazol-2-yl}pyrrolidine-1,2-dicarboxamide

(2*S*)-*N*^{1}-{4-metil-5-[2-(1,1,1-trifluoro-2-metilpropan-2-il)piridin-4-il]-1,3-tiazol-2-il}pirrolidina-1,2-dicarboxamida

Recommended International Nonproprietary Names (Rec. INN): List 78
Dénominations communes internationales recommandées (DCI Rec.): Liste 78
Denominaciones comunes internacionales recomendadas (DCI Rec.): Lista 78
(WHO Drug Information, Vol. 31, No. 3, 2017)

p. 517 **eltanexorum**

eltanexor	*replace the molecular formula by the following one*
eltanexor	*remplacer la formule moléculaire brute par la suivante*
eltanexor	*sustitúyase la fórmula molecular por la siguiente*

$C_{17}H_{10}F_6N_6O$

Recommended International Nonproprietary Names (Rec. INN): List 79
Dénominations communes internationales recommandées (DCI Rec.): Liste 79
Denominaciones comunes internacionales recomendadas (DCI Rec.): Lista 79
(WHO Drug Information, Vol. 32, No. 1, 2018)

p.109 **crenigacestatum**

crenigacestat	*replace the chemical name by the following one*
crénigacestat	*remplacer le nom chimique par le suivant*
crenigacestat	*sustitúyase el nombre químico por el siguiente*

4,4,4-trifluoro-*N*-[(2*S*)-1-{[(7*S*)-5-(2-hydroxyethyl)-6-oxo-6,7-dihydro-5*H*-pyrido[3,2-*a*][3]benzazepin-7-yl]amino}-1-oxopropan-2-yl]butanamide

4,4,4-trifluoro-*N*-[(2*S*)-1-{[(7*S*)-5-(2-hydroxyéthyl)-6-oxo-6,7-dihydro-5*H*-pyrido[3,2-*a*][3]benzazépin-7-yl]amino}-1-oxopropan-2-yl]butanamide

4,4,4-trifluoro-*N*-[(2*S*)-1-{[(7*S*)-5-(2-hidroxietil)-6-oxo-6,7-dihidro-5*H*-pirido[3,2-*a*][3]benzazepin-7-il]amino}-1-oxopropan-2-il]butanamida

p. 119 **estetrolum**

estetrol	*replace the molecular formula by the following one*
estétrol	*remplacer la formule moléculaire brute par la suivante*
estetrol	*sustitúyase la fórmula molecular por la siguiente*
	$C_{18}H_{24}O_4$

p. 179 **vecabrutinibum**

vecabrutinib	*replace the molecular formula by the following one*
vécabrutinib	*remplacer la formule moléculaire brute par la suivante*
vecabrutinib	*sustitúyase la fórmula molecular por la siguiente*
	$C_{22}H_{24}ClF_4N_7O_2$

Recommended International Nonproprietary Names (Rec. INN): List 80
Dénominations communes internationales recommandées (DCI Rec.): Liste 80
Denominaciones comunes internacionales recomendadas (DCI Rec.): Lista 80
(WHO Drug Information, Vol. 32, No. 3, 2018)

p. 429 **apraglutidum***

apraglutide	*replace the description and structure by the following ones*
apraglutide	*remplacer les description et structure par les suivantes*
apraglutida	*sustitúyase la descripción y la estructura por las siguientes*

[Ala^2>Gly,Met^{10}>Ahx,Asn^{11}>D-Phe,Asn^{16}>Leu]human glucagon-like peptide 2 (1-33)-peptide 33-amide:
L-histidylglycyl-L-α-aspartylglycyl-L-seryl-L-phenylalanyl-L-seryl-L-α-aspartyl-L-α-glutamyl-L-2-aminohexanoyl-D-phenylalanyl-L-threonyl-L-isoleucyl-L-leucyl-L-α-aspartyl-L-leucyl-L-leucyl-L-alanyl-L-alanyl-L-arginyl-L-α-aspartyl-L-phenylalanyl-L-isoleucyl-L-asparaginyl-L-tryptophyl-L-leucyl-L-isoleucyl-L-glutaminyl-L-threonyl-L-lysyl-L-isoleucyl-L-threonyl-L-isoasparagine

[Ala^2>Gly,Met^{10}>Ahx,Asn^{11}>D-Phe,Asn^{16}>Leu]peptide semblable au glucagon 2 humain (1-33)-peptide 33-amide:
L-histidylglycyl-L-α-aspartylglycyl-L-séryl-L-phénylalanyl-L-séryl-L-α-aspartyl-L-α-glutamyl-L-2-aminohexanoyl-D-phénylalanyl-L-thréonyl-L-isoleucyl-L-leucyl-L-α-aspartyl-L-leucyl-L-leucyl-L-alanyl-L-alanyl-L-arginyl-L-α-aspartyl-L-phénylalanyl-L-isoleucyl-L-asparaginyl-L-tryptophyl-L-leucyl-L-isoleucyl-L-glutaminyl-L-thréonyl-L-lysyl-L-isoleucyl-L-thréonyl-L-isoasparagine

[Ala^2>Gly,Met^{10}>Ahx,Asn^{11}>D-Phe,Asn^{16}>Leu]péptido similar al glucagón 2 humano (1-33)-péptido 33-amida:
L-histidilglicil-L-α-aspartilglicil-L-seril-L-fenilalanil-L-seril-L-α-aspartil-L-α-glutamil-L-2-aminohexanoil-D-fenilalanil-L-treonil-L-isoleucil-L-leucil-L-α-aspartil-L-leucil-L-leucil-L-alanil-L-alanil-L-arginil-L-α-aspartil-L-fenilalanil-L-isoleucil-L-asparaginil-L-triptofil-L-leucil-L-isoleucil-L-glutaminil-L-treonil-L-lisil-L-isoleucil-L-treonil-L-isoasparagina

H-His-Gly-Asp-Gly-Ser-Phe-Ser-Asp-Glu-Ahx-D-Phe-Thr-Ile-Leu-Asp-Leu-Leu-Ala-Ala-Arg-Asp-Phe-Ile-Asn-Trp-Leu-Ile-Gln-Thr-Lys-Ile-Thr-Asp-NH_2

p. 464 **lanraplenibum**

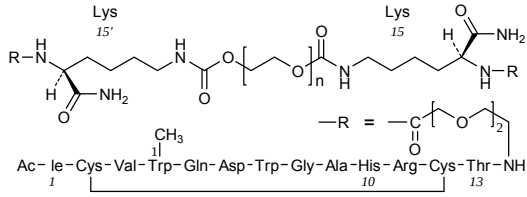
lanraplenib	*replace the molecular formula by the following one*
lanraplénib	*remplacer la formule moléculaire brute par la suivante*
lanraplenib	*sustitúyase la fórmula molecular por la siguiente*

$C_{23}H_{25}N_9O$

p. 479 **pegcetacoplanum**

pegcetacoplan	*replace the molecular formula and the structure by the following ones*
pegcétacoplan	*remplacer la formule moléculaire et la structure par les suivantes*
pegcetacoplán	*sustitúyase la fórmula molecular y la estructura por las siguientes*

$C_{170}H_{248}N_{50}O_{47}S_4(C_2H_4O)_n$ (n ~ 800-1100)



Procedure and Guiding Principles / Procédure et Directives / Procedimientos y principios generales

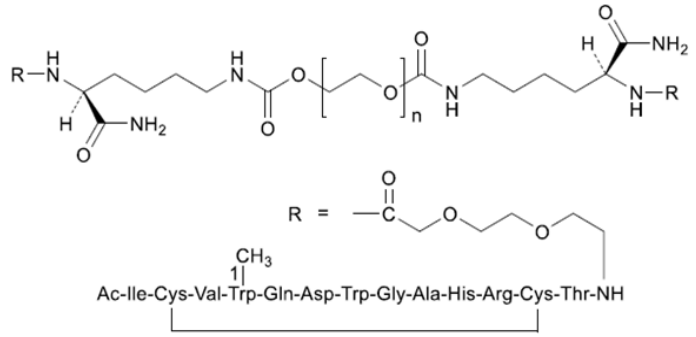
The text of the *Procedures for the Selection of Recommended International Nonproprietary Names for Pharmaceutical Substances* and *General Principles for Guidance in Devising International Nonproprietary Names for Pharmaceutical Substances* will be reproduced in proposed INN lists only.

Les textes de la *Procédure à suivre en vue du choix de dénominations communes internationales recommandées pour les substances pharmaceutiques* et des *Directives générales pour la formation de dénominations communes internationales applicables aux substances pharmaceutiques* seront publiés seulement dans les listes des DCI proposées.

El texto de los *Procedimientos de selección de denominaciones comunes internacionales recomendadas para las sustancias farmacéuticas* y de los *Principios generales de orientación para formar denominaciones comunes internacionales para sustancias farmacéuticas* aparece solamente en las listas de DCI propuestas.

目次

1.10　毒薬・劇薬等の指定審査資料のまとめ

化学名・別名	ペグセタコプランは PEG 化ペプチド（分子量：約 43,500）であり，補体 C3 に結合する 2 本の同一の合成ペプチドが，C 末端リシンアミドのε-アミノ基を介してポリエチレングリコール（分子量：約 39,600）の両端にそれぞれ結合している．ペプチド部分は 15 個のアミノ酸残基からなる．化学名は以下の通りである． *O,O'*-ビス[(*S*^{2},*S*^{12}-シクロ{*N*-アセチル-L-イソロイシル-L-システイニル-L-バリル-1-メチル-L-トリプトフィル-L-グルタミニル-L-α-アスパルチル-L-トリプトフィルグリシル-L-アラニル-L-ヒスチジル-L-アルギニル-L-システイニル-L-スレオニル-2-[2-(2-アミノエトキシ)エトキシ]アセチル-L-リシンアミド})-*N*$^{6\ 15}$-カルボニル]ポリエチレングリコール （別名：ペグセタコプラン）
構造式	 nは約800~1100である.
効能・効果	発作性夜間ヘモグロビン尿症
用法・用量	通常、成人には、ペグセタコプランとして 1 回 1080 mg を週 2 回皮下投与する。 なお、十分な効果が得られない場合には、1 回 1080 mg を 3 日に 1 回の間隔で皮下投与することができる。
劇薬等の指定	
市販名及び有効成分・分量	原体：ペグセタコプラン 製剤：エムパベリ皮下注 1080mg （1 バイアル中にペグセタコプラン 1080 mg を含む）

毒性

急性：

動物種	投与経路	投与量（mg/kg）	最大非致死量（mg/kg）
ウサギ#1	皮下	7、28、140	雌雄：140
サル#2	皮下	7、28、140	雌雄：140
サル#3	皮下	28、140	雄：140

#1 単回投与毒性試験は実施していない。ウサギを用いた 28 日間毒性試験（13CATX-003）の初回投与後の情報。

#2 単回投与毒性試験は実施していない。サルを用いた 28 日間毒性試験（13CATX-004）の初回投与後の情報。

#3 単回投与毒性試験は実施していない。サルを用いた安全性薬理試験（13CATX-005）の本剤投与後の情報。

亜急性：

動物種	投与経路	投与量（mg/kg/日）	投与スケジュール	無毒性量（mg/kg/日）	主な所見
ウサギ	皮下	7、28、140	1 日 1 回 28 日間	28	腎尿細管変性（140 mg/kg/日）
サル	皮下	7、28、140	1 日 1 回 28 日間	7	腎尿細管変性（28 mg/kg/日及び 140 mg/kg/日）

慢性：

動物種	投与経路	投与量（mg/kg/日）	投与スケジュール	無毒性量（mg/kg/日）	主な所見
ウサギ	皮下	1、7、28	1 日 1 回 6 ヵ月間	1 未満	腎尿細管変性（全投与量）
サル	皮下	1、7、28	1 日 1 回 9 ヵ月間	7	腎尿細管変性（28 mg/kg/日）

副作用

国際共同第 3 相臨床試験（APL2-302 試験）において、本剤投与を受けた 80 例中 39 例（48.8%）に副作用が認められた。

副作用の種類	例数
注射部位紅斑	12
注射部位硬結	5
注射部位そう痒感	5
注射部位反応	5
注射部位腫脹	5

会社

Swedish Orphan Biovitrum Japan 株式会社　製剤：輸入

1　　第3 部（モジュール3）：品質に関する文書

3.2.S 原薬

資料番号	表題	国内/海外	社内資料/公表論文	評価資料/参考資料
3.2.S.1 一般情報				
3.2.S.1.1	Nomenclature	海外	社内資料	評価資料
3.2.S.1.2	Structure	海外	社内資料	評価資料
3.2.S.1.3	General Properties	海外	社内資料	評価資料
3.2.S.2 製造				
3.2.S.2.1	Manufacturer(s)	海外	社内資料	評価資料
3.2.S.2.2	Description of Manufacturing Process and Process Controls	海外	社内資料	評価資料
3.2.S.2.3	Control of Materials	海外	社内資料	評価資料
3.2.S.2.4	Controls of Critical Steps and Intermediates	海外	社内資料	評価資料
3.2.S.2.5	Process Validation and/or Evaluation	海外	社内資料	評価資料
3.2.S.2.6	Manufacturing Process Development	海外	社内資料	評価資料
3.2.S.3 特性				
3.2.S.3.1	Elucidation of Structure and other Characteristics	海外	社内資料	評価資料
3.2.S.3.2	Impurities	海外	社内資料	評価資料
3.2.S.4 原薬の管理				
3.2.S.4.1	Specification	海外	社内資料	評価資料
3.2.S.4.2	Analytical Procedures	海外	社内資料	評価資料
3.2.S.4.3	Validation of Analytical Procedures	海外	社内資料	評価資料
3.2.S.4.4	Batch Analyses	海外	社内資料	評価資料
3.2.S.4.5	Justification of Specification	海外	社内資料	評価資料
3.2.S.5 標準品又は標準物質				
3.2.S.5	Reference Standards or Materials	海外	社内資料	評価資料
3.2.S.6 容器及び施栓系				
3.2.S.6	Container Closure System	海外	社内資料	評価資料
3.2.S.7 安定性				
3.2.S.7.1	Stability Summary and Conclusions	海外	社内資料	評価資料
3.2.S.7.2	Post-approval Stability Protocol and Stability Commitment	海外	社内資料	評価資料
3.2.S.7.3	Stability Data	海外	社内資料	評価資料

1　　第3 部（モジュール3）：品質に関する文書

3.2.P 製剤

資料番号	表題	国内/海外	社内資料/公表論文	評価資料/参考資料
3.2.P.1 製剤及び処方				
3.2.P.1	Description and Composition of the Drug Product	海外	社内資料	評価資料
3.2.P.2 製剤開発の経緯				
3.2.P.2.1	Components of the Drug Product	海外	社内資料	評価資料
3.2.P.2.2	Drug Product	海外	社内資料	評価資料
3.2.P.2.3	Manufacturing Process Development	海外	社内資料	評価資料
3.2.P.2.4	Container Closure System	海外	社内資料	評価資料
3.2.P.2.5	Microbiological Attributes	海外	社内資料	評価資料
3.2.P.2.6	Compatibility	海外	社内資料	評価資料
3.2.P.3 製造				
3.2.P.3.1	Manufacturers	海外	社内資料	評価資料
3.2.P.3.2	Batch Formula	海外	社内資料	評価資料
3.2.P.3.3	Description of Manufacturing Process and Process Controls	海外	社内資料	評価資料
3.2.P.3.4	Controls of Critical Steps	海外	社内資料	評価資料
3.2.P.3.5	Process Validation and/or Evaluation	海外	社内資料	評価資料
3.2.P.4 添加剤の管理				
3.2.P.4.1	Specifications	海外	社内資料	評価資料
3.2.P.4.2	Analytical Procedures	海外	社内資料	評価資料
3.2.P.4.3	Validation of Analytical Procedures	海外	社内資料	評価資料
3.2.P.4.4	Justification of Specifications	海外	社内資料	評価資料
3.2.P.4.5	Excipients of Human or Animal Origin	海外	社内資料	評価資料
3.2.P.4.6	Novel Excipients	海外	社内資料	評価資料
3.2.P.5 製剤の管理				
3.2.P.5.1	Specification	海外	社内資料	評価資料
3.2.P.5.2	Analytical Procedures	海外	社内資料	評価資料
3.2.P.5.3	Validation of Analytical Procedures	海外	社内資料	評価資料
3.2.P.5.4	Batch Analyses	海外	社内資料	評価資料
3.2.P.5.5	Characterisation of Impurities	海外	社内資料	評価資料
3.2.P.5.6	Justification of Specifications	海外	社内資料	評価資料
3.2.P.6 標準品又は標準物質				
3.2.P.6	Reference Standards or Materials	海外	社内資料	評価資料
3.2.P.7 容器及び施栓系				
3.2.P.7	Container Closure System	海外	社内資料	評価資料

1　　第3 部（モジュール3）：品質に関する文書

3.2.P 製剤

資料番号	表題	国内/海外	社内資料/公表論文	評価資料/参考資料
3.2.P.8 安定性				
3.2.P.8.1	Stability Summary and Conclusion	海外	社内資料	評価資料
3.2.P.8.2	Post-Approval Stability Protocol and Stability Commitment	海外	社内資料	評価資料
3.2.P.8.3	Stability Data	海外	社内資料	評価資料

1　　第3 部（モジュール3）：品質に関する文書

3.2.A その他

資料番号	表題	国内/海外	社内資料/公表論文	評価資料/参考資料
3.2.A.1	Facilities and Equipment	海外	社内資料	評価資料
3.2.A.2	Adventitious Agents Safety Evaluation	海外	社内資料	評価資料
3.2.A.3	Novel Excipients	海外	社内資料	評価資料

3.2.R 各極の要求資料：該当なし

3.3 参考文献：該当なし

2　　第4 部（モジュール4）：非臨床試験報告書

4.2.1 薬理試験

資料番号	試験番号	表題	国内/海外	社内資料/公表論文	評価資料/参考資料
4.2.1.1 効力を裏付ける試験					
4.2.1.1-1	18XTPH-001	Isothermal Titration Calorimetry: C3 and C3b	海外	社内資料	評価資料
4.2.1.1-2	19CFPH-001	APL-2 and APL-9 Inhibition of Alternative and Classical Pathway Complement Activation	海外	社内資料	評価資料
4.2.1.2 副次的薬理試験：該当なし					
4.2.1.3 安全性薬理試験					
4.2.1.3-1	13ZTX-001	In Vitro Effect of APL-2 and PEG40 on hERG Current (I_{Kr}) Expressed in Human Embryonic Kidney (HEK) Cells	海外	社内資料	評価資料
4.2.1.3-2	13CATX005	A Cardiovascular and Respiratory Safety Pharmacology Assessment of APL-2 Given by Subcutaneous Injection to Telemetered Cynomolgus Monkeys	海外	社内資料	評価資料
4.2.1.4 薬力学的薬物相互作用試験：該当なし					

2　　第4 部（モジュール4）：非臨床試験報告書

4.2.2 薬物動態試験

資料番号	試験番号	表題	国内/海外	社内資料/公表論文	評価資料/参考資料
4.2.2.1 分析法及びバリデーション報告書					
4.2.2.1-1	ARAPL2C	Method Validation Report for the Determination of APL-2 in Rabbit Serum Using LC-MS/MS	海外	社内資料	評価資料
4.2.2.1-2	BPAPL2C	BIOANALYTICAL PROCEDURE FOR THE DETERMINATION OF APL-2 IN RABBIT SERUM USING LC-MS/MS	海外	社内資料	参考資料
4.2.2.1-3	BPAPL-2A	BIOANALYTICAL PROCEDURE FOR THE DETERMINATION OF APL-2 IN MONKEY SERUM USING LC-MS/MS	海外	社内資料	参考資料
4.2.2.1-4	ARAPL2D	Method Validation Report for the Determination of APL-2 in Cynomolgus Monkey Serum Using LC-MS/MS	海外	社内資料	評価資料
4.2.2.1-5	BPAPL2D	BIOANALYTCAL PROCEDURE FOR THE DETERMINATION OF APL-2 IN CYNOMOLGUS MONKEY SERUM USING LC-MS/MS	海外	社内資料	参考資料
4.2.2.1-6	8378-758	Determination of APL-2 Concentration in Monkey Milk using LC-MS/MS	海外	社内資料	評価資料
4.2.2.1-7	1944-014-A-02	DETERMINATION OF APL-2 IN 5% DEXTROSE DOSE FORMULATIONS BY HPLC/UV	海外	社内資料	評価資料
4.2.2.1-8	1944-014	VALIDATION OF AN HPLC-UV ASSAY FOR APL-2 IN 5% DEXTROSE	海外	社内資料	評価資料
4.2.2.1-9	1944-033-A-04	DETERMINATION OF APL-2 AT LOW CONCENTRATIONS IN 5% DEXTROSE DOSE FORMULATIONS BY HPLC/UV	海外	社内資料	評価資料
4.2.2.1-10	1944-033	VALIDATION OF AN HPLC-UV ASSAY FOR APL-2 AT LOW CONCENTRATIONS IN 5% DEXTROSE	海外	社内資料	評価資料

2　　第4 部（モジュール4）：非臨床試験報告書

4.2.2 薬物動態試験

資料番号	試験番号	表題	国内/海外	社内資料/公表論文	評価資料/参考資料
4.2.2.1-11	APL-C0001-GTM0001.01	Reversed-Phase HPLC Method for Determining Identity, Assay, and Purity of APL-2 in Drug Substance and Drug Product	海外	社内資料	評価資料
4.2.2.1-12	APL-C0001-GTM0001.02	Reversed-Phase HPLC Method for Determining Identity, Assay (Concentration), and Purity of APL-2 in Drug Substance and Aqueous Drug Product	海外	社内資料	評価資料
4.2.2.1-13	APL-C0001-GTM0001.04	Reversed-Phase HPLC Method for Determining Identity, Concentration, Content, and Purity of APL-2 in Drug Substance, Drug Product, and Drug Solutions	海外	社内資料	評価資料
4.2.2.1-14	APL-C0001-GTM0001.05	Reversed-Phase HPLC Method for Determining Identity, Content, and Impurities of APL-2 in Drug Substance, Drug Product and Drug Solutions	海外	社内資料	評価資料
4.2.2.1-15	APL-C0001-GTM0001.07	Reversed-Phase HPLC Method for Determining Identity, Content, and Impurities of APL-2 in Drug Substance, Drug Product and Drug Solutions	海外	社内資料	評価資料
4.2.2.1-16	APL-C0001 -GMR0001.00	Phase 1 Validation of RP-HPLC Method APL-C000l-GTM000l for Identity, Concentration, and Purity Analysis of APL-2	海外	社内資料	評価資料
4.2.2.1-17	APL-C0001-GTM0011.00	Reversed-Phase HPLC Method for Determining Identity, Content (Concentration) and %Purity of APL-2 API and APL-2 Drug Product in ABSorb Vehicle	海外	社内資料	評価資料
4.2.2.1-18	APL-C0001-GTM0011.06	Reversed-Phase HPLC Method for Determining Identity, Assay and %Purity of APL-2 API and APL-2 Drug Product in ABSorb Vehicle	海外	社内資料	評価資料
4.2.2.1-19	APL-C0001-GMR0134.00	Phase 1Validation of RP-HPLC Test Method APL-C0001-GTM0011 for Determining Identity, Content (Concentration), %Purity, and Percentage Individual and Total Impurities of APL-2 in ABSorb Vehicle	海外	社内資料	評価資料
4.2.2.1-20	APL-C0001-GMR0134.01	Validation of RP-HPLC Test Method APL-C000l-GTM0011 for Determining Identity, Content (Concentration), %Purity, and Percentage Individual and Total Impurities of APL-2 in ABSorb Vehicle	海外	社内資料	評価資料

2　　第4 部（モジュール4）：非臨床試験報告書

4.2.2 薬物動態試験

資料番号	試験番号	表題	国内/海外	社内資料/公表論文	評価資料/参考資料
4.2.2.1-21	AL-PMP-0005	N-acylurea Impurity Method Procedure	海外	社内資料	評価資料
4.2.2.1-22	AF62SZ.GTCHEM.BTL	Validation of an APL-2 Analytical Method Using HPLC	海外	社内資料	評価資料
4.2.2.1-23	AF67HP.GTCHEM.BTL	Validation of an APi1603 Analytical Method Using HPLC	海外	社内資料	評価資料
4.2.2.2 吸収					
4.2.2.2-1	16CATX-003	Pharmacokinetics and Pharmacodynamics of APL-2 Following Two Intermittent 1-Hour Intravenous Infusions in Female Cynomolgus Monkeys	海外	社内資料	評価資料
4.2.2.2-2	17MTX-001	Pharmacokinetics, Excretion, and Tissue Distribution of Radioactivity in Male Cynomolgus Monkeys Administered a Single Subcutaneous or Intravitreal Dose of [^{3}H]APL-2	海外	社内資料	評価資料
4.2.2.2-3	19CAPK-001	An assessment of the pharmacokinetics of Apl-2 following a Single Subcutaneous Dose Administration to Male Cynomolgus Monkeys	海外	社内資料	評価資料
4.2.2.2-4	13APK-001	Dosing of APL-2 via Intravenous and Subcutaneous Administration in Female Cynomolgus Monkeys Followed by Serum Sample Collection for Analysis by the Sponsor	海外	社内資料	評価資料
4.2.2.3 分布：該当なし					
4.2.2.4 代謝					
4.2.2.4-1	17COTX-003	Evaluation of Inhibitory Potential of APL-2 towards Human Hepatic Microsomal Cytochrome P450 Enzymes	海外	社内資料	評価資料

2　　第4 部（モジュール4）：非臨床試験報告書

4.2.2 薬物動態試験

資料番号	試験番号	表題	国内/海外	社内資料/公表論文	評価資料/参考資料
4.2.2.4-2	17COTX-001	Evaluation of Cytochrome P450 Induction Following Exposure of Primary Cultures of Human Hepatocytes to APL-2	海外	社内資料	評価資料
4.2.2.4-3	17COTX-002	Evaluation of APL-2 as a Substrate and Inhibitor of a Panel of Human Drug Transporters	海外	社内資料	評価資料
4.2.2.5 排泄：該当なし					
4.2.2.6 薬物動態学的薬物相互作用（非臨床）：該当なし					
4.2.2.7 その他の薬物動態試験：該当なし					

2　　第4 部（モジュール4）：非臨床試験報告書

4.2.3 毒性試験

資料番号	試験番号	表題	国内/海外	社内資料/公表論文	評価資料/参考資料
4.2.3.1 単回投与毒性試験：該当なし					
4.2.3.2 反復投与毒性試験					
4.2.3.2-1	13CATX001	A 7-day Pilot Repeat Dose Toxicity Study of APL-2 by Subcutaneous Injection in New Zealand White Rabbits	海外	社内資料	参考資料
4.2.3.2-2	13CATX003	A 28-day Repeat Dose Toxicity Study of APL-2 by Subcutaneous Injection in New Zealand White Rabbits with a 28-day Recovery Period	海外	社内資料	評価資料
4.2.3.2-3	14CATX001	A 28-day Repeat Dose Toxicity Study of APL-2 by Subcutaneous or Intravenous Injection in New Zealand White Rabbits	海外	社内資料	評価資料
4.2.3.2-4	15CATX-003	A 6-Month Repeat Dose Toxicity Study of APL-2 by Subcutaneous Injection in New Zealand White Rabbits	海外	社内資料	評価資料
4.2.3.2-5	13CATX002	A 7-Day Pilot Repeat Dose Toxicity Study of APL-2 by Subcutaneous Injection in Cynomolgus Monkeys	海外	社内資料	参考資料
4.2.3.2-6	13CATX004	A 28-day Repeat Dose Toxicity Study of APL-2 by Subcutaneous Injection in Cynomolgus Monkeys with a 28-day Recovery Period	海外	社内資料	評価資料
4.2.3.2-7	14CATX002	A 28-day Repeat Dose Toxicity Study of APL-2 by Subcutaneous or Intravenous Injection in Cynomolgus Monkeys	海外	社内資料	評価資料
4.2.3.2-8	14CATX-005	A 28-day Repeat Dose Safety/Toxicity Study of APL-2 by Subcutaneous Injection in Cynomolgus Monkeys	海外	社内資料	評価資料
4.2.3.2-9	19CATX-003	A 28-Day Subcutaneous Injection Toxicity Study Comparing Heat-Degraded and Non-Degraded Pegcetacoplan Drug Product in the Cynomolgus Monkey	海外	社内資料	評価資料
4.2.3.2-10	15CATX-004	A 9-month Repeat Dose Toxicity Study of APL-2 by Subcutaneous Injection in Cynomolgus Monkeys with a 13-week Interim Necropsy	海外	社内資料	評価資料
4.2.3.3 遺伝毒性試験					

2　　第4 部（モジュール4）：非臨床試験報告書

4.2.3 毒性試験

資料番号	試験番号	表題	国内/海外	社内資料/公表論文	評価資料/参考資料
4.2.3.3.1 *In Vitro* 試験					
4.2.3.3.1-1	13BTX-001	*In Vitro* Bacterial Reverse Mutation Assay on APL-2 and PEG40	海外	社内資料	評価資料
4.2.3.3.1-2	14BTX-001	Bacterial Reverse Mutation Assay	海外	社内資料	評価資料
4.2.3.3.1-3	19BTX-002	Bacterial Reverse Mutation Assay with APL-2 Acetate	海外	社内資料	評価資料
4.2.3.3.1-4	19BTX-001	Bacterial Reverse Mutation Assay with APL-2	海外	社内資料	評価資料
4.2.3.3.1-5	19BTX-003	Bacterial Reverse Mutation Assay with APL-1-AEEAc-Lys-NH_2 Trifluoroacetate	海外	社内資料	評価資料
4.2.3.3.1-6	13BTX-002	*In Vitro* Mammalian Cell Micronucleus Assay in TK6 Cells	海外	社内資料	評価資料
4.2.3.3.2 *In Vivo* 試験					
4.2.3.3.2-1	13BTX-003	*In Vivo* Micronucleus Assay in Mice with PEG40 and APL-2	海外	社内資料	評価資料
4.2.3.4 がん原性試験：該当なし					
4.2.3.4.1 長期がん原性試験：該当なし					
4.2.3.4.2 短期又は中期がん原性試験：該当なし					
4.2.3.4.3 その他の試験：該当なし					
4.2.3.5 生殖発生毒性試験					
4.2.3.5.1 受胎能及び着床までの初期胚発生に関する試験：該当なし					
4.2.3.5.2 胚・胎児発生に関する試験					
4.2.3.5.2-1	15MTX-001	APL-2: A Pilot Prenatal Developmental Toxicity Study in Rats with a Serum Level Evaluation	海外	社内資料	参考資料

2　　第4 部（モジュール4）：非臨床試験報告書

4.2.3 毒性試験

資料番号	試験番号	表題	国内/海外	社内資料/公表論文	評価資料/参考資料
4.2.3.5.2-2	15MTX-002	APL-2: A Pilot Prenatal Developmental Toxicity Study in New Zealand White Rabbits with a Serum Level Evaluation	海外	社内資料	参考資料
4.2.3.5.2-3	17CATX-001	A Pilot Embryo-Fetal Development Study of APL-2 by Daily Subcutaneous Injection in Pregnant Cynomolgus Monkeys	海外	社内資料	参考資料
4.2.3.5.3 出生前及び出生後の発生並びに母体の機能に関する試験					
4.2.3.5.3-1	18CATX-001	Enhanced Pre-Postnatal Toxicity of APL-2 Administered by Daily Subcutaneous Injection in Pregnant Cynomolgus Monkeys with 6-Month Postnatal Evaluation	海外	社内資料	評価資料
4.2.3.5.4 新生児を用いた試験：該当なし					
4.2.3.6 局所刺激性試験：該当なし					
4.2.3.7 その他の毒性試験：該当なし					
4.2.3.7.1 抗原性試験：該当なし					
4.2.3.7.2 免疫毒性試験：該当なし					
4.2.3.7.3 毒性発現の機序に関する試験：該当なし					
4.2.3.7.4 依存性試験：該当なし					
4.2.3.7.5 代謝物の毒性試験：該当なし					
4.2.3.7.6 不純物の毒性試験：該当なし					
4.2.3.7.7 その他の試験：該当なし					

2　　第4 部（モジュール4）：非臨床試験報告書

4.3 参考文献

資料番号	表題/著者/掲載誌
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4.3-2	Chellman GJ, Makori N, Martin PL et al. Developmental and reproductive toxicity studies in nonhuman primates. *Birth Defects Res.(Part B)* 2009; 86: 446-462.
4.3-3	CHMP Safety Working Party of the European Medicinal Agency. (2012). EMA's pediatric committee regarding the use of PEGylated drug products in the pediatric population intended for long-term treatment. November 16, 2012. EMA/CHMP/SWP/647258/2012.
4.3-4	Dunkelberger JR, Song. Complement and its role in innate and adaptive immune responses. *Cell Res.* 2010, 20(1): 34-50.
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4.3-9	Martin PL, Breslin W, Rocca M, et al. Considerations in assessing the developmental and reproductive toxicity of pharmaceuticals. *Birth Defects Res. (Part B)* 2009; 86: 176-203.
4.3-10	Regal JF, Gilbert JS, Bunwick RM. The complement system and adverse pregnancy outcomes. Mol. Immunol. 2015; 67(1):56-70.
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4.3-15	Schellekens H, Hennink WE, Brinks V. The immunogenicity of polyethylene glycol:facts and fiction. *Pharm. Res.* 2013, 30:1729-1734.
4.3-16	Trouw LA, Daha MR. Role of complement in innate immunity and host defense. *Immunol Lett.* 2011, 138(1):35-37.
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2　　第4 部（モジュール4）：非臨床試験報告書

4.3 参考文献

資料番号	表題/著者/掲載誌
4.3-18	Xu H, Chen M.Targeting the complement system for the management of retinal inflammatory and degenerative diseases. *Eur J Pharmacol.* 2016;787:94-104. doi: 10.1016/j.ejphar.2016.03.001
4.3-19	Zhang R, Liu Q, Li T, et al. Role of the complement system in the tumor microenvironment. *Cancer Cell Int* . 2019;19:300.

3　　第5 部（モジュール5）：臨床試験報告書

5.2 臨床試験一覧表

資料番号	表題	国内/海外	社内資料/公表論文	評価資料/参考資料	申請電子データの有無
5.2	臨床試験一覧表	―	社内資料	―	無

3　　第5 部（モジュール5）：臨床試験報告書

5.3 試験報告書及び関連情報

資料番号	試験番号	表題	国内/海外	社内資料/公表論文	評価資料/参考資料	申請電子データの有無
5.3.1 生物薬剤学試験報告書						
5.3.1.1 バイオアベイラビリティ（BA）試験報告書：該当なし						
5.3.1.2 比較 BA 試験及び生物学的同等性（BE）試験報告書：該当なし						
5.3.1.3 *In Vitro-In Vivo* の関連を検討した試験報告書：該当なし						
5.3.1.4 生物学的及び理化学的分析法検討報告書						
5.3.1.4.1	VAL075	Validation of an Analytical Method for Determination of APL-2 in Human Serum by LC/MS/MS	海外	社内資料	参考資料	無
5.3.1.4.2	STAB056	Partial Validation of an LA/MA/MA Method for the Determination of APL-2 in Human Serum (Including LTS for UH-SQCDi and H-SQCDi)	海外	社内資料	参考資料	無
5.3.1.4.3-1	BIO.VR.0210-1989 01~03	Validation of an LC-MS/MS Assay for Determination of APL-2 in Human Serum	海外	社内資料	参考資料	無
5.3.1.4.3-2	BIO.VR.0210-1989.04	Validation of an LC-MS/MS Assay for Determination of APL-2 in Human Serum: Validation Report Amendment	海外	社内資料	参考資料	無
5.3.1.4.3-3	BIO.VR.0210-1989.05	Validation of an LC-MS/MS Assay for Determination of APL-2 in Human Serum: Validation Report Amendment	海外	社内資料	参考資料	無
5.3.1.4.4-1	ARAPL2F_MV Report (31222)-QCV04-QAV01	Method Validation Report for the Determination of APL-2 in Human Serum Using LC-MS/MS	海外	社内資料	参考資料	無
5.3.1.4.4-2	ARAPL2F_A1_MV Report (32131)-QCV03-QAV01	Method Validation Report for the Determination of APL-2 in Human Serum Using LC-MS/MS	海外	社内資料	参考資料	無
5.3.1.4.4-3	ARAPL2F.A2_MV Report (34636)-QCV03-QAV01	Method Validation Report for the Determination of APL-2 in Human Serum Using LC-MS/MS	海外	社内資料	参考資料	無
5.3.1.4.5-1	ARAPL2K_MV Report (32411)-QCV03-QAV01	Method Validation Report for the Determination of APL-2 In Human Serum (High Range) Using LC-MS/MS	海外	社内資料	参考資料	無
5.3.1.4.5-2	ARAPL2K.A1 MV Report (32411)-QCV02-QAV01	Method Validation Report for the Determination of APL-2 In Human Serum (High Range) Using LC-MS/MS	海外	社内資料	参考資料	無

3　　第5 部（モジュール5）：臨床試験報告書

5.3 試験報告書及び関連情報

資料番号	試験番号	表題	国内/海外	社内資料/公表論文	評価資料/参考資料	申請電子データの有無
5.3.1.4.6	AV21-190 (AV20-APL2-02)	HPLC/MS/MS Assay Validation for the Determination of APL-2 from Human Serum High Range	海外	社内資料	参考資料	無
5.3.1.4.7-1	BIO.VR.0210-2629.01	Cross-Validation of LC-MS/MS Assays for the Determination of APL-2 in Human Serum	海外	社内資料	参考資料	無
5.3.1.4.7-2	BIO.VR.0210-2629.02	Cross-Validation of LC-MS/MS Assays for the Determination of APL-2 in Human Serum	海外	社内資料	参考資料	無
5.3.1.4.8	AR5556	Qualitative Determination of Antibodies to APL-2 in Human Serum Using a Direct Enzyme Linked Immunosorbent Assay (ELISA)	海外	社内資料	参考資料	無
5.3.1.4.9-1	BAL-17-143-048-REP	Validation of a Direct Binding Electrochemiluminescent Assay for the Detection of Antibodies Against APL-2 in Human Serum	海外	社内資料	参考資料	無
5.3.1.4.9-2	BAL-17-143-048.01-REP	Addendum: Validation of a Direct Binding Electrochemiluminescent Assay for the Detection of Antibodies Against APL-2 in Human Serum	海外	社内資料	参考資料	無
5.3.1.4.9-3	BAL-17-143-048.02-REP	Addendum: Validation of a Direct Binding Electrochemiluminescent Assay for the Detection of Antibodies Against APL-2 in Human Serum	海外	社内資料	参考資料	無
5.3.1.4.9-4	BAL-17-143-048.03-REP	Addendum: Validation of a Direct Binding Electrochemiluminescent Assay for the Detection of Antibodies Against APL-2 in Human Serum	海外	社内資料	参考資料	無
5.3.1.4.9-5	BAL-17-143-048.04-REP	Addendum: Validation of a Direct Binding Electrochemiluminescent Assay for the Detection of Antibodies Against APL-2 in Human Serum	海外	社内資料	参考資料	無
5.3.1.4.10	190339VMES_APWM	Validation of an Electrochemiluminescence Method for the Detection of anti-APL-2 Antibodies in Human Serum	海外	社内資料	参考資料	無
5.3.1.4.11	BAL-21-143-121	Development and Optimization of an Electrochemiluminescent Assay for the Detection of Antibodies Against the Pegcetacoplan Peptide in Human Serum	海外	社内資料	参考資料	無
5.3.1.4.12-1	BAL-17-143-050-REP	Validation of a Direct Binding ELISA for the Detection of Antibodies Against PEG in Human Serum	海外	社内資料	参考資料	無

3　　第5 部（モジュール5）：臨床試験報告書

5.3 試験報告書及び関連情報

資料番号	試験番号	表題	国内/海外	社内資料/公表論文	評価資料/参考資料	申請電子データの有無
5.3.1.4.12-2	BAL-17-143-050.01-REP	Validation of a Direct Binding ELISA for the Detection of Antibodies Against PEG in Human Serum	海外	社内資料	参考資料	無
5.3.1.4.13	181686VRDW_APWM_R1	Validation of a Bead-Based Sandwich ELISA for the Detection of anti-PEG Antibodies in Human Serum	海外	社内資料	参考資料	無
5.3.1.4.14	BAL-17-143-027-REP	Validation of a Competitive Ligand Binding Assay that Employs Electrochemiluminescence to Detect Neutralizing Antibodies against APL-2 in Human Serum	海外	社内資料	参考資料	無
5.3.1.4.15	BAL-21-143-122	Development and Optimization of a Pegcetacoplan Peptide Neutralizing Antibody Assay in Human Serum	海外	社内資料	参考資料	無
5.3.1.4.16-1	c3-validation-rpt-dec-20[redacted]	Validation Report for the BNll Complement C3 Assay	海外	社内資料	参考資料	無
5.3.1.4.16-2	c3-validation-rpt-dec-20[redacted]	Complement C3 in Plasma by Nephelometry on Siemens BNII	海外	社内資料	参考資料	無
5.3.1.4.16-3	c3-amended-validation-rpt-jul-20[redacted]	Complement C3 in Serum and Plasma by Nephelometry on Siemens BNII	海外	社内資料	参考資料	無
5.3.1.4.16-4	GL-LA-08-SA	Complement C3 in Serum and Plasma by Nephelometry on Siemens BNII	海外	社内資料	参考資料	無
5.3.1.4.17	CL-VAL.002.001	SPAplus Verification Report	海外	社内資料	参考資料	無
5.3.1.4.18	CVL062708	Report of Validation of the CH50 Hemolytic Assay	海外	社内資料	参考資料	無
5.3.1.4.19	CVL071009	Report of Validation of the AH50, Alternative Hemolytic Function Assay	海外	社内資料	参考資料	無
5.3.1.4.20	MLM-VAL-1619	Validation of the Quantitative Analysis of Complement CH50 in Serum using the MicroVue Complement CH50 EIA Enzyme Immunoassay from Quidel	海外	社内資料	参考資料	無

3　　第5 部（モジュール5）：臨床試験報告書

5.3 試験報告書及び関連情報

資料番号	試験番号	表題	国内/海外	社内資料/公表論文	評価資料/参考資料	申請電子データの有無
5.3.1.4.21	MLM-VAL-1805	Validation of the Quantitative Analysis of Complement Factor C3c in Human Serum using Cobas 6000	海外	社内資料	参考資料	無
5.3.1.4.22	VAL080	Fit-for-Purpose Validation of an Assay to determine complement Alternative Pathway (AH50) in Human Plasma and Serum	海外	社内資料	参考資料	無
5.3.1.4.23	573697	PNH Panel-2 (CD59, CD235a, C3d)	海外	社内資料	参考資料	無
5.3.1.4.24	573702	PNH Panel-3 (CD14, CD15, CD24, CD45, CD64, FLAER)	海外	社内資料	参考資料	無
5.3.1.4.25	960854	Client-1470 PNH Panel-3 (CD14, CD15, CD24, CD45, CD64, FLAER)	海外	社内資料	参考資料	無
5.3.1.4.26	apl2-cp0713-1-ba-pk-rpt	Analytical Phase Report: A RANDOMIZED, DOUBLE-BLIND, PLACEBO-CONTROLED, SINGLE ASCENDING DOSE STUDY TO ASSESS THE SAFETY, TOLERABILITY, PHARMACOKINETICS AND PHARMACODYNAMICS OF SUBCUTANEOUS APL-2 IN HEALTHY ADULT SUBJECTS APL-CP0713-1	海外	社内資料	参考資料	無
5.3.1.4.27	apl2-cp1014-bioanalytical-pk-report (DAG)	Analysis Phase Report: A PHASE 1, DOUBLE-BLIND, RANDOMIZED, MULTIPLE ASCENDING APL-2 DOSE STUDY IN HEAL THY VOLUNTEERS APL-CP1014	海外	社内資料	参考資料	無
5.3.1.4.28	apl2-cp-hv-401-ba-pk-rpt (EAS)	Analytical Phase PK Report: PHASE 1, DOUBLE-BLIND, RANDOMIZED, PLACEBO-CONTROLLED, SINGLE ASCENDING DOSE STUDY OF INTRAVENOUS APL-2 IN HEALTHY VOLUNTEERS APL2-CP-HV-401	海外	社内資料	参考資料	無
5.3.1.4.29	apl2-101-fbe	LCMS Bioanalytical PK Report: PHASE I, DOUBLE BLIND, RANDOMIZED STUDY OF DAILY, TWICE-WEEKLY AND ONCE-WEEKLY APL-2 IN HEALTHY VOLUNTEERS APL2-101	海外	社内資料	参考資料	無
5.3.1.4.30	apl2-cp-pv-205-ba-pk-rpt	LCMS Bioanalytical Phase PK Report: A PHASE I, SINGLE DOSE, OPEN-LABEL STUDY TO EVALUATE THE EFFECT OF RENAL IMPAIRMENT ON THE PHARMACOKINETICS OF APL-2 APL2-CP-PV-205	海外	社内資料	参考資料	無
5.3.1.4.31	apl2-202-analyt-rpt (GAL)	Analytical Report: A PHASE IIA, OPEN LABEL, MULTIPLE DOSE STUDY TO ASSESS THE SAFETY, EFFICACY AND PHARMACOKINETICS OF SUBCUTANEOUSLY ADMINISTERED APL-2 IN SUBJECTS WITH PAROXYSMAL NOCTURNAL HEMOGLOBINURIA (PNH) APL2-202	海外	社内資料	参考資料	無

3　　第5 部（モジュール5）：臨床試験報告書

5.3 試験報告書及び関連情報

資料番号	試験番号	表題	国内/海外	社内資料/公表論文	評価資料/参考資料	申請電子データの有無
5.3.1.4.32	apl2-cp-pnh-204-analyt-rpt (DBY)	Analytical Report: A PHASE IB, OPEN LABEL, MULTIPLE ASCENDING DOSE, PILOT STUDY TO ASSESS THE SAFETY, PRELIMINARY EFFICACY AND PHARMACOKINETICS OF SUBCUTANEOUSLY ADMINISTERED APL-2 IN SUBJECTS WITH PAROXYSMAL NOCTURNAL HEMOGLOBINURIA (PNH) - PADDOCK- APL2-CP-PNH-204	海外	社内資料	参考資料	無
5.3.1.4.33-1	SAC-20[redacted]-037 (QCV05-QAV01)	Bioanalytical Report for the Analysis of APL-2 in Human Serum APL-CP0514	海外	社内資料	参考資料	無
5.3.1.4.33-2	SAC-20[redacted]-037	Chromatogram Report for the Analysis of APL-2 in Human Serum APL-CP0514	海外	社内資料	参考資料	無
5.3.1.4.34-1	SAC-20[redacted]-016 (QCV04-QAV01)	Bioanalytical Report for the Analysis of APL-2 in Human Serum APL2-102	海外	社内資料	参考資料	無
5.3.1.4.34-2	SAC-20[redacted]-016	Chromatogram Report for the Analysis of APL-2 in Human Serum APL2-102	海外	社内資料	参考資料	無
5.3.1.4.35-1	BIO.SR.0277-2221.01 (Interim Report)	Determination of APL-2 in Human Serum by LC-MS/MS Interim Sample Analysis Report APL2-302	海外	社内資料	参考資料	無
5.3.1.4.36	APL2-308 - AD21-1248 - [redacted]20[redacted]	Bioanalytical Sample Analysis for the Determination of APL-2 in Human Serum by HPLC/MS/MS	海外	社内資料	参考資料	無
5.3.1.4.37	6322	Qualitative Determination of Antibodies to APL-2 in Human Serum Using a Direct Enzyme Linked Immunosorbent Assay (ELISA) APL-CP1014	海外	社内資料	参考資料	無
5.3.1.4.38	6637	Qualitative Determination of Antibodies to APL-2 in Human Serum Using a Direct Enzyme Linked Immunosorbent Assay (ELISA) APL2-CP-HV-401	海外	社内資料	参考資料	無
5.3.1.4.39	5810	Qualitative Determination of Antibodies to APL-2 in Human Serum Using a Direct Enzyme Linked Immunosorbent Assay (ELISA) APL-CP0713-1	海外	社内資料	参考資料	無
5.3.1.4.40-1	BAL-19-143-073-REP	Detection of Anti-APL-2 Antibodies in Human Serum Samples from Clinical Trial APL2-101 Using a Validated Electrochemiluminescent Assay	海外	社内資料	参考資料	無

3　　第5 部（モジュール5）：臨床試験報告書

5.3 試験報告書及び関連情報

資料番号	試験番号	表題	国内/海外	社内資料/公表論文	評価資料/参考資料	申請電子データの有無
5.3.1.4.40-2	BAL-19-143-073.01-REP	Amendment for the Detection of Anti-APL-2 Antibodies in Human Serum Samples from Clinical Trial APL2-101 Using a Validated Electrochemiluminescent Assay	海外	社内資料	参考資料	無
5.3.1.4.41	AR-5805	Qualitative Determination of Antibodies to APL-2 In Human Serum Using a Direct Enzyme Linked lmmunosorbent Assay (ELISA) APL-CP0514	海外	社内資料	参考資料	無
5.3.1.4.42	BAL-17-143-033-REP	Detection of Anti-APL-2 Antibodies in Human Serum Samples from Clinical Trial APL2-CP-PV-205 Using a Validated Electrochemiluminescent Assay	海外	社内資料	参考資料	無
5.3.1.4.43-1	BAL-17-143-031-REP	Detection of Anti-APL-2 Antibodies in Human Serum Samples from Clinical Trial APL2-102 Using a Validated Electrochemiluminescent Assay	海外	社内資料	参考資料	無
5.3.1.4.43-2	BAL-17-143-031.01-REP	Detection of Anti-APL-2 Antibodies in Human Serum Samples from Clinical Trial APL2-102 Using a Validated Electrochemiluminescent Assay Amendment	海外	社内資料	参考資料	無
5.3.1.4.44	BAL-18-503-006-REP	Detection of Anti-APL-2 Antibodies in Human Serum Samples Using a Validated Electrochemiluminescent Assay APL2-302	海外	社内資料	参考資料	無
5.3.1.4.45	190703AMES_APWM	Immunogenicity Sample Analysis for the Detection of Anti-APL-2 Antibodies in Human Serum for Study APL2-202	海外	社内資料	参考資料	無
5.3.1.4.46	AR-6338	Qualitative Determination of Antibodies to APL-2 In Human Serum Using a Direct Enzyme Linked Immunosorbent Assay (ELISA) APL2-CP-PNH-204	海外	社内資料	参考資料	無
5.3.1.4.47	190697AMES_APWM	Immunogenicity Sample Analysis for the Detection of Anti-APL-2 Antibodies in Human Serum for Study APL2-CP-PNH-204	海外	社内資料	参考資料	無
5.3.1.4.48	BAL-19-143-074-REP	A Direct Binding ELISA for the Detection of Antibodies Against PEG in Human Serum APL2-101	海外	社内資料	参考資料	無
5.3.1.4.49	BAL-17-143-034-REP	A Direct Binding ELISA for the Detection of Antibodies Against PEG in Human Serum APL2-CP-PV-205	海外	社内資料	参考資料	無
5.3.1.4.50	BAL-17-143-032-REP	A Direct Binding ELISA for the Detection of Antibodies Against PEG in Human Serum APL2-102	海外	社内資料	参考資料	無

3　　第5 部（モジュール5）：臨床試験報告書

5.3 試験報告書及び関連情報

資料番号	試験番号	表題	国内/海外	社内資料/公表論文	評価資料/参考資料	申請電子データの有無
5.3.1.4.51	BAL-18-503-010	A Direct Binding ELISA for the Detection of Antibodies Against PEG in Human Serum APL2-302	海外	社内資料	参考資料	無
5.3.1.4.52	190704AMES_APWM	Immunogenicity Sample Analysis for the Detection of Anti-PEG Antibodies in Human Serum for Study APL2-202	海外	社内資料	参考資料	無
5.3.1.4.53	190706AMES_APWM	Immunogenicity Sample Analysis for the Detection of Anti-PEG Antibodies in Human Serum for Study APL2-CP-PNH-204	海外	社内資料	参考資料	無
5.3.1.4.54	BAL-19-143-075-REP	An Electrochemiluminescent Assay for the Detection of Anti-APL-2 Neutralizing Antibodies in Human Serum Samples in Support of Apellis Study APL2-101.	海外	社内資料	参考資料	無
5.3.1.4.55	BAL-20-503-011-REP	An Electrochemiluminescent Assay for the Detection of Anti-APL-2 Neutralizing Antibodies in Human Serum Samples APL2-302	海外	社内資料	参考資料	無
5.3.1.4.56	BAL-20-503-011.01-REP	An Electrochemiluminescent Assay for the Detection of Anti-APL-2 Neutralizing Antibodies in Human Serum Samples Amendment APL2-302	海外	社内資料	参考資料	無
5.3.1.4.57	BAL-20-143-093-REP	An Electrochemiluminescent Assay for the Detection of Anti-APL-2 Neutralizing Antibodies in Human Serum Samples APL2-CP-PNH-204	海外	社内資料	参考資料	無
5.3.1.4.58	apl2-cp1014-dar-analy-phase-re	Analytical Phase Report: PHASE 1, DOUBLE-BLIND, RANDOMIZED, MULTIPLE ASCENDING APL-2 DOSE STUDY IN HEALTHY VOLUNTEERS	海外	社内資料	参考資料	無
5.3.1.4.59	apl2-cp-hv-401-comple-report	REPORT OF COMPLEMENT TESTS OF SPECIMENS FROM APELLIS PHARMACEUTICALS, INC STUDY NO. APL2-CP-HV-401	海外	社内資料	参考資料	無
5.3.1.4.60	apl2-cp0713-1-cba-analyti-phase-rpt	Analytical Phase Report: A RANDOMIZED, DOUBLE-BLIND, PLACEBO-CONTROLED, SINGLE ASCENDING DOSE STUDY TO ASSESS THE SAFETY, TOLERABILITY, PHARMACOKINETICS AND PHARMACODYNAMICS OF SUBCUTANEOUS APL-2 IN HEAL THY ADULT SUBJECTS APL-CP0713-1	海外	社内資料	参考資料	無
5.3.1.4.61	apl2-101-comp-rpt	REPORT OF COMPLEMENT TESTS ON SPECIMENS FROM APELLIS PHARMACEUTICALS, INC. PROTOCOL NO. APL2-101	海外	社内資料	参考資料	無

3　　第5 部（モジュール5）：臨床試験報告書

5.3 試験報告書及び関連情報

資料番号	試験番号	表題	国内/海外	社内資料/公表論文	評価資料/参考資料	申請電子データの有無
5.3.1.4.62	apl2-102-comp-rpt	REPORT OF COMPLEMENT TESTS OF SPECIMENS FROM APELLIS PHARMACEUTICALS, INC STUDY NO. APL2-102	海外	社内資料	参考資料	無
5.3.1.4.63	GL-LA-23-SA	Complement C3 APL2-302	海外	社内資料	参考資料	無
5.3.1.4.64	2017-004268-36	Exsera Biolabs: A Phase III, Randomized, Multi-Center, Open- Label, Active-Comparator Controlled Study to Evaluate the Efficacy and Safety of APL-2 in Patients with Paroxysmal Nocturnal Hemoglobinuria (PNH) APL2-302	海外	社内資料	参考資料	無
5.3.1.4.65	MLM-APL-APL202	Analysis of PD Samples from the Study APL2-202	海外	社内資料	参考資料	無
5.3.1.4.66	apl2-202-gak-ba-rpt	Analytical Report: A PHASE IIA, OPEN LABEL, MULTIPLE DOSE STUDY TO ASSESS THE SAFETY, EFFICACY AND PHARMACOKINETICS OF SUBCUTANEOUSLY ADMINISTERED APL-2 IN SUBJECTS WITH PAROXYSMAL NOCTURNAL HEMOGLOBINURIA (PNH) APL2-202	海外	社内資料	参考資料	無
5.3.1.4.67	apl2-cp-pnh-204-dcp-bioanaly-re	Analytical Report: A PHASE 18, OPEN LABEL, MULTIPLE ASCENDING DOSE, PILOT STUDY TO ASSESS THE SAFETY, PRELIMINARY EFFICACY AND PHARMACOKINETICS OF SUBCUTANEOUSLY ADMINISTERED APL-2 IN SUBJECTS WITH PAROXYSMAL NOCTURNAL HEMOGLOBINURIA (PNH). - PADDOCK APL2-CP-PNH-204	海外	社内資料	参考資料	無
5.3.1.4.68	9B5-6-25-7	Certificate of Analysis: Polyethylene Glycol (PEG) Monoclonal Clone 985-6-25-7	海外	社内資料	参考資料	無
5.3.1.4.69	CJ .OO4	Certificate of Analysis: APi1514 (APL-2) Reference Standard	海外	社内資料	参考資料	無
5.3.1.4.70	coa-1509253-ap4	Certificate of Analysis: Affinity Purified Polyclonal Antibody	海外	社内資料	参考資料	無
5.3.1.4.71	MPEG-40k	Certificate of Analysis: Methoxy Polyethylene Glycol, MW 40,000	海外	社内資料	参考資料	無
5.3.1.4.72	PG1-BN-40k	Certificate of Analysis: Methoxyl polyethylene glycol biotin, mPEG-Biotin, MW 40000	海外	社内資料	参考資料	無

3　　第5 部（モジュール5）：臨床試験報告書

5.3 試験報告書及び関連情報

資料番号	試験番号	表題	国内/海外	社内資料/公表論文	評価資料/参考資料	申請電子データの有無
5.3.1.4.73	PBSA-00	Certificate of Analysis: Multi-PEGylated BSA (PEGylated with 20kDa mPEG-SVA)	海外	社内資料	参考資料	無
5.3.2 ヒト生体試料を用いた薬物動態関連の試験報告書：該当なし						
5.3.2.1 血漿蛋白結合試験報告書：該当なし						
5.3.2.2 肝代謝及び薬物相互作用試験報告書：該当なし						
5.3.2.3 他のヒト生体試料を用いた試験報告書：該当なし						
5.3.3 臨床薬物動態（PK）試験報告書						
5.3.3.1 健康被験者における PK 及び初期忍容性試験報告書						
5.3.3.1.1	APL-CP1014	Phase I, Double-Blind, Randomized, Multiple Ascending Pegcetacoplan Dose Study in Healthy Volunteers	海外	社内資料	評価資料	有
5.3.3.1.2	APL2-CP-HV-401	Phase 1, Double-Blind, Randomized, Placebo-Controlled, Single Ascending Dose Study of Intravenous Pegcetacoplan in Healthy Volunteers	海外	社内資料	評価資料	有
5.3.3.1.3	APL-CP0713-1	A Randomized, Double-Blind, Placebo-Controlled, Single Ascending Dose Study to Assess the Safety, Tolerability, Pharmacokinetics and Pharmacodynamics of Subcutaneous Pegcetacoplan in Healthy Adult Subjects	海外	社内資料	評価資料	有
5.3.3.1.4	APL2-101	Phase 1, Double-Blind, Randomized Study of Daily, Twice-Weekly, and Once-Weekly Pegcetacoplan in Healthy Volunteers	海外	社内資料	評価資料	有
5.3.3.2 患者における PK 及び初期忍容性試験報告書						
5.3.3.2.1	APL-CP0514	An Open Label, Single and Multiple Ascending Dose Study to Assess the Safety, Tolerability, Pharmacokinetics and Pharmacodynamics of APL-2 as an Add-On to Standard of Care in Subjects with Paroxysmal Nocturnal Hemoglobinuria (PNH)	海外	社内資料	評価資料	有
5.3.3.3 内因性要因を検討した PK 試験報告書						
5.3.3.3.1	APL2-CP-PV-205	A Phase I, Single-Dose, Open-Label Study to Evaluate the Effect of Renal Impairment on the Pharmacokinetics of Pegcetacoplan	海外	社内資料	評価資料	有
5.3.3.3.2	APL2-102	Phase I, Double-Blind, Randomized, Placebo-Controlled, Single Ascending Dose Study of APL-2 in Healthy Japanese Volunteers	海外	社内資料	評価資料	有
5.3.3.4 外因性要因を検討した PK 試験報告書：該当なし						
5.3.3.5 ポピュレーション PK 試験報告書						
5.3.3.5.1	APL-EX20-CP-002	DEVELOPMENT OF A POPULATION PHARMACOKINETIC MODEL FOR PEGCETACOPLAN (APL-2) IN PHASE 1, 2, AND 3 STUDIES IN HEALTHY SUBJECTS AND PATIENTS WITH PAROXYSMAL NOCTURNAL HEMOGLOBINURIA	海外	社内資料	評価資料	有
5.3.4 臨床薬力学（PD）試験報告書：該当なし						

3　　第5 部（モジュール5）：臨床試験報告書

5.3 試験報告書及び関連情報

資料番号	試験番号	表題	国内/海外	社内資料/公表論文	評価資料/ 参考資料	申請電子データ の有無
5.3.4.1 健康被験者における PD 試験及び PK/PD 試験報告書：該当なし						
5.3.4.2 患者における PD 試験及び PK/PD 試験報告書：該当なし						
5.3.5 有効性及び安全性試験報告書						
5.3.5.1 申請する適応症に関する比較対照試験報告書						
5.3.5.1.1-1	APL2-302	A Phase 3, Randomized, Multicenter, Open-label, Active-comparator Controlled Study to Evaluate the Efficacy and Safety of Pegcetacoplan in Patients with Paroxysmal Nocturnal Hemoglobinuria (PNH) -Week 16 Analysis-	海外	社内資料	評価資料	有
5.3.5.1.1-2	APL2-302	A Phase 3, Randomized, Multicenter, Open-label, Active-comparator Controlled Study to Evaluate the Efficacy and Safety of Pegcetacoplan in Patients with Paroxysmal Nocturnal Hemoglobinuria (PNH) -Week 48 Analysis-	海外	社内資料	評価資料	有
5.3.5.1.1-3	APL2-302	A Phase 3, Randomized, Multicenter, Open-label, Active-comparator Controlled Study to Evaluate the Efficacy and Safety of Pegcetacoplan in Patients with Paroxysmal Nocturnal Hemoglobinuria (PNH) -Japanese Subpopulation Report up to Week 48-	海外	社内資料	評価資料	無
5.3.5.2 非対照試験報告書						
5.3.5.2.1	APL2-202	A Phase 2a, Open-Label, Multiple Dose Study to Assess the Safety, Efficacy, and Pharmacokinetics of Subcutaneously Administered APL-2 in Subjects with Paroxysmal Nocturnal Hemoglobinuria (PNH)	海外	社内資料	評価資料	有
5.3.5.2.2	APL2-CP-PNH-204	A Phase 1b, Open-label, Multiple Ascending Dose, Pilot Study to Assess the Safety, Preliminary Efficacy, and Pharmacokinetics of Subcutaneously Administered Pegcetacoplan in Subjects with Paroxysmal Nocturnal Hemoglobinuria (PNH)	海外	社内資料	評価資料	有
5.3.5.3 複数の試験成績を併せて解析した報告書						
5.3.5.3.1	APL-EX20-CP-004	QT/QTc Evaluation for Pegcetacoplan (APL-2): A Phase III, Randomized, Multi-Center, Open-Label, Active-Comparator Controlled Study to Evaluate the Efficacy and Safety of Pegcetacoplan (APL-2) in Patients with Paroxysmal Nocturnal Hemoglobinuria (PNH) Protocol No: APL2-302 Phase I, Double-Blind, Randomized Study of Daily, Twice-Weekly and Once-Weekly Pegcetacoplan (APL-2) in Healthy Volunteers Protocol No: APL2-101	―	社内資料	評価資料	無
5.3.5.3.2	APL-EX20-CP-003	POPULATION MODELING ANALYSIS REPORT DEVELOPMENT OF EXPOSURE-RESPONSE MODELS FOR HEMOGLOBIN AND LACTATE DEHYDROGENASE IN PATIENTS WITH PAROXYSMAL NOCTURNAL HEMOGLOBINURIA TREATED WITH PEGCETACOPLAN (APL-2)	海外	社内資料	評価資料	有
5.3.5.4 その他の臨床試験報告書						
5.3.5.4.1	APL2-308	A Phase 3, Randomized, Multicenter, Open-Label, Controlled Study to Evaluate the Efficacy and Safety of Pegcetacoplan in Patients with Paroxysmal Nocturnal Hemoglobinuria (PNH) (Short Title: PRINCE)	海外	社内資料	参考資料	無

3　　第5 部（モジュール5）：臨床試験報告書

5.3 試験報告書及び関連情報

資料番号	試験番号	表題	国内/海外	社内資料/公表論文	評価資料/ 参考資料	申請電子データ の有無
5.3.5.4.2	APL2-307	An Open-label, Nonrandomized, Multicenter Extension Study to Evaluate the Long-term Safety and Efficacy of Pegcetacoplan in the Treatment of Paroxysmal Nocturnal Hemoglobinuria (PNH)	海外	社内資料	参考資料	無
5.3.6 市販後の使用経験に関する報告書：該当なし						
5.3.7 患者データ一覧表及び症例記録						
5.3.7.2	－	副作用一覧表	－	社内資料	－	－
5.3.7.3	－	重篤な有害事象一覧表	－	社内資料	－	－
5.3.7.4	－	臨床検査値異常変動一覧表	－	社内資料	－	－

3　　第5 部（モジュール5）：臨床試験報告書

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3　　第5 部（モジュール5）：臨床試験報告書

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3　　第5 部（モジュール5）：臨床試験報告書

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