International Nonproprietary Names for Pharmaceutical Substances (INN)

RECOMMENDED International Nonproprietary Names: List 86

Notice is hereby given that, in accordance with paragraph 7 of the Procedure for the Selection of Recommended International Nonproprietary Names for Pharmaceutical Substances [*Off. Rec. Wld Health Org.*, 1955, **60**, 3 (Resolution EB15.R7); 1969, **173**, 10 (Resolution EB43.R9); Resolution EB115.R4 (EB115/2005/REC/1)], the following names are selected as Recommended International Nonproprietary Names. The inclusion of a name in the lists of Recommended International Nonproprietary Names does not imply any recommendation of the use of the substance in medicine or pharmacy.

Lists of Proposed (1–117) and Recommended (1–78) International Nonproprietary Names can be found in *Cumulative List No. 17, 2017* (available in CD-ROM only).

Dénominations communes internationales des Substances pharmaceutiques (DCI)

Dénominations communes internationales RECOMMANDÉES: Liste 86

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 86

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*

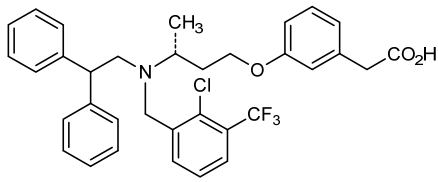
abequolixronum

abequolixron — (3-{(3*R*)-3-[{[2-chloro-3-(trifluoromethyl)phenyl]methyl}(2,2-diphenylethyl)amino]butoxy}phenyl)acetic acid

abéquolixron — acide (3-{(3*R*)-3-[{[2-chloro-3-(trifluorométhyl)phényl]méthyl}(2,2-diphényléthyl)amino]butoxy}phényl)acétique

abecuolixron — ácido (3-{(3*R*)-3-[{[2-cloro-3-(trifluorometil)fenil]metil}(2,2-difeniletil)amino]butoxi}fenil)acético

$C_{34}H_{33}ClF_3NO_3$



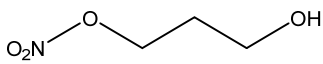
abrucomstatum

abrucomstat — 3-hydroxypropyl nitrate

abrucomstat — nitrate de 3-hydroxypropyle

abrucomstat — nitrato de 3-hidroxipropilo

$C_3H_7NO_4$



acasunlimabum #

acasunlimab — immunoglobulin G1-lambda/kappa, anti-[*Homo sapiens* CD274 (programmed death ligand 1, PDL1, PD-L1, B7 homolog 1, B7H1)], and anti-[*Homo sapiens* TNFRSF9 (tumor necrosis factor receptor (TNFR) superfamily member 9, 4-1BB, CD137)], humanized and *Homo sapiens* monoclonal antibody, bispecific;

	gamma1 heavy chain anti-CD274 humanized (1-450) [VH anti-CD274 humanized (*Homo sapiens* IGHV3-23*01 (87.6%) -(IGHD) -IGHJ1*01 (100%)) CDR-IMGT [8.8.14] (26-33.51-58.97-110) (1-121) -*Homo sapiens* IGHG1*03, G1m3, nG1m1, G1v41 CH2 F1.3, E1.2 (CH1 R120 (218) (122-219), hinge 1-15 (220-234), CH2 L1.3>F (238), L1.2>E (239), D27>A (269) (235-344), CH3 E12 (360), M14 (362), F85.1>L (409) (345-449), CHS K>del (450)) (122-450)], (224-213')-disulfide with lambda light chain anti-CD274 *Homo sapiens* (1'-214') [V-LAMBDA (*Homo sapiens* IGLV3-21*02 (97.9%) -IGLJ2*01 (100%)) CDR-IMGT [6.3.11] (26-31.49-51.88-98) (1'-108') -*Homo sapiens* IGLC2*01 (100%) (109'-214')]; gamma1 heavy chain anti-TNFRSF9 humanized (1''-446'') [VH anti-TNFRSF9 humanized (*Homo sapiens* IGHV3-49*04 (86%) -(IGHD) -IGHJ2*01 (92.9%)) CDR-IMGT [8.7.11] (26-33.51-57.96-106) (1''-117'') -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (214) (118''-215''), hinge 1-15 (216''-230''), CH2 L1.3>F (234), L1.2>E (235), D27>A (265) (231''-340''), CH3 E12 (356), M14 (358), K88>R (409) (341''-445''), CHS K>del (446)) (118''-446'')], (220''-217''')-disulfide with kappa light chain anti-TNFRSF9 humanized (1'''-217''') [V-KAPPA anti-TNFRSF9 humanized (*Homo sapiens* IGKV1-33*01 (85.7%) -IGKJ1*01 (90%)) CDR-IMGT [6.3.12] (27-32.50-52.89-100) (1'''-110''') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (156), V101 (194) (111'''-217''')]; dimer (230-226'':233-229'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa
acasunlimab	immunoglobuline G1-lambda/kappa, anti-[*Homo sapiens* CD274 (ligand 1 de mort programmée, PDL1, PD-L1, homologue 1 de B7, B7H1)] et anti-[*Homo sapiens* TNFRSF9 (membre 9 de la superfamille des récepteurs du facteur de nécrose tumorale, 4-1BB, CD137)], anticorps monoclonal humanisé et *Homo sapiens,* bispécifique; chaîne lourde gamma1 anti-CD274 humanisée (1-450) [VH anti-CD274 humanisé (*Homo sapiens* IGHV3-23*01 (87.6%) -(IGHD) -IGHJ1*01 (100%)) CDR-IMGT [8.8.14] (26-33.51-58.97-110) (1-121) -*Homo sapiens* IGHG1*03, G1m3, nG1m1, G1v41 CH2 F1.3, E1.2 (CH1 R120 (218) (122-219), charnière 1-15 (220-234), CH2 L1.3>F (238), L1.2>E (239), D27>A (269) (235-344), CH3 E12 (360), M14 (362), F85.1>L (409) (345-449), CHS K>del (450)) (122-450)], (224-213')-disulfure avec la chaîne légère lambda anti-CD274 *Homo sapiens* (1'-214') [V-LAMBDA (*Homo sapiens* IGLV3-21*02 (97.9%) -IGLJ2*01 (100%)) CDR-IMGT [6.3.11] (26-31.49-51.88-98) (1'-108') -*Homo sapiens* IGLC2*01 (100%) (109'-214')]; chaîne lourde gamma1 anti-TNFRSF9 humanisée (1''-446'') [VH anti-TNFRSF9 humanisé (*Homo sapiens* IGHV3-49*04 (86%) -(IGHD) -IGHJ2*01 (92.9%)) CDR-IMGT [8.7.11] (26-33.51-57.96-106) (1''-117'') -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (214) (118''-215''), charnière 1-15 (216''-230''), CH2 L1.3>F (234), L1.2>E (235), D27>A (265) (231''-340''), CH3 E12 (356), M14 (358), K88>R (409) (341''-445''), CHS K>del (446)) (118''-446'')], (220''-217''')-disulfure avec la chaîne légère kappa anti-TNFRSF9 humanisée (1'''-217''') [V-KAPPA anti-TNFRSF9 humanisé (*Homo sapiens* IGKV1-33*01 (85.7%) -IGKJ1*01 (90%)) CDR-IMGT [6.3.12] (27-32.50-52.89-100) (1'''-110''') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (156), V101 (194) (111'''-217''')]; dimère (230-226'':233-229'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa
acasunlimab	inmunoglobulina G1-lambda/kappa, anti-[*Homo sapiens* CD274 (ligando 1 de muerte programada, PDL1, PD-L1, homólogo 1 de B7, B7H1)] y anti-[*Homo sapiens* TNFRSF9 (miembro 9 de la superfamilia de los receptores del factor de necrosis tumoral, 4-1BB, CD137)], anticuerpo monoclonal humanizado y *Homo sapiens,* biespecífico;

cadena pesada gamma1 anti-CD274 humanizada (1-450) [VH anti-CD274 humanizado (*Homo sapiens* IGHV3-23*01 (87.6%) -(IGHD) -IGHJ1*01 (100%)) CDR-IMGT [8.8.14] (26-33.51-58.97-110) (1-121) -*Homo sapiens* IGHG1*03, G1m3, nG1m1, G1v41 CH2 F1.3, E1.2 (CH1 R120 (218) (122-219), bisagra 1-15 (220-234), CH2 L1.3>F (238), L1.2>E (239), D27>A (269) (235-344), CH3 E12 (360), M14 (362), F85.1>L (409) (345-449), CHS K>del (450)) (122-450)], (224-213')-disulfuro con la cadena ligera lambda anti-CD274 *Homo sapiens* (1'-214') [V-LAMBDA (*Homo sapiens* IGLV3-21*02 (97.9%) -IGLJ2*01 (100%)) CDR-IMGT [6.3.11] (26-31.49-51.88-98) (1'-108') -*Homo sapiens* IGLC2*01 (100%) (109'-214')];
cadena pesada gamma1 anti-TNFRSF9 humanizada (1"-446") [VH anti-TNFRSF9 humanizado (*Homo sapiens* IGHV3-49*04 (86%) -(IGHD) -IGHJ2*01 (92.9%)) CDR-IMGT [8.7.11] (26-33.51-57.96-106) (1"-117") -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (214) (118"-215"), bisagra 1-15 (216"-230"), CH2 L1.3>F (234), L1.2>E (235), D27>A (265) (231"-340"), CH3 E12 (356), M14 (358), K88>R (409) (341"-445"), CHS K>del (446)) (118"-446")], (220"-217"')-disulfuro con la cadena ligera kappa anti-TNFRSF9 humanizada (1"'-217"') [V-KAPPA anti-TNFRSF9 humanizado (*Homo sapiens* IGKV1-33*01 (85.7%) -IGKJ1*01 (90%)) CDR-IMGT [6.3.12] (27-32.50-52.89-100) (1"'-110"') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (156), V101 (194) (111"'-217"')]; dímero (230-226":233-229")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada (anti-CD274)

```
EVQLLEPGGG LVQPGGSLRL SCEASGSTFS TYAMSWVRQA PGKGLEWVSG  50
FSGSGGFTFY ADSVRGRFTI SRDSSKNTLF LQMSSLRAED TAVYYCAIPA 100
RGYNYGSFQH WGQGTLVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200
TYICNVNHKP SNTKVDKRVE PKSCDKTHTC PPCPAPEFEG GPSVFLFPPK 250
PKDTLMISRT PEVTCVVVAV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY 300
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP 350
QVYTLPPSRE EMTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP 400
VLDSDGSFLL YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG 450
```

Heavy chain / Chaîne lourde / Cadena pesada (anti-TNFRSF9)

```
EVQLVESGGG LVQPGRSLRL SCTASGFSLN DYWMSWVRQA PGKGLEWVGY  50
IDVGGSLYYA ASVKGRFTIS RDDSKSIAYL QMNSLKTEDT AVYYCARGGL 100
TYGFDLWGQG TLVTVSSAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF 150
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC 200
NVNHKPSNTK VDKRVEPKSC DKTHTCPPCP APEFEGGPSV FLFPPKPKDT 250
LMISRTPEVT CVVVAVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT 350
LPPSREEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS 400
DGSFFLYSRL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPG     446
```

Light chain / Chaîne légère / Cadena ligera (anti-CD274)

```
SYVLTQPPSV SVAPGQTARI TCGGNNIGSK SVHWYQQKPG QAPVLVVYDD  50
NDRPSGLPER FSGSNSGNTA TLTISRVEAG DEADYYCQVW DSSSDHVVFG 100
GGTKLTVLGQ PKAAPSVTLF PPSSEELQAN KATLVCLISD FYPGAVTVAW 150
KADSSPVKAG VETTTPSKQS NNKYAASSYL SLTPEQWKSH RSYSCQVTHE 200
GSTVEKTVAP TECS                                        214
```

Light chain / Chaîne légère / Cadena ligera (anti-TNFRSF9)

```
DIVMTQSPSS LSASVGDRVT ITCQASEDIS SYLAWYQQKP GKAPKRLIYG  50
ASDLASGVPS RFSASGSGTD YTFTISSLQP EDIATYYCHY YATISGLGVA 100
FGGGTKVEIK RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ 150
WKVDNALQSG NSQESVTEQD SKDSTYSLSS TLTLSKADYE KHKVYACEVT 200
HQGLSSPVTK SFNRGEC                                     217
```

Post-translational modifications

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

Intra-H (C23-C104) 22-96 148-204 265-325 371-429
22"-95" 144"-200" 261"-321" 367"-425"

Intra-L (C23-C104) 22'-87' 136'-195'
23'"-88'" 137'"-197'"

Inter-H-L (h 5-CL 126) 224-213' 220"-217'"

Inter-H-H (h 11, h 14) 230-226" 233-229"

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

H CH2 N84.4:
301, 297"

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

acavameranum #

acavameran — messenger RNA (mRNA), 5' capped, encoding tumour necrosis factor ligand superfamily member 4 (TNFSF4, OX40 ligand, OX40L, glycoprotein Gp34), flanked by 5' and 3' untranslated regions and a 3' polyA tail; contains N1-methylpseudouridine instead of uridine (*all*-U>$m^1\Psi$).

acavaméran — ARN messager (ARNm), protégé par une coiffe en 5', codant le membre 4 de la superfamille des ligands du facteur de nécrose tumorale (TNFSF4; ligand OX40, OX40L, glycoprotéine Gp34), flanqué de régions non traduites en 5' et 3' et d'une queue polyA en 3'; contient de la N1-méthylpseudouridine au lieu de l'uridine (*all*-U>$m^1\Psi$).

acavamerán — RNA mensajero (mRNA), protegido en 5', que codifica para el miembro 4 de la superfamilia de ligandos del factor de necrosis tumoral (TNFSF4, ligando de OX40, OX40L, glicoproteína Gp34), flanqueado por regiones no traducidas en 5' y 3' y una cola polyA en 3'; contiene N1-metilpseudouridina en lugar de uridina (*all*-U>$m^1\Psi$).

acazicolceptum #

acazicolcept — human inducible T-cell co-stimulator ligand (ICOS ligand) N-terminal fragment (1-122) (variant (N^{52}>H, N^{57}>Y, Q^{100}>R), fused via peptidyl linker ^{123}GGGGSGGGGS^{132} to a human immunoglobulin G1 Fc fragment (133-363) variant (L^{151}>A, L^{152}>E, G^{154}>A, C-terminal K^{364} deleted), dimer, glycosylated, produced in Chinese hamster ovary (CHO) cells;
[N^{52}>H, N^{57}>Y, Q^{100}>R] human inducible T-cell co-stimulator ligand (ICOS ligand, ICOSL, CD275) N-terminal fragment (1-122) fused via a $(G_4S)_2$ linker (123-132) to a human immunoglobulin G1 C-terminal K>del Fc fragment (133-363) [*Homo sapiens* IGHG1*01; hinge 133-147; CH2 148-257 (L151A, L152E, G154A); CH3 258-362; CHS 363], dimer (143-143':146-146')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

acazicolcept — fragment N-terminal (1-122) du ligand costimulateur de la cellule T inductible humaine (ligand ICOS) (variant (N^{52}>H, N^{57}>Y, Q^{100}>R), fusionné via un linker peptidique ^{123}GGGGSGGGGS^{132} à un fragment Fc (133-363) de l'immunoglobuline G1 humaine, variant (L^{151}>A, L^{152}>E, G^{154}>A, C-terminal K^{364} supprimé), dimère, glycosylé, produit dans des cellules ovariennes de hamster chinois (CHO);
fragment N-terminal (1-122) du ligand costimulateur de la cellule T inductible humaine (ligand d'ICOS, ICOSL, CD275) [N^{52}>H, N^{57}>Y, Q^{100}>R] fusionné via un linker $(G_4S)_2$ (123-132) au fragment Fc (133-363) C-terminal K>del de l'immunoglobuline G1 humaine [*Homo sapiens* IGHG1*01; charnière 133-147; CH2 148-257 (L151A, L152E, G154A); CH3 258-362; CHS 363], dimère (143-143':146-146')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

acazicolcept — ligando coestimulador de las células T inducible humano (ligando ICOS) fragmentoN-terminal (1-122) (variante (N^{52}>H, N^{57}>Y, Q^{100}>R), fusionado a través de un enlace peptidil ^{123}GGGGSGGGGS^{132} al fragmento de una inmunoglobulina humana G1 Fc (133-363) variante (L^{151}>A, L^{152}>E, G^{154}>A, C-terminal K^{364} eliminada), dímero, glicosilado, producido en células ováricas de hámster chino (CHO);

[N^{52}>H, N^{57}>Y, Q^{100}>R] ligando humano de coestimulador inducible de células T (ligando de ICOS, ICOSL, CD275), fragmento N-terminal (1-122), fusionado a través de un péptido $(G_4S)_2$ (123-132) con un fragmento Fc C-terminal K>del de la inmunoglobulina G1 humana (133-363) [*Homo sapiens* IGHG1*01; bisagra 133-147; CH2 148-257 (L151A, L152E, G154A); CH3 258-362; CHS 363], dímero (143-143':146-146')-bisdisulfuro, producido en células ováricas de hámster chino (CHO), glicoforma alfa

Sequence / Séquence / Secuencia

```
DTQEKEVRAM VGSDVELSCA CPEGSRFDLN DVYVYWQTSE SKTVVTYHIP    50
QHSSLEYVDS RYRNRALMSP AGMLRGDFSL RLFNVTPQDE QKFHCLVLSR   100
SLGFQEVLSV EVTLHVAANF SVGGGGSGGG GSEPKSSDKT HTCPPCPAPE   150
AEGAPSVFLF PPKPKDTLMI SRTPEVTCVV VDVSHEDPEV KFNWYVDGVE   200
VHNAKTKPRE EQYNSTYRVV SVLTVLHQDW LNGKEYKCKV SNKALPAPIE   250
KTISKAKGQP REPQVYTLPP SRDELTKNQV SLTCLVKGFY PSDIAVEWES   300
NGQPENNYKT TPPVLDSDGS FFLYSKLTVD KSRWQQGNVF SCSVMHEALH   350
NHYTQKSLSL SPG                                           363
```

Mutation sites / Sites de mutation / Posiciones de mutación
N52, N52'>H, N57, N57'>Y, Q100, Q100'>R, L151, L151'>A, L152, L152'>E, G154, G154'>A
K364, K364'>del

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posición del puentes disulfuro

intra-ICOSL	19-95		intra-Fc	178-238	284-342
	19'-95'			178'-238'	284'-342'
inter-Fc	143-143'	146-146'			

Glycosylation sites / Sites de glycosylation / Posiciones de glicosilación
ICOSL: N84, N119, N84', N119';
Fc: N214, N214'

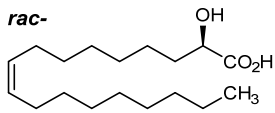
acidum idroxioleicum

idroxioleic acid — *rac*-(2*R*,9*Z*)-2-hydroxyoctadec-9-enoic acid

acide idroxioléique — acide *rac*-(2*R*,9*Z*)-2-hydroxyoctadéc-9-énoïque

ácido idroxioleico — ácido *rac*-(2*R*,9*Z*)-2-hidroxioctadec-9-enoico

$C_{18}H_{34}O_3$



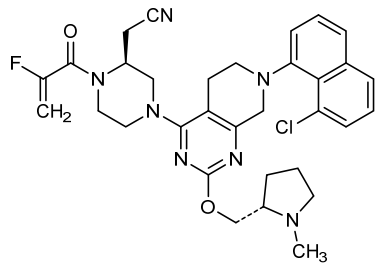
adagrasibum

adagrasib — {(2*S*)-4-[7-(8-chloronaphthalen-1-yl)-2-{[(2*S*)-1-methylpyrrolidin-2-yl]methoxy}-5,6,7,8-tetrahydropyrido[3,4-*d*]pyrimidin-4-yl]-1-(2-fluoroprop-2-enoyl)piperazin-2-yl}acetonitrile

adagrasib — {(2*S*)-4-[7-(8-chloronaphtalén-1-yl)-2-{[(2*S*)-1-méthylpyrrolidin-2-yl]méthoxy}-5,6,7,8-tétrahydropyrido[3,4-*d*]pyrimidin-4-yl]-1-(2-fluoroprop-2-énoyl)pipérazin-2-yl}acétonitrile

adagrasib — {(2*S*)-4-[7-(8-cloronaftalen-1-il)-2-{[(2*S*)-1-metilpirrolidin-2-il]metoxi}-5,6,7,8-tetrahidropirido[3,4-*d*]pirimidin-4-il]-1-(2-fluoroprop-2-enoil)piperazin-2-il}acetonitrilo

$C_{32}H_{35}ClFN_7O_2$



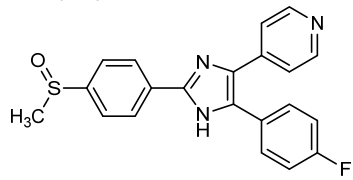
adezmapimodum

adezmapimod — *rac*-4-[5-(4-fluorophenyl)-2-{4-[(*R*)-methanesulfinyl]phenyl}-1*H*-imidazol-4-yl]pyridine

adezmapimod — *rac*-4-[5-(4-fluorophényl)-2-{4-[(*R*)-méthanesulfinyl]phényl}-1*H*-imidazol-4-yl]pyridine

adezmapimod — *rac*-4-[5-(4-fluorofenil)-2-{4-[(*R*)-metanosulfinil]fenil}-1*H*-imidazol-4-il]piridina

$C_{21}H_{16}FN_3OS$



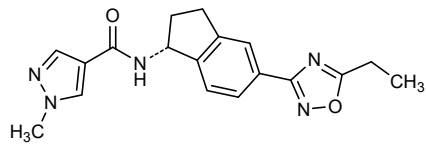
aficamtenum

aficamten — *N*-[(1*R*)-5-(5-ethyl-1,2,4-oxadiazol-3-yl)-2,3-dihydro-1*H*-inden-1-yl]-1-methyl-1*H*-pyrazole-4-carboxamide

aficamtène — *N*-[(1*R*)-5-(5-éthyl-1,2,4-oxadiazol-3-yl)-2,3-dihydro-1*H*-indén-1-yl]-1-méthyl-1*H*-pyrazole-4-carboxamide

aficamten — *N*-[(1*R*)-5-(5-etil-1,2,4-oxadiazol-3-il)-2,3-dihidro-1*H*-inden-1-il]-1-metil-1*H*-pirazol-4-carboxamida

$C_{18}H_{19}N_5O_2$

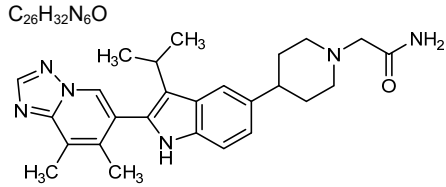


afimetoranum

afimetoran — 2-{4-[2-(7,8-dimethyl[1,2,4]triazolo[1,5-*a*]pyridin-6-yl)-3-(propan-2-yl)-1*H*-indol-5-yl]piperidin-1-yl}acetamide

afimétoran — 2-{4-[2-(7,8-diméthyl[1,2,4]triazolo[1,5-*a*]pyridin-6-yl)-3-(propan-2-yl)-1*H*-indol-5-yl]pipéridin-1-yl}acétamide

afimetorán — 2-{4-[2-(7,8-dimetil[1,2,4]triazolo[1,5-*a*]piridin-6-il)-3-(propan-2-il)-1*H*-indol-5-il]piperidin-1-il}acetamida



alomfilimabum #

alomfilimab	immunoglobulin G1-kappa, anti-[*Homo sapiens* ICOS (inducible T-cell costimulatory, activation-inducible lymphocyte immunomediatory molecule, AILIM, CD278)], *Homo sapiens* monoclonal antibody; gamma1 heavy chain *Homo sapiens* (1-454) [VH (*Homo sapiens* IGHV3-20*04 (94.9%) -(IGHD) -IGHJ4*01 (92.9%) T122>I (118)) CDR-IMGT [8.8.17] (26-33.51-58.97-113) (1-124) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 (CH1 K120 (221) (125-222), hinge 1-15 (223-237), CH2 (238-347), CH3 D12 (363), L14 (365) (348-452), CHS (453-454)) (125-454)], (227-215')-disulfide with kappa light chain *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (92.7%) -IGKJ3*01 (100%)) CDR-IMGT [7.3.9] (27-33.51-53.90-98) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (154), V101 (192) (109'-215')]; dimer (233-233'':236-236'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa
alomfilimab	immunoglobuline G1-kappa, anti-[*Homo sapiens* ICOS (costimulateur inductible du lymphocyte T, molécule immunomédiateur lymphocytaire inductible par activation, AILIM, CD278)], anticorps monoclonal *Homo sapiens*; chaîne lourde gamma1 *Homo sapiens* (1-454) [VH (*Homo sapiens* IGHV3-20*04 (94.9%) -(IGHD) -IGHJ4*01 (92.9%) T122>I (118)) CDR-IMGT [8.8.17] (26-33.51-58.97-113) (1-124) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 (CH1 K120 (221) (125-222), charnière 1-15 (223-237), CH2 (238-347), CH3 D12 (363), L14 (365) (348-452), CHS (453-454)) (125-454)], (227-215')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (92.7%) -IGKJ3*01 (100%)) CDR-IMGT [7.3.9] (27-33.51-53.90-98) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (154), V101 (192) (109'-215')]; dimère (233-233'':236-236'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa
alomfilimab	inmunoglobulina G1-kappa, anti-[*Homo sapiens* ICOS (coestimulador inducible del linfocito T, molécula inmunomediadora linfocitaria inducible por activación, AILIM, CD278)], anticuerpo monoclonal *Homo sapiens*; cadena pesada gamma1 *Homo sapiens* (1-454) [VH (*Homo sapiens* IGHV3-20*04 (94.9%) -(IGHD) -IGHJ4*01 (92.9%) T122>I (118)) CDR-IMGT [8.8.17] (26-33.51-58.97-113) (1-124) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 (CH1 K120 (221) (125-222), bisagra 1-15 (223-237), CH2 (238-347), CH3 D12 (363), L14 (365) (348-452), CHS (453-454)) (125-454)], (227-215')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (92.7%) -IGKJ3*01 (100%)) CDR-IMGT [7.3.9] (27-33.51-53.90-98) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (154), V101 (192) (109'-215')]; dímero (233-233'':236-236'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG VVRPGGSLRL SCVASGVTFD DYGMSWVRQA PGKGLEWVSG  50
INWNGGDTDY SDSVKGRFTI SRDNAKNSLY LQMNSLRAED TALYYCARDF 100
YGSGSYYHVP FDYWGQGILV TVSSASTKGP SVFPLAPSSK STSGGTAALG 150
CLVKDYFPEP VTVSWNSGAL TSGVHTFPAV LQSSGLYSLS SVVTVPSSSL 200
GTQTYICNVN HKPSNTKVDK KVEPKSCDKT HTCPPCPAPE LLGGPSVFLF 250
PPKPKDTLMI SRTPEVTCVV VDVSHEDPEV KFNWYVDGVE VHNAKTKPRE 300
EQYNSTYRVV SVLTVLHQDW LNGKEYKCKV SNKALPAPIE KTISKAKGQP 350
REPQVYTLPP SRDELTKNQV SLTCLVKGFY PSDIAVEWES NGQPENNYKT 400
TPPVLDSDGS FFLYSKLTVD KSRWQQGNVF SCSVMHEALH NHYTQKSLSL 450
SPGK                                                    454
```

Light chain / Chaîne légère / Cadena ligera

```
EIVLTQSPGT LSLSPGERAT LSCRASQSVS RSYLAWYQQK RGQAPRLLIY  50
GASSRATGIP DRFSGDGSGT DFTLSISRLE PEDFAVYYCH QYDMSPFTFG 100
PGTKVDIKRT 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) 22-96 151-207 268-328 374-432
22"-96" 151"-207" 268"-328" 374"-432"
Intra-L (C23-C104) 23'-89' 135'-195'
23'"-89'" 135'"-195'"
Inter-H-L (h 5-CL 126) 227-215' 227"-215'"
Inter-H-H (h 11, h 14) 233-233" 236-236"

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.

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2:
454, 454"

amlitelimabum #

amlitelimab — immunoglobulin G4-kappa, anti-[*Homo sapiens* TNFSF4 (tumor necrosis factor (TNF) superfamily member 4, OX40 ligand, OX-40L, TAX transcriptionally-activated glycoprotein 1, TXGP1, CD252)], monoclonal antibody;
gamma4 heavy chain (1-454) [VH (*Homo sapiens* IGHV3-23*04 (89.8%) -(IGHD) -IGHJ6*01 (100%)) CDR-IMGT [8.8.20] (26-33.51-58.97-116) (1-127)-*Homo sapiens* IGHG4*01, G4v5 h P10, G4v3 E1.2 (CH1 (128-225), hinge 1-12 S10>P (235) (226-237), CH2 L1.2>E (242) (238-347), CH3 (348-452), CHS (453-454)) (128-454)], (210-214')-disulfide with kappa light chain (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (96.8%) -IGKJ3*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (233-233":236-236")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

amlitélimab — immunoglobuline G4-kappa, anti-[*Homo sapiens* TNFSF4 (membre 4 de la superfamille des ligands du facteur de nécrose tumorale, ligand de OX40, OX40L, glycoprotéine 1 activée transcriptionellement par TAX, TXGP1, CD252)], anticorps monoclonal;
chaîne lourde gamma4 (1-454) [VH (*Homo sapiens* IGHV3-23*04 (89.8%) -(IGHD) -IGHJ6*01 (100%)) CDR-IMGT [8.8.20] (26-33.51-58.97-116) (1-127)-*Homo sapiens* IGHG4*01, G4v5 h P10, G4v3 E1.2 (CH1 (128-225), charnière 1-12 S10>P (235) (226-237), CH2 L1.2>E (242) (238-347), CH3 (348-452), CHS (453-454)) (128-454)], (210-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (96.8%) -IGKJ3*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (233-233":236-236")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

amlitelimab

inmunoglobulina G4-kappa, anti-[*Homo sapiens* TNFSF4 (miembro 4 de la superfamilia de los ligandos del factor de necrosis tumoral, ligando de OX40, OX40L, glicoproteína 1 activada transcripcionalmente por TAX, TXGP1, CD252)], anticuerpo monoclonal;
cadena pesada gamma4 (1-454) [VH (*Homo sapiens* IGHV3-23*04 (89.8%) -(IGHD) -IGHJ6*01 (100%)) CDR-IMGT [8.8.20] (26-33.51-58.97-116) (1-127)-*Homo sapiens* IGHG4*01, G4v5 h P10, G4v3 E1.2 (CH1 (128-225), bisagra 1-12 S10>P (235) (226-237), CH2 L1.2>E (242) (238-347), CH3 (348-452), CHS (453-454)) (128-454)], (210-214')-disulfuro con la cadena ligera kappa (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (96.8%) -IGKJ3*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (233-233'':236-236'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAASGFTFS NYAMNWVRQA PGKGLEWVST  50
ISGSGGATRY ADSVKGRFTI SRDNSRNTVY LQMNSLRVED TAVFYCTKDR 100
LIMATVRGPY YYGMDVWGQG TTVTVSSAST KGPSVFPLAP CSRSTSESTA 150
ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS 200
SSLGTKTYTC NVDHKPSNTK VDKRVESKYG PPCPPCPAPE FEGGPSVFLF 250
PPKPKDTLMI SRTPEVTCVV VDVSQEDPEV QFNWYVDGVE VHNAKTKPRE 300
EQFNSTYRVV SVLTVLHQDW LNGKEYKCKV SNKGLPSSIE KTISKAKGQP 350
REPQVYTLPP SQEEMTKNQV SLTCLVKGFY PSDIAVEWES NGQPENNYKT 400
TPPVLDSDGS FFLYSRLTVD KSRWQEGNVF SCSVMHEALH NHYTQKSLSL 450
SLGK                                                    454
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Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCRASQSIS SYLNWYQQKP GKAPNLLIYA  50
ASSLQSGVPS RFSGSGSETD FTLTISSLQP EDFATYYCQQ SHSVSFTFGP 100
GTKVDIKRTV 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	268-328	374-432
	22''-96''	154''-210''	268''-328''	374''-432''
Intra-L (C23-C104)	23'-88'	134'-194'		
	23'''-88'''	134'''-194''		
Inter-H-L (CH1 10-CL 126)	141-214'	141''-214'''		
Inter-H-H (h 8, h 11)	233-233''	236-236''		

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.

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2:
454, 454''

anbenitamabum #

anbenitamab

immunoglobulin G1-kappa, anti-[*Homo sapiens* ERBB2 (epidermal growth factor receptor 2, receptor tyrosine protein kinase erbB-2, EGFR2, HER2, HER-2, p185cerbB2, NEU, CD340)], humanized monoclonal antibody, biparatopic, tetravalent;
gamma1 heavy chain anti-ERBB2 domain II humanized (1-449) [VH anti-ERBB2 domain II (*Homo sapiens* IGHV3-66*01 (78.8%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.12] (26-33.51-58.97-108) (1-119) -*Homo sapiens* IGHG1*01, G1m7,1, G1v32 CH3 W22 (CH1 K120 (217) (120-217), hinge 1-15 (218-232), CH2 (233-342), CH3 D12 (358), L14 (360), T22>W (368), K88>A (411) (343-447), CHS (448-449)) (120-449)], (222-214')-disulfide with kappa light chain anti-ERBB2 humanized (1'-214') [V-KAPPA anti-ERBB2 humanized (*Homo sapiens* IGKV1-39*01 (86.3%) -IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (194) (108'-214')];

gamma1 heavy chain anti-ERBB2 domain IV humanized (1''-450'') [VH anti-ERBB2 domain IV (*Homo sapiens* IGHV3-66*01 (81.6%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1''-120'') -*Homo sapiens* IGHG1*01, G1m7,1, G1v33 CH3 S22, A24, V86 (CH1 K120 (217) (121''-218''), hinge 1-15 (219''-233''), CH2 (234''-343''), CH3 D12 (359), L14 (361) T22>S (369), L24>A (371), F85.1>K (408), Y86>V (410) (344''-448''), CHS (449''-450'')) (121''-450'')], (223''-214''')-disulfide with kappa light chain anti-ERBB2 humanized (1'''-214''') [V-KAPPA anti-ERBB2 humanized (*Homo sapiens* IGKV1-39*01 (86.3%) -IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'''-107''') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (194) (108'''-214''')]; dimer (228-229'':231-232'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

anbénitamab

immunoglobuline G1-kappa, anti-[*Homo sapiens* ERBB2 (récepteur 2 du facteur de croissance épidermique, récepteur tyrosine-protéine kinase erbB2, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], anticorps monoclonal humanisé, biparatopique, tétravalent;
chaîne lourde gamma1 anti-ERBB2 domaine II humanisée (1-449) [VH anti-ERBB2 domain II (*Homo sapiens* IGHV3-66*01 (78.8%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.12] (26-33.51-58.97-108) (1-119) -*Homo sapiens* IGHG1*01, G1m7,1, G1v32 CH3 W22 (CH1 K120 (217) (120-217), charnière 1-15 (218-232), CH2 (233-342), CH3 D12 (358), L14 (360), T22>W (368), K88>A (411) (343-447), CHS (448-449)) (120-449)], (222-214')-disulfure avec la chaîne légère lambda anti-ERBB2 humanisée (1'-214') [V-KAPPA anti-ERBB2 (*Homo sapiens* IGKV1-39*01 (86.3%) -IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (194) (108'-214')];
chaîne lourde gamma1 anti-ERBB2 domaine IV humanisée (1''-450'') [VH anti-ERBB2 domaine IV (*Homo sapiens* IGHV3-66*01 (81.6%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1''-120'') -*Homo sapiens* IGHG1*01, G1m7,1, G1v33 CH3 S22, A24, V86 (CH1 K120 (217) (121''-218''), charnière 1-15 (219''-233''), CH2 (234''-343''), CH3 D12 (359), L14 (361) T22>S (369), L24>A (371), F85.1>K (408), Y86>V (410) (344''-448''), CHS (449''-450'')) (121''-450'')], (223''-214''')-disulfure avec la chaîne légère kappa anti-ERBB2 humanisée (1'''-214''') [V-KAPPA anti-ERBB2 (*Homo sapiens* IGKV1-39*01 (86.3%) -IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'''-107''') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (194) (108'''-214''')]; dimère (228-229'':231-232'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

anbenitamab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* ERBB2 (receptor 2 del factor de crecimiento epidérmico, receptor tirosina-proteína kinasa erbB2, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], anticuerpo monoclonal humanizado, biparatópico, tetravalente;
cadena pesada gamma1 anti-ERBB2 dominio II humanizada (1-449) [VH anti-ERBB2 dominio II (*Homo sapiens* IGHV3-66*01 (78.8%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.12] (26-33.51-58.97-108) (1-119) -*Homo sapiens* IGHG1*01, G1m7,1, G1v32 CH3 W22 (CH1 K120 (217) (120-217), bisagra 1-15 (218-232), CH2 (233-342), CH3 D12 (358), L14 (360), T22>W (368), K88>A (411) (343-447), CHS (448-449)) (120-449)], (222-214')-disulfuro con la cadena ligera lambda anti-ERBB2 humanizada (1'-214') [V-KAPPA anti-ERBB2 (*Homo sapiens* IGKV1-39*01 (86.3%) -IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (194) (108'-214')];

cadena pesada gamma1 anti-ERBB2 domnio IV humanizada (1"-450") [VH anti-ERBB2 dominio IV (*Homo sapiens* IGHV3-66*01 (81.6%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1"-120") -*Homo sapiens* IGHG1*01, G1m7,1, G1v33 CH3 S22, A24, V86 (CH1 K120 (217) (121"-218"), bisagra 1-15 (219"-233"), CH2 (234"-343"), CH3 D12 (359), L14 (361) T22>S (369), L24>A (371), F85.1>K (408), Y86>V (410) (344"-448"), CHS (449"-450")) (121"-450")], (223"-214"')-disulfuro con la cadena ligera kappa anti-ERBB2 humanizada (1"'-214"') [V-KAPPA anti-ERBB2 (*Homo sapiens* IGKV1-39*01 (86.3%) -IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1"'-107"') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (194) (108"'-214"')]; dímero (228-229":231-232")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada (anti-ERBB2 domain II)

```
EVQLVESGGG LVQPGGSLRL SCAASGFTFT DYTMDWVRQA PGKGLEWVAD  50
VNPNSGGSIY NQRFKGRFTL SVDRSKNTLY LQMNSLRAED TAVYYCARNL 100
GPSFYFDYWG QGTLVTVSSA STKGPSVFPL APSSKSTSGG TAALGCLVKD 150
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY 200
ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP CPAPELLGGP SVFLFPPKPK 250
DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS 300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV 350
YTLPPSRDEL TKNQVSLWCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL 400
DSDGSFFLYS ALTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK  449
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Heavy chain / Chaîne lourde / Cadena pesada (anti-ERBB2 domain IV)

```
EVQLVESGGG LVQPGGSLRL SCAASGFNIK DTYIHWVRQA PGKGLEWVAR  50
IYPTNGYTRY ADSVKGRFTI SADTSKNTAY LQMNSLRAED TAVYYCSRWG 100
GDGFYAMDYW GQGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSRDE LTKNQVSLSC AVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFKLV SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK 450
```

Light chain / Chaîne légère / Cadena ligera (anti-ERBB2)

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

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 146-202 263-323 369-427
22"-96" 147"-203" 264"-324" 370"-428"
Intra-L (C23-C104) 23'-88' 134'-194'
23"'-88"' 134"'-194"'
Inter-H-L (h5-CL 126) 222-214' 223"-214"'
Inter-H-H (h11, h14) 228-229" 231-232"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
299, 300"
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 / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2:
449, 450"

ansuvimabum #
ansuvimab

immunoglobulin G1-kappa, anti-[*Zaire ebolavirus* (Zaire Ebola virus (EBOV)) envelope glycoprotein subunit 1 (GP1) glycan cap domain], monoclonal antibody;

	gamma1 heavy chain (1-449) [VH (*Homo sapiens* IGHV3-13*01 (78.4%) -(IGHD) -IGHJ5*01 (92.9%) T122>I (113)) CDR-IMGT [8.7.13] (26-33.51-57.96-108) (1-119) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 (CH1 K120 (216) (120-217), hinge 1-15 (218-232), CH2 (233-342), CH3 D12 (358), L14 (360) (343-447), CHS (448-449)) (120-449)], (222-214')-disulfide with kappa light chain (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-27*01 (87.4%) -IGKJ4*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (228-228'':231-231'')-bisdisulfide, produced in a Chinese hamster ovary (CHO)-DG44 cell line, glycoform alfa
ansuvimab	immunoglobuline G1-kappa, anti-[coiffe glycosylée de la sous-unité 1 de la glycoprotéine d'enveloppe (GP1) de *Zaire ebolavirus* (virus Ebola Zaïre (EBOV))], anticorps monoclonal; chaîne lourde gamma1 (1-449) [VH (*Homo sapiens* IGHV3-13*01 (78.4%) -(IGHD) -IGHJ5*01 (92.9%) T122>I (113)) CDR-IMGT [8.7.13] (26-33.51-57.96-108) (1-119) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 (CH1 K120 (216) (120-217), charnière 1-15 (218-232), CH2 (233-342), CH3 D12 (358), L14 (360) (343-447), CHS (448-449)) (120-449)], (222-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-27*01 (87.4%) -IGKJ4*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (228-228'':231-231'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO) lignée cellulaire CHO-DG44, glycoforme alfa
ansuvimab	inmunoglobulina G1-kappa, anti-[cubierta glicosilada de la subunidad 1 de la glicoproteína de envoltura (GP1) de *Zaire ebolavirus* (virus Ebola Zaïre (EBOV))], anticuerpo monoclonal; cadena pesada gamma1 (1-449) [VH (*Homo sapiens* IGHV3-13*01 (78.4%) -(IGHD) -IGHJ5*01 (92.9%) T122>I (113)) CDR-IMGT [8.7.13] (26-33.51-57.96-108) (1-119) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 (CH1 K120 (216) (120-217), bisagra 1-15 (218-232), CH2 (233-342), CH3 D12 (358), L14 (360) (343-447), CHS (448-449)) (120-449)], (222-214')-disulfuro con la cadena ligera kappa (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-27*01 (87.4%) -IGKJ4*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (228-228'':231-231'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular CHO-DG44, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LIQPGGSLRL SCAASGFALR MYDMHWVRQT IDKRLEWVSA  50
VGPSGDTTYA DSVKGRFAVS RENAKNSLSL QMNSLTAGDT AIYYCVRSDR 100
GVAGLFDSWG QGILVTVSSA STKGPSVFPL APSSKSTSGG TAALGCLVKD 150
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY 200
ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP CPAPELLGGP SVFLFPPKPK 250
DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS 300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV 350
YTLPPSRDEL TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL 400
DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK  449
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRIT ITCRASQAFD NYVAWYQQRP GKVPKLLISA  50
ASALHAGVPS RFSGSGSGTH FTLTISSLQP EDVATYYCQN YNSAPLTFGG 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) 22-95 146-202 263-323 369-427
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 / 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.

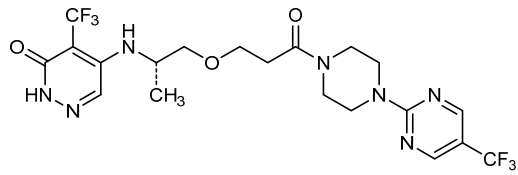
atamparibum

atamparib — 5-{[(2*S*)-1-(3-oxo-3-{4-[5-(trifluoromethyl)pyrimidin-2-yl]piperazin-1-yl}propoxy)propan-2-yl]amino}-4-(trifluoromethyl)pyridazin-3(2*H*)-one

atamparib — 5-{[(2*S*)-1-(3-oxo-3-{4-[5-(trifluorométhyl)pyrimidin-2-yl]pipérazin-1-yl}propoxy)propan-2-yl]amino}-4-(trifluorométhyl)pyridazin-3(2*H*)-one

atamparib — 5-{[(2*S*)-1-(3-oxo-3-{4-[5-(trifluorometil)pirimidin-2-il]piperazin-1-il}propoxi)propan-2-il]amino}-4-(trifluorometil)piridazin-3(2*H*)-ona

$C_{20}H_{23}F_6N_7O_3$



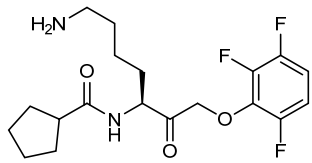
atuzaginstatum

atuzaginstat — *N*-[(3*S*)-7-amino-2-oxo-1-(2,3,6-trifluorophenoxy)heptan-3-yl]cyclopentanecarboxamide

atuzaginstat — *N*-[(3*S*)-7-amino-2-oxo-1-(2,3,6-trifluorophénoxy)heptan-3-yl]cyclopentanecarboxamide

atuzaginstat — *N*-[(3*S*)-7-amino-2-oxo-1-(2,3,6-trifluorofenoxi)heptan-3-il]ciclopentanocarboxamida

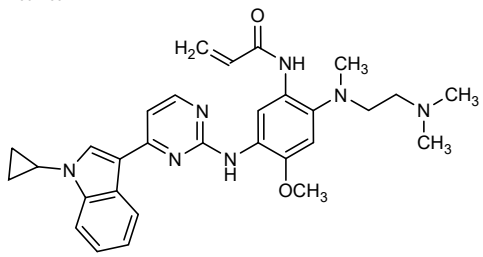
$C_{19}H_{25}F_3N_2O_3$



aumolertinibum

aumolertinib	*N*-(5-{[4-(1-cyclopropyl-1*H*-indol-3-yl)pyrimidin-2-yl]amino}-2-{[2-(dimethylamino)ethyl](methyl)amino}-4-methoxyphenyl)prop-2-enamide
aumolertinib	*N*-(5-{[4-(1-cyclopropyl-1*H*-indol-3-yl)pyrimidin-2-yl]amino}-2-{[2-(diméthylamino)éthyl](méthyl)amino}-4-méthoxyphényl)prop-2-énamide
aumolertinib	*N*-(5-{[4-(1-ciclopropil-1*H*-indol-3-il)pirimidin-2-il]amino}-2-{[2-(dimetilamino)etil](metil)amino}-4-metoxifenil)prop-2-enamida

$C_{30}H_{35}N_7O_2$



bevufenogenum nofeparvovecum #

bevufenogene nofeparvovec	A non-replicating, recombinant adeno-associated virus expressing codon-optimised human phenylalanine hydroxylase (PAH). A non-replicating, recombinant adeno-associated virus, hematopoietic stem cell serotype 15 (AAVHSC15) expressing codon-optimised human phenylalanine hydroxylase (PAH) under control of a liver-specific hybrid promoter [comprising human hepatic control region-1 (HCR-1) enhancer element, human alpha-1-antitrypsin (hAAT) promoter and the SV40 small t intron)] and an SV40 polyA signal sequence, flanked by adeno-associated virus 2 (AAV2) inverted terminal repeats (ITRs).
bévufénogène noféparvovec	Un virus adéno-associé recombinant, non-répliquant, exprimant la phénylalanine hydroxylase humaine (PAH) aux codons optimisés.

	Un virus adéno-associé recombinant, non-répliquant, de cellules souches hématopoïétiques de sérotype 15 (AAVHSC15) exprimant la phénylalanine hydroxylase humaine (PAH) aux codons optimisés sous le contrôle d'un promoteur hybride spécifique du foie [consistant en un élément activateur de la région 1 de contrôle hépatique humain (HCR-1), le promoteur de l'alpha-1-antitrypsine humaine (hAAT) et du petit intron t SV40] et d'une séquence signal polyA SV40, flanquée de répétitions terminales inversées (ITRs) du virus adéno-associé 2 (AAV2).
bevufenogén nofeparvovec	Un virus adeno-asociado recombinante, no replicativo, que expresa la fenilalanina hidroxilasa humana (PAH) con codones optimizados. Un virus adeno-asociado recombinante, no replicativo, derivado de células madre hematopoyéticas serotipo 15 (AAVHSC15) que expresa la fenilalanina hidroxilasa humana (PAH) con codones optimizados, bajo el control de un promotor híbrido específico de hígado [contiene un elemento potenciador de la región de control hepático 1 humana (HCR-1), un promotor de la alfa 1 antitripsina humana (hAAT) y el intrón pequeño t de SV40] y una secuencia señal de polyA de SV40, flanqueado por las repeticiones terminales invertidas (ITRs) del virus adeno-asociado 2 (AAV2).
botensilimabum #	
botensilimab	immunoglobulin G1-kappa, anti-[*Homo sapiens* CTLA4 (cytotoxic T-lymphocyte associated protein 4, CD152)], *Homo sapiens* monoclonal antibody; gamma1 heavy chain *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV3-21*01 (99.0%) -(IGHD) -IGHJ3*02 (92.9%) M123>L (113)) CDR-IMGT [8.8.11] (26-33.51-58.97-107) (1-118) -*Homo sapiens* IGHG1*03 G1m3, nG1m1, G1v8 CH2 D3, L115, E117 (CH1 R120 (215) (119-216), hinge 1-15 (217-231), CH2 S3>D (240), A115>L (331), I117>E (333) (232-341), CH3 E12 (357), M14 (359) (342-446), CHS K>del (447)) (119-447)], (221-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (94.8%) -IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (227-227'':230-230'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa
botensilimab	immunoglobuline G1-kappa, anti-[*Homo sapiens* CTLA4 (protéine 4 associée aux lymphocytes T cytotoxiques, CD152)], anticorps monoclonal *Homo sapiens*;

chaîne lourde gamma1 *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV3-21*01 (99%) -(IGHD) - IGHJ3*02 (92.9%) M123>L (113)) CDR-IMGT [8.8.11] (26-33.51-58.97-107) (1-118) -*Homo sapiens* IGHG1*03 G1m3, nG1m1, G1v8 CH2 D3, L115, E117 (CH1 R120 (215) (119-216), charnière 1-15 (217-231), CH2 S3>D (240), A115>L (331), I117>E (333) (232-341), CH3 E12 (357), M14 (359) (342-446), CHS K>del (447)) (119-447)], (221-214')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (94.8%) - IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (227-227'':230-230'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

botensilimab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CTLA4 (proteína 4 asociada con los linfocitos T citotóxicos, CD152)], anticuerpo monoclonal *Homo sapiens*;
cadena pesada gamma1 *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV3-21*01 (99%) -(IGHD) - IGHJ3*02 (92.9%) M123>L (113)) CDR-IMGT [8.8.11] (26-33.51-58.97-107) (1-118) -*Homo sapiens* IGHG1*03 G1m3, nG1m1, G1v8 CH2 D3, L115, E117 (CH1 R120 (215) (119-216), bisagra 1-15 (217-231), CH2 S3>D (240), A115>L (331), I117>E (333) (232-341), CH3 E12 (357), M14 (359) (342-446), CHS K>del (447)) (119-447)], (221-214')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (94.8%) - IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (227-227'':230-230'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVKPGGSLRL SCAASGFTFS SYSMNWVRQA PGKGLEWVSS  50
ISSSSSYIYY AESVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARVG 100
LFGPFDIWGQ GTLVTVSSAS 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 LPEEKTISKA KGQPREPQVY 350
TLPPSREEMT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD 400
SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPG    447
```

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.

cadonilimabum #

cadonilimab

immunoglobulin G1-kappa anti-[*Homo sapiens* PDCD1 (programmed cell death 1, PD-1, PD1, CD279)], each heavy chain being fused to a scFv anti-[*Homo sapiens* CTLA4 (cytotoxic T-lymphocyte-associated protein 4, CD152)], monoclonal antibody, bispecific, tetravalent;
gamma1 heavy chain anti-PDCD1 fused to scFv anti-CTLA4 (1-713) [gamma-1 heavy chain(1-448) [VH anti-PDCD1 (*Homo sapiens* IGHV3-23*04 (88.7%) -(IGHD) -IGHJ6*01 (90.9%) T123>L (113)) CDR-IMGT [8.8.11] (26-33.51-58.97-107) (1-118) - *Homo sapiens* IGHG1*01, G1m17,1, G1v14 CH2 A1.3, A1.2 (CH1 K120 (215) (119-216), hinge 1-15 (217-231), CH2 L1.3>A (235), L1.2>A (236), G1>A (238) (232-341), CH3 D12 (357), L14 (359) (342-446), CHS (447-448)) (119-448)] -20-mer tetrakis(tetraglycyl-seryl) linker (449-468) -scFv heavy-lambda anti-CTLA4 (469-713) [VH anti-CTLA4 G49>C (512) (*Homo sapiens* IGHV1-2*02 (84.7%) -(IGHD) -IGHJ5*01 (90.9%) S128>A (583)) CDR-IMGT [8.8.8] (494-501.519-526.565-572) (469-583) -20-mer tetrakis(tetraglycyl-seryl) linker (584-603) -V-LAMBDA anti-CTLA4 (*Homo sapiens* IGLV7-46*01 (85.3%) -IGLJ3*02 (91.7%) G120>C (705)) CDR-IMGT [9.3.9] (629-637.655-657.694-702) (604-713)]]; (221-214')-disulfide with kappa light chain anti-PDCD1 (1'-214') [V-KAPPA (*Mus musculus* IGKV14-111*01 (86.3%) -IGKJ5*01 (100%)/*Homo sapiens* IGKV1-16*01 (80.0%) -IGKJ2*01 (81.8%) Q120>A (100), I126>L (106)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (227-227'':230-230'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

cadonilimab

immunoglobuline G1-kappa anti-[*Homo sapiens* PDCD1 (protéine 1 de mort cellulaire programmée, PD-1, PD1, CD279)], chaque chaîne lourde étant fusionnée à un scFv anti-[*Homo sapiens* CTLA4 (protéine 4 associée aux lymphocytes T cytotoxiques, CD152)], anticorps monoclonal, bispécifique, tétravalent;
chaîne lourde gamma1 anti-PDCD1 fusionnée au scFv anti-CTLA4 (1-713) [chaîne lourde gamma-1 (1-448) [VH anti-PDCD1 (*Homo sapiens* IGHV3-23*04 (88.7%) -(IGHD) -IGHJ6*01 (90.9%) T123>L (113)) CDR-IMGT [8.8.11] (26-33.51-58.97-107) (1-118) - *Homo sapiens* IGHG1*01, G1m17,1, G1v14 CH2 A1.3, A1.2 (CH1 K120 (215) (119-216), charnière 1-15 (217-231), CH2 L1.3>A (235), L1.2>A (236), G1>A (238) (232-341), CH3 D12 (357), L14 (359) (342-446), CHS (447-448)) (119-448)] -20-mer tétrakis(tétraglycyl-séryl) linker (449-468) -scFv lourd-lambda anti-CTLA4 (469-713) [VH anti-CTLA4 G49>C (512) (*Homo sapiens* IGHV1-2*02 (84.7%) -(IGHD) -IGHJ5*01 (90.9%) S128>A (583)) CDR-IMGT [8.8.8] (494-501.519-526.565-572) (469-583) -20-mer tétrakis(tétraglycyl-séryl) linker (584-603) -V-LAMBDA anti-CTLA4 (*Homo sapiens* IGLV7-46*01 (85.3%) -IGLJ3*02 (91.7%) G120>C (705)) CDR-IMGT [9.3.9] (629-637.655-657.694-702) (604-713)]]; (221-214')-disulfure avec la chaîne légère kappa anti-PDCD1 (1'-214') [V-KAPPA (*Mus musculus* IGKV14-111*01 (86.3%) -IGKJ5*01 (100%)/*Homo sapiens* IGKV1-16*01 (80.0%) -IGKJ2*01 (81.8%) Q120>A (100), I126>L (106)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (227-227'':230-230'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

cadonilimab

inmunoglobulina G1-kappa anti-[*Homo sapiens* PDCD1 (proteína 1 de muerte celular programada, PD-1, PD1, CD279)], cada cadena pesada estando fusionada a un scFv anti-[*Homo sapiens* CTLA4 (proteína 4 asociada con los linfocitos T citotóxicos, CD152)], anticuerpo monoclonal, biespecífico, tetravalente; cadena pesada gamma1 anti-PDCD1 fusionada con scFv anti-CTLA4 (1-713) [cadena pesada gamma-1 (1-448) [VH anti-PDCD1 (*Homo sapiens* IGHV3-23*04 (88.7%) -(IGHD) -IGHJ6*01 (90.9%) T123>L (113)) CDR-IMGT [8.8.11] (26-33.51-58.97-107) (1-118) -*Homo sapiens* IGHG1*01, G1m17,1, G1v14 CH2 A1.3, A1.2 (CH1 K120 (215) (119-216), bisagra 1-15 (217-231), CH2 L1.3>A (235), L1.2>A (236), G1>A (238) (232-341), CH3 D12 (357), L14 (359) (342-446), CHS (447-448)) (119-448)] -20-mer tetrakis(tetraglicil-seril) linker (449-468) -scFv pesado-lambda anti-CTLA4 (469-713) [VH anti-CTLA4 G49>C (512) (*Homo sapiens* IGHV1-2*02 (84.7%) -(IGHD) -IGHJ5*01 (90.9%) S128>A (583)) CDR-IMGT [8.8.8] (494-501.519-526.565-572) (469-583) -20-mer tetrakis(tetraglicil-seril) linker (584-603) – V-LAMBDA anti-CTLA4 (*Homo sapiens* IGLV7-46*01 (85.3%) -IGLJ3*02 (91.7%) G120>C (705)) CDR-IMGT [9.3.9] (629-637.655-657.694-702) (604-713)]];
(221-214')-disulfuro con la cadena ligera kappa anti-PDCD1 (1'-214') [V-KAPPA (*Mus musculus* IGKV14-111*01 (86.3%) -IGKJ5*01 (100%)/*Homo sapiens* IGKV1-16*01 (80.0%) -IGKJ2*01 (81.8%) Q120>A (100), I126>L (106)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (227-227":230-230")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada (anti-PDCD1 and anti-CTLA4 (scFv))

```
EVQLVESGGG LVQPGGSLRL SCAASGFAFS SYDMSWVRQA PGKGLDWVAT  50
ISGGGRYTYY PDSVKGRFTI SRDNSKNNLY LQMNSLRAED TALYYCANRY 100
GEAWFAYWGQ GTLVTVSSAS TKGPSVFPLA PSSKSTSGGT AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTQTYI 200
CNVNHKPSNT KVDKKVEPKS CDKTHTCPPC PAPEAAGAPS VFLFPPKPKD 250
TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNST 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY 350
TLPPSRDELT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD 400
SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPGKGG 450
GGSGGGGSGG GGSGGGGSQV QLVESGAEVK KPGASVKVSC KASGYSFTGY 500
TMNWVRQAPG QCLEWIGLIN PYNNITNYAQ KFQGRVTFTV DTSISTAYME 550
LSRLRSDDTG VYFCARLDYR SYWGQGTLVT VSAGGGGSGG GGSGGGGSGG 600
GGSQAVVTQE PSLTVSPGGT VTLTCGSSTG AVTTSNFPNW VQQKPGQAPR 650
SLIGGTNNKA SWTPARFSGS LLGGKAALTI SGAQPEDEAE YYCALWYSNH 700
WVFGCGTKLT VLR                                         713
```

Light chain / Chaîne légère / Cadena ligera (anti-PDCD1)

```
DIQMTQSPSS MSASVGDRVT FTCRASQDIN TYLSWFQQKP GKSPKTLIYR  50
ANRLVSGVPS RFSGSGSGQD YTLTISSLQP EDMATYYCLQ YDEFPLTFGA 100
GTKLELKRTV 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) 22-96 145-201 262-322 368-426 490-564 625-693
22"-96" 145"-201" 262"-322" 368"-426" 490"-564" 625-693"
Intra-H (scFv VH C49 -VL IGLJ C120) 512-705
512"-705"
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"
H scFv VH CDR2 N63:
524, 524"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaire complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

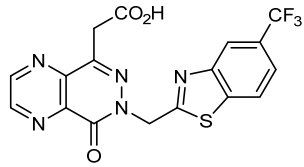
caficrestatum

caficrestat — (8-oxo-7-{[5-(trifluoromethyl)-1,3-benzothiazol-2-yl]methyl}-7,8-dihydropyrazino[2,3-*d*]pyridazin-5-yl)acetic acid

caficrestat — acide (8-oxo-7-{[5-(trifluorométhyl)-1,3-benzothiazol-2-yl]méthyl}-7,8-dihydropyrazino[2,3-*d*]pyridazin-5-yl)acétique

caficrestat — ácido (8-oxo-7-{[5-(trifluorometil)-1,3-benzotiazol-2-il]metil}-7,8-dihidropirazino[2,3-*d*]piridazin-5-il)acético

$C_{17}H_{10}F_3N_5O_3S$



cavrotolimodum

cavrotolimod — *all-P-ambo*-(17*RS*)-1-[(cholest-5-en-3β-yl)oxy]-17,20,40-trihydroxy-1,20,40-trioxo-6,9,12,15,19,21,24,27,30,33,36,39,41,44,47,50,53,56-octadecaoxa-2-aza-20λ^5,40λ^5-diphosphaoctapentacontan-58-yl *P*-thiothymidylyl-(3'→5')-2'-deoxy-*P*-thiocytidylyl-(3'→5')-2'-deoxy-*P*-thioguanylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-deoxy-*P*-thiocytidylyl-(3'→5')-2''-deoxy-*P*-thioguanylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-deoxy-*P*-thioguanylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-deoxy-*P*-thiocytidylyl-(3'→5')-2'-deoxy-*P*-thioguanylyl-(3'→5')-*P*-thiothymidylyl-(3'→5'')-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-deoxy-*P*-thioguanylyl-(3'→5')-2'-deoxy-*P*-thiocytidylyl-(3'→5')-2'-deoxy-*P*-thioguanylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-hydrogen 3'-thymidylate

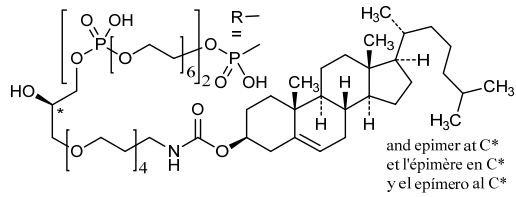
cavrotolimod — *tout-P-ambo-P*-thiothymidylyl-(3'→5')-2'-désoxy-*P*-thiocytidylyl-(3'→5')-2'-désoxy-*P*-thioguanylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-désoxy-*P*-thiocytidylyl-(3'→5')-2''-désoxy-*P*-thioguanylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-désoxy-*P*-thioguanylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-désoxy-*P*-thiocytidylyl-(3'→5')-2'-désoxy-*P*-thioguanylyl-(3'→5')-*P*-thiothymidylyl-(3'→5'')-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-désoxy-*P*-thioguanylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-désoxy-*P*-thiocytidylyl-(3'→5')-2'-désoxy-*P*-thioguanylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-hydrogéno-3'-thymidylate de (17*RS*)-1-[(cholest-5-én-3β-yl)oxy]-17,20,40-trihydroxy-1,20,40-trioxo-6,9,12,15,19,21,24,27,30,33,36,39,41,44,47,50,53,56-octadécaoxa-2-aza-20λ^5,40λ^5-diphosphaoctapentacontan-58-yle

cavrotolimod

todo-P-ambo-P-tiotimidilil-(3'→5')-2'-desoxi-*P*-tiocitidilil-(3'→5')-2'-desoxi-*P*-tioguanilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2'-desoxi-*P*-tiocitidilil-(3'→5')-2''-desoxi-*P*-tioguanilil-(3'→5')-*P*-tiotimidilil-(3'→5')-*P*-tiotimidilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2'-desoxi-*P*-tioguanilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2'-desoxi-*P*-tiocitidilil-(3'→5')-2'-desoxi-*P*-tioguanilil-(3'→5')-*P*-tiotimidilil-(3'→5'')-tiotimidilil-(3'→5')-*P*-tiotimidilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2'-desoxi-*P*-tioguanilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2'-desoxi-*P*-tiocitidilil-(3'→5')-2'-desoxi-*P*-tioguanilil-(3'→5')-*P*-tiotimidilil-(3'→5')-hidrógeno-3'-timidilato de (17*RS*)-1-[(colest-5-en-3β-il)oxi]-17,20,40-trihidroxi-1,20,40-trioxo-6,9,12,15,19,21,24,27,30,33,36,39,41,44,47,50,53,56-octadecaoxa-2-aza-20λ^5,40λ^5-difosfaoctapentacontan-58-ilo

$C_{300}H_{423}N_{71}O_{161}P_{26}S_{23}$

(3'-5')d(P-thio)(T-C-G-T-C-G-T-T-T-T-G-T-C-G-T-T-T-T-G-T-C-G-T-T)-R



cimpuciclibum

cimpuciclib

2^5-fluoro-1^2,4^6-dimethyl-1^3-(propan-2-yl)-1^3*H*-3,7-diaza-1(5)-benzimidazola-2(4,2)-pyrimidina-4(2,5)-pyridina-6(1,4)-piperidina-8(1)-cyclopropanaoctaphan-5-one

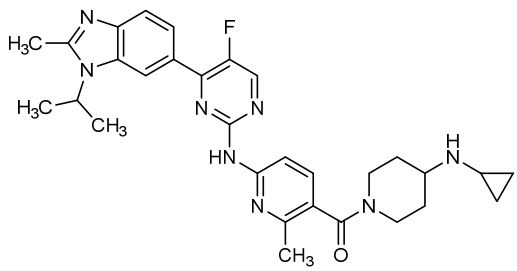
cimpuciclib

2^5-fluoro-1^2,4^6-diméthyl-1^3-(propan-2-yl)-1^3*H*-3,7-diaza-1(5)-benzimidazola-2(4,2)-pyrimidina-4(2,5)-pyridina-6(1,4)-pipéridina-8(1)-cyclopropanaoctaphan-5-one

cimpuciclib

2^5-fluoro-1^2,4^6-dimetil-1^3-(propan-2-il)-1^3*H*-3,7-diaza-1(5)-benzimidazola-2(4,2)-pirimidina-4(2,5)-piridina-6(1,4)-piperidina-8(1)-ciclopropanaoctafan-5-ona

$C_{30}H_{35}FN_8O$



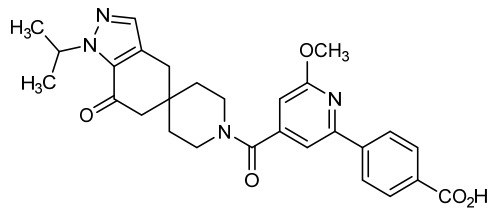
clesacostatum

clesacostat — 4-{6-methoxy-4-[7-oxo-1-(propan-2-yl)-1,4,6,7-tetrahydrospiro[indazole-5,4'-piperidine]-1'-carbonyl]pyridin-2-yl}benzoic acid

clésacostat — acide 4-{6-méthoxy-4-[7-oxo-1-(propan-2-yl)-1,4,6,7-tétrahydrospiro-[indazole-5,4'-pipéridine]-1'-carbonyl]pyridin-2-yl}benzoïque

clesacostat — ácido 4-{6-metoxi-4-[7-oxo-1-(propan-2-il)-1,4,6,7-tetrahidrospiro-[indazol-5,4'-piperidina]-1'-carbonil]piridin-2-il}benzoico

$C_{28}H_{30}N_4O_5$



cofirasersenum

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

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

cofirasersén — *todo-P-ambo*-2'-*O*,4'-*C*-[(1*S*)-etano-1,1-diil]-5-metil-*P*-tiocitidilil-(3'→5')-2'-*O*,4'-*C*-[(1*S*)-etano-1,1-diil]-5-metil-*P*-tiocitidilil-(3'→5')-2'-*O*,4'-*C*-[(1*S*)-etano-1,1-diil]-5-metil-*P*-tiocitidilil-(3'→5')-2'-desoxi-*P*-tioguanilil-(3'→5')-2'-desoxi-*P*-tioadenilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2'-desoxi-*P*-tioadenilil-(3'→5')-2'-desoxi-*P*-tioguanilil-

(3'→5')-2'-desoxi-5-metil-*P*-tiocitidilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2'-desoxi-*P*-tioguanilil-(3'→5')-2'-desoxi-*P*-tioguanilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2'-*O*,4'-*C*-[(1*S*)-etano-1,1-diil]-5-metil-*P*-tiouridilil-(3'→5')-2'-*O*,4'-*C*-[(1*S*)-etano-1,1-diil]-*P*-tioguanilil-(3'→5')-2'-*O*,4'-*C*-[(1*S*)-etano-1,1-diil]-5-metiluridina

$C_{172}H_{218}N_{57}O_{88}P_{15}S_{15}$

(3'-5') all *P*-thio C=C=C=C=d(G=A=T=A=G=C=T=G=G=T=)U=G=U

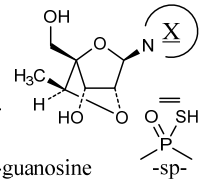
Legend:

A , G & T : 2'-deoxynucleotide

C : 2'-deoxy-5-methylcytidine

C & U : 2'-*O*,4'-*C*-[(1*S*)-ethane-1,1-diyl]-5-methylnucleotide

G : 2'-*O*,4'-*C*-[(1*S*)-ethane-1,1-diyl]-guanosine



-sp-

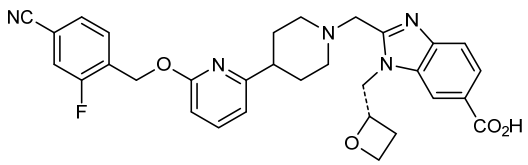
danuglipronum

danuglipron — (1^2*S*)-9^4-cyano-9^2-fluoro-7-oxa-3(1,2)-benzimidazola-6(2,6)-pyridina-5(1,4)-piperidina-1(2)-oxetana-9(1)-benzenanonaphane-3^6-carboxylic acid

danuglipron — acide (1^2*S*)-9^4-cyano-9^2-fluoro-7-oxa-3(1,2)-benzimidazola-6(2,6)-pyridina-5(1,4)-pipéridina-1(2)-oxétana-9(1)-benzénanonaphane-3^6-carboxylique

danugliprón — ácido (1^2*S*)-9^4-ciano-9^2-fluoro-7-oxa-3(1,2)-benzimidazola-6(2,6)-piridina-5(1,4)-piperidina-1(2)-oxetana-9(1)-bencenanonafano-3^6-carboxílico

$C_{31}H_{30}FN_5O_4$

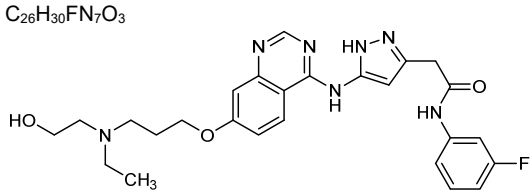


defosbarasertibum

defosbarasertib — 2-{5-[(7-{3-[ethyl(2-hydroxyethyl)amino]propoxy}quinazolin-4-yl)amino]-1*H*-pyrazol-3-yl}-*N*-(3-fluorophenyl)acetamide

défosbarasertib — 2-{5-[(7-{3-[éthyl(2-hydroxyéthyl)amino]propoxy}quinazolin-4-yl)amino]-1*H*-pyrazol-3-yl}-*N*-(3-fluorophényl)acétamide

defosbarasertib — 2-{5-[(7-{3-[etil(2-hidroxietil)amino]propoxi}quinazolin-4-il)amino]-1*H*-pirazol-3-il}-*N*-(3-fluorofenil)acetamida



delandistrogenum moxeparvovecum #

delandistrogene moxeparvovec	A non-replicating adeno-associated virus (AAV) vector encoding human micro-dystrophin. A recombinant, non-replicating, adeno-associated virus (AAV) serotype rh74 vector (AAVrh74) encoding codon-optimized human micro-dystrophin (a shortened functional version of human dystrophin), under control of a hybrid MHCK7 promoter consisting of enhancer/promoter regions of murine muscle creatine kinase (CK) and alpha-myosin heavy-chain genes, followed by a chimeric intron [including the SV40 late 16S/19S splice signals and a small 5′ UTR] and a small synthetic polyadenylation (polyA) signal sequence, flanked by adeno-associated virus 2 (AAV2) inverted terminal repeats (ITRs).
délandistrogène moxéparvovec	Un vecteur adéno-associé (AAV) non-répliquant codant la micro-dystrophine humaine. Un vecteur adéno-associé de sérotype rh74 (AAVrh74) recombinant, non-répliquant codant la micro-dystrophine humaine aux codons optimisés (une version fonctionnelle raccourcie de la dystrophine humaine), sous le contrôle d'un promoteur hybride MHCK7 consistant en régions activatrices/promotrices de la créatine kinase (CK) de muscle murin et des gènes de la chaîne lourde de l'alpha-myosine, suivi d'un intron chimérique [incluant les signaux d'épissage SV40 tardifs 16S/19S et une UTR courte en 5'] et d'une petite séquence signal synthétique de polyadénylation (polyA), flanquée de répétitions terminales inversées (ITRs) du virus adéno-associé 2 (AAV2).
delandistrogén moxeparvovec	Un vector de virus adeno-asociado (AAV) no replicativo que codifica para la micro distrofina humana. Un vector de virus adeno-asociado (AAV) recombinante de serotipo rh74 (AAVrh74), no replicativo que codifica para la micro distrofina humana (una versión funcional acortada de la distrofina humana), con codones optimizados, bajo el control de un promotor híbrido MHCK7 consistente en regiones potenciadoras/promotoras de los genes de la creatinina quinasa (CK) de músculo y de la cadena pesada de la miosina alfa murinas, seguido de un intrón quimérico [incluyendo las señales de procesamiento 16S/19S del SV40 tardío y una pequeña región 5' UTR] y una pequeña secuencia señal de poliadenilación (polyA) sintética, flanqueado por las repeticiones terminales invertidas (ITRs) del virus adeno-asociado 2 (AAV2).

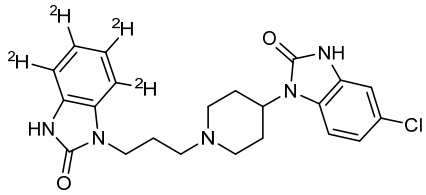
deudomperidonum

deudomperidone — 5-chloro-1-(1-{3-[2-oxo-2,3-dihydro-1*H*-(4,5,6,7-$^{2}H_4$)benzimidazol-1-yl]propyl}piperidin-4-yl)-1,3-dihydro-2*H*-benzimidazol-2-one

deudompéridone — 5-chloro-1-(1-{3-[2-oxo-2,3-dihydro-1*H*-(4,5,6,7-$^{2}H_4$)benzimidazol-1-yl]propyl}pipéridin-4-yl)-1,3-dihydro-2*H*-benzimidazol-2-one

deudomperidona — 5-cloro-1-(1-{3-[2-oxo-2,3-dihidro-1*H*-(4,5,6,7-$^{2}H_4$)benzimidazol-1-il]propil}piperidin-4-il)-1,3-dihidro-2*H*-benzimidazol-2-ona

$C_{22}H_{20}{}^{2}H_4ClN_5O_2$



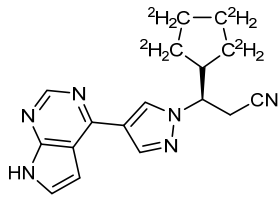
deuruxolitinibum

deuruxolitinib — (3*R*)-3-(2,2,3,3,4,4,5,5-$^{2}H_8$)cyclopentyl-3-[4-(7*H*-pyrrolo[2,3-*d*]pyrimidin-4-yl)-1*H*-pyrazol-1-yl]propanenitrile

deuruxolitinib — (3*R*)-3-(2,2,3,3,4,4,5,5-$^{2}H_8$)cyclopentyl-3-[4-(7*H*-pyrrolo[2,3-*d*]pyrimidin-4-yl)-1*H*-pyrazol-1-yl]propanenitrile

deuruxolitinib — (3*R*)-3-(2,2,3,3,4,4,5,5-$^{2}H_8$)ciclopentil-3-[4-(7*H*-pirrolo[2,3-*d*]pirimidin-4-il)-1*H*-pirazol-1-il]propanonitrilo

$C_{17}H_{10}{}^{2}H_8N_6$



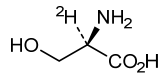
deutarserinum

deutarserine — D-(2-^{2}H)serine; (2*R*)-2-amino-3-hydroxy(2-^{2}H)propanoic acid

deutarsérine — D-(2-^{2}H)sérine; acide (2*R*)-2-amino-3-hydroxy(2-^{2}H)propanoïque

deutarserina — D-(2-^{2}H)serina; ácido (2*R*)-2-amino-3-hidroxi(2-^{2}H)proapoico

$C_3H_6{}^2HNO_3$



domvanalimabum #

domvanalimab	immunoglobulin G1-kappa, anti-[*Homo sapiens* TIGIT (T-cell immunoreceptor with Ig domain and ITIM, V-set Ig member 9, VSIG9, V-set and transmembrane member 3, VSTM3)], humanized monoclonal antibody; gamma1 heavy chain humanized (1-448) [VH (*Homo sapiens* IGHV3-48*01 (90.8%) -(IGHD) -IGHJ4*01 (92.3%)) CDR-IMGT [8.8.12] (26-33.51-58.97-108) (1-119) -*Homo sapiens* IGHG1*01, G1m17,1, G1v14 CH2 A1.3, A1.2 (CH1 K120 (216) (120-217), hinge 1-15 (218-232), CH2 L1.3>A (236), L1.2>A (237) (233-342), CH3 D12 (358), L14 (360) (343-447), CHS K>del (448)) (120-448)], (222-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-16*01 (89.5%) -IGKJ4*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (228-228'':231-231'')-bisdisulfide, produced in a Chinese hamster ovary (CHO)-K1 cell line, glycoform alfa
domvanalimab	immunoglobuline G1-kappa, anti-[*Homo sapiens* TIGIT (immunorécepteur des lymphocytes T avec domaine Ig et ITIM, membre 9 de l'Ig V-set, VSIG9, membre 3 de l'Ig V-set et région transmembranaire, VSTM3)], anticorps monoclonal humanisé; chaîne lourde gamma1 humanisée (1-448) [VH (*Homo sapiens* IGHV3-48*01 (90.8%) -(IGHD) - IGHJ4*01 (92.3%)) CDR-IMGT [8.8.12] (26-33.51-58.97-108) (1-119) -*Homo sapiens* IGHG1*01, G1m17,1, G1v14 CH2 A1.3, A1.2 (CH1 K120 (216) (120-217), charnière 1-15 (218-232), CH2 L1.3>A (236), L1.2>A (237) (233-342), CH3 D12 (358), L14 (360) (343-447), CHS K>del (448)) (120-448)], (222-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-16*01 (89.5%) -IGKJ4*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (228-228'':231-231'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO) lignée cellulaire CHO-K1, glycoforme alfa
domvanalimab	inmunoglobulina G1-kappa, anti-[*Homo sapiens* TIGIT (inmunoreceptor de los linfocitos T con dominio Ig e ITIM, miembro 9 de la Ig V-set, VSIG9, miembro 3 de la Ig V-set y región transmembrana, VSTM3)], anticuerpo monoclonal humanizado;

cadena pesada gamma1 humanizada (1-448) [VH (*Homo sapiens* IGHV3-48*01 (90.8%) -(IGHD) - IGHJ4*01 (92.3%)) CDR-IMGT [8.8.12] (26-33.51-58.97-108) (1-119) -*Homo sapiens* IGHG1*01, G1m17,1, G1v14 CH2 A1.3, A1.2 (CH1 K120 (216) (120-217), bisagra 1-15 (218-232), CH2 L1.3>A (236), L1.2>A (237) (233-342), CH3 D12 (358), L14 (360) (343-447), CHS K>del (448)) (120-448)], (222-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-16*01 (89.5%) -IGKJ4*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (228-228":231-231")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAASGFTFS NFGMHWVRQA PGKGLEWVAF  50
ISSGSSSIYY ADTVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARMR 100
LDYYAMDYWG QGTMVTVSSA STKGPSVFPL APSSKSTSGG TAALGCLVKD 150
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY 200
ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP CPAPEAAGGP SVFLFPPKPK 250
DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS 300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV 350
YTLPPSRDEL TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL 400
DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPG   448
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Light chain / Chaîne légère / Cadena ligera

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DIQMTQSPSS LSASVGDRVT ITCRASKSIS KYLAWYQQKP GKAPKLLIYS  50
GSTLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ HNEYPWTFGG 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) 22-96 146-202 263-323 369-427
22"-96" 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 / 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.

donidalorsenum
donidalorsen

all-P-ambo-5'-*O*-(28-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]-16,16-bis{[3-({6-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]hex-yl}amino)-3-oxopropoxy]methyl}-1-hydroxy-1,10,14,21-tetraoxo-2,18-dioxa-9,15,22-triaza-1λ^5-phosphaoctacosan-1-yl)-2'-*O*-(2-methoxyethyl)-5-methyl-*P*-thiouridylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-*P*-thioguanylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methylcytidylyl-(3'→5')-2'-*O*-(2-methoxyethyl)adenylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-*P*-thioadenylyl-(3'→5')-2'-deoxy-*P*-thioguanylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-deoxy-5-methyl-*P*-thiocytidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-deoxy-5-methyl-*P*-thiocytidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-deoxy-*P*-thioguanylyl-(3'→5')-2'-deoxy-*P*-thioguanylyl-(3'→5')-2'-deoxy-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-methoxyethyl)adenylyl-(3'→5')-2'-*O*-(2-methoxyethyl)adenylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-*P*-thioadenylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-methoxyethyl)adenosine

donidalorsen

tout-P-ambo-5'-*O*-(28-[(2-acétamido-2-désoxy-β-D-galactopyranosyl)oxy]-16,16-bis{[3-({6-[(2-acétamido-2-désoxy-β-D-galactopyranosyl)oxy]hexyl}amino)-3-oxopropoxy]méthyl}-1-hydroxy-1,10,14,21-tétraoxo-2,18-dioxa-9,15,22-triaza-1λ^5-phosphaoctacosan-1-yl)-2'-*O*-(2-méthoxyéthyl)-5-méthyl-*P*-thiouridylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-*P*-thioguanylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthylcytidylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)adénylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-*P*-thioadénylyl-(3'→5')-2'-désoxy-*P*-thioguanylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-désoxy-5-méthyl-*P*-thiocytidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-désoxy-5-méthyl-*P*-thiocytidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-désoxy-*P*-thioguanylyl-(3'→5')-2'-désoxy-*P*-thioguanylyl-(3'→5')-2'-désoxy-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)adénylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)adénylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-*P*-thioadénylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)adénosine

donidalorsén

todo-P-ambo-5'-*O*-(28-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]-16,16-bis{[3-({6-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]hexil}-amino)-3-oxopropoxi]metil}-1-hydroxi-1,10,14,21-tetraoxo-2,18-dioxa-9,15,22-triaza-1λ^5-fosfaoctacosan-1-il)-5-metil-2'-*O*-(2-metoxietil)-*P*-tio-uridilil-(3'→5')-2'-*O*-(2-metoxietil)-*P*-tioguanilil-(3'→5')-5-metil-2'-*O*-(2-metoxietil)citidilil-(3'→5')-2'-*O*-(2-metoxietil)adenilil-(3'→5')-2'-*O*-(2-metoxi-etil)-*P*-tioadenilil-(3'→5')-2'-desoxi-*P*-tioguanilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2'-desoxi-5-metil-*P*-tiocitidilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2'-desoxi-5-metil-*P*-tiocitidilil-(3'→5')-*P*-tiotimidilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2'-desoxi-*P*-tioguanilil-(3'→5')-2'-desoxi-*P*-tioguanilil-(3'→5')-2'-desoxi-5-metil-*P*-tiocitidilil-(3'→5')-2'-*O*-(2-metoxietil)adenilil-(3'→5')-2'-*O*-(2-metoxietil)adenilil-(3'→5')-2'-*O*-(2-metoxietil)-*P*-tioadenilil-(3'→5')-5-metil-2'-*O*-(2-metoxietil)-*P*-tiocitidilil-(3'→5')-2'-*O*-(2-metoxietil)adenosina

$C_{296}H_{435}N_{83}O_{151}P_{20}S_{15}$

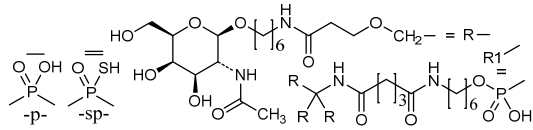
(3'-5') R1-U=G=C-A-A=d(G=T=C=T=C=T=T=G=G=C=)A-A-A=C=A

Legend:

G & T : 2'-deoxynucleotide C : 2'-deoxy-5-methylcytidine

A & G : 2'-*O*-(2-methoxyethyl)nucleotide

C & U : 2'-*O*-(2-methoxyethyl)-5-methylnucleotide



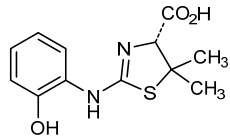
ebaresdaxum

ebaresdax

(4*R*)-2-(2-hydroxyanilino)-5,5-dimethyl-4,5-dihydro-1,3-thiazole-4-carboxylic acid

ébaresdax	acide (4*R*)-2-(2-hydroxyanilino)-5,5-diméthyl-4,5-dihydro-1,3-thiazole-4-carboxylique
ebaresdax	ácido (4*R*)-2-(2-hidroxianilino)-5,5-dimetil-4,5-dihidro-1,3-tiazol-4-carboxílico

$C_{12}H_{14}N_2O_3S$



ebdarokimabum #

ebdarokimab	immunoglobulin G1-kappa, anti-[*Homo sapiens* IL12B (interleukin 12B, CLMF, IL-12B, NKSF, CLMF2)], humanized monoclonal antibody; gamma1 heavy chain humanized(1-449) [VH (*Homo sapiens* IGHV5-51*01 (84.7%) -(IGHD) -IGHJ3*02 (92.9%)) CDR-IMGT [8.8.12] (26-33.51-58.97-108) (1-119) -*Homo sapiens* IGHG1*03v G1m3>G1m17, nG1m1 (CH1 R120>K (216) (120-217), hinge 1-15 (218-232), CH2 (233-342), CH3 E12 (358), M14 (360) (343-447), CHS (448-449) (120-449)], (222-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV3D-11*02 (86.7%) -IGKJ5*01 (100%)) CDR-IMGT [6.3.9](27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (228-228":231-231")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa
ebdarokimab	immunoglobuline G1-kappa, anti-[*Homo sapiens* IL12B (interleukine 12B, CLMF, IL-12B, NKSF, CLMF2)], anticorps monoclonal humanisé; chaîne lourde gamma1 humanisée (1-449) [VH (*Homo sapiens* IGHV5-51*01 (84.7%) -(IGHD) -IGHJ3*01 (92.9%)) CDR-IMGT [8.8.12] (26-33.51-58.97-108) (1-119) -*Homo sapiens* IGHG1*03v G1m3>G1m17, nG1m1 (CH1 R120>K (216) (120-217), charnière 1-15 (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 humanisée(1'-214') [V-KAPPA (*Homo sapiens* IGKV3D-11*02 (86.7%) -IGKJ5*01 (100%)) CDR-IMGT [6.3.9](27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (228-228":231-231")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa
ebdarokimab	inmunoglobulina G1-kappa, anti-[*Homo sapiens* IL12B (interleukina 12B, CLMF, IL-12B, NKSF, CLMF2)], anticuerpo monoclonal humanizado;

cadena pesada gamma1 humanizada (1-449) [VH (*Homo sapiens* IGHV5-51*01 (84.7%) -(IGHD) -IGHJ3*01 (92.9%)) CDR-IMGT [8.8.12] (26-33.51-58.97-108) (1-119) -*Homo sapiens* IGHG1*03v G1m3>G1m17, nG1m1 (CH1 R120>K (216) (120-217), bisagra 1-15 (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 humanizada(1'-214') [V-KAPPA (*Homo sapiens* IGKV3D-11*02 (86.7%) -IGKJ5*01 (100%)) CDR-IMGT [6.3.9](27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (228-228":231-231")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVQSGAE VKKPGESLKI SCQSSGYTFT SYWIGWVRQM PGQGLEWIGI  50
MSPVDSDIRY NPMFRGQVTM SVDKSSSTAY LQWSSLKASD TAMYYCARRR 100
PGQGYFDFWG QGTMVTVSSA STKGPSVFPL APSSKSTSGG TAALGCLVKD 150
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY 200
ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP CPAPELLGGP SVFLFPPKPK 250
DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS 300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV 350
YTLPPSREEM TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL 400
DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK  449
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Light chain / Chaîne légère / Cadena ligera

```
EIVLTQSPAT LSASPGERAT ISCRASQSVG TWVAWYQQKP GQAPRSLIYA  50
ASNLQSGIPA RFSGSGSGTD FTLTISSLEP EDFAVYYCQQ YNIYPYTFGQ 100
GTRLEIKRTV 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) 22-96 146-202 263-323 369-427
22"-96" 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 / 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 / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2:
449, 449"

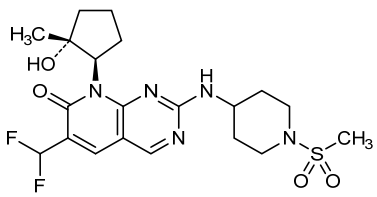
ebvaciclibum

ebvaciclib — 6-(difluoromethyl)-8-[(1*R*,2*R*)-2-hydroxy-2-methylcyclopentyl]-2-{[1-(methanesulfonyl)piperidin-4-yl]amino}pyrido[2,3-*d*]pyrimidin-7(8*H*)-one

ebvaciclib — 6-(difluorométhyl)-8-[(1*R*,2*R*)-2-hydroxy-2-méthylcyclopentyl]-2-{[1-(méthanesulfonyl)pipéridin-4-yl]amino}pyrido[2,3-*d*]pyrimidin-7(8*H*)-one

ebvaciclib — 6-(difluorometil)-8-[(1*R*,2*R*)-2-hidroxi-2-metilciclopentil]-2-{[1-(metanosulfonil)piperidin-4-il]amino}pirido[2,3-*d*]pirimidin-7(8*H*)-ona

$C_{20}H_{27}F_2N_5O_4S$



ecubectedinum

ecubectedin

(1'*R*,3'*S*,6*R*,6a*R*,7*R*,13*S*,14*S*,16*R*)-8,14-dihydroxy-3'-(hydroxymethyl)-9-methoxy-4,10,23-trimethyl-19-oxo-2',3',4',6,6a,7,9',13,14,16-decahydro-2*H*,12*H*-spiro[7,13-azano-6,16-(sulfanopropanooxymethano)[1,3]dioxolo[7,8]isoquino[3,2-*b*][3]benzazocine-20,1'-pyrido[3,4-*b*]indol]-5-yl acetate

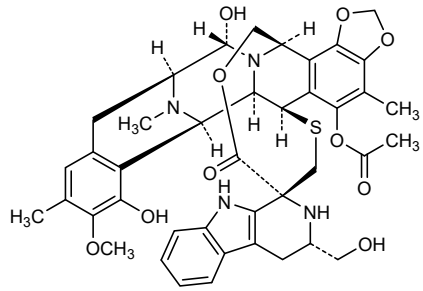
écubectédine

acétate de (1'*R*,3'*S*,6*R*,6a*R*,7*R*,13*S*,14*S*,16*R*)-8,14-dihydroxy-3'-(hydroxyméthyl)-9-méthoxy-4,10,23-triméthyl-19-oxo-2',3',4',6,6a,7,9',13,14,16-décahydro-2*H*,12*H*-spiro[7,13-azano-6,16-(sulfanopropanooxyméthano)[1,3]dioxolo[7,8]isoquino[3,2-*b*][3]benzazocine-20,1'-pyrido[3,4-*b*]indol]-5-yle

ecubectedina

acetato de (1'*R*,3'*S*,6*R*,6a*R*,7*R*,13*S*,14*S*,16*R*)-8,14-dihidroxi-3'-(hidroximetil)-4,10,23-trimetil-9-metoxi-19-oxo-2',3',4',6,6a,7,9',13,14,16-decahidro-2*H*,12*H*-spiro[7,13-azano-6,16-(sulfanopropanooximetano)[1,3]dioxolo[7,8]isoquino[3,2-*b*][3]benzazocina-20,1'-pirido[3,4-*b*]indol]-5-ilo

$C_{41}H_{44}N_4O_{10}S$



edaxeterkibum

edaxeterkib

6-[(3*R*)-1-benzylpiperidin-3-yl]-3-(2-methoxypyrimidin-5-yl)-1,5,6,8-tetrahydro-7*H*-pyrazolo[4,3-*g*]quinazolin-7-one

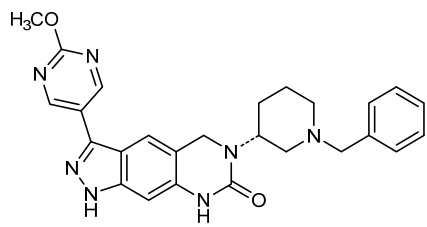
édaxéterkib

6-[(3*R*)-1-benzylpipéridin-3-yl]-3-(2-méthoxypyrimidin-5-yl)-1,5,6,8-tétrahydro-7*H*-pyrazolo[4,3-*g*]quinazolin-7-one

edaxeterkib

6-[(3*R*)-1-bencilpiperidin-3-il]-3-(2-metoxipirimidin-5-il)-1,5,6,8-tetrahidro-7*H*-pirazolo[4,3-*g*]quinazolin-7-ona

$C_{26}H_{27}N_7O_2$



eflimrufuspum alfa

eflimrufusp alfa	human vascular endothelial growth factor receptor 1 (VEGFR-1) immunoglobulin-like domain 2 containing fragment (132-232, 1-101 in the current sequence), fused via human vascular endothelial growth factor receptor 2 (VEGFR-2) immunoglobulin-like domain 3 containing fragment (227-327, 102-202 in the current sequence) to human fibroblast growth factor receptor 1 (FGFR-1) immunoglobulin-like domains 2 and 3 containing fragment (150-361, 203-414 in the current sequence), fused to human immunoglobulin G1 Fc fragment (415-641), dimer, glycosylated, produced in Chinese hamster ovary (CHO) cells; vascular endothelial growth factor receptor 1 (*Homo sapiens* VEGFR-1) (132-232)-peptide (1-101), containing the immunoglobulin-like domain 2, fused with vascular endothelial growth factor receptor 2 (*Homo sapiens* VEGFR-2) (227-327)-peptide (102-202), containing the immunoglobulin-like domain 3, with fibroblast growth factor receptor 1 (*Homo sapiens* FGFR-1) (150-361)-peptide (203-414), containing the immunoglobulin-like domains 2 and 3 (211-299 and 308-410), and with a C-terminal *Homo sapiens* immunoglobulin G1 227-peptide Fc fragment (415-641), [*Homo sapiens* IGHG1*01; hinge 415-424; CH2: 425-534; CH3: 535-639; CHS: 640-641]; dimer (420-420':423-423')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa
éflimrufusp alfa	domaine 2 analogue à l'immunoglobuline du récepteur 1 du facteur de croissance de l'endothélium vasculaire humain (VEGFR-1) contenant le fragment (132-232, 1-101 dans la séquence actuelle), fusionné via le domaine 3 analogue à l'immunoglobuline du récepteur 2 du facteur de croissance de l'endothélium vasculaire humain (VEGFR-2) contenant le fragment (227-327, 102-202 dans la séquence actuelle) aux domaines 2 et 3 analogues à l'immunoglobuline du récepteur 1 du facteur de croissance des fibroblastes humain 21 (FGFR-1) contenant le fragment (150-361, 203-414 dans la séquence actuelle), fusionné au fragment Fc (415-641) de l'immunoglobuline G1 humaine, dimère, glycosylé, produit dans des cellules ovariennes de hamster chinois (CHO); peptide 132-232 du récepteur 1 du facteur de croissance de l'endothélium vasculaire (VEGFR-1 d'*Homo sapiens*) (1-101), contenant le domaine 2 analogue à l'immunoglobuline, fusionné avec le peptide-(227-327) du récepteur 2 du facteur de croissance de l'endothélium vasculaire (VEGFR-2 d'*Homo sapiens*) (102-202), contenant le domaine 3 analogue à l'immunoglobuline, avec le peptide-(150-361) du récepteur 1 du facteur de croissance des fibroblastes (FGFR-1 d'*Homo sapiens*) (203-414), contenant les domaines 2 et 3 analogues à l'immunoglobuline (211-299 et 308-410), et avec le fragment Fc du peptide-227 C-terminal de l'immunoglobulines G1 d'*Homo sapiens* (415-641), [*Homo sapiens* IGHG1*01; charnière 415-424; CH2: 425-534; CH3: 535-639; CHS: 640-641]; dimère (420-420':423-423')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

eflimrufusp alfa

el receptor 1 del factor de crecimiento endotelial vascular humano (VEGFR-1) dominio 2 de inmunoglobulina conteniendo fragmento (132-232, 1-101 en la secuencia actual), fusionado a tráves del receptor 2 del factor de crecimiento endotelial vascular humano (VEGFR-2) dominio 3 de la inmunoglobulina conteniendo el fragmento (227-327, 102-202 en la secuencia actual) al receptor 1 del factor de crecimiento de fibroblastos humano (FGFR-1) dominio 2 y 3 de la inmunoglobulina conteniendo el fragmento (150-361, 203-414 en la secuencia actual), fusionado al fragmento de la inmunoglobulina humana G1 Fc (415-641), dímero, glicosilado, producido en células ováricas de hámster chino (CHO);
péptido 132-232 del receptor 1 del factor de crecimiento del endotelio vascular (VEGFR-1 de *Homo sapiens*) (1-101), que contiene el dominio 2 del tipo inmunoglobulina, fusionado con el péptido 227-327 del receptor 2 del factor de crecimiento del endotelio vascular (VEGFR-2 de *Homo sapiens*) (102-202), que contiene el dominio 3 del tipo inmunoglobulina, con el péptido 150-361 del receptor 1 del factor de crecimiento de fibroblastos (FGFR-1 de *Homo sapiens*) (203-414), que contiene los dominios 2 y 3 de tipo inmunoglobulina (211-299 y 308-410), y con el fragmento Fc 227-peptÍdico C-terminal de inmunoglobulinas G1 de *Homo sapiens* (415-641), [*Homo sapiens* IGHG1*01; bisagra 415-424; CH2: 425-534; CH3: 535-639; CHS: 640-641]; dímero (420-420':423-423')-bisdisulfuro, producido en células ováricas de hámster chino (CHO), glicoforma alfa

Sequence / Séquence / Secuencia

```
GRPFVEMYSE IPEIIHMTEG RELVIPCRVT SPNITVTLKK FPLDTLIPDG    50
KRIIWDSRKG FIISNATYKE IGLLTCEATV NGHLYKTNYL THRQTNTIID   100
VVLSPSHGIE LSVGEKLVLN CTARTELNVG IDFNWEYPSS KHQHKKLVNR   150
DLKTQSGSEM KKFLSTLTID GVTRSDQGLY TCAASSGLMT KKNSTFVRVH   200
EKPVAPYWTS PEKMEKKLHA VPAAKTVKFK CPSSGTPNPT LRWLKNGKEF   250
KPDHRIGGYK VRYATWSIIM DSVVPSDKGN YTCIVENEYG SINHTYQLDV   300
VERSPHRPIL QAGLPANKTV ALGSNVEFMC KVYSDPQPHI QWLKHIEVNG   350
SKIGPDNLPY VQILKTAGVN TTDKEMEVLH LRNVSFEDAG EYTCLAGNSI   400
GLSHHSAWLT VLEADKTHTC PPCPAPELLG GPSVFLFPPK PKDTLMISRT   450
PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY NSTYRVVSVL   500
TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP QVYTLPPSRD   550
ELTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP VLDSDGSFFL   600
YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG K            641
```

VEGFR-1 Ig-like 2 / *VEGFR-2 Ig-like 3* / **FGFR-1 Ig-like 2+3** / IgG1 Fc

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

Intra-VEGFR1:	27-76	Intra-VEGFR2:	121-182
	27'-76'		121'-182'
Intra-FGFR1:	231-283, 330-394	Intra-Fc:	455-515, 561-619
	231'-283', 330'-394'		455'-515', 561'-619'
Inter-Fc:	420-420', 423-423'		

Glycosylation sites / Sites de glycosylation / Posiciones de glicosilación
N33, N65, N120, N193, N280, N293, N317, N349, N370, N383, N491, N33', N65', N120', N193', N280', N293', N317', N349', N370', N383', N491'

C-terminal lysine clipping / Coupure de la lysine C-terminale / Supresión de lisina C-terminal
K641, K641'

efruxiferminum #
efruxifermin

human L-methionyl immunoglobulin G1 Fc fragment (1-228) fused via peptidyl linker ^{229}GGGGSGGGGSGGGGS^{243} to human fibroblast growth factor 21 (FGF-21) fragment (29-209, 244-424 in the current sequence) variant (L^{98}>R^{341}, P^{171}>G^{414}, A^{180}>E^{423}), dimer, produced in *Escherichia coli;*

	L-methionyl-immunoglobulin G1 (*Homo sapiens*) 33γ1-chain C-terminal 227-peptide Fc fragment (1-228) [*Homo sapiens* IGHG1*1; hinge 1-11; CH2 12-121; CH3 122-226; CHS 227-228] fused with the peptide linker $(G_4S)_3$ (229-243) and [$L^{98}>R^{341}$, $P^{171}>G^{414}$, $A^{180}>E^{423}$]-fibroblast growth factor 21 (*Homo sapiens* FGF-21) (244-424), dimer (7-7':10-10')-bisdisulfide, non-glycosylated, produced in *Escherichia coli*
éfruxifermine	fragment Fc L-méthionyl (1-228) de l'immunoglobuline G1 humaine fusionné via un linker peptidique ^{229}GGGGSGGGGSGGGGS^{243} au fragment (29-209, 244-424 dans la séquence actuelle) du facteur de croissance des fibroblastes 21 (FGF-21), variant ($L^{98}>R^{341}$, $P^{171}>G^{414}$, $A^{180}>E^{423}$), dimère, produit par *Escherichia coli*; L-méthionyl-fragment Fc (1-228) de l'immunoglobuline G1 (227-peptide C-terminal de la chaîne γ1 d'*Homo sapiens*) [*Homo sapiens* IGHG1*1; charnière 1-11; CH2 12-121; CH3 122-226; CHS 227-228] fusionné avec le linker peptidique $(G_4S)_3$ (229-243) et [$L^{98}>R^{341}$, $P^{171}>G^{414}$, $A^{180}>E^{423}$]-facteur 21 de croissance des fibroblastes (FGF-21 d'*Homo sapiens*) (244-424), dimère (7-7':10-10')-bisdisulfure, non-glycosylé, produit par *Escherichia coli*
efruxifermina	fragmento Fc L-metionil (1-228) de la inmunoglobulina G1 humana fusionada a través de un enlace peptidil ^{229}GGGGSGGGGSGGGGS^{243} al factor fibroblasto humano 21 (FGF-21) fragmento (29-209, 244-424 en la secuencia actual) variante ($L^{98}>R^{341}$, $P^{171}>G^{414}$, $A^{180}>E^{423}$), dímero, producido en *Escherichia coli;* L-metionil-fragmento Fc de inmunoglobulina G1 (227-péptido C-terminal de la cadena γ1 de *Homo sapiens*) (1-228) [*Homo sapiens* IGHG1*1; bisagra 1-11; CH2 12-121; CH3 122-226; CHS 227-228] fusionado con el péptido conector $(G_4S)_3$ (229-243) y [$L^{98}>R^{341}$, $P^{171}>G^{414}$, $A^{180}>E^{423}$]-factor 21 de crecimiento fibroblástico (FGF-21 de *Homo sapiens*) (244-424), dímero (7-7':10-10')-bisdisulfuro, no glicosilado, producido por *Escherichia coli*

Sequence / Séquence / Secuencia

```
MDKTHTCPPC PAPELLGGPS VFLFPPKPKD TLMISRTPEV TCVVVDVSHE    50
DPEVKFNWYV DGVEVHNAKT KPREEQYNST YRVVSVLTVL HQDWLNGKEY   100
KCKVSNKALP APIEKTISKA KGQPREPQVY TLPPSRDELT KNQVSLTCLV   150
KGFYPSDIAV EWESNGQPEN NYKTTPPVLD SDGSFFLYSK LTVDKSRWQQ   200
GNVFSCSVMH EALHNHYTQK SLSLSPGKGG GGSGGGGSGG GGSHPIPDSS   250
PLLQFGGQVR QRYLYTDDAQ QTEAHLEIRE DGTVGGAADQ SPESLLQLKA   300
LKPGVIQILG VKTSRFLCQR PDGALYGSLH FDPEACSFRE RLLEDGYNVY   350
QSEAHGLPLH LPGNKSPHRD PAPRGPARFL PLPGLPPAPP EPPGILAPQP   400
PDVGSSDPLS MVGGSQGRSP SYES                               424
```

Mutation sites / Sites de mutation / Posiciones de mutación
L341>R, P414>G, A423>E
L341'>R, P414'>G, A423'>E

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

Intra-Fc:	42-102, 148-206	Intra-FGF21:	318-336
	42'-102', 148'-206'		318'-336'
Inter-Fc	7-7', 10-10'		

Glycosylation sites / Sites de glycosylation / Posiciones de glicosilación
none / aucun / ninguna

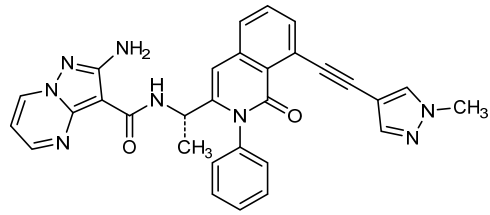
eganelisibum

eganelisib — 2-amino-*N*-[(1*S*)-1-{8-[(1-methyl-1*H*-pyrazol-4-yl)ethynyl]-1-oxo-2-phenyl-1,2-dihydroisoquinolin-3-yl}ethyl]pyrazolo[1,5-*a*]pyrimidine-3-carboxamide

éganélisib — 2-amino-*N*-[(1*S*)-1-{8-[(1-méthyl-1*H*-pyrazol-4-yl)éthynyl]-1-oxo-2-phényl-1,2-dihydroisoquinoléin-3-yl}éthyl]pyrazolo[1,5-*a*]pyrimidine-3-carboxamide

eganelisib — 2-amino-*N*-[(1*S*)-1-{2-fenil-8-[(1-metil-1*H*-pirazol-4-il)etinil]-1-oxo-1,2-dihidroisoquinolein-3-il}etil]pirazolo[1,5-*a*]pirimidina-3-carboxamida

$C_{30}H_{24}N_8O_2$



elasomeranum #

elasomeran — messenger RNA (mRNA), 5'-capped, encoding a full-length, codon-optimised pre-fusion stabilised conformation variant (K986P and V987P) of the SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2; GenBank ID MN908947.3) spike (S) glycoprotein, further optimized by two additional stop codons, flanked by an artificial 5' untranslated region (UTR) and a 3' UTR derived from the human alpha globin gene (HBA1) and terminated by a 3' poly(A) tail; contains N^1-methylpseudouridine instead of uridine (*all*-U>m$^1\Psi$).

élasoméran — ARN messager (ARNm), protégé d' une coiffe en 5', codant la séquence entière d' un variant de la glycoprotéine de spicule (S) du SARS-CoV-2 (coronavirus 2 du syndrome respiratoire aigu sévère; GenBank ID MN908947.3) à la conformation stabilisée par pré-fusion (K986P et V987P) et aux codons optimisés, optimisation renforcée par l'ajout de deux codons stop, flanqué d'une région non traduite (UTR) en 5' artificielle et d' une UTR en 3' dérivée du gène de l'alpha-globine humaine (HBA1) et terminé par une queue poly(A) en 3'; contient de la N^1-méthylpseudouridine au lieu de l'uridine (*all*-U>m$^1\Psi$).

elasomerán — ARN mensajero (ARNm), protegido en 5', que codifica para una variante estabilizada en conformación pre-fusión (K986P and V987P) de la glicoproteína de la espícula (S) del SARS-Cov-2 (coronavirus 2 del síndrome respiratorio agudo severo; GenBank ID MN908947.3) completa, con codones optimizados, con dos codones de terminación adicionales, flanqueado por una región 5' no traducida (UTR) artificial y una UTR en 3' derivada del gen de de la globina alfa humana (HBA1) y terminado por una cola poly(A) en 3'; contiene N^1-metilpseudouridina en lugar de uridina (*all*-U>m$^1\Psi$).

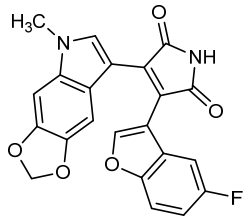
elraglusibum

elraglusib — 3-(5-fluoro-1-benzofuran-3-yl)-4-(5-methyl-5*H*-[1,3]dioxolo[4,5-*f*]indol-7-yl)-1*H*-pyrrole-2,5-dione

elraglusib — 3-(5-fluoro-1-benzofuran-3-yl)-4-(5-méthyl-5*H*-[1,3]dioxolo[4,5-*f*]indol-7-yl)-1*H*-pyrrole-2,5-dione

elraglusib — 3-(5-fluoro-1-benzofuran-3-il)-4-(5-metil-5*H*-[1,3]dioxolo[4,5-*f*]indol-7-il)-1*H*-pirrol-2,5-diona

$C_{22}H_{13}FN_2O_5$



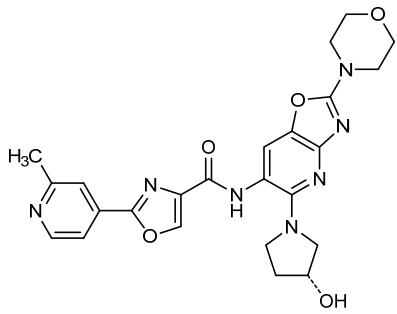
emavusertibum

emavusertib — *N*-{5-[(3*R*)-3-hydroxypyrrolidin-1-yl]-2-(morpholin-4-yl)[1,3]oxazolo[4,5-*b*]pyridin-6-yl}-2-(2-methylpyridin-4-yl)-1,3-oxazole-4-carboxamide

émavusertib — *N*-{5-[(3*R*)-3-hydroxypyrrolidin-1-yl]-2-(morpholin-4-yl)[1,3]oxazolo[4,5-*b*]pyridin-6-yl}-2-(2-méthylpyridin-4-yl)-1,3-oxazole-4-carboxamide

emavusertib — *N*-{5-[(3*R*)-3-hidroxipirrolidin-1-il]-2-(morfolin-4-il)[1,3]oxazolo[4,5-*b*]piridin-6-il}-2-(2-metilpiridin-4-il)-1,3-oxazol-4-carboxamida

$C_{24}H_{25}N_7O_5$



emvododstatum

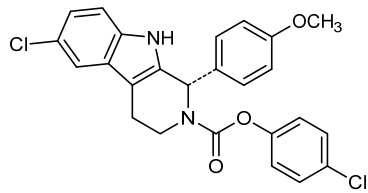
emvododstat — 4-chlorophenyl (1*S*)-6-chloro-1-(4-methoxyphenyl)-1,3,4,9-tetrahydro-2*H*-pyrido[3,4-*b*]indole-2-carboxylate

emvododstat — (1*S*)-6-chloro-1-(4-méthoxyphényl)-1,3,4,9-tétrahydro-2*H*-pyrido[3,4-*b*]indole-2-carboxylate de 4-chlorophényle

emvododstat

(1*S*)-6-cloro-1-(4-metoxifenil)-1,3,4,9-tetrahidro-2*H*-pirido[3,4-*b*]indol-2-carboxilato de 4-clorofenilo

$C_{25}H_{20}Cl_2N_2O_3$



encoberminogenum rezmadenovecum #

encoberminogene rezmadenovec

A replication-deficient recombinant adenovirus, serotype 5, encoding multiple human vascular endothelial growth factor (VEGF) isoforms.
A replication-deficient recombinant adenovirus, serotype 5 (Ad5), encoding multiple human vascular endothelial growth factor (VEGF) isoforms (VEGF121, VEGF165 and VEGF189) under the control of a cytomegalovirus immediate early promoter/enhancer (CMV) and the simian virus 40 (SV40) polyA sequence. Alternative splicing provides mRNA that encodes the three major isoforms of VEGF: VEGF121 (exons 1-5 and 8), VEGF165 (exons 1-5, 7 and 8) and VEGF189 (exons 1-5, 6A, 7 and 8). The VEGF transgene is inserted into the region from which the adenovirus early gene *E1A* is deleted and *E1B* is partially deleted; the *E3* gene is deleted between late gene *L5* and the early gene *E4*.

encoberminogène rezmadénovec

Un adénovirus recombinant déficient à la réplication, de sérotype 5, codant de multiples isoformes du facteur de croissance de l'endothélium vasculaire humain (VEGF).
Un adénovirus recombinant déficient à la réplication, de sérotype 5 (Ad5), codant de multiples isoformes (VEGF121, VEGF165 et VEGF189) du facteur de croissance de l'endothélium vasculaire humain (VEGF) sous le contrôle d'un promoteur/activateur précoce immédiat du cytomégalovirus (CMV) et d'une séquence polyA du virus simien (SV40). L'épissage alternatif génère un ARNm qui code trois isoformes majeures du VEGF : VEGF121 (exons 1-5 et 8), VEGF165 (exons 1-5, 7 et 8) et VEGF189 (exons 1-5, 6A, 7 et 8). Le transgène VEGF est inséré dans la région de laquelle le gène précoce de l'adénovirus *E1A* est supprimé et où *E1B* est partiellement supprimé; le gène E3 est supprimé entre le gène tardif *L5* et le gène précoce *E4*.

encoberminogén rezmadenovec

Un adenovirus recombinante, deficiente en replicación, serotipo 5, que codifica para múltiples isoformas del factor de crecimiento del endotelio vascular humano (VEGF).

Un adenovirus recombinante, deficiente en replicación, serotipo 5 (Ad5), que codifica para múltiples isoformas del factor de crecimiento del endotelio vascular humano (VEGF) (VEGF121, VEGF165 y VEGF189) bajo el control de un promotor/potenciador inmediato temprano del citomegalovirus (CMV) y una secuencia polyA del virus 40 de simios (SV40). El procesamiento alternativo proporciona mRNA que codifica para las tres principales isoformas de VEGF: VEGF121 (exones 1-5 y 8), VEGF165 (exones 1-5, 7 y 8) y VEGF189 (exones 1-5, 6A, 7 y 8). El transgén VEGF está insertado en la región en la que el gen temprano *E1A* del adenovirus está delecionado y *E1B* está parcialmente delecionado; el gen *E3* está delecionado entre el gen tardío *L5* y el gen temprano *E4*.

ensovibepum #

ensovibep

fusion protein consisting of two identical engineered ankyrin repeats-containing binding protein domains anti-(human albumin) (1-126 fused via peptidyl linker ^{127}GSPTPTPTTPTPTPTTPTPTPT^{148} to 149-274), fused via peptidyl linker ^{275}GSPTPTPTTPTPTPTTPTPTPT^{296} to three engineered ankyrin repeats-containing binding protein domains anti-(three different epitopes of the SARS-CoV-2 spike glycoprotein) (297-455 fused via peptidyl linker ^{456}GSPTPTPTTPTPTPTTPTPTPT^{477} to 478-636 in turn fused via peptidyl linker ^{637}GSPTPTPTTPTPTPTTPTPTPT^{658} to 659-817), produced in *Escherichia coli;*
fusion protein comprising five engineered protein-binding ankyrin repeat protein domains: two identical human serum albumin (HSA)-binding 126-peptides 1-126 and 149-274 plus three different 159-peptides 297-455, 478-636 and 659-817 that bind to three different epitopes of the spike glycoprotein (S protein, S1S2 protein) of SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2), connected by four $GS(PT)_3T(PT)_3T(PT)_3$ 22-peptide linkers 127-148, 275-296, 456-477 and 637-658, produced in *Escherichia coli*

ensovibep

protéine de fusion consistant de deux répétitions ankyrine identiques issues de l'ingénierie-contenant des domaines de protéines de liaison anti-(albumine humaine) (1-126 fusionné via un linker peptidique ^{127}GSPTPTPTTPTPTPTTPTPTPT^{148} au 149-274), fusionné via un linker peptidique ^{275}GSPTPTPTTPTPTPTTPTPTPT^{296} à trois répétitions ankyrine issues de l'ingénierie-contenant des domaines de protéines de liaison anti-(trois épitopes différents de la glycoprotéine de spicule) (297-455 fusionné via un linker peptidique ^{456}GSPTPTPTTPTPTPTTPTPTPT^{477} au 478-636 fusionné à son tour via un linker peptidique ^{637}GSPTPTPTTPTPTPTTPTPTPT^{658} au 659-817), produit chez *Escherichia coli*;
protéine de fusion consistant de cinq protéines issues de l'ingénierie-liant des domaines protéiques de répétitions ankyrine: deux albumines sériques humaines identiques (HAS)-liant 126-peptides 1-126 et 149-274 plus trois différents 159-peptides 297-455, 478-636 et 659-817 liés aux trois épitopes différents de la glycoprotéine de spicule (protéine S, protéine S1S2) du SARS-CoV-2 (coronavirus 2 du syndrome respiratoire aigu sévère), connectés par quatre $GS(PT)_3T(PT)_3T(PT)_3$ 22-linkers peptidiques 127-148, 275-296, 456-477 et 637-658, produit chez *Escherichia coli*

ensovibep

proteína de fusión consistente en dos dominios anti-(albúmina humana) diseñados de forma idéntica conteniendo repeticiones de anquirina (1-126 fusionada a través de un enlace peptidil ^{127}GSPTPTPTTPTPTPTTPTPTPT^{148} a 149-274), fusionado a través de un enlace peptidil ^{275}GSPTPTPTTPTPTPTTPTPTPT^{296} a tres dominios anti-(tres epítopos diferentes de SARS-CoV-2 glicoproteína espícula) diseñados conteniendo repeticiones de anquirina (297-455 fusionados a través del enlace pepitdil ^{456}GSPTPTPTTPTPTPTTPTPTPT^{477} a 478-636 por turno fusionado a través de un enlace peptidil ^{637}GSPTPTPTTPTPTPTTPTPTPT^{658} to 659-817), producido en *Escherichia coli*;
proteína de fusión que comprende cinco dominios diseñados conteniendo repeticiones de union a proteína anquirina: dos albúminas séricas idénticas humanas aglutinantes-(HSA) 126-péptidos 1-126 y 149-274 y además 159-péptidos 297-455, 478-636 y 659-817 que se une a 3 epítopos distintos de la glicoproteína espícula (S proteína, S1S2 proteína) de SARS-CoV-2 (síndrome severo agudo respiratorio del coronavirus 2) conectado por cuatro enlaces tipo péptido 127-148, 275-296, 456-477 y 637-658, producido en *Escherichia coli*

Sequence / Séquence / Secuencia

M 0

```
GSDLGKKLLE AARAGQDDEV RELLKAGADV NAKDYFSHTP LHLAARNGHL   50
KIVEVLLKAG ADVNAKDFAG KTPLHLAANE GHLEIVEVLL KAGADVNAQD  100
IFGKTPADIA ADAGHEDIAE VLQKAAGSPT PTPTTPTPTP TTPTPTPTGS  150
DLGKKLLEAA RAGQDDEVRE LLKAGADVNA KDYFSHTPLH LAARNGHLKI  200
VEVLLKAGAD VNAKDFAGKT PLHLAANEGH LEIVEVLLKA GADVNAQDIF  250
GKTPADIAAD AGHEDIAEVL QKAAGSPTPT PTTPTPTPTT PTPTPTGSDL  300
GKKLLQAARA GQLDEVRELL KAGADVNAKD REGITPLHLA AQHGHLEIVE  350
VLLKAGADVN AKDVWGRTPL HLAAWQGHLE IVEVLLKAGA DVNAKDLAGA  400
TPLHVAALYG HLEIVEVLLK AGADVNAQDK SGKTPADLAA RAGHQDIAEV  450
LQKAAGSPTP TPTTPTPTPT TPTPTPTGSD LGKKLLQAAR AGQLDEVREL  500
LKAGADVNAK DREGKTPLHV AAQEGHLEIV EVLLKAGADV NAKDVWGRTP  550
LHLAAWIGHL EIVEVLLKAG ADVNAKDVSG ATPLHAAALH GHLEIVEVLL  600
NAGADVNAQD KSGKTPADLA ARAGHQDIAE VLQKAAGSPT PTPTTPTPTP  650
TTPTPTPTGS DLGKKLLQAA RAGQLDEVRE LLKAGADVNA KDQEGITPLH  700
VAAHQGHLEI VEVLLKAGAD VNAKDVWGRT PLHLAAWRGH LEIVEVLLKA  750
GADVNAKDHA GATPLHAAAL SGHLEIVEVL LKAGADVNAQ DKSGKTPADL  800
AARAGHQDIA EVLQKAA                                      817
```

italicized *underlined* *letters*: 22-peptide linkers $GS(PT)_3T(PT)_3T(PT)_3$

Glycosylation sites / Sites de glycosylation / Posiciones de glicosilación:
none / aucune / ninguna

M: Met^0 is clipped

enuvaptanum

enuvaptan

3-({3-(4-chlorophenyl)-5-oxo-4-[(2S)-3,3,3-trifluoro-2-hydroxypropyl]-4,5-dihydro-1*H*-1,2,4-triazol-1-yl}methyl)-1-[3-(trifluoromethyl)pyridin-2-yl]-1*H*-1,2,4-triazole-5-carboxamide

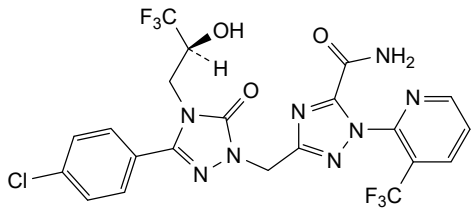
énuvaptan

3-({3-(4-chlorophényl)-5-oxo-4-[(2S)-3,3,3-trifluoro-2-hydroxypropyl]-4,5-dihydro-1*H*-1,2,4-triazol-1-yl}méthyl)-1-[3-(trifluorométhyl)pyridin-2-yl]-1*H*-1,2,4-triazole-5-carboxamide

enuvaptán

3-({3-(4-clorofenil)-5-oxo-4-[(2S)-3,3,3-trifluoro-2-hidroxipropil]-4,5-dihidro-1*H*-1,2,4-triazol-1-il}metil)-1-[3-(trifluorometil)piridin-2-il]-1*H*-1,2,4-triazol-5-carboxamida

$C_{21}H_{15}ClF_6N_8O_3$



eramkafuspum alfa #

eramkafusp alfa

chimeric immunoglobulin G1-kappa anti-(human B-lymphocyte antigen CD20) *(rituximab (77)(39)),* fused at the C-terminus of both heavy chains (1-451) via peptidyl linker ^{452}SGGGGS^{457} to human interferon α-2b (IFNα-2b) fragment (24-188, 458-622 in the current sequence) variant (^{23}K>R^{480}), dimer, glycosylated, produced in Chinese hamster ovary (CHO) cells;
immunoglobulin G1-kappa, anti-[*Homo sapiens* CD20 antigen (B-lymphocyte antigen CD20)], humanized monoclonal antibody *(rituximab (77)(39))*, gamma1 heavy chain humanized (1-451) [*Mus musculus* IGHV1-12*01; *Mus musculus* IGHJ1*01; *Homo sapiens* IGHG1*01; VH: 1-121; CH1: 122-219; hinge 220-234; CH2: 235-344; CH3: 345-449; CHS: 450-451; CDRKabatH1: SYNMH (31-35); CDRKabatH2: AIYPGNGDTSYNQKFKG (50-66); CDRKabatH3: STYYGGDWYFNV (99-110)], fused via a SG_4S linker (452-457) with interferon α-2b (*Homo sapiens*) [K^{23}>R^{480}]-variant (458-622), (224-213')-disulfide with kappa light chain humanized (1'-213') [*Mus musculus* IGKJ1*01; *Homo sapiens* IGKC*01; VL: 1-111; CL: 112-218; CDRKabatL1: RASSSVSYIH (24-33); CDRKabatL2: ATSNLAS (49-55); CDRKabatL3: QQWTSNPPT (88-96)]; dimer (230-230":233-233")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

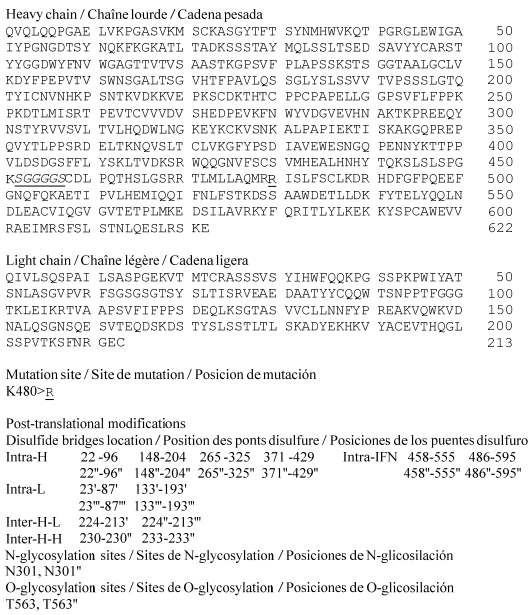
éramkafusp alfa

immunoglobuline chimérique G1-kappa anti-(antigène CD20 du lymphocyte B humain) (rituximab (77)(39)), fusionnée à la partie C-terminale des deux chaînes lourdes (1-451) via le linker peptidique 452SGGGGS457 du fragment (24-188, 458-622 de la séquence actuelle) de l'interféron α-2b (IFNα-2b) variant (23K>R480), dimère, glycosylée, produite dans des cellules ovariennes de hamster chinois (CHO);

immunoglobuline G1-kappa, anti-[antigène CD20 *Homo sapiens* des lymphocytes B), anticorps monoclonal humanisé *(rituximab (77)(39))*, chaîne lourde gamma1 humanisée (1-451) [*Mus musculus* IGHV1-12*01; *Mus musculus* IGHJ1*01; *Homo sapiens* IGHG1*01; VH: 1-121; CH1: 122-219; charnière 220-234; CH2: 235-344; CH3: 345-449; CHS: 450-451; CDRKabatH1: SYNMH (31-35); CDRKabatH2: AIYPGNGDTSYNQKFKG (50-66); CDRKabatH3: STYYGGDWYFNV (99-110)], fusionnée via le linker SG_4S (452-457) avec l'interféron α-2b (*Homo sapiens*) variant $K^{23}>R^{480}$ (458-622), (224-213')-disulfure avec la chaîne légère kappa humanisée (1'-213') [*Mus musculus* IGKJ1*01; *Homo sapiens* IGKC*01; VL: 1-111; CL: 112-218; CDRKabatL1: RASSSVSYIH (24-33); CDRKabatL2: ATSNLAS (49-55); CDRKabatL3: QQWTSNPPT (88-96)]; dimère (230-230":233-233")-bisdisulfure, produite dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

eramkafusp alfa

inmunoglobulina quimérica G1-kappa anti-(antígeno de linfocitos B CD20 humano) *(rituximab (77)(39)),* fusionado en la C-terminal de ambas cadenas pesadas (1-451) a través de un enlace peptidil $^{452}SGGGGS^{457}$ al fragmento del interferón α-2b (IFNα-2b) humano (24-188, 458-622 en la secuencia actual) variante ($^{23}K>R^{480}$), dímero, glicosilado, producido en células ováricas de hámster chino (CHO);
inmunoglobulina G1-kappa, anti-(*Homo sapiens* antígeno CD20 de los linfocitos B), anticuerpo monoclonal humanizado *(rituximab (77)(39))*, cadena pesada gamma1 humanizada (1-451) [*Mus musculus* IGHV1-12*01; *Mus musculus* IGHJ1*01; *Homo sapiens* IGHG1*01; VH: 1-121; CH1: 122-219; bisagra 220-234; CH2: 235-344; CH3: 345-449; CHS: 450-451; CDRKabatH1: SYNMH (31-35); CDRKabatH2: AIYPGNGDTSYNQKFKG (50-66); CDRKabatH3: STYYGGDWYFNV (99-110)], fusionado a través de un péptido conector SG_4S (452-457) con interferón α-2b (*Homo sapiens*) variante $K^{23}>R^{480}$ (458-622), (224-213')-disulfuro con la cadena ligera kappa humanizada (1'-213') [*Mus musculus* IGKJ1*01; *Homo sapiens* IGKC*01; VL: 1-111; CL: 112-218; CDRKabatL1: RASSSVSYIH (24-33); CDRKabatL2: ATSNLAS (49-55); CDRKabatL3: QQWTSNPPT (88-96)]; dímero (230-230":233-233")-bisdisulfuro, producido en células ováricas de hámster chino (CHO), glicoforma alfa



Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLQQPGAE LVKPGASVKM SCKASGYTFT SYNMHWVKQT PGRGLEWIGA    50
IYPGNGDTSY NQKFKGKATL TADKSSSTAY MQLSSLTSED SAVYYCARST   100
YYGGDWYFNV WGAGTTVTVS AASTKGPSVF PLAPSSKSTS GGTAALGCLV   150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ   200
TYICNVNHKP SNTKVDKKVE PKSCDKTHTC PPCPAPELLG GPSVFLFPPK   250
PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY   300
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP   350
QVYTLPPSRD ELTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP   400
VLDSDGSFFL YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG   450
KSGGGGSCDL PQTHSLGSRR TLMLLAQMRR ISLFSCLKDR HDFGFPQEEF   500
GNQFQKAETI PVLHEMIQQI FNLFSTKDSS AAWDETLLDK FYTELYQQLN   550
DLEACVIQGV GVTETPLMKE DSILAVRKYF QRITLYLKEK KYSPCAWEVV   600
RAEIMRSFSL STNLQESLRS KE                                 622
```

Light chain / Chaîne légère / Cadena ligera

```
QIVLSQSPAI LSASPGEKVT MTCRASSSVS YIHWFQQKPG SSPKPWIYAT    50
SNLASGVPVR FSGSGSGTSY SLTISRVEAE DAATYYCQQW TSNPPTFGGG   100
TKLEIKRTVA APSVFIFPPS DEQLKSGTAS VVCLLNNFYP REAKVQWKVD   150
NALQSGNSQE SVTEQDSKDS TYSLSSTLTL SKADYEKHKV YACEVTHQGL   200
SSPVTKSFNR GEC                                           213
```

Mutation site / Site de mutation / Posicion de mutación
K480>R

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

Intra-H	22 -96	148-204	265 -325	371 -429	Intra-IFN	458-555	486-595
	22"-96"	148"-204"	265"-325"	371"-429"		458"-555"	486"-595"
Intra-L	23'-87'	133'-193'					
	23'"-87'"	133'"-193'"					
Inter-H-L	224-213'	224"-213'"					
Inter-H-H	230-230"	233-233"					

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
N301, N301"
O-glycosylation sites / Sites de O-glycosylation / Posiciones de O-glicosilación
T563, T563"

erfonrilimabum #

erfonrilimab	immunoglobulin G1 VH-VH-h-CH2-CH3 dimer, anti-[*Homo sapiens* CD274 (programmed death ligand 1, PDL1, PD-L1, B7 homolog 1, B7H1)] and anti-[*Homo sapiens* CTLA4 (cytotoxic T-lymphocyte-associated protein 4, CD152)], chimeric and humanized monoclonal antibody, bispecific; gamma1 VH-VH-h-CH2-CH3 chain, chimeric and humanized (1-493) [VH anti-CD274 Vicpac/Homsap (*Vicugna pacos* IGHV3-3*01 (80.6%) -(IGHD) -IGHJ5*01 (92.3)/*Homo sapiens* IGHV3-64*04 (78.4%) -(IGHD) -IGHJ1*01 (92.9%)) CDR-IMGT [8.8.21] (26-33.51-58.97-117) (1-128)] -3-mer glycyl-alanyl-prolyl linker (129-131) -[VH anti-CTLA4 humanized (*Homo sapiens* IGHV3-NL1*01 (86.6%) -(IGHD) -IGHJ4*01 (92.9%)) CDR-IMGT [8.8.21] (157-164.182-189.228-248) (132-259)] -2-mer glycyl-seryl linker (260-261) -[*Homo sapiens* IGHG1*01, G1m1 D12, L14, G1v37 h S5, hinge-CH2-CH3 (100%) (hinge 1-15 C5>S (266) (262-276), CH2 (277-386), CH3 D12 (402), L14 (404) (387-491), CHS (492-493)) (262-493)], dimer (272-272":275-275")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa
erfonrilimab	immunoglobuline G1 VH-VH-h-CH2-CH3 dimère, anti-[*Homo sapiens* CD274 (ligand 1 de mort programmée, PDL1, PD-L1, homologue 1 de B7, B7H1)] et anti-[*Homo sapiens* CTLA4 (protéine 4 associée aux lymphocytes T cytotoxiques, CD152)], anticorps monoclonal chimérique et humanisé, bispécifique; gamma1 VH-VH-h-CH2-CH3 chaîne, chimérique et humanisée (1-493) [VH anti-CD274 Vicpac/Homsap (*Vicugna pacos* IGHV3-3*01 (80.6%) -(IGHD) -IGHJ5*01 (92.3)/*Homo sapiens* IGHV3-64*04 (78.4%) -(IGHD) -IGHJ1*01 (92.9%)) CDR-IMGT [8.8.21] (26-33.51-58.97-117) (1-128)] -3-mer glycyl-alanyl-prolyl linker (129-131) -[VH anti-CTLA4 humanisé (*Homo sapiens* IGHV3-NL1*01 (86.6%) -(IGHD) -IGHJ4*01 (92.9%)) CDR-IMGT [8.8.21] (157-164.182-189.228-248) (132-259)] -2-mer glycyl-séryl linker (260-261) -[*Homo sapiens* IGHG1*01, G1m1 D12, L14, G1v37 h S5, charnière-CH2-CH3 (100%) (charnière 1-15 C5>S (266) (262-276), CH2 (277-386), CH3 D12 (402), L14 (404) (387-491), CHS (492-493)) (262-493)], dimère (272-272":275-275")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa
erfonrilimab	inmunoglobulina G1 VH-VH-h-CH2-CH3 dímero, anti-[*Homo sapiens* CD274 (ligando 1 de muerte programada, PDL1, PD-L1, homólogo 1 de B7, B7H1)] y anti-[*Homo sapiens* CTLA4 (proteína 4 asociada con los linfocitos T citotóxicos, CD152)], anticuerpo monoclonal quimérico y humanizado, biespecífico; gamma1 VH-VH-h-CH2-CH3 cadena, quimérica y humanizada (1-493) [VH anti-CD274 Vicpac/Homsap (*Vicugna pacos* IGHV3-3*01 (80.6%) -(IGHD) -IGHJ5*01 (92.3)/*Homo sapiens* IGHV3-64*04 (78.4%) -(IGHD) -IGHJ1*01 (92.9%)) CDR-IMGT [8.8.21] (26-33.51-58.97-117) (1-128)] -3-mer glicil-alanil-prolil linker (129-131) -[VH anti-CTLA4 humanizado (*Homo sapiens* IGHV3-NL1*01 (86.6%) -(IGHD) -IGHJ4*01 (92.9%)) CDR-IMGT [8.8.21] (157-164.182-189.228-248) (132-259)] -2-mer glicil-seril linker (260-261) -[*Homo sapiens* IGHG1*01, G1m1 D12, L14, G1v37 h S5, bisagra-CH2-CH3 (100%) (bisagra 1-15 C5>S (266) (262-276), CH2 (277-386), CH3 D12 (402), L14 (404) (387-491), CHS (492-493)) (262-493)], dímero (272-272":275-275")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVESGGG LVQPGGSLRL SCAASGKMSS RRCMAWFRQA PGKERERVAK  50
LLTTSGSTYL ADSVKGRFTI SRDNSKNTVY LQMNSLRAED TAVYYCAADS 100
FEDPTCTLVT SSGAFQYWGQ GTLVTVSSGA PQVQLVESGG GLVQPGGSLR 150
LSCAASGYIY SAYCMGWFRQ APGKGLEGVA AIYIGGGSTY YADSVKGRFT 200
ISRDNSKNTL YLQMNSLRAE DTAVYYCAAD VIPTETCLGG SWSGPFGYWG 250
QGTLVTVSSG SEPKSSDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS 300
RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYNSTYRVVS 350
VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR EPQVYTLPPS 400
RDELTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT PPVLDSDGSF 450
FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLS PGK        493
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 153-227 307-367 413-471
22"-96" 153"-227" 307"-367" 413"-471"
Intra-H VH (C38-C111.3) 33-106 164-237
33"-106" 164-237"
Inter-H-H (h 11, h 14) 272-272" 275-275"

N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
H VH Q1:
1, 1"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
343, 343"
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 / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2:
493, 493"

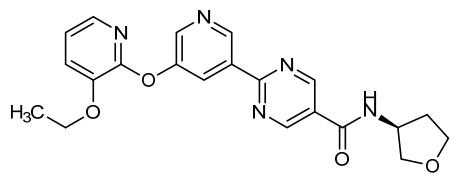
ervogastatum

ervogastat — 2-{5-[(3-ethoxypyridin-2-yl)oxy]pyridin-3-yl}-*N*-[(3*S*)-oxolan-3-yl]pyrimidine-5-carboxamide

ervogastat — 2-{5-[(3-éthoxypyridin-2-yl)oxy]pyridin-3-yl}-*N*-[(3*S*)-oxolan-3-yl]pyrimidine-5-carboxamide

ervogastat — 2-{5-[(3-etoxipiridin-2-il)oxi]piridin-3-yl}-*N*-[(3*S*)-oxolan-3-il]pirimidina-5-carboxamida

$C_{21}H_{21}N_5O_4$



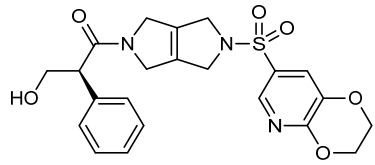
etavopivatum

etavopivat — (2*S*)-1-[5-(2,3-dihydro[1,4]dioxino[2,3-*b*]pyridine-7-sulfonyl)-3,4,5,6-tetrahydropyrrolo[3,4-*c*]pyrrol-2(1*H*)-yl]-3-hydroxy-2-phenylpropan-1-one

étavopivat — (2*S*)-1-[5-(2,3-dihydro[1,4]dioxino[2,3-*b*]pyridine-7-sulfonyl)-3,4,5,6-tétrahydropyrrolo[3,4-*c*]pyrrol-2(1*H*)-yl]-3-hydroxy-2-phénylpropan-1-one

etavopivat — (2*S*)-1-[5-(2,3-dihidro[1,4]dioxino[2,3-*b*]piridina-7-sulfonil)-3,4,5,6-tetrahidropirrolo[3,4-*c*]pirrol-2(1*H*)-il]-2-fenil-3-hidroxipropan-1-ona

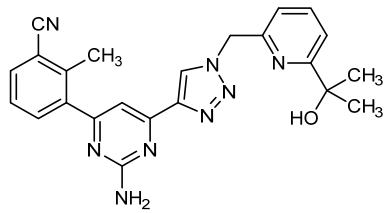
$C_{22}H_{23}N_3O_6S$



etrumadenantum

etrumadenant	3-[2-amino-6-(1-{[6-(2-hydroxypropan-2-yl)pyridin-2-yl]methyl}-1*H*-1,2,3-triazol-4-yl)pyrimidin-4-yl]-2-methylbenzonitrile
étrumadénant	3-[2-amino-6-(1-{[6-(2-hydroxypropan-2-yl)pyridin-2-yl]méthyl}-1*H*-1,2,3-triazol-4-yl)pyrimidin-4-yl]-2-méthylbenzonitrile
etrumadenant	3-[2-amino-6-(1-{[6-(2-hidroxipropan-2-il)piridin-2-il]metil}-1*H*-1,2,3-triazol-4-il)pirimidin-4-il]-2-metilbenzonitrilo

$C_{23}H_{22}N_8O$



exagamglogenum autotemcelum #

exagamglogene autotemcel	Autologous CD34+ cells isolated from mobilised peripheral blood by positive selection, modified by CRISPR/Cas9 (clustered regularly interspaced short palindromic repeats/CRISPR-associated protein 9) mediated gene editing consisting of a guide RNA (gRNA) introduced transiently as ribonucleoprotein (RNP) complex, targeting the erythroid lineage-specific enhancer region of *BCL11A* (B-cell lymphoma/leukemia 11A). The site-specific cleavage by Cas9 forms a double strand break (DSB), which is subsequently repaired by nonhomologous end-joining (NHEJ), leading to the transcriptional repression of *BCL11A*, a repressor of γ-globin gene transcription.
exagamglogène autotemcel	Cellules CD34+ autologues isolées du sang périphérique mobilisé par sélection positive, modifiées par CRISPR/Cas9 (courtes répétitions palindromiques groupées et régulièrement espacées / protéine 9 associée à CRISPR) induisant une édition génétique consistant de deux ARN guides (gRNA) introduisant transitoirement un complexe ribonucléoprotéique,

	ciblant la région activatrice spécifique du lignage des érythroïdes de *BCL11A* (lymphome des cellules B/ leucémie 11A). Le clivage site-spécifique par Cas9 forme une cassure double brin (DSB), qui est ensuite réparée par la jonction d'extrémités non homologues (NHEJ), menant à la répression transcriptionnelle de BCL11A, un répresseur de la transcription du gène γ-globine.
exagamglogén autotemcel	Células CD34+ autólogas aisladas de células movilizadas en sangre periférica mediante selección positiva, modificadas por CRISPR/Cas9 (repeticiones palindrómicas cortas agrupadas y regularmente espaciadas/proteína asociada a CRISPR 9) mediante edición geníca consistente en un RNA guía (gRNA) introducido transitoriamente como un complejo de ribonucleoproteína (RNP), dirigido a la región potenciadora específica de linaje eritroide de BCL11A (linfoma/leucemia de linfocitos B11A). El corte específico de sitio por Cas9 forma una rotura de la doble hélice (DSB) que es subsiguientemente reparada mediante unión de extremos no homóloga (NHEJ), lo que conduce a la represión transcripcional de BCL11A, un represor de la transcripción del gen de la γ-globina.

fesomersenum

fesomersen	*all-P-ambo*-5'-*O*-(28-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]-16,16-bis{[3-({6-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]hex-yl}amino)-3-oxopropoxy]methyl}-1-hydroxy-1,10,14,21-tetraoxo-2,18-dioxa-9,15,22-triaza-1λ^5-phosphaoctacosan-1-yl)-2'-*O*-(2-methoxyethyl)-*P*-thioadenylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methylcytidylyl-(3'→5')-2'-*O*-(2-methoxyethyl)guanylyl-(3'→5')-2'-*O*-(2-methoxyethyl)guanylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methylcytidylyl-(3'→5')-2'-deoxy-*P*-thioadenylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-deoxy-*P*-thioguanylyl-(3'→5')-2'-deoxy-*P*-thioguanylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-deoxy-*P*-thioguanylyl-(3'→5')-2'-deoxy-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-deoxy-*P*-thioadenylyl-(3'→5')-2'-deoxy-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-methoxyethyl)adenylyl-(3'→5')-2'-*O*-(2-methoxyethyl)guanylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyl-*P*-thiouridylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyl-*P*-thiouridylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyluridine
fésomersen	*tout-P-ambo*-5'-*O*-(28-[(2-acétamido-2-désoxy-β-D-galactopyranosyl)oxy]-16,16-bis{[3-({6-[(2-acétamido-2-désoxy-β-D-galactopyranosyl)oxy]hexyl}amino)-3-oxopropoxy]méthyl}-1-hydroxy-1,10,14,21-tétraoxo-2,18-dioxa-9,15,22-triaza-1λ^5-phosphaoctacosan-1-yl)-2'-*O*-(2-méthoxyéthyl)-*P*-thioadénylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthylcytidylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)guanylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)guanylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-

5-méthylcytidylyl-(3'→5')-2'-désoxy-*P*-thioadénylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-désoxy-*P*-thioguanylyl-(3'→5')-2'-désoxy-*P*-thioguanylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-désoxy-*P*-thioguanylyl-(3'→5')-2'-désoxy-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-désoxy-*P*-thioadénylyl-(3'→5')-2'-désoxy-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)adénylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)guanylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthyl-*P*-thiouridylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthyl-*P*-thiouridylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthyluridine

fesomersén

todo-P-ambo-5'-*O*-(28-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]-16,16-bis{[3-({6-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]hexil}-amino)-3-oxopropoxi]metil}-1-hidroxi-1,10,14,21-tetraoxo-2,18-dioxa-9,15,22-triaza-1λ^5-fosfaoctacosan-1-il)-2'-*O*-(2-metoxietil)-*P*-tioadenilil-(3'→5')-5-metil-2'-*O*-(2-metoxietil)citidilil-(3'→5')-2'-*O*-(2-metoxietil)guanilil-(3'→5')-2'-*O*-(2-metoxietil)guanilil-(3'→5')-5-metil-2'-*O*-(2-metoxietil)citidilil-(3'→5')-2'-desoxi-*P*-tioadenilil-(3'→5')-*P*-tiotimidilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2'-desoxi-*P*-tioguanilil-(3'→5')-2'-desoxi-*P*-tioguanilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2'-desoxi-*P*-tioguanilil-(3'→5')-2'-desoxi-5-metil-*P*-tiocitidilil-(3'→5')-2'-desoxi-*P*-tioadenilil-(3'→5')-2'-desoxi-5-metil-*P*-tiocitidilil-(3'→5')-2'-*O*-(2-metoxietil)adenilil-(3'→5')-2'-*O*-(2-metoxietil)guanilil-(3'→5')-5-metil-2'-*O*-(2-metoxietil)-*P*-tiouridilil-(3'→5')-5-metil-2'-*O*-(2-metoxietil)-*P*-tiouridilil-(3'→5')-5-metil-2'-*O*-(2-metoxietil)uridina

$C_{296}H_{434}N_{82}O_{156}P_{20}S_{13}$

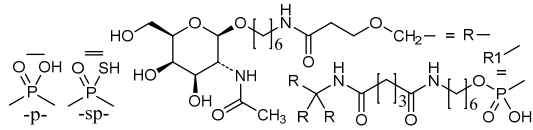
(3'-5') R1-A=C-G-G-C-d(A=T=T=G=G=T=G=C=A=C=)A-G-U=U=U

Legend:

A , G & T : 2'-deoxynucleotide C : 2'-deoxy-5-methylcytidine

A & G : 2'-*O*-(2-methoxyethyl)nucleotide

C & U : 2'-*O*-(2-methoxyethyl)-5-methylnucleotide



finotonlimabum #

finotonlimab

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

	gamma4 heavy chain (1-445) [VH (*Mus musculus* IGHV5-9-2*01 (88.8%) -(IGHD) -IGHJ4*01 (90.9%)/*Homo sapiens* IGHV3-23*04 (86.7%) -(IGHD) -IGHJ3*01 (90.9%)) CDR-IMGT [8.8.11] (26-33.51-58.97-107) (1-118)-*Homo sapiens* IGHG4*01, G4v5 h P10 (CH1 (119-216), hinge 1-12 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 (*Homo sapiens* IGKV3D-11*02 (81.9%) -IGKJ1*01 (100%)) CDR-IMGT [10.3.9] (27-36.54-56.93-101) (1'-111') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218')]; dimer (224-224":227-227")-bisdisulfide, produced in a Chinese hamster ovary (CHO)-DG44 cell line, glycoform alfa
finotonlimab	immunoglobuline G4-kappa, anti-[*Homo sapiens* PDCD1 (protéine 1 de mort cellulaire programmée, PD-1, PD1, CD279)], anticorps monoclonal; chaîne lourde gamma4 (1-445) [VH (*Mus musculus* IGHV5-9-2*01 (88.8%) -(IGHD) -IGHJ4*01 (90.9%)/*Homo sapiens* IGHV3-23*04 (86.7%) -(IGHD) -IGHJ3*01 (90.9%)) CDR-IMGT [8.8.11] (26-33.51-58.97-107) (1-118)-*Homo sapiens* IGHG4*01, G4v5 h P10 (CH1 (119-216), charnière 1-12 S10>P (226) (217-228), CH2 (229-338), CH3 (339-443), CHS (444-445)) (119-445)], (132-218')-disulfure avec la chaîne légère kappa humanisée(1'-218') [V-KAPPA (*Homo sapiens* IGKV3D-11*02 (81.9%) -IGKJ1*01 (100%)) CDR-IMGT [10.3.9] (27-36.54-56.93-101) (1'-111') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218')]; dimère (224-224":227-227")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO) lignée cellulaire CHO-DG44, glycoforme alfa
finotonlimab	inmunoglobulina G4-kappa, anti-[*Homo sapiens* PDCD1 (proteína 1 de muerte celular programada, PD-1, PD1, CD279)], anticuerpo monoclonal; cadena pesada gamma4 (1-445) [VH (*Mus musculus* IGHV5-9-2*01 (88.8%) -(IGHD) -IGHJ4*01 (90.9%)/*Homo sapiens* IGHV3-23*04 (86.7%) -(IGHD) -IGHJ3*01 (90.9%)) CDR-IMGT [8.8.11] (26-33.51-58.97-107) (1-118)-*Homo sapiens* IGHG4*01, G4v5 h P10 (CH1 (119-216), bisagra 1-12 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 humanizado (*Homo sapiens* IGKV3D-11*02 (81.9%) -IGKJ1*01 (100%)) CDR-IMGT [10.3.9] (27-36.54-56.93-101) (1'-111') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218')]; dímero (224-224":227-227")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular CHO-DG44, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVKPGGSLRL SCAASGFTFS SYGMSWVRQA PGKRLEWVAT  50
ISGGGRDTYY SDSVKGRFTI SRDNAKNNLY LQMNSLRAED TAVYYCSRQY 100
GTVWFFNWGQ GTLVTVSSAS 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

```
EIVLTQSPAT LSLSPGERAT LSCRASESVD SYGNSFMHWY QQKPGQPPRL 50
LIYAASNQGS GVPARFSGSG SGTDFTLTIS SLEPEDFAMY FCQQSKEVPW 100
TFGQGTKVEI 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.

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2:
445, 445"

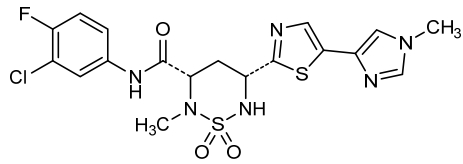
firzacorvirum

firzacorvir — (3*S*,5*R*)-*N*-(3-chloro-4-fluorophenyl)-2-methyl-5-[5-(1-methyl-1*H*-imidazol-4-yl)-1,3-thiazol-2-yl]-1,1-dioxo-1λ^6,2,6-thiadiazinane-3-carboxamide

firzacorvir — (3*S*,5*R*)-*N*-(3-chloro-4-fluorophényl)-2-méthyl-5-[5-(1-méthyl-1*H*-imidazol-4-yl)-1,3-thiazol-2-yl]-1,1-dioxo-1λ^6,2,6-thiadiazinane-3-carboxamide

firzacorvir — (3*S*,5*R*)-*N*-(3-cloro-4-fluorofenil)-2-metil-5-[5-(1-metil-1*H*-imidazol-4-il)-1,3-tiazol-2-il]-1,1-dioxo-1λ^6,2,6-tiadiazinano-3-carboxamida

$C_{18}H_{18}ClFN_6O_3S_2$



foscenvivintum

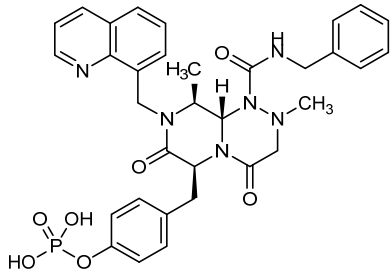
foscenvivint — 4-({(6*S*,9*S*,9a*S*)-1-(benzylcarbamoyl)-2,9-dimethyl-4,7-dioxo-8-[(quinolin-8-yl)methyl]octahydro-2*H*-pyrazino[2,1-*c*][1,2,4]triazin-6-yl}methyl)phenyl dihydrogen phosphate

foscenvivint — dihydrogénophosphate de 4-({(6*S*,9*S*,9a*S*)-1-(benzylcarbamoyl)-2,9-diméthyl-4,7-dioxo-8-[(quinoléin-8-yl)méthyl]octahydro-2*H*-pyrazino[2,1-*c*][1,2,4]triazin-6-yl}méthyl)phényle

foscenvivint

dihidrogenofosfato de 4-({(6*S*,9*S*,9a*S*)-1-(bencilcarbamoil)-2,9-dimetil-4,7-dioxo-8-[(quinolein-8-il)metil]octahidro-2*H*-pirazino[2,1-*c*][1,2,4]triazin-6-il}metil)fenilo

$C_{33}H_{35}N_6O_7P$



govorestatum

govorestat

(4-oxo-3-{[5-(trifluoromethyl)-1,3-benzothiazol-2-yl]methyl}-3,4-dihydrothieno[3,4-*d*]pyridazin-1-yl)acetic acid

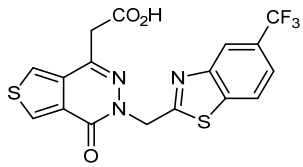
govorestat

acide (4-oxo-3-{[5-(trifluorométhyl)-1,3-benzothiazol-2-yl]méthyl}-3,4-dihydrothiéno[3,4-*d*]pyridazin-1-yl)acétique

govorestat

ácido (4-oxo-3-{[5-(trifluorometil)-1,3-benzotiazol-2-il]metil}-3,4-dihidrotieno[3,4-*d*]piridazin-1-il)acético

$C_{17}H_{10}F_3N_3O_3S_2$



guretolimodum

guretolimod

[({4-[(2-amino-4-{[(3*S*)-1-hydroxyhexan-3-yl]amino}-6-methylpyrimidin-5-yl)methyl]-3-methoxyphenyl}methyl)(2,2,2-trifluoroethyl)amino]acetic acid

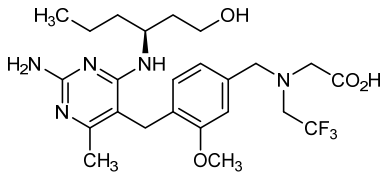
gurétolimod

acide [({4-[(2-amino-4-{[(3*S*)-1-hydroxyhexan-3-yl]amino}-6-méthylpyrimidin-5-yl)méthyl]-3-méthoxyphényl}méthyl)(2,2,2-trifluoroéthyl)amino]acétique

guretolimod

ácido [({4-[(2-amino-4-{[(3*S*)-1-hidroxihexan-3-il]amino}-6-metilpirimidin-5-il)metil]-3-metoxifenil}metil)(2,2,2-trifluoroetil)amino]acético

$C_{24}H_{34}F_3N_5O_4$



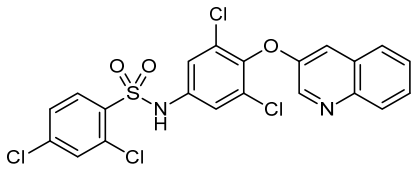
ibrigamparum

ibrigampar — 2,4-dichloro-*N*-{3,5-dichloro-4-[(quinolin-3-yl)oxy]phenyl}benzene-1-sulfonamide

ibrigampar — 2,4-dichloro-*N*-{3,5-dichloro-4-[(quinoléin-3-yl)oxy]phényl}benzène-1-sulfonamide

ibrigampar — 2,4-dicloro-*N*-{3,5-dicloro-4-[(quinolein-3-il)oxi]fenil}benceno-1-sulfonamida

$C_{21}H_{12}Cl_4N_2O_3S$



ilofotasum alfa #

ilofotase alfa — human intestinal-type alkaline phosphatase (IAP) variant (H^{279}>L, L^{328}>V, P^{478}>L), engineered by substituting its crown domain (366-430) with the human placental-type alkaline phosphatase (placental alkaline phosphatase 1, PLAP-1) crown domain (364-428, 366-430 in the current sequence), C-terminal linked glycosylphosphatidylinositol anchor removed, dimer, glycosylated, produced in Chinese hamster ovary (CHO) cells;
human intestinal-type alkaline phosphatase (ALPI, intestinal alkaline phosphatase, IAP) variant [H^{279}>L, L^{328}>V, P^{478}>L] (1-484) with its crown domain (65-peptide 366-430) being replaced by the human placental-type alkaline phosphatase (ALPP, alkaline phosphatase Regan isozyme, placental alkaline phosphatase 1, PLAP-1) crown domain (65-peptide 364-428) (366-430), dimer (481-481')-disulfide, without glycosylphosphatidylinositol (GPI) anchors at Asp-484 and Asp-484' (secretable, soluble enzyme), produced in Chinese hamster ovary (CHO) cells, glycoform alfa

ilofotase alfa — variant (H279>L, L328>V, P478>L) de la phosphatase alcaline humaine de type intestinal (IAP), conçu en substituant son domaine couronne (366-430) avec le domaine couronne (364-428, 366-430 dans la séquence actuelle) de la phosphatase alcaline humaine de type placentaire (phosphatase alcaline placentaire 1, PLAP-1), élimination de l'ancrage glycosylphosphatidylinositol lié à la partie C-terminale, dimère, glycosylé, produit dans des cellules ovariennes de hamster chinois (CHO);

phosphatase alcaline humaine de type intestinal (ALPI, phosphatase alcaline intestinale, IAP) variant [H279>L, L328>V, P478>L] (1-484), dont le domaine couronne (65-peptide 366-430) étant remplacé par le domaine couronne (65-peptide 364-428) de la phosphatase alcaline humaine de type placentaire (ALPP, isoenzyme Regan de la phosphatase alcaline, phosphatase alcaline placentaire 1, PLAP-1) (366-430), dimère (481-481')-disulfure, sans ancrage glycosylphosphatidylinositol (GPI) à Asp-484 et Asp-484' (sécrétable, enzyme soluble), produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

ilofotasa alfa

fosfatasa alcalina de tipo intestinal humana (IAP) variante (H^{279}>L, L^{328}>V, P^{478}>L), diseñada por sustitución de su propio dominio de corona (366-430) con la fosfatasa alcalina de tipo placentaria humana (fosfatasa alcalina placentaria 1, PLAP-1) dominio de corona (364-428, 366-430 en la secuencia actual), C-terminal unido al glicosilfosfatidilinositol anclaje eliminado, dímero, glicosilado, producido en células ováricas de hámster chino (CHO);
fosfatasa alcalina humana del tipo intestinal (ALPI, fosfatasa alcalina intestinal, IAP) variante [H^{279}>L, L^{328}>V, P^{478}>L](1-484) con su dominio corona (65-péptido 366-430) siendo reemplazado por el dominio corona (65-péptido 364-428) de la fosfatasa alcalina humana del tipo placentario (ALPP, isoenzima Regan de fosfatasa alcalina, fosfatasa alcalina placentaria 1, PLAP-1) (366-430), dímero (481-481')-disulfuro, sin anclajes de amidas de glicosilfosfatidilinositol (GPI) en Asp-484 y Asp-484' (soluble y secretable), producido en células ováricas de hámster chino (CHO), glicoforma alfa

Sequence / Séquence / Secuencia

```
VIPAEEENPA FWNRQAAEAL DAAKKLQPIQ KVAKNLILFL GDGLGVPTVT    50
ATRILKGQKN GKLGPETPLA MDRFPYLALS KTYNVDRQVP DSAATATAYL   100
CGVKANFQTI GLSAAARFNQ CNTTRGNEVI SVMNRAKQAG KSVGVVTTTR   150
VQHASPAGTY AHTVNRNWYS DADMPASARQ EGCQDIATQL ISNMDIDVIL   200
GGGRKYMFPM GTPDPEYPAD ASQNGIRLDG KNLVQEWLAK HQGAWYVWNR   250
TELMQASLDQ SVTHLMGLFE PGDTKYEILR DPTLDPSLME MTEAALRLLS   300
RNPRGFYLFV EGGRIDHGHH EGVAYQAVTE AVMFDDAIER AGQLTSEEDT   350
LTLVTADHSH VFSFGGYPLR GSSIFGLAPG KARDRKAYTV LLYGNGPGYV   400
LKDGARPDVT ESESGSPEYR QQSAVPLDEE THGGEDVAVF ARGPQAHLVH   450
GVQEQSFVAH VMAFAACLEP YTACDLALPA CTTD                    484
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Mutation sites / Sites de mutation / Posiciones de mutación
H279>L, L328>V, P478>L, crown domain replacement *G366-E430*
H279'>L, L328'>V, P478'>L, crown domain replacement *G366'-E430'*

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posición del puentes disulfuro
intra-monomer 121-183 467-474 121'-183' 467'-474' (Cys-SH: 101, 101')
inter-monomer 481-481'
Glycosylation sites / Sites de glycosylation / Posiciones de glicosilación
N122, N249, N122', N249'

iltamiocelum

iltamiocel

Autologous human skeletal muscle progenitor cells derived from muscle biopsy (*vastus lateralis*). The progenitor cells are isolated by enzymatic digestion and expanded in culture in growth media containing human recombinant basic fibroblast growth factor (rbFGF), human recombinant endothelial growth factor (rEGF) and fetal bovine serum (FBS). Cell function and phenotype are maintained through control of culture confluence. The cells are positive for the myogenic cell marker desmin (on average 89%), and other muscle specific genes. The final substance contains also non-myogenic cell populations, such as fibroblasts. The cells have been demonstrated to have myogenic cell differentiation capacity.

iltamiocel	Cellules progénitrices autologues humaines du muscle squelettique dérivées d'une biopsie de muscle (*vastus lateralis*). Les cellules progénitrices ont été isolées par digestion enzymatique et placées en culture d'expansion dans un milieu de croissance contenant le facteur de croissance basique recombinant des fibroblastes humain (rbFGF), le facteur de croissance recombinant de l'endothélium humain (rEGF) et le sérum bovin fœtal (FBS). Le phénotype et la fonction cellulaire ont été maintenus en contrôlant la confluence de la culture. Les cellules sont positives pour le marqueur cellulaire myogénique desmine (en moyenne 89%), et d'autres gènes spécifiques des muscles. La substance finale contient aussi des populations cellulaires non-myogéniques tels que les fibroblastes. Il a été démontré que les cellules ont une capacité de différenciation en cellules myogéniques.
iltamiocel	Células progenitoras de músculo esquelético humano autólogas derivadas de biopsia muscular (*vastus lateralis*). Las células progenitoras se aíslan mediante digestión enzimática y se expanden en cultivo con medio de crecimiento que contiene factor de crecimiento de fibroblastos básico humano recombinante (rbFGF), factor de crecimiento endotelial humano recombinante (rEGF) y suero bovino fetal (FBS). La función y el fenotipo celular se mantienen mediante el control de la confluencia del cultivo. Las células son positivas para el marcador de células miogénicas desmina (89% de media), y otros genes específicos de músculo. La substancia final contiene también poblaciones de células no miogénicas, tales como fibroblastos. Se ha demostrado que las células tienen capacidad de diferenciación de células miogénicas.
imsidolimabum #	
imsidolimab	immunoglobulin G4-kappa, anti-[*Homo sapiens* IL36R (interleukin 36 receptor)], monoclonal antibody; gamma4 heavy chain (1-447) [VH (*Homo sapiens* IGHV1-46*01 (84.7%) -(IGHD) -IGHJ1*01 (100%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120)-*Homo sapiens* IGHG4*01 (100%), G4v5 h P10 (CH1 (121-218), hinge 1-12 S10>P (228) (219-230), CH2 (231-340), CH3 (341-445), CHS (446-447) (121-447)], (134-219')-disulfide with kappa light chain (1'-219') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV2-109*01 (85%) -IGKJ1*01 (90.9%)/*Homo sapiens* IGKV2D-29*01 (84%) -IGKJ4*01 (100%)) CDR-IMGT [11.3.9] (27-37.55-57.94-102) (1'-112') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; dimer (226-226'':229-229'')-bisdisulfide, produced in a Chinese hamster ovary (CHO)-S cell line, glycoform alfa
imsidolimab	immunoglobuline G4-kappa, anti-[*Homo sapiens* IL36R (récepteur de l'interleukine 36)], anticorps monoclonal;

chaîne lourde gamma4 (1-447) [VH (*Homo sapiens* IGHV1-46*01 (84.7%) -(IGHD) -IGHJ1*01 (100%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120)-*Homo sapiens* IGHG4*01 (100%), G4v5 h P10 (CH1 (121-218), charnière 1-12 S10>P (228) (219-230), CH2 (231-340), CH3 (341-445), CHS (446-447) (121-447)], (134-219')-disulfure avec la chaîne légère kappa (1'-219') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV2-109*01 (85%) -IGKJ1*01 (90.9%)/*Homo sapiens* IGKV2D-29*01 (84%) -IGKJ4*01 (100%)) CDR-IMGT [11.3.9] (27-37.55-57.94-102) (1'-112') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; dimère (226-226'':229-229'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO) lignée cellulaire CHO-S, glycoforme alfa

imsidolimab

inmunoglobulina G4-kappa, anti-[*Homo sapiens* IL36R (receptor de la interleukina 36)], anticuerpo monoclonal; cadena pesada gamma4 (1-447) [VH (*Homo sapiens* IGHV1-46*01 (84.7%) -(IGHD) -IGHJ1*01 (100%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120)-*Homo sapiens* IGHG4*01 (100%), G4v5 h P10 (CH1 (121-218), bisagra 1-12 S10>P (228) (219-230), CH2 (231-340), CH3 (341-445), CHS (446-447) (121-447)], (134-219')-disulfuro con la cadena ligera kappa (1'-219') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV2-109*01 (85%) -IGKJ1*01 (90.9%)/*Homo sapiens* IGKV2D-29*01 (84%) -IGKJ4*01 (100%)) CDR-IMGT [11.3.9] (27-37.55-57.94-102) (1'-112') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; dímero (226-226'':229-229'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular CHO-S, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGASVKV SCKASGYTFT NYWMNWVRQA PRQGLEWMGM  50
FHPTGDVTRL NQKFKDRVTM TRDTSTSTVY MELSSLRSED TAVYYCARTT 100
SMIIGGFAYW 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
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Light chain / Chaîne légère / Cadena ligera

```
DIVMTQTPLS LSVTPGQPAS ISCRSSKSLL HRNAITYFYW YLHKPGQPPQ  50
LLIYQMSNLA SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCAQNLELP 100
LTFGGGTKVE IKRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK 150
VQWKVDNALQ SGNSQESVTE QDSKDSTYSL SSTLTLSKAD YEKHKVYACE 200
VTHQGLSSPV TKSFNRGEC                                   219
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Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 147-203 261-321 367-425
22"-96" 147"-203 261"-321" 367"-425"
Intra-L (C23-C104) 23'-93' 139'-199'
23"'-93"' 139"'-199"'
Inter-H-L (CH1 10-CL 126) 134-219' 134-219"'
Inter-H-H (h 8, h 11) 226-226" 229-229"

N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
H VH Q1:
1, 1"

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

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2:
447, 447"

inetagugenum geperpavecum #

inetagugene geperpavec	A replication-defective Herpes simplex virus encoding human transglutaminase 1 (TGM1). A recombinant replication-deficient, non-integrating Herpes simplex virus type 1 (HSV-1) (strain KOS) vector encoding two copies of codon-optimised human transglutaminase 1 [TGM1, (EC:2.3.2.13)], also known as protein-glutamine gamma-glutamyltransferase K (TGK) with both copies being expressed under the control of a human cytomegalovirus (hCMV) immediate early promoter and bovine growth hormone polyadenylation signal (bGH polyA). The vector was generated by deleting both copies of the viral immediate early (IE) gene ICP4 and inserting a copy of the TGM1 gene into each ICP4 locus. The vector is also deleted for the IE gene ICP22.
inétagugène géperpavec	Un virus Herpès simplex incompétent à la réplication codant la transglutaminase 1 humaine (TGM1). Un vecteur recombinant du virus Herpès simplex de type 1 (HSV-1) (lignée KOS) incompétent à la réplication, non intégrant, codant deux copies de la transglutaminase 1 humaine [TGM1, (EC:2.3.2.13)] aux codons optimisés aussi connue comme la gamma-glutamyltransférase protéine-glutamine K (TGK) avec deux copies étant exprimées sous le contrôle du promoteur précoce immédiat du cytomégalovirus humain (CMV) et du signal de polyadénylation de l'hormone de croissance bovine (bGH polyA). Le vecteur a été généré en supprimant les deux copies du ICP4, gène viral précoce immédiat (IE) et en insérant une copie du gène TGM1 dans chaque locus ICP4. Le vecteur a aussi été supprimé du ICP22, gène IE.
inetagugén geperpavec	Un virus Herpes simplex deficiente en replicación que codifica para la transglutaminasa humana 1 (TGM1). Un vector del virus Herpes simplex tipo 1 (HSV-1) (cepa KOS) recombinante, deficiente en replicación, no integrativo, que codifica dos copias de la transglutaminasa humana 1[TGM1, (EC:2.3.2.13)] , también conocida como proteína-glutamina gamma-glutamiltransferasa K (TGK), con codones optimizados, y ambas copias siendo expresadas bajo el control del promotor inmediato temprano del citomegalovirus humano (hCMV) y la señal de poliaadenilación de la hormona del crecimiento bovina (bGH polyA).El vector se generó mediante la deleción de ambas copias del gen inmediato temprano (IE) viral ICP4 y la inserción de una copia del gen TGM1 en cada locus ICP4. El vector tiene también delecionado el gen IE ICP22.

isaralgagenum civaparvovecum #

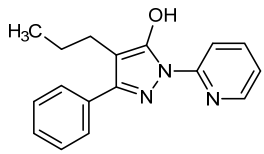
isaralgagene civaparvovec	A non-replicating adeno-associated viral vector encoding codon-optimised human alpha-galactosidase A (GLA). A recombinant, non-replicating adeno-associated viral vector serotype 6 (AAV6) encoding codon-optimised human alpha-galactosidase A (GLA) under control of liver-specific regulatory elements [comprising enhancer and hepatic control region from the human apolipoprotein E (ApoE) gene, the human α-1-antitrypsin (hAAT) promoter, a chimeric human β-globin/IgG (HBB-IGG) intron, as well as a WPREmut6 region] and a bovine growth hormone (bGH) poly A sequence, flanked by adeno-associated virus 2 (AAV2) inverted terminal repeats.

isaralgagène civaparvovec	Un vecteur viral adéno-associé non-répliquant codant la galactosidase alpha A humaine (GLA) aux codons optimisés. Un vecteur viral adéno-associé non-répliquant, recombinant, de sérotype 6 (AAV6) codant la galactosidase alpha A humaine (GLA) aux codons optimisés sous le contrôle d'éléments régulateurs spécifiques du foie [comprenant un activateur et une région de contrôle hépatique provenant du gène de l'apolipoprotéine E humaine (ApoE), le promoteur de l'alpha-1-antitrypsine humaine (hAAT), un intron chimérique de la β-globine/IgG humaine (HBB-IGG), ainsi qu'une région WPREmut6] et d'une séquence polyA de l'hormone de croissance bovine (bGH), flanquée de répétitions terminales inversées du virus adéno-associé 2 (AAV2).
isaralgagén civaparvovec	Un vector viral adeno-asociado, deficiente en replicación, que codifica para la alfa galactosidasa A (GLA) humana, con codones optimizados. Un vector viral adeno-asociado de serotipo 6 (AAV6) recombinante, no replicativo, que codifica para la alfa galactosidasa A (GLA) humana, con codones optimizados, bajo el control de elementos reguladores específicos de hígado [comprende el potenciador y la región de control hepático del gen de la apolipoproteína (ApoE) humana, el promotor de la α-1-antitripsina humana (hAAT), un intrón quimérico de β-globina humana/IgG (HBB-IGG), así como una región WPREmut6] y una secuencia polyA de la hormona decrecimiento bovina (bGH), flanqueado por la repeticiones terminales invertidas del virus adeno-asociado 2 (AAV2).

isuzinaxibum

isuzinaxib	3-phenyl-4-propyl-1-(pyridin-2-yl)-1*H*-pyrazol-5-ol
isuzinaxib	3-phényl-4-propyl-1-(pyridin-2-yl)-1*H*-pyrazol-5-ol
isuzinaxib	3-fenil-4-propil-1-(piridin-2-il)-1*H*-pirazol-5-ol

$C_{17}H_{17}N_3O$



labuvirtidum

labuvirtide	$N^{\alpha.1}$-acetyl-$N^{6.13}$-[(2-{2-[3-(2,5-dioxo-2,5-dihydro-1*H*-pyrrol-1-yl)propan-amido]ethoxy}ethoxy)acetyl]-[M^{118}>E^{2}, S^{129}>K^{13}, S^{133}>E^{17}]-(117-150)-peptide (1-34)-34-amide (non-glycosylated) of the transmembrane glycoprotein 41 (gp41) of the human immunodeficiency virus type 1 (HIV-1):

N-acetyl-L-tryptophyl-L-α-glutamyl-L-α-glutamyl-L-tryptophyl-L-α-aspartyl-L-arginyl-L-α-glutamyl-L-isoleucyl-L-asparaginyl-L-asparaginyl-L-tyrosyl-L-threonyl-N^6-[(2-{2-[3-(2,5-dioxo-2,5-dihydro-1*H*-pyrrol-1-yl)propanamido]-ethoxy}ethoxy)acetyl]-L-lysyl-L-leucyl-L-isoleucyl-L-histidyl-L-α-glutamyl-L-leucyl-L-isoleucyl-L-α-glutamyl-L-α-glutamyl-L-seryl-L-glutaminyl-L-asparaginyl-L-glutaminyl-L-glutaminyl-L-α-glutamyl-L-lysyl-L-asparaginyl-L-α-glutamyl-L-glutaminyl-L-α-glutamyl-L-leucyl-L-leucinamide

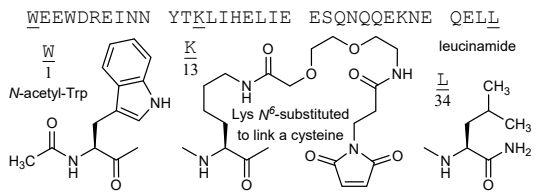
labuvirtide

$N^{\alpha.1}$-acétyl-$N^{6.13}$-[(2-{2-[3-(2,5-dioxo-2,5-dihydro-1*H*-pyrrol-1-yl)propan-amido]éthoxy}éthoxy)acétyl]-[M^{118}>E^2, S^{129}>K^{13}, S^{133}>E^{17}]-peptide 117-150 (1-34)-34-amide (non glycosylé) de la glycoprotéine transmembra-naire 41 (gp41) du virus de l'immunodéficience humaine de type 1 (VIH-1, HIV-1):
N-acétyl-L-tryptophyl-L-α-glutamyl-L-α-glutamyl-L-tryptophyl-L-α-aspartyl-L-arginyl-L-α-glutamyl-L-isoleucyl-L-asparaginyl-L-asparaginyl-L-tyrosyl-L-thréonyl-N^6-[(2-{2-[3-(2,5-dioxo-2,5-dihydro-1*H*-pyrrol-1-yl)propanamido]-éthoxy}éthoxy)acétyl]-L-lysyl-L-leucyl-L-isoleucyl-L-histidyl-L-α-glutamyl-L-leucyl-L-isoleucyl-L-α-glutamyl-L-α-glutamyl-L-séryl-L-glutaminyl-L-asparaginyl-L-glutaminyl-L-glutaminyl-L-α-glutamyl-L-lysyl-L-asparaginyl-L-α-glutamyl-L-glutaminyl-L-α-glutamyl-L-leucyl-L-leucinamide

labuvirtida

$N^{\alpha.1}$-acetil-$N^{6.13}$-[(2-{2-[3-(2,5-dioxo-2,5-dihidro-1*H*-pirrol-1-il)propan-amido]etoxi}etoxi)acetil]-[M^{118}>E^2, S^{129}>K^{13}, S^{133}>E^{17}]-péptido 117-150 (1-34)-34-amida (no glicosilado) de la glicoproteína transmembranaria 41 (gp41) del virus de inmunodeficiencia humana del tipo 1 (VIH-1, HIV-1):
N-acetil-L-triptofil-L-α-glutamil-L-α-glutamil-L-triptofil-L-α-aspartil-L-arginil-L-α-glutamil-L-isoleucil-L-asparaginil-L-asparaginil-L-tirosil-L-treonil-N^6-[(2-{2-[3-(2,5-dioxo-2,5-dihidro-1*H*-pirrol-1-il)propanamido]etoxi}etoxi)acetil]-L-lisil-L-leucil-L-isoleucil-L-histidil-L-α-glutamil-L-leucil-L-isoleucil-L-α-glutamil-L-α-glutamil-L-seril-L-glutaminil-L-asparaginil-L-glutaminil-L-glutaminil-L-α-glutamil-L-lisil-L-asparaginil-L-α-glutamil-L-glutaminil-L-α-glutamil-L-leucil-L-leucinamida

$C_{204}H_{306}N_{54}O_{72}$



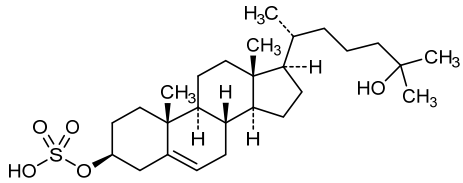
larsucosterolum

larsucosterol — 25-hydroxycholest-5-en-3β-yl hydrogen sulfate

larsucostérol — hydrogénosulfate de 25-hydroxycholest-5-én-3β-yle

larsucosterol — hidrogenosulfato de 25-hidroxicolest-5-en-3β-ilo

$C_{27}H_{46}O_5S$



latozinemabum #

latozinemab — immunoglobulin G1-kappa, anti-[*Homo sapiens* SORT1 (sortilin 1, Gp95, NT3)], *Homo sapiens* monoclonal antibody;
gamma1 heavy chain *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV4-38-2*01 (99.0%) -(IGHD) -IGHJ6*01 (100%)) CDR-IMGT [9.7.15] (26-34.52-58.97-111) (1-122) -*Homo sapiens* IGHG1*01 G1m17,1, G1v40 CH2 A1.3, A1.2, S116 (CH1 K120 (219) (123-220), hinge 1-15 (221-235), CH2 L1.3>A (239), L1.2>A (240), P116>S (336) (236-345), CH3 D12 (361), L14 (363) (346-450), CHS (451-452)) (123-452)], (225-219')-disulfide with kappa light chain *Homo sapiens* (1'-219') [V-KAPPA (*Homo sapiens* IGKV2-28*01 (93.0%) -IGKJ4*01 (100%)) CDR-IMGT [11.3.9] (27-37.55-57.94-102) (1'-112') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (158), V101 (196) (113'-219')]; dimer (231-231'':234-234'')-bisdisulfide, produced in Chinese hamster ovary (CHO)-K1SV cell line lacking the glutamine synthetase gene (GSKO), glycoform alfa

latozinémab — immunoglobuline G1-kappa, anti-[*Homo sapiens* SORT1 (sortiline 1, Gp95, NT3)], anticorps monoclonal *Homo sapiens*;
chaîne lourde gamma1 *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV4-38-2*01 (99.0%) -(IGHD) -IGHJ6*01 (100%)) CDR-IMGT [9.7.15] (26-34.52-58.97-111) (1-122) -*Homo sapiens* IGHG1*01 G1m17,1, G1v40 CH2 A1.3, A1.2, S116 (CH1 K120 (219) (123-220), charnière 1-15 (221-235), CH2 L1.3>A (239), L1.2>A (240), P116>S (336) (236-345), CH3 D12 (361), L14 (363) (346-450), CHS (451-452)) (123-452)], (225-219')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-219') [V-KAPPA (*Homo sapiens* IGKV2-28*01 (93.0%) -IGKJ4*01 (100%)) CDR-IMGT [11.3.9] (27-37.55-57.94-102) (1'-112') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (158), V101 (196) (113'-219')]; dimère (231-231'':234-234'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO) lignée cellulaire CHO-K1SV ne présentant pas le gène de la glutamine synthétase (GSKO), glycoforme alfa

latozinemab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* SORT1 (sortilina 1, Gp95, NT3)], anticuerpo monoclonal *Homo sapiens*;
cadena pesada gamma1 *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV4-38-2*01 (99.0%) -(IGHD) -IGHJ6*01 (100%)) CDR-IMGT [9.7.15] (26-34.52-58.97-111) (1-122) -*Homo sapiens* IGHG1*01 G1m17,1, G1v40 CH2 A1.3, A1.2, S116 (CH1 K120 (219) (123-220), bisagra 1-15 (221-235), CH2 L1.3>A (239), L1.2>A (240), P116>S (336) (236-345), CH3 D12 (361), L14 (363) (346-450), CHS (451-452)) (123-452)], (225-219')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-219') [V-KAPPA (*Homo sapiens* IGKV2-28*01 (93.0%) -IGKJ4*01 (100%)) CDR-IMGT [11.3.9] (27-37.55-57.94-102) (1'-112') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (158), V101 (196) (113'-219')]; dímero (231-231":234-234")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular CHO-K1SV en ausencia del gen glutamina sintetasa (GSKO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada
```
QVQLQESGPG LVKPSETLSL TCAVSGYSIS SGYYWGWIRQ PPGKGLEWIG  50
TIYHSGSTYY NPSLKSRVTI SVDTSKNQFS LKLSSVTAAD TAVYYCARQG 100
SIKQGYYGMD VWGQGTTVTV SSASTKGPSV FPLAPSSKST SGGTAALGCL 150
VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ SSGLYSLSSV VTVPSSSLGT 200
QTYICNVNHK PSNTKVDKKV EPKSCDKTHT CPPCPAPEAA GGPSVFLFPP 250
KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPASIEKT ISKAKGQPRE 350
PQVYTLPPSR DELTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP 400
PVLDSDGSFF LYSKLTVDKS RWQQGNVFSC SVMHEALHNH YTQKSLSLSP 450
GK                                                      452
```

Light chain / Chaîne légère / Cadena ligera
```
DIVMTQSPLS LPVTPGEPAS ISCRSSQSLL RSTGYNYLDW YLQKPGQSPQ  50
LLIYLGSNRA SGVPDRFSGS GSGTDFTLKI SRAEAEDVGV YYCMQQQEAP 100
LTFGGGTKVE 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) 22-96 149-205 266-326 372-430
22"-96" 149"-205" 266"-326" 372"-430"
Intra-L (C23-C104) 23'-93' 139'-199'
23'"-93'" 139'"-199'"
Inter-H-L (h 5-CL 126) 225-219' 225"-219'"
Inter-H-H (h 11, h 14) 231-231" 234-234"

N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
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.

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2:
452, 452"

ledelabricinum alfa #
ledelabricin alfa

human proteoglycan 4 (PRG4, lubricin, cartilage superficial zone proteoglycan, SZP, megakaryocyte-stimulating factor) isoform A, (S^{722}>C)-variant, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

lédélabricine alfa

protéoglycane 4 humain (PRG4, lubricine, protéoglycane de la zone superficielle du cartilage, SZP, facteur de stimulation des mégakaryocytes) isoforme A, (S^{722}>C)-variant, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

ledelabricina alfa

proteoglicano 4 humano (PRG4, lubricina, proteoglicano de la zona superficial del cartílago, SZP, factor de estimulación de los megacariocitos) isoforma A, (S^{722}>C)-variante, producido en las células ováricas de hamster chino (CHO), glicoforma alfa

Sequence / Séquence / Secuencia:

```
QDLSSCAGRC GEGYSRDATC NCDYNCQHYM ECCPDFKRVC TAELSCKGRC   50
FESFERGREC DCDAQCKKYD KCCPDYESFC AEVHNPTSPP SSKKAPPPSG  100
ASQTIKSTTK RSPKPPNKKK TKKVIESEEI TEEHSVSENQ ESSSSSSSS   150
SSSTIRKIKS SKNSAANREL QKKLKVKDNK KNRTKKKPTP KPPVVDEAGS  200
GLDNGDFKVT TPDTSTTQHN KVSTSPKITT AKPINPRPSL PPNSDTSKET  250
SLTVNKETTV ETKETTTTNK QTSTDGKEKT TSAKETQSIE KTSAKDLAPT  300
SKVLAKPTPK AETTTKGPAL TTPKEPTPTT PKEPASTTPK EPTPTTIKSA  350
PTTPKEPAPT TTKSAPTTPK EPAPTTTKEP APTTPKEPAP TTTKEPAPTT  400
TKSAPTTPKE PAPTTPKKPA PTTPKEPAPT TPKEPTPTTP KEPAPTTKEP  450
APTTPKEPAP TAPKKPAPTT PKEPAPTTPK EPAPTTTKEP SPTTPKEPAP  500
TTTKSAPTTT KEPAPTTTKS APTTPKEPSP TTTKEPAPTT PKEPAPTTPK  550
KPAPTTPKEP APTTPKEPAP TTTKKPAPTT PKEPAPTTPK ETAPTTPKKL  600
TPTTPEKLAP TTPEKPAPTT PEELAPTTPE EPTPTTPEEP APTTPKAAAP  650
NTPKEPAPTT PKEPAPTTPK EPAPTTPKET APTTPKGTAP TTLKEPAPTT  700
PKKPAPKELA PTTTKEPTST TCDKPAPTTP KGTAPTTPKE PAPTTPKEPA  750
PTTPKGTAPT TLKEPAPTTP KKPAPKELAP TTTKGPTSTT SDKPAPTTPK  800
ETAPTTPKEP APTTPKKPAP TTPETPPPTT SEVSTPTTTK EPTTIHKSPD  850
ESTPELSAEP TPKALENSPK EPGVPTTKTP AATKPEMTTT AKDKTTERDL  900
RTTPETTTAA PKMTKETATT TEKTTESKIT ATTTQVTSTT TQDTTPFKIT  950
TLKTTTLAPK VTTTKKTITT TEIMNKPEET AKPKDRATNS KATTPKPQKP 1000
TKAPKKPTST KKPKTMPRVR KPKTTPTPRK MTSTMPELNP TSRIAEAMLQ 1050
TTTRPNQTPN SKLVEVNPKS EDAGGAEGET PHMLLRPHVF MPEVTPDMDY 1100
LPRVPNQGII INPMLSDETN ICNGKPVDGL TTLRNGTLVA FRGHYFWMLS 1150
PFSPPSPARR ITEVWGIPSP IDTVFTRCNC EGKTFFFKDS QYWRFTNDIK 1200
DAGYPKPIFK GFGGLTGQIV AALSTAKYKN WPESVYFFKR GGSIQQYIYK 1250
QEPVQKCPGR RPALNYPVYG ETTQVRRRRF ERAIGPSQTH TIRIQYSPAR 1300
LAYQDKGVLH NEVKVSILWR GLPNVVTSAI SLPNIRKPDG YDYYAFSKDQ 1350
YYNIDVPSRT ARAITTRSGQ TLSKVWYNCP                        1380
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
6, 10, 20, 22, 26, 32, 33, 40, 46, 50, 60, 62, 66, 72, 73, 80, 1122, 1379
(linked pairs variable or undetermined)
Cys-SH: 722, 1257; unknown status: 1178, 1180

Glycosylation sites / Sites de glycosylation / Posiciones de glicosilación
N182, N1056, N1120, N1135
Fucosylated complex bi-antennary CHO-type glycans / Glycanes de type CHO bi-antennaires complexes fucosylés / Glicanos de tipo CHO biantenarios complejos fucosilados

Potential O-glycosylation sites
26 Ser, 174 Thr:
Sialylated and/or sulfated core 1 (Galβ1-3GalNAcβ1) CHO type O-glycans
Ser: 99, 102, 107, 112, 223, 225, 273, 282, 288, 293, 301, 336, 349, 364, 403, 491, 505, 529, 788, 848, 852, 857, 868, 938, 990, 1009;
Thr: 104, 108, 109, 216, 224, 229, 253, 258, 259, 265, 266, 267, 268, 272, 274, 280, 281, 286, 292, 300, 308, 321, 322, 327, 329, 330, 337, 338, 343, 345, 346, 352, 353, 360, 361, 362, 367, 368, 375, 376, 377, 383, 384, 391, 392, 393, 399, 400, 401, 406, 407, 414, 415, 422, 423, 430, 431, 436, 438, 439, 446, 447, 453, 454, 461, 469, 470, 477, 478, 485, 486, 487, 493, 494, 501, 502, 503, 508, 509, 510, 516, 517, 518, 523, 524, 531, 532, 533, 539, 540, 547, 548, 555, 556, 563, 564, 571, 572, 573, 579, 580, 587, 588, 592, 595, 603, 652, 659, 660, 667, 668, 675, 676, 680, 683, 688, 691, 692, 699, 700, 712, 733, 736, 737, 744, 745, 752, 753, 757, 760, 761, 768, 769, 781, 787, 789, 805, 813, 814, 843, 844, 853, 861, 876, 906, 907, 917, 919, 920, 921, 930, 932, 933, 934, 937, 939, 940, 941, 944, 951, 954, 955, 956, 962, 963, 964, 988, 1008, 1010, 1015, 1024, 1025, 1027, 1137

Gln1>Glp (pyroglutamyl, 5-oxoprolyl)

lemzoparlimabum #

lemzoparlimab	immunoglobulin G4-kappa, anti-[*Homo sapiens* CD47 (integrin associated protein, IAP, MER6, OA3)], monoclonal antibody; gamma4 heavy chain (1-445) [VH (*Homo sapiens* IGHV3-15*07 (93.9%) -(IGHD) -IGHJ3*02 (100%)) CDR-IMGT [8.10.9] (26-33.51-60.99-107) (1-118)-*Homo sapiens* IGHG4*01 (100%), G4v5 h P10 (CH1 (119-216), hinge 1-12 S10>P (226) (217-228), CH2 (229-338), CH3 (339-443), CHS (444-445)) (119-445)], (132-220')-disulfide with kappa light chain (1'-220') [V-KAPPA (*Homo sapiens* IGKV4-1*01 (89.1%) -IGKJ2*01 (90%) Q120>G (106)) CDR-IMGT [12.3.9] (27-38.56-58.95-103) (1'-113') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (159), V101 (197) (114'-220')]; dimer (224-224'':227-227'')-bisdisulfide, produced in a Chinese hamster ovary (CHO)-K1 cell line, glycoform alfa
lemzoparlimab	immunoglobuline G4-kappa, anti-[*Homo sapiens* CD47 (protéine associée à l'intégrine, IAP, MER6, OA3)], anticorps monoclonal; chaîne lourde gamma4 (1-445) [VH (*Homo sapiens* IGHV3-15*07 (93.9%) -(IGHD) -IGHJ3*02 (100%)) CDR-IMGT [8.10.9] (26-33.51-60.99-107) (1-118)-*Homo sapiens* IGHG4*01 (100%), G4v5 h P10 (CH1 (119-216), charnière 1-12 S10>P (226) (217-228), CH2 (229-338), CH3 (339-443), CHS (444-445)) (119-445)], (132-220')-disulfure avec la chaîne légère kappa (1'-220') [V-KAPPA (*Homo sapiens* IGKV4-1*01 (89.1%) -IGKJ2*01 (90%) Q120>G (106)) CDR-IMGT [12.3.9] (27-38.56-58.95-103) (1'-113') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (159), V101 (197) (114'-220')]; dimère (224-224'':227-227'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO) lignée cellulaire CHO-K1, glycoforme alfa
lemzoparlimab	inmunoglobulina G4-kappa, anti-[*Homo sapiens* CD47 (proteína asociada a la integrina, IAP, MER6, OA3)], anticuerpo monoclonal; cadena pesada gamma4 (1-445) [VH (*Homo sapiens* IGHV3-15*07 (93.9%) -(IGHD) -IGHJ3*02 (100%)) CDR-IMGT [8.10.9] (26-33.51-60.99-107) (1-118)-*Homo sapiens* IGHG4*01 (100%), G4v5 h P10 (CH1 (119-216), bisagra 1-12 S10>P (226) (217-228), CH2 (229-338), CH3 (339-443), CHS (444-445)) (119-445)], (132-220')-disulfuro con la cadena ligera kappa (1'-220') [V-KAPPA (*Homo sapiens* IGKV4-1*01 (89.1%) -IGKJ2*01 (90%) Q120>G (106)) CDR-IMGT [12.3.9] (27-38.56-58.95-103) (1'-113') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (159), V101 (197) (114'-220')]; dímero (224-224'':227-227'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVKPGGSLRL SCAASGLTFE RAWMNWVRQA PGKGLEWVGR  50
IKRKTDGETT DYAAPVKGRF SISRDDSKNT LYLQMNSLKT EDTAVYYCAG 100
SNRAFDIWGQ GTMVTVSSAS 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 INCKSSQSVL YAGNNRNYLA WYQQKPGQPP  50
KLLINQASTR ASGVPDRFSG SGSGTEFTLI ISSLQAEDVA IYYCQQYYTP 100
PLAFGGGTKL EIKRTVAAPS VFIFPPSDEQ LKSGTASVVC LLNNFYPREA 150
KVQWKVDNAL QSGNSQESVT EQDSKDSTYS LSSTLTLSKA DYEKHKVYAC 200
EVTHQGLSSP VTKSFNRGEC                                  220
```

Post-translational modifications

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

Intra-H (C23-C104) 22-98 145-201 259-319 365-423
22"-98" 145"-201" 259"-319" 365"-423"
Intra-L (C23-C104) 23'-94' 140'-200'
23'"-94'" 140'"-200'"
Inter-H-L (CH1 10-CL 126) 132-220' 132"-220'"
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.

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal

H CHS K2:
445, 445"

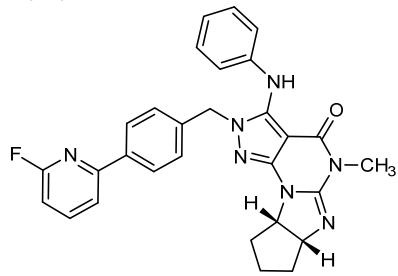
lenrispodunum

lenrispodun — (6a*R*,9a*S*)-3-anilino-2-{[4-(6-fluoropyridin-2-yl)phenyl]methyl}-5-methyl-5,6a,7,8,9,9a-hexahydrocyclopenta[4,5]imidazo[1,2-*a*]pyrazolo[4,3-*e*]pyrimidin-4(2*H*)-one

lenrispodun — (6a*R*,9a*S*)-3-anilino-2-{[4-(6-fluoropyridin-2-yl)phényl]méthyl}-5-méthyl-5,6a,7,8,9,9a-hexahydrocyclopenta[4,5]imidazo[1,2-*a*]pyrazolo[4,3-*e*]pyrimidin-4(2*H*)-one

lenrispodun — (6a*R*,9a*S*)-3-anilino-2-{[4-(6-fluoropiridin-2-yl)fenil]metil}-5-metil-5,6a,7,8,9,9a-hexahidrociclopenta[4,5]imidazo[1,2-*a*]pirazolo[4,3-*e*]pirimidin-4(2*H*)-ona

$C_{29}H_{26}FN_7O$



libvatrepum

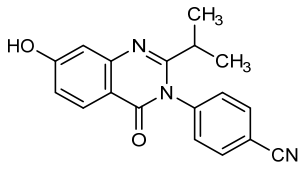
libvatrep — 4-[7-hydroxy-4-oxo-2-(propan-2-yl)quinazolin-3(4*H*)-yl]benzonitrile

libvatrep — 4-[7-hydroxy-4-oxo-2-(propan-2-yl)quinazolin-3(4*H*)-yl]benzonitrile

libvatrep

4-[7-hidroxi-4-oxo-2-(propan-2-il)quinazolin-3(4*H*)-il]benzonitrilo

$C_{18}H_{15}N_3O_2$



licaminlimabum #

licaminlimab

immunoglobulin scFv, anti-[*Homo sapiens* TNF (tumor necrosis factor, TNFSF2, DIF, TNF-alpha)], humanized monoclonal antibody single chain;
IG scFv humanized single chain (V-KAPPA-VH) (1-254) [V-KAPPA (*Homo sapiens* IGKV1-5*03 (79.2%) -(IGHD) - IGKJ2*02 (77.8%)) CDR-IMGT [8.3.11] (28-35.53-55.92-102) (1-112)] -21-mer glycyl-tetrakis(tetraglycyl-seryl) linker (113-133) -[VH (*Homo sapiens* IGHV3-66*01 (76%) - IGHJ6*01 (92.3%)) CDR-IMGT [8.8.14] (159-166.184-191.230-243) (134-254)], produced in the bacteria *Escherichia coli* (*E. coli*), non-glycosylated

licaminlimab

immunoglobuline scFv, anti-[*Homo sapiens* TNF (facteur de nécrose tumorale, TNFSF2, DIF, TNF-alpha)], anticorps monoclonal humanisé à chaîne unique;
IG scFv chaîne unique humanisée (V-KAPPA-VH) (1-254) [V-KAPPA (*Homo sapiens* IGKV1-5*03 (79.2%) -(IGHD) - IGKJ2*02 (77.8%)) CDR-IMGT [8.3.11] (28-35.53-55.92-102) (1-112)] -21-mer glycyl-tétrakis(tétraglycyl-séryl) linker (113-133) -[VH (*Homo sapiens* IGHV3-66*01 (76%) - IGHJ6*01 (92.3%)) CDR-IMGT [8.8.14] (159-166.184-191.230-243) (134-254)], produit dans la bactérie *Escherichia coli* (*E. coli*), non-glycosylé

licaminlimab

inmunoglobulina scFv, anti-[*Homo sapiens* TNF (factor de necrosis tumoral, TNFSF2, DIF, TNF-alfa)], anticuerpo monoclonal humanizado con cadena única;
IG scFv cadena única humanizada (V-KAPPA-VH) (1-254) [V-KAPPA (*Homo sapiens* IGKV1-5*03 (79.2%) -(IGHD) - IGKJ2*02 (77.8%)) CDR-IMGT [8.3.11] (28-35.53-55.92-102) (1-112)] -21-mer glicil-tetrakis(tetraglicil-seril) linker (113-133) -[VH (*Homo sapiens* IGHV3-66*01 (76%) - IGHJ6*01 (92.3%)) CDR-IMGT [8.8.14] (159-166.184-191.230-243) (134-254)], producido en la bacteria *Escherichia coli* (*E. coli*), no glicosilado

scFv chain / Chaîne scFv / Cadena scFv

```
MEIVMTQSPS TLSASVGDRV IITCQSSQSV YGNIWMAWYQ QKPGRAPKLL  50
IYQASKLASG VPSRFSGSGS GAEFTLTISS LQPDDFATYY CQGNFNTGDR 100
YAFGQGTKLT VLGGGGGSGG GGSGGGGSGG GGSEVQLVES GGGSVQPGGS 150
LRLSCTASGF TISRSYWICW VRQAPGKGLE WVGCIYGDND ITPLYANWAK 200
GRFTISRDTS KNTVYLQMNS LRAEDTATYY CARLGYADYA YDLWGQGTTV 250
TVSS                                                    254
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-scFv (C23-C104) 24-91 155-231 169-184

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

lirentelimabum #

lirentelimab	immunoglobulin G1-kappa, anti-[*Homo sapiens* SIGLEC8 (sialic acid binding Ig-like lectin 8, SIGLEC-8, SAF2, SIGLEC8L)], humanized monoclonal antibody; gamma1 heavy chain humanized (1-450) [VH (*Homo sapiens* IGHV3-66*01 (79.4%) -(IGHD) -IGHJ5*01 (90.9%)) CDR-IMGT [8.7.14] (26-33.51-57.96-109) (1-120) -*Homo sapiens* IGHG1*03 (100%) G1m3, nG1m1 (CH1 R120 (217) (121-218), hinge 1-15 (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-213')-disulfide with kappa light chain humanized (1'-213') [V-KAPPA (*Homo sapiens* IGKV3-11*01 (86.3%) -IGKJ3*01 (91.7%)) CDR-IMGT [5.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (152), V101 (190) (108'-213')]; dimer (229-229'':232-232'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa
lirentélimab	immunoglobuline G1-kappa, anti-[*Homo sapiens* SIGLEC8 (lectine 8 de type Ig-like liant l'acide sialique, SIGLEC-8, SAF2, SIGLEC8L)], anticorps monoclonal humanisé; chaîne lourde gamma1 humanisée (1-450) [VH (*Homo sapiens* IGHV3-66*01 (79.4%) -(IGHD) -IGHJ5*01 (90.9%)) CDR-IMGT [8.7.14] (26-33.51-57.96-109) (1-120) -*Homo sapiens* IGHG1*03 (100%) G1m3, nG1m1 (CH1 R120 (217) (121-218), charnière 1-15 (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-213')-disulfure avec la chaîne légère kappa humanisée (1'-213') [V-KAPPA (*Homo sapiens* IGKV3-11*01 (86.3%) -IGKJ3*01 (91.7%)) CDR-IMGT [5.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (152), V101 (190) (108'-213')]; dimère (229-229'':232-232'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa
lirentelimab	inmunoglobulina G1-kappa, anti-[*Homo sapiens* SIGLEC8 (lectina 8 de tipo Ig-like de unión al ácido siálico, SIGLEC-8, SAF2, SIGLEC8L)], anticuerpo monoclonal humanizado; cadena pesada gamma1 humanizada (1-450) [VH (*Homo sapiens* IGHV3-66*01 (79.4%) -(IGHD) -IGHJ5*01 (90.9%)) CDR-IMGT [8.7.14] (26-33.51-57.96-109) (1-120) -*Homo sapiens* IGHG1*03 (100%) G1m3, nG1m1 (CH1 R120 (217) (121-218), bisagra 1-15 (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-213')-disulfuro con la cadena ligera kappa humanizada (1'-213') [V-KAPPA (*Homo sapiens* IGKV3-11*01 (86.3%) -IGKJ3*01 (91.7%)) CDR-IMGT [5.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (152), V101 (190) (108'-213')]; dímero (229-229'':232-232'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAASGFSLT IYGAHWVRQA PGKGLEWVGV  50
IWAGGSTNYN SALMSRFTIS KDNSKNTVYL QMNSLRAEDT AVYYCARDGS 100
SPYYYSMEYW GQGTTVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKRVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK 450
```

Light chain / Chaîne légère / Cadena ligera

```
EIVLTQSPAT LSLSPGERAT LSCSATSSVS YMHWFQQKPG QAPRLLIYST  50
SNLASGIPAR FSGSGSGTDF TLTISSLEPE DFAVYYCQQR SSYPFTFGPG 100
TKLDIKRTVA APSVFIFPPS DEQLKSGTAS VVCLLNNFYP REAKVQWKVD 150
NALQSGNSQE SVTEQDSKDS TYSLSSTLTL SKADYEKHKV YACEVTHQGL 200
SSPVTKSFNR GEC                                         213
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-95 147-203 264-324 370-428
22"-95" 147"-203" 264"-324" 370"-428"
Intra-L (C23-C104) 23'-87' 133'-193'
23'"-87'" 133'"-193'"
Inter-H-L (h 5-CL 126) 223-213' 223"-213'"
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"
Afucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes afucosylés / glicanos de tipo CHO biantenarios complejos afucosilados.

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2:
450, 450"

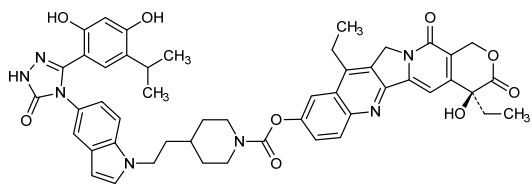
Iocnartecanum

locnartecan — (4*S*)-4,11-diethyl-4-hydroxy-3,14-dioxo-3,4,12,14-tetrahydro-1*H*-pyrano[3',4':6,7]indolizino[1,2-*b*]quinolin-9-yl 4-[2-(5-{3-[2,4-dihydroxy-5-(propan-2-yl)phenyl]-5-oxo-1,5-dihydro-4*H*-1,2,4-triazol-4-yl}-1*H*-indol-1-yl)ethyl]piperidine-1-carboxylate

locnartécan — 4-[2-(5-{3-[2,4-dihydroxy-5-(propan-2-yl)phényl]-5-oxo-1,5-dihydro-4*H*-1,2,4-triazol-4-yl}-1*H*-indol-1-yl)éthyl]pipéridine-1-carboxylate de (4*S*)-4,11-diéthyl-4-hydroxy-3,14-dioxo-3,4,12,14-tétrahydro-1*H*-pyrano[3',4':6,7]indolizino[1,2-*b*]quinoléin-9-yle

locnartecán — 4-[2-(5-{3-[2,4-dihidroxi-5-(propan-2-il)fenil]-5-oxo-1,5-dihidro-4*H*-1,2,4-triazol-4-il}-1*H*-indol-1-il)etil]piperidina-1-carboxilato de (4*S*)-4,11-dietil-4-hidroxi-3,14-dioxo-3,4,12,14-tetrahidro-1*H*-pirano[3',4':6,7]indolizino[1,2-*b*]quinolein-9-ilo

$C_{49}H_{49}N_7O_9$



Ionigutamabum

ionigutamab — immunoglobulin G1-kappa, anti-[*Homo sapiens* IGF1R (insulin like growth factor 1 receptor, IGF1-R, IGF-1R, CD221)], humanized monoclonal antibody;

	gamma1 heavy chain humanized (1-449) [VH humanized (*Homo sapiens* IGHV1-46*01 (92.8%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Homo sapiens* IGHG1*03 (100%) G1m3, nG1m1 (CH1 R120 (217) (121-218), hinge 1-15 (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS K>del (449)) (121-449)], (223-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA humanized (*Homo sapiens* IGKV1-39*01 (86.3%) -IGKJ4*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (229-229'':232-232'')-bisdisulfide, produced in Chinese hamster ovary (CHO)-K1SV cell line lacking the glutamine synthetase gene (GSKO), glycoform alfa
lonigutamab	immunoglobuline G1-kappa, anti-[*Homo sapiens* IGF1R (récepteur du facteur de croissance 1 analogue à l'insuline, IGF1-R, IGF-1R, CD221)], anticorps monoclonal humanisé; chaîne lourde gamma1 humanisée (1-449) [VH humanisé (*Homo sapiens* IGHV1-46*01 (92.8%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Homo sapiens* IGHG1*03 (100%) G1m3, nG1m1 (CH1 R120 (217) (121-218), charnière 11-15 (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS K>del (449)) (121-449)], (223-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA humanisé (*Homo sapiens* IGKV1-39*01 (86.3%) -IGKJ4*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (229-229'':232-232'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO) lignée cellulaire CHO-K1SV ne présentant pas le gène de la glutamine synthétase (GSKO), glycoforme alfa
lonigutamab	inmunoglobulina G1-kappa, anti-[*Homo sapiens* IGF1R (receptor del factor de crecimiento 1 análogo a la insulina, IGF1-R, IGF-1R, CD221)], anticuerpo monoclonal humanizado; cadena pesada gamma1 humanizada (1-449) [VH humanizado (*Homo sapiens* IGHV1-46*01 (92.8%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Homo sapiens* IGHG1*03 (100%) G1m3, nG1m1 (CH1 R120 (217) (121-218), bisagra 11-15 (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS K>del (449)) (121-449)], (223-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA humanizado (*Homo sapiens* IGKV1-39*01 (86.3%) -IGKJ4*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (229-229'':232-232'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular CHO-K1SV en ausencia del gen glutamina sintetasa (GSKO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGASVKV SCKASGYTFT SYYIHWVRQA PGQGLEWMGW  50
IWPGDGSTKY AQKFQGRVTM TRDTSTSTVY MELSSLRSED TAVYFCASPM 100
ITPNYAMDYW GQGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKRVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPG  449
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCRASQDIS KYLNWYQQKP GKAPKLLIYY  50
TSRLQSGVPS RFSGRGSGTD YSLTISSLQP EDFATYFCQQ GSTLPYTFGG 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

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

N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
H VH Q1:
1, 1"

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.

Ionigutamabum ugodotinum #

Ionigutamab ugodotin	immunoglobulin G1-kappa, anti-[*Homo sapiens* IGF1R (insulin like growth factor 1 receptor, IGF1-R, IGF-1R, CD221)], humanized monoclonal antibody conjugated to a dolastatin derivative (ugodotin groups); gamma1 heavy chain humanized (1-449) [VH humanized (*Homo sapiens* IGHV1-46*01 (92.8%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Homo sapiens* IGHG1*03 (100%) G1m3, nG1m1 (CH1 R120 (217) (121-218), hinge 1-15 (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS K>del (449)) (121-449)], (223-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA humanized (*Homo sapiens* IGKV1-39*01 (86.3%) -IGKJ4*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (229-229":232-232")-bisdisulfide, produced in Chinese hamster ovary (CHO)-K1SV cell line lacking the glutamine synthetase gene (GSKO), glycoform alfa; conjugated at the cysteines 223, 214', 223" and 214'" with four (3*S*,6*R*,7*R*,8^{2}*S*,11*R*,12*S*,15*S*,18*S*,30^{3}*RS*)-12-[(2*S*)-butan-2-yl]-3-carboxy-7,11-dimethoxy-6,13,19,23-tetramethyl-5,9,14,17,24,30^{2},30^{5}-heptaoxo-15,18-di(propan-2-yl)-4,13,16,19,23-pentaaza-8(2,1),30(1)-dipyrrolidina-1(1),22(1,4)-dibenzenatriacontaphan-30^{3}-yl (ugodotin) groups
Ionigutamab ugodotine	immunoglobuline G1-kappa, anti-[*Homo sapiens* IGF1R (récepteur du facteur de croissance 1 analogue à l'insuline, IGF1-R, IGF-1R, CD221)], anticorps monoclonal humanisé conjugué à un dérivé de dolastatine (groupes ugodotine);

	chaîne lourde gamma1 humanisée (1-449) [VH humanisé (*Homo sapiens* IGHV1-46*01 (92.8%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Homo sapiens* IGHG1*03 (100%) G1m3, nG1m1 (CH1 R120 (217) (121-218), charnière 1-15 (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS K>del (449)) (121-449)], (223-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA humanisé (*Homo sapiens* IGKV1-39*01 (86.3%) -IGKJ4*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (229-229'':232-232'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO) lignée cellulaire CHO-K1SV ne présentant pas le gène de la glutamine synthétase (GSKO), glycoforme alfa; conjugué aux cystéines 223, 214', 223'' et 214''' avec quatre groupes (3*S*,6*R*,7*R*,8^{2}*S*,11*R*,12*S*,15*S*,18*S*,30^{3}*RS*)-12-[(2*S*)-butan-2-yl]-3-carboxy-7,11-diméthoxy-6,13,19,23-tétraméthyl-5,9,14,17,24,30^{2},30^{5}-heptaoxo-15,18-di(propan-2-yl)-4,13,16,19,23-pentaaza-8(2,1),30(1)-dipyrrolidina-1(1),22(1,4)-dibenzénatriacontaphan-30^{3}-yle (ugodotine)
lonigutamab ugodotina	inmunoglobulina G1-kappa, anti-[*Homo sapiens* IGF1R (receptor del factor de crecimiento 1 análogo a la insulina, IGF1-R, IGF-1R, CD221)], anticuerpo monoclonal humanizado conjugado a un derivado de dolastatina (grupos ugodotina); cadena pesada gamma1 humanizada (1-449) [VH humanizado (*Homo sapiens* IGHV1-46*01 (92.8%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Homo sapiens* IGHG1*03 (100%) G1m3, nG1m1 (CH1 R120 (217) (121-218), bisagra 1-15 (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS K>del (449)) (121-449)], (223-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA humanizado (*Homo sapiens* IGKV1-39*01 (86.3%) -IGKJ4*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (229-229'':232-232'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular CHO-K1SV en ausencia del gen glutamina sintetasa (GSKO), forma glicosilada alfa; conjugado a cisteínas 223, 214', 223'' y 214''' con quatro grupos (3*S*,6*R*,7*R*,8^{2}*S*,11*R*,12*S*,15*S*,18*S*,30^{3}*RS*)-12-[(2*S*)-butan-2-il]-3-carboxi-6,13,19,23-tetrametil-7,11-dimetoxi-5,9,14,17,24,30^{2},30^{5}-heptaoxo-15,18-di(propan-2-il)-4,13,16,19,23-pentaaza-8(2,1),30(1)-dipirrolidina-1(1),22(1,4)-dibencenatriacontafan-30^{3}-il (ugodotina)

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGASVKV SCKASGYTFT SYYIHWVRQA PGQGLEWMGW  50
IWPGDGSTKY AQKFQGRVTM TRDTSTSTVY MELSSLRSED TAVYFCASPM 100
ITPNYAMDYW GQGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKRVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPG  449
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCRASQDIS KYLNWYQQKP GKAPKLLIYY  50
TSRLQSGVPS RFSGRGSGTD YSLTISSLQP EDFATYFCQQ GSTLPYTFGG 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

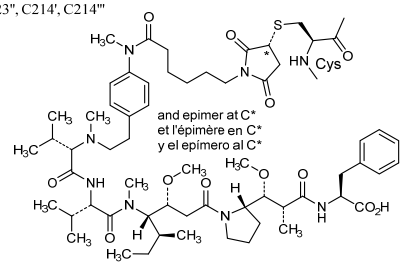
Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 147-203 264-324 370-428
22"-96" 147"-203" 264"-324" 370"-428"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194'"
Inter-H-L (h 5-CL 126)* 223-214'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

*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-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
H VH Q1:
1, 1"

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.

Conjugation sites / Sites de conjugaison / Posiciones de coniugación:
C223, C223", C214', C214'"



Iusvertikimabum #
lusvertikimab

immunoglobulin G4-kappa, anti-[*Homo sapiens* IL7R (interleukin 7 receptor, CD127, IL7RA)], humanized monoclonal antibody; gamma4 heavy chain humanized (1-449) [VH (*Homo sapiens* IGHV3-11*01 (90.8%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.15] (26-33.51-58.97-111) (1-122)-*Homo sapiens* IGHG4*01 (100%), G4v5 h P10 (CH1 (123-220), hinge 1-12 S10>P (230) (221-232), CH2 (233-342), CH3 (343-447), CHS (448-449)) (123-449)], (136-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-NL1*01 (86.3%) -IGKJ4*01 (91.7%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (228-228":231-231")-bisdisulfide, produced in a Chinese hamster ovary (CHO)-K1 cell line, glycoform alfa

lusvertikimab

immunoglobuline G4-kappa, anti-[*Homo sapiens* IL7R (récepteur de l'interleukine 7, CD127, IL7RA)], anticorps monoclonal humanisé;
chaîne lourde gamma4 humanisée (1-449) [VH (*Homo sapiens* IGHV3-11*01 (90.8%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.15] (26-33.51-58.97-111) (1-122)-*Homo sapiens* IGHG4*01 (100%), G4v5 h P10 (CH1 (123-220), charnière 1-12 S10>P (230) (221-232), CH2 (233-342), CH3 (343-447), CHS (448-449)) (123-449)], (136-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-NL1*01 (86.3%) -IGKJ4*01 (91.7%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (228-228":231-231")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO) lignée cellulaire CHO-K1, glycoforme alfa

lusvertikimab

inmunoglobulina G4-kappa, anti-[*Homo sapiens* IL7R (receptor de la interleukina 7, CD127, IL7RA)], anticuerpo monoclonal humanizado;
cadena pesada gamma4 humanizada (1-449) [VH (*Homo sapiens* IGHV3-11*01 (90.8%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.15] (26-33.51-58.97-111) (1-122)-*Homo sapiens* IGHG4*01 (100%), G4v5 h P10 (CH1 (123-220), bisagra 1-12 S10>P (230) (221-232), CH2 (233-342), CH3 (343-447), CHS (448-449)) (123-449)], (136-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-NL1*01 (86.3%) -IGKJ4*01 (91.7%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (228-228":231-231")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVESGGG LVKPGGSLRL SCAVSGFTLS DYYMAWIRQA PGKGLEWVST  50
ISASGLRTYY PDSVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARPL 100
SAHYGFNYFD YWGQGTLVTV SSASTKGPSV FPLAPCSRST SESTAALGCL 150
VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ SSGLYSLSSV VTVPSSSLGT 200
KTYTCNVDHK PSNTKVDKRV ESKYGPPCPP CPAPEFLGGP SVFLFPPKPK 250
DTLMISRTPE VTCVVVDVSQ EDPEVQFNWY VDGVEVHNAK TKPREEQFNS 300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKGL PSSIEKTISK AKGQPREPQV 350
YTLPPSQEEM TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL 400
DSDGSFFLYS RLTVDKSRWQ EGNVFSCSVM HEALHNHYTQ KSLSLSPGK  449
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCRTSEDIY QGLAWYQQKP GKAPKLLLYS  50
ANTLHIGVPS RFSGSGSGTD YTLTISSLQP EDFATYYCQQ YYDYPLAFGG 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    149-205    263-323    369-427
                    22"-96"  149"-205"  263"-323"  369"-427"
Intra-L (C23-C104)  23'-88'    134'-194'
                    23'"-88'"  134'"-194'"
Inter-H-L (CH1 10-CL 126)  136-214'  136"-214'"
Inter-H-H (h 8, h 11)          228-228"  231-231"
```

N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
H VH Q1:
1, 1"

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 / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2:
449, 449"

mevidalenum

mevidalen

2-(2,6-dichlorophenyl)-1-[(1*S*,3*R*)-3-(hydroxymethyl)-5-(3-hydroxy-3-methylbutyl)-1-methyl-3,4-dihydroisoquinolin-2(1*H*)-yl]ethan-1-one

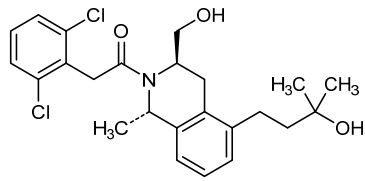
mévidalène

2-(2,6-dichlorophényl)-1-[(1*S*,3*R*)-3-(hydroxyméthyl)-5-(3-hydroxy-3-méthylbutyl)-1-méthyl-3,4-dihydroisoquinoléin-2(1*H*)-yl]éthan-1-one

mevidaleno

2-(2,6-diclorofenil)-1-[(1*S*,3*R*)-3-(hidroximetil)-5-(3-hidroxi-3-metilbutil)-1-metil-3,4-dihidroisoquinolein-2(1*H*)-il]etan-1-ona

$C_{24}H_{29}Cl_2NO_3$



mibavademabum #

mibavademab

immunoglobulin G4-kappa, anti-[*Homo sapiens* LEPR (leptin receptor, OBR, CD295)], monoclonal antibody; gamma4 heavy chain (1-446) [VH (*Homo sapiens* IGHV3-30*15 (86.7%) -(IGHD) -IGHJ2*01 (100%)) CDR-IMGT [8.8.12] (26-33.51-58.97-108) (1-119)-*Homo sapiens* IGHG4*01 (100%), G4v5 h P10 (CH1 (120-217), hinge 1-12 S10>P (227) (218-229), CH2 (230-339), CH3 (340-444), CHS (445-446)) (120-446)], (133-215')-disulfide with kappa light chain (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (100%) -IGKJ5*01 (100%)) CDR-IMGT [6.3.10] (27-32.50-52.89-98) (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')]; dimer (225-225'':228-228'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

mibavadémab

immunoglobuline G4-kappa, anti-[*Homo sapiens* LEPR (récepteur de la leptine, OBR, CD295)], anticorps monoclonal;
chaîne lourde gamma4 (1-446) [VH (*Homo sapiens* IGHV3-30*15 (86.7%) -(IGHD) -IGHJ2*01 (100%)) CDR-IMGT [8.8.12] (26-33.51-58.97-108) (1-119)-*Homo sapiens* IGHG4*01 (100%), G4v5 h P10 (CH1 (120-217), charnière 1-12 S10>P (227) (218-229), CH2 (230-339), CH3 (340-444), CHS (445-446)) (120-446)], (133-215')-disulfure avec la chaîne légère kappa (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (100%) -IGKJ5*01 (100%)) CDR-IMGT [6.3.10] (27-32.50-52.89-98) (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')]; dimère (225-225'':228-228'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

mibavademab

inmunoglobulina G4-kappa, anti-[*Homo sapiens* LEPR (receptor de la leptina, OBR, CD295)], anticuerpo monoclonal;
cadena pesada gamma4 (1-446) [VH (*Homo sapiens* IGHV3-30*15 (86.7%) -(IGHD) -IGHJ2*01 (100%)) CDR-IMGT [8.8.12] (26-33.51-58.97-108) (1-119)-*Homo sapiens* IGHG4*01 (100%), G4v5 h P10 (CH1 (120-217), bisagra 1-12 S10>P (227) (218-229), CH2 (230-339), CH3 (340-444), CHS (445-446)) (120-446)], (133-215')-disulfuro con la cadena ligera kappa (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (100%) -IGKJ5*01 (100%)) CDR-IMGT [6.3.10] (27-32.50-52.89-98) (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')]; dímero (225-225":228-228")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVESGGS VVQPGRSLRL SCAASGFTFS TYAMYWVRQT PGKGLEWVAV  50
LYSDGSNKYY IDSVKGRFTI SRDTSTNTLY LQMSSLRADD SALYYCARLN 100
WDYWYFDLWG RGTLVTVSSA STKGPSVFPL APCSRSTSES TAALGCLVKD 150
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTKTY 200
TCNVDHKPSN TKVDKRVESK YGPPCPPCPA PEFLGGPSVF LFPPKPKDTL 250
MISRTPEVTC VVVDVSQEDP EVQFNWYVDG VEVHNAKTKP REEQFNSTYR 300
VVSVLTVLHQ DWLNGKEYKC KVSNKGLPSS IEKTISKAKG QPREPQVYTL 350
PPSQEEMTKN QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD 400
GSFFLYSRLT VDKSRWQEGN VFSCSVMHEA LHNHYTQKSL SLSLGK     446
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCRASQSIS SYLNWYQQKP GKAPKLLIYA  50
ASSLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ SYSTPPITFG 100
QGTRLEIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK 150
VDNALQSGNS QESVTEQDSK DSTYSLSSTL TLSKADYEKH KVYACEVTHQ 200
GLSSPVTKSF NRGEC                                       215
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 146-202 260-320 366-424
22"-96" 146"-202" 260"-320" 366"-424"
Intra-L (C23-C104) 23'-88' 135'-195'
23'"-88'" 135'"-195'"
Inter-H-L (CH1 10-CL 126) 133-215' 133"-215'"
Inter-H-H (h 8, h 11) 225-225" 228-228"

N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
H VH Q1:
1, 1"

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 / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2:
446, 446"

mipicoledinum

mipicoledine

cholest-5-en-3β-yl 3,5-dichloro-2-methoxy-6-(trichloromethyl)pyridin-4-yl carbonate

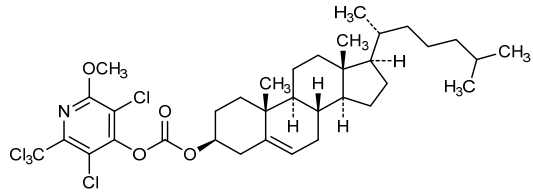
mipicolédine

carbonate de cholest-5-én-3β-yle et de 3,5-dichloro-2-méthoxy-6-(trichlorométhyl)pyridin-4-yle

mipicoledina

carbonato de colest-5-en-3β-ilo y de 3,5-dicloro-2-metoxi-6-(triclorometil)piridin-4-ilo

$C_{35}H_{48}Cl_5NO_4$



nadecnemabum #

nadecnemab	immunoglobulin G4-kappa, anti-[*Homo sapiens* GFRA3 (glial cell derived neurotrophic factor family receptor alpha 3, GFRa-3)], *Homo sapiens* monoclonal antibody; gamma4 heavy chain *Homo sapiens* (1-451) [VH (*Homo sapiens* IGHV3-23*04 (95.9%) -(IGHD) - IGHJ6*01 (94.4%)) CDR-IMGT [8.8.17] (26-33.51-58.97-113) (1-124)-*Homo sapiens* IGHG4*01 (100%), G4v5 h P10 (CH1 (125-222), hinge 1-12 S10>P (232) (223-234), CH2 (235-344), CH3 (345-449), CHS (450-451)) (125-451)], (138-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (98.9%) -IGKJ3*01 (91.7%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') - *Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (230-230'':233-233'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa
nadecnémab	immunoglobuline G4-kappa, anti-[*Homo sapiens* GFRA3 (récepteur-3 alfa de la famille du facteur neurotrophe dérivé de la glie, GFRa-3)], anticorps monoclonal *Homo sapiens*; chaîne lourde gamma4 *Homo sapiens* (1-451) [VH (*Homo sapiens* IGHV3-23*04 (95.9%) -(IGHD) - IGHJ6*01 (94.4%)) CDR-IMGT [8.8.17] (26-33.51-58.97-113) (1-124)-*Homo sapiens* IGHG4*01 (100%), G4v5 h P10 (CH1 (125-222), charnière 1-12 S10>P (232) (223-234), CH2 (235-344), CH3 (345-449), CHS (450-451)) (125-451)], (138-214')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (98.9%) - IGKJ3*01 (91.7%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (230-230'':233-233'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa
nadecnemab	inmunoglobulina G4-kappa, anti-[*Homo sapiens* GFRA3 (receptor-3 alfa de la familia del factor neurotrófico derivado de la glia, GFRa-3)], anticuerpo monoclonal *Homo sapiens*;

cadena pesada gamma4 *Homo sapiens* (1-451) [VH (*Homo sapiens* IGHV3-23*04 (95.9%) -(IGHD) - IGHJ6*01 (94.4%)) CDR-IMGT [8.8.17] (26-33.51-58.97-113) (1-124)-*Homo sapiens* IGHG4*01 (100%), G4v5 h P10 (CH1 (125-222), bisagra 1-12 S10>P (232) (223-234), CH2 (235-344), CH3 (345-449), CHS (450-451)) (125-451)], (138-214')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (98.9%) - IGKJ3*01 (91.7%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (230-230":233-233")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAASGFTFS SYAMSWVRQA PGKGLEWVSV  50
ISGSGGSTYY ADAVKGRFTI SRDNSKHTLY LQMNSLRAED TAVYYCTKPS 100
SYSSSNFYYG MDVWGQGTTV TVSSASTKGP SVFPLAPCSR STSESTAALG 150
CLVKDYFPEP VTVSWNSGAL TSGVHTFPAV LQSSGLYSLS SVVTVPSSSL 200
GTKTYTCNVD HKPSNTKVDK RVESKYGPPC PPCPAPEFLG GPSVFLFPPK 250
PKDTLMISRT PEVTCVVVDV SQEDPEVQFN WYVDGVEVHN AKTKPREEQF 300
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK GLPSSIEKTI SKAKGQPREP 350
QVYTLPPSQE EMTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP 400
VLDSDGSFFL YSRLTVDKSR WQEGNVFSCS VMHEALHNHY TQKSLSLSLG 450
K                                                       451
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS VSASVGDRVT ITCRASQGIS SWLAWYQQKP GKAPKLLIYA  50
ASSLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ TNSFPFPFGP 100
GTKVDIKRTV 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) 22-96 151-207 265-325 371-429
22"-96" 151"-207" 265"-325" 371"-429"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194'"
Inter-H-L (CH1 10-CL 126) 138-214' 138"-214'"
Inter-H-H (h 8, h 11) 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.

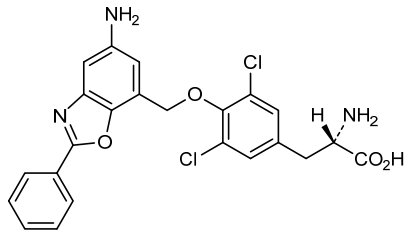
C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal

H CHS K2:
451, 451"

nanvuranlatum

nanvuranlat	*O*-[(5-amino-2-phenyl-1,3-benzoxazol-7-yl)methyl]-3,5-dichloro-L-tyrosine
nanvuranlat	*O*-[(5-amino-2-phényl-1,3-benzoxazol-7-yl)méthyl]-3,5-dichloro-L-tyrosine
nanvuranlat	*O*-[(5-amino-2-fenil-1,3-benzoxazol-7-il)metil]-3,5-dicloro-L-tirosina

$C_{23}H_{19}Cl_2N_3O_4$



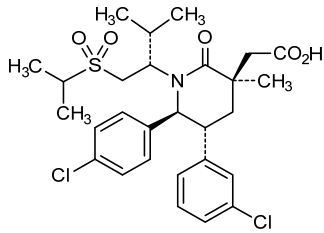
navtemadlinum

navtemadlin — {(3*R*,5*R*,6*S*)-5-(3-chlorophenyl)-6-(4-chlorophenyl)-3-methyl-1-[(2*S*)-3-methyl-1-(propane-2-sulfonyl)butan-2-yl]-2-oxopiperidin-3-yl}acetic acid

navtémadline — acide {(3*R*,5*R*,6*S*)-5-(3-chlorophényl)-6-(4-chlorophényl)-3-méthyl-1-[(2*S*)-3-méthyl-1-(propane-2-sulfonyl)butan-2-yl]-2-oxopipéridin-3-yl}acétique

navtemadlina — ácido {(3*R*,5*R*,6*S*)-5-(3-clorofenil)-6-(4-clorofenil)-3-metil-1-[(2*S*)-3-metil-1-(propano-2-sulfonil)butan-2-il]-2-oxopiperidin-3-il}acético

$C_{28}H_{35}Cl_2NO_5S$



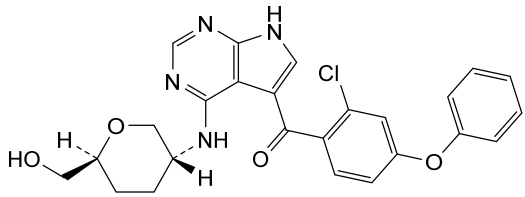
nemtabrutinibum

nemtabrutinib — (1^3R,1^6S)-5^2-chloro-1^6-(hydroxymethyl)-3^7H-6-oxa-2-aza-3(4,5)-pyrrolo[2,3-*d*]pyrimidina-1(3)-oxana-5(1,4),7(1)-dibenzenaheptaphan-4-one

nemtabrutinib — (1^3R,1^6S)-5^2-chloro-1^6-(hydroxyméthyl)-3^7H-6-oxa-2-aza-3(4,5)-pyrrolo[2,3-*d*]pyrimidina-1(3)-oxana-5(1,4),7(1)-dibenzénaheptaphan-4-one

nemtabrutinib — (1^3R,1^6S)-5^2-cloro-1^6-(hidroximetil)-3^7H-6-oxa-2-aza-3(4,5)-pirrolo[2,3-*d*]pirimidina-1(3)-oxana-5(1,4),7(1)-dibencenaheptafan-4-ona

$C_{25}H_{23}ClN_4O_4$



nendratareotidum

nendratareotide

S^2,S^7-cyclo(D-phenylalanyl-L-cysteinyl-L-tyrosyl-D-tryptophyl-L-lysyl-L-threonyl-L-cysteinyl-L-cysteinamide)

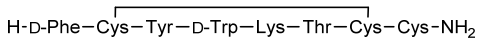
nendrataréotide

S^2,S^7-cyclo(D-phénylalanyl-L-cystéinyl-L-tyrosyl-D-tryptophyl-L-lysyl-L-thréonyl-L-cystéinyl-L-cystéinamide)

nendratareotida

S^2,S^7-ciclo(D-fenilalanil-L-cisteinil-L-tirosil-D-triptofil-L-lisil-L-treonil-L-cisteinil-L-cisteinamide)

$C_{48}H_{63}N_{11}O_{10}S_3$



nendratareotidum uzatansinum

nendratareotide uzatansine

S^2,S^7-cyclo{D-phenylalanyl-L-cysteinyl-L-tyrosyl-D-tryptophyl-L-lysyl-L-threonyl-L-cysteinyl-3-[(3-{[(2*S*)-1-{[(1^4*S*,1^6*S*,2*R*,3^2*S*,3^3*S*,4*S*,10*E*,12*E*,14*R*)-8^6-chloro-1^4-hydroxy-8^5,14-dimethoxy-2,3^3,7,10-tetramethyl-1^2,6-dioxo-7-aza-1(6,4)-[1,3]oxazinana-3(2,3)-oxirana-8(1,3)-benzenacyclotetradecaphane-10,12-dien-4-yl]oxy}-1-oxopropan-2-yl](methyl)amino}-3-oxopropyl)disulfanyl]-L-alaninamide}

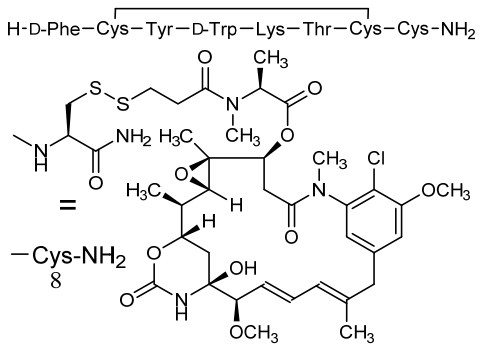
nendrataréotide uzatansine

S^2,S^7-cyclo{D-phénylalanyl-L-cystéinyl-L-tyrosyl-D-tryptophyl-L-lysyl-L-thréonyl-L-cystéinyl-3-[(3-{[(2*S*)-1-{[(1^4*S*,1^6*S*,2*R*,3^2*S*,3^3*S*,4*S*,10*E*,12*E*,14*R*)-8^6-chloro-1^4-hydroxy-8^5,14-diméthoxy-2,3^3,7,10-tétraméthyl-1^2,6-dioxo-7-aza-1(6,4)-[1,3]oxazinana-3(2,3)-oxirana-8(1,3)-benzénacyclotétradeca-phane-10,12-dién-4-yl]oxy}-1-oxopropan-2-yl](méthyl)amino}-3-oxopropyl)disulfanyl]-L-alaninamide}

nendratareotida uzatansina

S^2,S^7-ciclo{D-fenilalanil-L-cisteinil-L-tirosil-D-triptofil-L-lisil-L-treonil-L-cisteinil-3-[(3-{[(2*S*)-1-{[(1^4*S*,1^6*S*,2*R*,3^2*S*,3^3*S*,4*S*,10*E*,12*E*,14*R*)-8^6-cloro-1^4-hidroxi-2,3^3,7,10-tetrametil-8^5,14-dimetoxi-1^2,6-dioxo-7-aza-1(6,4)-[1,3]oxazinana-3(2,3)-oxirana-8(1,3)-bencenaciclotetradeca-fano-10,12-dien-4-il]oxi}-1-oxopropan-2-il](metil)amino}-3-oxopropil)disulfanil]-L-alaninamida}

$C_{83}H_{109}ClN_{14}O_{20}S_4$



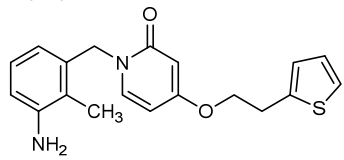
nilofabicinum

nilofabicin — 1-[(3-amino-2-methylphenyl)methyl]-4-[2-(thiophen-2-yl)ethoxy]pyridin-2(1*H*)-one

nilofabicine — 1-[(3-amino-2-méthylphényl)méthyl]-4-[2-(thiophén-2-yl)éthoxy]pyridin-2(1*H*)-one

nilofabicina — 1-[(3-amino-2-metilfenil)metil]-4-[2-(tiofen-2-il)etoxi]piridin-2(1*H*)-ona

$C_{19}H_{20}N_2O_2S$



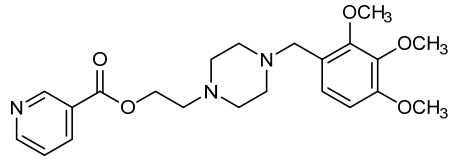
ninerafaxstatum

ninerafaxstat — 2-{4-[(2,3,4-trimethoxyphenyl)methyl]piperazin-1-yl}ethyl pyridine-3-carboxylate

ninérafaxstat — pyridine-3-carboxylate de 2-{4-[(2,3,4-triméthoxyphényl)méthyl]pipérazin-1-yl}éthyle

ninerafaxstat — piridina-3-carboxilato de 2-{4-[(2,3,4-trimetoxifenil)metil]piperazin-1-il}etilo

$C_{22}H_{29}N_3O_5$



nivadstrocelum

nivadstrocel — Allogeneic mesenchymal stromal cells derived from subcutaneous adipose tissue collected by liposuction. The cells are isolated from the adipose tissue by enzymatic digestion and are expanded in a three-dimensional hydrogel matrix with scaffold structure. The cells express cell surface markers CD105 and CD90 (≥95%), lack cell surface expression (<2% positive) of CD45, CD34, and do not express T cell co-stimulatory molecules CD40, CD80 or CD86 and major histocompatibility complex (MHC) class II (HLA-DR). The cells also secrete various growth factors (e.g. insulin-like growth factor (IGF), hepatocyte growth factor (HGF) and vascular endothelial growth factor (VEGF)) and express extracellular matrix proteins, in particular collagen type VII.

nivadstrocel — Cellules stromales mésenchymateuses allogéniques dérivées du tissu adipeux sous-cutané recueillies par liposuccion. Les cellules ont été isolées du tissu

adipeux par digestion enzymatique et ont été expansées dans une matrice d'hydrogel tridimensionnelle avec une structure d'échafaudage. Les cellules expriment les marqueurs cellulaires de surface CD105 et CD90 (≥95%), présentent une absence d'expression à la surface cellulaire (<2% positive) de CD45, CD34, et n'expriment pas les molécules co-stimulatrices des lymphocytes T CD40, CD80 ou CD86 ainsi que le complexe majeur d'histocompatibilité (MHC) de classe II (HLA-DR). Les cellules sécrètent aussi différents facteurs de croissance (p. ex. le facteur de croissance analogue à l'insuline (IGF), le facteur de croissance des hépatocytes (HGF) et le facteur de croissance de l'endothélium vasculaire (VEGF)) et expriment des protéines de la matrice extracellulaire, en particulier le collagène de type VII.

nivadstrocel — Células estromales mesenquimales alogénicas derivadas de tejido adiposo subcutáneo obtenido por liposucción. Las células se aíslan del tejido adiposo mediante digestión enzimática y se expanden en una matriz tridimensional de hidrogel con estructura de andamiaje. Las células expresan los marcadores de superficie CD105 y CD90 ((≥95%), carecen de expresión en la superficie celular (<2% positivo) de CD45, CD34 y no expresan las moléculas coestimuladoras de linfocitos T CD40, CD80 o CD86 ni complejo principal de histocompatibilidad (MHC) clase II (HLA-DR). Las células también secretan varios factores de crecimiento (por ejemplo el factor de crecimiento similar a insulina (IGF), el factor de crecimiento de hepatocitos (HGF) y el factor de crecimiento del endotelio vascular (VEGF)) y expresan proteínas de la matiz extracelular, en particular colágeno tipo VII.

nivatrotamabum #

nivatrotamab — immunoglobulin G1-kappa anti-[*Homo sapiens* GD2 (ganglioside GD2)], each kappa chain being fused to a scFv anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], monoclonal antibody, bispecific;
gamma1 heavy chain anti-GD2 (1-449) [VH (*Mus musculus* IGHV2-9*02 (79.2%) -(IGHD) -IGHJ3*01 (91.7%) A128>S (119)/*Homo sapiens* IGHV3-33*01 (72.2%) -(IGHD) -IGHJ4*01 (92.3%)) CDR-IMGT [8.7.13] (26-33.51-57.96-108) (1-119) -*Homo sapiens* IGHG1*08p (100%), G1m3,1, G1v29 CH2 A84.4, G1v20 CH2 A105 (CH1 R120 (216) (120-217), hinge 1-15 (218-232), CH2 N84.4>A (299), K105>A (324) (233-342), CH3 D12 (358), L14 (360) (343-447), CHS (448-449)) (120-449)], (222-211')-disulfide with kappa light chain anti-GD2 fused to scFv anti-CD3E (1'-484') [kappa light chain anti-GD2 (1'-211') [V-KAPPA anti-GD2 (*Mus musculus* IGKV6-32*02 (84.9%) -(IGHD) -IGKJ2*03 (90.0%) S120>Q (97)/*Homo sapiens* IGKV3-15*01 (78.9%) -IGKJ2*03 (100%)) CDR-IMGT [6.3.6] (27-32.50-52.89-94) (1'-104') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (150), V101 (188) (105'-211')]-17-mer threonyl-seryl-tris(tetraglycyl-seryl) linker (212'-228') -scFv heavy-kappa anti-CD3E (229'-484') [VH anti-CD3E G49>C (272), C114>S (333) (*Homo sapiens* IGHV3-30*10 (70.4%) -(IGHD) -IGHJ4*01 (85.7%) L123>P (342)) CDR-IMGT [8.8.12] (254-261.279-286.325-336) (229'-347') -30-mer hexakis(tetraglycyl-seryl) linker (348'-377') -V-KAPPA anti-CD3E (*Homo sapiens* IGKV1-33*01 (81.1%) -IGKJ2*02 (80.0%) Q120>C (476), E125>Q (481)) CDR-IMGT [5.3.9] (404-408.426-428.465-473) (378'-484')]]; dimer (228-228":231-231")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, non-glycosylated

nivatrotamab	immunoglobuline G1-kappa anti-[*Homo sapiens* GD2 (ganglioside GD2)], chaque chaîne kappa étant fusionnée à un scFv anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], anticorps monoclonal, bispécifique; chaîne lourde gamma1 anti-GD2 (1-449) [VH (*Mus musculus* IGHV2-9*02 (79.2%) -(IGHD) -IGHJ3*01 (91.7%) A128>S (119)/*Homo sapiens* IGHV3-33*01 (72.2%) -(IGHD) -IGHJ4*01 (92.3%)) CDR-IMGT [8.7.13] (26-33.51-57.96-108) (1-119) -*Homo sapiens* IGHG1*08p (100%), G1m3,1, G1v29 CH2 A84.4, G1v20 CH2 A105 (CH1 R120 (216) (120-217), charnière 1-15 (218-232), CH2 N84.4>A (299), K105>A (324) (233-342), CH3 D12 (358), L14 (360) (343-447), CHS (448-449)) (120-449)], (222-211')-disulfure avec la chaîne légère kappa anti-GD2 fusionnée au scFv anti-CD3E (1'-484') [chaîne légère kappa anti-GD2 (1'-211' [V-KAPPA anti-GD2 (*Mus musculus* IGKV6-32*02 (84.9%) -(IGHD) -IGKJ2*03 (90.0%) S120>Q (97)/*Homo sapiens* IGKV3-15*01 (78.9%) -IGKJ2*03 (100%)) CDR-IMGT [6.3.6] (27-32.50-52.89-94) (1'-104') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (150), V101 (188) (105'-211')]-17-mer thréonyl-séryl-tris(tétraglycyl-séryl) linker (212'-228') -scFv lourd-kappa anti-CD3E (229'-484') [VH anti-CD3E G49>C (272), C114>S (333) (*Homo sapiens* IGHV3-30*10 (70.4%) -(IGHD) -IGHJ4*01 (85.7%) L123>P (342)) CDR-IMGT [8.8.12] (254-261.279-286.325-336) (229'-347') -30-mer hexakis(tétraglycyl-séryl linker (348'-377') -V-KAPPA anti-CD3E (*Homo sapiens* IGKV1-33*01 (81.1%) -IGKJ2*02 (80.0%) Q120>C (476), E125>Q (481)) CDR-IMGT [5.3.9] (404-408.426-428.465-473) (378'-484')]]; dimère (228-228":231-231")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), non-glycosylé
nivatrotamab	inmunoglobulina G1-kappa anti-[*Homo sapiens* GD2 (ganglиósido GD2)], cada cadena kappa estando fusionada a un scFv anti-[*Homo sapiens* CD3E (CD3 épsilon, Leu-4)], anticuerpo monoclonal, biespecífico; cadena pesada gamma1 anti-GD2 (1-449) [VH (*Mus musculus* IGHV2-9*02 (79.2%) -(IGHD) -IGHJ3*01 (91.7%) A128>S (119)/*Homo sapiens* IGHV3-33*01 (72.2%) -(IGHD) -IGHJ4*01 (92.3%)) CDR-IMGT [8.7.13] (26-33.51-57.96-108) (1-119) -*Homo sapiens* IGHG1*08p (100%), G1m3,1, G1v29 CH2 A84.4, G1v20 CH2 A105 (CH1 R120 (216) (120-217), bisagra 1-15 (218-232), CH2 N84.4>A (299), K105>A (324) (233-342), CH3 D12 (358), L14 (360) (343-447), CHS (448-449)) (120-449)], (222-211')-disulfuro con la cadena ligera kappa anti-GD2 fusionada con scFv anti-CD3E (1'-484') [cadena ligera kappa anti-GD2 (1'-211' [V-KAPPA anti-GD2 (*Mus musculus* IGKV6-32*02 (84.9%) -(IGHD) -IGKJ2*03 (90.0%) S120>Q (97)/*Homo sapiens* IGKV3-15*01 (78.9%) -IGKJ2*03 (100%)) CDR-IMGT [6.3.6] (27-32.50-52.89-94) (1'-104') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (150), V101 (188) (105'-211')]-17-mer treonil-seril-tris(tetraglicil-seril) linker (212'-228') -scFv pesado-kappa anti-CD3E (229'-484') [VH anti-CD3E G49>C (272), C114>S (333) (*Homo sapiens* IGHV3-30*10 (70.4%) -(IGHD) -IGHJ4*01 (85.7%) L123>P (342)) CDR-IMGT

[8.8.12] (254-261.279-286.325-336) (229'-347') -30-mer hexakis(tetraglicil-seril linker (348'-377') -V-KAPPA anti-CD3E (*Homo sapiens* IGKV1-33*01 (81.1%) - IGKJ2*02 (80.0%) Q120>C (476), E125>Q (481)) CDR-IMGT [5.3.9] (404-408.426-428.465-473) (378'-484')]]; dímero (228-228":231-231")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), no glicosilado

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 TKPREEQYAS 300
TYRVVSVLTV LHQDWLNGKE YKCAVSNKAL 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 CTSGGGGSGG GGSGGGGSQV QLVQSGGGVV QPGRSLRLSC 250
KASGYTFTRY TMHWVRQAPG KCLEWIGYIN PSRGYTNYNQ KFKDRFTISR 300
DNSKNTAFLQ MDSLRPEDTG VYFCARYYDD HYSLDYWGQG TPVTVSSGGG 350
GSGGGGSGGG GSGGGGSGGG GSGGGGSDIQ MTQSPSSLSA SVGDRVTITC 400
SASSSVSYMN WYQQTPGKAP KRWIYDTSKL ASGVPSRFSG SGSGTDYTFT 450
ISSLQPEDIA TYYCQQWSSN PFTFGCGTKL QITR                  484
```

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' 250'-324' 400'-464'
23'"-88'" 131'"-191'" 250'"-324'" 400'"-464'"
Intra-L (scFv VH C49 -VL IGKJ C120) 272'-476'
272'"-476'"
Inter-H-L (h 5-CL 126) 222-211' 222"-211'"
Inter-H-H (h 11, h 14) 228-228" 231-231"

N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
L VH Q1:
1, 1"

No N-glycosylation sites / pas de sites de N-glycosylation / ningún posición de N-glicosilación
CH2 N84.4>A:
299, 299"
Aglycosylated

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2:
449, 449"

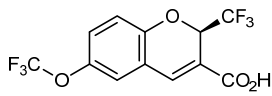
ocarocoxibum

ocarocoxib — *rac*-(2*R*)-6-(trifluoromethoxy)-2-(trifluoromethyl)-2*H*-1-benzopyran-3-carboxylic acid

ocarocoxib — acide *rac*-(2*R*)-6-(trifluorométhoxy)-2-(trifluorométhyl)-2*H*-1-benzopyrane-3-carboxylique

ocarocoxib — ácido *rac*-(2*R*)-2-(trifluorometil)-6-(trifluorometoxi)-2*H*-1-benzopirano-3-carboxílico

$C_{12}H_6F_6O_4$



and enantiomer
et énantiomère
y enantiómero

onilcamotidum

onilcamotide

RhoC (Rho-related GTP-binding protein RhoC, Ras homolog gene family member C protein) proprotein C-terminal (174-193)-peptide: L-alanyl-L-threonyl-L-arginyl-L-alanylglycyl-L-leucyl-L-glutaminyl-L-valyl-L-arginyl-L-lysyl-L-asparaginyl-L-lysyl-L-arginyl-L-arginyl-L-arginylglycyl-L-cysteinyl-L-prolyl-L-isoleucyl-L-leucine

onilcamotide

peptide 174-193 C-terminal de la proprotéine de RhoC (protéine RhoC de liaison au GTP RhoC apparentée à Rho, membre C des protéines de la famille de gènes homologues Ras): L-alanyl-L-thréonyl-L-arginyl-L-alanylglycyl-L-leucyl-L-glutaminyl-L-valyl-L-arginyl-L-lysyl-L-asparaginyl-L-lysyl-L-arginyl-L-arginyl-L-arginylglycyl-L-cystéinyl-L-prolyl-L-isoleucyl-L-leucine

onilcamotida

péptido 174-193 C-terminal de la proproteína del RhoC (proteína RhoC de unión a GTP relacionada con Rho, miembro C de proteínas en la familia de genes homólogos Ras): L-alanil-L-treonil-L-arginil-L-alanilglicil-L-leucil-L-glutaminil-L-valil-L-arginil-L-lisil-L-asparaginil-L-lisil-L-arginil-L-arginil-L-arginilglicil-L-cisteinil-L-prolil-L-isoleucil-L-leucina

$C_{96}H_{177}N_{39}O_{24}S$

H–Ala–Thr–Arg–Ala–Gly–Leu–Gln–Val–Arg–Lys–
10
Asn–Lys–Arg–Arg–Arg–Gly–Cys–Pro–Ile–Leu–OH
20

onzigolidum

onzigolide

S^2,*S*^{7}-cyclo[*N*^{2},*N*^{6}-bis({[(6-propylergolin-8β-yl)methyl]sulfanyl}acetyl)-D-lysyl-L-cysteinyl-L-tyrosyl-D-tryptophyl-L-lysyl-(2*S*)-2-aminobutanoyl-L-cysteinyl-L-threoninamide]

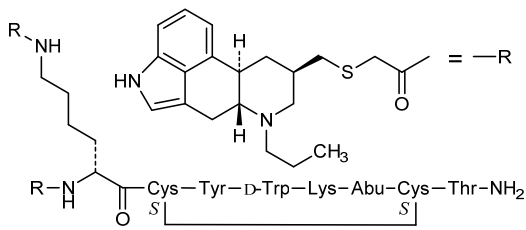
onzigolide

S^2,*S*^{7}-cyclo[*N*^{2},*N*^{6}-bis({[(6-propylergolin-8β-yl)méthyl]sulfanyl}acétyl)-D-lysyl-L-cystéinyl-L-tyrosyl-D-tryptophyl-L-lysyl-(2*S*)-2-aminobutanoyl-L-cystéinyl-L-thréoninamide]

onzigolida

S^2,*S*^{7}-ciclo[*N*^{2},*N*^{6}-bis({[(6-propilergolin-8β-il)metil]sulfanil}acetil)-D-lisil-L-cisteinil-L-tirosil-D-triptofil-L-lisil-(2*S*)-2-aminobutanoil-L-cisteinil-L-treoninamida]

$C_{86}H_{116}N_{16}O_{12}S_4$



opelconazolum

opelconazole

(6^2R,6^4R)-6^2-(2,4-difluorophenyl)-*N*-(4-fluorophenyl)-3^3-methyl-4-oxa-2(1,4)-piperazina-8(1)-[1,2,4]triazola-6(4,2)-oxolana-1(1),3(1,4)-dibenzenaoctaphane-1^4-carboxamide

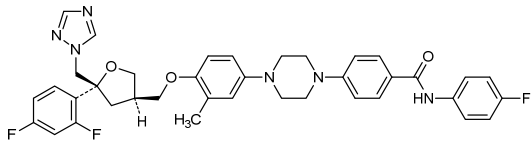
opelconazole

(6^2R,6^4R)-6^2-(2,4-difluorophényl)-*N*-(4-fluorophényl)-3^3-méthyl-4-oxa-2(1,4)-pipérazina-8(1)-[1,2,4]triazola-6(4,2)-oxolana-1(1),3(1,4)-dibenzénaoctaphane-1^4-carboxamide

opelconazol

(6^2R,6^4R)-6^2-(2,4-difluorofenil)-*N*-(4-fluorofenil)-3^3-metil-4-oxa-2(1,4)-piperazina-8(1)-[1,2,4]triazola-6(4,2)-oxolana-1(1),3(1,4)-dibencenaoctafano-1^4-carboxamida

$C_{38}H_{37}F_3N_6O_3$



ordesekimabum #

ordesekimab

immunoglobulin G1-kappa, anti-[*Homo sapiens* IL15 (interleukin 15, IL-15)], *Homo sapiens* monoclonal antibody;
gamma1 heavy chain *Homo sapiens* (1-448) [VH (*Homo sapiens* IGHV5-51*01 (95.9%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.11] (26-33.51-58.97-107) (1-118) -*Homo sapiens* IGHG1*08p (100%), G1m3,1 (CH1 R120 (215) (119-216), hinge 1-15 (217-231), CH2 (232-341), CH3 D12 (357), E14 (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 (97.9%) -IGKJ2*01 (100%)) CDR-IMGT [7.3.8] (27-33.51-53.90-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (227-227":230-230")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

ordésékimab

immunoglobuline G1-kappa, anti-[*Homo sapiens* IL15 (interleukine 15, IL-15)], anticorps monoclonal *Homo sapiens*;
chaîne lourde gamma1 *Homo sapiens* (1-448) [VH (*Homo sapiens* IGHV5-51*01 (95.9%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.11] (26-33.51-58.97-107) (1-118) -*Homo* IGHG1*08p (100%), G1m3,1 (CH1 R120 (215) (119-216), charnière 1-15 (217-231), CH2 (232-341), CH3 D12 (357), E14 (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 (97.9%) -IGKJ2*01 (100%)) CDR-IMGT [7.3.8] (27-33.51-53.90-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (227-227":230-230")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

ordesekimab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* IL15 (interleukina 15, IL-15)], anticuerpo monoclonal *Homo sapiens*;cadena pesada gamma1 *Homo sapiens* (1-448) [VH (*Homo sapiens* IGHV5-51*01 (95.9%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.11] (26-33.51-58.97-107) (1-118) -*Homo* IGHG1*08p (100%), G1m3,1 (CH1 R120 (215) (119-216), bisagra 1-15 (217-231), CH2 (232-341), CH3 D12 (357), E14 (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 (97.9%) -IGKJ2*01 (100%)) CDR-IMGT [7.3.8] (27-33.51-53.90-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (227-227'':230-230'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVQSGAE VKKPGESLKI SCKVSGYFFT TYWIGWVRQM PGKGLEYMGI  50
IYPGDSDTRY SPSFQGQVTI SADKSISTAY LQWSSLKASD TAMYYCARGG 100
NWNCFDYWGQ GTLVTVSSAS TKGPSVFPLA PSSKSTSGGT AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTQTYI 200
CNVNHKPSNT KVDKRVEPKS CDKTHTCPPC PAPELLGGPS VFLFPPKPKD 250
TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNST 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY 350
TLPPSRDELT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD 400
SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPGK   448
```

Light chain / Chaîne légère / Cadena ligera

```
EIVLTQSPGT LSLSPGERAT LSCRASQSVS SSYLAWYQQK PGQAPRLLIY  50
GASRRATGIP DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ RYGSSHTFGQ 100
GTKLEISRTV 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'-89' 134'-194'
23'"-89"' 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.

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2:
448, 448"

oremeperminum alfa #

oremepermin alfa

human hepatocyte growth factor isoform 3 (HGF3, hepatopoietin A isoform 3, five amino acid-deleted variant of hepatocyte growth factor, dHGF), heterodimer (alpha and beta chains), glycosylated, produced in Chinese hamster ovary (CHO) cells;
hepatocyte growth factor isoform 3 (*Homo sapiens* HGF3, hepatopoietin A isoform 3, des[SFLPS (130-134)]-hepatocyte growth factor, dHGF), produced in Chinese hamster ovary (CHO) cells, glycoform alfa

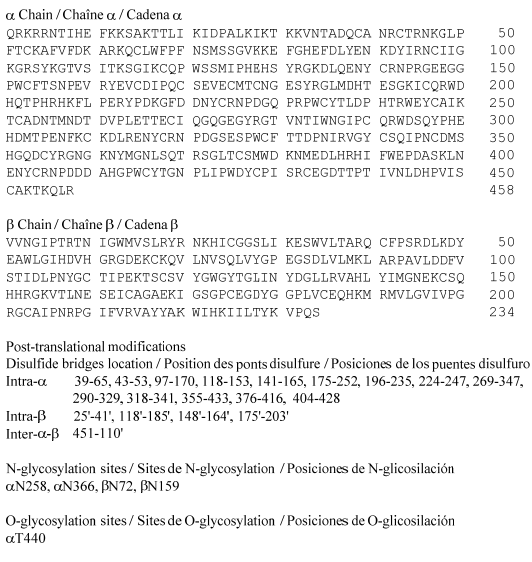
orémépermine alfa

isoforme 3 du factor de croissance des hépatocytes humains (HGF3, isoforme 3 de l'hépatopoïétine A, variant du facteur de croissance des hépatocytes avec cinq acides aminés supprimé, dHGF), hétérodimère (chaînes alpha et bêta), glycosylée, produite dans des cellules ovariennes de hamster (CHO);

isoforme 3 du facteur de croissance des hépatocytes (HGF3 *d'Homo sapiens*, isoforme 3 de l'hépatopoïétine A, dés[SFLPS (130-134)]-facteur de croissance des hépatocytes, dHGF), produite dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

oremepermina alfa

factor de crecimiento de hepatocitos humano isoforma 3 (HGF3, hepatopoyetina A isoforma 3, cinco aminoácidos eliminiados variante del factor de crecimiento de hepatocitos, dHGF), heterodímero (cadenas alfa y beta), glicosilado, producido en células ováricas de hámster chino (CHO);
factor de crecimiento de hepatocitos, isoforma 3 (HGF3 de *Homo sapiens*, isoforma 3 de hepatopoyetina A, des[SFLPS (130-134)]-factor de crecimiento de hepatocitos, dHGF), producido en células ováricas de hámster chino (CHO), glicoforma alfa



α Chain / Chaîne α / Cadena α

```
QRKRRNTIHE FKKSAKTTLI KIDPALKIKT KKVNTADQCA NRCTRNKGLP    50
FTCKAFVFDK ARKQCLWFPF NSMSSGVKKE FGHEFDLYEN KDYIRNCIIG   100
KGRSYKGTVS ITKSGIKCQP WSSMIPHEHS YRGKDLQENY CRNPRGEGG    150
PWCFTSNPEV RYEVCDIPQC SEVECMTCNG ESYRGLMDHT ESGKICQRWD   200
HQTPHRHKFL PERYPDKGFD DNYCRNPDGQ PRPWCYTLDP HTRWEYCAIK   250
TCADNTMNDT DVPLETTECI QGQGEGYRGT VNTIWNGIPC QRWDSQYPHE   300
HDMTPENFKC KDLRENYCRN PDGSESPWCF TTDPNIRVGY CSQIPNCDMS   350
HGQDCYRGNG KNYMGNLSQT RSGLTCSMWD KNMEDLHRHI FWEPDASKLN   400
ENYCRNPDDD AHGPWCYTGN PLIPWDYCPI SRCEGDTTPT IVNLDHPVIS   450
CAKTKQLR                                                 458
```

β Chain / Chaîne β / Cadena β

```
VVNGIPTRTN IGWMVSLRYR NKHICGGSLI KESWVLTARQ CFPSRDLKDY    50
EAWLGIHDVH GRGDEKCKQV LNVSQLVYGP EGSDLVLMKL ARPAVLDDFV   100
STIDLPNYGC TIPEKTSCSV YGWGYTGLIN YDGLLRVAHL YIMGNEKCSQ   150
HHRGKVTLNE SEICAGAEKI GSGPCEGDYG GPLVCEQHKM RMVLGVIVPG   200
RGCAIPNRPG IFVRVAYYAK WIHKIILTYK VPQS                    234
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-α 39-65, 43-53, 97-170, 118-153, 141-165, 175-252, 196-235, 224-247, 269-347, 290-329, 318-341, 355-433, 376-416, 404-428
Intra-β 25'-41', 118'-185', 148'-164', 175'-203'
Inter-α-β 451-110'

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
αN258, αN366, βN72, βN159

O-glycosylation sites / Sites de O-glycosylation / Posiciones de O-glicosilación
αT440

orludodstatum

orludodstat

N-(2-chloro-6-fluorophenyl)-4-[4-ethyl-3-(hydroxymethyl)-5-oxo-4,5-dihydro-1*H*-1,2,4-triazol-1-yl]-5-fluoro-2-{[(2*S*)-1,1,1-trifluoropropan-2-yl]oxy}benzamide

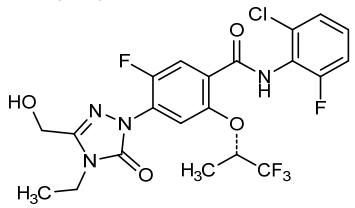
orludodstat

N-(2-chloro-6-fluorophényl)-4-[4-éthyl-3-(hydroxyméthyl)-5-oxo-4,5-dihydro-1*H*-1,2,4-triazol-1-yl]-5-fluoro-2-{[(2*S*)-1,1,1-trifluoropropan-2-yl]oxy}benzamide

orludodstat

N-(2-cloro-6-fluorofenil)-4-[4-etil-3-(hidroximetil)-5-oxo-4,5-dihidro-1*H*-1,2,4-triazol-1-il]-5-fluoro-2-{[(2*S*)-1,1,1-trifluoropropan-2-il]oxi}benzamida

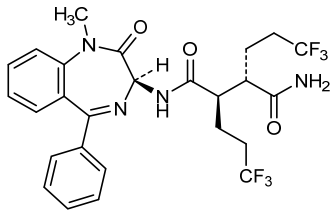
$C_{21}H_{18}ClF_5N_4O_4$



osugacestatum

osugacestat	(2*R*,3*S*)-*N*^{1}-[(3*S*)-1-methyl-2-oxo-5-phenyl-2,3-dihydro-1*H*-1,4-benzodiazepin-3-yl]-2,3-bis(3,3,3-trifluoropropyl)butanediamide
osugacestat	(2*R*,3*S*)-*N*^{1}-[(3*S*)-1-méthyl-2-oxo-5-phényl-2,3-dihydro-1*H*-1,4-benzodiazépin-3-yl]-2,3-bis(3,3,3-trifluoropropyl)butanediamide
osugacestat	(2*R*,3*S*)-*N*^{1}-[(3*S*)-5-fenil-1-metil-2-oxo-2,3-dihidro-1*H*-1,4-benzodiazepin-3-il]-2,3-bis(3,3,3-trifluoropropil)butanodiamida

$C_{26}H_{26}F_6N_4O_3$



ozarlimogenum inteplasmidum #

ozarlimogene inteplasmid	A DNA plasmid encoding *Streptococcus pyogenes* serotype M55 (emm55) cell surface protein (variant). A DNA plasmid encoding *Streptococcus pyogenes* serotype M55 (emm55) cell surface protein [variant, with 98% identity to the original source isolate A928171 (X72090.1)] under the control of a human cytomegalovirus (CMV) enhancer/promoter and an SV40 polyA signal sequence. Absence of the original stop codon results in the addition of 15 C-terminal plasmid-encoded amino acid residues. The plasmid also contains a bacterial origin (ori) of replication, F1 bacteriophage origin of replication, the SV40 virus origin of replication and a NeoR/KanR resistance coding sequence under the control of AmpR/SV40 promoters and a Herpes simplex virus (HSV) thymidine kinase (TK) poly(A) signal.
ozarlimogène intéplasmide	Un plasmide d'ADN codant pour une protéine de surface cellulaire (variant) du *Streptococcus pyogenes* de sérotype M55 (emm55). Un plasmide d'ADN codant pour une protéine de surface cellulaire du *Streptococcus pyogenes* de sérotype M55 (emm55) [variant, ayant une identité de 98% avec la source originelle de l'isolat A928171 (X72090.1)] sous le contrôle d'un activateur/promoteur du cytomégalovirus (CMV) humain et d'une séquence signal polyA SV40. L'absence du codon stop originel.

résulte de l'addition de 15 résidus d'acides aminés en C-terminal encodés par le plasmide. Le plasmide contient aussi une origine (ori) de réplication bactérienne, une origine de réplication du bactériophage F1, une origine de réplication du virus SV40 et une séquence codant une résistance NeoR/KanR sous le contrôle des promoteurs AmpR/SV40 et d'un signal poly(A) de la thymidine kinase (TK) du virus Herpès simplex (HSV).

ozarlimogén inteplásmido

Un plásmido de DNA que codifica para una variante de la proteína de superficie de *Streptococcus pyogenes* serotipo M55 (emm55).
Un plásmido de DNA que codifica para la proteína de superficie de *Streptococcus pyogenes* serotipo M55 (emm55) [variante, con un 98% de identidad con el aislado original A928171 (X72090.1)] bajo el control de un potenciador/promotor del citomegalovirus (CMV) humano y una secuencia señal polyA de SV40. La ausencia del codón de terminación original resulta en la adición a la región C-terminal de 15 residuos de aminoácidos codificados en el plásmido. El plásmido también contiene un origen de replicación (ori) bacteriano, un origen de replicación del bacteriófago F1, el origen de replicación del virus SV40 y una secuencia que codifica la resistencia NeoR/KanR, bajo el control de los promotores AmpR/SV40 y una señal poly(A) de la timidín quinasa (TK) del virus Herpes simplex (HSV).

pafolacianinum

pafolacianine

(2*E*,4^{3}*E*,8*S*)-14^{2}-amino-8-carboxy-4^{3}-{(2*E*)-2-[3,3-dimethyl-5-sulfo-1-(4-sulfobutyl)-1,3-dihydro-2*H*-indol-2-ylidene]ethylidene}-1^{3},1^{3}-dimethyl-10,14^{4}-dioxo-1^{1}-(4-sulfobutyl)-14^{3},14^{4}-dihydro-1^{3}*H*-5-oxa-9,12-diaza-14(6)-pteridina-1(2)-indola-6,11(1,4)-dibenzena-4(1,2)-cyclohexanatetradecaphane-2,4^{1}-dien-1^{1}-ium-1^{5}-sulfonate

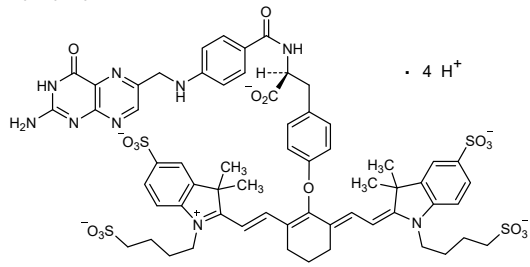
pafolacianine

(2*E*,4^{3}*E*,8*S*)-14^{2}-amino-8-carboxy-4^{3}-{(2*E*)-2-[3,3-diméthyl-5-sulfo-1-(4-sulfobutyl)-1,3-dihydro-2*H*-indol-2-ylidène]éthylidène}-1^{3},1^{3}-diméthyl-10,14^{4}-dioxo-1^{1}-(4-sulfobutyl)-14^{3},14^{4}-dihydro-1^{3}*H*-5-oxa-9,12-diaza-14(6)-ptéridina-1(2)-indola-6,11(1,4)-dibenzéna-4(1,2)-cyclohexanatétradécaphane-2,4^{1}-dién-1^{1}-ium-1^{5}-sulfonate

pafolacianina

(2*E*,4^{3}*E*,8*S*)-14^{2}-amino-8-carboxi-4^{3}-{(2*E*)-2-[3,3-dimetil-5-sulfo-1-(4-sulfobutil)-1,3-dihidro-2*H*-indol-2-ilideno]etilideno}-1^{3},1^{3}-dimetil-10,14^{4}-dioxo-1^{1}-(4-sulfobutil)-14^{3},14^{4}-dihidro-1^{3}*H*-5-oxa-9,12-diaza-14(6)-pteridina-1(2)-indola-6,11(1,4)-dibencena-4(1,2)-ciclohexanatetradecafano-2,4^{1}-dien-1^{1}-ium-1^{5}-sulfonato

$C_{61}H_{67}N_9O_{17}S_4$



palopegteriparatidum

palopegteriparatide

human parathyroid hormone (PTH) synthetic peptide fragment (1-34), conjugated at the N-terminal amino group via a cleavable linker to *O*-methylpolyethylene glycol (2 x 20 kDa mPEG);
2-methylalanyl-(1-34)-peptide of parathyroid hormone (*Homo sapiens* parathyrin, parathormone, PTH) conjugated with *O*-methylpolyethylene glycol via a cleavable linker at the N-terminal amino group:
N-({2-[(6-{[(3*RS*)-1-{3-[(3-{(2Ξ)-2,3-bis[α-methylpoly(oxyethylene)-ω-oxy]propoxy}propyl)amino]-3-oxopropyl}-2,5-dioxopyrrolidin-3-yl]sulfanyl}hexyl)amino]ethyl}carbamoyl)-2-methylalanyl-L-seryl-L-valyl-L-seryl-L-α-glutamyl-L-isoleucyl-L-glutaminyl-L-leucyl-L-methionyl-L-histidyl-L-asparaginyl-L-leucylglycyl-L-lysyl-L-histidyl-L-leucyl-L-asparaginyl-L-seryl-L-methionyl-L-α-glutamyl-L-arginyl-L-valyl-L-α-glutamyl-L-tryptophyl-L-leucyl-L-arginyl-L-lysyl-L-lysyl-L-leucyl-L-glutaminyl-L-α-aspartyl-L-valyl-L-histidyl-L-asparaginyl-L-phenylalanine

palopegtériparatide

fragment peptidique synthétique (1-34) de l'hormone parathyroïdienne humaine (HPT) conjugué au groupe aminé en N-terminal via un linker clivable au *O*-méthylpolyéthylène glycol (2 x 20 kDa mPEG);
2-methylalanyl-(1-34)-peptide de l'hormone parathyroïdienne d'*Homo sapiens* (parathyrine, parathormone, PTH), conjugué à un *O*-méthylpoly-éthylène glycol via un linker clivable au groupe aminé en N-terminal:
N-({2-[(6-{[(3*RS*)-1-{3-[(3-{(2Ξ)-2,3-bis[α-méthylpoly(oxyéthylène)-ω-oxy]propoxy}propyl)amino]-3-oxopropyl}-2,5-dioxopyrrolidine-3-yl]sulfanyl}hexyl)amino]éthyl}carbamoyl)-2-méthylalanyl-L-séryl-L-valyl-L-séryl-L-α-glutamyl-L-isoleucyl-L-glutaminyl-L-leucyl-L-méthionyl-L-histidyl-L-asparaginyl-L-leucylglycyl-L-lysyl-L-histidyl-L-leucyl-L-asparaginyl-L-séryl-L-méthionyl-L-α-glutamyl-L-arginyl-L-valyl-L-α-glutamyl-L-tryptophyl-L-leucyl-L-arginyl-L-lysyl-L-lysyl-L-leucyl-L-glutaminyl-L-α-aspartyl-L-valyl-L-histidyl-L-asparaginyl-L-phénylalanine

palopegteriparatida

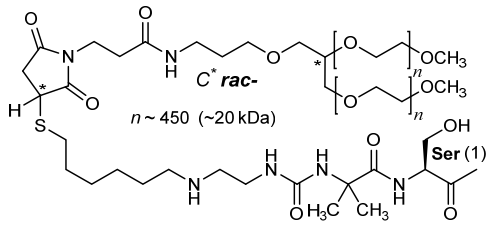
fragmento de péptido sintético (1-34) de la hormona paratiroidea humana (PTH) conjugado en el grupo amino N-terminal, a través de un enlace escindible, al glicol *O*-metilpolietileno (2 x 20 kDa mPEG);
2-metilalanil-péptido 1-34 de la hormona paratiroidiea del *Homo sapiens* (paratirina, parathormona, PTH), conjugado con O-metilpolietilenglicol a través de un grupo de unión separable escindible en el grupo amino N-terminal:
N-({2-[(6-{[(3*RS*)-1-{3-[(3-{(2Ξ)-2,3-bis[α-metilpoli(oxietileno)-ω-oxi]propoxi}propil)amino]-3-oxopropil}-2,5-dioxopirrolidin-3-il]sulfanil}hexil)amino]etil}carbamoil)-2-metilalanil-L-seril-L-valil-L-seril-L-α-glutamil-L-isoleucil-L-glutaminil-L-leucil-L-metionil-L-histidil-L-asparaginil-L-leucilglicil-L-lisil-L-histidil-L-leucil-L-asparaginil-L-seril-L-metionil-L-α-glutamil-L-arginil-L-valil-L-α-glutamil-L-triptofil-L-leucil-L-arginil-L-lisil-L-lisil-L-leucil-L-glutaminil-L-α-aspartil-L-valil-L-histidil-L-asparaginil-L-fenilalanina

$C_{209}H_{340}N_{60}O_{59}S_3(C_2H_4O)_{2n}$, n ≈ 450 (2 × ~20 kDa)

Sequence / Séquence / Secuencia

SVSEIQLMHN LGKHLNSMER VEWLRKKLQD VHNF 34

Modified residue / Résidu modifié / Resto modificado



peboctocogenum camaparvovecum #

peboctocogene camaparvovec

A non-replicating adeno-associated virus serotype hu37 (AAVhu37) vector encoding B-domain deleted human blood-coagulation factor VIII.
A recombinant, non-replicating, adeno-associated virus serotype hu37 (AAVhu37) vector, encoding a codon-optimised B-domain deleted SQ variant of human blood-coagulation factor VIII (hFVIII-SQ), under the control of a hybrid liver promoter (*Mus musculus* transthyretin enhancer-human transthyretin promoter) and a synthetic polyA signal sequence, flanked by AAV2 inverted terminal repeats; the A2 and A3 domains of hFVIII are linked by a DNA sequence encoding a 14-amino acid peptide (SQ) from the B domain.

péboctocogène camaparvovec

Un vecteur du virus adéno-associé de sérotype hu37 (AAVhu37) non-répliquant codant le facteur VIII de coagulation sanguine humaine avec délétion du domaine B.
Un vecteur du virus adéno-associé de sérotype hu37 (AAVhu37) non-répliquant, recombinant, codant un variant SQ aux codons optimisés avec délétion du domaine B du facteur VIII de coagulation sanguine humaine (hFVIII-SQ), sous le contrôle d'un promoteur hybride de foie (activateur de la transthyrétine de *Mus musculus* - promoteur de la transthyrétine humaine) et d'une séquence signal polyA synthétique, flanquée de répétitions terminales inversées du AAV2; les domaines A2 et A3 du hFVIII sont liés par une séquence d'ADN codant un peptide (SQ) de 14 acides aminés provenant du domaine B.

peboctocogén camaparvovec

Un vector de virus adeno-asociado de serotipo hu37 (AAVhu37) no replicativo que codifica para el factor de coagulación sanguínea VIII humano con el dominio B delecionado.
Un vector de virus adeno-asociado de serotipo hu37 (AAVhu37) recombinante, no replicativo, que codifica una variante SQ con el dominio B delecionado del factor de coagulación sanguínea VIII humano (hFVIII-SQ), con codones optimizados, bajo el control de un promotor híbrido de hígado (potenciador de transtiretina de *Mus musculus* - promotor de transtiretina humana) y una secuencia señal de polyA sintética, flanqueado por las repeticiones terminales invertidas de AAV2; los dominios A2 y A3 de hFVIII están ligados mediante una secuencia de DNA que codifica para un péptido de 14 aminoácidos (SQ) del dominio B.

pelgifatamabum corixetanum #

pelgifatamab corixetan

immunoglobulin G1-kappa, anti-[*Homo sapiens* FOLH1 (folate hydrolase, prostate specific membrane antigen, PSMA)], *Homo sapiens* monoclonal antibody conjugated to chelator *corixetan*;
gamma1 heavy chain *Homo sapiens* (1-453) [VH (*Homo sapiens* IGHV3-33*01 (96.9%) -(IGHD) -IGHJ6*01 (100%)) CDR-IMGT [8.8.16] (26-33.51-58.97-112) (1-123) -*Homo sapiens* IGHG1*03 (100%) G1m3, nG1m1 (CH1 R120 (220) (124-221), hinge 1-15 (222-236), CH2 (237-346), CH3 E12 (362), M14 (364) (347-451), CHS (452-453)) (124-453)], (226-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-27*01 (94.7%) -IGKJ3*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (232-232":235-235")-bisdisulfide, produced in a Chinese hamster ovary (CHO)-K1 cell line, glycoform alfa; conjugated to chelator *corixetan*, with an average of 0.8 chelator groups per antibody
For the *corixetan* part, please refer to the Proposed INN List 121, published in the *WHO Drug Information, Vol.33, No.2, 2019.*

pelgifatamab corixétan

immunoglobuline G1-kappa, anti-[*Homo sapiens* FOLH1 (folate hydrolase, antigène membranaire spécifique de la prostate, PSMA)], anticorps monoclonal *Homo sapiens* conjugué au chélateur *corixétan*;
chaîne lourde gamma1 *Homo sapiens* (1-453) [VH (*Homo sapiens* IGHV3-33*01 (96.9%) -(IGHD) -IGHJ6*01 (100%)) CDR-IMGT [8.8.16] (26-33.51-58.97-112) (1-123) -*Homo sapiens* IGHG1*03 (100%) G1m3, nG1m1 (CH1 R120 (220) (124-221), charnière 1-15 (222-236), CH2 (237-346), CH3 E12 (362), M14 (364) (347-451), CHS (452-453)) (124-453)], (226-214')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-27*01 (94.7%) -IGKJ3*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (232-232":235-235")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO) lignée cellulaire CHO-K1, glycoforme alfa; conjugué au chélateur *corixétan*, avec une moyenne de 0.8 groupes chélateurs par anticorps
Pour la partie *corixétan*, veuillez-vous référer à la Liste 121 des DCI proposées, publiée dans le *WHO Drug Information, Vol.33, No.2, 2019.*

pelgifatamab corixetán

inmunoglobulina G1-kappa, anti-[*Homo sapiens* FOLH1 (folato hidrolasa, antígeno membranario específico de la próstata, PSMA)], anticuerpo monoclonal *Homo sapiens* conjugado con el quelante *corixetán*;

cadena pesada gamma1 *Homo sapiens* (1-453) [VH *(Homo sapiens* IGHV3-33*01 (96.9%) -(IGHD) -IGHJ6*01 (100%)) CDR-IMGT [8.8.16] (26-33.51-58.97-112) (1-123) -*Homo sapiens* IGHG1*03 (100%) G1m3, nG1m1 (CH1 R120 (220) (124-221), bisagra 1-15 (222-236), CH2 (237-346), CH3 E12 (362), M14 (364) (347-451), CHS (452-453)) (124-453)], (226-214')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-27*01 (94.7%) -IGKJ3*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (232-232":235-235")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular CHO-K1, forma glicosilada alfa; conjugado con el quelante *corixetán*, con una media de 0.8 grupos quelantes por anticuerpo

Para la parte corixetán, por favor vaya a la Lista 121 de los DCI propuestas, publicada en el WHO Drug Information, Vol.33, No.2, 2019.

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVESGGG VVQPGRSLRL SCAASGFAFS RYGMHWVRQA PGKGLEWVAV  50
IWYDGSNKYY ADSVKGRFTI SRDNSKNTQY LQMNSLRAED TAVYYCARGG 100
DFLYYYYYGM DVWGQGTTVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC 150
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG 200
TQTYICNVNH KPSNTKVDKR VEPKSCDKTH TCPPCPAPEL LGGPSVFLFP 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 ITCRASQGIS NYLAWYQQKT GKVPKFLIYE  50
ASTLQSGVPS RFSGGGSGTD FTLTISSLQP EDVATYYCQN YNSAPFTFGP 100
GTKVDIKRTV 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) 22-96 150-206 267-327 373-431
22"-96" 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-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)

L VH Q1:
1, 1'"

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

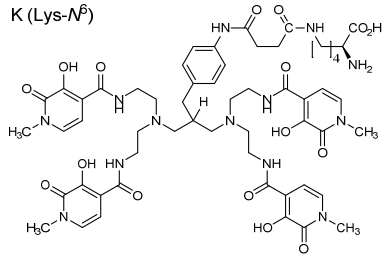
H CH2 N84.4:
303, 303"

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 / Coupure de la lysine C-terminale / Recorte de lisina C-terminal

H CHS K2:
453, 453"

Potential modified residues / résidus modifiés potentiels / restos modificados potenciales:



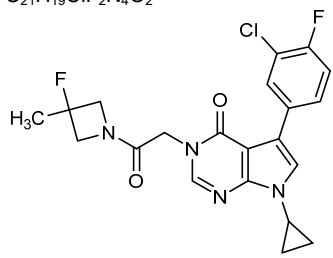
plazinemdorum

plazinemdor — 5-(3-chloro-4-fluorophenyl)-7-cyclopropyl-3-[2-(3-fluoro-3-methylazetidin-1-yl)-2-oxoethyl]-3,7-dihydro-4*H*-pyrrolo[2,3-*d*]pyrimidin-4-one

plazinemdor — 5-(3-chloro-4-fluorophényl)-7-cyclopropyl-3-[2-(3-fluoro-3-méthylazétidin-1-yl)-2-oxoéthyl]-3,7-dihydro-4*H*-pyrrolo[2,3-*d*]pyrimidin-4-one

plazinemdor — 7-ciclopropil-5-(3-cloro-4-fluorofenil)-3-[2-(3-fluoro-3-metilazetidin-1-il)-2-oxoetil]-3,7-dihidro-4*H*-pirrolo[2,3-*d*]pirimidin-4-ona

$C_{21}H_{19}ClF_2N_4O_2$



plonmarlimabum #

plonmarlimab — immunoglobulin G1-kappa, anti-[*Homo sapiens* CSF2 (colony stimulating factor 2 (granulocyte-macrophage), GM-CSF, GMCSF)], humanized monoclonal antibody; gamma1 heavy chain humanized (1-450) [VH (*Homo sapiens* IGHV1-2*02 (85.7%) -(IGHD) -IGHJ3*01 (92.9%) M123>T (115)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (217) (121-218), hinge 1-15 (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-9*01 (78.9%) -IGKJ4*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (229-229'':232-232'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

plonmarlimab — immunoglobuline G1-kappa, anti-[*Homo sapiens* CSF2 (facteur 2 stimulant les colonies (granulocyte-macrophage), GM-CSF, GMCSF)], anticorps monoclonal humanisé;
chaîne lourde gamma1 humanisée (1-450) [VH (*Homo sapiens* IGHV1-2*02 (85.7%) -(IGHD) -IGHJ3*01 (92.9%) M123>T (115)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (217) (121-218), charnière 1-15 (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfure avec la chaîne légère kappa

humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-9*01 (78.9%) -IGKJ4*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (229-229":232-232")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

plonmarlimab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CSF2 (factor 2 estimulante de las colonias (granulocito-macrófago), GM-CSF, GMCSF)], anticuerpo monoclonal humanizado;
cadena pesada gamma1 humanizada (1-450) [VH (*Homo sapiens* IGHV1-2*02 (85.7%) -(IGHD) -IGHJ3*01 (92.9%) M123>T (115)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (217) (121-218), bisagra 1-15 (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-9*01 (78.9%) -IGKJ4*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (229-229":232-232")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVQSGAE VKKPGASVKV SCKASGYTFT SHYLHWVRQA PGQGLEWMGW  50
IFPGDDKTKY NEKFKGRVTM TSDTSISTAY MELSRLRSDD TAVYYCARGT 100
KYLNWNFDVW GQGTTVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK 450
```

Light chain / Chaîne légère / Cadena ligera

```
DIQLTQSPSF LSASVGDRVT ITCKANQNVG TTLAWYQQKP GKSPKALIYS  50
ASYRYSGVPD RFSGSGSGTD FTLTISSLQP EDFATYFCHQ YTTYPLTFGG 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 147-203 264-324 370-428
22"-96" 147"-203" 264"-324" 370"-428"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194'"
Inter-H-L (h5-CL 126) 223-214' 223"-214'"
Inter-H-H (h11, h14) 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.

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2:
450, 450"

ponsegromabum #
ponsegromab

immunoglobulin G1-kappa, anti-[*Homo sapiens* GDF15 (growth differentiation factor 15, PLAB, MIC-1, PDF, MIC1, NAG-1, PTGFB)], monoclonal antibody;

	gamma1 heavy chain (1-449) [VH (*Homo sapiens* IGHV1-69*01 (93.9%) -(IGHD) -IGHJ1*01 (100%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) - *Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, G1v14 CH2 A1.3, A1.2 (CH1 R120>K (217) (121-218), hinge 1-15 (219-233), CH2 L1.3>A (237), L1.2>A (238), G1>A (240) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS K>del (449)) (121-449)], (223-214')-disulfide with kappa light chain (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-11*01 (91.6%) - IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (229-229'':232-232'')-bisdisulfide, produced in Chinese hamster ovary (CHO)-K1SV cell line lacking the glutamine synthetase gene (GSKO), glycoform alfa
ponségromab	immunoglobuline G1-kappa, anti-[*Homo sapiens* GDF15 (facteur 15 de croissance et de différenciation, PLAB, MIC-1, PDF, MIC1, NAG-1, PTGFB)], anticorps monoclonal; chaîne lourde gamma1 (1-449) [VH (*Homo sapiens* IGHV1-69*01 (93.9%) -(IGHD) -IGHJ1*01 (100%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) - *Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, G1v14 CH2 A1.3, A1.2 (CH1 R120>K (217) (121-218), charnière 1-15 (219-233), CH2 L1.3>A (237), L1.2>A (238), G1>A (240) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS K>del (449)) (121-449)], (223-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-11*01 (91.6%) - IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (229-229'':232-232'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO) lignée cellulaire CHO-K1SV ne présentant pas le gène de la glutamine synthétase (GSKO), glycoforme alfa
ponsegromab	inmunoglobulina G1-kappa, anti-[*Homo sapiens* GDF15 (factor 15 de crecimiento y de diferenciación, PLAB, MIC-1, PDF, MIC1, NAG-1, PTGFB)], anticuerpo monoclonal; cadena pesada gamma1 (1-449) [VH (*Homo sapiens* IGHV1-69*01 (93.9%) -(IGHD) -IGHJ1*01 (100%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) - *Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, G1v14 CH2 A1.3, A1.2 (CH1 R120>K (217) (121-218), bisagra 1-15 (219-233), CH2 L1.3>A (237), L1.2>A (238), G1>A (240) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS K>del (449)) (121-449)], (223-214')-disulfuro con la cadena ligera kappa (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-11*01 (91.6%) - IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (229-229'':232-232'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular CHO-K1SV en ausencia del gen glutamina sintetasa (GSKO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGSSVKV SCKASGYTFS SYNIDWVRQA PGQGLEWMGG  50
INPIFGTAFY NQKFQGRVTI TADESTSTAY MELSSLRSED TAVYYCAREA 100
ITTVGAMDHW GQGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPEAAGA PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPG  449
```

Light chain / Chaîne légère / Cadena ligera

```
EIVLTQSPAT LSLSPGERAT LSCRTSQSVH NYLAWYQQKP GQAPRLLIYD  50
ASTRADGIPA RFSGSGSGTD FTLTISSLEP EDFAVYYCQQ FWSWPWTFGQ 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

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

N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
H VH Q1:
1, 1"

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.

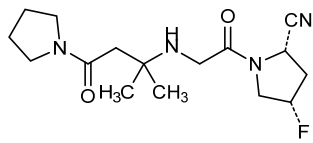
prusogliptinum

prusogliptin — (2*S*,4*S*)-4-fluoro-1-({[2-methyl-4-oxo-4-(pyrrolidin-1-yl)butan-2-yl]amino}acetyl)pyrrolidine-2-carbonitrile

prusogliptine — (2*S*,4*S*)-4-fluoro-1-({[2-méthyl-4-oxo-4-(pyrrolidin-1-yl)butan-2-yl]amino}acétyl)pyrrolidine-2-carbonitrile

prusogliptina — (2*S*,4*S*)-4-fluoro-1-({[2-metil-4-oxo-4-(pirrolidin-1-il)butan-2-il]amino}acetil)pirrolidina-2-carbonitrilo

$C_{16}H_{25}FN_4O_2$



pucotenlimabum #

pucotenlimab — immunoglobulin G4-kappa, anti-[*Homo sapiens* PDCD1 (programmed cell death 1, PD1, PD-1, CD279)], monoclonal antibody;
gamma4 heavy chain (1-445) [VH (*Mus musculus* IGHV5-9-2*01 (87.8%) -(IGHD) -IGHJ3*01 (93.3%)/*Homo sapiens* IGHV3-23*04 (86.7%) -(IGHD) -IGHJ6*01 (90.9%)) CDR-IMGT [8.8.11] (26-33.51-58.97-107) (1-118)-*Homo sapiens* IGHG4*01, G4v5 h P10, G4v22 CH2 T16, P91, CH3 A114 (CH1 (119-216), hinge 1-12 S10>P (226) (217-228), CH2 S16>T (252), V91>P (306) (229-338), CH3 N114>A (432) (339-443), CHS (444-445)) (119-445)], (132-218')-disulfide with kappa light chain (1'-218') [V-KAPPA (*Mus musculus* IGKV3-2*01 (92.9%) -IGKJ1*01 (100%)/*Homo sapiens* IGKV3D-11*02 (64.9%) -IGKJ4*01 (90.9%)) CDR-IMGT [10.3.9] (27-36.54-56.93-101) (1'-111') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218')]; dimer (224-224":227-227")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

pucotenlimab

immunoglobuline G4-kappa, anti-[*Homo sapiens* PDCD1 (protéine 1 de mort cellulaire programmée, PD-1, PD1, CD279)], anticorps monoclonal;
chaîne lourde gamma4 (1-445) [VH (*Mus musculus* IGHV5-9-2*01 (87.8%) -(IGHD) -IGHJ3*01 (93.3%)/*Homo sapiens* IGHV3-23*04 (86.7%) -(IGHD) -IGHJ6*01 (90.9%)) CDR-IMGT [8.8.11] (26-33.51-58.97-107) (1-118)-*Homo sapiens* IGHG4*01, G4v5 h P10, G4v22 CH2 T16, P91, CH3 A114 (CH1 (119-216), charnière 1-12 S10>P (226) (217-228), CH2 S16>T (252), V91>P (306) (229-338), CH3 N114>A (432) (339-443), CHS (444-445)) (119-445)], (132-218')-disulfure avec la chaîne légère kappa (1'-218') [V-KAPPA (*Mus musculus* IGKV3-2*01 (92.9%) -IGKJ1*01 (100%)/*Homo sapiens* IGKV3D-11*02 (64.9%) -IGKJ4*01 (90.9%)) CDR-IMGT [10.3.9] (27-36.54-56.93-101) (1'-111') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218')]; dimère (224-224'':227-227'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

pucotenlimab

inmunoglobulina G4-kappa, anti-[*Homo sapiens* PDCD1 (proteína 1 de muerte celular programada, PD-1, PD1, CD279)], anticuerpo monoclonal;
cadena pesada gamma4 (1-445) [VH (*Mus musculus* IGHV5-9-2*01 (87.8%) -(IGHD) -IGHJ3*01 (93.3%)/*Homo sapiens* IGHV3-23*04 (86.7%) -(IGHD) -IGHJ6*01 (90.9%)) CDR-IMGT [8.8.11] (26-33.51-58.97-107) (1-118)-*Homo sapiens* IGHG4*01, G4v5 h P10, G4v22 CH2 T16, P91, CH3 A114 (CH1 (119-216), bisagra 1-12 S10>P (226) (217-228), CH2 S16>T (252), V91>P (306) (229-338), CH3 N114>A (432) (339-443), CHS (444-445)) (119-445)], (132-218')-disulfuro con la cadena ligera kappa (1'-218') [V-KAPPA (*Mus musculus* IGKV3-2*01 (92.9%) -IGKJ1*01 (100%)/*Homo sapiens* IGKV3D-11*02 (64.9%) -IGKJ4*01 (90.9%)) CDR-IMGT [10.3.9] (27-36.54-56.93-101) (1'-111') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218')]; dímero (224-224'':227-227'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVQSGGG LVQPGGSLKL SCAASGFTFS SYGMSWVRQA PGKGLDWVAT  50
ISGGGRDTYY PDSVKGRFTI SRDNSKNNLY LQMNSLRAED TALYYCARQK 100
GEAWFAYWGQ GTLVTVSSAS TKGPSVFPLA PCSRSTSEST AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTKTYT 200
CNVDHKPSNT KVDKRVESKY GPPCPPCPAP EFLGGPSVFL FPPKPKDTLM 250
ITRTPEVTCV VVDVSQEDPE VQFNWYVDGV EVHNAKTKPR EEQFNSTYRV 300
VSVLTPLHQD WLNGKEYKCK VSNKGLPSSI EKTISKAKGQ PREPQVYTLP 350
PSQEEMTKNQ VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG 400
SFFLYSRLTV DKSRWQEGNV FSCSVMHEAL HAHYTQKSLS LSLGK      445
```

Light chain / Chaîne légère / Cadena ligera

```
DIVLTQSPAS LAVSPGQRAT ITCRASESVD NYGISFMNWF QQKPGQPPKL  50
LIYAASNKGT GVPARFSGSG SGTDFTLNIN PMEENDTAMY FCQQSKEVPW 100
TFGGGTKLEI 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"
```

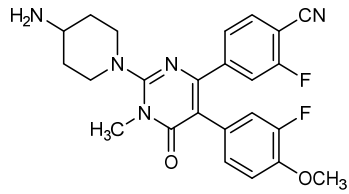
N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
295, 295"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2:
445, 445"

pulrodemstatum

pulrodemstat	4-[2-(4-aminopiperidin-1-yl)-5-(3-fluoro-4-methoxyphenyl)-1-methyl-6-oxo-1,6-dihydropyrimidin-4-yl]-2-fluorobenzonitrile
pulrodemstat	4-[2-(4-aminopipéridin-1-yl)-5-(3-fluoro-4-méthoxyphényl)-1-méthyl-6-oxo-1,6-dihydropyrimidin-4-yl]-2-fluorobenzonitrile
pulrodemstat	4-[2-(4-aminopiperidin-1-il)-5-(3-fluoro-4-metoxifenil)-1-metil-6-oxo-1,6-dihidropirimidin-4-il]-2-fluorobenzonitrilo

$C_{24}H_{23}F_2N_5O_2$



quaratusugenum ozeplasmidum #

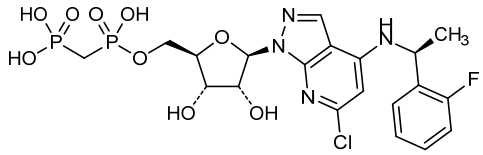
quaratusugene ozeplasmid	A DNA plasmid encoding tumour suppressor candidate 2 (TUSC2). A DNA plasmid encoding tumour suppressor candidate 2 (TUSC2), also referred to as fusion 1 protein (FUS1), under the control of an adenovirus E1 enhancer, human cytomegalovirus (hCMV) immediate early enhancer/ promoter and a bovine growth hormone (bGH) polyadenylation signal (polyA). The plasmid also contains a pMB1origin of replication and a NeoR/KanR antibiotic resistance coding sequence.
quaratusugène ozéplasmide	Un plasmide d'ADN codant pour le candidat 2 suppresseur de tumeur (TUSC2). Un plasmide d'ADN codant pour le candidat 2 suppresseur de tumeur (TUSC2), aussi appelé la protéine de fusion (FUS1), sous le contrôle d'un activateur de l'adénovirus E1, du promoteur/activateur précoce immédiat du cytomégalovirus humain (hCMV) et d'un signal de polyadénylation (polyA) de l'hormone de croissance bovine (bGH). Le plasmide contient aussi une origine de réplication pMB1 et une séquence codant une résistance aux antibiotiques NeoR/KanR.
quaratusugén ozeplásmido	Un plásmido de DNA que codifica para el candidato supresor de tumores 2 (TUSC2). Un plásmido de DNA que codifica para el candidato supresor de tumores 2 (TUSC2), también referido como proteína de fusión 1 (FUS1), bajo el control de un potenciador E1 de adenovirus, un potenciador/promotor inmediato temprano de citomegalovirus humano (hCMV) y una señal de poliadenilación (polyA) de la hormona de crecimiento bovina (bGH). El plásmido también contiene un origen de replicación pMB1 y una secuencia NeoR/KanR que codifica para la resistencia a antibióticos.

quemliclustatum
quemliclustat — 2-chloro-N^6-[(1*S*)-1-(2-fluorophenyl)ethyl]-8-aza-1,7-dicarbaadenosine 5'-(trihydrogen 2-carbadiphosphate)

quémliclustat — 2-chloro-N^6-[(1*S*)-1-(2-fluorophényl)éthyl]-8-aza-1,7-dicarbaadenosine 5'-(trihydrogéno-2-carbadiphosphate)

quemliclustat — 2-cloro-N^6-[(1*S*)-1-(2-fluorofenil)etil]-8-aza-1,7-dicarbaadenosina 5'-(trihidrógeno-2-carbadifosfato)

$C_{20}H_{24}ClFN_4O_9P_2$



retlirafuspum alfa #
retlirafusp alfa — human immunoglobulin G4-kappa anti-(human programmed cell death 1 ligand 1, PD-L1) variant (H^{52}>G, G^{57}>F, S^{227}>P, F^{233}>A, L^{234}>A, K^{446}>A in the heavy chain and N^{85}>E in the light chain), fused at the C-terminus of both heavy chains (1-446) via peptidyl linker ^{447}GGGGSGGGGSGGGGSGGGGSG^{467} to human transforming growth factor β type II (TGFR-2) extracellular fragment (20-136, 468-584 in the current sequence), dimer; glycosylated; produced in Chinese hamster ovary (CHO) cells;
immunoglobulin G4-kappa, anti-[*Homo sapiens* programmed cell death 1 ligand 1 (PD-L1, programmed death ligand 1, PDCD1 ligand 1, B7 homolog 1, B7-H1, CD274)], *Homo sapiens* monoclonal antibody, fused at the C-terminus of both heavy chains via a $(G_4S)_4G$ peptide linker (447-467) to fragment 20-136 of the extracellular domain of transforming growth factor β receptor type II (*Homo sapiens* TGF-β receptor 2, TGFR-2, TGFBR2) (468-584);
gamma4 heavy chain *Homo sapiens* (1-446) [*Homo sapiens* IGHV1-46*01; *Homo sapiens* IGHJ4*01; *Homo sapiens* IGHG4*01; VH: 1-119 (H52G G57F); CH1: 120-217; hinge 218-229 (S227P); CH2: 230-339 (F233A L234A); CH3: 340-444; CHS: 445-446 (K446A); CDRKabatH1: SYWMH (31-35); CDRKabatH2: RIGPNSGFTSYNEKFKN (50-66); CDRKabatH3: GGSSYDYFDY (99-108)], (133-218')-disulfide with kappa light chain *Homo sapiens* (1'-218') [*Homo sapiens* IGKV4-1*01; *Homo sapiens* IGKJ2*01; *Homo sapiens* IGKC*01; VL: 1-111 (N85E); CL: 112-218; CDRKabatL1: RASESVSIHGTHLMH (24-38); CDRKabatL2: AASNLES (54-60); CDRKabatL: QQSFEDPLT (93-101)]; dimer (225-225":228-228")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

rétlirafusp alfa	immunoglobuline G4-kappa humaine anti-(ligand 1 humain de mort cellulaire programmée 1, PD-L1) variant (H52>G, G57>F, S227>P, F233>A, L234>A, K446>A dans la chaîne lourde et N85>E dans la chaîne légère), fusionné à la partie C-terminale des deux chaînes lourdes (1-446) via le linker peptidique ^{447}GGGGSGGGGSGGGGSGGGGSG^{467} au fragment extracellulaire (20-136, 468-584 dans la séquence actuelle) du récepteur de type II du facteur β de croissance transformant humain (TGFR-2), dimère; glycosylé; produit dans des cellules ovariennes de hamster chinois (CHO); immunoglobuline G4-kappa, anti-[ligand 1 de mort cellulaire programmée 1 d'*Homo sapiens* (PD-L1, ligand 1 de PDCD1, homologue 1 de B7, B7-H1, CD274)], anticorps monoclonal d'*Homo sapiens*, fusionnée à la partie C-terminale des deux chaînes lourdes via un linker peptidique $(G_4S)_4G$ (447-467) au fragment 20-136 du domaine extracellulaire du récepteur de type II du facteur β de croissance transformant (récepteur 2 de TGF-β d'*Homo sapiens*, TGFR-2, TGFBR2) (468-584); chaîne lourde gamma4 d'*Homo sapiens* (1-446) [*Homo sapiens* IGHV1-46*01; *Homo sapiens* IGHJ4*01; *Homo sapiens* IGHG4*01; VH: 1-119 (H52G G57F); CH1: 120-217; charnière 218-229 (S227P); CH2: 230-339 (F233A L234A); CH3: 340-444; CHS: 445-446 (K446A); CDRKabatH1: SYWMH (31-35); CDRKabatH2: RIGPNSGFTSYNEKFKN (50-66); CDRKabatH3: GGSSYDYFDY (99-108)], (133-218')-disulfure avec la chaîne légère kappa d'*Homo sapiens* (1'-218') [*Homo sapiens* IGKV4-1*01; *Homo sapiens* IGKJ2*01; *Homo sapiens* IGKC*01; VL: 1-111 (N85E); CL: 112-218; CDRKabatL1: RASESVSIHGTHLMH (24-38); CDRKabatL2: AASNLES (54-60); CDRKabatL: QQSFEDPLT (93-101)]; dimère (225-225":228-228")-bisdisulfure, produite dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa
retlirafusp alfa	inmunoglobulina G4-kappa humana anti-(muerte celular programada 1 humana ligando 1, PD-L1) variante (H^{52}>G, G^{57}>F, S^{227}>P, F^{233}>A, L^{234}>A, K^{446}>A en la cadena pesada y N^{85}>E en la cadena ligera), fusionado al C-terminal de ambas cadenas pesadas (1-446) a través de un enlace peptidil ^{447}GGGGSGGGGSGGGGSGGGGSG^{467} al factor de crecimiento transformante β tipo II humano (TGFR-2) fragmento extracelular (20-136, 468-584 en la secuencia actual), dímero; glicosilado; producido en células ováricas de hámster chino (CHO); inmunoglobulina G4-kappa, anti-[*Homo sapiens* ligando 1 de muerte programada (PD-L1, ligando 1 de PDCD1, homólogo 1 de B7, B7-H1, CD274)], anticuerpo monoclonal *Homo sapiens*, fusionado en los residuos C-terminales de ambas cadenas pesadas a través de un péptido conector $(G_4S)_4G$ (447-467) con el fragmento 20-136 del dominio extracelular del receptor de tipo II del factor β de crecimiento transformante (receptor 2 de TGF-β de *Homo sapiens*, TGFR-2, TGFBR2) (468-584); cadena pesada gamma4 *Homo sapiens* (1-446) [*Homo sapiens* IGHV1-46*01; *Homo sapiens* IGHJ4*01; *Homo sapiens* IGHG4*01; VH: 1-119 (H52G G57F); CH1: 120-217; hinge 218-229 (S227P); CH2: 230-339 (F233A L234A); CH3: 340-444; CHS: 445-446 (K446A); CDRKabatH1: SYWMH (31-35); CDRKabatH2: RIGPNSGFTSYNEKFKN (50-66); CDRKabatH3: GGSSYDYFDY (99-108)], (133-218')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-214') [*Homo sapiens* IGKV4-1*01; *Homo sapiens* IGKJ2*01; *Homo sapiens* IGKC*01; VL: 1-111 (N85E); CL: 112-218; CDRKabatL1: RASESVSIHGTHLMH (24-38); CDRKabatL2: AASNLES (54-60); CDRKabatL: QQSFEDPLT (93-101)];dímero (225-225":228-228")-bisdisulfuro, producida en células ováricas de hámsters chinos (CHO), glicoforma alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGASVKV SCKASGYTFT SYWMHWVRQA PGQGLEWMGR   50
IGPNSGFTSY NEKFKNRVTM TRDTSTSTVY MELSSLRSED TAVYYCARGG  100
SSYDYFDYWG QGTTVTVSSA STKGPSVFPL APCSRSTSES TAALGCLVKD  150
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTKTY  200
TCNVDHKPSN TKVDKRVESK YGPPCPPCPA PEAAGGPSVF LFPPKPKDTL  250
MISRTPEVTC VVVDVSQEDP EVQFNWYVDG VEVHNAKTKP REEQFNSTYR  300
VVSVLTVLHQ DWLNGKEYKC KVSNKGLPSS IEKTISKAKG QPREPQVYTL  350
PPSQEEMTKN QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD  400
GSFFLYSRLT VDKSRWQEGN VFSCSVMHEA LHNHYTQKSL SLSLGAGGGG  450
SGGGGSGGGG SGGGGSGGAV KFPQLCKFCD VRFSTCDNQK SCMSNCSITS  500
ICEKPQEVCV AVWRKNDENI TLETVCHDPK LPYHDFILED AASPKCIMKE  550
KKKPGETFFM CSCSSDECND NIIFSEEYNT SNPD                    584
```

Light chain / Chaîne légère / Cadena ligera

```
DIVLTQSPAS LAVSPGQRAT ITCRASESVS IHGTHLMHWY QQKPGQPPKL    50
LIYAASNLES GVPARFSGSG SGTDFTLTIN PVEAEDTANY YCQQSFEDPL   100
TFGQGTKLEI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL NNFYPREAKV   150
QWKVDNALQS GNSQESVTEQ DSKDSTYSLS STLTLSKADY EKHKVYACEV   200
THQGLSSPVT KSFNRGEC                                      218
```

Mutation sites / Sites de mutation / Posiciones de mutación

H52>G, G57>F, S227>P, F233>A, L234>A, K446>A, N85">E
H52">G, G57">F, S227">P, F233">A, L234">A, K446">A, N85"">E

Post-translational modifications / Modifications post-traductionnelles / Modificaciones postraduccionales

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

Intra-H	22-96	146-202	260-320	366-424	
	22"-96"	146"-202"	260"-320"	366"-424"	
Intra-PDL1	476-509	479-496	486-492	502-526	546-561	563-568
	476"-509"	479"-496"	486"-492"	502"-526"	546"-561"	563"-568"
Intra-L	23'-92'	138'-198'				
	23'"-92'"	138'"-198'"				
Inter-H-L	133-218'	133"-218'"				
Inter-H-H	225-225"	228-228"				

Glycosylation sites / Sites de glycosylation / Posiciones de glicosilación

N296, N495, N519, N579,
N296", N495", N519", N579"

N-terminal pyroglutamyl / Pyroglutamyl N-terminal / Piroglutamil N-terminal

Q1,Q1">pE (5-oxo-L-prolyl, pyroglutamyl)

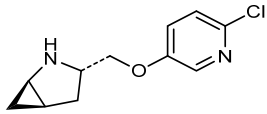
ropanicantum

ropanicant — (1*R*,3*S*,5*R*)-3-{[(6-chloropyridin-3-yl)oxy]methyl}-2-azabicyclo[3.1.0]hexane

ropanicant — (1*R*,3*S*,5*R*)-3-{[(6-chloropyridin-3-yl)oxy]méthyl}-2-azabicyclo[3.1.0]hexane

ropanicant — (1*R*,3*S*,5*R*)-3-{[(6-cloropiridin-3-il)oxi]metil}-2-azabiciclo[3.1.0]hexano

$C_{11}H_{13}ClN_2O$



runimotamabum

runimotamab — immunoglobulin G1-kappa, anti-[*Homo sapiens* ERBB2 (epidermal growth factor receptor 2, receptor tyrosine protein kinase erbB-2, EGFR2, HER2, HER-2, p185cerbB2, NEU, CD340)] and anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], monoclonal antibody, bispecific;
gamma1 heavy chain anti-ERBB2 (1-450) [VH anti-ERBB2 (*Homo sapiens* IGHV3-66*01 (81.6%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, G1v30 CH2 G84.4, G1v32 CH3 W22 (CH1 R120>K (217) (121-218), hinge 1-15 (219-233), CH2 N84.4>G (300) (234-343), CH3 E12 (359), M14 (361), T22>W (369) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfide with kappa light chain anti-ERBB2 (1'-214') [V-KAPPA anti-ERBB2 (*Homo sapiens* IGKV1-39*01 (86.3%) -IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')];

	gamma1 heavy chain anti-CD3E (1''-449'') [VH anti-CD3E (*Mus musculus* IGHV1-66*01 (82.7%) -(IGHD) -IGHJ2*01 (86.7%)/*Homo sapiens* anti-CD3E IGHV1-3*01(82.7%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.12] (26-33.51-58.97-108) (1''-119'') -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, G1v30 CH2 G84.4, G1v33 CH3 S22, A24, V86 (CH1 R120>K (216) (120''-217''), hinge 1-15 (218''-232''), CH2 N84.4>G (299) (233-342), CH3 E12 (358), M14 (360), T22>S (368), L24>A (370), Y86>V (409) (343''-447''), CHS (448''-449'')) (120''-449'')], (222''-219''')-disulfide with kappa light chain anti-CD3E (1'''-219''') [V-KAPPA anti-CD3E (*Homo sapiens* IGKV4-1*01 (91.8%) -IGKJ1*01 (100%)) CDR-IMGT [12.3.8] (27-38.56-58.95-102) (1'''-112''') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (158), V101 (196) (113'''-219''')]; dimer (229-228'':232-231'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, non-glycosylated
runimotamab	immunoglobuline G1-kappa, anti-[*Homo sapiens* ERBB2 (récepteur 2 du facteur de croissance épidermique, récepteur tyrosine-protéine kinase erbB2, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)] et anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], anticorps monoclonal, bispécifique; chaîne lourde gamma1 anti-ERBB2 (1-450) [VH anti-ERBB2 (*Homo sapiens* IGHV3-66*01 (81.6%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, G1v30 CH2 G84.4, G1v32 CH3 W22 (CH1 R120>K (217) (121-218), charnière1-15 (219-233), CH2 N84.4>G (300) (234-343), CH3 E12 (359), M14 (361), T22>W (369), (344-448), CHS (449-450)) (121-450)], (223-214')-disulfure avec la chaîne légère kappa anti-ERBB2 (1'-214') [V-KAPPA anti-ERBB2 (*Homo sapiens* IGKV1-39*01 (86.3%) -IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; chaîne lourde gamma1 anti-CD3E (1''-449'') [VH anti-CD3E (*Mus musculus* IGHV1-66*01 (82.7%) -(IGHD) -IGHJ2*01 (86.7%)/*Homo sapiens* IGHV1-3*01 (82.7%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.12] (26-33.51-58.97-108) (1''-119'') -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, G1v30 CH2 G84.4, G1v33 CH3 S22, A24, V86 (CH1 R120>K (216) (120''-217''), charnière1-15 (218''-232''), CH2 N84.4>G (299) (233-342), CH3 E12 (358), M14 (360), T22>S (368), L24>A (370), Y86>V (409) (343''-447''), CHS (448''-449'')) (120''-449'')], (222''-219''')-disulfure avec la chaîne légère kappa anti-CD3E (1'''-219''') [V-KAPPA anti-CD3E (*Homo sapiens* IGKV4-1*01 (91.8%) -IGKJ1*01 (100%)) CDR-IMGT [12.3.8] (27-38.56-58.95-102) (1'''-112''') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (158), V101 (196) (113'''-219''')]; dimère (229-228'':232-231'')-bidisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), non-glycosylé
runimotamab	inmunoglobulina G1-kappa, anti-[*Homo sapiens* ERBB2 (receptor 2 del factor de crecimiento epidérmico, receptor tirosina-proteína kinasa erbB2, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)] y anti-[*Homo sapiens* CD3E (CD3 épsilon, Leu-4)], anticuerpo monoclonal, biespecífico; cadena pesada gamma1 anti-ERBB2 (1-450) [VH anti-ERBB2 (*Homo sapiens* IGHV3-66*01 (81.6%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, G1v30 CH2 G84.4, G1v32 CH3 W22 (CH1 R120>K (217) (121-218), bisagra 1-15 (219-233), CH2 N84.4>G (300) (234-343), CH3 E12 (359), M14 (361), T22>W (369), (344-448), CHS (449-450)) (121-450)], (223-214')-disulfuro con la cadena ligera kappa anti-ERBB2 (1'-214') [V-KAPPA anti-ERBB2 (*Homo sapiens* IGKV1-39*01 (86.3%) -IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')];

cadena pesada gamma1 anti-CD3E (1"-449") [VH anti-CD3E (*Mus musculus* IGHV1-66*01 (82.7%) -(IGHD) -IGHJ2*01 (86.7%)/*Homo sapiens* IGHV1-3*01 (82.7%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.12] (26-33.51-58.97-108) (1"-119") -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, G1v30 CH2 G84.4, G1v33 CH3 S22, A24, V86 (CH1 R120>K (216) (120"-217"), bisagra 1-15 (218"-232"), CH2 N84.4>G (299) (233-342), CH3 E12 (358), M14 (360), T22>S (368), L24>A (370), Y86>V (409) (343"-447"), CHS (448"-449")) (120"-449")], (222"-219"')-disulfuro con la cadena ligera kappa anti-CD3E (1"'-219"') [V-KAPPA anti-CD3E (*Homo sapiens* IGKV4-1*01 (91.8%) -IGKJ1*01 (100%)) CDR-IMGT [12.3.8] (27-38.56-58.95-102) (1"'-112"') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (158), V101 (196) (113"'-219"')]; dímero (229-228":232-231")-bidisulfuro, producido en las células ováricas de hámster chino (CHO), no glicosilado

Heavy chain / Chaîne lourde / Cadena pesada (anti-ERBB2)
```
EVQLVESGGG LVQPGGSLRL SCAASGFNIK DTYIHWVRQA PGKGLEWVAR  50
IYPTNGYTRY ADSVKGRFTI SADTSKNTAY LQMNSLRAED TAVYYCSRWG 100
GDGFYAMDYW GQGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYG 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSREE MTKNQVSLWC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK 450
```

Heavy chain / Chaîne lourde / Cadena pesada (anti-CD3E)
```
EVQLVQSGAE VKKPGASVKV SCKASGYTFT NYYIHWVRQA PGQGLEWIGW  50
IYPGDGNTKY NEKFKGRATL TADTSTSTAY LELSSLRSED TAVYYCARDS 100
YSNYYFDYWG QGTLVTVSSA STKGPSVFPL APSSKSTSGG TAALGCLVKD 150
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY 200
ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP CPAPELLGGP SVFLFPPKPK 250
DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYGS 300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV 350
YTLPPSREEM TKNQVSLSCA VKGFYPSDIA VEWESNGQPE NNYKTTPPVL 400
DSDGSFFLVS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK  449
```

Light chain / Chaîne légère / Cadena ligera (anti-ERBB2)
```
DIQMTQSPSS LSASVGDRVT ITCRASQDVN TAVAWYQQKP GKAPKLLIYS  50
ASFLYSGVPS RFSGSRSGTD FTLTISSLQP EDFATYYCQQ HYTTPPTFGQ 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Light chain / Chaîne légère / Cadena ligera (anti-CD3E)
```
DIVMTQSPDS LAVSLGERAT INCKSSQSLL NSRTRKNYLA WYQQKPGQPP  50
KLLIYWASTR ESGVPDRFSG SGSGTDFTLT ISSLQAEDVA VYYCTQSFIL 100
RTFGQGTKVE 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) 22-96 147-203 264-324 370-428
22"-96" 146"-202" 263"-323" 369"-427"
Intra-L (C23-C104) 23'-88' 134'-194'
23"'-94"' 139"'-199"'
Inter-H-L (h 5-CL 126) 223-214' 222"-219"'
Inter-H-H (h 11, h 14) 229-228" 232-231"

No N-glycosylation sites / pas de sites de N-glycosylation / ningún posición de N-glicosilación
CH2 N84.4>G:
300, 299"
Aglycosylated

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2:
450, 449"

sapablursenum

sapablursen

all-P-ambo-5'-*O*-(28-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]-16,16-bis{[3-({6-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]hexyl}amino)-3-oxopropoxy]methyl}-1-hydroxy-1,10,14,21-tetraoxo-2,18-dioxa-9,15,22-triaza-1λ^5-phosphaoctacosan-1-yl)-2'-*O*-(2-methoxyethyl)-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyluridylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyluridylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyluridylyl-(3'→5')-2'-*O*-(2-methoxyethyl)adenylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-deoxy-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-deoxy-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-deoxy-*P*-thioadenylyl-(3'→5')-2'-deoxy-*P*-thioadenylyl-(3'→5')-2'-deoxy-*P*-thioadenylyl-(3'→5')-2'-deoxy-*P*-thioguanylyl-(3'→5')-2'-deoxy-*P*-thioguanylyl-(3'→5')-2'-deoxy-*P*-thioguanylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methylcytidylyl-(3'→5')-2'-*O*-(2-methoxyethyl)adenylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-*P*-thioguanylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyluridine

sapablursen

tout-P-ambo-5'-*O*-(28-[(2-acétamido-2-désoxy-β-D-galactopyranosyl)oxy]-16,16-bis{[3-({6-[(2-acétamido-2-désoxy-β-D-galactopyranosyl)oxy]hexyl}amino)-3-oxopropoxy]méthyl}-1-hydroxy-1,10,14,21-tétraoxo-2,18-dioxa-9,15,22-triaza-1λ^5-phosphaoctacosan-1-yl)-2'-*O*-(2-méthoxyéthyl)-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthyluridylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthyluridylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthyluridylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)adénylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-désoxy-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-désoxy-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-désoxy-*P*-thioadénylyl-(3'→5')-2'-désoxy-*P*-thioadénylyl-(3'→5')-2'-désoxy-*P*-thioadénylyl-(3'→5')-2'-désoxy-*P*-thioguanylyl-(3'→5')-2'-désoxy-*P*-thioguanylyl-(3'→5')-2'-désoxy-*P*-thioguanylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthylcytidylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)adénylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-*P*-thioguanylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthyluridine

sapablursén

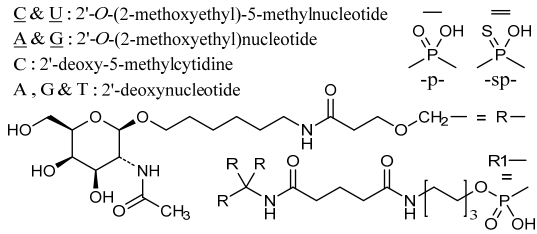
todo-P-ambo-5'-*O*-(28-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]-16,16-bis{[3-({6-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]hexil}amino)-3-oxopropoxi]metil}-1-hidroxi-1,10,14,21-tetraoxo-2,18-dioxa-9,15,22-triaza-1λ^5-fosfaoctacosan-1-il)-5-metil-2'-*O*-(2-metoxietil)-*P*-tiocitidilil-(3'→5')-5-metil-2'-*O*-(2-metoxietil)uridilil-(3'→5')-5-metil-2'-*O*-(2-metoxietil)uridilil-(3'→5')-5-metil-2'-*O*-(2-metoxietil)uridilil-(3'→5')-2'-*O*-(2-metoxietil)adenilil-(3'→5')-*P*-tiotimidilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2'-desoxi-5-metil-*P*-tiocitidilil-(3'→5')-2'-desoxi-5-metil-*P*-tiocitidilil-(3'→5')-2'-desoxi-*P*-tioadenilil-(3'→5')-2'-desoxi-*P*-tioadenilil-(3'→5')-2'-desoxi-*P*-tioadenilil-(3'→5')-2'-desoxi-*P*-tioguanilil-(3'→5')-2'-desoxi-*P*-tioguanilil-(3'→5')-2'-desoxi-*P*-tioguanilil-(3'→5')-5-metil-2'-*O*-(2-metoxietil)citidilil-(3'→5')-2'-*O*-(2-metoxietil)adenilil-(3'→5')-2'-*O*-(2-metoxietil)-*P*-tioguanilil-(3'→5')-5-metil-2'-*O*-(2-metoxietil)-*P*-tiocitidilil-(3'→5')-5-metil-2'-*O*-(2-metoxietil)uridina

$C_{296}H_{436}N_{80}O_{155}P_{20}S_{13}$

(3'-5') R1-C=U-U-U-A-d(T=T=C=C=A=A=A=G=C=G=)C-A-G=C=U

Legend:

C & U : 2'-*O*-(2-methoxyethyl)-5-methylnucleotide
A & G : 2'-*O*-(2-methoxyethyl)nucleotide
C : 2'-deoxy-5-methylcytidine
A , G & T : 2'-deoxynucleotide



sesiclenegenum cosaparvovecum #

sesiclenegene cosaparvovec

A non-replicating self-complementary adeno-associated virus (scAAV) vector encoding human ceroid-lipofuscinosis neuronal protein 6.
A recombinant non-replicating self-complementary adeno-associated virus serotype 9 (scAAV9) vector, encoding human ceroid-lipofuscinosis neuronal protein 6 (CLN6), under the control of a hybrid CMV enhancer/chicken-beta-actin promoter and a bovine growth hormone (bGH) polyA sequence, with an SV40 intron 5' to the transgene, and flanked by AAV2 inverted terminal repeats (ITRs). The vector genome is a head-to-head, self-complementary dimer, with the vector genome cassette located 5′ of the mutated internal inverted terminal repeat (Δ-ITR) in a reverse complementary orientation and 3′ of the Δ-ITR in a forward orientation.

sésiclénégène cosaparvovec

Un vecteur viral adéno-associé auto-complémentaire (scAAV) non-répliquant codant la protéine neuronale céroïde-lipofuscinose 6 humaine.
Un vecteur viral adéno-associé de sérotype 9 auto-complémentaire (scAAV9), recombinant, non-répliquant, codant la protéine neuronale céroïde-lipofuscinose 6 (CLN6) humaine, sous le contrôle de l'activateur hybride CMV/promoteur de la bêta-actine de poulet et d'une séquence polyA de l'hormone de croissance bovine (bGH), avec un intron SV40 dans la partie 5' du transgène, et flanquée de répétitions terminales inversées (ITRs) AAV2. Le génome du vecteur est un dimère en tête à tête, auto-complémentaire, avec la cassette génomique du vecteur localisée en 5' des répétitions terminales internes inversées mutées (Δ-ITR) en une orientation complémentaire inverse et en 3' de la Δ-ITR en une orientation en avant.

sesiclenegén cosaparvovec

Un vector de virus adeno-asociado auto complementario (scAAV), no replicativo, que codifica para la proteína 6 de la lipofuscinosis neuronal ceroidea humana.

Un vector de virus adeno-asociado serotipo 9 auto complementario (scAAV9), recombinante, no replicativo, que codifica para la proteína 6 de la lipofuscinosis neuronal ceroidea (CLN6) humana, bajo el control de un híbrido del potenciador de CMV/promotor de la beta actina de pollo y una secuencia polyA de la hormona de crecimiento bovina (bGH), con un intrón de SV40 en 5' del transgén, y flanqueado por las repeticiones terminales invertidas (ITRs) del AAV2. El genoma del vector es un dímero cabeza con cabeza auto complementario, con el casete del genoma del vector localizado 5' de la repetición terminal invertida mutada (Δ-ITR) en una orientación complementaria reversa y 3' de (Δ-ITR) en orientación hacia delante.

sibeprenlimabum #

sibeprenlimab

immunoglobulin G2-kappa, anti-[*Homo sapiens* TNFSF13 (tumor necrosis factor (TNF) superfamily member 13, APRIL, CD256)], humanized monoclonal antibody;
gamma2 heavy chain humanized (1-446) [VH (*Homo sapiens* IGHV1-46*01 (85.7%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Homo sapiens* IGHG2*01 (100%), G2m.. CH2 V45.1 (CH1 (121-218), hinge 1-12 (219-230), CH2 V45.1 (281) (231-339), CH3 (340-444), CHS (445-446)) (121-446)], (134-218')-disulfide with kappa light chain humanized (1'-218') [V-KAPPA (*Homo sapiens* IGKV3-15*01 (85.9%) -IGKJ4*01 (100%)) CDR-IMGT [10.3.9] (27-36.54-56.93-101) (1'-111') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218')]; dimer (222-222":223-223":226-226":229-229")-tetrakisdisulfide, produced in a Chinese hamster ovary (CHO)-K1 derived cell line, glycoform alfa

sibéprenlimab

immunoglobuline G2-kappa, anti-[*Homo sapiens* TNFSF13 (membre 13 de la superfamille du facteur de nécrose tumorale, APRIL, CD256)], anticorps monoclonal humanisé;
chaîne lourde gamma2 humanisée (1-446) [VH (*Homo sapiens* IGHV1-46*01 (85.7%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Homo sapiens* IGHG2*01 (100%), G2m.. CH2 V45.1 (CH1 (121-218), charnière 1-12 (219-230), CH2 V45.1 (281) (231-339), CH3 (340-444), CHS (445-446)) (121-446)], (134-218')-disulfure avec la chaîne légère kappa humanisée (1'-218') [V-KAPPA (*Homo sapiens* IGKV3-15*01 (85.9%) -IGKJ4*01 (100%)) CDR-IMGT [10.3.9] (27-36.54-56.93-101) (1'-111') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218')]; dimère (222-222":223-223":226-226":229-229")-tétrakisdisulfure, produite dans une lignée cellulaire dérivée des cellules ovariennes de hamster chinois (CHO)-K1, glycoforme alfa

sibeprenlimab

inmunoglobulina G2-kappa, anti-[*Homo sapiens* TNFSF13 (miembro 13 de la superfamilia del factor de necosis tumoral, APRIL, CD256)], anticuerpo monoclonal humanizado;
cadena pesada gamma2 humanizada (1-446) [VH (*Homo sapiens* IGHV1-46*01 (85.7%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.13] (26-33.51-58.97-109) (1-120) -*Homo sapiens* IGHG2*01 (100%), G2m.. CH2 V45.1 (CH1 (121-218), bisagra 1-12 (219-230), CH2 V45.1 (281) (231-339), CH3 (340-444), CHS (445-446)) (121-446)], (134-218')-disulfuro con la cadena ligera kappa humanizada (1'-218') [V-KAPPA (*Homo sapiens* IGKV3-15*01 (85.9%) - IGKJ4*01 (100%)) CDR-IMGT [10.3.9] (27-36.54-56.93-101) (1'-111') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218')]; dímero (222-222":223-223":226-226":229-229")-tetrakisdisulfuro, producido en una línea celular derivada de las células ováricas de hámster chino (CHO)-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGASVKV SCKASGYTFT DYTIHWVRQA TGQGLEWMGW  50
IYPLRGSINY AQKFQGRVTM TADKSISTVY MELSSLRSED TAVYFCARHG 100
AYYSNAFDYW GQGTLVTVSS ASTKGPSVFP LAPCSRSTSE STAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSNFGTQT 200
YTCNVDHKPS NTKVDKTVER KCCVECPPCP APPVAGPSVF LFPPKPKDTL 250
MISRTPEVTC VVVDVSHEDP EVQFNWYVDG VEVHNAKTKP REEQFNSTFR 300
VVSVLTVVHQ DWLNGKEYKC KVSNKGLPAP IEKTISKTKG QPREPQVYTL 350
PPSREEMTKN QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPMLDSD 400
GSFFLYSKLT VDKSRWQQGN VFSCSVMHEA LHNHYTQKSL SLSPGK     446
```

Light chain / Chaîne légère / Cadena ligera

```
EIVMTQSPAT LSVSPGERAT LSCRASESVD NDGIRFLHWY QQKPGQAPRL  50
LIYRASTRAT GIPARFSGSG SRTEFTLTIS SLQSEDFAVY YCQQSNKDPY 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) 22-96 147-203 260-320 366-424
22"-96" 147"-203" 260"-320" 366"-424"
Intra-L (C23-C104) 23'-92' 138'-198'
23'"-92'" 138'"-198'"
Inter-H-L (CH1 10-CL 126) 134-218' 134"-218'"
Inter-H-H (h 4, h 5, h 8, h 11) 222-222" 223-223" 226-226" 229-229"

N-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
H VH Q1:
1, 1"

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 / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2:
446, 446"

simpiniclinum

simpinicline

5-{(1*E*)-2-[(3*R*)-pyrrolidin-3-yl]ethen-1-yl}pyrimidine

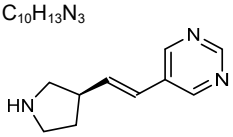
simpinicline

5-{(1*E*)-2-[(3*R*)-pyrrolidin-3-yl]éthén-1-yl}pyrimidine

simpiniclina

5-{(1*E*)-2-[(3*R*)-pirrolidin-3-il]eten-1-il}pirimidina

$C_{10}H_{13}N_3$



sirelretigenum suboparvovecum #

sirelretigene suboparvovec	A non-replicating self-complementary adeno-associated virus serotype 8 (scAAV8) vector, encoding human cellular retinaldehyde-binding protein (CRALBP). A recombinant non-replicating self-complementary adeno-associated virus serotype 8 (scAAV8) vector, encoding human cellular retinaldehyde-binding protein (CRALBP) under the control of the retinaldehyde-binding protein 1 promoter (pRLBP1) and terminated with SV40 poly adenylation (polyA) sequence. The vector genome is a head-to-head, self-complementary dimer, with the vector genome cassette located 5' of the mutated internal inverted terminal repeat (Δ-ITR) in a reverse complementary orientation and 3' of the Δ-ITR in a forward orientation.
sirelrétigène suboparvovec	Un vecteur du virus adéno-associé de sérotype 8 auto-complémentaire (scAAV8), non-répliquant, codant la protéinecellulaire humaine liée au rétinaldéhyde (CRALBP). Un vecteur du virus adéno-associé de sérotype 8 auto-complémentaire (scAAV8) recombinant, non-répliquant codant la protéine cellulaire humaine liée au rétinaldéhyde (CRALBP) sous le contrôle du promoteur de la protéine 1 liée au rétinaldéhyde (pRLBP1) et terminé par la séquence polyadénylée (polyA) SV40. Le génome du vecteur est un dimère en tête à tête, auto-complémentaire, avec la cassette génomique du vecteur localisée en 5' des répétitions terminales internes inversées mutées (Δ-ITR) en une orientation complémentaire inverse et en 3' de la Δ-ITR en une orientation en avant.
sirelretigén suboparvovec	Un vector de virus adeno-asociado serotipo 8 auto complementario (scAAV8), no replicativo, que codifica para la proteína de unión a retinaldehído celular (CRALBP) humana. Un vector de virus adeno-asociado serotipo 8 auto complementario (scAAV8) recombinante, no replicativo, que codifica para la proteína de unión a retinaldehído celular (CRALBP) humana bajo el control del promotor de la proteína de unión a retinaldehído 1 (pRLBP1) y terminado por la secuencia de poliadenilación (polyA) de SV40. El genoma del vector es un dímero cabeza con cabeza auto complementario, con el casete del genoma del vector localizado 5' de la repetición terminal invertida mutada (Δ-ITR) en una orientación complementaria reversa y 3' de (Δ-ITR) en orientación hacia delante.

sudubrilimabum #

sudubrilimab	immunoglobulin G1-kappa, anti-[*Homo sapiens* CD274 (programmed death ligand 1, PDL1, PD-L1, B7 homolog 1, B7H1)], monoclonal antibody;

	gamma1 heavy chain (1-447) [VH (*Homo sapiens* IGHV3-23*04 (85.7%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.11] (26-33.51-58.97-107) (1-118) - *Homo sapiens* IGHG1*03v G1m3>G1m17, nG1m1 (CH1 R120>K (215) (119-216), hinge 1-15 (217-231), CH2 N84.4>A (298) (232-341), CH3 E12 (357), M14 (359) (342-446), CHS K>del (447)) (119-447)], (221-214')-disulfide with kappa light chain (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (90.0%) -IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (227-227'':230-230'')-bisdisulfide, produced in a Chinese hamster ovary (CHO)-K1 cell line, non-glycosylated
sudubrilimab	immunoglobuline G1-kappa, anti-[*Homo sapiens* CD274 (ligand 1 de mort programmée, PDL1, PD-L1, homologue 1 de B7, B7H1)], anticorps monoclonal; chaîne lourde gamma1 (1-447) [VH (*Homo sapiens* IGHV3-23*04 (85.7%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.11] (26-33.51-58.97-107) (1-118) - *Homo sapiens* IGHG1*03v G1m3>G1m17, nG1m1 (CH1 R120>K (215) (119-216), charnière 1-15 (217-231), CH2 N84.4>A (298) (232-341), CH3 E12 (357), M14 (359) (342-446), CHS K>del (447)) (119-447)], (221-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (90.0%) -IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (227-227'':230-230'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO) lignée cellulaire CHO-K1, non-glycosylé
sudubrilimab	inmunoglobulina G1-kappa, anti-[*Homo sapiens* CD274 (ligando 1 de muerte programada, PDL1, PD-L1, homólogo 1 de B7, B7H1)], anticuerpo monoclonal; cadena pesada gamma1 (1-447) [VH (*Homo sapiens* IGHV3-23*04 (85.7%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.11] (26-33.51-58.97-107) (1-118) - *Homo sapiens* IGHG1*03v G1m3>G1m17, nG1m1 (CH1 R120>K (215) (119-216), bisagra 1-15 (217-231), CH2 N84.4>A (298) (232-341), CH3 E12 (357), M14 (359) (342-446), CHS K>del (447)) (119-447)], (221-214')-disulfuro con la cadena ligera kappa (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (90.0%) -IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (227-227'':230-230'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular CHO-K1, no glicosilado

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAASGFTFS ETWLHWVRQA PGKGLEWVAW  50
VSPFGGSTYY ADSVKGRFTI SADTSKNTAY LQMNSLRAED TAVYYCARRH 100
WPGGFDYWGQ GTLVTVSSAS TKGPSVFPLA PSSKSTSGGT AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTQTYI 200
CNVNHKPSNT KVDKKVEPKS CDKTHTCPPC PAPELLGGPS VFLFPPKPKD 250
TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYAST 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY 350
TLPPSREEMT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD 400
SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPG    447
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCRASQDVS TAVAWYQQKP GKAPKLLIYS  50
ASFLYSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ FLYHPATFGQ 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"

No N-glycosylation sites / Pas de sites de N-glycosylation / ningún posición de N-glicosilación
CH2 N84.4>A:
298, 298"
Aglycosylated

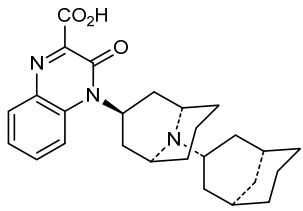
sunobinopum

sunobinop — 4-[(1*R*,1'*R*,3*r*,3'*r*,5*S*,5'*S*)-9'-aza[3,9'-bi(bicyclo[3.3.1]nonan)]-3'-yl]-3-oxo-3,4-dihydroquinoxaline-2-carboxylic acid

sunobinop — acide 4-[(1*R*,1'*R*,3*r*,3'*r*,5*S*,5'*S*)-9'-aza[3,9'-bi(bicyclo[3.3.1]nonan)]-3'-yl]-3-oxo-3,4-dihydroquinoxaline-2-carboxylique

sunobinop — ácido 4-[(1*R*,1'*R*,3*r*,3'*r*,5*S*,5'*S*)-9'-aza[3,9'-bi(biciclo[3.3.1]nonan)]-3'-il]-3-oxo-3,4-dihidroquinoxalina-2-carboxílico

$C_{26}H_{33}N_3O_3$



surzebiclimabum #

surzebiclimab — immunoglobulin G1-kappa, anti-[*Homo sapiens* HAVCR2 (hepatitis A virus cellular receptor 2, T-cell immunoglobulin mucin family member 3, Tim-3, TIM3, TIMD3, CD366)], monoclonal antibody; gamma1 heavy chain (1-448) [VH (*Homo sapiens* IGHV3-23*04 (93.8%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.7.13] (26-33.51-57.96-108) (1-119) -*Homo sapiens* IGHG1*01, G1m17,1, G1v4 CH2 A114 (CH1 K120 (217) (120-217), hinge 1-15 (218-232), linker (233-237), CH2 P114>A (330) (238-341), CH3 D12 (357), L14 (359) (342-446), CHS (447-448)) (120-448)], (222-218')-disulfide with kappa light chain (1'-218') [V-KAPPA (*Homo sapiens* IGKV3-15*01 (84%) -IGKJ4*01 (100%)) CDR-IMGT [10.3.9] (27-36.54-56.93-101) (1'-111') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (157), V101 (195) (112'-218')]; dimer (228-228":231-231")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

surzébiclimab

immunoglobuline G1-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;
chaîne lourde gamma1 (1-448) [VH (*Homo sapiens* IGHV3-23*04 (93.8%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.7.13] (26-33.51-57.96-108) (1-119) -*Homo sapiens* IGHG1*01, G1m17,1, G1v4 CH2 A114 (CH1 K120 (217) (120-217), charnière 1-15 (218-232), linker (233-237), CH2 P114>A (330) (238-341), CH3 D12 (357), L14 (359) (342-446), CHS (447-448)) (120-448)], (222-218')-disulfure avec la chaîne légère kappa (1'-218') [V-KAPPA (*Homo sapiens* IGKV3-15*01 (84.0%) -IGKJ4*01 (100%)) CDR-IMGT [10.3.9] (27-36.54-56.93-101) (1'-111') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (157), V101 (195) (112'-218')]; dimère (228-228":231-231")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

surzebiclimab

inmunoglobulina G1-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;
cadena pesada gamma1 (1-448) [VH (*Homo sapiens* IGHV3-23*04 (93.8%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.7.13] (26-33.51-57.96-108) (1-119) -*Homo sapiens* IGHG1*01, G1m17,1, G1v4 CH2 A114 (CH1 K120 (217) (120-217), bisagra 1-15 (218-232), linker (233-237), CH2 P114>A (330) (238-341), CH3 D12 (357), L14 (359) (342-446), CHS (447-448)) (120-448)], (222-218')-disulfuro con la cadena ligera kappa (1'-218') [V-KAPPA (*Homo sapiens* IGKV3-15*01 (84.0%) -IGKJ4*01 (100%)) CDR-IMGT [10.3.9] (27-36.54-56.93-101) (1'-111') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (157), V101 (195) (112'-218')]; dímero (228-228":231-231")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAASGFTFS RYAMSWVRQA PGKGLEWVAA  50
ISSGGSLYYP DSVKGRFTIS RDNAKNTLYL QMNSLRAEDT AVYYCARGRE 100
ADGGYFDYWG QGTLVTVSSA STKGPSVFPL APSSKSTSGG TAALGCLVKD 150
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY 200
ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP CPAPPAAGPS VFLFPPKPKD 250
TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNST 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKALA APIEKTISKA KGQPREPQVY 350
TLPPSRDELT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD 400
SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPGK   448
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Light chain / Chaîne légère / Cadena ligera

```
EIVLTQSPAT LSVSPGERAT LSCRASESVE YYGTSLMQWY QQKPGQAPRL  50
LIYAASNVES GIPARFSGSG SGTEFTLTIS SLQSEDFAVY YCQQSLKVPL 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) 22-95 146-202 262-322 368-426
22"-95" 146"-202" 262"-322" 368"-426"
Intra-L (C23-C104) 23'-92' 138'-198'
23'"-92'" 138'"-198'"
Inter-H-L (h 5-CL 126) 222-218' 222"-218'"
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:
298, 298"
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 / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2:
448, 448"

tacatresgenum autoleucelum #

tacatresgene autoleucel	Autologous T cells obtained from the peripheral blood of patients, collected by leukapheresis, modified by CRISPR/Cas9 (clustered regularly interspaced short palindromic repeats/CRISPR-associated protein 9) mediated gene editing consisting of two guide RNAs (gRNAs) introduced transiently as ribonucleoprotein (RNP) complex, and a neoepitope T cell receptor (neo-TCR) gene cassette encoded by plasmid DNA to replace the endogenous T cell receptor (TCR) with a single patient-derived tumour-specific neo-TCR per T cell, with a maximum of three different neo-TCRs in the final drug substance. The constant elements of the neo-TCR are identical for each patient and the neo-TCR gene expression is regulated by the native endogenous TCR promoter. The T cells are cultured in the presence of growth media containing IL-7 and IL-15 and a combination of membrane bound anti-CD3 and anti-CD28 for activation. The T cells are predominantly CD4 and CD8 T cells (generally >80%), including Tmsc (memory stem cells) and Tcm (central memory) phenotypes.
tacatresgène autoleucel	Lymphocytes T autologues obtenus du sang périphérique de patients, recueillis par leucophérèse, modifiés par CRISPR/Cas9 (courtes répétitions palindromiques groupées et régulièrement espacées / protéine 9 associée à CRISPR) induisant une édition génétique consistant en deux ARN guides (gRNAs) introduisant transitoirement un complexe ribonucléoprotéique, et la cassette du gène du récepteur néo-épitope du lymphocyte T (néo-TCR) encodés par un plasmide d'ADN pour remplacer le récepteur endogène du lymphocyte T (TCR) avec un seul néo-TCR tumeur-spécifique dérivé de patients pour chaque lymphocyte T, avec un maximum de trois néo-TCRs différents dans la substance médicamenteuse finale. Les éléments constants des néo-TCR sont identiques pour chaque patient et l'expression du gène néo-TCR est régulée par le promoteur natif endogène du TCR. Les lymphocytes T sont cultivés en présence de milieu de croissance contenant IL-7 et IL-15 et une combinaison d'anti-CD3 et anti-CD28 liés à la membrane pour l'activation. Les lymphocytes T sont majoritairement des lymphocytes T CD4 et CD8 (généralement >80%), incluant les phénotypes Tmsc (cellules souches à mémoire) et Tcm (à mémoire centrale).
tacatresgén autoleucel	Linfocitos T autólogos obtenidos de sangre periférica de pacientes, recogidos por leucoaféresis, modificados por CRISPR/Cas9 (repeticiones palindrómicas cortas agrupadas y regularmente espaciadas/proteína asociada a CRISPR 9) mediante edición genética consistente en dos RNAs guía (gRNAs) introducidos transitoriamente como un complejo de ribonucleoproteína (RNP), y un casete genético de un receptor de linfocitos T para un neoepítopo (neo-TCR) codificado en un plásmido de DNA, para reemplazar el receptor de linfocitos T (TCR) endógeno con un solo neo-TCR específico de tumor y derivado del paciente por linfocito T, con un máximo de tres neo-TCRs diferentes en el principio activo final. Los

elementos constantes de los neo-TCR son idénticos para cada paciente y la expresión del gen del neo-TCR está rgulada por el promotor nativo del TCR endógeno. Los linfocitos T se cultivan en presencia de medio de crecimiento que contiene IL-7 e IL-15 y una combinación de anti-CD3 y anti-CD28 de membrana para la activación. Los linfocitos T son predominantemente CD4 y CD8 (generalmente >80%), incluyendo fenotipos de Tmsc (células madre de memoria) y Tcm (memoria central).

tadnersenum

tadnersen	*all-P-ambo*-2'-*O*-(2-methoxyethyl)-*P*-thioguanylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methylcytidylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methylcytidylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-deoxy-5-methyl-*P*-thiocytidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-deoxy-*P*-thioadenylyl-(3'→5')-2'-deoxy-*P*-thioguanylyl-(3'→5')-2'-deoxy-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-deoxy-*P*-thioguanylyl-(3'→5')-2'-deoxy-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-deoxy-*P*-thioguanylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methylcytidylyl-(3'→5')-2'-*O*-(2-methoxyethyl)guanylyl-(3'→5')-2'-*O*-(2-methoxyethyl)adenylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyl-*P*-thiouridylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methylcytidine
tadnersen	*tout-P-ambo*-2'-*O*-(2-méthoxyéthyl)-*P*-thioguanylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthylcytidylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthylcytidylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-désoxy-5-méthyl-*P*-thiocytidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-désoxy-*P*-thioadénylyl-(3'→5')-2'-désoxy-*P*-thioguanylyl-(3'→5')-2'-désoxy-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-désoxy-*P*-thioguanylyl-(3'→5')-2'-désoxy-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-désoxy-*P*-thioguanylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthylcytidylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)guanylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)adénylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthyl-*P*-thiouridylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthylcytidine
tadnersén	*todo-P-ambo*-2'-*O*-(2-metoxietil)-*P*-tioguanilil-(3'→5')-5-metil-2'-*O*-(2-metoxietil)citidilil-(3'→5')-5-metil-2'-*O*-(2-metoxietil)citidilil-(3'→5')-5-metil-2'-*O*-(2-metoxietil)-*P*-tiocitidilil-(3'→5')-2'-deoxi-5-metil-*P*-tiocitidilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2'-deoxi-*P*-tioadenilil-(3'→5')-2'-deoxi-*P*-tioguanilil-(3'→5')-2'-deoxi-5-metil-*P*-tiocitidilil-(3'→5')-2'-deoxi-*P*-tioguanilil-(3'→5')-2'-deoxi-5-metil-*P*-tiocitidilil-(3'→5')-2'-deoxi-*P*-tioguanilil-(3'→5')-5-metil-2'-*O*-(2-metoxietil)citidilil-(3'→5')-2'-*O*-(2-metoxietil)guanilil-(3'→5')-2'-*O*-(2-metoxietil)adenilil-(3'→5')-5-metil-2'-*O*-(2-metoxietil)-*P*-tiocitidilil-(3'→5')-5-metil-2'-*O*-(2-metoxietil)-*P*-tiouridilil-(3'→5')-5-metil-2'-*O*-(2-metoxietil)citidina

$C_{210}H_{297}N_{66}O_{114}P_{17}S_{12}$

(3'-5') G=C=C−C−d(C=T=A=G=C=G=C=G=)C=G−A−C=U=C

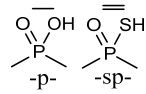
Legend:

A , G & T : 2'-deoxynucleotide

C : 2'-deoxy-5-methylnucleotide

A & G : 2'-*O*-(2-methoxyethyl)nucleotide

C & U : 2'-*O*-(2-methoxyethyl)-5-methylnucleotide



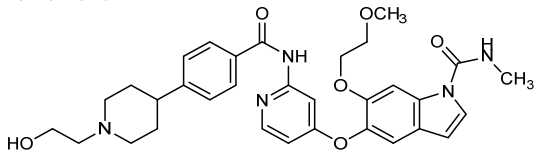
tasurgratinibum

tasurgratinib — 1^1-(2-hydroxyethyl)-7^6-(2-methoxyethoxy)-*N*-methyl-3-oxo-7^1*H*-6-oxa-4-aza-7(5)-indola-5(2,4)-pyridina-1(4)-piperidina-2(1,4)-benzenahepta-phane-7^1-carboxamide

tasurgratinib — 1^1-(2-hydroxyéthyl)-7^6-(2-méthoxyéthoxy)-*N*-méthyl-3-oxo-7^1*H*-6-oxa-4-aza-7(5)-indola-5(2,4)-pyridina-1(4)-pipéridina-2(1,4)-benzénahepta-phane-7^1-carboxamide

tasurgratinib — 1^1-(2-hidroxietil)-*N*-metil-7^6-(2-metoxietoxi)-3-oxo-7^1*H*-6-oxa-4-aza-7(5)-indola-5(2,4)-piridina-1(4)-piperidina-2(1,4)-bencenaheptafano-7^1-carboxamida

$C_{32}H_{37}N_5O_6$



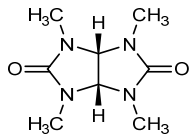
temgicolurilum

temgicoluril — *cis*-1,3,4,6-tetramethyltetrahydroimidazo[4,5-*d*]imidazole-2,5(1*H*,3*H*)-dione

temgicoluril — *cis*-1,3,4,6-tétraméthyltétrahydroimidazo[4,5-*d*]imidazole-2,5(1*H*,3*H*)-dione

temgicoluril — *cis*-1,3,4,6-tetrametiltetrahidroimidazo[4,5-*d*]imidazola-2,5(1*H*,3*H*)-diona

$C_8H_{14}N_4O_2$



tenofovirum amibufenamidum

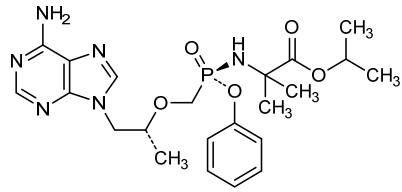
tenofovir amibufenamide — propan-2-yl 2-{[(*S*)-({[(2*R*)-1-(6-amino-9*H*-purin-9-yl)propan-2-yl]oxy}methyl)(phenoxy)phosphinoyl]amino}-2-methylpropanoate

ténofovir amibufénamide — 2-{[(*S*)-({[(2*R*)-1-(6-amino-9*H*-purin-9-yl)propan-2-yl]oxy}méthyl)(phénoxy)phosphinoyl]amino}-2-méthylpropanoate de propan-2-yle

tenofovir amibufenamida

2-{[(*S*)-({[(2*R*)-1-(6-amino-9*H*-purin-9-il)propan-2-il]oxi}metil)(fenoxi)fosfinoil]amino}-2-metilpropanoato de propan-2-ilo

$C_{22}H_{31}N_6O_5P$



tifcemalimabum #

tifcemalimab

immunoglobulin G4-kappa, anti-[*Homo sapiens* BTLA (B and T lymphocyte associated, BTLA1, CD272)], chimeric monoclonal antibody;
gamma4 heavy chain chimeric (1-446) [VH (*Mus musculus* IGHV14-3*02 (82.3%) -IGHJ3*01 (91.7%)/*Homo sapiens* IGHV1-3*01 (77.1%) -(IGHD) -IGHJ4*01 (92.9%)) CDR-IMGT [8.8.12] (26-33.51-58.97-108) (1-119) -*Homo sapiens* IGHG4*01, G4v5 h P10 (CH1 (120-217), hinge 1-12 S10>P (227) (218-229), CH2 (230-339), CH3 (340-444), CHS (445-446)) (120-446)], (133-219')-disulfide with kappa light chain chimeric (1'-219') [V-KAPPA (*Mus musculus* IGKV1-135*01 (92%) -IGKJ2*03 (91.7%)/*Homo sapiens* IGKV2-30*01 (87.0%) -IGKJ2*01 (100%)) CDR-IMGT [11.3.9] (27-47.55-57.94-102) (1'-112') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (158), V101 (196) (113'-219')];
dimer (225-225'':228-228'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

tifcémalimab

immunoglobuline G4-kappa, anti-[*Homo sapiens* BTLA (atténuateur des lymphocytes B et T, BTLA1, CD272)], anticorps monoclonal chimérique;
chaîne lourde gamma4 chimérique (1-446) [VH (*Mus musculus* IGHV14-3*02 (82.3%) -IGHJ3*01 (91.7%)/*Homo sapiens* IGHV1-3*01 (77.1%) -(IGHD) -IGHJ4*01 (92.9%)) CDR-IMGT [8.8.12] (26-33.51-58.97-108) (1-119) -*Homo sapiens* IGHG4*01, G4v5 h P10 (CH1 (120-217), charnière 1-12 S10>P (227) (218-229), CH2 (230-339), CH3 (340-444), CHS (445-446)) (120-446)], (133-219')-disulfure avec la chaîne légère kappa chimérique (1'-219') [V-KAPPA (*Mus musculus* IGKV1-135*01 (92%) -IGKJ2*03 (91.7%)/*Homo sapiens* IGKV2-30*01 (87.0%) -IGKJ2*01 (100%)) CDR-IMGT [11.3.9] (27-47.55-57.94-102) (1'-112') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (158), V101 (196) (113'-219')];
dimère (225-225'':228-228'')-bisdisulfure, produite dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

tifcemalimab

inmunoglobulina G4-kappa, anti-[*Homo sapiens* BTLA (atenuador de linfocitos B y T, BTLA1, CD272)], anticuerpo monoclonal quimérico;
cadena pesada gamma4 quimérica (1-446) [VH (*Mus musculus* IGHV14-3*02 (82.3%) -IGHJ3*01 (91.7%)/*Homo sapiens* IGHV1-3*01 (77.1%) -(IGHD) -IGHJ4*01 (92.9%)) CDR-IMGT [8.8.12] (26-33.51-58.97-108) (1-119) -*Homo sapiens* IGHG4*01, G4v5 h P10 (CH1 (120-217), bisagra 1-12 S10>P (227) (218-229), CH2 (230-339), CH3 (340-444), CHS (445-446)) (120-446)], (133-219')-disulfuro con la cadena ligera kappa quimérica (1'-219') [V-KAPPA (*Mus musculus* IGKV1-135*01 (92%) -IGKJ2*03 (91.7%)/*Homo sapiens* IGKV2-30*01 (87.0%) -IGKJ2*01 (100%)) CDR-IMGT [11.3.9] (27-47.55-57.94-102) (1'-112') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (158), V101 (196) (113'-219')];
dímero (225-225'':228-228'')-bisdisulfuro, producida por células ováricas de hamster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGASVKL SCKASGYNFK HTYAHWVRQA PGQGLEWIGR  50
IDPANGNTKY DPKFQGRATM TADTASNTAY LELSSLRSED TAVYYCVADH 100
YGSSLLDYWG QGTLVTVSSA STKGPSVFPL APCSRSTSES TAALGCLVKD 150
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTKTY 200
TCNVDHKPSN TKVDKRVESK YGPPCPPCPA PEFLGGPSVF LFPPKPKDTL 250
MISRTPEVTC VVVDVSQEDP EVQFNWYVDG VEVHNAKTKP REEQFNSTYR 300
VVSVLTVLHQ DWLNGKEYKC KVSNKGLPSS IEKTISKAKG QPREPQVYTL 350
PPSQEEMTKN QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD 400
GSFFLYSRLT VDKSRWQEGN VFSCSVMHEA LHNHYTQKSL SLSLGK     446
```

Light chain / Chaîne légère / Cadena ligera

```
DVVMTQTPLS LSVTPGQPAS ISCKSSQSLL DSDGKTYLNW FQQRPGQSPR  50
RLIYLVSKLD SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCWQGTYFP 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	146-202	260-320	366-424
	22''-96''	146''-202''	260''-320''	366''-424''
Intra-L (C23-C104)	23'-93'	139'-199'		
	23'''-93'''	139'''-199'''		
Inter-H-L (CH1 10-CL 126)	133-219'	133''-219'''		
Inter-H-H (h 8, h 11)	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

tigulixostatum

tigulixostat

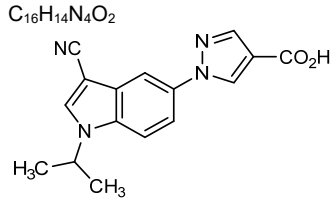
1-[3-cyano-1-(propan-2-yl)-1*H*-indol-5-yl]-1*H*-pyrazole-4-carboxylic acid

tigulixostat

acide 1-[3-cyano-1-(propan-2-yl)-1*H*-indol-5-yl]-1*H*-pyrazole-4-carboxylique

tigulixostat

ácido 1-[3-ciano-1-(propan-2-il)-1*H*-indol-5-il]-1*H*-pirazola-4-carboxílico



tirnovetmabum #

tirnovetmab	immunoglobulin G2-kappa, anti-[*Canis lupus familiaris* IL31 (interleukin 31)], caninized monoclonal antibody; gamma2 heavy chain caninized (1-453) [VH caninized (*Canis lupus familiaris* IGHV4-1*01 (61.2%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.7.12] (26-33.51-57.96-107) (1-118) -*Canis lupus familiaris* IGHG2*02 (100%) (CH1 (119-215), hinge 1-19 (216-234), CH2 (235-344), CH3 (345-451), CHS (452-453)) (119-453)], (133-217')-disulfide with kappa light chain caninized (1'-221') [V-KAPPA caninized (*Canis lupus familiaris* IGKV3-18*01 (63.8%) -IGKJ3*01 (83.3%) Q120>G (104)) CDR-IMGT [10.3.9](27-36.54-56.93-101) (1'-111') -*Canis lupus familiaris* IGKC*01 (100%) (112'-221')]; dimer (230-230":233-233")-bisdisulfide, produced in a Chinese hamster ovary (CHO)-K1 cell line, glycoform alfa
tirnovetmab	immunoglobuline G2-kappa, anti-[*Canis lupus familiaris* IL31 (interleukine 31)], anticorps monoclonal caninisé; chaîne lourde gamma2 caninisée (1-453) [VH caninisé (*Canis lupus familiaris* IGHV4-1*01 (61.2%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.7.12] (26-33.51-57.96-107) (1-118) CDR-IMGT [8.7.12] (26-33.51-57.96-107) (1-118) -*Canis lupus familiaris* IGHG2*02 (100%) (CH1 (119-215), charnière 1-19 (216-234), CH2 (235-344), CH3 (345-451), CHS (452-453)) (119-453)], (133-217')-disulfure avec la chaîne légère kappa caninisé (1'-221') [V-KAPPA caninisé (*Canis lupus familiaris* IGKV3-18*01 (63.8%) -IGKJ3*01 (83.3%) Q120>G (104)) CDR-IMGT [10.3.9](27-36.54-56.93-101) (1'-111') -*Canis lupus familiaris* IGKC*01 (100%) (112'-221')]; dimère (230-230":233-233")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO) lignée cellulaire CHO-K1, glycoforme alfa
tirnovetmab	inmunoglobulina G2-kappa, anti-[*Canis lupus familiaris* IL31 (interleukina 31)], anticuerpo monoclonal caninizado; cadena pesada gamma2 caninizada (1-453) [VH caninizado (*Canis lupus familiaris* IGHV4-1*01 (61.2%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.7.12] (26-33.51-57.96-107) (1-118) CDR-IMGT [8.7.12] (26-33.51-57.96-107) (1-118) -*Canis lupus familiaris* IGHG2*02 (100%) (CH1 (119-215), bisagra 1-19 (216-234), CH2 (235-344), CH3 (345-451), CHS (452-453)) (119-453)], (133-217')-disulfuro con la cadena ligera

kappa caninizada (1'-221') [V-KAPPA caninizado (*Canis lupus familiaris* IGKV3-18*01 (63.8%) -IGKJ3*01 (83.3%) Q120>G (104)) CDR-IMGT [10.3.9] (27-36.54-56.93-101) (1'-111') -*Canis lupus familiaris* IGKC*01 (100%) (112'-221')]; dímero (230-230":233-233")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGPS LVKPGGSLRL TCSVTGDSIT SGYWNWIRKF PGNKLEYMGY  50
ISYSGITDYN PSLKSRITIS RDTSKNQYYL QLNSVTTEDT ATYYCARYGN 100
YGYAMDYWGQ GTSVTVSSAS TTAPSVFPLA PSCGSTSGST VALACLVSGY 150
FPEPVTVSWN SGSLTSGVHT FPSVLQSSGL YSLSSMVTVP SSRWPSETFT 200
CNVAHPASKT KVDKPVPKRE NGRVPRPPDC PKCPAPEMLG GPSVFIFPPK 250
PKDTLLIART PEVTCVVVDL DPEDPEVQIS WFVDGKQMQT AKTQPREEQF 300
NGTYRVVSVL PIGHQDWLKG KQFTCKVNNK ALPSPIERTI SKARGQAHQP 350
SVYVLPPSRE ELSKNTVSLT CLIKDFFPPD IDVEWQSNGQ QEPESKYRTT 400
PPQLDEDGSY FLYSKLSVDK SRWQRGDTFI CAVMHEALHN HYTQESLSHS 450
PGK                                                     453
```

Light chain / Chaîne légère / Cadena ligera

```
DIVMTQSPAS LSVSLGQRAT ISCRASESVD TYGNSFMHWY QQKPGQSPKL  50
LIYRASNLES GIPARFGGSG SGTDFTLTID PVQADDVATY YCQQSYEDPW 100
TFGGGTKLEI KRNDAQPAVY LFQPSPDQLH TGSASVVCLL NSFYPKDINV 150
KWKVDGVIQD TGIQESVTEQ DKDSTYSLSS TLTMSSTEYL SHELYSCEIT 200
HKSLPSTLIK SFQRSECQRV D                                 221
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-95 145-201 265-325 371-431
22"-95" 145"-201" 265"-325" 371"-431"
Intra-L (C23-C104) 23'-92' 138'-197'
23'"-92'" 138'"-197'"
Inter-H-L (CH1 11-CL 126) 133-217' 133"-217'"
Inter-H-H (h 15, h 18) 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 / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2:
453, 453"

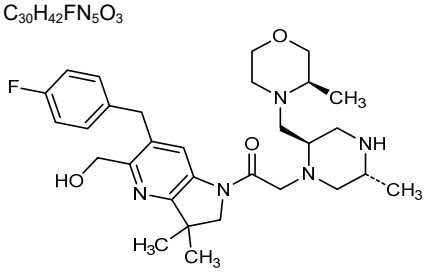
tolinapantum

tolinapant — (6^{2}*R*,6^{5}*R*,8^{3}*R*)-1^{4}-fluoro-3^{5}-(hydroxymethyl)-3^{3},3^{3},6^{5},8^{3}-tetramethyl-3^{2,3}-dihydro-3(6,1)-pyrrolo[3,2-*b*]pyridina-8(4)-morpholina-6(1,2)-piperazina-1(1)-benzenaoctaphan-4-one

tolinapant — (6^{2}*R*,6^{5}*R*,8^{3}*R*)-1^{4}-fluoro-3^{5}-(hydroxymethyl)-3^{3},3^{3},6^{5},8^{3}-tetramethyl-3^{2,3}-dihydro-3(6,1)-pyrrolo[3,2-*b*]pyridina-8(4)-morpholina-6(1,2)-piperazina-1(1)-benzenaoctaphan-4-one

tolinapant — (6^{2}*R*,6^{5}*R*,8^{3}*R*)-1^{4}-fluoro-3^{5}-(hidroximetil)-3^{3},3^{3},6^{5},8^{3}-tetrametil-3^{2,3}-dihidro-3(6,1)-pirrolo[3,2-*b*]piridina-8(4)-morfolina-6(1,2)-piperazina-1(1)-bencenaoctafan-4-ona

$C_{30}H_{42}FN_5O_3$



tomligisiranum

tomligisiran

all-P-ambo-*O*-[(2*R*,3*S*)-2-(hydroxymethyl)oxolan-3-yl] hydrogen 5'-*O*-({[(2*R*,3*S*)-3-{[({*cis*-4-[(3*S*,8*S*)-17-{[2-(acetylamino)-2-deoxy-β-D-galactopyranosyl]oxy}-3,8-bis{[2-(2-{[2-(acetylamino)-2-deoxy-β-D-galactopyranosyl]oxy}ethoxy)ethyl]carbamoyl}-6,11-dioxo-15-oxa-2,7,12-triazaheptadecan-1-oyl]cyclohexyl}oxy)hydroxyphosphorothioyl]oxy}-oxolan-2-yl]methoxy}hydroxyphosphorothioyl)-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-deoxy-2'-fluoroguanylyl-(3'→5')-2'-deoxy-2'-fluorocytidylyl-(3'→5')-2'-deoxy-2'-fluoroadenylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methyl-*P*-thio-3'-adenylate,
duplex with *all-P-ambo*-2'-*O*-methyl-*P*-thiouridylyl-(3'→5')-2'-deoxy-2'-fluoro-*P*-thioadenylyl-(3'→5')-2'-*O*-methyl-*P*-thiocytidylyl-(3'→5')-2'-deoxy-2'-fluorocytidylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-deoxy-2'-fluoroadenylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-deoxy-2'-fluorouridylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-deoxy-2'-fluoroadenylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-deoxy-2'-fluoroguanylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-deoxy-2'-fluorocytidylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-deoxy-2'-fluoroadenylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-deoxy-2'-fluoroadenylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-methylguanosine

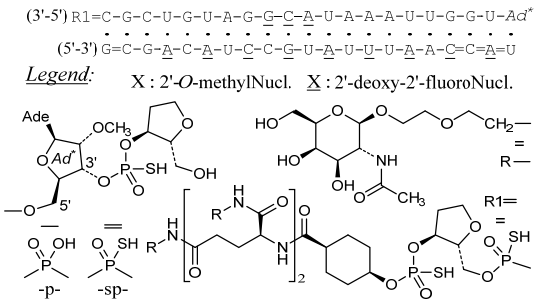
tomligisiran

tout-P-ambo-5'-*O*-({[(2*R*,3*S*)-3-{[({*cis*-4-[(3*S*,8*S*)-17-{[2-(acétylamino)-2-désoxy-β-D-galactopyranosyl]oxy}-3,8-bis{[2-(2-{[2-(acétylamino)-2-désoxy-β-D-galactopyranosyl]oxy}éthoxy)éthyl]carbamoyl}-6,11-dioxo-15-oxa-2,7,12-triazaheptadecan-1-oyl]cyclohexyl}oxy)hydroxyphos-phorothioyl]oxy}oxolan-2-yl]méthoxy}hydroxyphosphorothioyl)-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-désoxy-2'-fluoroguanylyl-(3'→5')-2'-désoxy-2'-fluorocytidylyl-(3'→5')-2'-désoxy-2'-fluoroadénylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-hydrogéno-2'-*O*-méthyl-*P*-thio-3'-adénylate de *O*-[(2*R*,3*S*)-2-(hydroxyméthyl)oxolan-3-yle],
duplex avec *tout-P-ambo*-2'-*O*-méthyl-*P*-thiouridylyl-(3'→5')-2'-désoxy-2'-fluoro-*P*-thioadénylyl-(3'→5')-2'-*O*-méthyl-*P*-thiocytidylyl-(3'→5')-2'-désoxy-2'-fluorocytidylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-désoxy-2'-fluoroadénylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-désoxy-2'-fluorouridylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-désoxy-2'-fluoroadénylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-désoxy-2'-fluoroguanylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-désoxy-2'-fluorocytidylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-désoxy-2'-fluoroadénylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-désoxy-2'-fluoroadénylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-méthylguanosine

tomligisirán

all-P-ambo-5'-*O*-({[(2*R*,3*S*)-3-{[({*cis*-4-[(3*S*,8*S*)-17-{[2-(acetilamino)-2-desoxi-β-D-galactopiranosil]oxi}-3,8-bis{[2-(2-{[2-(acetilamino)-2-desoxi-β-D-galactopiranosil]oxi}etoxi)etil]carbamoil}-6,11-dioxo-15-oxa-2,7,12-triazaheptadecan-1-oil]ciclohexil}oxi)hidroxifosforotioil]oxi}oxolan-2-il]metoxi}hidroxifosforotioil)-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-desoxi-2'-fluoroguanilil-(3'→5')-2'-desoxi-2'-fluorocitidilil-(3'→5')-2'-desoxi-2'-fluoroadenilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-hidrógeno-2'-*O*-metil-*P*-tio-3'-adenilato de *O*-[(2*R*,3*S*)-2-(hidroximetil)oxolan-3-ilo], dúplex con *todo-P-ambo*-2'-*O*-metil-*P*-tiouridilil-(3'→5')-2'-desoxi-2'-fluoro-*P*-tioadenilil-(3'→5')-2'-*O*-metil-*P*-tiocitidilil-(3'→5')-2'-desoxi-2'-fluorocitidilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-desoxi-2'-fluoroadenilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-desoxi-2'-fluorouridilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-desoxi-2'-fluoroadenilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-desoxi-2'-fluoroguanilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-desoxi-2'-fluorocitidilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-desoxi-2'-fluoroadenilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-desoxi-2'-fluoroadenilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metil-*P*-tiocitidilil-(3'→5')-2'-*O*-metilguanosina

$C_{492}H_{651}F_{12}N_{164}O_{310}P_{43}S_7$



torudokimabum #

torudokimab

immunoglobulin G4-kappa, anti-[*Homo sapiens* IL33 (interleukin 33, interleukin-1 family member 11, IL1F11, nuclear factor for high endothelial venules, NF-HEV)], monoclonal antibody; gamma4 heavy chain (1-449) [VH (*Homo sapiens* IGHV3-23*04 (95.9%) -(IGHD) -IGHJ3*02 (87.5%) M123>L (118)) CDR-IMGT [8.8.16] (26-33.51-58.97-112) (1-123)-*Homo sapiens* IGHG4*01 G4v5 h P10, G4v4 CH2 A1.3, A1.2 (CH1 (124-221), hinge 1-12 S10>P (231) (222-233), CH2 F1.3>A (237), L1.2>A (238) (234-343), CH3 (344-448), CHS K>del (449)) (124-449)], (137-215')-disulfide with kappa light chain (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (88.5%) -IGKJ4*01 (91.7%)) CDR-IMGT [6.3.10] (27-32.50-52.89-98) (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')]; dimer (229-229":232-232")-bisdisulfide, produced in a Chinese hamster ovary (CHO)-K1 cell line, glycoform alfa

torudokimab

immunoglobuline G4-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;
chaîne lourde gamma4 (1-449) [VH (*Homo sapiens* IGHV3-23*04 (95.9%) -(IGHD) - IGHJ3*02 (87.5%) M123>L (118)) CDR-IMGT [8.8.16] (26-33.51-58.97-112) (1-123)-*Homo sapiens* IGHG4*01 G4v5 h P10, G4v4 CH2 A1.3, A1.2 (CH1 (124-221), charnière 1-12 S10>P (231) (222-233), CH2 F1.3>A (237), L1.2>A (238) (234-343), CH3 (344-448), CHS K>del (449)) (124-449)], (137-215')-disulfure avec la chaîne légère kappa (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (88.5%) -IGKJ4*01 (91.7%)) CDR-IMGT [6.3.10] (27-32.50-52.89-98) (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')]; dimère (229-229":232-232")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO) lignée cellulaire CHO-K1, glycoforme alfa

torudokimab

inmunoglobulina G4-kappa, anti-[*Homo sapiens* IL33 (interleukina 33, miembro 11 de la familia 1 de interleukinas, IL1F11, factor nuclear de las vénulas del alto endotelio, NF-HEV)], anticuerpo monoclonal;
cadena pesada gamma4 *Homo sapiens* (1-449) [VH (*Homo sapiens* IGHV3-23*04 (95.9%) -(IGHD) - IGHJ3*02 (87.5%) M123>L (118)) CDR-IMGT [8.8.16] (26-33.51-58.97-112) (1-123)-*Homo sapiens* IGHG4*01 G4v5 h P10, G4v4 CH2 A1.3, A1.2 (CH1 (124-221), bisagra 1-12 S10>P (231) (222-233), CH2 F1.3>A (237), L1.2>A (238) (234-343), CH3 (344-448), CHS K>del (449)) (124-449)], (137-215')-disulfuro con la cadena ligera kappa (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (88.5%) -IGKJ4*01 (91.7%)) CDR-IMGT [6.3.10] (27-32.50-52.89-98) (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')]; dímero (229-229":232-232")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVETGGG LIQPGGSLRL SCAASGFTFS FYAMSWVRQA PGKGLEWVSA  50
ISGSGGSTYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARTI 100
HGIRAAYDAF IIWGQGTLVT VSSASTKGPS VFPLAPCSRS TSESTAALGC 150
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG 200
TKTYTCNVDH KPSNTKVDKR VESKYGPPCP PCPAPEAAGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS QEDPEVQFNW YVDGVEVHNA KTKPREEQFN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKG LPSSIEKTIS KAKGQPREPQ 350
VYTLPPSQEE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SRLTVDKSRW QEGNVFSCSV MHEALHNHYT QKSLSLSLG  449
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Light chain / Chaîne légère / Cadena ligera

```
EIVLTQSPGT LSLSPGERAT LSCRASQSVG INLSWYQQKP GQAPRLLIYG  50
ASHRLTGIPD RFSGSGSGTD FTLTISRLEP EDFAVYYCHQ YSQPPPFTFG 100
GGTKVEIKRT 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	264-324	370-428
	22"-96"	150"-206"	264"-324"	370"-428"
Intra-L (C23-C104)	23'-88'	135'-195'		
	23'"-88'"	135'"-195'"		
Inter-H-L (CH1 10-CL 126)	137-215'	137"-215'"		
Inter-H-H (h 8, h 11)	229-229"	232-232"		

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

tozorakimabum #

tozorakimab	immunoglobulin G1-lambda2, anti-[*Homo sapiens* IL33 (interleukin 33, DVS27, NF-HEV, IL1F11)], monoclonal antibody; gamma1 heavy chain (1-456) [VH (*Homo sapiens* IGHV3-23*01 (93.9%) -(IGHD) -IGHJ4*01 (85.7%) L123>M (121)) CDR-IMGT [8.8.19] (26-33.51-58.97-115) (1-126) -*Homo sapiens* IGHG1*03 (100%) G1m3, nG1m1 (CH1 R120 (223) (127-224), hinge 1-15 (225-239), CH2 (240-349), CH3 E12 (365), M14 (367) (350-454), CHS (455-456)) (127-456)], (229-211')-disulfide with lambda2 light chain (1'-212') [V-LAMBDA (*Homo sapiens* IGLV3-1*01 (86.2%) -IGLJ2*01 (100%)) CDR-IMGT [6.3.9] (26-31.49-51.88-96) (1'-106') -*Homo sapiens* IGLC2*01 (100%) (107'-212')]; dimer (235-235'':238-238'')-bisdisulfide, produced in a Chinese hamster ovary (CHO) cell line derived from CHO-K1, glycoform alfa
tozorakimab	immunoglobuline G1-lambda2, anti-[*Homo sapiens* IL33 (interleukine 33, DVS27, NF-HEV, IL1F11)], anticorps monoclonal; chaîne lourde gamma1 (1-456) [VH (*Homo sapiens* IGHV3-23*01 (93.9%) -(IGHD) -IGHJ4*01 (85.7%) L123>M (121)) CDR-IMGT [8.8.19] (26-33.51-58.97-115) (1-126) -*Homo sapiens* IGHG1*03 (100%) G1m3, nG1m1 (CH1 R120 (223) (127-224), charnière 1-15 (225-239), CH2 (240-349), CH3 E12 (365), M14 (367) (350-454), CHS (455-456)) (127-456)], (229-211')-disulfure avec la chaîne légère lambda2 (1'-212') [V-LAMBDA (*Homo sapiens* IGLV3-1*01 (86.2%) -IGLJ2*01 (100%)) CDR-IMGT [6.3.9] (26-31.49-51.88-96) (1'-106') -*Homo sapiens* IGLC2*01 (100%) (107'-212')]; dimère (235-235'':238-238'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO) dérivant de la lignée cellulaire CHO-K1, glycoforme alfa
tozorakimab	inmunoglobulina G1-lambda2, anti-[*Homo sapiens* IL33 (interleukina 33, DVS27, NF-HEV, IL1F11)], anticuerpo monoclonal; cadena pesada gamma1 (1-456) [VH (*Homo sapiens* IGHV3-23*01 (93.9%) -(IGHD) -IGHJ4*01 (85.7%) L123>M (121)) CDR-IMGT [8.8.19] (26-33.51-58.97-115) (1-126) -*Homo sapiens* IGHG1*03 (100%) G1m3, nG1m1 (CH1 R120 (223) (127-224), bisagra 1-15 (225-239), CH2 (240-349), CH3 E12 (365), M14 (367) (350-454), CHS (455-456)) (127-456)], (229-211')-disulfuro con la cadena ligera lambda2 (1'-212') [V-LAMBDA (*Homo sapiens* IGLV3-1*01 (86.2%) -IGLJ2*01 (100%)) CDR-IMGT [6.3.9] (26-31.49-51.88-96) (1'-106') -*Homo sapiens* IGLC2*01 (100%) (107'-212')]; dímero (235-235'':238-238'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular derivada de CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLLESGGG LVQPGGSLRL SCAASGFTFS SYAMSWVRQA PGKGLEWVSG  50
ISAIDQSTYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARQK 100
FMQLWGGGLR YPFGYWGQGT MVTVSSASTK GPSVFPLAPS SKSTSGGTAA 150
LGCLVKDYFP EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVVTVPSS 200
SLGTQTYICN VNHKPSNTKV DKRVEPKSCD KTHTCPPCPA PELLGGPSVF 250
LFPPKPKDTL MISRTPEVTC VVVDVSHEDP EVKFNWYVDG VEVHNAKTKP 300
REEQYNSTYR VVSVLTVLHQ DWLNGKEYKC KVSNKALPAP IEKTISKAKG 350
QPREPQVYTL PPSREEMTKN QVSLTCLVKG FYPSDIAVEW ESNGQPENNY 400
KTTPPVLDSD GSFFLYSKLT VDKSRWQQGN VFSCSVMHEA LHNHYTQKSL 450
SLSPGK                                                 456
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Light chain / Chaîne légère / Cadena ligera

```
SYVLTQPPSV SVSPGQTASI TCSGEGMGDK YAAWYQQKPG QSPVLVIYRD  50
TKRPSGIPER FSGSNSGNTA TLTISGTQAM DEADYYCGVI QDNTGVFGGG 100
TKLTVLGQPK AAPSVTLFPP SSEELQANKA TLVCLISDFY PGAVTVAWKA 150
DSSPVKAGVE TTTPSKQSNN KYAASSYLSL TPEQWKSHRS YSCQVTHEGS 200
TVEKTVAPTE CS                                          212
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Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 153-209 270-330 376-434
22"-96" 153"-209" 270"-330" 376"-434"
Intra-L (C23-C104) 22'-87' 134'-193'
22'"-87'" 134'"-193'"
Inter-H-L (h 5-CL 126) 229-211' 229"-211'"
Inter-H-H (h 11, h 14) 235-235" 238-238"

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

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2:
456, 456"

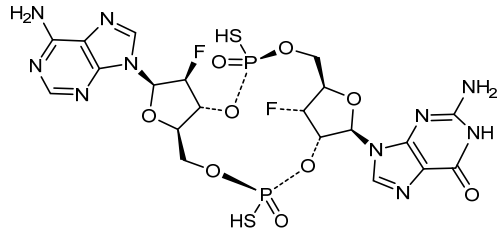
ulevostinagum

ulevostinag — cyclo[(*P*$^{3'}$*R*,2'*S*)-2'-deoxy-2'-fluoro-*P*-thioadenylyl-(3'→5')-(*P*$^{2'}$*R*)-3'-deoxy-3'-fluoro-*P*-thioguanylyl-(2'→5')]

ulévostinag — cyclo[(*P*$^{3'}$*R*,2'*S*)-2'-désoxy-2'-fluoro-*P*-thioadénylyl-(3'→5')-(*P*$^{2'}$*R*)-3'-désoxy-3'-fluoro-*P*-thioguanylyl-(2'→5')]

ulevostinag — cyclo[(*P*$^{3'}$*R*,2'*S*)-2'-désoxy-2'-fluoro-*P*-thioadénylyl-(3'→5')-(*P*$^{2'}$*R*)-3'-désoxy-3'-fluoro-*P*-thioguanylyl-(2'→5')]

$C_{20}H_{22}F_2N_{10}O_9P_2S_2$



uliledlimabum #

uliledlimab — immunoglobulin G1-kappa, anti-[*Homo sapiens* NT5E (5'-nucleotidase ecto, 5' nucleotidase, NT5, eN, eNT NTE, CALJA, CD73)], monoclonal antibody;

	gamma1 heavy chain (1-450) [VH (*Homo sapiens* IGHV4-38-2*01 (87.6%) -(IGHD) -IGHJ6*01 (100%)) CDR-IMGT [9.7.13] (26-34.52-58.97-109) (1-120) - *Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R>K 120 (217) (121-218), hinge 1-15 (219-233), CH2 N84.4>A (300) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS(449-450)) (121-450)], (223-213')-disulfide with kappa light chain (1'-215') [V-KAPPA (*Mus musculus* IGKV4-72*01 (81.1%) -IGKJ1*01 (90.9%) L124>V (103)/*Homo sapiens* IGKV3-11*01 (77.9%) -IGKJ4*01 (100%)) CDR-IMGT [5.3.9] (26-31.59-51.88-96) (1'-106') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (152), V101 (190) (107'-213')]; dimer (229-229'':232-232'')-bisdisulfide, produced in a Chinese hamster ovary (CHO)-K1 cell line, non-glycosylated
ulilédlimab	immunoglobuline G1-kappa, anti-[*Homo sapiens* NT5E (5' ecto nucléotidase, 5' nucléotidase, NT5, eN, eNT NTE, CALJA, CD73)], anticorps monoclonal; chaîne lourde gamma1 (1-450) [VH (*Homo sapiens* IGHV4-38-2*01 (87.6%) -(IGHD) -IGHJ6*01 (100%)) CDR-IMGT [9.7.13] (26-34.52-58.97-109) (1-120) - *Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R>K 120 (217) (121-218), charnière 1-15 (219-233), CH2 N84.4>A (300) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS(449-450)) (121-450)], (223-213')-disulfure avec la chaîne légère kappa (1'-215') [V-KAPPA (*Mus musculus* IGKV4-72*01 (81.1%) -IGKJ1*01 (90.9%) L124>V (103)/*Homo sapiens* IGKV3-11*01 (77.9%) -IGKJ4*01 (100%)) CDR-IMGT [5.3.9] (26-31.59-51.88-96) (1'-106') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (152), V101 (190) (107'-213')]; dimère (229-229'':232-232'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO) lignée cellulaire CHO-K1, non-glycosylé
ulileđlimab	inmunoglobulina G1-kappa, anti-[*Homo sapiens* NT5E (5' ecto nucleotidasa, 5' nucleotidasa, NT5, eN, eNT NTE, CALJA, CD73)], anticuerpo monoclonal; cadena pesada gamma1 (1-450) [VH (*Homo sapiens* IGHV4-38-2*01 (87.6%) -(IGHD) -IGHJ6*01 (100%)) CDR-IMGT [9.7.13] (26-34.52-58.97-109) (1-120) - *Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R>K 120 (217) (121-218), bisagra 1-15 (219-233), CH2 N84.4>A (300) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS(449-450)) (121-450)], (223-213')-disulfuro con la cadena ligera kappa (1'-215') [V-KAPPA (*Mus musculus* IGKV4-72*01 (81.1%) -IGKJ1*01 (90.9%) L124>V (103)/*Homo sapiens* IGKV3-11*01 (77.9%) -IGKJ4*01 (100%)) CDR-IMGT [5.3.9] (26-31.59-51.88-96) (1'-106') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (152), V101 (190) (107'-213')]; dímero (229-229'':232-232'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular CHO-K1, no glicosilado

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLQESGPG LVKPSETLSL TCAVSGYSIT SGYYWNWIRQ PPGKKLEWMG  50
YINYGGSNGY NPSLKSRITI SRDTSKNQFS LKLSSVTAAD TAVYYCARDY 100
DAYYEALDDW GQGTTVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYA 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK 450
```

Light chain / Chaîne légère / Cadena ligera

```
EIVLSQSPAT LSLSPGERAT LSCRASSRVN YMHWYQQKPG QSPRPWISAT  50
SNLASGVPAR FSGSGSGTSY TLTISSLEPE DFAVYYCQQW SSNPPTFGGG 100
TKVEIKRTVA APSVFIFPPS DEQLKSGTAS VVCLLNNFYP REAKVQWKVD 150
NALQSGNSQE SVTEQDSKDS TYSLSSTLTL SKADYEKHKV YACEVTHQGL 200
SSPVTKSFNR GEC                                         213
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 147-203 264-324 370-428
22"-96" 147"-203" 264"-324" 370"-428"
Intra-L (C23-C104) 23'-87' 133'-193'
23'"-87'" 133'"-193'"
Inter-H-L (h 5-CL 126) 223-213' 223"-213'"
Inter-H-H (h 11, h 14) 229-229" 232-232"

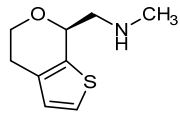
No N-glycosylation sites / pas de sites de N-glycosylation / ningún posición de N-glicosilación
CH2 N84.4>A:
300, 300"
Aglycosylated

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2:
450, 450"

ulotarontum

ulotaront	1-[(7*S*)-4,7-dihydro-5*H*-thieno[2,3-c]pyran-7-yl]-*N*-methylmethanamine
ulotaront	1-[(7*S*)-4,7-dihydro-5*H*-thiéno[2,3-c]pyran-7-yl]-*N*-méthylméthanamine
ulotaront	1-[(7*S*)-4,7-dihidro-5*H*-tieno[2,3-c]piran-7-il]-*N*-metilmetanamina

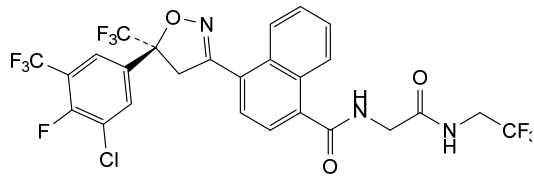
$C_9H_{13}NOS$



umifoxolanerum

umifoxolaner	4-[(5*S*)-5-[3-chloro-4-fluoro-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
umifoxolaner	4-[(5*S*)-5-[3-chloro-4-fluoro-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
umifoxolaner	4-[(5*S*)-5-[3-cloro-4-fluoro-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

$C_{26}H_{16}ClF_{10}N_3O_3$



unasnemabum #

unasnemab	immunoglobulin G1-kappa, anti-[*Homo sapiens* RGMA (repulsive guidance molecule BMP co-receptor a, RGM)], monoclonal antibody; gamma1 heavy chain (1-446) [VH (*Mus musculus* IGHV6-6*01 (87%) -(IGHD) -IGHJ1*01 (90.9%)/*Homo sapiens* IGHV3-49*04 (85%) -(IGHD) -IGHJ6*04 (100%)) CDR-IMGT [8.10.7] (26-33.51-60.99-105) (1-116) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 (CH1 K120 (213) (117-214), hinge 1-15 (215-229), CH2 (230-339), CH3 D12 (355), L14 (357) (340-444), CHS (445-446)) (117-446)], (219-214')-disulfide with kappa light chain (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (87.4%) -IGKJ4*01 (81.8%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (225-225'':228-228'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa
unasnémab	immunoglobuline G1-kappa, anti-[*Homo sapiens* RGMA (co-recepteur BMP de la molécule d'orientation répulsive a, RGM)], anticorps monoclonal; chaîne lourde gamma1 (1-446) [VH (*Mus musculus* IGHV6-6*01 (87%) -(IGHD) -IGHJ1*01 (90.9%)/*Homo sapiens* IGHV3-49*04 (85%) -(IGHD) -IGHJ6*04 (100%)) CDR-IMGT [8.10.7] (26-33.51-60.99-105) (1-116) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 (CH1 K120 (213) (117-214), charnière 1-15 (215-229), CH2 (230-339), CH3 D12 (355), L14 (357) (340-444), CHS (445-446)) (117-446)], (219-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (87.4%) -IGKJ4*01 (81.8%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (225-225'':228-228'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa
unasnemab	inmunoglobulina G1-kappa, anti-[*Homo sapiens* RGMA (co-réceptor BMP de la molécula de orientación repulsiva a, RGM)], anticuerpo monoclonal;

cadena pesada gamma1 (1-446) [VH (*Mus musculus* IGHV6-6*01 (87%) -(IGHD) -IGHJ1*01 (90.9%)/*Homo sapiens* IGHV3-49*04 (85%) -(IGHD) -IGHJ6*04 (100%)) CDR-IMGT [8.10.7] (26-33.51-60.99-105) (1-116) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 (CH1 K120 (213) (117-214), bisagra 1-15 (215-229), CH2 (230-339), CH3 D12 (355), L14 (357) (340-444), CHS (445-446)) (117-446)], (219-214')-disulfuro con la cadena ligera kappa (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (87.4%) -IGKJ4*01 (81.8%)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (225-225":228-228")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGRSLRL SCTASGFTFS DAWMDWVRQA PGKGLEWVAE  50
IRSKANNHAT YYAESVKGRF TISRDDSKSI VYLQMNSLRT EDTALYYCTR 100
RDGAYWGKGT TVTVSSASTK 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 VSASVGDRVT ITCRASQDIS SYLNWYQQKP GKAPKLLIYY  50
TSRLHSGVPS RFSGSGSGTD FTLTISSLQP EDFASYFCQQ LNTLPWTFGG 100
GTKVEMERTV 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) 22-98 143-199 260-320 366-424
22"-98" 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.

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2:
446, 446"

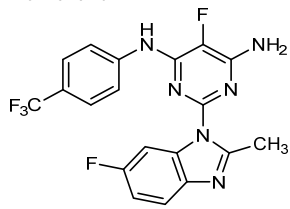
unesbulinum

unesbulin — 5-fluoro-2-(6-fluoro-2-methyl-1*H*-benzimidazol-1-yl)-N^4-[4-(trifluoromethyl)phenyl]pyrimidine-4,6-diamine

unesbuline — 5-fluoro-2-(6-fluoro-2-méthyl-1*H*-benzimidazol-1-yl)-N^4-[4-(trifluorométhyl)phényl]pyrimidine-4,6-diamine

unesbulina — 5-fluoro-2-(6-fluoro-2-metil-1*H*-benzimidazol-1-il)-N^4-[4-(trifluorometil)fenil]pirimidina-4,6-diamina

$C_{19}H_{13}F_5N_6$



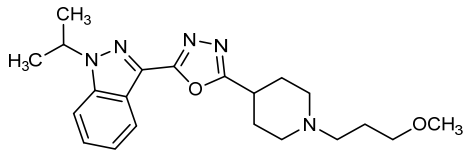
usmarapridum

usmarapride — 3-{5-[1-(3-methoxypropyl)piperidin-4-yl]-1,3,4-oxadiazol-2-yl}-1-(propan-2-yl)-1*H*-indazole

usmarapride — 3-{5-[1-(3-méthoxypropyl)pipéridin-4-yl]-1,3,4-oxadiazol-2-yl}-1-(propan-2-yl)-1*H*-indazole

usmaraprida — 3-{5-[1-(3-metoxipropil)piperidin-4-il]-1,3,4-oxadiazol-2-il}-1-(propan-2-il)-1*H*-indazol

$C_{21}H_{29}N_5O_2$



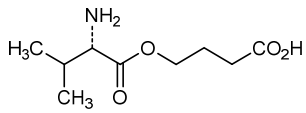
valiloxybatum

valiloxybate — 4-{[(2*S*)-2-amino-3-methylbutanoyl]oxy}butanoic acid, 4-(L-valyloxy)butanoic acid

valiloxybate — acide 4-{[(2*S*)-2-amino-3-méthylbutanoyl]oxy}butanoïque, acide 4-(L-valyloxy)butanoïque

valiloxibato — ácido 4-{[(2*S*)-2-amino-3-metilbutanoil]oxi}butanoico, ácido 4-(L-valiloxi)butanoico

$C_9H_{17}NO_4$



vanglusagenum ensiparvovecum #

vanglusagene ensiparvovec — A recombinant liver-directed adeno-associated virus vector expressing human acid alpha-glucosidase (GAA).
A recombinant liver-directed adeno-associated virus serotype rh74 (AAVrh74) vector that contains a bio-engineered capsid derived from AAVrh74 by four amino-acid substitutions and a codon-optimized transgene expression cassette to drive hepatic synthesis and secretion of the lysosomal enzyme human acid alpha-glucosidase (GAA, α-1,4-glucosidase, acid maltase) via an apolipoprotein E hepatic control region 1 (ApoE HCR1) enhancer/human alpha 1-antitrypsin (hAAT) promoter, a modified human beta-globin intron 2 (HBB2) and a bovine growth hormone (bGH) polyA signal sequence, flanked by adeno-associated virus 2 (AAV2) inverted terminal repeats (ITRs).

vanglusagène ensiparvovec — Un vecteur viral adéno-associé recombinant ciblant le foie exprimant l'alpha-glucosidase acide (GAA) humaine.

Un vecteur viral adéno-associé de sérotype rh74 recombinant (AAVrh74) ciblant le foie qui contient une capside issue de la bio-ingénierie dérivée du AAVrh74 par quatre substitutions d'acides aminés et une cassette d'expression d'un transgène aux codons optimisés pour induire la synthèse hépatique et la sécrétion de l'alpha-glucosidase acide (GAA, α-1,4-glucosidase, maltase acide) enzyme humaine des lysosomes via un activateur de la région 1 de contrôle hépatique de l'apolipoprotéine E (ApoE HCR1)/promoteur de l'alpha 1-antitrypsine humaine (hAAT), un intron 2 modifié de la bêta-globine humaine (HBB2) et une séquence signal polyA de l'hormone de croissance bovine (bGH), flanquée de répétitions terminales inversées (ITRs) du virus adéno-associé 2 (AAV2).

vanglusagén ensiparvovec

Un vector de virus adeno-asociado recombinante dirigido al hígado que expresa la alfa-glucosidasa ácida (GAA) humana.
Un vector de virus adeno-asociado serotipo rh74 (AAVrh74) recombinante dirigido al hígado que contiene una cápside bioingenierizada derivada de AAVrh74 mediante substituciones de cuatro aminoácidos y un casete de expresión con codones optimizados para dirigir la síntesis hepática y la secreción de la enzima lisosomal alfa-glucosidasa ácida humana (GAA, α-1,4-glucosidasa, maltasa ácida) mediante un potenciador de la región de control hepática 1 de la apolipoproteína E (ApoE HCR1)/promotor de alfa 1-antitripsina humana (hAAT), un intrón 2 modificado de la beta-globina humana (HBB2) y una secuencia señal polyA de la hormona de crecimiento bovina (bGH), flanqueado por las repeticiones terminales invertidas (ITRs) del virus adeno-asociado 2 (AAV2).

varoglutamstatum

varoglutamstat

(5*S*)-1-(1*H*-benzimidazol-5-yl)-5-(4-propoxyphenyl)imidazolidin-2-one

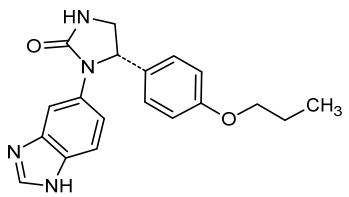
varoglutamstat

(5*S*)-1-(1*H*-benzimidazol-5-yl)-5-(4-propoxyphényl)imidazolidin-2-one

varoglutamstat

(5*S*)-1-(1*H*-benzimidazol-5-il)-5-(4-propoxifenil)imidazolidin-2-ona

$C_{19}H_{20}N_4O_2$



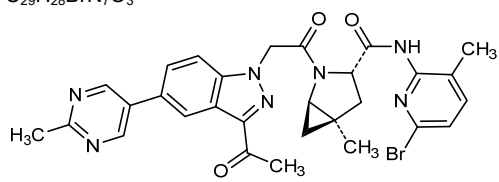
vemircopanum

vemircopan — (1*R*,3*S*,5*R*)-2-{[3-acetyl-5-(2-methylpyrimidin-5-yl)-1*H*-indazol-1-yl]acetyl}-*N*-(6-bromo-3-methylpyridin-2-yl)-5-methyl-2-azabicyclo[3.1.0]hexane-3-carboxamide

vémircopan — (1*R*,3*S*,5*R*)-2-{[3-acétyl-5-(2-méthylpyrimidin-5-yl)-1*H*-indazol-1-yl]acétyl}-*N*-(6-bromo-3-méthylpyridin-2-yl)-5-méthyl-2-azabicyclo[3.1.0]hexane-3-carboxamide

vemircopán — (1*R*,3*S*,5*R*)-2-{[3-acetil-5-(2-metilpirimidin-5-il)-1*H*-indazol-1-il]acetil}-*N*-(6-bromo-3-metilpiridin-2-il)-5-metil-2-azabiciclo[3.1.0]hexano-3-carboxamida

$C_{29}H_{28}BrN_7O_3$



vixtimotamabum #

vixtimotamab — immunoglobulin V-kappa-VH-V-lambda-VH' chain homodimer, anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)] and anti-[*Homo sapiens* CD33 (sialic acid binding Ig-like lectin 3, SIGLEC3, SIGLEC-3, gp67, p67)], monoclonal antibody V-kappa-VH-V-lambda-VH' chain noncovalent homodimer, bispecific, tetravalent; IG V-kappa-VH-V-lambda-VH' chain anti-CD3E and anti-CD33 (1-483) [anti-CD3E V-KAPPA (*Homo sapiens* IGKV1-17*01 (72.5%) -IGKJ1*01 (91.7%)) CDR-IMGT [9.3.9] (27-35.53-55.92-100) (1-110)] -6-mer bis(diglycyl-seryl) linker (111-116) -anti-CD33 VH (*Homo sapiens* IGHV1-8*01 (94.9%) -(IGHD) -IGHJ1*01 (100%)) CDR-IMGT [8.8.15] (142-149.167-174.213-227) (117-238) -4-mer diglycyl-seryl-glycyl linker (239-242) -anti-CD33 V-LAMBDA (*Homo sapiens* IGLV1-44*01 (95.9%) -IGLJ3*01 (86.7%)) CDR-IMGT [8.3.11] (268-275.293-295.332-342) (243-352)] -6-mer bis(diglycyl-seryl) linker (353-358) -anti-CD3E VH (*Mus musculus* IGHV10-1*02 (89.8%) -(IGHD) -IGHJ3*01 (86.7%)/*Homo sapiens* IGHV3-72*01 (88.0%) -(IGHD) -IGHJ4*01 (93.3%)) CDR-IMGT [8.10.16] (384-391.409-418.457-472) (359-483)]; noncovalent homodimer, produced in a Chinese hamster ovary (CHO)-derived cell line transfected with the glutamine synthetase (GS) gene, non-glycosylated

vixtimotamab — immunoglobuline chaîne V-kappa-VH-V-lambda-VH' homodimère, anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)] et anti-[*Homo sapiens* CD33 (lectine 3 de type Ig-like liant l'acide sialique, SIGLEC3, SIGLEC-3, gp67, p67)], anticorps monoclonal chaîne V-kappa-VH-V-lambda-VH' homodimère non-covalent, bispécifique, tétravalent;

IG chaîne V-kappa-VH-V-lambda-VH' anti-CD3E et anti-CD33 (1-483) [anti-CD3E V-KAPPA (*Homo sapiens* IGKV1-17*01 (72.5%) -IGKJ1*01 (91.7%)) CDR-IMGT [9.3.9] (27-35.53-55.92-100) (1-110)] -6-mer bis(diglycyl-séryl) linker (111-116) - anti-CD33 VH (*Homo sapiens* IGHV1-8*01 (94.9%) -(IGHD) - IGHJ1*01 (100%)) CDR-IMGT [8.8.15] (142-149.167-174.213-227) (117-238) -4-mer diglycyl-séryl-glycyl linker (239-242) - anti-CD33 V-LAMBDA (*Homo sapiens* IGLV1-44*01 (95.9%) - IGLJ3*01 (86.7%)) CDR-IMGT [8.3.11] (268-275.293-295.332-342) (243-352)] -6-mer bis(diglycyl-séryl) linker (353-358) - anti-CD3E VH (*Mus musculus* IGHV10-1*02 (89.8%) -(IGHD) - IGHJ3*01 (86.7%)/*Homo sapiens* IGHV3-72*01 (88.0%) - (IGHD) -IGHJ4*01 (93.3%)) CDR-IMGT [8.10.16] (384-391.409-418.457-472) (359-483)]; homodimère non-covalent, produite dans une lignée cellulaire dérivée des cellules ovariennes de hamster chinois (CHO) transfectée avec le gène de la glutamine synthétase (GS), non-glycosylé

vixtimotamab

inmunoglobulina cadena V-kappa-VH-V-lambda-VH' homodímero, anti-[*Homo sapiens* CD3E (CD3 épsilon, Leu-4)] y anti-[*Homo sapiens* CD33 (lectina 3 de tipo Ig-like de unión al ácido siálico, SIGLEC3, SIGLEC-3, gp67, p67)], anticuerpo monoclonal cadena V-kappa-VH-V-lambda-VH' homodímero no covalente, biespecífica, tetravalente;
IG cadena V-kappa-VH-V-lambda-VH' anti-CD3E y anti-CD33 (1-483) [anti-CD3E V-KAPPA (*Homo sapiens* IGKV1-17*01 (72.5%) -IGKJ1*01 (91.7%)) CDR-IMGT [9.3.9] (27-35.53-55.92-100) (1-110)] -6-mer bis(diglicil-seril) linker (111-116) - anti-CD33 VH (*Homo sapiens* IGHV1-8*01 (94.9%) -(IGHD) - IGHJ1*01 (100%)) CDR-IMGT [8.8.15] (142-149.167-174.213-227) (117-238) -4-mer diglicil-seril-glicil linker (239-242) -anti-CD33 V-LAMBDA (*Homo sapiens* IGLV1-44*01 (95.9%) - IGLJ3*01 (86.7%)) CDR-IMGT [8.3.11] (268-275.293-295.332-342) (243-352)] -6-mer bis(diglicil-seril) linker (353-358) -anti-CD3E VH (*Mus musculus* IGHV10-1*02 (89.8%) -(IGHD) - IGHJ3*01 (86.7%)/*Homo sapiens* IGHV3-72*01 (88.0%) - (IGHD) -IGHJ4*01 (93.3%)) CDR-IMGT [8.10.16] (384-391.409-418.457-472) (359-483)]; homodímero no covalente, producido en una línea celular derivada de las células ováricas de hámster chino (CHO) transfectada con el gen de la glutamina sintetasa (GS), no glicosilado

Chain / Chaîne / Cadena

```
DIQMTQSPSS LSASVGDRVT ITCRSSTGAV TTSNYANWVQ QKPGKAPKAL  50
IGGTNKRAPG VPSRFSGSLI GDKATLTISS LQPEDFATYY CALWYSNLWV 100
FGQGTKVEIK GGSGGSQVQL VQSGAEVKKP GASVKVSCKA SGYTFTSYDI 150
NWVRQAPGQG LEWMGWMNPN SGNTGFAQKF QGRVTMTRDT STSTVYMELS 200
SLRSEDTAVY YCARDRANTD YSLGMDVWGQ GTLVTVSSGG SGQSVLTQPP 250
SASGTPGQRV TISCSGSRSN IGSNTVNWYQ QLPGTAPKLL IYGNNQRPSG 300
VPDRFSGSKS GTSASLAISG LQSEDEADYY CATWDDSLIG WVFGGGTKLT 350
VLGGSGGSEV QLVESGGGLV QPGGSLRLSC AASGFTFSTY AMNWVRQAPG 400
KGLEWVGRIR SKYNNYATYY ADSVKDRFTI SRDDSKNSLY LQMNSLKTED 450
TAVYYCARHG NFGNSYVSYF AYWGQGTLVT VSS                   483
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-chain (C23-C104) 23-91 138-212 264-331 380-456

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

voxeralgagenum autotemcelum #

voxeralgagene autotemcel	Autologous CD34+ hematopoietic stem cells (HSCs) transduced *ex vivo* with a self-inactivating lentiviral vector encoding human alpha-galactosidase A (GLA). Autologous CD34+ hematopoietic stem cells (HSCs) obtained by apheresis, transduced with a non-replicating, self-inactivating lentiviral vector encoding codon-optimized human alpha-galactosidase A (GLA) under the control of the human elongation factor 1 alpha short (EFS-1 alpha) promoter and a modified woodchuck hepatitis virus posttranscriptional regulatory element (WPRE). The vector genome also contains a packaging signal, a partial *gag* sequence, a Rev response element (RRE), a central polypurine tract (cPPT) and a Kozak sequence.
voxéralgagène autotemcel	Cellules souches hématopoïétiques autologues CD34+ (HSCs) transduites *ex vivo* avec un vecteur lentiviral auto-inactivant codant pour la galactosidase-alpha A (GLA). Les cellules souches hématopoïétiques autologues CD34+ (HSCs) obtenues par aphérèse, transduites avec un vecteur lentiviral non-répliquant, auto-inactivant codant pour une galactosidase-alpha A humaine aux codons optimisés (GLA) sous le contrôle du promoteur humain du facteur d'élongation 1 alpha court (EFS-1 alpha) et un élément de régulation post-transcriptionnelle du virus de l'hépatite de la marmotte (WPRE). Le génome du vecteur contient aussi un signal de compaction, une séquence partielle *gag*, un élément de réponse Rev (RRE), un tractus central de polypurine (cPPT) et une séquence Kozak.
voxeralgagén autotemcel	Células madre hematopoyéticas (HSC) CD34+ autólogas transducidas *ex vivo* con un vector lentiviral auto inactivante que codifica para la galactosidasa alfa A (GLA) humana. Células madre hematopoyéticas (HSC) CD34+ autólogas obtenidas por aféresis, transducidas con un vector lentiviral no replicativo y auto inactivante que codifica para la galactosidasa alfa A (GLA) humana, con codones optimizados, bajo el control del promotor del factor de elongación corto 1 alfa (EFS-1 alfa) humano y un elemento regulador post-transcripcional del virus de la hepatitis de la marmota (WPRE) modificado. El genoma del vector también contiene una señal empaquetadora, una secuencia *gag* parcial, un elemento de respuesta Rev (RRE), un segmento central de polipurinas (cPPT) y una secuencia Kozak.

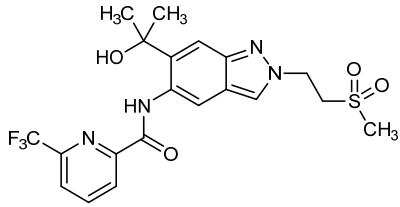
zabedosertibum

zabedosertib	*N*-{6-(2-hydroxypropan-2-yl)-2-[2-(methanesulfonyl)ethyl]-2*H*-indazol-5-yl}-6-(trifluoromethyl)pyridine-2-carboxamide
zabédosertib	*N*-{6-(2-hydroxypropan-2-yl)-2-[2-(méthanesulfonyl)éthyl]-2*H*-indazol-5-yl}-6-(trifluorométhyl)pyridine-2-carboxamide

zabedosertib

N-{6-(2-hidroxipropan-2-il)-2-[2-(metanosulfonil)etil]-2*H*-indazol-5-il}-6-(trifluorometil)piridina-2-carboxamida

$C_{20}H_{21}F_3N_4O_4S$



zaloglanstatum

zaloglanstat

N-[(4-chloro-3-{5-oxo-1-[4-(trifluoromethyl)phenyl]-2,5-dihydro-1*H*-1,2,4-triazol-3-yl}phenyl)methyl]-2,2-dimethylpropanamide

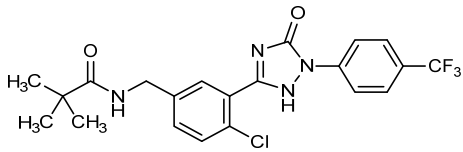
zaloglanstat

N-[(4-chloro-3-{5-oxo-1-[4-(trifluorométhyl)phényl]-2,5-dihydro-1*H*-1,2,4-triazol-3-yl}phényl)méthyl]-2,2-diméthylpropanamide

zaloglanstat

N-[(4-cloro-3-{5-oxo-1-[4-(trifluorometil)fenil]-2,5-dihidro-1*H*-1,2,4-triazol-3-il}fenil)metil]-2,2-dimetilpropanamida

$C_{21}H_{20}ClF_3N_4O_2$



zamtocabtagenum autoleucelum

zamtocabtagene autoleucel

Autologous T cells obtained from peripheral blood collected by leukapheresis, transduced with a non-replicating lentiviral vector, pseudotyped with vesicular stomatitis virus (VSV) glycoprotein (G), encoding a codon-optimized chimeric antigen receptor (CAR) targeting the human B-lymphocyte antigens CD19 and CD20. Cells are activated in the presence of a colloidal polymeric nanomatrix covalently attached to anti-CD3 and anti-CD28, transduced, and then cultured in the presence of IL-7 and IL-15. The T cells are predominantly central memory (>80%; CD4+/CD8+, CD62L+, CD45RO+) and effector memory T cells (CD4+/CD8+, CD62L-, CD45RO+). The target binding moieties of the CAR are two single-chain variable fragments (scFv), derived from a murine anti-human CD20 and a murine anti-human CD19 hybridoma clone linked with a $(GGGGS)_5$ sequence, fused to intracellular signalling domains from 4-1BB and CD3 zeta, under the control of the elongation factor 1 alpha (EF1α) promoter. The genome also contains a 5' splice donor site and a 3' splice acceptor site, a *gag* truncated open reading

	frame, an *env* truncated open reading frame, a Rev response element (RRE) 5' to the transgene, a non-coding artificial sequence for viral titre determination and a *nef* truncated open reading frame 3' to the transgene.
zamtocabtagène autoleucel	Lymphocytes T autologues du sang périphérique recueillis par leucophérèse, transduits avec un vecteur lentiviral non-répliquant, pseudotypés avec une glycoprotéine (G) du virus de la stomatite vésiculaire (VSV), codant un récepteur antigénique chimérique (CAR) aux codons optimisés ciblant les antigènes CD19 et CD20 du lymphocyte B humain. Les cellules sont activées en présence d'une nanomatrice polymérique colloïdale attachée de manière covalente à l'anti-CD3 et l'anti-CD28, transduites, et ensuite cultivées en présence d'IL-7 and IL-15. Les cellules sont majoritairement des lymphocytes T à mémoire centrale (>80%; CD4+/CD8+, CD62L+, CD45RO+) et à mémoire effectrice (CD4+/CD8+, CD62L-, CD45RO+). Les moitiés liées aux cibles du CAR sont deux fragments variables à chaîne simple (scFv), dérivées des clones murins antihumains d'hybridome CD19 et CD20 liés à la séquence $(GGGGS)_5$, fusionnées aux domaines de signalisation intracellulaire des zêta 4-1BB et CD3, sous le contrôle du promoteur du facteur 1 alpha d'élongation (EF1α). Le génome contient aussi un site d'épissage donneur en 5' et un site d'épissage accepteur en 3', un cadre de lecture ouvert *gag* tronqué, un cadre de lecture ouvert *env* tronqué, un élément de réponse Rev (RRE) dans la partie 5' du transgène, une séquence artificielle non-codante pour la détermination de la titration virale et un cadre de lecture *nef* tronqué dans la partie 3' du transgène.
zamtocabtagén autoleucel	Linfocitos T autólogos obtenidos de sangre periférica recogidos por leucoaféresis, transducidos con un vector lentiviral no replicativo, seudotipado con la glicoproteína (G) del virus de la estomatitis vesicular (VSV), que codifica, con codones optimizados, para un receptor de antígenos quimérico (CAR) dirigido a los antígenos CD19 y CD20 de los linfocitos B humanos. Las células se activan en presencia de una nanomatriz coloidal polimérica anclada covalentemente a anti-CD3 y anti-CD28, transducidas, y luego se cultivan en presencia de IL-7 e IL-15. Los linfocitos T son predominantemente de memoria central (>80%; CD4+/CD8+, CD62L+, CD45RO+) y memoria efectora (CD4+/CD8+, CD62L-, CD45RO+). Las fracciones de unión a la diana del CAR son dos fragmentos de cadena variable sencilla (scFv), derivados de un clon de hibridoma murino anti-CD20 humano y anti-CD19 humano ligados con una secuencia $(GGGGS)_5$, fusionada a los dominios de señalización intracelulares de 4-1BB y CD3 zeta, bajo el control del promotor del factor de elongación 1 alfa (EF1α). El genoma también contiene un sitio 5' donante del procesamiento y un sitio 3' aceptor del procesamiento, un marco de lectura abierto truncado *gag*, un marco de lectura abierto truncado *env*, un elemento de respuesta Rev (RRE) en 5' con respecto al transgén, una secuencia no codificante artificial para la determinación del título viral y un marco de lectura abierto truncado *nef* en 3' con respecto al transgén.

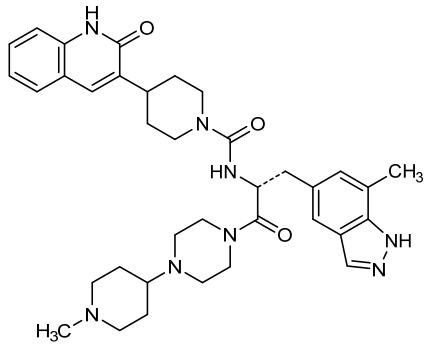
zavegepantum

zavegepant — *N*-{(2*R*)-3-(7-methyl-1*H*-indazol-5-yl)-1-[4-(1-methylpiperidin-4-yl)piperazin-1-yl]-1-oxopropan-2-yl}-4-(2-oxo-1,2-dihydroquinolin-3-yl)piperidine-1-carboxamide

zavégépant — *N*-{(2*R*)-3-(7-méthyl-1*H*-indazol-5-yl)-1-[4-(1-méthylpipéridin-4-yl)pipérazin-1-yl]-1-oxopropan-2-yl}-4-(2-oxo-1,2-dihydroquinoléin-3-yl)pipéridine-1-carboxamide

zavegepant — *N*-{(2*R*)-3-(7-metil-1*H*-indazol-5-il)-1-[4-(1-metilpiperidin-4-il)piperazin-1-il]-1-oxopropan-2-il}-4-(2-oxo-1,2-dihidroquinolein-3-il)piperidina-1-carboxamida

$C_{36}H_{46}N_8O_3$



zeluvalimabum #

zeluvalimab — immunoglobulin G1-kappa, anti-[*Homo sapiens* PDCD1 (programmed cell death 1, PD-1, PD1, CD279)], monoclonal antibody;
gamma1 heavy chain (1-450) [VH (*Homo sapiens* IGHV3-23*03 (92.8%) -(IGHD) -IGHJ3*01 (92.3%)) CDR-IMGT [8.8.13] (26-33.50-58.97-109) (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (217) (121-218), hinge 1-15 (219-233), CH2 R83>C (295), N84.4>G (300), V85>C (305) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfide with kappa light chain (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (96.8%) -IGKJ4*01 (100%)) CDR-IMGT [6.3.9](27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (229-229'':232-232'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, non-glycosylated

zéluvalimab — immunoglobuline G1-kappa, anti-[*Homo sapiens* PDCD1 (protéine 1 de mort cellulaire programmée, PD-1, PD1, CD279)], anticorps monoclonal;

chaîne lourde gamma1 (1-450) [VH (*Homo sapiens* IGHV3-23*03 (92.8%) -(IGHD) -IGHJ3*01 (92.3%)) CDR-IMGT [8.8.13] (26-33.50-58.97-109) (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (217) (121-218), charnière 1-15 (219-233), CH2 R83>C (295), N84.4>G (300), V85>C (305) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (96.8%) -IGKJ4*01 (100%)) CDR-IMGT [6.3.9](27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (229-229":232-232")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), non-glycosylé

zeluvalimab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* PDCD1 (proteína 1 de muerte celular programada, PD-1, PD1, CD279)], anticuerpo monoclonal; cadena pesada gamma1 (1-450) [VH (*Homo sapiens* IGHV3-23*03 (92.8%) -(IGHD) -IGHJ3*01 (92.3%)) CDR-IMGT [8.8.13] (26-33.50-58.97-109) (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (217) (121-218), bisagra 1-15 (219-233), CH2 R83>C (295), N84.4>G (300), V85>C (305) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfuro con la cadena ligera kappa (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (96.8%) -IGKJ4*01 (100%)) CDR-IMGT [6.3.9](27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (229-229":232-232")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), no glicosilado

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLLESGGG LVQPGGSLRL SCAASGFTFS SYDMSWVRQA PGKGLEWVSL  50
ISGGGSQTYY AESVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYFCASPS 100
GHYFYAMDVW GQGTTVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPCEEQYG 300
STYRCVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK 450
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Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS VSASVGDRVT ITCRASQGIS NWLAWYQQKP GKAPKLLIFA  50
ASSLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ AESFPHTFGG 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

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

Intra-H (C23-C104)	22-96	147-203	264-324	295-305	370-428
	22"-96"	147"-203"	264"-324"	295"-305"	370"-428"
Intra-L (C23-C104)	23'-88'	134'-194'			
	23'"-88'"	134'"-194'"			
Inter-H-L (h 5-CL 126)	223-214'	223"-214'"			
Inter-H-H (h 11, h14)	229-229"	232-232"			

No N-glycosylation sites / pas de sites de N-glycosylation / ningún posición de N-glicosilación
CH2 N84.4>G:
300, 300"
Aglycosylated

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2:
450, 450"

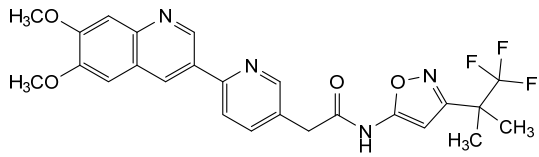
zeteletinibum

zeteletinib — 2-[6-(6,7-dimethoxyquinolin-3-yl)pyridin-3-yl]-*N*-[3-(1,1,1-trifluoro-2-methylpropan-2-yl)-1,2-oxazol-5-yl]acetamide

zételétinib — 2-[6-(6,7-diméthoxyquinoléin-3-yl)pyridin-3-yl]-*N*-[3-(1,1,1-trifluoro-2-méthylpropan-2-yl)-1,2-oxazol-5-yl]acétamide

zeteletinib — 2-[6-(6,7-dimetoxiquinolein-3-il)piridin-3-il]-*N*-[3-(1,1,1-trifluoro-2-metilpropan-2-il)-1,2-oxazol-5-il]acetamida

$C_{25}H_{23}F_3N_4O_4$



zilebesiranum

zilebesiran — [(2*S*,4*R*)-1-{1-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]-16,16-bis({3-[(3-{5-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]pentanamido}propyl)amino]-3-oxopropoxy}methyl)-5,11,18-trioxo-14-oxa-6,10,17-triazanonacosan-29-oyl}-4-hydroxypyrrolidin-2-yl]methyl *all-P-ambo*-2'-*O*-methyl-*P*-thioguanylyl-(3'→5')-2'-*O*-methyl-*P*-thiouridylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-deoxy-2'-fluorocytidylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-deoxy-2'-fluorocytidylyl-(3'→5')-2'-deoxy-2'-fluoroadenylyl-(3'→5')-2'-deoxy-2'-fluoroadenylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyl-3'-adenylate, duplex with *all-P-ambo*-2'-*O*-methyl-*P*-thioadenylyl-(5'→3')-2'-*O*-methyl-*P*-thioguanylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-*O*-methylguanylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-deoxy-2'-fluoroguanylyl-(5'→3')-2'-*O*-methylguanylyl-(5'→3')-2'-deoxy-2'-fluorouridylyl-(5'→3')-2'-*O*-methylguanylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→2')-1-de-β-D-ribofuranosyl-1-[(2*S*)-2,3-dihydroxypropyl]-5-methyluridylyl-(3'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-*O*-methyl-*P*-thiouridylyl-(5'→3')-2'-deoxy-2'-fluoro-*P*-thioguanylyl-(5'→3')-2'-*O*-methyluridine

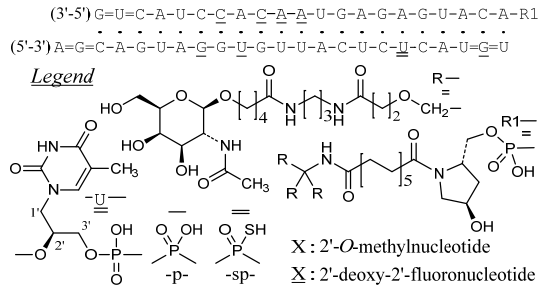
zilébésiran

tout-P-ambo-2'-*O*-méthyl-*P*-thioguanylyl-(3'→5')-2'-*O*-méthyl-*P*-thiouridylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-désoxy-2'-fluorocytidylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-désoxy-2'-fluorocytidylyl-(3'→5')-2'-désoxy-2'-fluoroadénylyl-(3'→5')-2'-désoxy-2'-fluoroadénylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyl-3'-adénylate de [(2*S*,4*R*)-1-{1-[(2-acétamido-2-désoxy-β-D-galactopyranosyl)oxy]-16,16-bis({3-[(3-{5-[(2-acétamido-2-désoxy-β-D-galactopyranosyl)oxy]pentanamido}propyl)amino]-3-oxopropoxy}méthyl)-5,11,18-trioxo-14-oxa-6,10,17-triazanonacosan-29-oyl}-4-hydroxypyrrolidin-2-yl]méthyle, duplex avec *tout-P-ambo*-2'-*O*-méthyl-*P*-thioadénylyl-(5'→3')-2'-*O*-méthyl-*P*-thioguanylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-*O*-méthylguanylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-désoxy-2'-fluoroguanylyl-(5'→3')-2'-*O*-méthylguanylyl-(5'→3')-2'-désoxy-2'-fluorouridylyl-(5'→3')-2'-*O*-méthylguanylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→2')-1-des-β-D-ribofuranosyl-1-[(2*S*)-2,3-dihydroxypropyl]-5-methyluridylyl-(3'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-*O*-méthyl-*P*-thiouridylyl-(5'→3')-2'-désoxy-2'-fluoro-*P*-thioguanylyl-(5'→3')-2'-*O*-méthyluridine

zilebesirán

todo-P-ambo-2'-*O*-metil-*P*-tioguanilil-(3'→5')-2'-*O*-metil-*P*-tiouridilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-desoxi-2'-fluorocitidilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-desoxi-2'-fluorocitidilil-(3'→5')-2'-desoxi-2'-fluoroadenilil-(3'→5')-2'-desoxi-2'-fluoroadenilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metil-3'-adenilato de [(2*S*,4*R*)-1-{1-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]-16,16-bis({3-[(3-{5-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]pentanamido}propil)amino]-3-oxopropoxi}metil)-5,11,18-trioxo-14-oxa-6,10,17-triazanonacosan-29-oil}-4-hidroxipirrolidin-2-il]metilo, dúplex con *todo-P-ambo*-2'-*O*-metil-*P*-tioadenilil-(5'→3')-2'-*O*-metil-*P*-tioguanilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-*O*-metilguanilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-desoxi-2'-fluoroguanilil-(5'→3')-2'-*O*-metilguanilil-(5'→3')-2'-desoxi-2'-fluorouridilil-(5'→3')-2'-*O*-metilguanilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-*O*-metilcitidilil-(5'→2')-1-des-β-D-ribofuranosil-1-[(2*S*)-2,3-dihidroxipropil]-5-metiluridilil-(3'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-*O*-metil-*P*-tiouridilil-(5'→3')-2'-desoxi-2'-fluoro-*P*-tioguanilil-(5'→3')-2'-*O*-metiluridina

$C_{532}H_{721}F_7N_{177}O_{321}P_{43}S_6$



zilovertamabum #

zilovertamab — immunoglobulin G1-kappa, anti-[*Homo sapiens* ROR1 (receptor tyrosine kinase like orphan receptor 1, NTRKR1)], humanized monoclonal antibody; gamma1 heavy chain humanized (1-446) [VH (*Homo sapiens* IGHV2-70*19 (65.0%) -(IGHD) -IGHJ4*01 (93.3%) Q120>H (108)) CDR-IMGT [8.7.10] (26-33.51-57.96-105) (1-116) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 (CH1 K120 (213) (117-214), hinge 1-15 (215-229), CH2 (230-339), CH3 D12 (355), L14 (357) (340-444), CHS (445-446)) (117-446)], (219-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV3D-11*02 (67.8%) -IGKJ4*01 (90.9%) G120>E (100)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (225-225'':228-228'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

zilovertamab — immunoglobuline G1-kappa, anti-[*Homo sapiens* ROR1 (récepteurs orphelins de type récepteur 1 à tyrosine kinase, NTRKR1)], anticorps monoclonal humanisé; chaîne lourde gamma1 humanisée (1-446) [VH (*Homo sapiens* IGHV2-70*19 (65%) -(IGHD) -IGHJ4*01 (93.3%) Q120>H (108)) CDR-IMGT [8.7.10] (26-33.51-57.96-105) (1-116) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 (CH1 K120 (213) (117-214), charnière 1-15 (215-229), CH2 (230-339), CH3 D12 (355), L14 (357) (340-444), CHS (445-446)) (117-446)], (219-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV3D-11*02 (67.8%) -IGKJ4*01 (90.9%) G120>E (100)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (225-225'':228-228'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

zilovertamab — inmunoglobulina G1-kappa, anti-[*Homo sapiens* ROR1 (receptores huérfanos de tipo receptor 1 con tirosina kinasa, NTRKR1)], anticuerpo monoclonal humanizado;

cadena pesada gamma1 humanizada (1-446) [VH (*Homo sapiens* IGHV2-70*19 (65%) -(IGHD) -IGHJ4*01 (93.3%) Q120>H (108)) CDR-IMGT [8.7.10] (26-33.51-57.96-105) (1-116) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 (CH1 K120 (213) (117-214), bisagra 1-15 (215-229), CH2 (230-339), CH3 D12 (355), L14 (357) (340-444), CHS (445-446)) (117-446)], (219-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV3D-11*02 (67.8%) -IGKJ4*01 (90.9%) G120>E (100)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (225-225":228-228")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLQESGPG LVKPSQTLSL TCTVSGYAFT AYNIHWVRQA PGQGLEWMGS  50
FDPYDGGSSY NQKFKDRLTI SKDTSKNQVV LTMTNMDPVD TATYYCARGW 100
YYFDYWGHGT 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

```
DIVMTQTPLS LPVTPGEPAS ISCRASKSIS KYLAWYQQKP GQAPRLLIYS  50
GSTLQSGIPP RFSGSGYGTD FTLTINNIES EDAAYYFCQQ HDESPYTFGE 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) 22-96 143-199 260-320 366-424
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-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
H VH Q1:
1, 1"

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 / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2:
446, 446"

zilovertamabum vedotinum #
zilovertamab vedotin

immunoglobulin G1-kappa, anti-[*Homo sapiens* ROR1 (receptor tyrosine kinase like orphan receptor 1, NTRKR1)], humanized monoclonal antibody conjugated to auristatin E; gamma1 heavy chain humanized (1-446) [VH (*Homo sapiens* IGHV2-70*19 (65.0%) -(IGHD) -IGHJ4*01 (93.3%) Q120>H (108)) CDR-IMGT [8.7.10] (26-33.51-57.96-105) (1-116) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 (CH1 K120 (213) (117-214), hinge 1-15 (215-229), CH2 (230-339), CH3 D12 (355), L14 (357) (340-444), CHS (445-446)) (117-446)], (219-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV3D-11*02 (67.8%) -IGKJ4*01 (90.9%) G120>E (100)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (225-225":228-228")-bisdisulfide, produced in *

	Chinese hamster ovary (CHO) cells, glycoform alfa; conjugated on an average of 4.0 ± 0.5 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"*
zilovertamab védotine	immunoglobuline G1-kappa, anti-[*Homo sapiens* ROR1 (récepteurs orphelins de type récepteur 1 à tyrosine kinase, NTRKR1)], anticorps monoclonal humanisé conjugué à l'auristatine E; chaîne lourde gamma1 humanisée (1-446) [VH (*Homo sapiens* IGHV2-70*19 (65%) -(IGHD) -IGHJ4*01 (93.3%) Q120>H (108)) CDR-IMGT [8.7.10] (26-33.51-57.96-105) (1-116) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 (CH1 K120 (213) (117-214), charnière 1-15 (215-229), CH2 (230-339), CH3 D12 (355), L14 (357) (340-444), CHS (445-446)) (117-446)], (219-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV3D-11*02 (67.8%) -IGKJ4*01 (90.9%) G120>E (100)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (225-225":228-228")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa; conjugué sur 4.0 ± 0.5 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"**
zilovertamab vedotina	inmunoglobulina G1-kappa, anti-[*Homo sapiens* ROR1 (receptores huérfanos de tipo receptor 1 con tirosina kinasa, NTRKR1)], anticuerpo monoclonal humanizado conjugado con la auristatina E; cadena pesada gamma1 humanizada (1-446) [VH (*Homo sapiens* IGHV2-70*19 (65%) -(IGHD) -IGHJ4*01 (93.3%) Q120>H (108)) CDR-IMGT [8.7.10] (26-33.51-57.96-105) (1-116) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 (CH1 K120 (213) (117-214), bisagra 1-15 (215-229), CH2 (230-339), CH3 D12 (355), L14 (357) (340-444), CHS (445-446)) (117-446)], (219-214')-disulfuro con la cadena ligera kappa humanizada 1'-214') [V-KAPPA (*Homo sapiens* IGKV3D-11*02 (67.8%) -IGKJ4*01 (90.9%) G120>E (100)) CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (225-225":228-228")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa; conjugado en 4.0 ± 0.5 restos cisteinil por término medio, con monometilauristatina E (MMAE), mediante un conector escindible de tipo maleimidocaproil-valil-citrulinil-*p*-aminobenziloxicarbonil (mc-val-cit-PABC) *Para la parte vedotina, por favor vaya al documento "INN for pharmaceutical substances: Names for radicals, groups and others"**

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLQESGPG LVKPSQTLSL TCTVSGYAFT AYNIHWVRQA PGQGLEWMGS  50
FDPYDGGSSY NQKFKDRLTI SKDTSKNQVV LTMTNMDPVD TATYYCARGW 100
YYFDYWGHGT 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

```
DIVMTQTPLS LPVTPGEPAS ISCRASKSIS KYLAWYQQKP GQAPRLLIYS  50
GSTLQSGIPP RFSGSGYGTD FTLTINNIES EDAAYYFCQQ HDESPYTFGE 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) 22-96 143-199 260-320 366-424
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"

*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-terminal glutaminyl cyclization to pyroglutamyl (pE, 5-oxoprolyl)
H VH Q1:
1, 1"

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 / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2:
446, 446"

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

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

Recommended International Nonproprietary Names (Rec. INN): List 5
(WHO Chronicle, Vol. 19, No. 4-5-6, 1965)

p.14 **oxymetholonum**
oxymetholone — *replace the chemical name by the following one*
17β-hydroxy-2-(hydroxymethylene)-17α-methyl-5α-androstan-3-one

Dénominations communes internationales recommandées (DCI Rec.): Liste 5
(Chronique OMS, Vol. 19, No 4-5-6, 1965)

p.14 **oxymetholonum**
oxymétholone — *remplacer le nom chimique par le suivant*
17β-hydroxy-2-(hydroxyméthylène)-17α-méthyl-5α-androstan-3-one

Denominaciones Comunes Internacionales Recommendadas (DCI Rec.): Lista 5
(Crónica de la OMS, Vol. 20, No 6, 1966)

p.263 **oxymetholonum**
oximetolona — *sustitúyase el nombre químico por el siguiente*
17β-hidroxi-2-(hidroximetileno)-17α-metil-5α-androstan-3-ona

Recommended International Nonproprietary Names (Rec. INN): List 9
(WHO Chronicle, Vol. 23, No. 10, 1969)

p.491 **androstanolonum**
androstanolone — *replace the chemical name by the following one*
17β-hydroxy-5α-androstan-3-one

Dénominations communes internationales recommandées (DCI Rec.): Liste 9
(Chronique OMS, Vol. 23, No 10, 1969)

p.513 **androstanolonum**
androstanolone — *remplacer le nom chimique par le suivant*
17β-hydroxy-5α-androstan-3-one

Denominaciones Comunes Internacionales Recommendadas (DCI Rec.): Lista 9
(Crónica de la OMS, Vol. 23, No 10, 1969)

p.531 **androstanolonum**
androstanolona — *sustitúyase el nombre químico por el siguiente*
17β-hidroxi-5α-androstan-3-ona

Recommended International Nonproprietary Names (Rec. INN): List 63
Dénominations communes internationales recommandées (DCI Rec.): Liste 63
Denominaciones Comunes Internacionales Recomendadas (DCI Rec.): Lista 63
(WHO Drug Information, Vol. 24, No. 1, 2010)

p.62	*suprimáse*	*insertese*
	iodine (^{124}I) girentuximab	iodo (^{124}I) girentuximab

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

p.123 **tirzepatidum**

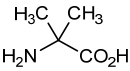
tirzepatide	*replace the structure by the following one*
tirzépatide	*remplacer la structure par la suivante*
tirzepatida	*sustitúyase la estructura por la siguiente*

Sequence / Séquence / Secuencia

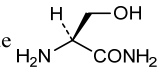
YXEGTFTSDY SIXLDKIAQK AFVQWLIAGG PSSGAPPPS 39

Modified residues / Résidus modifiés / Restos modificados

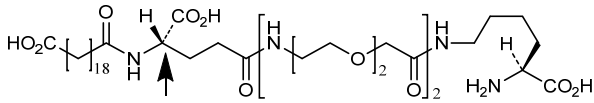
X (2, 13) 2-methylalanine (Aib)



S (39) L-serinamide



K (20): N^6-{*N*-(hydrogen icosanedioyl)-γ-Glu-bis[iminobis(ethylenoxy)acetyl]}-Lysine



Recommended International Nonproprietary Names (Rec. INN): List 83
Dénominations communes internationales recommandées (DCI Rec.): Liste 83
Denominaciones Comunes Internacionales Recomendadas (DCI Rec.): Lista 83
(WHO Drug Information, Vol. 34, No. 1, 2020)

p.34 **betibeglogenum autotemcelum #**

betibeglogene autotemcel	*replace the description by the following one*
bétibéglogène autotemcel	*remplacer la description par la suivante*
betibeglogén autotemcel	*sustitúyase la descripción por la siguiente*

autologous CD34+ hematopoietic stem cells **obtained from mobilised peripheral blood of patients with beta-thalassemia**, transduced *ex vivo* with *betibeglogene darolentivec (116)(78),* a self-inactivating human immunodeficiency virus-1 (HIV-1)-derived lentiviral vector encoding a T87Q-mutated form of the human hemoglobin subunit beta (HBB, beta-globin) gene under the control of a human β-globin promoter and a 3' β-globin enhancer.

cellules souches hématopoïétiques CD34+ autologues **obtenues à partir de sang périphérique mobilisé de patients atteints de bêta-thalassémie,** transduites *ex vivo*

avec le *bétibéglogène darolentivec (116)(78),* vecteur lentiviral auto-inactivant dérivé du virus de l'immunodéficience humaine-1 (HIV-1) codant pour une forme mutée (T87Q) du gène de la sous-unité bêta de l'hémoglobine humaine (HBB, bêta-globine) sous le contrôle d'un promoteur de la β-globine humaine et un activateur de la bêta-globine en position 3'.

células madre hematopoyéticas CD34+ autólogas **obtenidas a partir de sangre periférica mobilisada de pacientes con beta-talasemia,** transducidas *ex vivo* con *betibeglogén darolentivec (116)(78)*, un vector lentiviral, auto-inactivante, derivado del virus de la inmunodeficiencia humana-1 (VIH-1) que codifica para una forma mutada T87Q del gen de la subunidad beta de la hemoglobina humana (HBB, beta-globina) bajo el control del promotor de la beta-globina humana y un potenciador de la beta-globina localizado en posición 3'.

p. 124 **veverimerum**

veverimer

vévérimère

veverímero

replace the chemical name and the structure by the following ones

remplacer le nom chimique et la structure par les suivants

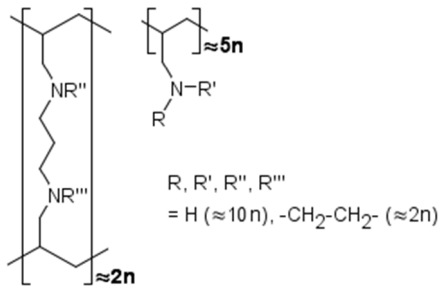
sustitúyase el nombre químico y la estructura por los siguientes

poly[*N*^{1},*N*^{3}-di(prop-2-en-1-yl)propane-1,3-diamine)-co-prop-2-en-1-amine], crosslinked with *N,N'*-ethane-1,2-diyl bridges (molar ratio ≈ 2:5:2)

poly[*N*^{1},*N*^{3}-di(prop-2-én-1-yl)propane-1,3-diamine)-co-prop-2-én-1-amine], réticulé avec des ponts *N,N'*-éthane-1,2-diyle (rapport molaire ≈ 2:5:2)

poli[*N*^{1},*N*^{3}-di(prop-2-en-1-il)propano-1,3-diamina)-co-prop-2-en-1-amina], reticulada con puentes *N,N'*-etano-1,2-diilo (cociente molar ≈ 2:5:2)

$[(C_9H_{18}N_2)_{\approx 2}\ (C_3H_7N)_{\approx 5}\ (C_2H_2)_{\approx 2}]_n$



p.127 **zagotenemabum #**
-128 zagotenemab *replace the structure by the following one*
zagoténémab *remplacer la structure par la suivante*
zagotenemab *sustitúyase la estructura por la siguiente*

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVQSGAE VKKPGESLKI SCKGSGYTFS NYWIEWVRQM PGKGLEWMGE  50
ILPGSDSIKY EKNFKGQVTI SADKSISTAY LQWSSLKASD TAMYYCARRG 100
NYVDDWGQGT LVTVSSASTK GPSVFPLAPC SRSTSESTAA LGCLVKDYFP 150
EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVVTVPSS SLGTKTYTCN 200
VDHKPSNTKV DKRVESKYGP PCPPCPAPEA AGGPSVFLFP PKPKDTLMIS 250
RTPEVTCVVV DVSQEDPEVQ FNWYVDGVEV HNAKTKPREE QFNSTYRVVS 300
VLTVLHQDWL NGKEYKCKVS NKGLPSSIEK TISKAKGQPR EPQVYTLPPS 350
QEEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT PPVLDSDGSF 400
FLYSRLTVDK SRWQEGNVFS CSVMHEALHN HYTQKSLSLS LG         442
```

Light chain / Chaîne légère / Cadena ligera

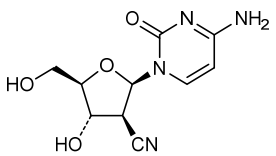
```
EIVLTQSPGT LSLSPGERAT LSCRSSQSLV HSNQNTYLHW YQQKPGQAPR  50
LLIYKVDNRF SGIPDRFSGS GSGTDFTLTI SRLEPEDFAV YYCSQSTLVP 100
LTFGGGTKVE IKRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK 150
VQWKVDNALQ SGNSQESVTE QDSKDSTYSL SSTLTLSKAD YEKHKVYACE 200
VTHQGLSSPV TKSFNRGEC                                   219
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 143-199 257-317 363-421
22"-96" 143"-199" 257"-317" 363"-421"
Intra-L (C23-C104) 23'-93' 139'-199'
23'"-93'" 139'"-199'"
Inter-H-L (CH1 10-CL 126) 130-219' 130"-219'"
Inter-H-H (h 8, h 11) 222-222" 225-225"

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

Recommended International Nonproprietary Names (Rec. INN): List 85
Dénominations communes internationales recommandées (DCI Rec.): Liste 85
Denominaciones Comunes Internacionales Recomendadas (DCI Rec.): Lista 85
(WHO Drug Information, Vol. 35, No. 1, 2021)

p.200 **radgocitabinum**
radgocitabine *replace the structure by the following one*
radgocitabine *remplacer la structure par la suivante*
radgocitabina *sustitúyase la estructura por la siguiente*



p.233 **zanidatamabum zovodotinum #**

-235 zanidatamab zovodotin *replace the description and the structure by the following ones*

zanidatamab zovodotine *remplacer la description et la structure par les suivantes*

zanidatamab zovodotina *sustitúyase la descripción y la estructura por las siguientes*

immunoglobulin half-IG G1-kappa/scFv-h-CH2-CH3, 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, biparatopic (targeting two different non-overlapping epitopes on ERBB2, on extracellular domains 2 (ECD2) and 4 (ECD4) ~~respectively~~), conjugated to **a derivative of** auristatin E;
gamma1 heavy chain, anti-ERBB2 extracellular domain 2 (ECD2), humanized (1-449) [VH humanized (*Homo sapiens* IGHV3-66*01 (78.8%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT-[8.8.12] (27-34.52-59.98-109) (1-120) -*Homo sapiens* IGHG1*01 G1m17,1 (CH1 K120 (217) (121-218), hinge 1-15 (219-233), CH2 (234-343), CH3 T6>V (353), L7>Y (354), D12 (359), L14 (361), F85.1>A (408), Y86>V (410) (344-448), CHS K2>del (449)) (121-449)], (223- 215')-disulfide with kappa light chain, anti ERBB2 ECD2, humanized (1'-215') [V-KAPPA humanized (*Homo sapiens* IGKV1-16*01 (84.2%) -IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (28-33.51-53.90-98) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (154), V101 (192) (109'-215')];
IG scFv-h-CH2-CH3 single chain, anti-ERBB2 extracellular domain 4 (ECD4), humanized (1"-481") [scFv V-kappa-VH anti-ERBB2 ECD4 (1'-248') [V-KAPPA humanized (*Homo sapiens* IGKV1-39*01 (86.3%) -IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (28-33.51-53.90-98) (1'-108') -20-mer pentakis(diglycyl-seryl-glycyl) linker (109"-128") -VH humanized (*Homo sapiens* IGHV3-66*01 (81.6%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.13] (154-161.179-186.225-237) (129"-248")] -dialanyl linker (249"-250") -*Homo sapiens* IGHG1*01 h-CH2-CH3, G1m1 (251"-481") [hinge 1-15, C5>S (255) (251-265), CH2 (266-375), CH3 T6>V (385), D12 (391), L14 (393), T22>L (401), K79>L (427), T81>W (429) (376-480), CHS K2>del (481)]]; dimer (229-261":232-264")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa, **conjugated, on an average of 2 to 3 cysteinyl, to an auristatin E derivative, via a cleavable 1-maleimido-3,6,9-trioxadodecan-12-oyl-valyl-citrullyl-*p*-aminobenzenesulfonyl linker**

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, biparatopique (ciblant deux épitopes différents non chevauchants sur ERBB2, ~~respectivement~~ sur les domaines extracellulaires 2 (ECD2) et 4 (ECD4)), conjugué à **un dérivé de** l'auristatine E;
chaîne lourde gamma1 anti-ERBB2 domaine extracellulaire 2 (ECD2), humanisée (1-449) [VH humanisé (*Homo sapiens* IGHV3-66*01 (78.8%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.12] (27-34.52-59.98-109) (1-120) -*Homo sapiens* IGHG1*01 G1m17,1 (CH1 K120 (217) (121-218), charnière 1-15 (219-233), CH2 (234- 343), CH3 T6>V (353), L7>Y (354), D12 (359), L14 (361), F85.1>A (408), Y86>V (410) (344-448), CHS K2>del (449)) (121-449)], (223-215')-disulfure avec la chaîne légère kappa, anti ERBB2 ECD2, humanisée (1'-215') [V-KAPPA humanisé (*Homo sapiens* IGKV1-

16*01 (84.2%) -IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (28-33.51-53.90-98) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (154), V101 (192) (109'-215')];
IG scFv-h-CH2-CH3 chaîne unique, anti-ERBB2 domaine extracellulaire 4 (ECD4), humanisée (1"-481") [scFv V-kappa-VH anti-ERBB2 ECD4 (1'-248') [V-KAPPA humanisé (*Homo sapiens* IGKV1-39*01 (86.3%) - IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (28-33.51-53.90-98) (1'-108') -20-mer pentakis(diglycyl-seryl-glycyl) linker (109"- 128") -VH humanisé (*Homo sapiens* IGHV3-66*01 (81.6%) -(IGHD) - IGHJ4*01 (100%)) CDR-IMGT [8.8.13] (154-161.179-186.225-237) (129"-248")] -dialanyl linker (249"-250") -*Homo sapiens* IGHG1*01 h-CH2-CH3, G1m1 (251"-481") [charnière 1-15 C5>S (255) (251- 265), CH2 (266-375), CH3 T6>V (385), D12 (391), L14 (393), T22>L (401), K79>L (427), T81>W (429) (376-480), CHS K2>del (481)]];
dimère (229-261":232- 264")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa; conjugué, sur 2 à 3 cystéinyl en moyenne, à **un dérivé de l'auristatine E**, via un linker clivable **1-maléimido-3,6,9-trioxadodécan-12-oyl-valyl-citrullyl-*p*-aminobenzènesulfonyle**.

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, biparatópico (dirigiendo dos epítopos diferentes no superpuestos sobre ERBB2, ~~respectivamente~~ sobre los dominios extracelulares 2 (ECD2) y 4 (ECD4)), conjugado **con un derivado de auristatina E**;
cadena pesada gamma1 anti-ERBB2 dominio extracelular 2 (ECD2), humanizada (1-449) [VH humanizado (*Homo sapiens* IGHV3-66*01 (78.8%) -(IGHD) -IGHJ4*01 (100%)) CDR-IMGT [8.8.12] (27-34.52-59.98-109) (1-120) -*Homo sapiens* IGHG1*01 G1m17,1 (CH1 K120 (217) (121-218), bisagra 1-15 (219-233), CH2 (234- 343), CH3 T6>V (353), L7>Y (354), D12 (359), L14 (361), F85.1>A (408), Y86>V (410) (344-448), CHS K2>del (449)) (121-449)], (223-215')-disulfuro con la cadena ligera kappa, anti ERBB2 ECD2, humanizada (1'-215') [V-KAPPA humanizado (*Homo sapiens* IGKV1-16*01 (84.2%) -IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (28-33.51-53.90-98) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1 (154), V101 (192) (109'-215')];
IG scFv-h-CH2-CH3 cadena única, anti-ERBB2 dominio extracelular 4 (ECD4), humanizada (1"-481") [scFv V-kappa-VH anti-ERBB2 ECD4 (1'-248') [V-KAPPA humanizado (*Homo sapiens* IGKV1-39*01 (86.3%) - IGKJ1*01 (100%)) CDR-IMGT [6.3.9] (28-33.51-53.90-98) (1'-108') -20-mer pentakis(diglicil-seril-glicil) linker (109"- 128") -VH humanizado (*Homo sapiens* IGHV3-66*01 (81.6%) -(IGHD) - IGHJ4*01 (100%)) CDR-IMGT [8.8.13] (154-161.179-186.225-237) (129"-248")] -dialanil linker (249"-250") -*Homo sapiens* IGHG1*01 h-CH2-CH3, G1m1 (251"-481") [bisagra 1-15 C5>S (255) (251- 265), CH2 (266-375), CH3 T6>V (385), D12 (391), L14 (393), T22>L (401), K79>L (427), T81>W (429) (376-480), CHS K2>del (481)]];
dímero (229-261":232- 264")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa; conjugado, sobre 2 a 3 restos cisteinilo en término medio, con **un derivado de auristatina E**, mediante un conector escindible **1-maleimido-3,6,9-trioxadodecan-12-oil-valil-citrullil-*p*-aminobencenesulfonilo.**

1.Heavy chain / Chaîne lourde / Cadena pesada (anti-ERBB2 ECD2)

```
GEVQLVESGG GLVQPGGSLR LSCAASGFTF ADYTMDWVRQ APGKGLEWVG  50
DVNPNSGGSI YNQRFKGRFT FSVDRSKNTL YLQMNSLRAE DTAVYYCARN 100
LGPSFYFDYW GQGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYVYPPSRDE LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFALV SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPG  449
```

2. Light chain / Chaîne légère / Cadena ligera (anti-ERBB2 ECD2)

```
GDIQMTQSPS SLSASVGDRV TITCKASQDV SIGVAWYQQK PGKAPKLLIY  50
SASYRYTGVP SRFSGSGSGT DFTLTISSLQ PEDFATYYCQ QYYIYPATFG 100
QGTKVEIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK 150
VDNALQSGNS QESVTEQDSK DSTYSLSSTL TLSKADYEKH KVYACEVTHQ 200
GLSSPVTKSF NRGEC                                      215
```

3. Chain / Chaîne / Cadena: IG scFv-h-CH2-CH3 (anti-ERBB2 ECD4)

```
GDIQMTQSPS SLSASVGDRV TITCRASQDV NTAVAWYQQK PGKAPKLLIY  50
SASFLYSGVP SRFSGSRSGT DFTLTISSLQ PEDFATYYCQ QHYTTPPTFG 100
QGTKVEIKGG SGGGSGGGSG GGSGGGSGEV QLVESGGGLV QPGGSLRLSC 150
AASGFNIKDT YIHWVRQAPG KGLEWVARIY PTNGYTRYAD SVKGRFTISA 200
DTSKNTAYLQ MNSLRAEDTA VYYCSRWGGD GFYAMDYWGQ GTLVTVSSAA 250
EPKSSDKTHT CPPCPAPELL GGPSVFLFPP KPKDTLMISR TPEVTCVVVD 300
VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ YNSTYRVVSV LTVLHQDWLN 350
GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYVLPPSR DELTKNQVSL 400
LCLVKGFYPS DIAVEWESNG QPENNYLTWP PVLDSDGSFF LYSKLTVDKS 450
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP G                     481
```

Post-translational modifications

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

Intra-H (C23-C104) 23-97 147-203 264-324 370-428

Intra-L (C23-C104) 24'-89' 135'-195'

Intra-chain 3 24"-89" 150"-224" 296"-356" 402"-460"

Inter-H-L (h 5-CL 126)* 223-215'

Inter-H-chain 3 (h 11, h 14)* 229-261" 232-264"

***The inter-chain disulfide bridges are partially reduced, an average of 2 to 3 cysteinyl being conjugated each via a thioether bond to a drug linker. * Les ponts disulfure inter-chaînes sont partiellement réduits, une moyenne de 2 à 3 cystéinyl étant chacun conjugué via une liaison thioéther à un linker-principe actif. * Los puentes disulfuro inter-catenarios están parcialmente reducidos, una media de 2 a 3 cisteinil está conjugada a conectores de principio activo a través de un enlace tioeter.**

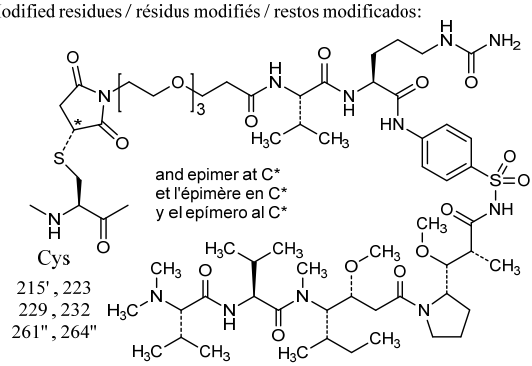
N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación

H CH2 N84.4:

300, 332"

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

Modified residues / résidus modifiés / restos modificados:



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.