International Nonproprietary Names for Pharmaceutical Substances (INN)

RECOMMENDED International Nonproprietary Names: List 82

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 (1–1117) 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)

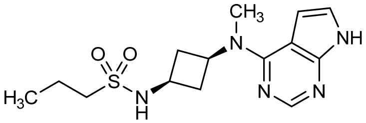
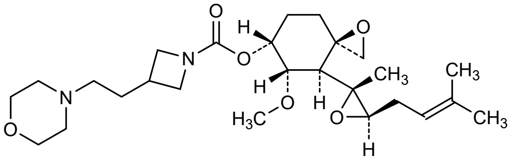
Dénominations communes internationales RECOMMANDÉES: Liste 82

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 82

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).

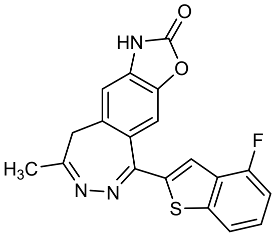
Latin, English, French, Spanish: *Recommended INN*	*Chemical name or description; Molecular formula; Graphic formula*
DCI Recommandée	*Nom chimique ou description; Formule brute; Formule développée*
DCI Recomendada	*Nombre químico o descripción; Fórmula molecular; Fórmula desarrollada*
abrocitinibum	
abrocitinib	*N*-{*cis*-3-[methyl(7*H*-pyrrolo[2,3-*d*]pyrimidin-4-yl)amino]cyclobutyl}propane-1-sulfonamide
abrocitinib	*N*-{*cis*-3-[méthyl(7*H*-pyrrolo[2,3-*d*]pyrimidin-4-yl)amino]cyclobutyl}propane-1-sulfonamide
abrocitinib	*N*-{*cis*-3-[metil(7*H*-pirrolo[2,3-*d*]pirimidin-4-il)amino]ciclobutil}propano-1-sulfonamida
	$C_{14}H_{21}N_5O_2S$ 
aclimostatum	
aclimostat	(3*R*,4*S*,5*S*,6*R*)-5-methoxy-4-[(2*R*,3*R*)-2-methyl-3-(3-methylbut-2-en-1-yl)oxiran-2-yl]-1-oxaspiro[2.5]octan-6-yl 3-[2-(morpholin-4-yl)ethyl]azetidine-1-carboxylate
aclimostat	3-[2-(morpholin-4-yl)éthyl]azétidine-1-carboxylate de (3*R*,4*S*,5*S*,6*R*)-5-méthoxy-4-[(2*R*,3*R*)-2-méthyl-3-(3-méthylbut-2-én-1-yl)oxiran-2-yl]-1-oxaspiro[2.5]octan-6-yle
aclimostat	3-[2-(morfolin-4-il)etil]azetidina-1-carboxilato de (3*R*,4*S*,5*S*,6*R*)-5-metoxi-4-[(2*R*,3*R*)-2-metil-3-(3-metilbut-2-en-1-il)oxiran-2-il]-1-oxaspiro[2.5]octan-6-ilo
	$C_{26}H_{42}N_2O_6$ 
adlinacogenum civaparvovecum #	
adlinacogene civaparvovec	a recombinant non-replicating adeno-associated virus type 2/6 (rAAV Rep2-Cap6) vector, which contains a promoter-less human coagulation factor IX (hF9, Factor IX or FIX) transgene cassette, encoding exons 2-8 and splice acceptor site sequence (SA) from hF9 exon 2, flanked by a sequence homologous to the zinc-finger nuclease (ZFN) cleavage site of the human albumin (hALB) intron 1

adlinacogène civaparvovec	vecteur viral adéno-associé de type 2/6 recombinant (rAAV Rep2-Cap6), non-répliquant, contenant la cassette avec le transgène du facteur de coagulation IX humain (hF9, Facteur IX, FIX) sans promoteur, codant pour les exons 2-8 et la séquence du site accepteur (SA) d'épissage de l'exon 2 de hF9, flanqué par une séquence homologue au site de clivage de la nucléase à doigts de zinc (ZFN) de l'intron 1 l'albumine humaine (hALB).
adlinacogén civaparvovec	un vector de virus adeno asociado tipo 2/6 recombinante (rAAV Rep2-Cap6), no replicativo, que contiene un casete con el transgen del factor de coagulación IX (hF9, Factor IX o FIX) humano sin promotor, que codifica para los exones 2-8 y la secuencia del sitio aceptor (SA) del splicing del exon 2 de hf9, flanqueado por una secuencia homóloga al sitio de rotura por la nuclease con dedos de zinc (ZFN) del intron 1 de la albúmina humana (hALB)

afizagabarum

afizagabar	5-(4-fluoro-1-benzothiophen-2-yl)-8-methyl-1,9-dihydro-2*H*-[1,3]oxazolo[4,5-*h*][2,3]benzodiazepin-2-one
afizagabar	5-(4-fluoro-1-benzothiophén-2-yl)-8-méthyl-1,9-dihydro-2*H*-[1,3]oxazolo[4,5-*h*][2,3]benzodiazépin-2-one
afizagabar	5-(4-fluoro-1-benzotiofen-2-il)-8-metil-1,9-dihidro-2*H*-[1,3]oxazolo[4,5-*h*][2,3]benzodiazepin-2-ona

$C_{19}H_{12}FN_3O_2S$



aldaferminum #

aldafermin	[Phe^{5}>Met,Ser^{6}>Arg,Ala^{8}>Ser,Gly^{9}>Ser,His^{11}>Leu] fibroblast growth factor 19 (human FGF19) (5-194)-peptide, produced in *Escherichia coli*
aldafermine	[Phe^{5}>Met,Ser^{6}>Arg,Ala^{8}>Ser,Gly^{9}>Ser,His^{11}>Leu] facteur de croissance des fibroblastes 19 (FGF19 humain) (5-194)-peptide, produit par *Escherichia coli*
aldafermina	[Phe^{5}>Met,Ser^{6}>Arg,Ala^{8}>Ser,Gly^{9}>Ser,His^{11}>Leu] factor de crecimiento de fibroblastos 19 (FGF19 humano) (5-194)-péptido, producido por *Escherichia coli*

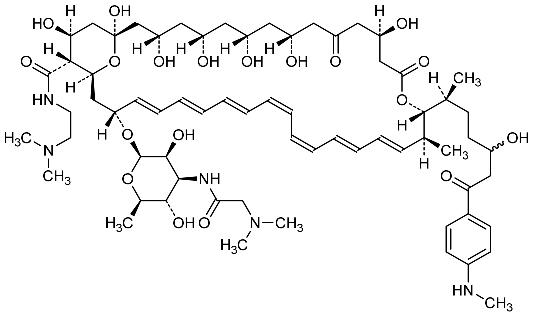
```
5   MRDSSP LVHYGWGDPI RLRHLYTSGP HGLSSCFLRI RADGVVDCAR  50
GQSAHSLLEI KAVALRTVAI KGVHSVRYLC MGADGKMQGL LQYSEEDCAF 100
EEEIRPDGYN VYRSEKHRLP VSLSSAKQRQ LYKNRGFLPL SHFLPMLPMV 150
PEEPEDLRGH LESDMFSSPL ETDSMDPFGL VTGLEAVRSP SFEK       194
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
36-48, 80-98

amcipatricinum

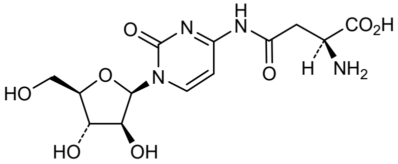
amcipatricin	$N^{3'}$-[(dimethylamino)acetyl]partricin-A 2-(dimethylamino)ethylamide: (1*R*,3*S*,5*S*,7*R*,9*R*,13*R*,17*R*,18*S*,19*E*,21*E*,23*Z*,25*Z*,27*E*,29*E*,31*E*,33*R*,35*S*,36*R*,37*S*)-33-({3,6-dideoxy-3-[2-(dimethylamino)acetamido]-β-D-mannopyranosyl}oxy)-*N*-[2-(dimethylamino)ethyl]-1,3,5,7,9,13,37-heptahydroxy-17-{(2*S*,5*Ξ*)-5-hydroxy-7-[4-(methylamino)phenyl]-7-oxoheptan-2-yl}-18-methyl-11,15-dioxo-16,39-dioxabicyclo[33.3.1]nonatriaconta-19,21,23,25,27,29,31-heptaene-36-carboxamide
amcipatricine	$N^{3'}$-[(diméthylamino)acétyl]partricin-A 2-(diméthylamino)éthylamide: (1*R*,3*S*,5*S*,7*R*,9*R*,13*R*,17*R*,18*S*,19*E*,21*E*,23*Z*,25*Z*,27*E*,29*E*,31*E*,33*R*,35*S*,36*R*,37*S*)-33-({3,6-didésoxy-3-[2-(diméthylamino)acétamido]-β-D-mannopyranosyl}oxy)-*N*-[2-(diméthylamino)éthyl]-1,3,5,7,9,13,37-heptahydroxy-17-{(2*S*,5*Ξ*)-5-hydroxy-7-[4-(méthylamino)phényl]-7-oxoheptan-2-yl}-18-méthyl-11,15-dioxo-16,39-dioxabicyclo[33.3.1]nonatriaconta-19,21,23,25,27,29,31-heptaène-36-carboxamide
amcipatricina	$N^{3'}$-[(dimetilamino)acetil]partricin-A 2-(dimetilamino)etilamida: (1*R*,3*S*,5*S*,7*R*,9*R*,13*R*,17*R*,18*S*,19*E*,21*E*,23*Z*,25*Z*,27*E*,29*E*,31*E*,33*R*,35*S*,36*R*,37*S*)-33-({3,6-didesoxi-3-[2-(dimetilamino)acetamido]-β-D-manopiranosil}oxi)-*N*-[2-(dimetilamino)etil]-1,3,5,7,9,13,37-heptahidroxi-17-{(2*S*,5*Ξ*)-5-hidroxi-7-[4-(metilamino)fenil]-7-oxoheptan-2-il}-18-metil-11,15-dioxo-16,39-dioxabiciclo[33.3.1]nonatriaconta-19,21,23,25,27,29,31-heptaeno-36-carboxamida

$C_{67}H_{103}N_5O_{19}$



aspacytarabinum

aspacytarabine	N^4-(1-β-D-arabinofuranosyl-2-oxo-1,2-dihydropyrimidin-4-yl)-L-asparagine
aspacytarabine	N^4-(1-β-D-arabinofuranosyl-2-oxo-1,2-dihydropyrimidin-4-yl)-L-asparagine

aspacitarabina	*N*^{4}-(1-β-D-arabinofuranosil-2-oxo-1,2-dihidropirimidin-4-il)-L-asparagina $C_{13}H_{18}N_4O_8$ 
atoltivimabum #	
atoltivimab	immunoglobulin G1-kappa, anti-[*Zaire ebolavirus* (Zaire Ebola virus (EBOV)) envelope glycoprotein (GP)], *Homo sapiens* monoclonal antibody; gamma1 heavy chain *Homo sapiens* (1-446) [VH (*Homo sapiens* IGHV3-33*01 (94.9%) -(IGHD) -IGHJ4*01 (100%)) [8.8.9] (1-116) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 (CH1 K120 (213) (117-214), hinge (215-229), CH2 (230-339), CH3 D12 (355), L14 (357) (340-444), CHS (445-446)) (117-446)], (219-215')-disulfide with kappa light chain *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (94.7%) -IGKJ2*01 (100%)) [6.3.10] (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')]; dimer (225-225'':228-228'')-bisdisulfide
atoltivimab	immunoglobuline G1-kappa, anti-[glycoprotéine d'enveloppe (GP) de *Zaire ebolaviru*s (virus Ebola Zaïre (EBOV))], anticorps monoclonal *Homo sapiens*; chaîne lourde gamma1 *Homo sapiens* (1-446) [VH (*Homo sapiens* IGHV3-33*01 (94.9%) -(IGHD) -IGHJ4*01 (100%)) [8.8.9] (1-116) -*Homo sapiens* IGHG1*01 01 (100%), G1m17,1 (CH1 K120 (213) (117-214), charnière (215-229), CH2 (230-339), CH3 D12 (355), L14 (357) (340-444), CHS (445-446)) (117-446)], (219-215')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (94.7%) -IGKJ2*01 (100%)) [6.3.10] (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')]; dimère (225-225'':228-228'')-bisdisulfure
atoltivimab	inmunoglobulina G1-kappa, anti-[glicoproteína de la envoltura (GP) de *Zaire ebolaviru*s (virus Ebola Zaïre (EBOV))], anticuerpo monoclonal *Homo sapiens*; cadena pesada gamma1 *Homo sapiens* (1-446) [VH (*Homo sapiens* IGHV3-33*01 (94.9%) -(IGHD) -IGHJ4*01 (100%)) [8.8.9] (1-116) -*Homo sapiens* IGHG1*01 01 (100%), G1m17,1 (CH1 K120 (213) (117-214), bisagra (215-229), CH2 (230-339), CH3 D12 (355), L14 (357) (340-444), CHS (445-446)) (117-446)], (219-215')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (94.7%) -IGKJ2*01 (100%)) [6.3.10] (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')]; dímero (225-225'':228-228'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVESGGG VVQPGRSLRL SCAASGFTFN NYGMHWVRQA PGMGLEWVAV  50
IWHDGSDKYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARNW 100
NLFDYWGQGT LVTVSSASTK GPSVFPLAPS SKSTSGGTAA LGCLVKDYFP 150
EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVVTVPSS SLGTQTYICN 200
VNHKPSNTKV DKKVEPKSCD KTHTCPPCPA PELLGGPSVF LFPPKPKDTL 250
MISRTPEVTC VVVDVSHEDP EVKFNWYVDG VEVHNAKTKP REEQYNSTYR 300
VVSVLTVLHQ DWLNGKEYKC KVSNKALPAP IEKTISKAKG QPREPQVYTL 350
PPSRDELTKN QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD 400
GSFFLYSKLT VDKSRWQQGN VFSCSVMHEA LHNHYTQKSL SLSPGK      446
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRIT ITCRASQSIS TYLHWYQQKP GKAPKLLIYA  50
ASTLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ SFSTPPINFG 100
QGTKLEIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK 150
VDNALQSGNS QESVTEQDSK DSTYSLSSTL TLSKADYEKH KVYACEVTHQ 200
GLSSPVTKSF NRGEC                                       215
```

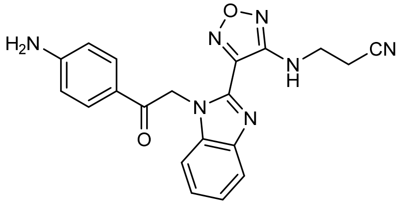
Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 143-199 260-320 366-424
22"-96" 143"-199" 260"-320" 366"-424"
Intra-L (C23-C104) 23'-88' 135'-195'
23'''-88''' 135'''-195'''
Inter-H-L (h 5-CL 126) 219-215' 219"-215'''
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

C-terminal lysine clipping:
H CHS K2:
446, 446"

avanbulinum	
avanbulin	3-[(4-{1-[2-(4-aminophenyl)-2-oxoethyl]-1*H*-benzimidazol-2-yl}-1,2,5-oxadiazol-3-yl)amino]propanenitrile
avanbuline	3-[(4-{1-[2-(4-aminophényl)-2-oxoéthyl]-1*H*-benzimidazol-2-yl}-1,2,5-oxadiazol-3-yl)amino]propanenitrile
avanbulina	3-[(4-{1-[2-(4-aminofenil)-2-oxoetil]-1*H*-benzimidazol-2-il}-1,2,5-oxadiazol-3-il)amino]propanonitrilo

$C_{20}H_{17}N_7O_2$



avexitidum	
avexitide	exendin 3 [*Heloderma horridum horridum* (Mexican beaded lizard)] (9-39)-peptide 39-amide: L-α-aspartyl-L-leucyl-L-seryl-L-lysyl-L-glutaminyl-L-methionyl-L-α-glutamyl-L-α-glutamyl-L-α-glutamyl-L-alanyl-L-valyl-L-arginyl-L-leucyl-L-phenylalanyl-L-isoleucyl-L-α-glutamyl-L-tryptophyl-L-leucyl-L-lysyl-L-asparaginylglycylglycyl-L-prolyl-L-seryl-L-serylglycyl-L-alanyl-L-prolyl-L-prolyl-L-prolyl-L-serinamide

avexitide

exendine 3 [*Heloderma horridum horridum* (lézard perlé mexicain)] (9-39)-peptide 39-amide: L-α-aspartyl-L-leucyl-L-séryl-L-lysyl-L-glutaminyl-L-méthionyl-L-α-glutamyl-L-α-glutamyl-L-α-glutamyl-L-alanyl-L-valyl-L-arginyl-L-leucyl-L-phénylalanyl-L-isoleucyl-L-α-glutamyl-L-tryptophyl-L-leucyl-L-lysyl-L-asparaginylglycylglycyl-L-prolyl-L-séryl-L-sérylglycyl-L-alanyl-L-prolyl-L-prolyl-L-prolyl-L-sérinamide

avexitida

exendina 3 [*Heloderma horridum horridum* (lagarto moteado mexicano)] (9-39)-péptido 39-amida: L-α-aspartil-L-leucil-L-seril-L-lisil-L-glutaminil-L-metionil-L-α-glutamil-L-α-glutamil-L-α-glutamil-L-alanil-L-valil-L-arginil-L-leucil-L-fenilalanil-L-isoleucil-L-α-glutamil-L-triptofil-L-leucil-L-lisil-L-asparaginilglicilglicil-L-prolil-L-seril-L-serilglicil-L-alanil-L-prolil-L-prolil-L-prolil-L-serinamida

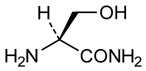
$C_{149}H_{234}N_{40}O_{47}S$

Sequence / Séquence / Secuencia

```
DLSKQMEEEA VRLFIEWLKN GGPSSGAPPP S        31
```

Modified residues / Résidus modifiés / Restos modificados

S (31)
L-serinamide



baloramotidum #

baloramotide

glycyl-L-prolyl-human cancer/testis antigen 1 (autoimmunogenic cancer/testis antigen NY-ESO-1, L antigen family member 2 (LAGE-2), cancer/testis antigen 6.1, CT6.1), produced by *Escherichia coli*

baloramotide

glycyl-L-prolyl-antigène 1 humain associé au cancer du testicule (antigène autoimmunogénique associé au cancer du testicule NY-ESO-1, membre 2 de la famille de l'antigène L (LAGE-2), antigène 6.1 associé au cancer du testicule, CT6.1), produit par *Escherichia coli*

baloramotida

glicil-L-prolil-antígeno 1 humano asociado al cáncer de testículo (antígeno autoinmunogénico asociado al cáncer de testículo NY-ESO-1, miembro 2 de la familia del antígeno L (LAGE-2), antígeno 6.1 asociado al cáncer de testículo, CT6.1), producido por *Escherichia coli*

```
GP                                          (N-terminal fused dipeptide)
MQAEGRGTGG STGDADGPGG PGIPDGPGGN AGGPGEAGAT GGRGPRGAGA   50
ARASGPGGGA PRGPHGGAAS GLNGCCRCGA RGPESRLLEF YLAMPFATPM  100
EAELARRSLA QDAPPLPVPG VLLKEFTVSG NILTIRLTAA DHRQLQLSIS  150
SCLQQLSLLM WITQCFLPVF LAQPPSGQRR                        180
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
potential intermolecular disulfide bonds (5 Cys: 75, 76, 78, 152, 165), preferred positions in the oligomers unknown

balstilimabum #

balstilimab

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

gamma4 heavy chain *Homo sapiens* (1-440) [VH (*Homo sapiens* IGHV3-33*01 (100%) -(IGHD) -IGHJ1*01 (100%)) [8.8.6] (1-113) -*Homo sapiens* IGHG4*01 (CH1 (114-211), hinge S10>P (221) (212-223), CH2 (224-333), CH3 (334-438), CHS (439-440)) (114-440)], (127-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-15*01 (100%) -IGKJ1*01 (100.0%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (219-219'':222-222'')-bisdisulfide

balstilimab

immunoglobuline G4-kappa, anti-[*Homo sapiens* PDCD1 (protéine 1 de mort cellulaire programmée, PD-1, PD1, CD279)], anticorps monoclonal *Homo sapiens*;
chaîne lourde gamma4 *Homo sapiens* (1-440) [VH (*Homo sapiens* IGHV3-33*01 (100%) -(IGHD) -IGHJ1*01 IGHJ1*01 (100%)) [8.8.6] (1-113) -*Homo sapiens* IGHG4*01 (CH1 (114-211), charnière S10>P (221) (212-223), CH2 (224-333), CH3 (334-438), CHS (439-440)) (114-440)], (127-214')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-15*01 (100%) -IGKJ1*01 (100.0%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (219-219'':222-222'')-bisdisulfure

balstilimab

inmunoglobulina G4-kappa, anti-[*Homo sapiens* PDCD1 (proteína 1 de muerte celular programada, PD-1, PD1, CD279)], anticuerpo monoclonal *Homo sapiens*;
cadena pesada gamma4 *Homo sapiens* (1-440) [VH (*Homo sapiens* IGHV3-33*01 (100%) -(IGHD) -IGHJ1*01 IGHJ1*01 (100%)) [8.8.6] (1-113) -*Homo sapiens* IGHG4*01 (CH1 (114-211), bisagra S10>P (221) (212-223), CH2 (224-333), CH3 (334-438), CHS (439-440)) (114-440)], (127-214')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-15*01 (100%) -IGKJ1*01 (100.0%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (219-219'':222-222'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVESGGG VVQPGRSLRL SCAASGFTFS SYGMHWVRQA PGKGLEWVAV  50
IWYDGSNKYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCASNG 100
DHWGQGTLVT VSSASTKGPS VFPLAPCSRS TSESTAALGC LVKDYFPEPV 150
TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG TKTYTCNVDH 200
KPSNTKVDKR VESKYGPPCP PCPAPEFLGG PSVFLFPPKP KDTLMISRTP 250
EVTCVVVDVS QEDPEVQFNW YVDGVEVHNA KTKPREEQFN STYRVVSVLT 300
VLHQDWLNGK EYKCKVSNKG LPSSIEKTIS KAKGQPREPQ VYTLPPSQEE 350
MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY 400
SRLTVDKSRW QEGNVFSCSV MHEALHNHYT QKSLSLSLGK            440
```

Light chain / Chaîne légère / Cadena ligera

```
EIVMTQSPAT LSVSPGERAT LSCRASQSVS SNLAWYQQKP GQAPRLLIYG  50
ASTRATGIPA RFSGSGSGTE FTLTISSLQS EDFAVYYCQQ YNNWPRTFGQ 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) 22-96 140-196 254-314 360-418
22''-96'' 140''-196'' 254''-314'' 360''-418''
Intra-L (C23-C104) 23'-88' 134'-194'
23'''-88''' 134'''-194'''
Inter-H-L (CH1 10-CL 126) 127-214' 127''-214'''
Inter-H-H (h 8, h 11) 219-219'' 222-222''

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
290, 290''
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

bedinvetmabum #

bedinvetmab

immunoglobulin G2-lambda, anti-[*Canis lupus familiaris* NGF (nerve growth factor beta polypeptide, NGFB)], *Canis lupus familiaris* monoclonal antibody;
gamma2 heavy chain *Canis lupus familiaris* (1-460) [VH (Canlupfam IGHV3-19*01 (91.8%) -(IGHD) -IGHJ4*01 (86.7%)) [8.8.18] (1-125) -Canlupfam IGHG2*02 (CH1 (126-222), hinge 1-19 (223-241), CH2 M1.3>A (245), L1.2>A (246), G1>A (248) (242-351), CH3 (352-458), CHS (459-460)) (126-460)], (140-215')-disulfide with lambda light chain *Canis lupus familiaris* (1'-216') [V-LAMBDA (Canlupfam IGLV1-141*01 (89.8%) -IGLJ3*01 (100%)) [8.3.11] (1'-108') -Canlupfam C-LAMBDA IGLC3*01 (109'-216')]; dimer (237-237'':240-240'')-bisdisulfide

bédinvetmab

immunoglobuline G2-lambda, anti-[*Canis familiaris* NGF (facteur de croissance du nerf polypeptide bêta)], anticorps monoclonal *Canis lupus familiaris*;
chaîne lourde gamma2 *Canis lupus familiaris* (1-460) [VH (Canlupfam IGHV3-19*01 (91.8%) -(IGHD) -IGHJ4*01 (86.7%)) [8.8.18] (1-125) -Canlupfam IGHG2*02 (CH1 (126-222), charnière 1-19 (223-241), CH2 M1.3>A (245), L1.2>A (246), G1>A (248) (242-351), CH3 (352-458), CHS (459-460)) (126-460)], (140-215')-disulfure avec la chaîne légère lambda *Canis lupus familiaris* (1'-216') [V-LAMBDA (Canlupfam IGLV1-141*01 (89.8%) -IGLJ3*01 (100%)) [8.3.11] (1'-108') -Canlupfam C-LAMBDA IGLC3*01 (109'-216')]; dimère (237-237'':240-240'')-bisdisulfure

bedinvetmab

inmunoglobulina G2-lambda, anti-[*Canis familiaris* NGF (factor de crecimiento del nervio polipéptido beta)], anticuerpo monoclonal *Canis lupus familiaris*;
cadena pesada gamma2 *Canis lupus familiaris* (1-460) [VH (Canlupfam IGHV3-19*01 (91.8%) -(IGHD) -IGHJ4*01 (86.7%)) [8.8.18] (1-125) -Canlupfam IGHG2*02 (CH1 (126-222), bisagra 1-19 (223-241), CH2 M1.3>A (245), L1.2>A (246), G1>A (248) (242-351), CH3 (352-458), CHS (459-460)) (126-460)], (140-215')-disulfuro con la cadena ligera lambda *Canis lupus familiaris* (1'-216') [V-LAMBDA (Canlupfam IGLV1-141*01 (89.8%) -IGLJ3*01 (100%)) [8.3.11] (1'-108') -Canlupfam C-LAMBDA IGLC3*01 (109'-216')]; dímero (237-237'':240-240'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGD LVKPGGSLRL SCVASGFTFS SHGMHWVRQS PGKGLQWVAV  50
INSGGSSTYY TDAVKGRFTI SRDNAKNTVY LQMNSLRAED TAMYYCAKES 100
VGGWEQLVGP HFDYWGQGTL VIVSSASTTA PSVFPLAPSC GSTSGSTVAL 150
ACLVSGYFPE PVTVSWNSGS LTSGVHTFPS VLQSSGLYSL SSMVTVPSSR 200
WPSETFTCNV AHPASKTKVD KPVPKRENGR VPRPPDCPKC PAPEAAGAPS 250
VFIFPPKPKD TLLIARTPEV TCVVVDLDPE DPEVQISWFV DGKQMQTAKT 300
QPREEQFNGT YRVVSVLPIG HQDWLKGKQF TCKVNNKALP SPIERTISKA 350
RGQAHQPSVY VLPPSREELS KNTVSLTCLI KDFFPPDIDV EWQSNGQQEP 400
ESKYRTTPPQ LDEDGSYFLY SKLSVDKSRW QRGDTFICAV MHEALHNHYT 450
QESLSHSPGK                                             460
```

Light chain / Chaîne légère / Cadena ligera

```
QSVLTQPTSV SGSLGQRVTI SCSGSTNNIG ILGASWYQLF PGKAPKLLVY  50
GNGNRPSGVP DRFSGADSGD SVTLTITGLQ AEDEADYYCQ SFDTTLGAHV 100
FGGGTHLTVL GQPKASPSVT LFPPSSEELG ANKATLVCLI SDFYPSGVTV 150
AWKADGSPVT QGVETTKPSK QSNNKYAASS YLSLTPDKWK SHSSFSCLVT 200
HEGSTVEKKV APAECS                                      216
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 152-208 272-332 378-438
22''-96'' 152''-208'' 272''-332'' 378''-438''
Intra-L (C23-C104) 22'-89' 138'-197'
22'''-89''' 138'''-197'''
Inter-H-L (CH1 11-CL 126) 140-215' 140''-215'''
Inter-H-H (h 15, h 18) 237-237'' 240-240''

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
308, 308''
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:
460, 460''

bermekimabum #

bermekimab	immunoglobulin G1-kappa, anti-[*Homo sapiens* IL1A (interleukin 1 alpha)], monoclonal antibody; gamma1 heavy chain (1-452) [VH (*Homo sapiens* IGHV3-30*03 (88.8%) -(IGHD) -IGHJ1*01 (91.7%)) [8.8.15] (1-122) -*Homo sapiens* IGHG1*03 (100%) G1m3, nG1m1 (CH1 R120 (219) (123-220), hinge (221-235), CH2 (236-345), CH3 E12 (361), M14 (363) (346-450), CHS (451-452)) (123-452)], (225-214')-disulfide with kappa light chain (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (92.6%) -IGKJ4*01 (83.3%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (231-231":234-234")-bisdisulfide
bermékimab	immunoglobuline G1-kappa, anti-[*Homo sapiens* IL1A (interleukine 1 alpha)], anticorps monoclonal; chaîne lourde gamma1 (1-452) [VH (*Homo sapiens* IGHV3-30*03 (88.8%) -(IGHD) -IGHJ1*01 (91.7%)) [8.8.15] (1-122) -*Homo sapiens* IGHG1*03 (100%) G1m3, nG1m1 (CH1 R120 (219) (123-220), charnière (221-235), CH2 (236-345), CH3 E12 (361), M14 (363) (346-450), CHS (451-452)) (123-452)], (225-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (92.6%) -IGKJ4*01 (83.3%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (231-231":234-234")-bisdisulfure
bermekimab	inmunoglobulina G1-kappa, anti-[*Homo sapiens* IL1A (interleukina 1 alfa)], anticuerpo monoclonal; cadena pesada gamma1 (1-452) [VH (*Homo sapiens* IGHV3-30*03 (88.8%) -(IGHD) -IGHJ1*01 (91.7%)) [8.8.15] (1-122) -*Homo sapiens* IGHG1*03 (100%) G1m3, nG1m1 (CH1 R120 (219) (123-220), bisagra (221-235), CH2 (236-345), CH3 E12 (361), M14 (363) (346-450), CHS (451-452)) (123-452)], (225-214')-disulfuro con la cadena ligera kappa (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (92.6%) -IGKJ4*01 (83.3%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (231-231":234-234")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVESGGG VVQPGRSLRL SCTASGFTFS MFGVHWVRQA PGKGLEWVAA  50
VSYDGSNKYY AESVKGRFTI SRDNSKNILF LQMDSLRLED TAVYYCARGR 100
PKVVIPAPLA HWGQGTLVTF SSASTKGPSV FPLAPSSKST SGGTAALGCL 150
VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ SSGLYSLSSV VTVPSSSLGT 200
QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL GGPSVFLFPP 250
KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE 350
PQVYTLPPSR EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP 400
PVLDSDGSFF LYSKLTVDKS RWQQGNVFSC SVMHEALHNH YTQKSLSLSP 450
GK                                                     452
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS VSASVGDRVT ITCRASQGIS SWLAWYQQKP GKAPKLLIYE  50
ASNLETGVPS RFSGSGSGSD FTLTISSLQP EDFATYYCQQ TSSFLLSFGG 100
GTKVEHKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

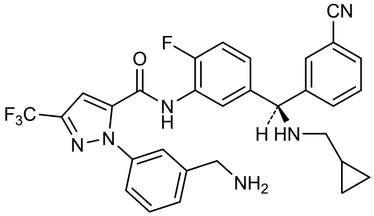
Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 149-205 266-326 372-430
22"-96" 149"-205" 266"-326" 372"-430"
Intra-L (C23-C104) 23'-88' 134'-194'
23'''-88''' 134'''-194'''
Inter-H-L (h 5-CL 126) 225-214' 225"-214'''
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

berotralstatum

berotralstat	1-[3-(aminomethyl)phenyl]-*N*-(5-{(*R*)-(3-cyanophenyl)[(cyclopropylmethyl)amino]methyl}-2-fluorophenyl)-3-(trifluoromethyl)-1*H*-pyrazole-5-carboxamide
bérotralstat	1-[3-(aminométhyl)phényl]-*N*-(5-{(*R*)-(3-cyanophényl)[(cyclopropylméthyl)amino]méthyl}-2-fluorophényl)-3-(trifluorométhyl)-1*H*-pyrazole-5-carboxamide
berotralstat	1-[3-(aminometil)fenil]-*N*-(5-{(*R*)-(3-cianofenil)[(ciclopropilmetil)amino]metil}-2-fluorofenil)-3-(trifluorometil)-1*H*-pirazol-5-carboxamida

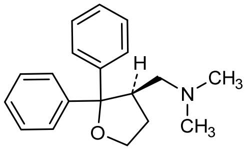
$C_{30}H_{26}F_4N_6O$



blarcamesinum

blarcamesine	*rac*-1-[(3*R*)-2,2-diphenyloxolan-3-yl]-*N*,*N*-dimethylmethanamine
blarcamésine	*rac*-1-[(3*R*)-2,2-diphényloxolan-3-yl]-*N*,*N*-diméthylméthanamine
blarcamesina	*rac*-1-[(3*R*)-2,2-difeniloxolan-3-il]-*N*,*N*-dimetilmetanamina

$C_{19}H_{23}NO$



and enantiomer
et énantiomère
y enantiómero

cadalimogenum ixalentivecum #

cadalimogene ixalentivec	a recombinant dendritic cell-targeting, non-replicating and integration-deficient lentiviral vector, encoding the cancer testis (CT) antigen NY-ESO-1, under the control of a eukaryotic ubiquitin intron-deleted promoter
cadalimogène ixalentivec	vecteur lentiviral recombinant dirigé contre les cellules dendritiques, non-répliquant et dont la capacité d'intégration est diminuée, codant pour l'antigène NY-ESO-1 du cancer du testicule (CT), sous le contrôle d'un promoteur eucaryotique de l'ubiquitine dont l'intron a été supprimé

cadalimogén ixalentivec	un vector lentiviral recombinante dirigido a células dendríticas, no replicativo y con capacidad de integración disminuida, que codifica para el antígeno de cáncer de testículo (CT) NY-ESO-1 bajo el control de un promotor eucariótico de ubiquitina con el intron delecionado
cendakimabum #	
cendakimab	immunoglobulin G1-kappa, anti-[*Homo sapiens* IL-13 (interleukin 13, IL-13)], humanized monoclonal antibody; gamma1 heavy chain humanized (1-453) [VH (*Homo sapiens* IGHV2-5*08 (80.6%) -(IGHD) -IGHJ4*01 (100%)) [10.7.15] (1-123) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (220) (124-221), hinge (222-236), CH2 L1.3>A (240), L1.2>A (241) (237-346), CH3 E12 (362), M14 (364) (347-451), CHS (452-453)) (124-453)], (226-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (85.3%) -IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%) A45.1 (153), V101 (191) (108'-214')]; dimer (232-232'':235-235'')-bisdisulfide
cendakimab	immunoglobuline G1-kappa, anti-[*Homo sapiens* IL-13 (interleukine 13, IL-13)], anticorps monoclonal humanisé; chaîne lourde gamma1 humanisée (1-453) [VH (*Homo sapiens* IGHV2-5*08 (80.6%) -(IGHD) - IGHJ4*01 (100%)) [10.7.15] (1-123) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (220) (124-221), charnière (222-236), CH2 L1.3>A (240), L1.2>A (241) (237-346), CH3 E12 (362), M14 (364) (347-451), CHS (452-453)) (124-453)], (226-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (85.3%) -IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%) A45.1 (153), V101 (191) (108'-214')]; dimère (232-232'':235-235'')-bisdisulfure
cendakimab	inmunoglobulina G1-kappa, anti-[*Homo sapiens* IL-13 (interleukina 13, IL-13)], anticuerpo monoclonal humanizado; cadena pesada gamma1 humanizada (1-453) [VH (*Homo sapiens* IGHV2-5*08 (80.6%) -(IGHD) -IGHJ4*01 (100%)) [10.7.15] (1-123) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (220) (124-221), bisagra (222-236), CH2 L1.3>A (240), L1.2>A (241) (237-346), CH3 E12 (362), M14 (364) (347-451), CHS (452-453)) (124-453)], (226-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (85.3%) -IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%) A45.1 (153), V101 (191) (108'-214')]; dímero (232-232'':235-235'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada
```
EVTLRESGPG LVKPTQTLTL TCTLYGFSLS TSDMGVDWIR QPPGKGLEWL  50
AHIWWDDVKR YNPALKSRLT ISKDTSKNQV VLKLTSVDPV DTATYYCART 100
VSSGYIYYAM DYWGQGTLVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC 150
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG 200
TQTYICNVNH KPSNTKVDKK VEPKSCDKTH TCPPCPAPEA AGGPSVFLFP 250
PKPKDTLMIS RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE 300
QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR 350
EPQVYTLPPS REEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT 400
PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLS 450
PGK                                                453
```

Light chain / Chaîne légère / Cadena ligera
```
DIQMTQSPSS LSASVGDRVT ISCRASQDIR NYLNWYQQKP GKAPKLLIFY  50
TSKLHSGVPS RFSGSGSGTD YTLTISSLQP EDIATYYCQQ GNTLPLTFGG 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)  22-97     150-206     267-327     373-431
                    22''-97''  150''-206''  267''-327''  373''-431''
Intra-L (C23-C104)  23'-88'   134'-194'
                    23'''-88'''  134'''-194'''
Inter-H-L (h 5-CL 126)  226-214'   226''-214'''
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.
C-terminal lysine clipping:
H CHS K2:
453, 453''

cetuximabum sarotalocanum

cetuximab sarotalocan	immunoglobulin G1-kappa, anti-[*Homo sapiens* EGFR (epidermal growth factor receptor, avian erythroblastic leukemia viral (v-erb-b) oncogene homolog, ERBB)], chimeric monoclonal antibody conjugated to IRDye 700DX (IR700) near-infrared photosensitizing dye; gamma1 heavy chain chimeric (1-449) [VH (*Mus musculus* IGHV2-2*03 (93.8%) -(IGHD) -IGHJ3*01 (100%)) [8.7.13] (1-119) -*Homo sapiens* IGHG1*03 (100%), 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)], (222-214')-disulfide with kappa light chain chimeric (1'-214') [V-KAPPA (*Mus musculus* IGKV5-48*01 (95.8%) -IGKJ5*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (228-228'':231-231'')-bisdisulfide; conjugated on an average of 2 or 3 lysyl to photosensitizing dye IRDye 700DX
cétuximab sarotalocan	immunoglobuline G1-kappa, anti-[*Homo sapiens* EGFR (récepteur du facteur de croissance épidermique, leucémie érythroblastique aviaire virale (v-erb-b) homologue d'oncogène, ERBB)], anticorps monoclonal chimérique conjugué au photosensibilisateur proche infrarouge IRDye 700DX (IR700); chaîne lourde gamma1 chimérique (1-449) [VH (*Mus musculus* IGHV2-2*03 (93.8%) -(IGHD) - IGHJ3*01 (100%)) [8.7.13] (1-119) -*Homo sapiens* IGHG1*03 (100%), 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)], (222-214')-disulfure avec la chaîne légère kappa chimérique (1'-214') [V-KAPPA (*Mus musculus* IGKV5-48*01 (95.8%) -IGKJ5*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (228-228'':231-231'')-bisdisulfure; conjugué sur 2 ou 3 lysyl en moyenne au photosensibilisateur IRDye 700DX

cetuximab sarotalocán

inmunoglobulina G1-kappa, anti-[*Homo sapiens* EGFR (receptor del factor de crecimiento epidérmico leucemia eritroblástica aviar viral (v-erb-b) homólogo del oncogen, ERBB)], anticuerpo monoclonal quimérico conjugado con el infrarrojo cercano fotosensibilizante IRDye 700DX (IR700); cadena pesada gamma1 quimérico (1-449) [VH (*Mus musculus* IGHV2-2*03 (93.8%) -(IGHD) - IGHJ3*01 (100%)) [8.7.13] (1-119) -*Homo sapiens* IGHG1*03 (100%), 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)], (222-214')-disulfuro con la cadena ligera kappa quimérica (1'-214') [V-KAPPA (*Mus musculus* IGKV5-48*01 (95.8%) -IGKJ5*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (228-228":231-231")-bisdisulfuro; conjugado con 2 o 3 restos lisil por término medio al fotosensibilizante IRDye 700DX

Heavy chain / chaîne lourde / cadena pesada

```
QVQLKQSGPG LVQPSQSLSI TCTVSGFSLT NYGVHWVRQS PGKGLEWLGV  50
IWSGGNTDYN TPFTSRLSIN KDNSKSQVFF KMNSLQSNDT AIYYCARALT 100
YYDYEFAYWG QGTLVTVSAA 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
```

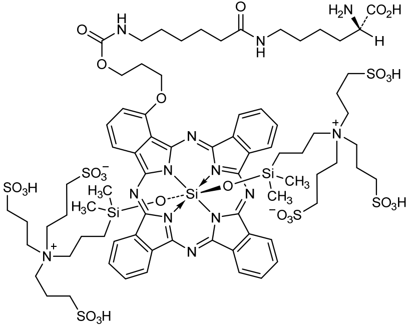
Light chain / chaîne légère / cadena ligera

```
DILLTQSPVI LSVSPGERVS FSCRASQSIG TNIHWYQQRT NGSPRLLIKY  50
ASESISGIPS RFSGSGSGTD FTLSINSVES EDIADYYCQQ NNNWPTTFGA 100
GTKLELKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                       214
```

Post-translational modifications
Disulfide bridges location
Intra-H (C23-C104) 22-95 146-202 263-323 369-427
22"-95" 146"-202" 263"-323" 369"-427"
Intra-L (C23-C104) 23'-88' 134'-194'
23'''-88''' 134'''-194'''
Inter-H-L (h 5-CL 126) 222-214' 222"-214'''
Inter-H-H (h 11, h 14) 228-228" 231-231"

N-glycosylation sites
H CH2 N84.4:
88, 88",
299, 299"
Fucosylated complex bi-antennary Sp2/0-type glycans

Modified lysines / lysines modifiées / lisinas modificadas



choriogonadotropinum beta #

choriogonadotropin beta	human chorionic gonadotropin, alpha and beta chains, non-covalent heterodimer, produced in recombinant human retinal cells containing an inserted sialyltransferase gene, glycoform beta
choriogonadotropine bêta	gonadotrophine chorionique humaine, chaînes alpha et bêta, hétérodimère non-covalent, produit dans des cellules rétinales humaines recombinantes contenant un gène de sialyltransférase, glycoforme bêta
coriogonadotropina beta	gonadotrofina coriónica humana, cadenas alfa y beta, heterodímero no covalente, producido en las células retinales humanas recombinantes que contienen un gen de sialiltransferasa, glicoforma beta

non-covalent heterodimer:
α-subunit
APDVQDCPEC TLQENPFFSQ PGAPILQCMG CCFSRAYPTP LRSKKTMLVQ 50
KNVTSESTCC VAKSYNRVTV MGGFKVENHT ACHCSTCYYH KS 92

β-subunit
SKEPLRPRCR PINATLAVEK EGCPVCITVN TTICAGYCPT MTRVLQGVLP 50
ALPQVVCNYR DVRFESIRLP GCPRGVNPVV SYAVALSCQC ALCRRSTTDC 100
GGPKDHPLTC DDPRFQDSSS SKAPPPSLPS PSRLPGPSDT PILPQ 145

Disulfide bridge location / Position de la pont disulfure / Posición del puente disulfuro
α: 7-31, 10-60, 28-82, 32-84, 59-87;
β: 9-57, 23-72, 26-110, 34-88, 38-90, 93-100

N-Glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
α: Asn52, Asn78; β: Asn13, Asn30
(highly sialylated glycans)

O-Glycosylation sites / Sites de O-glycosylation / Posiciones de O-glicosilación
β: Ser121, Ser127, Ser132, Ser138

cinpanemabum #

cinpanemab	immunoglobulin G1-lambda, anti-[*Homo sapiens* SNCA (synuclein alpha, alpha-synuclein, PARK1, PARK4, Parkinson disease (autosomal dominant, Lewy body) 4, non A4 component of amyloid precursor, NACP)], monoclonal antibody; gamma1 heavy chain (1-442) [VH (*Homo sapiens* IGHV3-15*01 (84.0%) -(IGHD) -IGHJ1*01 (100%)) [8.10.4] (1-113) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 (CH1 R120 (210) (114-211), hinge (212-226), CH2 (227-336), CH3 E12 (352), M14 (354) (337-441), CHS K2>del (442)) (114-442)], (216-213')-disulfide with lambda light chain (1'-214') [V-LAMBDA (*Homo sapiens* IGLV3-25*02 (85.4%) -IGLJ2*01 (100%)) [6.3.11] (1'-108') -*Homo sapiens* IGLC2*01 G1.5>S (109') (109'-214')]; dimer (222-222'':225-225'')-bisdisulfide
cinpanémab	immunoglobuline G1-lambda, anti-[*Homo sapiens* SNCA (synucléine alpha, alpha-synucléine, PARK1, PARK4, maladie de Parkinson (autosomique dominante, corps de Lewy) 4, composant non A4 du précurseur amyloïde, NACP)], anticorps monoclonal;

chaîne lourde gamma1 (1-442) [VH (*Homo sapiens* IGHV3-15*01 (84.0%) -(IGHD) - IGHJ1*01 (100%)) [8.10.4] (1-113) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 (CH1 R120 (210) (114-211), charnière (212-226), CH2 (227-336), CH3 E12 (352), M14 (354) (337-441), CHS K2>del (442)) (114-442)], (216-213')-disulfure avec la chaîne légère lambda (1'-214') [V-LAMBDA (*Homo sapiens* IGLV3-25*02 (85.4%) -IGLJ2*01 (100%)) [6.3.11] (1'-108') -*Homo sapiens* IGLC2*01 G1.5>S (109') (109'-214')]; dimère (222-222'':225-225'')-bisdisulfure

cinpanemab

inmunoglobulina G1-lambda, anti-[*Homo sapiens* SNCA (sinucleina alfa, alfa-sinucleína, PARK1, PARK4, enfermedad del Parkinson (autosómica dominante, cuerpos de Lewy) 4, componente no A4 del precusor amiloide, NACP)], anticuerpo monoclonal; cadena pesada gamma1 (1-442) [VH (*Homo sapiens* IGHV3-15*01 (84.0%) -(IGHD) - IGHJ1*01 (100%)) [8.10.4] (1-113) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 (CH1 R120 (210) (114-211), bisagra (212-226), CH2 (227-336), CH3 E12 (352), M14 (354) (337-441), CHS K2>del (442)) (114-442)], (216-213')-disulfuro con la cadena ligera lambda (1'-214') [V-LAMBDA (*Homo sapiens* IGLV3-25*02 (85.4%) -IGLJ2*01 (100%)) [6.3.11] (1'-108') -*Homo sapiens* IGLC2*01 G1.5>S (109') (109'-214')]; dímero (222-222'':225-225'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVEPGGSLRL SCAVSGFDFE KAWMSWVRQA PGQGLQWVAR  50
IKSTADGGTT SYAAPVEGRF IISRDDSRNM LYLQMNSLKT EDTAVYYCTS 100
AHWGQGTLVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC LVKDYFPEPV 150
TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG TQTYICNVNH 200
KPSNTKVDKR VEPKSCDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS 250
RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYNSTYRVVS 300
VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR EPQVYTLPPS 350
REEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT PPVLDSDGSF 400
FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLS PG         442
```

Light chain / Chaîne légère / Cadena ligera

```
SYELTQPPSV SVSPGQTARI TCSGEALPMQ FAHWYQQRPG KAPVIVVYKD  50
SERPSGVPER FSGSSSGTTA TLTITGVQAE DEADYYCQSP DSTNTYEVFG 100
GGTKLTVLSQ PKAAPSVTLF PPSSEELQAN KATLVCLISD FYPGAVTVAW 150
KADSSPVKAG VETTTPSKQS NNKYAASSYL SLTPEQWKSH RSYSCQVTHE 200
GSTVEKTVAP TECS                                        214
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-98 140-196 257-317 363-421
22''-98'' 140''-196'' 257''-317'' 363''-421''
Intra-L (C23-C104) 22'-87' 136'-195'
22'''-87''' 136'''-195'''
Inter-H-L (h 5-CL 126) 216-213' 216''-213'''
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''
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

clascoteronum
clascoterone

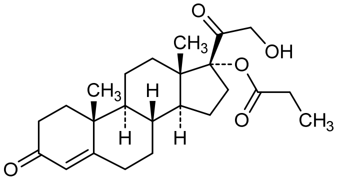
21-hydroxy-3,20-dioxopregn-4-en-17-yl propanoate

clascotérone

propanoate de 21-hydroxy-3,20-dioxoprégn-4-én-17-yle clascoterona

propanoato de 21-hidroxi-3,20-dioxopregn-4-en-17-ilo

$C_{24}H_{34}O_5$



clervonafuspum alfa #

clervonafusp alfa

immunoglobulin G1-kappa, cell-penetrating humanized Fab fragment targeting the equilibrative nucleoside transporter 2 (ENT2), fused with a human lysosomal α-glucosidase fragment, glycoform alfa:
gamma1 heavy chain VH-CH1 [humanized VH (*Homo sapiens* IGHV3-48*01 -(IGHD)-IGHJ4*01) [CDRKabatH1: NYGMH (31-35), CDRKabatH2: YISSGSSTIYYADSVKG (50-66), CDRKabatH3: RGLLLDY (99-105)] (1-116) -*Homo sapiens* IGHG1*01 (CH1 (117-214), hinge (215-224)) (117-224)] (1-224) fused by a $G_2SG_3SG_3SG_2$ linker (225-237) with human lysosomal α-glucosidase (acid α-glucosidase, GAA) pro-protein (67-952)-peptide (238-1123), (219-218')-disulfide with kappa light chain (1'-218') [humanized V-KAPPA (*Homo sapiens* IGKV1-39*01 -IGKJ2*02) [CDRKabatL1: RASKSVSTSSYSYMH (24-38), CDRKabatL2: YASYLQS (54-60), CDRKabatL3: QHSREFPWT (93-101)] (1'-111') -*Homo sapiens* IGKC*01 (112'-218')], produced in Chinese hamster ovary (CHO) cells, glycoform alfa

clervonafusp alfa

immunoglobuline G1-kappa, fragment Fab humanisé pénétrant les cellules et ciblant le transporteur équilibrant de type 2 de nucléosides (ENT2), fusionné avec un fragment de l'α-glucosidase lysosomale humaine, glycoforme alfa:
chaîne lourde gamma1 VH-CH1 [VH humanisé (*Homo sapiens* IGHV3-48*01 -(IGHD)-IGHJ4*01 [CDRKabatH1: NYGMH (31-35), CDRKabatH2: YISSGSSTIYYADSVKG (50-66), CDRKabatH3: RGLLLDY (99-105)] (1-116) -*Homo sapiens* IGHG1*01) (CH1 (117-214), charnière (215-224)) (117-224)] (1-224) fusionné via un linker $G_2SG_3SG_3SG_2$ (225-237) avec le précurseur de l'α-glucosidase lysosomale humaine (α-glucosidase acide, GAA) (67-952)-peptide (238-1123), (219-218')-disulfure avec la chaîne kappa légère (1'-218') [V-KAPPA humanisé (*Homo sapiens* IGKV1-39*01 -IGKJ2*02) [CDRKabatL1: RASKSVSTSSYSYMH (24-38), CDRKabatL2: YASYLQS (54-60), CDRKabatL3: QHSREFPWT (93-101)] (1'-111') -*Homo sapiens* IGKC*01 (112'-218')], produit dans des cellules ovariennes de hamsters chinois (CHO), glycoforme alfa

clervonafusp alfa

inmunoglobulina G1-kappa, fragmento Fab humanizado que penetra las células y cuya diana es el transportador que equilibra los nucleósidos de tipo 2 (ENT2), fusionado con un fragmento de la α-glucosidasa lisosomal humana, glicoforma alfa: cadena pesada gamma1 VH-CH1 [VH humanizado (*Homo sapiens* IGHV3-48*01 -(IGHD)-IGHJ4*01 [CDRKabatH1: NYGMH (31-35), CDRKabatH2: YISSGSSTIYYADSVKG (50-66), CDRKabatH3: RGLLLDY (99-105)] (1-116) -*Homo sapiens* IGHG1*01) (CH1 (117-214), bisagra (215-224)) (117-224)] (1-224) fusionada mediante un conector $G_2SG_3SG_3SG_2$ (225-237) con el precusor de la α-glucosidasa lisosomal humana (α-glucosidasa ácida, GAA) (67-952)-péptido (238-1123), (219-218')-disulfuro con la cadena kappa ligera (1'-218') [V-KAPPA humanizada (*Homo sapiens* IGKV1-39*01 -IGKJ2*02) [CDRKabatL1: RASKSVSTSSYSYMH (24-38), CDRKabatL2: YASYLQS (54-60), CDRKabatL3: QHSREFPWT (93-101)] (1'-111') -*Homo sapiens* IGKC*01 (112'-218')], producido en las células ováricas de hamsters chinos (CHO), glicoforma alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLQESGGG VVQPGGSLRL SCAASGFTFS NYGMHWIRQA PGKGLEWVSY   50
ISSGSSTIYY ADSVKGRFTI SRDNSKNTLY LQMNSLRSED TAVYYCARRG  100
LLLDYWGQGT LVTVSSASTK GPSVFPLAPS SKSTSGGTAA LGCLVKDYFP  150
EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVVTVPSS SLGTQTYICN  200
VNHKPSNTKV DKKVEPKSCD KTHTGGSGGG SGGGSGGDAQ AHPGRPRAVP  250
TQCDVPPNSR FDCAPDKAIT QEQCEARGCC YIPAKQGLQG AQMGQPWCFF  300
PPSYPSYKLE NLSSSEMGYT ATLTRTTPTF FPKDILTLRL DVMMETENRL  350
HFTIKDPANR RYEVPLETPH VHSRAPSPLY SVEFSEEPFG VIVRRQLDGR  400
VLLNTTVAPL FFADQFLQLS TSLPSQYITG LAEHLSPLML STSWTRITLW  450
NRDLAPTPGA NLYGSHPFYL ALEDGGSAHG VFLLNSNAMD VVLQPSPALS  500
WRSTGGILDV YIFLGPEPKS VVQQYLDVVG YPFMPPYWGL GFHLCRWGYS  550
STAITRQVVE NMTRAHFPLD VQWNDLDYMD SRRDFTFNKD GFRDFPAMVQ  600
ELHQGGRRYM MIVDPAISSS GPAGSYRPYD EGLRRGVFIT NETGQPLIGK  650
VWPGSTAFPD FTNPTALAWW EDMVAEFHDQ VPFDGMWIDM NEPSNFIRGS  700
EDGCPNNELE NPPYVPGVVG GTLQAATICA SSHQFLSTHY NLHNLYGLTE  750
AIASHRALVK ARGTRPFVIS RSTFAGHGRY AGHWTGDVWS SWEQLASSVP  800
EILQFNLLGV PLVGADVCGF LGNTSEELCV RWTQLGAFYP FMRNHNSLLS  850
LPQEPYSFSE PAQQAMRKAL TLRYALLPHL YTLFHQAHVA GETVARPLFL  900
EFPKDSSTWT VDHQLLWGEA LLITPVLQAG KAEVTGYFPL GTWYDLQTVP  950
VEALGSLPPP PAAPREPAIH SEGQWVTLPA PLDTINVHLR AGYIIPLQGP 1000
GLTTTESRQQ PMALAVALTK GGEARGELFW DDGESLEVLE RGAYTQVIFL 1050
ARNNTIVNEL VRVTSEGAGL QLQKVTVLGV ATAPQQVLSN GVPVSNFTYS 1100
PDTKVLDICV SLLMGEQFLV SWC                              1123
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ISCRASKSVS TSSYSYMHWY QQKPEKAPKL  50
LIKYASYLQS GVPSRFSGSG SGTDFTLTIS SLQPEDVATY YCQHSREFPW 100
TFGAGTKLEL 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: IgG1:  22-96,     143-199,
          GAA:  253-280,   263-279,   274-298,
                704-729,   818-829,   1109-1123
intra-L:        23'-92',   138'-198'
inter-H-L:      219-218'
```

N-Glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
Asn311, Asn404, Asn561, Asn641 , Asn823, Asn1053, Asn1096

cobolimabum #
cobolimab

immunoglobulin G4-kappa, anti-[*Homo sapiens* HAVCR2 (hepatitis A virus cellular receptor 2, T-cell immunoglobulin mucin family member 3, Tim-3, TIM3, TIMD3, CD366)], humanized monoclonal antibody;

gamma4 heavy chain humanized (1-440) [VH (*Homo sapiens* IGHV3-23*01 25^26>ins^A (25) (92.8%) -(IGHD) -IGHJ6*01 (92.9%)) [8.8.5] (1-113) -*Homo sapiens* IGHG4*01 (CH1 (114-211), hinge S10>P (221) (212-223), CH2 (224-333), CH3 (334-438), CHS (439-440)) (114-440)], (127-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (90.5%) -IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (219-219":222-222")-bisdisulfide

cobolimab

immunoglobuline G4-kappa, anti-[*Homo sapiens* HAVCR2 (récepteur cellulaire 2 du virus de l'hépatite A, CD366, membre 3 de la famille mucine immunoglobuline des cellules T, Tim-3, TIM3, TIMD3, CD366)], anticorps monoclonal humanisé; chaîne lourde gamma4 humanisée (1-440) [VH (*Homo sapiens* IGHV3-23*01 25^26>ins^A (25) (92.8%) -(IGHD) -IGHJ6*01 (92.9%)) [8.8.5] (1-113) -*Homo sapiens* IGHG4*01 (CH1 (114-211), charnière S10>P (221) (212-223), CH2 (224-333), CH3 (334-438), CHS (439-440)) (114-440)], (127-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (90.5%) -IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191), (108'-214')]; dimère (219-219":222-222")-bisdisulfure

cobolimab

inmunoglobulina G4-kappa, anti-[*Homo sapiens* HAVCR2 (receptor celular 2 del virus de la hepatitis A, CD366, miembro 3 de la familia mucina inmunoglobulina de las células T, Tim-3, TIM3, TIMD3, CD366)], anticuerpo monoclonal humanizado; cadena pesada gamma4 humanizada (1-440) [VH (*Homo sapiens* IGHV3-23*01 25^26>ins^A (25) (92.8%) -(IGHD) -IGHJ6*01 (92.9%)) [8.8.5] (1-113) -*Homo sapiens* IGHG4*01 (CH1 (114-211), bisagra S10>P (221) (212-223), CH2 (224-333), CH3 (334-438), CHS (439-440)) (114-440)], (127-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (90.5%) -IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191), (108'-214')]; dímero (219-219":222-222")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLLESGGG LVQPGGSLRL SCAAASGFTF SSYDMSWVRQ APGKGLDWVS  50
TISGGGTYTY YQDSVKGRFT ISRDNSKNTL YLQMNSLRAE DTAVYYCASM 100
DYWGQGTTVT VSSASTKGPS VFPLAPCSRS TSESTAALGC LVKDYFPEPV 150
TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG TKTYTCNVDH 200
KPSNTKVDKR VESKYGPPCP PCPAPEFLGG PSVFLFPPKP KDTLMISRTP 250
EVTCVVVDVS QEDPEVQFNW YVDGVEVHNA KTKPREEQFN STYRVVSVLT 300
VLHQDWLNGK EYKCKVSNKG LPSSIEKTIS KAKGQPREPQ VYTLPPSQEE 350
MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY 400
SRLTVDKSRW QEGNVFSCSV MHEALHNHYT QKSLSLSLGK            440
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCRASQSIR RYLNWYHQKP GKAPKLLIYG  50
ASTLQSGVPS RFSGSGSGTD FTLTISSLQP EDFAVYYCQQ SHSAPLTFGG 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

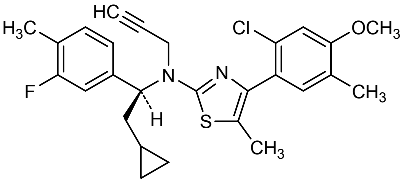
Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-97 140-196 254-314 360-418
22"-97" 140"-196" 254"-314" 360"-418"
Intra-L (C23-C104) 23'-88' 134'-194'
23'''-88''' 134'''-194'''
Inter-H-L (CH1 10-CL 126) 127-214' 127"-214'''
Inter-H-H (h 8, h 11) 219-219" 222-222"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
290, 290"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

crinecerfontum

crinecerfont	4-(2-chloro-4-methoxy-5-methylphenyl)-*N*-[(1*S*)-2-cyclopropyl-1-(3-fluoro-4-methylphenyl)ethyl]-5-methyl-*N*-(prop-2-yn-1-yl)-1,3-thiazol-2-amine
crinécerfont	4-(2-chloro-4-méthoxy-5-méthylphényl)-*N*-[(1*S*)-2-cyclopropyl-1-(3-fluoro-4-méthylphényl)éthyl]-5-méthyl-*N*-(prop-2-yn-1-yl)-1,3-thiazol-2-amine
crinecerfont	4-(2-cloro-4-metoxi-5-metilfenil)-*N*-[(1*S*)-2-ciclopropil-1-(3-fluoro-4-metilfenil)etil]-5-metil-*N*-(prop-2-in-1-il)-1,3-tiazol-2-amino

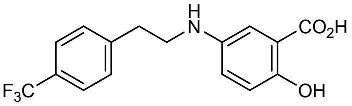
$C_{27}H_{28}ClFN_2OS$



crisdesalazinum

crisdesalazine	2-hydroxy-5-({2-[4-(trifluoromethyl)phenyl]ethyl}amino)benzoic acid
crisdésalazine	acide 2-hydroxy-5-({2-[4-(trifluorométhyl)phényl]éthyl}amino)benzoïque
crisdesalazina	ácido 2-hidroxi-5-({2-[4-(trifluorometil)fenil]etil}amino)ben-zoico

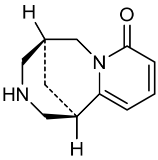
$C_{16}H_{14}F_3NO_3$



cytisiniclinum

cytisinicline	(1*R*,5*S*)-1,2,3,4,5,6-hexahydro-8*H*-1,5-methanopyrido[1,2-*a*][1,5]diazocin-8-one (cytisine)
cytisinicline	(1*R*,5*S*)-1,2,3,4,5,6-hexahydro-8*H*-1,5-méthanopyrido[1,2-*a*][1,5]diazocin-8-one (cytisine)
citisiniclina	(1*R*,5*S*)-1,2,3,4,5,6-hexahidro-8*H*-1,5-metanopirido[1,2-*a*][1,5]diazocin-8-ona (citisina)

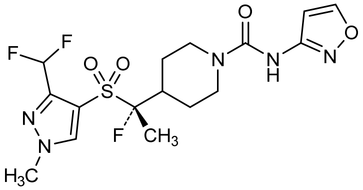
$C_{11}H_{14}N_2O$



danicamtivum

danicamtiv	4-{(1*R*)-1-[3-(difluoromethyl)-1-methyl-1*H*-pyrazole-4-sulfonyl]-1-fluoroethyl}-*N*-(1,2-oxazol-3-yl)piperidine-1-carboxamide
danicamtiv	4-{(1*R*)-1-[3-(difluorométhyl)-1-méthyl-1*H*-pyrazole-4-sulfonyl]-1-fluoroéthyl}-*N*-(1,2-oxazol-3-yl)pipéridine-1-carboxamide
danicamtiv	4-{(1*R*)-1-[3-(difluorometil)-1-metil-1*H*-pirazol-4-sulfonil]-1-fluoroetil}-*N*-(1,2-oxazol-3-il)piperidina-1-carboxamida

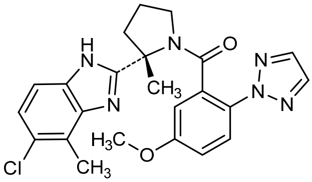
$C_{16}H_{20}F_3N_5O_4S$



daridorexantum

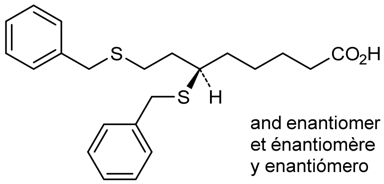
daridorexant	[(2*S*)-2-(5-chloro-4-methyl-1*H*-benzimidazol-2-yl)-2-methylpyrrolidin-1-yl][5-methoxy-2-(2*H*-1,2,3-triazol-2-yl)phenyl]methanone
daridorexant	[(2*S*)-2-(5-chloro-4-méthyl-1*H*-benzimidazol-2-yl)-2-méthylpyrrolidin-1-yl][5-méthoxy-2-(2*H*-1,2,3-triazol-2-yl)phényl]méthanone
daridorexant	[(2*S*)-2-(5-cloro-4-metil-1*H*-benzimidazol-2-il)-2-metilpirrolidin-1-il][5-metoxi-2-(2*H*-1,2,3-triazol-2-il)fenil]metanona

$C_{23}H_{23}ClN_6O_2$



devafidugenum civaparvovecum #

devafidugene civaparvovec	a recombinant non-replicating adeno-associated virus type 2/6 (rAAV Rep2-Cap6) vector, which contains a promoter-less human alpha-L-iduronidase (hIDUA) transgene cassette, encoding partial exon 1 and full exons 2-14 with the first 28 amino acids removed, and splice acceptor site sequence (SA) from hF9 exon 2, flanked by a sequence homologous to the zinc-finger nuclease (ZFN) cleavage site of the human albumin (hALB) intron 1

devafidugène civaparvovec	vecteur viral adéno-associé de type 2/6 recombinant (rAAV Rep2-Cap6), non-répliquant, contenant la cassette du transgène de l'alpha-L-iduronidase humaine (hIDUA) sans promoteur, codant partiellement l'exon 1 et entièrement les exons 2-14 dont la partie correspondant aux 28 premiers acides aminés a été retirée, et la séquence du site accepteur (SA) d'épissage de l'exon 2 de l'hF9, flanqué d'une séquence homologue au site de clivage de la nucléase à doigts de zinc (ZFN) de l'intron 1 de l'albumine humaine (hALB)
devafidugén civaparvovec	un vector de virus adeno asociado tipo 2/6 recombinante (rAAV Rep2-Cap6), no replicativo, que contiene un casete con el transgen de la alfa-L-iduronidasa humana (hIDUA) sin promotor, que codifica para el exón 1 parcial y los exones 2-14 completos con los primeros 28 amino ácidos eliminados, y la secuencia del sitio aceptor (SA) del splicing del exón 2 de hF9, flanqueado por una secuencia homóloga al sitio de rotura por la nuclease con dedos de zinc (ZFN) del intron 1 de la albúmina humana (hALB)
devimistatum	
devimistat	*rac*-(6*R*)-6,8-bis(benzylsulfanyl)octanoic acid
dévimistat	acide *rac*-(6*R*)-6,8-bis(benzylsulfanyl)octanoïque
devimistat	ácido *rac*-(6*R*)-6,8-bis(bencilsulfanil)octanoico
	$C_{22}H_{28}S_2O_2$  and enantiomer et énantiomère y enantiómero
disitamabum #	
disitamab	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; gamma1 heavy chain humanized (1-445) [VH (*Homo sapiens* IGHV1-69-2*01 (83.5%) -(IGHD) -IGHJ1*01 (92.9%)) [8.8.8] (1-115) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (212) (116-213), hinge (214-228), CH2 (229-338), CH3 E12 (354), M14 (357) (339-443), CHS (444-445)) (116-445)] (218-212')-disulfide with kappa light chain humanized (1'-212') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (83.3%) -IGKJ4*01 (100%))[6.3.7] (1'-105') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (151), V101 (189) (106'-212')]; dimer (224-224'':227-227'')-bisdisulfide

disitamab

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 (1-445) [VH (*Homo sapiens* IGHV1-69-2*01 (83.5%) -(IGHD) -IGHJ1*01 (92.9%)) [8.8.8] (1-115) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (212) (116-213), charnière (214-228), CH2 (229-338), CH3 E12 (354), M14 (357) (339-443), CHS (444-445)) (116-445)] (218-212')-disulfure avec la chaîne légère kappa humanisée (1'-212') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (83.3%) -IGKJ4*01 (100%)) [6.3.7] (1'-105') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (151), V101 (189) (106'-212')]; dimère (224-224":227-227")-bisdisulfure

disitamab

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 (1-445) [VH (*Homo sapiens* IGHV1-69-2*01 (83.5%) -(IGHD) -IGHJ1*01 (92.9%)) [8.8.8] (1-115) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (212) (116-213), bisagra (214-228), CH2 (229-338), CH3 E12 (354), M14 (357) (339-443), CHS (444-445)) (116-445)] (218-212')-disulfuro con la cadena ligera kappa humanizada (1'-212') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (83.3%) -IGKJ4*01 (100%)) [6.3.7] (1'-105') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (151), V101 (189) (106'-212')]; dímero (224-224":227-227")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVQSGAE VKKPGATVKI SCKVSGYTFT DYYIHWVQQA PGKGLEWMGR  50
VNPDHGDSYY NQKFKDKATI TADKSTDTAY MELSSLRSED TAVYFCARNY 100
LFDHWGQGTL 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
PSREEMTKNQ VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG 400
SFFLYSKLTV DKSRWQQGNV FSCSVMHEAL HNHYTQKSLS LSPGK      445
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS VSASVGDRVT ITCKASQDVG TAVAWYQQKP GKAPKLLIYW  50
ASIRHTGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCHQ FATYTFGGGT 100
KVEIKRTVAA PSVFIFPPSD EQLKSGTASV VCLLNNFYPR EAKVQWKVDN 150
ALQSGNSQES VTEQDSKDST YSLSSTLTLS KADYEKHKVY ACEVTHQGLS 200
SPVTKSFNRG EC                                         212
```

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'-88' 132'-192'
23'''-88''' 132'''-192'''
Inter-H-L (h 5-CL 126) 218-212' 218"-212'''
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"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

disitamabum vedotinum #

disitamab vedotin

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 conjugated to auristatin E;
gamma1 heavy chain humanized (1-445) [VH (*Homo sapiens* IGHV1-69-2*01 (83.5%) -(IGHD) -IGHJ1*01 (92.9%)) [8.8.8] (1-115) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (212) (116-213), hinge (214-228), CH2 (229-338), CH3 E12 (354), M14 (357) (339-443), CHS (444-445)) (116-445)] (218-212')-disulfide with kappa light chain humanized (1'-212') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (83.3%) -IGKJ4*01 (100%))[6.3.7] (1'-105') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (151), V101 (189) (106'-212')]; dimer (224-224'':227-227'')-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"*.*

disitamab védotine

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 conjugué à l'auristatine E;
chaîne lourde gamma1 humanisée (1-445) [VH (*Homo sapiens* IGHV1-69-2*01 (83.5%) -(IGHD) -IGHJ1*01 (92.9%)) [8.8.8] (1-115) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (212) (116-213), charnière (214-228), CH2 (229-338), CH3 E12 (354), M14 (357) (339-443), CHS (444-445)) (116-445)] (218-212')-disulfure avec lachaîne légère kappa humanisée (1'-212') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (83.3%) -IGKJ4*01 (100%)) [6.3.7] (1'-105') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (151), V101 (189) (106'-212')]; dimère (224-224'':227-227'')-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"*.*

disitamab vedotina

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 conjugado com la auristatina E;
cadena pesada gamma1 humanizada (1-445) [VH (*Homo sapiens* IGHV1-69-2*01 (83.5%) -(IGHD) -IGHJ1*01 (92.9%)) [8.8.8] (1-115) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (212) (116-213), bisagra (214-228), CH2 (229-338), CH3 E12 (354), M14 (357) (339-443), CHS (444-445)) (116-445)] (218-212')-disulfuro con la cadena ligera

kappa humanizada (1'-212') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (83.3%) -IGKJ4*01 (100%)) [6.3.7] (1'-105') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (151), V101 (189) (106'-212')]; dímero (224-224":227-227")-bisdisulfuro; conjugado con 4 restos cisteinil, por término médio, con monometilauristatina E (MMAE), mediante un conector escindible del tipo maleimidocaproil-valil-citrulinil-*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 VKKPGATVKI SCKVSGYTFT DYYIHWVQQA PGKGLEWMGR  50
VNPDHGDSYY NQKFKDKATI TADKSTDTAY MELSSLRSED TAVYFCARNY 100
LFDHWGQGTL 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
PSREEMTKNQ VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG 400
SFFLYSKLTV DKSRWQQGNV FSCSVMHEAL HNHYTQKSLS LSPGK      445
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS VSASVGDRVT ITCKASQDVG TAVAWYQQKP GKAPKLLIYW  50
ASIRHTGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCHQ FATYTFGGGT 100
KVEIKRTVAA PSVFIFPPSD EQLKSGTASV VCLLNNFYPR EAKVQWKVDN 150
ALQSGNSQES VTEQDSKDST YSLSSTLTLS KADYEKHKVY ACEVTHQGLS 200
SPVTKSFNRG EC                                          212
```

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'-88' 132'-192'
23'''-88''' 132'''-192'''
Inter-H-L (h 5-CL 126)* 218-212' 218"-212'''
Inter-H-H (h 11, h 14)* 224-224" 227-227"

*At least two of the four inter-chain disulfide bridges are not present, an average of 4 cysteinyl being conjugated each via a thioether bond to a drug linker.
*Au moins deux des quatre ponts disulfures inter-chaînes ne sont pas présents, 4 cystéinyl en moyenne étant chacun conjugué via une liaison thioéther à un linker-principe actif.
*Al menos dos de los cuatro puentes disulfuro inter-catenarios no estan presentes, 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:
295, 295"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

donanemabum #
donanemab

immunoglobulin G1-kappa, anti-[*Homo sapiens* APP (amyloid beta A4 precursor protein) A beta 3-pyroglutamyl peptides, Aβ 3 (3-x)], humanized monoclonal antibody;
gamma1 heavy chain humanized (1-444) [VH (*Homo sapiens* IGHV1-3*01 (84.7%) -(IGHD) -IGHJ4*01 (91.7%)) [8.8.8] (1-115) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 (CH1 K120 (212) (116-213), hinge (214-228), CH2 (229-338), CH3 D12 (354), L14 (356) (339-443), CHS K2>del (444)) (116-444)], (218-219')-disulfide with kappa light chain humanized (1'-219') [V-KAPPA (*Homo sapiens* IGKV2-29*02 (89.0%) -IGKJ2*02 (100%)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (158), V101 (196) (113'-219')]; dimer (224-224":227-227")-bisdisulfide

donanémab	immunoglobuline G1-kappa, anti-[*Homo sapiens* APP (précurseur de la protéine amyloïde bêta A4) peptides A bêta3-pyroglutamyl*,* Aβ 3 (3-X)], anticorps monoclonal humanisé; chaîne lourde gamma1 humanisée (1-444) [VH (*Homo sapiens* IGHV1-3*01 (84.7%) -(IGHD) -IGHJ4*01 (91.7%)) [8.8.8] (1-115) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 (CH1 K120 (212) (116-213), charnière (214-228), CH2 (229-338), CH3 D12 (354), L14 (356) (339-443), CHS K2>del (444)) (116-444)], (218-219')-disulfure avec la chaîne légère kappa humanisée (1'-219') [V-KAPPA (*Homo sapiens* IGKV2-29*02 (89.0%) -IGKJ2*02 (100%)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (158), V101 (196) (113'-219')]; dimère (224-224'':227-227'')-bisdisulfure
donanemab	inmunoglobulina G1-kappa, anti-[*Homo sapiens* APP (precursor de la proteína amiloide beta A4) péptidos A beta3-piroglutamil*,* Aβ 3 (3-X)], anticuerpo monoclonal humanizado; cadena pesada gamma1 humanizada (1-444) [VH (*Homo sapiens* IGHV1-3*01 (84.7%) -(IGHD) -IGHJ4*01 (91.7%)) [8.8.8] (1-115) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 (CH1 K120 (212) (116-213), bisagra (214-228), CH2 (229-338), CH3 D12 (354), L14 (356) (339-443), CHS K2>del (444)) (116-444)], (218-219')-disulfuro con la cadena ligera kappa humanizada (1'-219') [V-KAPPA (*Homo sapiens* IGKV2-29*02 (89.0%) -IGKJ2*02 (100%)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (158), V101 (196) (113'-219')]; dímero (224-224'':227-227'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGSSVKV SCKASGYDFT RYYINWVRQA PGQGLEWMGW  50
INPGSGNTKY NEKFKGRVTI TADESTSTAY MELSSLRSED TAVYYCAREG 100
ITVYWGQGTT 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 LSPG       444
```

Light chain / Chaîne légère / Cadena ligera

```
DIVMTQTPLS LSVTPGQPAS ISCKSSQSLL YSRGKTYLNW LLQKPGQSPQ  50
LLIYAVSKLD SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCVQGTHYP 100
FTFGQGTKLE IKRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK 150
VQWKVDNALQ SGNSQESVTE QDSKDSTYSL SSTLTLSKAD YEKHKVYACE 200
VTHQGLSSPV TKSFNRGEC                                   219
```

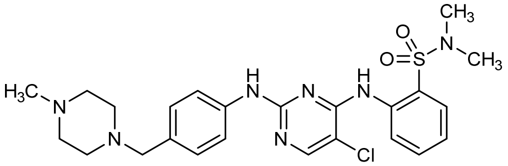
Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 142-198 259-319 365-423
22''-96'' 142''-198'' 259''-319'' 365''-423''
Intra-L (C23-C104) 23'-93' 139'-199'
23'''-93''' 139'''-199'''
Inter-H-L (h 5-CL 126) 218-219' 218''-219'''
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''
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

dubermatinibum

dubermatinib	3^5-chloro-*N*,*N*,7^4-trimethyl-2,4-diaza-3(4,2)-pyrimidina-7(1)-piperazina-1(1),5(1,4)-dibenzenaheptaphane-1^2-sulfonamide
dubermatinib	3^5-chloro-*N*,*N*,7^4-triméthyl-2,4-diaza-3(4,2)-pyrimidina-7(1)-piperazina-1(1),5(1,4)-dibenzenaheptaphane-1^2-sulfonamide
dubermatinib	3^5-cloro-*N*,*N*,7^4-trimetil-2,4-diaza-3(4,2)-pirimidina-7(1)-piperazina-1(1),5(1,4)-dibencenaheptafano-1^2-sulfonamida

$C_{24}H_{30}ClN_7O_2S$



efaprinerminum alfa #

efaprinermin alfa	tumor necrosis factor ligand superfamily protein TNFSF18 (human) extracellular (71-199)-peptide trimer [three fused copies (1-129, 130-258, 259-387)] fusion protein with immunoglobulin G1 (human) Fc fragment (227 C-terminal residues) (388-614), natural [D^{523}>E,L^{525}>M] variant [*Homo sapiens* IGHG1*03, hinge (388-397), CH2 (398-507), CH3 (508-612), CHS (613-614)], (393-393',396-396')-bisdisulfide dimer, produced in Chinese hamster ovary (CHO) cells, glycoform alfa
éfaprinermine alfa	membre 18 de la superfamille des ligands du facteur de nécrose tumorale humain TNFSF18, domaine extracellulaire (71-199)-trimère de peptides [trois copies fusionnées (1-129, 130-258, 259-387)], protéine de fusion avec le fragment Fc de l'immunoglobuline G1 humaine (227 résidus C-terminaux), (388-614), variant [D^{523}>E,L^{525}>M] naturel [*Homo sapiens* IGHG1*03, charnière (388-397), CH2 (398-507), CH3 (508-612), CHS (613-614)], (393-393',396-396')- dimère bisdisulfure, produit dans des cellules ovariennes de hamsters chinois (CHO), glycoforme alfa
efaprinermina alfa	miembro 18 de la superfamilia de los ligandos del factor de necrosis tumoral humano TNFSF18 dominio extracelular (71-199)-trímero de péptidos [tres copias fusionadas (1-129, 130-258, 259-387)], proteína de fusión con el fragmento Fc de la inmunoglobulina G1 humana (227 residuo C-terminal), (388-614), variante [D^{523}>E,L^{525}>M] naturel [*Homo sapiens* IGHG1*03, bisagra (388-397), CH2 (398-507), CH3 (508-612), CHS (613-614)], (393-393',396-396')- dímero bisdisulfuro, producido en las células ováricas de hamsters chinos (CHO), glicoforma alfa

```
LQLETAKEPC MAKFGPLPSK WQMASSEPPC VNKVSDWKLE ILQNGLYLIY  50
GQVAPNANYN DVAPFEVRLY KNKDMIQTLT NKSKIQNVGG TYELHVGDTI 100
DLIFNSEHQV LKNNTYWGII LLANPQFISL QLETAKEPCM AKFGPLPSKW 150
QMASSEPPCV NKVSDWKLEI LQNGLYLIYG QVAPNANYND VAPFEVRLYK 200
NKDMIQTLTN KSKIQNVGGT YELHVGDTID LIFNSEHQVL KNNTYWGIIL 250
LANPQFISLQ LETAKEPCMA KFGPLPSKWQ MASSEPPCVN KVSDWKLEIL 300
QNGLYLIYGQ VAPNANYNDV APFEVRLYKN KDMIQTLTNK SKIQNVGGTY 350
ELHVGDTIDL IFNSEHQVLK NNTYWGIILL ANPQFISDKT HTCPPCPAPE 400
LLGGPSVFLF PPKPKDTLMI SRTPEVTCVV VDVSHEDPEV KFNWYVDGVE 450
VHNAKTKPRE EQYNSTYRVV SVLTVLHQDW LNGKEYKCKV SNKALPAPIE 500
KTISKAKGQP REPQVYTLPP SREEMKTNQV SLTCLVKGFY PSDIAVEWES 550
NGQPENNYKT TPPVLDSDGS FFLYSKLTVD KSRWQQGNVF SCSVMHEALH 600
NHYTQKSLSL SPGK                                        614
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
intra-chain: 10-30, 139-159, 268-288, 428-488, 534-592,
10'-30', 139'-159', 268'-288', 428'-488', 534'-592'
inter-chain: 393-393', 396-396'

N-Glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
81, 113, 210, 242, 339, 371; 464

efgivanerminum alfa

efgivanermin alfa	immunoglobulin γ1 chain Fc fragment [*Homo sapiens* IGHG1*03 {hinge 1,4-del, C^{5}>L(1), CH2 (12-121), CH3 (122-226), CHS (227-228)}-(1-228)] fusion protein with pentakis(tetraglycyl-L-seryl)[*Homo sapiens* coronin-1A precursor (tryptophan aspartate-containing coat protein, TACO) fragment 430-461 (254-285)]-(229-285) fusion protein with tetraglycyl[*Homo sapiens* tumor necrosis factor ligand superfamily member 18 (glucocorticoid-induced TNF-related ligand) [N^{183}>D(401)]precursor fragment 72-199 (290-417)]-(286-417); hexamer stabilized with hexakisdisulfide bridges between 12 cysteines at position 7 and 10; produced in Chinese hamster ovary (CHO) cells, glycoform alfa
efgivanermine alfa	fragment Fc de l'immunoglobuline G1 [*Homo sapiens* IGHG1*03 {charnière 1,4-del, C^{5}>L(1), CH2 (12-121), CH3 (122-226), CHS (227-228)}-(1-228)] protéine de fusion avec le pentakis(tétraglycyl-L-séryl)[précurseur de la coronine-1A (protéine manteau contenant du tryptophane aspartate, TACO) *Homo sapiens* fragment 430-461 (254-285)]-(229-285) protéine de fusion avec le tétraglycyl[membre 18 de la superfamille des ligands du facteur de nécrose tumorale *Homo sapiens* (ligand apparenté au TNF induit par les glucocorticoïdes) [N^{183}>D(401)]précurseur fragment 72-199 (290-417)]-(286-417); hexamère stabilisé par des ponts hexakisdisulfure entre les 12 cystéines des positions 7 et 10, produit dans des cellules ovariennes de hamsters chinois (CHO), glycoforme alfa
efgivanermina alfa	fragmento Fc de la inmunoglobulina G1 [*Homo sapiens* IGHG1*03 {bisagra 1,4-del, C^{5}>L(1), CH2 (12-121), CH3 (122-226), CHS (227-228)}-(1-228)] proteína de fusión con pentakis(tetraglicil-L-seril)[precursor de la coronina-1A (proteína manteau que contiene triptófano aspartato, TACO) *Homo sapiens* fragmento 430-461 (254-285)]-(229-285) proteína de fusión con tetraglicil[miembro 18 de la

superfamilia de los ligandos del factor de necrosis tumoral *Homo sapiens* (ligando relacionado con TNF inducido por los glucocorticoides) [N^{183}>D(401)]precursor fragmento 72-199 (290-417)]-(286-417); hexámero estabilizado por los puentes hexakisdisulfuro entre las 12 cisteínas de las posiciones 7 y 10, producido en las células ováricas de hamsters chinos (CHO), glicoforma alfa

```
LDKTHTCPPC PAPELLGGPS VFLFPPKPKD TLMISRTPEV TCVVVDVSHE 50
DPEVKFNWYV DGVEVHNAKT KPREEQYNST YRVVSVLTVL HQDWLNGKEY 100
KCKVSNKALP APIEKTISKA KGQPREPQVY TLPPSREEMT KNQVSLTCLV 150
KGFYPSDIAV EWESNGQPEN NYKTTPPVLD SDGSFFLYSK LTVDKSRWQQ 200
GNVFSCSVMH EALHNHYTQK SLSLSPGKGG GGSGGGGSGG GGSGGGGSGG 250
GGSVSRLEEE MRKLQATVQE LQKRLDRLEE TVQAKGGGGQ LETAKEPCMA 300
KFGPLPSKWQ MASSEPPCVN KVSDWKLEIL QNGLYLIYGQ VAPNANYNDV 350
APFEVRLYKN KDMIQTLTNK SKIQNVGGTY ELHVGDTIDL IFNSEHQVLK 400
DNTYWGIILL ANPQFIS                                     417
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Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
intra-chain: 42-102 148-206 298-318 (in each chain of the hexamer)
inter-chain: 7-7' 10-10' (in each of the three dimeric subunits)

N-Glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
Asn-78

elipovimabum #

elipovimab

immunoglobulin G1-lambda, anti-[human immunodeficiency virus type 1 (HIV-1) gp120 envelope glycoprotein (HIV-1 gp120)], *Homo sapiens* monoclonal antibody;
gamma1 heavy chain *Homo sapiens* (1-462) [VH (*Homo sapiens* IGHV4-59*01 (78.4%) -(IGHD) - IGHJ3*01(84.6%)) [8.7.26] (1-132) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (229) (133-230), hinge (231-245), CH2 G1.1>A (251), S3>D (254), A115>L (345), I117>E (347) (246-355), CH3 E12 (371), M14 (373), M107>L (443), N114>S (449) (356-460), CHS (461-462)) (133-462)], (235-210')-disulfide with lambda light chain *Homo sapiens* (1'-211') [V-LAMBDA (*Homo sapiens* IGLV3-21*01 (67.4%) -IGLJ3*02 (91.7%)) [6.3.13] (1'-105') -*Homo sapiens* IGLC2*01 (100%) (106'-211')]; dimer (241-241'':244-244'')-bisdisulfide

élipovimab

immunoglobuline G1-lambda, anti-[virus de l'immunodéficience humaine de type 1 (HIV-1) protéine d'enveloppe gp120 (HIV-1 gp120)], anticorps monoclonal *Homo sapiens*;
chaîne lourde gamma1 *Homo sapiens* (1-462) [VH (*Homo sapiens* IGHV4-59*01 (78.4%) -(IGHD) - IGHJ3*01(84.6%)) [8.7.26] (1-132) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (229) (133-230), charnière (231-245), CH2 G1.1>A (251), S3>D (254), A115>L (345), I117>E (347) (246-355), CH3 E12 (371), M14 (373), M107>L (443), N114>S (449) (356-460), CHS (461-462)) (133-462)], (235-210')-disulfure avec la chaîne légère lambda *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV3-21*01 (67.4%) -IGLJ3*02 (91.7%)) [6.3.13] (1'-105') -*Homo sapiens* IGLC2*01 (100%) (106'-211')]; dimère (241-241'':244-244'')-bisdisulfure

elipovimab

inmunoglobulina G1-lambda, anti-[virus de la inmunodeficiencia humana de tipo 1 (HIV-1) proteína de la envoltura gp120 (HIV-1 gp120)], anticuerpo monoclonal *Homo sapiens*;
cadena pesada gamma1 *Homo sapiens* (1-462) [VH (*Homo sapiens* IGHV4-59*01 (78.4%) -(IGHD) - IGHJ3*01(84.6%)) [8.7.26] (1-132) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (229) (133-230), bisagra (231-245), CH2 G1.1>A (251), S3>D (254), A115>L (345), I117>E (347) (246-355), CH3 E12 (371), M14 (373), M107>L (443), N114>S (449) (356-460), CHS (461-462)) (133-462)], (235-210')-disulfuro con la cadena ligera lambda *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV3-21*01 (67.4%) -IGLJ3*02 (91.7%)) [6.3.13] (1'-105') -*Homo sapiens* IGLC2*01 (100%) (106'-211')]; dímero (241-241'':244-244'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QMQLQESGPG LVKPSETLSL TCSVSGASIS DSYWSWIRRS PGKGLEWIGY  50
VHKSGDTNYN PSLKSRVHLS LDTSKNQVSL SLTGVTAADS GKYYCARTLH 100
GRRIYGIVAF NEWFTYFYMD VWGTGTQVTV SSASTKGPSV FPLAPSSKST 150
SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ SSGLYSLSSV 200
VTVPSSSLGT QTYICNVNHK PSNTKVDKKV EPKSCDKTHT CPPCPAPELL 250
AGPDVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH 300
NAKTKPREEQ YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPLPEEKT 350
ISKAKGQPRE PQVYTLPPSR EEMTKNQVSL TCLVKGFYPS DIAVEWESNG 400
QPENNYKTTP PVLDSDGSFF LYSKLTVDKS RWQQGNVFSC SVLHEALHSH 450
YTQKSLSLSP GK                                          462
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Light chain / Chaîne légère / Cadena ligera

```
SDISVAPGET ARISCGEKSL GSRAVQWYQH RAGQAPSLII YNNQDRPSGI  50
PERFSGSPDS RPGTTATLTI TSVEAGDEAD YYCHIWDSRV PTKWVFGGGT 100
TLTVLGQPKA APSVTLFPPS SEELQANKAT LVCLISDFYP GAVTVAWKAD 150
SSPVKAGVET TTPSKQSNNK YAASSYLSLT PEQWKSHRSY SCQVTHEGST 200
VEKTVAPTEC S                                           211
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Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-95 159-215 276-336 382-440
22''-95'' 159''-215'' 276''-336'' 382''-440''
Intra-L (C23-C104) 15'-83' 133'-192'
15'''-83''' 133'''-192'''
Inter-H-L (h 5-CL 126) 235-210' 235''-210'''
Inter-H-H (h 11, h 14) 241-241'' 244-244''

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

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.
C-terminal lysine clipping:
H CHS K2:
462, 462''

envafolimabum #
envafolimab

immunoglobulin VH-h-CH2-CH3 gamma1 chain dimer, anti-[*Homo sapiens* CD274 (programmed death ligand 1, PDL1, PD-L1, B7 homolog 1, B7H1)], monoclonal antibody;
gamma1 heavy chain VH-h-CH2-CH3 (1-360) [VH (*Vicugna pacos* IGHV3-3*01 (80.6%) -(IGHD) -IGHJ5*01 (92.3%)/*Homo sapiens* IGHV3-64*04 (78.4%) -(IGHD) -IGHJ1*01 (92.3%)) [8.8.21] (1-128) -*Homo sapiens* IGHG1*01 G1m1 (hinge 1-15, C5>S (133) (129-143), CH2 (144-253) D27>A (178), P116>G (244), CH3 D12 (269) L14 (271) (254-358), CHS (359-360)) (129-360)]; dimer (139-139'':142-142'')-bisdisulfide

envafolimab

immunoglobuline dimère de chaînes gamma1 VH-h-CH2-CH3, anti-[*Homo sapiens* CD274 (ligand 1 de mort programmée, PDL1, PD-L1, homologue 1 de B7, B7H1)], anticorps monoclonal;
chaîne lourde gamma1 VH-h-CH2-CH3 (1-360) [VH (*Vicugna pacos* IGHV3-3*01 (80.6%) -(IGHD) -IGHJ5*01 (92.3%)/*Homo sapiens* IGHV3-64*04 (78.4%) -(IGHD) -IGHJ1*01 (92.3%)) [8.8.21] (1-128) -*Homo sapiens* IGHG1*01 G1m1 (charnière 1-15, C5>S (133) (129-143), CH2 (144-253) D27>A (178), P116>G (244), CH3 D12 (269) L14 (271) (254-358), CHS (359-360)) (129-360)]; dimère (139-139":142-142")-bisdisulfure

envafolimab

inmunoglobulina dímero de cadenas gamma1 VH-h-CH2-CH3, anti-[*Homo sapiens* CD274 (ligando 1 de muerte programada, PDL1, PD-L1, homólogo 1 de B7, B7H1)], anticuerpo monoclonal;
cadena pesada gamma1 VH-h-CH2-CH3 (1-360) [VH (*Vicugna pacos* IGHV3-3*01 (80.6%) -(IGHD) -IGHJ5*01 (92.3%)/*Homo sapiens* IGHV3-64*04 (78.4%) -(IGHD) -IGHJ1*01 (92.3%)) [8.8.21] (1-128) -*Homo sapiens* IGHG1*01 G1m1 (bisagra 1-15, C5>S (133) (129-143), CH2 (144-253) D27>A (178), P116>G (244), CH3 D12 (269) L14 (271) (254-358), CHS (359-360)) (129-360)]; dímero (139-139":142-142")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVESGGG LVQPGGSLRL SCAASGKMSS RRCMAWFRQA PGKERERVAK   50
LLTTSGSTYL ADSVKGRFTI SRDNSKNTVY LQMNSLRAED TAVYYCAADS  100
FEDPTCTLVT SSGAFQYWGQ GTLVTVSSEP KSSDKTHTCP PCPAPELLGG  150
PSVFLFPPKP KDTLMISRTP EVTCVVVAVS HEDPEVKFNW YVDGVEVHNA  200
KTKPREEQYN STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAGIEKTIS  250
KAKGQPREPQ VYTLPPSRDE LTKNQVSLTC LVKGFYPSDI AVEWESNGQP  300
ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT  350
QKSLSLSPGK                                              360
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Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 33-106 174-234 280-338
22"-96" 33"-106" 174"-234" 280"-338"
Inter-H-H (h 11, h 14) 139-139" 142-142"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
210, 210"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

esafoxolanerum

esafoxolaner

4-[(5*S*)-5-[3-chloro-5-(trifluoromethyl)phenyl]-5-(trifluoromethyl)-4,5-dihydro-1,2-oxazol-3-yl]-*N*-{2-oxo-2-[(2,2,2-trifluoroethyl)amino]ethyl}naphthalene-1-carboxamide

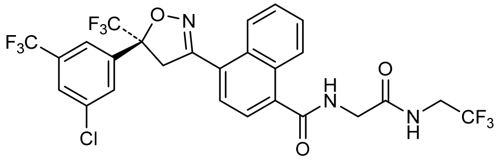
ésafoxolaner

4-[(5*S*)-5-[3-chloro-5-(trifluorométhyl)phényl]-5-(trifluorométhyl)-4,5-dihydro-1,2-oxazol-3-yl]-*N*-{2-oxo-2-[(2,2,2-trifluoroéthyl)amino]éthyl}naphtalène-1-carboxamide

esafoxolaner

4-[(5*S*)-5-[3-cloro-5-(trifluorometil)fenil]-5-(trifluorometil)-4,5-dihidro-1,2-oxazol-3-il]-*N*-{2-oxo-2-[(2,2,2-trifluoroetil)amino]etil}naftaleno-1-carboxamida

$C_{26}H_{17}ClF_9N_3O_3$



etokimabum #

etokimab	immunoglobulin G1-kappa, anti-[*Homo sapiens* IL33 (interleukin 33, interleukin-1 family member 11, IL1F11, nuclear factor for high endothelial venules, NF-HEV)], humanized monoclonal antibody; gamma1 heavy chain humanized (1-452) [VH (*Homo sapiens* IGHV1-46*01 (87.8%) -(IGHD) -IGHJ1*01 (100%)) [8.8.15] (1-122) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 (CH1 K120 (219) (123-220), hinge (221-235), CH2 D12 (361), L14 (363) (236-345), CH3 (346-450), CHS (451-452)) (123-452)], (225-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-9*01 (85.3%) -IGKJ2*02 (90.9%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (231-231":234-234")-bisdisulfide
étokimab	immunoglobuline G1-kappa, anti-[*Homo sapiens IL33* (interleukine 33*,* membre 11 de la famille 1 d'interleukines, IL1F11, facteur nucléaire des veinules à haut endothélium, NF-HEV*)*], anticorps monoclonal humanisé; chaîne lourde gamma1 humanisée (1-452) [VH (*Homo sapiens* IGHV1-46*01 (87.8%) -(IGHD) -IGHJ1*01 (100%)) [8.8.15] (1-122) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 (CH1 K120 (219) (123-220), charnière (221-235), CH2 D12 (361), L14 (363) (236-345), CH3 (346-450), CHS (451-452)) (123-452)], (225-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-9*01 (85.3%) -IGKJ2*02 (90.9%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (231-231":234-234")-bisdisulfure
etokimab	inmunoglobulina G1-kappa, anti-[*Homo sapiens IL33* (interleukina 33, miembro 11 de la familia 1 de interleukinas, IL1F11, factor nuclear de las vénulas del endotelio alto NF-HEV*)*], anticuerpo monoclonal humanizado; cadena pesada gamma1 humanizada (1-452) [VH (*Homo sapiens* IGHV1-46*01 (87.8%) -(IGHD) -IGHJ1*01 (100%)) [8.8.15] (1-122) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 (CH1 K120 (219) (123-220), bisagra (221-235), CH2 D12 (361), L14 (363) (236-345), CH3 (346-450), CHS (451-452)) (123-452)], (225-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-9*01 (85.3%) -IGKJ2*02 (90.9%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (231-231":234-234")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada
```
QVQLMQSGAE VKKPGASVKV SCKASGYTFT SYWMHWVRQA PGQGLEWMGT  50
IYPRNSNTDY NQKFKARVTM TRDTSTSTVY MELSSLRSED TAVYYCARPL 100
YYYLTSPPTL FWGQGTLVTV 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
```
DIQLTQSPSF LSASVGDRVT ITCKASQDVG TAVAWYQQKP GKAPKLLIYW  50
ASTRHTGVPS RFSGSGSGTE FTLTISSLQP EDFATYYCQQ AKTYPFTFGS 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) 22-96 149-205 266-326 372-430
22''-96'' 149''-205'' 266''-326'' 372''-430''
Intra-L (C23-C104) 23'-88' 134'-194'
23'''-88''' 134'''-194'''
Inter-H-L (h 5-CL 126) 225-214' 225''-214'''
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.
C-terminal lysine clipping:
H CHS K2:
452, 452''

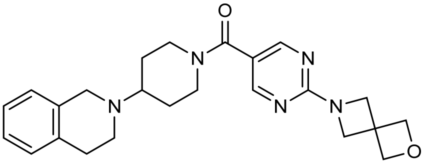
etranacogenum dezaparvovecum #

etranacogene dezaparvovec	a recombinant non-replicating adeno-associated virus serotype 5 (AAV5) expressing the Padua variant (R338L) of human coagulation factor IX (F9, Factor IX, or FIX), under the control of the liver-specific promoter (LP1); the genomic inverted terminal repeats (ITR) are derived from AAV serotype 2 (AAV2) ITRs while the vector is encapsidated in a serotype 5 AAV protein capsid.
étranacogène dezaparvovec	vecteur viral adéno-associé de sérotype 5 (AAV5) recombinant, non-répliquant, exprimant le variant Padua (R338L) du facteur de coagulation IX humain (F9, Facteur IX, FIX), sous le contrôle du promoteur spécifique du foie (LP1); les séquences inverses terminales répétées (ITR) dérivent des ITR de l'AAV de sérotype 2 (AAV2) alors que le vecteur est encapsulé dans la capside protéique d'un AAV de sérotype 5.
etranacogén dezaparvovec	un virus adeno asociado serotipo 5 (AAV5) recombinante, no replicativo, que expresa la variante Padua (R338L) del factor de coagulación IX (F9, Factor IX, o FIX) humano, bajo el control del promotor específico de hígado (LP1); las secuencias terminales invertidas (ITR) derivan de las ITR del AAV serotipo 2 (AAV2) mientras que el vector está encapsidado en la cápside proteíca de AAV serotipo 5

fadaltranum

fadaltran	[4-(3,4-dihydroisoquinolin-2(1*H*)-yl)piperidin-1-yl][2-(2-oxa-6-azaspiro[3.3]heptan-6-yl)pyrimidin-5-yl]methanone
fadaltran	[4-(3,4-dihydroisoquinoléin-2(1*H*)-yl)pipéridin-1-yl][2-(2-oxa-6-azaspiro[3.3]heptan-6-yl)pyrimidin-5-yl]méthanone
fadaltran	[4-(3,4-dihidroisoquinolein-2(1*H*)-il)piperidin-1-il][2-(2-oxa-6-azaspiro[3.3]heptan-6-il)pirimidin-5-il]metanona

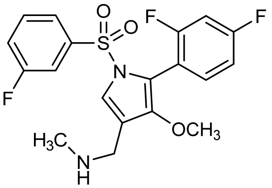
$C_{24}H_{29}N_5O_2$



fexuprazanum

fexuprazan	1-[5-(2,4-difluorophenyl)-1-(3-fluorobenzene-1-sulfonyl)-4-methoxy-1*H*-pyrrol-3-yl]-*N*-methylmethanamine
fexuprazan	1-[5-(2,4-difluorophényl)-1-(3-fluorobenzène-1-sulfonyl)-4-méthoxy-1*H*-pyrrol-3-yl]-*N*-méthylméthanamine
fexuprazán	1-[5-(2,4-difluorofenil)-1-(3-fluorobenceno-1-sulfonil)-4-metoxi-1*H*-pirrol-3-il]-*N*-metilmetanamina

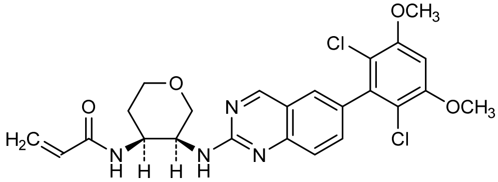
$C_{19}H_{17}F_3N_2O_3S$



fisogatinibum

fisogatinib	*N*-[(3*S*,4*S*)-3-{[6-(2,6-dichloro-3,5-dimethoxyphenyl)quinazolin-2-yl]amino}oxan-4-yl]prop-2-enamide
fisogatinib	*N*-[(3*S*,4*S*)-3-{[6-(2,6-dichloro-3,5-diméthoxyphényl)quinazolin-2-yl]amino}oxan-4-yl]prop-2-énamide
fisogatinib	*N*-[(3*S*,4*S*)-3-{[6-(2,6-dicloro-3,5-dimetoxifenil)quinazolin-2-il]amino}oxan-4-il]prop-2-enamida

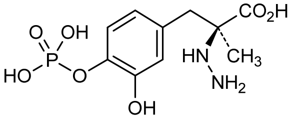
$C_{24}H_{24}Cl_2N_4O_4$



foscarbidopum

foscarbidopa	(2*S*)-2-hydrazinyl-3-[3-hydroxy-4-(phosphonooxy)phenyl]-2-methylpropanoic acid
foscarbidopa	acide (2*S*)-2-hydrazinyl-3-[3-hydroxy-4-(phosphonooxy)phényl]-2-méthylpropanoïque
foscarbidopa	ácido (2*S*)-2-hidrazinil-3-[3-hidroxi-4-(fosfonooxi)fenil]-2-metilpropanoico

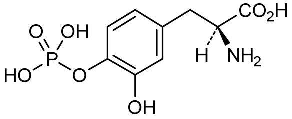
$C_{10}H_{15}N_2O_7P$



foslevodopum

foslevodopa	3-hydroxy-*O*-phosphono-L-tyrosine
foslévodopa	3-hydroxy-*O*-phosphono-L-tyrosine
foslevodopa	3-hidroxi-*O*-fosfono-L-tirosina

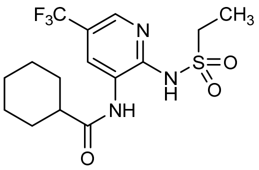
$C_9H_{12}NO_7P$



fuzapladibum

fuzapladib	*N*-[2-(ethanesulfonamido)-5-(trifluoromethyl)pyridin-3-yl]cyclohexanecarboxamide
fuzapladib	*N*-[2-(éthanesulfonamido)-5-(trifluorométhyl)pyridin-3-yl]cyclohexanecarboxamide
fuzapladib	*N*-[2-(etanosulfonamido)-5-(trifluorometil)piridin-3-il]ciclohexanocarboxamida

$C_{15}H_{20}F_3N_3O_3S$



garadacimabum #

garadacimab

immunoglobulin G4-lambda, anti-[*Homo sapiens* F12 (coagulation factor XII, Hageman factor) activated (F12a, FXIIa)], monoclonal antibody;
gamma1 heavy chain (1-456) [VH (*Homo sapiens* IGHV3-23*01 (87.8%) -(IGHD) - IGHJ1*01 (90.0%)) [8.8.22] (1-128) -1-mer seryl linker (129) -*Homo sapiens* IGHG4*01 (CH1 (130-227), hinge S10>P (237) (228-239), CH2 (240-349), CH3 (350-454), CHS (455-456)) (130-456)], (143-214')-disulfide with lambda light chain (1'-215') [V-LAMBDA (*Homo sapiens* IGLV1-47*02 (96.9%) -IGLJ2*01 (100%)) [8.3.10] (1'-109') -*Homo sapiens* IGLC2*01 (100%) (110'-215')]; dimer (235-235'':238-238'')-bisdisulfide

garadacimab

immunoglobuline G4-lambda, anti-[*Homo sapiens* F12 (facteur de coagulation XII, Facteur Hageman) activé (F12a, FXIIa)], anticorps monoclonal;
chaîne lourde gamma1 (1-456) [VH (*Homo sapiens* IGHV3-23*01 (87.8%) (IGHD) - IGHJ1*01 (90.0%)) [8.8.22] (1-128) -1-mer séryl linker (129) -*Homo sapiens* IGHG4*01 (CH1 (130-227), charnière S10>P (237) (228-239), CH2 (240-349), CH3 (350-454), CHS (455-456)) (130-456)], (143-214')-disulfure avec la chaîne légère lambda (1'-215') [V-LAMBDA (*Homo sapiens* IGLV1-47*02 (96.9%) - IGLJ2*01(100%)) [8.3.10] (1'-109') -*Homo sapiens* IGLC2*01 (100%) (110'-215')]; dimère (235-235'':238-238'')-bisdisulfure

garadacimab

inmunoglobulina G4-lambda, anti-[*Homo sapiens* F12 (factor de coagulación XII, Factor Hageman) activado (F12a, FXIIa)], anticuerpo monoclonal;
cadena pesada gamma1 (1-456) [VH (*Homo sapiens* IGHV3-23*01 (87.8%) (IGHD) - IGHJ1*01 (90.0%)) [8.8.22] (1-128) -1-mer seril conector (129) -*Homo sapiens* IGHG4*01 (CH1 (130-227), bisagra S10>P (237) (228-239), CH2 (240-349), CH3 (350-454), CHS (455-456)) (130-456)], (143-214')-disulfuro con la cadena ligera lambda (1'-215') [V-LAMBDA (*Homo sapiens* IGLV1-47*02 (96.9%) - IGLJ2*01(100%)) [8.3.10] (1'-109') -*Homo sapiens* IGLC2*01 (100%) (110'-215')]; dímero (235-235'':238-238'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLLESGGG LVQPGGSLRL SCAASGFTFS KYIMQWVRQA PGKGLEWVSG  50
IDIPTKGTVY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARAL 100
PRSGYLISPH YYYYALDVWG QGTTVTVSSA STKGPSVFPL APCSRSTSES 150
TAALGCLVKD YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV 200
PSSSLGTKTY TCNVDHKPSN TKVDKRVESK YGPPCPPCPA PEFLGGPSVF 250
LFPPKPKDTL MISRTPEVTC VVVDVSQEDP EVQFNWYVDG VEVHNAKTKP 300
REEQFNSTYR VVSVLTVLHQ DWLNGKEYKC KVSNKGLPSS IEKTISKAKG 350
QPREPQVYTL PPSQEEMTKN QVSLTCLVKG FYPSDIAVEW ESNGQPENNY 400
KTTPPVLDSD GSFFLYSRLT VDKSRWQEGN VFSCSVMHEA LHNHYTQKSL 450
SLSLGK                                                 456
```

Light chain / Chaîne légère / Cadena ligera

```
QSVLTQPPSA SGTPGQRVTI SCSGSSSNIG RNYVYWYQQL PGTAPKLLIY  50
SNNQRPSGVP DRFSGSKSGT SASLAISGLR SEDEADYYCA AWDASLRGVF 100
GGGTKLTVLG QPKAAPSVTL FPPSSEELQA NKATLVCLIS DFYPGAVTVA 150
WKADSSPVKA GVETTTPSKQ SNNKYAASSY LSLTPEQWKS HRSYSCQVTH 200
EGSTVEKTVA PTECS                                       215
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 156-212 270-330 376-434
22''-96'' 156''-212'' 270''-330'' 376''-434''
Intra-L (C23-C104) 22'-89' 137'-196'
22'''-89''' 137'''-196'''
Inter-H-L (CH1 10-CL 126) 143-214' 143''-214'''
Inter-H-H (h 8, h 11) 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

garetosmabum #

garetosmab

immunoglobulin G4-kappa, anti-[*Homo sapiens* INHBA (inhibin subunit beta A, activin A (INHBA homodimer), activin AB (INHBA/INHBB dimer) and activin AC (INHBA/INHBC dimer)], monoclonal antibody;
gamma4 heavy chain (1-453) [VH (*Homo sapiens* IGHV4-59*01 (88.7%) -(IGHD) -IGHJ3*02 (93.3%)) [8.7.20] (1-126) -*Homo sapiens* IGHG4*01 (CH1 (127-224), hinge S10>P (234) (225-236), CH2 (237-346), CH3 (347-451), CHS (452-453)) (127-453)], (140-215')-disulfide with kappa light chain (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (100%) -IGKJ1*01 (100%)) [7.3.9] (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V (192) (109'-215')]; dimer (232-232'':235-235'')-bisdisulfide

garétosmab

immunoglobuline G4-kappa, anti-[*Homo sapiens* INHBA (sous-unité inhibine bêta A, activine A (homodimère INHBA), activine AB (dimère INHBA/INHBB) et activine AC (dimère INHBA/INHBC)], anticorps monoclonal;
chaîne lourde gamma4 (1-453) [*Homo sapiens* VH (IGHV4-59*01 (88.7%) -(IGHD) -IGHJ3*02 (93.3%)) [8.7.20] (1-126) -*Homo sapiens* IGHG4*01 (CH1 (127-224), charnière S10>P (234) (225-236), CH2 (237-346), CH3 (347-451), CHS (452-453)) (127-453)], (140-215')-disulfure avec la chaîne légère kappa (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (100%) -IGKJ1*01 (100%)) [7.3.9] (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V (192) (109'-215')]; dimère (232-232'':235-235'')-bisdisulfure

garetosmab

inmunoglobulina G4-kappa, anti-[*Homo sapiens* INHBA (subunidad inhibina beta A, activina A (homodímero INHBA), activina AB (dímero INHBA/INHBB) y activina AC (dímero INHBA/INHBC)], anticuerpo monoclonal;
cadena pesada gamma4 (1-453) [*Homo sapiens* VH (IGHV4-59*01 (88.7%) -(IGHD) -IGHJ3*02 (93.3%)) [8.7.20] (1-126) -*Homo sapiens* IGHG4*01 (CH1 (127-224), bisagra S10>P (234) (225-236), CH2 (237-346), CH3 (347-451), CHS (452-453)) (127-453)], (140-215')-disulfuro con la cadena ligera kappa (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (100%) -IGKJ1*01 (100%)) [7.3.9] (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V (192) (109'-215')]; dímero (232-232'':235-235'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLQESGPG LVKPSETLSL TCTVSGGSFS SHFWSWIRQP PGKGLEWIGY  50
ILYTGGTSFN PSLKSRVSMS VGTSKNQFSL KLSSVTAADT AVYYCARARS 100
GITFTGIIVP GSFDIWGQGT MVTVSSASTK GPSVFPLAPC SRSTSESTAA 150
LGCLVKDYFP EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVVTVPSS 200
SLGTKTYTCN VDHKPSNTKV DKRVESKYGP PCPPCPAPEF LGGPSVFLFP 250
PKPKDTLMIS RTPEVTCVVV DVSQEDPEVQ FNWYVDGVEV HNAKTKPREE 300
QFNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKGLPSSIEK TISKAKGQPR 350
EPQVYTLPPS QEEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT 400
PPVLDSDGSF FLYSRLTVDK SRWQEGNVFS CSVMHEALHN HYTQKSLSLS 450
LGK                                                   453
```

Light chain / Chaîne légère / Cadena ligera

```
EIVLTQSPGT LSLSPGERAT LSCRASQSVS SSYLAWYQQK PGQAPRLLIY  50
GASSRATGIP DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QYGSSPWTFG 100
QGTKVEIKRT 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) 22-95 153-209 267-327 373-431
22''-95'' 153''-209'' 267''-327'' 373''-431''
Intra-L (C23-C104) 23'-89' 135'-195'
23'''-89''' 135'''-195'''
Inter-H-L (CH1 10-CL 126) 140-215' 140''-215'''
Inter-H-H (h 8, h 11) 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

C-terminal lysine clipping:
H CHS K2:
453, 453''

glenzocimabum #

glenzocimab

immunoglobulin Fab G1-kappa, anti-[*Homo sapiens* GP6 (glycoprotein VI platelet, glycoprotein VI (platelet), GPVI, platelet glycoprotein VI)], humanized monoclonal antibody;
gamma1 heavy chain VH-CH1 humanized (1-227) [VH (*Homo sapiens* IGHV1-46*01 (92.9%) -(IGHD) -IGHJ4*01 (93.3%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*01, G1m17 (CH1 K120 (217) (121-218), hinge 1-9 (219-227)) (121-227)], (223-214')-disulfide with kappa light chain humanized (1'-219') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (80.0%) -IGKJ1*01 (100%)) [11.3.9] (1'-111') -1-mer (112') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]

glenzocimab

immunoglobuline Fab G1-kappa, anti-[*Homo sapiens* GP6 (glycoprotéine VI de la plaquette, glycoprotéine VI (plaquette), GPVI, glycoprotéine plaquettaire VI)], anticorps monoclonal humanisé;
chaîne lourde gamma1 VH-CH1 humanisée (1-227) [VH (*Homo sapiens* IGHV1-46*01 (92.9%) -(IGHD) -IGHJ4*01 (93.3%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*01, G1m17 (CH1 K120 (217) (121-218), charnière 1-9 (219-227)) (121-227)], (223-214')-disulfure avec la chaîne légère kappa humanisée (1'-219') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (80.0%) -IGKJ1*01 (100%)) [11.3.9] (1'-111') -1-mer (112') -*Homo sapiens* IGKC*01 (100%), Km3, A45.1 (158), V101 (196) (113'-219')]

glenzocimab

inmunoglobulina Fab G1-kappa, anti-[*Homo sapiens* GP6 (glicoproteína VI de la plaqueta, glicoproteína VI (plaqueta), GPVI, glicoproteína plaquetaria VI)], anticuerpo monoclonal humanizado;
cadena pesada gamma1 VH-CH1 humanizada (1-227) [VH (*Homo sapiens* IGHV1-46*01 (92.9%) -(IGHD) -IGHJ4*01 (93.3%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*01, G1m17 (CH1 K120 (217) (121-218), bisagra 1-9 (219-227)) (121-227)], (223-214')-disulfuro con la cadena ligera kappa humanizada (1'-219') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (80.0%) -IGKJ1*01 (100%)) [11.3.9] (1'-111') -1-mer (112') -*Homo sapiens* IGKC*01 (100%), Km3, A45.1 (158), V101 (196) (113'-219')]

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGASVKV SCKASGYTFT SYNMHWVRQA PGQGLEWMGG  50
IYPGNGDTSY NQKFQGRVTM TRDTSTSTVY MELSSLRSED TAVYYCARGT 100
VVGDWYFDVW GQGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKKVEP KSCDKTH                          227
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCRSSQSLE NSNGNTYLNW YQQKPGKAPK  50
LLIYRVSNRF SGVPSRFSGS GSGTDFTFTI SSLQPEDIAT YYCLQLTHVP 100
WTFGQGTKVE ITRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK 150
VQWKVDNALQ SGNSQESVTE QDSKDSTYSL SSTLTLSKAD YEKHKVYACE 200
VTHQGLSSPV TKSFNRGEC                                   219
```

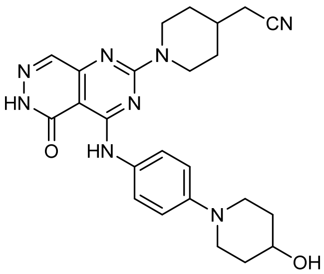
Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 147-203
Intra-L (C23-C104) 23'-93' 139'-199'
Inter-H-L (h 5-CL 126) 223-219'

No N-glycosylation sites / pas de sites de N-glycosylation / ningún positión de N-glicosilación

gusacitinibum

gusacitinib

(1-{4-[4-(4-hydroxypiperidin-1-yl)anilino]-5-oxo-5,6-dihydropyrimido[4,5-*d*]pyridazin-2-yl}piperidin-4-yl)acetonitrile

gusacitinib	(1-{4-[4-(4-hydroxypipéridin-1-yl)anilino]-5-oxo-5,6-dihydropyrimido[4,5-*d*]pyridazin-2-yl}pipéridin-4-yl)acetonitrile
gusacitinib	(1-{4-[4-(4-hidroxipiperidin-1-il)anilino]-5-oxo-5,6-dihidropirimido[4,5-*d*]piridazin-2-il}piperidin-4-il)acetonitrile $C_{24}H_{28}N_8O_2$ 

ieramilimabum #

ieramilimab	immunoglobulin G4-kappa, anti-[*Homo sapiens* LAG3 (lymphocyte activating 3, lymphocyte-activation 3, CD223)], humanized monoclonal antibody; gamma4 heavy chain humanized (1-451) [VH (*Homo sapiens* IGHV7-4-1*02 (85.7%) -(IGHD) -IGHJ4*01 (92.3%)) [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 K2>del (451)) (126-451)], (139-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGVK1-33*01 (83.2%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (231-231'':234-234'')-bisdisulfide
iéramilimab	immunoglobuline G4-kappa, anti-[*Homo sapiens* LAG3 (activateur 3 des lymphocytes, lymphocyte-activation 3, CD223)], anticorps monoclonal humanisé; chaîne lourde gamma4 humanisée (1-451) [VH (*Homo sapiens* IGHV7-4-1*02 (85.7%) -(IGHD) - IGHJ4*01 (92.3%)) [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 K2>del (451)) (126-451)], (139-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGVK1-33*01 (83.2%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (231-231'':234-234'')-bisdisulfure
ieramilimab	inmunoglobulina G4-kappa, anti-[*Homo sapiens* LAG3 (activador 3 de los linfocitos, linfocito-activación 3, CD223)], anticuerpo monoclonal humanizado;

cadena pesada gamma4 humanizada (1-451) [VH (*Homo sapiens* IGHV7-4-1*02 (85.7%) -(IGHD) -IGHJ4*01 (92.3%)) [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 K2>del (451)) (126-451)], (139-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (83.2%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (231-231'':234-234'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGASVKV SCKASGFTLT NYGMNWVRQA RGQRLEWIGW  50
INTDTGEPTY ADDFKGRFVF SLDTSVSTAY LQISSLKAED TAVYYCARNP 100
PYYYGTNNAE AMDYWGQGTT 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
G                                                     451
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCSSSQDIS NYLNWYLQKP GQSPQLLIYY  50
TSTLHLGVPS RFSGSGSGTE FTLTISSLQP DDFATYYCQQ YYNLPWTFGQ 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) 22-96 152-208 266-326 372-430
22''-96'' 152''-208'' 266''-326'' 372''-420''
Intra-L (C23-C104) 23'-88' 134'-194'
23'''-88''' 134'''-194'''
Inter-H-L (CH1 10-CL 126) 139-214' 139''-214'''
Inter-H-H (h 8, h 11) 231-231'' 234-234''

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

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

inbakiceptum

inbakicept

interleukin 15 receptor subunit alpha (human IL15Rα) (1-65)-peptide (sushi domain-containing) fusion protein with human immunoglobulin G1 Fc fragment (232 C-terminal residues) (66-297) [*Homo sapiens* IGHG1*01, hinge (71-80), CH2 (81-190), CH3 (191-295), CHS (296-297)], (76-76':79-79')-bisdisulfide dimer, produced in Chinese hamster ovary (CHO) cells

inbakicept

sous-unité alpha du recepteur de l’interleukine 15 (1-65)-peptide (IL15Rα) humain (contenant le domaine sushi) fusionné à un fragment Fc de l'immunoglobuline G1 humaine (232 résidus C-terminaux) (66-297) [*Homo sapiens* IGHG1*01, charnière (71-80), CH2 (81-190), CH3 (191-295), CHS (296-297)], dimère (76-76':79-79')-bisdisulfure, produit par des cellules ovariennes de hamsters chinois (CHO) inbakicept

(1-65)-péptido de la subunidad alfa del receptor de interleukina 15 (IL15Rα humana) (que contiene el dominio sushi) fusionado a un fragmento Fc de la inmunoglobulina G1 humana (232 restos C-terminales) (66-297) [*Homo sapiens* IGHG1*01, bisagra (71-80), CH2 (81-190), CH3 (191-295), CHS (296-297)], dímero (76-76':79-79')-bisdisulfuro, producido por las células ováricas de hamsters chinos (CHO)

```
ITCPPPMSVE HADIWVKSYS LYSRERYICN SGFKRKAGTS SLTECVLNKA  50
TNVAHWTTPS LKCIREPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT 100
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 150
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT 200
LPPSRDELTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS 250
DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPGK    297
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
intra: 3-45, 29-63, 111-171, 217-275
3'-45', 29'-63', 111'-171', 217'-275'
inter: 76-76', 79-79'

N-Glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
Asn147, Asn147'

O-Glycosylation sites / Sites de O-glycosylation / Posiciones de O-glicosilación
Thr2, Thr2'

C-terminal lysine (K) clipping
Lys297, Lys297'

inlezifigenum civaparvovecum #

inlezifigene civaparvovec

a recombinant non-replicating adeno-associated virus type 2/6 (rAAV Rep2-Cap6) vector, expressing a cDNA that targets 447-461 bp of the albumin locus (relative to the transcription initiation site), fused to the obligate heterodimeric FokI nuclease domain ELD, under the control of an apolipoprotein E hepatic control region and human alpha-1-antitrypsin promoter (ApoE/hAAT)

inlezifigène civaparvovec

vecteur viral adéno-associé de type 2/6 recombinant (rAAV Rep2-Cap6), non-répliquant, exprimant un ADNc ciblant les paires de bases 447-461 du locus de l'albumine (en relation avec le site initial de transcription), fusionné au domaine hétérodimérique ELD de la nucléase FokI, sous le contrôle d'une région de contrôle de l'apolipoprotéine E (ApoE) spécifique du foie et du promoteur de l'alpha1-antitrypsine humaine (ApoE/hAAT)

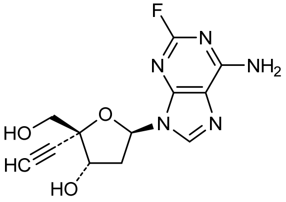
inlezifigén civaparvovec

un vector de virus adeno asociado tipo 2/6 recombinante (rAAV Rep2-Cap6), no replicativo, que expresa un cDNA dirigido a unirse a los pares de bases 447-461 (en relación al sitio de iniciación de la transcripción) del locus de la albúmina, fusionado al dominio heterodimérico ELD de la nuclease FokI, bajo el control de una región de control hepático de la apolipoproteína E y el promotor de la alfa 1 antitripsina humana (ApoE/hAAT)

inodiftagenum vixteplasmidum #

inodiftagene vixteplasmid

plasmid DNA vector encoding the diphtheria toxin A (DT-A) gene under transcriptional regulation of the promoter region of the human H19 gene (an imprinted maternally expressed non-protein coding gene)

inodiftagène vixteplasmide	vecteur d'ADN plasmidique contenant le gène de la toxine diphtérique A (DT-A) sous la régulation transcriptionelle d'un promoteur du gène humain H19 (gène d'empreinte maternelle ne codant pas de protéine)
inodiftagén vixteplasmida	vector de DNA plasmídico que codifica para el gen de la toxina diftérica A (DT-A) bajo la regulación transcripcional de la región promotora del gen H19 humano (un gen no codificante de proteína expresado con impronta materna)
islatravirum	
islatravir	2'-deoxy-4'-*C*-ethynyl-2-fluoroadenosine
islatravir	2'-désoxy-4'-*C*-éthynyl-2-fluoroadénosine
islatravir	2'-desoxi-4'-*C*-etinil-2-fluoroadenosina
	$C_{12}H_{12}FN_5O_3$ 
lacutamabum #	
lacutamab	immunoglobulin G1-kappa, anti-[*Homo sapiens* KIR3DL2 (killer cell immunoglobulin-like receptor, three Ig domains, long cytoplasmic tail 2)], monoclonal antibody; gamma1 heavy chain (1-448) [VH (*Homo sapiens* IGHV7-4-1*02 (84.7%) -(IGHD) -IGHJ6*01 (92.9%)) [8.8.11] (1-118) -*Homo sapiens* IGHG1*03 (G1v7) (CH1 R120 (215) (119-216), hinge (217-231), CH2 S3>D (240), I117>E (333) (232-341), CH3 E12 (357), M14 (359) (342-446), CHS (447-448)) (119-448)], (221-214')-disulfide with kappa light chain (1'-214') [V-KAPPA (*Mus musculus* IGKV6-25*01 (87.4%) -IGKJ1*01 (91.7%)/*Homo sapiens* IGKV1-NL1*01 (77.9%) -IGKJ4*01 (100%)) [6.3.6] (1'-107') -*Homo sapiens* IGKC*01 (100%) A45.1 (153), V101 (191) (108'-214')]; dimer (227-227'':230-230'')-bisdisulfide
lacutamab	immunoglobuline G1-kappa, anti-[*Homo sapiens* KIR3DL2 (récepteur 2 des cellules tueuses à trois domaines Ig-like et longue région cytoplasmique)], anticorps monoclonal; chaîne lourde gamma1 (1-448) [VH (*Homo sapiens* IGHV7-4-1*02 (84.7%) -(IGHD) -IGHJ6*01 (92.9%)) [8.8.11] (1-118) -*Homo sapiens* IGHG1*03 (G1v7) (CH1 R120 (215) (119-216), charnière (217-231), CH2 S3>D (240), I117>E (333) (232-341), CH3 E12 (357), M14 (359) (342-446), CHS (447-448)) (119-448)], (221-214')-disulfure avec la chaîne légère kappa

(1'-214') [V-KAPPA (*Mus musculus* IGKV6-25*01 (87.4%) -IGKJ1*01 (91.7%)/*Homo sapiens* IGKV1-NL1*01 (77.9%) -IGKJ4*01 (100%)) [6.3.6] (1'-107') -*Homo sapiens* IGKC*01 (100%) A45.1 (153), V101 (191) (108'-214')]; dimère (227-227":230-230")-bisdisulfure

lacutamab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* KIR3DL2 (receptor 2 de las células asesinas de los tres dominios Ig-like y región larga citoplasmática)], anticuerpo monoclonal;
cadena pesada gamma1 (1-448) [VH (*Homo sapiens* IGHV7-4-1*02 (84.7%) -(IGHD) -IGHJ6*01 (92.9%)) [8.8.11] (1-118) -*Homo sapiens* IGHG1*03 (G1v7) (CH1 R120 (215) (119-216), bisagra (217-231), CH2 S3>D (240), I117>E (333) (232-341), CH3 E12 (357), M14 (359) (342-446), CHS (447-448)) (119-448)], (221-214')-disulfuro con la cadena ligera kappa (1'-214') [V-KAPPA (*Mus musculus* IGKV6-25*01 (87.4%) -IGKJ1*01 (91.7%)/*Homo sapiens* IGKV1-NL1*01 (77.9%) -IGKJ4*01 (100%)) [6.3.6] (1'-107') -*Homo sapiens* IGKC*01 (100%) A45.1 (153), V101 (191) (108'-214')]; dímero (227-227":230-230")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QIQLVQSGSE LKKPGASVKV SCKASGYTFT TAGMQWVRQA PGQGLEWIGW  50
INSHSGVPKY AEDFKGRFVF SLDTSVSTAY LQISSLKAED TAVYFCARGG 100
DEGVMDYWGQ GTTVTVSSAS TKGPSVFPLA PSSKSTSGGT AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTQTYI 200
CNVNHKPSNT KVDKRVEPKS CDKTHTCPPC PAPELLGGPD VFLFPPKPKD 250
TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNST 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APEEKTISKA KGQPREPQVY 350
TLPPSREEMT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD 400
SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPGK   448
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSF LSASVGDRVT ITCKASQDVS TAVAWYQQKP GQPPKLLIYW  50
TSTRHTGVPD RFSGSGSGTD YTLTISSLQA EDVAVYYCQQ HYSTPWTFGG 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) 22-96 145-201 262-322 368-426
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.

lademirsenum
lademirsen

all-*P*-*ambo*-2'-*O*-(2-methoxyethyl)-*P*-thioadenylyl-(3'→5')-2'-*O*,4'-*C*-[(1*S*)-ethane-1,1-diyl]-*P*-thiocytidylyl-(3'→5')-2'-deoxy-*P*-thioadenylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-*O*,4'-*C*-[(1*S*)-ethane-1,1-diyl]-*P*-thiocytidylyl-(3'→5')-2'-deoxy-*P*-thioadenylyl-(3'→5')-2'-deoxy-*P*-thioguanylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-*O*,4'-*C*-[(1*S*)-ethane-1,1-diyl]-*P*-thiocytidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-deoxy-*P*-thioguanylyl-(3'→5')-2'-deoxy-*P*-thioadenylyl-(3'→5')-2'-*O*,4'-*C*-[(1*S*)-ethane-1,1-diyl]-*P*-thiouridylyl-(3'→5')-2'-deoxy-*P*-thioadenylyl-(3'→5')-2'-deoxy-*P*-thioadenylyl-(3'→5')-2'-deoxy-*P*-thioguanylyl-(3'→5')-2'-*O*,4'-*C*-[(1*S*)-ethane-1,1-diyl]-*P*-thiocytidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-*O*-(2-methoxyethyl)adenosine lademirsen

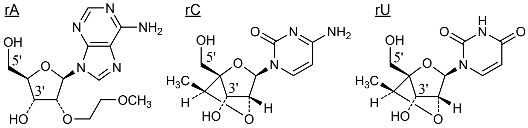
tout-P-ambo-2'-*O*-(2-méthoxyéthyl)-*P*-thioadénylyl-(3'→5')-2'-*O*,4'-*C*-[(1*S*)-éthane-1,1-diyl]-*P*-thiocytidylyl-(3'→5')-2'-désoxy-*P*-thioadénylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-*O*,4'-*C*-[(1*S*)-éthane-1,1-diyl]-*P*-thiocytidylyl-(3'→5')-2'-désoxy-*P*-thioadénylyl-(3'→5')-2'-désoxy-*P*-thioguanylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-*O*,4'-*C*-[(1*S*)-éthane-1,1-diyl]-*P*-thiocytidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-désoxy-*P*-thioguanylyl-(3'→5')-2'-désoxy-*P*-thioadénylyl-(3'→5')-2'-*O*,4'-*C*-[(1*S*)-éthane-1,1-diyl]-*P*-thiouridylyl-(3'→5')-2'-désoxy-*P*-thioadénylyl-(3'→5')-2'-désoxy-*P*-thioadénylyl-(3'→5')-2'-désoxy-*P*-thioguanylyl-(3'→5')-2'-*O*,4'-*C*-[(1*S*)-éthane-1,1-diyl]-*P*-thiocytidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)adenosine

lademirsen

todo-P-ambo-2'-*O*-(2-metoxietil)-*P*-tioadenilil-(3'→5')-2'-*O*,4'-*C*-[(1*S*)-etano-1,1-diil]-*P*-tiocitidilil-(3'→5')-2'-desoxi-*P*-tioadenilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2'-*O*,4'-*C*-[(1*S*)-etano-1,1-diil]-*P*-tiocitidilil-(3'→5')-2'-desoxi-*P*-tioadenilil-(3'→5')-2'-desoxi-*P*-tioguanilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2'-*O*,4'-*C*-[(1*S*)-etano-1,1-diil]-*P*-tiocitidilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2'-desoxi-*P*-tioguanlil-(3'→5')-2'-desoxi-*P*-tioadenilil-(3'→5')-2'-*O*,4'-*C*-[(1*S*)-etano-1,1-diil]-*P*-tiouridilil-(3'→5')-2'-desoxi-*P*-tioadenilil-(3'→5')-2'-desoxi-*P*-tioadenilil-(3'→5')-2'-desoxi-*P*-tioguanilil-(3'→5')-2'-*O*,4'-*C*-[(1*S*)-etano-1,1-diil]-*P*-tiocitidilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2'-*O*-(2-metoxietil)adenosine

$C_{201}H_{254}N_{72}O_{101}P_{18}S_{18}$

(3'-5')d(*P*-thio)(rA-rC-A-T-rC-A-G-T-rC-T-G-A-rU-A-A-G-rC-T-rA)



lapretolimodum

lapretolimod

2-deoxy-6-*O*-{2-deoxy-4-*O*-phosphono-2-[(3*R*)-3-(tetradecanoyloxy)tetradecanamido]-3-*O*-[(3*R*)-3-(tetradecanoyloxy)tetradecanoyl]-β-D-glucopyranosyl}-2-[(3*R*)-3-hydroxytetradecanamido]-α-D-glucopyranose 3-[(3*R*)-3-hydroxytetradecanoate]

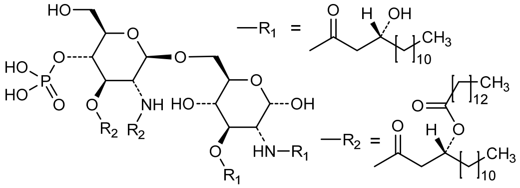
laprétolimod

3-[(3*R*)-3-hydroxytétradécanoate] de 2-désoxy-6-*O*-{2-désoxy-4-*O*-phosphono-2-[(3*R*)-3-(tétradécanoyloxy)tétradécanamido]-3-*O*-[(3*R*)-3-(tétradécanoyloxy)tétradécanoyl]-β-D-glucopyranosyl}-2-[(3*R*)-3-hydroxytétradécanamido]-α-D-glucopyranose

lapretolimod

3-[(3*R*)-3-hidroxitetradecanoato] de 2-desoxi-6-*O*-{2-desoxi-4-*O*-fosfono-2-[(3*R*)-3-(tetradecanoiloxi)tetradecanamido]-3-*O*-[(3*R*)-3-(tetradecanoiloxi)tetradecanoil]-β-D-glucopiranosil}-2-[(3*R*)-3-hidroxitetradecanamido]-α-D-glucopiranosa

$C_{96}H_{181}N_2O_{22}P$

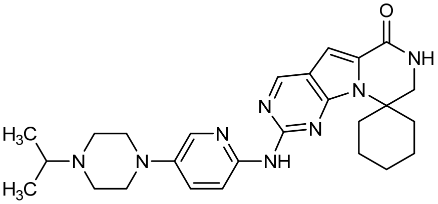


lerociclibum
lerociclib 2'-({5-[4-(propan-2-yl)piperazin-1-yl]pyridin-2-yl}amino)-7',8'-dihydro-6'*H*-spiro[cyclohexane-1,9'-pyrazino[1',2':1,5]pyrrolo[2,3-*d*]pyrimidin]-6'-one

lérociclib 2'-({5-[4-(propan-2-yl)pipérazin-1-yl]pyridin-2-yl}amino)-7',8'-dihydro-6'*H*-spiro[cyclohexane-1,9'-pyrazino[1',2':1,5]pyrrolo[2,3-*d*]pyrimidin]-6'-one

lerociclib 2'-({5-[4-(propan-2-il)piperazin-1-il]piridin-2-il}amino)-7',8'-dihidro-6'*H*-spiro[ciclohexano-1,9'-pirazino[1',2':1,5]pirrolo[2,3-*d*]pirimidin]-6'-ona

$C_{26}H_{34}N_8O$



levilimabum #
levilimab immunoglobulin G1-kappa, anti-[*Homo sapiens* IL6R (interleukin 6 receptor, IL-6R, CD126)], monoclonal antibody;
gamma1 heavy chain (1-450) [VH (*Camelus dromedarius* IGHV1S4*01(91.6%)/*Homo sapiens* IGHV3-23*02 (85.7%) -(IGHD) -IGHJ1*01 (100%)) [8.7.14] (1-120) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (217) (121-218), hinge (219-233), CH2 E1.4>P (236), L1.3>V (237), L1.2>A (238), M13>Y (255), S16>T (257), T18>E (259) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-218')-disulfide with kappa light chain (1'-218') [V-KAPPA *(Homo sapiens* IGKV4-1*01 (79.2%) -IGKJ2*01 (100%)) [10.3.9] (1'-111') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (157), V101 (195) (112'-218')]; dimer (229-229":232-232")-bisdisulfide

lévilimab immunoglobuline G1-kappa, anti-[*Homo sapiens* IL6R (récepteur de l'interleukine 6, IL-6R, CD126)], anticorps monoclonal;

chaîne lourde gamma1 (1-450) [VH (*Camelus dromedarius* IGHV1S4*01(91.6%)/*Homo sapiens* IGHV3-23*02 (85.7%) -(IGHD) -IGHJ1*01 (100%)) [8.7.14] (1-120) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (217) (121-218), charnière (219-233), CH2 E1.4>P (236), L1.3>V (237), L1.2>A (238), M13>Y (255), S16>T (257), T18>E (259) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-218')-disulfure avec la chaîne légère kappa (1'-218') [V-KAPPA *(Homo sapiens* IGKV4-1*01 (79.2%) -IGKJ2*01 (100%)) [10.3.9] (1'-111') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (157), V101 (195) (112'-218')]; dimère (229-229":232-232")-bisdisulfure

levilimab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* IL6R (receptor de la interleukina 6, IL-6R, CD126)], anticuerpo monoclonal;
cadena pesada gamma1 (1-450) [VH (*Camelus dromedarius* IGHV1S4*01(91.6%)/*Homo sapiens* IGHV3-23*02 (85.7%) -(IGHD) -IGHJ1*01 (100%)) [8.7.14] (1-120) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (217) (121-218), bisagra (219-233), CH2 E1.4>P (236), L1.3>V (237), L1.2>A (238), M13>Y (255), S16>T (257), T18>E (259) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-218')-disulfuro con la cadena ligera kappa (1'-218') [V-KAPPA *(Homo sapiens* IGKV4-1*01 (79.2%) -IGKJ2*01 (100%)) [10.3.9] (1'-111') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (157), V101 (195) (112'-218')]; dímero (229-229":232-232")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada
```
QVQLVQSGGG LVQPGGSLRL SCAASGFTFS SYYMSWVRQA PGKGLEWVSG  50
IYSDGTTHYG DSVKGRFTIS RDNAKNTVYL QLNSLRAEDT AMYYCAKGAG 100
PTWWYALDAW GQGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKRVEP KSCDKTHTCP PCPAPPVAGG PSVFLFPPKP 250
KDTLYITREP 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
```
DIQLTQSPSS VSVSVGERVT IDCKSSQSVL SASNTYLNWY QQKPGQAPQL  50
LIYYASTRES GVPDRFSGSG SGTDFTLTIS SLQAEDAAVY YCQQAYRAPV 100
TFGQGTKLEI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL NNFYPREAKV 150
QWKVDNALQS GNSQESVTEQ DSKDSTYSLS STLTLSKADY EKHKVYACEV 200
THQGLSSPVT KSFNRGEC                                   218
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-95 147-203 264-324 370-428
22"-95" 147"-203" 264"-324" 370"-428"
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 (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.

lorukafuspum alfa #

lorukafusp alfa	immunoglobulin G1-kappa, anti-(human ganglioside GD2) chimeric monoclonal antibody, fused with interleukin 2, glycoform alfa: gamma1 heavy chain [*Mus musculus* VH (*Mus musculus* IGHV1S135*01 (79.2%) -(IGHD)-IGHJ4*01 (92.9%)) [CDRKabatH1: GYNMN (31-35); CDRKabatH2: AIDPYYGGTSYNQKFKG (50-66); CDRKabatH3: GMEY (99-102)] (1-113) - *Homo sapiens* IGHG1*03 (CH1 (114-211), hinge (212-226), CH2 (227-336), CH3 (337-441), CHS (442-443))] (1-443) fused with interleukin 2 (IL2, human) (444-576), (216-220')-disulfide with kappa light chain [V-KAPPA (*Mus musculus* IGKV1-110*01 (94.0%) -IGKJ5*01 (100.0%)) [CDRKabatL1: RSSQSLVHRNGNTYLH (24-39); CDRKabatL2: KVSNRFS (55-61); CDRKabatL3: SQSTHVPPLT (94-103)] (1'-113') - *Homo sapiens* IGKC*01 (114'-220')] (1'-220'), (222-222'':225-225'')-bisdisulfide dimer, produced in mouse myeloma NS0 cells, glycoform alfa
lorukafusp alfa	immunoglobuline G1-kappa, anticorps monoclonal chimérique anti-(ganglioside GD2 humain), fusionné avec l'interleukine 2, glycoforme alfa: chaîne lourde gamma1 [*Mus musculus* VH (*Mus musculus* IGHV1S135*01 (79.2%) -(IGHD)-IGHJ4*01 (92.9%)) [CDRKabatH1: GYNMN (31-35); CDRKabatH2: AIDPYYGGTSYNQKFKG (50-66); CDRKabatH3: GMEY (99-102)] (1-113) - *Homo sapiens* IGHG1*03 (CH1 (114-211), charnière (212-226), CH2 (227-336), CH3 (337-441), CHS (442-443))] (1-443) fusionné avec l'interleukine 2 (IL2, humaine) (444-576), (216-220')-disulfure avec la chaîne kappa légère [V-KAPPA (*Mus musculus* IGKV1-110*01 (94.0%) -IGKJ5*01 (100.0%)) [CDRKabatL1: RSSQSLVHRNGNTYLH (24-39); CDRKabatL2: KVSNRFS (55-61); CDRKabatL3: SQSTHVPPLT (94-103)] (1'-113') - *Homo sapiens* IGKC*01 (114'-220')] (1'-220'), (222-222'':225-225'')- dimère bisdisulfure, produit dans des cellules du myélome murin NS0, glycoforme alfa
lorukafusp alfa	inmunoglobulina G1-kappa, anticuerpo monoclonal quimérico anti-(gangliósido GD2 humano), fusionado con la interleukina 2, glicoforma alfa: cadena pesada gamma1 [*Mus musculus* VH (*Mus musculus* IGHV1S135*01 (79.2%) -(IGHD)-IGHJ4*01 (92.9%)) [CDRKabatH1: GYNMN (31-35); CDRKabatH2: AIDPYYGGTSYNQKFKG (50-66); CDRKabatH3: GMEY (99-102)] (1-113) - *Homo sapiens* IGHG1*03 (CH1 (114-211), bisagra (212-226), CH2 (227-336), CH3 (337-441), CHS (442-443))] (1-443) fusionado con la interleukina 2 (IL2, humana) (444-576), (216-220')-disulfuro con la cadena kappa ligera [V-KAPPA (*Mus musculus* IGKV1-110*01 (94.0%) -IGKJ5*01 (100.0%)) [CDRKabatL1: RSSQSLVHRNGNTYLH (24-39); CDRKabatL2: KVSNRFS (55-61); CDRKabatL3: SQSTHVPPLT (94-103)] (1'-113') - *Homo sapiens* IGKC*01 (114'-220')] (1'-220'), (222-222'':225-225'')- dímero bisdisulfuro, producido en las células del mieloma murino NS0, glicoforma alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVQSGAE VEKPGASVKI SCKASGSSFT GYNMNWVRQN IGKSLEWIGA  50
IDPYYGGTSY NQKFKGRATL TVDKSTSTAY MHLKSLRSED TAVYYCVSGM 100
EYWGQGTSVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC LVKDYFPEPV 250
TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG TQTYICNVNH 200
KPSNTKVDKR VEPKSCDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS 250
RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYNSTYRVVS 300
VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR EPQVYTLPPS 350
REEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT PPVLDSDGSF 400
FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLS PGKAPTSSST 450
KKTQLQLEHL LLDLQMILNG INNYKNPKLT RMLTFKFYMP KKATELKHLQ 500
CLEEELKPLE EVLNLAQSKN FHLRPRDLIS NINVIVLELK GSETTFMCEY 550
ADETATIVEF LNRWITFCQS IISTLT                          576
```

Light chain / Chaîne légère / Cadena ligera

```
DVVMTQTPLS LPVTPGEPAS ISCRSSQSLV HRNGNTYLHW YLQKPGQSPK  50
LLIHKVSNRF SGVPDRFSGS GSGTDFTLKI SRVEAEDLGV YFCSQSTHVP 100
PLTFGAGTKL ELKRTVAAPS 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: IgG1: 22-96, 140-196, 257-317, 363-421,
22''-96'', 140''-196'', 257''-317'', 363''-421''
IL2: 501-548, 501''-548'' (structure A, natural, 80 %)
548-568, 548''-568'' (structure B, 20 %)
intra-L: 23'-93', 140'-200', 23'''-93''', 140'''-200'''
inter-H-L: 216-220', 216''-220'''
inter-H-H: 222-222'', 225-225''

Glycosylation sites / Sites de glycosylation / Posiciones de glicosilación
Asn293, Asn293'': complex biantennary core-fucosylated glycans
Thr446, Thr446'': no O-glycosylation

maftivimabum #

maftivimab

immunoglobulin G1-kappa, anti-[*Zaire ebolavirus* (Zaire Ebola virus (EBOV)) glycoprotein], *Homo sapiens* monoclonal antibody;
gamma1 heavy chain *Homo sapiens* (1-448) [VH (*Homo sapiens* IGHV3-23*04 (95.9%) -(IGHD) - IGHJ3*02(93.3%)) [8.8.11] (1-118) -*Homo sapiens* IGHG1*01 (100%), 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)], (221-213')-disulfide with kappa light chain *Homo sapiens* (1'-213') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (98.9%) -IGKJ5*01(91.7%)) [6.3.8] (1'-106') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (152), V101 (190) (106'-213')]; dimer (227-227'':230-230'')-bisdisulfide

maftivimab

immunoglobuline G1-kappa, anti-[glycoprotéine de *Zaire ebolavirus* (virus Ebola Zaïre (EBOV))], anticorps monoclonal *Homo sapiens*;
chaîne lourde gamma1 *Homo sapiens* (1-448) [VH (*Homo sapiens* IGHV3-23*04 (95.9%) -(IGHD) - IGHJ3*02(93.3%)) [8.8.11] (1-118) -*Homo sapiens* IGHG1*01 (100%), 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)], (221-213')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-213') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (98.9%) -IGKJ5*01(91.7%)) [6.3.8] (1'-106') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (152), V101 (190) (106'-213')]; dimère (227-227'':230-230'')-bisdisulfure

maftivimab

inmunoglobulina G1-kappa, anti-[glicoproteína de *Zaire ebolavirus* (virus Ebola Zaïre (EBOV))], anticuerpo monoclonal *Homo sapiens*;

cadena pesada gamma1 *Homo sapiens* (1-448) [VH (*Homo sapiens* IGHV3-23*04 (95.9%) -(IGHD) -IGHJ3*02(93.3%)) [8.8.11] (1-118) -*Homo sapiens* IGHG1*01 (100%), 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)], (221-213')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-213') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (98.9%) -IGKJ5*01(91.7%)) [6.3.8] (1'-106') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (152), V101 (190) (106'-213')]; dímero (227-227'':230-230'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAASGFTSS SYAMNWVRQA PGKGLEWVST  50
ISGMGGSTYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKRG 100
YPHSFDIWGQ GTMVTVSSAS 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

```
DIQMTQSPSS LSASVGDRVT ITCRASQSIS SFLNWYQQKP GKAPKLLIYA  50
ASSLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ SYSTLTFGQG 100
TRLEIKRTVA 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) 22-96 145-201 262-322 368-426
22''-96'' 145''-201'' 262''-322'' 368''-426''
Intra-L (C23-C104) 23'-88' 133'-193'
23'''-88''' 135'''-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

magrolimabum #

magrolimab

immunoglobulin G4-kappa, anti-[*Homo sapiens* CD47 (integrin associated protein, IAP, MER6, OA3)], monoclonal antibody;
gamma4 heavy chain (1-444) [VH (*Homo sapiens* IGHV1-3*01 (87.8%) -(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)], (131-219')-disulfide with kappa light chain (1'-219') [V-KAPPA (*Mus musculus* IGKV1-117*01 (89.0%) -IGKJ2*03 (91.7%)/*Homo sapiens* IGKV2-28*01 (86%) -IGKJ2*01 (100%)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; dimer (223-223'':226-226'')-bisdisulfide

magrolimab

immunoglobuline G4-kappa, anti-[*Homo sapiens* CD47 (protéine associée à l'intégrine, IAP, MER6, OA3)], anticorps monoclonal;
chaîne lourde gamma4 (1-444) [VH (*Homo sapiens* IGHV1-3*01 (87.80%) -(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)], (131-219')-disulfure avec la chaîne légère kappa

(1'-219') [V-KAPPA (*Mus musculus* IGKV1-117*01 (89.0%) -IGKJ2*03 (91.7%)/*Homo sapiens* IGKV2-28*01 (86%) -IGKJ2*01 (100%)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; dimère (223-223'':226-226'')-bisdisulfure

magrolimab

inmunoglobulina G4-kappa, anti-[*Homo sapiens* CD47 (proteína asociada a la integrina, IAP, MER6, OA3)], anticuerpo monoclonal;
cadena pesada gamma4 (1-444) [VH (*Homo sapiens* IGHV1-3*01 (87.80%) -(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)], (131-219')-disulfuro con la cadena ligera kappa (1'-219') [V-KAPPA (*Mus musculus* IGKV1-117*01 (89.0%) -IGKJ2*03 (91.7%)/*Homo sapiens* IGKV2-28*01 (86%) -IGKJ2*01 (100%)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; dímero (223-223'':226-226'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGASVKV SCKASGYTFT NYNMHWVRQA PGQRLEWMGT  50
IYPGNDDTSY NQKFKDRVTI TADTSASTAY MELSSLRSED TAVYYCARGG 100
YRAMDYWGQG 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

```
DIVMTQSPLS LPVTPGEPAS ISCRSSQSIV YSNGNTYLGW YLQKPGQSPQ  50
LLIYKVSNRF SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCFQGSHVP 100
YTFGQGTKLE 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

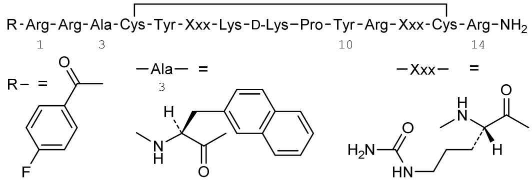
mocemestrocelum

mocemestrocel

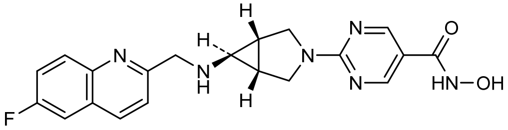
human culture expanded sub-fractionated allogeneic adherent mesenchymal-like stromal cells derived from bone marrow of healthy living donors. Cells express cell surface markers CD105, CD73, CD90 and human leukocyte antigen (HLA) class-I, and express transforming growth factor beta 1 (TGF-β1), soluble tumour necrosis factor receptor 1 (sTNF-R1), interleukin-10 (IL-10), interleukin 17 (IL-17), acetylcholine (ACh), ICOS ligand (B7 homolog 2, B7-H2, ICOSL, antigen CD275), and indoleamine 2,3-dioxygenase 1 (IDO-1). The cells are negative for CD34, CD45, CD14 and HLA-DR markers.

mocémestrocel	cellules stromales adhérentes allogéniques humaines semblables aux cellules mésenchymales, subfractionnées, en culture d'expansion, dérivées de moëlle osseuse de donneurs sains vivants. Les cellules expriment les marqueurs de surface CD105, CD73, CD90 et l'antigène de classe I de leukocytes humains (HLA, CMH, complexe majeur d'histocompatibilité), et expriment le facteur de croissance transformant bêta 1 ((TGF-β1), la partie soluble du récepteur 1 du facteur de nécrose tumorale (sTNF-R1), l'interleukine 1 (IL-1), l'interleukine 17 (IL-17), l'acétylcholine (ACh), le ligand ICOS (homologue 2 de B7, B7-H2, ICOSL, CD275) et l'indolamine 2,3-dioxygénase 1 (IDO-1). Les cellules sont négatives pour les marqueurs CD34, CD45, CD14 et HLA-DR .
mocemestrocel	células adherentes estromales alogénicas humanas similares a células mesenquimales subfraccionadas, expandidas en cultivo, derivadas de la médula ósea de donantes vivos sanos. Las células expresan los marcadores de superficie CD105, CD73, CD90 y HLA clase I, y expresan factor transformador del crecimiento beta 1 (TGF-b1), receptor 1 soluble del factor de necrosis tumoral 1 (sTNF-R1), interleuquina 10 (IL-10), interleuquina 17 (IL-17), acetilcolina (Ach), ligando de ICOS (homólogo 2 de B7, B7-H2, ICOSL, antígeno CD275), e indoleamina 2,3-dioxigenasa 1 (IDO-1). Las células son negativas para los marcadores CD34, CD45, CD14 y HLA-DR.
motixafortidum	
motixafortide	$S^{3.4}$,$S^{3.13}$-cyclo[N^{α}-(4-fluorobenzoyl)-L-arginyl-L-arginyl-3-(naphthalen-2-yl)-L-alanyl-L-cysteinyl-L-tyrosyl-N^{5}-carbamoyl-L-ornithyl-L-lysyl-D-lysyl-L-prolyl-L-tyrosyl-L-arginyl-N^{5}-carbamoyl-L-ornithyl-L-cysteinyl-L-argininamide]
motixafortide	$S^{3.4}$,$S^{3.13}$-cyclo[N^{α}-(4-fluorobenzoyl)-L-arginyl-L-arginyl-3-(naphtalén-2-yl)-L-alanyl-L-cystéinyl-L-tyrosyl-N^{5}-carbamoyl-L-ornithyl-L-lysyl-D-lysyl-L-prolyl-L-tyrosyl-L-arginyl-N^{5}-carbamoyl-L-ornithyl-L-cystéinyl-L-argininamide]
motixafortida	$S^{3.4}$,$S^{3.13}$-ciclo[N^{α}-(4-fluorobenzoil)-L-arginil-L-arginil-3-(naftalen-2-il)-L-alanil-L-cisteinil-L-tirosil-N^{5}-carbamoil-L-ornitil-L-lisil-D-lisil-L-prolil-L-tirosil-L-arginil-N^{5}-carbamoil-L-ornitil-L-cysteinil-L-argininamida]

$C_{97}H_{144}FN_{33}O_{19}S_2$



nanatinostatum

nanatinostat	2-[(1*R*,5*S*,6*s*)-6-{[(6-fluoroquinolin-2-yl)methyl]amino}-3-azabicyclo[3.1.0]hexan-3-yl]-*N*-hydroxypyrimidine-5-carboxamide
nanatinostat	2-[(1*R*,5*S*,6*s*)-6-{[(6-fluoroquinoléin-2-yl)méthyl]amino}-3-azabicyclo[3.1.0]hexan-3-yl]-*N*-hydroxypyrimidine-5-carboxamide
nanatinostat	2-[(1*R*,5*S*,6*s*)-6-{[(6-fluoroquinolein-2-il)metil]amino}-3-azabiciclo[3.1.0]hexan-3-il]-*N*-hidroxipirimidina-5-carboxamida $C_{20}H_{19}FN_6O_2$ 

naxitamabum #

naxitamab	immunoglobulin G1-kappa, anti-[*Homo sapiens* ganglioside GD2 (disialoganglioside GD2)], monoclonal antibody; gamma1 heavy chain (1-449) [VH (*Mus musculus* IGHV2-9*02 (79.2%) -(IGHD) -IGHJ3*01 (91.7%)/*Homo sapiens* IGHV3-33*01 (72.2%) -(IGHD) -IGHJ4*01 (92.9%)) [8.7.13] (1-119) -*Homo sapiens* IGHG1*08p, G1m3,1 (CH1 R120 (216) (120-217), hinge (218-232), CH2 (233-342), CH3 D12 (358), L14 (360) (343-447), CHS (448-449)) (120-449)], (222-211')-disulfide with kappa light chain (1'-211') [V-KAPPA (*Mus musculus* IGKV6-32*02 (84.9%) -IGKJ2*03 (90.0%)/*Homo sapiens* IGKV3-15*01 (78.7%) -IGKJ2*03 (100%)) [6.3.6] (1'-104') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (150), V101 (188) (105'-211')]; dimer (228-228":231-231")-bisdisulfide
naxitamab	immunoglobuline G1-kappa, anti-[*Homo sapiens ganglioside GD2 (disialoganglioside GD2)*], anticorps monoclonal; chaîne lourde gamma1 (1-449) [VH (*Mus musculus* IGHV2-9*02 (79.2%) -(IGHD) -IGHJ3*01 (91.7%)/*Homo sapiens* IGHV3-33*01 (72.2%) -(IGHD) -IGHJ4*01 (92.9%)) [8.7.13] (1-119) -*Homo sapiens* IGHG1*08p, G1m3,1 (CH1 R120 (216) (120-217), charnière (218-232), CH2 (233-342), CH3 D12 (358), L14 (360) (343-447), CHS (448-449)) (120-449)], (222-211')-disulfure avec la chaîne légère kappa (1'-211') [V-KAPPA (*Mus musculus* IGKV6-32*02 (84.9%) -IGKJ2*03 (90.0%)/*Homo sapiens* IGKV3-15*01 (78.7%) -IGKJ2*03 (100%)) [6.3.6] (1'-104') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (150), V101 (188) (105'-211')]; dimère (228-228":231-231")-bisdisulfure

naxitamab

inmunoglobulina G1-kappa, anti-[*Homo sapiens gangliósido GD2 (disialogangliósido GD2)*], anticuerpo monoclonal;
cadena pesada gamma1 (1-449) [VH (*Mus musculus* IGHV2-9*02 (79.2%) -(IGHD) -IGHJ3*01 (91.7%)/*Homo sapiens* IGHV3-33*01 (72.2%) -(IGHD) -IGHJ4*01 (92.9%)) [8.7.13] (1-119) -*Homo sapiens* IGHG1*08p, G1m3,1 (CH1 R120 (216) (120-217), bisagra (218-232), CH2 (233-342), CH3 D12 (358), L14 (360) (343-447), CHS (448-449)) (120-449)], (222-211')-disulfuro con la cadena ligera kappa (1'-211') [V-KAPPA (*Mus musculus* IGKV6-32*02 (84.9%) -IGKJ2*03 (90.0%)/*Homo sapiens* IGKV3-15*01 (78.7%) -IGKJ2*03 (100%)) [6.3.6] (1'-104') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (150), V101 (188) (105'-211')]; dímero (228-228":231-231")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVESGPG VVQPGRSLRI SCAVSGFSVT NYGVHWVRQP PGKGLEWLGV  50
IWAGGITNYN SAFMSRLTIS KDNSKNTVYL QMNSLRAEDT AMYYCASRGG 100
HYGYALDYWG 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
YTLPPSRDEL TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL 400
DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK  449
```

Light chain / Chaîne légère / Cadena ligera

```
EIVMTQTPAT LSVSAGERVT ITCKASQSVS NDVTWYQQKP GQAPRLLIYS  50
ASNRYSGVPA RFSGSGYGTE FTFTISSVQS EDFAVYFCQQ DYSSFGQGTK 100
LEIKRTVAAP SVFIFPPSDE QLKSGTASVV CLLNNFYPRE AKVQWKVDNA 150
LQSGNSQESV TEQDSKDSTY SLSSTLTLSK ADYEKHKVYA CEVTHQGLSS 200
PVTKSFNRGE C                                           211
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-95 146-202 263-323 369-427
22"-95" 146"-202" 263"-323" 369"-427"
Intra-L (C23-C104) 23'-88' 131'-191'
23'''-88''' 131'''-191'''
Inter-H-L (h 5-CL 126) 222-211' 222"-211'''
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.
C-terminal lysine clipping:
H CHS K2:
449, 449"

nimacimabum #

nimacimab

immunoglobulin G4-kappa, anti-[*Homo sapiens* CNR1 (cannabinoid receptor 1, CANN6, CNR)], humanized monoclonal antibody;
gamma4 heavy chain humanized (1-444) [VH (*Homo sapiens* IGHV1-69*02 (86.7%) -(IGHD) -IGHJ4*01 (90.9%)) [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 (443-444)) (118-444)], (131-215')-disulfide with kappa light chain humanized (1'-215') [V-KAPPA (*Homo sapiens* IGKV3D-11*02 (90.1%) -IGKJ1*01 (100%)) [7.3.9] (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (204), V101 (192) (109'-215')]; dimer (223-223":226-226")-bisdisulfide

nimacimab

immunoglobuline G4-kappa, anti-[*Homo sapiens* CNR1 (récepteur cannabinoïde 1, CANN6, CNR)], anticorps monoclonal humanisé;

chaîne lourde gamma4 humanisée (1-444) [VH (*Homo sapiens* IGHV1-69*02 (86.7%) -(IGHD) -IGHJ4*01 (90.9%)) [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 (443-444)) (118-444)], (131-215')-disulfure avec la chaîne légère kappa humanisée (1'-219') [V-KAPPA (*Homo sapiens* IGKV3D-11*02 (90.1%) -IGKJ1*01 (100%)) [7.3.9] (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (204), V101 (192) (109'-215')]; dimère (223-223":226-226")-bisdisulfure

nimacimab

inmunoglobulina G4-kappa, anti-[*Homo sapiens* CNR1 (receptor cannabinoide 1, CANN6, CNR)], anticuerpo monoclonal humanizado;
cadena pesada gamma4 humanizada (1-444) [VH (*Homo sapiens* IGHV1-69*02 (86.7%) -(IGHD) -IGHJ4*01 (90.9%)) [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 (443-444)) (118-444)], (131-215')-disulfuro con la cadena ligera kappa humanizada (1'-219') [V-KAPPA (*Homo sapiens* IGKV3D-11*02 (90.1%) -IGKJ1*01 (100%)) [7.3.9] (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (204), V101 (192) (109'-215')]; dímero (223-223":226-226")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGSSVKV SCKASGYEFS YYWMNWVRQA PGQGLEWMGQ  50
IYPGDGETKY AQKFQGRVTI TADKSTSTAY MELSSLRSED TAVYYCARSH 100
GNYLPYWGQG 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

```
EIVLTQSPAT LSLSPGERAT LSCRASQSVS SSYLHWYQQK PGQAPRLLIY  50
STSNLASGIP ARFSGSGSGT DFTLTISRLE PEDFAVYYCH QYHRSPPTFG 100
QGTKVEIKRT 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) 22-96 144-200 258-318 364-422
22"-96" 144"-200" 258"-318" 364"-422"
Intra-L (C23-C104) 23'-89' 135'-195'
23'"-89'" 135'"-195'"
Inter-H-L (CH1 10-CL 126) 131-215' 131"-215'"
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

C-terminal lysine clipping:
H CHS K2:
444, 444"

olutasidenibum

olutasidenib

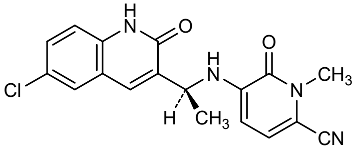
5-{[(1*S*)-1-(6-chloro-2-oxo-1,2-dihydroquinolin-3-yl)ethyl]amino}-1-methyl-6-oxo-1,6-dihydropyridine-2-carbonitrile

olutasidénib

5-{[(1*S*)-1-(6-chloro-2-oxo-1,2-dihydroquinoléin-3-yl)éthyl]amino}-1-méthyl-6-oxo-1,6-dihydropyridine-2-carbonitrile olutasidenib

5-{[(1*S*)-1-(6-cloro-2-oxo-1,2-dihidroquinolein-3-il)etil]amino}-1-metil-6-oxo-1,6-dihidropiridina-2-carbonitrilo

$C_{18}H_{15}ClN_4O_2$



pabinafuspum alfa #

pabinafusp alfa

immunoglobulin G1-kappa, anti-(human transferrin receptor 1, TfR1) humanized monoclonal antibody, fused with human iduronate-2-sulfatase, glycoform alfa:
gamma1 heavy chain [humanized VH (*Homo sapiens* IGHV5-51*01 -(IGHD)-IGHJ4*01) [CDRKabatH1[1]: NYWLG (31-35); CDRKabatH2[1]: DIYPGGDYPTYSEKFKV (50-66); CDRKabatH3[1]: SGNYDEVAY (99-107)] (1-118) - *Homo sapiens* IGHG1*01 (CH1 (119-216), hinge (217-231), CH2 (232-341), CH3 (342-446), CHS (447-448))] (1-448) fused by a GS linker (449-450) with human iduronate-2-sulfatase pro-protein (451-975), (221-219')-disulfide with kappa light chain [V-KAPPA (*Mus musculus* IGKV1-110*01) -*Homo sapiens* IGKJ1*01 [CDRKabatL1: RSSQSLVHSNGNTYLH (24-39); CDRKabatL2: KVSNRFS (55-61); CDRKabatL3: SQSTHVPWT (94-102)] (1'-112') - *Homo sapiens* IGKC*01 (113'-219')] (1'-219'), (227-227'',230-230'')-bisdisulfide dimer, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

pabinafusp alfa

immunoglobuline G1-kappa, anticorps monoclonal humanisé anti-(récepteur de type 1 de la transferrine humain, TfR1), fusionné à l'iduronate 2-sulfatase humaine, glycoforme alfa:
chaîne lourde gamma1 [VH humanisé (*Homo sapiens* IGHV5-51*01 -(IGHD)-IGHJ4*01) [CDRKabatH1[1]: NYWLG (31-35); CDRKabatH2[1]: DIYPGGDYPTYSEKFKV (50-66); CDRKabatH3[1]: SGNYDEVAY (99-107)] (1-118) - *Homo sapiens* IGHG1*01 (CH1 (119-216), charnière (217-231), CH2 (232-341), CH3 (342-446), CHS (447-448))] (1-448) fusionné via un linker GS (449-450) au précurseur de l'iduronate 2-sulfatase humaine (451-975), (221-219')-disulfure avec la chaîne légère kappa [V-KAPPA (*Mus musculus* IGKV1-110*01 -*Homo sapiens* IGKJ1*01) [CDRKabatL1: RSSQSLVHSNGNTYLH (24-39); CDRKabatL2: KVSNRFS (55-61); CDRKabatL3: SQSTHVPWT (94-102)] (1'-112') - *Homo sapiens* IGKC*01 (113'-219')] (1'-219'), (227-227'',230-230'')-dimère bisdisulfure, produit dans des cellules ovariennes de hamsters chinois (CHO), glycoforme alfa

pabinafusp alfa

inmunoglobulina G1-kappa, anticuerpo monoclonal humanizado anti-(receptor tipo 1 de la transferrina humana, TfR1), fusionado con la iduronato 2-sulfatasa humana, glicoforma alfa:
cadena pesada gamma1 [VH humanizado (*Homo sapiens* IGHV5-51*01 -(IGHD)-IGHJ4*01) [CDRKabatH1[1]: NYWLG (31-35); CDRKabatH2[1]: DIYPGGDYPTYSEKFKV (50-66); CDRKabatH3[1]: SGNYDEVAY (99-107)] (1-118) - *Homo sapiens* IGHG1*01 (CH1 (119-216), bisagra (217-231), CH2 (232-341), CH3 (342-446), CHS (447-448))] (1-448) fusionado mediante un conector GS (449-450) con el precusor de la iduronato 2-sulfatasa humana (451-975), (221-219')-disulfuro con la cadena ligera kappa [V-KAPPA (*Mus musculus* IGKV1-110*01 -*Homo sapiens* IGKJ1*01) [CDRKabatL1: RSSQSLVHSNGNTYLH (24-39); CDRKabatL2: KVSNRFS (55-61); CDRKabatL3: SQSTHVPWT (94-102)] (1'-112') - *Homo sapiens* IGKC*01 (113'-219')] (1'-219'), (227-227'',230-230'')-dímero bisdisulfuro, producido en las células ováricas de hamsters chinos (CHO), glicoforma alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVQSGAE VKKPGESLKI SCKGSGYSFT NYWLGWVRQM PGKGLEWMGD  50
IYPGGDYPTY SEKFKVQVTI SADKSISTAY LQWSSLKASD TAMYYCARSG 100
NYDEVAYWGQ GTLVTVSSAS 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 SLSLSPGKGS 450
SETQANSTTD ALNVLLIIVD DLRPSLGCYG DKLVRSPNID QLASHSLLFQ 500
NAFAQQAVCA PSRVSFLTGR RPDTTRLYDF NSYWRVHAGN FSTIPQYFKE 550
NGYVTMSVGK VFHPGISSNH TDDSPYSWSF PPYHPSSEKY ENTKTCRGPD 600
GELHANLLCP VDVLDVPEGT LPDKQSTEQA IQLLEKMKTS ASPFFLAVGY 650
HKPHIPFRYP KEFQKLYPLE NITLAPDPEV PDGLPPVAYN PWMDIRQRED 700
VQALNISVPY GPIPVDFQRK IRQSYFASVS YLDTQVGRLL SALDDLQLAN 750
STIIAFTSDH GWALGEHGEW AKYSNFDVAT HVPLIFYVPG RTASLPEAGE 800
KLFPYLDPFD SASQLMEPGR QSMDLVELVS LFPTLAGLAG LQVPPRCPVP 850
SFHVELCREG KNLLKHFRFR DLEEDPYLPG NPRELIAYSQ YPRPSDIPQW 900
NSDKPSLKDI KIMGYSIRTI DYRYTVWVGF NPDEFLANFS DIHAGELYFV 950
DSDPLQDHNM YNDSQGGDLF QLLMP                            975
```

Light chain / Chaîne légère / Cadena ligera

```
DIVMTQTPLS LSVTPGQPAS ISCRSSQSLV HSNGNTYLHW YLQKPGQSPQ  50
LLIYKVSNRF SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCSQSTHVP 100
WTFGQGTKVE 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: IgG1: 22-96, 145-201, 262-322, 368-426,
22''-96'', 145''-201'', 262''-322'', 368''-426'',
IDS: 596-609, 847-857, 596''-609'', 847''-857''
intra-L: 23'-93', 139'-199', 23'''-93''', 139'''-199'''
inter-H-L: 221-219', 221''-219'''
inter-H-H: 227-227'', 230-230''

N-Glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
298, 456, 540, 569, 671, 705, 750, 938, 962,
298'', 456'', 540'', 569'', 671'', 705'', 750'', 938'', 962''

Other modifications / Autres modifications / Otras modificaciones
Cys509, Cys509'' → 3-oxoalanyl (2-formylglycyl)

pecavaptanum
pecavaptan

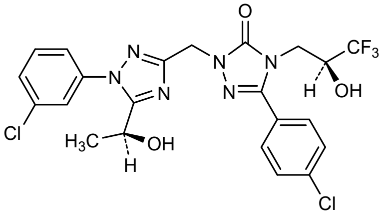
5-(4-chlorophenyl)-2-({1-(3-chlorophenyl)-5-[(1*S*)-1-hydroxyethyl]-1*H*-1,2,4-triazol-3-yl}methyl)-4-[(2*S*)-3,3,3-trifluoro-2-hydroxypropyl]-2,4-dihydro-3*H*-1,2,4-triazol-3-one pécavaptan

5-(4-chlorophényl)-2-({1-(3-chlorophényl)-5-[(1*S*)-1-hydroxyéthyl]-1*H*-1,2,4-triazol-3-yl}méthyl)-4-[(2*S*)-3,3,3-trifluoro-2-hydroxypropyl]-2,4-dihydro-3*H*-1,2,4-triazol-3-one

pecavaptan

5-(4-clorofenil)-2-({1-(3-clorofenil)-5-[(1*S*)-1-hidroxietil]-1*H*-1,2,4-triazol-3-il}metil)-4-[(2*S*)-3,3,3-trifluoro-2-hidroxipropil]-2,4-dihidro-3*H*-1,2,4-triazol-3-ona

$C_{22}H_{19}Cl_2F_3N_6O_3$



pegbelferminum #

pegbelfermin

L-methionyl-[108-{4-[*N*-(2-{[ω-methoxypoly(oxyethylene)-α-carbonyl]amino}ethoxy)ethanimidoyl]-L-phenylalanine}(108Q>X)] human fibroblast growth factor 21 (FGF21) natural L^{146}>P variant, produced in *Escherichia coli*

pegbelfermine

L-méthionyl-[108-{4-[*N*-(2-{[ω-méthoxypoly(oxyéthylène)-α-carbonyl]amino}éthoxy)éthanimidoyl]-L-phénylalanine}(108Q>X)] facteur de croissance des fibroblastes 21 (FGF21) humain, variant naturel L^{146}>P, produit par *Escherichia coli*

pegbelfermina

L-metionil-[108-{4-[*N*-(2-{[ω-metoxipoli(oxietileno)-α-carbonil]amino}etoxi)etanimidoil]-L-fenilalanina}(108Q>X)] factor de crecimiento de fibroblastos 21 (FGF21) humano, variante natural L^{146}>P, producido por *Escherichia coli*

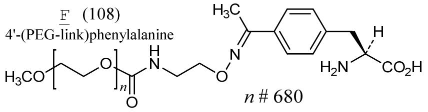
Sequence / Séquence / Secuencia

```
                                                     M    0
HPIPDSSPLL QFGGQVRQRY LYTDDAQQTE AHLEIREDGT VGGAADQSPE   50
SLLQLKALKP GVIQILGVKT SRFLCQRPDG ALYGSLHFDP EACSFRELLL  100
EDGYNVYFSE AHGLPLHLPG NKSPHRDPAP RGPARFLPLP GLPPAPPEPP  150
GILAPQPPDV GSSDPLSMVG PSQGRSPSYA S                      181
```

Disulfide bridge location / Position du pont disulfure / Posición del puente disulfuro

75-93

Modified residue / Résidu modifié / Resto modificado

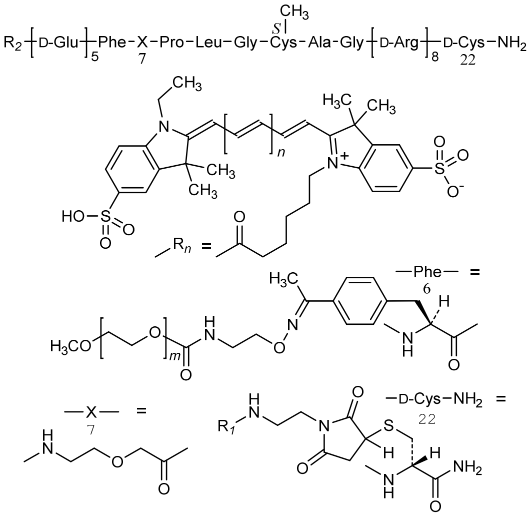

F (108)
4'-(PEG-link)phenylalanine

n # 680

pegloprastidum

pegloprastide	$N^{2.1}$-(6-{2-[7-(1-ethyl-3,3-dimethyl-5-sulfo-1,3-dihydro-2*H*-indol-2-ylidene)hepta-1,3,5-trien-1-yl]-3,3-dimethyl-5-sulfonato-3*H*-indol-1-ium-1-yl}hexanoyl)penta-D-α-glutamyl-4-[*N*-(2-{[ω-methoxypoly(oxyethylene)-α-carbonyl]amino}ethoxy)ethanimidoyl]-L-phenylalanyl-2-(2-aminoethoxy)acetyl-L-prolyl-L-leucylglycyl-*S*-methyl-L-cysteinyl-L-alanylglycylocta-D-arginyl-*S*-{(3*Ξ*)-1-[2-(6-{2-[5-(1-ethyl-3,3-dimethyl-5-sulfo-1,3-dihydro-2*H*-indol-2-ylidene)penta-1,3-dien-1-yl]-3,3-dimethyl-5-sulfonato-3*H*-indol-1-ium-1-yl}hexanamido)ethyl]-2,5-dioxopyrrolidin-3-yl}-D-cysteinamide
péglóprastide	$N^{2.1}$-(6-{2-[7-(1-éthyl-3,3-diméthyl-5-sulfo-1,3-dihydro-2*H*-indol-2-ylidène)hepta-1,3,5-trién-1-yl]-3,3-diméthyl-5-sulfonato-3*H*-indol-1-ium-1-yl}hexanoyl)penta-D-α-glutamyl-4-[*N*-(2-{[ω-méthoxypoly(oxyéthylène)-α-carbonyl]amino}éthoxy)éthanimidoyl]-L-phénylalanyl-2-(2-aminoéthoxy)acétyl-L-prolyl-L-leucylglycyl-*S*-méthyl-L-cystéinyl-L-alanylglycylocta-D-arginyl-*S*-{(3*Ξ*)-1-[2-(6-{2-[5-(1-éthyl-3,3-diméthyl-5-sulfo-1,3-dihydro-2*H*-indol-2-ylidène)penta-1,3-dién-1-yl]-3,3-diméthyl-5-sulfonato-3*H*-indol-1-ium-1-yl}hexanamido)éthyl]-2,5-dioxopyrrolidin-3-yl}-D-cystéinamide
pegloprastida	$N^{2.1}$-(6-{2-[7-(1-etil-3,3-dimetil-5-sulfo-1,3-dihidro-2*H*-indol-2-ilideno)hepta-1,3,5-trien-1-il]-3,3-dimetil-5-sulfonato-3*H*-indol-1-ium-1-il}hexanoil)penta-D-α-glutamil-4-[*N*-(2-{[ω-metoxipoli(oxietileno)-α-carbonil]amino}etoxi)etanimidoil]-L-fenilalanil-2-(2-aminoetoxi)acetil-L-prolil-L-leucilglicil-*S*-metil-L-cisteinil-L-alanilglicilocta-D-arginil-*S*-{(3*Ξ*)-1-[2-(6-{2-[5-(1-etil-3,3-dimetil-5-sulfo-1,3-dihidro-2*H*-indol-2-ilideno)penta-1,3-dien-1-il]-3,3-dimetil-5-sulfonato-3*H*-indol-1-ium-1-il}hexanamido)etil]-2,5-dioxopirrolidin-3-il}-D-cisteinamida

$C_{191}H_{287}N_{55}O_{52}S_6(C_2H_4O)_m$, m ~ 45



pepinemabum #

pepinemab

immunoglobulin G4-kappa, anti-[*Homo sapiens* SEMA4D (semaphorin 4D, CD100)], monoclonal antibody;
gamma4 heavy chain (1-445) [VH (*Homo sapiens* IGHV1-46*01 (82.7%) -(IGHD) -IGHJ3*01 (92.9%)) [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 (444-445)) (119-445)], (132-218')-disulfide with kappa light chain (1'-218') [V-KAPPA (*Mus musculus* IGKV3-4*01 (85.9%) -(IGHD) -IGKJ2*03 (91.7%)/*Homo sapiens* IGKV4-1*01 (83.2%) -IGKJ2*01 (100%)) [10.3.9] (1'-111') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218')]; dimer (224-224'':227-227'')-bisdisulfide

pépinémab

immunoglobuline G4-kappa, anti-[*Homo sapiens* SEMA4D (sémaphorine 4D, CD100)], anticorps monoclonal;
chaîne lourde gamma4 (1-445) [VH (*Homo sapiens* IGHV1-46*01 (82.7%) -(IGHD) - IGHJ3*01 (92.9%)) [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 (444-445)) (119-445)], (132-218')-disulfure avec la chaîne légère kappa (1'-218') [V-KAPPA (*Mus musculus* IGKV3-4*01 (85.9%) -(IGHD) -IGKJ2*03 (91.7%)/*Homo sapiens* IGKV4-1*01 (83.2%) -IGKJ2*01 (100%)) [10.3.9] (1'-111') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218')]; dimère (224-224'':227-227'')-bisdisulfure

pepinemab

inmunoglobulina G4-kappa, anti-[*Homo sapiens* SEMA4D (semaforina 4D, CD100)], anticuerpo monoclonal;
cadena pesada gamma4 (1-445) [VH (*Homo sapiens*IGHV1-46*01 (82.7%) -(IGHD) - IGHJ3*01 (92.9%)) [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 (444-445)) (119-445)], (132-218')-disulfuro con la cadena ligera kappa (1'-218') [V-KAPPA (*Mus musculus* IGKV3-4*01 (85.9%) -(IGHD) -IGKJ2*03 (91.7%)/*Homo sapiens* IGKV4-1*01 (83.2%) -IGKJ2*01 (100%)) [10.3.9] (1'-111') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218')]; dímero (224-224'':227-227'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

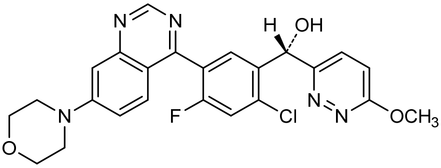
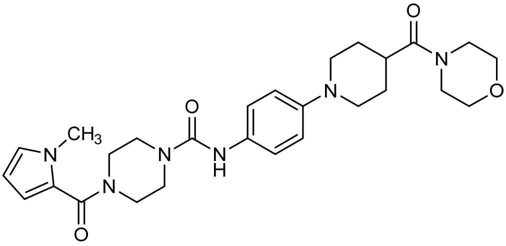
```
QVQLVQSGAE VKKPGSSVKV SCKASGYSFS DYYMHWVRQA PGQGLEWMGQ  50
INPTTGGASY NQKFKGKATI TVDKSTSTAY MELSSLRSED TAVYYCARYY 100
YGRHFDVWGQ GTTVTVSSAS TKGPSVFPLA PCSRSTSEST AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTKTYT 200
CNVDHKPSNT KVDKRVESKY GPPCPPCPAP EFLGGPSVFL FPPKPKDTLM 250
ISRTPEVTCV VVDVSQEDPE VQFNWYVDGV EVHNAKTKPR EEQFNSTYRV 300
VSVLTVLHQD WLNGKEYKCK VSNKGLPSSI EKTISKAKGQ PREPQVYTLP 350
PSQEEMTKNQ VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG 400
SFFLYSRLTV DKSRWQEGNV FSCSVMHEAL HNHYTQKSLS LSLGK      445
```

Light chain / Chaîne légère / Cadena ligera

```
DIVMTQSPDS LAVSLGERAT INCKASQSVD YDGDSYMNWY QQKPGQPPKL  50
LIYAASNLES GVPDRFSGSG SGTDFTLTIS SLQAEDVAVY YCQQSNEDPY 100
TFGQGTKLEI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL NNFYPREAKV 150
QWKVDNALQS GNSQESVTEQ DSKDSTYSLS STLTLSKADY EKHKVYACEV 200
THQGLSSPVT KSFNRGEC                                   218
```

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'-92' 138'-198'
23'''-92''' 138'''-198'''
Inter-H-L (CH1 10-CL 126) 132-218' 132''-218'''
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

peposertibum	
peposertib	(*S*)-{2-chloro-4-fluoro-5-[7-(morpholin-4-yl)quinazolin-4-yl]phenyl}(6-methoxypyridazin-3-yl)methanol
péposertib	(*S*)-{2-chloro-4-fluoro-5-[7-(morpholin-4-yl)quinazolin-4-yl]phényl}(6-méthoxypyridazin-3-yl)methanol
peposertib	(*S*)-{2-cloro-4-fluoro-5-[7-(morfolin-4-il)quinazolin-4-il]fenil}(6-metoxipiridazin-3-il)methanol
	$C_{24}H_{21}ClFN_5O_3$
	
pizuglanstatum	
pizuglanstat	4-(1-methyl-1*H*-pyrrole-2-carbonyl)-*N*-{4-[4-(morpholine-4-carbonyl)piperidin-1-yl]phenyl}piperazine-1-carboxamide
pizuglanstat	4-(1-méthyl-1*H*-pyrrole-2-carbonyl)-*N*-{4-[4-(morpholine-4-carbonyl)pipéridin-1-yl]phényl}pipérazine-1-carboxamide
pizuglanstat	4-(1-metil-1*H*-pirrolo-2-carbonil)-*N*-{4-[4-(morfolina-4-carbonil)piperidin-1-il]fenil}piperazina-1-carboxamida
	$C_{27}H_{36} N_6O_4$
	
plamotamabum #	
plamotamab	immunoglobulin half-G1-kappa/scFv-h-CH2-CH3, anti-[*Homo sapiens* MS4A1 (membrane-spanning 4-domains subfamily A member 1, CD20) and *Homo sapiens* CD3 epsilon (CD3E, Leu-4)], monoclonal antibody, bispecific; gamma1 heavy chain anti-MS4A1 (1-450) [VH (*Homo sapiens* IGHV1-3*01 (88.8%) -(IGHD) -IGHJ2*01 (81.2%)) [8.8.14] (1-121) -*Homo sapiens* IGHG1*03v (CH1 N114>D (212), R120>K (218) (122-219), hinge 1-15 (220-234), CH2 E1.4>P (237), L1.2>V (238), G1.1>A (239), S29>K (270), Q84.2>E (298) (235-343), CH3 E12 (359), M14 (361), L24>D (371), K26>S (373), N44>D (387), Q97>E (421), N100>D (424) (344-448), CHS (449-450)) (122-450)],(224-213')-disulfide with

with kappa light chain anti-MS4A1 (1'-213') [V-KAPPA (*Homo sapiens* IGKV1-16*01 (80.9%) -IGKJ4*01 (100%)) [5.3.9] (1'-106') -*Homo sapiens* IGKC*01 (100%) A45.1 (152), V101 (190) (107'-213')];
heavy chain scFv-h-CH2-CH3, anti-CD3E (1-485) [VH (*Homo sapiens* IGHV3-73*01 (87.0%) -(IGHD) -IGHJ6*01 (90.9%)) [8.10.16] (1-125) -20-mer linker (126-145) -V-LAMBDA (*Mus musculus* IGLV1*01 (80.6%) -IGLJ1*01 (100%)/*Homo sapiens* IGLV7-46*01 (76.8%) -IGHJ3*02 (100%)) [9.3.9] (146-254) -IGHG1*03 (hinge 1-15 C5>S (259) (255-269) -CH2 E1.4>P (272), L1.2>V (273), G1.1>A (274), S29>K (305) (270-378),CH3 E12 (394), E13>Q (395), M14 (396), S20>K (402)(379-483), CHS (484-485)) (1-485)]; (230-265":233-268")-bisdisulfide

plamotamab

immunoglobuline demi-G1-kappa/scFv-h-CH2-CH3, anti-[*Homo sapiens* MS4A1 (membre 1 de la sous-famille A à 4 domaines transmembranaires, CD20) et *Homo sapiens* CD3 epsilon (CD3E, Leu-4)], anticorps monoclonal, bispécifique;
chaîne lourde gamma1 anti-MS4A1 (1-450) [VH (*Homo sapiens* IGHV1-3*01 (88.8%) -(IGHD) -IGHJ2*01 (81.2%)) [8.8.14] (1-121) -*Homo sapiens* IGHG1*03v (CH1 N114>D (212), R120>K (122-219), charnière 1-15 (220-234), CH2 E1.4>P (237), L1.2>V (238), G1.1>A (239), S29>K (270), Q84.2>E (298) (235-343), CH3 E12 (359), M14 (361), L24>D (371), K26>S (373), N44>D (387), Q97>E (421), N100>D (424) (344-448), CHS (449-450)) (122-450)],(224-213')-disulfure avec la chaîne légère kappa (1'-213') [V-KAPPA (*Homo sapiens* IGKV1-16*01 (80.9%) -IGKJ4*01 (100%)) [5.3.9] (1'-106') -*Homo sapiens* IGKC*01 (107'-213')];
chaîne lourde scFv-h-CH2-CH3, anti-CD3E (1-485) [VH (*Homo sapiens* IGHV3-73*01 (87.0%) -(IGHD) -IGHJ6*01 (90.9%)) [8.10.16] (1-125) -20-mer linker (126-145) -V-LAMBDA (*Mus musculus* IGLV1*01 (80.6%) -IGLJ1*01 (100%)/*Homo sapiens* IGLV7-46*01 (76.8%) -IGHJ3*02 (100%)) [9.3.9] (146-254) -IGHG1*03 (charnière 1-15 C5>S (259) (255-269) -CH2 E1.4>P (272), L1.2>V (273), G1.1>A (274), S29>K (305) (270-378), CH3 E12 (394), E13>Q (395), M14 (396), S20>K (402)(379-483), CHS (484-485)) (1-485)]; dimère (230-265":233-268")-bisdisulfure

plamotamab

inmunoglobulina demi-G1-kappa/scFv-h-CH2-CH3, anti-[*Homo sapiens* MS4A1 (miembro 1 de la subfamilia A con 4 dominios transmembranarios, CD20) y *Homo sapiens* CD3 épsilon (CD3E, Leu-4)], anticuerpo monoclonal, biespecífico;
cadena pesada gamma1 anti-MS4A1 (1-450) [VH (*Homo sapiens* IGHV1-3*01 (88.8%) -(IGHD) -IGHJ2*01 (81.2%)) [8.8.14] (1-121) -*Homo sapiens* IGHG1*03v (CH1 N114>D (212), R120>K (122-219), bisagra 1-15 (220-234), CH2 E1.4>P (237), L1.2>V (238), G1.1>A (239), S29>K (270), Q84.2>E (298) (235-343), CH3 E12 (359), M14 (361), L24>D (371), K26>S (373), N44>D (387), Q97>E (421), N100>D (424) (344-448), CHS (449-450)) (122-450)],(224-213')-disulfuro con la cadena ligera kappa (1'-213') [V-KAPPA (*Homo sapiens* IGKV1-16*01 (80.9%) -IGKJ4*01 (100%)) [5.3.9] (1'-106') -*Homo sapiens* IGKC*01 (107'-213')];
cadena pesada scFv-h-CH2-CH3, anti-CD3E (1-485) [VH (*Homo sapiens* IGHV3-73*01 (87.0%) -(IGHD) -IGHJ6*01 (90.9%)) [8.10.16] (1-125) -20-mer ligante (126-145) -V-LAMBDA (*Mus musculus* IGLV1*01 (80.6%) -IGLJ1*01 (100%)/*Homo sapiens* IGLV7-46*01 (76.8%) -IGHJ3*02 (100%)) [9.3.9] (146-254) -IGHG1*03 (bisagra 1-15 C5>S (259) (255-269) -CH2 E1.4>P (272), L1.2>V (273), G1.1>A (274), S29>K (305) (270-378), CH3 E12 (394), E13>Q (395), M14 (396), S20>K (402)(379-483), CHS (484-485)) (1-485)]; dímero (230-265":233-268")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada (anti-MS4A1)

```
QVQLVQSGAE VKKPGASVKV SCKASGYTFT SYNMHWVRQA PGQGLEWMGA  50
IYPGNGDTSY NQKFQGRVTI TADKSISTAY MELSSLRSED TAVYYCARST 100
YYGGDWYFNV WGAGTLVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200
TYICNVNHKP SDTKVDKKVE PKSCDKTHTC PPCPAPPVAG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVK HEDPEVKFNW YVDGVEVHNA KTKPREEEYN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSREE MTKNQVSLTC DVSGFYPSDI AVEWESDGQP ENNYKTTPPV 400
LDSDGSFFLY SKLTVDKSRW EQGDVFSCSV MHEALHNHYT QKSLSLSPGK 450
```

Light chain / Chaîne légère / Cadena ligera (anti-MS4A1)

```
QIVLTQSPSS LSASVGDRVT ITCRASSSVS YIHWFQQKPG KSPKPLIYAT  50
SNLASGVPVR FSGSGSGTDY TLTISSLQPE DFATYYCQQW TSNPPTFGGG 100
TKVEIKRTVA APSVFIFPPS DEQLKSGTAS VVCLLNNFYP REAKVQWKVD 150
NALQSGNSQE SVTEQDSKDS TYSLSSTLTL SKADYEKHKV YACEVTHQGL 200
SSPVTKSFNR GEC          213
```

Heavy chain / Chaîne lourde / Cadena pesada scFv-h-CH2-CH3 (anti-CD3E)

```
EVQLVESGGG LVQPGGSLRL SCAASGFTFS TYAMNWVRQA PGKGLEWVGR  50
IRSKYNNYAT YYADSVKGRF TISRDDSKNT LYLQMNSLRA EDTAVYYCVR 100
HGNFGDSYVS WFAYWGQGTL VTVSSGKPGS GKPGSGKPGS GKPGSQAVVT 150
QEPSLTVSPG GTVTLTCGSS TGAVTTSNYA NWVQQKPGKS PRGLIGGTNK 200
RAPGVPARFS GSLLGGKAAL TISGAQPEDE ADYYCALWYS NHWVFGGGTK 250
LTVLEPKSSD KTHTCPPCPA PPVAGPSVFL FPPKPKDTLM ISRTPEVTCV 300
VVDVKHEDPE VKFNWYVDGV EVHNAKTKPR EEQYNSTYRV VSVLTVLHQD 350
WLNGKEYKCK VSNKALPAPI EKTISKAKGQ PREPQVYTLP PSREQMTKNQ 400
VKLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG SFFLYSKLTV 450
DKSRWQQGNV FSCSVMHEAL HNHYTQKSLS LSPGK      485
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 148-204 264-324 370-428
Intra-H scFv-h-CH2-CH3 22''-98'' 167''-235'' 299''-359'' 405''-463''
Intra-L (C23-C104) 23'-87' 133'-193'
Inter-H-L (h 5-CL 126) 224-213'
Inter-H-H (h 11, h 14) 230-265'' 233-268''

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
300, 335''
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

pozelimabum #

pozelimab

immunoglobulin G4-kappa, anti-[*Homo sapiens* C5 (complement C5)], *Homo sapiens* monoclonal antibody;
gamma4 heavy chain *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV4-59*02 (94.8%) -(IGHD) -IGHJ4*01 (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 *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-6*01 (96.8%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (226-226'':229-229'')-bisdisulfide

pozélimab

immunoglobuline G4-kappa, anti-[*Homo sapiens* C5 (complément C5)], anticorps monoclonal *Homo sapiens*;
chaîne lourde gamma4 *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV4-59*02 (94.8%) -(IGHD) -IGHJ4*01 (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 *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-6*01 (96.8%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (226-226'':229-229'')-bisdisulfure

pozelimab

inmunoglobulina G4-kappa, anti-[*Homo sapiens* C5 (complemento C5)], anticuerpo monoclonal *Homo sapiens*; cadena pesada gamma4 *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV4-59*02 (94.8%) -(IGHD) -IGHJ4*01 (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 *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-6*01 (96.8%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (226-226":229-229")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLQESGPG LVKPSETLSL TCTVSGDSVS SSYWTWIRQP PGKGLEWIGY  50
IYYSGSSNYN PSLKSRATIS VDTSKNQFSL KLSSVTAADT AVYYCAREGN 100
VDTTMIFDYW 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

```
AIQMTQSPSS LSASVGDRVT ITCRASQGIR NDLGWYQQKP GKAPKLLIYA  50
ASSLQSGVPS RFAGRGSGTD FTLTISSLQP EDFATYYCLQ DFNYPWTFGQ 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) 22-95 147-203 261-321 367-425
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

pralsetinibum

pralsetinib

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

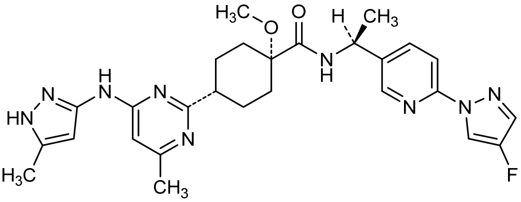
pralsétinib

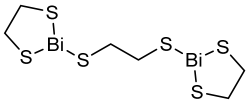
cis-*N*-{(1*S*)-1-[6-(4-fluoro-1*H*-pyrazol-1-yl)pyridin-3-yl]éthyl}-1-méthoxy-4-{4-méthyl-6-[(5-méthyl-1*H*-pyrazol-3-yl)amino]pyrimidin-2-yl}cyclohexane-1-carboxamide

pralsetinib

cis-*N*-{(1*S*)-1-[6-(4-fluoro-1*H*-pirazol-1-il)piridin-3-il]etil}-1-metoxi-4-{4-metil-6-[(5-metil-1*H*-pirazol-3-il)amino]pirimidin-2-il}ciclohexano-1-carboxamida

$C_{27}H_{32}FN_9O_2$



pravibismanum	
pravibismane	2,2'-[ethane-1,2-diylbis(sulfanediyl)]bis(1,3,2-dithiabismolane)
pravibismane	2,2'-[éthane-1,2-diylbis(sulfanediyl)]bis(1,3,2-dithiabismolane)
pravibismano	2,2'-[etano-1,2-diilbis(sulfanediil)]bis(1,3,2-ditiabismolano)
	$C_6H_{12}Bi_2S_6$ 
quetmolimabum #	
quetmolimab	immunoglobulin G2-kappa, anti-[*Homo sapiens* CX3CL1 (chemokine C-X3-C motif ligand 1, SCYD1, small inducible cytokine subfamily D Cys-X3-Cysmember 1, fractalkine, FKN, neurotactin, NTN)], monoclonal antibody; gamma2 heavy chain (1-445) [VH (*Mus musculus* IGHV1S56*01 (80.4%) -(IGHD) -IGHJ2*01 (93.3%)/*Homo sapiens* IGHV1-46*01 (76.3%) -(IGHD) -IGHJ4*01 (93.3%)) [8.8.12] (1-119) -*Homo sapiens* IGHG2*01 (CH1 (120-217), hinge (218-229), CH2 V1.2>A (233), G1>A (235) (230-338), CH3 (339-443), CHS (444-445)) (120-445)], (133-214')-disulfide with kappa light chain (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-NL1*01 (85.3%) -IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (221-221":222-222":225-225":228-228")-tetrakisdisulfide
quetmolimab	immunoglobuline G2-kappa, anti-[*Homo sapiens* CX3CL1 (chimiokine ligand 1 de motif C-X3-C, SCYD1, membre 1 de la sous-famille D Cys-X3-Cys des petites cytokines inductibles, fractalkine, FKN, neurotactine, NTN)], anticorps monoclonal; chaîne lourde gamma2 (1-445) [VH (*Mus musculus* IGHV1S56*01 (80.4%) -(IGHD) -IGHJ2*01 (93.3%)/*Homo sapiens* IGHV1-46*01 (76.3%) -(IGHD) -IGHJ4*01 (93.3%)) [8.8.12] (1-119) -*Homo sapiens* IGHG2*01 (CH1 (120-217), charnière (218-229), CH2 V1.2>A (233), G1>A (235) (230-338), CH3 (339-443), CHS (444-445)) (120-445)], (133-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-NL1*01 (85.3%) -IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (221-221":222-222":225-225":228-228")-tétrakisdisulfure
quetmolimab	inmunoglobulina G2-kappa, anti-[*Homo sapiens* CX3CL1 (quimiokina ligando 1 de motif C-X3-C, SCYD1, miembro 1 de la subfamilia D Cys-X3-Cys de las pequeñas citoquinas inducibles, fractalquina, FKN, neurotactina, NTN)], anticuerpo monoclonal;

cadena pesada gamma2 (1-445) [VH (*Mus musculus* IGHV1S56*01 (80.4%) -(IGHD) -IGHJ2*01 (93.3%)/*Homo sapiens* IGHV1-46*01 (76.3%) -(IGHD) -IGHJ4*01 (93.3%)) [8.8.12] (1-119) -*Homo sapiens* IGHG2*01 (CH1 (120-217), bisagra (218-229), CH2 V1.2>A (233), G1>A (235) (230-338), CH3 (339-443), CHS (444-445)) (120-445)], (133-214')-disulfuro con la cadena ligera kappa (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-NL1*01 (85.3%) -IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (221-221":222-222":225-225":228-228")-tetrakisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGASVKV SCKASGYTFT NYYIHWVKQA PGQGLEWIGW  50
IYPGDGSPKF NERFKGRTTL TADKSTNTAY MLLSSLRSED TAVYFCATGP 100
TDGDYFDYWG QGTTVTVSSA STKGPSVFPL APCSRSTSES TAALGCLVKD 150
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSNFGTQTY 200
TCNVDHKPSN TKVDKTVERK CCVECPPCPA PPAAAPSVFL FPPKPKDTLM 250
ISRTPEVTCV VVDVSHEDPE VQFNWYVDGV EVHNAKTKPR EEQFNSTFRV 300
VSVLTVVHQD WLNGKEYKCK VSNKGLPAPI EKTISKTKGQ PREPQVYTLP 350
PSREEMTKNQ VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPMLDSDG 400
SFFLYSKLTV DKSRWQQGNV FSCSVMHEAL HNHYTQKSLS LSPGK      445
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCRASGNIH NFLAWYQQKP GKAPKLLIYN  50
EKTLADGVPS RFSGSGSGTD YTLTISSLQP EDFATYFCQQ FWSTPYTFGG 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) 22-96 146-202 259-319 365-423
22"-96" 146"-202" 259"-319" 365"-423"
Intra-L (C23-C104) 23'-88' 134'-194'
23'''-88''' 134'''-194'''
Inter-H-L (CH1 10-CL 126) 133-214' 133"-214'''
Inter-H-H (h 4, h 5, h 8, h 11) 221-221" 222-222" 225-225" 228-228"

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.

ranuzifigenum civaparvovecum #

ranuzifigene civaparvovec	a recombinant non-replicating adeno-associated virus type 2/6 (rAAV Rep2-Cap6) vector, expressing a cDNA that targets 468-485 bp of the albumin locus (relative to the transcription initiation site), fused to the obligate heterodimeric FokI nuclease domain KKR, under the control of an apolipoprotein E hepatic control region and human alpha-1-antitrypsin promoter (ApoE/hAAT)
ranuzifigène civaparvovec	vecteur viral adéno-associé de type 2/6 recombinant (rAAV Rep2-Cap6), non-répliquant, exprimant un ADNc ciblant les paires de bases 468-485 du locus de l'albumine (en relation avec le site initial de transcription), fusionné au domaine hétérodimérique KKR de la nucléase FokI, sous le contrôle d'une région de contrôle de l'apolipoprotéine E (ApoE) spécifique du foie et du promoteur de l'alpha1-antitrypsine humaine (ApoE/hAAT)

ranuzifigén civaparvovec	un vector de virus adeno asociado tipo 2/6 recombinante (rAAV Rep2-Cap6), no replicativo, que expresa un cDNA dirigido a unirse a los pares de bases 468-485 (en relación al sitio de iniciación de la transcripción) del locus de la albúmina, fusionado al dominio heterodimérico KKR de la nuclease FokI, bajo el control de una región de control hepático de la apolipoproteína E y el promotor de la alfa 1 antitripsina humana (ApoE/hAAT)
relfovetmabum #	
relfovetmab	immunoglobulin G1-kappa, anti-[*Felis catus* NGF (nerve growth factor beta polypeptide, NGFB)], felinized monoclonal antibody; gamma1 heavy chain felinized (1-453) [VH (*Homo sapiens* IGHV3-74*01 (74.5%) -(IGHD) -IGHJ4*01(93.3%)) [8.8.11] (1-118) -*Felis catus* IGHG1*01 (CH1 (119-216), hinge (217-234), CH2 (235-344), CH3 (345-451), CHS (452-453)) (119-453)], (133-214')-disulfide with kappa light chain felinized (1'-217') [V-KAPPA (*Homo sapiens* IGKV1-27*01 (81.1%) -IGKJ2*02 (90.9%)) [6.3.9] (1'-107') -*Felis catus* IGKC*01 N122>Q (210) (108'-217')]; dimer (228-228'':230-230'':233-233'')-trisdisdisulfide
relfovetmab	immunoglobuline G1-kappa, anti-[*Felis catus* NGF (facteur de croissance du nerf polypeptide bêta)], anticorps monoclonal félinisé; chaîne lourde gamma1 félinisée (1-453) [VH (*Homo sapiens* IGHV3-74*01 (74.5%) -(IGHD) -IGHJ4*01(93.3%)) [8.8.11] (1-118) -*Felis catus* IGHG1*01 (CH1 (119-216), charnière (217-234), CH2 (235-344), CH3 (345-449), CHS (450-451)) (119-451)], (133-214')-disulfure avec la chaîne légère kappa félinisée (1'-217') [V-KAPPA (*Homo sapiens* IGKV1-27*01 (81.1%) -IGKJ2*02 (90.9%)) [6.3.9] (1'-107') -*Felis catus* IGKC*01 N122>Q (210) (108'-217')]; dimère (228-228'':230-230'':233-233'')-trisdisulfure
relfovetmab	inmunoglobulina G1-kappa, anti-[*Felis catus* NGF (factor de crecimiento del nervio polipéptido beta)], anticuerpo monoclonal felinizado; cadena pesada gamma1 felinizada (1-453) [VH (*Homo sapiens* IGHV3-74*01 (74.5%) -(IGHD) -IGHJ4*01(93.3%)) [8.8.11] (1-118) -*Felis catus* IGHG1*01 (CH1 (119-216), bisagra (217-234), CH2 (235-344), CH3 (345-449), CHS (450-451)) (119-451)], (133-214')-disulfuro con la cadena ligera kappa felinizada (1'-217') [V-KAPPA (*Homo sapiens* IGKV1-27*01 (81.1%) -IGKJ2*02 (90.9%)) [6.3.9] (1'-107') -*Felis catus* IGKC*01 N122>Q (210) (108'-217')]; dímero (228-228'':230-230'':233-233'')-trisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
DVQLVESGGD LVKPGGSLRL TCVASGFTYS NYWMHWVRQA PGKGLQWVAR  50
IDPYGGGTKH NEKFKRRFTI SRDNAKNTLY LQMNSLKTED TATYYCVRSG 100
YDYYFDVWGQ GTLVTVSSAS TTAPSVFPLA PSCGTTSGAT VALACLVLGY 150
FPEPVTVSWN SGALTSGVHT FPAVLQASGL YSLSSMVTVP SSRWLSDTFT 200
CNVAHPPSNT KVDKTVRKTD HPPGPKPCDC PKCPPPEMLG GPSIFIFPPK 250
PKDTLSISRT PEVTCLVVDL GPDDSDVQIT WFVDNTQVYT AKTSPREEQF 300
NSTYRVVSVL PILHQDWLKG KEFKCKVNSK SLPSPIERTI SKAKGQPHEP 350
QVYVLPPAQE ELSRNKVSVT CLIKSFHPPD IAVEWEITGQ PEPENNYRTT 400
PPQLDSDGTY FVYSKLSVDR SHWQRGNTYT CSVSHEALHS HHTQKSLTQS 450
PGK                                                   453
```

Light chain / Chaîne légère / Cadena ligera

```
EIQMTQSPSS LSASPGDRVT ITCRASENIY SFLAWYQQKP GKVPKLLIYN  50
ANTLAEGVPS RFSGSGSGTD FTLTISSLEP EDAATYYCQH HFGTPFTFGS 100
GTKLEIKRSD AQPSVFLFQP SLDELHTGSA SIVCILNDFY PKEVNVKWKV 150
DGVVQNKGIQ ESTTEQNSKD STYSLSSTLT MSSTEYQSHE KFSCEVTHKS 200
LASTLVKSFQ RSECQRE                                    217
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 145-201 265-325 371-431
22"-96" 145"-201" 265"-325" 371"-431"
Intra-L (C23-C104) 23'-88' 134'-194'
23'''-88''' 134'''-194'''
Inter-H-L (CH1 11-CL 126) 133-214' 133"-214'''
Inter-H-H (h 12, h14, h 17) 228-228" 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:
453, 453"

renadirsenum

renadirsen	*O*-(2-hydroxyethyl) *all-P-ambo*-2'-*O*,4'-*C*-(ethane-1,2-diyl)-5-methyl-*P*-thiocytidylyl-(3'→5')-2-*O*'-methyl-*P*-thioguanylyl-(3'→5')-2'-*O*,4'-*C*-(ethane-1,2-diyl)-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*,4'-*C*-(ethane-1,2-diyl)-5-methyl-*P*-thiouridylyl-(3'→5')-2-*O*'-methyl-*P*-thioguanylyl-(3'→5')-2'-*O*-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*,4'-*C*-(ethane-1,2-diyl)-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*,4'-*C*-(ethane-1,2-diyl)-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-methyl-*P*-thioadenylyl-(3'→5')-2'-*O*-methyl-*P*-thioadenylyl-(3'→5')-2'-*O*,4'-*C*-(ethane-1,2-diyl)-5-methyl-*P*-thiouridylyl-(3'→5')-2-*O*'-methyl-*P*-thioguanylyl-(3'→5')-2'-*O*,4'-*C*-(ethane-1,2-diyl)-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*,4'-*C*-(ethane-1,2-diyl)-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-methyl-*P*-thioadenylyl-(3'→5')-2'-*O*-methyl-*P*-thiouridylyl-(3'→5')-2'-*O*,4'-*C*-(ethane-1,2-diyl)-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*,4'-*C*-(ethane-1,2-diyl)-5-methyl-*P*-thio-3'-cytidylate
rénadirsen	*tout-P-ambo*-2'-*O*,4'-*C*-(éthane-1,2-diyl)-5-méthyl-*P*-thiocytidylyl-(3'→5')-2-*O*'-méthyl-*P*-thioguanylyl-(3'→5')-2'-*O*,4'-*C*-(éthane-1,2-diyl)-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-*O*,4'-*C*-(éthane-1,2-diyl)-5-méthyl-*P*-thiouridylyl-(3'→5')-2-*O*'-méthyl-*P*-thioguanylyl-(3'→5')-2'-*O*-méthyl-*P*-thiocytidylyl-(3'→5')-2'-*O*,4'-*C*-(éthane-1,2-diyl)-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-*O*,4'-*C*-(éthane-1,2-diyl)-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-méthyl-*P*-thioadenylyl-(3'→5')-2'-*O*-méthyl-*P*-thioadenylyl-(3'→5')-2'-*O*,4'-*C*-(éthane-1,2-diyl)-5-méthyl-*P*-thiouridylyl-(3'→5')-2-*O*'-méthyl-*P*-thioguanylyl-(3'→5')-2'-*O*,4'-*C*-(éthane-1,2-diyl)-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-*O*,4'-*C*-(éthane-1,2-diyl)-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-méthyl-*P*-thioadenylyl-(3'→5')-2'-*O*-methyl-*P*-thiouridylyl-(3'→5')-2'-*O*,4'-*C*-(éthane-1,2-diyl)-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-*O*,4'-*C*-(éthane-1,2-diyl)-5-méthyl-*P*-thio-3'-cytidylate de *O*-(2-hydroxyéthyle)

renadirsén

todo-*P*-*ambo*-2'-*O*,4'-*C*-(etano-1,2-diil)-5-metil-*P*-tiocitidilil-(3'→5')-2-*O*'-metil-*P*-tioguanilil-(3'→5')-2'-*O*,4'-*C*-(etano-1,2-diil)-5-metil-*P*-tiocitidilil-(3'→5')-2'-*O*,4'-*C*-(etano-1,2-diil)-5-metil-*P*-tiouridilil-(3'→5')-2-*O*'-metil-*P*-thoguanilil-(3'→5')-2'-*O*-metil-*P*-tiocitidilil-(3'→5')-2'-*O*,4'-*C*-(etano-1,2-diil)-5-metil-*P*-tiocitidilil-(3'→5')-2'-*O*,4'-*C*-(etano-1,2-diil)-5-metil-*P*-tiocitidilil-(3'→5')-2'-*O*-metil-*P*-tioadenilil-(3'→5')-2'-*O*-metil-*P*-tioadenilil-(3'→5')-2'-*O*,4'-*C*-(etano-1,2-diil)-5-metil-*P*-tiouridilil-(3'→5')-2-*O*'-metil-*P*-tioguanilil-(3'→5')-2'-*O*,4'-*C*-(etano-1,2-diil)-5-metil-*P*-tiocitidilil-(3'→5')-2'-*O*,4'-*C*-(etano-1,2-diil)-5-metil-*P*-tiocitidilil-(3'→5')-2'-*O*-metil-*P*-tioadenilil-(3'→5')-2'-*O*-metil-*P*-tiouridilil-(3'→5')-2'-*O*,4'-*C*-(etano-1,2-diil)-5-metil-*P*-tiocitidilil-(3'→5')-2'-*O*,4'-*C*-(etano-1,2-diil)-5-metil-*P*-tio-3'-citidilato de *O*-(2-hidroxietilo)

$C_{208}H_{275}N_{63}O_{110}P_{18}S_{18}$

(3'-5')-(*P*-thio)[m^{5}C(*Et*)-Gm-m^{5}C(*Et*)-m^{5}U(*Et*)-Gm-Cm-m^{5}C(*Et*)-m^{5}C(*Et*)-Am-Am-m^{5}U(*Et*)-Gm -m^{5}C(*Et*)-m^{5}C(*Et*)-Am-Um-m^{5}C(*Et*)-m^{5}C(*Et*)-(CH_2-CH_2-OH)]

Legend:
(Et) as suffix = 2'-O,4'-C-(ethan-1,2-diyl)
m as suffix = 2'-O-methyl
m5 as prefix = 5-methyl

repotrectinibum

repotrectinib

(3*R*,6*S*)-4^5-fluoro-3,6-dimethyl-5-oxa-2,8-diaza-1(5,3)-pyrazolo[1,5-*a*]pyrimidina-4(1,2)-benzenacyclononaphan-9-one

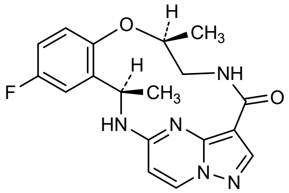
répotrectinib

(3*R*,6*S*)-4^5-fluoro-3,6-diméthyl-5-oxa-2,8-diaza-1(5,3)-pyrazolo[1,5-*a*]pyrimidina-4(1,2)-benzénacyclononaphan-9-one

repotrectinib

(3*R*,6*S*)-4^5-fluoro-3,6-dimetil-5-oxa-2,8-diaza-1(5,3)-pirazolo[1,5-*a*]pirimidina-4(1,2)-bencenaciclononafan-9-ona

$C_{18}H_{18}FN_5O_2$



resamirigenum bilparvovecum #

resamirigene bilparvovec

a recombinant non-replicating adeno-associated virus serotype 8 (AAV8) vector expressing human myotubularin 1 (MTM1), under the control of the human desmin gene promoter

résamirigène bilparvovec

vecteur viral adéno-associé de sérotype 8 (AAV8) recombinant, non-répliquant, exprimant la myotubularine 1 (MTM1) sous le contrôle du promoteur du gène de la desmine

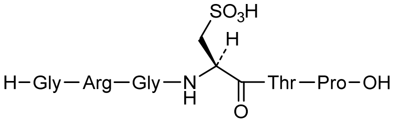
resamirigén bilparvovec

un vector de virus adeno asociado serotipo 8 (AAV8) recombinante, no replicativo, que expresa miotubularina 1 (MTM1) bajo el control del promotor del gen de la desmina humana

risuteganibum

risuteganib	glycyl-L-arginylglycyl-3-sulfo-L-alanyl-L-threonyl-L-proline
risutéganib	glycyl-L-arginylglycyl-3-sulfo-L-alanyl-L-thréonyl-L-proline
risuteganib	glicil-L-arginilglicil-3-sulfo-L-alanil-L-treonil-L-prolina

$C_{22}H_{39}N_9O_{11}S$



rovoctocogenum durparvovecum #

rovoctocogene durparvovec	a recombinant intronless non-replicating adeno-associated virus 2 vector (AAV2) with a bio-engineered capsid derived by DNA shuffling of 10 AAV capsid sequences (AAV1, 2, 3B, 4, 5, 6 8, 9, avian and bovine AAV) followed by *in vivo* selection in *Fah−/−/Rag2−/−/Il2rg−/−* (FRG) mice partially repopulated with human hepatocytes. The vector has AAV2 genomic inverted terminal repeats (ITR) and encodes a human B-domain-deleted blood coagulation factor VIII (hF8, factor VIII, FVIII) under the control of a modified transthyretin (TTRm) promoter.
rovoctocogène durparvovec	vecteur viral adéno-associé de sérotype 2 (AAV2) recombinant, sans intron, non répliquant, avec une capside issue de la bioingénierie, dérivée de séquences d'ADN remaniées de 10 capsides d'AVV (AAV1, 2, 3B, 4, 5, 6, 8, 9, AAV aviaire et bovin), suivie de sélection chez les souris *Fah−/−/Rag2−/−/Il2rg−/−* (FRG) *in vivo,* partiellement repeuplé d'hépatocytes humains. Le vecteur a les deux séquences inverses terminales répétées (ITR) du génome de AAV2 et code pour le facteur de coagulation VIII humain (hF8, facteur VIIIFVIII) dont le domaine B est supprimé, sous le contrôle d'un promoteur de la transthyrétine modifié (TTRm).
rovoctocogén durparvovec	un virus adeno asociado serotipo 2 (AAV2) recombinante, sin intrón, no replicativo con una cápside bio-ingenierizada derivada mediante barajado de secuencias de DNA de 10 cápsides de AAV (AAV1, 2, 3B, 4, 5, 6, 8, 9, AAV aviar y bovino) seguido de selección *in vivo* en ratones *Fah−/−/Rag2−/−/Il2rg−/−* (FRG) parcialmente repoblados con hepatocitos humanos. El vector tiene secuencias terminales invertidas (ITR) genómicas de AAV2 y codifica para el factor de coagulación VIII humano (hF8, factor VIII, FVIII) con el dominio B delecionado, bajo el control de un promotor modificado de transtiretina (TTRm).

rozibafuspum alfa #

rozibafusp alfa	immunoglobulin G2-kappa, anti-[human inducible costimulator (ICOS) ligand protein] human monoclonal antibody, fused with two copies of a tumor necrosis factor ligand superfamily member 13B (TNFSF13B, B-cell activating factor, BAFF)-binding peptide, glycoform alfa:

gamma2 heavy chain [*Homo sapiens* VH (*Homo sapiens* IGHV3-7*01 -(IGHD)-IGHJ1*01) [CDRKabatH1: SYWMS (31-35); CDRKabatH2: YIKQDGNEKYYVDSVKG (50-66); CDRKabatH3: EGILWFGDLPTF (99-110)] (1-121) - *Homo sapiens* IGHG2*01 (CH1 (122-219), hinge (220-231), CH2 (232-340), CH3 (341-445), CHS (446-447))] (1-447) fused by a G_5 linker (448-452) and a $(GS)_2ATG(GS)_2VASS(GS)_2ATHL$ linker (471-493) with two copies of a synthetic human tumor necrosis factor ligand superfamily member 13B (TNFSF13B, B cell-activating factor, BAFF)-binding peptide (453-470, 494-511), (135-214')-disulfide with kappa light chain [V-KAPPA (*Homo sapien*s IGKV1D-16*01 -IGKJ1*01) [CDRKabatL1: RASQGISNWLA (24-34); CDRKabatL2: AASSLQS (50-56); CDRKabatL3: QQYDSYPRT (89-97)] (1'-107') - *Homo sapiens* IGKC*01 (108'-214')] (1'-214'), (223-223'',224-224'',227-227'',230-230'')-tetrakisdisulfide dimer, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

rozibafusp alfa

immunoglobuline G2-kappa, anticorps monoclonal humain anti-[ligand de la protéine inductible de co-stimulation (ICOS), humain], fusionné à deux copies du peptide se liant au membre 13B de la superfamille des ligands du facteur de nécrose tumorale humain (TNFSF13B, facteur d'activation des lymphocytes B, BAFF), glycoforme alfa:
chaîne lourde gamma2 [*Homo sapiens* VH (*Homo sapiens* IGHV3-7*01 -(IGHD)-IGHJ1*01) [CDRKabatH1: SYWMS (31-35); CDRKabatH2: YIKQDGNEKYYVDSVKG (50-66); CDRKabatH3: EGILWFGDLPTF (99-110)] (1-121) - *Homo sapiens* IGHG2*01 (CH1 (122-219), charnière (220-231), CH2 (232-340), CH3 (341-445), CHS (446-447))] (1-447) fusionné via un linker G_5 (448-452) et un linker $(GS)_2ATG(GS)_2VASS(GS)_2ATHL$ (471-493) à deux copies du peptide se liant au membre 13B de la superfamille des ligands du facteur de nécrose tumorale humain (TNFSF13B, facteur d'activation des lymphocytes B, BAFF) (453-470, 494-511), (135-214')-disulfure avec la chaîne légère kappa [V-KAPPA (*Homo sapien*s IGKV1D-16*01 -IGKJ1*01) [CDRKabatL1: RASQGISNWLA (24-34); CDRKabatL2: AASSLQS (50-56); CDRKabatL3: QQYDSYPRT (89-97)] (1'-107') - *Homo sapiens* IGKC*01 (108'-214')] (1'-214'), (223-223'',224-224'',227-227'',230-230'')-dimère tétrakisdisulfure, produit dans des cellules ovariennes de hamsters chinois (CHO), glycoforme alfa

rozibafusp alfa

inmunoglobulina G2-kappa, anticuerpo monoclonal humano anti-[ligando de la proteína inductible de coestimulación (ICOS), humano], fusionado con diez copias del péptido que se une al miembro 13B de la superfamilia de los ligandos del factor de necrosis tumoral humano (TNFSF13B, factor de activación de los linfocitos B, BAFF), glicoforma alfa:
cadena pesada gamma2 [*Homo sapiens* VH (*Homo sapiens* IGHV3-7*01 -(IGHD)-IGHJ1*01) [CDRKabatH1: SYWMS (31-35); CDRKabatH2: YIKQDGNEKYYVDSVKG (50-66); CDRKabatH3: EGILWFGDLPTF (99-110)] (1-121) - *Homo sapiens* IGHG2*01 (CH1 (122-219), bisagra (220-231), CH2 (232-340), CH3 (341-445), CHS (446-447))] (1-447) fusionado mediante un conector G_5 (448-452) y un conector $(GS)_2ATG(GS)_2VASS(GS)_2ATHL$ (471-493) con diez copias del péptido que se une al miembro 13B de la superfamilia de los ligandos del factor de necrosis tumoral humano (TNFSF13B, factor de activación de los linfocitos B, BAFF) (453-470, 494-511), (135-214')-disulfuro con la cadena ligera kappa [V-KAPPA (*Homo sapien*s IGKV1D-16*01 -IGKJ1*01) [CDRKabatL1: RASQGISNWLA (24-34); CDRKabatL2: AASSLQS (50-56); CDRKabatL3: QQYDSYPRT (89-97)] (1'-107') - *Homo sapiens* IGKC*01 (108'-214')] (1'-214'), (223-223'',224-224'',227-227'',230-230'')-dímero tetrakisdisulfuro, producido en las células ováricas de hamsters chinos (CHO), glicoforma alfa

Heavy chain / Chaîne lourde / Cadena pesada
```
EVQLVESGGG LVQPGGSLRL SCAASGFTFS SYWMSWVRQA PGKGLEWVAY  50
IKQDGNEKYY VDSVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCAREG 100
ILWFGDLPTF WGQGTLVTVS SASTKGPSVF PLAPCSRSTS ESTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSNFGTQ 200
TYTCNVDHKP SNTKVDKTVE RKCCVECPPC PAPPVAGPSV FLFPPKPKDT 250
LMISRTPEVT CVVVDVSHED PEVQFNWYVD GVEVHNAKTK PREEQFNSTF 300
RVVSVLTVVH QDWLNGKEYK CKVSNKGLPA PIEKTISKTK GQPREPQVYT 350
LPPSREEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPMLDS 400
DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPGKGGG 450
GGLPGCKWDL LIKQWVCDPL GSGSATGGSG SVASSGSGSA THLLPGCKWD 500
LLIKQWVCDP L                                          511
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Light chain / Chaîne légère / Cadena ligera
```
DIQMTQSPSS LSASVGDRVT ITCRASQGIS NWLAWYQQKP EKAPKSLIYA  50
ASSLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YDSYPRTFGQ 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                       214
```

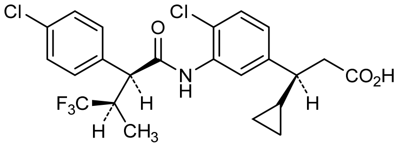
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
```
intra-H: IgG2:  22-96,     148-204,    261-321,    367-425,
                22''-96'',  148''-204'', 261''-321'',  367''-425'',
       BAFF:  456-467,   497-508,    456''-467'',   497''-508''
intra-L:        23'-88',   134'-194',    23'''-88''',   134'''-194'''
inter-H-L:    135-214',   135''-214'''
inter-H-H:    223-223'',  224-224'',  227-227'',   230-230''
```

N-Glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
Asn297, Asn297''

runcaciguatum

runcaciguat	(3*S*)-3-{4-chloro-3-[(2*S*,3*R*)-2-(4-chlorophenyl)-4,4,4-trifluoro-3-methylbutanamido]phenyl}-3-cyclopropylpropanoic acid
runcaciguat	acide (3*S*)-3-{4-chloro-3-[(2*S*,3*R*)-2-(4-chlorophényl)-4,4,4-trifluoro-3-méthylbutanamido]phényl}-3-cyclopropylpropanoïque
runcaciguat	ácido (3*S*)-3-{4-cloro-3-[(2*S*,3*R*)-2-(4-clorofenil)-4,4,4-trifluoro-3-metilbutanamido]fenil}-3-ciclopropilpropanoico

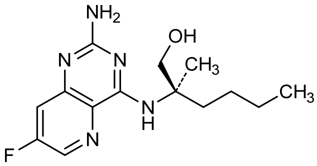
$C_{23}H_{22}Cl_2F_3NO_3$



selgantolimodum

selgantolimod	(2*R*)-2-[(2-amino-7-fluoropyrido[3,2-*d*]pyrimidin-4-yl)amino]-2-methylhexan-1-ol
selgantolimod	(2*R*)-2-[(2-amino-7-fluoropyrido[3,2-*d*]pyrimidin-4-yl)amino]-2-méthylhexan-1-ol
selgantolimod	(2*R*)-2-[(2-amino-7-fluoropirido[3,2-*d*]pirimidin-4-il)amino]-2-metilhexan-1-ol

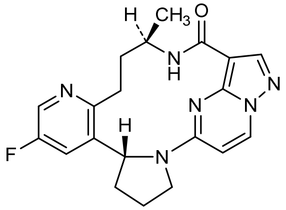
$C_{14}H_{20}FN_5O$



selitrectinibum

selitrectinib	(2^{2}*R*,6*R*)-3^{5}-fluoro-6-methyl-1(5,3)-pyrazolo[1,5-*a*]pyrimidina-3(3,2)-pyridina-2(1,2)-pyrrolidinacyclooctaphan-8-one
sélitrectinib	(2^{2}*R*,6*R*)-3^{5}-fluoro-6-méthyl-1(5,3)-pyrazolo[1,5-*a*]pyrimidina-3(3,2)-pyridina-2(1,2)-pyrrolidinacyclooctaphan-8-one
selitrectinib	(2^{2}*R*,6*R*)-3^{5}-fluoro-6-metil-1(5,3)-pirazolo[1,5-*a*]pirimidina-3(3,2)-piridina-2(1,2)-pirrolidinaciclooctafan-8-ona

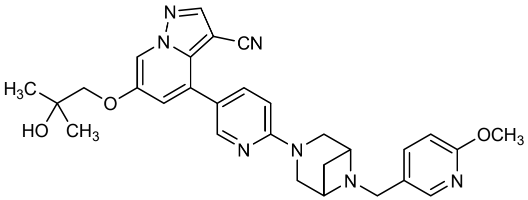
$C_{20}H_{21}FN_6O$



selpercatinibum

selpercatinib	6-(2-hydroxy-2-methylpropoxy)-4-(6-{6-[(6-methoxypyridin-3-yl)methyl]-3,6-diazabicyclo[3.1.1]heptan-3-yl}pyridin-3-yl)pyrazolo[1,5-*a*]pyridine-3-carbonitrile
selpercatinib	6-(2-hydroxy-2-méthylpropoxy)-4-(6-{6-[(6-méthoxypyridin-3-yl)méthyl]-3,6-diazabicyclo[3.1.1]heptan-3-yl}pyridin-3-yl)pyrazolo[1,5-*a*]pyridine-3-carbonitrile
selpercatinib	6-(2-hidroxi-2-metilpropoxi)-4-(6-{6-[(6-metoxipiridin-3-il)metil]-3,6-diazabiciclo[3.1.1]heptan-3-il}piridin-3-il)pirazolo[1,5-*a*]piridina-3-carbonitrilo

$C_{29}H_{31}N_7O_3$



semorinemabum #

semorinemab	immunoglobulin G4-kappa, anti-[*Homo sapiens* MAPT (microtubule-associated protein tau, tau)], monoclonal antibody;

gamma4 heavy chain (1-444) [VH (*Homo sapiens* IGHV3-23*03 (88.7%) -(IGHD) -IGHJ4*01 (100%)) [8.8.10] (1-117) -*Homo sapiens* IGHG4*01 (CH1 (118-215), hinge S10>P (225) (216-227), CH2 M15.1>Y (249), S16>T (251), T18>E (253) (228-337), CH3 (338-442), CHS (443-444)) (118-444)], (131-219')-disulfide with kappa light chain (1'-219') [V-KAPPA (*Mus musculus* IGKV1-117*01 (90.0%) -IGKJ4*01(83.3%)/*Homo sapiens* IGKV2-4*01 (85.4%) -IGKJ1*01 (100%)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; dimer (223-223'':226-226'')-bisdisulfide

sémorinémab

immunoglobuline G4-kappa, anti-[*Homo sapiens* MAPT (protéine tau associée aux microtubules, tau)], anticorps monoclonal;
chaîne lourde gamma4 (1-444) [VH (*Homo sapiens* IGHV3-23*03 (88.7%) -(IGHD) - IGHJ4*01 (100%)) [8.8.10] (1-117) -*Homo sapiens* IGHG4*01 (CH1 (118-215), charnière S10>P (225) (216-227), CH2 M15.1>Y (249), S16>T (251), T18>E (253) (228-337), CH3 (338-442), CHS (443-444)) (118-444)], (131-219')-disulfure avec la chaîne légère kappa (1'-219') [V-KAPPA (*Mus musculus* IGKV1-117*01 (90.0%) -IGKJ4*01(83.3%)/*Homo sapiens* IGKV2-40*01 (85.4%) -IGKJ1*01 (100%)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; dimère (223-223'':226-226'')-bisdisulfure

semorinemab

inmunoglobulina G4-kappa, anti-[*Homo sapiens* MAPT (proteína tau asociada a los microtúbulos, tau)], anticuerpo monoclonal;
cadena pesada gamma4 (1-444) [VH (*Homo sapiens* IGHV3-23*03 (88.7%) -(IGHD) - IGHJ4*01 (100%)) [8.8.10] (1-117) -*Homo sapiens* IGHG4*01 (CH1 (118-215), bisagra S10>P (225) (216-227), CH2 M15.1>Y (249), S16>T (251), T18>E (253) (228-337), CH3 (338-442), CHS (443-444)) (118-444)], (131-219')-disulfuro con la cadena ligera kappa (1'-219') [V-KAPPA (*Mus musculus* IGKV1-117*01 (90.0%) -IGKJ4*01(83.3%)/*Homo sapiens* IGKV2-40*01 (85.4%) -IGKJ1*01 (100%)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; dímero (223-223'':226-226'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAASGLIFR SYGMSWVRQA PGKGLEWVAT  50
INSGGTYTYY PDSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCANSY 100
SGAMDYWGQG TLVTVSSAST KGPSVFPLAP CSRSTSESTA ALGCLVKDYF 150
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTKTYTC 200
NVDHKPSNTK VDKRVESKYG PPCPPCPAPE FLGGPSVFLF PPKPKDTLYI 250
TREPEVTCVV 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

```
DDVLTQTPLS LPVTPGQPAS ISCRSSQSIV HSNGNTYLEW YLQKPGQSPQ  50
LLIYKVSNRF SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCFQGSLVP 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) 22-96 144-200 258-318 364-422
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

C-terminal lysine clipping:
H CHS K2:
444, 444''

serclutamabum #

serclutamab

immunoglobulin G1-kappa, anti-[*Homo sapiens* EGFR (epidermal growth factor receptor, receptor tyrosine-protein kinase erbB-1, ERBB1, HER1, HER-1, ERBB)], monoclonal antibody;
gamma1 heavy chain (1-446) [VH (*Homo sapiens* IGHV4-30-4*01 (81.4%) -(IGHD) -IGHJ4*01 (92.9%)) [9.7.9] (1-116) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (213) (117-214), hinge (215-229), CH2 S3>C (238) (230-339), CH3 E12 (355), M 14 (357) (340-444), CHS (445-446)) (117-446)], (219-214')-disulfide with kappa light chain (1'-214') [V-KAPPA (*Mus musculus* IGKV14-100*01 (86.3%) -IGKJ1*01 (100%)/*Homo sapiens* IGKV1-12*01 (74.7%) -IGKJ4*01 (90.9%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (225-225'':228-228'')-bisdisulfide

serclutamab

immunoglobuline G1-kappa, anti-[*Homo sapiens* EGFR (récepteur du facteur de croissance épidermique, récepteur tyrosine-protéine kinase erb-1, ERBB1, HER1, HER-1, ERBB)], anticorps monoclonal;
chaîne lourde gamma1 (1-227) [VH (*Homo sapiens* IGHV4-30-4*01 (81.4%) -(IGHD) -IGHJ4*01 (92.9%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (213) (117-214), charnière (215-229), CH2 S3>C (238) (230-339), CH3 E12 (355), M 14 (357) (340-444), CHS (445-446)) (117-446)], (219-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA (*Mus musculus* IGKV14-100*01 (86.3%) -IGKJ1*01 (100%)/*Homo sapiens* IGKV1-12*01 (74.7%) -IGKJ4*01 (90.9%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (225-225'':228-228'')-bisdisulfure

serclutamab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* EGFR (receptor del factor de crecimiento epidérmico receptor tirosina-proteína kinasa erb-1, ERBB1, HER1, HER-1, ERBB)], anticuerpo monoclonal;
cadena pesada gamma1 (1-227) [VH (*Homo sapiens* IGHV4-30-4*01 (81.4%) -(IGHD) -IGHJ4*01 (92.9%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (213) (117-214), bisagra (215-229), CH2 S3>C (238) (230-339), CH3 E12 (355), M 14 (357) (340-444), CHS (445-446)) (117-446)], (219-214')-disulfuro con la cadena ligera kappa (1'-214') [V-KAPPA (*Mus musculus* IGKV14-100*01 (86.3%) -IGKJ1*01 (100%)/*Homo sapiens* IGKV1-12*01 (74.7%) -IGKJ4*01 (90.9%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (225-225'':228-228'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLQESGPG LVKPSQTLSL TCTVSGYSIS RDFAWNWIRQ PPGKGLEWMG  50
YISYNGNTRY QPSLKSRITI SRDTSKNQFF LKLNSVTAAD TATYYCVTAS 100
RGFPYWGQGT LVTVSSASTK GPSVFPLAPS SKSTSGGTAA LGCLVKDYFP 150
EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVVTVPSS SLGTQTYICN 200
VNHKPSNTKV DKKVEPKSCD KTHTCPPCPA PELLGGPCVF LFPPKPKDTL 250
MISRTPEVTC VVVDVSHEDP EVKFNWYVDG VEVHNAKTKP REEQYNSTYR 300
VVSVLTVLHQ DWLNGKEYKC KVSNKALPAP IEKTISKAKG QPREPQVYTL 350
PPSREEMTKN QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD 400
GSFFLYSKLT VDKSRWQQGN VFSCSVMHEA LHNHYTQKSL SLSPGK      446
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS MSVSVGDRVT ITCHSSQDIN SNIGWLQQKP GKSFKGLIYH  50
GTNLDDGVPS RFSGSGSGTD YTLTISSLQP EDFATYYCVQ YAQFPWTFGG 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) 22-96 143-199 260-320 366-424
22''-96'' 143''-199'' 260''-320'' 366''-424''
Intra-L (C23-C104) 23'-88' 134'-194'
23'''-88''' 134'''-194'''
Inter-H-L (h 5-CL 126) 219-214' 219''-214'''
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

serclutamabum talirinum

serclutamab talirine	immunoglobulin G1-kappa, anti-[*Homo sapiens* EGFR (epidermal growth factor receptor, receptor tyrosine-protein kinase erbB-1, ERBB1, HER1, HER-1, ERBB)], monoclonal antibody conjugated to the pyrrolobenzodiazepine (PDB) dimer SGD-1882; gamma1 heavy chain (1-446) [VH (*Homo sapiens* IGHV4-30-4*01 (81.4%) -(IGHD) -IGHJ4*01 (92.9%)) [9.7.9] (1-116) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (213) (117-214), hinge (215-229), CH2 S3>C (238) (230-339), CH3 E12 (355), M 14 (357) (340-444), CHS (445-446)) (117-446)], (219-214')-disulfide with kappa light chain (1'-214') [V-KAPPA (*Mus musculus* IGKV14-100*01 (86.3%) -IGKJ1*01 (100%)/*Homo sapiens* IGKV1-12*01 (74.7%) -IGKJ4*01 (90.9%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (225-225'':228-228'')-bisdisulfide; conjugated, on two site-specific drug attachment engineered cysteines (C238, C238''), to pyrrolobenzodiazepine (PDB) dimers SGD-1882, via a cathepsin-cleavable maleimidocaproyl-valine-alanine (MC-Val-Ala) type linker
serclutamab talirine	immunoglobuline G1-kappa, anti-[*Homo sapiens* EGFR (récepteur du facteur de croissance épidermique, récepteur tyrosine-protéine kinase erb-1, ERBB1, HER1, HER-1, ERBB)], anticorps monoclonal conjugué au dimère de pyrrolobenzodiazépine (PDB) SGD-1882; chaîne lourde gamma1 (1-227) [VH (*Homo sapiens* IGHV4-30-4*01 (81.4%) -(IGHD) -IGHJ4*01 (92.9%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (213) (117-214), charnière (215-229), CH2 S3>C (238) (230-339), CH3 E12 (355), M 14 (357) (340-444), CHS (445-446)) (117-446)], (219-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA (*Mus musculus* IGKV14-100*01 (86.3%) -IGKJ1*01 (100%)/*Homo sapiens* IGKV1-12*01 (74.7%) -IGKJ4*01 (90.9%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (225-225'':228-228'')-bisdisulfure; conjugué, sur deux cystéines sites de

fixation spécifique du linker-produit actif (C238, C238''), à 2 dimères de pyrrolobenzodiazépine (PDB) SGD-1882, via un linker cathepsin-clivable de type maléimidocaproyl-valine-alanine (MC-Val-Ala)

serclutamab talirina

inmunoglobulina G1-kappa, anti-[*Homo sapiens* EGFR (receptor del factor de crecimiento epidérmico receptor tirosina-proteína kinasa erb-1, ERBB1, HER1, HER-1, ERBB)], anticuerpo monoclonal conjugado con el dímero de pirrolobenzodiazepina (PDB) SGD-1882;
cadena pesada gamma1 (1-227) [VH (*Homo sapiens* IGHV4-30-4*01 (81.4%) -(IGHD) -IGHJ4*01 (92.9%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (213) (117-214), bisagra (215-229), CH2 S3>C (238) (230-339), CH3 E12 (355), M 14 (357) (340-444), CHS (445-446)) (117-446)], (219-214')-disulfuro con la cadena ligera kappa (1'-214') [V-KAPPA (*Mus musculus* IGKV14-100*01 (86.3%) -IGKJ1*01 (100%)/*Homo sapiens* IGKV1-12*01 (74.7%) -IGKJ4*01 (90.9%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (225-225'':228-228'')-bisdisulfuro; conjugado, en dos lugares de fijación específicos de cisteina del enlace activo producido (C238, C238''), a 2 dímeros de pirrolobenzodiazepina (PDB) SGD-1882, mediante un enlace de catepsina escindible de tipo maleimidocaproil-valina-alanina (MC-Val-Ala)

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLQESGPG LVKPSQTLSL TCTVSGYSIS RDFAWNWIRQ PPGKGLEWMG  50
YISYNGNTRY QPSLKSRITI SRDTSKNQFF LKLNSVTAAD TATYYCVTAS 100
RGFPYWGQGT LVTVSSASTK GPSVFPLAPS SKSTSGGTAA LGCLVKDYFP 150
EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVVTVPSS SLGTQTYICN 200
VNHKPSNTKV DKKVEPKSCD KTHTCPPCPA PELLGGPCVF LFPPKPKDTL 250
MISRTPEVTC VVVDVSHEDP EVKFNWYVDG VEVHNAKTKP REEQYNSTYR 300
VVSVLTVLHQ DWLNGKEYKC KVSNKALPAP IEKTISKAKG QPREPQVYTL 350
PPSREEMTKN QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD 400
GSFFLYSKLT VDKSRWQQGN VFSCSVMHEA LHNHYTQKSL SLSPGK      446
```

Light chain / Chaîne légère / Cadena ligera

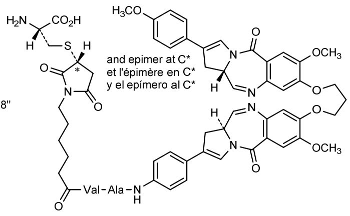
```
DIQMTQSPSS MSVSVGDRVT ITCHSSQDIN SNIGWLQQKP GKSFKGLIYH  50
GTNLDDGVPS RFSGSGSGTD YTLTISSLQP EDFATYYCVQ YAQFPWTFGG 100
GTKLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 143-199 260-320 366-424
22''-96'' 143''-199'' 260''-320'' 366''-424''
Intra-L (C23-C104) 23'-88' 134'-194'
23'''-88''' 134'''-194'''
Inter-H-L (h 5-CL 126) 219-214' 219''-214'''
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

Modidfied residues / résidus modifiés / restos modificados

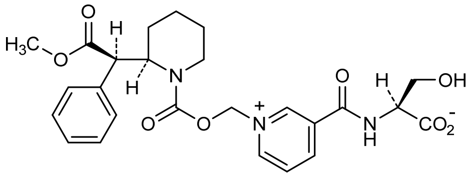
C 238, 238''



serdexmethylphenidatum

serdexmethylphenidate	*N*-{1-[({(2*R*)-2-[(1*R*)-2-methoxy-2-oxo-1-phenylethyl]piperidine-1-carbonyl}oxy)methyl]pyridin-1-ium-3-carbonyl}-L-serinate
serdexméthylphénidate	*N*-{1-[({(2*R*)-2-[(1*R*)-2-méthoxy-2-oxo-1-phényléthyl]pipéridine-1-carbonyl}oxy)méthyl]pyridin-1-ium-3-carbonyl}-L-sérinate
serdexmetilfenidato	*N*-{1-[({(2*R*)-2-[(1*R*)-2-metoxi-2-oxo-1-feniletil]piperidina-1-carbonil}oxi)metil]piridin-1-ium-3-carbonil}-L-serinato

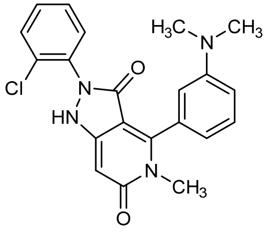
$C_{25}H_{29}N_3O_8$



setanaxibum

setanaxib	2-(2-chlorophenyl)-4-[3-(dimethylamino)phenyl]-5-methyl-1*H*-pyrazolo[4,3-*c*]pyridine-3,6(2*H*,5*H*)-dione
sétanaxib	2-(2-chlorophényl)-4-[3-(diméthylamino)phényl]-5-méthyl-1*H*-pyrazolo[4,3-*c*]pyridine-3,6(2*H*,5*H*)-dione
setanaxib	2-(2-clorofenil)-4-[3-(dimetilamino)fenil]-5-metil-1*H*-pirazolo[4,3-*c*]piridina-3,6(2*H*,5*H*)-diona

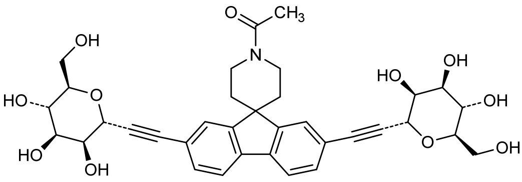
$C_{21}H_{19}ClN_4O_2$



sibofimlocum

sibofimloc	1-[2,7-bis(2,6-anhydro-7,8-dideoxy-D-*glycero*-D-*manno*-oct-7-ynitol-8-yl)spiro[fluorene-9,4'-piperidin]-1'-yl]ethan-1-one
sibofimloc	1-[2,7-bis(2,6-anhydro-7,8-didésoxy-D-*glycéro*-D-*manno*-oct-7-ynitol-8-yl)spiro[fluorène-9,4'-pipéridin]-1'-yl]éthan-1-one
sibofimloc	1-[2,7-bis(2,6-anhidro-7,8-didesoxi-D-*glicero*-D-*mano*-oct-7-initol-8-il)spiro[fluoreno-9,4'-piperidin]-1'-il]etan-1-ona

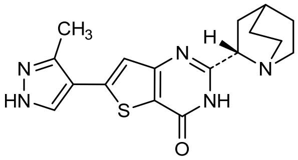
$C_{35}H_{39}NO_{11}$



simurosertibum

simurosertib	2-[(2*S*)-1-azabicyclo[2.2.2]octan-2-yl]-6-(3-methyl-1*H*-pyrazol-4-yl)thieno[3,2-*d*]pyrimidin-4(3*H*)-one
simurosertib	2-[(2*S*)-1-azabicyclo[2.2.2]octan-2-yl]-6-(3-méthyl-1*H*-pyrazol-4-yl)thiéno[3,2-*d*]pyrimidin-4(3*H*)-one
simurosertib	2-[(2*S*)-1-azabiciclo[2.2.2]octan-2-il]-6-(3-metil-1*H*-pirazol-4-il)tieno[3,2-*d*]pirimidin-4(3*H*)-ona

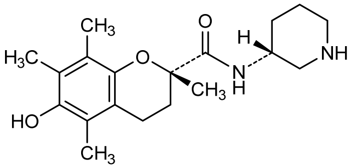
$C_{17}H_{19}N_5OS$



sonlicromanolum

sonlicromanol	(2*S*)-6-hydroxy-2,5,7,8-tetramethyl-*N*-[(3*R*)-piperidin-3-yl]-3,4-dihydro-2*H*-1-benzopyran-2-carboxamide
sonlicromanol	(2*S*)-6-hydroxy-2,5,7,8-tétraméthyl-*N*-[(3*R*)-pipéridin-3-yl]-3,4-dihydro-2*H*-1-benzopyran-2-carboxamide
sonlicromanol	(2*S*)-6-hydroxi-2,5,7,8-tetrametil-*N*-[(3*R*)-piperidin-3-il]-3,4-dihidro-2*H*-1-benzopiran-2-carboxamida

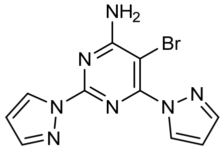
$C_{19}H_{28}N_2O_3$



taminadenantum

taminadenant	5-bromo-2,6-di(1*H*-pyrazol-1-yl)pyrimidin-4-amine
taminadénant	5-bromo-2,6-di(1*H*-pyrazol-1-yl)pyrimidin-4-amine
taminadenant	5-bromo-2,6-di(1*H*-pirazol-1-il)pirimidin-4-amino

$C_{10}H_8BrN_7$



tamrintamabum #

tamrintamab	immunoglobulin G1-kappa, anti-[*Homo sapiens* DPEP3 (dipeptidase 3)], humanized monoclonal antibody; gamma1 heavy chain humanized (1-452) [VH (*Homo sapiens* IGHV1-69*01 (85.7%) -(IGHD) -IGHJ6*01 (90.9%)) [8.8.16] (1-123) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (220) (124-221), hinge C5>S (226) (222-236), CH2 (237-346), CH3 D12 (362), L14 (364) (347-451), CHS K>del (452)) (124-452)], non-covalently associated with kappa light chain humanized (1'-215') [V-KAPPA (*Homo sapiens* IGKV3D-20*01 (86.50%) -IGKJ2*01 (100.0%)) [7.3.9] (1'-108'),-*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')]; dimer (232-232'':235-235'')-bisdisulfide
tamrintamab	immunoglobuline G1-kappa, anti-[*Homo sapiens* DPEP3 (dipeptidase 3)], anticorps monoclonal humanisé; chaîne lourde gamma1 humanisée (1-452) [VH (*Homo sapiens* IGHV1-69*01 (85.7%) -(IGHD) -IGHJ6*01 (90.9%)) [8.8.16] (1-123) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (220) (124-221), charnière C5>S (226) (222-236), CH2 (237-346), CH3 D12 (362), L14 (364) (347-451), CHS K>del (452)) (124-452)], associée de manière non-covalente avec la chaîne légère kappa humanisée (1'-215') [V-KAPPA (*Homo sapiens* IGKV3D-20*01 (86.50%) -IGKJ2*01 (100.0%)) [7.3.9] (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')]; dimère (232-232'':235-235'')-bisdisulfure
tamrintamab	inmunoglobulina G1-kappa, anti-[*Homo sapiens* DPEP3 (dipeptidasa 3)], anticuerpo monoclonal humanizado; cadena pesada gamma1 humanizada (1-452) [VH (*Homo sapiens* IGHV1-69*01 (85.7%) -(IGHD) -IGHJ6*01 (90.9%)) [8.8.16] (1-123) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (220) (124-221), bisagra C5>S (226) (222-236), CH2 (237-346), CH3 D12 (362), L14 (364) (347-451), CHS K>del (452)) (124-452)], asociada de forma no-covalente con la cadena ligera kappa humanizada (1'-215') [V-KAPPA (*Homo sapiens* IGKV3D-20*01 (86.50%) -IGKJ2*01 (100.0%)) [7.3.9] (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')]; dímero (232-232'':235-235'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGSSVKV SCKASGGTFS SYWIEWVRQA PGQGLEWMGE  50
ILPGSGNTYY NERFKDRVTI TADESTSTAY MELSSLRSED TAVYYCARRA 100
AAYYSNPEWF AYWGQGTLVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC 150
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG 200
TQTYICNVNH KPSNTKVDKK VEPKSSDKTH TCPPCPAPEL LGGPSVFLFP 250
PKPKDTLMIS RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE 300
QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR 350
EPQVYTLPPS RDELTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT 400
PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLS 450
PG                                                    452
```

Light chain / Chaîne légère / Cadena ligera

```
EIVLTQSPAT LSLSPGERAT LSCTASSSVN SFYLHWYQQK PGLAPRLLIY  50
STSNLASGIP DRFSGSGSGT DFTLTISRLE PEDFAVYYCH QYHRSPYTFG 100
QGTKLEIKRT 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) 22-96 150-206 267-327 373-431
22''-96'' 150''-206'' 267''-327'' 373''-431''
Intra-L (C23-C104) 23'-89' 135'-195'
23'''-89''' 135'''-195'''
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

tamrintamabum pamozirinum #

tamrintamab pamozirine

immunoglobulin G1-kappa, anti-[*Homo sapiens* DPEP3 (dipeptidase 3)], humanized monoclonal antibody conjugated to a pyrrolobenzodiazepine dimer (PBD) SC-DR002 via light Cys215;
gamma1 heavy chain humanized (1-452) [VH (*Homo sapiens* IGHV1-69*01 (85.7%) -(IGHD) -IGHJ6*01 (90.9%)) [8.8.16] (1-123) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (220) (124-221), hinge C5>S (226) (222-236), CH2 (237-346), CH3 D12 (362), L14 (364) (347-451), CHS K>del (452)) (124-452)], non-covalently associated with kappa light chain humanized (1'-215') [V-KAPPA (*Homo sapiens* IGKV3D-20*01 (86.50%) -IGKJ2*01 (100.0%)) [7.3.9] (1'-108'),-*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')]; dimer (232-232'':235-235'')-bisdisulfide; conjugated at each CL C126 (215', 215''') to a pyrrolobenzodiazepine dimer (PBD) SC-DR002 via a protease-cleavable maleimide linker (LD6.23)

tamrintamab pamozirine

immunoglobuline G1-kappa, anti-[*Homo sapiens* DPEP3 (dipeptidase 3)], anticorps monoclonal humanisé conjugué sur chaque chaîne kappa à un dimère de pyrrolobenzodiazépine (PDB) SC-DR002;
chaîne lourde gamma1 humanisée (1-452) [VH (*Homo sapiens* IGHV1-69*01 (85.7%) -(IGHD) -IGHJ6*01 (90.9%)) [8.8.16] (1-123) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (220) (124-221), charnière C5>S (226) (222-236), CH2 (237-346), CH3 D12 (362), L14 (364) (347-451), CHS K>del (452)) (124-452)], associée de manière non-covalente avec la chaîne légère kappa humanisée (1'-215') [V-KAPPA (*Homo sapiens* IGKV3D-20*01 (86.50%) -IGKJ2*01 (100.0%)) [7.3.9] (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')]; dimère (232-232'':235-235'')-bisdisulfure; conjugué à chaque CL C126 (215', 215''') à un dimère de pyrrolobenzodiazépine (PBD) SC-DR002 via un linker protéase-clivable de type maléimide (LDL6.23)

tamrintamab pamozirina

inmunoglobulina G1-kappa, anti-[*Homo sapiens* DPEP3 (dipeptidasa 3)], anticuerpo monoclonal humanizado conjugado sobre cada cadena kappa a un dímero de pirrolobenzodiazepina (PDB) SC-DR-002; cadena pesada gamma1 humanizada (1-452) [VH (*Homo sapiens* IGHV1-69*01 (85.7%) -(IGHD) -IGHJ6*01 (90.9%)) [8.8.16] (1-123) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (220) (124-221), bisagra C5>S (226) (222-236), CH2 (237-346), CH3 D12 (362), L14 (364) (347-451), CHS K>del (452)) (124-452)], asociada de forma no-covalente con la cadena ligera kappa humanizada (1'-215') [V-KAPPA (*Homo sapiens* IGKV3D-20*01 (86.50%) -IGKJ2*01 (100.0%)) [7.3.9] (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')]; dímero (232-232'':235-235'')-bisdisulfuro; conjugado con cada CL C126 (215', 215''') a un dímero de pirrolobenzodiazepina (PBD) SC-DR002 mediante un conector escindible de proteasa de tipo maleimida (LDL6.23)

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGSSVKV SCKASGGTFS SYWIEWVRQA PGQGLEWMGE  50
ILPGSGNTYY NERFKDRVTI TADESTSTAY MELSSLRSED TAVYYCARRA 100
AAYYSNPEWF AYWGQGTLVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC 150
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG 200
TQTYICNVNH KPSNTKVDKK VEPKSSDKTH TCPPCPAPEL LGGPSVFLFP 250
PKPKDTLMIS RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE 300
QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR 350
EPQVYTLPPS RDELTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT 400
PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLS 450
PG                                                    452
```

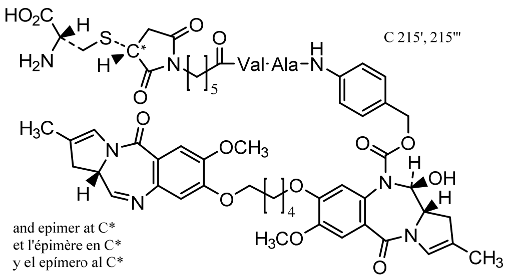
Light chain / Chaîne légère / Cadena ligera

```
EIVLTQSPAT LSLSPGERAT LSCTASSSVN SFYLHWYQQK PGLAPRLLIY  50
STSNLASGIP DRFSGSGSGT DFTLTISRLE PEDFAVYYCH QYHRSPYTFG 100
QGTKLEIKRT 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 disulfu
Intra-H (C23-C104) 22-96 150-206 267-327 373-431
22''-96'' 150''-206'' 267''-327'' 373''-431''
Intra-L (C23-C104) 23'-89' 135'-195'
23'''-89''' 135'''-195'''
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-antennai
complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

Modidfied residues / résidus modifiés / restos modificados



and epimer at C*
et l'épimère en C*
y el epímero al C*

tanfanerceptum #

tanfanercept

L-methionyl-[L^{28}>V,S^{52}>M,H^{55}>F,R^{57}>P,H^{58}>G,K^{121}>N] tumor necrosis factor (TNF) binding protein variant 1 (TBP-1) with C-terminal extension by further 10 residues of the pro-protein, human, unglycosylated, produced in *Escherichia coli*

tanfanercept

L-méthionyl-[L^{28}>V,S^{52}>M,H^{55}>F,R^{57}>P,H^{58}>G,K^{121}>N] protéine de liaison au facteur de nécrose tumorale, variant 1 humain (TBP-1) avec extension C-terminale par 10 autres résidus du précurseur, non glycosylée, produite par *Escherichia coli*

tanfanercept

L-metionil-[L^{28}>V,S^{52}>M,H^{55}>F,R^{57}>P,H^{58}>G,K^{121}>N] proteína de union al factor de necrosis tumoral, variante 1 humano (TBP-1) con extensión C-terminal por otros 10 residuos de la pro-proteína, no glicosilada, producida por *Escherichia coli*

```
M                                                        0
DSVCPQGKYI HPQNNSICCT KCHKGTYVYN DCPGPGQDTD CRECESGSFT  50
AMENFLPGCL SCSKCRKEMG QVEISSCTVD RDTVCGCRKN QYRHYWSENL 100
FQCFNCSLCL NGTVHLSCQE NQNTVCTCHA GFFLRENECV SCSNCKKSLE 150
CTKLCLPQIE NVKGTEDSGT T                                171
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
4-18, 19-32, 22-41, 44-59, 62-77, 65-85, 87-103, 106-118, 109-126,
128-139, 142-155, 145-151

teclistamabum #

teclistamab

immunoglobulin G4-lambda, anti-[*Homo sapiens* TNFRSF17 (TNF receptor superfamily member 17, tumor necrosis factor receptor superfamily, member 17, B cell maturation antigen, BCMA, BCM, TNFRSF13A, CD269)] and anti-[*Homo sapiens* CD3 epsilon (CD3E, Leu-4)], monoclonal antibody, bispecific;
gamma4 heavy chain anti-TNFRSF17 (1-448) [VH (*Homo sapiens* IGHV4-39*01 (97.0%) -(IGHD) -IGHJ4*01 (100%)) [10.7.13] (1-121) -*Homo sapiens* IGHG4*01 (CH1 (122-219), hinge S10>P (229) (220-231), CH2 L1.3>A (235), L1.2>A (236) (232-341), CH3 (342-446), CHS (447-448)) (122-448)], (135-213')-disulfide with lambda light chain anti-TNFRSF17 (1'-214') [V-LAMBDA (*Homo sapiens* IGLV3-21*02 (96.9%) -IGLJ2*01 (100.0%)) [6.3.11] (1'-108') -*Homo sapiens* IGLC2*01 (99.1%) A43>G (152) (109'-214')];
gamma4 heavy chain anti-CD3E (1''-452'') [VH (*Mus musculus* IGHV10-1*02 (89.8%) -(IGHD) -IGHJ3*01 (93.3%)/*Homo sapiens* IGHV3-72*01 (88.0%) -(IGHD) -IGHJ6*01 (90.9%)) [8.10.16] (1''-125'') -*Homo sapiens* IGHG4*01 (CH1 (126-223), hinge S10>P (233) (224-235), CH2 L1.3>A (239), L1.2 (240) (236-345), CH3 F85.1>L (410), R88>K (414) (346-450), CHS (451-452)) (126''-452'')], (139''-214''')-disulfide with lambda light chain anti-CD3 (1'''-215''') [V-LAMBDA (*Homo sapiens* IGLV7-43*01 (81.9%) -IGLJ3*02 (100%)) [9.3.9] (1'''-109''') -*Homo sapiens* IGLC2*01 (100%) (110'''-215''')];
dimer (227-231'':230-234'')-bisdisulfide

téclistamab	immunoglobuline G4-lambda, anti-[*Homo sapiens* TNFRSF17 (membre 17 de la superfamille des récepteurs du TNF, membre 17 de la superfamille des récepteurs du facteur de nécrose tumorale, antigène de maturation de cellule B, BCMA, BCM, TNFRSF13A, CD269)] et anti-[*Homo sapiens* CD3 epsilon (CD3E, Leu-4)], anticorps monoclonal, bispécifique; chaîne lourde gamma4 anti-TNFRSF17(1-448) [VH (*Homo sapiens* IGHV4-39*01 (97.0%) -(IGHD) -IGHJ4*01 (100%)) [10.7.13] (1-121) -*Homo sapiens* IGHG4*01 (CH1 (122-219), charnière S10>P (229) (220-231), CH2 L1.3>A (235), L1.2 (236) (232-341), CH3 (342-446), CHS (447-448)) (122-448)], (135-213')-disulfure avec la chaîne légère lambda anti-TNFRSF17 (1'-214') [V-LAMBDA (*Homo sapiens* IGLV3-21*02 (96.9%) -IGLJ2*01 (100.0%)) [6.3.11] (1'-108') -*Homo sapiens* IGLC2*01 (99.1%) A43>G (152) (109'-214')]; chaîne lourde gamma4 anti-CD3E (1"-452") [VH (*Mus musculus* IGHV10-1*02 (89.8%) -(IGHD) -IGHJ3*01 (93.3%)/*Homo sapiens* IGHV3-72*01 (88.0%) -(IGHD) -IGHJ6*01 (90.9%)) [8.10.16] (1"-125") -*Homo sapiens* IGHG4*01 (CH1 (126-223), charnière S10>P (233) (224-235), CH2 L1.3>A (239), L1.2 (240) (236-345), CH3 F85.1>L (410), R88>K (414) (346-450), CHS (451-452)) (126"-452")], (139"-214''')-disulfure avec la chaîne légère lambda anti-CD3 (1'''-215''') [V-LAMBDA (*Homo sapiens* IGLV7-43*01 (81.9%) -IGLJ3*02 (100%)) [9.3.9] (1'''-109''') -*Homo sapiens* IGLC2*01 (100%) (110'''-215''')]; dimère (227-231":230-234")-bisdisulfure
teclistamab	inmunoglobulina G4-lambda, 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 la célula B, BCMA, BCM, TNFRSF13A, CD269)] y anti-[*Homo sapiens CD3 épsilon (CD3E, Leu-4)*], anticuerpo monoclonal, biespecífico; cadena pesada gamma4 anti-TNFRSF17(1-448) [VH (*Homo sapiens* IGHV4-39*01 (97.0%) -(IGHD) -IGHJ4*01 (100%)) [10.7.13] (1-121) -*Homo sapiens* IGHG4*01 (CH1 (122-219), bisagra S10>P (229) (220-231), CH2 L1.3>A (235), L1.2 (236) (232-341), CH3 (342-446), CHS (447-448)) (122-448)], (135-213')-disulfuro con la cadena ligera lambda anti-TNFRSF17 (1'-214') [V-LAMBDA (*Homo sapiens* IGLV3-21*02 (96.9%) -IGLJ2*01 (100.0%)) [6.3.11] (1'-108') -*Homo sapiens* IGLC2*01 (99.1%) A43>G (152) (109'-214')]; cadena pesada gamma4 anti-CD3E (1"-452") [VH (*Mus musculus* IGHV10-1*02 (89.8%) -(IGHD) -IGHJ3*01 (93.3%)/*Homo sapiens* IGHV3-72*01 (88.0%) -(IGHD) -IGHJ6*01 (90.9%)) [8.10.16] (1"-125") -*Homo sapiens* IGHG4*01 (CH1 (126-223), bisagra S10>P (233) (224-235), CH2 L1.3>A (239), L1.2 (240) (236-345), CH3 F85.1>L (410), R88>K (414) (346-450), CHS (451-452)) (126"-452")], (139"-214''')-disulfuro con la cadena ligera lambda anti-CD3 (1'''-215''') [V-LAMBDA (*Homo sapiens* IGLV7-43*01 (81.9%) -IGLJ3*02 (100%)) [9.3.9] (1'''-109''') -*Homo sapiens* IGLC2*01 (100%) (110'''-215''')]; dímero (227-231":230-234")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada (anti-TNFRSF17)

```
QLQLQESGPG LVKPSETLSL TCTVSGGSIS SGSYFWGWIR QPPGKGLEWI  50
GSIYYSGITY YNPSLKSRVT ISVDTSKNQF SLKLSSVTAA DTAVYYCARH 100
DGAVAGLFDY WGQGTLVTVS SASTKGPSVF PLAPCSRSTS ESTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTK 200
TYTCNVDHKP SNTKVDKRVE SKYGPPCPPC PAPEAAGGPS VFLFPPKPKD 250
TLMISRTPEV TCVVVDVSQE DPEVQFNWYV DGVEVHNAKT KPREEQFNST 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKGLP SSIEKTISKA KGQPREPQVY 350
TLPPSQEEMT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD 400
SDGSFFLYSR LTVDKSRWQE GNVFSCSVMH EALHNHYTQK SLSLSLGK   448
```

Light chain / Chaîne légère / Cadena ligera (anti-TNFRSF17)

```
SYVLTQPPSV SVAPGQTARI TCGGNNIGSK SVHWYQQPPG QAPVVVVYDD  50
SDRPSGIPER FSGSNSGNTA TLTISRVEAG DEAVYYCQVW DSSSDHVVFG 100
GGTKLTVLGQ PKAAPSVTLF PPSSEELQAN KATLVCLISD FYPGAVTVAW 150
KGDSSPVKAG VETTTPSKQS NNKYAASSYL SLTPEQWKSH RSYSCQVTHE 200
GSTVEKTVAP TECS                                        214
```

Heavy chain / Chaîne lourde / Cadena pesada (anti-CD3E)

```
EVQLVESGGG LVQPGGSLRL SCAASGFTFN TYAMNWVRQA PGKGLEWVAR  50
IRSKYNNYAT YYAASVKGRF TISRDDSKNS LYLQMNSLKT EDTAVYYCAR 100
HGNFGNSYVS WFAYWGQGTL 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
PVLDSDGSFL LYSKLTVDKS RWQEGNVFSC SVMHEALHNH YTQKSLSLSL 450
GK                                                     452
```

Light chain / Chaîne légère / Cadena ligera (anti-CD3E)

```
QTVVTQEPSL TVSPGGTVTL TCRSSTGAVT TSNYANWVQQ KPGQAPRGLI  50
GGTNKRAPGT PARFSGSLLG GKAALTLSGV QPEDEAEYYC ALWYSNLWVF 100
GGGTKLTVLG QPKAAPSVTL FPPSSEELQA NKATLVCLIS DFYPGAVTVA 150
WKADSSPVKA GVETTTPSKQ SNNKYAASSY LSLTPEQWKS HRSYSCQVTH 200
EGSTVEKTVA PTECS                                       215
```

Post-translational modifications

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

Intra-H (C23-C104)	22-97	148-204	262-322	368-426
	22''-98''	152''-208''	266''-326''	372''-430''
Intra-L (C23-C104)	22'-87'	136'-195'		
	22'''-90'''	137'''-196'''		
Inter-H-L (CH1 10-CL 126)	135-213'	139''-214'''		
Inter-H-H (h 8, h 11)	227-231''	230-234''		

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
298, 302''
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

tefidsogenum civaparvovecum #

tefidsogene civaparvovec	a recombinant non-replicating adeno-associated virus type 2/6 (rAAV Rep2-Cap6) vector, which contains a promoter-less human iduronate 2-sulfatase (hIDS) transgene cassette, encoding parts of exon 1 plus exons 2-9 from hIDS and a splice acceptor site (SA) derived from human coagulation factor IX (hF9, factor IX or FIX) exon 2, flanked by a sequence homologous to the zinc-finger nuclease (ZFN) cleavage site of the human albumin (hALB) intron 1
tefidsogène civaparvovec	vecteur viral adéno-associé de type 2/6 recombinant (rAAV Rep2-Cap6), non-répliquant, contenant la cassette du transgène de l'iduronate 2-sulfatase humaine (hIDS) sans promoteur, codant partiellement l'exon 1 et les exons 2-9 de hIDS, et la séquence du site accepteur (SA) d'épissage dérivé de l'exon 2 du facteur de coagulation IX humain (hF9, facteur IX, FIX), flanqué d'une séquence homologue au site de clivage de la nucléase à doigts de zinc (ZFN) de l'intron 1 de l'albumine humaine (hALB)

tefidsogén civaparvovec	un vector de virus adeno asociado tipo 2/6 recombinante (rAAV Rep2-Cap6), no replicativo, que contiene un casete con el transgen de la iduronato 2-sulfatasa humana (hIDS) sin promotor, que codifica para partes del exón 1 más los exones 2-9 de hIDS y un sitio aceptor del splicing derivado del exón 2 del factor de coagulación IX humano (hF9, factor IX o FIX), flanqueado por una secuencia homóloga al sitio de rotura por la nuclease con dedos de zinc (ZFN) del intron 1 de la albúmina humana (hALB)
telitaciceptum #	
telitacicept	[L^{120}>A,L^{121}>E,G^{123}>A,A^{216}>S,P^{217}>S]-TACI (transmembrane activator and CAML interactor, tumor necrosis factor receptor superfamily protein TNFRSF13B) human extracellular domain fragment (13-118)-peptide (1-106) fusion protein with human immunoglobulin G1-(227 C-terminal residues)-peptide (γ1-chain Fc fragment) (107-333) [*Homo sapiens* IGHG1*01, hinge (107-116), CH2 L^{120}>A, L^{121}>E, G^{123}>A, A^{216}>S, P^{217}>S (117-226), CH3 (227-331), CHS (332-333)], (112-112':115-115')-bisdisulfide dimer, produced in Chinese hamster ovary (CHO) cells
télitacicept	[L^{120}>A,L^{121}>E,G^{123}>A,A^{216}>S,P^{217}>S]-protéine de fusion du fragment de domaine extracellulaire humain de TACI (activateur transmembranaire et interacteur CAML, membre 13B de la superfamille des récepteurs du facteur de nécrose tumorale TNFRSF13B)-(13-118)-peptide (1-106) avec l'immunoglobuline G1 humaine-(227 résidus C-terminaux)-peptide (fragment Fc de la chaîne γ1) (107-333) [*Homo sapiens* IGHG1*01, charnière (107-116), CH2 L^{120}>A, L^{121}>E, G^{123}>A, A^{216}>S, P^{217}>S (117-226), CH3 (227-331), CHS (332-333)], dimère (112-112':115-115')-bisdisulfure, produite par des cellules ovariennes de hamsters chinois (CHO)
telitacicept	[L^{120}>A,L^{121}>E,G^{123}>A,A^{216}>S,P^{217}>S]-proteína de fusión del fragmento de dominio extracelular humano de TACI (activador transmembrana y CAML-interactor, miembro 13B de la superfamilia de receptores del factor de necrosis tumoral TNFRSF13B)-(13-118)-péptido (1-106) con la inmunoglobulina G1 humana-(227 restos C-terminales)-péptido (fragmento Fc de la cadena γ1) (107-333) [*Homo sapiens* IGHG1*01, bisagra (107-116), CH2 L^{120}>A, L^{121}>E, G^{123}>A, A^{216}>S, P^{217}>S (117-226), CH3 (227-331), CHS (332-333)], dímero (112-112':115-115')-bisdisulfuro, producida por las células ováricas de hamsters chinos (CHO)

```
SRVDQEERFP QGLWTGVAMR SCPEEQYWDP LLGTCMSCKT ICNHQSQRTC  50
AAFCRSLSCR KEQGKFYDHL LRDCISCASI CGQHPKQCAY FCENKLRSPV 100
NLPPELDKTH TCPPCPAPEA EGAPSVFLFP PKPKDTLMIS RTPEVTCVVV 150
DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYNSTYRVVS VLTVLHQDWL 200
NGKEYKCKVS NKALPSSIEK TISKAKGQPR EPQVYTLPPS RDELTKNQVS 250
LTCLVKGFYP SDIAVEWESN GQPENNYKTT PPVLDSDGSF FLYSKLTVDK 300
SRWQQGNVFS CSVMHEALHN HYTQKSLSLS PGK                   333
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
intra-TACI: 22-35, 38-50, 42-54, 59-74, 77-88, 81-92
intra-IgG1 Fc: 147-207, 253-311
inter-IgG1 Fc: 112-112', 115-115'

Glycosylation sites / Sites de glycosylation / Posiciones de glicosilación
Asn183, Asn183'

tidutamabum #

tidutamab

immunoglobulin half-G1-kappa/scFv-h-CH2-CH3, anti-[*Homo sapiens* SSTR2 (somatostatin receptor 2) and *Homo sapiens* CD3 epsilon (CD3E, Leu-4)], monoclonal antibody, bispecific;
gamma1 heavy chain anti-SSTR2 (1-451) [VH (*Homo sapiens* IGHV3-48*03 (90.8%) -(IGHD) -IGHJ4*01 (100%)) [8.8.15] (1-122) -*Homo sapiens* IGHG1*03v (CH1 N114>D (213), R120>K (219) (123-220), hinge 1-15 (221-235), CH2 E1.4>P (238), L1.2>V (239), G1.1>A (240), S29>K (271), Q84.2>E (299) (236-344), CH3 E12 (360), M14 (362), L24>D (372), K26>S (374), N44>D (388), Q97>E (422), N100>D (425) (345-449), CHS (450-451)) (123-451)], (225-219')-disulfide with kappa light chain anti-SSTR2 (1'-219') [V-KAPPA (*Homo sapiens* IGKV4-1*01 (91.8%) -IGKJ4*01 (100.0%)) [12.3.8] (1'-112') -*Homo sapiens* IGKC*01 (100%) A45.1 (158), V101 (196) (113'-219')];
heavy chain scFv-h-CH2-CH3, anti-CD3E (1-485) [VH (*Homo sapiens* IGHV3-73*01 (87.0%) -(IGHD) -IGHJ6*01 (90.9%)) [8.10.16] (1-125) -20-mer linker (126-145) -V-LAMBDA (*Mus musculus* IGLV1*01 (80.6%) -IGLJ1*01 (100%)/*Homo sapiens* IGLV7-46*01 (76.8%) -IGHJ3*02 (100%)) [9.3.9] (146-254) -IGHG1*03 (hinge 1-15 C5>S (259) (255-269) -CH2 E1.4>P (272), L1.2>V (273), G1.1>A (274), S29>K (305) (270-378),CH3 E12 (394), E13>Q (395), M14 (396), S20>K (402)(379-483), CHS (484-485)) (1-485)]; (231-265'':234-268'')-bisdisulfide

tidutamab

immunoglobuline demi-G1-kappa/scFv-h-CH2-CH3, anti-[*Homo sapiens* SSTR2 (récepteur de la somatostatine 2) et *Homo sapiens* CD3 epsilon (CD3E, Leu-4)], anticorps monoclonal, bispécifique;
chaîne lourde gamma1 anti-SSTR2 (1-451) [VH (*Homo sapiens* IGHV3-48*03 (90.8%) -(IGHD) -IGHJ4*01 (100%)) [8.8.15] (1-122) -*Homo sapiens* IGHG1*03v (CH1 N114>D (213), R120>K (219) (123-220), charnière 1-15 (221-235), CH2 E1.4>P (238), L1.2>V (239), G1.1>A (240), S29>K (271), Q84.2>E (299) (236-344), CH3 E12 (360), M14 (362), L24>D (372), K26>S (374), N44>D (388), Q97>E (422), N100>D (425) (345-449), CHS (450-451)) (123-451)], (225-219')-disulfure avec la chaîne légère kappa anti-SSTR2 (1'-219') [V-KAPPA (*Homo sapiens* IGKV4-1*01 (91.8%) -IGKJ4*01 (100%)) [12.3.8] (1'-112') -*Homo sapiens* IGKC*01 (100%) A45.1 (158), V101 (196) (113'-219')];
chaîne lourde scFv-h-CH2-CH3, anti-CD3E (1-485) [VH (*Homo sapiens* IGHV3-73*01 (87.0%) -(IGHD) -IGHJ6*01 (90.9%)) [8.10.16] (1-125) -20-mer linker (126-145)-V-LAMBDA (*Mus musculus* IGLV1*01 (80.6%) -IGLJ1*01 (100%)/*Homo sapiens* IGLV7-46*01 (76.8%) -IGHJ3*02 (100%)) [9.3.9] (146-254) -IGHG1*03 (charnière 1-15 C5>S (259) (255-269) -CH2 E1.4>P (272), L1.2>V (273), G1.1>A (274), S29>K (305) (270-378), CH3 E12 (394), E13>Q (395), M14 (396), S20>K (402)(379-483), CHS (484-485)) (1-485)]; dimère (231-265'':234-268'')-bisdisulfure

tidutamab

inmunoglobulina demi-G1-kappa/scFv-h-CH2-CH3, anti-[*Homo sapiens* SSTR2 (receptor de la somatostatina 2) y *Homo sapiens* CD3 épsilon (CD3E, Leu-4)], anticuerpo monoclonal, biespecífico;
cadena pesada gamma1 anti-SSTR2 (1-451) [VH (*Homo sapiens* IGHV3-48*03 (90.8%) -(IGHD) -IGHJ4*01 (100%)) [8.8.15] (1-122) -*Homo sapiens* IGHG1*03v (CH1 N114>D (213), R120>K (219) (123-220), bisagra 1-15 (221-235), CH2 E1.4>P (238), L1.2>V (239), G1.1>A (240), S29>K (271), Q84.2>E (299) (236-344), CH3 E12 (360), M14 (362), L24>D (372), K26>S (374), N44>D (388), Q97>E (422), N100>D (425) (345-449), CHS (450-451)) (123-451)], (225-219')-disulfuro con la cadena ligera kappa anti-SSTR2 (1'-219') [V-KAPPA (*Homo sapiens* IGKV4-1*01 (91.8%) -IGKJ4*01 (100%)) [12.3.8] (1'-112') -*Homo sapiens* IGKC*01 (100%) A45.1 (158), V101 (196) (113'-219')];
cadena pesada scFv-h-CH2-CH3, anti-CD3E (1-485) [VH (*Homo sapiens* IGHV3-73*01 (87.0%) -(IGHD) -IGHJ6*01 (90.9%)) [8.10.16] (1-125) -20-mer ligante (126-145) -V-LAMBDA (*Mus musculus* IGLV1*01 (80.6%) -IGLJ1*01 (100%)/*Homo sapiens* IGLV7-46*01 (76.8%) -IGHJ3*02 (100%)) [9.3.9] (146-254) -IGHG1*03 (bisagra 1-15 C5>S (259) (255-269) -CH2 E1.4>P (272), L1.2>V (273), G1.1>A (274), S29>K (305) (270-378), CH3 E12 (394), E13>Q (395), M14 (396), S20>K (402)(379-483), CHS (484-485)) (1-485)];
dímero (231-265":234-268")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada (anti-SSTR2)

```
EVQLVESGGG LVQPGGSLRL SCAASGFTFS DYGMAWFRQA PGKGLEWVSF  50
ISNLGYSIYY ADSVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARAP 100
YDYDSFDPMD YWGQGTLVTV SSASTKGPSV FPLAPSSKST SGGTAALGCL 150
VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ SSGLYSLSSV VTVPSSSLGT 200
QTYICNVNHK PSDTKVDKKV EPKSCDKTHT CPPCPAPPVA GPSVFLFPPK 250
PKDTLMISRT PEVTCVVVDV KHEDPEVKFN WYVDGVEVHN AKTKPREEEY 300
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP 350
QVYTLPPSRE EMTKNQVSLT CDVSGFYPSD IAVEWESDGQ PENNYKTTPP 400
VLDSDGSFFL YSKLTVDKSR WEQGDVFSCS VMHEALHNHY TQKSLSLSPG 450
K                                                      451
```

Light chain / Chaîne légère / Cadena ligera (anti-SSTR2)

```
DIVMTQSPDS LAVSLGERAT INCKSSQSLL NSRNRKNYLA WYQQKPDQSP  50
KLLIYWASTR ESGVPDRFSG SGSGTDFTLT ISSLQAEDVA VYYCKQSYYL 100
WTFGGGTKVE IKRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK 150
VQWKVDNALQ SGNSQESVTE QDSKDSTYSL SSTLTLSKAD YEKHKVYACE 200
VTHQGLSSPV TKSFNRGEC                                   219
```

Heavy chain / Chaîne lourde / Cadena pesada scFv-h-CH2-CH3 (anti-CD3E)

```
EVQLVESGGG LVQPGGSLRL SCAASGFTFS TYAMNWVRQA PGKGLEWVGR  50
IRSKYNNYAT YYADSVKGRF TISRDDSKNT LYLQMNSLRA EDTAVYYCVR 100
HGNFGDSYVS WFAYWGQGTL VTVSSGKPGS GKPGSGKPGS GKPGSQAVVT 150
QEPSLTVSPG GTVTLTCGSS TGAVTTSNYA NWVQQKPGKS PRGLIGGTNK 200
RAPGVPARFS GSLLGGKAAL TISGAQPEDE ADYYCALWYS NHWVFGGGTK 250
LTVLEPKSSD KTHTCPPCPA PPVAGPSVFL FPPKPKDTLM ISRTPEVTCV 300
VVDVKHEDPE VKFNWYVDGV EVHNAKTKPR EEQYNSTYRV VSVLTVLHQD 350
WLNGKEYKCK VSNKALPAPI EKTISKAKGQ PREPQVYTLP PSREQMTKNQ 400
VKLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG SFFLYSKLTV 450
DKSRWQQGNV FSCSVMHEAL HNHYTQKSLS LSPGK                 485
```

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

Intra-H (C23-C104)	22-96	149-205	265-325	371-429
Intra-L (C23-C104)	23'-94'	139'-199'		
Intra-H scFv-h-CH2-CH3	22"-98"	167"-235"	299"-359"	405"-463"
Inter-H-L (h 5-CL 126)	225-219'			
Inter-H-H (h 11, h 14)	231-265"	234-268"		

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
301, 335"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

tilavonemabum #

tilavonemab

immunoglobulin G4-kappa, anti-[*Homo sapiens* MAPT (microtubule-associated protein tau, tau)], monoclonal antibody;
gamma4 heavy chain (1-442) [VH (*Mus musculus* IGHV6-3*01 (91.9%) -(IGHD) -IGHJ4*01 (92.3%)/*Homo sapiens* IGHV3-7*01 (71.4%) -(IGHD) -IGHJ4*01 (92.3%)) [8.10.6] (1-115) -*Homo sapiens* IGHG4*01 (CH1 (116-213), hinge S10>P (223) (214-225), CH2 (226-335), CH3 (336-440), CHS (441-442)) (115-442)], (129-218')-disulfide with kappa light chain (1'-218') [V-KAPPA (*Mus musculus* IGKV3-7*01 (90.9%) -IGKJ2*03 (90.9%)/*Homo sapiens* IGKV4-1*01 (69.3%) -IGKJ2*01 (100%)) [10.3.9] (1'-111') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218')]; dimer (221-221'':224-224'')-bisdisulfide

tilavonémab

immunoglobuline G4-kappa, anti-[*Homo sapiens* MAPT (protéine tau associée aux microtubules, tau)], anticorps monoclonal;
chaîne lourde gamma4 (1-442) [VH (*Mus musculus* IGHV6-3*01 (91.9%) -(IGHD) -IGHJ4*01 (92.3%)/*Homo sapiens* IGHV3-7*01 (71.4%) -(IGHD) -IGHJ4*01 (92.3%)) [8.10.6] (1-115) -*Homo sapiens* IGHG4*01 (CH1 (116-213), charnière S10>P (223) (214-225), CH2 (226-335), CH3 (336-440), CHS (441-442)) (115-442)], (129-218')-disulfure avec la chaîne légère kappa (1'-218') [V-KAPPA (*Mus musculus* IGKV3-7*01 (90.9%) -IGKJ2*03 (90.9%)/*Homo sapiens* IGKV4-1*01 (69.3%) -IGKJ2*01 (100%)) [10.3.9] (1'-111') -*Homo sapiens* IGKC*01 (100%), Km3 (100%), Km3 A45.1 (157), V101 (195) (112'-218')]; dimère (221-221'':224-224'')-bisdisulfure

tilavonemab

inmunoglobulina G4-kappa, anti-[*Homo sapiens* MAPT (proteína tau asociada a los microtúbulos, tau)], anticuerpo monoclonal;
cadena pesada gamma4 (1-442) [VH (*Mus musculus* IGHV6-3*01 (91.9%) -(IGHD) -IGHJ4*01 (92.3%)/*Homo sapiens* IGHV3-7*01 (71.4%) -(IGHD) -IGHJ4*01 (92.3%)) [8.10.6] (1-115) -*Homo sapiens* IGHG4*01 (CH1 (116-213), bisagra S10>P (223) (214-225), CH2 (226-335), CH3 (336-440), CHS (441-442)) (115-442)], (129-218')-disulfuro con la cadena ligera kappa (1'-218') [V-KAPPA (*Mus musculus* IGKV3-7*01 (90.9%) -IGKJ2*03 (90.9%)/*Homo sapiens* IGKV4-1*01 (69.3%) -IGKJ2*01 (100%)) [10.3.9] (1'-111') -*Homo sapiens* IGKC*01 (100%), Km3 (100%), Km3 A45.1 (157), V101 (195) (112'-218')]; dímero (221-221'':224-224'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVKVVESGGG LVQPGGSMKL SCVVSGFTFS NYWVNWVRQA PGKGLEWVAQ  50
IRLKSDNYAT HYEESVKGRF TISRDDSKSS VYLQMNNLRA EDSGIYYCTN 100
WEDYWGQGTT VTVSSASTKG PSVFPLAPCS RSTSESTAAL GCLVKDYFPE 150
PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL SSVVTVPSSS LGTKTYTCNV 200
DHKPSNTKVD KRVESKYGPP CPPCPAPEFL GGPSVFLFPP KPKDTLMISR 250
TPEVTCVVVD VSQEDPEVQF NWYVDGVEVH NAKTKPREEQ FNSTYRVVSV 300
LTVLHQDWLN GKEYKCKVSN KGLPSSIEKT ISKAKGQPRE PQVYTLPPSQ 350
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF 400
LYSRLTVDKS RWQEGNVFSC SVMHEALHNH YTQKSLSLSL GK         442
```

Light chain / Chaîne légère / Cadena ligera

```
DIVLTQSPDS LAVSLGERAT ISCRASQSVS TSRYSYIHWY QQKPGQPPKL  50
LIKYASNLES GVPSRFSGSG SGTDFTLNIH PLEPEDFATY YCHHSWEIPL 100
TFGQGTKLEI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL NNFYPREAKV 150
QWKVDNALQS GNSQESVTEQ DSKDSTYSLS STLTLSKADY EKHKVYACEV 200
THQGLSSPVT KSFNRGEC                                   218
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-98 142-198 256-316 362-420
22''-98'' 142''-198'' 256''-316'' 362''-420''
Intra-L (C23-C104) 23'-92' 138'-198'
23'''-92''' 138'''-198'''
Inter-H-L (CH1 10-CL 126) 129-218' 129''-218'''
Inter-H-H (h 8, h 11) 221-221'' 224-224''

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
292, 292''
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

tomaralimabum #

tomaralimab	immunoglobulin G4-kappa, anti-[*Homo sapiens* TLR2 (toll like receptor 2, toll-like receptor 2, TIL4, CD282)], monoclonal antibody; gamma4 heavy chain (1-445) [VH (*Mus musculus* IGHV1-85*01 (80.6%) -(IGHD) -IGHJ4*01 (85.7%)/*Homo sapiens* IGHV1-8*03 (73.5%) -(IGHD) -IGHJ6*01 (85.7%)) [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 (444-445)) (118-445)], (132-218')-disulfide with kappa light chain (1'-218') [V-KAPPA (*Mus musculus* IGKV3-1*01 (81.8%) -IGKJ1*01 (91.7%)/*Homo sapiens* IGKV3D-11*02 (70.2%) -(IGHD) -IGKJ4*01 (100%)) [10.3.9] (1'-111') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218')]; dimer (224-224'':227-227'')-bisdisulfide
tomaralimab	immunoglobuline G4-kappa, anti-[*Homo sapiens* TLR2 (récepteur 2 de type Toll, récepteur 2 toll-like, TIL4, CD282)], anticorps monoclonal; chaîne lourde gamma4 (1-445) [VH (*Mus musculus* IGHV1-85*01 (80.6%) -(IGHD) -IGHJ4*01 (85.7%)/*Homo sapiens* IGHV1-8*03 (73.5%) -(IGHD) -IGHJ6*01 (85.7%)) [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 (444-445)) (118-445)], (132-218')-disulfure avec la chaîne légère kappa (1'-218') [V-KAPPA (*Mus musculus* IGKV3-1*01 (81.8%) -IGKJ1*01 (91.7%)/*Homo sapiens* IGKV3D-11*02 (70.2%) -(IGHD) -IGKJ4*01 (100%)) [10.3.9] (1'-111') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218')]; dimère (224-224'':227-227'')-bisdisulfure
tomaralimab	inmunoglobulina G4-kappa, anti-[*Homo sapiens* TLR2 (receptor 2 de tipo Toll, receptor 2 toll-like, TIL4, CD282)], anticuerpo monoclonal; cadena pesada gamma4 (1-445) [VH (*Mus musculus* IGHV1-85*01 (80.6%) -(IGHD) -IGHJ4*01 (85.7%)/*Homo sapiens* IGHV1-8*03 (73.5%) -(IGHD) -IGHJ6*01 (85.7%)) [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 (444-445)) (118-445)], (132-218')-disulfuro con la cadena ligera kappa (1'-218') [V-KAPPA (*Mus musculus* IGKV3-1*01 (81.8%) -IGKJ1*01 (91.7%)/*Homo sapiens* IGKV3D-11*02 (70.2%) -(IGHD) -IGKJ4*01 (100%)) [10.3.9] (1'-111') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218')]; dímero (224-224'':227-227'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVQSGSE LKKPGASVKL SCKASGFTFT TYGINWVRQA PGQGLEWIGW  50
IYPRDGSTNF NENFKDRATI TVDTSASTAY MELSSLRSED TAVYFCARLT 100
GGTFLDYWGQ 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 LSLGK      445
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Light chain / Chaîne légère / Cadena ligera

```
DIVLTQSPAT LSLSPGERAT LSCRASESVE YYGTSLMQWY QQKPGQPPKL  50
LIFGASNVES GVPDRFSGSG SGTDFTLKIS RVEAEDVGMY FCQQSRKLPW 100
TFGGGTKVEI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL NNFYPREAKV 150
QWKVDNALQS GNSQESVTEQ DSKDSTYSLS STLTLSKADY EKHKVYACEV 200
THQGLSSPVT KSFNRGEC                                    218
```

Post-translational modifications

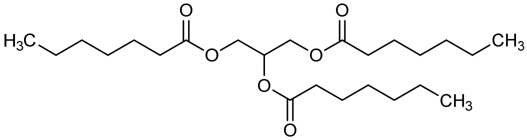
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 145-201 259-319 365-423
22''-96'' 145''-201'' 259''-319'' 365''-423''
Intra-L (C23-C104) 23'-92' 138'-198'
23'''-92''' 138'''-198'''
Inter-H-L (CH1 10-CL 126) 132-218' 132''-218'''
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

triheptanoinum

triheptanoin	propane-1,2,3-triyl triheptanoate
triheptanoïne	triheptanoate de propane-1,2,3-triyle
triheptanoína	triheptanoato de propano-1,2,3-triilo

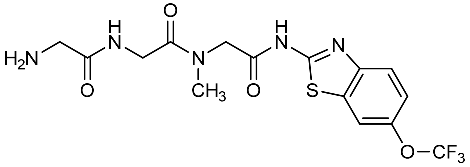
$C_{24}H_{44}O_6$



troriluzolum

troriluzole	glycylglycyl-N^2-methyl-N^1-[6-(trifluoromethoxy)-1,3-benzothiazol-2-yl]glycinamide
troriluzole	glycylglycyl-N^2-méthyl-N^1-[6-(trifluorométhoxy)-1,3-benzothiazol-2-yl]glycinamide
troriluzole	glicilglicil-N^2-metil-N^1-[6-(trifluorometoxi)-1,3-benzotiazol-2-il]glicinamida

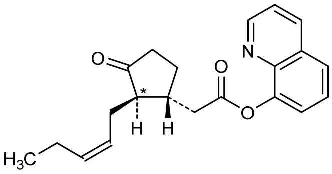
$C_{15}H_{16}F_3N_5O_4S$



tuvatexibum

tuvatexib	*rac*-quinolin-8-yl {(1*R*,2*R*)-3-oxo-2-[(2*Z*)-pent-2-en-1-yl]cyclopentyl}acetate (predominant epimer)
tuvatexib	*rac*-{(1*R*,2*R*)-3-oxo-2-[(2*Z*)-pent-2-én-1-yl]cyclopentyl}acétate de quinoléin-8-yle (épimère prédominant)
tuvatexib	*rac*-{(1*R*,2*R*)-3-oxo-2-[(2*Z*)-pent-2-en-1-il]ciclopentil}acetato de quinolein-8-ilo (epímero predominante)

$C_{21}H_{23}NO_3$



and its epimer at C*
and their enantiomers

et son épimère en C*
et leurs énantiomères

y su epímero al C*
y sus enantiómeros

vibecotamabum

vibecotamab	immunoglobulin half-G1-kappa/scFv-h-CH2-CH3, anti-[*Homo sapiens* IL3RA (interleukin 3 receptor subunit alpha, interleukin 3 receptor, alpha (low affinity), CD123) and *Homo sapiens* CD3 epsilon (CD3E, Leu-4)], monoclonal antibody, bispecific; gamma1 heavy chain anti-IL3RA (1-449) [VH (*Mus musculus* IGHV1-26*01(83.7%) -(IGHD) -IGHJ3*01(93.3%)/*Homo sapiens* IGHV1-46*01 (78.6%) -(IGHD) -IGHJ6*01 (90.9%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*03v (CH1 N114>D (211), R120>K (217) (121-218), hinge 1-15 (219-233), CH2 E1.4>P (236), L1.2>V (237), G1.1>A (238), S29>K (269), Q84.2>E (297) (234-342), CH3 E12 (358), M14 (360), L24>D (370), K26>S (372), N44>D (386), Q97>E (420), N100>D (423) (343- 447), CHS (448-449)) (121-449)], (223-220')-disulfide with kappa light chain anti IL3RA (1'-220') [V-KAPPA (*Homo sapiens* IGKV4-1*01 (89.1%) -IGKJ2*01 (91.7%)) [12.3.9] (1'-113') -*Homo sapiens* IGKC*01 (100%) A45.1 (159), V101 (197) (114'-220')]; heavy chain scFv-h-CH2-CH3, anti-CD3E (1-485) [VH (*Homo sapiens* IGHV3-73*01 (87.0%) -(IGHD) -IGHJ6*01 (90.9%)) [8.10.16] (1-125) -20-mer linker (126-145) -V-LAMBDA (*Mus musculus* IGLV1*01 (80.6%) -IGLJ1*01 (100%)/*Homo sapiens* IGLV7-46*01 (76.8%) -IGHJ3*02 (100%)) [9.3.9] (146-254) -IGHG1*03 (hinge 1-15 C5>S (259) (255-269) -CH2 E1.4>P (272), L1.2>V (273), G1.1>A (274), S29>K (305) (270-378),CH3 E12 (394), E13>Q (395), M14 (396), S20>K (402)(379-483), CHS (484-485)) (1-485)]; dimer (229-265'':232-268'')-bisdisulfide
vibécotamab	immunoglobuline demi-G1-kappa/scFv-h-CH2-CH3, anti-[*Homo sapiens* IL3RA (sous-unité alpha du récepteur de l'interleukine 3, récepteur alpha (faible affinité) de l'interleukine 3, CD123) et *Homo sapiens* CD3 epsilon (CD3E, Leu-4)], anticorps monoclonal, bispécifique; chaîne lourde gamma1 anti-IL3RA (1-449) [VH (*Mus musculus* IGHV1-26*01(83.7%) -(IGHD) -IGHJ3*01(93.3%)/*Homo sapiens* IGHV1-46*01 (78.6%) -(IGHD) -IGHJ6*01 (90.9%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*03v (CH1 N114>D (211), R120>K (217) (121-218), charnière 1-15 (219-233), CH2 E1.4>P (236), L1.2>V (237), G1.1>A (238), S29>K (269), Q84.2>E (297) (234-342), CH3 E12 (358), M14 (360), L24>D (370), K26>S (372), N44>D (386), Q97>E (420), N100>D (423) (343- 447), CHS (448-449)) (121-449)], (223-220')-disulfure avec la chaîne légère kappa (1'-220') [V-KAPPA (*Homo sapiens* IGKV4-1*01 (89.1%) -IGKJ2*01 (91.7%)) [12.3.9] (1'-113') -*Homo sapiens* IGKC*01 (100%) A45.1 (159), V101 (197) (114'-220')]; chaîne lourde scFv-h-CH2-CH3, anti-CD3E (1-485) [VH (*Homo sapiens* IGHV3-73*01 (87.0%) -(IGHD) -IGHJ6*01 (90.9%)) [8.10.16] (1-125) -20-mer linker (126-145) -V-LAMBDA (*Mus musculus* IGLV1*01 (80.6%) -IGLJ1*01 (100%)/*Homo sapiens* IGLV7-46*01 (76.8%) -IGHJ3*02 (100%)) [9.3.9] (146-254) -IGHG1*03 (charnière 1-15 C5>S (259) (255-269) -CH2 E1.4>P (272), L1.2>V (273), G1.1>A (274), S29>K (305) (270-378), CH3 E12 (394), E13>Q (395), M14 (396), S20>K (402)(379-483), CHS (484-485)) (1-485)]; dimère (229-265'':232-268'')-bisdisulfure

vibecotamab

inmunoglobulina demi-G1-kappa/scFv-h-CH2-CH3, anti-[*Homo sapiens* IL3RA (subunidad alfa del receptor de la interleukina 3, receptor alfa (baja afinidad) de la interleukina 3, CD123) et *Homo sapiens*CD3 épsilon (CD3E, Leu-4)], anticuerpo monoclonal, biespecífico;
cadena pesada gamma1 anti-IL3RA (1-449) [VH (*Mus musculus* IGHV1-26*01(83.7%) -(IGHD) -IGHJ3*01(93.3%)/*Homo sapiens* IGHV1-46*01 (78.6%) -(IGHD) -IGHJ6*01 (90.9%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*03v (CH1 N114>D (211), R120>K (217) (121-218), bisagra 1-15 (219-233), CH2 E1.4>P (236), L1.2>V (237), G1.1>A (238), S29>K (269), Q84.2>E (297) (234-342), CH3 E12 (358), M14 (360), L24>D (370), K26>S (372), N44>D (386), Q97>E (420), N100>D (423) (343- 447), CHS (448-449)) (121-449)], (223-220')-disulfuro con la cadena ligera kappa (1'-220') [V-KAPPA (*Homo sapiens* IGKV4-1*01 (89.1%) -IGKJ2*01 (91.7%)) [12.3.9] (1'-113') -*Homo sapiens* IGKC*01 (100%) A45.1 (159), V101 (197) (114'-220')];
cadena pesada scFv-h-CH2-CH3, anti-CD3E (1-485) [VH (*Homo sapiens* IGHV3-73*01 (87.0%) -(IGHD) -IGHJ6*01 (90.9%)) [8.10.16] (1-125) -20-mer ligante (126-145) -V-LAMBDA (*Mus musculus* IGLV1*01 (80.6%) -IGLJ1*01 (100%)/*Homo sapiens* IGLV7-46*01 (76.8%) -IGHJ3*02 (100%)) [9.3.9] (146-254) -IGHG1*03 (bisagra 1-15 C5>S (259) (255-269) -CH2 E1.4>P (272), L1.2>V (273), G1.1>A (274), S29>K (305) (270-378), CH3 E12 (394), E13>Q (395), M14 (396), S20>K (402)(379-483), CHS (484-485)) (1-485)];
dímero (229-265":232-268")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada (anti-IL3RA)

```
QVQLQQSGAE VKKPGASVKV SCKASGYTFT DYYMKWVKQS HGKSLEWMGD  50
IIPSNGATFY NQKFKGKATL TVDRSTSTAY MELSSLRSED TAVYYCARSH 100
LLRASWFAYW GQGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS DTKVDKKVEP KSCDKTHTCP PCPAPPVAGP SVFLFPPKPK 250
DTLMISRTPE VTCVVVDVKH EDPEVKFNWY VDGVEVHNAK TKPREEEYNS 300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV 350
YTLPPSREEM TKNQVSLTCD VSGFYPSDIA VEWESDGQPE NNYKTTPPVL 400
DSDGSFFLYS KLTVDKSRWE QGDVFSCSVM HEALHNHYTQ KSLSLSPGK  449
```

Light chain / Chaîne légère / Cadena (anti-IL3RA)

```
DFVMTQSPDS LAVSLGERAT INCKSSQSLL NTGNQKNYLT WYQQKPGQPP  50
KLLIYWASTR ESGVPDRFTG SGSGTDFTLT ISSLQAEDVA VYYCQNDYSY 100
PYTFGGGTKL EIKRTVAAPS VFIFPPSDEQ LKSGTASVVC LLNNFYPREA 150
KVQWKVDNAL QSGNSQESVT EQDSKDSTYS LSSTLTLSKA DYEKHKVYAC 200
EVTHQGLSSP VTKSFNRGEC                                 220
```

Heavy chain / Chaîne lourde / Cadena pesada scFv-h-CH2-CH3 (anti-CD3E)

```
EVQLVESGGG LVQPGGSLRL SCAASGFTFS TYAMNWVRQA PGKGLEWVGR  50
IRSKYNNYAT YYADSVKGRF TISRDDSKNT LYLQMNSLRA EDTAVYYCVR 100
HGNFGDSYVS WFAYWGQGTL VTVSSGKPGS GKPGSGKPGS GKPGSQAVVT 150
QEPSLTVSPG GTVTLTCGSS TGAVTTSNYA NWVQQKPGKS PRGLIGGTNK 200
RAPGVPARFS GSLLGGKAAL TISGAQPEDE ADYYCALWYS NHWVFGGGTK 250
LTVLEPKSSD KTHTCPPCPA PPVAGPSVFL FPPKPKDTLM ISRTPEVTCV 300
VVDVKHEDPE VKFNWYVDGV EVHNAKTKPR EEQYNSTYRV VSVLTVLHQD 350
WLNGKEYKCK VSNKALPAPI EKTISKAKGQ PREPQVYTLP PSREQMTKNQ 400
VKLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG SFFLYSKLTV 450
DKSRWQQGNV FSCSVMHEAL HNHYTQKSLS LSPGK                485
```

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

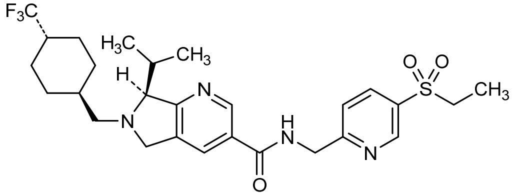
Intra-H (C23-C104)	22-96	147-203	263-323	369-427
Intra-L (C23-C104)	23'-94'	140'-200'		
Intra-H scFv-h-CH2-CH3	22"-98"	167"-235"	299"-359"	405"-463"
Inter-H-L (h 5-CL 126)	223-220'			
Inter-H-H (h 11, h 14)	229-265"	232-268"		

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
299, 335"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

vimirogantum

vimirogant	(7*S*)-*N*-{[5-(ethanesulfonyl)pyridin-2-yl]methyl}-7-(propan-2-yl)-6-{[*trans*-4-(trifluoromethyl)cyclohexyl]methyl}-6,7-dihydro-5*H*-pyrrolo[3,4-*b*]pyridine-3-carboxamide
vimirogant	(7*S*)-*N*-{[5-(éthanesulfonyl)pyridin-2-yl]méthyl}-7-(propan-2-yl)-6-{[*trans*-4-(trifluorométhyl)cyclohexyl]méthyl}-6,7-dihydro-5*H*-pyrrolo[3,4-*b*]pyridine-3-carboxamide
vimirogant	(7*S*)-*N*-{[5-(etanosulfonil)piridin-2-il]metil}-7-(propan-2-il)-6-{[*trans*-4-(trifluorometil)ciclohexil]metil}-6,7-dihidro-5*H*-pirrolo[3,4-*b*]piridina-3-carboxamida

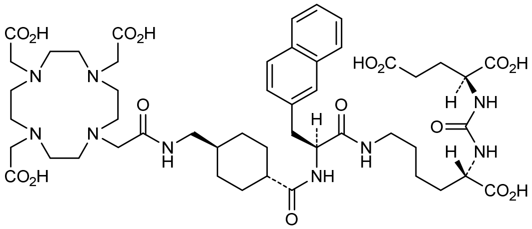
$C_{27}H_{35}F_3N_4O_3S$



vipivotidum tetraxetanum

vipivotide tetraxetan	*N*-[(N^6-{3-(naphthalen-2-yl)-*N*-[*trans*-4-({2-[4,7,10-tris(carboxymethyl)-1,4,7,10-tetraazacyclododecan-1-yl]acetamido}methyl)cyclohexane-1-carbonyl]-L-alanyl}-L-lysin-N^2-yl)carbonyl]-L-glutamic acid
vipivotide tétraxétan	acide *N*-[(N^6-{3-(naphtalén-2-yl)-*N*-[*trans*-4-({2-[4,7,10-tris(carboxyméthyl)-1,4,7,10-tétraazacyclododécan-1-yl]acétamido}méthyl)cyclohexane-1-carbonyl]-L-alanyl}-L-lysin-N^2-yl)carbonyl]-L-glutamique
vipivotida tetraxetãn	ácido *N*-[(N^6-{3-(naftalen-2-il)-*N*-[*trans*-4-({2-[4,7,10-tetraazaciclododecan-1-il]acetamido}metil)ciclohexano-1-carbonil]-L-alanil}-L-lisin-N^2-il)carbonil]-L-glutámico

$C_{49}H_{71}N_9O_{16}$



vofatamabum #

vofatamab	immunoglobulin G1-kappa, anti-[*Homo sapiens* FGFR3 (fibroblast growth factor receptor 3, CD333)], monoclonal antibody;

gamma1 heavy chain (1-457) [VH (*Homo sapiens* IGHV3-66*01 (85.7%) -(IGHD) -IGHJ4*01 (100%)) [8.8.20] (1-127) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (224) (128-225), hinge (226-240), CH2 (241-350), CH3 E12 (366), M14 (368) (351-455), CHS (456-457)) (128-457)], (230-214')-disulfide with kappa light chain (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5*01 (86.7%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (236-236'':239-239'')-bisdisulfide

vofatamab

immunoglobuline G1-kappa, anti-[*Homo sapiens* FGFR3 (récepteur 3 du facteur de croissance des fibroblastes, CD333)], anticorps monoclonal;
chaîne lourde gamma1 (1-457) [VH (*Homo sapiens* IGHV3-66*01 (85.7%) -(IGHD) -IGHJ4*01 (100%)) [8.8.20] (1-127) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (224) (128-225), charnière (226-240), CH2 (241-350), CH3 E12 (366), M14 (368) (351-455), CHS (456-457)) (128-457)], (230-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5*01 (86.7%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (236-236'':239-239'')-bisdisulfure

vofatamab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* FGFR3 (receptor 3 del factor de crecimiento de los fibroblastos, CD333)], anticuerpo monoclonal;
cadena pesada gamma1 (1-457) [VH (*Homo sapiens* IGHV3-66*01 (85.7%) -(IGHD) -IGHJ4*01 (100%)) [8.8.20] (1-127) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (224) (128-225), bisagra (226-240), CH2 (241-350), CH3 E12 (366), M14 (368) (351-455), CHS (456-457)) (128-457)], (230-214')-disulfuro con la cadena ligera kappa (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5*01 (86.7%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (236-236'':239-239'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAASGFTFT STGISWVRQA PGKGLEWVGR  50
IYPTSGSTNY ADSVKGRFTI SADTSKNTAY LQMNSLRAED TAVYYCARTY 100
GIYDLYVDYT EYVMDYWGQG TLVTVSSAST KGPSVFPLAP SSKSTSGGTA 150
ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS 200
SSLGTQTYIC NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV 250
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK 300
PREEQYNSTY RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK 350
GQPREPQVYT LPPSREEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN 400
YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS 450
LSLSPGK                                                457
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Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCRASQDVD TSLAWYKQKP GKAPKLLIYS  50
ASFLYSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ STGHPQTFGQ 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) 22-96 154-210 271-331 377-435
22''-96'' 154''-210'' 271''-331'' 377''-435''
Intra-L (C23-C104) 23'-88' 134'-194'
23'''-88''' 134'''-194'''
Inter-H-L (h 5-CL 126) 230-214' 230''-214'''
Inter-H-H (h 11, h 14) 236-236'' 239-239''

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
307, 307''
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

volagidemabum #

volagidemab	immunoglobulin G2-kappa, anti-[*Homo sapiens* GCGR (glucagon receptor)], *Homo sapiens* monoclonal antibody; gamma2 heavy chain *Homo sapiens* (1-454) [VH (*Homo sapiens* IGHV3-33*01 (95.9%) -(IGHD) -IGHJ1*01(90.9%)) [8.8.21] (1-128) -*Homo sapiens* IGHG2*01 (CH1 (129-226), hinge (227-238), CH2 (239-347), CH3 (348-452), CHS (453-454)) (129-454)], (142-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-17*01 (96.8%) -IGKJ4*01 (100.0%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (230-230":231-231":234-234":237-237")-tetrakisdisulfide
volagidémab	immunoglobuline G2-kappa, anti-[*Homo sapiens* GCGR (récepteur du glucagon)], anticorps monoclonal *Homo sapiens*; chaîne lourde gamma2 *Homo sapiens* (1-454) [VH (*Homo sapiens* IGHV3-33*01 (95.9%) -(IGHD) - IGHJ1*01(90.9%)) [8.8.21] (1-128) -*Homo sapiens* IGHG2*01 (CH1 (129-226), charnière (227-238), CH2 (239-347), CH3 (348-452), CHS (453-454)) (129-454)], (142-214')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-17*01 (96.8%) -IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (230-230":231-231":234-234":237-237")-tétrakisdisulfure
volagidemab	inmunoglobulina G2-kappa, anti-[*Homo sapiens* GCGR (receptor del glucagón)], anticuerpo monoclonal *Homo sapiens*; cadena pesada gamma2 *Homo sapiens* (1-454) [VH (*Homo sapiens* IGHV3-33*01 (95.9%) -(IGHD) - IGHJ1*01(90.9%)) [8.8.21] (1-128) -*Homo sapiens* IGHG2*01 (CH1 (129-226), bisagra (227-238), CH2 (239-347), CH3 (348-452), CHS (453-454)) (129-454)], (142-214')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-17*01 (96.8%) -IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (230-230":231-231":234-234":237-237")-tetrakisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVESGGG VVQPGRSLRL SCAASGFTFS SYGMHWVRQA PGKGLEWVAV  50
MWYDGSNKDY VDSVKGRFTI SRDNSKNTLY LQMNRLRAED TAVYYCAREK 100
DHYDILTGYN YYYGLDVWGQ GTTVTVSSAS TKGPSVFPLA PCSRSTSEST 150
AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP 200
SSNFGTQTYT CNVDHKPSNT KVDKTVERKC CVECPPCPAP PVAGPSVFLF 250
PPKPKDTLMI SRTPEVTCVV VDVSHEDPEV QFNWYVDGVE VHNAKTKPRE 300
EQFNSTFRVV SVLTVVHQDW LNGKEYKCKV SNKGLPAPIE KTISKTKGQP 350
REPQVYTLPP SREEMTKNQV SLTCLVKGFY PSDIAVEWES NGQPENNYKT 400
TPPMLDSDGS FFLYSKLTVD KSRWQQGNVF SCSVMHEALH NHYTQKSLSL 450
SPGK                                                  454
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCRASQGIR NDLGWYQQKP GKAPKRLIYA  50
ASSLQSGVPS RFSGSGSGTE FTLTISSVQP EDFVTYYCLQ HNSNPLTFGG 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) 22-96 155-211 268-328 374-432
22"-96" 155"-211" 268"-328" 374"-432"
Intra-L (C23-C104) 23'-88' 134'-194'
23'''-88''' 134'''-194'''
Inter-H-L (CH1 10-CL 126) 142-214' 142"-214'''
Inter-H-H (h 4, h 5, h 8, h 11) 230-230" 231-231" 234-234" 237-237"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
304, 304"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

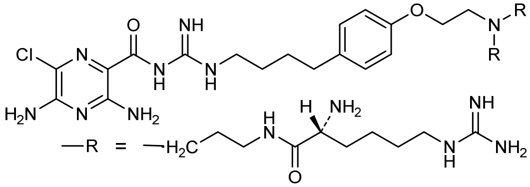
volrubigenum ralaparvovecum #

volrubigene ralaparvovec	recombinant non-replicating adeno-associated viral serotype 8 (AAV8) vector encoding the 1A1 isoform of the uridine-diphosphate (UDP) glucuronosyltransferase (UGT1A1) gene under the control of a chimeric thyroxine binding globulin promoter
volrubigène ralaparvovec	vecteur viral adéno-associé de sérotype 8 (AAV8) recombinant, non-répliquant, codant le gène de l'isoforme 1A1 de l'uridine-diphosphate (UDP) glucuronosyltransférase (UGT1A1) sous le contrôle du promoteur chimérique de la globuline liant la tyroxine
volrubigèn ralaparvovec	un vector de virus adeno asociado serotipo 8(AAV8) recombinante, no replicativo, que codifica para la isoforma 1A1 del gen de la uridina difosfato glucuronosiltransferasa (UGT1A1) bajo el control de un promotor quimérico de la globulina fijadora de tiroxina

voluloridum

voluloride	3,5-diamino-*N*-[*N*-(4-{4-[2-(bis{3-[(2*R*)-2-amino-6-(carbamimidoylamino)hexanamido]propyl}amino)ethoxy]phenyl}butyl)carbamimidoyl]-6-chloropyrazine-2-carboxamide
voluloride	3,5-diamino-*N*-[*N*-(4-{4-[2-(bis{3-[(2*R*)-2-amino-6-(carbamimidoylamino)hexanamido]propyl}amino)éthoxy]phényl}butyl)carbamimidoyl]-6-chloropyrazine-2-carboxamide
volulorida	3,5-diamino-*N*-[*N*-(4-{4-[2-(bis{3-[(2*R*)-2-amino-6-(carbamimidoilamino)hexanamido]propil}amino)etoxi]fenil}butil)carbamimidoil]-6-cloropirazina-2-carboxamida

$C_{38}H_{67}ClN_{18}O_4$



zalifrelimabum #

zalifrelimab	immunoglobulin G1-kappa, anti-[*Homo sapiens* CTLA4 (cytotoxic T-lymphocyte-associated protein 4, CD152)], *Homo sapiens* monoclonal antibody; gamma1 heavy chain *Homo sapiens* (1-448) [VH (*Homo sapiens* IGHV3-21*01 (100%) -(IGHD) -IGHJ3*02 (100%)) [8.8.11] (1-118) -*Homo sapiens* IGHG1*03 (100%) (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 *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (94.8%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (227-227'':230-230'')-bisdisulfide

zalifrélimab

immunoglobuline G1-kappa, anti-[*Homo sapiens* CTLA4 (protéine 4 associée aux lymphocytes T cytotoxiques, CD152)], anticorps monoclonal *Homo sapiens*;
chaîne lourde gamma1 *Homo sapiens* (1-448) [VH (*Homo sapiens* IGHV3-21*01 (100%) -(IGHD) - IGHJ3*02 (100%)) [8.8.11] (1-118) -*Homo sapiens* IGHG1*03 (100%) (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 *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (94.8%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (227-227'':230-230'')-bisdisulfure

zalifrelimab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CTLA4 (proteína 4 asociada a los linfocitos T citotóxicos CD152)], anticuerpo monoclonal *Homo sapiens*;
cadena pesada gamma1 *Homo sapiens* (1-448) [VH (*Homo sapiens* IGHV3-21*01 (100%) -(IGHD) - IGHJ3*02 (100%)) [8.8.11] (1-118) -*Homo sapiens* IGHG1*03 (100%) (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 *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (94.8%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (227-227'':230-230'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVKPGGSLRL SCAASGFTFS SYSMNWVRQA PGKGLEWVSS  50
ISSSSSYIYY ADSVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARVG 100
LMGPFDIWGQ GTMVTVSSAS 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

```
EIVLTQSPGT LSLSPGERAT LSCRASQSVS RYLGWYQQKP GQAPRLLIYG  50
ASTRATGIPD RFSGSGSGTD FTLTITRLEP EDFAVYYCQQ YGSSPWTFGQ 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) 22-96 145-201 262-322 368-426
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

ziresovirum

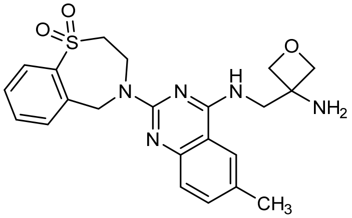
ziresovir

4-(4-{[(3-aminooxetan-3-yl)methyl]amino}-6-methylquinazolin-2-yl)-2,3,4,5-tetrahydro-1*H*-1λ^{6},4-benzothiazepine-1,1-dione

zirésovir

4-(4-{[(3-aminooxétan-3-yl)méthyl]amino}-6-méthylquinazolin-2-yl)-2,3,4,5-tétrahydro-1*H*-1λ^{6},4-benzothiazépine-1,1-dione ziresovir 4-(4-{[(3-aminooxetán-3-il)metil]amino}-6-metilquinazolin-2-il)-2,3,4,5-tetrahidro-1*H*-$1\lambda^6$,4-benzotiazepina-1,1-diona

$C_{22}H_{25}N_5O_3S$



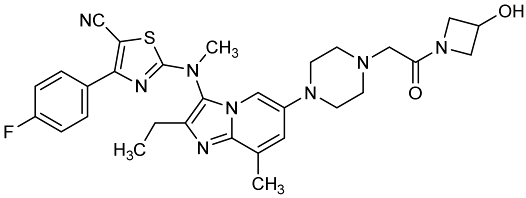
ziritaxestatum

ziritaxestat 4^2-ethyl-1^4-fluoro-8^3-hydroxy-3,4^8-dimethyl-7-oxo-3-aza-4(3,6)-imidazo[1,2-*a*]pyridina-5(1,4)-piperazina-2(4,2)-[1,3]thiazola-8(1)-azetidina-1(1)-benzenaoctaphane-2^5-carbonitrile

ziritaxestat 4^2-éthyl-1^4-fluoro-8^3-hydroxy-3,4^8-diméthyl-7-oxo-3-aza-4(3,6)-imidazo[1,2-*a*]pyridina-5(1,4)-pipérazina-2(4,2)-[1,3]thiazola-8(1)-azétidina-1(1)-benzénaoctaphane-2^5-carbonitrile

ziritaxestat 4^2-etil-1^4-fluoro-8^3-hidroxi-3,4^8-dimetil-7-oxo-3-aza-4(3,6)-imidazo[1,2-*a*]piridina-5(1,4)-piperazina-2(4,2)-[1,3]tiazola-8(1)-azetidina-1(1)-bencenaoctafano-2^5-carbonitrilo

$C_{30}H_{33}FN_8O_2S$



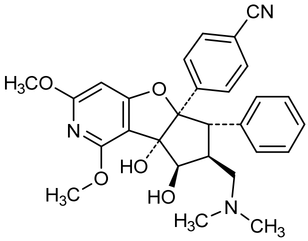
zotatifinum

zotatifin 4-{(5a*R*,6*S*,7*S*,8*R*,8a*S*)-7-[(dimethylamino)methyl]-8,8a-dihydroxy-1,3-dimethoxy-6-phenyl-6,7,8,8a-tetrahydro-5a*H*-cyclopenta[4,5]furo[3,2-*c*]pyridin-5a-yl}benzonitrile

zotatifine 4-{(5a*R*,6*S*,7*S*,8*R*,8a*S*)-7-[(diméthylamino)méthyl]-8,8a-dihydroxy-1,3-diméthoxy-6-phényl-6,7,8,8a-tétrahydro-5a*H*-cyclopenta[4,5]furo[3,2-*c*]pyridin-5a-yl}benzonitrile

zotatifina 4-{(5a*R*,6*S*,7*S*,8*R*,8a*S*)-7-[(dimetilamino)metil]-8,8a-dihidroxi-1,3-dimetoxi-6-fenil-6,7,8,8a-tetrahidro-5a*H*-ciclopenta[4,5]furo[3,2-*c*]piridin-5a-il}benzonitrilo

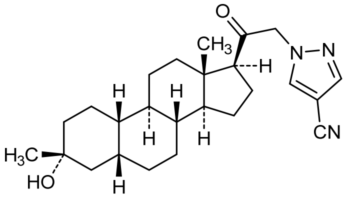
$C_{28}H_{29}N_3O_5$



zuranolonum

zuranolone	1-(3α-hydroxy-3β-methyl-20-oxo-19-nor-5β-pregnan-21-yl)-1*H*-pyrazole-4-carbonitrile
zuranolone	1-(3α-hydroxy-3β-méthyl-20-oxo-19-nor-5β-prégnan-21-yl)-1*H*-pyrazole-4-carbonitrile
zuranolone	1-(3α-hidroxi-3β-metil-20-oxo-19-nor-5β-pregnan-21-il)-1*H*-pirazolo-4-carbonitrilo

$C_{25}H_{35}N_3O_2$



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

Denominaciones comunes internacionales recomendadas (DCI Rec.): Lista 11
(Crónica de la OMS, 1971, Vol. 25, No. 10)

p. 4	*suprimáse*	*insertese*
	fluocinónido	fluocinonida

Denominaciones comunes internacionales recomendadas (DCI Rec.): Lista 13
(Crónica de la OMS, 1974, Vol. 28, No. 10)

p. 3	*suprimáse*	*insertese*
	cicortónido	cicortonida

Denominaciones comunes internacionales recomendadas (DCI Rec.): Lista 15
(Crónica de la OMS, 1975, Vol. 29, No. 10)

p. 2	*suprimáse*	*insertese*
	amcinónido	amcinonida

Denominaciones comunes internacionales recomendadas (DCI Rec.): Lista 17
(Crónica de la OMS, 1977, Vol. 31, No. 10)

p. 2	*suprimáse*	*insertese*
	budesónido	budesonida

Recommended International Nonproprietary Names (Rec. INN): List 57
Dénominations communes internationales recommandées (DCI Rec.): Liste 57
Denominaciones Comunes Internacionales recomendedas (DCI Rec.): Lista 57
(WHO Drug Information, Vol. 20, No. 2, 2007)

p. 68	**imisopasemum manganum**	
	imisopasem manganese	*replace the chemical name by the following*
	imisopasem manganèse	*remplacer le nom chimique par le suivant*
	imisopasem manganeso	*sustitúyase el nombre químico por el siguiente*

(*PBPY*-7-11-2344'3')-dichlorido[($1^{1}R,1^{2}R,7^{1}R,7^{2}R$)-2,6,8,11-tetraaza-4(2,6)-pyridina-1,7(1,2)-dicyclohexanacycloundecaphane-$\kappa^{5}N^{2},N^{1.4},N^{6},N^{8},N^{11}$]manganese

(*PBPY*-7-11-2344'3')-dichlorido[($1^{1}R,1^{2}R,7^{1}R,7^{2}R$)-2,6,8,11-tetraaza-4(2,6)-pyridina-1,7(1,2)-dicyclohexanacycloundécaphane-$\kappa^{5}N^{2},N^{1.4},N^{6},N^{8},N^{11}$]manganèse

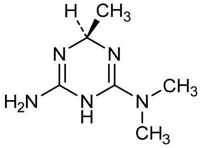
(*PBPY*-7-11-2344'3')-dicloridо[($1^{1}R,1^{2}R,7^{1}R,7^{2}R$)-2,6,8,11-tetraaza-4(2,6)-piridina-1,7(1,2)-diciclohexanacicloundecafano-$\kappa^{5}N^{2},N^{1.4},N^{6},N^{8},N^{11}$]manganeso

Recommended International Nonproprietary Names (Rec. INN): List 60
Dénominations communes internationales recommandées (DCI Rec.): Liste 60
Denominaciones Comunes Internacionales recomendedas (DCI Rec.): Lista 60
(WHO Drug Information, Vol. 22, No. 3, 2008)

p. 234 **imegliminum**

imeglimin	*replace the chemical name and the structure by the following ones*
iméglimine	*remplacer le nom chimique et la structure par les suivants*
imeglimina	*sustitúyase el nombre químico y la estructura por los siguientes*

(6*R*)-N^2,N^2,6-trimethyl-3,6-dihydro-1,3,5-triazine-2,4-diamine
(6*R*)-N^2,N^2,6-triméthyl-3,6-dihydro-1,3,5-triazine-2,4-diamine
(6*R*)-N^2,N^2,6-trimetil-3,6-dihidro-1,3,5-triazina-2,4-diamina



Recommended International Nonproprietary Names (Rec. INN): List 61
Dénominations communes internationales recommandées (DCI Rec.): Liste 61
Denominaciones Comunes Internacionales recomendedas (DCI Rec.): Lista 61
(WHO Drug Information, Vol. 23, No. 1, 2009)

p. 59	*suprimáse*	*insertese*
	derquantel	dercuantel

Recommended International Nonproprietary Names (Rec. INN): List 67
Dénominations communes internationales recommandées (DCI Rec.): Liste 67
Denominaciones Comunes Internacionales recomendedas (DCI Rec.): Lista 67
(WHO Drug Information, Vol. 26, No. 1, 2012)

p. 87 **solithromycin**

solithromycin	*replace the chemical name by the following one*
solithromycine	*remplacer le nom chimique par le suivant*
solitromicina	*sustitúyase el nombre químico por el siguiente*

(3a*S*,4*R*,7*S*,9*R*,10*R*,11*R*,13*R*,15*R*,15a*R*)-1-{4-[4-(3-aminophenyl)-1*H*-1,2,3-triazol-1-yl]butyl}-4-ethyl-7-fluoro-11-methoxy-3a,7,9,11,13,15-hexamethyl-10-{[3,4,6-trideoxy-3-(dimethylamino)-β-D-*xylo*-hexopyranosyl]oxy}octahydro-2*H*-[1]oxacyclotetradecino[4,3-*d*][1,3]oxazole-2,6,8,14(1*H*,7*H*,9*H*)-tetrone

(3a*S*,4*R*,7*S*,9*R*,10*R*,11*R*,13*R*,15*R*,15a*R*)-1-{4-[4-(3-aminophényl)-1*H*-1,2,3-triazol-1-yl]butyl}-4-éthyl-7-fluoro-11-méthoxy-3a,7,9,11,13,15-hexaméthyl-10-{[3,4,6-tridésoxy-3-(diméthylamino)-β-D-*xylo*-hexopyranosyl]oxy}octahydro-2*H*-[1]oxacyclotétradécino[4,3-*d*]oxazole-2,6,8,14(1*H*,7*H*,9*H*)-tétrone

(3a*S*,4*R*,7*S*,9*R*,10*R*,11*R*,13*R*,15*R*,15a*R*)-1-{4-[4-(3-aminofenil)-1*H*-1,2,3-triazol-1-il]butil}-4-etil-7-fluoro-3a,7,9,11,13,15-hexametil-11-metoxi-10-{[3,4,6-tridesoxi-3-(dimetilamino)-β-D-*xilo*-hexopiranosil]oxi}octahidro-2*H*-[1]oxaciclotetradecino[4,3-*d*][1,3]oxazol-2,6,8,14(1*H*,7*H*,9*H*)-tetrona

Recommended International Nonproprietary Names (Rec. INN): List 79
Dénominations communes internationales recommandées (DCI Rec.): Liste 79
Denominaciones Comunes Internacionales recomendedas (DCI Rec.): Lista 79
(WHO Drug Information, Vol. 31, No. 2, 2017)

p. 95-96	**avalglucosidasum alfa #**	
	avalglucosidase alfa	*replace the description by the following one*
	avalglucosidase alfa	*remplacer la description par la suivante*
	avalglucosidasa alfa	*sustitúyase la descripción por la siguiente*

modified human acid α-glucosidase produced in Chinese hamster ovary (CHO) cells, glycoform alfa, conjugated to a synthetic branched hexasaccharide containing two terminal mannose-6-phosphate (M6P), via aminooxy linkers;
prepro-lysosomal α-glucosidase (EC=3.2.1.20) (human) (57-952)-peptide, natural [Arg^{143},His^{167},Ile^{724}] variant, expressed in CHO cells, glycoform alfa, with 5~9 sialyl end groups of glycan residues being oxidized and chemically modified to 5-acetamido-3,5,7-trideoxy-7-[(*E*)-(2-oxo-2-{2-[4-({*O*-(6-*O*-phosphono-α-D-mannopyranosyl)-(1→2)-*O*-α-D-mannopyranosyl-(1→6)-*O*-α-D-mannopyranosyl-(1→6)-*O*-[*O*-(6-*O*-phosphono-α-D-mannopyranosyl)-(1→2)-*O*-α-D-mannopyranosyl-(1→3)]-β-D-mannopyranosyl}oxy)butanoyl]hydrazinyl}ethoxy)imino]-β-L-*arabino*-2-heptulo-2,6-pyranosylonic acid groups

α-glucosidase acide humaine modifiée, produite dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa, liée à un hexasaccharide de synthèse dont les résidus terminaux sont deux mannose-6-phosphates via un groupe aminoxy;
prépro-α-glucosidase lysosomale (EC=3.2.1.20) (humaine) (57-952)-peptide, variant naturel [Arg^{143},His^{167},Ile^{724}], exprimé dans des cellules CHO, glycoforme alfa: 5~9 résidus sialyl terminaux sont oxidés et chimiquement modifiés en acide 5-acétamido-3,5,7-tridésoxy-7-[(*E*)-(2-oxo-2-{2-[4-({*O*-(6-*O*-phosphono-α-D-mannopyranosyl)-(1→2)-*O*-α-D-mannopyranosyl-(1→6)-*O*-α-D-mannopyranosyl-(1→6)-*O*-[*O*-(6-*O*-phosphono-α-D-mannopyranosyl)-(1→2)-*O*-α-D-mannopyranosyl-(1→3)]-β-D-mannopyranosyl}oxy)butanoyl]hydrazinyl}éthoxy)imino]-β-L-*arabino*-2-heptulo-2,6-pyranosylonique

α-glucosidasa ácida humana modificada, producida en las células ováricas de hamster chino (CHO), glicoforma alfa, conjugada con un glicano hexasacarídico sintético que contiene dos manosa-6-fosfatos (M6Ps) terminales, vía un grupo aminoxi;
prepro-α-glucosidasa lisosomal (EC=3.2.1.20) (humana) (57-952)-péptido, variante natural [Arg^{143},His^{167},Ile^{724}], expresada en las células CHO, glicoforma alfa, con los 5~9 restos sialil terminales están oxidados y químicamente modificados en ácido 5-acetamido-3,5,7-tridesoxi-7-[(*E*)-(2-oxo-2-{2-[4-({*O*-(6-*O*-fosfono-α-D-manopiranosil)-(1→2)-*O*-α-D-manopiranosil-(1→6)-*O*-α-D-manopiranosil-(1→6)-*O*-[*O*-(6-*O*-fosfono-α-D-manopiranosil)-(1→2)-*O*-α-D-manopiranosil-(1→3)]-β-D-manopiranosil}oxi)butanoil]hidrazinil}etoxi)imino]-β-L-*arabino*-2-heptulo-2,6-piranosilónico

Recommended International Nonproprietary Names (Rec. INN): List 81
Dénominations communes internationales recommandées (DCI Rec.): Liste 81
Denominaciones Comunes Internacionales recomendedas (DCI Rec.): Lista 81
(WHO Drug Information, Vol. 33, No. 1, 2019)

p. 49-50	**avoplacelum**	
	avoplacel	*replace the description by the following one*
	avoplacel	*remplacer la description par la suivante*
	avoplacel	*sustitúyase la descripción por la siguiente*

human culture expanded allogenic mesenchymal-like adherent stromal cells for cell-based therapy. Cells are of fetal origin and derived from placentae of healthy donors following a cesarean section. Cells express cell surface markers CD29, CD73, and CD105 and secrete the factors IL-6, IL-8 and MCP-1.

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 de donneuses en bonne santé, à la suite d'une césarienne. Les cellules expriment les marqueurs de surface CD29, CD73 et CD105 et secrètent les facteurs IL-6, IL-8 et MCP-1.

células similares a mesenquimales, estromales, alogénicas, humanas, adherentes, expandidas en cultivo para terapia celular. Las células son de origen fetal y derivadas de placentas de donantes sanas tras una cesárea. Las células expresan los marcadores de superficie CD29, CD73 y CD105, y secretan los factores IL-6, IL-8 y MCP-1.

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.