International Nonproprietary Names for Pharmaceutical Substances (INN)

RECOMMENDED International Nonproprietary Names: List 92

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 92

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 92

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*

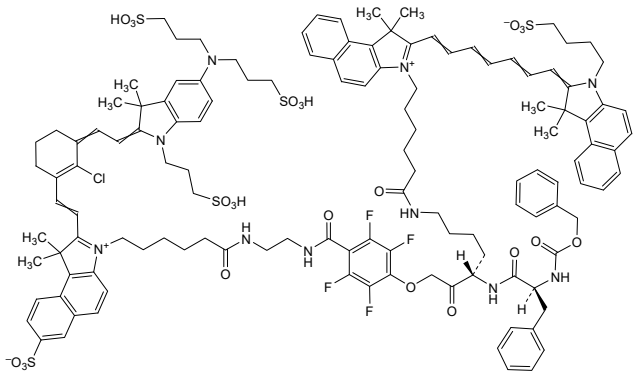
abenacianinum

abenacianine — (1^{2}(2)Ξ,3(4^{1})Ξ,4^{2}Ξ,5Ξ,23*S*,36Ξ,38Ξ,40Ξ,42(43^{2})Ξ)-23-[(2*S*)-2-{[(benzyloxy)carbonyl]amino}-3-phenylpropanamido]-1^{5}-[bis(3-sulfopropyl)amino]-4^{2}-chloro-19^{2},19^{3},19^{5},19^{6}-tetrafluoro-1^{3},1^{3},7^{1},7^{1},35^{1},35^{1},43^{1},43^{1}-octamethyl-13,18,22,29-tetraoxo-43^{3}-(4-sulfonatobutyl)-1^{1}-(3-sulfopropyl)-1^{1},1^{3},43^{1},43^{3}-tetrahydro-7^{1}*H*,35^{1}*H*-20-oxa-14,17,28-triaza-7(2,3),35(3,2),43(2)-tris(benzo[*e*]indola)-1(2)-indola-19(1,4)-benzena-4(1,3)-cyclohexanatritetracontaphane-1^{2}(2),3(4^{1}),4^{2},5,36,38,40,42(43^{2})-octaene-7^{3},35^{3}-diium-7^{7}-sulfonate

abénacianine — (1^{2}(2)Ξ,3(4^{1})Ξ,4^{2}Ξ,5Ξ,23*S*,36Ξ,38Ξ,40Ξ,42(43^{2})Ξ)-23-[(2*S*)-2-{[(benzyloxy)carbonyl]amino}-3-phénylpropanamido]-1^{5}-[bis(3-sulfopropyl)amino]-4^{2}-chloro-19^{2},19^{3},19^{5},19^{6}-tétrafluoro-1^{3},1^{3},7^{1},7^{1},35^{1},35^{1},43^{1},43^{1}-octaméthyl-13,18,22,29-tétraoxo-43^{3}-(4-sulfonatobutyl)-1^{1}-(3-sulfopropyl)-1^{1},1^{3},43^{1},43^{3}-tétrahydro-7^{1}*H*,35^{1}*H*-20-oxa-14,17,28-triaza-7(2,3),35(3,2),43(2)-tris(benzo[*e*]indola)-1(2)-indola-19(1,4)-benzéna-4(1,3)-cyclohexanatritétracontaphane-1^{2}(2),3(4^{1}),4^{2},5,36,38,40,42(43^{2})-octaène-7^{3},35^{3}-diium-7^{7}-sulfonate

abenacianina — (1^{2}(2)Ξ,3(4^{1})Ξ,4^{2}Ξ,5Ξ,23*S*,36Ξ,38Ξ,40Ξ,42(43^{2})Ξ)-23-[(2*S*)-2-{[(benziloxi)carbonil]amino}-3-fenilpropanamido]-1^{5}-[bis(3-sulfopropil)amino]-4^{2}-cloro-19^{2},19^{3},19^{5},19^{6}-tetrafluoro-1^{3},1^{3},7^{1},7^{1},35^{1},35^{1},43^{1},43^{1}-octametil-13,18,22,29-tetraoxo-43^{3}-(4-sulfonatobutil)-1^{1}-(3-sulfopropil)-1^{1},1^{3},43^{1},43^{3}-tetrahidro-7^{1}*H*,35^{1}*H*-20-oxa-14,17,28-triaza-7(2,3),35(3,2),43(2)-tris(benzo[*e*]indola)-1(2)-indola-19(1,4)-bencena-4(1,3)-ciclohexanatritetracontafano-1^{2}(2),3(4^{1}),4^{2},5,36,38,40,42(43^{2})-octaeno-7^{3},35^{3}-diio-7^{7}-sulfonato

$C_{127}H_{145}ClF_4N_{10}O_{23}S_5$



adakitugum #

adakitug	immunoglobulin G1-kappa, anti-[*Homo sapiens* CXCL8 (C-X-C motif chemokine ligand 8, interleukin 8, IL8)], *Homo sapiens* monoclonal antibody; H-gamma1 heavy chain *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV3-30-5*03 (93.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14(CH1 R120 (214) (118-215), hinge 1-15 (216-230), CH2 (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-214')-disulfide with L-kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (95.8%) -IGKJ3*01 (91.7%), 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 (226-226":229-229")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa
adakitug	immunoglobuline G1-kappa, anti-[*Homo sapiens* CXCL8 (C-X-C motif chimiokine ligand 8, interleukine 8, IL8)], anticorps monoclonal *Homo sapiens*; chaîne lourde H-gamma1 *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV3-30-5*03 (93.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (214) (118-215), charnière 1-15 (216-230), CH2 (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-214')-disulfure avec la chaîne légère L-kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (95.8%) -IGKJ3*01 (91.7%), 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 (226-226":229-229")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa
adakitug	inmunoglobulina G1-kappa, anti-[*Homo sapiens* CXCL8 (C-X-C ligando 8 del motivo quimiocina, interleukina 8, IL8)], anticuerpo monoclonal *Homo sapiens*; cadena pesada H-gamma1 *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV3-30-5*03 (93.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens*IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (214) (118-215), bisagra 1-15 (216-230), CH2 (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-214')-disulfuro con la cadena ligera L-kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (95.8%) -IGKJ3*01 (91.7%), 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 (226-226":229-229")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVESGGG VVQPGRSLRL SCTASGFTFS HYGMYWVRQA PGKGLEWVAV  50
IWYDGSYEYN ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARDR 100
VGLFDYWGQG TLVTVSSAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF 150
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC 200
NVNHKPSNTK VDKRVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT 250
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT 350
LPPSREEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS 400
DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPGK    447
```

Light chain / Chaîne légère / Cadena ligera

```
EIVLTQSPGT LSLSPGERAT LSCRASQSIS SSYLAWYQQK PGQAPRLLIY  50
GPSSRATGIP DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QYAGSLTFGP 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) 22-96 144-200 261-321 367-425
22"-96" 144"-200" 261"-321" 367"-425"
Intra-L (C23-C104) 23'-89' 134'-194'
23'"-89'" 134'"-194'"
Inter-H-L (h 5-CL 126) 220-214' 220"-214'"
Inter-H-H (h 11, h 14) 226-226" 229-229"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)
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"

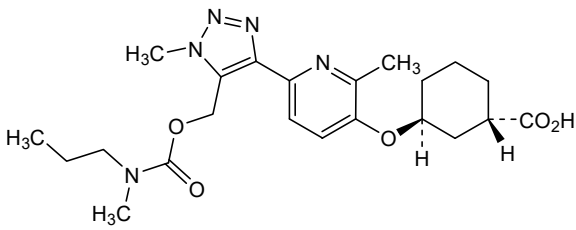
admilparantum

admilparant — (1*S*,3*S*)-3-({2-methyl-6-[1-methyl-5-({[methyl(propyl)carbamoyl]oxy}methyl)-1*H*-1,2,3-triazol-4-yl]pyridin-3-yl}oxy)cyclohexane-1-carboxylic acid

admilparant — acide (1*S*,3*S*)-3-({2-méthyl-6-[1-méthyl-5-({[méthyl(propyl)carbamoyl]oxy}méthyl)-1*H*-1,2,3-triazol-4-yl]pyridin-3-yl}oxy)cyclohexane-1-carboxylique

admilparant — ácido (1*S*,3*S*)-3-({6-[1-metil-5-({[metil(propil)carbamoil]oxi}metil)-1*H*-1,2,3-triazol-4-il]-2-metilpiridin-3-il}oxi)ciclohexano-1-carboxílico

$C_{22}H_{31}N_5O_5$



albipagrastimum alfa #

albipagrastim alfa — human serum albumin (1-585 in the current sequence) fused to human granulocyte colony-stimulating factor (P09919-2) [T^{1}>A^{586}, ^{3}LGP^{5}>^{588}TYR^{590}, C^{17}>S^{602}]-variant (1-174, 586-759 in the current sequence), produced in *Pichia pastoris* (*Komagataella phaffii*), glycoform alfa

albipagrastim alfa — albumine sérique humaine (1-585 dans la séquence actuelle) fusionnée au facteur de stimulation des colonies de granulocytes humains (P09919-2) [T^{1}>A^{586}, ^{3}LGP^{5}>^{588}TYR^{590}, C^{17}>S^{602}]-variant (1-174, 586-759 dans la séquence actuelle), produit chez *Pichia pastoris* (*Komagataella phaffii*), glycoforme alfa

albipagrastim alfa — albúmina sérica humana (1-585 en la secuencia actual) fusionada al factor estimulador de colonias del granulocito humano (P09919-2) [T^{1}>A^{586}, ^{3}LGP^{5}>^{588}TYR^{590}, C^{17}>S^{602}]-variante (1-174, 586-759 en la secuencia actual), producido en *Pichia pastoris* (*Komagataella phaffii*), glicoforma alfa

Sequence / Séquence / Secuencia

```
DAHKSEVAHR FKDLGEENFK ALVLIAFAQY LQQCPFEDHV KLVNEVTEFA   50
KTCVADESAE NCDKSLHTLF GDKLCTVATL RETYGEMADC CAKQEPERNE  100
CFLQHKDDNP NLPRLVRPEV DVMCTAFHDN EETFLKKYLY EIARRHPYFY  150
APELLFFAKR YKAAFTECCQ AADKAACLLP KLDELRDEGK ASSAKQRLKC  200
ASLQKFGERA FKAWAVARLS QRFPKAEFAE VSKLVTDLTK VHTECCHGDL  250
LECADDRADL AKYICENQDS ISSKLKECCE KPLLEKSHCI AEVENDEMPA  300
DLPSLAADFV ESKDVCKNYA EAKDVFLGMF LYEYARRHPD YSVVLLLRLA  350
KTYETTLEKC CAAADPHECY AKVFDEFKPL VEEPQNLIKQ NCELFEQLGE  400
YKFQNALLVR YTKKVPQVST PTLVEVSRNL GKVGSKCCKH PEAKRMPCAE  450
DYLSVVLNQL CVLHEKTPVS DRVTKCCTES LVNRRPCFSA LEVDETYVPK  500
EFNAETFTFH ADICTLSEKE RQIKKQTALV ELVKHKPKAT KEQLKAVMDD  550
FAAFVEKCCK ADDKETCFAE EGKKLVAASQ AALGLAPTYR ASSLPQSFLL  600
KSLEQVRKIQ GDGAALQEKL CATYKLCHPE ELVLLGHSLG IPWAPLSSCP  650
SQALQLAGCL SQLHSGLFLY QGLLQALEGI SPELGPTLDT LQLDVADFAT  700
TIWQQMEELG MAPALQPTQG AMPAFASAFQ RRAGGVLVAS HLQSFLEVSY  750
RVLRHLAQP                                               759
```

Mutations / Mutations / Mutaciónes

T^{1}>**A**^{586}, ^{3}LGP^{5}>^{588}**TYR**^{590}, C^{17}>**S**^{602}

Post-translational modifications

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
53-62, 75-91, 90-101, 124-169, 168-177, 200-246, 245-253,265-279,278-289, 316-361, 360-369, 392-438, 437-448, 461-477, 476-487, 514-559, 558-567, 621-627, 649-659

Oxidation sites / Sites d'oxydation / Posiciones de oxidación
M123, M298, M329, M548, W703, M711, M722

Deamidation sites / Sites de désamidation / Posiciones de desamidación
N18, Q29, Q32, Q33, N61

aldastotugum #

aldastotug — immunoglobulin G1-kappa, anti-[*Homo sapiens* SIGLEC15 (sialic acid-binding Ig-like lectin 15, CD33-like 3, CD33L3)], *Homo sapiens* monoclonal antibody;
H-gamma1 heavy chain *Homo sapiens* (1-449) [VH (*Homo sapiens* IGHV5-10-1*01 (95.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (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)], (222-215')-disulfide with

L-kappa light chain *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (94.8%) -IGKJ1*01 (90.9%) I126>F (107'), 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 (228-228":231-231")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa

aldastotug

immunoglobuline G1-kappa, anti-[*Homo sapiens* SIGLEC15 (Ig-like lectine 15 liant l'acide sialique, CD33-like 3, CD33L3)], anticorps monoclonal *Homo sapiens*;
chaîne lourde H-gamma1 *Homo sapiens* (1-449) [VH (*Homo sapiens* IGHV5-10-1*01 (95.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (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)], (222-215')-disulfure avec la chaîne légère L-kappa *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (94.8%) -IGKJ1*01 (90.9%) I126>F (107'), 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 (228-228":231-231")-bisdisulfide, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa

aldastotug

inmunoglobulina G1-kappa, anti-[*Homo sapiens* SIGLEC15 (Ig-like lectina 15 que une el ácido siálico, CD33-like 3, CD33L3)], anticuerpo monoclonal *Homo sapiens*;
cadena pesada H-gamma1 *Homo sapiens* (1-449) [VH (*Homo sapiens* IGHV5-10-1*01 (95.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (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)], (222-215')-disulfuro con la cadena ligera L-kappa *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (94.8%) -IGKJ1*01 (90.9%) I126>F (107'), 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 (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

```
EVQLVQSGAE VKKPGESLRI SCKGSGYSFT TYWISWVRQM PGKGLEWMGL  50
IDPSDSYTNY SPSFKGHVTI STDKSISTAY LQWSSLKASD TAMYYCARGG 100
YYGSEEDYWG QGTLVTVSSA STKGPSVFPL APSSKSTSGG TAALGCLVKD 150
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY 200
ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP CPAPELLGGP SVFLFPPKPK 250
DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS 300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV 350
YTLPPSRDEL TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL 400
DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK  449
```

Light chain / Chaîne légère / Cadena ligera

```
EIVLTQSPGT LSLSPGERAT LSCRASQSVS SSRLAWFQQK SGQAPRLLIF  50
DASSRATGIP DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QYGSSPRTFG 100
QGTKVEFKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK 150
VDNALQSGNS QESVTEQDSK DSTYSLSSTL TLSKADYEKH KVYACEVTHQ 200
GLSSPVTKSF NRGEC                                       215
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 146-202 263-323 369-427
22"-96" 146"-202" 263"-323" 369"-427"
Intra-L (C23-C104) 23'-89' 135'-195'
23'"-89'" 135'"-195'"
Inter-H-L (h 5-CL 126) 222-215' 222"-215'"
Inter-H-H (h 11, h 14) 228-228" 231-231"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H VH 66: 59, 59" (very low N-glycosylation)
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"

amlenetugum #

amlenetug	immunoglobulin G1-kappa, anti-[*Homo sapiens* SNCA (synuclein alpha, PARK1, PARK4, Parkinson disease (autosomal dominant, Lewy body) 4, synuclein alpha (non A4 component of amyloid precursor))], *Homo sapiens* monoclonal antibody; H-gamma1 heavy chain *Homo sapiens* (1-445) [VH (*Homo sapiens* IGHV3-23*01 (90.8%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.8.9] (26-33.51-58.97-105)) (1-116) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (213) (117-214), hinge 1-15 (215-229), CH2 (230-339), CH3 E12 (355), M14 (357) (340-444), CHS K2>del (445)) (117-445)], (219-215')-disulfide with L-kappa light chain *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (100%) -IGKJ1*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 (225-225'':228-228'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1SV, lacking the glutamine synthetase (GS-KO) gene, glycoform alfa
amlénetug	immunoglobuline G1-kappa, anti-[*Homo sapiens* SNCA (synucléine alpha, alpha-synucléine, PARK1, PARK4, maladie de Parkinson (autosomique dominante, corps de Lewy) 4, synucléine alpha (composant non A4 du précurseur amyloïde))], anticorps monoclonal *Homo sapiens*; chaîne lourde H-gamma1 *Homo sapiens* (1-445) [VH (*Homo sapiens* IGHV3-23*01 (90.8%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.8.9] (26-33.51-58.97-105)) (1-116) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (213) (117-214), charnière 1-15 (215-229), CH2 (230-339), CH3 E12 (355), M14 (357) (340-444), CHS K2>del (445)) (117-445)], (219-215')-disulfure avec la chaîne légère L-kappa *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (100%) -IGKJ1*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 (225-225'':228-228'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1SV, ne présentant pas le gène de la glutamine synthétase (GS-KO), glycoforme alfa
amlenetug	inmunoglobulina G1-kappa, anti-[*Homo sapiens* SNCA (sinucleína alfa, PARK1, PARK4, enfermedad de Parkinson (autosómico dominante, cuerpos de Lewy) 4, sinucleína alfa (que se compone de precusor amieloide no A4))], anticuerpo monoclonal *Homo sapiens*; cadena pesada H-gamma1 *Homo sapiens* (1-445) [VH (*Homo sapiens* IGHV3-23*01 (90.8%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.8.9] (26-33.51-58.97-105)) (1-116) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (213) (117-214), bisagra 1-15 (215-229), CH2 (230-339), CH3 E12 (355), M14 (357) (340-444), CHS K2>del (445)) (117-445)], (219-215')-disulfuro con la cadena ligera L-kappa *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (100%) -IGKJ1*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 (225-225'':228-228'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1SV en ausencia del gen glutamina sintetasa (GS-KO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLLESGGG LVQTGGSLRL SCAASGFTFS SYAMTWVRQA PGKGLEWVSA  50
IRSQGDRTDY ADSVKGRFTI SRDNSQNTLY LQMNSLRAED TAVYYCAKNW 100
APFDSWGQGT LVTVSSASTK GPSVFPLAPS SKSTSGGTAA LGCLVKDYFP 150
EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVVTVPSS SLGTQTYICN 200
VNHKPSNTKV DKRVEPKSCD KTHTCPPCPA PELLGGPSVF LFPPKPKDTL 250
MISRTPEVTC VVVDVSHEDP EVKFNWYVDG VEVHNAKTKP REEQYNSTYR 300
VVSVLTVLHQ DWLNGKEYKC KVSNKALPAP IEKTISKAKG QPREPQVYTL 350
PPSREEMTKN QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD 400
GSFFLYSKLT VDKSRWQQGN VFSCSVMHEA LHNHYTQKSL SLSPG      445
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Light chain / Chaîne légère / Cadena ligera

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EIVLTQSPGT LSLSPGERAT LSCRASQSVS SSYLAWYQQK PGQAPRLLIY  50
GASSRATGIP DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QYGSSPWTFG 100
QGTKVEIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK 150
VDNALQSGNS QESVTEQDSK DSTYSLSSTL TLSKADYEKH KVYACEVTHQ 200
GLSSPVTKSF NRGEC                                       215
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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	143-199	260-320	366-424
	22"-96"	143"-199"	260"-320"	366"-424"
Intra-L (C23-C104)	23'-89'	135'-195'		
	23'"-89'"	135'"-195'"		
Inter-H-L (h 5-CL 126)	219-215'	219"-215'"		
Inter-H-H (h 11, 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

amostomigum #
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immunoglobulin G1-lambda, anti-[*Homo sapiens* CD47 (CD47 molecule, integrin associated protein, IAP, MER6, OA3)] and anti-[*Homo sapiens* CD274 (programmed cell death 1 ligand 1, PDL1, PD-L1, B7 homolog 1, B7H1, B7-H1, PDCD1LG1)], humanized monoclonal antibody, bispecific;
H-gamma1 heavy chain anti-CD47 humanized (1-464) [VH (*Homo sapiens* IGHV3-23*04 (83.8%) -(IGHD) -IGHJ4*01 (92.3%) L123>T (129), CDR-IMGT [8.10.20] (26-33.51-60.104-123)) (1-134)-*Homo sapiens* IGHG1*01v, G1m17,1>G1m3,1 CH1 R120, CH3 D12, L14, G1v14 CH2 A1.3, A1.2, G1v74 CH3 C10, G1v32 CH3 W22 (knob) (CH1 R120 (231) (135-232), hinge 1-15 (233-247), CH2 L1.3>A (251), L1.2>A (252) (248-357), CH3 D12 (373), L14 (375), S10>C (371), T22>W (383) (358-462), CHS (463-464)) (135-464)], (237-215')-disulfide with common L-lambda2 light chain humanized (1'-216') [V-LAMBDA (*Homo sapiens* IGLV8-61*01 (85.6%) -IGLJ2*01 (90.9%), CDR-IMGT [9.3.10] (26'-34'.52'-54'.91'-100')) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')];
H-gamma1 heavy chain anti-CD274 humanized (1"-453") [VH (*Homo sapiens* IGHV3-20*01 (92.9%) -(IGHD) -IGHJ5*01 (100%), CDR-IMGT [8.8.15] (26"-33".51"-58".97"-111")) (1"-122")-*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, CH1 K120, CH3 E12, M14, G1v14 CH2 A1.3, A1.2, G1v75 CH3 C5, G1v33 CH3 S22, A24, V86 (hole) (CH1 R120>K (219") (123"-220"), hinge 1-15 K7>G (227"), T8>P (228"), H9>GG (229"-230") (221"-236"), CH2 L1.3>A (240"), L1.2>A (241") (237"-346"), CH3 E12 (362"), M14 (364"), Y5>C (355"), T22>S (372"), L24>A (374"), Y86>V (413") (347"-451"), CHS (452"-453")) (123"-453")], (225"-215"')-disulfide with common L-lambda2 light chain humanized (1'"-216'") [V-LAMBDA (*Homo sapiens* IGLV8-61*01 (85.6%) -IGLJ2*01 (90.9%), CDR-IMGT [9.3.10] (26'"-34'".52'"-54'".91'"-100'")) (1'"-110'") -*Homo sapiens* IGLC2*01 (100%) (111'"-216'")]; dimer (243-232":246-235")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-S, glycoform alfa

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immunoglobuline G1-lambda, anti-[*Homo sapiens* CD47 (CD47 molécule, protéine associée à l'intégrine, IAP, MER6, OA3)] et anti-[*Homo sapiens* CD274 (ligand 1 de mort cellulaire programmée 1, PDL1, PD-L1, B7 homologue 1, B7H1, B7-H1, PDCD1LG1)], anticorps monoclonal humanisé, bispécifique;
chaîne lourde H-gamma1 anti-CD47 humanisée (1-464) [VH (*Homo sapiens* IGHV3-23*04 (83.8%) -(IGHD) -IGHJ4*01 (92.3%) L123>T (129), CDR-IMGT [8.10.20] (26-33.51-60.104-123)) (1-134)-*Homo sapiens* IGHG1*01v, G1m17,1>G1m3,1 CH1 R120, CH3 D12, L14, G1v14 CH2 A1.3, A1.2, G1v74 CH3 C10, G1v32 CH3 W22 (knob) (CH1 R120 (231) (135-232), charnière 1-15 (233-247), CH2 L1.3>A (251), L1.2>A (252) (248-357), CH3 D12 (373), L14 (375), S10>C (371), T22>W (383) (358-462), CHS (463-464)) (135-464)], (237-215')-disulfure avec la chaîne commune légère L-lambda2 humanisée (1'-216') [V-LAMBDA (*Homo sapiens* IGLV8-61*01 (85.6%) -IGLJ2*01 (90.9%), CDR-IMGT [9.3.10] (26'-34'.52'-54'.91'-100')) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')];
chaîne lourde H-gamma1 anti-CD274 humanisée (1''-453'') [VH (*Homo sapiens* IGHV3-20*01 (92.9%) -(IGHD) -IGHJ5*01 (100%), CDR-IMGT [8.8.15] (26''-33''.51''-58''.97''-111'')) (1''-122'')-*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, CH1 K120, CH3 E12, M14, G1v14 CH2 A1.3, A1.2, G1v75 CH3 C5, G1v33 CH3 S22, A24, V86 (hole) (CH1 R120>K (219'') (123''-220''), charnière 1-15 K7>G (227''), T8>P (228''), H9>G (229''-230'') (221''-236''), CH2 L1.3>A (240''), L1.2>A (241'') (237''-346''), CH3 E12 (362''), M14 (364''), Y5>C (355''), T22>S (372''), L24>A (374''), Y86>V (413'') (347''-451''), CHS (452''-453'')) (123''-453'')], (225''-215''')-disulfure avec la chaîne commune légère L-lambda2 humanisée (1'''-216''') [V-LAMBDA (*Homo sapiens* IGLV8-61*01 (85.6%) -IGLJ2*01 (90.9%), CDR-IMGT [9.3.10] (26'''-34'''.52'''-54'''.91'''-100''')) (1'''-110''') -*Homo sapiens* IGLC2*01 (100%) (111'''-216''')]; dimère (243-232'':246-235'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-S, glycoforme alfa

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inmunoglobulina G1-lambda, anti-[*Homo sapiens* CD47 (CD47 molécula, proteína asociada a la integrina, IAP, MER6, OA3)] y anti-[*Homo sapiens* CD274 (ligando 1 de muerte celular programada 1, PDL1, PD-L1, B7 homólogo 1, B7H1, B7-H1, PDCD1LG1)], anticuerpo monoclonal humanizado, biespecífico;
cadena pesada H-gamma1 anti-CD47 humanizada (1-464) [VH (*Homo sapiens* IGHV3-23*04 (83.8%) -(IGHD) -IGHJ4*01 (92.3%) L123>T (129), CDR-IMGT [8.10.20] (26-33.51-60.104-123)) (1-134)-*Homo sapiens* IGHG1*01v, G1m17,1>G1m3,1 CH1 R120, CH3 D12, L14, G1v14 CH2 A1.3, A1.2, G1v74 CH3 C10, G1v32 CH3 W22 (knob) (CH1 R120 (231) (135-232), bisagra 1-15 (233-247), CH2 L1.3>A (251), L1.2>A (252) (248-357), CH3 D12 (373), L14 (375), S10>C (371), T22>W (383) (358-462), CHS (463-464)) (135-464)], (237-215')-disulfuro con la cadena común ligera L-lambda2 humanizada (1'-216') [V-LAMBDA (*Homo sapiens* IGLV8-61*01 (85.6%) -IGLJ2*01 (90.9%), CDR-IMGT [9.3.10] (26'-34'.52'-54'.91'-100')) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')];
cadena pesada H-gamma1 anti-CD274 humanizada (1''-453'') [VH (*Homo sapiens* IGHV3-20*01 (92.9%) -(IGHD) -IGHJ5*01 (100%), CDR-IMGT [8.8.15] (26''-33''.51''-58''.97''-111'')) (1''-122'')-*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, CH1 K120, CH3 E12, M14, G1v14 CH2 A1.3, A1.2, G1v75 CH3 C5, G1v33 CH3 S22, A24, V86 (hole) (CH1 R120>K (219'') (123''-220''), bisagra 1-15 K7>G (227''), T8>P (228''), H9>G (229''-230'') (221''-236''), CH2 L1.3>A (240''), L1.2>A (241'') (237''-346''), CH3 E12 (362''), M14 (364''), Y5>C (355''), T22>S (372''), L24>A (374''), Y86>V (413'') (347''-451''), CHS (452''-453'')) (123''-453'')], (225''-215''')-disulfuro con la cadena común ligera L-lambda2 humanizada (1'''-216''') [V-LAMBDA (*Homo sapiens* IGLV8-61*01 (85.6%) -IGLJ2*01 (90.9%), CDR-IMGT [9.3.10] (26'''-34'''.52'''-54'''.91'''-100''')) (1'''-110''') -*Homo sapiens* IGLC2*01 (100%) (111'''-216''')]; dímero (243-232'':246-235'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-S, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada : H-gamma1 (H) anti-CD47 (knob)

```
QVQLVESGGG LVQPGGSLRL SCAASGFTFS RYWMYWVRQA PGKGLEWVSS  50
IEDSSINTGG GTETTYYTDS VKGRFTISRD NAKNTLYLQM NSLRAEDTAV 100
YYCAKGDYYC TTYECQHYYG MDYWGQGTTV TVSSASTKGP SVFPLAPSSK 150
STSGGTAALG CLVKDYFPEP VTVSWNSGAL TSGVHTFPAV LQSSGLYSLS 200
SVVTVPSSSL GTQTYICNVN HKPSNTKVDK RVEPKSCDKT HTCPPCPAPE 250
AAGGPSVFLF PPKPKDTLMI SRTPEVTCVV VDVSHEDPEV KFNWYVDGVE 300
VHNAKTKPRE EQYNSTYRVV SVLTVLHQDW LNGKEYKCKV SNKALPAPIE 350
KTISKAKGQP REPQVYTLPP CRDELTKNQV SLWCLVKGFY PSDIAVEWES 400
NGQPENNYKT TPPVLDSDGS FFLYSKLTVD KSRWQQGNVF SCSVMHEALH 450
NHYTQKSLSL SPGK                                        464
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Heavy chain / Chaîne lourde / Cadena pesada : H-gamma1 (H") CD274 (hole)

```
EVQLVESGGG VVRPGGSLRL SCAASGFTFD DYAMSWVRQA PGKGLEWVSD  50
ISWSGSNTNY ADSVKGRFTI SRDNAKNSLY LQMNSLRAED TALYHCARAP 100
LLLAMTFGVG SWGQGTLVTV SSASTKGPSV FPLAPSSKST SGGTAALGCL 150
VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ SSGLYSLSSV VTVPSSSLGT 200
QTYICNVNHK PSNTKVDKKV EPKSCDGPGG TCPPCPAPEA AGGPSVFLFP 250
PKPKDTLMIS RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE 300
QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR 350
EPQVCTLPPS REEMTKNQVS LSCAVKGFYP SDIAVEWESN GQPENNYKTT 400
PPVLDSDGSF FLVSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLS 450
PGK                                                    453
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Light chain / Chaîne légère / Cadena ligera : L-lambda2 (L', L'") common

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QTVVTQEPSL SVSPGGTVTL TCGLSSGTVT AINYPGWYQQ TPGQAPRTLI  50
YNTNTRHSGV PDRFSGSISG NKAALTITGA QAEDEADYYC ALYMGNGGHM 100
FGGGTKLTVL GQPKAAPSVT LFPPSSEELQ ANKATLVCLI SDFYPGAVTV 150
AWKADSSPVK AGVETTTPSK QSNNKYAASS YLSLTPEQWK SHRSYSCQVT 200
HEGSTVEKTV APTECS                                      216
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-103 161-217 278-338 384-442
22"-96" 149"-205" 267"-327" 373"-431"
Intra-H CDR3 110-115
Intra-L (C23-C104) 22'-90' 138'-197'
22'"-90'" 138'"-197'"
Inter-H-L (h 5-CL 126) 237-215' 225"-215'"
Inter-H-H (h 11, h 14) 243-232" 246-235"
Inter-H-H (CH3 C10-C5)* 371-355"
*variants G1v74 (CH3 C10) and G1v75 (CH3 C5) creating an additional inter-H-H disulfide bond
*variantes G1v74 (CH3 C10) et G1v75 (CH3 C5) créant une liaison disulfure inter-H-H supplémentaire
*variantes G1v74 (CH3 C10) y G1v74 (CH3 C5) que crean un enlace disulfuro inter-H-H adicional

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)
H VH Q1: 1
L VL V-LAMBDA Q1: 1', 1'"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4: 314, 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: 464, 453"

amulirafuspum alfa

amulirafusp alfa

human signal regulatory protein alpha (SIRPα) fragment, anti-(human CD47, integrin associated protein (IAP)), fused via a $(G_4S)_2$ peptide linker to the N-terminus of both heavy chains of a chimeric immunoglobulin G1-kappa anti-(human B-lymphocyte antigen CD20), glycoform alfa;
human signal regulatory protein alpha (SIRP alpha variant V2 extracellular D1 domain, SIRP alpha V2D1) fragment 31-163, comprising the first two extracellular loops of the D1 domain, [N^{110}>A^{80}]-variant, anti-(human CD47, integrin associated protein (IAP)) (1-133 in the current sequence) fused via a $(G_4S)_2$ peptide

	linker (134-143) to gamma 1 heavy chain (144-594) [VH (*Mus musculus* IGHV1-12*01 -(IGHD) -IGHJ1*01, CDR-Kabat [5.17.12] (174-178.193-209.242-253)) (144-264) -*Homo sapiens* IGHG1*03 (CH1 (265-362), hinge (363-377), CH2 S^{445}>A, E^{480}>A, K^{481}>A (378-487), CH3 (488-592), CHS (593-594)) (265-594)], (367-213')-disulfide with kappa light chain (1'-213') [V-KAPPA (*Mus musculus* IGKV4-72*01 -IGKJ1*01, CDR-Kabat [10.7.9] (24'-33'.49'-55'.88'-96')) (1'-106') -*Homo sapiens* IGKC*01 (107'-213')]; dimer (373-373'':376-376'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa
amulirafusp alfa	fragment de la protéine humaine de régulation du signal alpha (SIRPα), anti-(CD47 humain, protéine associée à l'intégrine (IAP)), fusionné, via un peptide liant $(G_4S)_2$, à l'extrémité N-terminale des deux chaînes lourdes d'une immunoglobuline chimérique G1-kappa anti-(antigène CD20 des lymphocytes B humains), glycoforme alfa; fragment 31-163 de la protéine humaine de régulation du signal alpha (variant V2 SIRP alpha du domaine extracellulaire D1, SIRP alpha V2D1), comprenant les deux premières boucles extracellulaires du domaine D1, [N^{110}>A^{80}]-variant, anti-(CD47 humain, protéine associée à l'intégrine (IAP)) (1-133 dans la séquence actuelle) fusionné via un peptide liant $(G_4S)_2$ (134-143) à la chaîne lourde gamma 1 (144-594) [VH (*Mus musculus* IGHV1-12*01 -(IGHD) -IGHJ1*01, CDR-Kabat [5. 17.12] (174-178.193-209. 242-253)) (144-264) -*Homo sapiens* IGHG1*03 (CH1 (265-362), charnière (363-377), CH2 S^{445}>A, E^{480}>A, K^{481}>A (378-487), CH3 (488-592), CHS (593-594)) (265-594)], (367-213')-disulfure avec la chaîne légère kappa (1'-213') [V-KAPPA (*Mus musculus* IGKV4-72*01 -IGKJ1*01, CDR-Kabat [10. 7.9] (24'-33'.49'-55'.88'-96')) (1'-106') -*Homo sapiens* IGKC*01 (107'-213')]; dimère (373-373'':376-376'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa
amulirafusp alfa	fragmento de proteína reguladora de señal alfa (SIRPα) humana, anti-(CD47 humano, integrina asociada a proteína (IAP)), fusionada, a través de un enlace peptídico $(G_4S)_2$, al terminal N de ambas cadenas pesadas de una inmunoglobulina quimérica G1-kappa anti-(antígeno de linfocito B humano CD20), glicoforma alfa; proteína reguladora de señal alfa humana (SIRP alpha variante V2 extracelular dominio D1, SIRP alpha V2D1) fragmento 31-163, que comprende los dos primeros loops extracelulares del dominio D1, [N^{110}>A^{80}]-variante, anti-(CD47 humano, integrina asociada a proteína (IAP)) (1-133 en la actual secuencia) fusionada a través de un enlace peptídico $(G_4S)_2$ (134-143) a una cadena pesada gamma 1 (144-594) [VH (*Mus musculus* IGHV1-12*01 -(IGHD) -IGHJ1*01, CDR-Kabat [5.17.12] (174-178.193-209.242-253)) (144-264) -*Homo sapiens* IGHG1*03 (CH1 (265-362), bisagra (363-377), CH2 S^{445}>A, E^{480}>A, K^{481}>A (378-487), CH3 (488-592), CHS (593-594)) (265-594)], (367-213')-disulfuro con cadena ligera kappa (1'-213') [V-KAPPA (*Mus musculus* IGKV4-72*01 -IGKJ1*01, CDR-Kabat [10.7.9] (24'-33'.49'-55'.88'-96')) (1'-106') -*Homo sapiens* IGKC*01 (107'-213')]; dímero (373-373'':376-376'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, glicoforma alfa

Sequence / Séquence / Secuencia
SIRPα IgG1 heavy chain

```
EEELQVIQPD KSVSVAAGES AILHCTVTSL IPVGPIQWFR GAGPARELIY   50
NQKEGHFPRV TTVSESTKRE NMDFSISISA ITPADAGTYY CVKFRKGSPD  100
TEFKSGAGTE LSVRAKPSAP VVSGPAARAT PQHGGGGSGG GGSQVQLQQP  150
GAELVKPGAS VKMSCKASGY TFTSYNMHWV KQTPGRGLEW IGAIYPGNGD  200
TSYNQKFKGK ATLTADKSSS TAYMQLSSLT SEDSAVYYCA RSTYYGGDWY  250
FNVWGAGTTV TVSAASTKGP SVFPLAPSSK STSGGTAALG CLVKDYFPEP  300
VTVSWNSGAL TSGVHTFPAV LQSSGLYSLS SVVTVPSSSL GTQTYICNVN  350
HKPSNTKVDK RVEPKSCDKT HTCPPCPAPE LLGGPSVFLF PPKPKDTLMI  400
SRTPEVTCVV VDVSHEDPEV KFNWYVDGVE VHNAKTKPRE EQYNATYRVV  450
SVLTVLHQDW LNGKEYKCKV SNKALPAPIA ATISKAKGQP REPQVYTLPP  500
SREEMTKNQV SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS  550
FFLYSKLTVD KSRWQQGNVF SCSVMHEALH NHYTQKSLSL SPGK        594
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IgG1 light chain

```
QIVLSQSPAI LSASPGEKVT MTCRASSSVS YIHWFQQKPG SSPKPWIYAT   50
SNLASGVPVR FSGSGSGTSY SLTISRVEAE DAATYYCQQW TSNPPTFGGG  100
TKHELKRTVA APSVFIFPPS DEQLKSGTAS VVCLLNNFYP REAKVQWKVD  150
NALQSGNSQE SVTEQDSKDS TYSLSSTLTL SKADYEKHKV YACEVTHQGL  200
SSPVTKSFNR GEC                                          213
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Mutation / Mutation / Mutación
SIRPα IgG1 heavy chain: N^{110}>A^{80},A$^{80''}$, S^{445},$S^{445''}$>A, E^{480},$E^{480''}$>A, K^{481},$K^{481''}$>A

Peptide linker / Peptide liant / Péptido de unión
^{134}GGGGSGGGGS^{143}

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra SIRPα heavy chain: 25-91, 165-239, 291-347, 408-468, 514-572, 25"-91", 165"-239", 291"-347", 408"-468", 514"-572"
Intra light chain: 23'-87', 133'-193'; 23'"-87'", 133'"-193'"
Inter light chain-SIRPα heavy chain: 213'-367; 213'"-367"
Inter SIRPα heavy chain: 373-373", 376-376"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
SIRPα IgG1 heavy chain: 444, 444"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
kappa chain Q1',Q1'" > pyroglutamyl (pE, 5-oxo-L-prolyl)

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS: 594, 594"

ansipastobartum

ansipastobart	immunoglobulin G1-lambda2, anti-[*Homo sapiens* NT5E (5'-nucleotidase ecto, 5' nucleotidase, NT5, eN, eNT NTE, CALJA, CD73)], *Homo sapiens* monoclonal antibody; H-gamma1 heavy chain *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV3-23*01 (93.9%) -(IGHD) -IGHJ2*01 (92.3%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens* IGHG1*03,G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v39 CH2 F1.3, E1.2, S116 (CH1 R120 (214) (118-215), hinge 1-15 (216-230), CH2 L1.3>F (234), L1.2>E (235), P116>S (331) (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-215')-disulfide with L-lambda2 light chain *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV1-44*01 (89.8%) -IGLJ2*01 (100%), CDR-IMGT [8.3.11] (26'-33'.51'-53'.90'-100')) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')]; dimer (226-226":229-229")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-DG44, glycoform alfa
ansipastobart	immunoglobuline G1-lambda2, anti-[*Homo sapiens* NT5E (5' ecto nucléotidase, 5' nucléotidase, NT5, eN, eNT NTE, CALJA, CD73)], anticorps monoclonal *Homo sapiens*;

chaîne lourde H-gamma1 *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV3-23*01 (93.9%) -(IGHD) -IGHJ2*01 (92.3%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v39 CH2 F1.3, E1.2, S116 (CH1 R120 (214) (118-215), charnière 1-15 (216-230), CH2 L1.3>F (234), L1.2>E (235), P116>S (331) (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-215')-disulfure avec la chaîne légère L-lambda2 *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV1-44*01 (89.8%) -IGLJ2*01 (100%), CDR-IMGT [8.3.11] (26'-33'.51'-53'.90'-100')) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')]; dimère (226-226":229-229")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-DG44, glycoforme alfa

ansipastobart

inmunoglobulina G1-lambda2, anti-[*Homo sapiens* NT5E (5' ecto nucleotidasa, 5' nucleotidasa, NT5, eN, eNT NTE, CALJA, CD73)], anticuerpo monoclonal *Homo sapiens*;
cadena pesada H-gamma1 *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV3-23*01 (93.9%) -(IGHD) -IGHJ2*01 (92.3%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v39 CH2 F1.3, E1.2, S116 (CH1 R120 (214) (118-215), bisagra 1-15 (216-230), CH2 L1.3>F (234), L1.2>E (235), P116>S (331) (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-215')-disulfuro con la cadena ligera L-lambda2 *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV1-44*01 (89.8%) -IGLJ2*01 (100%), CDR-IMGT [8.3.11] (26'-33'.51'-53'.90'-100')) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')]; dímero (226-226":229-229")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-DG44, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada : H-gamma1 (H, H") anti-NT5E

```
EVQLLESGGG LVQPGGSLRL SCAASGSSFS SYAYSWVRQA PGKGLEWISA  50
ISGSGGRTYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARLG 100
YSRADEWGRG TLVTVSSAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF 150
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC 200
NVNHKPSNTK VDKRVEPKSC DKTHTCPPCP APEFEGGPSV FLFPPKPKDT 250
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA SIEKTISKAK GQPREPQVYT 350
LPPSREEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS 400
DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPGK    447
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Light chain / Chaîne légère / Cadena ligera : L-lambda2 (L', L'") anti-NT5E

```
QSVLTQPPSA SGTPGQRVTI SCSGSISNIG RNPVNWYQQL PGTAPKLLIY  50
LDNLRLSGVP DRFSGSKSGT SASLAISGLQ SEDEADYYCA TWDDSHPGWT 100
FGGGTKLTVL GQPKAAPSVT LFPPSSEELQ ANKATLVCLI SDFYPGAVTV 150
AWKADSSPVK AGVETTTPSK QSNNKYAASS YLSLTPEQWK SHRSYSCQVT 200
HEGSTVEKTV APTECS                                      216
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Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 144-200 261-321 367-425
22"-96" 144"-200" 261"-321" 367"-425"
Intra-L (C23-C104) 22'-89' 138'-197'
22"'-89"' 138"'-197"'
Inter-H-L (h 5-CL 126) 220-215' 220"-215"'
Inter-H-H (h 11, h 14) 226-226" 229-229"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)
L VL V-LAMBDA 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"

aplitabartum #

aplitabart — immunoglobulin M-kappa cyclic pentamer bisdisulfide with the JCHAIN (joining chain of multimeric IgA and IgM), anti-[*Homo sapiens* TNFRSF10B (TNF receptor superfamily member 10B, death receptor 5, DR5, TNF-related apoptosis-inducing ligand TRAIL receptor 2, TRAILR2, TRAIL-R2, TR-2, CD262)], humanized monoclonal antibody, monospecific, decavalent, agonist;
H-mu heavy chain anti-TNFRSF10B humanized (1-572) [VH (*Homo sapiens* IGHV3-23*03 (90.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHM*03 (100%) (CH1 (120-223), CH2 (224-335), CH3 (336-441), CH4 (442-552), CHS (553-572)) (120-572)], (133-213')-disulfide with L-kappa light chain anti-TNFRSF10B humanized (1'-213') [V-KAPPA (*Homo sapiens* IGKV1-13*02 (84.9%) -IGKJ1*01 (100%), CDR-IMGT [6.3.8] (27'-32'.50'-52'.89'-96')) (1'-106') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (152'), V101 (190') (107'-213')]; dimer (333-333'':410-410'')-bisdisulfide, 5 [H-mu_L-kappa]2 dimers forming a cyclic pentamer, disulfide 4 x (571''-571), and 1x (571''-15'''':69''''-571)-bisdisulfide with the JCHAIN Y102>A (102'''') (1''''-137''''), produced in a cell line derived from Chinese hamster ovary (CHO) cells, glycoform alfa

aplitabart — immunoglobuline M-kappa pentamère cyclique bisdisulfure avec la JCHAIN (chaîne de jonction des IgA et IgM multimériques), anti-[*Homo sapiens* TNFRSF10B (membre 10B de la superfamille des récepteurs du TNF, récepteur de mort 5, DR5, récepteur 2 du ligand TRAIL apparenté au TNF induisant l'apoptose, TRAIL-R2, TR2, CD262)], anticorps monoclonal humanisé, monospécifique, décavalent, agoniste;
chaîne lourde H-mu anti-TNFRSF10B (1-572) [VH (*Homo sapiens* IGHV3-23*03 (90.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHM*03 (100%) (CH1 (120-223), CH2 (224-335), CH3 (336-441), CH4 (442-552), CHS (553-572)) (120-572)], (133-213')-disulfure avec la chaîne légère L-kappa anti-TNFRSF10B humanisée (1'-213') [V-KAPPA (*Homo sapiens* IGKV1-13*02 (84.9%) -IGKJ1*01 (100%), CDR-IMGT [6.3.8] (27'-32'.50'-52'.89'-96')) (1'-106') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (152'), V101 (190') (107'-213')]; dimère (333-333'':410-410'')-bisdisulfure, 5 dimères [H-mu_L-kappa]2 formant un pentamère cyclique disulfure 4x (571''-571), et 1x (571''-15'''':69''''-571)-bisdisulfure avec la JCHAIN Y102>A (102'''') (1''''-137''''), produite dans une lignée cellulaire dérivée des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

aplitabart — inmunoglobulina M-kappa pentámero cíclico bisdisulfuro con la JCHAIN (cadena de unión de las IgA e IgM multiméricas), anti-[*Homo sapiens* TNFRSF10B (miembro 10B de la superfamilia de los receptores del TNF, receptor de muerte 5, DR5, receptor 2 del ligando TRAIL relacionado con TNF que induce la apotosis, TRAIL-R2, TR2, CD262)], anticuerpo monoclonal humanizado, monoespecífico, decavalente, agonista;
cadena pesada H-mu anti-TNFRSF10B (1-572) [VH (*Homo sapiens* IGHV3-23*03 (90.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHM*03 (100%) (CH1 (120-223), CH2 (224-335), CH3 (336-441), CH4 (442-552), CHS (553-572)) (120-572)], (133-213')-disulfuro con la cadena ligera L-kappa anti-TNFRSF10B humanizada (1'-213') [V-KAPPA (*Homo sapiens* IGKV1-13*02 (84.9%) -IGKJ1*01 (100%), CDR-IMGT [6.3.8] (27'-32'.50'-52'.89'-96')) (1'-106') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (152'), V101 (190') (107'-213')]; dímero (333-333'':410-410'')-bisdisulfuro, 5 dímeros [H-mu_L-kappa]2 que forman un pentámreo cíclico disulfuro 4x (571''-571), y 1x (571''-15'''':69''''-571)-bisdisulfuro con la JCHAIN Y102>A (102'''') (1''''-137''''), producido en una línea celular derivada de las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada : H-mu (H, H'') anti-TNFRSF10B (x10)

```
EVQLVESGGG LVQPGGSLRL SCAASGFTFS SYVMSWVRQA PGKGLEWVAT  50
ISSGGSYTYY PDSVKGRFTI SRDNAKNTLY LQMNSLRAED TAVYYCARRG 100
DSMITTDYWG QGTLVTVSSG SASAPTLFPL VSCENSPSDT SSVAVGCLAQ 150
DFLPDSITFS WKYKNNSDIS STRGFPSVLR GGKYAATSQV LLPSKDVMQG 200
TDEHVVCKVQ HPNGNKEKNV PLPVIAELPP KVSVFVPPRD GFFGNPRKSK 250
LICQATGFSP RQIQVSWLRE GKQVGSGVTT DQVQAEAKES GPTTYKVTST 300
LTIKESDWLS QSMFTCRVDH RGLTFQQNAS SMCVPDQDTA IRVFAIPPSF 350
ASIFLTKSTK LTCLVTDLTT YDSVTISWTR QNGEAVKTHT NISESHPNAT 400
FSAVGEASIC EDDWNSGERF TCTVTHTDLP SPLKQTISRP KGVALHRPDV 450
YLLPPAREQL NLRESATITC LVTGFSPADV FVQWMQRGQP LSPEKYVTSA 500
PMPEPQAPGR YFAHSILTVS EEEWNTGETY TCVVAHEALP NRVTERTVDK 550
STGKPTLYNV SLVMSDTAGT CY                              572
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Light chain / Chaîne légère / Cadena ligera : L-kappa (L', L''') anti-TNFRSF10B (x10)

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DIQMTQSPSS LSASVGDRVT ITCKASQDVG TAVAWYQQKP GKAPKLLIYW  50
ASTRHTGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YSSYRTFGQG 100
TKVEIKRTVA APSVFIFPPS DEQLKSGTAS VVCLLNNFYP REAKVQWKVD 150
NALQSGNSQE SVTEQDSKDS TYSLSSTLTL SKADYEKHKV YACEVTHQGL 200
SSPVTKSFNR GEC                                       213
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Joining chain / Chaîne de jonction / Cadena de unión : JCHAIN (J"") (x1)

```
QEDERIVLVD NKCKCARITS RIIRSSEDPN EDIVERNIRI IVPLNNRENI  50
SDPTSPLRTR FVYHLSDLCK KCDPTEVELD NQIVTATQSN ICDEDSATET 100
CATYDRNKCY TAVVPLVYGG ETKMVETALT PDACYPD               137
```

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

Intra-H (C23-C104)	22-96	147-207	253-316	363-422	470-532	5x5
	22"-96"	147"-207"	253"-316"	363"-422"	470"-532"	5x5
Intra-L (C23-C104)	23'-88'	133'-193'				2x5
	23'"-88'"	133'"-193'"				2x5
Intra-J (JCHAIN)	13""-101""	72""-92""	109""-134""			3
Inter-H-L (CH1 10-CL 126)	133-213'	133"-213'"				2x5
Inter-H-H (CH2 125)	333-333"					5
Inter-H-H (CH3 92)	410-410"					4*
Inter-H-H (CHS 147)	571"-571					4
Inter-H-J (CHS 147-J) (J-CHS 147)	571"-15""	69""-571				2
Total S-S per pentamer						98

*two unpaired cysteines 410, 410"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)
J chain Q1: 1""

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH1 N45, CH2 N120, CH3 N81, N84.4, CHS N7 (50 sites per pentamer):
N165, N328, N391, N398, N559 (5x)
N165", N328", N391", N398", N559" (5x)
J JCHAIN (1x): 49""
Fucosylated complex bi-antennary CHO-type glycans or high mannose glycans / glycanes de type CHO bi-antennaires complexes fucosylés ou glycanes riche en mannose / glicanos de tipo CHO biantenarios complejos fucosilados o glicanos ricos en manosa

arlocabtagenum autoleucelum

arlocabtagene autoleucel

autologous T lymphocytes obtained from peripheral blood mononuclear cells (PBMCs) by leukapheresis, transduced with a self-inactivating, non-replicating lentiviral vector encoding a chimeric antigen receptor (CAR) targeting G protein-coupled receptor, class C group 5 member D (GPRC5D). The expressed transgene comprises a human CD33 leader sequence, a human GPRC5D-specific single chain variable fragment (scFv) binding domain (clone ET150-8), an IgG4 hinge region, CD28 transmembrane domain, 4-1BB co-stimulatory domain and CD3ζ signalling domain, under control of a hybrid human elongation factor 1 alpha (EF-1α) promoter / human T-cell leukemia virus type 1 (HTLV-1) R enhancer. The construct is flanked by 5' and 3' long terminal repeats (LTRs) and also contains a ψ packaging signal, partial *gag*, a Rev response element (RRE), a Flap structure and a Woodchuck hepatitis virus posttranscriptional regulatory element (WPRE). The vector is pseudotyped with the vesicular stomatitis virus (VSV) G envelope protein.

	The PBMCs are enriched for CD8+ and CD4+ T lymphocytes, which are subsequently cultured together, activated with a magnetic-based CD3/CD28 activation reagent, and then transduced with the lentiviral vector encoding the GPRC5D-specific CAR. The cells are expanded in serum-free media containing interleukin-2, interleukin-7 and interleukin-15 to obtain the necessary number of CD3+ CAR+ cells and then harvested. The cells are ≥80% CD3+, with ≥10% CAR+. The cells respond to GPRC5D-expressing target cells by producing an array of pro-inflammatory cytokines and demonstrate cytotoxicity against the target tumour cells
arlocabtagène autoleucel	lymphocytes T autologues obtenus à partir de cellules mononucléaires de sang périphérique (PBMC) par leucaphérèse, transduits avec un vecteur lentiviral auto-inactivant et non répliquant codant un récepteur antigénique chimérique (CAR) ciblant le récepteur couplé à la protéine G, classe C groupe 5 membre D (GPRC5D). Le transgène exprimé comprend une séquence de tête CD33 humaine, un domaine de liaison du fragment variable à chaîne unique (scFv) spécifique du GPRC5D humain (clone ET150-8), une région charnière IgG4, un domaine transmembranaire CD28, un domaine de costimulation 4-1BB et un domaine de signalisation CD3ζ, sous le contrôle d'un promoteur hybride du facteur d'élongation 1 alpha humain (EF-1α) / d'un amplificateur R du virus de la leucémie à cellules T humaines de type 1 (HTLV-1). La construction est flanquée de répétitions terminales longues (LTR) en 5' et 3' et contient également un signal d'encapsidation ψ, un *gag* partiel, un élément de réponse Rev (RRE), une structure Flap et un élément de régulation post-transcriptionnelle du virus de l'hépatite de la marmotte (WPRE). Le vecteur est pseudotypé avec la protéine d'enveloppe G du virus de la stomatite vésiculaire (VSV). Les PBMCs sont enrichis en lymphocytes T CD8+ et CD4+ qui sont ensuite cultivés ensemble, activés avec un réactif d'activation CD3/CD28 à base magnétique, puis transduits avec le vecteur lentiviral codant le CAR spécifique du GPRC5D. Les cellules sont amplifiées dans un milieu sans sérum contenant de l'interleukine-2, de l'interleukine-7 et de l'interleukine-15 afin d'obtenir le nombre de cellules CD3+ CAR+ nécessaire, puis elles sont prélevées. Les cellules sont ≥80 % CD3+, avec ≥10 % CAR+. Les cellules répondent aux cellules cibles exprimant le GPRC5D en produisant une série de cytokines pro-inflammatoires et démontrent une cytotoxicité contre les cellules tumorales cibles
arlocabtagén autoleucel	linfocitos T autólogos obtenidos de células mononucleares de sangre periférica (PBMC) mediante leucoaféresis, transducidos con un vector lentiviral no replicativo, auto inactivante, que codifica para un receptor de antígenos quimérico (CAR) dirigido al receptor acoplado a proteína G, clase C, grupo 5, miembro D (GPRC5D). El transgén expresado contiene una secuencia líder del CD33 humano, un dominio de unión como fragmento variable de cadena sencilla (scFv) específico de GPRC5D humano (clon ET150-8), una región bisagra de IgG4, un dominio transmembrana de CD28, un dominio coestimulador de 4-1BB y un dominio de señalización de CD3ζ, bajo el control de un promotor híbrido del factor de elongación 1 alfa (EF-1α) humano / potenciador R del virus de la leucemia de linfocitos T tipo 1 (HTLV-1) humano. El constructo está flanqueado por repeticiones terminales largas (LTRs) en 5' y 3' y también contiene una señal de empaquetamiento ψ, *gag* parcial, un elemento de respuesta Rev (RRE), una estructura Flap y un

elemento regulador post-transcripcional del virus de la hepatitis de la marmota (WPRE). El vector está seudotipado con la proteína G de la envuelta del virus de la estomatitis vesicular (VSV).
Las PBMCs se enriquecen para linfocitos T CD4+ y CD8+ que son después cultivados juntos, activados con un reactivo de activación CD3/CD28 de base magnética y después transducidos con el vector lentiviral que codifica para el CAR específico de GPRC5D. Las células se expanden en medio sin suero que contiene interleuquina 2, interleuquina 7 e interleuquina 15 para obtener el número de células CD3+ CAR+ necesario y después se cosechan. Las células son ≥80% CD3+, con ≥10% CAR+. Las células responden a células diana que expresan GPRC5D produciendo un conjunto de citoquinas proinflamatorias y demuestran citotoxicidad contra las células diana tumorales

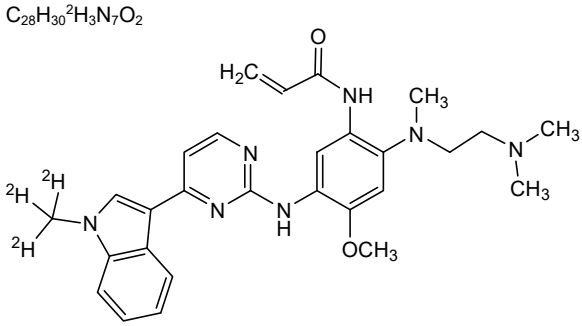
asandeutertinibum

asandeutertinib — *N*-[2-{[2-(dimethylamino)ethyl](methyl)amino}-4-methoxy-5-({4-[1-($^2H_3$)methyl-1*H*-indol-3-yl]pyrimidin-2-yl}amino)phenyl]prop-2-enamide

asandeutertinib — *N*-[2-{[2-(diméthylamino)éthyl](méthyl)amino}-4-méthoxy-5-({4-[1-($^2H_3$)méthyl-1*H*-indol-3-yl]pyrimidin-2-yl}amino)phényl]prop-2-énamide

asandeutertinib — *N*-[2-{[2-(dimetilamino)etil](metil)amino}-5-({4-[1-($^2H_3$)metil-1*H*-indol-3-il]pirimidin-2-il}amino)-4-metoxifenil]prop-2-enamida

$C_{28}H_{30}{}^2H_3N_7O_2$



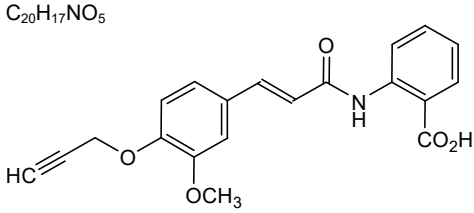
asengeprastum

asengeprast — 2-[(2*E*)-3-{3-methoxy-4-[(prop-2-yn-1-yl)oxy]phenyl}prop-2-enamido]benzoic acid

asengéprast — acide 2-[(2*E*)-3-{3-méthoxy-4-[(prop-2-yn-1-yl)oxy]phényl}prop-2-énamido]benzoïque

asengeprast — ácido 2-[(2*E*)-3-{3-metoxi-4-[(prop-2-in-1-il)oxi]fenil}prop-2-enamido]benzoico

$C_{20}H_{17}NO_5$



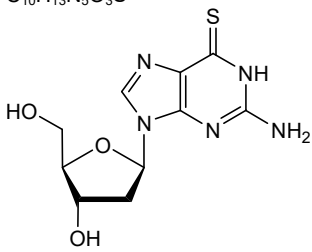
ateganosinum

ateganosine — 2′-deoxy-6-thioguanosine

atéganosine — 2′-désoxy-6-thioguanosine

ateganosina — 2′-desoxi-6-tioguanosina

$C_{10}H_{13}N_5O_3S$



atigotatugum #

atigotatug — immunoglobulin G1-kappa, anti-[Fucosyl-GM1 (fucosylated monosialoganglioside 1)], *Homo sapiens* monoclonal antibody;
H-gamma1 heavy chain *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV3-48*02 (90.7%) -(IGHD) -IGHJ3*01 (92.3%) M123>T (117), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (219) (123-220), hinge 1-15 (221-235), CH2 (236-345), CH3 E12 (361), M14 (363) (346-450), CHS (451-452)) (123-452)], (225-214')-disulfide with L-kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1D-16*01 (100%) -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 (231-231":234-234")-bisdisulfide, produced in a Chinese hamster ovary (CHO) cell line lacking the enzyme alpha-(1,6)-fucosyltransferase (FUT8), glycoform alfa

atigotatug — immunoglobuline G1-kappa, anti-[Fucosyl-GM1 (monosialoganglioside 1 fucosylé)], anticorps monoclonal *Homo sapiens*;
chaîne lourde H-gamma1 *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV3-48*02 (90.7%) -(IGHD) -IGHJ3*01 (92.3%) M123>T (117), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (219) (123-220), charnière 1-15 (221-235), CH2 (236-345), CH3 E12 (361), M14 (363) (346-450), CHS (451-452)) (123-452)], (225-214')-disulfure avec la chaîne légère L-kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1D-16*01 (100%) -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 (231-231":234-234")-bisdisulfure, produit dans une lignée cellulaire des cellules ovariennes de hamster chinois (CHO) ne présentant pas l'enzyme alpha-(1,6)-fucosyltransférase (FUT8), glycoforme alfa

atigotatug — inmunoglobulina G1-kappa, anti-[Fucosil-GM1 (monosialogangliósido 1 fucosilado)], anticuerpo monoclonal *Homo sapiens*;

cadena pesada H-gamma1 *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV3-48*02 (90.7%) -(IGHD) -IGHJ3*01 (92.3%) M123>T (117), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (219) (123-220), bisagra 1-15 (221-235), CH2 (236-345), CH3 E12 (361), M14 (363) (346-450), CHS (451-452)) (123-452)], (225-214')-disulfuro con la cadena ligera L-kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1D-16*01 (100%) -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 (231-231":234-234")-bisdisulfuro, producido en una línea celular de las células ováricas de hámster chino (CHO) en ausencia de la enzima alfa-1,6-fucosiltransferasa (FUT8), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG SVQPGESLRL SCVASGFTFS RYKMNWVRQA PGKGLEWVSY  50
ISRSGRDIYY ADSVKGRFTI SRDNAKNSLY LQMNSLRDED TAVYYCAGTV 100
TTYYYDFGMD VWGQGTTVTV SSASTKGPSV FPLAPSSKST SGGTAALGCL 150
VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ SSGLYSLSSV VTVPSSSLGT 200
QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL GGPSVFLFPP 250
KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE 350
PQVYTLPPSR EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP 400
PVLDSDGSFF LYSKLTVDKS RWQQGNVFSC SVMHEALHNH YTQKSLSLSP 450
GK                                                      452
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Light chain / Chaîne légère / Cadena ligera

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DIQMTQSPSS LSASVGDRVT ITCRASQGIS SWLAWYQQKP EKAPKSLIYA  50
ASSLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YNSYPPTFGG 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) 22-96 149-205 266-326 372-430
22"-96" 149"-205" 266"-326" 372"-430"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194'"
Inter-H-L (h 5-CL 126) 225-214' 225"-214'"
Inter-H-H (h 11, h 14) 231-231" 234-234"

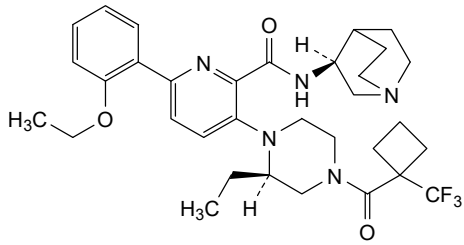
N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4: 302, 302"
Afucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes afucosylés / glicanos de tipo CHO biantenarios complejos afucosilados

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

atumelnantum

atumelnant	*N*-[(3*S*)-1-azabicyclo[2.2.2]octan-3-yl]-6-(2-ethoxyphenyl)-3-{(2*R*)-2-ethyl-4-[1-(trifluoromethyl)cyclobutane-1-carbonyl]piperazin-1-yl}pyridine-2-carboxamide
atumelnant	*N*-[(3*S*)-1-azabicyclo[2.2.2]octan-3-yl]-6-(2-éthoxyphényl)-3-{(2*R*)-2-éthyl-4-[1-(trifluorométhyl)cyclobutane-1-carbonyl]pipérazin-1-yl}pyridine-2-carboxamide
atumelnant	*N*-[(3*S*)-1-azabiciclo[2.2.2]octan-3-il]-3-{(2*R*)-2-etil-4-[1-(trifluorometil)ciclobutano-1-carbonil]piperazin-1-il}-6-(2-etoxifenil)piridina-2-carboxamida

$C_{33}H_{42}F_3N_5O_3$



avitotamigum #

avitotamig

immunoglobulin G1_L-kappa-scFvhk, anti-[*Homo sapiens* CD33 (sialic acid binding Ig-like lectin 3, SIGLEC3, SIGLEC-3, gp67, p67)] and anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], humanized monoclonal antibody, bipecific, tetravalent;
H-gamma1 heavy chain anti-CD33 humanized (1-449) [VH (*Homo sapiens* IGHV1-2*02 (85.7%) -(IGHD) -IGHJ4*01 (86.7%) T122>S (113), L123>S (114), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119)-*Homo sapiens* IGHG1*01v, G1m17,1>G1m3,1 CH1 R120, CH3 D12, L14, 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)], (222-213')-disulfide with the L-kappa-scFvhk chain humanized (1'-486') [L-kappa light chain anti-CD33 humanized (1'-213') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (88.3%) -IGKJ2*01 (88.3%) Q120>A (99'), I126>L (105') , CDR-IMGT [6.3.8] (27'-32'.50'-52'.89'-96')) (1'-106') -*Homo sapiens* IGKC*01 (100%), Km3, A45.1 (152'), V101 (190') (107'-213')] -17-mer threonyl-seryl-tris(tetraglycyl-seryl) linker (214'-230') -scFvhk anti-CD3E humanized (231'-486') [VH (*Homo sapiens* IGHV3-30*10 (70.4%) -(IGHD) -IGHJ4*01 (85.7%) L123>P (344'), CDR-IMGT [8.8.12] (255'-263'.281'-288'.327'-338') C114>S (335')) (231'-349') -30-mer hexakis(tetraglycyl-seryl) linker (350'-379') -V-KAPPA (*Homo sapiens* IGKV1-33*01 (81.1%) -(IGHD) -IGKJ2*02 (80.0%) Q120>C (478'), E125>Q (483'), CDR-IMGT [5.3.9] (406'-410'.428'-430'.467'-475')) (380'-486')]]; dimer (228-228'':231-231'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-DG44, non-glycosylated

avitotamig

immunoglobuline G1_L-kappa-scFvhk, anti-[*Homo sapiens* CD33 (lectine 3 de type Ig-like liant l'acide sialique, SIGLEC3, SIGLEC-3, gp67, p67)] et anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], anticorps monoclonal humanisé, bispécifique, tétravalent;
chaîne lourde H-gamma1 anti-CD33 humanisée (1-449) [VH (*Homo sapiens* IGHV1-2*02 (85.7%) -(IGHD) -IGHJ4*01 (86.7%) T122>S (113), L123>S (114), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119)-*Homo sapiens* IGHG1*01v, G1m17,1>G1m3,1 CH1 R120, CH3 D12, L14, 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)], (222-213')-disulfure avec

	la chaîne L-kappa-scFvhk humanisée (1'-486') [L-kappa chaîne légère anti-CD33 humanisée (1'-213') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (88.3%) -IGKJ2*01 (88.3%) Q120>A (99'), I126>L (105') , CDR-IMGT [6.3.8] (27'-32'.50'-52'.89'-96')) (1'-106') -*Homo sapiens* IGKC*01 (100%), Km3, A45.1 (152'), V101 (190') (107'-213')] -17-mer thréonyl-séryl-tris(tétraglycyl-séryl) linker (214'-230') -scFvhk anti-CD3E humanisé (231'-486') [VH (*Homo sapiens* IGHV3-30*10 (70.4%) -(IGHD) -IGHJ4*01 (85.7%) L123>P (344'), CDR-IMGT [8.8.12] (255'-263'.281'-288'.327'-338') C114>S (335')) (231'-349') -30-mer hexakis(tétraglycyl-séryl) linker (350'-379') -V-KAPPA (*Homo sapiens* IGKV1-33*01 (81.1%) -(IGHD) -IGKJ2*02 (80.0%) Q120>C (478'), E125>Q (483'), CDR-IMGT [5.3.9] (406'-410'.428'-430'.467'-475')) (380'-486')]]; dimère (228-228'':231-231'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-DG44, non-glycosylé
avitotamig	inmunoglobulina G1_L-kappa-scFvhk, anti-[*Homo sapiens* CD33 (lectina 3 de tipo Ig que se une al ácido siálico, SIGLEC3, SIGLEC-3, gp67, p67)] y anti-[*Homo sapiens* CD3E (CD3 épsilon, Leu-4)], anticuerpo monoclonal humanizado, biespecífico, tetravalente; cadena pesada H-gamma1 anti-CD33 humanizada (1-449) [VH (*Homo sapiens* IGHV1-2*02 (85.7%) -(IGHD) -IGHJ4*01 (86.7%) T122>S (113), L123>S (114), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119)-*Homo sapiens* IGHG1*01v, G1m17,1>G1m3,1 CH1 R120, CH3 D12, L14, 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)], (222-213')-disulfuro con la cadena L-kappa-scFvhk humanizada (1'-486') [L-kappa cadena ligera anti-CD33 humanizada (1'-213') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (88.3%) -IGKJ2*01 (88.3%) Q120>A (99'), I126>L (105') , CDR-IMGT [6.3.8] (27'-32'.50'-52'.89'-96')) (1'-106') -*Homo sapiens* IGKC*01 (100%), Km3, A45.1 (152'), V101 (190') (107'-213')] -17-mer treonil-seril-tris(tetraglicil-seril) enlace (214'-230') -scFvhk anti-CD3E humanizado (231'-486') [VH (*Homo sapiens* IGHV3-30*10 (70.4%) -(IGHD) -IGHJ4*01 (85.7%) L123>P (344'), CDR-IMGT [8.8.12] (255'-263'.281'-288'.327'-338') C114>S (335')) (231'-349') -30-mer hexakis(tetraglicil-seril) enlace (350'-379') -V-KAPPA (*Homo sapiens* IGKV1-33*01 (81.1%) -(IGHD) -IGKJ2*02 (80.0%) Q120>C (478'), E125>Q (483'), CDR-IMGT [5.3.9] (406'-410'.428'-430'.467'-475')) (380'-486')]]; dímero (228-228'':231-231'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-DG44, no glicosilado

Heavy chain / Chaîne lourde / Cadena pesada : H-gamma1 (H, H") anti-CD3

```
QVQLQQSGAE VVKPGASVKV SCKASGYSFT DYNMYWVRQA PGQGLEWMGY  50
IDPYKGGTIY NQKFQGRATL TRDTSISTAY MELSRLRSDD TAVYYCAREM 100
ITAYYFDYWG QGSSVTVSSA 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
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Light chain / Chaîne légère / Cadena ligera : L-kappa (L', L'") anti-CD33 - scFvhk anti-CD3E

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DIQMTQSPSS LSASVGDRVT ITCKASQDIN KYIAWYQHKP GKAPKLLIYY  50
ASNLQPGVPS RFSGSGSGRD FTFTISSLQP EDIATYYCLQ YDNLLTFGAG 100
TKLELKRTVA APSVFIFPPS DEQLKSGTAS VVCLLNNFYP REAKVQWKVD 150
NALQSGNSQE SVTEQDSKDS TYSLSSTLTL SKADYEKHKV YACEVTHQGL 200
SSPVTKSFNR GECTSGGGGS GGGGSGGGGS QVQLVQSGGG VVQPGRSLRL 250
SCKASGYTFT RYTMHWVRQA PGKCLEWIGY INPSRGYTNY NQKFKDRFTI 300
SRDNSKNTAF LQMDSLRPED TGVYFCARYY DDHYSLDYWG QGTPVTVSSG 350
GGGSGGGGSG GGGSGGGGSG GGGSGGGGSD IQMTQSPSSL SASVGDRVTI 400
TCSASSSVSY MNWYQQTPGK APKRWIYDTS KLASGVPSRF SGSGSGTDYT 450
FTISSLQPED IATYYCQQWS SNPFTFGCGT KLQITR                 486
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Post-translational modifications

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

Intra-H (C23-C104) 22-96 146-202 263-323 369-427
22"-96" 146"-202" 263"-323" 369"-427"
Intra-L (C23-C104) 23'-88' 133'-193' 252'-326' 402'-466'
23'"-88'" 133'"-193'" 252'"-326'" 402'"-466'"
Intra-L scFv C49 (VH)-C120 (VL)* 274'-478'
274'"-478'"
Inter-H-L (h 5-CL 126) 222-213' 222"-213'"
Inter-H-H (h 11, h 14) 228-228" 231-231"
* Engineered additional disulfide bond to stabilize the scFv.

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)
H VH Q1: 1, 1"

No N-glycosylation sites / pas de sites de N-glycosylation / ningùm posición de N-glycosilación
H CH2 N84.4>A (G1v29): 299, 299"

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

azirkitugum #

azirkitug — immunoglobulin G1-kappa, anti-[*Homo sapiens* CCR8 (C-C motif chemokine receptor 8, CKR-L1, CDw198)], humanized monoclonal antibody;
H-gamma1 heavy chain humanized (1-450) [VH (*Homo sapiens* IGHV3-73*01 (84.8%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.10.11] (26-33.51-60.99-109)) (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (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 L-kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-11*01 (78.9%) -IGKJ2*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 a Chinese hamster ovary (CHO) cell line, derived from the cell line CHO-DUX-B11, lacking the enzyme dihydrofolate reductase (DHFR), and co-expressing the RMD enzyme (GDP-6-deoxy-D-lyxo-4-hexulose reductase), glycoform alfa

azirkitug — immunoglobuline G1-kappa, anti-[*Homo sapiens* CCR8 (récepteur 8 de chimiokine C-C motif, CKR-L1, CDw198)], anticorps monoclonal humanisé;

chaîne lourde H-gamma1 humanisée (1-450) [VH (*Homo sapiens* IGHV3-73*01 (84.8%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.10.11] (26-33.51-60.99-109)) (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (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 L-kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-11*01 (78.9%) -IGKJ2*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 une lignée cellulaire des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-DUX-B11, ne présentant pas l'enzyme dihydrofolate réductase (DHFR), et co-exprimant l'enzyme RMD (GDP-6-désoxy-D-lyxo-4-hexulose réductase), glycoforme alfa

azirkitug

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CCR8 (receptor 8 de quimiocina C-C motivo, CKR-L1, CDw198)], anticuerpo monoclonal humanizado;
cadena pesada H-gamma1 humanizada (1-450) [VH (*Homo sapiens* IGHV3-73*01 (84.8%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.10.11] (26-33.51-60.99-109)) (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (217) (121-218), bisagra1-15 (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfuro con la cadena ligera L-kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-11*01 (78.9%) -IGKJ2*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 una línea celular de las células ováricas de hámster chino (CHO), línea celular derivada de CHO-DUX-B11, en ausencia de la enzima dihidrofolato reductasa (DHFR), y coexpresando la enzima RMD (GDP-6-desoxi-D-lixo-4-hexulosa reductasa), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

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EVQLVESGGG LVQPGGSLKL SCAASGFIFS NAVMYWVRQA SGKGLEWVAR  50
IKTKFNNYAT YYADAVKGRF TISRDDSKNM VYLQMNSLKT EDTAVYYCTA 100
GDRNKPFAYW GQGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK 450
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Light chain / Chaîne légère / Cadena ligera

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ETVVTQSPAT LSLSPGERAT LSCRASTSVI TLLHWFQQKP GQAPRLLIHG  50
ASNLESRVPA RFSGSGSGTD FTLTISSLEP EDFATYFCQQ SWNDPYTFGQ 100
GTKLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
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Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-98 147-203 264-324 370-428
22"-98" 147"-203" 264"-324" 370"-428"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194'"
Inter-H-L (h 5-CL 126) 223-214' 223"-214'"
Inter-H-H (h 11, h 14) 229-229" 232-232"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4: 300, 300"
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"

belacabnagenum franleucelum #

belacabnagene franleucel

allogeneic natural killer (NK) cells obtained from peripheral blood mononuclear cells (PBMC) by leukapheresis, transduced with a non-replicating gamma (γ)-retroviral vector encoding a chimeric antigen receptor (CAR) targeting CD19 together with a membrane bound form of human interleukin-15 (mbIL15). The expressed transgene comprises a CD8 alpha (CD8α) leader sequence, a humanized anti-CD19 single-chain variable fragment derived from murine FMC63, a CD8α transmembrane domain, an OX40 costimulatory domain, and a CD3ζ signalling domain, separated by a self-cleaving T2A peptide from IL-15 fused to a CD8α transmembrane domain, which creates a membrane bound form of IL-15 (mbIL-15) under control of a promoter derived from the U3 region of the murine stem cell virus (MSCV) 5' long terminal repeat (LTR).
The construct is flanked by 5' and 3' long terminal repeats (LTRs) and also contains a murine embryonic stem cell virus packaging signal.
The CD56+ CD3- NK cells are isolated by leukapheresis and co-cultured with a modified and irradiated K562 cell line. Specifically, the NK cells are isolated through a series of steps, first to reduce platelets and red blood cells, followed by a CD3+ depletion step, and lastly a positive selection using CD56+ enrichment. The cells are cultured in serum replacement media containing interleukin-12 (IL-12), interleukin-18 (IL-18) and interleukin-2 (IL-2) and co-cultured with a modified and irradiated K562 cell line. The cells are then transduced with the retroviral vector, and the transduced NK cells are further expanded in media containing human AB serum and IL-2.
The final substance consists of ≥90% CD56+CD3-NK cells with ≥20% CD56+ cells expressing the transgene. Cells secrete granulocyte-macrophage colony-stimulating factor (GM-CSF), interferon gamma (IFN-γ), and tumor necrosis factor alpha (TNF-α) when co-cultured with CD19-beads

bélacabnagène franleucel

cellules tueuses naturelles (NK) allogéniques obtenues par leucaphérèse à partir de cellules mononucléaires de sang périphérique (PBMC), transduites avec un vecteur non répliquant rétroviral-gamma (γ) codant un récepteur antigénique chimérique (CAR) ciblant le CD19 ainsi qu'une forme liée à la membrane de l'interleukine-15 humaine (mbIL15). Le transgène exprimé comprend une séquence de tête CD8 alpha (CD8α), un fragment à chaîne unique variable humanisé anti-CD19 dérivé du FMC63 murin, un domaine transmembranaire CD8α, un domaine co-stimulateur OX40 et un domaine de signalisation CD3ζ, séparée par un peptide T2A auto-clivant de l'IL-15 fusionné à un domaine transmembranaire CD8α, qui crée une forme d'IL-15 liée à la membrane (mbIL-15) sous le contrôle d'un promoteur dérivé de la région U3 du virus des cellules souches murines (MSCV). La construction est flanquée de répétitions terminales longues (LTR) en 5' et 3' et contient également un signal d'encapsidation du MSCV.
Les cellules NK CD56+ CD3- sont isolées par leucaphérèse et co-cultivées avec une lignée cellulaire K562 modifiée et irradiée. Plus précisément, les cellules NK sont isolées par une série d'étapes, d'abord pour réduire les plaquettes et les globules rouges, puis par une étape d'élimination des CD3+, et enfin d'une sélection positive par enrichissement des CD56+. Les cellules sont cultivées dans un milieu de remplacement du sérum contenant de l'interleukine-12 (IL-12), de l'interleukine-18 (IL-18) et de l'interleukine-2 (IL-2) et co-cultivées avec une lignée cellulaire K562 modifiée et irradiée. Les cellules sont ensuite transduites avec le vecteur rétroviral et les cellules NK transduites sont encore amplifiées dans un milieu contenant du sérum AB humain et de l'IL-2.

	La substance finale est constituée de ≥90% de cellules CD56+CD3-NK dont ≥20% des cellules CD56+ expriment le transgène. Les cellules sécrètent du facteur de stimulation des granulocytes et des macrophages (GM-CSF), de l'interféron gamma (IFN-γ) et du facteur de nécrose tumorale alpha (TNF-α) lorsqu'elles sont co-cultivées avec des billes CD19
belacabnagén franleucel	células natural killer (NK) alogénicas obtenidas de células mononucleares de sangre periférica (PBMC) mediante leucoaféresis, transducidas con un vector gamma (γ)-retroviral no replicativo que codifica para un receptor de antígeno quimérico (CAR) dirigido a CD19 junto con una forma unida a membrana de la interleuquina 15 humana (mbIL-15). El transgén expresado cotiene una secuencia líder de CD8 alfa (CD8α), un fragmento variable de cadena sencilla (scFv) humanizado anti-CD19 derivado del FMC63 murino, un domino transmembrana de CD8α, un domino coestimulador de OX40 y un dominio de señalización de CD3ζ, separado mediante un péptido de autoexcisión T2A de IL-15 fusionada a un domino transmembrana de CD8α, lo que crea una forma unida a membrana de IL-15 (mbIL-15), bajo el control de un promotor derivado de la región U3 de la repetición terminal larga (LTR) 5' del virus de células madre murino (MSCV). El constructo está flanqueado por repeticiones terminales largas (LTRs) en 5' y 3' y también contiene una señal de empaquetamiento del virus de células madre embrionarias murino. Las células NK CD56+ CD3- se aíslan por leucoaféresis y se cocultivan con una línea celular K562 modificada e irradiada. Específicamente, las células NK se aíslan mediante una serie de pasos, primero para reducir las plaquetas y los eritrocitos, seguido de un paso de depleción de CD3+ y finalmente una selección positiva usando un enriquecimiento en CD56+. Las células se cultivan en medio con substituto de suero que contiene interleuquina 12 (IL-12), interleuquina 18 (IL-18) e interleuquina 2 (IL-2) y se cocultivan con una línea celular K562 modificada e irradiada. Las células se transducen después con un vector retroviral y las células NK transducidas se expanden en medio que contiene suero humano AB e IL-2. La substancia final consiste en ≥90% células NK CD56+CD3- con ≥20% de las células CD56+ que expresan el transgén. Las células secretan factor estimulador de colonias granulocito-macrófago (GM-CSF), interferón gamma (IFN-γ) y factor de necrosis tumoral alfa (TNF-α) cuando se cocultivan con bolas CD19

bemremeranum

bemremeran	messenger RNA (mRNA), 5'-capped, encoding the codon-optimized receptor binding domain (RBD) of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) spike (S) glycoprotein (Omicron variant XBB.1.5; based upon GISAID EPI_ISL_16433058), with a cysteine to serine substitution at residue 233 (corresponding to cys534 in the full-length spike glycoprotein), expressed as a fusion protein with the S glycoprotein signal peptide derived from SARS-CoV-2 Wuhan-Hu 1 strain (GenBank: MN908947.3), flanked by 5' and 3' untranslated regions (UTRs) derived from the human β-globin gene and a 3' polyadenylation (polyA) tail; contains 5-methyluridine instead of uridine (*all*-U>5-Me-U) and 5-methylcytidine instead of cytidine (*all*-C>5-Me-C)

bemréméran	ARN messager (ARNm), protégé d'une coiffe en 5', codant le domaine de liaison au récepteur (RBD) aux codons optimisés de la glycoprotéine de spicule (S) du coronavirus 2 du syndrome respiratoire aigu sévère (SRAS-CoV-2) (sous-ligne Omicron XBB.1.5; d'après GISAID: EPI_ISL_16433058), avec substitution de la cystéine 233 par la sérine (correspondant à cys534 dans la glycoprotéine de spicule de pleine longueur), exprimé sous la forme d'une protéine de fusion avec le peptide signal de la glycoprotéine S dérivée de la souche SRAS-CoV-2 Wuhan-Hu 1 (GenBank: MN908947.3), flanquée des régions non traduites (UTR) en 5' et 3' dérivées du gène de la β-globine humaine et d'une queue de polyadénylation (polyA) en 3'; contient de la 5-méthyluridine en lieu de l'uridine (*tout*-U>5-Me-U) et de la 5-méthylcytidine en lieu de la cytidine (*tout*-C>5-Me-C)
bemremerán	ARN mensajero (ARNm), protegido en 5', que codifica, con codones optimizados, para el dominio de unión al receptor (RBD) de la glicoproteína de la espícula (S) del coronavirus 2 del síndrome respiratorio agudo severo (SRAS-CoV-2) (sublinaje XBB.1.5 de Omicron; basado en GISAID: EPI_ISL_16433058), con una substitución de la cisteína 233 a serina (correspondiente a cys534 en la glicoproteína de la espícula de longitud completa), expresado como una proteína de fusión con el péptido señal de la glicoproteína S derivada de la cepa Wuhan-Hu 1 de SRAS-CoV-2 (GenBank: MN908947.3), flanqueado por regiones 5' y 3' no traducidas (UTRs) derivadas del gen de la β-globina humana y una cola poliadenilación (poliA) en 3'; contiene 5-metiluridina en lugar de uridina (*todo*-U>5-Me-U) y 5-metilcitidina en lugar de citidina (*todo*-C>5-Me-C)

beretemcelum

beretemcel	allogeneic stem cells derived from donor adult liver tissue. The liver biopsy is digested, and the released cells placed in culture media containing fetal bovine serum (FBS), fibroblast growth factor-2 (FGF-2) and epidermal growth factor (EGF). The cells are frozen to generate a master cell bank (MCB) at an early passage, and then resuscitated and culture-expanded. The cells are characterized as adherent with an elongated morphology, the presence (≥70%) of cellular markers CD29, CD73, CD90, CD105, CD44 and albumin, and the absence of CD34 (<5%), CD45 (<2%) and CD14 (<5%). The cells differentiate into functional hepatocytes in a rotary cell culture system in media containing fetal calf serum (FCS), hepatocyte growth factor (HGF), and fibroblast growth factor 4 (FGF4) with the ability to transport indocyanine green (ICG)
bérétemcel	cellules souches allogéniques dérivées du tissu hépatique de donneurs adultes. La biopsie du foie est digérée et les cellules libérées sont placées dans un milieu de culture contenant du sérum bovin fœtal (FBS), du facteur de croissance des fibroblastes 2 (FGF-2) et du facteur de croissance épidermique (EGF). Les cellules sont congelées à un passage précoce pour générer une banque cellulaire maîtresse (MCB), puis ressuscitées et mises en culture. Les cellules se caractérisent par leur adhérence et leur morphologie allongée, la présence (≥70 %) des marqueurs cellulaires CD29, CD73, CD90, CD105, CD44 et de l'albumine, et l'absence de CD34 (<5%), CD45 (<2%) et CD14 (<5 %). Les cellules se différencient en hépatocytes fonctionnels dans un système de culture cellulaire rotatif dans un milieu contenant du sérum de veau fœtal (SVF), du facteur de croissance des hépatocytes (HGF) et du facteur de croissance des fibroblastes 4 (FGF4) avec la capacité de transporter du vert d'indocyanine (ICG)

beretemcel	células madre alogénicas derivadas de tejido de hígado de donante adulto. La biopsia de hígado se digiere y las células se liberadas se ponen en medio de cultivo que contiene suero bovino fetal (FBS), factor 2 de crecimiento de fibroblastos (FGF-2) y factor de crecimiento epidérmico (EGF). Las células se congelan para general un banco de células maestro (MCB) en un pase temprano y después se resucitan y se expanden en cultivo. Las células se caracterizan por ser adherentes con morfología alargada, la presencia (≥ 70%) de los marcadores celulares CD29, CD73, CD90, CD105, CD44 y albúmina, y la ausencia de CD34 (<5%), CD45 (<2%) y CD14 (<5%). Las células se diferencian a hepatocitos funcionales en un sistema de cultivo celular rotativo en medio que contiene suero de ternera fetal (FCS), factor de crecimiento de hepatocitos (HGF) y factor 4 de crecimiento de fibroblastos (FGF4) con la capacidad de transportar indocianina verde (ICG)

bexatamigum #

bexatamig	immunoglobulin (H-gamma1-VH-G1CH1h_L-kappa)_L-kappa-G1hCH2CH3, anti-[*Homo sapiens* IL3RA (interleukin 3 receptor subunit alpha, interleukin 3 receptor alpha (low affinity), CD123)] and anti-[*Homo sapiens* NCR1 (natural cytotoxicity triggering receptor 1, NKP46, NKp46, NK cell-activating receptor, LY94, CD335)], humanized monoclonal antibody, bispecific; [H-gamma1-VH-G1CH1h chain anti-IL3RA and anti-NCR1 humanized (1-681) [H-gamma1 anti-IL3RA [VH (*Homo sapiens* IGHV5-10-1*04 (82.7%) -(IGHD) -IGHJ6*01 (90.9%) T123>M (115), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (217) (121-218), hinge 1-15 (219-233), CH2 (234-343), CH3 (344-448), CHS K2>del (449) (121-449))] -4-mer-seryl-threonyl-glycyl-seryl linker (450-453) -VH-G1CH1h anti-NCR1 humanized (454-681) [VH (*Homo sapiens* IGHV1-69*08 (83.7%) -(IGHD) -IGHJ4*01 (92.3%) L123>T (568), CDR-IMGT [8.8.13] (479-486.504-511.550-562)) (454-573) -IGHG1*03 CH1-h (100%), G1m3 CH1 R120 (CH1 R120 (670) (574-671), hinge 1-10 (672-681)) (574-681)]; (676-214')-disulfide with L-kappa light chain anti-NCR1 humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (88.4%) -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')]; (223-220'':229-226'':232-229'')-trisdisulfide with the L-kappa-G1hCH2CH3 chain anti-IL3RA humanized (1-447'') [L-kappa anti-IL3RA (1''-220'') [V-KAPPA (*Homo sapiens* IGKV4-1*01 (90.1%) -IGKJ2*01 (100%), CDR-IMGT [12.3.9] (27''-38''.56''-58''.95''-103'')) (1''-113'') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 A45.1 (159''), V101 (197'') (114''-220'')] -G1hCH2CH3 (221''-447'') [*Homo sapiens* IGHG1*03 h-CH2-CH3-CHS (100%), nG1m1 CH3 E12, M14 (hinge 6-15 (221''-230''), CH2 (231''-340''), CH3 E12 (356''), M14 (358'') (341''-445''), CHS (446''-447''))]], produced in a cell line from Chinese hamster ovary (CHO) cells, derived from the cell line CHO-DXB11, glycoform alfa
bexatamig	immunoglobuline (H-gamma1-VH-G1CH1h_L-kappa)_L-kappa-G1hCH2CH3, anti-[*Homo sapiens* IL3RA (sous-unité alpha du récepteur de l'interleukine 3, récepteur alpha (faible affinité) de l'interleukine 3, CD123)] et anti-[*Homo sapiens* NCR1 (récepteur 1 déclenchant la cytotoxicité naturelle, NKP46, NKp46, récepteur d'activation des cellules NK, LY94, CD335)], anticorps monoclonal humanisé, bispécifique;

[chaîne H-gamma1-VH-G1CH1h anti-IL3RA and anti-NCR1 humanisée (1-681) [H-gamma1 anti-IL3RA [VH (*Homo sapiens* IGHV5-10-1*04 (82.7%) -(IGHD) -IGHJ6*01 (90.9%) T123>M (115), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (217) (121-218), charnière 1-15 (219-233), CH2 (234-343), CH3 (344-448), CHS K2>del (449) (121-449))] -4-mer-séryl-thréonyl-glycyl-séryl linker (450-453) -VH-G1CH1h anti-NCR1 humanisé (454-681) [VH (*Homo sapiens* IGHV1-69*08 (83.7%) -(IGHD) -IGHJ4*01 (92.3%) L123>T (568), CDR-IMGT [8.8.13] (479-486.504-511.550-562)) (454-573) -IGHG1*03 CH1-h (100%), G1m3 CH1 R120 (CH1 R120 (670) (574-671), charnière 1-10 (672-681)) (574-681)];
(676-214')-disulfure avec la chaîne légère L-kappa anti-NCR1 humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (88.4%) -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')];
(223-220":229-226":232-229")-trisdisulfure avec la chaîne L-kappa-G1hCH2CH3 anti-IL3RA humanisée (1-447") [L-kappa anti-IL3RA (1"-220") [V-KAPPA (*Homo sapiens* IGKV4-1*01 (90.1%) -IGKJ2*01 (100%), CDR-IMGT [12.3.9] (27"-38".56"-58".95"-103")) (1"-113") -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 A45.1 (159"), V101 (197") (114"-220")] -G1hCH2CH3 (221"-447") [*Homo sapiens* IGHG1*03 h-CH2-CH3-CHS (100%), nG1m1 CH3 E12, M14 (charnière 6-15 (221"-230"), CH2 (231"-340"), CH3 E12 (356"), M14 (358") (341"-445"), CHS (446"-447"))]], produit dans une lignée cellulaire des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-DXB11, glycoforme alfa

bexatamig

inmunoglobulina (H-gamma1-VH-G1CH1h_L-kappa)_L-kappa-G1hCH2CH3, anti-[*Homo sapiens* IL3RA (subunidad alfa del receptor de la interleukina 3, receptor alfa (baja afinidad) de la interleukina 3, CD123)] y anti-[*Homo sapiens* NCR1 (receptor 1 desencadenante de la citotoxicidad natural, NKP46, NKp46, receptor de la activación de las células NK, LY94, CD335)], anticuerpo monoclonal humanizado, biespecífico;
[cadena H-gamma1-VH-G1CH1h anti-IL3RA y anti-NCR1 humanizada (1-681) [H-gamma1 anti-IL3RA [VH (*Homo sapiens* IGHV5-10-1*04 (82.7%) -(IGHD) -IGHJ6*01 (90.9%) T123>M (115), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (217) (121-218), bisagra 1-15 (219-233), CH2 (234-343), CH3 (344-448), CHS K2>del (449) (121-449))] -4-mer-seril-treonil-glicil-seril enlace (450-453) -VH-G1CH1h anti-NCR1humanizado (454-681) [VH (*Homo sapiens* IGHV1-69*08 (83.7%) -(IGHD) -IGHJ4*01 (92.3%) L123>T (568), CDR-IMGT [8.8.13] (479-486.504-511.550-562)) (454-573) -IGHG1*03 CH1-h (100%), G1m3 CH1 R120 (CH1 R120 (670) (574-671), bisagra 1-10 (672-681)) (574-681)];
(676-214')-disulfuro con la cadena ligera L-kappa anti-NCR1 humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (88.4%) -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')];
(223-220":229-226":232-229")-trisdisulfuro con la cadena L-kappa-G1hCH2CH3 anti-IL3RA humanizada (1-447") [L-kappa anti-IL3RA (1"-220") [V-KAPPA (*Homo sapiens* IGKV4-1*01 (90.1%) -IGKJ2*01 (100%), CDR-IMGT [12.3.9] (27"-38".56"-58".95"-103")) (1"-113") -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 A45.1 (159"), V101 (197") (114"-220")] -G1hCH2CH3 (221"-447") [*Homo sapiens* IGHG1*03 h-CH2-CH3-CHS (100%), nG1m1 CH3 E12, M14 (bisagra 6-15 (221"-230"), CH2 (231"-340"), CH3 E12 (356"), M14 (358") (341"-445"), CHS (446"-447"))]], producido en una línea celular de las células ováricas de hámster chino (CHO), línea celular derivada de CHO-DXB11, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada : H-gamma1 (anti-IL3RA) -VH-G1CH1h (anti-NCR1) (H)

```
EVQLVQSGAE VKKPGESLKI SCKGSGYSFT DYYMKWARQM PGKGLEWMGD  50
IIPSSGATFY NQKFKGQVTI SADKSISTTY LQWSSLKASD TAMYYCARSH 100
LLRASWFAYW GQGTMVTVSS 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 QKSLSLSPGS 450
TGSQVQLVQS GAEVKKPGSS VKVSCKASGY TFSDYVINWV RQAPGQGLEW 500
MGEIYPGSGT NYYNEKFKAK ATITADKSTS TAYMELSSLR SEDTAVYYCA 550
RRGRYGLYAM DYWGQGTTVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC 600
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG 650
TQTYICNVNH KPSNTKVDKR VEPKSCDKTH S                     681
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Light chain / Chaîne légère / Cadena ligera : L-kappa anti-NCR1 (L')

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DIQMTQSPSS LSASVGDRVT ITCRASQDIS NYLNWYQQKP GKAPKLLIYY  50
TSRLHSGVPS RFSGSGSGTD FTFTISSLQP EDIATYFCQQ GNTRPWTFGG 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Heavy chain / Chaîne lourde / Cadena pesada : L-kappa-G1hCH2CH3 (anti-IL3RA) (LH")

```
DIVMTQSPDS LAVSLGERAT INCESSQSLL SSGNQKNYLT WYQQKPGQPP  50
KPLIYWASTR ESGVPDRFSG SGSGTDFTLT ISSLQAEDVA VYYCQNDYSY 100
PYTFGQGTKL EIKRTVAAPS VFIFPPSDEQ LKSGTASVVC LLNNFYPREA 150
KVQWKVDNAL QSGNSQESVT EQDSKDSTYS LSSTLTLSKA DYEKHKVYAC 200
EVTHQGLSSP VTKSFNRGEC DKTHTCPPCP APELLGGPSV FLFPPKPKDT 250
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT 350
LPPSREEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS 400
DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPGK    447
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 147-203 264-324 370-428 475-549 600-656
Intra-LH (C23-C104) 23"-94" 140"-200" 261"-321" 367"-425"
Intra-L (C23-C104) 23'-88' 134'-194'
Inter-H-L (h5-CL126) 676-214'
Inter-H-LH (h5-CL126*) or (-h5*) 223-220"
Inter-H-LH (h11, h14) 229-226" 232-229"
* 220" may be identified as CL126, last amino acid of the L part of LH (anti-ILR3A Fab arm) or as h5, first amino acid of the H part of LH (hinge).

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4: 300, 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"

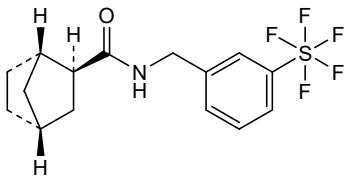
bimokalnerum

bimokalner (1*S*,2*S*,4*R*)-*N*-{[3-(pentafluoro-λ^6-sulfanyl)phenyl]methyl}bicyclo[2.2.1]heptane-2-carboxamide

bimokalner (1*S*,2*S*,4*R*)-*N*-{[3-(pentafluoro-λ^6-sulfanyl)phényl]méthyl}bicyclo[2.2.1]heptane-2-carboxamide

bimokalner (1*S*,2*S*,4*R*)-*N*-{[3-(pentafluoro-λ^6-sulfanil)fenil]metil}biciclo[2.2.1]heptano-2-carboxamida

$C_{15}H_{18}F_5NOS$



bofanglutidum

bofanglutide — L-histidylglycyl-L-α-glutamylglycyl-L-threonyl-L-phenylalanyl-L-threonyl-L-seryl-L-α-aspartyl-L-valyl-L-seryl-L-seryl-L-tyrosyl-L-leucyl-L-α-glutamylglycyl-L-glutaminyl-L-alanyl-L-alanyl-*N*^{6}-[(22*S*)-22,44-dicarboxy-10,19,24-trioxo-3,6,12,15-tetraoxa-9,18,23-triazatetratetracontan-1-oyl]-L-lysyl-L-α-glutamyl-L-phénylalanyl-L-isoleucyl-L-alanyl-L-tryptophyl-L-leucyl-L-valyl-L-arginylglycyl-L-arginylglycine

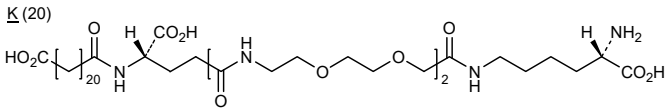
bofanglutide — L-histidylglycyl-L-α-glutamylglycyl-L-thréonyl-L-phénylalanyl-L-thréonyl-L-séryl-L-α-aspartyl-L-valyl-L-séryl-L-séryl-L-tyrosyl-L-leucyl-L-α-glutamylglycyl-L-glutaminyl-L-alanyl-L-alanyl-*N*^{6}-[(22*S*)-22,44-dicarboxy-10,19,24-trioxo-3,6,12,15-tétraoxa-9,18,23-triazatétratétracontan-1-oyl]-L-lysyl-L-α-glutamyl-L-phénylalanyl-L-isoleucyl-L-alanyl-L-tryptophyl-L-leucyl-L-valyl-L-arginylglycyl-L-arginylglycine

bofanglutida — L-histidilglicil-L-α-glutamilglicil-L-treonil-L-fenilalanil-L-treonil-L-seril-L-α-aspartil-L-valil-L-seril-L-seril-L-tirosil-L-leucil-L-α-glutamilglicil-L-glutaminil-L-alanil-L-alanil-*N*^{6}-[(22*S*)-22,44-dicarboxi-10,19,24-trioxo-3,6,12,15-tetraoxa-9,18,23-triazatetratetracontan-1-oil]-L-lisil-L-α-glutamil-L-fenilalanil-L-isoleucil-L-alanil-L-triptofil-L-leucil-L-valil-L-arginilglicil-L-arginilglicina

$C_{189}H_{295}N_{45}O_{59}$

HGEGTFTSDV SSYLEGQAAK EFIAWLVRGR G 31

Modified residue / Résidu modifié / Resto modificado



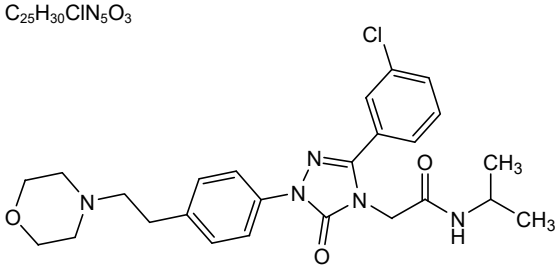
brezivaptanum

brezivaptan — 2-[3-(3-chlorophenyl)-1-{4-[2-(morpholin-4-yl)ethyl]phenyl}-5-oxo-1,5-dihydro-4*H*-1,2,4-triazol-4-yl]-*N*-(propan-2-yl)acetamide

brézivaptan — 2-[3-(3-chlorophényl)-1-{4-[2-(morpholin-4-yl)éthyl]phényl}-5-oxo-1,5-dihydro-4*H*-1,2,4-triazol-4-yl]-*N*-(propan-2-yl)acétamide

brezivaptán — 2-[3-(3-clorofenil)-1-{4-[2-(morfolin-4-il)etil]fenil}-5-oxo-1,5-dihidro-4*H*-1,2,4-triazol-4-il]-*N*-(propan-2-il)acetamida

$C_{25}H_{30}ClN_5O_3$



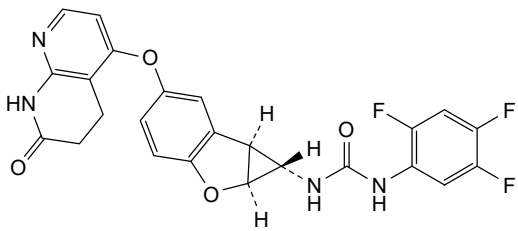
brimarafenibum

brimarafenib — *N*-{(1*S*,1a*S*,6b*S*)-5-[(7-oxo-5,6,7,8-tetrahydro-1,8-naphthyridin-4-yl)oxy]-1a,6b-dihydro-1*H*-cyclopropa[*b*]benzofuran-1-yl}-*N*′-(2,4,5-trifluorophenyl)urea

brimarafénib *N*-{(1*S*,1a*S*,6b*S*)-5-[(7-oxo-5,6,7,8-tétrahydro-1,8-naphtyridin-4-yl)oxy]-1a,6b-dihydro-1*H*-cyclopropa[*b*]benzofuran-1-yl}-*N*'-(2,4,5-trifluorophényl)urée

brimarafenib *N*-{(1*S*,1a*S*,6b*S*)-5-[(7-oxo-5,6,7,8-tetrahidro-1,8-naftiridin-4-il)oxi]-1a,6b-dihidro-1*H*-ciclopropa[*b*]benzofuran-1-il}-*N*'-(2,4,5-trifluorofenil)urea

$C_{24}H_{17}F_3N_4O_4$



brivekimigum #

brivekimig immunoglobulin IG single chain of 5 VH (VH-VH-VH'-VH''-VH') monomer, anti-[*Homo sapiens* TNFSF4 (TNF superfamily member 4, tumor necrosis factor superfamily member 4, OX40 ligand, OX40L, TAX transcriptionally-activated glycoprotein 1, TXGP1, gp34, CD252)], anti-[*Homo sapiens* TNF (tumor necrosis factor, TNF superfamily member 2, TNFSF2, TNF-alpha, TNFA)] and anti-[*Homo sapiens* ALB (albumin, human serum albumin, HSA)], monoclonal antibody VH-VH-VH'-VH''-VH', trispecific, pentavalent;
IG single chain VH-VH-VH'-VH''-VH' (1-630) [VH anti-TNFSF4 Vicpac/Homsap (*Vicugna pacos* IGHV3-3*01 (89.8%) -(IGHD) -IGHJ7*01 (92.3%) K120>Q (116)/*Homo sapiens* IGHV3-23*04 (82.7%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [9.8.16] (26-34.52-59.98-113)) (1-124) -9-mer (tetraglycyl-seryl-triglycyl-seryl) linker (125-133) -VH anti-TNFSF4 Vicpac/Homsap (*Vicugna pacos* IGHV3-3*01 (88.9%) -(IGHD) -IGHJ7*01 (92.3%) K120>Q (249)/*Homo sapiens* IGHV3-23*04 (83.7%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [9.8.16] (159-167.185-192.231-246)) (134-257) -9-mer (tetraglycyl-seryl-triglycyl-seryl) linker (258-266) -VH anti-TNF (*Homo sapiens* IGHV3-20*04 (87.8%) -(IGHD) -IGHJ1*01 (91.9%) W118>R (371), CDR-IMGT [8.8.8] (292-299.317-324.363-370)) (267-381) -9-mer (tetraglycyl-seryl-triglycyl-seryl) linker (382-390) -VH anti-ALB (*Homo sapiens* IGHV3-23*04 (88.5%) -(IGHD) -IGHJ1*01 (81.8%) W118>S (495), G119>S (496), CDR-IMGT [8.8.8] (416-423.441-448.487-494)) (391-505) -9-mer (tetraglycyl-seryl-triglycyl-seryl) linker (506-514) -VH anti-TNF (*Homo sapiens* IGHV3-20*04 (87.8%) -(IGHD) -IGHJ1*01 (90.0%) W118>R (619), CDR-IMGT [8.8.18] (540-547.565-572.611-618)) (515-630)], produced in the yeast *Pichia pastoris* (*Komagataella phaffii*), non-glycosylated

brivékimig immunoglobuline IG chaîne unique de 5 VH (VH-VH-VH'-VH''-VH') monomère, anti-[*Homo sapiens* TNFSF4 (membre 4 de la superfamille du TNF membre 4 de la superfamille du facteur de nécrose tumorale, OX40 ligand, OX40L, glycoprotéine 1 activée transcriptionellement par TAX, TXGP1, gp34, CD252)], anti-[*Homo sapiens* TNF (facteur de nécrose tumorale, membre 2 de la superfamille du TNF, TNFSF2, TNF-alpha, TNFA)] et anti-[*Homo sapiens* ALB (albumine, sérum albumine humaine, SAH), anticorps monoclonal VH-VH-VH'-VH''-VH', trispécifique, pentavalent;

	IG chaîne unique VH-VH-VH'-VH''-VH' (1-630) [VH anti-TNFSF4 Vicpac/Homsap (*Vicugna pacos* IGHV3-3*01 (89.8%) -(IGHD) -IGHJ7*01 (92.3%) K120>Q (116)/*Homo sapiens* IGHV3-23*04 (82.7%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [9.8.16] (26-34.52-59.98-113)) (1-124) -9-mer (tétraglycyl-séryl-triglycyl-séryl) linker (125-133) -VH anti-TNFSF4 Vicpac/Homsap (*Vicugna pacos* IGHV3-3*01 (88.9%) -(IGHD) -IGHJ7*01 (92.3%) K120>Q (249)/*Homo sapiens* IGHV3-23*04 (83.7%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [9.8.16] (159-167.185-192.231-246)) (134-257) -9-mer (tétraglycyl-séryl-triglycyl-séryl) linker (258-266) -VH anti-TNF (*Homo sapiens* IGHV3-20*04 (87.8%) -(IGHD) -IGHJ1*01 (91.9%) W118>R (371), CDR-IMGT [8.8.8] (292-299.317-324.363-370)) (267-381) -9-mer (tétraglycyl-séryl-triglycyl-séryl) linker (382-390) -VH anti-ALB (*Homo sapiens* IGHV3-23*04 (88.5%) -(IGHD) -IGHJ1*01 (81.8%) W118>S (495), G119>S (496), CDR-IMGT [8.8.8] (416-423.441-448.487-494)) (391-505) -9-mer (tétraglycyl-séryl-triglycyl-séryl) linker (506-514) -VH anti-TNF (*Homo sapiens* IGHV3-20*04 (87.8%) -(IGHD) -IGHJ1*01 (90.0%) W118>R (619), CDR-IMGT [8.8.18] (540-547.565-572.611-618)) (515-630)], produit dans la levure *Pichia pastoris* (*Komagataella phaffii*), non-glycosylé
brivekimig	inmunoglobulina IG cadena única de 5 VH (VH-VH-VH'-VH''-VH') monómero, anti-[*Homo sapiens* TNFSF4 (miembro 4 de la superfamília del TNF miembro 4 de la superfamília del fator de necrosis tumoral, OX40 ligando, OX40L, glicoproteína 1 activada transcripcionalmente por TAX, TXGP1, gp34, CD252)], anti-[*Homo sapiens* TNF (factor de necrosis tumoral, miembro 2 de la superfamilia del TNF, TNFSF2, TNF-alfa, TNFA)] y anti-[*Homo sapiens* ALB (albúmina, albumina sérica humana, SAH), anticuerpo monoclonal VH-VH-VH'-VH''-VH', triespecífico, pentavalente; IG cadena única VH-VH-VH'-VH''-VH' (1-630) [VH anti-TNFSF4 Vicpac/Homsap (*Vicugna pacos* IGHV3-3*01 (89.8%) -(IGHD) -IGHJ7*01 (92.3%) K120>Q (116)/*Homo sapiens* IGHV3-23*04 (82.7%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [9.8.16] (26-34.52-59.98-113)) (1-124) -9-mer (tetraglicil-seril-triglicil-seril) enlace (125-133) -VH anti-TNFSF4 Vicpac/Homsap (*Vicugna pacos* IGHV3-3*01 (88.9%) -(IGHD) -IGHJ7*01 (92.3%) K120>Q (249)/*Homo sapiens* IGHV3-23*04 (83.7%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [9.8.16] (159-167.185-192.231-246)) (134-257) -9-mer (tetraglicil-seril-triglicil-seril) enlace (258-266) -VH anti-TNF (*Homo sapiens* IGHV3-20*04 (87.8%) -(IGHD) -IGHJ1*01 (91.9%) W118>R (371), CDR-IMGT [8.8.8] (292-299.317-324.363-370)) (267-381) -9-mer (tetraglicil-seril-triglicil-seril) enlace (382-390) -VH anti-ALB (*Homo sapiens* IGHV3-23*04 (88.5%) -(IGHD) -IGHJ1*01 (81.8%) W118>S (495), G119>S (496), CDR-IMGT [8.8.8] (416-423.441-448.487-494)) (391-505) -9-mer (tetraglicil-seril-triglicil-seril) enlace (506-514) -VH anti-TNF (*Homo sapiens* IGHV3-20*04 (87.8%) -(IGHD) -IGHJ1*01 (90.0%) W118>R (619), CDR-IMGT [8.8.18] (540-547.565-572.611-618)) (515-630)], producido en la levadura *Pichia pastoris* (*Komagataella phaffii*), no glicosilado

Single chain / Chaîne unique / Cadena única : VH-VH-VH'-VH"-VH' (anti-TNFSF4, anti-TNF, anti-ALB)

```
DVQLVESGGG VVQPGGSLRL SCAASGRTFS SIYAKGWFRQ APGKEREFVA  50
AISRSGRSTS YADSVKGRFT ISRDNSKNTV YLQMNSLRPE DTALYYCAAV 100
GGATTVTASE WDYWGQGTLV TVSSGGGGSG GGSEVQLVES GGGVVQPGGS 150
LRLSCAASGR TFSSIYAKGW FRQAPGKERE FVAAISRSGR STSYADSVKG 200
RFTISRDNSK NTVYLQMNSL RPEDTALYYC AAVGGATTVT ASEWDYWGQG 250
TLVTVSSGGG GSGGGSEVQL VESGGGVVQP GGSLRLSCAA SGFTFSDYWM 300
YWVRQAPGKG LEWVSEINTN GLITKYPDSV KGRFTISRDN AKNTLYLQMN 350
SLRPEDTALY YCARSPSGFN RGQGTLVTVS SGGGGSGGGS EVQLVESGGG 400
VVQPGGSLRL SCAASGFTFR SFGMSWVRQA PGKGPEWVSS ISGSGSDTLY 450
ADSVKGRFTI SRDNSKNTLY LQMNSLRPED TALYYCTIGG SLSRSSQGTL 500
VTVSSGGGGS GGGSEVQLVE SGGGVVQPGG SLRLSCAASG FTFSDYWMYW 550
VRQAPGKGLE WVSEINTNGL ITKYPDSVKG RFTISRDNAK NTLYLQMNSL 600
RPEDTALYYC ARSPSGFNRG QGTLVKVSSA                        630
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Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra chain (C23-C104) 22-97 155-230 288-362 412-486 536-610

cafelkibartum #

cafelkibart	immunoglobulin G1-kappa, anti-[*Homo sapiens* CCR8 (C-C motif chemokine receptor 8, CKR-L1, CDw198)]; H-gamma1 heavy chain (1-453) [VH Musmus/Homsap (*Mus musculus* IGHV10-1*02 (92.9%) -(IGHD) -IGHJ4*01 (93.8%) S123>L (118)/*Homo sapiens* IGHV3-73*01 (88.0%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.10.14] (26-33.51-60.99-112)) (1-123) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, G1v7 CH2 D3, E117 (CH1 K120 (220) (124-221), hinge 1-15 (222-236), CH2 S3>D (245), I117>E (338) (237-346), CH3 D12 (362), L14 (364) (347-451), CHS (452-453)) (124-453)], (226-219')-disulfide with L-kappa light chain (1'-219') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV2-137*01 (91.0%) -IGKJ4*01 (91.7%) S120>Q (115')/*Homo sapiens* IGKV2-28*01 (87.0%) -IGKJ2*02 (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 (232-232":235-235")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa
cafelkibart	immunoglobuline G1-kappa, anti-[*Homo sapiens* CCR8 (récepteur 8 de chimiokine C-C motif, CKR-L1, CDw198)]; chaîne lourde H-gamma1 (1-453) [VH Musmus/Homsap (*Mus musculus* IGHV10-1*02 (92.9%) -(IGHD) -IGHJ4*01 (93.8%) S123>L (118)/*Homo sapiens* IGHV3-73*01 (88.0%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.10.14] (26-33.51-60.99-112)) (1-123) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, G1v7 CH2 D3, E117 (CH1 K120 (220) (124-221), charnière 1-15 (222-236), CH2 S3>D (245), I117>E (338) (237-346), CH3 D12 (362), L14 (364) (347-451), CHS (452-453)) (124-453)], (226-219')-disulfure avec la chaîne légère L-kappa (1'-219') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV2-137*01 (91.0%) -IGKJ4*01 (91.7%) S120>Q (115')/*Homo sapiens* IGKV2-28*01 (87.0%) -IGKJ2*02 (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 (232-232":235-235")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa
cafelkibart	inmunoglobulina G1-kappa, anti-[*Homo sapiens* CCR8 (receptor 8 de quimiocina C-C motivo, CKR-L1, CDw198)];

cadena pesada H-gamma1 (1-453) [VH Musmus/Homsap (*Mus musculus* IGHV10-1*02 (92.9%) -(IGHD) -IGHJ4*01 (93.8%) S123>L (118)/*Homo sapiens* IGHV3-73*01 (88.0%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.10.14] (26-33.51-60.99-112)) (1-123) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, G1v7 CH2 D3, E117 (CH1 K120 (220) (124-221), bisagra 1-15 (222-236), CH2 S3>D (245), I117>E (338) (237-346), CH3 D12 (362), L14 (364) (347-451), CHS (452-453)) (124-453)], (226-219')-disulfuro con la cadena ligera L-kappa (1'-219') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV2-137*01 (91.0%) -IGKJ4*01 (91.7%) S120>Q (115')/*Homo sapiens* IGKV2-28*01 (87.0%) -IGKJ2*02 (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 (232-232":235-235")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada : H-gamma1 (H, H") anti-CCR8

```
EVQLVESGGG LVQPGGSLKL SCAASGFTFN TYAMNWVRQA SGKGLEWVAR  50
IRSKANNYAT YYADSVKDRF TISRDDSKNT LYLQMNNLKT EDTAVYYCVR 100
DRSRGEDYAM DYWGQGTLVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC 150
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG 200
TQTYICNVNH KPSNTKVDKK VEPKSCDKTH TCPPCPAPEL LGGPDVFLFP 250
PKPKDTLMIS RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE 300
QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALPAPEEK TISKAKGQPR 350
EPQVYTLPPS RDELTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT 400
PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLS 450
PGK                                                     453
```

Light chain / Chaîne légère / Cadena ligera : L-kappa (L', L'") anti-CCR8

```
DIVMTQSPLS LPVTPGEPAS ISCRSSKSLL HSNANTYLYW FLQKPGQSPQ  50
LLIYRMSNLA SGVPDRFSGS GSGTAFTLKI SRVEAEDVGV YYCMQHLEYP 100
FTFGQGTKLE IKRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK 150
VQWKVDNALQ SGNSQESVTE QDSKDSTYSL SSTLTLSKAD YEKHKVYACE 200
VTHQGLSSPV TKSFNRGEC                                    219
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-98 150-206 267-327 373-431
22"-98" 150"-206" 267"-327" 373"-431"
Intra-L (C23-C104) 23'-93' 139'-199'
23'"-93'" 139'"-199'"
Inter-H-L (h 5-CL 126) 226-219' 226"-219'"
Inter-H-H (h 11, h 14) 232-232" 235-235"

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

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2: 453, 453"

calotatugum #
calotatug

immunoglobulin G1-kappa, anti-[*Homo sapiens* ERBB2 (receptor tyrosine-protein kinase erbB-2, epidermal growth factor receptor 2, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], *Homo sapiens* monoclonal antibody;
H-gamma1 heavy chain *Homo sapiens* (1-446) [VH (*Homo sapiens* IGHV3-48*01 (100%) -(IGHD) -IGHJ2*01 (100%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (214) (118-215), hinge 1-15 (216-230), CH2 (231-340), CH3 D12 (356), L14 (358) (341-445), CHS K2>del (446)) (118-446)], (220-215')-disulfide with L-kappa light chain *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (97.9%) -IGKJ4*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 (226-226":229-229")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1SV, glycoform alfa

calotatug

immunoglobuline G1-kappa, anti-[*Homo sapiens* ERBB2 (récepteur tyrosine-protéine kinase erbB-2, récepteur 2 du facteur de croissance épidermique, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], anticorps monoclonal *Homo sapiens*;
chaîne lourde H-gamma1 *Homo sapiens* (1-446) [VH (*Homo sapiens* IGHV3-48*01 (100%) -(IGHD) -IGHJ2*01 (100%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (214) (118-215), charnière 1-15 (216-230), CH2 (231-340), CH3 D12 (356), L14 (358) (341-445), CHS K2>del (446)) (118-446)], (220-215')-disulfure avec la chaîne légère L-kappa *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (97.9%) -IGKJ4*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 (226-226":229-229")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1SV, glycoforme alfa

calotatug

inmunoglobulina G1-kappa, anti-[*Homo sapiens* ERBB2 (receptor tirosina-proteína kinasa erbB-2, receptor 2 del factor de crecimiento epidérmico, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], anticuerpo monoclonal *Homo sapiens*;
cadena pesada H-gamma1 *Homo sapiens* (1-446) [VH (*Homo sapiens* IGHV3-48*01 (100%) -(IGHD) -IGHJ2*01 (100%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (214) (118-215), bisagra 1-15 (216-230), CH2 (231-340), CH3 D12 (356), L14 (358) (341-445), CHS K2>del (446)) (118-446)], (220-215')-disulfuro con la cadena ligera L-kappa *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (97.9%) -IGKJ4*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 (226-226":229-229")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1SV, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAASGFTFS SYSMNWVRQA PGKGLEWVSY  50
ISSSSSTIYY ADSVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARGG 100
HGYFDLWGRG TLVTVSSAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF 150
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC 200
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT 250
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT 350
LPPSRDELTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS 400
DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPG     446
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Light chain / Chaîne légère / Cadena ligera

```
EIVLTQSPGT LSLSPGERAT LSCRASQSVS SSYLAWYQQK PGQAPRLLIY  50
GASSRATGIP DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QYHHSPLTFG 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) 22-96 144-200 261-321 367-425
22"-96" 144"-200" 261"-321" 367"-425"
Intra-L (C23-C104) 23'-89' 135'-195'
23'"-89'" 135'"-195'"
Inter-H-L (h 5-CL 126) 220-215' 220"-215'"
Inter-H-H (h 11, h 14) 226-226" 229-229"

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

camalprinum alfa

camalprin alfa — human alpha-1-antitrypsin (alpha-1 protease inhibitor, alpha-1-antiproteinase, serpin A1) [C^{232}>S, ^{357}PMS^{359}>KRK]-variant, produced in Chinese hamster ovary (CHO) cells, cell line CHO-GS, glycoform alfa

camalprine alfa — alpha-1-antitrypsine humaine (inhibiteur de la protéase alpha-1, alpha-1-antiprotéinase, serpine A1), [C^{232}>S, ^{357}PMS^{359}>KRK]-variant, produite dans des cellules ovariennes de hamster chinois (CHO) lignée cellulaire CHO-GS, glycoforme alfa

camalprina alfa — antitripsina alfa 1 humana (inhibidor de la proteasa alfa-1, antiproteinasa alfa-1, serpin A1) [C^{232}>S, ^{357}PMS^{359}>KRK]-variante, producido en las células ováricas de hámster chino (CHO), línea celular CHO-GS, glicoforma alfa

Sequence / Séquence / Secuencia

```
EDPQGDAAQK TDTSHHDQDH PTFNKITPNL AEFAFSLYRQ LAHQSNSTNI   50
FFSPVSIATA FAMLSLGTKA DTHDEILEGL NFNLTEIPEA QIHEGFQELL  100
RTLNQPDSQL QLTTGNGLFL SEGLKLVDKF LEDVKKLYHS EAFTVNFGDT  150
EEAKKQINDY VEKGTQGKIV DLVKELDRDT VFALVNYIFF KGKWERPFEV  200
KDTEEEDFHV DQVTTVKVPM MKRLGMFNIQ HSKKLSSWVL LMKYLGNATA  250
IFFLPDEGKL QHLENELTHD IITKFLENED RRSASLHLPK LSITGTYDLK  300
SVLGQLGITK VFSNGADLSG VTEEAPLKLS KAVHKAVLTI DEKGTEAAGA  350
MFLEAIKRKI PPEVKFNKPF VFLMIEQNTK SPLFMGKVVN PTQK        394
```

Mutation / Mutation / Mutación
C^{232}>**S**, ^{357}PMS^{359}>**KRK**

Post-translation modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
none / aucun / ninguna

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
N46, N83, N247

Oxidation sites / Sites d'oxydation / Posiciones de oxidación
M226, M242, M351, M374

Deamidation sites / Sites de désamidation / Posiciones de desamidación
N104, N116, N314, N378

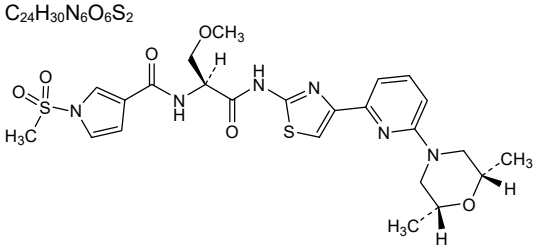
camibirstatum

camibirstat — *N*-{(2*S*)-1-[(4-{6-[(2*R*,6*S*)-2,6-dimethylmorpholin-4-yl]pyridin-2-yl}-1,3-thiazol-2-yl)amino]-3-methoxy-1-oxopropan-2-yl}-1-(methanesulfonyl)-1*H*-pyrrole-3-carboxamide

camibirstat — *N*-{(2*S*)-1-[(4-{6-[(2*R*,6*S*)-2,6-diméthylmorpholin-4-yl]pyridin-2-yl}-1,3-thiazol-2-yl)amino]-3-méthoxy-1-oxopropan-2-yl}-1-(méthanesulfonyl)-1*H*-pyrrole-3-carboxamide

camibirstat — *N*-{(2*S*)-1-[(4-{6-[(2*R*,6*S*)-2,6-dimetilmorfolin-4-il]piridin-2-il}-1,3-tiazol-2-il)amino]-3-metoxi-1-oxopropan-2-il}-1-(metanosulfonil)-1*H*-pirrol-3-carboxamida

$C_{24}H_{30}N_6O_6S_2$



cesnicabtagenum autoleucelum #

cesnicabtagene autoleucel	autologous T lymphocytes obtained from peripheral blood mononuclear cells (PBMC) by leukapheresis, transduced with a self-inactivating, non-replicating lentiviral vector encoding a chimeric antigen receptor (CAR) targeting the B-cell maturation antigen (BCMA). The expressed transgene comprises an IgGκ chain V-III leader sequence, a humanized anti-BCMA single chain variable fragment (scFv, clone J22.9), a CD8α hinge and transmembrane domain, and a 4-1BB co-stimulatory domain and CD3ζ signalling domain, under control of the human elongation factor 1 alpha (EF-1α) promoter. The construct is flanked by 5' and 3' long terminal repeats (LTRs) and also contains a ψ packaging signal, a Rev response element (RRE), a central polypurine tract (cPPT) sequence and a Woodchuck hepatitis virus posttranscriptional regulatory element (WPRE). The vector is pseudotyped with the vesicular stomatitis virus (VSV) G envelope protein. The leukapheresis material is enriched for CD4+ and CD8+ T lymphocytes by positive immunoselection prior to activation with CD3 and CD28 agonists in growth media containing interleukin 7 (IL-7) and interleukin 5 (IL-5). The cells are then transduced with the lentiviral vector and expanded in growth media containing interleukin 7 (IL-7) and interleukin 5 (IL-5). The cell suspension consists of T lymphocytes (>70%), with greater than 20% of the T lymphocytes expressing the CAR-BCMA transgene. The transduced T lymphocytes demonstrate cytotoxicity against BCMA-expressing cells
cesnicabtagène autoleucel	lymphocytes T autologues obtenus à partir de cellules mononucléaires de sang périphérique (PBMC) par leucaphérèse, transduits avec un vecteur lentiviral auto-inactivant et non répliquant codant un récepteur antigénique chimérique (CAR) ciblant l'antigène de maturation des cellules B (BCMA). Le transgène exprimé comprend une séquence de tête de la chaîne IgGκ V-III, un fragment variable à chaîne unique (scFv) humanisé anti-BCMA (clone J22.9), une charnière CD8α et un domaine transmembranaire, ainsi qu'un domaine de costimulation 4-1BB et un domaine de signalisation CD3ζ, sous le contrôle du promoteur du facteur d'élongation 1 alpha humain (EF-1α). La construction est flanquée de répétitions terminales longues (LTR) en 5' et 3' et contient également un signal d'encapsidation ψ, un élément de réponse Rev (RRE), une séquence du tractus polypurine central (cPPT) et un élément de régulation post-transcriptionnelle du virus de l'hépatite de la marmotte (WPRE). Le vecteur est pseudotypé avec la protéine d'enveloppe G du virus de la stomatite vésiculaire (VSV). Le matériel de leucaphérèse est enrichi en lymphocytes T CD4+ et CD8+ par immunosélection positive avant d'être activé avec des agonistes CD3 et CD28 dans des milieux de croissance contenant de l'interleukine 7 (IL-7) et de l'interleukine 5 (IL-5). Les cellules sont ensuite transduites avec le vecteur lentiviral et amplifiées dans un milieu de croissance contenant de l'interleukine 7 (IL-7) et de l'interleukine 5 (IL-5). La suspension cellulaire est composée de lymphocytes T (>70%), dont plus de 20% expriment le transgène CAR-BCMA. Les lymphocytes T transduits présentent une cytotoxicité contre les cellules exprimant le BCMA

cesnicabtagén autoleucel	linfocitos T autólogos obtenidos de células mononucleares de sangre periférica (PBMC) mediante leucoaféresis, transducidos con un vector lentiviral no replicativo, auto inactivante, que codifica para un receptor de antígenos quimérico (CAR) dirigido al antígeno de maduración de linfocitos B (BCMA). El transgén expresado contiene una secuencia líder de la cadena IgGκV-III, un fragmento variable de cadena sencilla (scFv) humanizado anti-BCMA (clon J22.9), un dominio bisagra y transmembrana de CD8α, y un dominio coestimulador de 4-1BB y un dominio de señalización de CD3ζ, bajo el control del promotor del factor de elongación 1 alfa (EF-1α) humano. El constructo está flanqueado por repeticiones terminales largas (LTRs) en 5' y 3' y también contiene una señal de empaquetamiento ψ, un elemento de respuesta Rev (RRE), una secuencia de tracto de polipurina central (cPPT) y un elemento regulador post-transcripcional del virus de la hepatitis de la marmota (WPRE). El vector está seudotipado con la proteína G de la envuelta del virus de la estomatitis vesicular (VSV). El material de leucoaféresis se enriquece para linfocitos T CD4+ y CD8+ mediante inmunoselección positiva antes de la activación con agonistas de CD3 y CD28 en medio de crecimiento que contiene interleuquina 7 (IL-7) e interleuquina 5 (IL-5). Las células se transducen después con el vector lentiviral y se expanden en medio de cultivo que contiene interleuquina 7 (IL-7) e interleuquina 5 (IL-5). La suspensión celular consiste en linfocitos T (>70%), con más del 20% de los linfocitos T que expresan el transgén CAR-BCMA. Los linfocitos T transducidos demuestran citotoxicidad contra células que expresan BCMA

ciracigenum golparvovecum #

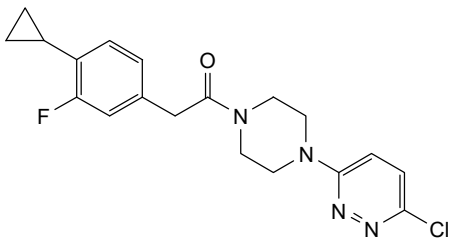
ciracigene golparvovec	recombinant, self-complementary non-replicating adeno-associated virus vector with Olig-001* capsid (rAAV-Olig-001) encoding codon-optimized human aspartoacylase (ASPA, ASP, ACY2) under control of a cytomegalovirus (CMV) enhancer/chicken β-actin (CBh) hybrid promoter and terminated by a bovine growth hormone polyadenylation signal, flanked by adeno-associated virus 2 (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. *The Olig-001 capsid is a chimeric mixture of AAV1, 2, 6, 8 and 9 that facilitates entry into oligodendrocytes.
ciracigène golparvovec	vecteur recombinant, auto-complémentaire et non répliquant avec une capside Olig-001* du virus adéno-associé (rAAV-Olig-001) codant une aspartoacylase humaine aux codons optimisés (ASPA, ASP, ACY2) sous le contrôle d'un amplificateur du cytomégalovirus (CMV)/promoteur hybride de la β-actine de poulet (CBh) et terminé par un signal de polyadénylation de l'hormone de croissance bovine, flanqué de répétitions terminales inversées (ITR) du virus adéno-associé 2 (AAV2). Le génome du vecteur est un dimère tête à tête, auto-complémentaire, avec la cassette du génome du vecteur localisée en 5' de la répétition terminale inversée interne mutée (Δ-ITR) dans une orientation complémentaire inverse et en 3' de la Δ-ITR dans une orientation vers l'avant *La capside d'Olig-001 est un mélange chimérique d'AAV1, 2, 6, 8 et 9 qui facilite l'entrée dans les oligodendrocytes.

ciracigén golparvovec	vector de virus adenoasociado con cápsida Olig-001* recombinante (rAAV-Olig-001), auto complementario, no replicativo, que codifica, con codones optimizados, para la aspartoacilasa humana (ASPA, ASP, ACY2) bajo el control de un potenciador del citomegalovirus/promotor híbrido de la β-actina de pollo (CBh) y terminado por una señal de poliadenilación de la hormona de crecimiento bovina, flanqueado por repeticiones terminales invertidas (ITRs) del virus adenoasociado 2 (AAV2). El genoma del vector es un dímero auto complementario en disposición cabeza con cabeza, con el casete del genoma del vector localizado en posición 5' de la repetición terminal invertida interna mutada (Δ-ITR) en una orientación complementaria inversa y 3' de la Δ-ITR) en una orientación directa *La cápsida Olig-001 es una mezcla quimérica de AAV1, 2, 6, 8 y 9 que facilita la entrada en oligodendrocitos.

claziprotamidum

claziprotamide	1-[4-(6-chloropyridazin-3-yl)piperazin-1-yl]-2-(4-cyclopropyl-3-fluorophenyl)ethan-1-one
claziprotamide	1-[4-(6-chloropyridazin-3-yl)pipérazin-1-yl]-2-(4-cyclopropyl-3-fluorophényl)éthan-1-one
claziprotamida	2-(4-ciclopropil-3-fluorofenil)-1-[4-(6-cloropiridazin-3-il)piperazin-1-il]etan-1-ona

$C_{19}H_{20}ClFN_4O$



comekibartum #

comekibart	immunoglobulin G4-kappa, anti-[*Homo sapiens* IL4R (interleukin 4 receptor, IL4RA, IL-4RA, interleukin 13 receptor, CD124)], humanized monoclonal antibody; H-gamma4 heavy chain humanized (1-448) [VH (*Homo sapiens* IGHV3-48*01 (93.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122)-*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, G4v5 h P10, G4v24 CH3 L107, S114 (CH1 (123-220), hinge 1-12 S10>P (230) (221-232), CH2 L92 (311) (233-342), CH3 M107>L (430), N114>S (436) (343-447), CHS K2>del (448)) (123-448)], (136-214')-disulfide with L-kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (89.5%) -IGKJ2*02 (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'-114')]; dimer (228-228":231-231")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa

comékibart

immunoglobuline G4-kappa, anti-[*Homo sapiens* IL4R (récepteur de l'interleukine 4, IL4RA, IL-4RA, récepteur de l'interleukine 13, CD124)], anticorps monoclonal humanisé;
chaîne lourde H-gamma4 humanisée (1-448) [VH (*Homo sapiens* IGHV3-48*01 (93.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122)-*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, G4v5 h P10, G4v24 CH3 L107, S114 (CH1 (123-220), charnière 1-12 S10>P (230) (221-232), CH2 L92 (311) (233-342), CH3 M107>L (430), N114>S (436) (343-447), CHS K2>del (448)) (123-448)], (136-214')-disulfure avec la chaîne légère L-kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (89.5%) -IGKJ2*02 (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'-114')]; dimère (228-228":231-231")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa

comekibart

inmunoglobulina G4-kappa, anti-[*Homo sapiens* IL4R (receptor de la interleukina 4, IL4RA, IL-4RA, receptor de la interleukina 13, CD124)], anticuerpo monoclonal humanizado;
cadena pesada H-gamma4 humanizada (1-448) [VH (*Homo sapiens* IGHV3-48*01 (93.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122)-*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, G4v5 h P10, G4v24 CH3 L107, S114 (CH1 (123-220), bisagra 1-12 S10>P (230) (221-232), CH2 L92 (311) (233-342), CH3 M107>L (430), N114>S (436) (343-447), CHS K2>del (448)) (123-448)], (136-214')-disulfuro con la cadena ligera L-kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (89.5%) -IGKJ2*02 (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'-114')]; 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 : H-gamma4 (H, H") anti-IL4R

```
EVQLVESGGG LVQPGGSLRL SCAASGFTFS DYGMHWVRQA PGKGLEWVSY  50
ISSGSTTIYY ADTVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARIS 100
TVVAKRYAMD 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 EGNVFSCSVL HEALHSHYTQ KSLSLSLG   448
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Light chain / Chaîne légère / Cadena ligera : L-kappa (L', L'") anti-IL4R

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DIQMTQSPSS LSASVGDRVT ITCRASQDIS NYLNWYQQKP GKAPKLLIYY  50
TSRLHSGVPS RFSGSGSGTD FTLTISSLQP EDIATYYCQQ INALPFTFGQ 100
GTKLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

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

Intra-H (C23-C104)	22-96	149-205	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-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

crebankitugum #

crebankitug	immunoglobulin G1-lambda2, anti-[*Homo sapiens* IL7R (interleukin 7 receptor, IL7RA, CD127)], *Homo sapiens* monoclonal antibody; H-gamma1 heavy chain *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV3-43D*03 (87.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens* IGHG1*03v (100%), G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (214) (118-215), hinge 1-15 (216-230), CH2 (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-215')-disulfide with L-lambda2 light chain *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV6-57*01 (96.8%) -IGLJ3*02 (100%), CDR-IMGT [8.3.9] (26'-33'.51'-53'.92'-100')) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')]; dimer (226-226'':229-229'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1SV, glycoform alfa
crébankitug	immunoglobuline G1-lambda2, anti-[*Homo sapiens* IL7R (récepteur de l'interleukine 7, IL7RA, CD127)], anticorps monoclonal *Homo sapiens*; chaîne lourde H-gamma1 *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV3-43D*03 (87.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens* IGHG1*03v (100%), G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (214) (118-215), charnière 1-15 (216-230), CH2 (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-215')-disulfure avec la chaîne légère L-lambda2 *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV6-57*01 (96.8%) -IGLJ3*02 (100%), CDR-IMGT [8.3.9] (26'-33'.51'-53'.92'-100')) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')]; dimère (226-226'':229-229'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1SV, glycoforme alfa
crebankitug	inmunoglobulina G1-lambda2, anti-[*Homo sapiens* IL7R (receptor de la interleukina 7, IL7RA, CD127)], anticuerpo monoclonal *Homo sapiens*; cadena pesada H-gamma1 *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV3-43D*03 (87.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens* IGHG1*03v (100%), G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (214) (118-215), bisagra 1-15 (216-230), CH2 (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-215')-disulfuro con la cadena ligera L-lambda2 *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV6-57*01 (96.8%) -IGLJ3*02 (100%), CDR-IMGT [8.3.9] (26'-33'.51'-53'.92'-100')) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')]; dímero (226-226'':229-229'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1SV, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVKPGGSLRL SCAASGFTFD DSVMHWVRQA PGKGLEWVSL  50
VGWDGFFTYY ADSVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARQG 100
DYMGNNWGQG TLVTVSSAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF 150
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC 200
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT 250
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT 350
LPPSREEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS 400
DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPGK    447
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Light chain / Chaîne légère / Cadena ligera

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NFMLTQPHSV SESPGKTVTI SCTRSSGSID SSYVQWYQQR PGSSPTTVIY  50
EDDQRPSGVP DRFSGSIDSS SNSASLTISG LKTEDEADYY CQSYDFHHLV 100
FGGGTKLTVL GQPKAAPSVT LFPPSSEELQ ANKATLVCLI SDFYPGAVTV 150
AWKADSSPVK AGVETTTPSK QSNNKYAASS YLSLTPEQWK SHRSYSCQVT 200
HEGSTVEKTV APTECS                                      216
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 144-200 261-321 367-425
22"-96" 144"-200" 261"-321" 367"-425"
Intra-L (C23-C104) 22'-91' 138'-197'
22'"-91'" 138'"-197'"
Inter-H-L (h 5-CL 126) 220-215' 220"-215'"
Inter-H-H (h 11, h 14) 226-226" 229-229"

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

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

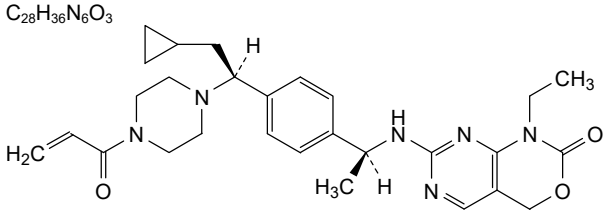
crelosidenibum

crelosidenib — 7-{[(1*S*)-1-(4-{(1*S*)-1-[4-(prop-2-enoyl)piperazin-1-yl]-2-cyclopropylethyl}phenyl)ethyl]amino}-1-ethyl-1,4-dihydro-2*H*-pyrimido[4,5-*d*][1,3]oxazin-2-one

crélosidénib — 7-{[(1*S*)-1-(4-{(1*S*)-1-[4-(prop-2-énoyl)pipérazin-1-yl]-2-cyclopropyléthyl}phényl)éthyl]amino}-1-éthyl-1,4-dihydro-2*H*-pyrimido[4,5-*d*][1,3]oxazin-2-one

crelosidenib — 7-{[(1*S*)-1-(4-{(1*S*)-1-[4-(prop-2-enoil)piperazin-1-il]-2-ciclopropiletil}fenil)etil]amino}-1-etil-1,4-dihidro-2*H*-pirimido[4,5-*d*][1,3]oxazin-2-ona

$C_{28}H_{36}N_6O_3$



cugrastomigum

cugrastomig — immunoglobulin IG fused to 2 scFv (H-gamma1-scFvhk_L'-kappa) dimer bisdisulfide, anti-[*Homo sapiens* LAG3 (lymphocyte activating 3, lymphocyte-activation 3, CD223)] and scFv anti-[*Homo sapiens* PDCD1 (programmed cell death 1, PD-1, PD1, CD279)], *Homo sapiens*, humanized and chimeric monoclonal antibody, bispecific, tetravalent;

	H-gamma1 heavy chain anti-LAG3 fused to a scFv anti-PDCD1 (1-716) [H-gamma1 heavy chain anti-LAG3 *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV4-34*01 (90.6%) -(IGHD) -IGHJ5*02 (93.8%), CDR-IMGT [8.7.14] (26-33.51-57.96-109)) (1-120)-*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, G1v14-1 CH2 A1.3, A1.2, A1 (CH1 K120 (217) (121-218), hinge 1-15 (219-233), CH2 L1.3>A (237), L1.2>A (238), G1>A (240)(234-343), CH3 D12 (359), L14 (361) (344-448), CHS (449-450)) (121-450)] -20-mer tetrakis(tetraglycyl-seryl) linker (451-470) -scFvhk anti-PDCD1 humanized and chimeric (471-716) [humanized VH (*Homo sapiens* IGHV3-23*04 (88.7%) -IGHD -IGHJ6*01 (90.9%) T123>L (583), CDR-IMGT [8.8.11] (496-503.521-528.567-577)) (471-588) -20-mer tetrakis(tetraglycyl-seryl) linker (589-608) -V-KAPPA Musmus/Homsap (*Mus musculus* IGKV14-111*01 (86.3%) -IGKJ5*01 (100%)/*Homo sapiens* IGKV1-16*01 (80.0%) -IGKJ2*01 (81.8%) Q120>A (708), I126>L (714), CDR-IMGT [6.3.9] (635-640.658-660.697-705)) (609-716)]]; (223-214')-disulfide with L-kappa light chain anti-LAG3 *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-11*01 (97.9%) -IGKJ5*01 (91.7%) R123>N (103'), 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
cugrastomig	immunoglobuline IG fusionnée à 2 scFv (H-gamma1-scFvhk_L'-kappa) dimère bisdisulfure, anti-[*Homo sapiens* LAG3 (activateur 3 des lymphocytes, lymphocyte-activation 3, CD223) et scFv anti-[*Homo sapiens* PDCD1 (protéine 1 de mort cellulaire programmée, PD-1, PD1, CD279)], anticorps monoclonal *Homo sapiens*, humanisé et chimérique, bispécifique, tétravalent; chaîne lourde H-gamma1 anti-LAG3 fusionnée à un scFv anti-PDCD1 (1-716) [chaîne lourde H-gamma1 anti-LAG3 *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV4-34*01 (90.6%) -(IGHD) -IGHJ5*02 (93.8%), CDR-IMGT [8.7.14] (26-33.51-57.96-109)) (1-120)-*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, G1v14-1 CH2 A1.3, A1.2, A1 (CH1 K120 (217) (121-218), charnière 1-15 (219-233), CH2 L1.3>A (237), L1.2>A (238), G1>A (240) (234-343), CH3 D12 (359), L14 (361) (344-448), CHS (449-450)) (121-450)] -20-mer tétrakis(tétraglycyl-séryl) linker (451-470) -scFv heavy-kappa anti-PDCD1 humanisé et chimérique (471-716) [VH humanisé (*Homo sapiens* IGHV3-23*04 (88.7%) -IGHD -IGHJ6*01 (90.9%) T123>L (583), CDR-IMGT [8.8.11] (496-503.521-528.567-577)) (471-588) -20-mer tétrakis(tétraglycyl-séryl) linker (589-608) -V-KAPPA Musmus/Homsap (*Mus musculus* IGKV14-111*01 (86.3%) -IGKJ5*01 (100%)/*Homo sapiens* IGKV1-16*01 (80.0%) -IGKJ2*01 (81.8%) Q120>A (708), I126>L (714), CDR-IMGT [6.3.9] (635-640.658-660.697-705)) (609-716)]]; (223-214')-disulfure avec la chaîne légère L-kappa anti-LAG3 *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-11*01 (97.9%) -IGKJ5*01 (91.7%) R123>N (103'), 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

cugrastomig

inmunoglobulina IG fusionada con 2 scFv (H-gamma1-scFvhk_L'-kappa) dímero bisdisulfuro, anti-[*Homo sapiens* LAG3 (activador 3 de los linfocitos, linfocito-activación 3, CD223) y scFv anti-[*Homo sapiens* PDCD1 (proteína 1 de muerte celular programada, PD-1, PD1, CD279)], anticuerpo monoclonal *Homo sapiens*, humanizado y quimérico, biespecífico, tetravalente; cadena pesada H-gamma1 anti-LAG3 fusionada con un scFv anti-PDCD1 (1-716) [cadena pesada H-gamma1 anti-LAG3 *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV4-34*01 (90.6%) -(IGHD) -IGHJ5*02 (93.8%), CDR-IMGT [8.7.14] (26-33.51-57.96-109)) (1-120)-*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, G1v14-1 CH2 A1.3, A1.2, A1 (CH1 K120 (217) (121-218), bisagra 1-15 (219-233), CH2 L1.3>A (237), L1.2>A (238), G1>A (240) (234-343), CH3 D12 (359), L14 (361) (344-448), CHS (449-450)) (121-450)] -20-mer tetrakis(tetraglicil-seril) enlace (451-470) -scFv pesada-kappa anti-PDCD1 humanizada y quimérica (471-716) [VH humanizada (*Homo sapiens* IGHV3-23*04 (88.7%) -IGHD -IGHJ6*01 (90.9%) T123>L (583), CDR-IMGT [8.8.11] (496-503.521-528.567-577)) (471-588) -20-mer tetrakis(tetraglicil-seril) enlace (589-608) -V-KAPPA Musmus/Homsap (*Mus musculus* IGKV14-111*01 (86.3%) -IGKJ5*01 (100%)/*Homo sapiens* IGKV1-16*01 (80.0%) -IGKJ2*01 (81.8%) Q120>A (708), I126>L (714), CDR-IMGT [6.3.9] (635-640.658-660.697-705)) (609-716)]]; (223-214')-disulfuro con la cadena ligera L-kappa anti-LAG3 *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-11*01 (97.9%) -IGKJ5*01 (91.7%) R123>N (103'), 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 : H-gamma1 (H, H") anti-LAG3 fused to scFvhk anti-PDCD1

```
QVQLQQWGAG LLKPSETLSL TCAVYGGSIS DYYWNWIRQP PGKGLEWIGE  50
INHRGTTNSN PSLKSRVTLS LDTSKNQFSL KLRSVTAADT AVYYCAFGYS 100
DYEYDWFDPW 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
VYTLPPSRDE LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK 450
GGGGSGGGGS GGGGSGGGGS EVQLVESGGG LVQPGGSLRL SCAASGFAFS 500
SYDMSWVRQA PGKGLDWVAT ISGGGRYTYY PDSVKGRFTI SRDNSKNNLY 550
LQMNSLRAED TALYYCANRY GEAWFAYWGQ GTLVTVSSGG GGSGGGGSGG 600
GGSGGGGSDI QMTQSPSSMS ASVGDRVTFT CRASQDINTY LSWFQQKPGK 650
SPKTLIYRAN RLVSGVPSRF SGSGSGQDYT LTISSLQPED MATYYCLQYD 700
EFPLTFGAGT KLELKR                                     716
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Light chain / Chaîne légère / Cadena ligera: L-kappa (L', L'") anti-LAG3

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

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-95 147-203 264-324 370-428
22"-95" 147"-203" 264"-324" 370"-428"
492-566 631-696
492"-566" 631"-696"
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 / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)
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

cuprum (^{64}Cu) adarulatidum tetraxetanum

copper (^{64}Cu) adarulatide tetraxetan

[*N*-({4,10-bis[(carboxylato-κ*O*)methyl]-7-(carboxymethyl)-1,4,7,10-tetraazacyclododecan-1-yl-κ^4*N*^{1},*N*^{4},*N*^{7},*N*^{10}}acetyl)-L-α-aspartyl-3-cyclohexyl-L-alanyl-L-phenylalanyl-D-seryl-D-arginyl-L-tyrosyl-L-leucyl-L-tryptophyl-L-serine](^{64}Cu)copper

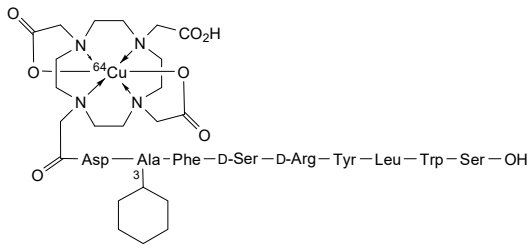
cuivre (^{64}Cu) adarulatide tétraxétan

[*N*-({4,10-bis[(carboxylato-κ*O*)méthyl]-7-(carboxyméthyl)-1,4,7,10-tétraazacyclododécan-1-yl-κ^4*N*^{1},*N*^{4},*N*^{7},*N*^{10}}acétyl)-L-α-aspartyl-3-cyclohexyl-L-alanyl-L-phénylalanyl-D-séryl-D-arginyl-L-tyrosyl-L-leucyl-L-tryptophyl-L-sérine](^{64}Cu)cuivre

cobre (^{64}Cu) adarulatida tetraxetán

[*N*-({4,10-bis[(carboxilato-κ*O*)metil]-7-(carboximetil)-1,4,7,10-tetraazaciclododecan-1-il-κ^4*N*^{1},*N*^{4},*N*^{7},*N*^{10}}acetil)-L-α-aspartil-3-ciclohexil-L-alanil-L-fenilalanil-L-seril-L-arginil-L-tirosil-L-leucil-L-triptofil-L-serina](^{64}Cu)cobre

$C_{76}H_{107}{}^{64}CuN_{17}O_{22}$



dapolsertibum

dapolsertib

5,6-dibromo-4-nitro-2-(piperidin-4-yl)-1-(propan-2-yl)-1*H*-1,3-benzimidazole

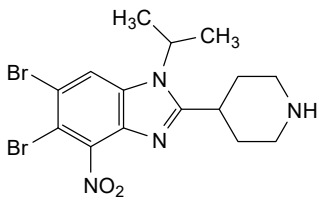
dapolsertib

5,6-dibromo-4-nitro-2-(pipéridin-4-yl)-1-(propan-2-yl)-1*H*-1,3-benzimidazole

dapolsertib

5,6-dibromo-4-nitro-2-(piperidin-4-il)-1-(propan-2-il)-1*H*-1,3-benzimidazol

$C_{15}H_{18}Br_2N_4O_2$



darbinuradum

darbinurad

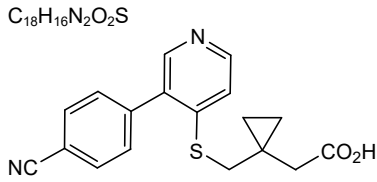
[1-({[3-(4-cyanophenyl)pyridin-4-yl]sulfanyl}methyl)cyclopropyl]acetic acid

darbinurad

acide [1-({[3-(4-cyanophényl)pyridin-4-yl]sulfanyl}méthyl)cyclopropyl]acétique

darbinurad

ácido [1-({[3-(4-cianofenil)piridin-4-il]sulfanil}metil)ciclopropil]acético



denikitugum #

denikitug

immunoglobulin G1-kappa, anti-[*Homo sapiens* CCR8 (C-C motif chemokine receptor 8, CKR-L1, CDw198)]; H-gamma1 heavy chain (1-451) [VH Musmus/Homsap (*Mus musculus* IGHV10-1*02 (90.9%) -(IGHD) -IGHJ1*01 (82.4%) A120>Q (113)/*Homo sapiens* IGHV3-73*01 (90.0%) -(IGHD) -IGHJ3*01 (92.9%) M123>T (116), CDR-IMGT [8.10.12] (26-33.51-60.99-110)) (1-121) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (218) (122-219), hinge 1-15 (220-234), CH2 (235-344), CH3 E12 (360), M14 (362) (345-449), CHS (450-451)) (122-451)], (224-219')-disulfide with L-kappa light chain (1'-219') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV2-137*01 (91.3%) -IGKJ1*02 (90.0%) L124>V (109')/*Homo sapiens* IGKV2-28*01 (89.0%) -IGKJ4*01 (91.7%), 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 (230-230'':233-233'')-bisdisulfide, produced in a Chinese hamster ovary (CHO) cell line, derived from the cell line CHO-K1SV, co-expressing the enzyme glutamine synthetase (GS), and lacking the enzyme alpha-(1,6)-fucosyltransferase (FUT8), glycoform alfa

dénikitug

immunoglobuline G1-kappa, anti-[*Homo sapiens* CCR8 (récepteur 8 de chimiokine C-C motif, CKR-L1, CDw198)];
chaîne lourde H-gamma1 (1-451) [VH Musmus/Homsap (*Mus musculus* IGHV10-1*02 (90.9%) -(IGHD) -IGHJ1*01 (82.4%) A120>Q (113)/*Homo sapiens* IGHV3-73*01 (90.0%) -(IGHD) -IGHJ3*01 (92.9%) M123>T (116), CDR-IMGT [8.10.12] (26-33.51-60.99-110)) (1-121) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (218) (122-219), charnière 1-15 (220-234), CH2 (235-344), CH3 E12 (360), M14 (362) (345-449), CHS (450-451)) (122-451)], (224-219')-disulfure avec la chaîne légère L-kappa (1'-219') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV2-137*01 (91.3%) -IGKJ1*02 (90.0%) L124>V (109)/*Homo sapiens* IGKV2-28*01 (89.0%) -IGKJ4*01 (91.7%), 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 (230-230'':233-233'')-bisdisulfure, produit dans une lignée cellulaire des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1SV, co-exprimant l'enzyme glutamine synthétase (GS), et ne présentant pas l'enzyme alpha-(1,6)-fucosyltransférase (FUT8), glycoforme alfa

denikitug

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CCR8 (receptor 8 de quimiocina C-C motivo, CKR-L1, CDw198)];
cadena pesada H-gamma1 (1-451) [VH Musmus/Homsap (*Mus musculus* IGHV10-1*02 (90.9%) -(IGHD) -IGHJ1*01 (82.4%) A120>Q (113)/*Homo sapiens* IGHV3-73*01 (90.0%) -(IGHD) -IGHJ3*01 (92.9%) M123>T (116), CDR-IMGT [8.10.12] (26-33.51-60.99-110)) (1-121) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (218) (122-219), bisagra 1-15 (220-234), CH2 (235-344), CH3 E12 (360), M14 (362) (345-449), CHS (450-451)) (122-451)], (224-219')-disulfuro con la cadena ligera L-kappa (1'-219') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV2-137*01 (91.3%) -IGKJ1*02 (90.0%) L124>V (109)/*Homo sapiens* IGKV2-28*01 (89.0%) -IGKJ4*01 (91.7%), 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 (230-230":233-233")-bisdisulfuro, producido en una línea celular de las células ováricas de hámster chino (CHO), derivada de la línea celular CHO-K1SV, co-expresando la enzima glutamina sintetasa (GS), y en ausencia de la enzima alfa-1,6-fucosiltransferasa (FUT8), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLKL SCAASGFTFN TYAMNWVRQA SGKGLEWVGR  50
IRSKSNNYAT YYADSVKDRF TISRDDSKNT AYLQMNSLKT EDTAVYYCVR 100
GLLRYRFFDV WGQGTTVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200
TYICNVNHKP SNTKVDKKVE PKSCDKTHTC PPCPAPELLG GPSVFLFPPK 250
PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY 300
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP 350
QVYTLPPSRE EMTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP 400
VLDSDGSFFL YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG 450
K                                                       451
```

Light chain / Chaîne légère / Cadena ligera

```
DIVMTQSPLS LPVTPGEPAS ISCRSSKSLL HSNGNTYLYW FLQKPGQSPQ  50
LLIYRMSNLA SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCMQHLEYP 100
FTFGGGTKVE IKRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK 150
VQWKVDNALQ SGNSQESVTE QDSKDSTYSL SSTLTLSKAD YEKHKVYACE 200
VTHQGLSSPV TKSFNRGEC                                    219
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-98 148-204 265-325 371-429
22"-98" 148"-204" 265"-325" 371"-429"
Intra-L (C23-C104) 23'-93' 139'-199'
23'"-93'" 139'"-199'"
Inter-H-L (h 5-CL 126) 224-219' 224"-219'"
Inter-H-H (h 11, h 14) 230-230" 233-233"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4: 301, 301"
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: 451, 451"

dibotatugum #

dibotatug

immunoglobulin G1-kappa, anti-[*Homo sapiens* KLRD1 (killer cell lectin-like receptor D1, CD94)], *Homo sapiens* monoclonal antibody;
H-gamma1 heavy chain *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV3-21*01 (95.9%) -(IGHD) -IGHJ6*04 (94.4%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14 (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)], (223-214')-disulfide with L-kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1D-16*01 (92.6%) -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 (229-229":232-232")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1SV, glycoform alfa

dibotatug

immunoglobuline G1-kappa, anti-[*Homo sapiens* KLRD1 (récepteur D1 lectine-like des cellules tueuses, CD94)], anticorps monoclonal *Homo sapiens*;
chaîne lourde H-gamma1 *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV3-21*01 (95.9%) -(IGHD) -IGHJ6*04 (94.4%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14 (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)], (223-214')-disulfure avec la chaîne légère L-kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1D-16*01 (92.6%) -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 (229-229":232-232")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1SV, glycoforme alfa

dibotatug

inmunoglobulina G1-kappa, anti-[*Homo sapiens* KLRD1 (receptor D1 tipo lectine de las células asesinas, CD94)], anticuerpo monoclonal *Homo sapiens*;
cadena pesada H-gamma1 *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV3-21*01 (95.9%) -(IGHD) -IGHJ6*04 (94.4%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (217) (121-218), pesada 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 L-kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1D-16*01 (92.6%) -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 (229-229":232-232")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular derivada de CHO-K1SV, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLLESGGG LVKPGGSLRL SCAASGFTFS SYSMNWVRQA PGKGLEWVSS  50
ISTSSNFIYY ADSVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARDL 100
GRYYYYMDVW GKGTTVTVSS 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

```
DIVMTQSPSS LSASVGDRVT ITCRASQSIS SWLAWYQQKP GKAPKSLIYA  50
ASSLQSGVPS KFSGSGSGTD FTLTISSLQP EDVATYYCQK 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) 22-96 147-203 264-324 370-428
22"-96" 147"-203" 264"-324" 370"-428"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194'"
Inter-H-L (h 5-CL 126) 223-214' 223"-214'"
Inter-H-H (h 11, h 14) 229-229" 232-232"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4: 300, 300"
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"

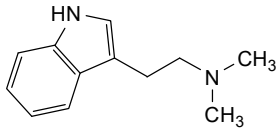
dimethyltryptaminum

dimethyltryptamine — 2-(1*H*-indol-3-yl)-*N*,*N*-dimethylethan-1-amine

diméthyltryptamine — 2-(1*H*-indol-3-yl)-*N*,*N*-diméthyléthan-1-amine

dimetiltriptamina — 2-(1*H*-indol-3-il)-*N*,*N*-dimetiletan-1-amina

$C_{12}H_{16}N_2$



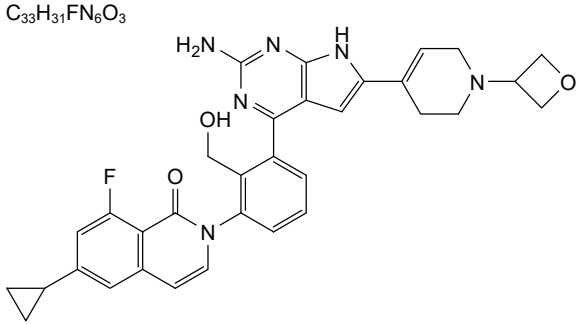
docirbrutinibum

docirbrutinib — 2-[3-{2-amino-6-[1-(oxetan-3-yl)-1,2,3,6-tetrahydropyridin-4-yl]-7*H*-pyrrolo[2,3-*d*]pyrimidin-4-yl}-2-(hydroxymethyl)phenyl]-6-cyclopropyl-8-fluoroisoquinolin-1(2*H*)-one

docirbrutinib — 2-[3-{2-amino-6-[1-(oxétan-3-yl)-1,2,3,6-tétrahydropyridin-4-yl]-7*H*-pyrrolo[2,3-*d*]pyrimidin-4-yl}-2-(hydroxyméthyl)phényl]-6-cyclopropyl-8-fluoroisoquinoléin-1(2*H*)-one

docirbrutinib — 2-[3-{2-amino-6-[1-(oxetan-3-il)-1,2,3,6-tetrahidropiridin-4-il]-7*H*-pirrolo[2,3-*d*]pirimidin-4-il}-2-(hidroximetil)fenil]-6-ciclopropil-8-fluoroisoquinolein-1(2*H*)-ona

$C_{33}H_{31}FN_6O_3$



donitabartum #

donitabart — immunoglobulin G1-kappa, anti-[*Homo sapiens* GD2 (disialoganglioside GD2)];
H-gamma1 heavy chain (1-443) [VH (*Homo sapiens* IGHV1-2*06 (82.3%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.6] (26-33.51-58.97-102)) (1-113) -*Homo sapiens* IGHG1*01v, G1m17,1>G1m3,1 CH1 R120, CH3 D12, L14, G1v21 CH2 Y15.1, T16, E18, G1v20 A105 (CH1 R120 (210) (114-211), hinge 1-15 (212-226), CH2 M15.1>Y (248), S16>T (250), T18>E (252), K105>A (318) (227-336), CH3 D12 (352), L14 (354) (337-441), CHS (442-443)) (114-443)], (216-220')-disulfide with L-kappa light chain (1'-220') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV1-110*01 (87.0%) -IGKJ5*01 (91.7%) A120>Q (105')/*Homo sapiens* IGKV2D-29*02 (81.0%) -IGKJ2*01 (90.9%) I126>L (112'), CDR-IMGT [11.3.10] (27'-37'.55'-57'.94'-103')) (1'-113') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (159'), V101 (197') (114'-220')]; dimer (222-222":225-225")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-S, glycoform alfa

donitabart

immunoglobuline G1-kappa, anti-[*Homo sapiens* GD2 (disialoganglioside GD2)];
chaîne lourde H-gamma1 (1-443) [VH (*Homo sapiens* IGHV1-2*06 (82.3%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.6] (26-33.51-58.97-102)) (1-113) -*Homo sapiens* IGHG1*01v, G1m17,1>G1m3,1 CH1 R120, CH3 D12, L14, G1v21 CH2 Y15.1, T16, E18, G1v20 A105 (CH1 R120 (210) (114-211), charnière 1-15 (212-226), CH2 M15.1>Y (248), S16>T (250), T18>E (252), K105>A (318) (227-336), CH3 D12 (352), L14 (354) (337-441), CHS (442-443)) (114-443)], (216-220')-disulfure avec la chaîne légère L-kappa (1'-220') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV1-110*01 (87.0%) -IGKJ5*01 (91.7%) A120>Q (105')/*Homo sapiens* IGKV2D-29*02 (81.0%) -IGKJ2*01 (90.9%) I126>L (112'), CDR-IMGT [11.3.10] (27'-37'.55'-57'.94'-103')) (1'-113') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (159'), V101 (197') (114'-220')]; dimère (222-222":225-225")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-S, glycoforme alfa

donitabart

inmunoglobulina G1-kappa, anti-[*Homo sapiens* GD2 (disialogangliósido GD2)];
cadena pesada H-gamma1 (1-443) [VH (*Homo sapiens* IGHV1-2*06 (82.3%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.6] (26-33.51-58.97-102)) (1-113) -*Homo sapiens* IGHG1*01v, G1m17,1>G1m3,1 CH1 R120, CH3 D12, L14, G1v21 CH2 Y15.1, T16, E18, G1v20 A105 (CH1 R120 (210) (114-211), bisagra 1-15 (212-226), CH2 M15.1>Y (248), S16>T (250), T18>E (252), K105>A (318) (227-336), CH3 D12 (352), L14 (354) (337-441), CHS (442-443)) (114-443)], (216-220')-disulfuro con la cadena ligera L-kappa (1'-220') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV1-110*01 (87.0%) -IGKJ5*01 (91.7%) A120>Q (105')/*Homo sapiens* IGKV2D-29*02 (81.0%) -IGKJ2*01 (90.9%) I126>L (112'), CDR-IMGT [11.3.10] (27'-37'.55'-57'.94'-103')) (1'-113') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (159'), V101 (197') (114'-220')]; dímero (222-222":225-225")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-S, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada : H-gamma1 (H, H") anti-GD2

```
QVQLVQSGAE VKKPGASVKV SCKASGSSFT GKNMNWVRQN IGQGLEWMGA  50
IDPFYGGTSY NQKFKGRVTL TVDKSISTAY MELSRLRSDD TAVYYCVSGM 100
FYWGQGTLVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC LVKDYFPEPV 150
TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG TQTYICNVNH 200
KPSNTKVDKR VEPKSCDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLYIT 250
REPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYNSTYRVVS 300
VLTVLHQDWL NGKEYKCAVS NKALPAPIEK TISKAKGQPR EPQVYTLPPS 350
RDELTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT PPVLDSDGSF 400
FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLS PGK         443
```

Light chain / Chaîne légère / Cadena ligera : L-kappa (L', L'") anti-GD2

```
DIVMTQTPLS LSVTPGERAS LSCRSSQNLV HRNGNTYLHW YLQKPGQSPK  50
LLIHKVNNRF SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YFCGQSTHVP 100
PLTFGQGTKL ELKRTVAAPS 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) 22-96 140-196 257-317 363-421
22"-96" 140"-196" 257"-317" 363"-421"
Intra-L (C23-C104) 23'-93' 140'-200'
23'"-93'" 140'"-200'"
Inter-H-L (h 5-CL 126) 216-220' 216"-220'"
Inter-H-H (h 11, h 14) 222-222" 225-225"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)
H VH Q1: 1, 1"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4: 293, 293"
Mainly (>90%) afucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes principalement (>90%) afucosylés / glicanos de tipo CHO biantenarios complejos principalmente (>90%) afucosilados

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2: 443, 443"

duvalgagenum otiparvovecum #

duvalgagene otiparvovec	recombinant, non-replicating adeno-associated virus serotype 2 variant 4D-C102 (rAAV2 [4D-C102]) vector encoding codon optimized human alpha-galactosidase A (GLA) under control of a CAG promoter (cytomegalovirus (CMV) immediate-early enhancer/chicken β-actin exon 1 plus intron 1/rabbit β-globin splice acceptor) and a simian virus 40 (SV40) late polyadenylation signal, flanked by adeno-associated virus 2 (AAV2) inverted terminal repeats (ITRs)
duvalgagène otiparvovec	vecteur recombinant et non répliquant du virus adéno-associé de sérotype 2, variant 4D-C102 (rAAV2 [4D-C102]) codant l'alpha-galactosidase A (GLA) humaine aux codons optimisés sous le contrôle d'un promoteur CAG (amplificateur immédiat et précoce du cytomégalovirus (CMV)/exon 1 plus intron 1 de la β-actine de poulet/accepteur d'épissage de la β-globine de lapin) et d'un signal de polyadénylation tardive du virus simien 40 (SV40), flanqué de répétitions terminales inversées (ITR) du virus adéno-associé 2 (AAV2)
duvalgagén otiparvovec	vector de virus adenoasociado del serotipo 2 variante 4D-C102 recombinante (rAAV2 [4D-C102]), no replicativo, que codifica, con codones optimizados, para la alfa-galactosidasa A (GLA) humana bajo el control de un promotor CAG (potenciador inmediato-temprano de citomegalovirus (CMV)/exón 1 más intrón 1 de la β-actina de pollo/aceptor del procesamiento de la β-globina de conejo) y una señal de poliadenilación del gen tardío del virus simio 40 (SV40), flanqueado por repeticiones terminales invertidas (ITRs) del virus adenoasociado 2 (AAV2)

ebrasodebartum #

ebrasodebart	immunoglobulin G4-lambda2, anti-[*Homo sapiens* TMEM219 (transmembrane protein 219, insulin-like growth factor-binding protein 3 receptor, IGFBP-3R) extracellular domain], *Homo sapiens* monoclonal antibody; H-gamma4 heavy chain *Homo sapiens* (1-444) [VH (*Homo sapiens* IGHV1-18*01 (99.0%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118)-*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, G4v5 h P10, G4v3 CH2 E1.2 (CH1 (119-216), hinge 1-12 S10>P (226) (217-228), CH2 L92 (307), L1.2>E (233) (229-338), CH3 (339-443), CHS K2>del (444)) (119-444)], (132-213')-disulfide with L-lambda2 light chain *Homo sapiens* (1'-214') [V-LAMBDA (*Homo sapiens* IGLV3-1*01 (90.1%) -IGLJ2*01 (100%), CDR-IMGT [6.3.11] (26'-31'.49'-51'.88'-98')) (1'-108') -*Homo sapiens* IGLC2*01 (100%) (109'-214')]; dimer (224-224'':227-227'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1SV lacking the glutamine synthetase (GS-KO) gene, glycoform alfa
ébrasodébart	immunoglobuline G4-lambda2, anti-[*Homo sapiens* TMEM219 (protéine transmembranaire 219, récepteur de la protéine 3 liant le facteur de croissance analogue à l'insuline, IGFBP-3R) domaine extracellulaire], anticorps monoclonal *Homo sapiens*;

chaîne lourde H-gamma4 *Homo sapiens* (1-444) [VH (*Homo sapiens* IGHV1-18*01 (99.0%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118)-*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, G4v5 h P10, G4v3 CH2 E1.2 (CH1 (119-216), charnière 1-12 S10>P (226) (217-228), CH2 L92 (307), L1.2>E (233) (229-338), CH3 (339-443), CHS K2>del (444)) (119-444)], (132-213')-disulfure avec la chaîne légère L-lambda2 *Homo sapiens* (1'-214') [V-LAMBDA (*Homo sapiens* IGLV3-1*01 (90.1%) -IGLJ2*01 (100%), CDR-IMGT [6.3.11] (26'-31'.49'-51'.88'-98')) (1'-108') -*Homo sapiens* IGLC2*01 (100%) (109'-214')]; dimère (224-224":227-227")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1SV ne présentant pas le gène de la glutamine synthétase (GS-KO), glycoforme alfa

ebrasodebart

inmunoglobulina G4-lambda2, anti-[*Homo sapiens* TMEM219 (proteína transmembranaria 219, receptor de la proteína 3 de unión al factor de crecimiento análogo a la insulina, IGFBP-3R) dominio extracelular], anticuerpo monoclonal *Homo sapiens*;
cadena pesada H-gamma4 *Homo sapiens* (1-444) [VH (*Homo sapiens* IGHV1-18*01 (99.0%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118)-*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, G4v5 h P10, G4v3 CH2 E1.2 (CH1 (119-216), bisagra 1-12 S10>P (226) (217-228), CH2 L92 (307), L1.2>E (233) (229-338), CH3 (339-443), CHS K2>del (444)) (119-444)], (132-213')-disulfuro con la cadena ligera L-lambda2 *Homo sapiens* (1'-214') [V-LAMBDA (*Homo sapiens* IGLV3-1*01 (90.1%) -IGLJ2*01 (100%), CDR-IMGT [6.3.11] (26'-31'.49'-51'.88'-98')) (1'-108') -*Homo sapiens* IGLC2*01 (100%) (109'-214')]; dímero (224-224":227-227")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1SV en ausencia del gen glutamina sintetasa (GS-KO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada: H-gamma4 (H, H") anti-TMEM219
```
QIQLVQSGAE VKKPGASVKV SCKASGYTFT SYGISWVRQA PGQGLEWMGW  50
ISAYNGNTNY AQKLQGRVTM TTDTSTSTAY MELRSLRSDD TAVYYCARWG 100
RWLAHDYWGQ GTLVTVSSAS TKGPSVFPLA PCSRSTSEST AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTKTYT 200
CNVDHKPSNT KVDKRVESKY GPPCPPCPAP EFEGGPSVFL FPPKPKDTLM 250
ISRTPEVTCV VVDVSQEDPE VQFNWYVDGV EVHNAKTKPR EEQFNSTYRV 300
VSVLTVLHQD WLNGKEYKCK VSNKGLPSSI EKTISKAKGQ PREPQVYTLP 350
PSQEEMTKNQ VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG 400
SFFLYSRLTV DKSRWQEGNV FSCSVMHEAL HNHYTQKSLS LSLG        444
```

Light chain / Chaîne légère / Cadena ligera : L-lambda2 (L', L'") anti-TMEM219
```
QAVLTQPPSV SVSPGQTASI TCSGDKLGNK NAYWYQQKPG QSPVLVMYQS  50
TRRPSGIPER FSASNSGNTA TLTISGTQAM DEADYYCQAW DSSSGWEVFG 100
GGTKLTVLGQ PKAAPSVTLF PPSSEELQAN KATLVCLISD FYPGAVTVAW 150
KADSSPVKAG VETTTPSKQS NNKYAASSYL SLTPEQWKSH RSYSCQVTHE 200
GSTVEKTVAP TECS                                        214
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 145-201 259-319 365-423
22"-96" 145"-201" 259"-319" 365"-423"
Intra-L (C23-C104) 22'-87' 136'-195'
22'"-87'" 136'"-195'"
Inter-H-L (CH1 10-CL 126) 132-213' 132"-213'"
Inter-H-H (h 8, h 11) 224-224" 227-227"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)
H VH Q1: 1, 1"
L VL V-LAMBDA Q1: 1', 1'"

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

ebribafuspum alfa #

ebribafusp alfa

chimeric immunoglobulin G4-kappa anti-(human complement C3d) fused at the C-terminus of the heavy chain, via a $(G_4S)_2$ peptide linker to human complement factor H fragment, glycoform alfa;
gamma 4 heavy chain (1-437) [VH (*Homo sapiens* IGHV1-46*01 -(IGHD) -IGHJ4*01, CDR-Kabat [5.17.2] (31-35.50-66.99-100)) (1-111) -*Homo sapiens* IGHG4*01 (CH1 (112-209), hinge S^{219}>P (210-221), CH2 L^{226}>E (222-331), CH3 M^{419}>L, N^{425}>S (332-436), CHS K^{438}>del (437)) (112-437)] fused via a $(G_4S)_2$ peptide linker (438-447) to human complement factor H fragment 1-305 (448-752 in the current sequence, containing the first five consensus repeat Sushi domains, residues 1-304, plus the adjacent K^{305}), (125-219')-disulfide with kappa light chain (1'-219') [V-KAPPA (*Homo sapiens* IGKV2-30*01 -IGKJ4*01, CDR-Kabat [16.7.9] (24'-39'.55'-61'.94'-102')) (1'-112') -*Homo sapiens* IGKC*01 (113'-219')]; dimer (217-217":220-220")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-M, glycoform alfa

ébribafusp alfa

immunoglobuline chimérique G4-kappa anti-(complément humain C3d) fusionnée à l'extrémité C-terminale de la chaîne lourde, via un peptide liant $(G_4S)_2$, à un fragment du facteur H du complément humain, glycoforme alfa;
chaîne lourde gamma 4 (1-437) [VH (*Homo sapiens* IGHV1-46*01 -(IGHD) -IGHJ4*01, CDR-Kabat [5.17.2] (31-35.50-66. 99-100)) (1-111) -*Homo sapiens* IGHG4*01 (CH1 (112-209), charnière S^{219}>P (210-221), CH2 L^{226}>E (222-331), CH3 M^{419}>L, N^{425}>S (332-436), CHS K^{438}>del (437)) (112-437)] fusionnée, via un peptide liant $(G_4S)_2$ (438-447), au fragment 1-305 du facteur H du complément humain (448-752 dans la séquence actuelle), contenant les cinq premiers domaines Sushi à répétition consensuelle, résidus 1-304, plus le K^{305} adjacent), (125-219')-disulfure avec la chaîne légère kappa (1'-219') [V-KAPPA (*Homo sapiens* IGKV2-30*01 -IGKJ4*01, CDR-Kabat [16. 7.9] (24'-39'.55'-61'.94'-102')) (1'-112') -*Homo sapiens* IGKC*01 (113'-219')]; dimère (217-217":220-220")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-M, glycoforme alfa

ebribafusp alfa

inmunoglobulina quimérica G4-kappa anti-(complemento C3d humano) fusionado en el terminal C de la cadena pesada, a través del enlace peptídico $(G_4S)_2$ al fragmento del factor H del complemento humano, glicoforma alfa;
cadena pesada gamma 4 (1-437) [VH (*Homo sapiens* IGHV1-46*01 -(IGHD) -IGHJ4*01, CDR-Kabat [5.17.2] (31-35.50-66.99-100)) (1-111) -*Homo sapiens* IGHG4*01 (CH1 (112-209), bisagra S^{219}>P (210-221), CH2 L^{226}>E (222-331), CH3 M^{419}>L, N^{425}>S (332-436), CHS K^{438}>del (437)) (112-437)] fusionado a través del $(G_4S)_2$ enlace peptídico (438-447) al fragmento del factor H del complemento humano 1-305 (448-752 en la secuencia actual, que contiene los primeros cinco dominios de repetición consensuada Sushi, residuos 1-304, además del adyacente K^{305}), (125-219')-disulfuro con la cadena ligera kappa (1'-219') [V-KAPPA (*Homo sapiens* IGKV2-30*01 -IGKJ4*01, CDR-Kabat [16.7.9] (24'-39'.55'-61'.94'-102')) (1'-112') -*Homo sapiens* IGKC*01 (113'-219')]; dímero (217-217":220-220")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-M, glicoforma alfa

Sequence / Séquence / Secuencia
IgG4 heavy chain-human Factor H

```
QVQLVQSGAE VKKPGASVKV SCKASGYTFT NYYINWVRQA PGQGLEWMGV   50
INPYSGGTSY NQKFKGRVTM TVDTSTSTAY MELSSLRSED TAVYFCSSPY  100
WGQGTLVTVS SASTKGPSVF PLAPCSRSTS ESTAALGCLV KDYFPEPVTV  150
SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTK TYTCNVDHKP  200
SNTKVDKRVE SKYGPPCPPC PAPEFEGGPS VFLFPPKPKD TLMISRTPEV  250
TCVVVDVSQE DPEVQFNWYV DGVEVHNAKT KPREEQFNST YRVVSVLTVL  300
HQDWLNGKEY KCKVSNKGLP SSIEKTISKA KGQPREPQVY TLPPSQEEMT  350
KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD SDGSFFLYSR  400
LTVDKSRWQE GNVFSCSVLH EALHSHYTQK SLSLSLGGGG GSGGGGSEDC  450
NELPPRRNTE ILTGSWSDQT YPEGTQAIYK CRPGYRSLGN VIMVCRKGEW  500
VALNPLRKCQ KRPCGHPGDT PFGTFTLTGG NVFEYGVKAV YTCNEGYQLL  550
GEINYRECDT DGWTNDIPIC EVVKCLPVTA PENGKIVSSA MEPDREYHFG  600
QAVRFVCNSG YKIEGDEEMH CSDDGFWSKE KPKCVEISCK SPDVINGSPI  650
SQKIIYKENE RFQYKCNMGY EYSERGDAVC TESGWRPLPS CEEKSCDNPY  700
IPNGDYSPLR IKHRTGDEIT YQCRNGFYPA TRGNTAKCTS TGWIPAPRCT  750
LK                                                      752
```

IgG4 light chain

```
DVVMTQSPLS LPVTLGQPAS ISCKSSQSLL DSDGKTYLNW FQQRPGQSPR   50
RLIYLVSKLD SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCWQGTHFP  100
RTFGGGTKVE IKRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK  150
VQWKVDNALQ SGNSQESVTE QDSKDSTYSL SSTLTLSKAD YEKHKVYACE  200
VTHQGLSSPV TKSFNRGEC                                    219
```

Mutations / Mutations / Mutaciónes
IgG4 heavy chain: S^{219},$S^{219"}$>**P**, L^{226},$L^{226"}$>**E**, M^{419},$M^{419"}$>**L**, N^{425},$N^{425"}$>S, K^{438},$K^{438"}$>del

Peptide linker / Peptide liant / Péptido de unión
IgG4 heavy chain-human Factor H: ^{438}*GGGGSGGGGS*^{447}

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra IgG4 heavy chain: 22-96, 138-194, 252-312, 358-416,
22"-96", 138"-194", 252"-312", 358"-416"
Intra Factor H: 450-495, 481-509, 514-558, 543-570, 575-621, 607-634, 639-680, 666-691, 696-738, 723-749,
450"-495", 481"-509", 514"-558", 543"-570", 575"-621", 607"-634", 639"-680", 666"-691", 696"-738", 723"-749"
Intra IgG4 light chain: 23'-93', 139'-199', 23'"-93'", 139'"-199'"
Inter IgG4 heavy-light chain: 125-219', 125"-129'"
Inter IgG4 heavy-heavy chain: 217-217", 220-220"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
IgG4 heavy chain - Factor H: 288, 288"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
IgG1-heavy chain Q1,Q1" > pyroglutamyl (pE, 5-oxo-L-prolyl)

efimosferminum alfa

efimosfermin alfa	Fc fragment of human immunoglobulin G1 (1-227) [*Homo sapiens* IGHG1*03 (hinge (1-10), CH2 L^{14}>A, L^{15}>A (11-120), CH3 (121-226), CHS (226-227))] fused via peptide linker ^{228}GS^{229} to human fibroblast growth factor 21 (FGF-21) fragment 33-209 [Q^{55}>C^{252}, R^{105}>K^{302}, G^{148}>C^{345}, K^{150}>R^{347}, P^{158}>S^{355}, S^{195}>A^{392}, P^{199}>G^{396}, G^{202}>A^{399}]-variant (230-406 in the current sequence); dimer (6-6', 9-9')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-DG44, glycoform alfa
éfimosfermine alfa	fragment Fc de l'immunoglobuline G1 humaine (1-227) [*Homo sapiens* IGHG1*03 (charnière (1-10), CH2 L^{14}>A, L^{15}>A (11-120), CH3 (121-226), CHS (226-227))] fusionné, via un peptide liant ^{228}GS^{229}, au fragment 33-209 du facteur de croissance des

fibroblastes 21 (FGF-21) humain, [Q^{55}>C^{252}, R^{105}>K^{302}, G^{148}>C^{345}, K^{150}>R^{347}, P^{158}>S^{355}, S^{195}>A^{392}, P^{199}>G^{396}, G^{202}>A^{399}]-variant (230-406 dans la séquence actuelle); dimère (6-6', 9-9')-bidisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-DG44, glycoforme alfa

efimosfermina alfa

fragmento Fc de la inmunoglobulina G1 humana (1-227) [*Homo sapiens* IGHG1*03 (bisagra (1-10), CH2 L^{14}>A, L^{15}>A (11-120), CH3 (121-226), CHS (226-227))] fusionada, a través de enlace peptídico ^{228}GS^{229}, al factor de crecimiento humano de fibroblasto 21 (FGF-21) fragmento 33-209 [Q^{55}>C^{252}, R^{105}>K^{302}, G^{148}>C^{345}, K^{150}>R^{347}, P^{158}>S^{355}, S^{195}>A^{392}, P^{199}>G^{396}, G^{202}>A^{399}]-variante (230-406 en la secuencia actual); dímero (6-6', 9-9')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-DG44, glicoforma alfa

Sequence / Séquence / Secuencia

```
DKTHTCPPCP APEAAGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED  50
PEVKFNWYVD GVEVHNAKTK PREEQYNSTY RVVSVLTVLH QDWLNGKEYK 100
CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSREEMTK NQVSLTCLVK 150
GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG 200
NVFSCSVMHE ALHNHYTQKS LSLSPGKGSD SSPLLQFGGQ VRQRYLYTDD 250
ACQTEAHLEI REDGTVGGAA DQSPESLLQL KALKPGVIQI LGVKTSRFLC 300
QKPDGALYGS LHFDPEACSF RELLLEDGYN VYQSEAHGLP LHLPCNRSPH 350
RDPASRGPAR FLPLPGLPPA LPEPPGILAP QPPDVGSSDP LAMVGGSQAR 400
SPSYAS                                                 406
```

Mutation / Mutation / Mutación

L^{14},$L^{14'}$>**A**, L^{15},$L^{15'}$>**A**, Q^{55}>**C**^{252},**C**$^{252'}$, R^{105}>**K**^{302},**K**$^{302'}$, G^{148}>**C**^{345},**C**$^{345'}$, K^{150}>**R**^{347},**R**$^{347'}$, P^{158}>**S**^{355},**S**$^{355'}$, S^{195}>**A**^{392},**A**$^{392'}$, P^{199}>**G**^{396},**G**$^{396'}$, G^{202}>**A**^{399},**A**$^{399'}$

Peptide linker / Peptide liant / Péptido de unión

^{228}*GS*^{229}

Post-translation modifications

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

Intra chain: 41-101, 147-205, 252-345, 300-318,
41'-101', 147'-205', 252'-345', 300'-318'

Inter chain: 6-6', 9-9'

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

77, 77'

efparepoetinum alfa

efparepoetin alfa

human erythropoietin [R^{166}>del]-variant (1-165 in the current sequence) fused via peptide linker ^{166}GSGGGSGGGGSGGGGS^{181} to a Fc fragment of immunoglobulin G2 (182-407) [*Homo sapiens* IGHG1*01 (hinge N-terminal EPKSC deleted (182-191)), *Homo sapiens* IGHG2*01 (CH2 P^{291}>S (192-300), CH3 (301-405), CHS (406-407))]; dimer (187-187', 190-190')-bisdisulfide, produced in Chinese ovary hamster (CHO) cells, glycoform alfa

efparépoétine alfa

[R^{166}>del]-variant de l'érythropoïétine humaine (1-165 dans la séquence actuelle) fusionné, via un peptide liant ^{166}GSGGGSGGGGSGGGGS^{181}, à un fragment Fc de l'immunoglobuline G2 (182-407) [*Homo sapiens* IGHG1*01 (charnière N-terminale EPKSC supprimée (182-191)), *Homo sapiens* IGHG2*01 (CH2 P^{291}>S (192-300), CH3 (301-405), CHS (406-407))]; dimère (187-187', 190-190')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

efparepoetina alfa

[R^{166}>del]-variante de la eritropoyetina humana (1-165 en la secuencia actual) fusionado a través de un enlace peptídico ^{166}GSGGGSGGGGSGGGGS^{181} a un fragmento Fc de la inmunoglobulina G2 (182-407) [*Homo sapiens* IGHG1*01 (bisagra N-terminal EPKSC eliminada (182-191)), *Homo sapiens* IGHG2*01 (CH2 P^{291}>S (192-300), CH3 (301-405), CHS (406-407))]; dímero (187-187', 190-190')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), glicoforma alfa

Sequence / Séquence / Secuencia

```
APPRLICDSR VLERYLLEAK EAENITTGCA EHCSLNENIT VPDTKVNFYA   50
WKRMEVGQQA VEVWQGLALL SEAVLRGQAL LVNSSQPWEP LQLHVDKAVS  100
GLRSLTTLLR ALGAQKEAIS PPDAASAAPL RTITADTFRK LFRVYSNFLR  150
GKLKLYTGEA CRTGDGSGGG SGGGGSGGGG SDKTHTCPPC PAPPVAGPSV  200
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVQFNWYVD GVEVHNAKTK  250
PREEQFNSTF RVVSVLTVVH QDWLNGKEYK CKVSNKGLPA SIEKTISKTK  300
GQPREPQVYT LPPSREEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN  350
YKTTPPMLDS DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS  400
LSLSPGK                                                 407
```

Mutation / Mutation / Mutación
P^{291}, P$^{291'}$>**S**

Peptide linker / Peptide liant / Péptido de unión
^{166}*GSGGGSGGGGSGGGGS*^{181}

Post-translation modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-chain: 7-161, 29-33, 221-281, 327-385,
7'-161', 29'-33', 221'-281', 327'-385'
Inter-chain: 187-187', 190-190'

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
24, 38, 83, 257; 24', 38', 83', 257'

O-glycosylation sites / Sites de O-glycosylation / Posiciones de O-glicosilación
S126 , S126'

Oxidation sites / Sites d'oxydation / Posiciones de oxidación
M54, M212, M357, M388; M54', M212', M357', M388'

Deamidation sites / Sites de désamidation / Posiciones de desamidación
Q115, N147, (^{321}NQ^{322})*, Q115', N147' ($^{321'}$NQ$^{322'}$)*
*Deamidation can be in any of the listed amino acids

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS: 407, 407'

elsunersenum

elsunersen

(*all-P-ambo*)-2'-*O*-(2-methoxyethyl)-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methylcytidylyl-(3'→5')-2'-*O*-(2-methoxyethyl)adenylyl-(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'-deoxy-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-deoxy-*P*-thioadenylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-deoxy-*P*-thioadenylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-deoxy-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyluridylyl-(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

elsunersen

(*tout-P-ambo*)-2'-*O*-(2-méthoxyéthyl)-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthylcytidylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)adénylyl-(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'-désoxy-5-méthyl-*P*-

thiocytidylyl-(3'→5')-2'-désoxy-*P*-thioadénylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-désoxy-*P*-thioadénylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-désoxy-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthyluridylyl-(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

elsunersén

(*todo-P-ambo*)-5-metil-2'-*O*-(2-metoxietil)-*P*-tiocitidilil-(3'→5')-5-metil-2'-*O*-(2-metoxietil)citidilil-(3'→5')-2'-*O*-(2-metoxietil)adenilil-(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')-2'-desoxi-5-metil-*P*-tiocitidilil-(3'→5')-2'-desoxi-*P*-tioadenilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2'-desoxi-*P*-tioadenilil-(3'→5')-*P*-tiotimidilil-(3'→5')-*P*-tiotimidilil-(3'→5')-*P*-tiotimidilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2'-desoxi-5-metil-*P*-tiocitidilil-(3'→5')-5-metil-2'-*O*-(2-metoxietil)uridilil-(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

$C_{230}H_{320}N_{67}O_{126}P_{19}S_{13}$

(3'-5')m^{5}Cmoe=m^{5}Cmoe-Amoe-m^{5}Cmoe-Gmoe-Amoe-m^{5}C$_d$=dA=dT=dA=dT=dT==dT=dT=dT=m^{5}C$_d$=m^{5}Umoe-Amoe=m^{5}Cmoe=Amoe

N : nucleoside / nucléoside / nucleósido
dN & N$_d$: 2'-deoxy-N / 2'-désoxy-N / 2'-desoxi-N
m^{5}N : 5-methyl-N / 5-méthyl-N / 5-metil-N
Nmoe : 2'-*O*-methoxyethyl-N / 2'-*O*-méthoxyéthyl-N / 2'-*O*-metoxietil-N
− : −PO(OH)− = : −PO(SH)−

elzocabtagenum autoleucelum #

elzocabtagene autoleucel

autologous T lymphocytes from peripheral blood obtained by leukapheresis, transduced with four self-inactivating, non-replicating lentiviral vectors encoding (i) a chimeric antigen receptor (CAR) targeting guanylyl cyclase C (GC-C, GUCY2C), (ii) a chimeric antigen receptor (CAR) targeting CD19 co-expressing interferon gamma (IFN-γ), (iii) a chimeric antigen receptor (CAR) targeting CD19 co-expressing interleukin-6 (IL-6), (iv) a chimeric antigen receptor (CAR) targeting CD19 co-expressing interleukin-12 (IL-12) fused to a von Hippel-Lindau tumour suppressor (VHL) recognition sequence.
Each CAR transgene comprises a signal peptide derived from the CD8 alpha chain, a single chain variable fragment (scFv) binding domain, a CD8 hinge and transmembrane domain, a 4-1BB co-stimulatory domain and a CD3ζ signalling domain, under control of the human elongation factor 1 alpha (EF-1α) core promoter. For the three vectors that also encode a cytokine, each cytokine gene is preceded by an NFAT enhancer and is under the control of a minimal IL-2 promoter. For the IL-12-VHL expressing vector, a recognition sequence of the von Hippel-Lindau tumour suppressor protein (VHL) is fused to the 3' end of the IL-12 gene via an EA rich linker.
Each construct is flanked by 5' and 3' long terminal repeats (LTRs) and also contains a ψ packaging signal, a Rev response element (RRE), a central polypurine tract (CPPT) and central termination sequence (CTS) and a Woodchuck hepatitis virus post-transcriptional regulatory element (WPRE). Each vector is pseudotyped with the vesicular stomatitis virus (VSV) G envelope protein.

	The leukapheresis material is enriched for CD4/CD8 T lymphocytes by positive immunoselection, activated by CD3 and CD28 agonists and transduced with the vector. The cells are then expanded in media with serum replacement and interleukin 2 (IL-2). The T lymphocytes (>75%) are positive for the transgenes (>5% CAR positive), with less than 0.5 % CD19+ cells. The cells produce cytokines (interleukin-6, interleukin-12, and interferon gamma) in co-culture with B lymphocytes
elzocabtagène autoleucel	lymphocytes T autologues issus de sang périphérique obtenus par leucaphérèse, transduits avec quatre vecteurs lentivirus auto-inactivants et non-répliquants codant (i) un récepteur chimérique d'antigène (CAR) ciblant la guanylyl cyclase C (GC-C, GUCY2C), (ii) un récepteur chimérique d'antigène (CAR) ciblant le CD19 coexprimant l'interféron gamma (IFN-γ), (iii) un récepteur chimérique d'antigène (CAR) ciblant le CD19 coexprimant l'interleukine-6 (IL-6), (iv) un récepteur chimérique d'antigène (CAR) ciblant le CD19 coexprimant l'interleukine-12 (IL-12) fusionné à une séquence de reconnaissance du suppresseur de tumeur de von Hippel-Lindau (VHL). Chaque transgène CAR comprend un peptide signal dérivé de la chaîne alpha du CD8, un domaine de liaison à un fragment variable à chaîne unique (scFv), une charnière CD8 et un domaine transmembranaire, un domaine de co-stimulation 4-1BB et un domaine de signalisation CD3ζ, sous le contrôle du promoteur central du facteur d'élongation 1 alpha (EF-1α) humain. Pour les trois vecteurs qui codent également une cytokine, chaque gène de cytokine est précédé d'un amplificateur NFAT et est sous le contrôle d'un promoteur minimal IL-2. Pour le vecteur exprimant l'IL-12-VHL, une séquence de reconnaissance de la protéine suppresseur de tumeur de von Hippel-Lindau (VHL) est fusionnée à l'extrémité 3' du gène de l'IL-12 via un lieur riche en EA. Chaque construction est flanquée de répétitions terminales longues (LTR) en 5' et 3' et contient également un signal d'encapsidation ψ, un élément de réponse Rev (RRE), un tractus polypurine central (CPPT) et une séquence de terminaison centrale (CTS), ainsi qu'un élément de régulation post-transcriptionnelle du virus de l'hépatite de la marmotte (WPRE). Chaque vecteur est pseudotypé avec la protéine d'enveloppe G du virus de la stomatite vésiculaire (VSV). Le matériel de leucaphérèse est enrichi en lymphocytes T CD4/CD8 par immunosélection positive, activé par des agonistes CD3 et CD28 et transduit avec le vecteur. Les cellules sont ensuite amplifées dans un milieu contenant du sérum de substitution et de l'interleukine 2 (IL-2). Les lymphocytes T (>75%) sont positifs pour les transgènes (>5% CAR positif), avec moins de 0.5 % de cellules CD19+. Les cellules produisent des cytokines (interleukine-6, interleukine-12 et interféron gamma) en co-culture avec des lymphocytes B
elzocabtagén autoleucel	linfocitos T autólogos de sangre periférica obtenidos por leucoaféresis, transducidos con cuatro vectores lentivirales auto inactivantes, no replicativos, que codifican para (i) un receptor de antígenos quimérico (CAR) dirigido a la guanidil ciclasa C (GC-C, GUCY2C), (ii) un receptor de antígenos quimérico (CAR) dirigido a CD19 coexpresando interferón gamma (IFN-γ), (iii) un receptor de antígenos quimérico (CAR) dirigido a CD19 coexpresando interleuquina 6 (IL-6), (iv) un receptor de antígenos quimérico (CAR) dirigido a CD19 coexprensando interleuquina 12 (IL-12) fusionado a una secuencia de reconocimiento del supresor tumoral von Hippel-Lindau (VHL).

Cada transgén CAR contiene un péptido señal derivado de la cadena alfa de CD8, un dominio de unión de fragmento variable de cadena sencilla (scFv), un dominio bisagra y transmembrana de CD8, un dominio coestimulador de 4-1BB y un dominio de señalización de CD3ζ, bajo el control del promotor mínimo del factor de elongación 1 alfa (EF-1α) humano. Para los tres vectores que también codifican una citoquina, cada gen de citoquina está precedido por un potenciador NFAT y está bajo el control de un promotor mínimo de IL-2. Para el vector que expresa IL-12-VHL, una secuencia de reconocimiento de la proteína supresora tumoral von Hippel-Lindau (VHL) está fusionada a la región 3' del gen de IL-12 mediante un enlazador rico en EA.
Cada constructo está flanqueado por repeticiones terminales largas (LTRs) en 5' y 3' y también contiene una señal de empaquetamiento ψ, un elemento de respuesta Rev (RRE), un tracto de polipurina central (CPPT) y una secuencia de terminación central (CTS) y un elemento regulador post-transcripcional del virus de la hepatitis de la marmota (WPRE). Cada vector está seudotipado con la proteína G de la envuelta del virus de la estomatitis vesicular (VSV).
El material de leucoaféresis se enriquece en linfocitos T CD4/CD8 mediante inmunoselección positiva, se activa mediante agonistas de CD3 y CD28 y se transduce con el vector. Las células después se expanden en medio con substituto de suero e interleuquina 2 (IL-2). Los linfocitos T (>75%) son positivos para los transgénes (>5% CAR positivos), con menos de 0.5% de células CD19+. Las células producen citoquinas (interleuquina 6, interleuquina 12 e interferón gamma) en cocultivo con linfocitos B

emiltatugum #

emiltatug — immunoglobulin G1-kappa, anti-[*Homo sapiens* VTCN1(V-set domain containing T cell activation inhibitor 1, B7 family member H4, B7H4, B7-H4)], *Homo sapiens* monoclonal antibody;
H-gamma1 heavy chain *Homo sapiens* (1-445) [VH (*Homo sapiens* IGHV3-53*01 (91.8%) -(IGHD) -IGHJ6*01 (93.8%), CDR-IMGT [8.7.10] (26-33.51-57.96-105)) (1-116) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (213) (117-214), hinge 1-15 (215-229), CH2 (230-339), CH3 D12 (355), L14 (357) (340-444), CHS K2>del (445)) (117-445)], (219-216')-disulfide with L-kappa light chain *Homo sapiens* (1'-216') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (100%) -IGKJ2*01 (100%), CDR-IMGT [7.3.10] (27'-33'.51'-53'.90'-99')) (1'-109') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (155'), V101 (193') (110'-216')]; dimer (225-225'':228-228'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-DG44, glycoform alfa

émiltatug — immunoglobuline G1-kappa, anti-[*Homo sapiens* VTCN1 (inhibiteur 1 de l'activation des cellules T contenant un domaine V-like, membre H4 de la famille B7, B7-H4, B7H4)], anticorps monoclonal *Homo sapiens*; chaîne lourde H-gamma1 *Homo sapiens* (1-445) [VH (*Homo sapiens* IGHV3-53*01 (91.8%) -(IGHD) -IGHJ6*01 (93.8%), CDR-IMGT [8.7.10] (26-33.51-57.96-105)) (1-116) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (213) (117-214), charnière 1-15 (215-229), CH2 (230-339), CH3 D12 (355), L14 (357) (340-444), CHS K2>del (445)) (117-445)], (219-216')-disulfure avec la

chaîne légère L-kappa *Homo sapiens* (1'-216') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (100%) -IGKJ2*01 (100%), CDR-IMGT [7.3.10] (27'-33'.51'-53'.90'-99')) (1'-109') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (155'), V101 (193') (110'-216')]; dimère (225-225":228-228")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-DG44, glycoforme alfa

emiltatug

inmunoglobulina G1-kappa, anti-[*Homo sapiens* VTCN1 (inhibidor 1 de la activación de las células T que contienen un dominio V-like, miembro H4 de la familia B7, B7-H4, B7H4)], anticuerpo monoclonal *Homo sapiens*;
cadena pesada H-gamma1 *Homo sapiens* (1-445) [VH (*Homo sapiens* IGHV3-53*01 (91.8%) -(IGHD) -IGHJ6*01 (93.8%), CDR-IMGT [8.7.10] (26-33.51-57.96-105)) (1-116) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (213) (117-214), bisagra 1-15 (215-229), CH2 (230-339), CH3 D12 (355), L14 (357) (340-444), CHS K2>del (445)) (117-445)], (219-216')-disulfuro con la cadena ligera L-kappa *Homo sapiens* (1'-216') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (100%) -IGKJ2*01 (100%), CDR-IMGT [7.3.10] (27'-33'.51'-53'.90'-99')) (1'-109') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (155'), V101 (193') (110'-216')]; dímero (225-225":228-228")-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 SCAASGFIVS RNYMNWVRQA PGKGLEWVSV  50
IYGSGRTDSA DSVKGRFTIS RDNSKNTLYL QMNSLRAEDT AVYYCARDAD 100
YGLDVWGQGT 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 SLSPG      445
```

Light chain / Chaîne légère / Cadena ligera

```
EIVLTQSPGT LSLSPGERAT LSCRASQSVS SSYLAWYQQK PGQAPRLLIY  50
GASSRATGIP DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QYGSSPLYTF 100
GQGTKLEIKR TVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQW 150
KVDNALQSGN SQESVTEQDS KDSTYSLSST LTLSKADYEK HKVYACEVTH 200
QGLSSPVTKS FNRGEC                                      216
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-95 143-199 260-320 366-424
22"-95" 143"-199" 260"-320" 366"-424"
Intra-L (C23-C104) 23'-89' 136'-196'
23'"-89'" 136'"-196'"
Inter-H-L (h 5-CL 126) 219-216' 219"-216'"
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

emiltatugum ledadotinum #

emiltatug ledadotin

immunoglobulin G1-kappa, anti-[*Homo sapiens* VTCN1(V-set domain containing T cell activation inhibitor 1, B7 family member H4, B7H4, B7-H4)], *Homo sapiens* monoclonal antibody; conjugated at glycosylated asparaginyl residues to a derivative of auristatin, with a ratio of 1 to 6, via a cleavable linker;
H-gamma1 heavy chain *Homo sapiens* (1-445) [VH (*Homo sapiens* IGHV3-53*01 (91.8%) -(IGHD) -IGHJ6*01 (93.8%), CDR-IMGT [8.7.10] (26-33.51-57.96-105)) (1-116) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (213) (117-214), hinge 1-15 (215-229), CH2 (230-339), CH3 D12 (355), L14 (357) (340-444), CHS K2>del (445)) (117-445)], (219-216')-disulfide

	with L-kappa light chain *Homo sapiens* (1'-216') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (100%) -IGKJ2*01 (100%), CDR-IMGT [7.3.10] (27'-33'.51'-53'.90'-99')) (1'-109') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (155'), V101 (193') (110'-216')]; dimer (225-225'':228-228'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-DG44, glycoform alfa; substituted at the side chain nitrogen atom of L-asparaginyl residues 296 and 296'' with a radical group consisting of 2-acetamido-[(5a*RS*,6*SR*,6a*SR*)-6-[(45*S*)-22,22-bis[(28*S*)-28-[(9*S*,14*S*)-9-carboxy-19-{[*N*,*N*-dimethyl-L-valyl-L-valyl-(3*R*,4*S*,5*S*)-3-methoxy-5-methyl-4-(methylamino)heptanoyl-(2*R*,3*R*)-3-methoxy-2-methyl-3-[(2*S*)-pyrrolidin-2-yl]propanoyl-L-phenylalanyl]amino}-14-methyl-3,7,12,15-tetraoxo-2,16-dioxa-4,8,13-triazanonadecan-1-yl]-27,30,33,36,39,42,46-heptaoxo-2,5,8,11,14,17,20,23,49-nonaoxa-26,29,32,35,38,41,45-heptaazapentacontan-50-yl]-45-[(9*S*,14*S*)-9-carboxy-19-{[*N*,*N*-dimethyl-L-valyl-L-valyl-(3*R*,4*S*,5*S*)-3-methoxy-5-methyl-4-(methylamino)heptanoyl-(2*R*,3*R*)-3-methoxy-2-methyl-3-[(2*S*)-pyrrolidin-2-yl]propanoyl-L-phenylalanyl]amino}-14-methyl-3,7,12,15-tetraoxo-2,16-dioxa-4,8,13-triazanonadecan-1-yl]-3,14,17,20,27,31,34,37,40,43,46-undecaoxo-2,7,10,24,50,53,56,59,62,65,68,71-dodecaoxa-4,13,18,21,28,32,35,38,41,45,47-undecaazadoheptacontan-1-yl]-1,4,5,5a,6,6a,7,8-octahydrocyclopropa[5,6]cycloocta[1,2-*d*][1,2,3]triazol-1-yl]-2,6-dideoxy-β-D-galactopyranosyl-(1→4)-2-acetamido-2-deoxy-6-*O*-(H *or* 6-deoxy-α-L-galactopyranosyl)-β-D-glucopyranosyl (*ledadotin*)
émiltatug lédadotine	immunoglobuline G1-kappa, anti-[*Homo sapiens* VTCN1 (inhibiteur 1 de l'activation des cellules T contenant un domaine V-like, membre H4 de la famille B7, B7-H4, B7H4)], anticorps monoclonal *Homo sapiens*; conjugué, par des résidus asparaginyles glycosylés, à un dérivé de l'auristatine, via un linker clivable avec un rapport de 1 pour 6; chaîne lourde H-gamma1 *Homo sapiens* (1-445) [VH (*Homo sapiens* IGHV3-53*01 (91.8%) -(IGHD) -IGHJ6*01 (93.8%), CDR-IMGT [8.7.10] (26-33.51-57.96-105)) (1-116) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (213) (117-214), charniére 1-15 (215-229), CH2 (230-339), CH3 D12 (355), L14 (357) (340-444), CHS K2>del (445)) (117-445)], (219-216')-disulfure avec la chaîne légère L-kappa *Homo sapiens* (1'-216') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (100%) -IGKJ2*01 (100%), CDR-IMGT [7.3.10] (27'-33'.51'-53'.90'-99')) (1'-109') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (155'), V101 (193') (110'-216')]; dimère (225-225'':228-228'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-DG44, glycoforme alfa; substitué sur l'atome d'azote de la chaîne latérale des résidus L-asparaginyle 296 et 296'' avec un

	groupement radical 2-acétamido-[(5a*RS*,6*SR*,6a*SR*)-6-[(45*S*)-22,22-bis[(28*S*)-28-[(9*S*,14*S*)-9-carboxy-19-{[*N*,*N*-diméthyl-L-valyl-L-valyl-(3*R*,4*S*,5*S*)-3-méthoxy-5-méthyl-4-(méthylamino)heptanoyl-(2*R*,3*R*)-3-méthoxy-2-méthyl-3-[(2*S*)-pyrrolidin-2-yl]propanoyl-L-phénylalanyl]amino}-14-méthyl-3,7,12,15-tétraoxo-2,16-dioxa-4,8,13-triazanonadécan-1-yl]-27,30,33,36,39,42,46-heptaoxo-2,5,8,11,14,17,20,23,49-nonaoxa-26,29,32,35,38,41,45-heptaazapentacontan-50-yl]-45-[(9*S*,14*S*)-9-carboxy-19-{[*N*,*N*-diméthyl-L-valyl-L-valyl-(3*R*,4*S*,5*S*)-3-méthoxy-5-méthyl-4-(méthylamino)heptanoyl-(2*R*,3*R*)-3-méthoxy-2-méthyl-3-[(2*S*)-pyrrolidin-2-yl]propanoyl-L-phénylalanyl]amino}-14-méthyl-3,7,12,15-tétraoxo-2,16-dioxa-4,8,13-triazanonadécan-1-yl]-3,14,17,20,27,31,34,37,40,43,46-undécaoxo-2,7,10,24,50,53,56,59,62,65,68,71-dodécaoxa-4,13,18,21,28,32,35,38,41,45,47-undécaazadoheptacontan-1-yl]-1,4,5,5a,6,6a,7,8-octahydrocyclopropa[5,6]cycloocta[1,2-*d*][1,2,3]triazol-1-yl]-2,6-didésoxy-β-D-galactopyranosyl-(1→4)-2-acétamido-2-désoxy-6-*O*-(H *ou* 6-désoxy-α-L-galactopyranosyl)-β-D-glucopyranosyle (*lédadotine*)
emiltatug ledadotina	inmunoglobulina G1-kappa, anti-[*Homo sapiens* VTCN1 (inhibidor 1 de la activación de las células T que contienen un dominio V-like, miembro H4 de la familia B7, B7-H4, B7H4)], anticuerpo monoclonal *Homo sapiens*; conjugado, por los residuos asparaginilos glicosilados, con un derivado de la auristatina, a través de un enlace escindible con un ratio de 1 por 6; cadena pesada H-gamma1 *Homo sapiens* (1-445) [VH (*Homo sapiens* IGHV3-53*01 (91.8%) -(IGHD) -IGHJ6*01 (93.8%), CDR-IMGT [8.7.10] (26-33.51-57.96-105)) (1-116) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (213) (117-214), bisagra 1-15 (215-229), CH2 (230-339), CH3 D12 (355), L14 (357) (340-444), CHS K2>del (445)) (117-445)], (219-216')-disulfuro con la cadena ligera L-kappa *Homo sapiens* (1'-216') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (100%) -IGKJ2*01 (100%), CDR-IMGT [7.3.10] (27'-33'.51'-53'.90'-99')) (1'-109') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (155'), V101 (193') (110'-216')]; dímero (225-225'':228-228'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-DG44, forma glicosilada alfa; substituido en el átomo de nitrógeno de la cadena lateral de los residuos L-asparaginilo 296 y 296'' con un grupo radical 2-acetamido-[(5a*RS*,6*SR*,6a*SR*)-6-[(45*S*)-22,22-bis[(28*S*)-28-[(9*S*,14*S*)-9-carboxi-19-{[*N*,*N*-dimetil-L-valil-L-valil-(3*R*,4*S*,5*S*)-3-metoxi-5-metil-4-(metilamino)heptanoil-(2*R*,3*R*)-3-metoxi-2-metil-3-[(2*S*)-pirrolidin-2il]propanoil-L-fenilalanil]amino}-14-metil-3,7,12,15-tetraoxo-2,16-dioxa-4,8,13-triazanonadecan-1-il]-27,30,33,36,39,42,46-heptaoxo-2,5,8,11,14,17,20,23,49-nonaoxa-26,29,32,35,38,41,45-heptaazapentacontan-50-il]-45-[(9*S*,14*S*)-9-carboxi-19-{[*N*,*N*-dimetil-L-valil-L-valil-(3*R*,4*S*,5*S*)-3-metoxi-5-metil-4-(metilamino)heptanoil-(2*R*,3*R*)-3-metoxi-2-metil-3-[(2*S*)-pirrolidin-2-il]propanoil-L-fenilalanil]amino}-14-metil-3,7,12,15-tetraoxo-2,16-dioxa-4,8,13-triazanonadecan-1-il]-3,14,17,20,27,31,34,37,40,43,46-undecaoxo-2,7,10,24,50,53,56,59,62,65,68,71-dodecaoxa-4,13,18,21,28,32,35,38,41,45,47-undecaazadoheptacontan-1-il]-1,4,5,5a,6,6a,7,8-octahidrociclopropa[5,6]ciclooctа[1,2-*d*][1,2,3]triazol-1-il]-2,6-didesoxi-β-D-galactopiranosil-(1→4)-2-acetamido-2-desoxi-6-*O*-(H *ou* 6-desoxi-α-L-galactopiranosil)-β-D-glucopiranosilo (*ledadotina*)

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LIQPGGSLRL SCAASGFIVS RNYMNWVRQA PGKGLEWVSV  50
IYGSGRTDSA DSVKGRFTIS RDNSKNTLYL QMNSLRAEDT AVYYCARDAD 100
YGLDVWGQGT 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 SLSPG       445
```

Light chain / Chaîne légère / Cadena ligera

```
EIVLTQSPGT LSLSPGERAT LSCRASQSVS SSYLAWYQQK PGQAPRLLIY  50
GASSRATGIP DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QYGSSPLYTF 100
GQGTKLEIKR TVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQW 150
KVDNALQSGN SQESVTEQDS KDSTYSLSST LTLSKADYEK HKVYACEVTH 200
QGLSSPVTKS FNRGEC                                      216
```

Post-translational modifications

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

Intra-H (C23-C104) 22-95 143-199 260-320 366-424
22"-95" 143"-199" 260"-320" 366"-424"
Intra-L (C23-C104) 23'-89' 136'-196'
23'"-89'" 136'"-196'"
Inter-H-L (h 5-CL 126) 219-216' 219"-216'"
Inter-H-H (h 11, h 14) 225-225" 228-228"

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

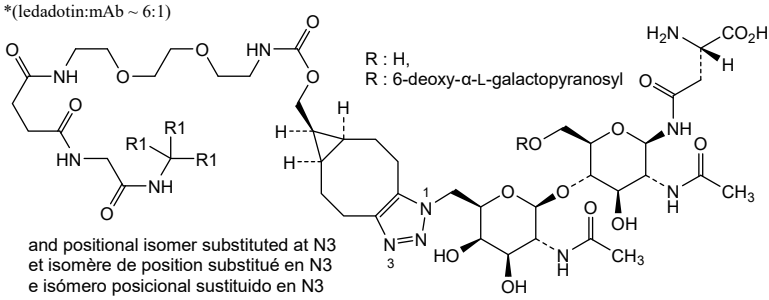
H CH2 N84.4: 296, 296"

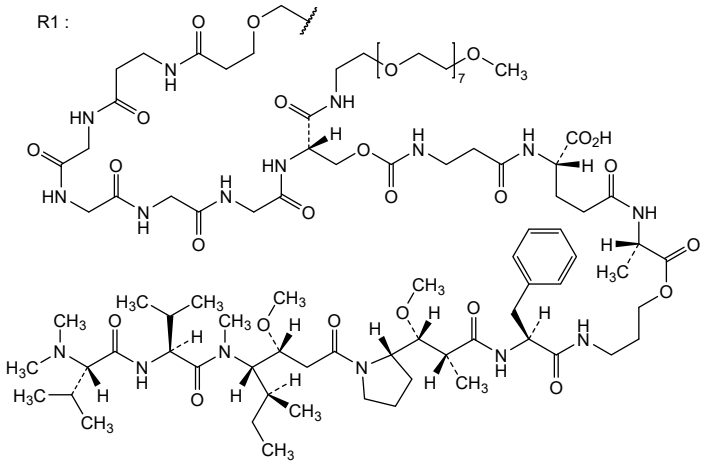
Specific conjugation sites to remodeled fucosylated CHO-type glycans / sites de conjugaison spécifiques aux glycanes de type CHO fucosylés remodelés / Sitios de conjugación específicos para glicanos tipo CHO fucosilados remodelados

Modified residues / résidus modifiés / restos modificados*

N (296, 296")

*(ledadotin:mAb ~ 6:1)





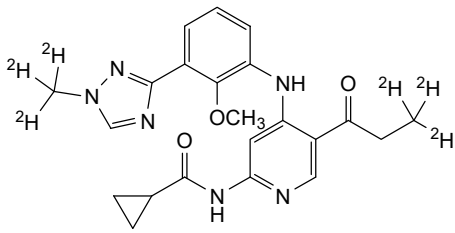
envudeucitinibum

envudeucitinib — *N*-[4-{2-methoxy-3-[1-($^2H_3$)methyl-1*H*-1,2,4-triazol-3-yl]anilino}-5-(3,3,3-$^2H_3$)propanoylpyridin-2-yl]cyclopropanecarboxamide

envudeucitinib — *N*-[4-{2-méthoxy-3-[1-($^2H_3$)méthyl-1*H*-1,2,4-triazol-3-yl]anilino}-5-(3,3,3-$^2H_3$)propanoylpyridin-2-yl]cyclopropanecarboxamide

envudeucitinib — *N*-[4-{3-[1-($^2H_3$)metil-1*H*-1,2,4-triazol-3-il]-2-metoxianilino}-5-(3,3,3-$^2H_3$)propanoilpiridin-2-il]ciclopropanocarboxamida

$C_{22}H_{18}{}^2H_6N_6O_3$



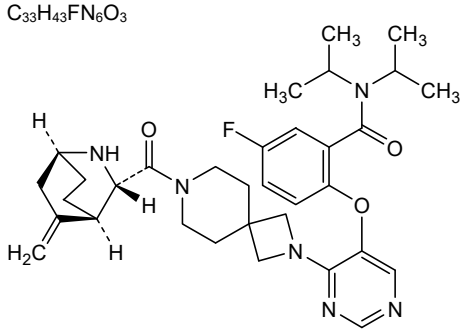
enzomenibum

enzomenib — 5-fluoro-2-[(4-{7-[(1*S*,3*S*,4*R*)-5-methylidene-2-azabicyclo[2.2.2]octane-3-carbonyl]-2,7-diazaspiro[3.5]nonan-2-yl}pyrimidin-5-yl)oxy]-*N*,*N*-di(propan-2-yl)benzamide

enzoménib — 5-fluoro-2-[(4-{7-[(1*S*,3*S*,4*R*)-5-méthylidène-2-azabicyclo[2.2.2]octane-3-carbonyl]-2,7-diazaspiro[3.5]nonan-2-yl}pyrimidin-5-yl)oxy]-*N*,*N*-di(propan-2-yl)benzamide

enzomenib — 5-fluoro-2-[(4-{7-[(1*S*,3*S*,4*R*)-5-metilideno-2-azabiciclo[2.2.2]octano-3-carbonil]-2,7-diazaespiro[3.5]nonan-2-il}pirimidin-5-il)oxi]-*N*,*N*-di(propan-2-il)benzamida

$C_{33}H_{43}FN_6O_3$



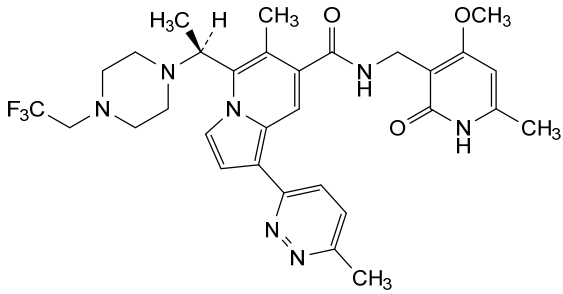
epsametostatum

epsametostat — *N*-[(4-methoxy-6-methyl-2-oxo-1,2-dihydropyridin-3-yl)methyl]-6-methyl-1-(6-methylpyridazin-3-yl)-5-{(1*S*)-1-[4-(2,2,2-trifluoroethyl)piperazin-1-yl]ethyl}indolizine-7-carboxamide

epsamétostat — *N*-[(4-méthoxy-6-méthyl-2-oxo-1,2-dihydropyridin-3-yl)méthyl]-6-méthyl-1-(6-méthylpyridazin-3-yl)-5-{(1*S*)-1-[4-(2,2,2-trifluoroéthyl)pipérazin-1-yl]éthyl}indolizine-7-carboxamide

epsametostat — 6-metil-*N*-[(6-metil-4-metoxi-2-oxo-1,2-dihidropiridin-3-il)metil]-1-(6-metilpiridazin-3-il)-5-{(1*S*)-1-[4-(2,2,2-trifluoroetil)piperazin-1-il]etil}indolizina-7-carboxamida

$C_{31}H_{36}F_3N_7O_3$



etakafuspum alfa #

etakafusp alfa — humanized immunoglobulin G1-kappa anti-(human CD8) fused at the C-terminus of one heavy chain, via peptide linker ^{449}SGGGGSGGGGSGGGGS^{464}, to a variant of human interleukin-2, glycoform alfa;
gamma 1 heavy chain (1-448) [VH (*Homo sapiens* IGHV1-69*01 -(IGHD) -IGHJ4*01, CDR-Kabat [5.17.10] (31-35.50-66.99-108)) (1-119) -*Homo sapiens* IGHG1*03v (CH1 (120-217), hinge (218-232), CH2 L^{236}>A, L^{237}>A, G^{239}>A (233-342), CH3 S^{356}>C, T^{368}>S, L^{370}>A, Y^{409}>V (343-447), CHS K^{449}>del (448)) (120-448)] fused via a peptide linker ^{449}SGGGGSGGGGSGGGGS^{464} to human interleukin-2 (IL-2, T-cell growth factor (TCGF)) [H^{16}>E^{480}, R^{38}>E^{502}, F^{42}>A^{506}, C^{125}>A^{589}]-variant (1-133, 465-597 in the current sequence), (222-214')-disulfide with kappa light chain (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*01 -IGKJ4*01, CDR-Kabat [11.7.9] (24'-34'.50'-56'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (108'-214')]; (228-228'':231-231'':356-351'')-trisdisulfide with gamma 1 heavy chain (1''-449'') [VH (*Homo sapiens* IGHV1-69*01 -(IGHD) -IGHJ4*01, CDR-Kabat [5.17.10] (31''-35''.50''-66''.99''-108'')) (1''-119'') -*Homo sapiens* IGHG1*03v (CH1 (120''-217''), hinge (218''-232''), CH2 L$^{236''}$>A, L$^{237''}$>A, G$^{239''}$>A (233''-342''), CH3 Y$^{351''}$>C, T$^{368''}$>W (343''-447''), CHS (448''-449'')) (120''-449'')], (222''-214''')-disulfide with kappa light chain (1'''-214''') [V-KAPPA (*Homo sapiens* IGKV1-39*01 -IGKJ4*01, CDR-Kabat [11.7.9] (24'''-34'''.50'''-56'''.89'''-97''')) (1'''-107''') -*Homo sapiens* IGKC*01 (108'''-214''')]; produced in Chinese hamster ovary (CHO) cells, glycoform alfa

étakafusp alfa — immunoglobuline G1-kappa humanisée anti-(CD8 humain) fusionnée à l'extrémité C-terminale d'une chaîne lourde, via un peptide liant ^{449}SGGGGSGGGGSGGGGS^{464}, à un variant de l'interleukine-2 humaine, glycoforme alfa;

	chaîne lourde gamma 1 (1-448) [VH (*Homo sapiens* IGHV1-69*01 -(IGHD) -IGHJ4*01, CDR-Kabat [5.17.10] (31-35.50-66. 99-108)) (1-119) -*Homo sapiens* IGHG1*03v (CH1 (120-217), charnière (218-232), CH2 L^{236}>A, L^{237}>A, G^{239}>A (233-342), CH3 S^{356}>C, T^{368}>S, L^{370}>A, Y^{409}>V (343-447), CHS K^{449}>del (448)) (120-448)] fusionnée via un peptide liant ^{449}SGGGGSGGGGSGGGGS^{464} à l'interleukine-2 humaine (IL-2, facteur de croissance des lymphocytes T (TCGF)), [H^{16}>E^{480}, R^{38}>E^{502}, F^{42}>A^{506}, C^{125}>A^{589}]-variant (1-133, 465-597 dans la séquence actuelle), (222-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*01 -IGKJ4*01, CDR-Kabat [11. 7.9] (24'-34'.50'-56'. 89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (108'-214')]; (228-228'':231-231'':356-351'')-trisdisulfure avec la chaîne lourde gamma 1 (1''-449'') [VH (*Homo sapiens* IGHV1-69*01 -(IGHD) -IGHJ4*01, CDR-Kabat [5. 17.10] (31''-35''.50''-66''. 99''-108'')) (1''-119'') -*Homo sapiens* IGHG1*03v (CH1 (120''-217''), charnière (218''-232''), CH2 $L^{236''}$>A, $L^{237''}$>A, $G^{239''}$>A (233''-342''), CH3 $Y^{351''}$>C, $T^{368''}$>W (343''-447''), CHS (448''-449'')) (120''-449'')], (222''-214'')-disulfure avec la chaîne légère kappa (1'''-214'') [V-KAPPA (*Homo sapiens* IGKV1-39*01 -IGKJ4*01, CDR-Kabat [11. 7.9] (24'''-34'''.50'''-56'''.89'''-97''')) (1'''-107''') -*Homo sapiens* IGKC*01 (108'''-214''')]; produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa
etakafusp alfa	inmunoglobulina G1-kappa humanizada anti-(human CD8) fusionada en el terminal C de una cadena pesada, a través de un enlace peptídico ^{449}SGGGGSGGGGSGGGGS^{464}, a una variante de interleukina 2 humana, glicoforma alfa; cadena pesada gamma 1 (1-448) [VH (*Homo sapiens* IGHV1-69*01 -(IGHD) -IGHJ4*01, CDR-Kabat [5.17.10] (31-35.50-66.99-108)) (1-119) -*Homo sapiens* IGHG1*03v (CH1 (120-217), bisagra (218-232), CH2 L^{236}>A, L^{237}>A, G^{239}>A (233-342), CH3 S^{356}>C, T^{368}>S, L^{370}>A, Y^{409}>V (343-447), CHS K^{449}>del (448)) (120-448)] fusionado a través de un enlace ^{449}SGGGGSGGGGSGGGGS^{464} a interleukina 2 humana (IL-2, factor de crecimiento de células T (TCGF)) [H^{16}>E^{480}, R^{38}>E^{502}, F^{42}>A^{506}, C^{125}>A^{589}]-variante (1-133, 465-597 en la secuencia actual), (222-214')-disulfuro con cadena ligera (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*01 -IGKJ4*01, CDR-Kabat [11.7.9] (24'-34'.50'-56'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (108'-214')]; (228-228'':231-231'':356-351'')-trisdisulfuro con cadena pesada gamma 1 (1''-449'') [VH (*Homo sapiens* IGHV1-69*01 -(IGHD) -IGHJ4*01, CDR-Kabat [5.17.10] (31''-35''.50''-66''.99''-108'')) (1''-119'') -*Homo sapiens* IGHG1*03v (CH1 (120''-217''), bisagra (218''-232''), CH2 $L^{236''}$>A, $L^{237''}$>A, $G^{239''}$>A (233''-342''), CH3 $Y^{351''}$>C, $T^{368''}$>W (343''-447''), CHS (448''-449'')) (120''-449'')], (222''-214''')-disulfuro con cadena ligera kappa (1'''-214''') [V-KAPPA (*Homo sapiens* IGKV1-39*01 -IGKJ4*01, CDR-Kabat [11.7.9] (24'''-34'''.50'''-56'''.89'''-97''')) (1'''-107''') -*Homo sapiens* IGKC*01 (108'''-214''')]; producido en las células ováricas de hámster chino (CHO), glicoforma alfa

Sequence / Séquence / Secuencia
IgG1 heavy chain-IL2

```
QVQLVQSGAE VKKPGSSVKV SCKASGGTFS SYAISWVRQA PGQGLEWMGG   50
IIPGYATANY AQKFQGRVTI TADESTSTAY MELSSLRSED TAVYYCARDA  100
AGIRLFADWG QGTLVTVSSA STKGPSVFPL APSSKSTSGG TAALGCLVKD  150
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY  200
ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP CPAPEAAGAP SVFLFPPKPK  250
DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS  300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV  350
YTLPPCREEM TKNQVSLSCA VKGFYPSDIA VEWESNGQPE NNYKTTPPVL  400
DSDGSFFLVS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGSG  450
GGGSGGGGSG GGGSAPTSSS TKKTQLQLEE LLLDLQMILN GINNYKNPKL  500
TEMLTAKFYM PKKATELKHL QCLEEELKPL EEVLNLAQSK NFHLRPRDLI  550
SNINVIVLEL KGSETTFMCE YADETATIVE FLNRWITFAQ SIISTLT     597
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IgG1 heavy chain

```
QVQLVQSGAE VKKPGSSVKV SCKASGGTFS SYAISWVRQA PGQGLEWMGG   50
IIPGYATANY AQKFQGRVTI TADESTSTAY MELSSLRSED TAVYYCARDA  100
AGIRLFADWG QGTLVTVSSA STKGPSVFPL APSSKSTSGG TAALGCLVKD  150
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY  200
ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP CPAPEAAGAP SVFLFPPKPK  250
DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS  300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV  350
CTLPPSREEM TKNQVSLWCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL  400
DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK   449
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IgG1 light chain

```
DIQMTQSPSS LSASVGDRVT ITCRASQSIY GALNWYQQKP GKAPKLLIYG   50
ASNLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQS TYTAPWTFGG  100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV  150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG  200
LSSPVTKSFN RGEC                                         214
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Mutations / Mutations / Mutaciónes
IgG1 heavy chain-IL-2: L^{236}>**A**, L^{237}>**A**, G^{239}>**A**, S^{356}>**C**, T^{368}>**S**, L^{370}>**A**, Y^{409}>**V**, K^{449}>del, H^{16}>**E**^{480}, R^{38}>**E**^{502}, F^{42}>**A**^{506}, C^{125}>**A**^{589}
IgG1 heavy chain: $L^{236''}$>**A**, $L^{237''}$>**A**, $G^{239''}$>**A**, $Y^{351''}$>C, $T^{368''}$>**W**

Peptide linker / Peptide liant / Péptido de unión
IgG1 heavy chain-IL2: ^{449}*SGGGGSGGGGSGGGGS*^{464}

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra IgG1 heavy chain-IL2: 22-96, 146-202, 263-323, 369-427, 522-569
Intra IgG1 heavy chain: 22''-96'', 146''-202'', 263''-323'', 369''-427''
Intra IgG1 light chain: 23'-88', 134'-194', 23'''-88''', 134'''-194'''
Inter IgG1 heavy chain-IL2-heavy chain: 228-228", 231-231", 356-351"
Inter IgG1 heavy chain-light chain: 222-214', 222''-214'''

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
N299, N299''

O-glycosylation sites / Sites de O-glycosylation / Posiciones de O-glicosilación
T467

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
IgG1-heavy chain Q1,Q1'' > pyroglutamyl (pE, 5-oxo-L-prolyl)

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

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immunoglobulin G4-kappa, anti-[*Homo sapiens* CD3E (CD3 epsilon)] and anti-[*Homo sapiens* TNFRSF17 (TNF receptor superfamily member 17, BCMA, TNFRSF13A, CD269)], *Homo sapiens* and humanized monoclonal antibody, bispecific, trivalent;
gamma4 heavy chain anti-CD3E *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV3-9*01 (100%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens* IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10, G4v4 CH2 A1.3, A1.2, G1v32 CH3 W22 (knob) (CH1 (124-221), hinge 1-12 S10>P (231) (222-233), CH2 F1.3>A (237), L1.2>A (238), L92 (312) (234-343), CH3 T22>W (369) (344-448), CHS (449-450)) (124-450)], (137-214')-disulfide with a fixed kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-15*01 (100%) -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')];

	bivalent (1"-472") [VH humanized (*Homo sapiens* IGHV3-23*01 (93.9%) -(IGHD) -IGHJ1*01 W118>R (109) (85.7%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1"-119")-5-mer tetraglycyl-seryl linker (120"-124") -[VH humanized (*Homo sapiens* IGHV3-23*01 (93.9%) -(IGHD) -IGHJ1*01 W118>R (233) (85.7%), CDR-IMGT [8.8.12] (150-157.175-182.221-232)) (125"-243") -*Homo sapiens* IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10, G4v4 CH2 A1.3, A1.2, G1v33 CH3 S22, A24, V86 (hole) (hinge 1-12 S10>P (253) (244"-255"), CH2 F1.3>A (259), L1.2>A (260), L92 (334) (256"-365"), CH3 T22>S (391), L24>A (393), Y86>V (432) (366"-470"), CHS (471"-472")) (244"-472")] ; dimer (229-251":232-254")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa
étentamig	immunoglobuline G4-kappa, anti-[*Homo sapiens* CD3E (CD3 epsilon)] et anti-[*Homo sapiens* TNFRSF17 (membre 17 de la superfamille des récepteurs du TNF, BCMA, TNFRSF13A, CD269)], anticorps monoclonal *Homo sapiens* et humanisé, bispécifique, trivalent; chaîne lourde gamma4 anti-CD3E *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV3-9*01 (100%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens* IGHG4*01, G4v5 h P10, nG4m(a) CH2 L92, G4v4 CH2 A1.3, A1.2,G1v32 CH3 W22 (knob) (CH1 (124-221), charnière 1-12 S10>P (231) (222-233), CH2 F1.3>A (237), L1.2>A (238), L92 (312) (234-343), CH3 T22>W (369) (344-448), CHS (449-450)) (124-450)], (137-214')-disulfure avec une chaîne légère kappa fixe *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-15*01 (100%) -IGKJ1*01 (100%), CDR-IMGT [6.3.10] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; chaîne lourde gamma4 anti-TNFRSF17 humanisée, bivalente (1"-472") [VH humanisé (*Homo sapiens* IGHV3-23*01 (93.9%) -(IGHD) -IGHJ1*01 W118>R (109) (85.7%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1"-119") -5-mer tétraglycyl-séryl linker (120"-124") -[VH humanisé (*Homo sapiens* IGHV3-23*01 (93.9%) -(IGHD) -IGHJ1*01 W118>R (233) (85.7%), CDR-IMGT [8.8.12] (150-157.175-182.221-232)) (125"-243") -*Homo sapiens* IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10,G4v4 CH2 A1.3, A1.2,G1v33 CH3 S22, A24, V86 (hole) (charnière 1-12 S10>P (253) (244"-255"), CH2 F1.3>A (259), L1.2>A (260), L92 (334) (256"-365"), CH3 T22>S (391), L24>A (393), Y86>V (432) (366"-470"), CHS (471"-472")) (244"-472")]; dimère (229-251":232-254")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa
etentamig	inmunoglobulina G4-kappa, anti-[*Homo sapiens* CD3E (CD3 épsilon)] y anti-[*Homo sapiens* TNFRSF17 (miembro 17 de la superfamilia de los receptores del TNF, BCMA, TNFRSF13A, CD269)], anticuerpo monoclonal *Homo sapiens* y humanizado, biespecífico, trivalente; cadena pesada gamma4 anti-CD3E *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV3-9*01 (100%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens* IGHG4*01, G4v5 h P10, nG4m(a) CH2 L92, G4v4 CH2 A1.3, A1.2,G1v32 CH3 W22 (knob) (CH1 (124-221), bisagra 1-12 S10>P (231) (222-233), CH2 F1.3>A (237), L1.2>A (238), L92 (312) (234-343), CH3 T22>W (369) (344-448), CHS (449-450)) (124-450)], (137-214')-disulfuro con una cadena ligera kappa fija *Homo sapiens*(1'-214') [V-KAPPA (*Homo sapiens* IGKV3-15*01 (100%) -IGKJ1*01 (100%), CDR-IMGT [6.3.10] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')];

cadena pesada gamma4 anti-TNFRSF17 humanizada, bivalente (1"-472") [VH humanizado (*Homo sapiens* IGHV3-23*01 (93.9%) -(IGHD) -IGHJ1*01 W118>R (109) (85.7%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1"-119") -5-mer tetraglicil-seril enlace (120"-124") -[VH humanizado (*Homo sapiens* IGHV3-23*01 (93.9%) -(IGHD) -IGHJ1*01 W118>R (233) (85.7%), CDR-IMGT [8.8.12] (150-157.175-182.221-232)) (125"-243")-*Homo sapiens* IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10,G4v4 CH2 A1.3, A1.2,G1v33 CH3 S22, A24, V86 (hole) (bisagra 1-12 S10>P (253) (244"-255"), CH2 F1.3>A (259), L1.2>A (260), L92 (334) (256"-365"), CH3 T22>S (391), L24>A (393), Y86>V (432) (366"-470"), CHS (471"-472")) (244"-472")]; dímero (229-251":232-254")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, forma glicosilada alfa

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

```
EVQLVESGGG LVQPGRSLRL SCAASGFTFD DYAMHWVRQA PGKGLEWVSG  50
ISWNSGSIGY ADSVKGRFTI SRDNAKNSLY LQMNSLRAED TALYYCAKDS 100
RGYGDYRLGG AYWGQGTLVT 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 MTKNQVSLWC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SRLTVDKSRW QEGNVFSCSV MHEALHNHYT QKSLSLSLGK 450
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Heavy chain / Chaîne lourde / Cadena pesada: anti-TNFRSF17, bivalent (H")

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EVQLLESGGG LVQPGGSLRL SCAASGFTVS SYGMSWVRQA PGKGPEWVSG  50
IRGSDGSTYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKQG 100
ENDGPFDHRG QGTLVTVSSG GGGSEVQLLE SGGGLVQPGG SLRLSCAASG 150
FTVSSYGMSW VRQAPGKGPE WVSGIRGSDG STYYADSVKG RFTISRDNSK 200
NTLYLQMNSL RAEDTAVYYC AKQGENDGPF DHRGQGTLVT VSSESKYGPP 250
CPPCPAPEAA GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSQEDPEVQF 300
NWYVDGVEVH NAKTKPREEQ FNSTYRVVSV LTVLHQDWLN GKEYKCKVSN 350
KGLPSSIEKT ISKAKGQPRE PQVYTLPPSQ EEMTKNQVSL SCAVKGFYPS 400
DIAVEWESNG QPENNYKTTP PVLDSDGSFF LVSRLTVDKS RWQEGNVFSC 450
SVMHEALHNH YTQKSLSLSL GK                               472
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Light chain / Chaîne légère / Cadena ligera: (L')

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EIVMTQSPAT LSVSPGERAT LSCRASQSVS SNLAWYQQKP GQAPRLLIYG  50
ASTRATGIPA RFSGSGSGTE FTLTISSLQS EDFAVYYCQQ YNNWPWTFGQ 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) 22-96 150-206 264-324 370-428
22"-96" 146"-220" 286"-346" 392"-450"
Intra-L (C23-C104) 23'-88' 134'-194'
Inter-H-L (CH1 10-CL 126) 137-214'
Inter-H-H (h 8, h 11) 229-251" 232-254"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4: 300, 322"
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, 472"

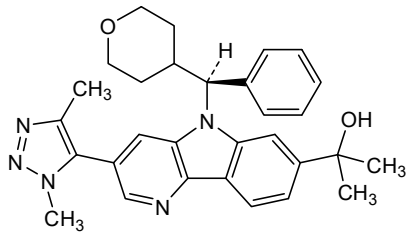
ezobresibum

ezobresib — 2-{3-(1,4-dimethyl-1*H*-1,2,3-triazol-5-yl)-5-[(*S*)-(oxan-4-yl)(phenyl)methyl]-5*H*-pyrido[3,2-*b*]indol-7-yl}propan-2-ol

ézobrésib — 2-{3-(1,4-diméthyl-1*H*-1,2,3-triazol-5-yl)-5-[(*S*)-(oxan-4-yl)(phényl)méthyl]-5*H*-pyrido[3,2-*b*]indol-7-yl}propan-2-ol

ezobresib — 2-{3-(1,4-dimetil-1*H*-1,2,3-triazol-5-il)-5-[(*S*)-fenil(oxan-4-il)metil]-5*H*-pirido[3,2-*b*]indol-7-il}propan-2-ol

$C_{30}H_{33}N_5O_2$



ficerafuspum alfa #

ficerafusp alfa

chimeric immunoglobulin G1-kappa anti-(human epidermal growth factor receptor) fused at the C-terminus of both light chains, via a $(G_4S)_3$ peptide linker, to a fragment of the extracellular domain of human TGF-beta receptor type-2 (TGFR-2, TGF-beta type II receptor, transforming growth factor-beta receptor type II), glycoform alfa;
gamma 1 heavy chain (1-448) [VH (*Mus musculus* IGHV2-2*03 -(IGHD) -IGHJ3*01, CDR-Kabat [5.16.11] (31-35.50-65.98-108)) (1-119) -*Homo sapiens* IGHG1*08 (CH1 (120-217), hinge (218-232), CH2 (233-342), CH3 (343-447), CHS K^{449}>del (448)) (120-448)], (222-214')-disulfide with kappa light chain (1'-214') [V-KAPPA (*Mus musculus* IGKV5-48*01 -IGKJ5*01, CDR-Kabat [11.7.9] (24'-34'.50'-56'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (108'-214')] fused via a $(G_4S)_3$ peptide linker (215'-229') to human TGF-beta receptor type-2 (TGFR-2, TGF-beta type II receptor, transforming growth factor-beta receptor type II) extracellular domain fragment 1-137 (230-366 in the current sequence); dimer (228-228'', 231-231'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

ficérafusp alfa

immunoglobuline chimérique G1-kappa anti-(récepteur du facteur de croissance épidermique humain) fusionnée à l'extrémité C-terminale des deux chaînes légères, via un peptide liant $(G_4S)_3$, à un fragment du domaine extracellulaire du récepteur humain du TGF-bêta de type 2 (TGFR-2, récepteur du TGF-bêta de type II, récepteur du facteur de croissance transformant-bêta de type II), glycoforme alfa;
chaîne lourde gamma 1 (1-448) [VH (*Mus musculus* IGHV2-2*03 -(IGHD) -IGHJ3*01, CDR-Kabat [5.16.11] (31-35.50-65. 98-108)) (1-119) -*Homo sapiens* IGHG1*08 (CH1 (120-217), charnière (218-232), CH2 (233-342), CH3 (343-447), CHS K^{449}>del (448)) (120-448)], (222-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA (*Mus musculus* IGKV5-48*01 -IGKJ5*01, CDR-Kabat [11. 7.9] (24'-34'.50'-56'. 89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (108'-214')] fusionné, via un peptide liant $(G_4S)_3$ (215'-229'), au récepteur humain du TGF-bêta de type 2 (TGFR-2, récepteur du TGF-bêta de type II, récepteur du facteur de croissance transformant bêta de type II), fragment 1-137 du domaine extracellulaire (230-366 dans la séquence actuelle); dimère (228-228'', 231-231'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

ficerafusp alfa

inmunoglobulina quimérica G1-kappa anti-(receptor del factor de crecimiento epidérmico humano) fusionada en el terminal C de ambas cadenas ligeras, a través de un enlace peptídico $(G_4S)_3$, a un fragmento del dominio extracelular de receptor TGF-beta humano de tipo 2 (TGFR-2, receptor TGF-beta de tipo II, receptor de factor de crecimiento beta de transformación de tipo II), glicoforma alfa;

cadena pesada gamma 1 (1-448) [VH (*Mus musculus* IGHV2-2*03 -(IGHD) -IGHJ3*01, CDR-Kabat [5.16.11] (31-35.50-65.98-108)) (1-119) -*Homo sapiens* IGHG1*08 (CH1 (120-217), bisagra (218-232), CH2 (233-342), CH3 (343-447), CHS K^{449}>del (448)) (120-448)], (222-214')-disulfuro con cadena ligera kappa (1'-214') [V-KAPPA (*Mus musculus* IGKV5-48*01 -IGKJ5*01, CDR-Kabat [11.7.9] (24'-34'.50'-56'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (108'-214')] fusionado a través de un enlace peptídico $(G_4S)_3$ (215'-229') a un receptor TGF-beta humano de tipo 2 (TGFR-2, receptor TGF-beta de tipo II, receptor de factor de crecimiento beta de transformación de tipo II) fragmento de dominio extracelular 1-137 (230-366 en la secuencia actual); dímero (228-228":231-231")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), glicoforma alfa

Sequence / Séquence / Secuencia
IgG1 heavy chain

```
QVQLKQSGPG LVQPSQSLSI TCTVSGFSLT NYGVHWVRQS PGKGLEWLGV   50
IWSGGNTDYN TPFTSRLSIN KDNSKSQVFF KMNSLQSNDT AIYYCARALT  100
YYDYEFAYWG QGTLVTVSAA STKGPSVFPL APSSKSTSGG TAALGCLVKD  150
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY  200
ICNVNHKPSN TKVDKRVEPK SCDKTHTCPP CPAPELLGGP SVFLFPPKPK  250
DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS  300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV  350
YTLPPSRDEL TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL  400
DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPG    448
```

IgG1 light chain-TGFBRII

```
DILLTQSPVI LSVSPGERVS FSCRASQSIG TNIHWYQQRT NGSPRLLIKY   50
ASESISGIPS RFSGSGSGTD FTLSINSVES EDIADYYCQQ NNNWPTTFGA  100
GTKLELKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV  150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG  200
LSSPVTKSFN RGEC[GGGGSG GGGSGGGGS]T IPPHVQKSVN NDMIVTDNNG  250
AVKFPQLCKF CDVRFSTCDN QKSCMSNCSI TSICEKPQEV CVAVWRKNDE  300
NITLETVCHD PKLPYHDFIL EDAASPKCIM KEKKKPGETF FMCSCSSDEC  350
NDNIIFSEEY NTSNPD                                       366
```

Mutation / Mutation / Mutación
IgG1 heavy chain C-term K^{449}>del

Peptide linker / Peptide liant / Péptido de unión
IgG1 light chain-TGFBRII: ^{215}*GGGGSGGGGSGGGGS*^{229}

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra heavy chain: 22-95, 146-202, 263-323, 369-427; 22"-95", 146"-202", 263"-323", 369"-427"
Intra light chain-TGFBRII: 23'-88', 134'-194', 258'-261', 268'-274', 278'-284', 291'-308', 328'-343', 345'-350'; 23'"-88'", 134'"-194'", 258'"-261'", 268'"-274'", 278'"-284'", 291'"-308'", 328'"-343'", 345'"-350'"
Inter heavy chain - light chain-TGFBRII: 222-214', 222"-214'"
Inter heavy chain: 228-228", 231-231"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
IgG1 heavy chain: 88, 299, 88", 299"
IgG1 light chain-TGFBRII: 277', 301', 361', 277'", 301'", 361'"

O-glycosylation sites / Sites de O-glycosylation / Posiciones de O-glicosilación
Peptide linker: (S219', S224', S229'; S219'", S224'", S229'")*
*Glycosylation can be in any of the listed amino acids
IgG1 light chain-TGFBRII: S238', S238'"

Oxidation sites / Sites d'oxydation / Posiciones de oxidación
IgG1 heavy chain: M254, M254"
IgG1 light chain-TGFBRII: M243', M243'"

Deamidation sites / Sites de désamidation / Posiciones de desamidación
IgG1 heavy chain: N386, N386"; IgG1 light chain-TGFBRII: N249', N249'"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
IgG1-heavy chain Q1,Q1" > pyroglutamyl (pE, 5-oxo-L-prolyl)

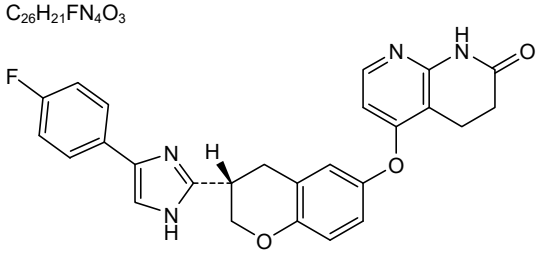
flezurafenibum

flezurafenib — 5-({(3*S*)-3-[4-(4-fluorophenyl)-1*H*-imidazol-2-yl]-3,4-dihydro-2*H*-1-benzopyran-6-yl}oxy)-3,4-dihydro-1,8-naphthyridin-2(1*H*)-one

flézurafénib — 5-({(3*S*)-3-[4-(4-fluorophényl)-1*H*-imidazol-2-yl]-3,4-dihydro-2*H*-1-benzopyran-6-yl}oxy)-3,4-dihydro-1,8-naphtyridin-2(1*H*)-one

flezurafenib — 5-({(3*S*)-3-[4-(4-fluorofenil)-1*H*-imidazol-2-il]-3,4-dihidro-2*H*-1-benzopiran-6-il}oxi)-3,4-dihidro-1,8-naftiridin-2(1*H*)-ona

$C_{26}H_{21}FN_4O_3$



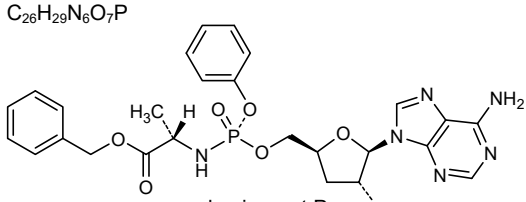
fosdesdenosinum sipalabenamidum

fosdesdenosine sipalabenamide — benzyl *N*-(*P*-*ambo*-3'-deoxy-O^P-phenyl-5'-adenylyl)-L-alaninate

fosdesdénosine sipalabénamide — *N*-(*P*-*ambo*-3'-désoxy-O^P-phényl-5'-adénylyl)-L-alaninate de benzyle

fosdesdenosina sipalabenamida — *N*-(*P*-*ambo*-3'-desoxi-O^P-fenil-5'-adenilil)-L-alaninato de bencilo

$C_{26}H_{29}N_6O_7P$



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

foselutoclaxum

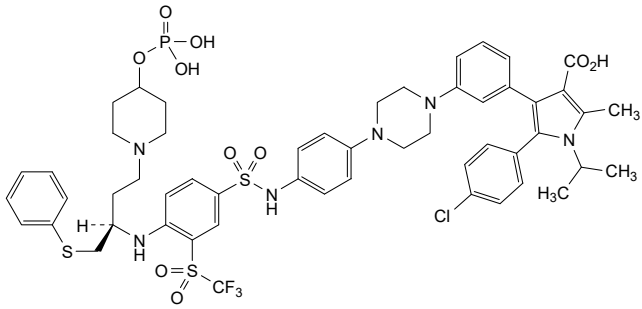
foselutoclax — (10*R*)-1^4-chloro-2^5-methyl-7,7-dioxo-10-[(phenylsulfanyl)methyl]-13^4-(phosphonooxy)-2^1-(propan-2-yl)-8^3-(trifluoromethanesulfonyl)-2^1*H*-7λ^6-thia-6,9-diaza-4(1,4)-piperazina-13(1)-piperidina-2(2,3)-pyrrola-1(1),3(1,3),5,8(1,4)-tetrabenzenatridecaphane-2^4-carboxylic acid

fosélutoclax — acide (10*R*)-1^4-chloro-2^5-méthyl-7,7-dioxo-10-[(phénylsulfanyl)méthyl]-13^4-(phosphonooxy)-2^1-(propan-2-yl)-8^3-(trifluorométhanesulfonyl)-2^1*H*-7λ^6-thia-6,9-diaza-4(1,4)-pipérazina-13(1)-pipéridina-2(2,3)-pyrrola-1(1),3(1,3),5,8(1,4)-tétrabenzénatridécaphane-2^4-carboxylique

foselutoclax

ácido (10*R*)-1^{4}-cloro-10-[(fenilsulfanil)metil]-13^{4}-(fosfonooxi)-2^{5}-metil-7,7-dioxo-2^{1}-(propan-2-il)-8^{3}-(trifluorometanosulfonil)-2^{1}*H*-7λ^{6}-tia-6,9-diaza-4(1,4)-piperazina-13(1)-piperidina-2(2,3)-pirrola-1(1),3(1,3),5,8(1,4)-tetrabencenatridecafano-2^{4}-carboxílico

$C_{53}H_{59}ClF_3N_6O_{10}PS_3$



fovinaciclibum

fovinaciclib

7-cyclopentyl-*N*,*N*-dimethyl-2-({5-[4-(4-methylpiperazin-1-yl)piperidin-1-yl]pyridin-2-yl}amino)thieno[3,2-*d*]pyrimidine-6-carboxamide

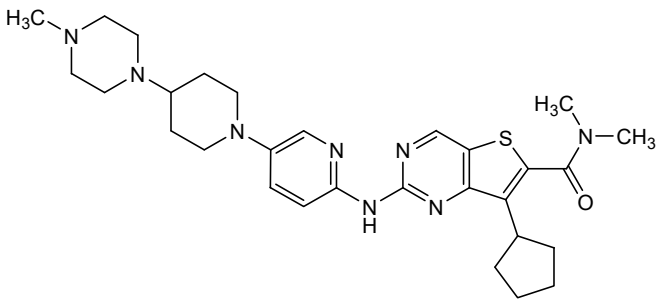
fovinaciclib

7-cyclopentyl-*N*,*N*-diméthyl-2-({5-[4-(4-méthylpipérazin-1-yl)pipéridin-1-yl]pyridin-2-yl}amino)thiéno[3,2-*d*]pyrimidine-6-carboxamide

fovinaciclib

7-ciclopentil-*N*,*N*-dimetil-2-({5-[4-(4-metilpiperazin-1-il)piperidin-1-il]piridin-2-il}amino)tieno[3,2-*d*]pirimidina-6-carboxamida

$C_{29}H_{40}N_8OS$



frevecitinibum

frevecitinib

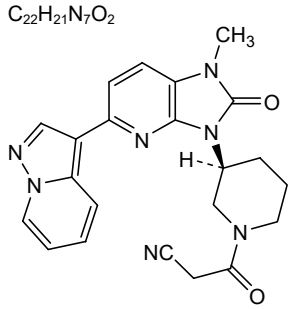
3-{(3*S*)-3-[1-methyl-2-oxo-5-(pyrazolo[1,5-*a*]pyridin-3-yl)-1,2-dihydro-3*H*-imidazo[4,5-*b*]pyridin-3-yl]piperidin-1-yl}-3-oxopropanenitrile

frévécitinib

3-{(3*S*)-3-[1-méthyl-2-oxo-5-(pyrazolo[1,5-*a*]pyridin-3-yl)-1,2-dihydro-3*H*-imidazo[4,5-*b*]pyridin-3-yl]pipéridin-1-yl}-3-oxopropanenitrile

frevecitinib

3-{(3*S*)-3-[1-metil-2-oxo-5-(pirazolo[1,5-*a*]piridin-3-il)-1,2-dihidro-3*H*-imidazo[4,5-*b*]piridin-3-il]piperidin-1-il}-3-oxopropanonitrilo

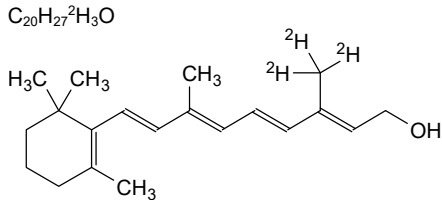


gildeuretinolum

gildeuretinol — (2*E*,4*E*,6*E*,8*E*)-3-($^2H_3$)methyl-7-methyl-9-(2,6,6-trimethylcyclohex-1-en-1-yl)nona-2,4,6,8-tetraen-1-ol; (20,20,20-$^2H_3$)retinol

gildeurétinol — (2*E*,4*E*,6*E*,8*E*)-3-($^2H_3$)méthyl-7-méthyl-9-(2,6,6-triméthylcyclohex-1-én-1-yl)nona-2,4,6,8-tétraén-1-ol; (20,20,20-$^2H_3$)rétinol

gildeuretinol — (2*E*,4*E*,6*E*,8*E*)-3-($^2H_3$)metil-7-metil-9-(2,6,6-trimetilciclohex-1-en-1-il)nona-2,4,6,8-tetraen-1-ol; (20,20,20-$^2H_3$)retinol



gimistotugum #

gimistotug — immunoglobulin G1-kappa, anti-[*Homo sapiens* TNFRSF4 (tumor necrosis factor receptor (TNFR) superfamily member 4, OX40, CD134)], humanized monoclonal antibody;
H-gamma1 heavy chain humanized (1-450) [VH (*Homo sapiens* IGHV1-46*01 (84.7%) -(IGHD) - IGHJ4*01 (92.3%) L123>T (115), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (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 L-kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*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 (229-229":232-232")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

gimistotug — immunoglobuline G1-kappa, anti-[*Homo sapiens* TNFRSF4 (membre 4 de la superfamille des récepteurs du facteur de nécrose tumorale (TNFR), OX40, CD134)], anticorps monoclonal humanisé;

chaîne lourde H-gamma1 humanisée (1-450) [VH (*Homo sapiens* IGHV1-46*01 (84.7%) -(IGHD) -IGHJ4*01 (92.3%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (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 L-kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*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 (229-229":232-232")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

gimistotug

inmunoglobulina G1-kappa, anti-[*Homo sapiens* TNFRSF4 (miembro 4 de la superfamilia de los receptores del factor de necrosis tumoral (TNFR), OX40, CD134)], anticuerpo monoclonal humanizado;
cadena pesada H-gamma1 humanizada (1-450) [VH (*Homo sapiens* IGHV1-46*01 (84.7%) -(IGHD) -IGHJ4*01 (92.3%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (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 L-kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*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 (229-229":232-232")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGSSVKV SCKASGYKFT SYIIHWVRQA PGQGLEWMGY  50
INPYNEGTRY NQKFQGRVTL TADKSTSTAY MELSSLRSED TAVYYCARGY 100
YGSSYAMDYW 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
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Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCRASQGIS NYLNWYQQKP DGAIKLLIYD  50
ASTLYSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YSKLPYTFGG 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 / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)
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

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

girocitinibum

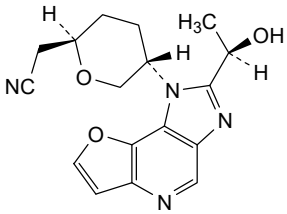
girocitinib

[(2*R*,5*S*)-5-{2-[(1*R*)-1-hydroxyethyl]-1*H*-furo[3,2-*b*]imidazo[4,5-*d*]pyridin-1-yl}oxan-2-yl]acetonitrile

girocitinib [(2*R*,5*S*)-5-{2-[(1*R*)-1-hydroxyéthyl]-1*H*-furo[3,2-*b*]imidazo[4,5-*d*]pyridin-1-yl}oxan-2-yl]acétonitrile

girocitinib [(2*R*,5*S*)-5-{2-[(1*R*)-1-hidroxietil]-1*H*-furo[3,2-*b*]imidazo[4,5-*d*]piridin-1-il}oxan-2-il]acetonitrilo

$C_{17}H_{18}N_4O_3$



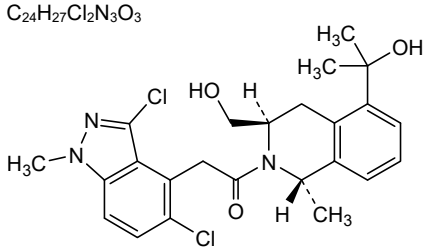
glovadalenum

glovadalen 2-(3,5-dichloro-1-methyl-1*H*-indazol-4-yl)-1-[(1*S*,3*R*)-3-(hydroxymethyl)-5-(2-hydroxypropan-2-yl)-1-methyl-3,4-dihydroisoquinolin-2(1*H*)-yl]ethan-1-one

glovadalène 2-(3,5-dichloro-1-méthyl-1*H*-indazol-4-yl)-1-[(1*S*,3*R*)-3-(hydroxyméthyl)-5-(2-hydroxypropan-2-yl)-1-méthyl-3,4-dihydroisoquinoléin-2(1*H*)-yl]éthan-1-one

glovadalén 2-(3,5-dicloro-1-metil-1*H*-indazol-4-il)-1-[(1*S*,3*R*)-3-(hidroximetil)-5-(2-hidroxipropan-2-il)-1-metil-3,4-dihidroisoquinolin-2(1*H*)-il]etan-1-ona

$C_{24}H_{27}Cl_2N_3O_3$



gocatamigum #

gocatamig immunoglobulin single chain scFvhl-VH-VH', anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], anti-[*Homo sapiens* ALB (albumin, human serum albumin, HSA)] and anti-[*Homo sapiens* DLL3 (delta-like ligand 3, delta like canonical Notch ligand 3)], trispecific;
IG single chain scFvhl-VH-VH' (1-505) [scFvhl anti-CD3E (1-149) [VH Musmus/Homsap (*Mus musculus* IGHV10-1*02 (89.9%) -(IGHD) -IGHJ3*01 (100%)/*Homo sapiens* IGHV3-73*01 (85.0%) -(IGHD) -IGHJ5*01 (100%), CDR-IMGT [8.10.16] (26-33.51-60.99-114)) (1-125) -15-mer-tris(tetraglycyl-seryl) linker (126-140) -V-LAMBDA (*Homo sapiens* IGLV7-43*01 (86.2%) -IGLJ3*02 (100%), CDR-IMGT [9.3.9] (166-174.192-194.231-239)) (141-249)] -9-mer-tetraglycyl-seryl-triglycyl-seryl linker (250-258) -VH anti-ALB (*Homo sapiens* IGHV3-23*04 (88.5%) -(IGHD) -IGHJ1*01 (81.8%) W118>S (363), G119>S (364), CDR-IMGT [8.8.8] (284-291.309-316.355-362)) (259-373) -9-mer-tetraglycyl-seryl-triglycyl-seryl linker (374-382) -VH anti-DLL3 Vicpac /Homsap (*Vicugna pacos* IGHV3S53*01 (77.3%) -(IGHD) -IGHJ5*01 (100%)/*Homo sapiens* IGHV3-7*01 (77.1%) -(IGHD) -IGHJ4*01 (100%), (CDR-IMGT [8.7.11] (408-415.433-440.478-488)) (383-499) -hexahistidine tag (500-505)], produced in Chinese hamster ovary (CHO) cells, cell line CHO-DG44, lacking the enzyme dihydrofolate reductase (DHFR), non-glycosylated

gocatamig	immunoglobuline à chaîne unique scFvhl-VH-VH', anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], anti-[*Homo sapiens* ALB (albumine, sérum albumine humaine, SAH)] et anti-[*Homo sapiens* DLL3 (delta-like ligand 3, delta like canonical Notch ligand 3)], trispécifique; IG à chaîne unique scFvhl-VH-VH' (1-505) [scFvhl anti-CD3E (1-149) [VH Musmus/Homsap (*Mus musculus* IGHV10-1*02 (89.9%) -(IGHD) -IGHJ3*01 (100%)/*Homo sapiens* IGHV3-73*01 (85.0%) -(IGHD) -IGHJ5*01 (100%), CDR-IMGT [8.10.16] (26-33.51-60.99-114)) (1-125) -15-mer-tris(tétraglycyl-séryl) linker (126-140) -V-LAMBDA (*Homo sapiens* IGLV7-43*01 (86.2%) -IGLJ3*02 (100%)), CDR-IMGT [9.3.9] (166-174.192-194.231-239)) (141-249)] -9-mer-tétraglycyl-séryl-triglycyl-séryl linker (250-258) -VH anti-ALB (*Homo sapiens* IGHV3-23*04 (88.5%) -(IGHD) -IGHJ1*01 (81.8%) W118>S (363), G119>S (364), CDR-IMGT [8.8.8] (284-291.309-316.355-362)) (259-373) -9-mer-tétraglycyl-séryl-triglycyl-séryl linker (374-382) -VH' anti-DLL3 Vicpac /Homsap (*Vicugna pacos* IGHV3S53*01 (77.3%) -(IGHD) -IGHJ5*01 (100%)/*Homo sapiens* IGHV3-7*01 (77.1%) -(IGHD) -IGHJ4*01 (100%), (CDR-IMGT [8.7.11] (408-415.433-440.478-488)) (383-499) -hexahistidine tag (500-505)], produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-DG44, ne présentant pas l'enzyme dihydrofolate réductase (DHFR), non-glycosylé
gocatamig	inmunoglobulina con cadena única scFvhl-VH-VH', anti-[*Homo sapiens* CD3E (CD3 épsilon, Leu-4)], anti-[*Homo sapiens* ALB (albúmina, albumina sérica humana, SAH)] y anti-[*Homo sapiens* DLL3 (ligando 3 tipo delta, delta like canonical Notch ligand 3)], triespecífico; IG con cadena única scFvhl-VH-VH' (1-505) [scFvhl anti-CD3E (1-149) [VH Musmus/Homsap (*Mus musculus* IGHV10-1*02 (89.9%) -(IGHD) -IGHJ3*01 (100%)/*Homo sapiens* IGHV3-73*01 (85.0%) -(IGHD) -IGHJ5*01 (100%), CDR-IMGT [8.10.16] (26-33.51-60.99-114)) (1-125) -15-mer-tris(tetraglicil-seril) enlace (126-140) -V-LAMBDA (*Homo sapiens* IGLV7-43*01 (86.2%) -IGLJ3*02 (100%)), CDR-IMGT [9.3.9] (166-174.192-194.231-239)) (141-249)] -9-mer-tetraglicil-seril-triglicil-seril enlace (250-258) -VH anti-ALB (*Homo sapiens* IGHV3-23*04 (88.5%) -(IGHD) -IGHJ1*01 (81.8%) W118>S (363), G119>S (364), CDR-IMGT [8.8.8] (284-291.309-316.355-362)) (259-373) -9-mer-tetraglicil-seril-triglicil-seril enlace (374-382) -VH' anti-DLL3 Vicpac /Homsap (*Vicugna pacos* IGHV3S53*01 (77.3%) -(IGHD) -IGHJ5*01 (100%)/*Homo sapiens* IGHV3-7*01 (77.1%) -(IGHD) -IGHJ4*01 (100%), (CDR-IMGT [8.7.11] (408-415.433-440.478-488)) (383-499) -hexahistidina tag (500-505)], producido en las células ováricas de hámster chino (CHO), línea celular CHO-DG44,en ausencia de la enzima dihidrofolato reductasa (DHFR), no glicosilado

Heavy chain / Chaîne lourde / Cadena pesada : scFvhl (anti-CD3E) -VH (anti-ALB) -VH' (anti-DLL3)

```
EVQLVESGGG LVQPGGSLKL SCAASGFTFN KYAINWVRQA PGKGLEWVAR  50
IRSKYNNYAT YYADQVKDRF TISRDDSKNT AYLQMNNLKT EDTAVYYCVR 100
HANFGNSYIS YWAYWGQGTL VTVSSGGGGS GGGGSGGGGS QTVVTQEPSL 150
TVSPGGTVTL TCASSTGAVT SGNYPNWVQQ KPGQAPRGLI GGTKFLVPGT 200
PARFSGSLLG GKAALTLSGV QPEDEAEYYC TLWYSNRWVF GGGTKLTVLG 250
GGGSGGGSEV QLVESGGGLV QPGNSLRLSC AASGFTFSKF GMSWVRQAPG 300
KGLEWVSSIS GSGRDTLYAD SVKGRFTISR DNAKTTLYLQ MNSLRPEDTA 350
VYYCTIGGSL SVSSQGTLVT VSSGGGGSGG GSEVQLVESG GGLVQPGGSL 400
TLSCAASSSS VSLLSLAWYR QAPGKKRELV AGISDDGSIV YMDSVKGRFT 450
ISRDNAKNSV YLQMNSLRAE DTAVYYCYAY SWITRSPYWG QGTLVTVSSH 500
HHHHH                                                   505
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-chain (C23-C104) 22-98 162-230 280-354 404-477

No N-glycosylation sites / pas de sites de N-glycosylation / ningùm posición de N-glycosilación

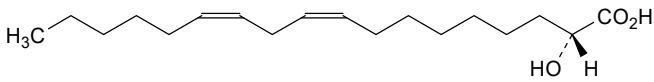
ibrilatazarum

ibrilatazar — *rac*-(2*R*)-(9*Z*,12*Z*)-2-hydroxyoctadeca-9,12-dienoic acid

ibrilatazar — acide *rac*-(2*R*)-(9*Z*,12*Z*)-2-hydroxyoctadéca-9,12-diénoïque

ibrilatazar — ácido *rac*-(2*R*)-(9*Z*,12*Z*)-2-hidroxioctadeca-9,12-dienoico

$C_{18}H_{32}O_3$



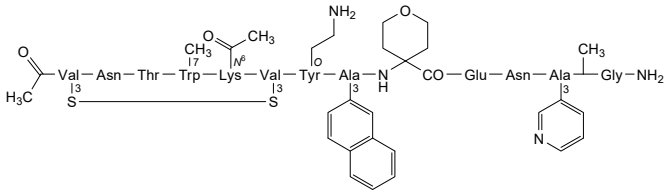
icotrokinrum

icotrokinra — *S*$^{3.1}$,*S*$^{3.6}$-cyclo[*N*-acetyl-3-sulfanyl-L-valyl-L-asparaginyl-L-threonyl-7-methyl-L-tryptophyl-*N*^{6}-acetyl-L-lysyl-3-sulfanyl-L-valyl-*O*-(2-aminoethyl)-L-tyrosyl-3-(naphthalen-2-yl)-L-alanyl-4-aminooxan-4-carbonyl-L-α-glutamyl-L-asparaginyl-3-(pyridin-3-yl)-L-alanyl-*N*^{2}-methylglycinamide]

icotrokinra — *S*$^{3.1}$,*S*$^{3.6}$-cyclo[*N*-acétyl-3-sulfanyl-L-valyl-L-asparaginyl-L-thréonyl-7-méthyl-L-tryptophyl-*N*^{6}-acétyl-L-lysyl-3-sulfanyl-L-valyl-*O*-(2-aminoéthyl)-L-tyrosyl-3-(naphthalén-2-yl)-L-alanyl-4-aminooxan-4-carbonyl-L-α-glutamyl-L-asparaginyl-3-(pyridin-3-yl)-L-alanyl-*N*^{2}-méthylglycinamide]

icotrokinra — *S*$^{3.1}$,*S*$^{3.6}$-cyclo[*N*-acetil-3-sulfanil-L-valil-L-asparaginil-L-treonil-7-metil-L-triptofil-*N*^{6}-acetil-L-lisil-3-sulfanil-L-valil-*O*-(2-aminoetil)-L-tirosil-3-(naftalen-2-il)-L-alanil-4-aminooxan-4-carbonil-L-α-glutamil-L-asparaginil-3-(piridin-3-il)-L-alanil-*N*^{2}-metilglicinamida]

$C_{90}H_{120}N_{20}O_{22}S_2$



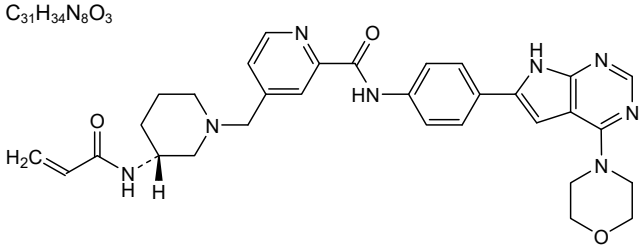
icovamenibum

icovamenib — *N*-{4-[4-(morpholin-4-yl)-7*H*-pyrrolo[2,3-*d*]pyrimidin-6-yl]phenyl}-4-{[(3*R*)-3-(prop-2-enamido)piperidin-1-yl]methyl}pyridine-2-carboxamide

icovaménib — *N*-{4-[4-(morpholin-4-yl)-7*H*-pyrrolo[2,3-*d*]pyrimidin-6-yl]phényl}-4-{[(3*R*)-3-(prop-2-énamido)pipéridin-1-yl]méthyl}pyridine-2-carboxamide

icovamenib — *N*-{4-[4-(morfolin-4-il)-7*H*-pirrolo[2,3-*d*]pirimidin-6-il]fenil}-4-{[(3*R*)-3-(prop-2-enamido)piperidin-1-il]metil}piridina-2-carboxamida

$C_{31}H_{34}N_8O_3$



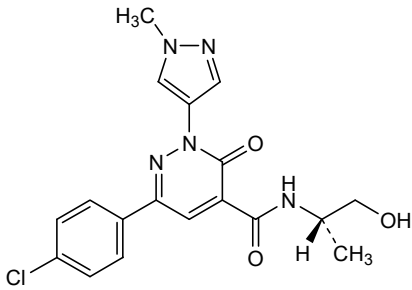
ilantimodum

ilantimod — 6-(4-chlorophenyl)-*N*-[(2*S*)-1-hydroxypropan-2-yl]-2-(1-methyl-1*H*-pyrazol-4-yl)-3-oxo-2,3-dihydropyridazine-4-carboxamide

ilantimod — 6-(4-chlorophényl)-*N*-[(2*S*)-1-hydroxypropan-2-yl]-2-(1-méthyl-1*H*-pyrazol-4-yl)-3-oxo-2,3-dihydropyridazine-4-carboxamide

ilantimod — 6-(4-clorofenil)-*N*-[(2*S*)-1-hidroxipropan-2-il]-2-(1-metil-1*H*-pirazol-4-il)-3-oxo-2,3-dihidropiridazina-4-carboxamida

$C_{18}H_{18}ClN_5O_3$



imdusiranum

imdusiran — *all-P-ambo*-2'-*O*-methyl-*P*-thioguanylyl-(3'→5')-2'-*O*-methyl-*P*-thiouridylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-deoxy-2'-fluoroadenylyl-(3'→5')-2'-deoxy-2'-fluorocytidylyl-(3'→5')-2'-deoxy-2'-fluorouridylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-3'-*O*-[{[(3*RS*,4*SR*)-1-(10-{[(2*S*)-1,5-bis{[2-(3,5-bis{[2-(2-{2-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]ethoxy}ethoxy)ethyl]carbamoyl}anilino)-2-oxoethyl]amino}-1,5-dioxopentan-2-yl]amino}-10-oxodecanoyl)-4-(hydroxymethyl)-3,4-dimethylpyrrolidin-3-yl]methoxy}(hydroxy)phosphoryl]-2'-*O*-methyladenosine

duplex with *all-P-ambo*-uridylyl-(5'→3')-2'-*O*-methyl-*P*-thioguanylyl-(5'→3')-2'-*O*-methyl-*P*-thioguanylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-(5'→3')-2'-*O*-methyladenylyl-2'-*O*-methylcytidylyl-(5'→3')-2'-deoxy-2'-fluoroadenylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-deoxy-2'-fluoroguanylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-*O*-methylguanylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-*O*-methylguanylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-*O*-methylguanylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-*O*-methylguanylyl-(5'→3')-2'-*O*-methyl-*P*-thiouridylyl-(5'→3')-2'-deoxy-2'-fluoro-*P*-thioguanylyl-(5'→3')-2'-*O*-methyluridine

imdusiran

tout-P-ambo-2'-*O*-méthyl-*P*-thioguanylyl-(3'→5')-2'-*O*-méthyl-*P*-thiouridylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-désoxy-2'-fluoroadénylyl-(3'→5')-2'-désoxy-2'-fluorocytidylyl-(3'→5')-2'-désoxy-2'-fluorouridylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-3'-*O*-[{[(3*RS*,4*SR*)-1-(10-{[(2*S*)-1,5-bis{[2-(3,5-bis{[2-(2-{2-[(2-acétamido-2-désoxy-β-D-galactopyranosyl)oxy]éthoxy}éthoxy)éthyl]carbamoyl}anilino)-2-oxoéthyl]amino}-1,5-dioxopentan-2-yl]amino}-10-oxodécanoyl)-4-(hydroxyméthyl)-3,4-diméthylpyrrolidin-3-yl]méthoxy}(hydroxy)phosphoryl]-2'-*O*-méthyladénosine
duplex avec *tout-P-ambo*-uridylyl-(5'→3')-2'-*O*-méthyl-*P*-thioguanylyl-(5'→3')-2'-*O*-méthyl-*P*-thioguanylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-(5'→3')-2'-*O*-méthyladenylyl-2'-*O*-méthylcytidylyl-(5'→3')-2'-désoxy-2'-fluoroadénylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-désoxy-2'-fluoroguanylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-*O*-méthylguanylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-*O*-méthylguanylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-*O*-méthylguanylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-*O*-méthylguanylyl-(5'→3')-2'-*O*-méthyl-*P*-thiouridylyl-(5'→3')-2'-désoxy-2'-fluoro-*P*-thioguanylyl-(5'→3')-2'-*O*-méthyluridine

imdusirán

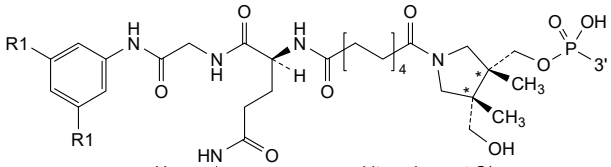
todo-P-ambo-2'-*O*-metil-*P*-tioguanilil-(3'→5')-2'-*O*-metil-*P*-tiouridilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-desoxi-2'-fluoroadenilil-(3'→5')-2'-desoxi-2'-fluorocitidilil-(3'→5')-2'-desoxi-2'-fluorouridilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-3'-*O*-[{[(3*RS*,4*SR*)-1-(10-{[(2*S*)-1,5-bis{[2-(3,5-bis{[2-(2-{2-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]etoxi}etoxi)etil]carbamoil}anilino)-2-oxoetil]amino}-1,5-dioxopentan-2-il]amino}-10-oxodecanoil)-4-(hidroximetil)-3,4-dimetilpirrolidin-3-il]metoxi}(hidroxi)fosforil]-2'-*O*-metiladenosina
dúplex con *todo-P-ambo*-uridilil-(5'→3')-2'-*O*-metil-*P*-tioguanilil-(5'→3')-2'-*O*-metil-*P*-tioguanilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-(5'→3')-2'-*O*-metiladenilil-2'-*O*-metilcitidilil-(5'→3')-2'-desoxi-2'-fluoroadenilil-(5'→3')-2'-*O*-metilcitidill-(5'→3')-2'-desoxi-2'-fluoroguanilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-*O*-metilguanilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-*O*-metilguanilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-*O*-metilguanilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-*O*-metilguanilil-(5'→3')-2'-*O*-metil-*P*-tiouridilil-(5'→3')-2'-desoxi-2'-fluoro-*P*-tioguanilil-(5'→3')-2'-*O*-metiluridina

$C_{502}H_{678}F_6N_{162}O_{303}P_{38}S_6$

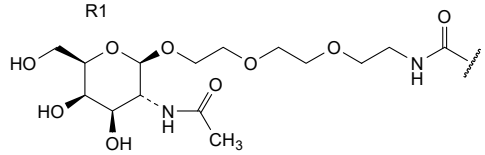
(3'-5')*G*=*U*=*G*−*C*−A−C−U−*U*−*C*−*G*−*C*−*U*−*U*−*C*−*A*−*C*−*A*−R
(5'-3')U−*G*=*G*=*C*−*A*−*C*−A−*C*−G−*U*−*G*−*A*−*A*−*G*−*C*−*G*−*A*−*A*−*G*−*U*=G=*U*

N : A,C,G,U
N : 2'-*O*-methyl-N / 2'-*O*-méthyl-N / 2'-*O*-metil-N
N : 2'-deoxy-2'-fluoro-N / 2'-désoxy-2'-fluoro-N / 2'-desoxi-2'-fluoro-N
− : –PO(OH)– = : –PO(SH)–

R- :



R1 :



imelcimentum #

imelciment — immunoglobulin (H-gamma4_L-kappa)_G4hCH2CH3, anti-[*vixticibart*, monoclonal antibody allosteric agonist of *Homo sapiens* NPR1 (atrial natriuretic peptide receptor 1)], *Homo sapiens* monoclonal antibody;
H-gamma4 heavy chain anti-*vixticibart Homo sapiens* (1-448) [VH (*Homo sapiens* IGHV3-30-5*03 (94.9%) -(IGHD) -IGHJ4*01 (92.9%) T122>I (115), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1-121)-*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, G4v5 h P10, G4v8 CH3 R115, F116, P125 (CH1 (122-219), hinge 1-12 S10>P (229) (220-231), CH2 L92 (310) (232-341), CH3 H115>R (436), Y116>F (437), L125>P (446) (342-446), CHS (447-448)) (122-448)], (135-213')-disulfide with L-kappa light chain anti-*vixticibart Homo sapiens* (1'-213') [V-KAPPA (*Homo sapiens* IGKV1-5*03 (98.9%) -IGKJ1*01 (91.7%) Q120>P (99'), CDR-IMGT [6.3.8] (27'-32'.50'-52'.89'-96')) (1'-106') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (152'), V101 (190') (107'-213')];
G4hCH2CH3 chain *Homo sapiens* (1"-229") [*Homo sapiens* IGHG4*01 (100%), *nG4m(a)* CH2 L92, G4v5 h P10 (hinge 1-12 S10>P (10") (1"-12"), CH2 L92 (310") (13"-122"), CH3 (123"-227"), CHS (228"-229"))]; dimer (227-8":230-11")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa

imelciment — immunoglobuline (H-gamma4_L-kappa)_G4hCH2CH3), anti-[*vixticibart*, anticorps monoclonal allostérique agoniste de *Homo sapiens* NPR1 (récepteur 1 du peptide natriurétique atrial)], anticorps monoclonal *Homo sapiens*;

chaîne lourde H-gamma4 anti-*vixticibart Homo sapiens* (1-448) [VH (*Homo sapiens* IGHV3-30-5*03 (94.9%) -(IGHD) -IGHJ4*01 (92.9%) T122>I (115), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1-121)-*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, G4v5 h P10, G4v8 CH3 R115, F116, P125 (CH1 (122-219), charnière 1-12 S10>P (229) (220-231), CH2 L92 (310) (232-341), CH3 H115>R (436), Y116>F (437), L125>P (446) (342-446), CHS (447-448)) (122-448)], (135-213')-disulfure avec la chaîne légère L-kappa anti-*vixticibart Homo sapiens* (1'-213') [V-KAPPA (*Homo sapiens* IGKV1-5*03 (98.9%) -IGKJ1*01 (91.7%) Q120>P (99'), CDR-IMGT [6.3.8] (27'-32'.50'-52'.89'-96')) (1'-106') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (152'), V101 (190') (107'-213')]; chaîne G4hCH2CH3 *Homo sapiens* (1''-229'') [*Homo sapiens* IGHG4*01 (100%), *nG4m(a)* CH2 L92, G4v5 h P10 (charnière 1-12 S10>P (10'') (1''-12''), CH2 L92 (310'') (13''-122''), CH3 (123''-227''), CHS (228''-229''))]; dimère (227-8'':230-11'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa

imelciment

inmunoglobulina (H-gamma4_L-kappa)_G4hCH2CH3), anti-[*vixticibart*, anticerpo monoclonal alostérico agonista de *Homo sapiens* NPR1 (recepto 1 del péptido natriurético atrial)], anticuerpo monoclonal *Homo sapiens*; cadena pesada H-gamma4 anti-*vixticibart Homo sapiens* (1-448) [VH (*Homo sapiens* IGHV3-30-5*03 (94.9%) -(IGHD) -IGHJ4*01 (92.9%) T122>I (115), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1-121)-*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, G4v5 h P10, G4v8 CH3 R115, F116, P125 (CH1 (122-219), bisagra 1-12 S10>P (229) (220-231), CH2 L92 (310) (232-341), CH3 H115>R (436), Y116>F (437), L125>P (446) (342-446), CHS (447-448)) (122-448)], (135-213')-disulfuro con la cadena ligera L-kappa anti-vixticibart *Homo sapiens* (1'-213') [V-KAPPA (*Homo sapiens* IGKV1-5*03 (98.9%) -IGKJ1*01 (91.7%) Q120>P (99'), CDR-IMGT [6.3.8] (27'-32'.50'-52'.89'-96')) (1'-106') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (152'), V101 (190') (107'-213')]; cadena G4hCH2CH3 *Homo sapiens* (1''-229'') [*Homo sapiens* IGHG4*01 (100%), *nG4m(a)* CH2 L92, G4v5 h P10 (bisagra 1-12 S10>P (10'') (1''-12''), CH2 L92 (310'') (13''-122''), CH3 (123''-227''), CHS (228''-229''))]; dímero (227-8'':230-11'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada : H-gamma4 (H) anti-vixticibart
```
QVQLVESGGG VVQPGRSLRL SCAASGFTFS SYGMHWVRQA PGKGLEWVAL  50
IWFDGGYKYY ADSVKGRFTI SRDNSKNTLY LQMNSLRADD TAVYYCARGS 100
AAAGHVPFDY WGQGILVTVS SASTKGPSVF PLAPCSRSTS ESTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTK 200
TYTCNVDHKP SNTKVDKRVE SKYGPPCPPC PAPEFLGGPS VFLFPPKPKD 250
TLMISRTPEV TCVVVDVSQE DPEVQFNWYV DGVEVHNAKT KPREEQFNST 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKGLP SSIEKTISKA KGQPREPQVY 350
TLPPSQEEMT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD 400
SDGSFFLYSR LTVDKSRWQE GNVFSCSVMH EALHNRFTQK SLSLSPGK   448
```

Light chain / Chaîne légère / Cadena ligera : L-kappa (L') anti-vixticibart
```
DIQMTQSPST LSASVGDRVT ITCRASQSIS SWLAWYQQKP GKAPKLLIYK  50
ASSLESGVPS RFSGSGSETE FTLTISSLQP DDFATYYCQQ YNSYWTFGPG 100
TKVEIKRTVA APSVFIFPPS DEQLKSGTAS VVCLLNNFYP REAKVQWKVD 150
NALQSGNSQE SVTEQDSKDS TYSLSSTLTL SKADYEKHKV YACEVTHQGL 200
SSPVTKSFNR GEC                                         213
```

Heavy chain / Chaîne lourde / Cadena pesada : G4hCH2CH3 (H'')
```
ESKYGPPCPP CPAPEFLGGP SVFLFPPKPK DTLMISRTPE VTCVVVDVSQ  50
EDPEVQFNWY VDGVEVHNAK TKPREEQFNS TYRVVSVLTV LHQDWLNGKE 100
YKCKVSNKGL PSSIEKTISK AKGQPREPQV YTLPPSQEEM TKNQVSLTCL 150
VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS RLTVDKSRWQ 200
EGNVFSCSVM HEALHNHYTQ KSLSLSLGK                        229
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 148-204 262-322 368-426
no VH no CH1 43''-103'' 149''-207''
Intra-L (C23-C104) 23'-88' 133'-193'
Inter-H-L (CH1 10-CL 126) 135-213'
Inter-H-H (h 8, h 11) 227-8'' 230-11''

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)
H VH Q1: 1

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4: 298, 79''
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, 229''

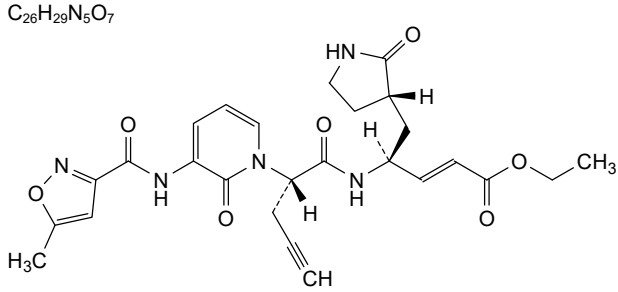
imocitrelvirum

imocitrelvir — ethyl (2*E*,4*S*)-4-{(2*S*)-2-[3-(5-methyl-1,2-oxazole-3-carboxamido)-2-oxopyridin-1(2*H*)-yl]pent-4-ynamido}-5-[(3*S*)-2-oxopyrrolidin-3-yl]pent-2-enoate

imocitrelvir — (2*E*,4*S*)-4-{(2*S*)-2-[3-(5-méthyl-1,2-oxazole-3-carboxamido)-2-oxopyridin-1(2*H*)-yl]pent-4-ynamido}-5-[(3*S*)-2-oxopyrrolidin-3-yl]pent-2-énoate d'éthyle

imocitrelvir — (2*E*,4*S*)-4-{(2*S*)-2-[3-(5-metil-1,2-oxazol-3-carboxamido)-2-oxopiridin-1(2*H*)-il]pent-4-inamido}-5-[(3*S*)-2-oxopirrolidin-3-il]pent-2-enoato de etilo

$C_{26}H_{29}N_5O_7$



indenebartum #

indenebart — immunoglobulin G1-lambda2, anti-[*Homo sapiens* SNCA (synuclein alpha, PARK1, PARK4, Parkinson disease (autosomal dominant, Lewy body) 4, synuclein alpha (non A4 component of amyloid precursor))], *Homo sapiens* monoclonal antibody;
H-gamma1 heavy chain *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV3-23*01 (96.9%) -(IGHD) -IGHJ6*01 (94.4%)) [8.8.15] (26-33.51-58.97-111) (1-122) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v39 CH2 F1.3, E1.2, S116 (CH1 R120 (219) (123-220), hinge 1-15 (221-235), CH2 L1.3>F (239), L1.2>E (240), P116>S (336) (236-345), CH3 E12 (361), M14 (363) (346-450), CHS (451-452)) (123-452)], (225-220')-disulfide with L-lambda2 light chain *Homo sapiens* (1'-221') [V-LAMBDA (*Homo sapiens* IGLV5-45*01 (91.9%) -IGLJ2*01 (100%), CDR-IMGT [9.7.9] (26'-34'.52'-58'.97'-105')) (1'-115') -*Homo sapiens* IGLC2*01 (100%) (116'-221')]; dimer (231-231'':234-234'')-bisdisulfide, produced in a cell line from Chinese hamster ovary (CHO) cells,derived from the cell line CHO-K1, glycoform alfa

indénebart — immunoglobuline G1-lambda2, anti-[*Homo sapiens* SNCA (synucléine alpha, alpha-synucléine, PARK1, PARK4, maladie de Parkinson (autosomique dominante, corps de Lewy) 4, synucléine alpha (composant non A4 du précurseur amyloïde))], anticorps monoclonal *Homo sapiens*; chaîne lourde H-gamma1 *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV3-23*01 (96.9%) -(IGHD) -IGHJ6*01 (94.4%)) [8.8.15] (26-33.51-58.97-111) (1-122) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v39 CH2 F1.3, E1.2, S116 (CH1 R120 (219) (123-220), charnière 1-15 (221-235), CH2 L1.3>F (239), L1.2>E (240), P116>S (336) (236-345), CH3 E12 (361), M14 (363) (346-450), CHS (451-452)) (123-452)], (225-220')-disulfure avec la chaîne légère L-lambda2 *Homo sapiens* (1'-221') [V-LAMBDA (*Homo sapiens* IGLV5-45*01 (91.9%) -IGLJ2*01 (100%), CDR-IMGT [9.7.9] (26'-34'.52'-58'.97'-105')) (1'-115') -*Homo sapiens* IGLC2*01 (100%) (116'-221')]; dimère (231-231'':234-234'')-bisdisulfure, produite dans une lignée cellulaire des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1, glycoforme alfa

indenebart

inmunoglobulina G1-lambda2, anti-[*Homo sapiens* SNCA (sinucleína alfa, alfa-sinucleína, PARK1, PARK4, enfermedad de Parkinson (autosómico dominante, cuerpos de Lewy) 4, sinucleína alfa (compuesto no A4 del precusor amieloide))], anticuerpo monoclonal *Homo sapiens*;
cadena pesada H-gamma1 *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV3-23*01 (96.9%) -(IGHD) -IGHJ6*01 (94.4%)) [8.8.15] (26-33.51-58.97-111) (1-122) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v39 CH2 F1.3, E1.2, S116 (CH1 R120 (219) (123-220), bisagra 1-15 (221-235), CH2 L1.3>F (239), L1.2>E (240), P116>S (336) (236-345), CH3 E12 (361), M14 (363) (346-450), CHS (451-452)) (123-452)], (225-220')-disulfuro con la cadena ligera L-lambda2 *Homo sapiens* (1'-221') [V-LAMBDA (*Homo sapiens* IGLV5-45*01 (91.9%) -IGLJ2*01 (100%), CDR-IMGT [9.7.9] (26'-34'.52'-58'.97'-105')) (1'-115') -*Homo sapiens* IGLC2*01 (100%) (116'-221')]; dímero (231-231":234-234")-bisdisulfuro, producido en una línea celular de las células ováricas de hámster chino (CHO), derivada de la línea celular de CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada : H-gamma1 (H, H") anti-SNCA
```
EVQLLESGGG LVQPGGSLRL SCAASGFTFS SYAMSWVRQA PGKGLEWVSS  50
ISHLGGSTYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAGGA 100
NHGKYYYGMD KWGQGTTVTV SSASTKGPSV FPLAPSSKST SGGTAALGCL 150
VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ SSGLYSLSSV VTVPSSSLGT 200
QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPEFE GGPSVFLFPP 250
KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPASIEKT ISKAKGQPRE 350
PQVYTLPPSR EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP 400
PVLDSDGSFF LYSKLTVDKS RWQQGNVFSC SVMHEALHNH YTQKSLSLSP 450
GK                                                      452
```

Light chain / Chaîne légère / Cadena ligera : L-lambda2 (L', L'") anti-SNCA
```
QAVLTQPASL SASPGASASL TCTLRSGAPL PKYRIYWYQQ KPGSPPQYLL  50
RYKSDADKHQ GSGVPSRFSG SKDASANAGI LLISGLQSED EADYYCMVWD 100
HGVWYFGGGT KLTVLGQPKA APSVTLFPPS SEELQANKAT LVCLISDFYP 150
GAVTVAWKAD SSPVKAGVET TTPSKQSNNK YAASSYLSLT PEQWKSHRSY 200
SCQVTHEGST VEKTVAPTEC S                                 221
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 149-205 266-326 372-430
22"-96" 149"-205" 266"-326" 372"-430"
Intra-L (C23-C104) 22'-96' 143'-202'
22'"-96'" 143'"-202'"
Inter-H-L (h 5-CL 126) 225-220' 225"-220'"
Inter-H-H (h 11, h 14) 231-231" 234-234"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)
L VL V-LAMBDA 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"

inlexisertibum

inlexisertib

2^3-ethyl-1^4-methyl-4^5-(trifluoromethyl)-3,5-diaza-9(4)-[1,4]oxazepana-4(2,4)-pyrimidina-1(1)-piperazina-2(1,4)-benzenanonaphan-9^5-one

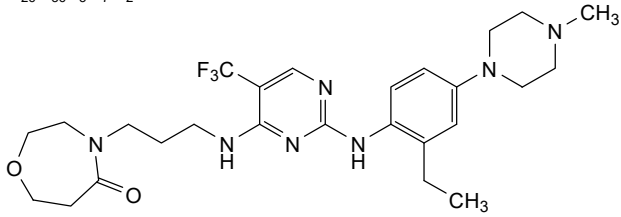
inlexisertib

2^3-éthyl-1^4-méthyl-4^5-(trifluorométhyl)-3,5-diaza-9(4)-[1,4]oxazépana-4(2,4)-pyrimidina-1(1)-pipérazina-2(1,4)-benzénanonaphan-9^5-one

inlexisertib

2^3-etil-1^4-metil-4^5-(trifluorometil)-3,5-diaza-9(4)-[1,4]oxazepana-4(2,4)-pirimidina-1(1)-piperazina-2(1,4)-bencenanonafan-9^5-ona

$C_{26}H_{36}F_3N_7O_2$



invikafuspum alfa #

invikafusp alfa

humanized immunoglobulin G1-kappa anti-(human T cell receptor germline-encoded variable chain Vβ6/β10) monomer disulfide bridged to human interleukin 2 (IL-2, T-cell growth factor) (C^{125}>A)-variant fused via $(G_4S)_2$ peptide linker to immunoglobulin G1 Fc fragment, glycoform alfa;
gamma 1 heavy chain (1-447) [VH (*Homo sapiens* IGHV1-3*01 -(IGHD) -IGHJ4*01, CDR-Kabat [5.17.10] (31-35.50-66.99-108)) (1-119) -*Homo sapiens* IGHG1*03 (CH1 (120-217), hinge (218-232), CH2 N^{299}>A (233-342), CH3 Y^{351}>C, T^{368}>S, L^{370}>A, Y^{409}>V (343-447), CHS G^{448}>del, K^{449}>del)) (120-447)], (222-214')-disulfide with kappa light chain (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-9*01 -IGKJ2*01, CDR-Kabat [11.7.9] (24'-34'.50'-56'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (108'-214')]; (228-149'':231:152'': 351:277'')-trisdisulfide with human interleukin 2 (IL-2, T-cell growth factor) (C^{125}>A)-variant (1-133) fused via $(G_4S)_2$ peptide linker (134-143) to a Fc fragment of human immunoglobulin G1 (144-368) [*Homo sapiens* IGHG1*03, hinge N-terminal EPKSC deleted (144-153), CH2 N^{220}>A (154-263), CH3 S^{277}>C, T^{289}>W (264-368), CHS G^{369}>del, K^{370}>del]; produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa

invikafusp alfa

immunoglobuline G1-kappa humanisée anti-(chaîne variable Vβ6/β10 codée par la lignée germinale du récepteur de lymphocytes T humain) monomère à pont disulfure avec un (C^{125}>A)-variant d'interleukine 2 humaine (IL-2, facteur de croissance des lymphocytes T) fusionné, via un peptide liant $(G_4S)_2$, avec un fragment Fc de l'immunoglobuline G1, glycoforme alfa;
chaîne lourde gamma 1 (1-447) [VH (*Homo sapiens* IGHV1-3*01 -(IGHD) -IGHJ4*01, CDR-Kabat [5.17.10] (31-35.50-66. 99-108)) (1-119) -*Homo sapiens* IGHG1*03 (CH1 (120-217), charnière (218-232), CH2 N^{299}>A (233-342), CH3 Y^{351}>C, T^{368}>S, L^{370}>A, Y^{409}>V (343-447), CHS G^{448}>del, K^{449}>del)) (120-447)], (222-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-9*01 -IGKJ2*01, CDR-Kabat [11. 7.9] (24'-34'.50'-56'. 89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (108'-214')]; (228-149'':231:152'':351:277'')-trisdisulfure avec un (C^{125}>A)-variant de l'interleukine 2 humaine (IL-2, facteur de croissance des lymphocytes T) (1-133) fusionné, via un peptide liant $(G_4S)_2$ (134-143), à un fragment Fc de l'immunoglobuline G1 humaine (144-368) [Homo sapiens IGHG1*03, charnière N-terminale EPKSC supprimée (144-153), CH2 N^{220}>A (154-263), CH3 S^{277}>C, T^{289}>W (264-368), CHS G^{369}>del, K^{370}>del]; produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa

invikafusp alfa

inmunoglobulina G1-kappa humanizada anti-(cadena variable Vβ6/β10 codificada en la línea germinal del receptor humano de células T) monómero con puente disulfuro a (C^{125}>A)-variante de interleukina 2 humana (IL-2, factor de crecimiento de los linfocitos T) fusionado a través de un enlace peptídico $(G_4S)_2$ al fragmento Fc de la inmunoglobulina G1, glicoforma alfa;
cadena pesada gamma 1 (1-447) [VH (*Homo sapiens* IGHV1-3*01 -(IGHD) -IGHJ4*01, CDR-Kabat [5.17.10] (31-35.50-66.99-108)) (1-119) -*Homo sapiens* IGHG1*03 (CH1 (120-217), bisagra (218-232), CH2 N^{299}>A (233-342), CH3 Y^{351}>C, T^{368}>S, L^{370}>A, Y^{409}>V (343-447), CHS G^{448}>del, K^{449}>del)) (120-447)], (222-214')-disulfuro con cadena ligera kappa (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-9*01 -IGKJ2*01, CDR-Kabat [11.7.9] (24'-34'.50'-56'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (108'-214')]; (228-149":231:152": 351:277")-trisdisulfuro con interleukina 2 humana (IL-2, factor de crecimiento de los linfocitos T) (C^{125}>A)-variante (1-133) fusionado a través del enlace peptídico $(G_4S)_2$ (134-143) a un fragmento Fc de la inmunoglobulina humana G1 (144-368) [*Homo sapiens* IGHG1*03, bisagra terminal N EPKSC eliminada (144-153), CH2 N^{220}>A (154-263), CH3 S^{277}>C, T^{289}>W (264-368), CHS G^{369}>del, K^{370}>del]; producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, glicoforma alfa

Sequence / Séquence / Secuencia
IgG1 heavy chain

```
QVQLVQSGAE VKKPGSSVKV SCKASGHDFR LTYIHWVRQA PGQGLEWMGR   50
VSAGSGNVKY NEKFKGRVTI TADTSTSTAY MELSSLRSED TAVYYCAVSY  100
YSYDVLDYWG QGTTVTVSSA STKGPSVFPL APSSKSTSGG TAALGCLVKD  150
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY  200
ICNVNHKPSN TKVDKRVEPK SCDKTHTCPP CPAPELLGGP SVFLFPPKPK  250
DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYAS  300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV  350
CTLPPSREEM TKNQVSLSCA VKGFYPSDIA VEWESNGQPE NNYKTTPPVL  400
DSDGSFFLVS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSP     447
```

IgG1 Light Chain

```
DIQMTQSPSF LSASVGDRVT ITCKASQNVA DRVVWHQQKP GKAPKALIYS   50
SSHRYKGVPS RFSGSGSGTE FTLTISSLQP EDFATYFCQQ FKSYPLTFGQ  100
GTKLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV  150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG  200
LSSPVTKSFN RGEC                                        214
```

IL2- IgG1Fc

```
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA   50
TELKHLQCLE EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE  100
TTFMCEYADE TATIVEFLNR WITFAQSIIS TLTGGGGSGG GGSDKTHTCP  150
PCPAPELLGG PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW  200
YVDGVEVHNA KTKPREEQYA STYRVVSVLT VLHQDWLNGK EYKCKVSNKA  250
LPAPIEKTIS KAKGQPREPQ VYTLPPCREE MTKNQVSLWC LVKGFYPSDI  300
AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV  350
MHEALHNHYT QKSLSLSP                                    368
```

Mutation / Mutation / Mutación
IgG1 heavy chain: N>A^{299}, Y>C^{351}, T>S^{368}, L>A^{370}, Y>V^{409}, G^{448}>del, K^{449}>del
IL2-IgG1Fc: N>A$^{220"}$, S>C$^{277"}$, T>W$^{289"}$, G$^{369"}$>del, K$^{370"}$>del

Peptide linker / Peptide liant / Péptido de unión
IL2- IgG1Fc: $^{134"}$*GGGGSGGGGS*$^{143"}$

Post-translation modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra heavy chain: 22-96, 146-202, 263-323, 369-427
Intra light chain: 23'-88', 134'-194'
Intra IL2-Fc: 58"-105", 184"-244", 290"-348"
Inter light chain-heavy chain: 214'-222
Inter IL2-Fc-heavy chain: 149"-228, 152"-231, 277"-351

O-glycosylation sites / Sites de O-glycosylation / Posiciones de O-glicosilación
IL2-IgG1Fc: (^{3}TSSST^{7})*
*Glycosylation can be in any of the listed amino acids

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
IgG1 heavy chain Q1> pyroglutamyl (pE, 5-oxo-L-prolyl)

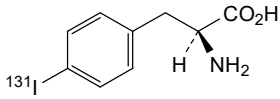
iodofalanum (^{131}I)

iodofalan (^{131}I) 4-(^{131}I)iodo-L-phenylalanine

iodofalan (^{131}I) 4-(^{131}I)iodo-L-phénylalanine

iodofalán (^{131}I) 4-(^{131}I)iodo-L-fenilalanina

$C_9H_{10}{}^{131}INO_2$



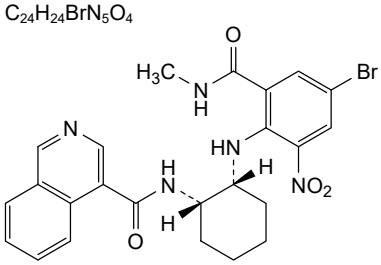
iscartrelvirum

iscartrelvir *N*-{(1*S*,2*R*)-2-[4-bromo-2-(methylcarbamoyl)-6-nitroanilino]cyclohexyl}isoquinoline-4-carboxamide

iscartrelvir *N*-{(1*S*,2*R*)-2-[4-bromo-2-(méthylcarbamoyl)-6-nitroanilino]cyclohexyl}isoquinoléine-4-carboxamide

iscartrelvir *N*-{(1*S*,2*R*)-2-[4-bromo-2-(metilcarbamoil)-6-nitroanilino]ciclohexil}isoquinoleína-4-carboxamida

$C_{24}H_{24}BrN_5O_4$



lanerkitugum #

lanerkitug immunoglobulin G1-lambda2, anti-[*Homo sapiens* CCR8 (C-C motif chemokine receptor 8, CKR-L1, CDw198)], *Homo sapiens* monoclonal antibody;
H-gamma1 heavy chain *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV3-23*01 (92.9%) -(IGHD) -IGHJ4*01 (93.3%)) [8.8.15] (26-33.51-58.97-111) (1-122) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (219) (123-220), hinge 1-15 (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS (451-452)) (123-452)], (225-216')-disulfide with L-lambda2 light chain *Homo sapiens* (1'-217') [V-LAMBDA (*Homo sapiens* IGLV1-47*02 (89.9%) -IGLJ3*02 (100%), CDR-IMGT [9.3.11] (26'-34'.52'-54'.91'-101')) (1'-111') -*Homo sapiens* IGLC2*01 (100%) (112'-217')]; dimer (231-231":234-234")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from CHO-K1 cell line, lacking the glutamine synthetase (GS-KO) gene, and co-expressing the RMD enzyme (GDP-6-deoxy-D-lyxo-4-hexulose reductase), glycoform alfa

lanerkitug immunoglobuline G1-lambda2, anti-[*Homo sapiens* CCR8(récepteur 8 de chimiokine C-C motif, CKR-L1, CDw198)], anticorps monoclonal *Homo sapiens*;

chaîne lourde H-gamma1 *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV3-23*01 (92.9%) -(IGHD) -IGHJ4*01 (93.3%)) [8.8.15] (26-33.51-58.97-111) (1-122) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (219) (123-220), charnière 1-15 (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS (451-452)) (123-452)], (225-216')-disulfure avec la chaîne légère L-lambda2 *Homo sapiens* (1'-217') [V-LAMBDA (*Homo sapiens* IGLV1-47*02 (89.9%) -IGLJ3*02 (100%), CDR-IMGT [9.3.11] (26'-34'.52'-54'.91'-101')) (1'-111') -*Homo sapiens* IGLC2*01 (100%) (112'-217')]; dimère (231-231":234-234")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1, ne présentant pas le gène de la glutamine synthétase (GS-KO), et co-exprimant l'enzyme RMD (GDP-6-désoxy-D-lyxo-4-hexulose réductase), glycoforme alfa

lanerkitug

inmunoglobulina G1-lambda2, anti-[*Homo sapiens* CCR8 (receptor 8 de quimiocina C-C motivo, CKR-L1, CDw198)], anticuerpo monoclonal *Homo sapiens*;
cadena pesada H-gamma1 *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV3-23*01 (92.9%) -(IGHD) -IGHJ4*01 (93.3%)) [8.8.15] (26-33.51-58.97-111) (1-122) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (219) (123-220), bisagra 1-15 (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS (451-452)) (123-452)], (225-216')-disulfuro con la cadena ligera L-lambda2 *Homo sapiens* (1'-217') [V-LAMBDA (*Homo sapiens* IGLV1-47*02 (89.9%) -IGLJ3*02 (100%), CDR-IMGT [9.3.11] (26'-34'.52'-54'.91'-101')) (1'-111') -*Homo sapiens* IGLC2*01 (100%) (112'-217')]; dímero (231-231":234-234")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular derivada de CHO-K1, en ausencia del gen glutamina sintetasa (GS-KO), y co-expresando la enzima RMD (GDP-6-desoxi-D-lixo-4-hexulosa reductasa), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

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EVQLLESGGG LVQPGGSLRL SCAASGFTFS SYGMHWVRQA PGKGLEWVSA  50
INWNGGSTGY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARGH 100
HSGYDGRFFD YWGQGTLVTV SSASTKGPSV FPLAPSSKST SGGTAALGCL 150
VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ SSGLYSLSSV VTVPSSSLGT 200
QTYICNVNHK PSNTKVDKKV EPKSCDKTHT CPPCPAPELL GGPSVFLFPP 250
KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE 350
PQVYTLPPSR DELTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP 400
PVLDSDGSFF LYSKLTVDKS RWQQGNVFSC SVMHEALHNH YTQKSLSLSP 450
GK                                                      452
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Light chain / Chaîne légère / Cadena ligera

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QSVLTQPPSV SGAPGQRVTI SCTGSSSNIG AGYNVHWYQQ LPGTAPKLLI  50
YTNNRRPSGV PDRFSGSKSG TSASLAISGL RSEDEADYYC AAWDASLSGW 100
VFGGGTKLTV LGQPKAAPSV TLFPPSSEEL QANKATLVCL ISDFYPGAVT 150
VAWKADSSPV KAGVETTTPS KQSNNKYAAS SYLSLTPEQW KSHRSYSCQV 200
THEGSTVEKT VAPTECS                                      217
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Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 149-205 266-326 372-430
22"-96" 149"-205" 266"-326" 372"-430"
Intra-L (C23-C104) 22'-90' 139'-198'
22'"-90'" 139'"-198'"
Inter-H-L (h 5-CL 126) 225-216' 225"-216'"
Inter-H-H (h 11, h 14) 231-231" 234-234"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)
L VL V-LAMBDA Q1: 1', 1'"

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

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

lefelsiranum

lefelsiran

all-P-ambo-2'-*O*-methyl-*P*-thioguanylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-deoxy-2'-fluoroguanylyl-(3'→5')-2'-deoxy-2'-fluoroadenylyl-(3'→5')-2'-deoxy-2'-fluoroadenylyl-(3'→5')-2'-deoxy-2'-fluoroadenylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-{[2-(2-{5-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]pentanamido}ethoxy)ethoxy]methyl}adenylyl-(3'→5')-2'-*O*-{[2-(2-{5-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]pentanamido}ethoxy)ethoxy]methyl}adenylyl-(3'→5')-2'-*O*-{[2-(2-{5-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]pentanamido}ethoxy)ethoxy]methyl}adenylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylcytidine
duplex with *all-P-ambo*-2'-*O*-methyl-*P*-thioguanylyl-(5'→3')-2'-*O*-methyl-*P*-thioguanylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-deoxy-2'-fluoroadenylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-*O*-methylguanylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-deoxy-2'-fluoroguanylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-deoxy-2'-fluorocytidylyl-(5'→3')-deoxy-2'-fluoro-*P*-thioadenylyl-(5'→3')-2'-deoxy-2'-fluoro-*P*-thioadenylyl-(5'→3')-2'-deoxy-2'-fluoro-*P*-thioadenylyl-(5'→3')-4'-de(hydroxymethyl)-4'-{[hydroxy(methoxy)phosphoryl]methoxy}-2'-*O*-methyluridine

léfelsiran

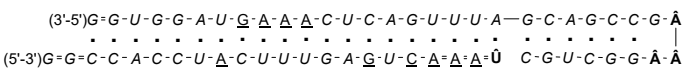
tout-P-ambo-2'-*O*-méthyl-*P*-thioguanylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-désoxy-2'-fluoroguanylyl-(3'→5')-2'-désoxy-2'-fluoroadénylyl-(3'→5')-2'-désoxy-2'-fluoroadénylyl-(3'→5')-2'-désoxy-2'-fluoroadénylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-{[2-(2-{5-[(2-acétamido-2-désoxy-β-D-galactopyranosyl)oxy]pentanamido}éthoxy)éthoxy]méthyl}adénylyl-(3'→5')-2'-*O*-{[2-(2-{5-[(2-acétamido-2-désoxy-β-D-galactopyranosyl)oxy]pentanamido}éthoxy)éthoxy]méthyl}adénylyl-(3'→5')-2'-*O*-{[2-(2-{5-[(2-acétamido-2-désoxy-β-D-galactopyranosyl)oxy]pentanamido}éthoxy)éthoxy]méthyl}adénylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthylcytidine

duplex avec *tout-P-ambo*-2'-*O*-méthyl-*P*-thioguanylyl-(5'→3')-2'-*O*-méthyl-*P*-thioguanylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-désoxy-2'-fluoroadénylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-*O*-méthylguanylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-désoxy-2'-fluoroguanylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-désoxy-2'-fluorocytidylyl-(5'→3')-désoxy-2'-fluoro-*P*-thio adénylyl-(5'→3')-2'-désoxy-2'-fluoro-*P*-thioadénylyl-(5'→3')-2'-désoxy-2'-fluoro-*P*-thioadénylyl-(5'→3')-4'-dés(hydroxyméthyl)-4'-{[hydroxy(méthoxy)phosphoryl]méthoxy}-2'-*O*-méthyluridine

lefelsirán

todo-P-ambo-2'-*O*-metil-*P*-tioguanilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-desoxi-2'-fluoroguanilil-(3'→5')-2'-desoxi-2'-fluoroadenilil-(3'→5')-2'-desoxi-2'-fluoroadenilil-(3'→5')-2'-desoxi-2'-fluoroadenilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-{[2-(2-{5-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]pentanamido}etoxi)etoxi]metil}adenilil-(3'→5')-2'-*O*-{[2-(2-{5-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]pentanamido}etoxi)etoxi]metil}adenilil-(3'→5')-2'-*O*-{[2-(2-{5-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]pentanamido}etoxi)etoxi]-metil}adenilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilcitidina
dúplex con *todo-P-ambo*-2'-*O*-metil-*P*-tioguanilil-(5'→3')-2'-*O*-metil-*P*-tioguanilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-desoxi-2'-fluoroadenilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-*O*-metilguanilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-desoxi-2'-fluoroguanilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-desoxi-2'-fluorocitidilil-(5'→3')-desoxi-2'-fluoro-*P*-tioadenilil-(5'→3')-2'-desoxi-2'-fluoro-*P*-tioadenilil-(5'→3')-2'-desoxi-2'-fluoro-*P*-tioadenilil-(5'→3')-4'-des(hidroximetil)-4'-{[hidroxi(metoxi)fosforil]metoxi}-2'-*O*-metiluridina

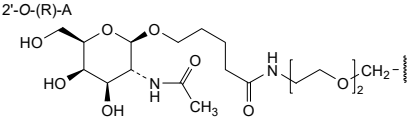
$C_{654}H_{864}N_{231}O_{413}P_{57}S_6$



N : A,C,G,U
N : 2'-*O*-methyl-N / 2'-*O*-méthyl-N / 2'-*O*-metil-N
N : 2'-deoxy-2'-fluoro-N / 2'-désoxy-2'-fluoro-N / 2'-desoxi-2'-fluoro-N
– : –PO(OH)– = : –PO(SH)–

Â : 2'-*O*-(R)-A

R :



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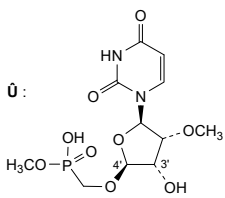


lepodisiranum

lepodisiran

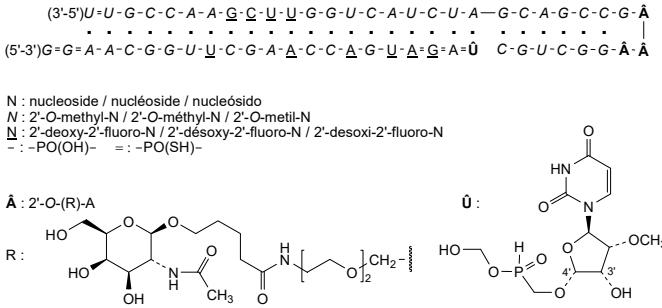
all-P-ambo-2'-*O*-methyl-*P*-thiouridylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-deoxy-2'-fluoroguanylyl-(3'→5')-2'-deoxy-2'-fluorocytidylyl-(3'→5')-2'-deoxy-2'-fluorouridylyl-(3'→5')-2'-deoxy-2'-fluorouridylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-{[2-(2-{5-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]pentanamido}ethoxy)ethoxy]methyl}adenylyl-(3'→5')-2'-*O*-{[2-(2-{5-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]pentanamido}ethoxy)ethoxy]methyl}adenylyl-(3'→5')-2'-*O*-{[2-(2-{5-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]pentanamido}ethoxy)ethoxy]methyl}adenylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylcytidine
duplex with *all-P-ambo*-2'-*O*-methyl-*P*-thioguanylyl-(5'→3')-2'-*O*-methyl-*P*-thioguanylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-*O*-methylguanylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-deoxy-2'-fluorouridylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-*O*-methylguanylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-deoxy-2'-fluoroadenylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-deoxy-2'-fluoroadenylyl-(5'→3')-2'-*O*-methylguanylyl-(5'→3')-2'-deoxy-2'-fluorouridylyl-(5'→3')-2'-deoxy-2'-fluoro-*P*-thioadenylyl-(5'→3')-2'-deoxy-2'-fluoro-*P*-thioguanylyl-(5'→3')-2'-deoxy-2'-fluoro-*P*-thioadenylyl-(5'→3')-4'-de(hydroxymethyl)-4'-{[hydroxy(methoxy)phosphoryl]methoxy}-2'-*O*-methyluridine

lépodisiran

tout-P-ambo-2'-*O*-méthyl-*P*-thiouridylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-désoxy-2'-fluoroguanylyl-(3'→5')-2'-désoxy-2'-fluorocytidylyl-(3'→5')-2'-désoxy-2'-fluorouridylyl-(3'→5')-2'-désoxy-2'-fluorouridylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-{[2-(2-{5-[(2-acétamido-2-désoxy-β-D-galactopyranosyl)oxy]pentanamido}éthoxy)éthoxy]méthyl}adénylyl-(3'→5')-2'-*O*-{[2-(2-{5-[(2-acétamido-2-désoxy-β-D-galactopyranosyl)oxy]pentanamido}éthoxy)éthoxy]méthyl}adénylyl-(3'→5')-2'-*O*-{[2-(2-{5-[(2-acétamido-2-désoxy-β-D-galactopyranosyl)oxy]pentanamido}éthoxy)éthoxy]méthyl}adénylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthylcytidine

	duplex avec *tout-P-ambo*-2'-*O*-méthyl-*P*-thioguanylyl-(5'→3')-2'-*O*-méthyl-*P*-thioguanylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-*O*-méthylguanylyl-(5'→3')-2'-*O*-méthylguanylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-désoxy-2'-fluorouridylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-*O*-méthylguanylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-désoxy-2'-fluoroadénylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-désoxy-2'-fluoroadénylyl-(5'→3')-2'-*O*-méthylguanylyl-(5'→3')-2'-désoxy-2'-fluorouridylyl-(5'→3')-2'-désoxy-2'-fluoro-*P*-thioadénylyl-(5'→3')-2'-désoxy-2'-fluoro-*P*-thioguanylyl-(5'→3')-2'-désoxy-2'-fluoro-*P*-thioadénylyl-(5'→3')-4'-de(hydroxyméthyl)-4'-{[hydroxy(méthoxy)phosphoryl]méthoxy}-2'-*O*-méthyluridine
lepodisirán	*todo-P-ambo*-2'-*O*-metil-*P*-tiouridilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-desoxi-2'-fluoroguanilil-(3'→5')-2'-desoxi-2'-fluorocitidilil-(3'→5')-2'-desoxi-2'-fluorouridilil-(3'→5')-2'-desoxi-2'-fluorouridilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-{[2-(2-{5-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]pentanamido}etoxi)etoxi]metil}adenilil-(3'→5')-2'-*O*-{[2-(2-{5-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]pentanamido}etoxi)etoxi]metil}adenilil-(3'→5')-2'-*O*-{[2-(2-{5-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]pentanamido}etoxi)etoxi]metil}adenilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilcitidina dúplex con *todo-P-ambo*-2'-*O*-metil-*P*-tioguanilil-(5'→3')-2'-*O*-metil-*P*-tioguanilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-*O*-metilguanilil-(5'→3')-2'-*O*-metilguanilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-desoxi-2'-fluorouridilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-*O*-metilguanilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-desoxi-2'-fluoroadenilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-desoxi-2'-fluoroadenilil-(5'→3')-2'-*O*-metilguanilil-(5'→3')-2'-desoxi-2'-fluorouridilil-(5'→3')-2'-desoxi-2'-fluoro-*P*-tioadenilil-(5'→3')-2'-desoxi-2'-fluoro-*P*-tioguanilil-(5'→3')-2'-desoxi-2'-fluoro-*P*-tioadenilil-(5'→3')-4'-de(hidroximetil)-4'-{[hidroxi(metoxi)phosforil]metoxi}-2'-*O*-metiluridina

$C_{654}H_{864}F_{11}N_{232}O_{412}P_{57}S_6$



lesigerceptum #

lesigercept	human high affinity immunoglobulin epsilon receptor subunit alpha (Fc-epsilon RI-alpha (FcERI), IgE Fc receptor subunit alpha) extracellular domain fragment 26-205 (1-180 in the current sequence), fused to a Fc fragment of an hybrid human immunoglobulin D/G4 (181-425) [*Homo sapiens* IGHD*01 (hinge K^{192}>G, E^{193}>S (181-210)), *Homo sapiens* IGHG4*01 (CH2 E^{211}>S, F^{212}>H, L^{213}>T, G^{214}>Q, G^{215}>P, P^{216}>L, S^{217}>G (209-217 matches IGHD*01) (211-318), CH3 (319-423), CHS (424-425))]; dimer (209-209')-disulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa
lésigercept	fragment 26-205 (1-180 dans la séquence actuelle) du domaine extracellulaire de la sous-unité alpha du récepteur de l'immunoglobuline epsilon à haute affinité humaine (Fc-epsilon RI-alpha (FcERI), sous-unité alpha du récepteur Fc de l'IgE), fusionné à un fragment Fc d'une immunoglobuline D/G4 (181-425) hybride humaine [*Homo sapiens* IGHD*01 (charnière K^{192}>G, E^{193}>S (181-210)), *Homo sapiens* IGHG4*01 (CH2 E^{211}>S, F^{212}>H, L^{213}>T, G^{214}>Q, G^{215}>P, P^{216}>L, S^{217}>G (209-217 correspond à IGHD*01) (211-318), CH3 (319-423), CHS (424-425))]; dimère (209-209')-disulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa
lesigercept	fragmento del dominio extracelular 26-205 (1-180 en la secuencia actual) de la subunidad alfa del receptor épsilon de la inmunoglobulina humana de alta afinidad (Fc-épsilon RI-alfa (FcERI), IgE receptor Fc de la subunidad alfa) fusionado al fragmento Fc de una inmunoglobulina humana híbrida D/G4 (181-425) [*Homo sapiens* IGHD*01 (bisagra K^{192}>G, E^{193}>S (181-210)), *Homo sapiens* IGHG4*01 (CH2 E^{211}>S, F^{212}>H, L^{213}>T, G^{214}>Q, G^{215}>P, P^{216}>L, S^{217}>G (209-217 que combina IGHD*01) (211-318), CH3 (319-423), CHS (424-425))]; dímero (209-209')-disulfuro, producido en las células ováricas de hámster chino (CHO), glicoforma alfa

Sequence / Séquence / Secuencia

```
VPQKPKVSLN PPWNRIFKGE NVTLTCNGNN FFEVSSTKWF HNGSLSEETN   50
SSLNIVNAKF EDSGEYKCQH QQVNESEPVY LEVFSDWLLL QASAEVVMEG  100
QPLFLRCHGW RNWDVYKVIY YKDGEALKYW YENHNISITN ATVEDSGTYY  150
CTGKVWQLDY ESEPLNITVI KAPREKYWLQ RNTGRGGEEK KGSKEKEEQE  200
ERETKTPECP SHTQPLGVFL FPPKPKDTLM ISRTPEVTCV VVDVSQEDPE  250
VQFNWYVDGV EVHNAKTKPR EEQFNSTYRV VSVLTVLHQD WLNGKEYKCK  300
VSNKGLPSSI EKTISKAKGQ PREPQVYTLP PSQEEMTKNQ VSLTCLVKGF  350
YPSDIAVEWE SNGQPENNYK TTPPVLDSDG SFFLYSRLTV DKSRWQEGNV  400
FSCSVMHEAL HNHYTQKSLS LSLGK                             425
```

Mutation / Mutation / Mutación

K^{192},$K^{192'}$>**G**, E^{193},$E^{193'}$>**S**, E^{211},$E^{211'}$>**S**, F^{212},$F^{212'}$>**H**, L^{213},$L^{213'}$>**T**, G^{214},$G^{214'}$>**Q**, G^{215},$G^{215'}$>**P**, P^{216},$P^{216'}$>**L**, S^{217},$S^{217'}$>**G**

Post-translational modifications

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

Intra-chain: 26-68, 107-151, 239-299, 345-403,
26'-68',107'-151', 239'-299', 345'-403'

Inter-chain: 209-209'

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

21, 42, 50, 74, 135, 140, 166, 275; 21', 42', 50', 74', 135', 140', 166', 275'

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

H CHS: 425, 425'

libevitugum

libevitug	immunoglobulin G1-lambda2, anti-[Hepatitis B virus (HBV) surface antigen (HbsAg, surface envelope protein, large envelope protein) pre-S1 domain], *Homo sapiens* monoclonal antibody; H-gamma1 heavy chain *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV6-1*01 (100%) -(IGHD) -IGHJ1*01 (100%)) [10.9.10] (26-35.53-61.100-109) (1-120) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (217) (121-218), hinge 1-15 (219-233), CH2 (234-343), CH3 D12 (359), L14 (361) (344-448), CHS (449-450)) (121-450)], (223-215')-disulfide with L-lambda2 light chain *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV1-40*01 (90.9%) -IGLJ2*01 (91.7%), CDR-IMGT [8.3.11] (26'-33'.51'-53'.90'-100')) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')]; dimer (229-229":232-232")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa
libévitug	immunoglobuline G1-lambda2, anti-[domaine pré-S1 de l'antigène de surface (HbsAg, protéine d'enveloppe de surface, grande protéine d'enveloppe) du virus de l'hépatite B (HBV)], anticorps monoclonal *Homo sapiens*; chaîne lourde H-gamma1 *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV6-1*01 (100%) -(IGHD) -IGHJ1*01 (100%)) [10.9.10] (26-35.53-61.100-109) (1-120) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (217) (121-218), charnière 1-15 (219-233), CH2 (234-343), CH3 D12 (359), L14 (361) (344-448), CHS (449-450)) (121-450)) (121-450)], (223-215')-disulfure avec la chaîne légère L-lambda2 *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV1-40*01 (90.9%) -IGLJ2*01 (91.7%), CDR-IMGT [8.3.11] (26'-33'.51'-53'.90'-100')) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')]; dimère (229-229":232-232")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa

libevitug

inmunoglobulina G1-lambda2, anti-[dominio pre-S1 del antígeno de superficie (HbsAg, proteína de envoltura de superficie, proteína grande de envoltura) del virus de la hepatitis B (HBV)], anticuerpo monoclonal *Homo sapiens*;
cadena pesada H-gamma1 *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV6-1*01 (100%) -(IGHD) -IGHJ1*01 (100%)) [10.9.10] (26-35.53-61.100-109) (1-120) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (217) (121-218), bisagra 1-15 (219-233), CH2 (234-343), CH3 D12 (359), L14 (361) (344-448), CHS (449-450)) (121-450)) (121-450)], (223-215')-disulfuro con la cadena ligera L-lambda2 *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV1-40*01 (90.9%) -IGLJ2*01 (91.7%), CDR-IMGT [8.3.11] (26'-33'.51'-53'.90'-100')) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')]; 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

```
QVQLQQSGPG LVKPSQTLSL TCAISGDSVS SNSAAWNWIR QSPSRGLEWL  50
GRTYYRSKWY NDYAVSVKSR ITINPDTSKN QFSLQLNSVT PEDTAVYYCA 100
RGTRWGMDVW 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 LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK 450
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Light chain / Chaîne légère / Cadena ligera

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QSVLTQPPSA SGTPGQRVTI SCSGSSSNIG SYYVYWYQQL PGTAPKLLIY  50
GNNQRPSGVP DRFSGSKSGT SASLAITGLQ AEDEADYYCQ SYDSSLSGVI 100
FGGGTKLTVL GQPKAAPSVT LFPPSSEELQ ANKATLVCLI SDFYPGAVTV 150
AWKADSSPVK AGVETTTPSK QSNNKYAASS YLSLTPEQWK SHRSYSCQVT 200
HEGSTVEKTV APTECS                                      216
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-99 147-203 264-324 370-428
22"-99" 147"-203" 264"-324" 370"-428"
Intra-L (C23-C104) 22'-89' 138'-197'
22'"-89'" 138'"-197'"
Inter-H-L (h 5-CL 126) 223-215' 223"-215'"
Inter-H-H (h 11, h 14) 229-229" 232-232"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)
H VH Q1: 1, 1"
L VL V-LAMBDA 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

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

limnetrelvirum

limnetrelvir

N-{(3*R*)-1-[4-cyano-2-(morpholine-4-carbonyl)-6-(trifluoromethyl)phenyl]pyrrolidin-3-yl}-8-fluoro-2-oxo-1,2-dihydroquinoline-4-carboxamide

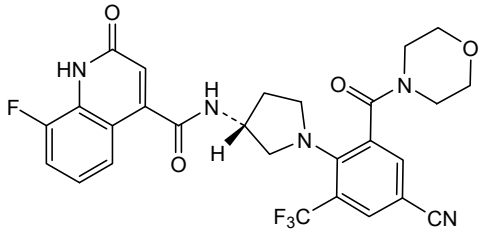
limnétrelvir

N-{(3*R*)-1-[4-cyano-2-(morpholine-4-carbonyl)-6-(trifluorométhyl)phényl]pyrrolidin-3-yl}-8-fluoro-2-oxo-1,2-dihydroquinoléine-4-carboxamide

limnetrelvir

N-{(3*R*)-1-[4-ciano-2-(morfolina-4-carbonil)-6-(trifluorometil)fenil]pirrolidin-3-il}-8-fluoro-2-oxo-1,2-dihidroquinolina-4-carboxamida

$C_{27}H_{23}F_4N_5O_4$



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immunoglobulin G1-kappa, anti-[*Homo sapiens* LY6G6D (lymphocyte antigen 6 family member G6D, G6D, LY6-D, MEGT1, NG25)] and anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], humanized monoclonal antibody, bispecific;
H-gamma1 heavy chain anti-LY6G6D humanized, G1v84-1 VH E44, CH1 K86 (1-442) [VH E44 (*Homo sapiens* IGHV3-23*01 (77.6%) -(IGHD) -IGHJ2*01 (92.3%) R120>P (104), CDR-IMGT [8.8.5] (26-33.51-58.97-101)) (1-112) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, CH1 K120, CH3 E12, M14, CH1 K86, G1v30 CH2 G84.4, G1v32 CH3 W22 (knob) (CH1 R120>K (209), S86>K (178) (113-210), hinge 1-15 (211-225), CH2 N84.4>G (292) (226-335), CH3 E12 (351), M14 (353), T22>W (361) (336-440), CHS (441-442)) (123-442)], (215-218')-disulfide with L-kappa light chain humanized, Kv84-1 VK K44, CK E22 (1'-218') [V-KAPPA K44 (*Homo sapiens* IGKV1-5*01 (89.8%) -IGKJ4*01 (100%), CDR-IMGT [6.3.13] (27'-32'.50'-52'.89'-101')) (1'-111') -*Homo sapiens* IGKC*01 (99.1%) V22>E (137), Km3 A45.1 (157), V101 (195) (112'-218')];
H-gamma1 heavy chain anti-CD3E humanized, G1v84-2 VH K44, CH1 E86 (1"-449") [VH K44 (*Homo sapiens* IGHV1-3*01 (81.6%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.12] (26"-33".51"-58".97"-108")) (1"-119") -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, CH1 E86, G1v30 CH2 G84.4, G1v33 CH3 S22, A24, V86 (hole) (CH1 R120>K (216") S86>E (185") (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 L-kappa light chain humanized, Kv84-2 VK E44, CK K22 (1"'-219"') [V-KAPPA E44 (*Homo sapiens* IGKV4-1*01 (90.8%) -IGKJ1*01 (100%), CDR-IMGT [12.3.8] (27"'-38"'.56"'-58"'.95"'-102"')) (1"'-112"') -*Homo sapiens* IGKC*01 (99.1%) V22>K (138"), Km3 A45.1 (158"'), V101 (196"') (113"'-219"')]; dimer (221-228":224-231")-bisdisulfide, produced in a cell line from Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, glycoform alfa

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immunoglobuline G1-kappa, anti-[*Homo sapiens* LY6G6D (lymphocyte antigène 6 membre de la famille G6D, G6D, LY6-D, MEGT1, NG25)] et anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], anticorps monoclonal humanisé, bispécifique;
chaîne lourde H-gamma1 anti-LY6G6D humanisée, G1v84-1 VH E44, CH1 K86 (1-442) [VH E44 (*Homo sapiens* IGHV3-23*01 (77.6%) -(IGHD) -IGHJ2*01 (92.3%) R120>P (104), CDR-IMGT [8.8.5] (26-33.51-58.97-101)) (1-112) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, CH1 K86, G1v30 CH2 G84.4, G1v32 CH3 W22 (knob) (CH1 R120>K (209), S86>K (178) (113-210), charnière 1-15 (211-225), CH2 N84.4>G (292) (226-335), CH3 E12 (351), M14 (353), T22>W (361) (336-440), CHS (441-442)) (123-442)], (215-218')-disulfure avec la chaîne légère L-kappa humanisée, Kv84-1 VK K44, CK E22 (1'-218') [V-KAPPA K44 (*Homo sapiens* IGKV1-5*01 (89.8%) -IGKJ4*01 (100%), CDR-IMGT [6.3.13] (27'-32'.50'-52'.89'-101')) (1'-111') -*Homo sapiens* IGKC*01 (99.1%) V22>E (137), Km3 A45.1 (157), V101 (195) (112'-218')];

	chaîne lourde H-gamma1 anti-CD3E humanisée, G1v84-2 VH K44, CH1 E86 (1"-449") [VH K44 (*Homo sapiens* IGHV1-3*01 (81.6%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.12] (26"-33".51"-58".97"-108")) (1"-119") -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, CH1 E86, G1v30 CH2 G84.4, G1v33 CH3 S22, A24, V86 (hole) (CH1 R120>K (216") S86>E (185") (120"-217"), charnière 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"')-disulfure avec la chaîne légère L-kappa humanisée, Kv84-2 VK E44, CK K22(1"'-219"') [V-KAPPA E44 (*Homo sapiens* IGKV4-1*01 (90.8%) -IGKJ1*01 (100%), CDR-IMGT [12.3.8] (27"'-38"'.56"'-58"'.95"'-102"')) (1"'-112"') -*Homo sapiens* IGKC*01 (99.1%) V22>K (138"), Km3 A45.1 (158"'), V101 (196"') (113"'-219"')]; dimère (221-228":224-231")-bisdisulfure, produit dans une lignée cellulaire des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1, glycoforme alfa
linclatamig	inmunoglobulina G1-kappa, anti-[*Homo sapiens* LY6G6D (linfocito antígeno 6 miembro de la familia G6D, G6D, LY6-D, MEGT1, NG25)] y anti-[*Homo sapiens* CD3E (CD3 épsilon, Leu-4)], anticuerpo monoclonal humanizado, biespecífico; cadena pesada H-gamma1 anti-LY6G6D humanizada, G1v84-1 VH E44, CH1 K86 (1-442) [VH E44 (*Homo sapiens* IGHV3-23*01 (77.6%) -(IGHD) -IGHJ2*01 (92.3%) R120>P (104), CDR-IMGT [8.8.5] (26-33.51-58.97-101)) (1-112) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, CH1 K86, G1v30 CH2 G84.4, G1v32 CH3 W22 (knob) (CH1 R120>K (209), S86>K (178) (113-210), bisagra 1-15 (211-225), CH2 N84.4>G (292) (226-335), CH3 E12 (351), M14 (353), T22>W (361) (336-440), CHS (441-442)) (123-442)], (215-218')-disulfuro con la cadena ligera L-kappa humanizada, Kv84-1 VK K44, CK E22 (1'-218') [V-KAPPA K44 (*Homo sapiens* IGKV1-5*01 (89.8%) -IGKJ4*01 (100%), CDR-IMGT [6.3.13] (27'-32'.50'-52'.89'-101')) (1'-111') -*Homo sapiens* IGKC*01 (99.1%) V22>E (137), Km3 A45.1 (157), V101 (195) (112'-218')]; cadena pesada H-gamma1 anti-CD3E humanizada, G1v84-2 VH K44, CH1 E86 (1"-449") [VH K44 (*Homo sapiens* IGHV1-3*01 (81.6%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.12] (26"-33".51"-58".97"-108")) (1"-119") -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, CH1 E86, G1v30 CH2 G84.4, G1v33 CH3 S22, A24, V86 (hole) (CH1 R120>K (216") S86>E (185") (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 L-kappa humanizada, Kv84-2 VK E44, CK K22(1"'-219"') [V-KAPPA E44 (*Homo sapiens* IGKV4-1*01 (90.8%) -IGKJ1*01 (100%), CDR-IMGT [12.3.8] (27"'-38"'.56"'-58"'.95"'-102"')) (1"'-112"') -*Homo sapiens* IGKC*01 (99.1%) V22>K (138"), Km3 A45.1 (158"'), V101 (196"') (113"'-219"')]; dímero (221-228":224-231")-bisdisulfuro, producido en una línea celular de las células ováricas de hámster chino (CHO), línea celular derivada de CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada : H-gamma1 (H) anti-LY6G6D (knob)

```
EVQLLESGGG LVQPGGSLRL SCAASGFDFV NNAMIWVREA PGKGLEWVSA  50
LSFADNTAYY ATWASGRFTI SRDSSKTTVY LQMNSLRAED TAVYYCMRGD 100
LWGPGTLVTV SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT 150
VSWNSGALTS GVHTFPAVLQ SSGLYSLKSV VTVPSSSLGT QTYICNVNHK 200
PSNTKVDKKV EPKSCDKTHT CPPCPAPELL GGPSVFLFPP KPKDTLMISR 250
TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ YGSTYRVVSV 300
LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR 350
EEMTKNQVSL WCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF 400
LYSKLTVDKS RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GK          442
```

Light chain / Chaîne légère / Cadena ligera : L-kappa (L') anti-LY6G6D

```
DIQMTQSPST LSASVGDRVT ITCQASESIT RYLNWYQKKP GKAPKLLIYD  50
ASKLPSGVPS RFSGSGSGTE FTLTISSLQP DDFATYYCQS TSFRGRSYQN 100
TFGGGTKVEI KRTVAAPSVF IFPPSDEQLK SGTASVECLL NNFYPREAKV 150
QWKVDNALQS GNSQESVTEQ DSKDSTYSLS STLTLSKADY EKHKVYACEV 200
THQGLSSPVT KSFNRGEC                                    218
```

Heavy chain / Chaîne lourde / Cadena pesada : H-gamma1 (H") anti-CD3E (hole)

```
EVQLVQSGAE VKKPGASVKV SCKASGFTFT SYYIHWVRKA PGQGLEWIGW  50
IYPENDNTKY NEKFKDRVTI TADTSTSTAY LELSSLRSED TAVYYCARDG 100
YSRYYFDYWG QGTLVTVSSA STKGPSVFPL APSSKSTSGG TAALGCLVKD 150
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLESVVTV 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 : L-kappa (L'") anti-CD3E

```
DIVMTQSPDS LAVSLGERAT INCKSSQSLL NSRTRKNYLA WYQEKPGQPP  50
KLLIYWASTR ESGVPDRFSG SGSGTDFTLT ISSLQAEDVA VYYCTQSFIL 100
RTFGQGTKVE IKRTVAAPSV FIFPPSDEQL KSGTASVKCL 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) 22-96 139-195 256-316 362-420
22"-96" 146"-202" 263"-323" 369"-427"

Intra-L (C23-C104) 23'-88' 138'-198'
23'"-94'" 139'"-199'"

Inter-H-L (h 5-CL 126) 215-218' 222"-219'"

Inter-H-H (h 11, h 14) 221-228" 224-231"

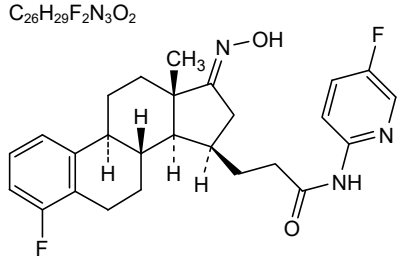
No N-glycosylation sites / pas de sites de N-glycosylation / ningùm posición de N-glycosilación
H CH2 N84.4>G (G1v30): 292, 299"

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2: 442, 449"

linustedastatum

linustedastat	3-[(17*E*)-4-fluoro-17-(hydroxyimino)estra-1,3,5(10)-trien-15β-yl]-*N*-(5-fluoropyridin-2-yl)propanamide
linustédastat	3-[(17*E*)-4-fluoro-17-(hydroxyimino)estra-1,3,5(10)-trién-15β-yl]-*N*-(5-fluoropyridin-2-yl)propanamide
linustedastat	3-[(17*E*)-4-fluoro-17-(hidroxiimino)estra-1,3,5(10)-trien-15β-il]-*N*-(5-fluoropiridin-2-il)propanamida

$C_{26}H_{29}F_2N_3O_2$



lirodegimodum

lirodegimod

[(3*S*,6^{2}*S*,6^{4}*R*,8*S*,17*S*,20^{5}*S*,20^{8}*S*,20^{10a}*R*)-20^{3}-acetyl-17-(3-amino-3-oxopropyl)-8-*tert*-butyl-14^{2}-chloro-6^{4}-hydroxy-1^{4},3-dimethyl-5,7,10,19,20^{6},22-hexaoxo-20^{1},20^{2},20^{3},20^{4},20^{5},20^{6},20^{8},20^{9},20^{10},20^{10a}-decahydro-23^{1}*H*-15-oxa-4,9,18,21-tetraaza-20(8,5)-pyrrolo[1,2-*a*][1,5]diazocina-23(2)-indola-1(5)-[1,3]thiazola-6(2,1)-pyrrolidina-2(1,4),14(1,3)-dibenzenatricosaphane-23^{5}-carbonyl]phosphonic acid

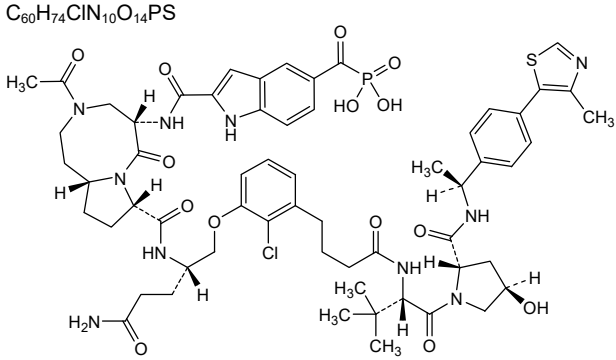
lirodégimod

acide [(3*S*,6^{2}*S*,6^{4}*R*,8*S*,17*S*,20^{5}*S*,20^{8}*S*,20^{10a}*R*)-20^{3}-acétyl-17-(3-amino-3-oxopropyl)-8-*tert*-butyl-14^{2}-chloro-6^{4}-hydroxy-1^{4},3-diméthyl-5,7,10,19,20^{6},22-hexaoxo-20^{1},20^{2},20^{3},20^{4},20^{5},20^{6},20^{8},20^{9},20^{10},20^{10a}-décahydro-23^{1}*H*-15-oxa-4,9,18,21-tétraaza-20(8,5)-pyrrolo[1,2-*a*][1,5]diazocina-23(2)-indola-1(5)-[1,3]thiazola-6(2,1)-pyrrolidina-2(1,4),14(1,3)-dibenzénatricosaphane-23^{5}-carbonyl]phosphonique

lirodegimod

ácido [(3*S*,6^{2}*S*,6^{4}*R*,8*S*,17*S*,20^{5}*S*,20^{8}*S*,20^{10a}*R*)-20^{3}-acetil-17-(3-amino-3-oxopropil)-8-*terc*-butil-14^{2}-cloro-6^{4}-hidroxi-1^{4},3-dimetil-5,7,10,19,20^{6},22-hexaoxo-20^{1},20^{2},20^{3},20^{4},20^{5},20^{6},20^{8},20^{9},20^{10},20^{10a}-decahidro-23^{1}*H*-15-oxa-4,9,18,21-tetraaza-20(8,5)-pirrolo[1,2-*a*][1,5]diazocina-23(2)-indola-1(5)-[1,3]tiazola-6(2,1)-pirrolidina-2(1,4),14(1,3)-dibencenatricosafano-23^{5}-carbonil]fosfónico

$C_{60}H_{74}ClN_{10}O_{14}PS$



lomedeucitinibum

lomedeucitinib

4-{[3-(methanesulfonyl)pyridin-2-yl]amino}-*N*-($^{2}H_3$)methyl-6-[(1*R*)-spiro[2.2]pentane-1-carboxamido]pyridazine-3-carboxamide

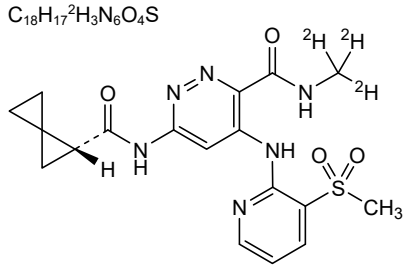
lomédeucitinib

4-{[3-(méthanesulfonyl)pyridin-2-yl]amino}-*N*-($^{2}H_3$)méthyl-6-[(1*R*)-spiro[2.2]pentane-1-carboxamido]pyridazine-3-carboxamide

lomedeucitinib

6-[(1*R*)-espiro[2.2]pentano-1-carboxamido]-4-{[3-(metanosulfonil)piridin-2-il]amino}-*N*-($^{2}H_3$)metilpiridazina-3-carboxamida

$C_{18}H_{17}{}^{2}H_3N_6O_4S$



Ionimecgenum renparvovecum #

Ionimecgene renparvovec	recombinant, self-complementary (dimeric), non-replicating adeno-associated virus serotype 9 (scAAV9) vector encoding a miniaturised form of human methyl-CpG binding protein 2 (MECP2) containing the methyl-CpG-binding domain (MBD) and the NCoR/SMRT (silencing mediator of retinoic acid and thyroid hormone receptor) interaction domain (NID), under the control of a fragment of the mouse MECP2 promoter. The 3' untranslated region is designed to decrease protein expression through RNA interference by containing a microRNA (miR) Responsive Auto-Regulatory Element (miRARE) inserted into the replication dependent histone 1 (RDH1) polyadenylation region. The construct is flanked by adeno-associated virus 2 (AAV2) inverted terminal repeats (ITRs)
Ionimecgène renparvovec	vecteur recombinant, auto-complémentaire (dimère), non répliquant du virus adéno-associé de sérotype 9 (scAAV9) codant une forme miniaturisée de la protéine 2 humaine de liaison au méthyl-CpG (MECP2) contenant le domaine de liaison au méthyl-CpG (MBD) et le domaine d'interaction (NID) des NCOR/SMRT (corépresseurs transcriptionnels des récepteurs des hormones thyroïdiennes et de l'acide), sous le contrôle d'un fragment du promoteur de la MECP2 de souris. La région 3' non traduite a été conçue pour diminuer l'expression protéique grâce à l'interférence ARN en contenant un élément autorégulateur sensible aux micro-ARN (MiR) (miRARE) inséré dans la région de polyadénylation de l'histone 1 dépendante de la réplication (RDH1). La construction est flanquée de répétitions terminales inversées (ITR) du virus adéno-associé 2 (AAV2)
Ionimecgén renparvovec	vector de virus adenoasociado serotipo 9 recombinante, autocomplementario (dimérico), no replicativo (scAAV9) que codifica para una forma miniaturizada de la proteína 2 de unión a metil-CpG (MECP2) humana que contiene el dominio de unión a metil-CpG (MBD) y el domino de interacción (NID) NCOR/SMRT (mediador de silenciamiento de ácido retinoico y receptor de hormona tioridea), bajo el control de un fragmento del promotor MECP2 de ratón. La región no traducida 3' está diseñada para reducir la expresión de proteína a través de interferencia de ARN mediante la presencia de un elemento auto-regulador que responde a microARN (miR) (miRARE) insertado en la región de poliadenilación de la histona dependiente de replicación 1 (RDH1). El constructo está flanqueado por repeticiones terminales invertidas (ITRs) del virus adenoasociado 2 (AAV2)

Ionvoguranum

Ionvoguran	*all-P-ambo*-2'-*O*-methyl-*P*-thioguanylyl-(3'→5')-2'-*O*-methyl-*P*-thioguanylyl-(3'→5')-2'-*O*-methyl-*P*-thioadenylyl-(3'→5')-uridylyl-

(3'→5')-uridylyl-(3'→5')-guanylyl-(3'→5')-cytidylyl-(3'→5')-guanylyl-(3'→5')-uridylyl-(3'→5')-adenylyl-(3'→5')-uridylyl-(3'→5')-guanylyl-(3'→5')-guanylyl-(3'→5')-guanylyl-(3'→5')-adenylyl-(3'→5')-cytidylyl-(3'→5')-adenylyl-(3'→5')-cytidylyl-(3'→5')-adenylyl-(3'→5')-adenylyl-(3'→5')-guanylyl-(3'→5')-uridylyl-(3'→5')-uridylyl-(3'→5')-uridylyl-(3'→5')-uridylyl-(3'→5')-adenylyl-(3'→5')-guanylyl-(3'→5')-adenylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-adenylyl-(3'→5')-adenylyl-(3'→5')-guanylyl-(3'→5')-uridylyl-(3'→5')-uridylyl-(3'→5')-adenylyl-(3'→5')-adenylyl-(3'→5')-adenylyl-(3'→5')-adenylyl-(3'→5')-uridylyl-(3'→5')-adenylyl-(3'→5')-adenylyl-(3'→5')-guanylyl-(3'→5')-guanylyl-(3'→5')-cytidylyl-(3'→5')-uridylyl-(3'→5')-adenylyl-(3'→5')-guanylyl-(3'→5')-uridylyl-(3'→5')-cytidylyl-(3'→5')-cytidylyl-(3'→5')-guanylyl-(3'→5')-uridylyl-(3'→5')-uridylyl-(3'→5')-adenylyl-(3'→5')-guanylyl-(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*-methyladenylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyl-*P*-thiouridylyl-(3'→5')-2'-*O*-methyl-*P*-thiouridylyl-(3'→5')-2'-*O*-methyl-*P*-thiouridylyl-(3'→5')-2'-*O*-methyluridine

lonvoguran *tout-P-ambo*-2'-*O*-méthyl-*P*-thioguanylyl-(3'→5')-2'-*O*-méthyl-*P*-thioguanylyl-(3'→5')-2'-*O*-méthyl-*P*-thioadénylyl-(3'→5')-uridylyl-(3'→5')-uridylyl-(3'→5')-guanylyl-(3'→5')-cytidylyl-(3'→5')-guanylyl-(3'→5')-uridylyl-(3'→5')-adénylyl-(3'→5')-uridylyl-(3'→5')-guanylyl-(3'→5')-guanylyl-(3'→5')-guanylyl-(3'→5')-adénylyl-(3'→5')-cytidylyl-(3'→5')-adénylyl-(3'→5')-cytidylyl-(3'→5')-adénylyl-(3'→5')-adénylyl-(3'→5')-guanylyl-(3'→5')-uridylyl-(3'→5')-uridylyl-(3'→5')-uridylyl-(3'→5')-uridylyl-(3'→5')-adénylyl-(3'→5')-guanylyl-(3'→5')-adénylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-adénylyl-(3'→5')-adénylyl-(3'→5')-adénylyl-(3'→5')-adénylyl-(3'→5')-adénylyl-(3'→5')-adénylyl-(3'→5')-guanylyl-(3'→5')-guanylyl-(3'→5')-cytidylyl-(3'→5')-uridylyl-(3'→5')-adénylyl-(3'→5')-guanylyl-(3'→5')-uridylyl-(3'→5')-cytidylyl-(3'→5')-cytidylyl-(3'→5')-guanylyl-(3'→5')-uridylyl-(3'→5')-adénylyl-(3'→5')-uridylyl-(3'→5')-cytidylyl-(3'→5')-adénylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyl-*P*-thiouridylyl-(3'→5')-2'-*O*-méthyl-*P*-thiouridylyl-(3'→5')-2'-*O*-méthyl-*P*-thiouridylyl-(3'→5')-2'-*O*-méthyluridine

lonvogurán

todo-P-ambo- 2'-*O*-metil-*P*-tioguanilil-(3'→5')-2'-*O*-metil-*P*-tioguanilil-(3'→5')-2'-*O*-metil-*P*-tioadenilil-(3'→5')-uridilil-(3'→5')-uridilil-(3'→5')-guanilil-(3'→5')-citidilil-(3'→5')-guanilil-(3'→5')-uridilil-(3'→5')-adenilil-(3'→5')-uridilil-(3'→5')-guanilil-(3'→5')-guanilil-(3'→5')-guanilil-(3'→5')-adenilil-(3'→5')-citidilil-(3'→5')-adenilil-(3'→5')-citidilil-(3'→5')-adenilil-(3'→5')-adenilil-(3'→5')-guanilil-(3'→5')-uridilil-(3'→5')-uridilil-(3'→5')-uridilil-(3'→5')-uridilil-(3'→5')-adenilil-(3'→5')-guanilil-(3'→5')-adenilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilcitidilil-(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*-metiladenilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-adenilil-(3'→5')-adenilil-(3'→5')-guanilil-(3'→5')-uridilil-(3'→5')-uridilil-(3'→5')-adenilil-(3'→5')-adenilil-(3'→5')-adenilil-(3'→5')-adenilil-(3'→5')-uridilil-(3'→5')-adenilil-(3'→5')-adenilil-(3'→5')-guanilil-(3'→5')-guanilil-(3'→5')-citidilil-(3'→5')-uridilil-(3'→5')-adenilil-(3'→5')-guanilil-(3'→5')-uridilil-(3'→5')-citidilil-(3'→5')-citidilil-(3'→5')-guanilil-(3'→5')-uridilil-(3'→5')-uridilil-(3'→5')-adenilil-(3'→5')-uridilil-(3'→5')-citidilil-(3'→5')-adenilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metil-*P*-tiouridilil-(3'→5')-2'-*O*-metil-*P*-tiouridilil-(3'→5')-2'-*O*-metil-*P*-tiouridilil-(3'→5')-2'-*O*-metiluridina

$C_{1005}H_{1268}N_{389}O_{687}P_{99}S_6$

```
    1                  10                  20                  30
(3'-5')G=G=A=U-U-G-C-G-U-A-U-G-G-G-A-C-A-C-A-A-G-U-U-U-U-A-G-A-G-C-
                      40                  50                  60
   -U-A-G-A-A-A-U-A-G-C-A-A-G-U-U-A-A-A-A-U-A-A-G-G-C-U-A-G-U-C-
                      70                  80                  90
   -C-G-U-U-A-U-C-A-A-C-U-U-G-A-A-A-A-G-U-G-G-C-A-C-C-G-A-G-U-
                     100
   -C-G-G-U-G-C-U=U=U=U
```

N : nucleoside / nucléoside / nucleósido
N : 2'-*O*-methyl-N / 2'-*O*-méthyl-N / 2'-*O*-metil-N
- : -PO(OH)- = : -PO(SH)-

Iorutengitidum

lorutengitide

(4*R*)-4-hydroxy-L-prolylglycyl-L-glutaminyl-L-α-glutamyl-2-methylalanyl-L-leucyl-L-alanine

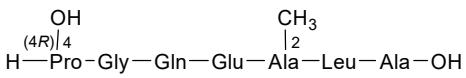
lorutengitide

(4*R*)-4-hydroxy-L-prolylglycyl-L-glutaminyl-L-α-glutamyl-2-méthylalanyl-L-leucyl-L-alanine

lorutengitida

(4*R*)-4-hidroxi-L-prolilglicil-L-glutaminil-L-α-glutamil-2-metilalanil-L-leucil-L-alanina

$C_{30}H_{50}N_8O_{12}$



lucorafuspum alfa #

lucorafusp alfa

humanized immunoglobulin G4-kappa, anti-[human TIGIT (T cell immunoreceptor with Ig domain and ITIM, V-set Ig member 9, VSIG9, V-set and transmembrane member 3, VSTM3)] fused at the C-terminus of the heavy chain, via a $(G_4S)_4$ peptide linker, to a fragment of the mature extracellular domain of human TGF-beta receptor type-2, glycoform alfa; gamma 4 heavy chain (1-447) [VH (*Homo sapiens* IGHV4-30-4*01 -(IGHD) -IGHJ4*01, CDR-Kabat [6.16.12] (31-36.51-66.99-110)) (1-121) -*Homo sapiens* IGHG4*01 (CH1 (122-219), hinge S^{229}>P (220-231), CH2 F^{235}>A, L^{236}>A (232-341), CH3 (342-446), CHS K^{448}>del (447)) (122-447)] fused via a $(G_4S)_4$ peptide linker (448-467) to human TGF-beta receptor type-2 (TGFR-2, TGFBR2, transforming growth factor-beta receptor type II, TGFβ type II receptor, TGFβRII) extracellular domain fragment 23-159 (1-137 of the mature protein), [T^{23}>G^{468}, ^{S31}>T^{476}]-variant (468-604 in the current sequence), (135-214')-disulfide with kappa light chain (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*01 -IGKJ1*01, CDR-Kabat [11.7.9] (24'-34'.50'-56'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (108'-214')]; dimer (227-227'':230-230'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

lucorafusp alfa

immunoglobuline G4-kappa humanisée, anti-[TIGIT humain (immunorécepteur des lymphocytes T avec les domaines Ig et ITIM, membre 9 de l'Ig du groupe V, VSIG9, membre 3 transmembranaire du groupe V (V-set), VSTM3)] fusionnée à l'extrémité C-terminale de la chaîne lourde, via un peptide liant $(G_4S)_4$, à un fragment du domaine extracellulaire mature du récepteur humain du TGF-bêta de type 2, glycoforme alfa;
chaîne lourde gamma 4 (1-447) [VH (*Homo sapiens* IGHV4-30-4*01 -(IGHD) -IGHJ4*01, CDR-Kabat [6.16.12] (31-36.51-66. 99-110)) (1-121) -*Homo sapiens* IGHG4*01 (CH1 (122-219), charnière S^{229}>P (220-231), CH2 F^{235}>A, L^{236}>A (232-341), CH3 (342-446), CHS K^{448}>del (447)) (122-447)] fusionné via un peptide liant $(G_4S)_4$ (448-467) au récepteur humain du TGF-bêta de type 2 (TGFR-2, TGFBR2, récepteur de type II du facteur de croissance transformant bêta, récepteur TGFβ type II, TGFβRII) fragment 23-159 du domaine extracellulaire (1-137 de la protéine mature), [T^{23}>G^{468}, ^{S31}>T^{476}]-variant (468-604 dans la séquence actuelle), (135-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*01 -IGKJ1*01, CDR-Kabat [11. 7.9] (24'-34'.50'-56'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (108'-214')]; dimère (227-227'':230-230'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

lucorafusp alfa

inmunoglobulina G4-kappa humanizada, anti-[humana TIGIT (inmunoreceptor de células T con dominio Ig e ITIM, V-set Ig miembro 9, VSIG9, V-set y transmembrana miembro 3, VSTM3)] fusionado en el terminal C de la cadena pesada, a través del enlace peptídico $(G_4S)_4$, a un fragmento de dominio extracelular maduro del receptor humano TGF-beta tipo-2, glicoforma alfa;
cadena pesada gamma 4 (1-447) [VH (*Homo sapiens* IGHV4-30-4*01 -(IGHD) -IGHJ4*01, CDR-Kabat [6.16.12] (31-36.51-66.99-110)) (1-121) -*Homo sapiens* IGHG4*01 (CH1 (122-219), bisagra S^{229}>P (220-231), CH2 F^{235}>A, L^{236}>A (232-341), CH3 (342-446), CHS K^{448}>del (447)) (122-447)] fusionado a través de un $(G_4S)_4$ enlace peptídico (448-467) al receptor tipo 2 humano TGF-beta (TGFR-2, TGFBR2, receptor del factor de crecimiento transformador beta de tipo II, receptor tipo III TGFβ, TGFβRII) fragmento del dominio extracelular 23-159 (1-137 de la proteína madura), [T^{23}>G^{468}, ^{S31}>T^{476}]-variante (468-604 en la secuencia actual), (135-214')-disulfuro con la cadena ligera kappa (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*01 -IGKJ1*01, CDR-Kabat [11.7.9] (24'-34'.50'-56'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (108'-214')]; dímero (227-227'':230-230'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), glicoforma alfa

Sequence / Séquence / Secuencia
IgG4-TGFBR2 heavy chain

```
DVQLQESGPG LVKPSQTLSL TCTVSGHSFT SDYAWSWIRQ PPGKGLEWIG  050
YISYSDSTNY NPSLKSRVTI SRDTSKNQFS LKLSSVTAAD TAVYYCARLD  100
YGNYGGAMDY WGQGTSVTVS SASTKGPSVF PLAPCSRSTS ESTAALGCLV  150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTK  200
TYTCNVDHKP SNTKVDKRVE SKYGPPCPPC PAPEAAGGPS VFLFPPKPKD  250
TLMISRTPEV TCVVVDVSQE DPEVQFNWYV DGVEVHNAKT KPREEQFNST  300
YRVVSVLTVL HQDWLNGKEY KCKVSNKGLP SSIEKTISKA KGQPREPQVY  350
TLPPSQEEMT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD  400
SDGSFFLYSR LTVDKSRWQE GNVFSCSVMH EALHNHYTQK SLSLSLGGGG  450
GSGGGGSGGG GSGGGGSGIP PHVQKTVNND MIVTDNNGAV KFPQLCKFCD  500
VRFSTCDNQK SCMSNCSITS ICEKPQEVCV AVWRKNDENI TLETVCHDPK  550
LPYHDFILED AASPKCIMKE KKKPGETFFM CSCSSDECND NIIFSEEYNT  600
SNPD                                                    604
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IgG4 light chain

```
DIQMTQSPSS LSASVGDRVT ITCRSSQHVS TALAWYQQKP GKSPKLLIYS  050
ASSRYSGVPD RFSGSGSGTD FTFTISSLQP EDFATYYCQQ HYITPWTFGG  100
GTKLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV  150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG  200
LSSPVTKSFN RGEC                                         214
```

Mutation / Mutation / Mutación
S^{229},$S^{229"}$>**P**, F^{235},$F^{235"}$>**A**, L^{236},$L^{236"}$>**A**, T^{23}>**G**^{468},**G**$^{468"}$, S^{31}>**T**^{476},**T**$^{476"}$, K^{448},$K^{448"}$>del

Peptide linker / Peptide liant / Péptido de unión
IgG4-TGFBR2: ^{448}*GGGGSGGGGSGGGGSGGGGS*^{467}

Post-translation modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra heavy chain: 22-96, 148-204, 262-322, 368-426
22"-96", 148"-204", 262"-322", 368"-426"
Intra light chain: 23'-88', 134'-194'; 23'"- 88'", 134'"-194'"
Inter heavy-light chain: 135-214', 135"-214'"
Inter heavy-heavy chain 227-227", 230-230"
Intra TGFBR2: 496-529, 499-516, 506-512, 522-546, 566-581, 583-588
496"-529", 499"-516", 506"-512", 522"-546", 566"-581", 583"-588"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
IgG4-TGFBR2: 298, 515, 539; 298", 515", 539"

lumistobartum

lumistobart — immunoglobulin G1-kappa, anti-[*Homo sapiens* SIRPA (signal regulatory protein alpha, SHPS1, protein tyrosine phosphatase non-receptor type substrate 1, PTPNS1, SIRP, SIRP alpha, CD172a)], humanized monoclonal antibody;
H-gamma1 heavy chain humanized (1-448) [VH (*Homo sapiens* IGHV4-31*02 (93.9%) -(IGHD) -IGHJ4*01 (86.7%) L123>T (113), CDR-IMGT [9.7.11] (26-34.52-58.97-107)) (1-118) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, G1v29 CH2 A84.4 (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 (447-448)) (119-448)], (221-220')-disulfide with L-kappa light chain humanized (1'-220') [V-KAPPA (*Homo sapiens* IGKV4-1*01 (91.1%) -IGKJ2*01 (100%), 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 (227-227":230-230")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-S, non-glycosylated

lumistobart — immunoglobuline G1-kappa, anti-[*Homo sapiens* SIRPA (protéine alpha régulatrice du signal, SHPS1, substrat 1 de protéine tyrosine phosphatase de type non-récepteur, PTPNS1, SIRP, SIRP alpha, CD172a)]; anticorps monoclonal humanisé;

chaîne lourde H-gamma1 humanisée (1-448) [VH (*Homo sapiens* IGHV4-31*02 (93.9%) -(IGHD) -IGHJ4*01 (86.7%) L123>T (113), CDR-IMGT [9.7.11] (26-34.52-58.97-107)) (1-118) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, G1v29 CH2 A84.4 (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 (447-448)) (119-448)], (221-220')-disulfure avec la chaîne légère L-kappa humanisée (1'-220') [V-KAPPA (*Homo sapiens* IGKV4-1*01 (91.1%) -IGKJ2*01 (100%), 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 (227-227'':230-230'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-S, non-glycosylé

lumistobart

inmunoglobulina G1-kappa, anti-[*Homo sapiens* SIRPA (proteína alfa reguladora de la señal, SHPS1, sustrato 1 de proteína tirosina fosfatasa de tipop no receptor, PTPNS1, SIRP alfa, CD172a)]; anticuerpo monoclonal humanizado;
cadena pesada H-gamma1 humanizada (1-448) [VH (*Homo sapiens* IGHV4-31*02 (93.9%) -(IGHD) -IGHJ4*01 (86.7%) L123>T (113), CDR-IMGT [9.7.11] (26-34.52-58.97-107)) (1-118) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, G1v29 CH2 A84.4 (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 (447-448)) (119-448)], (221-220')-disulfuro con la cadena ligera L-kappa humanizada (1'-220') [V-KAPPA (*Homo sapiens* IGKV4-1*01 (91.1%) -IGKJ2*01 (100%), 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 (227-227'':230-230'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-S, no glicosilado

Heavy chain / Chaîne lourde / Cadena pesada : H-gamma1 (H, H'') anti-SIRPA

```
QVQLQESGPG LVKPSQTLSL TCTVSGGSIS SGYYWSWIRQ HPGKGLEWIG  50
YISYDGSRYN NPSLKNRVTI SVDTSKNQFS LKLSSVTAAD TAVYYCAREE 100
YANYFAYWGQ GTTVTVSSAS 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 SLSLSPGK   448
```

Light chain / Chaîne légère / Cadena ligera : L-kappa (L', L'") anti-SIRPA

```
DIVMTQSPDS LAVSLGERAT INCKSSQSLF YSSNQKNFLA WYQQKPGQPP  50
KLLIYWASTR ESGVPDRFTG SGSGTDFTLT ISSVKAEDLA VYYCQQYYSY 100
PPTFGQGTKL 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) 22-96 145-201 262-322 368-426
22"-96" 145"-201" 262"-322" 368"-426"
Intra-L (C23-C104) 23'-94' 140'-200'
23'"-94'" 140'"-200'"
Inter-H-L (h 5-CL 126) 221-220' 221"-220'"
Inter-H-H (h 11, h 14) 227-227" 230-230"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)
H VH Q1: 1, 1"

No N-glycosylation sites / pas de sites de N-glycosylation / ningùm posición de N-glycosilación
H CH2 N84.4>A (G1v29): 298, 298"

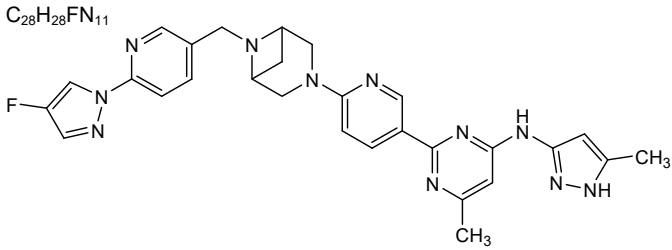
C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2: 448, 448"

lunbotinibum

lunbotinib — 2-[6-(6-{[6-(4-fluoro-1*H*-pyrazol-1-yl)pyridin-3-yl]methyl}-3,6-diazabicyclo[3.1.1]heptan-3-yl)pyridin-3-yl]-6-methyl-*N*-(5-methyl-1*H*-pyrazol-3-yl)pyrimidin-4-amine

lunbotinib — 2-[6-(6-{[6-(4-fluoro-1*H*-pyrazol-1-yl)pyridin-3-yl]méthyl}-3,6-diazabicyclo[3.1.1]heptan-3-yl)pyridin-3-yl]-6-méthyl-*N*-(5-méthyl-1*H*-pyrazol-3-yl)pyrimidin-4-amine

lunbotinib — 2-[6-(6-{[6-(4-fluoro-1*H*-pirazol-1-il)piridin-3-il]metil}-3,6-diazabiciclo[3.1.1]heptan-3-il)piridin-3-il]-6-metil-*N*-(5-metil-1*H*-pirazol-3-il)pirimidin-4-amina

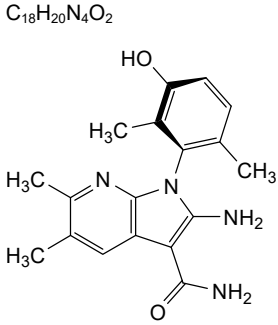


lunresertibum

lunresertib — (1*P*)-2-amino-1-(3-hydroxy-2,6-dimethylphenyl)-5,6-dimethyl-1*H*-pyrrolo[2,3-*b*]pyridine-3-carboxamide

lunrésertib — (1*P*)-2-amino-1-(3-hydroxy-2,6-diméthylphényl)-5,6-diméthyl-1*H*-pyrrolo[2,3-*b*]pyridine-3-carboxamide

lunresertib — (1*P*)-2-amino-1-(3-hidroxi-2,6-dimetilfenil)-5,6-dimetil-1*H*-pirrolo[2,3-*b*]piridina-3-carboxamida



lutetium (^{177}Lu) rosopatamabum tetraxetanum #

lutetium (^{177}Lu) rosopatamab tetraxetan

immunoglobulin G1-kappa, anti-[*Homo sapiens* FOLH1 (folate hydrolase, prostate specific membrane antigen, PSMA)], lutetium (^{177}Lu) radiolabelled *tetraxetan* conjugate ;
H-gamma1 heavy chain (1-445) [VH Musmus/Homsap (*Mus musculus* IGHV1-26*01 (78.4%) -(IGHD) -IGHJ2*01 (92.9%) T123>L (110)/*Homo sapiens* IGHV1-69-2*01 (76.3%) -(IGHD) -IGHJ4*01 (92.9%) V124>L (111), CDR-IMGT [8.8.8] (26-33.51-58.97-104)) (1-115) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (212) (116-213), hinge 1-15 (214-228), CH2 (229-338), CH3 D12 (354), L14 (356) (339-443), CHS (444-445)) (116-445)], (218-214')-disulfide with L-kappa light

chain (1'-214') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV6-23*01 (81.8%) -IGKJ2*03 (72.7%) S120>P (100), L124>V (104), E125>D (105)/*Homo sapiens* IGKV1-13*02 (78.7%) -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 (224-224'':227-227'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa; conjugated via the side chain nitrogen of an average of 4 lysine residues to lutetium (^{177}Lu) radiolabelled 2-[4,7,10-tris(carboxymethyl)-1,4,7,10-tetraazacyclodecan-1-yl]acetyl (*tetraxetan*, DOTA)

lutécium (^{177}Lu) rosopatamab tétraxétan

immunoglobuline G1-kappa, anti-[*Homo sapiens* FOLH1 (folate hydrolase, antigène membranaire spécifique de la prostate, PSMA)], conjugué au *tétraxétan* et radiomarqué au lutécium (^{177}Lu); chaîne lourde H-gamma1 (1-445) [VH Musmus/Homsap (*Mus musculus* IGHV1-26*01 (78.4%) -(IGHD) -IGHJ2*01 (92.9%) T123>L (110)/*Homo sapiens* IGHV1-69-2*01 (76.3%) -(IGHD) -IGHJ4*01 (92.9%) V124>L (111), CDR-IMGT [8.8.8] (26-33.51-58.97-104)) (1-115) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (212) (116-213), charnière 1-15 (214-228), CH2 (229-338), CH3 D12 (354), L14 (356) (339-443), CHS (444-445)) (116-445)], (218-214')-disulfure avec la chaîne légère L-kappa (1'-214') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV6-23*01 (81.8%) -IGKJ2*03 (72.7%) S120>P (100), L124>V (104), E125>D (105)/*Homo sapiens* IGKV1-13*02 (78.7%) -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 (224-224'':227-227'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa; conjugué par l'azote de la chaîne latérale de 4 résidus lysine en moyenne au 2-[4,7,10-tris(carboxyméthyl)-1,4,7,10-tétraazacyclodécan-1-yl]acétyle (*tétraxétan,* DOTA) et radiomarqué au lutécium (^{177}Lu)

lutecio (^{177}Lu) rosopatamab tetraxetán

inmunoglobulina G1-kappa, anti-[*Homo sapiens* FOLH1 (folato hidrolasa, antígeno membranario específico de la próstata, PSMA)], conjugado al *tetraxetán* radiomarcado con lutecio (^{177}Lu); cadena pesada H-gamma1 (1-445) [VH Musmus/Homsap (*Mus musculus* IGHV1-26*01 (78.4%) -(IGHD) -IGHJ2*01 (92.9%) T123>L (110)/*Homo sapiens* IGHV1-69-2*01 (76.3%) -(IGHD) -IGHJ4*01 (92.9%) V124>L (111), CDR-IMGT [8.8.8] (26-33.51-58.97-104)) (1-115) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (212) (116-213), bisagra 1-15 (214-228), CH2 (229-338), CH3 D12 (354), L14 (356) (339-443), CHS (444-445)) (116-445)], (218-214')-disulfuro con la cadena ligera L-kappa (1'-214') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV6-23*01 (81.8%) -IGKJ2*03 (72.7%) S120>P (100), L124>V (104), E125>D (105)/*Homo sapiens* IGKV1-13*02 (78.7%) -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 (224-224'':227-227'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, forma glicosilada alfa; conjugado por el nitrógeno de la cadena lateral de 4 residuos de lisina en promedio al 2-[4,7,10-tris(carboximetil)-1,4,7,10-tetraazaciclodecan-1-il]acetilo (*tetraxetán,* DOTA) y radiomarcado con lutecio (^{177}Lu)

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVQSGPE VKKPGATVKI SCKTSGYTFT EYTIHWVKQA PGKGLEWIGN  50
INPNNGGTTY NQKFEDKATL TVDKSTDTAY MELSSLRSED TAVYYCAAGW 100
NFDYWGQGTL LTVSSASTKG PSVFPLAPSS KSTSGGTAAL GCLVKDYFPE 150
PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL SSVVTVPSSS LGTQTYICNV 200
NHKPSNTKVD KKVEPKSCDK THTCPPCPAP ELLGGPSVFL FPPKPKDTLM 250
ISRTPEVTCV VVDVSHEDPE VKFNWYVDGV EVHNAKTKPR EEQYNSTYRV 300
VSVLTVLHQD WLNGKEYKCK VSNKALPAPI EKTISKAKGQ PREPQVYTLP 350
PSRDELTKNQ VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG 400
SFFLYSKLTV DKSRWQQGNV FSCSVMHEAL HNHYTQKSLS LSPGK      445
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Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSTSVGDRVT LTCKASQDVG TAVDWYQQKP GPSPKLLIYW  50
ASTRHTGIPS RFSGSGSGTD FTLTISSLQP EDFADYYCQQ YNSYPLTFGP 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) 22-96 142-198 259-319 365-423
22"-96" 142"-198" 259"-319" 365"-423"

Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194'"

Inter-H-L (h 5-CL 126) 218-214' 218"-214'"

Inter-H-H (h 11, h 14) 224-224" 227-227"

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

H CH2 N84.4: 295, 295"

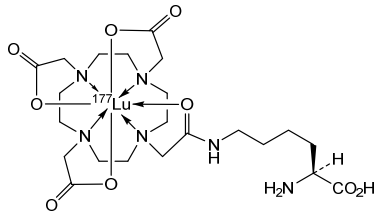
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

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

H CHS K2: 445, 445"

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

K



*(N^6-(^{177}Lu-lutetium tetraxetan)-L-lysine:mAb ~ 4:1)

luvomeranum

luvomeran	messenger RNA (mRNA), 5' capped, encoding codon-optimised human cystic fibrosis transmembrane conductance regulator (hCFTR; channel conductance-controlling ATPase, cAMP-dependent chloride channel, ATP-binding cassette sub-family C member 7), flanked by 5' and 3' untranslated regions based on the *Mus musculus* histone H1.5 gene and the human haemoglobin subunit alpha (HBA1) gene, followed by a 3' polyadenylation (polyA) tail (containing a 100-nucleotide polyA sequence, a 5-nucleotide XbaI scar and a 20-nucleotide polyA sequence ending with an inverted dT); contains N^1-methylpseudouridine instead of uridine (*all*-U>m$^1\Psi$)
luvoméran	ARN messager (ARNm), coiffé en 5', codant le régulateur de conductance transmembranaire de la mucoviscidose humaine aux codons optimisés (hCFTR; canal ATPase contrôlant la conductance, canal chlorure dépendant de l'AMPc, membre 7 de la sous-famille C des cassettes de liaison à l'ATP), flanqué de régions 5' et 3' non traduites basées sur le gène de l'histone H1.5 de *Mus musculus* et du gène de la sous-unité alpha de l'hémoglobine

humaine (HBA1), suivies d'une queue de polyadénylation (polyA) en 3' (contenant une séquence polyA de 100 nucléotides, une cicatrice XbaI de 5 nucléotides et une séquence polyA de 20 nucléotides se terminant par un dT inversé); contient de la N^1-méthylpseudouridine à la place de l'uridine (*tout*-U>m$^1\Psi$)

luvomerán — ARN mensajero (ARNm), protegido en 5', que codifica, con codones optimizados, para el regulador de conductancia transmembrana de la fibrosis quística humana (hCFTR; ATPasa controladora de la conductancia de canal, canal de cloro dependiente de cAMP, miembro 7 de la subfamilia C del casete de unión a ATP), flanqueado por regiones sin traducir 5' y 3' basadas en el gen de la histona H1.5 de *Mus musculus* y el gen de la subunidad alfa de la hemoglobina humana (HBA1), seguido de una cola de poliadenilación (Poli A) en 3' (que contiene una secuencia poli A de 100 nucleótidos, una cicatriz XbaI de 5 nucleótidos y una secuencia poli A de 20 nucleótidos que termina en un dT invertido); contiene N^1-metilpseudouridina en lugar de uridina (*todo*-U>m$^1\Psi$)

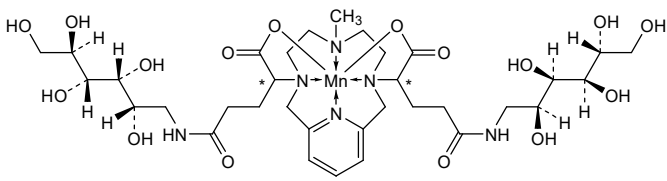
mangaciclanolum

mangaciclanol — [1,1'-([6-methyl-3,6,9-triaza-1(2,6)-pyridinacyclodecaphane-3,9-diyl-κ^4*N*^{1},*N*^{3},*N*^{6},*N*^{9}]bis{[(4Ξ)-4-(carboxylato-κ*O*)-1-oxobutane-4,1-diyl]azanediyl})bis(1-deoxy-D-glucitol)]manganese

mangaciclanol — [1,1'-([6-méthyl-3,6,9-triaza-1(2,6)-pyridinacyclodécaphane-3,9-diyl-κ^4*N*^{1},*N*^{3},*N*^{6},*N*^{9}]bis{[(4Ξ)-4-(carboxylato-κ*O*)-1-oxobutane-4,1-diyl]azanediyl})bis(1-désoxy-D-glucitol)]manganèse

mangaciclanol — [1,1'-([6-metil-3,6,9-triaza-1(2,6)-piridinaciclodecafano-3,9-diil-κ^4*N*^{1},*N*^{3},*N*^{6},*N*^{9}]bis{[(4Ξ)-4-(carboxilato-κ*O*)-1-oxobutano-4,1-diil]azanodiil})bis(1-desoxi-D-glucitol)]manganeso

$C_{34}H_{56}MnN_6O_{16}$



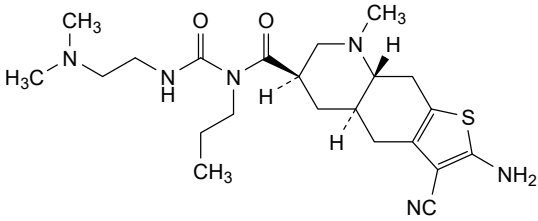
matsupexolum

matsupexole — (4a*R*,6*R*,8a*R*)-2-amino-3-cyano-*N*-{[2-(dimethylamino)ethyl]carbamoyl}-8-methyl-*N*-propyl-4,4a,5,6,7,8,8a,9-octahydrothieno[3,2-*g*]quinoline-6-carboxamide

matsupexole — (4a*R*,6*R*,8a*R*)-2-amino-3-cyano-*N*-{[2-(diméthylamino)éthyl]carbamoyl}-8-méthyl-*N*-propyl-4,4a,5,6,7,8,8a,9-octahydrothiéno[3,2-*g*]quinoléine-6-carboxamide

matsupexol — (4a*R*,6*R*,8a*R*)-2-amino-3-ciano-*N*-{[2-(dimetilamino)etil]carbamoil}-8-metil-*N*-propil-4,4a,5,6,7,8,8a,9-octahidrotieno[3,2-*g*]quinoleína-6-carboxamida

$C_{22}H_{34}N_6O_2S$



micvotabartum #

micvotabart — immunoglobulin G1-kappa, anti-[*Homo sapiens* FN1 (fibronectin 1) extra domain B (ED-B) splice variant], *Homo sapiens* monoclonal antibody; H-gamma1 heavy chain *Homo sapiens* (1-445) [VH (*Homo sapiens* IGHV3-23*01 (93.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.9] (26-33.51-58.97-105)) (1-116) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, CH2 C81 (CH1 R120>K (213) (117-214), hinge 1-15 (215-229), CH2 K81>C (289) (230-339), CH3 E12 (355), M14 (357) (340-444), CHS K2>del (445)) (117-445)], (219-215')-disulfide with L-kappa light chain *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (94.8%) -IGKJ1*01 (100%), CDR-IMGT [7.3.9] (27'-33'.51'-53'.90'-98')) (1'-108') -*Homo sapiens* IGKC*01 (99.1%) K93>C (184'), Km3 A45.1 (154'), V101 (192') (109'-215')]; dimer (225-225":228-228")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa

micvotabart — immunoglobuline G1-kappa, anti-[*Homo sapiens* FN1 (fibronectine 1) extra domaine B (ED-B) variant d'épissage], anticorps monoclonal *Homo sapiens*;
chaîne lourde H-gamma1 *Homo sapiens* (1-445) [VH (*Homo sapiens* IGHV3-23*01 (93.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.9] (26-33.51-58.97-105)) (1-116) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, CH2 C81 (CH1 R120>K (213) (117-214), charnière 1-15 (215-229), CH2 K81>C (289) (230-339), CH3 E12 (355), M14 (357) (340-444), CHS K2>del (445)) (117-445)], (219-215')-disulfure avec la chaîne légère L-kappa *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (94.8%) -IGKJ1*01 (100%), CDR-IMGT [7.3.9] (27'-33'.51'-53'.90'-98')) (1'-108') -*Homo sapiens* IGKC*01 (99.1%) K93>C (184'), Km3 A45.1 (154'), V101 (192') (109'-215')]; dimère (225-225":228-228")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa

micvotabart — inmunoglobulina G1-kappa, anti-[*Homo sapiens* FN1 (fibronectina 1) extra dominio B (ED-B) variante de empalme], anticuerpo monoclonal *Homo sapiens*;
cadena pesada H-gamma1 *Homo sapiens* (1-445) [VH (*Homo sapiens* IGHV3-23*01 (93.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.9] (26-33.51-58.97-105)) (1-116) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, CH2 C81 (CH1 R120>K (213) (117-214), bisagra 1-15 (215-229), CH2 K81>C (289) (230-339), CH3 E12 (355), M14 (357) (340-444), CHS K2>del (445)) (117-445)], (219-215')-disulfuro con la cadena ligera L-kappa *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (94.8%) -IGKJ1*01 (100%), CDR-IMGT [7.3.9] (27'-33'.51'-53'.90'-98')) (1'-108') -*Homo sapiens* IGKC*01 (99.1%) K93>C (184'), Km3 A45.1 (154'), V101 (192') (109'-215')]; dímero (225-225":228-228")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLLESGGG LVQPGGSLRL SCAASGFTFS SFSMSWVRQA PGKGLEWVSS  50
ISGSSGTTYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARPF 100
PYFDYWGQGT LVTVSSASTK GPSVFPLAPS SKSTSGGTAA LGCLVKDYFP 150
EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVVTVPSS SLGTQTYICN 200
VNHKPSNTKV DKKVEPKSCD KTHTCPPCPA PELLGGPSVF LFPPKPKDTL 250
MISRTPEVTC VVVDVSHEDP EVKFNWYVDG VEVHNAKTCP REEQYNSTYR 300
VVSVLTVLHQ DWLNGKEYKC KVSNKALPAP IEKTISKAKG QPREPQVYTL 350
PPSREEMTKN QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD 400
GSFFLYSKLT VDKSRWQQGN VFSCSVMHEA LHNHYTQKSL SLSPG      445
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Light chain / Chaîne légère / Cadena ligera

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EIVLTQSPGT LSLSPGERAT LSCRASQSVS SSFLAWYQQK PGQAPRLLIY  50
YASSRATGIP DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QTGRIPPTFG 100
QGTKVEIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK 150
VDNALQSGNS QESVTEQDSK DSTYSLSSTL TLSCADYEKH KVYACEVTHQ 200
GLSSPVTKSF NRGEC                                       215
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Post-translational modifications

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

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

Conjugation specific sites / Sites spécifiques de conjugaison / Sitios de conjugación específicos

H CH2 K81>C: 289, 289"

L C-KAPPA K93>C: 184', 184'"

micvotabartum pelidotinum

micvotabart pelidotin

immunoglobulin G1-kappa, anti-[*Homo sapiens* FN1 (fibronectin 1) extra domain B (ED-B) splice variant], *Homo sapiens* monoclonal antibody, conjugated through four cysteinyl residues to a derivative of auristatin;
H-gamma1 heavy chain *Homo sapiens* (1-445) [VH (*Homo sapiens* IGHV3-23*01 (93.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.9] (26-33.51-58.97-105)) (1-116) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, G1v81 CH2 C81 (CH1 R120>K(213) (117-214), hinge 1-15 (215-229), CH2 K81>C (230-339), CH3 E12 (355), M14 (357) (340-444), CHS K2>del (445)) (117-445)], (219-215')-disulfide with L-kappa light chain *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (94.8%) -IGKJ1*01 (100%), CDR-IMGT [7.3.9] (27'-33'.51'-53'.90'-98')) (1'-108') -*Homo sapiens* IGKC*01 (99.1%) Km3 A45.1 (154'), V101 (192'), KCv93 K93>C (184') (109'-215')]; dimer (225-225":228-228")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa; substituted at the sulfur atom of L-cysteinyl residues 289, 184', 289" and 184'" with four (2*S*,5*R*,6*R*,7^{2}*S*,10*R*,11*S*,14*S*,25*S*,28*S*,36^{3}*RS*)-2-benzyl-11-[(2*S*)-butan-2-yl]-25-[3-(carbamoylamino)propyl]-6,10-dimethoxy-5,12,17,17-tetramethyl-4,8,13,16,19,24,27,30,36^{2},36^{5}-decaoxo-14,28-di(propan-2-yl)-20-oxa-3,12,15,18,23,26,29-heptaaza-1(2)-[1,3]thiazola-7(2,1),36(1)-dipyrrolidina-22(1,4)-benzenahexatriacontaphan-36^{3}-yl (*pelidotin*) groups

micvotabart pélidotine

immunoglobuline G1-kappa, anti-[*Homo sapiens* FN1 (fibronectine 1) extra domaine B (ED-B) variant d'épissage], anticorps monoclonal *Homo sapiens*, conjugué, par quatre résidus cystéinyle, à un dérivé de l'auristatine;

	chaîne lourde H-gamma1 *Homo sapiens* (1-445) [VH (*Homo sapiens* IGHV3-23*01 (93.9%) -(IGHD) - IGHJ4*01 (100%), CDR-IMGT [8.8.9] (26-33.51-58.97-105)) (1-116) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, G1v81 CH2 C81 (CH1 R120>K (213) (117-214), charnière 1-15 (215-229), CH2 K81>C (230-339), CH3 E12 (355), M14 (357) (340-444), CHS K2>del (445)) (117-445)], (219-215')-disulfure avec la chaîne légère L-kappa *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (94.8%) -IGKJ1*01 (100%), CDR-IMGT [7.3.9] (27'-33'.51'-53'.90'-98')) (1'-108') - *Homo sapiens* IGKC*01 (99.1%) Km3 A45.1 (154'), V101 (192'), KCv93 K93>C (184'), (109'-215')]; dimère (225-225":228-228")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa; substitué sur l'atome de soufre des résidus L-cystéinyle 289, 184', 289" et 184"' avec quatre groupes (2*S*,5*R*,6*R*,7^{2}*S*,10*R*,11*S*,14*S*,25*S*,28*S*,36^{3}*RS*)-2-benzyl-11-[(2*S*)-butan-2-yl]-25-[3-(carbamoylamino)propyl]-6,10-diméthoxy-5,12,17,17-tétraméthyl-4,8,13,16,19,24,27,30,36^{2},36^{5}-décaoxo-14,28-di(propan-2-yl)-20-oxa-3,12,15,18,23,26,29-heptaaza-1(2)-[1,3]thiazola-7(2,1),36(1)-dipyrrolidina-22(1,4)-benzénahexatriacontaphan-36^{3}-yle (*pélidotine*)
micvotabart pelidotina	inmunoglobulina G1-kappa, anti-[*Homo sapiens* FN1 (fibronectina 1) extra dominio B (ED-B) variante de empalme], anticuerpo monoclonal *Homo sapiens*, conjugado, por cuatro residuos cisteinilo, a un derivado de la auristatina; cadena pesada H-gamma1 *Homo sapiens* (1-445) [VH (*Homo sapiens* IGHV3-23*01 (93.9%) -(IGHD) - IGHJ4*01 (100%), CDR-IMGT [8.8.9] (26-33.51-58.97-105)) (1-116) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, G1v81 CH2 C81 (CH1 R120>K (213) (117-214), bisagra 1-15 (215-229), CH2 K81>C (230-339), CH3 E12 (355), M14 (357) (340-444), CHS K2>del (445)) (117-445)], (219-215')-disulfuro con la cadena ligera L-kappa *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (94.8%) -IGKJ1*01 (100%), CDR-IMGT [7.3.9] (27'-33'.51'-53'.90'-98')) (1'-108') - *Homo sapiens* IGKC*01 (99.1%) Km3 A45.1 (154'), V101 (192'), KCv93 K93>C (184'), (109'-215')]; dímero (225-225":228-228")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, forma glicosilada alfa; sustituido en el átomo de azufre de los residuos L-cisteinilo 289, 184', 289" y 184" con cuatro grupos (2*S*,5*R*,6*R*,7^{2}*S*,10*R*,11*S*,14*S*,25*S*,28*S*,36^{3}*RS*)-2-bencil-11-[(2*S*)-butan-2-il]-25-[3-(carbamoilamino)propil]-6,10-dimetoxi-5,12,17,17-tetrametil-4,8,13,16,19,24,27,30,36^{2},36^{5}-decaoxo-14,28-di(propan-2-il)-20-oxa-3,12,15,18,23,26,29-heptaaza-1(2)-[1,3]tiazola-7(2,1),36(1)-dipirrolidina-22(1,4)-bencenahexatriacontafan-36^{3}-ilo (*pelidotina*)

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLLESGGG LVQPGGSLRL SCAASGFTFS SFSMSWVRQA PGKGLEWVSS  50
ISGSSGTTYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARPF 100
PYFDYWGQGT LVTVSSASTK GPSVFPLAPS SKSTSGGTAA LGCLVKDYFP 150
EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVVTVPSS SLGTQTYICN 200
VNHKPSNTKV DKKVEPKSCD KTHTCPPCPA PELLGGPSVF LFPPKPKDTL 250
MISRTPEVTC VVVDVSHEDP EVKFNWYVDG VEVHNAKTCP REEQYNSTYR 300
VVSVLTVLHQ DWLNGKEYKC KVSNKALPAP IEKTISKAKG QPREPQVYTL 350
PPSREEMTKN QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD 400
GSFFLYSKLT VDKSRWQQGN VFSCSVMHEA LHNHYTQKSL SLSPG      445
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Light chain / Chaîne légère / Cadena ligera

```
EIVLTQSPGT LSLSPGERAT LSCRASQSVS SSFLAWYQQK PGQAPRLLIY  50
YASSRATGIP DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QTGRIPPTFG 100
QGTKVEIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK 150
VDNALQSGNS QESVTEQDSK DSTYSLSSTL TLSCADYEKH KVYACEVTHQ 200
GLSSPVTKSF NRGEC                                       215
```

Post-translational modifications

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

Intra-H (C23-C104) 22-96 143-199 260-320 366-424
22"-96" 143"-199" 260"-320" 366"-424"
Intra-L (C23-C104) 23'-89' 135'-195'
23'"-89'" 135'"-195'"
Inter-H-L (h 5-CL 126) 219-215' 219"-215'"
Inter-H-H (h 11, h 14) 225-225" 228-228"

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

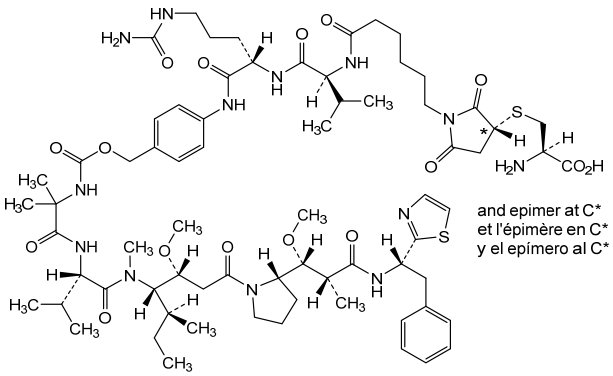
H CH2 N84.4: 296, 296"

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

Specific conjugation sites / Sites spécifiques de conjugaison / Sitios de conjugación específicos

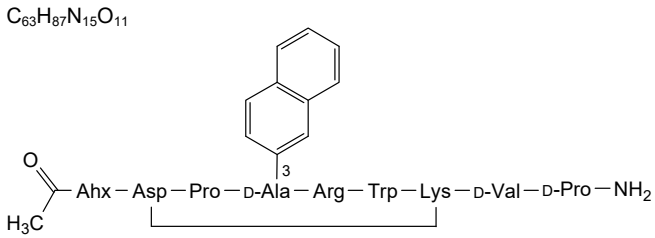
H CH2 K81>C (G1v81): 289, 289"

L C-KAPPA K93>C (KCv93): 184', 184'"



mifomelatidum

mifomelatide	2,*N*$^{6.7}$-anhydro[(2*S*)-2-acetamidohexanoyl-L-α-aspartyl-L-prolyl-3-(naphthalen-2-yl)-D-alanyl-L-arginyl-L-tryptophyl-L-lysyl-D-valyl-D-prolinamide]
mifomélatide	2,*N*$^{6.7}$-anhydro[(2*S*)-2-acétamidohexanoyl-L-α-aspartyl-L-prolyl-3-(naphtalén-2-yl)-D-alanyl-L-arginyl-L-tryptophyl-L-lysyl-D-valyl-D-prolinamide]
mifomelatida	2,*N*$^{6.7}$-anhidro[(2*S*)-2-acetamidohexanoil-L-α-aspartil-L-prolil-3-(naftalen-2-il)-D-alanil-L-arginil-L-triptofil-L-lisil-D-valil-D-prolinamida]



Ahx = (2*S*)-2-aminohexanoic acid

mipletamigum #

mipletamig

immunoglobulin IG chain scFvkh-G1hCH2CH3-scFvhk dimer bisdisulfide, anti-[*Homo sapiens* IL3RA (interleukin 3 receptor subunit alpha, interleukin 3 receptor alpha (low affinity), CD123)] and anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], *Homo sapiens* and humanized monoclonal antibody, bispecific, tetravalent;
IG chain scFvkh-G1hCH2CH3-scFvhk *Homo sapiens* and humanized (1-757) [scFvkh anti-IL3RA *Homo sapiens* (1-259) [V-KAPPA (*Homo sapiens* IGKV4-1*01 (99.0%) -IGKJ4*01 (100%), CDR-IMGT [12.3.10] (27-38.56-58.95-104)) (1-114) -20-mer tetrakis(tetraglycyl-seryl) linker (115-134) -VH (*Homo sapiens* IGHV3-23*01 (98.0%) -(IGHD) -IGHJ3*02 (100%), CDR-IMGT [8.8.17] (160-167.185-192.231-247)) (135-259)] -*Homo sapiens* IGHG1*01, G1m17,1CH3 D12, L14, G1v14-1 CH2 A1.3, A1.2, A1, G1v20 A105, G1v37 h S5 (hinge 1-15 C5>S (264) (260-274), CH2 L1.3>A (278), L1.2>A (279), G1>A (281), K105>A (366) (275-384), CH3 D12 (400), L14 (402) (385-489), CHS K2>del (490)) (260-490)] -18-mer (seryl-tris(glycyl-seryl)-prolyl-seryl) linker (491-508) -scFvhk anti-CD3E humanized (509-757) [VH (*Homo sapiens* IGHV1-69*02 (82.7%) -IGHD -IGHJ4*01 (92.9%), CDR-IMGT [8.8.14] (534-541.559-566.605-618)) (509-629) -20-mer tetrakis(tetraglycyl-seryl) linker (630-649) -V-KAPPA (*Homo sapiens* IGKV1-5*01 (81.5%) -IGKJ4*01 (100%), CDR-IMGT [5.3.9] (676-680.698-700.737-745)) (650-757)]]; dimer (270-270':273-273')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa

miplétamig

immunoglobuline IG chaîne scFvkh-G1hCH2CH3-scFvhk dimère bisdisulfure, anti-[*Homo sapiens* IL3RA (sous-unité alpha du récepteur de l'interleukine 3, récepteur alpha (faible affinité) de l'interleukine 3, CD123)] et anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], anticorps monoclonal *Homo sapiens* et humanisé, bispécifique, tétravalent;
IG chaîne scFvkh-G1hCH2CH3-scFvhk *Homo sapiens* et humanisée (1-757) [scFvkh anti-IL3RA *Homo sapiens* (1-259) [V-KAPPA(*Homo sapiens* IGKV4-1*01 (99.0%) -IGKJ4*01 (100%), CDR-IMGT [12.3.10] (27-38.56-58.95-104)) (1-114) -20-mer tétrakis(tétraglycyl-séryl) linker (115-134) -VH (*Homo sapiens* IGHV3-23*01 (98.0%) -(IGHD) -IGHJ3*02 (100%), CDR-IMGT [8.8.17] (160-167.185-192.231-247)) (135-259)] -*Homo sapiens* IGHG1*01, G1m17,1CH3 D12, L14, G1v14-1 CH2 A1.3, A1.2, A1, G1v20 A105, G1v37 h S5 (charnière 1-15 C5>S (264) (260-274), CH2 L1.3>A (278), L1.2>A (279), G1>A (281), K105>A (366) (275-384), CH3 D12 (400), L14 (402) (385-489), CHS K2>del (490)) (260-490)] -18-mer (séryl-tris(glycyl-séryl)-prolyl-séryl) linker (491-508) -scFvhk anti-CD3E humanisé (509-757) [VH (*Homo sapiens* IGHV1-69*02 (82.7%) -IGHD -IGHJ4*01 (92.9%), CDR-IMGT [8.8.14] (534-541.559-566.605-618)) (509-629) -20-mer tétrakis(tétraglycyl-séryl) linker (630-649) -V-KAPPA (*Homo sapiens* IGKV1-5*01 (81.5%) -IGKJ4*01 (100%), CDR-IMGT [5.3.9] (676-680.698-700.737-745)) (650-757)]]; dimère (270-270':273-273')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa

mipletamig

inmunoglobulina IG cadena scFvkh-G1hCH2CH3-scFvhk dímero bisdisulfuro, anti-[*Homo sapiens* IL3RA (subunidade alfa del receptor de la interleukina 3, receptor alfa (baja afinidad) de la interleukina 3, CD123)] y anti-[*Homo sapiens* CD3E (CD3 épsilon, Leu-4)], anticuerpo monoclonal *Homo sapiens* y humanizado, biespecífico, tetravalente;
IG cadena scFvkh-G1hCH2CH3-scFvhk *Homo sapiens* y humanizada (1-757) [scFvkh anti-IL3RA *Homo sapiens* (1-259) [V-KAPPA(*Homo sapiens* IGKV4-1*01 (99.0%) -IGKJ4*01 (100%), CDR-IMGT [12.3.10] (27-38.56-58.95-104)) (1-114) -20-mer tetrakis(tetraglicil-seril) enlace (115-134) -VH (*Homo sapiens* IGHV3-23*01 (98.0%) -(IGHD) -IGHJ3*02 (100%), CDR-IMGT [8.8.17] (160-167.185-192.231-247)) (135-259)] -*Homo sapiens* IGHG1*01, G1m17,1CH3 D12, L14, G1v14-1 CH2 A1.3, A1.2, A1, G1v20 A105, G1v37 h S5 (bisagra 1-15 C5>S (264) (260-274), CH2 L1.3>A (278), L1.2>A (279), G1>A (281), K105>A (366) (275-384), CH3 D12 (400), L14 (402) (385-489), CHS K2>del (490)) (260-490)] -18-mer (seril-tris(glicil-seril)-prolil-seril) enlace (491-508) -scFvhk anti-CD3E humanizado (509-757) [VH (*Homo sapiens* IGHV1-69*02 (82.7%) -IGHD -IGHJ4*01 (92.9%), CDR-IMGT [8.8.14] (534-541.559-566.605-618)) (509-629) -20-mer tetrakis(tetraglicil-seril) enlace (630-649) -V-KAPPA (*Homo sapiens* IGKV1-5*01 (81.5%) -IGKJ4*01 (100%), CDR-IMGT [5.3.9] (676-680.698-700.737-745)) (650-757)]]; dímero (270-270':273-273')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, forma glicosilada alfa

Chain / Chaîne / Cadena : scFvkh (anti-IL3RA) -G1hCH2CH3 -scFvhk (anti-CD3E)

```
DIVMTQSPDS LAVSLGERAT INCKSSHSVL YSSNNKNYLA WYQQKPGQPP  50
KLLIYWASTR ESGVPDRFSG SGSGTDFTLT ISSLQAEDVA VYYCQQYYST 100
PPTTFGGGTK VEIKGGGGSG GGGSGGGGSG GGGSEVQLLE SGGGLVQPGG 150
SLRLSCAASG FTFSSYGMSW VRQAPGKGLE GVSAISGSGG STYYADSVKG 200
RFTISRDNSK NTLYLQMNSL RAEDTAVYYC AKEKLRYFDW LSDAFDIWGQ 250
GTMVTVSSSE PKSSDKTHTC PPCPAPEAAG APSVFLFPPK PKDTLMISRT 300
PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY NSTYRVVSVL 350
TVLHQDWLNG KEYKCAVSNK ALPAPIEKTI SKAKGQPREP QVYTLPPSRD 400
ELTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP VLDSDGSFFL 450
YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG SGGGGSGGGG 500
SGGGGSPSQV QLVQSGPEVK KPGSSVKVSC KASGYTFSRS TMHWVRQAPG 550
QGLEWIGYIN PSSAYTNYNQ KFKDRVTITA DKSTSTAYME LSSLRSEDTA 600
VYYCARPQVH YDYNGFPYWG QGTLVTVSSG GGGSGGGGSG GGGSGGGGSD 650
IQMTQSPSTL SASVGDRVTM TCSASSSVSY MNWYQQKPGK APKRWIYDSS 700
KLASGVPSRF SGSGSGTDYT LTISSLQPDD FATYYCQQWS RNPPTFGGGT 750
KVEIKRS                                               757
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Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 23-94 156-230 305-365 411-469
23'-94' 156'-230' 305'-365' 411'-469'
530-604 672-736
530'-604' 672'-736'
Inter-H-H (h 11, h 14) 270-270' 273-273'

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4: 341, 341"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

misitatugum #

misitatug

immunoglobulin G1-kappa, anti-[*Homo sapiens* MSLN (mesothelin, pre-pro-megakaryocyte-potentiating factor, megakaryocyte-potentiating factor, MPF, CAK1)];

	H-gamma1 heavy chain (1-454) [VH Musmus/Homsap (*Mus musculus* IGHV4-1*02 (91.8%) -(IGHD) -IGHJ1*01 (100%)/*Homo sapiens* IGHV3-74*03 (80.6%) -(IGHD) -IGHJ3*01 (85.7%) Q120>A (116), M123>T (119), CDR-IMGT [8.8.17] (26-33.51-58.97-113)) (1-124) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (221) (125-222), hinge 1-15 (223-237), CH2 (238-347), CH3 E12 (363), M14 (365) (348-452), CHS (453-454)) (125-454)], (227-213')-disulfide with L-kappa light chain (1'-213') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV4-55*01 (84.0%) -IGKJ1*01 (90.9%) L124>V (103)/*Homo sapiens* IGKV6-21*02 (68.4%) -IGKJ4*01 (100%), CDR-IMGT [5.3.9] (27'-31'.49'-51'.88'-96')) (1'-106') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (152'), V101 (190') (107'-213')]; dimer (233-233":236-236")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa
misitatug	immunoglobuline G1-kappa, anti-[*Homo sapiens* MSLN (mésothéline, facteur de potentialisation du pré-pro-mégacaryocyte, facteur de potentialisation des mégacaryocytes, MPF, CAK1)]; chaîne lourde H-gamma1 (1-454) [VH Musmus/Homsap (*Mus musculus* IGHV4-1*02 (91.8%) -(IGHD) -IGHJ1*01 (100%)/*Homo sapiens* IGHV3-74*03 (80.6%) -(IGHD) -IGHJ3*01 (85.7%) Q120>A (116), M123>T (119), CDR-IMGT [8.8.17] (26-33.51-58.97-113)) (1-124) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (221) (125-222), charnière 1-15 (223-237), CH2 (238-347), CH3 E12 (363), M14 (365) (348-452), CHS (453-454)) (125-454)], (227-213')-disulfure avec la chaîne légère L-kappa (1'-213') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV4-55*01 (84.0%) -IGKJ1*01 (90.9%) L124>V (103)/*Homo sapiens* IGKV6-21*02 (68.4%) -IGKJ4*01 (100%), CDR-IMGT [5.3.9] (27'-31'.49'-51'.88'-96')) (1'-106') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (152'), V101 (190') (107'-213')]; dimère (233-233":236-236")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa
misitatug	inmunoglobulina G1-kappa, anti-[*Homo sapiens* MSLN (mesotelina, factor de potenciación del pre-pro-megacariocito, factor de potenciación de los megacariocitos, MPF, CAK1)]; cadena pesada H-gamma1 (1-454) [VH Musmus/Homsap (*Mus musculus* IGHV4-1*02 (91.8%) -(IGHD) -IGHJ1*01 (100%)/*Homo sapiens* IGHV3-74*03 (80.6%) -(IGHD) -IGHJ3*01 (85.7%) Q120>A (116), M123>T (119), CDR-IMGT [8.8.17] (26-33.51-58.97-113)) (1-124) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (221) (125-222), bisagra 1-15 (223-237), CH2 (238-347), CH3 E12 (363), M14 (365) (348-452), CHS (453-454)) (125-454)], (227-213')-disulfuro con la cadena ligera L-kappa (1'-213') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV4-55*01 (84.0%) -IGKJ1*01 (90.9%) L124>V (103)/*Homo sapiens* IGKV6-21*02 (68.4%) -IGKJ4*01 (100%), CDR-IMGT [5.3.9] (27'-31'.49'-51'.88'-96')) (1'-106') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (152'), V101 (190') (107'-213')]; dímero (233-233":236-236")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

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EVQLVESGGG LVQPGGSLRL SCAASGFDFS RYWMSWVRQA PGKGLEWIGE  50
INPDSSTIVY TPSLKDKFII SRDNAKNTLY LQMNSLRAED TALYYCARRG 100
SHYYGYRTGY FDVWGAGTTV 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 SREEMTKNQV SLTCLVKGFY PSDIAVEWES NGQPENNYKT 400
TPPVLDSDGS FFLYSKLTVD KSRWQQGNVF SCSVMHEALH NHYTQKSLSL 450
SPGK                                                    454
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Light chain / Chaîne légère / Cadena ligera

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DVVMTQSPAF LSVTPGEKVT MTCSASSSVS YMYWHQQKPD QAPKLLIYDT  50
SNLASGVPVR FSGSGSGTDF TFTISRMEAE DAATYYCQQW SSYPPTFGGG 100
TKVEIKRTVA APSVFIFPPS DEQLKSGTAS VVCLLNNFYP REAKVQWKVD 150
NALQSGNSQE SVTEQDSKDS TYSLSSTLTL SKADYEKHKV YACEVTHQGL 200
SSPVTKSFNR GEC                                          213
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Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 151-207 268-328 374-432
22"-96" 151"-207" 268"-328" 374"-432"
Intra-L (C23-C104) 23'-87' 133'-193'
23'"-87'" 133'"-193'"
Inter-H-L (h 5-CL 126) 227-213' 227"-213'"
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"

misitatugum blivedotinum

misitatug blivedotin — immunoglobulin G1-kappa, anti-[*Homo sapiens* MSLN (mesothelin, pre-pro-megakaryocyte-potentiating factor, megakaryocyte-potentiating factor, MPF, CAK1)]; conjugated on an average of 4 cysteinyl residues to monomethylauristatin E (MMAE), with a ratio of 1 to 2, via a cleavable divalent linker*;*
H-gamma1 heavy chain (1-454) [VH Musmus/Homsap (*Mus musculus* IGHV4-1*02 (91.8%) -(IGHD) -IGHJ1*01 (100%)/*Homo sapiens* IGHV3-74*03 (80.6%) Q120>A (116), M123>T (119) -(IGHD) -IGHJ3*01 (85.7%), CDR-IMGT [8.8.17] (26-33.51-58.97-113)) (1-124) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (221) (125-222), hinge 1-15 (223-237), CH2 (238-347), CH3 E12 (363), M14 (365) (348-452), CHS (453-454)) (125-454)], (227-213')-disulfide with L-kappa light chain (1'-213') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV4-55*01 (84.0%) -IGKJ1*01 (90.9%) L124>V (103)/*Homo sapiens* IGKV6-21*02 (68.4%) -IGKJ4*01 (100%), CDR-IMGT [5.3.9] (27'-31'.49'-51'.88'-96')) (1'-106') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (152'), V101 (190') (107'-213')]; dimer (233-233":236-236")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa; substituted at the sulfur atoms of four L-cysteinyl residues on an average among 227, 233, 236, 213', 227", 233", 236" and 213'" with two divalent radical groups consisting of 3,3'-[(2*S*,3*R*,6*R*,7*R*,8^{2}*S*,11*R*,12*S*,15*S*,18*S*,26*S*,29*S*)-12-[(2*S*)-butan-2-yl]-26-[3-(carbamoylamino)propyl]-2-hydroxy-7,11-dimethoxy-3,6,13,19-tetramethyl-5,9,14,17,20,25,28,31,36-nonaoxo-15,18,29-tri(propan-2-yl)-21-oxa-33-thia-4,13,16,19,24,27,30-heptaaza-37(1)-[1,3,5]triazinana-8(2,1)-pyrrolidina-1(1),23(1,4)-dibenzenaheptatriacontaphane-37^{3},37^{5}-diyl]bis(3-oxopropyl) (*blivedotin*)

misitatug blivédotine — immunoglobuline G1-kappa, anti-[*Homo sapiens* MSLN (mésothéline, facteur de potentialisation du pré-pro-mégacaryocyte, facteur de potentialisation des mégacaryocytes, MPF, CAK1)]; conjugué, par 4 résidus cystéinyle en moyenne, au monométhylauristatine E (MMAE), via un linker clivable divalent avec un rapport de 1 pour 2;

	chaîne lourde H-gamma1 (1-454) [VH Musmus/Homsap (*Mus musculus* IGHV4-1*02 (91.8%) -(IGHD) -IGHJ1*01 (100%)/*Homo sapiens* IGHV3-74*03 (80.6%) Q120>A (116), M123>T (119) -(IGHD) -IGHJ3*01 (85.7%), CDR-IMGT [8.8.17] (26-33.51-58.97-113)) (1-124) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (221) (125-222), charnière 1-15 (223-237), CH2 (238-347), CH3 E12 (363), M14 (365) (348-452), CHS (453-454)) (125-454)], (227-213')-disulfure avec la chaîne légère L-kappa (1'-213') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV4-55*01 (84.0%) -IGKJ1*01 (90.9%) L124>V (103)/*Homo sapiens* IGKV6-21*02 (68.4%) -IGKJ4*01 (100%), CDR-IMGT [5.3.9] (27'-31'.49'-51'.88'-96')) (1'-106') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (152'), V101 (190') (107'-213')]; dimère (233-233'':236-236'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa; substitué sur l'atome de soufre de 4 résidus L-cystéinyle en moyenne parmi 227, 233, 236, 213', 227'', 233'', 236'' et 213''' avec deux groupements radicaux divalents 3,3'-[(2*S*,3*R*,6*R*,7*R*,8^{2}*S*,11*R*,12*S*,15*S*,18*S*,26*S*,29*S*)-12-[(2*S*)-butan-2-yl]-26-[3-(carbamoylamino)propyl]-2-hydroxy-7,11-diméthoxy-3,6,13,19-tétraméthyl-5,9,14,17,20,25,28,31,36-nonaoxo-15,18,29-tri(propan-2-yl)-21-oxa-33-thia-4,13,16,19,24,27,30-heptaaza-37(1)-[1,3,5]triazinana-8(2,1)-pyrrolidina-1(1),23(1,4)-dibenzénaheptatriacontaphane-37^{3},37^{5}-diyl]bis(3-oxopropyle) (*blivédotine*)
misitatug blivedotina	inmunoglobulina G1-kappa, anti-[*Homo sapiens* MSLN (mesotelina, factor de potenciación del pre-pro-megacariocito, factor de potenciación de los megacariocitos, MPF, CAK1)]; conjugado, por 4 residuos de cisteinilo en promedio, a la monometilauristatina E (MMAE), mediante un conector escindible divalente con una proporción de 1 a 2; cadena pesada H-gamma1 (1-454) [VH Musmus/Homsap (*Mus musculus* IGHV4-1*02 (91.8%) -(IGHD) -IGHJ1*01 (100%)/*Homo sapiens* IGHV3-74*03 (80.6%) Q120>A (116), M123>T (119) -(IGHD) -IGHJ3*01 (85.7%), CDR-IMGT [8.8.17] (26-33.51-58.97-113)) (1-124) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (221) (125-222), bisagra 1-15 (223-237), CH2 (238-347), CH3 E12 (363), M14 (365) (348-452), CHS (453-454)) (125-454)], (227-213')-disulfuro con la cadena ligera L-kappa (1'-213') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV4-55*01 (84.0%) -IGKJ1*01 (90.9%) L124>V (103)/*Homo sapiens* IGKV6-21*02 (68.4%) -IGKJ4*01 (100%), CDR-IMGT [5.3.9] (27'-31'.49'-51'.88'-96')) (1'-106') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (152'), V101 (190') (107'-213')]; dímero (233-233'':236-236'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa; sustituido en el átomo de azufre de 4 residuos de L-cisteinilo en promedio de 227, 233, 236, 213', 227'', 233'', 236'' y 213''' con dos grupos radicales divalentes 3,3'-[(2*S*,3*R*,6*R*,7*R*,8^{2}*S*,11*R*,12*S*,15*S*,18*S*,26*S*,29*S*)-12-[(2*S*)-butan-2-il]-26-[3-(carbamoilamino)propil]-2-hidroxi-7,11-dimetoxi-3,6,13,19-tetrametil-5,9,14,17,20,25,28,31,36-nonaoxo-15,18,29-tri(propan-2-il)-21-oxa-33-tia-4,13,16,19,24,27,30-heptaaza-37(1)-[1,3,5]triazinana-8(2,1)-pirrolidina-1(1),23(1,4)-dibencenaheptatriacontafano-37^{3},37^{5}-diil]bis(3-oxopropilo) (*blivedotina*)

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAASGFDFS RYWMSWVRQA PGKGLEWIGE  50
INPDSSTIVY TPSLKDKFII SRDNAKNTLY LQMNSLRAED TALYYCARRG 100
SHYYGYRTGY FDVWGAGTTV 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 SREEMTKNQV SLTCLVKGFY PSDIAVEWES NGQPENNYKT 400
TPPVLDSDGS FFLYSKLTVD KSRWQQGNVF SCSVMHEALH NHYTQKSLSL 450
SPGK                                                    454
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Light chain / Chaîne légère / Cadena ligera

```
DVVMTQSPAF LSVTPGEKVT MTCSASSSVS YMYWHQQKPD QAPKLLIYDT  50
SNLASGVPVR FSGSGSGTDF TFTISRMEAE DAATYYCQQW SSYPPTFGGG 100
TKVEIKRTVA APSVFIFPPS DEQLKSGTAS VVCLLNNFYP REAKVQWKVD 150
NALQSGNSQE SVTEQDSKDS TYSLSSTLTL SKADYEKHKV YACEVTHQGL 200
SSPVTKSFNR GEC                                         213
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Post-translational modifications

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

Intra-H (C23-C104) 22-96 151-207 268-328 374-432
22"-96" 151"-207" 268"-328" 374"-432"

Intra-L (C23-C104) 23'-87' 133'-193'
23'"-87'" 133'"-193'"

Inter-H-L (h 5-CL 126) * 227-213' 227"-213'"

Inter-H-H (h 11, h 14) * 233-233" 236-236"

*At least two of the four inter-chain disulfide bridges are not present, an average of 4 cysteinyl being conjugated each via a thioether bond to a drug linker.

*Au moins deux des quatre ponts disulfures inter-chaînes ne sont pas présents, 4 cystéinyl en moyenne étant chacun conjugué via une liaison thioéther à un linker-principe actif.

*Al menos dos de los cuatro puentes disulfuro inter-catenarios no estan presentes, una media de 4 cisteinil está conjugada a conectores de principio activo.

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

H CH2 N84.4: 304, 304"

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

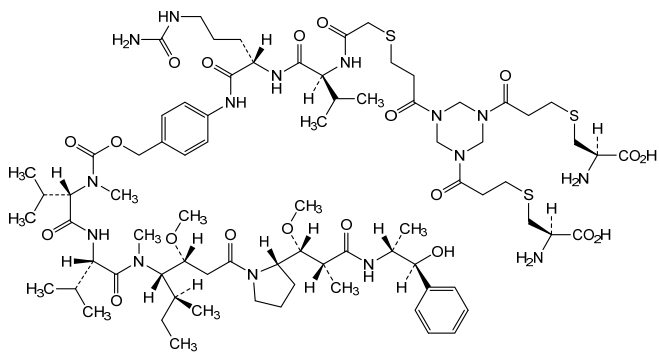
C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal

H CHS K2: 454, 454"

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

C (227,233,236,213',227",233",236",213'")

*(blivedotin:mAb ~ 2:1)



mozistobartum #

mozistobart

immunoglobulin G1-kappa, anti-[*Homo sapiens* CD22 (sialic acid binding Ig-like lectin 2, SIGLEC2, SIGLEC-2, B-lymphocyte cell adhesion molecule, BL-CAM, Leu-14)], humanized monoclonal antibody;

H-gamma1 heavy chain humanized (1-460) [VH (*Homo sapiens* IGHV3-48*03 (89.8%) -(IGHD) -IGHJ4*01 (85.7%) Q120>R (115), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, G1v14-1 CH2 A1.3, A1.2, A1 (CH1 R120>K (220) (124-221), hinge 1-15 (222-236), CH2 L1.3>A (240), L1.2>A (241), G1>A (243) (237-346), CH3 E12 (362), M14 (364) (347-451), CHS K2>del (452),

	fused 8-mer RPQGFGPP (453-460)) (124-460)], (226-214')-disulfide with L-kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (87.4%) -IGKJ2*02 (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 Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, glycoform alfa
mozistobart	immunoglobuline G1-kappa, anti-[*Homo sapiens* CD22 (Ig-like lectine 2 liant l'acide sialique, SIGLEC2, SIGLEC-2, molécule d'adhésion cellulaire du lymphocyte B, BL-CAM, Leu-14)], anticorps monoclonal humanisé; chaîne lourde H-gamma1 humanisée (1-460) [VH (*Homo sapiens* IGHV3-48*03 (89.8%) -(IGHD) -IGHJ4*01 (85.7%) Q120>R (115), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, G1v14-1 CH2 A1.3, A1.2, A1 (CH1 R120>K (220) (124-221), charnière 1-15 (222-236), CH2 L1.3>A (240), L1.2>A (241), G1>A (243) (237-346), CH3 E12 (362), M14 (364) (347-451), CHS K2>del (452), 8-mer fusionné RPQGFGPP (453-460)) (124-460)], (226-214')-disulfure avec la chaîne légère L-kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (87.4%) -IGKJ2*02 (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), dérivant de la lignée cellulaire CHO-K1, glycoforme alfa
mozistobart	inmunoglobulina G1-kappa, anti-[*Homo sapiens* CD22 (Ig-like lectina 2 que se une al ácido siálico, SIGLEC2, SIGLEC-2, molécula de adhesión celular del linfocito B, BL-CAM, Leu-14)], anticuerpo monoclonal humanizado; cadena pesada H-gamma1 humanizada (1-460) [VH (*Homo sapiens* IGHV3-48*03 (89.8%) -(IGHD) -IGHJ4*01 (85.7%) Q120>R (115), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, G1v14-1 CH2 A1.3, A1.2, A1 (CH1 R120>K (220) (124-221), bisagra 1-15 (222-236), CH2 L1.3>A (240), L1.2>A (241), G1>A (243) (237-346), CH3 E12 (362), M14 (364) (347-451), CHS K2>del (452), 8-mer fusionada RPQGFGPP (453-460)) (124-460)], (226-214')-disulfuro con la cadena ligera L-kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (87.4%) -IGKJ2*02 (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 derivada de CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLLESGGG VVQPGGSLRL SCAASGFAFS IYDMNWVRQA PGKGLEWVSA  50
ISSGGGTTYY ADSVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARHS 100
GYGTHWGVLF AYWGRGTLVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC 150
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG 200
TQTYICNVNH KPSNTKVDKK VEPKSCDKTH TCPPCPAPEA AGAPSVFLFP 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
PGRPQGFGPP                                              460
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Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCRASQDIH GYLNWYQQKP GKAPKLLIYY  50
TSILHSGVPS RFSGSGSGTD FTLTISSLQP EDFATYFCQQ GSTLPWTFGQ 100
GTKLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Post-translational modifications

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

Intra-H (C23-C104) 22-96 150-206 267-327 373-431
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 / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)
H 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

mozistobartum zoratolimodum

mozistobart zoratolimod

immunoglobulin G1-kappa, anti-[*Homo sapiens* CD22 (sialic acid binding Ig-like lectin 2, SIGLEC2, SIGLEC-2, B-lymphocyte cell adhesion molecule, BL-CAM, Leu-14)], humanized monoclonal antibody; conjugated at one glutamine residue with *zoratolimod*; H-gamma1 heavy chain humanized (1-460) [VH (*Homo sapiens* IGHV3-48*03 (89.8%) -(IGHD) -IGHJ4*01 (85.7%) Q120>R (115), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, G1v14-1 CH2 A1.3, A1.2, A1 (CH1 R120>K (220) (124-221), hinge 1-15 (222-236), CH2 L1.3>A (240), L1.2>A (241), G1>A (243) (237-346), CH3 E12 (362), M14 (364) (347-451), CHS K2>del (452), fused 8-mer RPQGFGPP (453-460)) (124-460)], (226-214')-disulfide with L-kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (87.4%) -IGKJ2*02 (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 Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, glycoform alfa; substituted at N^6 of L-glutamine residue 255 with radical group (1*RS*)-1-{[*all-P-ambo*-5-bromo-2'-deoxy-*P*-thiouridylyl-(3'→5')-2'-deoxy-*P*-thiocytidylyl-(3'→5')-2'-deoxy-*P*-thioguanylyl-(3'→5')-3'-deoxythymidin-3'-yl]oxy}-1-{[*all-P-ambo*-3'-*O*-[hydroxy(3-hydroxypropyl)phosphorothioyl]-5,2'-*O*-dimethyl-*P*-thiouridylyl-(5'→3')-5,2'-*O*-dimethyl-*P*-thiouridylyl-(5'→3')-*P*-thiothymidylyl-(5'→3')-2'-deoxy-*P*-thioguanylyl-(5'→3')-2'-deoxy-*P*-dithiocytidylyl-(5'→3')-*P*-thiothymidylyl-(5'→3')-2'-deoxy-*P*-thioguanylyl-(5'→3')-*P*-thiothymidylyl-(5'→3')-2'-deoxy-*P*-thioguanylyl-(5'→3')-2',3'-dideoxycytidin-3'-yl]oxy}phosphorothioyl]oxy}-12-oxo-1-sulfanylidene-2,5,8,15,18,21,24,27,30,33,36,39,42,45,48,51,54,57,60,63,66,69,72,75,78,81,84-heptacosaoxa-11-aza-1-phosphahexaoctacontan-86-yl (*zoratolimod*)

mozistobart zoratolimod

immunoglobuline G1-kappa, anti-[*Homo sapiens* CD22 (Ig-like lectine 2 liant l'acide sialique, SIGLEC2, SIGLEC-2, molécule d'adhésion cellulaire du lymphocyte B, BL-CAM, Leu-14)], anticorps monoclonal humanisé; conjugué sur une glutamine *au zoratolimod*;
chaîne lourde H-gamma1 humanisée (1-460) [VH (*Homo sapiens* IGHV3-48*03 (89.8%) -(IGHD) -IGHJ4*01 (85.7%) Q120>R (115), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, G1v14-1 CH2 A1.3, A1.2, A1 (CH1 R120>K (220) (124-221), charnière 1-15 (222-236), CH2 L1.3>A (240), L1.2>A (241), G1>A (243) (237-346), CH3 E12 (362), M14 (364) (347-451), CHS K2>dél (452), 8-mer fusionné RPQGFGPP (453-460)) (124-460)], (226-214')-disulfure avec la chaîne légère L-kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (87.4%) -IGKJ2*02 (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), dérivant de la lignée cellulaire CHO-K1, glycoforme alfa; substitué en N^5 du résidu L-glutamine 255 par un groupe radical (1*RS*)-1-{[*tout*-*P*-*ambo*-5-bromo-2'-désoxy-*P*-thiouridylyl-(3'→5')-2'-désoxy-*P*-thiocytidylyl-(3'→5')-2'-désoxy-*P*-thioguanylyl-(3'→5')-3'-désoxythymidin-3'-yl]oxy}-1-{[*tout*-*P*-*ambo*-3'-*O*-[hydroxy(3-hydroxypropyl)phosphorothioyl]-5,2'-*O*-diméthyl-*P*-thiouridylyl-(5'→3')-5,2'-*O*-diméthyl-*P*-thiouridylyl-(5'→3')-*P*-thiothymidylyl-(5'→3')-2'-désoxy-*P*-thioguanylyl-(5'→3')-2'-désoxy-*P*-dithiocytidylyl-(5'→3')-*P*-thiothymidylyl-(5'→3')-2'-désoxy-*P*-thioguanylyl-(5'→3')-*P*-thiothymidylyl-(5'→3')-2'-désoxy-*P*-thioguanylyl-(5'→3')-2',3'-didésoxycytidin-3'-yl]oxy}-12-oxo-1-sulfanylidène-2,5,8,15,18,21,24,27,30,33,36,39,42,45,48,51,54,57,60,63,66,69,72,75,78,81,84-heptacosaoxa-11-aza-1-phosphahexaoctacontan-86-yle (*zoratolimod*)

mozistobart zoratolimod

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CD22 (Ig-like lectina 2 de unión al ácido siálico, SIGLEC2, SIGLEC-2, molécula de adhesión celular del infocito B, BL-CAM, Leu-14)], anticuerpo monoclonal humanizado; conjugado por un único residuo de glutamina con el *zoratolimod*;
cadena pesada H-gamma1 humanizada (1-460) [VH (*Homo sapiens* IGHV3-48*03 (89.8%) -(IGHD) -IGHJ4*01 (85.7%) Q120>R (115), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, G1v14-1 CH2 A1.3, A1.2, A1 (CH1 R120>K (220) (124-221), bisagra 1-15 (222-236), CH2 L1.3>A (240), L1.2>A (241), G1>A (243) (237-346), CH3 E12 (362), M14 (364) (347-451), CHS K2>del (452), 8-mer fusionada RPQGFGPP (453-460)) (124-460)], (226-214')-disulfuro con la cadena ligera L-kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (87.4%) -IGKJ2*02 (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 derivada de CHO-K1, forma glicosilada alfa; sustituido en N^5 del residuo L-glutamina 255 por un grupo radical (1*RS*)-1-{[*todo*-*P*-*ambo*-5-bromo-2'-desoxi-*P*-tiouridilil-(3'→5')-2'-desoxi-*P*-tiocitidilil-(3'→5')-2'-desoxi-*P*-tioguanilil-(3'→5')-3'-desoxitimidin-3'-il]oxi}-1-{[*todo*-*P*-*ambo*-3'-*O*-[hidroxi(3-hidroxipropil)fosforotioil]-5,2'-*O*-dimetil-*P*-tiouridilil-(5'→3')- 5,2'-*O*-dimetil-*P*-tiouridilil-(5'→3')-*P*-tiotimidilil-(5'→3')-2'-desoxi-*P*-tioguanilil-(5'→3')-2'-desoxi-*P*-ditiocitidilil-(5'→3')-*P*-tiotimidilil-(5'→3')-2'-desoxi-*P*-tioguanilil-(5'→3')-*P*-tiotimidilil-(5'→3')-2'-desoxi-*P*-tioguanilil-(5'→3')-2',3'-didesoxicitidin-3'-il]oxi}-12-oxo-1-sulfanilideno-2,5,8,15,18,21,24,27,30,33,36,39,42,45,48,51,54,57,60,63,66,69,72,75,78,81,84-heptacosaoxa-11-aza-1-fosfahexaoctacontan-86-ilo (*zoratolimod*)

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLLESGGG VVQPGGSLRL SCAASGFAFS IYDMNWVRQA PGKGLEWVSA  50
ISSGGGTTYY ADSVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARHS 100
GYGTHWGVLF AYWGRGTLVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC 150
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG 200
TQTYICNVNH KPSNTKVDKK VEPKSCDKTH TCPPCPAPEA AGAPSVFLFP 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
PGRPQGFGPP                                              460
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Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCRASQDIH GYLNWYQQKP GKAPKLLIYY  50
TSILHSGVPS RFSGSGSGTD FTLTISSLQP EDFATYFCQQ GSTLPWTFGQ 100
GTKLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Post-translational modifications

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

Intra-H (C23-C104) 22-96 150-206 267-327 373-431
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 / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal

Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)

H VH Q1: 1, 1"

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

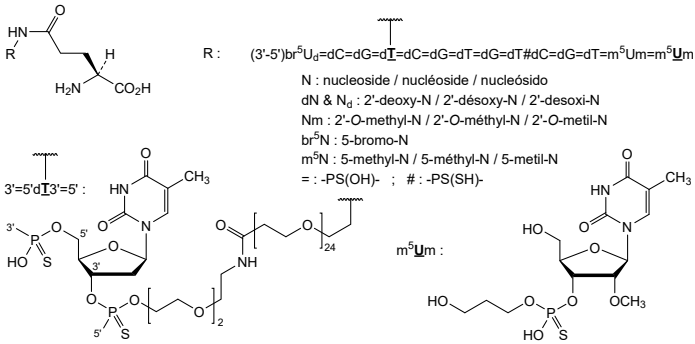
H CH2 N84.4: 303, 303"

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

Modified residue / résidu modifié / restos modificados*

Q (455)

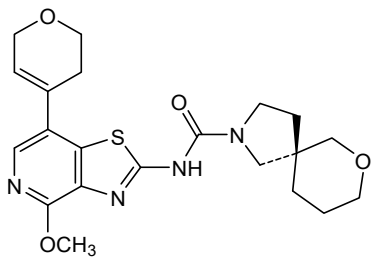
*(zoratolimod:mAb ~ 1:1)



muvadenantum

muvadenant	(5*S*)-*N*-[7-(3,6-dihydro-2*H*-pyran-4-yl)-4-methoxy[1,3]thiazolo[4,5-*c*]pyridin-2-yl]-7-oxa-2-azaspiro[4.5]decane-2-carboxamide
muvadénant	(5*S*)-*N*-[7-(3,6-dihydro-2*H*-pyran-4-yl)-4-méthoxy[1,3]thiazolo[4,5-*c*]pyridin-2-yl]-7-oxa-2-azaspiro[4.5]décane-2-carboxamide
muvadenant	(5*S*)-*N*-[7-(3,6-dihidro-2*H*-piran-4-il)-4-metoxi[1,3]tiazolo[4,5-*c*]piridin-2-il]-7-oxa-2-azaespiro[4.5]decano-2-carboxamida

$C_{21}H_{26}N_4O_4S$



navenibartum #

navenibart	immunoglobulin G1-kappa, anti-[*Homo sapiens* KLKB1 (kallikrein B 1, plasma prekallikrein (zymogen), kininogenin, Fletcher factor, KLK3) proteolytically cleaved by F12 (factor FXII), active plasma kallikrein (EC 3.4.21.34)], humanized monoclonal antibody; H-gamma1 heavy chain humanized (1-450) [VH (*Homo sapiens* IGHV1-69*08 (81.4%) -(IGHD) -IGHJ4*01 (92.9%) L123>T (116), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1-121) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v21 CH2 Y15.1, T16, E18 (CH1 R120 (218) (122-219), hinge 1-15 (220-234), CH2 M15.1>Y (256), S16>T (258), T18>E (260) (235-344), CH3 E12 (360), M14 (362) (345-449), CHS K2>del (450)) (122-450)], (224-214')-disulfide with L-kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-16*01 (82.1%) -IGKJ2*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 (230-230":233-233")-bisdisulfide, produced in a Chinese hamster ovary (CHO) cell line, derived from CHO-K1 cell line, lacking the glutamine synthetase (GS-KO) gene, glycoform alfa
navénibart	immunoglobuline G1-kappa, anti-[*Homo sapiens* KLKB1 (kallikréine B 1, prékallikréine plasmatique (zymogène), kininogénine, facteur de Fletcher, KLK3) clivé protéolytiquement par F12 (facteur FXII), kallikréine plasmatique active (EC 3.4.21.34)], anticorps monoclonal humanisé; chaîne lourde H-gamma1 humanisée (1-450) [VH (*Homo sapiens* IGHV1-69*08 (81.4%) -(IGHD) -IGHJ4*01 (92.9%) L123>T (116), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1-121) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v21 CH2 Y15.1, T16, E18 (CH1 R120 (218) (122-219), charniére 1-15 (220-234), CH2 M15.1>Y (256), S16>T (258), T18>E (260) (235-344), CH3 E12 (360), M14 (362) (345-449), CHS K2>del (450)) (122-450)], (224-214')-disulfure avec la chaîne légère L-kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-16*01 (82.1%) -IGKJ2*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 (230-230":233-233")-bisdisulfure, produit dans une lignée cellulaire des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1, ne présentant pas le gène de la glutamine synthétase (GS-KO), glycoforme alfa
navenibart	inmunoglobulina G1-kappa, anti-[*Homo sapiens* KLKB1 (calicreína B 1, precalicreína plasmática (zimogén), kininogenina, factor de Fletcher, KLK3) escindido proteolíticamente por F12 (factor FXII), calicreína plasmática activa (EC 3.4.21.34)], anticuerpo monoclonal humanizado;

cadena pesada H-gamma1 humanizada (1-450) [VH (*Homo sapiens* IGHV1-69*08 (81.4%) -(IGHD) -IGHJ4*01 (92.9%) L123>T (116), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1-121) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v21 CH2 Y15.1, T16, E18 (CH1 R120 (218) (122-219), bisagra 1-15 (220-234), CH2 M15.1>Y (256), S16>T (258), T18>E (260) (235-344), CH3 E12 (360), M14 (362) (345-449), CHS K2>del (450)) (122-450)], (224-214')-disulfuro con la cadena ligera L-kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-16*01 (82.1%) -IGKJ2*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 (230-230":233-233")-bisdisulfuro, producido en una línea celular de las células ováricas de hámster chino (CHO), derivada de la línea celular CHO-K1, en ausencia del gen glutamina sintetasa (GS-KO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada : H-gamma1 (H, H") anti-KLKB1

```
QVQLVQSGAE VKKPGSSVKV SCKASGYAFS SYWMNWVRQA PGQGLEWIGQ  50
IYPGDDDTNY NAKFQGRVTI TVDKSTTTAY MELSSLRSED TAVYFCAGSL 100
MVTTGAPFDY WGQGTTVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200
TYICNVNHKP SNTKVDKRVE PKSCDKTHTC PPCPAPELLG GPSVFLFPPK 250
PKDTLYITRE PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY 300
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP 350
QVYTLPPSRE EMTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP 400
VLDSDGSFFL YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG 450
```

Light chain / Chaîne légère / Cadena ligera : L-kappa (L', L'") anti-KLKB1

```
DIQMTQSPSS LSASVGDRVT ITCKASQDVG IAVAWYQQKP GKAPKFLIYY  50
ASHRGWGVPD RFSGSGSGTD FTLTISSLQP EDFATYFCQQ YRSYPLTFGQ 100
GTKLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 148-204 265-325 371-429
22"-96" 148"-204" 265"-325" 371"-429"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194'"
Inter-H-L (h 5-CL 126) 224-214' 224"-214"'
Inter-H-H (h 11, h 14) 230-230" 233-233"

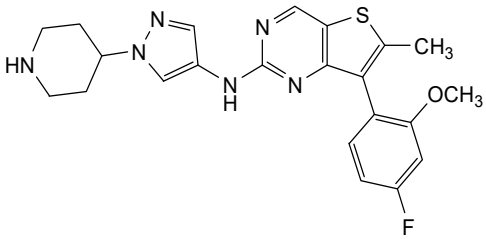
N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)
H VH Q1: 1, 1"

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

nefextinibum

nefextinib	7-(4-fluoro-2-methoxyphenyl)-6-methyl-*N*-[1-(piperidin-4-yl)-1*H*-pyrazol-4-yl]thieno[3,2-*d*]pyrimidin-2-amine
néfextinib	7-(4-fluoro-2-méthoxyphényl)-6-méthyl-*N*-[1-(pipéridin-4-yl)-1*H*-pyrazol-4-yl]thiéno[3,2-*d*]pyrimidin-2-amine
nefextinib	7-(4-fluoro-2-metoxifenil)-6-metil-*N*-[1-(piperidin-4-il)-1*H*-pirazol-4-il]tieno[3,2-*d*]pirimidin-2-amina

$C_{22}H_{23}FN_6OS$



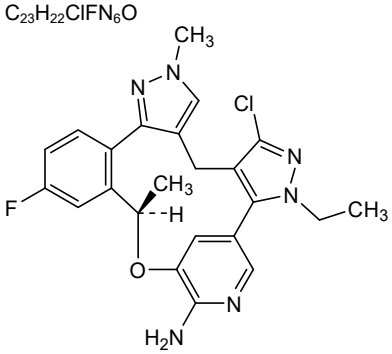
neladalkibum

neladalkib — (6*R*)-2^5-chloro-2^2-ethyl-5^4-fluoro-4^1,6-dimethyl-2^2*H*,4^1*H*-7-oxa-1(3,5)-pyridina-2(3,4),4(4,3)-dipyrazola-5(1,2)-benzenacycloheptaphan-1^6-amine

néladalkib — (6*R*)-2^5-chloro-2^2-éthyl-5^4-fluoro-4^1,6-diméthyl-2^2*H*,4^1*H*-7-oxa-1(3,5)-pyridina-2(3,4),4(4,3)-dipyrazola-5(1,2)-benzénacycloheptaphan-1^6-amine

neladalkib — (6*R*)-2^5-cloro-2^2-etil-5^4-fluoro-4^1,6-dimetil-2^2*H*,4^1*H*-7-oxa-1(3,5)-piridina-2(3,4),4(4,3)-dipirazola-5(1,2)-bencenacicloheptafan-1^6-amina

$C_{23}H_{22}ClFN_6O$



nendocabtagenum onogedleucelum #

nendocabtagene onogedleucel — allogeneic T lymphocytes obtained from peripheral blood mononuclear cells by leukapheresis of healthy volunteer donors, transduced with a self-inactivating, non-replicating lentiviral vector encoding a chimeric antigen receptor (CAR) targeting human B-cell maturation antigen (BCMA). The cells are also genetically modified using transcription activator-like (TAL) effector nucleases that are transiently delivered into the cell as mRNAs via electroporation and code for two pairs: one pair is designed for disruption of the T-cell receptor α constant (TRAC) and the other for disruption of the CD52 locus.

The expressed transgene comprises a human CD8α leader sequence, an anti-BCMA single chain variable fragment (scFv) derived from the anti-human BCMA (clone P5A2), a CD8α hinge and transmembrane domain, and 4-1BB (CD137) and CD3ζ (CD247) intracellular costimulatory domains, under control of the human elongation factor 1 alpha (EF1α) promoter. The extracellular region of the CAR also contains 2 mimotopes that confer susceptibility to *rituximab*. The construct is flanked by 5' and 3' long terminal repeats (LTRs) and also contains a ψ packaging signal, a truncated *gag*, a Rev response element (RRE), a central polypurine tract (cPPT) sequence and a mutated

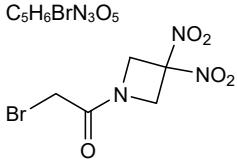
	Woodchuck hepatitis virus post-transcriptional regulatory element (WPRE). The vector is pseudotyped with vesicular stomatitis virus (VSV) glycoprotein G. The leukapheresis material is activated by CD3 and CD28 agonists to stimulate T lymphocyte growth in media containing serum and interleukin 2 (IL-2), transduced with the lentiviral vector, genetically modified, and then culture expanded. At the end of expansion, TCR- cells are enriched by positive selection and residual TCR+ cells are depleted using magnetic bead purification. The T lymphocytes consist of ≥20% TCR αβ- T lymphocytes expressing the CAR-BCMA transgene, ≥50% CD52- and ≤3.0% TCR αβ+ T lymphocytes. The cells respond to BCMA-expressing target cells by releasing interferon gamma (IFN-γ) and demonstrate cytotoxicity against cells expressing BCMA
nendocabtagène onogedleucel	lymphocytes T allogéniques obtenus par leucaphérèse à partir de cellules mononucléaires de sang périphérique provenant de donneurs volontaires sains, transduits avec un vecteur lentiviral auto-inactivant et non répliquant codant un récepteur antigénique chimérique (CAR) ciblant l'antigène humain de maturation des cellules B (BCMA). Les cellules sont également modifiées génétiquement à l'aide de nucléases effectrices de type activateur de transcription (TAL) qui sont délivrées transitoirement dans la cellule sous forme d'ARNm par électroporation et qui codent deux paires: une paire conçue pour la perturbation du récepteur α constant des cellules T (TRAC) et l'autre pour la perturbation du locus CD52. Le transgène exprimé comprend une séquence de tête CD8α humaine, un fragment variable à chaîne unique anti-BCMA (scFv) dérivé de l'anti-BCMA humain (clone P5A2), une charnière et un domaine transmembranaire CD8α, ainsi que les domaines co-stimulateurs intracellulaires 4-1BB (CD137) et CD3ζ (CD247), sous le contrôle du promoteur du facteur d'élongation 1 alpha (EF1α) humain. La région extracellulaire du CAR contient également 2 mimotopes qui lui confèrent une sensibilité au *rituximab*. La construction est flanquée de longues répétitions terminales (LTR) en 5' et 3' et contient également un signal d'encapsidation ψ, un *gag* tronqué, un élément de réponse Rev (RRE), une séquence du tractus polypurine central (cPPT) et un élément muté de régulation post-transcriptionnelle du virus de l'hépatite de la marmotte (WPRE). Le vecteur est pseudotypé avec la glycoprotéine G du virus de la stomatite vésiculaire (VSV). Le matériel de leucaphérèse est activé par des agonistes CD3 et CD28 pour stimuler la croissance des lymphocytes T dans des milieux contenant du sérum et de l'interleukine 2 (IL-2), transduits avec le vecteur lentiviral, génétiquement modifiés, puis amplifiés en culture. À la fin de l'amplification, les cellules TCR- sont enrichies par sélection positive et les cellules TCR+ résiduelles sont éliminées par purification sur billes magnétiques. Les lymphocytes T sont constitués de ≥20 % de lymphocytes T TCR αβ- exprimant le transgène CAR-BCMA, de ≥50% de lymphocytes CD52- et de ≤3.0% de lymphocytes T TCR αβ+. Les cellules répondent aux cellules cibles exprimant le BCMA en libérant de de l'interféron gamma (IFN-γ) et démontrent une cytotoxicité contre les cellules exprimant le BCMA

nendocabtagén onogedleucel	linfocitos T alogénicos obtenidos de células mononucleares de sangre periférica mediante leucoaféresis de donantes voluntarios sanos, transducidos con un vector lentiviral no replicativo, auto inactivante, que codifica para un receptor de antígenos quimérico (CAR) dirigido al antígeno de maduración de linfocitos B (BCMA). Las células también se modifican genéticamente usando nucleasas efectoras similares al activador de la transcripción (TAL) que se administran transitoriamente a la célula en forma de ARNm mediante electroporación y que codifican para dos pares: un par está diseñado para la ruptura de la cadena constante α del receptor de linfocitos T (TRAC) y el otro para la ruptura del locus de CD52. El transgén expresado contiene una secuencia líder del CD8α humano, un fragmento variable de cadena sencilla (scFv) anti-BCMA derivado del anti-BCMA humano (clon P5A2), un dominio bisagra y transmembrana de CD8α, y dominios coestimuladores intracelulares de 4-1BB (CD137) y de CD3ζ(CD247), bajo el control del promotor del factor de elongación 1 alfa (EF-1α) humano. La región extracelular del CAR también contiene 2 mimotopos que confieren susceptibilidad a *rituximab*. El constructo está flanqueado por repeticiones terminales largas (LTRs) en 5' y 3' y también contiene una señal de empaquetamiento ψ, un *gag* truncado, un elemento de respuesta Rev (RRE), una secuencia de tracto de polipurina central (cPPT) y un elemento regulador post-transcripcional del virus de la hepatitis de la marmota (WPRE) mutado. El vector está seudotipado con la glicoproteína G del virus de la estomatitis vesicular (VSV). El material de leucoaféresis se activa con agonistas de CD3 y CD28 para estimular el crecimiento de linfocitos T en medio que contiene suero e interleuquina 2 (IL-2), se transducen con el vector lentiviral, se modifican genéticamente y se expanden en cultivo. Al final de la expansión, los linfocitos TCR- se enriquecen mediante selección positiva y los linfocitos TCR+ residuales se deplecionan usando purificación con bolas magnéticas. Los linfocitos T consisten en ≥20% de linfocitos T TCR αβ- que expresan el transgén del CAR-BCMA, ≥50% de linfocitos T CD52- y ≤3.0% de linfocitos T TCR αβ+. Las células responden a células diana que expresan BCMA liberando interferón gamma (IFN-γ) y demuestran citotoxicidad frente a células que expresan BCMA

nibrozetonum

nibrozetone	2-bromo-1-(3,3-dinitroazetidin-1-yl)ethan-1-one
nibrozétone	2-bromo-1-(3,3-dinitroazétidin-1-yl)éthan-1-one
nibrozetona	2-bromo-1-(3,3-dinitroazetidin-1-il)etan-1-ona

$C_5H_6BrN_3O_5$



noraramtidum

noraramtide

1,13-anhydro-*S*^{24},*S*^{34}-cyclo[L-alanyl-L-arginyl-(2*S*)-2-aminoheptanoyl-L-tyrosyl-L-histidyl-L-α-aspartylglycyl-L-valyl-L-leucyl-4-phenyl-L-phenylalanyl-(2*S*)-2-aminoheptanoyl-L-α-aspartyl-*S*-(carboxymethyl)-L-cysteinyl-1-({[(5a*RS*,6*SR*,6a*SR*)-1-(20-amino-3,6,9,12,15,18-hexaoxaicosan-1-yl)-1,4,5,5a,6,6a,7,8-octahydrocyclopropa[5,6]cycloocta[1,2-*d*][1,2,3]triazol-6-yl]methoxy}carbonyl)piperidine-4-carbonylglycyl-D-γ-glutamyl-D-γ-glutamyl-D-α-glutamyl-D-γ-glutamyl-D-γ-glutamylglycylglycyl-L-α-aspartyl-L-cysteinyl-L-alanyl-L-tryptophyl-L-histidyl-L-leucylglycyl-L-α-glutamyl-L-leucyl-L-valyl-L-tryptophyl-L-cysteinyl-L-threonine]

noraramtide

1,13-anhydro-*S*^{24},*S*^{34}-cyclo[L-alanyl-L-arginyl-(2*S*)-2-aminoheptanoyl-L-tyrosyl-L-histidyl-L-α-aspartylglycyl-L-valyl-L-leucyl-4-phényl-L-phénylalanyl-(2*S*)-2-aminoheptanoyl-L-α-aspartyl-*S*-(carboxyméthyl)-L-cystéinyl-1-({[(5a*RS*,6*SR*,6a*SR*)-1-(20-amino-3,6,9,12,15,18-hexaoxaicosan-1-yl)-1,4,5,5a,6,6a,7,8-octahydrocyclopropa[5,6]cycloocta[1,2-*d*][1,2,3]triazol-6-yl]méthoxy}carbonyl)pipéridine-4-carbonylglycyl-D-γ-glutamyl-D-γ-glutamyl-D-α-glutamyl-D-γ-glutamyl-D-γ-glutamylglycylglycyl-L-α-aspartyl-L-cystéinyl-L-alanyl-L-tryptophyl-L-histidyl-L-leucylglycyl-L-α-glutamyl-L-leucyl-L-valyl-L-tryptophyl-L-cystéinyl-L-thréonine]

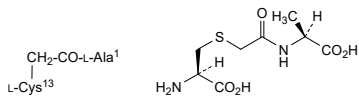
noraramtida

1,13-anhidro-*S*^{24},*S*^{34}-ciclo[L-alanil-L-arginil-(2*S*)-2-aminoheptanoil-L-tirosil-L-histidil-L-α-aspartilglicil-L-valil-L-leucil-3-([1,1′-bifenil]-4-il)-L-alanil-(2*S*)-2-aminoheptanoil-L-α-aspartil-*S*-(carboximetil)-L-cisteinil-1-({[(5a*RS*,6*SR*,6a*SR*)-1-(20-amino-3,6,9,12,15,18-hexaoxaicosan-1-il)-1,4,5,5a,6,6a,7,8-octahidrociclopropa[5,6]ciclooctа[1,2-*d*][1,2,3]triazol-6-il]metoxi}carbonil)piperidina-4-carbonilglicil-D-γ-glutamil-D-γ-glutamil-D-α-glutamil-D-γ-glutamil-D-γ-glutamilglicilglicil-L-α-aspartil-L-cisteinil-L-alanil-L-triptofil-L-histidil-L-leucilglicil-L-α-glutamil-L-leucil-L-valil-L-triptofil-L-cisteinil-L-treonina]

$C_{210}H_{300}N_{48}O_{65}S_3$

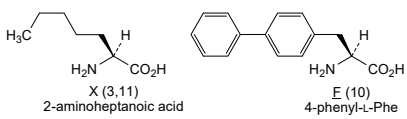
ARXYHDGVLF XDCXGEEÊEE GGDCAWHLGE LVWCT 35

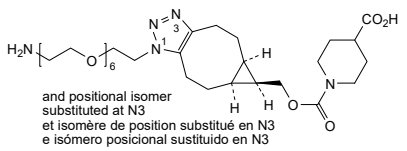
Amide bridge location / Position du pont amide / Posición del puente amido
C^{13}-A^{1}



Disulfide bridge location / Position du pont disulfure / posición del puente disulfuro
C^{24}-C^{34} (Cys^{24}-Cys^{34})

Modified residues / Résidus modifiés / Restos modificados





nucresiranum

nucresiran *all-P-ambo*-2'-*O*-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-methyl-*P*-thioadenylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-deoxy-2'-fluorouridylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-deoxy-2'-fluorouridylyl-(3'→5')-2'-deoxy-2'-fluorouridylyl-(3'→5')-2'-deoxy-2'-fluorocytidylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-3'-*O*-[{[(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]methoxy}(hydroxy)phosphoryl]-2'-*O*-methyluridine
duplex with *all-P-ambo*-2'-*O*-methyl-*P*-thiouridylyl-(5'→3')-2'-*O*-methyl-*P*-thioguanylyl-(5'→3')-2'-*O*-methylguanylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-deoxy-2'-fluorocytidylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-deoxy-2'-fluorouridylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-*O*-methylguanylyl-(5'→3')-2'-*O*-methylguanylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-deoxy-2'-fluoroadenylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-*O*-methyl-*P*-thiouridylyl-(5'→3')-2'-deoxy-2'-fluoro-*P*-thioguanylyl-(5'→3')-2'-*O*-methyladenosine

nucrésiran *tout-P-ambo*-2'-*O*-méthyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-méthyl-*P*-thioadénylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-désoxy-2'-fluorouridylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-désoxy-2'-fluorouridylyl-(3'→5')-2'-désoxy-2'-fluorouridylyl-(3'→5')-2'-désoxy-2'-fluorocytidylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-3'-*O*-[{[(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]methoxy}(hydroxy)phosphoryl]-2'-*O*-méthyl-3'-uridine
duplex avec *tout-P-ambo*-2'-*O*-méthyl-*P*-thiouridylyl-(5'→3')-2'-*O*-méthyl-*P*-thioguanylyl-(5'→3')-2'-*O*-méthylguanylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-désoxy-2'-fluorocytidylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-désoxy-2'-fluorouridylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-*O*-méthylguanylyl-(5'→3')-2'-*O*-méthylguanylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-désoxy-2'-fluoroadénylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-*O*-méthyl-*P*-thiouridylyl-(5'→3')-2'-désoxy-2'-fluoro-*P*-thioguanylyl-(5'→3')-2'-*O*-méthyladénosine

nucresirán *todo-P-ambo*-2'-*O*-metil-*P*-tiocitidilil-(3'→5')-2'-*O*-metil-*P*-tioadenilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-desoxi-2'-fluorouridilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-desoxi-2'-fluorouridilil-(3'→5')-2'-desoxi-2'-fluorouridilil-(3'→5')-2'-desoxi-2'-fluorocitidilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-3'-*O*-[{[(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]metoxi}(hidroxi)fosforil]-2'-*O*-metil-3'-uridina

dúplex con *todo-P-ambo*-2'-*O*-metil-*P*-tiouridilil-(5'→3')-2'-*O*-metil-*P*-tioguanilil-(5'→3')-2'-*O*-metilguanilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-desoxi-2'-fluorocitidilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-desoxi-2'-fluorouridilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-*O*-metilguanilil-(5'→3')-2'-*O*-metilguanilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-desoxi-2'-fluoroadenilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-*O*-metil-*P*-tiouridilil-(5'→3')-2'-desoxi-2'-fluoro-*P*-tioguanilil-(5'→3')-2'-*O*-metiladenosina

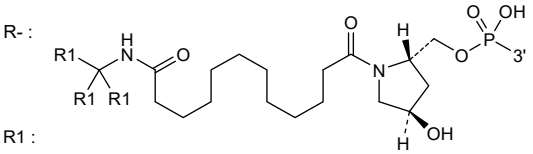
$C_{532}H_{716}F_8N_{171}O_{324}P_{43}S_6$

(3'-5')*C*=*A*=*A*−*G*−*A*−*G*−U−*A*−U−U−C−*C*−*A*−*U*−*U*−*U*−*U*−*U*−*A*−*C*−*U*−R

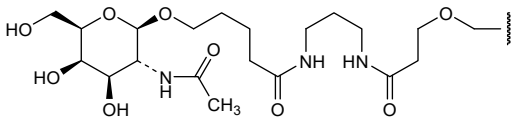
(5'-3')*U*=*G*=*G*−*U*−*U*−*C*−*U*−C−*A*−U−*A*−*A*−*G*−*G*−*U*−*A*−*A*−A−*A*−*A*−*U*=G=*A*

N : A,C,G,U
N : 2'-*O*-methyl-N / 2'-*O*-méthyl-N / 2'-*O*-metil-N
N : 2'-deoxy-2'-fluoro-N / 2'-désoxy-2'-fluoro-N / 2'-desoxi-2'-fluoro-N
– : –PO(OH)– = : –PO(SH)–

R- :



R1 :



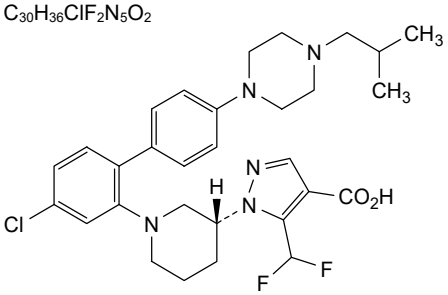
nurandociguatum

nurandociguat — 1-[(3*R*)-1-{4-chloro-4'-[4-(2-methylpropyl)piperazin-1-yl][1,1'-biphenyl]-2-yl}piperidin-3-yl]-5-(difluoromethyl)-1*H*-pyrazole-4-carboxylic acid

nurandociguat — acide 1-[(3*R*)-1-{4-chloro-4'-[4-(2-méthylpropyl)pipérazin-1-yl][1,1'-biphényl]-2-yl}piperidin-3-yl]-5-(difluoromethyl)-1*H*-pyrazole-4-carboxylique

nurandociguat — ácido 1-[(3*R*)-1-{4-cloro-4'-[4-(2-metilpropil)piperazin-1-il][1,1'-bifenil]-2-il}piperidin-3-il]-5-(difluorometil)-1*H*-pirazol-4-carboxílico

$C_{30}H_{36}ClF_2N_5O_2$



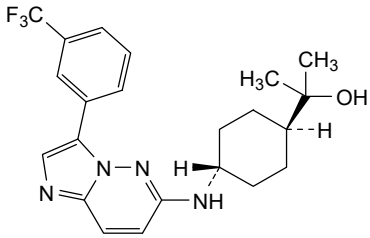
nuvisertibum

nuvisertib — 2-[(1*r*,4*r*)-4-({3-[3-(trifluoromethyl)phenyl]imidazo[1,2-*b*]pyridazin-6-yl}amino)cyclohexyl]propan-2-ol

nuvisertib — 2-[(1*r*,4*r*)-4-({3-[3-(trifluorométhyl)phényl]imidazo[1,2-*b*]pyridazin-6-yl}amino)cyclohexyl]propan-2-ol

nuvisertib — 2-[(1*r*,4*r*)-4-({3-[3-(trifluorometil)fenil]imidazo[1,2-*b*]piridazin-6-il}amino)ciclohexil]propan-2-ol

$C_{22}H_{25}F_3N_4O$



obrixtamigum #

obrixtamig — immunoglobulin L-kappa-H-gamma1_L-lambda-H-gamma1, anti-[*Homo sapiens* DLL3 (delta-like ligand 3, delta like canonical Notch ligand 3)] and anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], bispecific;
L-kappa-H-gamma1 (knob) chain anti-DLL3 (1-705) [L-kappa anti-DLL3 (1-214) [V-KAPPA (*Homo sapiens* IGKV1-17*03 (94.9%) -IGKJ2*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')] -38-mer (GGGGSE GKSSGSGSES KSTEGKSSGS GSESKSTGGGGS) linker (215-252) -H-gamma-1 heavy chain anti-DLL3 (253-705) [VH (*Homo sapiens* IGHV1-46*01 (92.9%) -(IGHD) -IGHJ6*01 (94.7%), CDR-IMGT [8.8.17] (278-285.303-310.349-365)) (253-376)-*Homo sapiens* IGHG1*03, G1m3, nG1m1, CH1 R120, CH3 E12, M14, G1v14 CH2 A1.3, A1.2, G1v32 CH3 W22 (knob) (CH1 R120 (473) (377-474), hinge 1-15 (475-489), CH2 L1.3>A (493), L1.2>A (494) (490-599), CH3 E12 (615), M14 (617), T22>W (625) (600-704), CHS K2>del (705)) (377-705)]];
L-lambda6-H-gamma1 (hole) chain anti-CD3E (1-707) [L-lambda6 anti-CD3 (1'-215') [V-LAMBDA Musmus/Homsap (*Mus musculus* IGLV1*01 (82.3%) -IGLJ1*01 (100%)/*Homo sapiens* IGLV7-46*01 (76.8%) -IGLJ3*02 (100%), CDR-IMGT [9.3.9] (26'-34'.52'-54'.91'-99')) (1'-109') -*Homo sapiens* IGLC6*01 (100%) (110'-215')] -38-mer (GGGGSE GKSSGSGSES KSTEGKSSGSGSESKSTGGGGS) linker (216'-253') -H-gamma-1 anti-CD3E (254'-707') [VH Musmus/Homsap (*Mus musculus* IGHV10-1*02 (92.9%) -(IGHD) -IGHJ3*01 (100%)/*Homo sapiens* IGHV3-73*01 (87.0%) -(IGHD) -IGHJ6*01 (81.8%) T123>L (373'), S128>A (378'), CDR-IMGT [8.10.16] (279'-286'.304'-313'.352'-367')) (254'-378')-*Homo sapiens* IGHG1*03, G1m3, nG1m1, CH1 R120, CH3 E12, M14, G1v14 CH2 A1.3, A1.2, G1v33 CH3 S22, A24, V86 (hole), G1v83 CH3 R115, F116 (CH1 R120 (475') (379'-476'), hinge 1-15 (477'-491'), CH2 L1.3>A (495'), L1.2>A (496') (492'-601'), CH3 E12 (617'), M14 (619'), T22>S (627'), L24>A (629'), Y86>V (686'), H115>R (696'), Y116>F (697') (602'-706'), CHS K2>del (707')) (379'-707')]]; dimer (485-487':488-490')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa

obrixtamig — immunoglobuline L-kappa-H-gamma1_L-lambda-H-gamma1, anti-[*Homo sapiens* DLL3 (delta-like ligand 3, delta like canonical Notch ligand 3)] et anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], bispécifique;

chaîne (knob) L-kappa-H-gamma1 anti-DLL3 (1-705) [L-kappa anti-DLL3 (1-214) [V-KAPPA (*Homo sapiens* IGKV1-17*03 (94.9%) -IGKJ2*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')] -38-mer (GGGGSE GKSSGSGSES KSTEGKSSGS GSESKSTGGGGS) linker (215-252) -H-gamma1 anti-DLL3 (253-705) [VH (*Homo sapiens* IGHV1-46*01 (92.9%) -(IGHD) -IGHJ6*01 (94.7%), CDR-IMGT [8.8.17] (278-285.303-310.349-365)) (253-376)-*Homo sapiens* IGHG1*03, G1m3, nG1m1, CH1 R120, CH3 E12, M14, G1v14 CH2 A1.3, A1.2, G1v32 CH3 W22 (knob) (CH1 R120 (473) (377-474), charnière 1-15 (475-489), CH2 L1.3>A (493), L1.2>A (494) (490-599), CH3 E12 (615), M14 (617), T22>W (625) (600-704), CHS K2>del (705)) (377-705)]];
chaîne (hole) L-lambda6-H-gamma1 anti-CD3E (1-707) [L-lambda6 anti-CD3 (1'-215') [V-LAMBDA Musmus/Homsap (*Mus musculus* IGLV1*01 (82.3%) -IGLJ1*01 (100%)/*Homo sapiens* IGLV7-46*01 (76.8%) -IGLJ3*02 (100%), CDR-IMGT [9.3.9] (26'-34'.52'-54'.91'-99')) (1'-109') -*Homo sapiens* IGLC6*01 (100%) (110'-215')] -38-mer (GGGGSE GKSSGSGSES KSTEGKSSGSGSESKSTGGGGS) linker (216'-253') -H-gamma1 anti-CD3E (254'-707') [VH Musmus/Homsap (*Mus musculus* IGHV10-1*02 (92.9%) -(IGHD) -IGHJ3*01 (100%)/*Homo sapiens* IGHV3-73*01 (87.0%) -(IGHD) -IGHJ6*01 (81.8%) T123>L (373'), S128>A (378'), CDR-IMGT [8.10.16] (279'-286'.304'-313'.352'-367')) (254'-378')-*Homo sapiens* IGHG1*03, G1m3, nG1m1, CH1 R120, CH3 E12, M14, G1v14 CH2 A1.3, A1.2, G1v33 CH3 S22, A24, V86 (hole), G1v83 CH3 R115, F116 (CH1 R120 (475') (379'-476'), charnière 1-15 (477'-491'), CH2 L1.3>A (495'), L1.2>A (496') (492'-601'), CH3 E12 (617'), M14 (619'), T22>S (627'), L24>A (629'), Y86>V (686'), H115>R (696'), Y116>F (697') (602'-706'), CHS K2>del (707')) (379'-707')]];
dimère (485-487':488-490')- bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa

obrixtamig

inmunoglobulina L-kappa-H-gamma1_L-lambda-H-gamma1, anti-[*Homo sapiens* DLL3 (ligando 3 tipo delta, delta like canonical Notch ligand 3)] y anti-[*Homo sapiens* CD3E (CD3 épsilon, Leu-4)], biespecífico;
cadena (knob) L-kappa-H-gamma1 anti-DLL3 (1-705) [L-kappa anti-DLL3 (1-214) [V-KAPPA (*Homo sapiens* IGKV1-17*03 (94.9%) -IGKJ2*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')] -38-mer (GGGGSE GKSSGSGSES KSTEGKSSGS GSESKSTGGGGS) enlace (215-252) -H-gamma1 anti-DLL3 (253-705) [VH (*Homo sapiens* IGHV1-46*01 (92.9%) -(IGHD) -IGHJ6*01 (94.7%), CDR-IMGT [8.8.17] (278-285.303-310.349-365)) (253-376)-*Homo sapiens* IGHG1*03, G1m3, nG1m1, CH1 R120, CH3 E12, M14, G1v14 CH2 A1.3, A1.2, G1v32 CH3 W22 (knob) (CH1 R120 (473) (377-474), bisagra 1-15 (475-489), CH2 L1.3>A (493), L1.2>A (494) (490-599), CH3 E12 (615), M14 (617), T22>W (625) (600-704), CHS K2>del (705)) (377-705)]];
cadena (hole) L-lambda6-H-gamma1 anti-CD3E (1-707) [L-lambda6 anti-CD3 (1'-215') [V-LAMBDA Musmus/Homsap (*Mus musculus* IGLV1*01 (82.3%) -IGLJ1*01 (100%)/*Homo sapiens* IGLV7-46*01 (76.8%) -IGLJ3*02 (100%), CDR-IMGT [9.3.9] (26'-34'.52'-54'.91'-99')) (1'-109') -*Homo sapiens* IGLC6*01 (100%) (110'-215')] -38-mer (GGGGSE GKSSGSGSES KSTEGKSSGSGSESKSTGGGGS) enlace (216'-253') -H-gamma1 anti-CD3E (254'-707') [VH Musmus/Homsap (*Mus musculus* IGHV10-1*02 (92.9%) -(IGHD) -IGHJ3*01 (100%)/*Homo sapiens* IGHV3-73*01 (87.0%) -(IGHD) -IGHJ6*01 (81.8%) T123>L (373'), S128>A (378'), CDR-IMGT [8.10.16] (279'-286'.304'-313'.352'-367')) (254'-378')-*Homo sapiens* IGHG1*03, G1m3, nG1m1, CH1 R120, CH3 E12, M14, G1v14 CH2 A1.3, A1.2, G1v33 CH3 S22, A24, V86 (hole), G1v83 CH3 R115, F116 (CH1 R120 (475') (379'-476'), bisagra 1-15 (477'-491'), CH2 L1.3>A (495'), L1.2>A (496') (492'-601'), CH3 E12 (617'), M14 (619'), T22>S (627'), L24>A (629'), Y86>V (686'), H115>R (696'), Y116>F (697') (602'-706'), CHS K2>del (707')) (379'-707')]];
dímero (485-487':488-490')- bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, forma glicosilada alfa

Light-heavy chain / chaîne légère-lourde / cadena ligera-pesada : L-kappa-H-gamma1 (L-H) anti-DLL3 (knob)

```
DIQMTQSPSA MSASVGDRVT ITCRASQGIS NYLVWFQQKP GKAPKRLIYA  50
VSSLYSGVPS RFSGSGSGTE FTLTISSLQP EDFATYYCLQ HDSYPYTFGQ 100
GTKLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGECGGGGSE GKSSGSGSES KSTEGKSSGS GSESKSTGGG 250
GSQVQLVQSG AEVKKPGASV KVSCKASGYT FTSYYVHWVR QAPGQGLEWM 300
VIINPGGGTT SYAQKFLGRV TMTRDTSTNT VYMELKSLRS EDTAVYYCAR 350
GEAVTGNYFY YGMDVWGQGT TVTVSSASTK GPSVFPLAPS SKSTSGGTAA 400
LGCLVKDYFP EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVVTVPSS 450
SLGTQTYICN VNHKPSNTKV DKRVEPKSCD KTHTCPPCPA PEAAGGPSVF 500
LFPPKPKDTL MISRTPEVTC VVVDVSHEDP EVKFNWYVDG VEVHNAKTKP 550
REEQYNSTYR VVSVLTVLHQ DWLNGKEYKC KVSNKALPAP IEKTISKAKG 600
QPREPQVYTL PPSREEMTKN QVSLWCLVKG FYPSDIAVEW ESNGQPENNY 650
KTTPPVLDSD GSFFLYSKLT VDKSRWQQGN VFSCSVMHEA LHNHYTQKSL 700
SLSPG                                                   705
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Light-heavy chain / chaîne légère-lourde / cadena ligera-pesada : L-lambda6-H-gamma1 (L'-H') anti-CD3E (hole)

```
EAVVTQEPSL TVSPGGTVTL TCRSSTGAVT TSNYANWVQE KPGQLPRGLI  50
GGTNKRAPWV PARFSGSLLG GKAALTLSGA QPEDEAEYFC ALWYSNLWVF 100
GGGTKLTVLG QPKAAPSVTL FPPSSEELQA NKATLVCLIS DFYPGAVKVA 150
WKADGSPVNT GVETTTPSKQ SNNKYAASSY LSLTPEQWKS HRSYSCQVTH 200
EGSTVEKTVA PAECSGGGGS EGKSSGSGSE SKSTEGKSSG SGSESKSTGG 250
GGSEVQLVES GGGLVQPGGS LKLSCAASGF TFNTYAMNWV RQAPGKGLEW 300
VARIRSKYNN YATYYADSVK DRFTISRDDS KNTAYLQMNN LKTEDTAVYY 350
CVRHGNFGNS YVSWFAYWGQ GTLVTVSAAS TKGPSVFPLA PSSKSTSGGT 400
AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP 450
SSSLGTQTYI CNVNHKPSNT KVDKRVEPKS CDKTHTCPPC PAPEAAGGPS 500
VFLFPPKPKD TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT 550
KPREEQYNST YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA 600
KGQPREPQVY TLPPSREEMT KNQVSLSCAV KGFYPSDIAV EWESNGQPEN 650
NYKTTPPVLD SDGSFFLVSK LTVDKSRWQQ GNVFSCSVMH EALHNRFTQK 700
SLSLSPG                                                 707
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-L (C23-C104) 23-88 134-194
22'-90' 137'-196'
Intra-H (C23-C104) 274-348 403-459 520-580 626-684
275'-351' 405'-461' 522'-582' 628'-686'
Intra-H-L (h 5-CL 126) 479-214 481'-214'
Inter-H-H (h 11, h 14) 485-487' 488-490'

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4: 556, 558"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

ocankitugum #

ocankitug — immunoglobulin G1-kappa, anti-[*Homo sapiens* TSLP (thymic stromal lymphopoietin)], humanized monoclonal antibody; H-gamma1 heavy chain humanized (1-447) [VH (*Homo sapiens* IGHV1-46*01 (87.8%) -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14(CH1 R120 (214) (118-215), hinge 1-15 (216-230), CH2 (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-214')-disulfide with L-kappa light chain humanized (1'-214') [V-KAPPA (*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')]; dimer (226-226":229-229")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, lacking the glutamine synthetase (GS-KO) gene, glycoform alfa

ocankitug — immunoglobuline G1-kappa, anti-[*Homo sapiens* TSLP (lymphopoïétine stromale thymique)], anticorps monoclonal humanisé;
chaîne lourde H-gamma1 humanisée (1-447) [VH (*Homo sapiens* IGHV1-46*01 (87.8%) -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (214) (118-215), charnière 1-15 (216-230), CH2 (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-214')-disulfure avec la chaîne légère L-kappa humanisée (1'-214') [V-KAPPA (*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')]; dimère

(226-226":229-229")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1, ne présentant pas le gène de la glutamine synthétase (GS-KO), glycoforme alfa

ocankitug

inmunoglobulina G1-kappa, anti-[*Homo sapiens* TSLP (linfopoyetina estromal tímica)], anticuerpo monoclonal humanizado;
cadena pesada H-gamma1 humanizada (1-447) [VH (*Homo sapiens* IGHV1-46*01 (87.8%) -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens*IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (214) (118-215), bisagra 1-15 (216-230), CH2 (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-214')-disulfuro con la cadena ligera L-kappa humanizada (1'-214') [V-KAPPA (*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')]; dímero (226-226":229-229")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular derivada de CHO-K1, en ausencia del gen glutamina sintetasa (GS-KO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGSSVKV SCKASGYTFT DYWMHWVRQA PGQGLEWMGI  50
IDPSDSDTSL NQKFQGRVTI TADTSTSTAY MELSSLRSED TAVYYCARSL 100
DGYYDYWGQG TLVTVSSAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF 150
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC 200
NVNHKPSNTK VDKRVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT 250
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT 350
LPPSREEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS 400
DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPGK    447
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCRTSENIY SYLAWYQQKP GKAPKLLIYF  50
AKTLTDGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQH HYGTPWTFGQ 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) 22-96 144-200 261-321 367-425
22"-96" 144"-200" 261"-321" 367"-425"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194'"
Inter-H-L (h 5-CL 126) 220-214' 220"-214'"
Inter-H-H (h 11, h 14) 226-226" 229-229"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)
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"

odentegravirum

odentegravir

(7*S*)-12-hydroxy-1,11-dioxo-*N*-[(2,4,6-trifluorophenyl)methyl]-1,4,5,6,7,11-hexahydro-3*H*-2,7-methanopyrido[1,2-*a*][1,4]diazonine-10-carboxamide

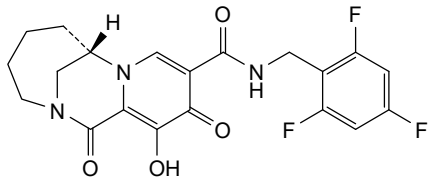
odentégravir

(7*S*)-12-hydroxy-1,11-dioxo-*N*-[(2,4,6-trifluorophényl)méthyl]-1,4,5,6,7,11-hexahydro-3*H*-2,7-méthanopyrido[1,2-*a*][1,4]diazonine-10-carboxamide

odentegravir

(7*S*)-12-hidroxi-1,11-dioxo-*N*-[(2,4,6-trifluorofenil)metil]-1,4,5,6,7,11-hexahidro-3*H*-2,7-metanopirido[1,2-*a*][1,4]diazonina-10-carboxamida

$C_{20}H_{18}F_3N_3O_4$



ofirnoflastum

ofirnoflast

N-[4-(4-amino-7-cyclopropyl-7*H*-pyrrolo[2,3-*d*]pyrimidin-5-yl)-2-fluorophenyl]-*N*'-{5-[1-(trifluoromethyl)cyclopropyl]-1,2-oxazol-3-yl}urea

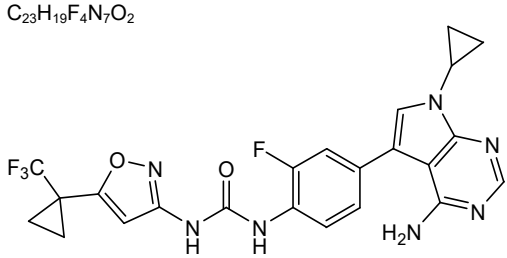
ofirnoflast

N-[4-(4-amino-7-cyclopropyl-7*H*-pyrrolo[2,3-*d*]pyrimidin-5-yl)-2-fluorophényl]-*N*'-{5-[1-(trifluorométhyl)cyclopropyl]-1,2-oxazol-3-yl}urée

ofirnoflast

N-[4-(4-amino-7-ciclopropil-7*H*-pirrolo[2,3-*d*]pirimidin-5-il)-2-fluorofenil]-*N*'-{5-[1-(trifluorometil)ciclopropil]-1,2-oxazol-3-il}urea

$C_{23}H_{19}F_4N_7O_2$



olatorepatidum

olatorepatide

L-tyrosyl-2-methylalanyl-L-α-glutamylglycyl-L-threonyl-L-phenylalanyl-L-threonyl-L-seryl-L-α-aspartyl-L-tyrosyl-L-seryl-L-isoleucyl-L-tyrosyl-L-leucyl-L-α-glutamyl-L-lysyl-L-isoleucyl-L-alanyl-L-alanyl-L-glutaminyl-L-α-glutamyl-L-phenylalanyl-L-valyl-L-asparaginyl-L-tryptophyl-L-leucyl-L-leucyl-L-alanylglycylglycyl-L-prolyl-L-seryl-L-serylglycyl-L-alanyl-L-prolyl-L-prolyl-L-prolyl-L-seryl-N^6-[(22*S*)-22,42-dicarboxy-10,19,24-trioxo-3,6,12,15-tetraoxa-9,18,23-triazadotetracontan-1-oyl]-L-lysinamide

olatorépatide

L-tyrosyl-2-méthylalanyl-L-α-glutamylglycyl-L-thréonyl-L-phénylalanyl-L-thréonyl-L-séryl-L-α-aspartyl-L-tyrosyl-L-séryl-L-isoleucyl-L-tyrosyl-L-leucyl-L-α-glutamyl-L-lysyl-L-isoleucyl-L-alanyl-L-alanyl-L-glutaminyl-L-α-glutamyl-L-phénylalanyl-L-valyl-L-asparaginyl-L-tryptophyl-L-leucyl-L-leucyl-L-alanylglycylglycyl-L-prolyl-L-séryl-L-sérylglycyl-L-alanyl-L-prolyl-L-prolyl-L-prolyl-L-séryl-N^6-[(22*S*)-22,42-dicarboxy-10,19,24-trioxo-3,6,12,15-tétraoxa-9,18,23-triazadotétracontan-1-oyl]-L-lysinamide

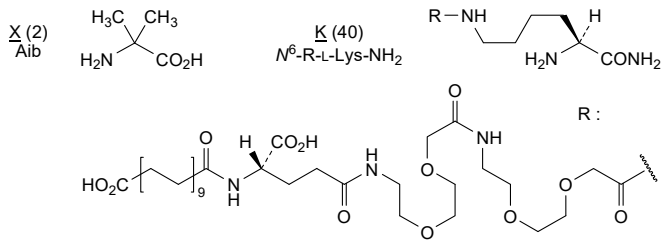
olatorepatida

L-tirosil-2-metilalanil-L-α-glutamilglicil-L-treonil-L-fenilalanil-L-treonil-L-seril-L-α-aspartil-L-tirosil-L-seril-L-isoleucil-L-tirosil-L-leucil-L-α-glutamil-L-lisil-L-isoleucil-L-alanil-L-alanil-L-glutaminil-L-α-glutamil-L-fenilalanil-L-valil-L-asparaginil-L-triptofil-L-leucil-L-leucil-L-alanilglicilglicil-L-prolil-L-seril-L-serilglicil-L-alanil-L-prolil-L-prolil-L-prolil-L-seril-N^6-[(22*S*)-22,42-dicarboxi-10,19,24-trioxo-3,6,12,15-tetraoxa-9,18,23-triazadotetracontan-1-oil]-L-lisinamida

$C_{235}H_{357}N_{49}O_{72}$

YXEGTFTSDY SIYLEKIAAQ EFVNWLLAGG PSSGAPPPSK 40

Modified residues / Résidus modifiés / Restos modificados



olintatugum #

olintatug

immunoglobulin G1-kappa, anti-[*Homo sapiens* KAAG1 (kidney associated DCDC2 antisense RNA 1, kidney associated antigen 1, RU2AS, RU2 antisense gene protein)], humanized and chimeric monoclonal antibody;
H-gamma1 heavy chain humanized (1-445) [VH (*Homo sapiens* IGHV1-46*01 (80.6%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.9] (26-33.51-58.97-105)) (1-116) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (213) (117-214), hinge 1-15 (215-229), CH2 (230-339), CH3 D12 (355), L14 (357) (340-444), CHS K2>del (445)) (117-445)], (219-219')-disulfide with L-kappa light chain chimeric(1'-219') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV1-117*01 (89.0%) -IGKJ2*03 (90.9%) S120>Q (105)/*Homo sapiens* IGKV2-29*02 (89.0%) -IGKJ2*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 (225-225'':228-228'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-DG44, glycoform alfa

olintatug

immunoglobuline G1-kappa, anti-[*Homo sapiens* KAAG1 (antisense DCD2 ARN 1 associé au rein, antigène 1 associé au rein, RU2AS, protéine du gène antisens RU2)], anticorps monoclonal humanisé et chimérique;
chaîne lourde H-gamma1 humanisée (1-445) [VH (*Homo sapiens* IGHV1-46*01 (80.6%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.9] (26-33.51-58.97-105)) (1-116) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (213) (117-214), charnière 1-15 (215-229), CH2 (230-339), CH3 D12 (355), L14 (357) (340-444), CHS K2>del (445)) (117-445)], (219-219')-disulfure avec la chaîne légère L-kappa chimérique (1'-219') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV1-117*01 (89.0%) -IGKJ2*03 (90.9%) S120>Q (105)/*Homo sapiens* IGKV2-29*02 (89.0%) -IGKJ2*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 (225-225'':228-228'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-DG44, glycoforme alfa

olintatug

inmunoglobulina G1-kappa, anti-[*Homo sapiens* KAAG1 (antisentido DCD2 ARN 1 asociado con la renina, antígeno 1 asociado con la renina, RU2AS, proteína del gen antisentido RU2)], anticuerpo monoclonal humanizado y quimérico;
cadena pesada H-gamma1 humanizada (1-445) [VH (*Homo sapiens* IGHV1-46*01 (80.6%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.9] (26-33.51-58.97-105)) (1-116) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (213) (117-214), bisagra 1-15 (215-229), CH2 (230-339), CH3 D12 (355), L14 (357) (340-444), CHS K2>del (445)) (117-445)], (219-219')-disulfuro con la cadena ligera L-kappa quimérica (1'-219') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV1-117*01 (89.0%) -IGKJ2*03 (90.9%) S120>Q (105)/*Homo sapiens* IGKV2-29*02 (89.0%) -IGKJ2*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 (225-225":228-228")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-DG44, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QIQLVQSGAE VKKPGASVKV SCKASGYTFT DDYMSWVKQA PGQGLEWIGD  50
INPYNGDTNY NQKFKGKATL TVDKSTSTAY MELSSLRSED TAVYYCARDP 100
GAMDYWGQGT 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 SLSPG      445
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Light chain / Chaîne légère / Cadena ligera

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DIVMTQTPLS LPVTPGEPAS ISCRSSQSLL HSNGNTYLEW YLQKPGQSPQ  50
LLIYTVSNRF SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCFQGSHVP 100
LTFGQGTKLE IKRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK 150
VQWKVDNALQ SGNSQESVTE QDSKDSTYSL SSTLTLSKAD YEKHKVYACE 200
VTHQGLSSPV TKSFNRGEC                                   219
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 143-199 260-320 366-424
22"-96" 143"-199" 260"-320" 366"-424"
Intra-L (C23-C104) 23'-93' 139'-199'
23'"-93'" 139'"-199'"
Inter-H-L (h 5-CL 126) 219-219' 219"-219'"
Inter-H-H (h 11, h 14) 225-225" 228-228"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)
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

olintatugum tesirinum #

olintatug tesirine

immunoglobulin G1-kappa, anti-[*Homo sapiens* KAAG1 (kidney associated DCDC2 antisense RNA 1, kidney associated antigen 1, RU2AS, RU2 antisense gene protein)], humanized and chimeric monoclonal antibody, conjugated on an average of 2-3 cysteinyl residues to *tesirine*;
H-gamma1 heavy chain humanized (1-445) [VH (*Homo sapiens* IGHV1-46*01 (80.6%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.9] (26-33.51-58.97-105)) (1-116) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (213) (117-214), hinge 1-15 (215-229), CH2 (230-339), CH3 D12 (355), L14 (357) (340-444), CHS K2>del (445)) (117-445)], (219-219')-disulfide with L-kappa light chain chimeric(1'-219') [V-KAPPA Musmus/Homsap (*Mus musculus*

IGKV1-117*01 (89.0%) -IGKJ2*03 (90.9%) S120>Q (105)/*Homo sapiens* IGKV2-29*02 (89.0%) -IGKJ2*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 (225-225'':228-228'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-DG44, glycoform alfa; substituted at the sulfur atoms of 2-3 L-cysteinyl residues on an average among 219, 225, 228, 219', 219'', 225'', 228'' and 219''' with radical group ($1^{11a}S$,$9^{11}S$,$9^{11a}S$,16*S*,19*S*,$52^{3}RS$)-9^{11}-hydroxy-1^{7},9^{7}-dimethoxy-1^{2},9^{2},16-trimethyl-1^{5},9^{5},10,15,18,21,49,52^{2},52^{5}-nonaoxo-19-(propan-2-yl)-1^{5},1^{11a},9^{11},9^{11a}-tetrahydro-$1^{1}H$,$9^{1}H$,$9^{5}H$-2,8,11,24,27,30,33,36,39,42,45-undecaoxa-14,17,20,48-tetraaza-1(8),9(8,10)-bis(pyrrolo[2,1-*c*][1,4]benzodiazepina)-52(1)-pyrrolidina-13(1,4)benzenadopentacontaphan-52^{3}-yl (*tesirine*)

olintatug tésirine

immunoglobuline G1-kappa, anti-[*Homo sapiens* (antisense DCD2 ARN 1 associé au rein, antigène 1 associé au rein, RU2AS, protéine du gène antisens RU2)], anticorps monoclonal humanisé et chimérique, conjugué par 2-3 résidus cystéinyle en moyenne à la *tésirine*;
chaîne lourde H-gamma1 humanisée (1-445) [VH (*Homo sapiens* IGHV1-46*01 (80.6%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.9] (26-33.51-58.97-105)) (1-116) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (213) (117-214), charnière 1-15 (215-229), CH2 (230-339), CH3 D12 (355), L14 (357) (340-444), CHS K2>del (445)) (117-445)], (219-219')-disulfure avec la chaîne légère L-kappa chimérique (1'-219') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV1-117*01 (89.0%) -IGKJ2*03 (90.9%) S120>Q (105)/*Homo sapiens* IGKV2-29*02 (89.0%) -IGKJ2*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 (225-225'':228-228'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-DG44, glycoforme alfa; substitué sur l'atome de soufre de 2-3 résidus L-cystéinyle en moyenne parmi 219, 225, 228, 219', 219'', 225'', 228'' et 219''' avec un groupement radical ($1^{11a}S$,$9^{11}S$,$9^{11a}S$,16*S*,19*S*,$52^{3}RS$)-9^{11}-hydroxy-1^{7},9^{7}-diméthoxy-1^{2},9^{2},16-triméthyl-1^{5},9^{5},10,15,18,21,49,52^{2},52^{5}-nonaoxo-19-(propan-2-yl)-1^{5},1^{11a},9^{11},9^{11a}-tétrahydro-$1^{1}H$,$9^{1}H$,$9^{5}H$-2,8,11,24,27,30,33,36,39,42,45-undécaoxa-14,17,20,48-tétraaza-1(8),9(8,10)-bis(pyrrolo[2,1-*c*][1,4]benzodiazépina)-52(1)-pyrrolidina-13(1,4)benzénadopentacontaphan-52^{3}-yle (*tésirine*)

olintatug tesirina

inmunoglobulina G1-kappa, anti-[*Homo sapiens* (antisentido DCD2 ARN 1 asociado con la renina, antígeno 1 asociado con la renina, RU2AS, proteína del gen antisentido RU2)], anticuerpo monoclonal humanizado y quimérico, conjugado a 2-3 residuos cisteinilo por término medio a la *tesirina*;
cadena pesada H-gamma1 humanizada (1-445) [VH (*Homo sapiens* IGHV1-46*01 (80.6%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.9] (26-33.51-58.97-105)) (1-116) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (213) (117-214), bisagra 1-15 (215-229), CH2 (230-339), CH3 D12 (355), L14 (357) (340-444), CHS K2>del (445)) (117-445)], (219-219')-disulfuro con la cadena ligera L-kappa quimérica (1'-219') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV1-117*01 (89.0%) -IGKJ2*03 (90.9%) S120>Q (105)/*Homo sapiens* IGKV2-29*02 (89.0%) -IGKJ2*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 (225-225'':228-228'')-bisdisulfuro,

producido en las células ováricas de hámster chino (CHO), línea celular CHO-DG44, forma glicosilada alfa; sustituido en el átomo de azufre de 2-3 residuos L-cisteinilo en promedio entre 219, 225, 228, 219', 219", 225", 228" y 219" con un grupo radical (111aS, 911S, 911aS,16S,19S,523RS)-911-hidroxi-12,92,16-trimetil-17,97-dimetoxi-15,95,10,15,18,21,49,522,525-nonaoxo-19-(propan-2- il)-15,111a,911,911a-tetrahidro-11H,91H,95H-2,8,11,24,27,30,33,36,39,42,45-undecaoxa-14,17,20,48-tetraaza -1(8),9(8,10)-bis(pirrolo[2,1-c][1,4]benzodiazepina)-52(1)-pirrolidina-13(1,4)bencenadopentacontafano-523-ilo (*tesirina*)

Heavy chain / Chaîne lourde / Cadena pesada

```
QIQLVQSGAE VKKPGASVKV SCKASGYTFT DDYMSWVKQA PGQGLEWIGD  50
INPYNGDTNY NQKFKGKATL TVDKSTSTAY MELSSLRSED TAVYYCARDP 100
GAMDYWGQGT 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 SLSPG      445
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Light chain / Chaîne légère / Cadena ligera

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DIVMTQTPLS LPVTPGEPAS ISCRSSQSLL HSNGNTYLEW YLQKPGQSPQ  50
LLIYTVSNRF SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCFQGSHVP 100
LTFGQGTKLE IKRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK 150
VQWKVDNALQ SGNSQESVTE QDSKDSTYSL SSTLTLSKAD YEKHKVYACE 200
VTHQGLSSPV TKSFNRGEC                                   219
```

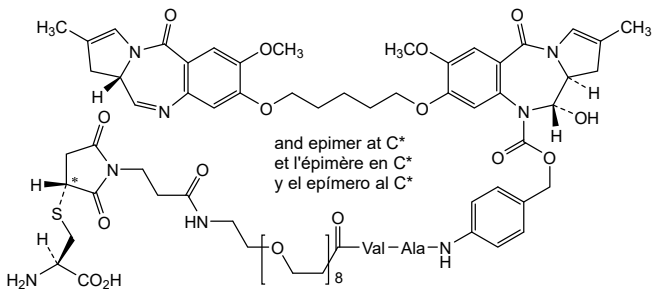
Post-translational modifications

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 143-199 260-320 366-424
22"-96" 143"-199" 260"-320" 366"-424"
Intra-L (C23-C104) 23'-93' 139'-199'
23'"-93'" 139'"-199'"
Inter-H-L (h 5-CL 126) 219-219' 219"-219'"
Inter-H-H (h 11, h 14) 225-225" 228-228"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)
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

Potential modified residues / résidus modifiés potentiels / restos modificados potenciales*
C (219,225,228,219',219",225",228",219'")
*(tesirine:mAb ~ 2.5:1)



opugotamigum #

opugotamig — immunoglobulin (G1_L-kappa)_scFvkh-G1(h-CH2-CH3), anti-[*Homo sapiens* FOLR1 (folate receptor 1, folate receptor alpha, FR-alpha, adult folate-binding protein, FBP, ovarian tumor-associated antigen MOv18)], biparatopic, bivalent;
H-gamma1 heavy chain, anti-FOLR1 (1-447) [VH (*Mus musculus* IGHV1-37*01 (87.8%) -(IGHD) -IGHJ4*01 (93.3%) S123>T (113), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, G1v33 CH3 S22, A24, V86 (hole) (CH1 R120>K (215) (119-216), hinge 1-15 (217-231), CH2 (232-341), CH3 E12 (357), M14 (359), T22>S (367), L24>A (369), Y86>V (408) (342-446), CHS K2>del (447)) (119-447)], (221-218')-disulfide with L-kappa light chain, anti-FOLR1 (1'-218') [V-KAPPA (*Mus musculus* IGKV3-9*01 (80.8%) -IGKJ2*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')];
scFvkh-G1(h-CH2-CH3) heavy chain, anti-FOLR1 (1''-479'') [V-KAPPA (*Mus musculus* IGKV5-43*01 (86.3%) -IGKJ2*03 (91.7%) S120>C (101''), CDR-IMGT [6.3.10] (27''-32''.50''-52''.89''-98'')) (1''-108'')-20-mer tetrakis(tetraglycyl-seryl) linker (109''-128'') -VH (*Mus musculus* IGHV5-17*02 (88.8%) -(IGHD) -IGHJ3*01 (91.7%) A128>S (246''), CDR-IMGT [8.8.11] (154''-161''.179''-186''.225''-235'')) (129''-246'') -2-mer (glycyl-seryl) linker (247''-248'') -*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 CH3 E12, M14, G1v37 h S5, G1v32 CH3 W22 (knob) (hinge 1-15 C5>S (253'') (249''-263''), CH2 (264''-373''), CH3 T22>W (399'') (374''-478''), CHS K2>del (479'')) (249''-479'')]; dimer (227-259'': 230-262'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa

opugotamig — immunoglobuline (G1_L-kappa)_scFvkh-G1(h-CH2-CH3), anti-[*Homo sapiens* FOLR1 (récepteur 1 du folate, récepteur alpha du folate, FR-alpha, protéine de l'adulte liant le folate, FBP, antigène MOv18 associé à des tumeurs ovariennes)], biparatopique, bivalent;
chaîne lourde H-gamma1, anti-FOLR1 (1-447) [VH (*Mus musculus* IGHV1-37*01 (87.8%) -(IGHD) -IGHJ4*01 (93.3%) S123>T (113), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, G1v33 CH3 S22, A24, V86 (hole) (CH1 R120>K (215) (119-216), charnière 1-15 (217-231), CH2 (232-341), CH3 E12 (357), M14 (359), T22>S (367), L24>A (369), Y86>V (408) (342-446), CHS K2>del (447)) (119-447)], (221-218')-disulfure avec la chaîne légère L-kappa, anti-FOLR1 (1'-218') [V-KAPPA (*Mus musculus* IGKV3-9*01 (80.8%) -IGKJ2*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')];
chaîne lourde scFvkh-G1(h-CH2-CH3), anti-FOLR1 (1''-479'') [V-KAPPA (*Mus musculus* IGKV5-43*01 (86.3%) -IGKJ2*03 (91.7%) S120>C (101''), CDR-IMGT [6.3.10] (27''-32''.50''-52''.89''-98'')) (1''-108'')-20-mer tétrakis(tétraglycyl-séryl) linker (109''-128'') -VH (*Mus musculus* IGHV5-17*02 (88.8%) -(IGHD) -IGHJ3*01 (91.7%) A128>S (246), CDR-IMGT [8.8.11] (154''-161''.179''-186''.225''-235'')) (129''-246'') -2-mer (glycyl-séryl) linker (247''-248'') -*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 CH3 E12, M14, G1v37 h S5, G1v32 CH3 W22 (knob) (charnière 1-15 C5>S (253'') (249''-263''), CH2 (264''-373''), CH3 T22>W (399'') (374''-478''), CHS K2>del (479'')) (249''-479'')]; dimère (227-259'': 230-262'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa

opugotamig — inmunoglobulina (G1_L-kappa)_scFvkh-G1(h-CH2-CH3), anti-[*Homo sapiens* FOLR1 (receptor 1 del folato, receptor alfa del folato, FR-alfa, proteína del adulto que se une al folato, FBP, antígeno MOv18 asociado con dos tumores ováricos)], biparatópico y bivalente;

cadena pesada H-gamma1, anti-FOLR1 (1-447) [VH (*Mus musculus* IGHV1-37*01 (87.8%) -(IGHD) -IGHJ4*01 (93.3%) S123>T (113), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, G1v33 CH3 S22, A24, V86 (hole) (CH1 R120>K (215) (119-216),bisagra 1-15 (217-231), CH2 (232-341), CH3 E12 (357), M14 (359), T22>S (367), L24>A (369), Y86>V (408) (342-446), CHS K2>del (447)) (119-447)], (221-218')-disulfuro con la cadena ligera L-kappa, anti-FOLR1 (1'-218') [V-KAPPA (*Mus musculus* IGKV3-9*01 (80.8%) -IGKJ2*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')];
cadena pesada scFvkh-G1(h-CH2-CH3), anti-FOLR1 (1"-479") [V-KAPPA (*Mus musculus* IGKV5-43*01 (86.3%) -IGKJ2*03 (91.7%) S120>C (101"), CDR-IMGT [6.3.10] (27"-32".50"-52".89"-98")) (1"-108")-20-mer tetrakis(tetraglicil-seril) enlace (109"-128") -VH (*Mus musculus* IGHV5-17*02 (88.8%) -(IGHD) -IGHJ3*01 (91.7%) A128>S (246), CDR-IMGT [8.8.11] (154"-161".179"-186".225"-235")) (129"-246") -2-mer (glicil-seril) enlace (247"-248") -*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 CH3 E12, M14, G1v37 h S5, G1v32 CH3 W22 (knob) (bisagra1-15 C5>S (253") (249"-263"), CH2 (264"-373"), CH3 T22>W (399") (374"-478"), CHS K2>del (479")) (249"-479")]; dímero (227-259": 230-262")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada: anti-FOLR1-hole (H)

```
QVQLVQSGAE VVKPGASVKI SCKASGYTFT GYFMNWVKQS PGQSLEWIGR  50
IHPYDGDTFY NQKFQGKATL TVDKSSNTAH MELLSLTSED FAVYYCTRYD 100
GSRAMDYWGQ GTTVTVSSAS TKGPSVFPLA PSSKSTSGGT AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTQTYI 200
CNVNHKPSNT KVDKKVEPKS CDKTHTCPPC PAPELLGGPS VFLFPPKPKD 250
TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNST 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY 350
TLPPSREEMT KNQVSLSCAV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD 400
SDGSFFLVSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPG    447
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Light chain / Chaîne légère / Cadena ligera: anti-FOLR1 (L')

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DIVLTQSPLS LAVSLGQPAI ISCKASQSVS FAGTSLMHWY HQKPGQQPRL  50
LIYRASNLEA GVPDRFSGSG SKTDFTLTIS PVEAEDAATY YCQQSREYPY 100
TFGGGTKLEI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL NNFYPREAKV 150
QWKVDNALQS GNSQESVTEQ DSKDSTYSLS STLTLSKADY EKHKVYACEV 200
THQGLSSPVT KSFNRGEC                                    218
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Heavy chain / Chaîne lourde / Cadena pesada: anti-FOLR1-knob (H")

```
EIVLTQSPAT LSVTPGDRVS LSCRASQNIN NNLHWYQQKP GQSPRLLIKY  50
VSQSVSGIPD RFSGSGSGTD FTLSISSVEP EDEGMYFCQQ SNSWPHYTFG 100
CGTKLEIKGG GGSGGGGSGG GGSGGGGSEV QLVQSGGGLV QPGGSRRLSC 150
AASGFTFSSF GMHWVRQAPG KCLEWVAYIS SGSSTISYAD SVKGRFTISR 200
DNSKKTLLLQ MTSLRAEDTA MYYCAREAYG SSMEYWGQGT LVTVSSGSEP 250
KSSDKTHTCP PCPAPELLGG PSVFLFPPKP KDTLMISRTP EVTCVVVDVS 300
HEDPEVKFNW YVDGVEVHNA KTKPREEQYN STYRVVSVLT VLHQDWLNGK 350
EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSREE MTKNQVSLWC 400
LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW 450
QQGNVFSCSV MHEALHNHYT QKSLSLSPG                        479
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Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 145-201 262-322 368-426
23"-88" 150"-224" 294"-354" 400"-458"
Intra-H scFv VL120-VH49* 101"-172"
Intra-L (C23-C104) 2 3'-92' 138'-198'
Inter-H-L (CH1 10-CL 126) 221-218'
Inter-H-H (h 8, h 11) 227-259" 230-262"
*Engineered additional disulfide bond to stabilize the scFv.

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)
H VH Q1: 1

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4: 298, 330"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

opugotamigum olatansinum

opugotamig olatansine

immunoglobulin (G1_L-kappa)_scFvkh-G1(h-CH2-CH3), anti-[*Homo sapiens* FOLR1 (folate receptor 1, folate receptor alpha, FR-alpha, adult folate-binding protein, FBP, ovarian tumor-associated antigen MOv18)], biparatopic, assymetric, bivalent; conjugated, on an average of 3 to 4 lysinyl residues to *olatansine*;
H-gamma1 heavy chain, anti-FOLR1 (1-447) [VH (*Mus musculus* IGHV1-37*01 (87.8%) -(IGHD) -IGHJ4*01 (93.3%) S123>T (113) , CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, G1v33 CH3 S22, A24, V86 (hole) (CH1 R120>K (215) (119-216), hinge 1-15 (217-231), CH2 (232-341), CH3 E12 (357), M14 (359), T22>S (367), L24>A (369), Y86>V (408) (342-446), CHS K2>del (447)) (119-447)], (221-218')-disulfide with L-kappa light chain, anti-FOLR1 (1'-218') [V-KAPPA (*Mus musculus* IGKV3-9*01 (80.8%) -IGKJ2*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')];
scFvkh-G1(h-CH2-CH3) heavy chain, anti-FOLR1 (1''-479'') [V-KAPPA (*Mus musculus* IGKV5-43*01 (86.3%) -IGKJ2*03 (91.7%) S120>C (101''), CDR-IMGT [6.3.10] (27''-32''.50''-52''.89''-98'')) (1''-108'')-20-mer tetrakis(tetraglycyl-seryl) linker (109''-128'') -VH (*Mus musculus* IGHV5-17*02 (88.8%) -(IGHD) -IGHJ3*01 (91.7%) A128>S (246''), CDR-IMGT [8.8.11] (154''-161''.179''-186''.225''-235'')) (129''-246'') -2-mer (glycyl-seryl) linker (247''-248'') -*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 CH3 E12, M14, G1v37 h S5, G1v32 CH3 W22 (knob) (hinge 1-15 C5>S (253'') (249''-263''), CH2 (264''-373''), CH3 T22>W (399'') (374''-478''), CHS K2>del (479'')) (249''-479'')]; dimer (227-259'': 230-262'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa; substituted at the side chain nitrogen atom of an average of 3 to 4 L-lysinyl residues with radical group 4-[(3*RS*)-3-{[(2*S*,14*S*,17*R*,20*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}-2,3,14,17,20-pentamethyl-1,4,13,16,19,22-hexaoxo-10-thia-3,12,15,18,21-pentaazapentacosan-25-yl]sulfanyl}-2,5-dioxopyrrolidin-1-yl]butanoyl (*olatansine*)

opugotamig olatansine

immunoglobuline (G1_L-kappa)_scFvkh-G1(h-CH2-CH3), anti-[*Homo sapiens* FOLR1 (récepteur 1 du folate, récepteur alpha du folate, FR-alpha, protéine de l'adulte liant le folate, FBP, antigène MOv18 associé à des tumeurs ovariennes)], biparatopique, asymétrique, bivalent; conjugué par 3 à 4 résidus lysinyle en moyenne à l'*olatansine*;
chaîne lourde H-gamma1, anti-FOLR1 (1-447) [VH (*Mus musculus* IGHV1-37*01 (87.8%) -(IGHD) -IGHJ4*01 (93.3%) S123>T (113), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, G1v33 CH3 S22, A24, V86 (hole) (CH1 R120>K (215) (119-216), charnière 1-15 (217-231), CH2 (232-341), CH3 E12 (357), M14 (359), T22>S (367), L24>A (369), Y86>V (408) (342-446), CHS K2>del (447)) (119-447)], (221-218')-disulfure avec la

	chaîne légère L-kappa, anti-FOLR1 (1'-218') [V-KAPPA (*Mus musculus* IGKV3-9*01 (80.8%) -IGKJ2*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')]; chaîne lourde scFvkh-G1(h-CH2-CH3), anti-FOLR1 (1''-479'') [V-KAPPA (*Mus musculus* IGKV5-43*01 (86.3%) -IGKJ2*03 (91.7%) S120>C (101''), CDR-IMGT [6.3.10] (27''-32''.50''-52''.89''-98'')) (1''-108'')-20-mer tétrakis(tétraglycyl-séryl) linker (109''-128'') -VH (*Mus musculus* IGHV5-17*02 (88.8%) -(IGHD) -IGHJ3*01 (91.7%) A128>S (246), CDR-IMGT [8.8.11] (154''-161''.179''-186''.225''-235'')) (129''-246'') -2-mer (glycyl-séryl) linker (247''-248'') -*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 CH3 E12, M14, G1v37 h S5, G1v32 CH3 W22 (knob) (charnière 1-15 C5>S (253'') (249''-263''), CH2 (264''-373''), CH3 T22>W (399'') (374''-478''), CHS K2>del (479'')) (249''-479'')]; dimère (227-259'': 230-262'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa; substitué sur l'atome d'azote de la chaîne latérale de 3 à 4 résidus lysinyle en moyenne avec un groupement radical 4-[(3*RS*)-3-{[(2*S*,14*S*,17*R*,20*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)-benzénacyclotétradécaphane-10,12-dién-4-yl]oxy}-2,3,14,17,20-pentaméthyl-1,4,13,16,19,22-hexaoxo-10-thia-3,12,15,18,21-pentaazapentacosan-25-yl]sulfanyl}-2,5-dioxopyrrolidin-1-yl]butanoyle (*olatansine*)
opugotamig olatansina	inmunoglobulina (G1_L-kappa)_scFvkh-G1(h-CH2-CH3), anti-[*Homo sapiens* FOLR1 (receptor 1 del folato, receptor alfa del folato, FR-alfa, proteína del adulto que se une al folato, FBP, antígeno MOv18 asociado con los tumores ováricos)], biparatópico, asimétrico, bivalente; conjugado por 3 a 4 residuos lisinilo en promedio a la *olatansina*; cadena pesada H-gamma1, anti-FOLR1 (1-447) [VH (*Mus musculus* IGHV1-37*01 (87.8%) -(IGHD) -IGHJ4*01 (93.3%) S123>T (113), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, G1v33 CH3 S22, A24, V86 (hole) (CH1 R120>K (215) (119-216), bisagra 1-15 (217-231), CH2 (232-341), CH3 E12 (357), M14 (359), T22>S (367), L24>A (369), Y86>V (408) (342-446), CHS K2>del (447)) (119-447)], (221-218')-disulfuro con la cadena ligera L-kappa, anti-FOLR1 (1'-218') [V-KAPPA (*Mus musculus* IGKV3-9*01 (80.8%) -IGKJ2*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')]; cadena pesada scFvkh-G1(h-CH2-CH3), anti-FOLR1 (1''-479'') [V-KAPPA (*Mus musculus* IGKV5-43*01 (86.3%) -IGKJ2*03 (91.7%) S120>C (101''), CDR-IMGT [6.3.10] (27''-32''.50''-52''.89''-98'')) (1''-108'')-20-mer tetrakis(tetraglicil-seril) enlace (109''-128'') -VH (*Mus musculus* IGHV5-17*02 (88.8%) -(IGHD) -IGHJ3*01 (91.7%) A128>S (246), CDR-IMGT [8.8.11] (154''-161''.179''-186''.225''-235'')) (129''-246'') -2-mer (glicil-seril) enlace (247''-248'') -*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 CH3 E12, M14, G1v37 h S5, G1v32 CH3 W22 (knob) (bisagra 1-15 C5>S (253'') (249''-263''), CH2 (264''-373''), CH3 T22>W (399'') (374''-478''), CHS K2>del (479'')) (249''-479'')]; dímero (227-259'': 230-262'')-bisdisulfuro,

producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, forma glicosilada alfa; sustituido en el átomo de nitrógeno de la cadena lateral de 3 a 4 residuos lisinilo en promedio con un grupo radical 4-[(3*RS*)-3-{[(2*S*,14*S*,17*R*,20*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-8^{5},14-dimetoxi-2,3^{3},7,10-tetrametil-1^{2},6-dioxo-7-aza-1(6,4)-[1,3]oxazinana-3(2,3)-oxirana-8(1,3)-bencenaciclotetradecafano-10,12-dien-4-il]oxi}-2,3,14,17,20-pentametil-1,4,13,16,19,22-hexaoxo-10-tia-3,12,15,18,21-pentaazapentacosan-25-il]sulfanil}-2,5-dioxopirrolidin-1-il]butanoilo (*olatansina*)

Heavy chain / Chaîne lourde / Cadena pesada: anti-FOLR1-hole (H)

```
QVQLVQSGAE VVKPGASVKI SCKASGYTFT GYFMNWVKQS PGQSLEWIGR  50
IHPYDGDTFY NQKFQGKATL TVDKSSNTAH MELLSLTSED FAVYYCTRYD 100
GSRAMDYWGQ GTTVTVSSAS TKGPSVFPLA PSSKSTSGGT AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTQTYI 200
CNVNHKPSNT KVDKKVEPKS CDKTHTCPPC PAPELLGGPS VFLFPPKPKD 250
TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNST 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY 350
TLPPSREEMT KNQVSLSCAV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD 400
SDGSFFLVSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPG    447
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Light chain / Chaîne légère / Cadena ligera: anti-FOLR1 (L')

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DIVLTQSPLS LAVSLGQPAI ISCKASQSVS FAGTSLMHWY HQKPGQQPRL  50
LIYRASNLEA GVPDRFSGSG SKTDFTLTIS PVEAEDAATY YCQQSREYPY 100
TFGGGTKLEI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL NNFYPREAKV 150
QWKVDNALQS GNSQESVTEQ DSKDSTYSLS STLTLSKADY EKHKVYACEV 200
THQGLSSPVT KSFNRGEC                                    218
```

Heavy chain / Chaîne lourde / Cadena pesada: anti-FOLR1-knob (H")

```
EIVLTQSPAT LSVTPGDRVS LSCRASQNIN NNLHWYQQKP GQSPRLLIKY  50
VSQSVSGIPD RFSGSGSGTD FTLSISSVEP EDEGMYFCQQ SNSWPHYTFG 100
CGTKLEIKGG GGSGGGGSGG GGSGGGGSEV QLVQSGGGLV QPGGSRRLSC 150
AASGFTFSSF GMHWVRQAPG KCLEWVAYIS SGSSTISYAD SVKGRFTISR 200
DNSKKTLLLQ MTSLRAEDTA MYYCAREAYG SSMEYWGQGT LVTVSSGSEP 250
KSSDKTHTCP PCPAPELLGG PSVFLFPPKP KDTLMISRTP EVTCVVVDVS 300
HEDPEVKFNW YVDGVEVHNA KTKPREEQYN STYRVVSVLT VLHQDWLNGK 350
EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSREE MTKNQVSLWC 400
LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW 450
QQGNVFSCSV MHEALHNHYT QKSLSLSPG                        479
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Post-translational modifications

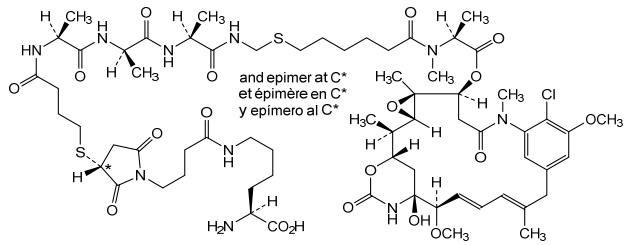
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

Intra-H (C23-C104) 22-96 145-201 262-322 368-426
23"-88" 150"-224" 294"-354" 400"-458"
Intra-H scFv VL120-VH49* 101"-172"
Intra-L (C23-C104) 23'-92' 138'-198'
Inter-H-L (CH1 10-CL 126) 221-218'
Inter-H-H (h 8, h 11) 227-259" 230-262"
*Engineered additional disulfide bond to stabilize the scFv.

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)
H VH Q1: 1

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
298, 330"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

Potential modified residues / résidus modifiés potentiels / restos modificados potenciales*
K (Lys)
*(olatansine:mAb ~ 3.5:1)



osencabtagenum autoleucelum #

osencabtagene autoleucel	autologous T lymphocytes obtained from peripheral blood by leukapheresis, transduced with two self-inactivating, non-replicating lentiviral vectors encoding: (i) a chimeric antigen receptor (CAR) targeting human CD7: the expressed transgene comprises a granulocyte-macrophage colony-stimulating factor (GM-CSF) receptor signal sequence, a single-domain antibody derived from a humanized nano-antibody (HuVHH6) targeting CD7, an immunoglobulin G4 (IgG4) Fc hinge, an inducible T lymphocyte costimulator (ICOS) transmembrane and intracellular domain, a 4-1BB intracellular costimulatory domain and a CD3ζ intracellular activation domain, under control of the human elongation factor 1 alpha (EF1α) promoter. (ii) a CD7-blocking gene comprising a granulocyte-macrophage colony-stimulating factor (GM-CSF) receptor signal sequence, a bivalent CD7 nano-antibody sequence (VHH6-linker-VHH6) fused to an endoplasmic reticulum (ER) retention sequence (KDEL sequence), under control of the cytomegalovirus promoter. In both constructs, the transgene is flanked by 5' and 3' long terminal repeats (LTRs) and also contains a ψ packaging signal, a Rev response element (RRE) and a central polypurine tract (cPPT) sequence 5' to the transgene, and a Woodchuck hepatitis virus post-transcriptional regulatory element (WPRE)3' to the transgene. Both vectors are pseudotyped with vesicular stomatitis virus (VSV) G glycoprotein. The leukapheresis material is enriched for CD4+ and CD8+ T lymphocytes by positive immunoselection prior to activation with CD3 and CD28 agonists in growth media containing interleukin 7 (IL-7) and interleukin 15 (IL-15). The cells are then transduced with the lentiviral vectors and expanded in growth media containing IL-7 and IL-15. The cell suspension consists of CD3+ T lymphocytes (≥90%; of which CD3+CD7- T lymphocytes account for more than 95%), with greater than 5% of the T lymphocytes expressing the CAR transgene. The transduced T lymphocytes release interferon gamma (IFN-γ) by co-culture with target cells *in vitro*
osencabtagène autoleucel	lymphocytes T autologues obtenus à partir de sang périphérique par leucaphérèse, transduits avec deux vecteurs lentivirus auto-inactivants et non-répliquants codant: (i) un récepteur antigénique chimérique (CAR) ciblant le CD7 humain : le transgène exprimé comprend une séquence signal du récepteur du facteur de stimulation des granulocytes et macrophages (GM-CSF), un anticorps à domaine unique dérivé d'un nano-anticorps humanisé (HuVHH6) ciblant CD7, une charnière Fc de l'immunoglobuline G4 (IgG4), un domaine transmembranaire et intracellulaire de costimulation des lymphocytes T inductibles (ICOS), un domaine intracellulaire de costimulation 4-1BB et un domaine d'activation intracellulaire CD3ζ, sous le contrôle du promoteur du facteur d'élongation 1 alpha (EF1α) humain.

(ii) un gène bloquant CD7 comprenant une séquence signal du récepteur du facteur de stimulation des granulocytes et macrophages (GM-CSF), une séquence bivalente de nano-anticorps CD7 (VHH6-linker-VHH6) fusionnée à une séquence de rétention du réticulum endoplasmique (séquence KDEL), sous le contrôle du promoteur du cytomégalovirus (CMV).
Dans les deux constructions, le transgène est flanqué de longues répétitions terminales (LTR) en 5' et 3' et contient également un signal d'encapsidation ψ, un élément de réponse Rev (RRE) et une séquence du tractus polypurine central (cPPT) en 5' du transgène, et un élément de régulation post-transcriptionnelle du virus de l'hépatite de la marmotte (WPRE) en 3' du transgène. Les deux vecteurs sont pseudotypés avec la glycoprotéine G du virus de la stomatite vésiculaire (VSV).
Le matériel de leucaphérèse est enrichi en lymphocytes T CD4+ et CD8+ par immunosélection positive avant d'être activé avec des agonistes CD3 et CD28 dans un milieu de croissance contenant de l'interleukine 7 (IL-7) et de l'interleukine 15 (IL-15). Les cellules sont ensuite transduites avec les vecteurs lentivirus et amplifiées dans un milieu de croissance contenant de l'IL-7 et de l'IL-15. La suspension cellulaire est constituée de lymphocytes T CD3+ (≥90 %, dont plus de 95% de lymphocytes T CD3+CD7-), avec plus de 5% des lymphocytes T exprimant le transgène CAR. Les lymphocytes T transduits libèrent de l'interféron gamma (IFN-γ) par co-culture avec des cellules cibles *in vitro*

osencabtagén autoleucel

linfocitos T autólogos obtenidos de sangre periférica mediante leucoaféresis, transducidos con dos vectores lentivirales no replicativos, auto inactivantes, que codifican para:
(i) un receptor de antígenos quimérico (CAR) dirigido a CD7 humano: el transgén expresado contiene una secuencia señal del receptor del factor estimulador de colonias granulocito-macrófago (GM-CSF), un anticuerpo de dominio único derivado de un nano-anticuerpo humanizado (HuVHH6) frente a CD7, una bisagra del Fc de la inmunoglobulina 4 (IgG4), un dominio transmembrana e intracelular del coestimulador inducible de linfocitos T (ICOS), un dominio coestimulador intracelular de 4-1BB y un dominio de activación intracelular de CD3ζ, bajo el control del promotor del factor de elongación 1 alfa (EF1α) humano.
(ii) un gen bloqueante de CD7 que contiene una secuencia señal del receptor del factor estimulador de colonias granulocito-macrófago (GM-CSF), una secuencia de nano-anticuerpo bivalente frente a CD7 (VHH6-linker-VHH6) fusionada a una secuencia de retención en retículo endoplasmático (secuencia KDEL), bajo el control del promotor de citomegalovirus.
En ambos constructos, el transgén está flanqueado por repeticiones terminales largas (LTRs) en 5' y 3' y también contiene una señal de empaquetamiento ψ, un elemento de respuesta Rev (RRE) y una secuencia de tracto de polipurina central (cPPT) en 5' del transgén y un elemento regulador post-transcripcional del virus de la hepatitis de la marmota (WPRE) en 3' del transgén. Ambos vectores están seudotipados con la glicoproteína G del virus de la estomatitis vesicular (VSV).
El material de leucoaféreis se enriquece en linfocitos T CD4+ y CD8+ mediante inmunoslección positiva antes de la activación con agonistas de CD3 y CD28 en medio de crecimiento que contiene interleuquina 7 (IL-7) e interleuquina 15 (IL-15). A continuación, las células se transducen con los vectores lentivirales y se expandiden en medio de crecimiento que contiene IL-7 e IL-15. La suspensión celular consiste en linfocitos T CD3+ (≥90%; de los cuales los linfocitos T CD3+CD7- son más del 95%), con más del 5% de los linfocitos T que expresan el transgén CAR. Los linfocitos T transducidos liberan interferón gamma (IFN-γ) mediante su cocultivo con células diana *in vitro*

ozureprubartum #

ozureprubart	immunoglobulin G1-kappa, anti-[*Homo sapiens* IGHE (immunoglobulin constant epsilon) region of IgE heavy chain, Fc region of IgE)], humanized monoclonal antibody; H-gamma1 heavy chain humanized (1-451) [VH (*Homo sapiens* IGHV3-66*01 (84.7%) -(IGHD) -IGHJ3*01 (85.7%) M123>L (116), CDR-IMGT [9.7.14] (26-34.52-58.97-110)) (1-121) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, G1v21 CH2 Y15.1, T16, E18 (CH1 R120>K (218) (122-219), hinge 1-15 (220-234), CH2 M15.1>Y (256), S16>T (258), T18>E (260) (235-344), CH3 E12 (360), M14 (362) (345-449), CHS (450-451)) (122-451)], (224-218')-disulfide with L-kappa light chain humanized (1'-218') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (87.9%) -IGKJ2*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 (230-230'':233-233'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-S, glycoform alfa
ozuréprubart	immunoglobuline G1-kappa, anti-[*Homo sapiens* IGHE (immunoglobuline constante epsilon) région de la chaîne lourde des IgE, région Fc des IgE)], anticorps monoclonal humanisé; chaîne lourde H-gamma1 humanisée (1-451) [VH (*Homo sapiens* IGHV3-66*01 (84.7%) -(IGHD) -IGHJ3*01 (85.7%) M123>L (116), CDR-IMGT [9.7.14] (26-34.52-58.97-110)) (1-121) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, G1v21 CH2 Y15.1, T16, E18 (CH1 R120>K (218) (122-219), charnière 1-15 (220-234), CH2 M15.1>Y (256), S16>T (258), T18>E (260) (235-344), CH3 E12 (360), M14 (362) (345-449), CHS (450-451)) (122-451)], (224-218')-disulfure avec la chaîne légère L-kappa humanisée (1'-218') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (87.9%) -IGKJ2*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 (230-230'':233-233'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-S, glycoforme alfa
ozureprubart	inmunoglobulina G1-kappa, anti-[*Homo sapiens* IGHE (inmunoglobulina constante épsilon) región de la cadena pesada de las IgE, región Fc de las IgE)], anticuerpo monoclonal humanizado; cadena pesada H-gamma1 humanizada (1-451) [VH (*Homo sapiens* IGHV3-66*01 (84.7%) -(IGHD) -IGHJ3*01 (85.7%) M123>L (116), CDR-IMGT [9.7.14] (26-34.52-58.97-110)) (1-121) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, G1v21 CH2 Y15.1, T16, E18 (CH1 R120>K (218) (122-219), bisagra 1-15 (220-234), CH2 M15.1>Y (256), S16>T (258), T18>E (260) (235-344), CH3 E12 (360), M14 (362) (345-449), CHS (450-451)) (122-451)], (224-218')-disulfuro con la cadena ligera L-kappa humanizada (1'-218') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (87.9%) -IGKJ2*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 (230-230'':233-233'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-S, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada : H-gamma1 (H, H'') anti-IGHE

```
EVQLVESGGG LVQPGGSLRL SCAVSGYSIT SGYSWNWVRQ APGKGLEWVS  50
VITYAGSTNY ADSVKGRFTI SRDDSKNTFY LQMNSLRAED TAVYYCARGT 100
HYFGHWHFAV WGQGTLVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200
TYICNVNHKP SNTKVDKKVE PKSCDKTHTC PPCPAPELLG GPSVFLFPPK 250
PKDTLYITRE PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY 300
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP 350
QVYTLPPSRE EMTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP 400
VLDSDGSFFL YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG 450
K                                                       451
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Light chain / Chaîne légère / Cadena ligera : L-kappa (L', L''') anti-IGHE

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DIQLTQSPSS LSASVGDRVT ITCRASQSVG DEADSYMNWY QQKPGKAPKL  50
LIYAASYLQS GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSHEDPY 100
TFGQGTKLEI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL NNFYPREAKV 150
QWKVDNALQS GNSQESVTEQ DSKDSTYSLS STLTLSKADY EKHKVYACEV 200
THQGLSSPVT KSFNRGEC                                     218
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Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 148-204 265-325 371-429
22"-96" 148"-204" 265"-325" 371"-429"
Intra-L (C23-C104) 23'-92' 138'-198'
23'"-92'" 138'"-198'"
Inter-H-L (h 5-CL 126) 224-218' 224"-218'"
Inter-H-H (h 11, h 14) 230-230" 233-233"

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

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2: 451, 451"

pacibekitugum

pacibekitug — immunoglobulin G2-kappa, anti-[*Homo sapiens* IL6 (interleukin 6, IL-6)], *Homo sapiens* monoclonal antibody;
H-gamma2 heavy chain *Homo sapiens* (1-442) [VH (*Homo sapiens* IGHV4-34*12 (95.9%) -(IGHD) -IGHJ3*02 (93.8%), CDR-IMGT [8.7.10] (26-33.51-57.96-105)) (1-116) -*Homo sapiens* IGHG2*01 (100%), G2m.. CH2 V45.1 (CH1 (117-214), hinge 1-12 (215-226), CH2 V45.1 (277) (227-335), CH3 (336-440), CHS (441-442)) (117-442)], (130-214')-disulfide with L-kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1D-16*01 (98.9%) -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 (218-218":219-219":222-222":225-225")-tetrakisdisulfide, produced in Chinese hamster ovary (CHO)-K1SV cell line, lacking the glutamine synthetase gene (GS-KO), glycoform alfa

pacibékitug — immunoglobuline G2-kappa, anti-[*Homo sapiens* IL6 (interleukine 6, IL-6)], anticorps monoclonal *Homo sapiens*;
chaîne lourde H-gamma2 *Homo sapiens* (1-442) [VH (*Homo sapiens*IGHV4-34*12 (95.9%) -(IGHD) -IGHJ3*02 (93.8%), CDR-IMGT [8.7.10] (26-33.51-57.96-105)) (1-116) -*Homo sapiens* IGHG2*01 (100%), G2m.. CH2 V45.1 (CH1 (117-214), charnière 1-12 (215-226), CH2 V45.1 (277) (227-335), CH3 (336-440), CHS (441-442)) (117-442)], (130-214')-disulfure avec la chaîne légère L-kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1D-16*01 (98.9%) -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 (218-218":219-219":222-222":225-225")- tétrakisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO) lignée cellulaire CHO-K1SV, ne présentant pas le gène de la glutamine synthétase (GS-KO), glycoforme alfa

pacibekitug

inmunoglobulina G2-kappa, anti-[*Homo sapiens* IL6 (interleukina 6, IL-6)], anticuerpo monoclonal *Homo sapiens*;
cadena pesada H-gamma2 *Homo sapiens* (1-442) [VH (*Homo sapiens* IGHV4-34*12 (95.9%) -(IGHD) -IGHJ3*02 (93.8%), CDR-IMGT [8.7.10] (26-33.51-57.96-105)) (1-116) -*Homo sapiens* IGHG2*01 (100%), G2m.. CH2 V45.1 (CH1 (117-214), bisagra 1-12 (215-226), CH2 V45.1 (277) (227-335), CH3 (336-440), CHS (441-442)) (117-442)], (130-214')-disulfuro con la cadena ligera L-kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1D-16*01 (98.9%) -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 (218-218":219-219":222-222":225-225")- tetrakisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular CHO-K1SV, en ausencia del gen glutamina sintetasa (GS-KO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLQQWGAG LLKPSETLSL TCAIYGGSFR EYYWSWIRQP PGKGLEWIGE  50
IFHSGSTNYN PSLKSRVTIS VDTSKNQFSL KLSSVTAADT AVYYCAREEL 100
DDFDIWGQGT MVTVSSASTK GPSVFPLAPC SRSTSESTAA LGCLVKDYFP 150
EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVVTVPSS NFGTQTYTCN 200
VDHKPSNTKV DKTVERKCCV ECPPCPAPPV AGPSVFLFPP KPKDTLMISR 250
TPEVTCVVVD VSHEDPEVQF NWYVDGVEVH NAKTKPREEQ FNSTFRVVSV 300
LTVVHQDWLN GKEYKCKVSN KGLPAPIEKT ISKTKGQPRE PQVYTLPPSR 350
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PMLDSDGSFF 400
LYSKLTVDKS RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GK          442
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCRASQGIS SWLAWYQQKP EKAPKSLIYA  50
ASSLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YKSYPRTFGQ 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) 22-95 143-199 256-316 362-420
22"-95" 143"-199" 256"-316" 362"-420"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88"' 134'"-194"'
Inter-H-L (CH1 10-CL 126) 130-214' 130"-214'"
Inter-H-H (h 4, h 5, h 8, h11) 218-218" 219-219" 222-222" 225-225"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)
H VH Q1: 1, 1"

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

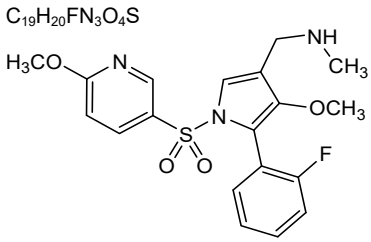
C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2: 442, 442"

padoprazanum

padoprazan — 1-[5-(2-fluorophenyl)-4-methoxy-1-(6-methoxypyridine-3-sulfonyl)-1*H*-pyrrol-3-yl]-*N*-methylmethanamine

padoprazan — 1-[5-(2-fluorophényl)-4-méthoxy-1-(6-méthoxypyridine-3-sulfonyl)-1*H*-pyrrol-3-yl]-*N*-méthylméthanamine

padoprazán — 1-[5-(2-fluorofenil)-4-metoxi-1-(6-metoxipiridina-3-sulfonil)-1*H*-pirrol-3-il]-*N*-metilmetanamina

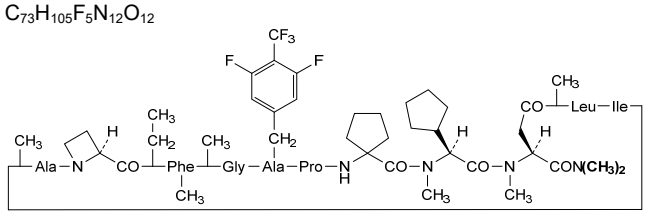


paluratidum

paluratide — 1,11-anhydro[*N*-methyl-L-alanyl-(2*S*)-azetidine-2-carbonyl-*N*-ethyl-4-methyl-L-phenylalanyl-*N*-methylglycyl-(2*S*)-2-amino-4-[3,5-difluoro-4-(trifluoromethyl)phenyl]butanoyl-L-prolyl-2-aminocyclopentane-1-carbonyl-(2*S*)-2-cyclopentyl-*N*-methylglycyl-N^1,N^1,N^2-trimethyl-L-isoasparaginyl-*N*-methyl-L-leucyl-L-isoleucine]

paluratide — 1,11-anhydro[*N*-méthyl-L-alanyl-(2*S*)-azétidine-2-carbonyl-*N*-éthyl-4-méthyl-L-phénylalanyl-*N*-méthylglycyl-(2*S*)-2-amino-4-[3,5-difluoro-4-(trifluorométhyl)phényl]butanoyl-L-prolyl-2-aminocyclopentane-1-carbonyl-(2*S*)-2-cyclopentyl-*N*-méthylglycyl-N^1,N^1,N^2-triméthyl-L-isoasparaginyl-*N*-méthyl-L-leucyl-L-isoleucine]

paluratida — 1,11-anhidro[*N*-metil-L-alanil-(2*S*)-azetidina-2-carbonil-*N*-etil-4-metil-L-fenilalanil-*N*-metilglicil-(2*S*)-2-amino-4-[3,5-difluoro-4-(trifluorometil)fenil]butanoil-L-prolil-2-aminociclopentano-1-carbonil-(2*S*)-2-ciclopentil-*N*-metilglicil-N^1,N^1,N^2-trimetil-L-isoasparaginil-*N*-metil-L-leucil-L-isoleucina]



palverafuspum alfa #

palverafusp alfa — human vascular endothelial growth factor receptor 1 (VEGFR-1) fragment, anti-(human vascular endothelial growth factor (VEGF), fused via a $(G_4S)_3$ peptide linker to the N-terminus of both heavy chains of a humanized immunoglobulin G1-kappa anti-(human programmed cell death 1 ligand 1 [PD-L1, programmed death ligand 1, PDCD1 ligand 1, B7 homolog 1, B7-H1, CD274]), glycoform alfa;
human vascular endothelial growth factor receptor 1 (VEGFR-1) fragment 129-228 comprising the second extracellular domain of the VEGF receptor (VEGFR-D2), [N^{196}>A^{68}]-variant, anti-(human vascular endothelial growth factor (VEGF) (1-100 in the current sequence) fused, via a $(G_4S)_3$ peptide linker (101-115), to gamma 1 heavy chain (116-563) [VH (*Homo sapiens* IGHV3-23*04 -(IGHD) -IGHJ4*01, CDR-Kabat [5.17.9] (146-150.165-181.214-222)) (116-233) -*Homo sapiens* IGHG1*03 (CH1 (234-331), hinge (332-346), CH2 S^{414}>A, E^{449}>A, K^{450}>A (347-456), CH3 (457-561), CHS (562-563)) (234-563)], (336-214')-disulfide with kappa light chain

	(1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 -IGKJ1*01, CDR-Kabat [11.7.9] (24'-34'.50'-56'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (108'-214')]; dimer (342-342'', 345-345'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa
palvérafusp alfa	fragment du récepteur 1 du facteur de croissance de l'endothélium vasculaire humain (VEGFR-1), anti-(facteur de croissance de l'endothélium vasculaire humain (VEGF), fusionné via un peptide liant $(G_4S)_3$ à l'extrémité N-terminale des deux chaînes lourdes d'une immunoglobuline G1-kappa humanisée anti-(ligand 1 humain de mort cellulaire programmée [PD-L1, ligand 1 de mort programmée, ligand 1 de PDCD1, homologue 1 B7, B7-H1, CD274]), glycoforme alfa; fragment 129-228 du récepteur 1 du facteur de croissance de l'endothélium vasculaire humain (VEGFR-1) comprenant le deuxième domaine extracellulaire du récepteur du VEGF (VEGFR-D2), [N^{196}>A^{68}]-variant, anti-(facteur de croissance de l'endothélium vasculaire humain (VEGF) (1-100 dans la séquence actuelle) fusionné, via un peptide liant $(G_4S)_3$ (101-115), à la chaîne lourde gamma 1 (116-563) [VH (*Homo sapiens* IGHV3-23*04 -(IGHD) -IGHJ4*01, CDR-Kabat [5. 17.9] (146-150.165-181. 214-222)) (116-233) -*Homo sapiens* IGHG1*03 (CH1 (234-331), charnière (332-346), CH2 S^{414}>A, E^{449}>A, K^{450}>A (347-456), CH3 (457-561), CHS (562-563)) (234-563)], (336-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 -IGKJ1*01, CDR-Kabat [11. 7.9] (24'-34'.50'-56'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (108'-214')]; dimère (342-342'', 345-345'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa
palverafusp alfa	fragmento del receptor 1 del factor de crecimiento endotelial vascular humano (VEGFR-1), anti-(factor de crecimiento endotelial vascular humano (VEGF), fusionado a través de un enlace peptídico $(G_4S)_3$ al terminal N de ambas cadenas pesadas de una inmunoglobulina G1-kappa humanizada anti-(ligando humano de la muerte celular programada 1 [PD-L1, ligando de la muerte programada 1, PDCD1 ligando 1, homólogo B7, B7-H1, CD274]), glicoforma alfa; fragmento del receptor 1 del factor de crecimiento endotelial vascular humano (VEGFR-1) 129-228 que comprende el segundo dominio extracelular del receptor VEGF (VEGFR-D2), [N^{196}>A^{68}]-variante, anti-(factor de crecimiento endotelial vascular humano (VEGF) (1-100 en la secuencia actual) fusionado, a través de un enlace peptídico $(G_4S)_3$ (101-115), a la cadena pesada gamma 1 (116-563) [VH (*Homo sapiens* IGHV3-23*04 -(IGHD) -IGHJ4*01, CDR-Kabat [5.17.9] (146-150.165-181.214-222)) (116-233) -*Homo sapiens* IGHG1*03 (CH1 (234-331), bisagra (332-346), CH2 S^{414}>A, E^{449}>A, K^{450}>A (347-456), CH3 (457-561), CHS (562-563)) (234-563)], (336-214')-disulfuro con cadena ligera kappa (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 -IGKJ1*01, CDR-Kabat [11.7.9] (24'-34'.50'-56'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (108'-214')]; dimer (342-342'', 345-345'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, glicoforma alfa

Sequence / Séquence / Secuencia
VEGFR1 IgG1 heavy chain

```
SDTGRPFVEM YSEIPEIIHM TGRELVIPC RVTSPNITVT LKKFPLDTLI   50
PDGKRIIWDS RKGFIISAAT YKEIGLLTCE ATVNGHLYKT NYLTHRQTNT  100
GGGGSGGGGS GGGGSEVQLV ESGGGLVQPG GSLRLSCAAS GFTFSDSWIH  150
WVRQAPGKGL EWVAWISPYG GSTYYADSVK GRFTISADTS KNTAYLQMNS  200
LRAEDTAVYY CARRHWPGGF DYWGQGTLVT VSSASTKGPS VFPLAPSSKS  250
TSGGTAALGC LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS  300
VVTVPSSSLG TQTYICNVNH KPSNTKVDKR VEPKSCDKTH TCPPCPAPEL  350
LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV  400
HNAKTKPREE QYNATYRVVS VLTVLHQDWL NGKEYKCKVS NKALPAPIAA  450
TISKAKGQPR EPQVYTLPPS REEMTKNQVS LTCLVKGFYP SDIAVEWESN  500
GQPENNYKTT PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN  550
HYTQKSLSLS PGK                                          563
```

IgG1 light chain

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

Mutation / Mutation / Mutación
VEGFR1 IgG1 heavy chain: N^{196}>A^{68},A$^{68''}$, S^{414},$S^{414''}$>A, E^{449},$E^{449''}$>A, K^{450},$K^{450''}$>A

Peptide linker / Peptide liant / Péptido de unión
VEGFR1 IgG1 heavy chain: ^{101}*GGGGSGGGGSGGGGS*^{115}

Post-translation modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra VEGFR1 IgG1 heavy chain: 30-79, 137-211, 260-316, 377-437, 483-541, 30"-79", 137"-211", 260"-316", 377"-437", 483"-541"
Intra IgG1 light chain: 23'-88', 134'"-194'"
Inter IgG1 light chain-VEGFR1 IgG1 heavy chain: 214'-336, 214'"-336"
Inter VEGFR1 IgG1 heavy chain: 342-342", 345-345"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
VEGFR1 IgG1 heavy chain: 36, 413, 36", 413"

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS: 563, 563"

pegrizeprumentum #
pegrizeprument

immunoglobulin Fab VH-G1CH1h_L-kappa, anti-[*Homo sapiens* CD28 (T cell specific surface glycoprotein CD28, TP44)], conjugated to a bi-branched polyethylene glycol (PEG) chain; VH-CH1 chain (1-232) [VH Musmus/Homsap (*Mus musculus* IGHV1-62-2*01 (84.0%) -(IGHD) -IGHJ3*01 (100%)/*Homo sapiens* IGHV1-2*02 (63.3%) -(IGHD) -IGHJ4*01 (91.7%) S128>A (121), CDR-IMGT [8.8.14] (26-34.51-58.97-110)) (1-121) -*Homo sapiens* IGHG1*01 CH1-h, G1m17 CH1 K120 (CH1 K120 (218) (122-219), hinge 1-11 (220-230) -2-mer bisalanyl (231-232)) (122-232)], (224-214')-disulfide with L-kappa light chain (1'-214') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV12-46*01 (83.2%) -IGKJ1*01 (100%)/*Homo sapiens* IGKV1-NL1*01 (74.4%) -IGKJ2*02 (91.7%) Q120>G (100'), CDR-IMGT [6.3.9] (27'-32'.51'-53'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153'), V101 (191') (108'-214')], produced in Chinese hamster ovary (CHO) cells, expressing the enzyme glutamine synthetase (GS), non-glycosylated; substituted at the sulfur atoms of L-cysteinyl residue 230 with group (3Ξ)-1-{3-[(3-{(2Ξ)-2,3-bis[ω-methoxypoly(oxyethylene)-α-yl]propoxy}propyl)amino]-3-oxopropyl}-2,5-dioxopyrrolidin-3-yl

pégrizéprument	immunoglobuline Fab VH-G1CH1h_L-kappa, anti-[*Homo sapiens* CD28 (glycoprotéine de surface CD28 spécifique des lymphocytes T, TP44)], conjuguée à une chaîne polyéthylène glycol (PEG) composée de deux branches; chaîne VH-CH1 (1-232) [VH Musmus/Homsap (*Mus musculus* IGHV1-62-2*01 (84.0%) -(IGHD) -IGHJ3*01 (100%)/*Homo sapiens* IGHV1-2*02 (63.3%) -(IGHD) -IGHJ4*01 (91.7%) S128>A (121), CDR-IMGT [8.8.14] (26-34.51-58.97-110)) (1-121) -*Homo sapiens* IGHG1*01 CH1-h, G1m17 CH1 K120 (CH1 K120 (218) (122-219), charnière 1-11 (220-230) -2-mer bisalanyl (231-232)) (122-232)], (224-214')-disulfure avec la chaîne légère L-kappa (1'-214') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV12-46*01 (83.2%) -IGKJ1*01 (100%)/*Homo sapiens* IGKV1-NL1*01 (74.4%) -IGKJ2*02 (91.7%) Q120>G (100'), CDR-IMGT [6.3.9] (27'-32'.51'-53'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153'), V101 (191') (108'-214')], produit dans des cellules ovariennes de hamster chinois (CHO), exprimant l'enzyme glutamine synthétase (GS), non-glycosylé; substitué sur l'atome de soufre du résidu L-cystéinyle 230 avec un groupe (3Ξ)-1-{3-[(3-{(2Ξ)-2,3-bis[ω-méthoxypoly(oxyéthylène)-α-yl]propoxy}propyl)amino]-3-oxopropyl}-2,5-dioxopyrrolidin-3-yle
pegrizeprument	inmunoglobulina Fab VH-G1CH1h_L-kappa , anti-[*Homo sapiens* CD28 (glicoproteína de superficie CD28 específica de los linfocitos T, TP44)], conjugado con una cadena de polietilenglicol (PEG) compuesto por dos cadenas; cadena VH-CH1 (1-232) [VH Musmus/Homsap (*Mus musculus* IGHV1-62-2*01 (84.0%) -(IGHD) -IGHJ3*01 (100%)/*Homo sapiens* IGHV1-2*02 (63.3%) -(IGHD) -IGHJ4*01 (91.7%) S128>A (121), CDR-IMGT [8.8.14] (26-34.51-58.97-110)) (1-121) -*Homo sapiens* IGHG1*01 CH1-h, G1m17 CH1 K120 (CH1 K120 (218) (122-219), bisagra 1-11 (220-230) -2-mer bisalanil (231-232)) (122-232)], (224-214')-disulfuro con la cadena ligera L-kappa (1'-214') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV12-46*01 (83.2%) -IGKJ1*01 (100%)/*Homo sapiens* IGKV1-NL1*01 (74.4%) -IGKJ2*02 (91.7%) Q120>G (100'), CDR-IMGT [6.3.9] (27'-32'.51'-53'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153'), V101 (191') (108'-214')], producido en las células ováricas de hámster chino (CHO), expresando la enzima glutamina sintetasa (GS), no glicosilado; substituído por el átomo de azufre del resíduo L-cisteína 230 con un grupo (3Ξ)-1-{3-[(3-{(2Ξ)-2,3-bis[ω-methxipoli(oxietileno)-α-il]propoxi}propil)amino]-3-oxopropil}-2,5-dioxopirrolidin-3-ilo

Heavy chain / Chaîne lourde / Cadena pesada : VH-G1CH1h (H)

```
QVQLQQSGAE LKKPGASVKV SCKASGYTFT EYIIHWIKLR SGQGLEWIGW  50
FYPGSNDIQY NAQFKGKATL TADKSSSTVY MELTGLTPED SAVYFCARRD 100
DFSGYDALPY WGQGTLVTVS AASTKGPSVF PLAPSSKSTS GGTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200
TYICNVNHKP SNTKVDKKVE PKSCDKTHTC AA                    232
```

Light chain / Chaîne légère / Cadena ligera : L-kappa (L)

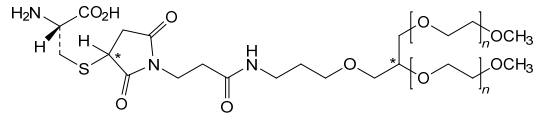
```
DIQMTQSPSS LSASVGDRVT ITCKTNENIY SNLAWYQQKD GKSPQLLIYA  50
ATHLVEGVPS RFSGSGSGTQ YSLTISSLQP EDFGNYYCQH FWGTPCTFGG 100
GTKLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Post-translational modifications

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 148-204
Intra-L (C23-C104) 23'-88' 134'-194'
Inter-H-L (h 5-CL 126) 224-214'

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)
H VH Q1:1

Pegylation site / Site de pegylation / Posiciones de pegilación
H hinge h11: C230



n~230 (~2x10 kDa)

pesorimcovateinum

pesorimcovatein — severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), omicron lineage BQ.1.1.1 (Gisaid: EPI_ISL_14752457) spike (S) glycoprotein fragment (1-1190), stable prefusion conformation variant (H^{663}>P, R^{664}>G, R^{665}>S, R^{667}>S, F^{799}>P, A^{874}>P, A^{881}>P, A^{924}>P, K^{968}>P, V^{969}>P) fused to the enterobacteria phage T4 fibritin foldon domain fragment (458-484, 1191-1217 in the current sequence), trimer, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

pésorimcovatéine — coronavirus 2 du syndrome respiratoire aigu sévère (SRAS-CoV-2), fragment de la glycoprotéine de spicule (S) (1-1190) de la lignée omicron BQ.1 .1. 1 (Gisaid : EPI_ISL_14752457), variant de conformation stabilisée par préfusion (H^{663}>P, R^{664}>G, R^{665}>S, R^{667}>S, F^{799}>P, A^{874}>P, A^{881}>P, A^{924}>P, K^{968}>P, V^{969}>P) fusionné au fragment du domaine foldon de la fibritine de l'entérobactérie du phage T4 (458-484, 1191-1217 dans la séquence actuelle), trimère, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

pesorimcovateína — síndrome respiratorio agudo grave coronavirus 2 (SARS-CoV-2), linaje BQ.1.1.1 de ómicron (Gisaid: EPI_ISL_14752457) fragmento de la glicoproteína de espícula (S) (1-1190), variante de conformación de prefusión estable (H^{663}>P, R^{664}>G, R^{665}>S, R^{667}>S, F^{799}>P, A^{874}>P, A^{881}>P, A^{924}>P, K^{968}>P, V^{969}>P) fusionado al fragmento del dominio plegable de fibritina del fago T4 de las enterobacterias (458-484, 1191-1217 en la secuencia acual), trímero, producido en células ováricas de hamster Chino (CHO), glicoforma alfa

Monomer sequence / Séquence du monomère / Secuencia del monómero

```
QCVNLITRTQ SYTNSFTRGV YYPDKVFRSS VLHSTQDLFL PFFSNVTWFH    50
AISGTNGTKR FDNPVLPFND GVYFASTEKS NIIRGWIFGT TLDSKTQSLL   100
IVNNATNVVI KVCEFQFCND PFLDVYYHKN NKSWMESEFR VYSSANNCTF   150
EYVSQPFLMD LEGKQGNFKN LREFVFKNID GYFKIYSKHT PINLGRDLPQ   200
GFSALEPLVD LPIGINITRF QTLLALHRSY LTPGDSSSGW TAGAAAYYVG   250
YLQPRTFLLK YNENGTITDA VDCALDPLSE TKCTLKSFTV EKGIYQTSNF   300
RVQPTESIVR FPNITNLCPF DEVFNATTFA SVYAWNRKRI SNCVADYSVL   350
YNFAPFFAFK CYGVSPTKLN DLCFTNVYAD SFVIRGNEVS QIAPGQTGNI   400
ADYNYKLPDD FTGCVIAWNS NKLDSTVGGN YNYRYRLFRK SKLKPFERDI   450
STEIYQAGNK PCNGVAGVNC YFPLQSYGFR PTYGVGHQPY RVVVLSFELL   500
HAPATVCGPK KSTNLVKNKC VNFNFNGLTG TGVLTESNKK FLPFQQFGRD   550
IADTTDAVRD PQTLEILDIT PCSFGGVSVI TPGTNTSNQV AVLYQGVNCT   600
EVPVAIHADQ LTPTWRVYST GSNVFQTRAG CLIGAEYVNN SYECDIPIGA   650
GICASYQTQT KSPGSASSVA SQSIIAYTMS LGAENSVAYS NNSIAIPTNF   700
TISVTTEILP VSMTKTSVDC TMYICGDSTE CSNLLLQYGS FCTQLKRALT   750
GIAVEQDKNT QEVFAQVKQI YKTPPIKYFG GFNFSQILPD PSKPSKRSPI   800
EDLLFNKVTL ADAGFIKQYG DCLGDIAARD LICAQKFNGL TVLPPLLTDE   850
MIAQYTSALL AGTITSGWTF GAGPALQIPF PMQMAYRFNG IGVTQNVLYE   900
NQKLIANQFN SAIGKIQDSL SSTPSALGKL QDVVNHNAQA LNTLVKQLSS   950
KFGAISSVLN DILSRLDPPE AEVQIDRLIT GRLQSLQTYV TQQLIRAAEI  1000
RASANLAATK MSECVLGQSK RVDFCGKGYH LMSFPQSAPH GVVFLHVTYV  1050
PAQEKNFTTA PAICHDGKAH FPREGVFVSN GTHWFVTQRN FYEPQIITTD  1100
NTFVSGNCDV VIGIVNNTVY DPLQPELDSF KEELDKYFKN HTSPDVDLGD  1150
ISGINASVVN IQKEIDRLNE VAKNLNESLI DLQELGKYEQ GYIPEAPRDG  1200
QAYVRKDGEW VLLSTFL                                      1217
```

Mutation / Mutation / Mutación
H663>P, R664>G, R665>S, R667>S, F799>P, A874>P, A881>P, A924>P, K968>P, V969>P

Foldon domain / Foldon domaine / Foldon dominio
GYIPEAPRDG QAYVRKDGEW VLLSTFL 1191-1217

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-chain: 2-113, 118-148, 273-283, 318-343, 361-414, 373-507, 462-470, 520-572,
599-631, 644-653, 720-742, 725-731, 822-833, 1014-1025, 1064-1108
2'-113', 118'-148', 273'-283', 318'-343', 361'-414', 373'-507', 462'-470', 520'-572',
599'-631', 644'-653', 720'-742', 725'-731', 822'-833', 1014'-1025', 1064'-1108'
2"-113", 118"-148", 273"-283", 318"-343", 361"-414", 373"-507", 462"-470", 520"-572",
599"-631", 644"-653", 720"-742", 725"-731", 822"-833", 1014"-1025", 1064"-1108"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
N45, N56, N104, N131, N147, N216, N264, N313, N325, N585, N598, N639, N691, N699, N783, N1056, N1080, N1116, N1140, N1155, N1176

N45', N56', N104', N131', N147', N216', N264', N313', N325', N585', N598', N639', N691', N699', N783', N1056', N1080', N1116', N1140', N1155', N1176'

N45", N56", N104", N131", N147", N216", N264", N313", N325", N585", N598", N639", N691", N699", N783", N1056", N1080", N1116", N1140", N1155", N1176"

O-glycosylation sites / Sites de O-glycosylation / Posiciones de O-glicosilación
T305, S307, T305', S307', T305", S307"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
Q1, Q1', Q1" >pyroglutamyl (pE, 5-oxoprolyl)

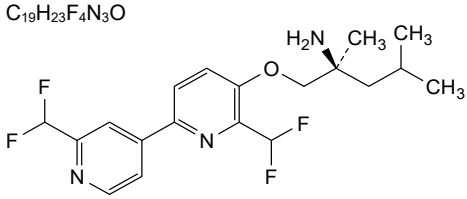
pilavapadinum

pilavapadin — (2*S*)-1-{[2',6-bis(difluoromethyl)[2,4'-bipyridin]-5-yl]oxy}-2,4-dimethylpentan-2-amine

pilavapadine — (2*S*)-1-{[2',6-bis(difluorométhyl)[2,4'-bipyridin]-5-yl]oxy}-2,4-diméthylpentan-2-amine

pilavapadina — (2*S*)-1-{[2',6-bis(difluorometil)[2,4'-bipiridin]-5-il]oxi}-2,4-dimetilpentan-2-amina

$C_{19}H_{23}F_4N_3O$



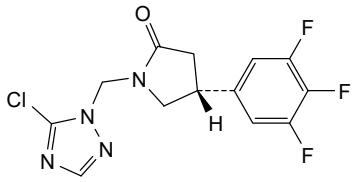
plosaracetamum

plosaracetam — (4*R*)-1-[(5-chloro-1*H*-1,2,4-triazol-1-yl)methyl]-4-(3,4,5-trifluorophenyl)pyrrolidin-2-one

plosaracétam (4*R*)-1-[(5-chloro-1*H*-1,2,4-triazol-1-yl)méthyl]-4-(3,4,5-trifluorophényl)pyrrolidin-2-one

plosaracetam (4*R*)-1-[(5-cloro-1*H*-1,2,4-triazol-1-il)metil]-4-(3,4,5-trifluorofenil)pirrolidin-2-ona

$C_{13}H_{10}ClF_3N_4O$



plozasiranum

plozasiran *all-P-ambo*-3′-*O*-[({(1*s*,4*s*)-4-[(3*S*,8*S*)-17-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]-3,8-bis[(2-{2-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]ethoxy}ethyl)carbamoyl]-6,11-dioxo-15-oxa-2,7,12-triazaheptadecan-1-oyl]cyclohexyl}oxy)(sulfanyl)phosphoryl]-1'-de(6-amino-9*H*-purin-9-yl)-2'-deoxy-*P*-thioadenylyl-(5'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-deoxy-2'-fluoroguanylyl-(3'→5')-2'-deoxy-2'-fluorouridylyl-(3'→5')-2'-deoxy-2'-fluoroadenylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methylinosinylyl-(3'→5')-2'-*O*-methyl-*P*-thioadenylyl-(3'→3')-1'-de(6-amino-9*H*-purin-9-yl)-2'-deoxyadenosine
duplex with *all-P-ambo*-2'-*O*-methyl-*P*-thiouridylyl-(5'→3')-2'-deoxy-2'-fluoroguanylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-deoxy-2'-fluorocytidylyl-(3'→5')-2'-*O*-methylcytidylyl-(5'→3')-2'-deoxy-2'-fluorouridylyl-2'-*O*-methylguanylyl-(5'→3')-2'-deoxy-2'-fluorouridylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-deoxy-2'-fluoroadenylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-*O*-methylguanylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-deoxy-2'-fluoroguanylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-deoxy-2'-fluoro-*P*-thiocytidylyl-(5'→3')-2'-*O*-methyl-*P*-thioadenylyl-(5'→3')-2'-deoxy-2'-fluoro-*P*-thiocytidylyl-(5'→3')-2'-*O*-methyluridine

plozasiran *tout-P-ambo*-3′-*O*-[({(1*s*,4*s*)-4-[(3*S*,8*S*)-17-[(2-acétamido-2-désoxy-β-D-galactopyranosyl)oxy]-3,8-bis[(2-{2-[(2-acétamido-2-désoxy-β-D-galactopyranosyl)oxy]éthoxy}éthyl)carbamoyl]-6,11-dioxo-15-oxa-2,7,12-triazaheptadécan-1-oyl]cyclohexyl}oxy)(sulfanyl)phosphoryl]-1'-dés(6-amino-9*H*-purin-9-yl)-2'-désoxy-*P*-thioadénylyl-(5'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-désoxy-2'-fluoroguanylyl-(3'→5')-2'-désoxy-2'-fluorouridylyl-(3'→5')-2'-désoxy-2'-fluoroadénylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*- méthylcytidylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthylinosinylyl-(3'→5')-2'-*O*-méthyl-*P*-thioadénylyl-(3'→3')-1'-dés(6-amino-9*H*-purin-9-yl)-2'-désoxyadénosine

duplex avec *tout-P-ambo*-2'-*O*-méthyl-*P*-thiouridylyl-(5'→3')-2'-désoxy-2'-fluoroguanylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-désoxy-2'-fluorocytidylyl-(3'→5')-2'-*O*-méthylcytidylyl-(5'→3')-2'-désoxy-2'-fluorouridylyl-2'-*O*-méthylguanylyl-(5'→3')-2'-désoxy-2'-fluorouridylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-désoxy-2'-fluoroadénylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-*O*-méthylguanylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-désoxy-2'-fluoroguanylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-désoxy-2'-fluoro-*P*-thiocytidylyl-(5'→3')-2'-*O*-méthyl-*P*-thioadénylyl-(5'→3')-2'-désoxy-2'-fluoro-*P*-thiocytidylyl-(5'→3')-2'-*O*-méthyluridine

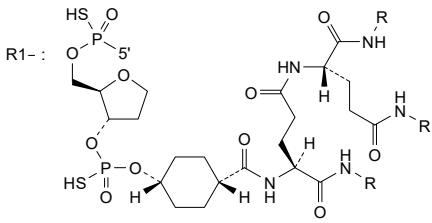
plozasirán

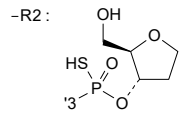
todo-P-ambo-3'-*O*-[({(1*s*,4*s*)-4-[(3*S*,8*S*)-17-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]-3,8-bis[(2-{2-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]etoxi}etil)carbamoil]-6,11-dioxo-15-oxa-2,7,12-triazaheptadecan-1-oil]ciclohexil}oxi)(sulfanil)fosforil]-1'-des(6-amino-9*H*-purin-9-il)-2'-desoxi-*P*-tioadenilil-(5'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-desoxi-2'-fluoroguanilil-(3'→5')-2'-desoxi-2'-fluorouridilil-(3'→5')-2'-desoxi-2'-fluoroadenilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metilinosinilil-(3'→5')-2'-*O*-metil-*P*-tioadenilil-(3'→3')-1'-des(6-amino-9*H*-purin-9-il)-2'-desoxiadenosina
dúplex con *todo-P-ambo*-2'-*O*-metil-*P*-tiouridilil-(5'→3')-2'-desoxi-2'-fluoroguanilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-desoxi-2'-fluorocitidilil-(3'→5')-2'-*O*-metilcitidilil-(5'→3')-2'-desoxi-2'-fluorouridilil-2'-*O*-metilguanilil-(5'→3')-2'-desoxi-2'-fluorouridilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-desoxi-2'-fluoroadenilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-*O*-metilguanilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-desoxi-2'-fluoroguanilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-desoxi-2'-fluoro-*P*-tiocitidilil-(5'→3')-2'-*O*-metil-*P*-tioadenilil-(5'→3')-2'-desoxi-2'-fluoro-*P*-tiocitidilil-(5'→3')-2'-*O*-metiluridina

$C_{493}H_{654}F_{11}N_{164}O_{311}P_{43}S_7$

(3'-5') R1-*A*-*C*-*G*-*G*-*G*-*A*-*C*-*A*-G-U-A-*U*-*U*-*C*-*U*-*C*-*A*-*G*-*U*-*I*-*A*-R2
(5'-3')*U*=G-*C*-C-*C*-*C*-U-*G*-U-*C*-A-*U*-*A*-*A*-*G*-*A*-G-*U*-C-*A*=C=*U*

N : A,C,G,U, I
N : 2'-*O*-methyl-N / 2'-*O*-méthyl-N / 2'-*O*-metil-N
N : 2'-deoxy-2'-fluoro-N / 2'-désoxy-2'-fluoro-N / 2'-desoxi-2'-fluoro-N
– : –PO(OH)– = : –PO(SH)–





podentamigum #

podentamig immunoglobulin single chain VH-VH'-scFvhl, anti-[*Homo sapiens* TNFRSF17 (TNF receptor superfamily member 17, BCMA, TNFRSF13A, CD269)], anti-[*Homo sapiens* ALB (albumin, human serum albumin, HSA)] and anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], trispecific;
IG single chain VH-VH'-scFvhl (1-507) [VH anti-TNFRSF17 Vicpac /Homsap (*Vicugna pacos* IGHV3S53*01 (83.3%) -(IGHD) -IGHJ4*01 (100%)/*Homo sapiens* IGHV3-23*04 (73.5%) -(IGHD) -IGHJ4*01 (91.7%) L123>Q (114), (CDR-IMGT [8.6.14] (27-33.51-56.95-108)) (1-119) -9-mer-tetraglycyl-seryl-triglycyl-seryl linker (120-128) -VH anti-ALB (*Homo sapiens* IGHV3-23*04 (88.5%) -(IGHD) -IGHJ1*01 (81.8%) W118>S (333), G119>S (334), CDR-IMGT [8.8.8] (154-161.179-186.225-232)) (129-243) -9-mer-tetraglycyl-seryl-triglycyl-seryl linker (244-252) - scFvhl anti-CD3E (253-507) [VH Musmus/Homsap (*Mus musculus* IGHV10-1*02 (89.9%) -(IGHD) -IGHJ3*01 (100%)/*Homo sapiens* IGHV3-73*01 (85.0%) -(IGHD) -IGHJ5*01 (100%), CDR-IMGT [8.10.16] (278-285.303-312.351-366)) (253-377) -15-mer-tris(tetraglycyl-seryl) linker (378-392) -V-LAMBDA (*Homo sapiens* IGLV7-43*01 (86.2%) -IGLJ3*02 (100%), CDR-IMGT [9.3.9] (418-426.444-446.483-491)) (393-501)] -hexahistidine tag (502-507)], produced in Chinese hamster ovary (CHO) cells, cell line CHO-DG44, lacking the enzyme dihydrofolate reductase (DHFR), non-glycosylated

podentamig immunoglobuline à chaîne unique VH-VH'-scFvhl, anti-[*Homo sapiens* TNFRSF17 (membre 17 de la superfamille des récepteurs du TNF, BCMA, TNFRSF13A, CD269)], anti-[*Homo sapiens* ALB (albumine, sérum albumine humaine, SAH)] et anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], trispécifique;
IG à chaîne unique VH-VH'-scFvhl (1-507) [VH anti-TNFRSF17 Vicpac /Homsap (*Vicugna pacos* IGHV3S53*01 (83.3%) -(IGHD) -IGHJ4*01 (100%)/*Homo sapiens* IGHV3-23*04 (73.5%) -(IGHD) -IGHJ4*01 (91.7%) L123>Q (114), (CDR-IMGT [8.6.14] (27-33.51-56.95-108)) (1-119) -9-mer-tétraglycyl-séryl-triglycyl-séryl linker (120-128) -VH anti-ALB (*Homo sapiens* IGHV3-23*04 (88.5%) -(IGHD) -IGHJ1*01 (81.8%) W118>S (333), G119>S (334), CDR-IMGT [8.8.8] (154-161.179-186.225-232)) (129-243) -9-mer-tétraglycyl-séryl-triglycyl-séryl linker (244-252) -scFvhl anti-CD3E (253-507) [VH Musmus/Homsap (*Mus musculus* IGHV10-1*02 (89.9%) -(IGHD) -IGHJ3*01 (100%)/*Homo sapiens* IGHV3-73*01 (85.0%) -(IGHD) -IGHJ5*01 (100%), CDR-IMGT [8.10.16] (278-285.303-312.351-366)) (253-377) -15-mer-tris(tétraglycyl-séryl) linker (378-392) -V-LAMBDA (*Homo sapiens* IGLV7-43*01 (86.2%) -IGLJ3*02 (100%), CDR-IMGT [9.3.9] (418-426.444-446.483-491)) (393-501)] -hexahistidine tag (502-507)], produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-DG44, ne présentant pas l'enzyme dihydrofolate réductase (DHFR), non-glycosylé

podentamig inmunoglobulina con cadena única VH-VH'-scFvhl, anti-[*Homo sapiens* TNFRSF17 (miembro 17 de la superfamilia de los receptores del TNF, BCMA, TNFRSF13A, CD269)], anti-[*Homo sapiens* ALB (albúmina, albumina sérica humana, SAH)] y anti-[*Homo sapiens* CD3E (CD3 épsilon, Leu-4)], triespecífico;
IG con cadena única VH-VH'-scFvhl (1-507) [VH anti-TNFRSF17 Vicpac /Homsap (*Vicugna pacos* IGHV3S53*01 (83.3%) -(IGHD) -IGHJ4*01 (100%)/*Homo sapiens* IGHV3-23*04 (73.5%) -(IGHD) -IGHJ4*01 (91.7%) L123>Q (114), (CDR-IMGT [8.6.14] (27-33.51-56.95-108)) (1-119) -9-mer-tetraglicil-seril-triglicil-seril enlace (120-128) -VH anti-ALB (*Homo sapiens* IGHV3-23*04 (88.5%) -(IGHD) -IGHJ1*01 (81.8%) W118>S (333), G119>S (334), CDR-IMGT [8.8.8] (154-161.179-186.225-232)) (129-243) -9-mer-tetraglicil-seril-triglicil-seril enlace (244-252) -scFvhl anti-CD3E (253-507) [VH Musmus/Homsap (*Mus musculus* IGHV10-1*02 (89.9%) -(IGHD) -IGHJ3*01 (100%)/*Homo sapiens* IGHV3-73*01 (85.0%) -(IGHD) -IGHJ5*01 (100%), CDR-IMGT [8.10.16] (278-285.303-312.351-366)) (253-377) -15-mer-tris(tetraglicil-seril) enlace (378-392) -V-LAMBDA (*Homo sapiens* IGLV7-43*01 (86.2%) -IGLJ3*02 (100%), CDR-IMGT [9.3.9] (418-426.444-446.483-491)) (393-501)] -hexahistidina tag (502-507)], producido en las células ováricas de hámster chino (CHO), línea celular CHO-DG44, en ausencia de la enzima dihidrofolato reductasa (DHFR), no glicosilado

Heavy chain / Chaîne lourde / Cadena pesada : VH (anti-TNFRSF17) -VH' (anti-ALB) -scFvhl (anti-CD3E)

```
EVQLVESGGG LVQPGRSLTL SCAASTNIFS ISPYGWYRQA PGKQRELVAA 50
IHGTSTLYAD SVKGRFTISR DNAKNSIYLQ MNSLRPEDTA LYYCNKVPWG 100
DYHPGNVYWG QGTQVTVSSG GGGSGGGSEV QLVESGGGLV QPGNSLRLSC 150
AASGFTFSKF GMSWVRQAPG KGLEWVSSIS GSGRDTLYAD SVKGRFTISR 200
DNAKTTLYLQ MNSLRPEDTA VYYCTIGGSL SVSSQGTLVT VSSGGGGSGG 250
GSEVQLVESG GGLVQPGGSL KLSCAASGFT FNKYAINWVR QAPGKGLEWV 300
ARIRSKYNNY ATYYADQVKD RFTISRDDSK NTAYLQMNNL KTEDTAVYYC 350
VRHANFGNSY ISYWAYWGQG TLVTVSSGGG GSGGGGSGGG GSQTVVTQEP 400
SLTVSPGGTV TLTCASSTGA VTSGNYPNWV QQKPGQAPRG LIGGTKFLVP 450
GTPARFSGSL LGGKAALTLS GVQPEDEAEY YCTLWYSNRW VFGGGTKLTV 500
LHHHHHH                                               507
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-chain (C23-C104) 22-94 150-224 274-350 414-482

No N-glycosylation sites / pas de sites de N-glycosylation / ningùm posición de N-glycosilación

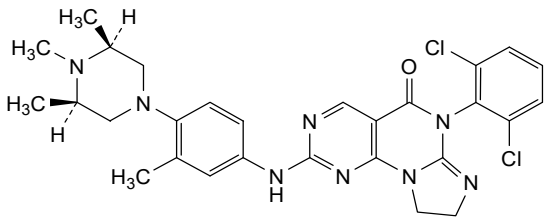
potrasertibum

potrasertib — 6-(2,6-dichlorophenyl)-2-{3-methyl-4-[(3*R*,5*S*)-3,4,5-trimethylpiperazin-1-yl]anilino}-8,9-dihydroimidazo[1,2-*a*]pyrimido[5,4-*e*]pyrimidin-5(6*H*)-one

potrasertib — 6-(2,6-dichlorophényl)-2-{3-méthyl-4-[(3*R*,5*S*)-3,4,5-triméthylpipérazin-1-yl]anilino}-8,9-dihydroimidazo[1,2-*a*]pyrimido[5,4-*e*]pyrimidin-5(6*H*)-one

potrasertib — 6-(2,6-diclorofenil)-2-{3-metil-4-[(3*R*,5*S*)-3,4,5-trimetilpiperazin-1-il]anilino}-8,9-dihidroimidazo[1,2-*a*]pirimido[5,4-*e*]pirimidin-5(6*H*)-ona

$C_{28}H_{30}Cl_2N_8O$



precemtabartum #

precemtabart — immunoglobulin G1-kappa, anti-[*Homo sapiens* CEACAM5 (carcinoembryonic antigen-related cell adhesion molecule 5, CEA, CD66e)], *Homo sapiens* monoclonal antibody; H-gamma1 heavy chain *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV4-31*02 (90.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [10.7.11] (26-35.53-59.98-108)) (1-119) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14,G1v50 delE1.4, P1.3, V1.2, A1.1, G1v60 CH2 S115, S116 (CH1 R120 (216) (120-217), hinge 1-15(218-232), CH2 E1.4>del, L1.3>P (235), L1.2>V (236), G1.1>A (237), A115>S (331), P116>S (332) (233-341), CH3 E12 (357), M14 (359) (342-446), CHS K2>del (447)) (120-447)], (222-214')-disulfide with L-kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-15*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 (228-228":231-231")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1SV, glycoform alfa

précemtabart

immunoglobuline G1-kappa, anti-[*Homo sapiens* CEACAM5 (molécule d'adhésion cellulaire 5 apparentée à l'antigène carcinoembryonaire, CEA, CD66e)], anticorps monoclonal *Homo sapiens*;
chaîne lourde H-gamma1 *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV4-31*02 (90.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [10.7.11] (26-35.53-59.98-108)) (1-119) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14,G1v50 CH2 delE1.4, P1.3, V1.2, A1.1, G1v60 CH2 S115, S116 (CH1 R120 (216) (120-217), charnière 1-15 (218-232), CH2 E1.4>del, L1.3>P (235), L1.2>V (236), G1.1>A (237), A115>S (331), P116>S (332) (233-341), CH3 E12 (357), M14 (359) (342-446), CHS K2>del (447)) (120-447)], (222-214')-disulfure avec la chaîne légère L-kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-15*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 (228-228":231-231")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1SV, glycoforme alfa

precemtabart

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CEACAM5 (molécula de adhesión celular 5 parecida al antígeno carcinoembrionario, CEA, CD66e)], anticuerpo monoclonal *Homo sapiens*;
cadena pesada H-gamma1 *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV4-31*02 (90.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [10.7.11] (26-35.53-59.98-108)) (1-119) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14,G1v50 CH2 delE1.4, P1.3, V1.2, A1.1, G1v60 CH2 S115, S116 (CH1 R120 (216) (120-217), bisagra 1-15 (218-232), CH2 E1.4>del, L1.3>P (235), L1.2>V (236), G1.1>A (237), A115>S (331), P116>S (332) (233-341), CH3 E12 (357), M14 (359) (342-446), CHS K2>del (447)) (120-447)], (222-214')-disulfuro con la cadena ligera L-kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-15*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 (228-228":231-231")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1SV, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLQESGPG LVKPSQTLSL TCTVSDGSVS RGGYYLTWIR QHPGKGLEWI  50
GYIYYSGSTY FNPSLRSRVT MSVDTSKNQF SLKLSSVTAA DTAVYYCARG 100
IAVAPFDYWG QGTLVTVSSA STKGPSVFPL APSSKSTSGG TAALGCLVKD 150
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY 200
ICNVNHKPSN TKVDKRVEPK SCDKTHTCPP CPAPPVAGPS VFLFPPKPKD 250
TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNST 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKALP SSIEKTISKA KGQPREPQVY 350
TLPPSREEMT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD 400
SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPG    447
```

Light chain / Chaîne légère / Cadena ligera

```
EIVLTQSPAT LSVSPGERAT LSCRTSQSVR SNLAWYQQKP GQAPRLLIYA  50
ASTRATGIPA RFSGSGSGTE FTLTISSLQS EDFAVYYCQQ YTNWPFTFGP 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) 22-97 146-202 262-322 368-426
22"-97" 146"-202" 262"-322" 368"-426"
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 VH N68 (no glycosylation X being P69 in NXS/T motif): 62, 62"
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

precemtabartum tocentecanum #

precemtabart tocentecan

immunoglobulin G1-kappa, anti-[*Homo sapiens* CEACAM5 (carcinoembryonic antigen-related cell adhesion molecule 5, CEA, CD66e)], *Homo sapiens* monoclonal antibody,conjugated on an average of 8 cysteinyl residues to *tocentecan*, comprising a linker and a camptothecin derivative (*exatecan*);
H-gamma1 heavy chain *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV4-31*02 (90.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [10.7.11] (26-35.53-59.98-108)) (1-119) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v50 CH2 delE1.4, P1.3, V1.2, A1.1, G1v60 CH2 S115, S116 (CH1 R120 (216) (120-217), hinge 1-15(218-232), CH2 E1.4>del, L1.3>P (235), L1.2>V (236), G1.1>A (237), A115>S (331), P116>S (332) (233-341), CH3 E12 (357), M14 (359) (342-446), CHS K2>del (447)) (120-447)], (222-214')-disulfide with L-kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-15*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 (228-228'':231-231'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1SV, glycoform alfa; substituted at the sulfur atoms of an average of 8 L-cysteinyl residues among 222, 228, 231, 214', 222'', 228'', 231'' and 214''' with radical group 1-{3-[(2-{5-[({[(1*S*,9*S*)-9-ethyl-5-fluoro-9-hydroxy-4-methyl-10,13-dioxo-2,3,9,10,13,15-hexahydro-1*H*,12*H*-benzo[*de*]pyrano[3',4':6,7]indolizino[1,2-*b*]quinolin-1-yl]carbamoyl}oxy)methyl]-2-(β-D-glucopyranuronosyloxy)anilino}-2-oxoethyl)amino]-3-oxopropyl}-2,5-dioxopyrrolidin-3-yl (*tocentecan*)

précemtabart tocentécan

immunoglobuline G1-kappa, anti-[*Homo sapiens* CEACAM5 (molécule d'adhésion cellulaire 5 apparentée à l'antigène carcinoembryonaire, CEA, CD66e)]; anticorps monoclonal *Homo sapiens*, conjugué par 8 résidus cystéinyle en moyenne au *tocentécan*, comprenant un linker et un dérivé de la camptothécine (*exatécan*);
chaîne lourde H-gamma1 *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV4-31*02 (90.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [10.7.11] (26-35.53-59.98-108)) (1-119) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v50 CH2 delE1.4, P1.3, V1.2, A1.1, G1v60 CH2 S115, S116 (CH1 R120 (216) (120-217), charnière 1-15 (218-232), CH2 E1.4>del, L1.3>P (235), L1.2>V (236), G1.1>A(237), A115>S (331), P116>S (332) (233-341), CH3 E12 (357), M14 (359) (342-446), CHS K2>del (447)) (120-447)], (222-214')-disulfure avec la chaîne légère L-kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-15*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 (228-228'':231-231'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1SV, glycoforme alfa; substitué sur l'atome de soufre de 8 résidus L-cystéinyle en moyenne parmi 222, 228, 231, 214', 222'', 228'', 231'' et 214''' avec un groupement radical 1-{3-[(2-{5-[({[(1*S*,9*S*)-9-éthyl-5-fluoro-9-hydroxy-4-méthyl-10,13-dioxo-2,3,9,10,13,15-hexahydro-1*H*,12*H*-benzo[*de*]pyrano[3',4':6,7]indolizino[1,2-*b*]quinoléin-1-yl]carbamoyl}oxy)méthyl]-2-(β-D-glucopyranuronosyloxy)anilino}-2-oxoéthyl)amino]-3-oxopropyl}-2,5-dioxopyrrolidin-3-yle (*tocentécan*)

precemtabart tocentecán

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CEACAM5 (molécula de adhesión celular 5 parecida al antígeno carcinoembrionario, CEA, CD66e)]; anticuerpo monoclonal *Homo sapiens*, conjugado por 8 residuos cisteinilo en promedio al *tocentecán*, que comprende un conector y un derivado de la camptotecina (*exatecán*);

cadena pesda H-gamma1 *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV4-31*02 (90.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [10.7.11] (26-35.53-59.98-108)) (1-119) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v50 CH2 delE1.4, P1.3, V1.2, A1.1, G1v60 CH2 S115, S116 (CH1 R120 (216) (120-217), bisagra 1-15 (218-232), CH2 E1.4>del, L1.3>P (235), L1.2>V (236), G1.1>A(237), A115>S (331), P116>S (332) (233-341), CH3 E12 (357), M14 (359) (342-446), CHS K2>del (447)) (120-447)], (222-214')-disulfuro con la cadena ligera L-kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-15*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 (228-228'':231-231'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1SV, forma glicosilada alfa; sustituido en el átomo de azufre de 8 residuos L-cisteinilo en promedio entre 222, 228, 231, 214', 222'', 228'', 231'' y 214'' con un grupo radical 1-{3-[(2-{5-[({[(1*S*,9*S*)-9-etil-5-fluoro-9-hidroxi-4-metil-10,13-dioxo-2,3,9,10,13,15-hexahidro-1*H*,12*H*-benzo[de]pirano[3',4':6,7]indolizino[1,2-b]quinolin-1-il]carbamoil}oxi)metil]-2-(β-D-glucopiranuronosiloxi)anilino}-2-oxoetil)amino]-3-oxopropil}-2,5-dioxopirrolidin-3-ilo (*tocentecán*)

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLQESGPG LVKPSQTLSL TCTVSDGSVS RGGYYLTWIR QHPGKGLEWI  50
GYIYYSGSTY FNPSLRSRVT MSVDTSKNQF SLKLSSVTAA DTAVYYCARG 100
IAVAPFDYWG QGTLVTVSSA STKGPSVFPL APSSKSTSGG TAALGCLVKD 150
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY 200
ICNVNHKPSN TKVDKRVEPK SCDKTHTCPP CPAPPVAGPS VFLFPPKPKD 250
TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNST 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKALP SSIEKTISKA KGQPREPQVY 350
TLPPSREEMT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD 400
SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPG    447
```

Light chain / Chaîne légère / Cadena ligera

```
EIVLTQSPAT LSVSPGERAT LSCRTSQSVR SNLAWYQQKP GQAPRLLIYA  50
ASTRATGIPA RFSGSGSGTE FTLTISSLQS EDFAVYYCQQ YTNWPFTFGP 100
GTKVDIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Post-translational modifications

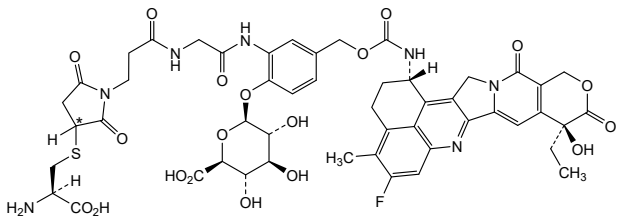
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

Intra-H (C23-C104) 22-97 146-202 262-322 368-426
22''-97'' 146''-202'' 262''-322'' 368''-426''
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''

*The four inter-chain disulfide bridges are not present, an average of 8 cysteinyl being conjugated each via a thioether bond to a drug linker.
*Les quatre ponts disulfures inter-chaînes ne sont pas présents, 8 cystéinyl en moyenne étant chacun conjugué via une liaison thioéther à un linker-principe actif.
*Los cuatro puentes disulfuro inter-catenarios no estan presentes, una media de 8 cisteinil está conjugada a conectores de principio activo.

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H VH N68 (no glycosylation X being P69 in NXS/T motif): 62, 62''
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

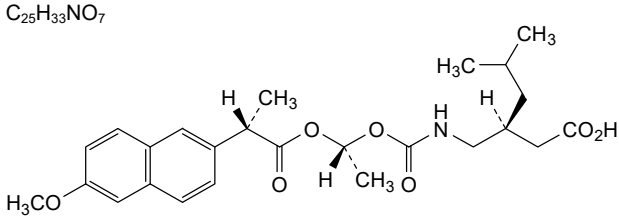
Potential modified residues / résidus modifiés potentiels / restos modificados potenciales*
C (222,228,231,214',222'',228'',231'',214''')
*(tocentecan:mAb ~ 8:1)



pregabalinum naproxencarbilum

pregabalin naproxencarbil	(3*S*)-3-[({[(1*R*)-1-{[(2*S*)-2-(6-methoxynaphthalen-2-yl)propanoyl]oxy}ethoxy]carbonyl}amino)methyl]-5-methylhexanoic acid
prégabaline naproxencarbil	acide (3*S*)-3-[({[(1*R*)-1-{[(2*S*)-2-(6-méthoxynaphtalén-2-yl)propanoyl]oxy}éthoxy]carbonyl}amino)méthyl]-5-méthylhexanoïque
pregabalina naproxencarbilo	ácido (3*S*)-5-metil-3-[({[(1*R*)-1-{[(2*S*)-2-(6-metoxinaftalen-2-il)propanoil]oxi}etoxi]carbonil}amino)metil]hexanoico

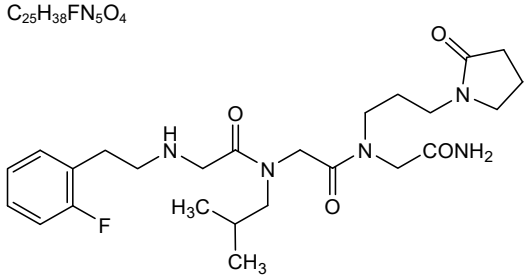
$C_{25}H_{33}NO_7$



privosegtorum

privosegtor	*N*-[2-(2-fluorophenyl)ethyl]glycyl-*N*-(2-methylpropyl)glycyl-N^2-[3-(2-oxopyrrolidin-1-yl)propyl]glycinamide
privosegtor	*N*-[2-(2-fluorophényl)éthyl]glycyl-*N*-(2-méthylpropyl)glycyl-N^2-[3-(2-oxopyrrolidin-1-yl)propyl]glycinamide
privosegtor	*N*-[2-(2-fluorofenil)etil]glicil-*N*-(2-metilpropil)glicil-N^2-[3-(2-oxopirrolidin-1-il)propil]glicinamida

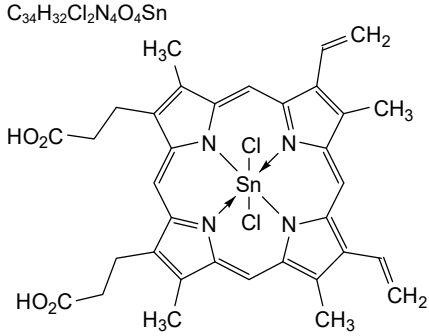
$C_{25}H_{38}FN_5O_4$



protoporfinum stannicum

stannic protoporfin	(*OC*-6-13)-[2,18-bis(2-carboxyethyl)-8,13-diethenyl-3,7,12,17-tetramethylporphyrin-21,23-diido-$\kappa^4N^{21},N^{22},N^{23},N^{24}$]dichloridotin
protoporfine stannique	(*OC*-6-13)-[2,18-bis(2-carboxyéthyl)-8,13-diéthényl-3,7,12,17-tétraméthylporphyrine-21,23-diido-$\kappa^4N^{21},N^{22},N^{23},N^{24}$]dichloridoétain
protoporfina estanica	(*OC*-6-13)-[2,18-bis(2-carboxietil)-8,13-dietenil-3,7,12,17-tetrametilporfirina-21,23-diido-$\kappa^4N^{21},N^{22},N^{23},N^{24}$]dicloridoestaño

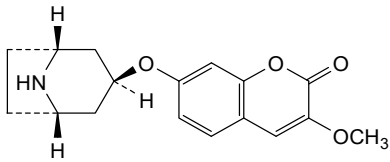
$C_{34}H_{32}Cl_2N_4O_4Sn$



pudafensinum

pudafensine	7-{[(1*R*,3*s*,5*S*)-8-azabicyclo[3.2.1]octan-3-yl]oxy}-3-methoxy-2*H*-1-benzopyran-2-one
pudafensine	7-{[(1*R*,3*s*,5*S*)-8-azabicyclo[3.2.1]octan-3-yl]oxy}-3-méthoxy-2*H*-1-benzopyran-2-one
pudafensina	7-{[(1*R*,3*s*,5*S*)-8-azabiciclo[3.2.1]octan-3-il]oxi}-3-metoxi-2*H*-1-benzopiran-2-ona

$C_{17}H_{19}NO_4$



redalsomatropinum alfa #

redalsomatropin alfa	human somatotropin (growth hormone (GH), growth hormone 1, pituitary growth hormone) (1-191) fused to human serum albumin (1-585, 192-776 in the current sequence) [$A^{320}>T^{511}$]-variant, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa
rédalsomatropine alfa	somatotropine humaine (hormone de croissance (GH), hormone de croissance 1, hormone de croissance hypophysaire) (1-191) fusionnée à l'albumine sérique humaine (1-585, 192-776 dans la séquence actuelle), [$A^{320}>T^{511}$]-variant, produite dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa
redalsomatropina alfa	somatotropina humana (hormona de crecimiento (GH), hormona de crecimiento 1, hormona de crecimiento pituitaria) (1-191) fusionada a la albúmina sérica humana (1-585, 192-776 en la secuencia actual) [$A^{320}>T^{511}$]-variante, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, glicoforma alfa

Sequence / Séquence / Secuencia

```
FPTIPLSRLF DNAMLRAHRL HQLAFDTYQE FEEAYIPKEQ KYSFLQNPQT   50
SLCFSESIPT PSNREETQQK SNLELLRISL LLIQSWLEPV QFLRSVFANS  100
LVYGASDSNV YDLLKDLEEG IQTLMGRLED GSPRTGQIFK QTYSKFDTNS  150
HNDDALLKNY GLLYCFRKDM DKVETFLRIV QCRSVEGSCG FDAHKSEVAH  200
RFKDLGEENF KALVLIAFAQ YLQQCPFEDH VKLVNEVTEF AKTCVADESA  250
ENCDKSLHTL FGDKLCTVAT LRETYGEMAD CCAKQEPERN ECFLQHKDDN  300
PNLPRLVRPE VDVMCTAFHD NEETFLKKYL YEIARRHPYF YAPELLFFAK  350
RYKAAFTECC QAADKAACLL PKLDELRDEG KASSAKQRLK CASLQKFGER  400
AFKAWAVARL SQRFPKAEFA EVSKLVTDLT KVHTECCHGD LLECADDRAD  450
LAKYICENQD SISSKLKECC EKPLLEKSHC IAEVENDEMP ADLPSLAADF  500
VESKDVCKNY TEAKDVFLGM FLYEYARRHP DYSVVLLLRL AKTYETTLEK  550
CCAAADPHEC YAKVFDEFKP LVEEPQNLIK QNCELFEQLG EYKFQNALLV  600
RYTKKVPQVS TPTLVEVSRN LGKVGSKCCK HPEAKRMPCA EDYLSVVLNQ  650
LCVLHEKTPV SDRVTKCCTE SLVNRRPCFS ALEVDETYVP KEFNAETFTF  700
HADICTLSEK ERQIKKQTAL VELVKHKPKA TKEQLKAVMD DFAAFVEKCC  750
KADDKETCFA EEGKKLVAAS QAALGL                            776
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Mutation / Mutation / Mutación

$A^{320}>\underline{T}^{511}$

Post-translational modifications

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

53-165, 182-189, 244-253, 266-282, 281-292, 315-360, 359-368, 391-437, 436-444, 456-470, 469-480 507-552, 551-560, 583-629, 628-639, 652-668, 667-678, 705-750, 749-758

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

509

remvulimorgenum autoleucelum

remvulimorgene autoleucel	autologous peripheral blood mononuclear cells (PBMCs) obtained by apheresis and engineered into enhanced antigen presenting cells (eAPCs) by loading with five messenger RNAs (mRNAs) individually encoding human papillomavirus type 16 (HPV16) E6 protein, HPV16 E7 protein, human CD86, membrane-bound interleukin 2 (mbIL-2) and membrane-bound interleukin 12 (mbIL-12). Interleukin 2 (IL-2) and interleukin 12 (IL-12) are rendered membrane-bound (mb) by fusion to the transmembrane domain of the transferrin receptor with an interceding $(G_4S)_3$ linker. The mRNAs are delivered using a microfluidic membrane deformation technique that temporarily disrupts the cell membrane. Each mRNA comprises a 5'-cap, a synthetic 5' untranslated region containing a Kozak sequence, a coding region and a 3' untranslated region (UTR) derived from the murine alpha globin UTR. The cell population phenotype is CD45+, comprising primarily T lymphocytes (CD3+), monocytes (CD14+), natural killer (NK) cells (CD56+), and B lymphocytes (CD19+)
remvulimorgène autoleucel	cellules mononucléaires de sang périphérique (PBMC) autologues obtenues par aphérèse et transformées en cellules présentatrices d'antigènes amplifiées (eAPC) par chargement de cinq ARN messagers (ARNm) codant individuellement la protéine E6 du papillomavirus humain de type 16 (HPV16), la protéine E7 du HPV16, le CD86 humain, l'interleukine 2 liée à la membrane (mbIL-2) et l'interleukine 12 liée à la membrane (mbIL-12). L'interleukine 2 (IL-2) et l'interleukine 12 (IL-12) sont capable de se lier à la membrane (mb) grâce à la fusion au domaine transmembranaire du récepteur de la transferrine avec un linker $(G_4S)_3$ intercalé. Les ARNm sont délivrés au moyen d'une technique microfluidique de déformation de la membrane qui perturbe temporairement la membrane cellulaire. Chaque ARNm comprend une coiffe en 5', une région synthétique non traduite en 5' contenant une séquence Kozak, une région codante et une région non traduite (UTR) en 3' dérivée de l'UTR de l'alpha-globine murine.

remvulimorgén autoleucel	células mononucleares de sangre periférica (PBMCs) autólogas, obtenidas por aféresis y modificadas para convertirlas en células presentadoras de antígeno potenciadas (eAPCs) mediante su carga con cinco ARN mensajeros (ARNm) que codifican individualmente para la proteína E6 del virus del papiloma humano tipo 16 (HPV16), la proteína E7 del HPV16, el CD86 humano, la interleuquina 2 unida a membrana (mbIL-2) y la interleuquina 12 unida a membrana (mbIL-12). La interleuquina 2 (IL-2) y la interleuquina 12 (IL-12) se convierten en unidas a membrana (mb) mediante la fusión del domino transmembrana del receptor de transferrina con un enlazador intercesor $(G_4S)_3$. Los ARNm se administran usando una técnica de deformación de membrana microfuida que interrumpe temporalmente la membrana celular. Cada ARNm contiene un 5'-cap, una región sintética no traducida en 5'que contiene la secuencia Kozak, una región codificante y una región no traducida (UTR) en 3' derivada de la UTR de la globina alfa murina. El fenotipo de la población celular es CD45+, consistiendo principalmente en linfocitos T (CD3+), monocitos (CD14+), células NK (CD56+) y linfocitos B (CD19+)

rinatabartum #

rinatabart	immunoglobulin G1-kappa, anti-[*Homo sapiens* FOLR1 (folate receptor 1, folate receptor alpha, FR-alpha, adult folate-binding protein, FBP, ovarian tumor-associated antigen MOv18)], *Homo sapiens* monoclonal antibody; H-gamma1 heavy chain *Homo sapiens* (1-453) [VH (*Homo sapiens* IGHV3-30*03 (96.9%) -(IGHD) -IGHJ4*01 (92.9%) L123>Q (118), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, G1v14 CH2 A1.3, A1.2 (CH1 K120 (220) (124-221), hinge 1-15 (222-236), CH2 L1.3>A (240), L1.2>A (241) (237-346), CH3 D12 (362), L14 (364) (347-451), CHS (452-453)) (124-453)], (226-214')-disulfide with L-kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (93.7%) -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 (232-232'':235-235'')-bisdisulfide, produced in a cell line from Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, glycoform alfa
rinatabart	immunoglobuline G1-kappa, anti-[*Homo sapiens* FOLR1 (récepteur 1 du folate, récepteur alpha du folate, FR-alpha, protéine de l'adulte liant le folate, FBP, antigène MOv18 associé à des tumeurs ovariennes)], anticorps monoclonal *Homo sapiens*; chaîne lourde H-gamma1 *Homo sapiens* (1-453) [VH (*Homo sapiens* IGHV3-30*03 (96.9%) -(IGHD) -IGHJ4*01 (92.9%) L123>Q (118), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, G1v14 CH2 A1.3, A1.2 (CH1 K120 (220) (124-221), charnière 1-15 (222-236), CH2 L1.3>A (240), L1.2>A (241) (237-346), CH3 D12 (362), L14 (364) (347-451), CHS (452-453)) (124-453)], (226-214')-disulfure avec la chaîne légère L-kappa *Homo*

sapiens (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (93.7%) - 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 (232-232":235-235")-bisdisulfure, produit dans une lignée cellulaire des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1, glycoforme alfa

rinatabart

inmunoglobulina G1-kappa, anti-[*Homo sapiens* FOLR1 (receptor 1 del folato, receptor alfa del folato, FR-alfa, proteína del adulto que se une al folato, FBP, antígeno MOv18 asociado a dos tumores ováricos)], anticuerpo monoclonal *Homo sapiens*;
cadena pesada H-gamma1 *Homo sapiens* (1-453) [VH (*Homo sapiens* IGHV3-30*03 (96.9%) -(IGHD) -IGHJ4*01 (92.9%) L123>Q (118), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, G1v14 CH2 A1.3, A1.2 (CH1 K120 (220) (124-221), bisagra 1-15 (222-236), CH2 L1.3>A (240), L1.2>A (241) (237-346), CH3 D12 (362), L14 (364) (347-451), CHS (452-453)) (124-453)], (226-214')-disulfuro con la cadena ligera L-kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (93.7%) -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 (232-232":235-235")-bisdisulfuro, producido en una línea celular de las células ováricas de hámster chino (CHO), línea celular derivada de CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLLESGGG VVQPGRSLRL SCAASGFTFS SYGMHWVRQA PGKGLEWVAV  50
ISYDGSNKYY ADSVKGRFTI SRANSKNTLY LQMNSLRAED TAVYYCARPR 100
AYYGAYGSSF DYWGQGTQVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC 150
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG 200
TQTYICNVNH KPSNTKVDKK VEPKSCDKTH TCPPCPAPEA AGGPSVFLFP 250
PKPKDTLMIS RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE 300
QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR 350
EPQVYTLPPS RDELTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT 400
PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLS 450
PGK                                                     453
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Light chain / Chaîne légère / Cadena ligera

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EIVMTQSPSS VSASVGDRVA ITCRASQGIS SWLAWYQQKP GKAPKLLIYA  50
ASSLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ SYSTPLTFGG 100
GTKVDIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                         214
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Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 150-206 267-327 373-431
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-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-antennaire 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"

rinatabartum sesutecanum #

rinatabart sesutecan

immunoglobulin G1-kappa, anti-[*Homo sapiens* FOLR1 (folate receptor 1, folate receptor alpha, FR-alpha, adult folate-binding protein, FBP, ovarian tumor-associated antigen MOv18)], *Homo sapiens* monoclonal antibody, conjugated on an average of 8 cysteinyl residues to *sesutecan*, comprising a linker and a camptothecin derivative (*exatecan*);
H-gamma1 heavy chain *Homo sapiens* (1-453) [VH (*Homo sapiens* IGHV3-30*03 (96.9%) -(IGHD) -IGHJ4*01 (92.9%) L123>Q (118), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, G1v14 CH2 A1.3, A1.2 (CH1 K120 (220) (124-221), hinge 1-15 (222-236), CH2 L1.3>A (240), L1.2>A (241) (237-346), CH3 D12 (362), L14 (364) (347-451), CHS (452-453)) (124-453)], (226-214')-disulfide with L-kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (93.7%) -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 (232-232'':235-235'')-bisdisulfide, produced in a cell line from Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, glycoform alfa; substituted at the sulfur atoms of an average of 8 L-cysteinyl residues among 226, 232, 235, 214', 226'', 232'', 235'' and 214''' with radical group 1-[(2*R*,3*R*,4*R*,5*S*,52*S*)-1,2,3,4,5-pentahydroxy-52-{[(2*S*)-1-{[(2*S*)-5-carbamoylamino-1-oxo-1-{3-[({[(1*S*,9*S*)-9-ethyl-5-fluoro-9-hydroxy-4-methyl-10,13-dioxo-2,3,9,10,13,15-hexahydro-1*H*,12*H*-benzo[*de*]pyrano[3',4':6,7]indolizino[1,2-*b*]quinolin-1-yl]carbamoyl}oxy)methyl]anilino}pentan-2-yl]amino}-3-methyl-1-oxobutan-2-yl]carbamoyl}-7-[(2*S*,3*R*,4*R*,5*R*)-2,3,4,5,6-pentahydroxyhexyl]-46,54-dioxo-10,13,16,19,22,25,28,31,34,37,40,43-dodecaoxa-7,47,53-triazanonapentacontan-59-yl]-2,5-dioxopyrrolidin-3-yl (*sesutecan*)

rinatabart sésutécan

immunoglobuline G1-kappa, anti-[*Homo sapiens* FOLR1 (récepteur 1 du folate, récepteur alpha du folate, FR-alpha, protéine de l'adulte liant le folate, FBP, antigène MOv18 associé à des tumeurs ovariennes)], anticorps monoclonal *Homo sapiens*, conjugué via un linker clivable par 8 résidus cystéinyle en moyenne au *sésutécan*, comprenant un linker et un dérivé de la camptothécine (*exatécan*);
chaîne lourde H-gamma1 *Homo sapiens* (1-453) [VH (*Homo sapiens* IGHV3-30*03 (96.9%) -(IGHD) -IGHJ4*01 (92.9%) L123>Q (118), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, G1v14 CH2 A1.3, A1.2 (CH1 K120 (220) (124-221), charnière 1-15 (222-236), CH2 L1.3>A (240), L1.2>A (241) (237-346), CH3 D12 (362), L14 (364) (347-451), CHS (452-453)) (124-453)], (226-214')-disulfure avec la chaîne légère L-kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (93.7%) -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 (232-232'':235-235'')-bisdisulfure, produit dans une lignée cellulaire des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1, glycoforme alfa;

	substitué sur un atome de soufre de 8 résidus L-cystéinyle en moyenne parmi 226, 232, 235, 214', 226'', 232'', 235'' et 214''' avec un groupement radical 1-[(2*R*,3*R*,4*R*,5*S*,52*S*)-1,2,3,4,5-pentahydroxy-52-{[(2*S*)-1-{[(2*S*)-5-carbamoylamino-1-oxo-1-{3-[({[(1*S*,9*S*)-9-éthyl-5-fluoro-9-hydroxy-4-méthyl-10,13-dioxo-2,3,9,10,13,15-hexahydro-1*H*,12*H*-benzo[*de*]pyrano[3',4':6,7]indolizino[1,2-*b*]quinoléin-1-yl]carbamoyl}oxy)méthyl]anilino}pentan-2-yl]amino}-3-méthyl-1-oxobutan-2-yl]carbamoyl}-7-[(2*S*,3*R*,4*R*,5*R*)-2,3,4,5,6-pentahydroxyhexyl]-46,54-dioxo-10,13,16,19,22,25,28,31,34,37,40,43-dodécaoxa-7,47,53-triazanonapentacontan-59-yl]-2,5-dioxopyrrolidin-3-yle (*sésutécan*)
rinatabart sesutecán	inmunoglobulina G1-kappa, anti-[*Homo sapiens* FOLR1 (receptor 1 del folato, receptor alfa del folato, FR-alfa, proteína del adulto que se une al folato, FBP, antígeno MOv18 asociado a los tumores ováricos)], anticuerpo monoclonal *Homo sapiens*, conjugado mediante un conector escindible por 8 residuos cisteinilo en promedio a *sesutecán*, que comprende un conector y un derivado de la camptotecina (*exatecán*); cadena pesada H-gamma1 *Homo sapiens* (1-453) [VH (*Homo sapiens* IGHV3-30*03 (96.9%) -(IGHD) - IGHJ4*01 (92.9%) L123>Q (118), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, G1v14 CH2 A1.3, A1.2 (CH1 K120 (220) (124-221), bisagra 1-15 (222-236), CH2 L1.3>A (240), L1.2>A (241) (237-346), CH3 D12 (362), L14 (364) (347-451), CHS (452-453)) (124-453)], (226-214')-disulfuro con la cadena ligera L-kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (93.7%) - 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 (232-232'':235-235'')-bisdisulfuro, producido en una línea celular de las células ováricas de hámster chino (CHO), línea celular derivada de CHO-K1, forma glicosilada alfa; sustituido en un átomo de azufre de 8 residuos L-cisteinilo en promedio entre 226, 232, 235, 214', 226'', 232'', 235'' y 214''' con un grupo radical 1-[(2*R*,3*R*,4*R*,5*S*,52*S*)-1,2,3,4,5-pentahidroxi-52-{[(2*S*)-1-{[(2*S*)-5-carbamoilamino-1-oxo-1-{3-[({[(1*S*,9*S*)-9-etil-5-fluoro-9-hidroxi-4-metil-10,13-dioxo-2,3,9,10,13,15-hexahidro-1*H*,12*H*-benzo[*de*]pirano[3',4':6,7]indolizino[1,2-*b*]quinolein-1-il]carbamoil}oxi)metil]anilino}pentan-2-il]amino}-3-metil-1-oxobutan-2-il]carbamoil}-7-[(2*S*,3*R*,4*R*,5*R*)-2,3,4,5,6-pentahidroxihexil]-46,54-dioxo-10,13,16,19,22,25,28,31,34,37,40,43-dodecaoxa-7,47,53-triazanonapentacontan-59-il]-2,5-dioxopirrolidin-3-ilo (*sesutecán*)

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLLESGGG VVQPGRSLRL SCAASGFTFS SYGMHWVRQA PGKGLEWVAV  50
ISYDGSNKYY ADSVKGRFTI SRANSKNTLY LQMNSLRAED TAVYYCARPR 100
AYYGAYGSSF DYWGQGTQVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC 150
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG 200
TQTYICNVNH KPSNTKVDKK VEPKSCDKTH TCPPCPAPEA AGGPSVFLFP 250
PKPKDTLMIS RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE 300
QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR 350
EPQVYTLPPS RDELTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT 400
PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLS 450
PGK                                                     453
```

Light chain / Chaîne légère / Cadena ligera

```
EIVMTQSPSS VSASVGDRVA ITCRASQGIS SWLAWYQQKP GKAPKLLIYA  50
ASSLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ SYSTPLTFGG 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"

*The four inter-chain disulfide bridges are not present, an average of 8 cysteinyl being conjugated each via a thioether bond to a drug linker.

*Les quatre ponts disulfures inter-chaînes ne sont pas présents, 8 cystéinyl en moyenne étant chacun conjugué via une liaison thioéther à un linker-principe actif.

*Los cuatro puentes disulfuro inter-catenarios no estan presentes, una media de 8 cisteinil está conjugada a conectores de principio activo.

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

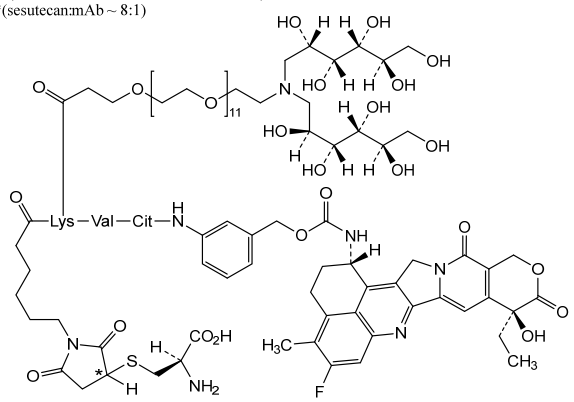
C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal

H CHS K2: 453, 453"

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

C (226,232,235,214',226",232",235",214'")

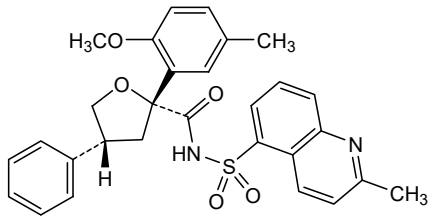
*(sesutecan:mAb ~ 8:1)



riselcaftorum

riselcaftor	(2*R*,4*R*)-2-(2-methoxy-5-methylphenyl)-*N*-(2-methylquinoline-5-sulfonyl)-4-phenyloxolane-2-carboxamide
riselcaftor	(2*R*,4*R*)-2-(2-méthoxy-5-méthylphényl)-*N*-(2-méthylquinoléine-5-sulfonyl)-4-phényloxolane-2-carboxamide
riselcaftor	(2*R*,4*R*)-4-fenil-2-(5-metil-2-metoxifenil)-*N*-(2-metilquinoleína-5-sulfonil)oxolano-2-carboxamida

$C_{29}H_{28}N_2O_5S$



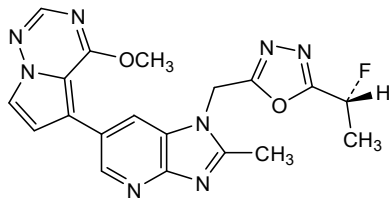
rogocekibum

rogocekib — 1-({5-[(1*R*)-1-fluoroethyl]-1,3,4-oxadiazol-2-yl}methyl)-6-(4-methoxypyrrolo[2,1-*f*][1,2,4]triazin-5-yl)-2-methyl-1*H*-imidazo[4,5-*b*]pyridine

rogocékib — 1-({5-[(1*R*)-1-fluoroéthyl]-1,3,4-oxadiazol-2-yl}méthyl)-6-(4-méthoxypyrrolo[2,1-*f*][1,2,4]triazin-5-yl)-2-méthyl-1*H*-imidazo[4,5-*b*]pyridine

rogocekib — 1-({5-[(1*R*)-1-fluoroetil]-1,3,4-oxadiazol-2-il}metil)-2-metil-6-(4-metoxipirrolo[2,1-*f*][1,2,4]triazin-5-il)-1*H*-imidazo[4,5-*b*]piridina

$C_{19}H_{17}FN_8O_2$



rondaptivonum pegolum

rondaptivon pegol — *all-P-ambo*-5'-*O*-(1-hydroxy-14-[α-methylpoly(oxyethylene)-ω-oxy]-12-{[α-methylpoly(oxyethylene)-ω-oxy]ethyl}-1,10,13-trioxo-2-oxa-9,12-diaza-1λ^5-phosphatetradecan-1-yl)-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyladenylyl-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→3')-thymidine

rondaptivon pégol

tout-P-ambo-5'-*O*-(1-hydroxy-14-[α-méthylpoly(oxyéthylène)-ω-oxy]-12-{[α-méthylpoly(oxyéthylène)-ω-oxy]éthyl}-1,10,13-trioxo-2-oxa-9,12-diaza-1λ^5-phosphatétradécan-1-yl)-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyladénylyl-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→3')-thymidine

rondaptivón pegol

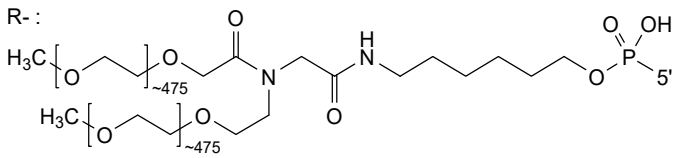
todo-P-ambo-5'-*O*-(1-hidroxi-14-[α-metilpoli(oxietileno)-ω-oxi]-12-{[α-metilpoli(oxietileno)-ω-oxi]etil}-1,10,13-trioxo-2-oxa-9,12-diaza-1λ^5-fosfatetradecan-1-il)-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metiladenilil-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilcitidilil-(3'→3')-timidina

$C_{329}H_{443}N_{117}O_{212}P_{30}(C_2H_4O)_{2n}$

(3'-5')R-*G*-*C*-*C*-*A*-*G*-*G*-*G*-*A*-*C*-*C*-*U*-*A*-*A*-*G*-*A*-*C*-*A*-*C*-*A*-*U*-*G*-*U*-*C*-*C*-*C*-*U*-*G*-*G*-*C*3'-3'dT

N : A, C, G, U, T
N : 2'-*O*-methyl-N / 2'-*O*-méthyl-N / 2'-*O*-metil-N
dN : 2'-deoxy-N / 2'-désoxy-N / 2'-desoxi-N

R- :



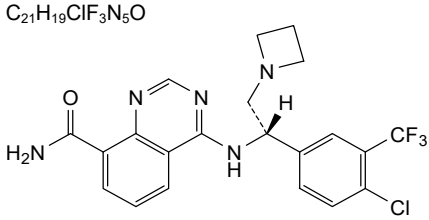
rupitasertibum

rupitasertib

4-({(1*S*)-2-(azetidin-1-yl)-1-[4-chloro-3-(trifluoromethyl)phenyl]ethyl}amino)quinazoline-8-carboxamide

rupitasertib	4-({(1*S*)-2-(azétidin-1-yl)-1-[4-chloro-3-(trifluorométhyl)phényl]éthyl}amino)quinazoline-8-carboxamide
rupitasertib	4-({(1*S*)-2-(azetidin-1-il)-1-[4-cloro-3-(trifluorometil)fenil]etil}amino)quinazolina-8-carboxamida

$C_{21}H_{19}ClF_3N_5O$



samatatugum

samatatug	immunoglobulin G1-kappa, anti-[*Homo sapiens* F3 (coagulation factor III (thromboplastin, tissue factor), CD142)], *Homo sapiens* monoclonal antibody; H-gamma1 heavy chain *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV1-18*01 (94.9%) -(IGHD) -IGHJ3*01 (92.3%) M123>T (118), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (220) (124-221), hinge 1-15 (222-236), CH2 (237-346), CH3 E12 (362), M14 (364) (347-451), CHS K2>del (452)) (124-452)], (226-215')-disulfide with L-kappa light chain *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-5*03 (91.4%) -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 (232-232":235-235")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from the cell line CHO-DG44, co-expressing the enzyme dihydrofolate reductase (DHFR), glycoform alfa
samatatug	immunoglobuline G1-kappa, anti-[*Homo sapiens* F3 (facteur de coagulation III (thromboplastine, facteur tissulaire), CD142)], anticorps monoclonal *Homo sapiens*; chaîne lourde H-gamma1 *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV1-18*01 (94.9%) -(IGHD) -IGHJ3*01 (92.3%) M123>T (118), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (220) (124-221), charnière 1-15 (222-236), CH2 (237-346), CH3 E12 (362), M14 (364) (347-451), CHS K2>del (452)) (124-452)], (226-215')-disulfure avec la chaîne légère L-kappa *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-5*03 (91.4%) -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 (232-232":235-235")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-DG44, co-exprimant l'enzyme dihydrofolate réductase (DHFR), glycoforme alfa

samatatug

inmunoglobulina G1-kappa, anti-[*Homo sapiens* F3 (factor de coagulación III (tromboplastina, factor tisular), CD142)], anticuerpo monoclonal *Homo sapiens*;
cadena pesada H-gamma1 *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV1-18*01 (94.9%) -(IGHD) -IGHJ3*01 (92.3%) M123>T (118), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (220) (124-221), bisagra 1-15 (222-236), CH2 (237-346), CH3 E12 (362), M14 (364) (347-451), CHS K2>del (452)) (124-452)], (226-215')-disulfureo con la cadena ligera L-kappa *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-5*03 (91.4%) -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 (232-232":235-235")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular derivada de CHO-DG44, co-expresando la enzima dihidrofolato reductasa (DHFR) forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGASVKV SCKASGYTFD VYGISWVRQA PGQGLEWMGW  50
IAPYSGNTNY AQKLQGRVTM TTDTSTSTAY MELRSLRSDD TAVYYCARDA 100
GTYSPFGYGM 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
PG                                                      452
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Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPST LSASVGDRVT ITCQASQSIN NWLAWYQQKP GKAPKLLIYK  50
AYNLESGVPS RFSGSGSGTE FTLTISSLQP DDFATYYCQL FQSLPPFTFG 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) 22-96 150-206 267-327 373-431
22"-96" 150"-206" 267"-327" 373"-431"
Intra-L (C23-C104) 23'-88' 135'-195'
23'"-88'" 135'"-195'"
Inter-H-L (h 5-CL 126) 226-215' 226"-215'"
Inter-H-H (h 11, h 14) 232-232" 235-235"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)
H 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

samatatugum zovodotinum

samatatug zovodotin

immunoglobulin G1-kappa, anti-[*Homo sapiens* F3 (coagulation factor III (thromboplastin, tissue factor), CD142)], *Homo sapiens* monoclonal antibody, conjugated on an average of 4 cysteinyl residues via a cleavable linker to a derivative of auristatin;
H-gamma1 heavy chain *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV1-18*01 (94.9%) -(IGHD) -IGHJ3*01 (92.3%) M123>T (118), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (220) (124-221), hinge 1-15 (222-236), CH2 (237-346), CH3 E12 (362), M14 (364) (347-451), CHS K2>del (452)) (124-452)], (226-215')-disulfide with L-kappa light chain *Homo sapiens*

	(1'-215') [V-KAPPA (*Homo sapiens* IGKV1-5*03 (91.4%) -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 (232-232":235-235")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from the cell line CHO-DG44, co-expressing the enzyme dihydrofolate reductase (DHFR), glycoform alfa; substituted at the sulfur atoms of four L-cysteinyl residues on an average among 226, 232, 235, 215', 226", 232", 235" and 215"' with radical group (3*RS*)-1-[(6*S*,9*S*)-1-amino-6-{[4-({*N*,*N*-dimethyl-L-valyl-L-valyl-(3*R*,4*S*,5*S*)-3-methoxy-5-methyl-4-(methylamino)heptanoyl-(2*R*,3*R*)-3-methoxy-2-methyl-3-[(2*S*)-pyrrolidin-2-yl]propanoyl}sulfamoyl)phenyl]carbamoyl}-1,8,11-trioxo-9-(propan-2-yl)-14,17,20-trioxa-2,7,10-triazadocosan-22-yl]-2,5-dioxopyrrolidin-3-yl (*zovodotin*)
samatatug zovodotine	immunoglobuline G1-kappa, anti-[*Homo sapiens* F3 (facteur de coagulation III (thromboplastine, facteur tissulaire), CD142)], anticorps monoclonal *Homo sapiens*, conjugué, par 4 résidus cystéinyle en moyenne, à un dérivé de l'auristatine, via un linker clivable; chaîne lourde H-gamma1 *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV1-18*01 (94.9%) -(IGHD) -IGHJ3*01 (92.3%) M123>T (118), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (220) (124-221), charnière 1-15 (222-236), CH2 (237-346), CH3 E12 (362), M14 (364) (347-451), CHS K2>del (452)) (124-452)], (226-215')-disulfure avec la chaîne légère L-kappa *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-5*03 (91.4%) -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 (232-232":235-235")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-DG44, co-exprimant l'enzyme dihydrofolate réductase (DHFR), glycoforme alfa; substitué sur l'atome de soufre de 4 résidus L-cystéinyle en moyenne parmi 226, 232, 235, 215', 226", 232", 235" et 215"' avec un groupement radical (3*RS*)-1-[(6*S*,9*S*)-1-amino-6-{[4-({*N*,*N*-diméthyl-L-valyl-L-valyl-(3*R*,4*S*,5*S*)-3-méthoxy-5-méthyl-4-(méthylamino)heptanoyl-(2*R*,3*R*)-3-méthoxy-2-méthyl-3-[(2*S*)-pyrrolidin-2-yl]propanoyl}sulfamoyl)phényl]carbamoyl}-1,8,11-trioxo-9-(propan-2-yl)-14,17,20-trioxa-2,7,10-triazadocosan-22-yl]-2,5-dioxopyrrolidin-3-yle (*zovodotine*)
samatatug zovodotina	inmunoglobulina G1-kappa, anti-[*Homo sapiens* F3 (factor de coagulación III (tromboplastina, factor tisular), CD142)], anticuerpo monoclonal *Homo sapiens*, conjugado, por 4 restos cisteinilo por término medio, con un derivado de la auristatina a través de un enclace escindible; cadena pesada H-gamma1 *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV1-18*01 (94.9%) -(IGHD) -IGHJ3*01 (92.3%) M123>T (118), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (220) (124-221), bisagra1-15 (222-236), CH2 (237-346), CH3 E12 (362), M14 (364) (347-451), CHS K2>del (452)) (124-452)], (226-215')-disulfuro con la cadena ligera L-kappa *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-5*03 (91.4%) -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 (232-232":235-235")-bisdisulfuro, producido en las células ováricas de hámster chino

(CHO), línea celular derivada de CHO-DG44, co-expresando la enzima dihidrofolato reductasa (DHFR)forma glicosilada alfa; sustituido en el átomo de azufre de 4 residuos de L-cisteinilo en promedio de 226, 232, 235, 215', 226'', 232'', 235'' y 215'' con un grupo radical (3*RS*)-1-[(6*S*,9*S*)-1-amino-6-{[4-({*N*,*N*-dimetil-L-valil-L-valil-(3*R*,4*S*,5*S*)-5-metil-3-metoxi-4-(metilamino)heptanoil-(2*R*,3*R*)-2-metil-3-metoxi-3-[(2*S*)-pirrolidin-2-il]propanoil}sulfamoil)fenil]carbamoil}-1,8,11-trioxo-9 -(propan-2-il)-14,17,20-trioxa-2,7,10-triazadocosan-22-il]-2,5-dioxopirrolidin-3-ilo (*zovodotina*)

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGASVKV SCKASGYTFD VYGISWVRQA PGQGLEWMGW  50
IAPYSGNTNY AQKLQGRVTM TTDTSTSTAY MELRSLRSDD TAVYYCARDA 100
GTYSPFGYGM 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
PG                                                      452
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPST LSASVGDRVT ITCQASQSIN NWLAWYQQKP GKAPKLLIYK  50
AYNLESGVPS RFSGSGSGTE FTLTISSLQP DDFATYYCQL FQSLPPFTFG 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) 22-96 150-206 267-327 373-431
22''-96'' 150''-206'' 267''-327'' 373''-431''

Intra-L (C23-C104) 23'-88' 135'-195'
23'''-88''' 135'''-195'''

Inter-H-L (h 5-CL 126)* 226-215' 226''-215'''

Inter-H-H (h 11, h 14)* 232-232'' 235-235''

*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 / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal

Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)

H VH Q1: 1, 1''

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

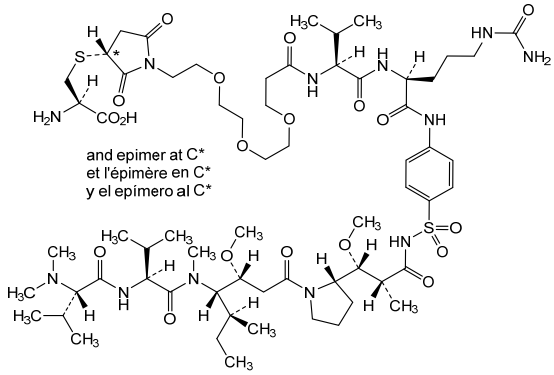
H CH2 N84.4: 303, 303''

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

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

C (226, 232, 235, 215', 226'', 232'', 235'',215''')

*(zovodotin:mAb ~ 4:1)



sefaxersenum

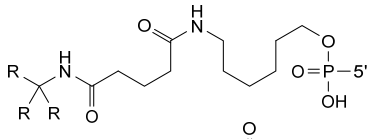
sefaxersen	*all-P-ambo*-5'-*O*-(28-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]-16,16-bis{[3-({6-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]hexyl}amino)-3-oxopropoxy]methyl}-1-hydroxy-1,10,14,21-tetraoxo-2,18-dioxa-9,15,22-triaza-1λ^5-phosphaoctacosan-1-yl)-2'-*O*-(2-methoxyethyl)-*P*-thioadenylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyl-*P*-thiouridylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-deoxy-*P*-thioadenylyl-(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-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-deoxy-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-deoxy-5-methyl-*P*-thiocytidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-deoxy-*P*-thioguanylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-*P*-thioadenylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-*P*-thioguanylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methylcytidine
séfaxersen	*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-méthyl-*P*-thiouridylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-désoxy-*P*-thioadénylyl-(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-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-désoxy-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-désoxy-5-méthyl-*P*-thiocytidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-désoxy-*P*-thioguanylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-*P*-thioadénylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-*P*-thioguanylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthylcytidine
sefaxersén	*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')-2'-*O*-(2-metoxietil)-5-metil-*P*-tiouridilil-(3'→5')-2'-*O*-(2-metoxietil)-5-metil-*P*-tiocitidilil-(3'→5')-2'-*O*-(2-metoxietil)-5-metil-*P*-tiocitidilil-(3'→5')-2'-*O*-(2-metoxietil)-5-metil-*P*-tiocitidilil-(3'→5')-2'-desoxi-*P*-tioadenilil-(3'→5')-2'-desoxi-5-metil-*P*-tiocitidilil-(3'→5')-2'-desoxi-*P*-tioguanilil-(3'→5')-2'-desoxi-5-metil-*P*-tiocitidilil-(3'→5')-2'-desoxi-5-metil-*P*-tiocitidilil-(3'→5')-2'-desoxi-5-metil-*P*-tiocitidilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2'-desoxi-*P*-tioguanilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2'-*O*-(2-metoxietil)-5-metil-*P*-tiocitidilil-(3'→5')-2'-*O*-(2-metoxietil)-5-metil-*P*-tiocitidilil-(3'→5')-2'-*O*-(2-metoxietil)-*P*-tioadenilil-(3'→5')-2'-*O*-(2-metoxietil)-*P*-tioguanilil-(3'→5')-2'-*O*-(2-metoxietil)-5-metilcitidina

$C_{296}H_{445}N_{77}O_{148}P_{20}S_{19}$

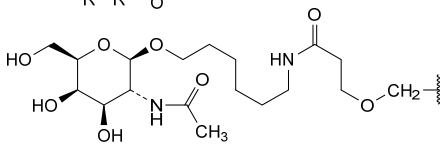
R1-Amoe=m^{5}Umoe=m^{5}Cmoe=m^{5}Cmoe=m^{5}Cmoe=dA=m^{5}C$_d$=dG=m^{5}C$_d$=m^{5}C$_d$=
m^{5}C$_d$=m^{5}C$_d$=dT=dG=dT=m^{5}Cmoe=m^{5}Cmoe=Amoe=Gmoe=m^{5}Cmoe

N : A,C,G,T,U
m^{5}N : 5-methyl-N / 5-méthyl-N / 5-metil-N
dN & N$_d$: 2'-deoxy-N / 2'-désoxy-N / 2'-desoxi-N
Nmoe : 2'-*O*-(2-methoxyethyl)-N / 2'-*O*-(2-méthoxyéthyl)-N / 2'-*O*-(2-metoxietil)-N
– : –PO(OH)– =: –PO(SH)–

R1- :



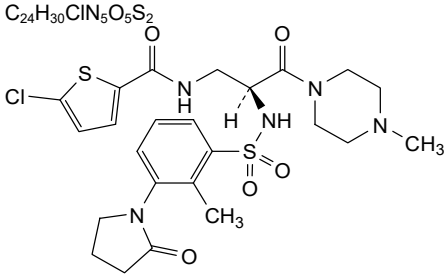
R :



segatroxabanum

segatroxaban	5-chloro-*N*-{(2*S*)-2-[2-methyl-3-(2-oxopyrrolidin-1-yl)benzene-1-sulfonamido]-3-(4-methylpiperazin-1-yl)-3-oxopropyl}thiophene-2-carboxamide
ségatroxaban	5-chloro-*N*-{(2*S*)-2-[2-méthyl-3-(2-oxopyrrolidin-1-yl)benzène-1-sulfonamido]-3-(4-méthylpipérazin-1-yl)-3-oxopropyl}thiophène-2-carboxamide
segatroxabán	5-cloro-*N*-{(2*S*)-2-[2-metil-3-(2-oxopirrolidin-1-il)benceno-1-sulfonamido]-3-(4-metilpiperazin-1-il)-3-oxopropil}tiofeno-2-carboxamida

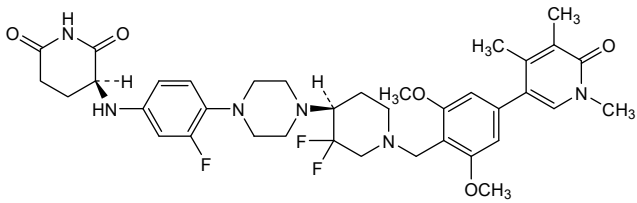
$C_{24}H_{30}ClN_5O_5S_2$



sendegobresibum

sendegobresib	(4^4S,8^3S)-4^3,4^3,6^2-trifluoro-2^3,2^5-dimethoxy-1^1,1^4,1^5-trimethyl-7-aza-5(1,4)-piperazina-1(3)-pyridina-4(1,4),8(3)-dipiperidina-2,6(1,4)-dibenzenaoctaphane-1^6(1^1H),8^2,8^6-trione
sendégobrésib	(4^4S,8^3S)-4^3,4^3,6^2-trifluoro-2^3,2^5-diméthoxy-1^1,1^4,1^5-triméthyl-7-aza-5(1,4)-pipérazina-1(3)-pyridina-4(1,4),8(3)-dipipéridina-2,6(1,4)-dibenzénaoctaphane-1^6(1^1H),8^2,8^6-trione
sendegobresib	(4^4S,8^3S)-4^3,4^3,6^2-trifluoro-1^1,1^4,1^5-trimetil-2^3,2^5-dimetoxi-7-aza-5(1,4)-piperazina-1(3)-piridina-4(1,4),8(3)-dipiperidina-2,6(1,4)-dibencenaoctafano-1^6(1^1H),8^2,8^6-triona

$C_{37}H_{45}F_3N_6O_5$



setidegrasibum

setidegrasib

(7*S*,9^2*S*,9^4*R*)-2^6-cyclopropyl-2^4-[(1*S*,4*S*)-2,5-diazabicyclo[2.2.1]heptan-2-yl]-1^6-fluoro-9^4-hydroxy-*N*-{(1*R*)-2-hydroxy-1-[4-(4-methyl-1,3-thiazol-5-yl)phenyl]ethyl}-1^5-methyl-2^2-[(oxan-4-yl)oxy]-8-oxo-7-(propan-2-yl)-1^1*H*-3-oxa-2(7,8)-quinazolina-1(4)-indazola-6(4,1)-[1,2,3]triazola-9(1)-pyrrolidina-5(1,4)-benzenanonaphane-9^2-carboxamide

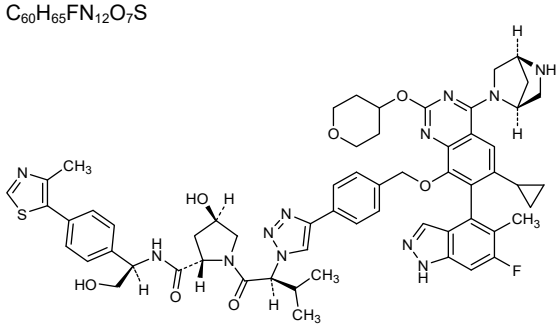
sétidégrasib

(7*S*,9^2*S*,9^4*R*)-2^6-cyclopropyl-2^4-[(1*S*,4*S*)-2,5-diazabicyclo[2.2.1]heptan-2-yl]-1^6-fluoro-9^4-hydroxy-*N*-{(1*R*)-2-hydroxy-1-[4-(4-méthyl-1,3-thiazol-5-yl)phényl]éthyl}-1^5-méthyl-2^2-[(oxan-4-yl)oxy]-8-oxo-7-(propan-2-yl)-1^1*H*-3-oxa-2(7,8)-quinazolina-1(4)-indazola-6(4,1)-[1,2,3]triazola-9(1)-pyrrolidina-5(1,4)-benzénanonaphane-9^2-carboxamide

setidegrasib

(7*S*,9^2*S*,9^4*R*)-2^6-ciclopropil-2^4-[(1*S*,4*S*)-2,5-diazabiciclo[2.2.1]heptan-2-il]-1^6-fluoro-9^4-hidroxi-*N*-{(1*R*)-2-hidroxi-1-[4-(4-metil-1,3-tiazol-5-il)fenil]etil}-1^5-metil-2^2-[(oxan-4-il)oxi]-8-oxo-7-(propan-2-il)-1^1*H*-3-oxa-2(7,8)-quinazolina-1(4)-indazola-6(4,1)-[1,2,3]triazola-9(1)-pirrolidina-5(1,4)-bencenanonafano-9^2-carboxamida

$C_{60}H_{65}FN_{12}O_7S$



siltartoxatugum #

siltartoxatug

immunoglobulin G1-kappa, anti-[*Clostridium tetani* tetanus toxin (TeNT)], *Homo sapiens* monoclonal antibody; H-gamma1 heavy chain *Homo sapiens* (1-448) [VH (*Homo sapiens* IGHV4-34*09 (86.6%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.7.12] (26-33.51-57.96-107)) (1-118) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (215) (119-216), hinge 1-15 (217-231), CH2 (232-341), CH3 E12 (357), M14 (359) (342-446), CHS (447-448)) (119-448)], (221-214')-disulfide with L-kappa light

	chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5*03 (90.4%) -IGKJ2*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, cell line CHO-K1 lacking the glutamine synthetase (GS-KO) gene, glycoform alfa, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1 lacking the glutamine synthetase (GS-KO) gene, glycoform alfa
siltartoxatug	immunoglobuline G1-kappa, anti-[*Clostridium tetani* toxine tétanique (TeNt)]; anticorps monoclonal *Homo sapiens*; chaîne lourde H-gamma1 *Homo sapiens* (1-448) [VH (*Homo sapiens* IGHV4-34*09 (86.6%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.7.12] (26-33.51-57.96-107)) (1-118) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (215) (119-216), charnière 1-15 (217-231), CH2 (232-341), CH3 E12 (357), M14 (359) (342-446), CHS (447-448)) (119-448)], (221-214')-disulfure avec la chaîne légère L-kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5*03 (90.4%) -IGKJ2*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 ne présentant pas le gène de la glutamine synthétase (GS-KO), glycoforme alfa
siltartoxatug	inmunoglobulina G1-kappa, anti-[*Clostridium tetani* toxina tetánica (TeNt)]; anticuerpo monoclonal *Homo sapiens*; cadena pesada H-gamma1 *Homo sapiens* (1-448) [VH (*Homo sapiens* IGHV4-34*09 (86.6%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.7.12] (26-33.51-57.96-107)) (1-118) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (215) (119-216), bisagra 1-15 (217-231), CH2 (232-341), CH3 E12 (357), M14 (359) (342-446), CHS (447-448)) (119-448)], (221-214')-disulfuro con la cadena ligera L-kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5*03 (90.4%) -IGKJ2*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 en ausencia del gen glutamina sintetasa (GS-KO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLQESGAG LVKPSETLSL TCGVAGGPFT GSYLSWIRQP PGKGLEWIGE  50
VSQSGSTSYN PSLKSRVTIS VDTSKSQFSL KLSSVTAADT AVYYCARLTK 100
HYINSAYWGQ GTLVTVSSAS TKGPSVFPLA PSSKSTSGGT AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTQTYI 200
CNVNHKPSNT KVDKRVEPKS CDKTHTCPPC PAPELLGGPS VFLFPPKPKD 250
TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNST 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY 350
TLPPSREEMT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD 400
SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPGK   448
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSI LSASVGDRVT ITCRASQIIG SWLAWYQQKP GKAPTLVIYK  50
ASRLDSGVPS RFSGTESGTE FTLTISSLQP DDFATYYCQQ YNSYPYTFGQ 100
GTKLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Post-translational modifications

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

Intra-H (C23-C104) 22-95 145-201 262-322 368-426
22"-95" 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-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)
H VH Q1: 1, 1"

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"

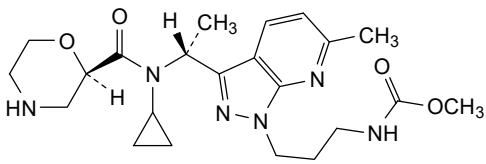
sitokirenum

sitokiren — methyl [3-(3-{(1*R*)-1-[(2*R*)-*N*-cyclopropylmorpholine-2-carboxamido]ethyl}-6-methyl-1*H*-pyrazolo[3,4-*b*]pyridin-1-yl)propyl]carbamate

sitokirène — [3-(3-{(1*R*)-1-[(2*R*)-*N*-cyclopropylmorpholine-2-carboxamido]éthyl}-6-méthyl-1*H*-pyrazolo[3,4-*b*]pyridin-1-yl)propyl]carbamate de méthyle

sitokireno — [3-(3-{(1*R*)-1-[(2*R*)-ciclopropilmorfolina-2-carboxamido]etil}-6-metil-1*H*-pirazolo[3,4-*b*]piridin-1-il)propil]carbamato de metilo

$C_{22}H_{32}N_6O_4$



sonavibartum #

sonavibart — immunoglobulin G1-kappa, anti-[influenza A virus hemagglutinin HA], *Homo sapiens* monoclonal antibody;
H-gamma1 heavy chain *Homo sapiens* (1-458) [VH (*Homo sapiens* IGHV6-1*01 (95.0%) -(IGHD) -IGHJ3*02 (93.8%), CDR-IMGT [10.9.18] (26-35.53-61.100-117)) (1-128) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v24 CH3 L107, S114 (CH1 R120 (225) (129-226), hinge 1-15 (227-241), CH2 (242-351), CH3 E12 (367), M14 (369), M107>L (439), N114>S (445) (352-456), CHS (457-458)) (129-458)], (231-210')-disulfide with L-kappa

light chain *Homo sapiens* (1'-210') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (91.4%) -IGKJ1*01 (100%), CDR-IMGT [6.3.5] (27'-32'.50'-52'.89'-93')) (1'-103') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (149'), V101 (187') (104'-210')]; dimer (237-237'':240-240'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa

sonavibart — immunoglobuline G1-kappa, anti-[hémagglutinine HA du virus de la grippe A], anticorps monoclonal *Homo sapiens*;
chaîne lourde H-gamma1 *Homo sapiens* (1-458) [VH (*Homo sapiens* IGHV6-1*01 (95.0%) -(IGHD) -IGHJ3*02 (93.8%), CDR-IMGT [10.9.18] (26-35.53-61.100-117)) (1-128) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v24 CH3 L107, S114 (CH1 R120 (225) (129-226), charnière 1-15 (227-241), CH2 (242-351), CH3 E12 (367), M14 (369), M107>L (439), N114>S (445) (352-456), CHS (457-458)) (129-458)], (231-210')-disulfure avec la chaîne légère L-kappa *Homo sapiens* (1'-210') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (91.4%) -IGKJ1*01 (100%), CDR-IMGT [6.3.5] (27'-32'.50'-52'.89'-93')) (1'-103') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (149'), V101 (187') (104'-210')]; dimère (237-237'':240-240'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa

sonavibart — inmunoglobulina G1-kappa, anti-[hemaglutinina HA del virus de la gripe A], anticuerpo monoclonal *Homo sapiens*;
cadena pesada H-gamma1 *Homo sapiens* (1-458) [VH (*Homo sapiens* IGHV6-1*01 (95.0%) -(IGHD) -IGHJ3*02 (93.8%), CDR-IMGT [10.9.18] (26-35.53-61.100-117)) (1-128) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v24 CH3 L107, S114 (CH1 R120 (225) (129-226), bisagra 1-15 (227-241), CH2 (242-351), CH3 E12 (367), M14 (369), M107>L (439), N114>S (445) (352-456), CHS (457-458)) (129-458)], (231-210')-disulfuro con la cadena ligera L-kappa *Homo sapiens* (1'-210') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (91.4%) -IGKJ1*01 (100%), CDR-IMGT [6.3.5] (27'-32'.50'-52'.89'-93')) (1'-103') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (149'), V101 (187') (104'-210')]; dímero (237-237'':240-240'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada : H-gamma1 (H, H'') anti-influenza A virus hemagglutinin HA

```
QVQLQQSGPG LVKPSQTLSL TCAISGDSVS SYNAVWNWIR QSPSRGLEWL  50
GRTYYRSGWY NDYAESVKSR ITINPDTSKN QFSLQLNSVT PEDTAVYYCA 100
RSGHITVFGV NVDAFDMWGQ GTMVTVSSAS TKGPSVFPLA PSSKSTSGGT 150
AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP 200
SSSLGTQTYI CNVNHKPSNT KVDKRVEPKS CDKTHTCPPC PAPELLGGPS 250
VFLFPPKPKD TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT 300
KPREEQYNST YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA 350
KGQPREPQVY TLPPSREEMT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN 400
NYKTTPPVLD SDGSFFLYSK LTVDKSRWQQ GNVFSCSVLH EALHSHYTQK 450
SLSLSPGK                                              458
```

Light chain / Chaîne légère / Cadena ligera : L-kappa (L', L''') anti-influenza A virus hemagglutinin HA

```
DIQMTQSPSS LSASVGDRVT ITCRTSQSLS SYTHWYQQKP GKAPKLLIYA  50
ASSRGSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ SRTFGQGTKV 100
EIKRTVAAPS VFIFPPSDEQ LKSGTASVVC LLNNFYPREA KVQWKVDNAL 150
QSGNSQESVT EQDSKDSTYS LSSTLTLSKA DYEKHKVYAC EVTHQGLSSP 200
VTKSFNRGEC                                            210
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-99 155-211 272-332 378-436
22''-99'' 155''-211'' 272''-332'' 378''-436''
Intra-L (C23-C104) 23'-88' 130'-190'
23'''-88''' 130'''-190'''
Inter-H-L (h 5-CL 126) 231-210' 231''-210'''
Inter-H-H (h 11, h 14) 237-237'' 240-240''

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)
H VH Q1: 1, 1''

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4: 308, 308''
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2: 458, 458''

sonefpeglutidum #

sonefpeglutide

glucagon-like peptide 2 (GLP-2) analogue, conjugated through a 3.4 kDa polyethylene glycol (PEG) linker (n ~ 75) to an Fc portion dimer of human immunoglobulin G4 (IgG4);
N$^{1.1}$-(3-{α-[3-({[Ala^{2}>*N*-[(1*H*-imidazol-4-yl)acetyl]Gly^{1},Lys^{30}>Arg^{29}]glucagon like peptide 2 (2-33)-peptidyl (1-32)-L-lysine (33)}-*N*$^{6.33}$-yl)propyl]poly(oxyethylene)-ω-oxy}propyl)[immunoglobulin G4 heavy chain constant region C-terminal 221-peptide dimer (3-3')-disulfide], non-glycosylated, immunoglobulin fragment dimer produced in *Escherichia coli*

sonefpéglutide

analogue du peptide-2 similaire au glucagon (GLP-2), conjugué par un linker polyéthylène glycol (PEG) de 3,4 kDa (n ~ 75) à un dimère de fragment Fc d'immunoglobuline G4 (IgG4) humaine;
N$^{1.1}$-(3-{α-[3-({[Ala^{2}>*N*-[(1*H*-imidazol-4-yl)acétyl]Gly^{1},Lys^{30}>Arg^{29}]peptide-2 similaire au glucagon (2-33)-peptidyl (1-32)-L-lysine (33)}-*N*$^{6.33}$-yl)propyl]poly(oxyéthylène)-ω-oxy}propyl)[peptide de 221 acides aminés de la région constante C-terminale de la chaîne lourde d'immunoglobuline G4, dimère (3-3')-disulfure], non-glycosylé, dimère du fragment d'immunoglobuline produit par *Escherichia coli*

sonefpeglutida

análogo del péptido similar al glucagón tipo 2 (GLP-2), conjugado a través de un enlace polietileno glicol (PEG) de 3,4 kDa (n ~ 75) a un dímero del fragmento Fc de la inmunoglobulina G4 (IgG4) humana;
N$^{1.1}$-(3-{α-[3-({[Ala^{2}>*N*-[(1*H*-imidazol-4-il)acetil]Gli^{1},Lis^{30}>Arg^{29}]péptido similar al glucagón tipo 2 (2-33)-peptidil (1-32)-L-lisina (33)}-*N*$^{6.33}$-yl)propil]poli(oxietileno)-ω-oxi}propil)[péptido de 221 aminoácidos de la región constante C-terminal de la cadena pesada de la inmunoglobulina G4, dímero (3-3')-disulfuro], no glicosilado, dímero del fragmento de la inmunoglobulina producido por *Escherichia coli*

Monomer / Monomère / Monómero IgG4 Fc

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

Conjugated peptide / Peptide conjugué / Péptido conjugado

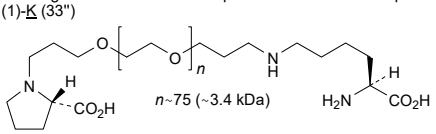
```
GDGSFSDEMN TILDNLAARD FINWLIQTRI TDK 33
```

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

Intra-chain	35-95	141-199
	35'-95'	141'-199'
Inter-chain	3-3'	

PEG bridge location / Position du pont PEG / Posición del puente PEG

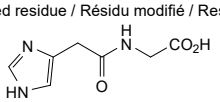
P (1)-K (33")



P (1) K (33")

Modified residue / Résidu modifié / Resto modificado

G (1")



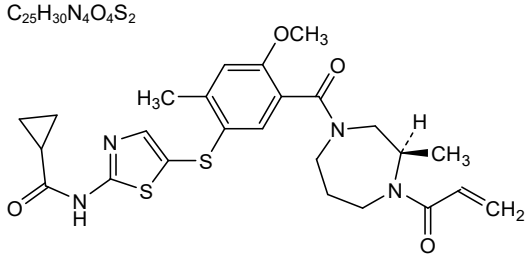
soquelitinibum

soquelitinib — *N*-[5-({4-methoxy-2-methyl-5-[(3*R*)-3-methyl-4-(prop-2-enoyl)-1,4-diazepane-1-carbonyl]phenyl}sulfanyl)-1,3-thiazol-2-yl]cyclopropane-1-carboxamide

soquélitinib — *N*-[5-({4-méthoxy-2-méthyl-5-[(3*R*)-3-méthyl-4-(prop-2-énoyl)-1,4-diazépane-1-carbonyl]phényl}sulfanyl)-1,3-thiazol-2-yl]cyclopropane-1-carboxamide

soquelitinib — *N*-[5-({2-metil-5-[(3*R*)-3-metil-4-(prop-2-enoil)-1,4-diazepano-1-carbonil]-4-metoxifenil}sulfanil)-1,3-tiazol-2-il]ciclopropano-1-carboxamida

$C_{25}H_{30}N_4O_4S_2$



spunoleucelum

spunoleucel — allogeneic peripheral blood mononuclear cells (PBMCs) isolated by apheresis from donors seropositive for respiratory syncytial virus (RSV), influenza A virus, human metapneumovirus (hMPV) and parainfluenza virus (PIV). The PBMCs are co-cultured with viral peptide mixes spanning immunogenic antigens from RSV (N, F), influenza A (NP1, MP1), PIV (M, HN, N, F), and hMPV (F, N, M2-1, M) in media containing human AB serum, interleukin 4 (IL-4) and interleukin 7 (IL-7).
The final cell population consists of ≥ 90% CD3+ T lymphocytes (mix of CD4+/CD8+ T lymphocytes). The cells produce interferon gamma (IFN-γ) in response to stimulation with RSV, influenza A, hMPV and PIV specific peptides. Cells are stored according to human leukocyte antigen (HLA) type.

spunoleucel — cellules mononucléaires de sang périphérique (PBMC) allogéniques isolées par aphérèse à partir de donneurs séropositifs pour le virus respiratoire syncytial (VRS), le virus de la grippe A, le métapneumovirus humain (MPVh) et le virus de la parainfluenza (PIV). Les PBMC sont co-cultivées avec des mélanges de peptides viraux couvrant les antigènes immunogènes du VRS (N, F), de la grippe A (NP1, MP1), du PIV (M, HN, N, F) et du MPVh (F, N, M2-1, M) dans des milieux contenant du sérum AB humain, de l'interleukine 4 (IL-4) et de l'interleukine 7 (IL-7).
La population cellulaire finale est composée de ≥90% de lymphocytes T CD3+ (mélange de lymphocytes T CD4+/CD8+). Les cellules produisent de l'interféron gamma (IFN-γ) en réponse à une stimulation par des peptides spécifiques du VRS, de la grippe A, du MPVh et du PIV. Les cellules sont stockées en fonction du type d'antigène leucocytaire humain (HLA).

espunoleucel

células mononucleares de sangre periférica (PBMCs) alogénicas aisladas mediante aféresis de donantes seropositivos para el virus respiratorio sincitial (VRS), el virus inluenza A, el metaneumovirus humano (hMPV) y el virus parainfluenza (PIV). Las PBMCs se cocultivan con mezclas de péptidos virales que cubren antígenos inmunogénicos de VRS (N, F), influenza A (NP1, MP1), PIV (M, HN, N, F) y hMPV (F, N, M2-1, M) en medio que contiene suero AB humano, interleuquina 4 (IL-4) e interleuquina 7 (IL-7).
La población celular final consiste en ≥90% linfocitos T CD3+ (mezcla de linfocitos T CD4+/CD8+). Las células producen interferón gamma (IFN-γ) en respuesta a la estimulación con péptidos específicos de VRS, influenza A, hMPV y PIV. Las células se almacenan de acuerdo al tipo de antígeno leucocitario humano (HLA).

sumecigrelum

sumecigrel

methyl (*S*)-[2-(acetyloxy)-6,7-dihydrothieno[3,2-*c*]pyridin-5(4*H*)-yl](2-chlorophenyl)acetate

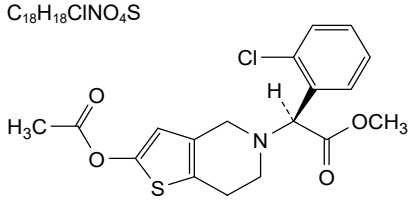
sumécigrel

(*S*)-[2-(acétyloxy)-6,7-dihydrothiéno[3,2-*c*]pyridin-5(4*H*)-yl](2-chlorophényl)acétate de méthyle

sumecigrel

(*S*)-[2-(acetiloxi)-6,7-dihidrotieno[3,2-*c*]piridin-5(4*H*)-il](2-clorofenil)acetato de metilo

$C_{18}H_{18}ClNO_4S$



surabgenum lomparvovecum #

surabgene lomparvovec

recombinant, non-replicating adeno-associated virus serotype 8 (rAAV8) vector encoding a soluble humanised anti-vascular endothelial growth factor (VEGF) antibody fragment (Fab) under control of a hybrid cytomegalovirus (CMV) immediate-early enhancer/chicken β-actin promoter, enhanced by a chicken β-actin intron and terminated by a rabbit β-globin polyadenylation signal. The heavy and light chains of the Fab are separated by a self-cleaving furin /F2A linker and the transgene is flanked by adeno-associated virus 2 (AAV2) inverted terminal repeats (ITRs)

surabgène lomparvovec

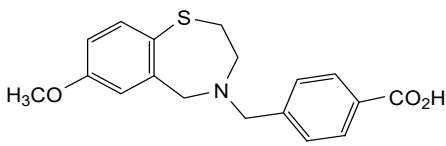
vecteur recombinant et non répliquant du virus adéno-associé de sérotype 8 (rAAV8) codant un fragment d'anticorps humanisé soluble dirigé contre le facteur de croissance de l'endothélium vasculaire (VEGF) sous le contrôle d'un amplificateur immédiat et précoce hybride du cytomégalovirus (CMV)/promoteur de la

	β-actine de poulet, amplifié par un intron de la β-actine de poulet et terminé par un signal de polyadénylation de la β-globine de lapin. Les chaînes lourdes et légères du Fab sont séparées par un coupleur furine/F2A auto-clivante et le transgène est flanqué de répétitions terminales inversées (ITR) du virus adéno-associé 2 (AAV2)
surabgén lomparvovec	vector de virus adenoasociado del serotipo 8 recombinante (rAAV8), no replicativo, que codifica para un fragmento soluble de anticuerpo (Fab) humanizado anti-factor de crecimiento del endotelio vascular (VEGF) bajo el control de un híbrido del potenciador inmediato-temprano de citomegalovirus (CMV) /promotor de la β-actina de pollo, potenciado por un intron de la β-actina de pollo y terminado con una señal de poliadenilación de la β-globina de conejo. Las cadenas pesada y ligera del Fab están separadas por un enlazador de auto-escisión de furina/F2A y el transgén está flanqueado por repeticiones terminales invertidas (ITRs) del virus adenoasociado 2 (AAV2)

surlorianum

surlorian	4-[(7-methoxy-2,3-dihydro-1,4-benzothiazepin-4(5*H*)-yl)methyl]benzoic acid
surlorian	acide 4-[(7-méthoxy-2,3-dihydro-1,4-benzothiazépin-4(5*H*)-yl)méthyl]benzoïque
surlorián	ácido 4-[(7-metoxi-2,3-dihidro-1,4-benzotiazepin-4(5*H*)-il)metil]benzoico

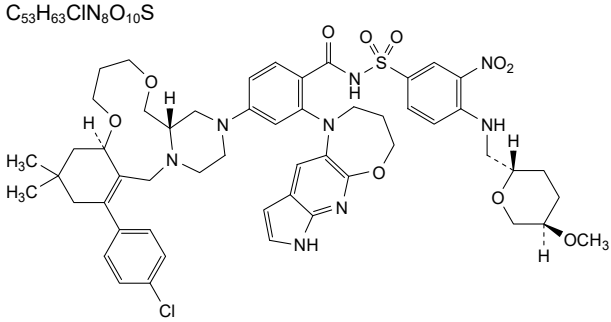
$C_{18}H_{19}NO_3S$



surzetoclaxum

surzetoclax	4-[(4a*S*,10a*R*)-14-(4-chlorophenyl)-12,12-dimethyl-1,2,4a,5,8,9,10a,11,13,15-decahydro-7*H*,12*H*-pyrazino[2,1-*g*][1,5,8]benzodioxaazacycloundecin-3(4*H*)-yl]-2-(3,4-dihydro-2*H*-pyrrolo[3',2':5,6]pyrido[2,3-*b*][1,4]oxazepin-1(7*H*)-yl)-*N*-[4-({[(2*S*,5*R*)-5-methoxyoxan-2-yl]methyl}amino)-3-nitrobenzene-1-sulfonyl]benzamide
surzétoclax	4-[(4a*S*,10a*R*)-14-(4-chlorophényl)-12,12-diméthyl-1,2,4a,5,8,9,10a,11,13,15-décahydro-7*H*,12*H*-pyrazino[2,1-*g*][1,5,8]benzodioxaazacycloundécin-3(4*H*)-yl]-2-(3,4-dihydro-2*H*-pyrrolo[3',2':5,6]pyrido[2,3-*b*][1,4]oxazépin-1(7*H*)-yl)-*N*-[4-({[(2*S*,5*R*)-5-méthoxyoxan-2-yl]méthyl}amino)-3-nitrobenzène-1-sulfonyl]benzamide
surzetoclax	4-[(4a*S*,10a*R*)-14-(4-clorofenil)-12,12-dimetil-1,2,4a,5,8,9,10a,11,13,15-decahidro-7*H*,12*H*-pirazino[2,1-*g*][1,5,8]benzodioxaazaciclоundecin-3(4*H*)-il]-2-(3,4-dihidro-2*H*-pirrolo[3',2':5,6]pirido[2,3-*b*][1,4]oxazepin-1(7*H*)-il)-*N*-[4-({[(2*S*,5*R*)-5-metoxioxan-2-il]metil}amino)-3-nitrobenceno-1-sulfonil]benzamida

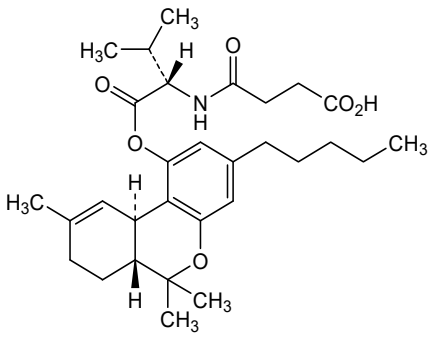
$C_{53}H_{63}ClN_8O_{10}S$



suvadronabinolum

suvadronabinol	4-{[(2*S*)-3-methyl-1-oxo-1-{[(6a*R*,10a*R*)-6,6,9-trimethyl-3-pentyl-6a,7,8,10a-tetrahydro-6*H*-dibenzo[*b*,*d*]pyran-1-yl]oxy}butan-2-yl]amino}-4-oxobutanoic acid
suvadronabinol	acide 4-{[(2*S*)-3-méthyl-1-oxo-1-{[(6a*R*,10a*R*)-6,6,9-triméthyl-3-pentyl-6a,7,8,10a-tétrahydro-6*H*-dibenzo[*b*,*d*]pyran-1-yl]oxy}butan-2-yl]amino}-4-oxobutanoïque
suvadronabinol	ácido 4-{[(2*S*)-3-metil-1-oxo-1-{[(6a*R*,10a*R*)-6,6,9-trimetil-3-pentil-6a,7,8,10a-tetrahidro-6*H*-dibenzo[*b*,*d*]piran-1-il]oxi}butan-2-il]amino}-4-oxobutanoico

$C_{30}H_{43}NO_6$



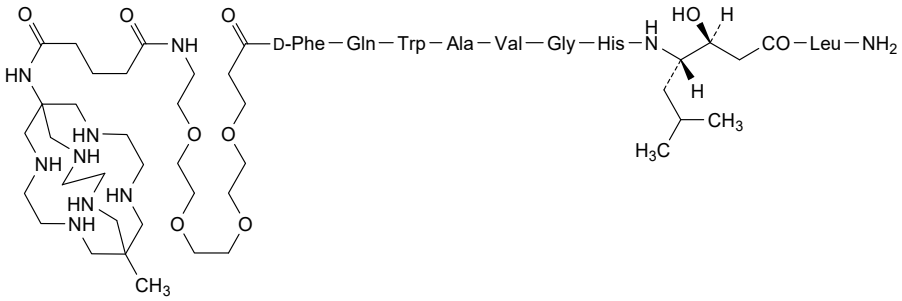
talogreptidum mesaroxetanum

talogreptide mesaroxetan	*N*-{21-[(8-methyl-3,6,10,13,16,19-hexaazabicyclo[6.6.6]icosan-1-yl)amino]-17,21-dioxo-4,7,10,13-tetraoxa-16-azahenicosan-1-oyl}-D-phenylalanyl-L-glutaminyl-L-tryptophyl-L-alanyl-L-valylglycyl-L-histidyl-(3*S*,4*S*)-4-amino-3-hydroxy-6-methylheptanoyl-L-leucinamide
talogreptide mésaroxetan	*N*-{21-[(8-méthyl-3,6,10,13,16,19-hexaazabicyclo[6.6.6]icosan-1-yl)amino]-17,21-dioxo-4,7,10,13-tétraoxa-16-azahénicosan-1-oyl}-D-phénylalanyl-L-glutaminyl-L-tryptophyl-L-alanyl-L-valylglycyl-L-histidyl-(3*S*,4*S*)-4-amino-3-hydroxy-6-méthylheptanoyl-L-leucinamide

talogreptida mesaroxetán

N-{21-[(8-metil-3,6,10,13,16,19-hexaazabiciclo[6.6.6]icosan-1-il)amino]-17,21-dioxo-4,7,10,13-tetraoxa-16-azahenicosan-1-oil}-D-fenilalanil-L-glutaminil-L-triptofil-L-alanil-L-valilglicil-L-histidil-(3*S*,4*S*)-4-amino-3-hidroxi-6-metilheptanoil-L-leucinamida

$C_{86}H_{140}N_{22}O_{18}$



talorasibum

talorasib

[(2*S*)-4-[(7*S*)-7-(8-chloronaphthalen-1-yl)-2-{[(2*S*)-1-methylpyrrolidin-2-yl]methoxy}-7,8-dihydro-5*H*-pyrano[4,3-*d*]pyrimidin-4-yl]-1-(2-fluoroprop-2-enoyl)piperazin-2-yl]acetonitrile

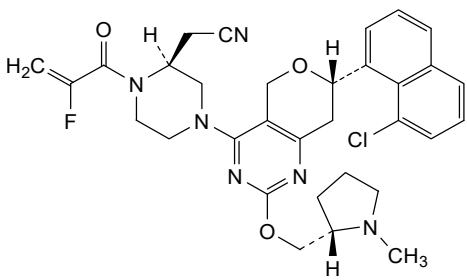
talorasib

[(2*S*)-4-[(7*S*)-7-(8-chloronaphtalén-1-yl)-2-{[(2*S*)-1-méthylpyrrolidin-2-yl]méthoxy}-7,8-dihydro-5*H*-pyrano[4,3-*d*]pyrimidin-4-yl]-1-(2-fluoroprop-2-énoyl)pipérazin-2-yl]acétonitrile

talorasib

[(2*S*)-4-[(7*S*)-7-(8-cloronaftalen-1-il)-2-{[(2*S*)-1-metilpirrolidin-2-il]metoxi}-7,8-dihidro-5*H*-pirano[4,3-*d*]pirimidin-4-il]-1-(2-fluoroprop-2-enoil)piperazin-2-il]acetonitrilo

$C_{32}H_{34}ClFN_6O_3$



tambiciclibum

tambiciclib

(1^1r,1^4r)-3^5-chloro-1^4-{[(2*R*)-1-methoxypropan-2-yl]amino}-2,5-diaza-3(2,4)-pyridina-4(4,2)-[1,3]thiazola-7(4)-oxana-1(1)-cyclohexanaheptaphane-7^4-carbonitrile

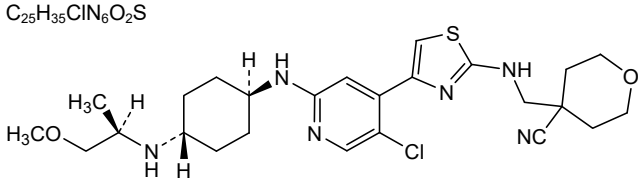
tambiciclib

(1^1r,1^4r)-3^5-chloro-1^4-{[(2*R*)-1-méthoxypropan-2-yl]amino}-2,5-diaza-3(2,4)-pyridina-4(4,2)-[1,3]thiazola-7(4)-oxana-1(1)-cyclohexanaheptaphane-7^4-carbonitrile

tambiciclib

(1^1*r*,1^4*r*)-3^5-cloro-1^4-{[(2*R*)-1-metoxipropan-2-il]amino}-2,5-diaza-3(2,4)-piridina-4(4,2)-[1,3]tiazola-7(4)-oxana-1(1)-ciclohexanaheptafano-7^4-carbonitrilo

$C_{25}H_{35}ClN_6O_2S$



tazlestobartum #

tazlestobart

immunoglobulin G1-kappa, anti-[*Homo sapiens* CTLA4 (cytotoxic T-lymphocyte associated protein 4, CTLA-4, CD152)], humanized monoclonal antibody;
H-gamma1 heavy chain humanized (1-448) [VH (*Homo sapiens* IGHV3-30*01 (94.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v6 CH2 A85.4, A118, A119 (CH1 R120 (215) (119-216), hinge 1-15 (217-231), CH2 S85.4>A (299), E118>A (334), K119>A (335), (232-341), CH3 E12 (357), M14 (359) (342-446), CHS (447-448)) (119-448)], (221-215')-disulfide with L-kappa light chain humanized (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (97.9%) -IGKJ1*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 (227-227":230-230")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa

tazlestobart

immunoglobuline G1-kappa, anti-[*Homo sapiens* CTLA4 (protéine 4 associée aux lymphocytes T cytotoxiques, CTLA-4, CD152)], anticorps monoclonal humanisé;
chaîne lourde H-gamma1 humanisée (1-448) [VH (*Homo sapiens* IGHV3-30*01 (94.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v6 CH2 A85.4, A118, A119 (CH1 R120 (215) (119-216), charnière 1-15 (217-231), CH2 S85.4>A (299), E118>A (334), K119>A (335), (232-341), CH3 E12 (357), M14 (359) (342-446), CHS (447-448)) (119-448)], (221-215')-disulfure avec la chaîne légère L-kappa humanisée (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (97.9%) -IGKJ1*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 (227-227":230-230")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa

tazlestobart

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CTLA4 (proteína 4 asociada con los linfocitos T citotóxicos, CTLA-4, CD152)], anticuerpo monoclonal humanizado;
cadena pesada H-gamma1 humanizada (1-448) [VH (*Homo sapiens* IGHV3-30*01 (94.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo*

sapiens IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v6 CH2 A85.4, A118, A119 (CH1 R120 (215) (119-216), bisagra 1-15 (217-231), CH2 S85.4>A (299), E118>A (334), K119>A (335), (232-341), CH3 E12 (357), M14 (359) (342-446), CHS (447-448)) (119-448)], (221-215')-disulfuro con la cadena ligera L-kappa humanizada (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (97.9%) -IGKJ1*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 (227-227'':230-230'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada : H-gamma1 (H, H'') anti-CTLA4
```
QVQLVESGGG VVQPGRSLRL SCAASGFTFS SYTMHWVRQA PGKGLEWVTF  50
ISYDGNNKYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAIYYCARTG 100
WLGPFDYWGQ GTLVTVSSAS TKGPSVFPLA PSSKSTSGGT AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTQTYI 200
CNVNHKPSNT KVDKRVEPKS CDKTHTCPPC PAPELLGGPS VFLFPPKPKD 250
TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNAT 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIAATISKA KGQPREPQVY 350
TLPPSREEMT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD 400
SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPGK   448
```

Light chain / Chaîne légère / Cadena ligera : L-kappa (L', L'") anti-CTLA4
```
EIVLTQSPGT LSLSPGERAT LSCRASQSVG SSYLAWYQQK PGQAPRLLIY  50
GAFSRATGIP DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QYGSSPWTFG 100
QGTKVEIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK 150
VDNALQSGNS QESVTEQDSK DSTYSLSSTL TLSKADYEKH KVYACEVTHQ 200
GLSSPVTKSF NRGEC                                       215
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 145-201 262-322 368-426
22''-96'' 145''-201'' 262''-322'' 368''-426''
Intra-L (C23-C104) 23'-89' 135'-195'
23'''-89''' 135'''-195'''
Inter-H-L (h 5-CL 126) 221-215' 221''-215'''
Inter-H-H (h 11, h 14) 227-227'' 230-230''

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)
H VH Q1: 1, 1''

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''

tecotabartum #

tecotabart — immunoglobulin G1-kappa, anti-[*Homo sapiens* CLDN18 (claudin 18, claudin-18, surfactant associated protein J, SFTPJ)], humanized monoclonal antibody;
H-gamma1 heavy chain humanized (1-449) [VH (*Homo sapiens* IGHV3-48*01 (88.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, G1v7 CH2 D3, E117 (CH1 K120 (216) (120-217), hinge 1-15 (218-232), CH2 S3>D (241), I117>E (334) (233-342), CH3 D12 (358), L14 (360) (343-447), CHS (448-449)) (120-449)], (222-220')-disulfide with L-kappa light chain humanized (1'-220') [V-KAPPA (*Homo sapiens* IGKV4-1*01 (90.1%) -IGKJ2*02 (90.9%), 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 (228-228'':231-231'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa

técotabart — immunoglobuline G1-kappa, anti-[*Homo sapiens* CLDN18 (claudine 18, claudine-18, protéine J associée au surfactant, SFTPJ)]; anticorps monoclonal humanisé;

chaîne lourde H-gamma1 humanisée (1-449) [VH (*Homo sapiens* IGHV3-48*01 (88.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, G1v7 CH2 D3, E117 (CH1 K120 (216) (120-217), charnière 1-15 (218-232), CH2 S3>D (241), I117>E (334) (233-342), CH3 D12 (358), L14 (360) (343-447), CHS (448-449)) (120-449)], (222-220')-disulfure avec la chaîne légère L-kappa humanisée (1'-220') [V-KAPPA (*Homo sapiens* IGKV4-1*01 (90.1%) -IGKJ2*02 (90.9%), 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 (228-228":231-231")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa

tecotabart

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CLDN18 (claudina 18, claudina-18, proteína J asociada al surfactante, SFTPJ)]; anticuerpo monoclonal humanizado;
cadena pesada H-gamma1 humanizada (1-449) [VH (*Homo sapiens* IGHV3-48*01 (88.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, G1v7 CH2 D3, E117 (CH1 K120 (216) (120-217), bisagra 1-15 (218-232), CH2 S3>D (241), I117>E (334) (233-342), CH3 D12 (358), L14 (360) (343-447), CHS (448-449)) (120-449)], (222-220')-disulfuro con la cadena ligera L-kappa humanizada (1'-220') [V-KAPPA (*Homo sapiens* IGKV4-1*01 (90.1%) -IGKJ2*02 (90.9%), 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 (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 TFGMHWVRQA PGKGLEWVSY  50
ITSGESPIYF TDTVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARSS 100
YYGNSMDYWG QGTLVTVSSA STKGPSVFPL APSSKSTSGG TAALGCLVKD 150
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY 200
ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP CPAPELLGGP DVFLFPPKPK 250
DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS 300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPEEKTISK AKGQPREPQV 350
YTLPPSRDEL TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL 400
DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK  449
```

Light chain / Chaîne légère / Cadena ligera

```
DIVMTQSPDS LAVSLGERAT INCRSSQSLL NAGNRKNYLT WYQQKPGQPP  50
KLLIYWASTR ESGVPDRFSG SGSGTDFTLT ISSLQAEDVA VYYCQNAYSY 100
PFTFGGGTKL 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) 22-96 146-202 263-323 369-427
22"-96" 146"-202" 263"-323" 369"-427"
Intra-L (C23-C104) 23'-94' 140'-200'
23'"-94'" 140'"-200'"
Inter-H-L (h 5-CL 126) 222-220' 222"-220'"
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"

tecotabartum vedotinum #

tecotabart vedotin

immunoglobulin G1-kappa, anti-[*Homo sapiens* CLDN18 (claudin 18, claudin-18, surfactant associated protein J, SFTPJ)], humanized monoclonal antibody; conjugated on an average of 4 cysteinyl residues via a cleavable linker to monomethylauristatin E (MMAE); H-gamma1 heavy chain humanized (1-449) [VH (*Homo sapiens* IGHV3-48*01 (88.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, G1v7 CH2 D3, E117 (CH1 K120 (216) (120-217), hinge 1-15 (218-232), CH2 S3>D (241), I117>E (334) (233-342), CH3 D12 (358), L14 (360) (343-447), CHS (448-449)) (120-449)], (222-220')-disulfide with L-kappa light chain humanized (1'-220') [V-KAPPA (*Homo sapiens* IGKV4-1*01 (90.1%) -IGKJ2*02 (90.9%), 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 (228-228'':231-231'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa; substituted at the sulfur atoms of four L-cysteinyl residues on an average among 222, 228, 231, 220', 222'', 228'', 231'' and 220''' with radical group (3*RS*)-1-(6-{[(2*S*)-1-{[(2*S*)-5-(carbamoylamino)-1-{4-[({[(2*S*)-1-{[(2*S*)-1-{[(3*R*,4*S*,5*S*)-1-{(2*S*)-2-[(1*R*,2*R*)-3-{[(1*S*,2*R*)-1-hydroxy-1-phenylpropan-2-yl]amino}-1-methoxy-2-methyl-3-oxopropyl]pyrrolidin-1-yl}-3-methoxy-5-methyl-1-oxoheptan-4-yl](methyl)amino}-3-methyl-1-oxobutan-2-yl]amino}-3-methyl-1-oxobutan-2-yl](methyl)carbamoyl}oxy)methyl]anilino}-1-oxopentan-2-yl]amino}-3-methyl-1-oxobutan-2-yl]amino}-6-oxohexyl)-2,5-dioxopyrrolidin-3-yl (*vedotin*)

técotabart védotine

immunoglobuline G1-kappa, anti-[*Homo sapiens* CLDN18 (claudine 18, claudine-18, protéine J associée au surfactant, SFTPJ)]; anticorps monoclonal humanisé; conjugué, sur 4 résidus cystéinyle en moyenne, au monométhylauristatine E (MMAE), via un linker clivable ;
chaîne lourde H-gamma1 humanisée (1-449) [VH (*Homo sapiens* IGHV3-48*01 (88.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, G1v7 CH2 D3, E117 (CH1 K120 (216) (120-217), charnière 1-15 (218-232), CH2 S3>D (241), I117>E (334) (233-342), CH3 D12 (358), L14 (360) (343-447), CHS (448-449)) (120-449)], (222-220')-disulfure avec la chaîne légère L-kappa humanisée (1'-220') [V-KAPPA (*Homo sapiens* IGKV4-1*01 (90.1%) -IGKJ2*02 (90.9%), 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 (228-228'':231-231'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois

	(CHO), lignée cellulaire CHO-K1, glycoforme alfa; substitué sur un atome de soufre de 4 résidus L-cystéinyle en moyenne parmi 222, 228, 231, 220', 222", 228", 231" et 220"' avec un groupement radical (3*RS*)-1-(6-{[(2*S*)-1-{[(2*S*)-5-(carbamoylamino)-1-{4-[({[(2*S*)-1-{[(2*S*)-1-{[(3*R*,4*S*,5*S*)-1-{(2*S*)-2-[(1*R*,2*R*)-3-{[(1*S*,2*R*)-1-hydroxy-1-phénylpropan-2-yl]amino}-1-méthoxy-2-méthyl-3-oxopropyl]pyrrolidin-1-yl}-3-méthoxy-5-méthyl-1-oxoheptan-4-yl](méthyl)amino}-3-méthyl-1-oxobutan-2-yl]amino}-3-méthyl-1-oxobutan-2-yl](méthyl)carbamoyl}oxy)méthyl]anilino}-1-oxopentan-2-yl]amino}-3-méthyl-1-oxobutan-2-yl]amino}-6-oxohexyl)-2,5-dioxopyrrolidin-3-yle (*védotine*)
tecotabart vedotina	inmunoglobulina G1-kappa, anti-[*Homo sapiens* CLDN18 (claudina 18, claudine-18, proteína J asociada con surfactante, SFTPJ)]; anticuerpo monoclonal humanizado; conjugado, por 4 residuos cisteinilo por término medio, a la monometilauristatina E (MMAE), a través de un enlace escindible; cadena pesada H-gamma1 humanizada (1-449) [VH (*Homo sapiens* IGHV3-48*01 (88.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, G1v7 CH2 D3, E117 (CH1 K120 (216) (120-217), bisagra 1-15 (218-232), CH2 S3>D (241), I117>E (334) (233-342), CH3 D12 (358), L14 (360) (343-447), CHS (448-449)) (120-449)], (222-220')-disulfuro con la cadena ligera L-kappa humanizada (1'-220') [V-KAPPA (*Homo sapiens* IGKV4-1*01 (90.1%) -IGKJ2*02 (90.9%), 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 (228-228":231-231")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, forma glicosilada alfa; sustituido en un átomo de azufre de 4 residuos L-cisteinilo en promedio de 222, 228, 231, 220', 222", 228", 231" y 220" con un grupo radical (3*RS*)-1-(6-{[(2*S*)-1-{[(2*S*)-5-(carbamoilamino)-1-{4-[({[(2*S*)-1-{[(2*S*)-1-{[(3*R*,4*S*,5*S*)-1-{(2*S*)-2-[(1*R*,2*R*)-3-{[(1*S*,2*R*)-1-hidroxi-1-fenilpropan-2-il]amino}-2-metil-1-metoxi-3-oxopropil]pirrolidin-1-il}-5-metil-3-metoxi-1-oxoheptan-4-il](metil)amino}-3-metil-1-oxobutan-2-il]amino}-3-metil-1-oxobutan-2-il](metil)carbamoil}oxi)metil]anilino}-1-oxopentan-2-il]amino}-3-metil-1-oxobutan-2-il]amino}-6-oxohexil)-2,5-dioxopirrolidin-3-ilo (*vedotina*)

Heavy chain / Chaîne lourde / Cadena pesada

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EVQLVESGGG LVQPGGSLRL SCAASGFTFS TFGMHWVRQA PGKGLEWVSY  50
ITSGESPIYF TDTVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARSS 100
YYGNSMDYWG QGTLVTVSSA STKGPSVFPL APSSKSTSGG TAALGCLVKD 150
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY 200
ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP CPAPELLGGP DVFLFPPKPK 250
DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS 300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPEEKTISK AKGQPREPQV 350
YTLPPSRDEL TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL 400
DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK  449
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Light chain / Chaîne légère / Cadena ligera

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DIVMTQSPDS LAVSLGERAT INCRSSQSLL NAGNRKNYLT WYQQKPGQPP  50
KLLIYWASTR ESGVPDRFSG SGSGTDFTLT ISSLQAEDVA VYYCQNAYSY 100
PFTFGGGTKL EIKRTVAAPS VFIFPPSDEQ LKSGTASVVC LLNNFYPREA 150
KVQWKVDNAL QSGNSQESVT EQDSKDSTYS LSSTLTLSKA DYEKHKVYAC 200
EVTHQGLSSP VTKSFNRGEC                                   220
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Post-translational modifications

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

Intra-H (C23-C104) 22-96 146-202 263-323 369-427
22"-96" 146"-202" 263"-323" 369"-427"

Intra-L (C23-C104) 23'-94' 140'-200'
23'"-94'" 140'"-200'"

Inter-H-L (h 5-CL 126) * 222-220' 222"-220'"

Inter-H-H (h 11, h 14) * 228-228" 231-231"

*At least two of the four inter-chain disulfide bridges are not present, an average of 4 cysteinyl being conjugated each via a thioether bond to a drug linker.

*Au moins deux des quatre ponts disulfures inter-chaînes ne sont pas présents, 4 cystéinyl en moyenne étant chacun conjugué via une liaison thioéther à un linker-principe actif.

*Al menos dos de los cuatro puentes disulfuro inter-catenarios no estan presentes, una media de 4 cisteinil está conjugada a conectores de principio activo.

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

H CH2 N84.4: 299, 299"

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

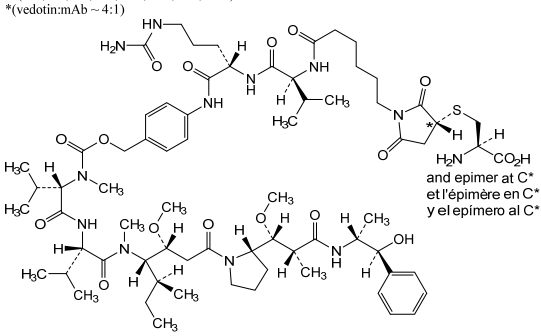
C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal

H CHS K2: 449, 449"

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

C (222,228,231,220',222",228",231",220'")

*(vedotin:mAb ~ 4:1)



telisotuzumabum adizutecanum #

telisotuzumab adizutecan

immunoglobulin G1-kappa, anti-[*Homo sapiens* MET (met proto-oncogene, hepatocyte growth factor (HGF) receptor, HGFR, scatter factor (SF) receptor, HGF/SF receptor, receptor tyrosine-protein kinase c-met, papillary renal cell carcinoma 2, RCCP2)], humanized monoclonal antibody, conjugated on an average of 6 cysteinyl residues to a*dizutecan*, comprising a linker and a camptothecin derivative;
H-gamma1 heavy chain humanized (1-445) [VH (*Homo sapiens* IGHV1-2*02 (92.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (215) (119-216), hinge 1-15 K7>del, T8>C (223), T10>del (217-229), CH2 (230-339), CH3 E12 (355), M14 (357) (340-444), CHS K2>del (445)) (119-445)], (221-218')-disulfide

	with L-kappa light chain humanized (1'-218') [V-KAPPA (*Homo sapiens* IGKV4-1*01 (85.1%) -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 (223-223''-225-225'':228-228'')-trisdisulfide, produced in a cell line from Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1SV, expressing the enzyme glutamine synthetase (GS), glycoform alfa; substituted at the sulfur atoms of an average of 6 L-cysteinyl residues among 221, 223, 225, 228, 218', 221'', 223'', 225'', 228'' and 218''' with radical group 2-{[(2*S*)-1-{[(2S)-1-({3-[(7*S*)-7-ethyl-7-hydroxy-14-methyl-8,11-dioxo-7,8,11,13-tetrahydro-2*H*,10*H*-[1,3]dioxolo[4,5-*g*]pyrano[3',4':6,7]indolizino[1,2-*b*]quinolin-14-yl]bicyclo[1.1.1]pentan-1-yl}amino)-1-oxopropan-2-yl]amino}-3-methyl-1-oxobutan-2-yl]amino}-2-oxoethyl (*adizutecan*)
télisotuzumab adizutécan	immunoglobuline G1-kappa, anti-[*Homo sapiens* MET (proto-oncogène met, récepteur du facteur de croissance hépatocytaire, HGFR, récepteur du facteur de dispersion, récepteur de l'HGF/SF, récepteur protéine-tyrosine kinase c-Met, carcinome papillaire à cellules rénales 2, RCCP2)], anticorps monoclonal humanisé, conjugué, par 6 résidus cystéinyle en moyenne à l'*adizutécan*, comprenant un linker et un dérivé de la camptothécine; chaîne lourde H-gamma1 humanisée (1-445) [VH (*Homo sapiens* IGHV1-2*02 (92.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (215) (119-216), charnière 1-15 K7>del, T8>C (223), T10>del (217-229), CH2 (230-339), CH3 E12 (355), M14 (357) (340-444), CHS K2>del (445)) (119-445)], (221-218')-disulfure avec la chaîne légère L-kappa humanisée (1'-218') [V-KAPPA (*Homo sapiens* IGKV4-1*01 (85.1%) -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 (223-223''-225-225'':228-228'')-trisdisulfure, produit dans une lignée cellulaire des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1SV, exprimant l'enzyme glutamine synthétase (GS), glycoforme alfa; substitué sur l'atome de soufre de 6 résidus L-cystéinyle en moyenne parmi 221, 223, 225, 228, 218', 221'', 223'', 225'', 228'' et 218''' avec un groupement radical 2-{[(2*S*)-1-{[(2*S*)-1-({3-[(7*S*)-7-éthyl-7-hydroxy-14-méthyl-8,11-dioxo-7,8,11,13-tétrahydro-2*H*,10*H*-[1,3]dioxolo[4,5-*g*]pyrano[3',4':6,7]indolizino[1,2-*b*]quinoléin-14-yl]bicyclo[1.1.1]pentan-1-yl}amino)-1-oxopropan-2-yl]amino}-3-méthyl-1-oxobutan-2-yl]amino}-2-oxoéthyle (*adizutécan*)
telisotuzumab adizutecán	inmunoglobulina G1-kappa, anti-[*Homo sapiens* MET (proto-oncogén met, receptor del factor de crecimiento hepatocitario, HGFR, receptor del factor de dispersión, receptor del HGF/SF, receptor proteína-tirosina kinasa c-Met, carcinoma papilar con células renales 2, RCCP2)], anticuerpo monoclonal humanizado, conjugado, por 6 residuos cisteinilo en promedio, al *adizutecán*, que comprende un conector y un derivado de camptotecina; cadena pesada H-gamma1 humanizada (1-445) [VH (*Homo sapiens* IGHV1-2*02 (92.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (215) (119-216), bisagra 1-15 K7>del, T8>C (223), T10>del (217-229), CH2 (230-339), CH3 E12 (355), M14 (357) (340-444), CHS K2>del (445)) (119-445)], (221-218')-disulfuro con la cadena ligera

L-kappa humanizada (1'-218') [V-KAPPA (*Homo sapiens* IGKV4-1*01 (85.1%) -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 (223-223"-225-225":228-228")-trisdisulfuro, producido en una línea cellular de las células ováricas de hámster chino (CHO), línea celular derivada de CHO-K1SV, expresando la enzima glutamina sintetasa (GS), forma glicosilada alfa; sustituido en el átomo de azufre de 6 residuos L-cisteinilo en promedio de 221, 223, 225, 228, 218', 221", 223", 225", 228" y 218"' con un grupo radical 2-{[(2*S*)-1-{[(2*S*)-1-({3-[(7*S*)-7-etil-7-hidroxi-14-metil-8,11-dioxo-7,8,11,13-tetrahidro-2*H*,10*H*-[1,3]dioxolo[4,5-*g*]pirano[3',4':6,7]indolizino[1,2-*b*]quinolein-14-il]biciclo[1.1.1]pentan-1-il}amino)-1-oxopropan-2-il]amino}-3-metil-1-oxobutan-2-il]amino}-2-oxoetilo (*adizutecán*)

Heavy chain / Chaîne lourde / Cadena pesada

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QVQLVQSGAE VKKPGASVKV SCKASGYIFT AYTMHWVRQA PGQGLEWMGW  50
IKPNNGLANY AQKFQGRVTM TRDTSISTAY MELSRLRSDD TAVYYCARSE 100
ITTEFDYWGQ GTLVTVSSAS TKGPSVFPLA PSSKSTSGGT AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTQTYI 200
CNVNHKPSNT KVDKRVEPKS CDCHCPPCPA PELLGGPSVF LFPPKPKDTL 250
MISRTPEVTC VVVDVSHEDP EVKFNWYVDG VEVHNAKTKP REEQYNSTYR 300
VVSVLTVLHQ DWLNGKEYKC KVSNKALPAP IEKTISKAKG QPREPQVYTL 350
PPSREEMTKN QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD 400
GSFFLYSKLT VDKSRWQQGN VFSCSVMHEA LHNHYTQKSL SLSPG      445
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Light chain / Chaîne légère / Cadena ligera

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DIVMTQSPDS LAVSLGERAT INCKSSESVD SYANSFLHWY QQKPGQPPKL  50
LIYRASTRES GVPDRFSGSG SGTDFTLTIS SLQAEDVAVY YCQQSKEDPL 100
TFGGGTKVEI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL NNFYPREAKV 150
QWKVDNALQS GNSQESVTEQ DSKDSTYSLS STLTLSKADY EKHKVYACEV 200
THQGLSSPVT KSFNRGEC                                    218
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Post-translational modifications

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

Intra-H (C23-C104) 22-96 145-201 260-320 366-424
22"-95" 145"-201" 260"-320" 366"-424"
Intra-L (C23-C104) 23'-92' 138'-198'
23"'-92"' 138"'-198"'
Inter-H-L (h 5-CL 126)* 221-218' 221"-218"'
Inter-H-H (h 11, h 14)* 225-225" 228-228" (h8>C)* 223-223"

*At least three inter-chain disulfide bridges are not present, an average of 6 cysteinyl being conjugated each via a thioether bond to a drug linker.

*Au moins trois ponts disulfures inter-chaînes ne sont pas présents, 6 cystéinyl en moyenne étant chacun conjugué via une liaison thioéther à un linker-principe actif.

*Al menos tros puentes disulfuro inter-catenarios no estan presentes, una media de 6 cisteinil está conjugada a conectores de principio activo.

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal

Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)
H VH Q1: 1, 1"

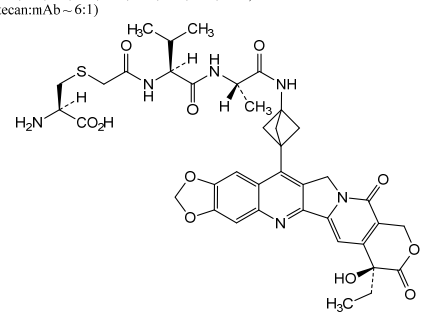
N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación

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

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

C (221,223,225,228,218',221",223",225",228",218"')
*(adizutecan:mAb ~ 6:1)



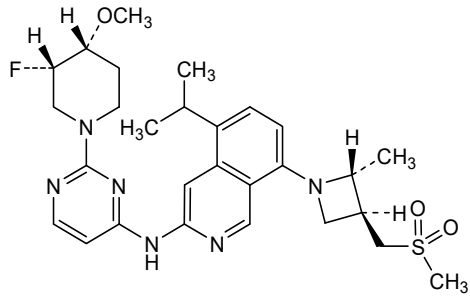
tigozertinibum

tigozertinib — *N*-{2-[(3*S*,4*R*)-3-fluoro-4-methoxypiperidin-1-yl]pyrimidin-4-yl}-8-{(2*R*,3*S*)-3-[(methanesulfonyl)methyl]-2-methylazetidin-1-yl}-5-(propan-2-yl)isoquinolin-3-amine

tigozertinib — *N*-{2-[(3*S*,4*R*)-3-fluoro-4-méthoxypipéridin-1-yl]pyrimidin-4-yl}-8-{(2*R*,3*S*)-3-[(méthanesulfonyl)méthyl]-2-méthylazétidin-1-yl}-5-(propan-2-yl)isoquinoléin-3-amine

tigozertinib — *N*-{2-[(3*S*,4*R*)-3-fluoro-4-metoxipiperidin-1-il]pirimidin-4-il}-8-{(2*R*,3*S*)-3-[(metanosulfonil)metil]-2-metilazetidin-1-il}-5-(propan-2-il)isoquinolein-3-amina

$C_{28}H_{37}FN_6O_3S$



tilatamigum #

tilatamig — immunoglobulin G1-kappa/G1-lambda, anti-[*Homo sapiens* MET (met proto-oncogene, hepatocyte growth factor (HGF) receptor, HGFR, scatter factor (SF) receptor, HGF/SF receptor, receptor tyrosine-protein kinase c-met, papillary renal cell carcinoma 2, RCCP2)] and anti-[*Homo sapiens* EGFR (epidermal growth factor receptor, receptor tyrosine-protein kinase erbB-1, ERBB1, HER1, HER-1, ERBB)], *Homo sapiens* monoclonal antibody, bispecific;
H-gamma1 heavy chain anti-MET *Homo sapiens* (1-446) [VH (*Homo sapiens* IGHV1-8*01 (95.9%) -(IGHD) -IGHJ3*01 (100%), CDR-IMGT [8.8.9] (26-33.51-58.97-105)) (1-116)-*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v39 CH2 F1.3, E1.2, S116, G1v33 CH3 S22, A24, V86 (hole), G1v75 CH3 C5 (CH1 R120 (213) (117-214), hinge 1-15 (215-229), CH2 L1.3>F (233), L1.2>E (234), P116>S (330) (230-339), CH3 Y5>C (348), E12 (355), M14 (357) T22>S (365), L24>A (367), Y86>V (406) (hole) (340-444), CHS (445-446)) (117-446)], (219-214')-disulfide with L-kappa light chain anti-MET *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5*03 (92.6%) -IGKJ4*01 (90.9%) V124>L (104'), 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')];
H-gamma1 heavy chain anti-EGFR *Homo sapiens* (1''-454'') [VH (*Homo sapiens* IGHV1-69*06 (83.7%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.8.17] (26''-33''.51''-58''.97''-113'')) (1''-124'') -*Homo sapiens*

	IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v39 CH2 F1.3, E1.2, S116, G1v32 CH3 W22 (knob), G1v74 CH3 C10, G1v58 CH1 C5, h V5 (CH1 F5>C (133"), R120 (221") (125"-222"), hinge 1-15 C5>V (227") (223"-237"), CH2 L1.3>F (241"), L1.2>E (242"), P116>S (338") (238"-347"), CH3 S10>C (361"), E12 (363"), M14 (365"), T22>W (373") (348"-452"), CHS (453"-454")) (125"-454")], (133"-126"')-disulfide with L-lambda2 light chain anti-EGFR *Homo sapiens* (1"'-217"') [V-LAMBDA (*Homo sapiens* IGLV2-14*05 (94.9%) -IGLJ2*01 (90.9%), CDR-IMGT [9.3.11] (26"'-34"'.52"'-54"'.91"'-101"')) (1"'-111"') -*Homo sapiens* IGLC2*01 (98.1%), LC2v58 C10, V126, S10>C (126"'), C126>V (216"') (112"'-217"')]; dimer (225-233":228-236")-bisdisulfide, produced in a cell line from Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, glycoform alfa
tilatamig	immunoglobuline G1-kappa/G1-lambda, anti-[*Homo sapiens* MET (proto-oncogène met, récepteur du facteur de croissance hépatocytaire, HGFR, récepteur du facteur de dispersion (SF), récepteur de l'HGF/SF, récepteur protéine-tyrosine kinase c-met, carcinome papillaire à cellules rénales 2, RCCP2)] et anti-[*Homo sapiens* EGFR (récepteur du facteur de croissance épidermique, récepteur tyrosine-protéine kinase erbB-1, ERBB1, HER1, HER-1, ERBB)], anticorps monoclonal *Homo sapiens*, bispécifique; chaîne lourde H-gamma1 anti-MET *Homo sapiens* (1-446) [VH (*Homo sapiens* IGHV1-8*01 (95.9%) -(IGHD) -IGHJ3*01 (100%), CDR-IMGT [8.8.9] (26-33.51-58.97-105)) (1-116)-*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v39 CH2 F1.3, E1.2, S116, G1v33 CH3 S22, A24, V86 (hole), G1v75 CH3 C5 (CH1 R120 (213) (117-214), charnière 1-15 (215-229), CH2 L1.3>F (233), L1.2>E (234), P116>S (330) (230-339), CH3 Y5>C (348), E12 (355), M14 (357), T22>S (365), L24>A (367), Y86>V (406) (hole) (340-444), CHS (445-446)) (117-446)], (219-214')-disulfure avec la chaîne légère L-kappa anti-MET *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5*03 (92.6%) -IGKJ4*01 (90.9%) V124>L (104), 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 H-gamma1 anti-EGFR *Homo sapiens* 1"-454") [VH (*Homo sapiens* IGHV1-69*06 (83.7%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.8.17] (26"-33".51"-58".97"-113")) (1"-124") -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v39 CH2 F1.3, E1.2, S116, G1v32 CH3 W22 (knob), G1v74 CH3 C10, G1v58 CH1 C5, h V5 (CH1 F5>C (133"), R120 (221") (125"-222"), charnière 1-15 C5>V (227") (223"-237"), CH2 L1.3>F (241"), L1.2>E (242"), P116>S (338") (238"-347"), CH3 S10>C (361"), E12 (363"), M14 (365"), T22>W (373") (348"-452"), CHS (453"-454")) (125"-454")], (133"-126"')-

	disulfure avec la chaîne légère L-lambda2 anti-EGFR *Homo sapiens* (1'"-217'") [V-LAMBDA (*Homo sapiens* IGLV2-14*05 (94.9%) -IGLJ2*01 (90.9%), CDR-IMGT [9.3.11] (26'"-34'".52'"-54'".91'"-101'")) (1'"-111'") -*Homo sapiens* IGLC2*01 (98.1%), LC2v58 C10, V126, S10>C (126'"), C126>V (216'") (112'"-217'")]; dimère (225-233":228-236")-bisdisulfure, produit dans une lignée cellulaire des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1, glycoforme alfa
tilatamig	inmunoglobulina G1-kappa/G1-lambda, anti-[*Homo sapiens* MET (proto-oncogén met, receptor del factor de crecimiento hepatocitario, HGFR, receptor del factor de dispersión (SF), receptor del HGF/SF, receptor proteína-tirosina kinasa c-met, carcinoma papilar con células renales 2, RCCP2)] y anti-[*Homo sapiens* EGFR (receptor del factor de crecimiento epidérmico, receptor tirosina-proteína kinasa erbB-1, ERBB1, HER1, HER-1, ERBB)], anticuerpo monoclonal *Homo sapiens*, biespecífico; cadena pesada H-gamma1 anti-MET *Homo sapiens* (1-446) [VH (*Homo sapiens* IGHV1-8*01 (95.9%) -(IGHD) -IGHJ3*01 (100%), CDR-IMGT [8.8.9] (26-33.51-58.97-105)) (1-116)-*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v39 CH2 F1.3, E1.2, S116, G1v33 CH3 S22, A24, V86 (hole), G1v75 CH3 C5 (CH1 R120 (213) (117-214), bisagra 1-15 (215-229), CH2 L1.3>F (233), L1.2>E (234), P116>S (330) (230-339), CH3 Y5>C (348), E12 (355), M14 (357), T22>S (365), L24>A (367), Y86>V (406) (hole) (340-444), CHS (445-446)) (117-446)], (219-214')-disulfuro con la cadena ligera L-kappa anti-MET *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5*03 (92.6%) -IGKJ4*01 (90.9%) V124>L (104), 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 H-gamma1 anti-EGFR *Homo sapiens* 1"-454") [VH (*Homo sapiens* IGHV1-69*06 (83.7%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.8.17] (26"-33".51"-58".97"-113")) (1"-124") -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v39 CH2 F1.3, E1.2, S116, G1v32 CH3 W22 (knob), G1v74 CH3 C10, G1v58 CH1 C5, h V5 (CH1 F5>C (133"), R120 (221") (125"-222"), bisagra 1-15 C5>V (227") (223"-237"), CH2 L1.3>F (241"), L1.2>E (242"), P116>S (338") (238"-347"), CH3 S10>C (361"), E12 (363"), M14 (365"), T22>W (373") (348"-452"), CHS (453"-454")) (125"-454")], (133"-126'")-disulfuro con la cadena ligera L-lambda2 anti-EGFR *Homo sapiens* (1'"-217'") [V-LAMBDA (*Homo sapiens* IGLV2-14*05 (94.9%) -IGLJ2*01 (90.9%), CDR-IMGT [9.3.11] (26'"-34'".52'"-54'".91'"-101'")) (1'"-111'") -*Homo sapiens* IGLC2*01 (98.1%), LC2v58 C10, V126, S10>C (126'"), C126>V (216'") (112'"-217'")]; dímero (225-233":228-236")-bisdisulfuro, producido en una línea celular de las células ováricas de hámster chino (CHO), línea celular derivada de CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada: anti-MET (hole) (H)

```
QVQLVQSGAE VKKPGASVKV SCKASGYTFT DYYIHWVRQA TGQGLEWMGW  50
MNPNSGNTGY AQKFQGRVTM TRDTSISTAY MELSSLRSED TAVYYCARGQ 100
GYTHSWGQGT MVTVSSASTK GPSVFPLAPS SKSTSGGTAA LGCLVKDYFP 150
EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVVTVPSS SLGTQTYICN 200
VNHKPSNTKV DKRVEPKSCD KTHTCPPCPA PEFEGGPSVF LFPPKPKDTL 250
MISRTPEVTC VVVDVSHEDP EVKFNWYVDG VEVHNAKTKP REEQYNSTYR 300
VVSVLTVLHQ DWLNGKEYKC KVSNKALPAS IEKTISKAKG QPREPQVCTL 350
PPSREEMTKN QVSLSCAVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD 400
GSFFLVSKLT VDKSRWQQGN VFSCSVMHEA LHNHYTQKSL SLSPGK     446
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Light chain / Chaîne légère / Cadena ligera: anti-MET (L')

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DIQMTQSPST LSASVGDRVT ITCRASEGIY HWLAWYQQKP GKAPKLLIYK  50
ASSLASGVPS RFSGSGSGTE FTLTISSLQP DDFATYYCQQ YSNYPPTFGG 100
GTKLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
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Heavy chain / Chaîne lourde / Cadena pesada: anti-EGFR (knob) (H")

```
QVQLVQSGAE VKKPGSSVKV SCKASGGTFS DNDFSWVRQA PGQGLEWMGA  50
IVAVFRTETY AQKFQDRVKI TADISTRTTY MELSSLRSED TAVYYCARRL 100
MSAISGPGAP LLMWGQGTLV TVSSASTKGP SVCPLAPSSK STSGGTAALG 150
CLVKDYFPEP VTVSWNSGAL TSGVHTFPAV LQSSGLYSLS SVVTVPSSSL 200
GTQTYICNVN HKPSNTKVDK RVEPKSVDKT HTCPPCPAPE FEGGPSVFLF 250
PPKPKDTLMI SRTPEVTCVV VDVSHEDPEV KFNWYVDGVE VHNAKTKPRE 300
EQYNSTYRVV SVLTVLHQDW LNGKEYKCKV SNKALPASIE KTISKAKGQP 350
REPQVYTLPP CREEMTKNQV SLWCLVKGFY PSDIAVEWES NGQPENNYKT 400
TPPVLDSDGS FFLYSKLTVD KSRWQQGNVF SCSVMHEALH NHYTQKSLSL 450
SPGK                                                   454
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Light chain / Chaîne légère / Cadena ligera: anti-EGFR (L'")

```
QSALTQPRSV SGSPGQSVTI SCTGTSSDVG GYNYVSWYQQ HPGKAPKLMI  50
YDVSKRPSGV PDRFSGSKSG NTASLTISGL QAEDEADYYC SSYTSSDTLE 100
IFGGGTKLTV LGQPKAAPSV TLFPPCSEEL QANKATLVCL ISDFYPGAVT 150
VAWKADSSPV KAGVETTTPS KQSNNKYAAS SYLSLTPEQW KSHRSYSCQV 200
THEGSTVEKT VAPTEVS                                     217
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Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 143-199 260-320 366-424
22"-96" 151"-207" 268"-328" 374"-432"
Intra-L (C23-C104) 23'-88' 134'-194'
22"'-90"' 139"'-198"'
Inter-H-L (h 5-CL 126) 219-214' 133"-126"'
Inter-H-H (h 11, h 14) 225-233" 228-236"
Inter-H-H (CH3 C5-C10)* 348-361"
*variants G1v75 (CH3 C5) and G1v74 (CH3 C10) creating an additional inter-H-H disulfide bond
*variantes G1v75 (CH3 C5) et G1v74 (CH3 C10) créant une liaison disulfure inter-H-H supplémentaire
*variantes G1v75 (CH3 C5) y G1v74 (CH3 C10) que crean un enlace disulfuro inter-H-H adicional

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)
H VH Q1: 1, 1"
L VL Q1: 1"'

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4: 296, 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: 446, 454"

tilatamigum samrotecanum

tilatamig samrotecan — immunoglobulin G1-kappa/G1-lambda, anti-[*Homo sapiens* MET (met proto-oncogene, hepatocyte growth factor (HGF) receptor, HGFR, scatter factor (SF) receptor, HGF/SF receptor, receptor tyrosine-protein kinase c-met, papillary renal cell carcinoma 2, RCCP2)] and anti-[*Homo sapiens* EGFR (epidermal growth factor receptor, receptor tyrosine-protein kinase erbB-1, ERBB1, HER1, HER-1, ERBB)], *Homo sapiens* monoclonal antibody, bispecific, conjugated on 6 cysteinyl residues to *samrotecan*;
H-gamma1 heavy chain anti-MET *Homo sapiens* (1-446) [VH (*Homo sapiens* IGHV1-8*01 (95.9%) -(IGHD) -IGHJ3*01 (100%), CDR-IMGT [8.8.9] (26-33.51-58.97-105)) (1-116)-*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v39 CH2 F1.3, E1.2, S116, G1v33 CH3 S22, A24, V86 (hole), G1v75 CH3 C5 (CH1 R120 (213)

(117-214), hinge 1-15 (215-229), CH2 L1.3>F (233), L1.2>E (234), P116>S (330) (230-339), CH3 Y5>C (348), E12 (355), M14 (357) T22>S (365), L24>A (367), Y86>V (406) (hole) (340-444), CHS (445-446)) (117-446)], (219-214')-disulfide with L-kappa light chain anti-MET *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5*03 (92.6%) -IGKJ4*01 (90.9%) V124>L (104'), 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')];
H-gamma1 heavy chain anti-EGFR *Homo sapiens* (1"-454") [VH (*Homo sapiens* IGHV1-69*06 (83.7%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.8.17] (26"-33".51"-58".97"-113")) (1"-124") -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v39 CH2 F1.3, E1.2, S116, G1v32 CH3 W22 (knob), G1v74 CH3 C10, G1v58 CH1 C5, h V5 (CH1 F5>C (133"), R120 (221") (125"-222"), hinge 1-15 C5>V (227") (223"-237"), CH2 L1.3>F (241"), L1.2>E (242"), P116>S (338") (238"-347"), CH3 S10>C (361"), E12 (363"), M14 (365"), T22>W (373") (348"-452"), CHS (453"-454")) (125"-454")], (133"-126"')-disulfide with L-lambda2 light chain anti-EGFR *Homo sapiens* (1"'-217"') [V-LAMBDA (*Homo sapiens* IGLV2-14*05 (94.9%) -IGLJ2*01 (90.9%), CDR-IMGT [9.3.11] (26"'-34"'.52"'-54"'.91"'-101"')) (1"'-111"') -*Homo sapiens* IGLC2*01 (98.1%), LC2v58 C10, V126, S10>C (126"'), C126>V (216"') (112"'-217"')]; dimer (225-233":228-236")-bisdisulfide, produced in a cell line from Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, glycoform alfa; substituted at the sulfur atoms of L-cysteinyl residues 233, 236, 219", 225", 228" and 214"' with radical group 1-[(2*S*,5*S*)-1-{[(9*S*)-9-ethyl-9-hydroxy-10,13-dioxo-2,3,9,10,13,15-hexahydro-1*H*,12*H*-benzo[*de*]pyrano[3',4':6,7]indolizino[1,2-*b*]quinolin-4-yl]amino}-2-methyl-1,4,7,35-tetraoxo-5-(propan-2-yl)-10,13,16,19,22,25,28,31-octaoxa-3,6,34-triazaheptatriacontan-37-yl]-2,5-dioxopyrrolidin-3-yl (*samrotecan*)

tilatamig samrotécan

immunoglobuline G1-kappa/G1-lambda, anti-[*Homo sapiens* MET (proto-oncogène met, récepteur du facteur de croissance hépatocytaire, HGFR, récepteur du facteur de dispersion (SF), récepteur de l'HGF/SF, récepteur protéine-tyrosine kinase c-met, carcinome papillaire à cellules rénales 2, RCCP2)] et anti-[*Homo sapiens* EGFR (récepteur du facteur de croissance épidermique, récepteur tyrosine-protéine kinase erbB-1, ERBB1, HER1, HER-1, ERBB)], anticorps monoclonal *Homo sapiens*, bispécifique, conjugué par 6 résidus cystéinyle au *samrotécan*;
chaîne lourde H-gamma1 anti-MET *Homo sapiens* (1-446) [VH (*Homo sapiens* IGHV1-8*01 (95.9%) -(IGHD) -IGHJ3*01 (100%), CDR-IMGT [8.8.9] (26-33.51-58.97-105)) (1-116)-*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v39 CH2 F1.3, E1.2, S116, G1v33 CH3 S22, A24, V86 (hole), G1v75 CH3 C5 (CH1 R120 (213) (117-214), charnière 1-15 (215-229), CH2 L1.3>F (233), L1.2>E (234), P116>S (330) (230-339), CH3 Y5>C (348), E12 (355), M14 (357), T22>S (365), L24>A (367), Y86>V (406) (hole) (340-444), CHS (445-446)) (117-446)], (219-214')-disulfure avec la chaîne légère L-kappa anti-MET *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5*03 (92.6%) -IGKJ4*01 (90.9%) V124>L (104), 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 H-gamma1 anti-EGFR *Homo sapiens* 1"-454") [VH (*Homo sapiens* IGHV1-69*06 (83.7%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.8.17] (26"-33".51"-58".97"-113")) (1"-124") -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v39 CH2 F1.3, E1.2, S116, G1v32 CH3 W22 (knob), G1v74 CH3 C10, G1v58 CH1 C5, h V5 (CH1 F5>C (133"), R120 (221") (125"-222"),

charnière 1-15 C5>V (227") (223"-237"), CH2 L1.3>F (241"), L1.2>E (242"), P116>S (338") (238"-347"), CH3 S10>C (361"), E12 (363"), M14 (365"), T22>W (373") (348"-452"), CHS (453"-454")) (125"-454")], (133"-126"')-disulfure avec la chaîne légère L-lambda2 anti-EGFR *Homo sapiens* (1"'-217"') [V-LAMBDA (*Homo sapiens* IGLV2-14*05 (94.9%) -IGLJ2*01 (90.9%), CDR-IMGT [9.3.11] (26"'-34"'.52"'-54"'.91"'-101"')) (1"'-111"') -*Homo sapiens* IGLC2*01 (98.1%), LC2v58 C10, V126, S10>C (126"'), C126>V (216"') (112"'-217"')]; dimère (225-233":228-236")-bisdisulfure, produit dans une lignée cellulaire des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1, glycoforme alfa; substitué sur l'atome de soufre des résidus L-cystéinyle 233, 236, 219", 225", 228" et 214"' avec un groupement radical 1-[(2*S*,5*S*)-1-{[(9*S*)-9-éthyl-9-hydroxy-10,13-dioxo-2,3,9,10,13,15-hexahydro-1*H*,12*H*-benzo[*de*]pyrano[3',4':6,7]indolizino[1,2-*b*]quinoléin-4-yl]amino}-2-méthyl-1,4,7,35-tétraoxo-5-(propan-2-yl)-10,13,16,19,22,25,28,31-octaoxa-3,6,34-triazaheptatriacontan-37-yl]-2,5-dioxopyrrolidin-3-yle (*samrotécan*)

tilatamig samrotecán

inmunoglobulina G1-kappa/G1-lambda, anti-[*Homo sapiens* MET (proto-oncogén met, receptor del factor de crecimiento hepatocitario, HGFR, receptor del factor de dispersión (SF), receptor del HGF/SF, receptor proteína-tirosina kinasa c-met, carcinoma papilar con células renales 2, RCCP2)] y anti-[*Homo sapiens* EGFR (receptor del factor de crecimiento epidérmico, receptor tirosina-proteína kinasa erbB-1, ERBB1, HER1, HER-1, ERBB)], anticuerpo monoclonal *Homo sapiens*, biespecífico, conjugué par 6 résidus cystéinyle au *samrotécan*;
cadena pesada H-gamma1 anti-MET *Homo sapiens* (1-446) [VH (*Homo sapiens* IGHV1-8*01 (95.9%) -(IGHD) -IGHJ3*01 (100%), CDR-IMGT [8.8.9] (26-33.51-58.97-105)) (1-116)-*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v39 CH2 F1.3, E1.2, S116, G1v33 CH3 S22, A24, V86 (hole), G1v75 CH3 C5 (CH1 R120 (213) (117-214), bisagra 1-15 (215-229), CH2 L1.3>F (233), L1.2>E (234), P116>S (330) (230-339), CH3 Y5>C (348), E12 (355), M14 (357), T22>S (365), L24>A (367), Y86>V (406) (hole) (340-444), CHS (445-446)) (117-446)], (219-214')-disulfuro con la cadena ligera L-kappa anti-MET *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5*03 (92.6%) -IGKJ4*01 (90.9%) V124>L (104), 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 H-gamma1 anti-EGFR *Homo sapiens* 1"-454") [VH (*Homo sapiens* IGHV1-69*06 (83.7%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.8.17] (26"-33".51"-58".97"-113")) (1"-124") -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v39 CH2 F1.3, E1.2, S116, G1v32 CH3 W22 (knob), G1v74 CH3 C10, G1v58 CH1 C5, h V5 (CH1 F5>C (133"), R120 (221") (125"-222"), bisagra 1-15 C5>V (227") (223"-237"), CH2 L1.3>F (241"), L1.2>E (242"), P116>S (338") (238"-347"), CH3 S10>C (361"), E12 (363"), M14 (365"), T22>W (373") (348"-452"), CHS (453"-454")) (125"-454")], (133"-126"')-disulfuro con la cadena ligera L-lambda2 anti-EGFR *Homo sapiens* (1"'-217"') [V-LAMBDA (*Homo sapiens* IGLV2-14*05 (94.9%) -IGLJ2*01 (90.9%), CDR-IMGT [9.3.11] (26"'-34"'.52"'-54"'.91"'-101"')) (1"'-111"') -*Homo sapiens* IGLC2*01 (98.1%), LC2v58 C10, V126, S10>C (126"'), C126>V (216"') (112"'-217"')]; dímero (225-233":228-236")-bisdisulfuro, producido en una línea celular de las células ováricas de hámster chino (CHO), línea celular derivada de CHO-K1, forma glicosilada alfa; substitué sur l'atome de soufre des résidus L-cystéinyle 233, 236, 219", 225", 228" et 214"' avec un groupement

Heavy chain / Chaîne lourde / Cadena pesada: anti-MET (hole) (H)

```
QVQLVQSGAE VKKPGASVKV SCKASGYTFT DYYIHWVRQA TGQGLEWMGW  50
MNPNSGNTGY AQKFQGRVTM TRDTSISTAY MELSSLRSED TAVYYCARGQ 100
GYTHSWGQGT MVTVSSASTK GPSVFPLAPS SKSTSGGTAA LGCLVKDYFP 150
EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVVTVPSS SLGTQTYICN 200
VNHKPSNTKV DKRVEPKSCD KTHTCPPCPA PEFEGGPSVF LFPPKPKDTL 250
MISRTPEVTC VVVDVSHEDP EVKFNWYVDG VEVHNAKTKP REEQYNSTYR 300
VVSVLTVLHQ DWLNGKEYKC KVSNKALPAS IEKTISKAKG QPREPQVCTL 350
PPSREEMTKN QVSLSCAVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD 400
GSFFLVSKLT VDKSRWQQGN VFSCSVMHEA LHNHYTQKSL SLSPGK     446
```

Light chain / Chaîne légère / Cadena ligera: anti-MET (L')

```
DIQMTQSPST LSASVGDRVT ITCRASEGIY HWLAWYQQKP GKAPKLLIYK  50
ASSLASGVPS RFSGSGSGTE FTLTISSLQP DDFATYYCQQ YSNYPPTFGG 100
GTKLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Heavy chain / Chaîne lourde / Cadena pesada: anti-EGFR (knob) (H")

```
QVQLVQSGAE VKKPGSSVKV SCKASGGTFS DNDFSWVRQA PGQGLEWMGA  50
IVAVFRTETY AQKFQDRVKI TADISTRTTY MELSSLRSED TAVYYCARRL 100
MSAISGPGAP LLMWGQGTLV TVSSASTKGP SVCPLAPSSK STSGGTAALG 150
CLVKDYFPEP VTVSWNSGAL TSGVHTFPAV LQSSGLYSLS SVVTVPSSSL 200
GTQTYICNVN HKPSNTKVDK RVEPKSVDKT HTCPPCPAPE FEGGPSVFLF 250
PPKPKDTLMI SRTPEVTCVV VDVSHEDPEV KFNWYVDGVE VHNAKTKPRE 300
EQYNSTYRVV SVLTVLHQDW LNGKEYKCKV SNKALPASIE KTISKAKGQP 350
REPQVYTLPP CREEMTKNQV SLWCLVKGFY PSDIAVEWES NGQPENNYKT 400
TPPVLDSDGS FFLYSKLTVD KSRWQQGNVF SCSVMHEALH NHYTQKSLSL 450
SPGK                                                   454
```

Light chain / Chaîne légère / Cadena ligera: anti-EGFR (L'")

```
QSALTQPRSV SGSPGQSVTI SCTGTSSDVG GYNYVSWYQQ HPGKAPKLMI  50
YDVSKRPSGV PDRFSGSKSG NTASLTISGL QAEDEADYYC SSYTSSDTLE 100
IFGGGTKLTV LGQPKAAPSV TLFPPCSEEL QANKATLVCL ISDFYPGAVT 150
VAWKADSSPV KAGVETTTPS KQSNNKYAAS SYLSLTPEQW KSHRSYSCQV 200
THEGSTVEKT VAPTEVS                                     217
```

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" 151"-207" 268"-328" 374"-432"

Intra-L (C23-C104) 23'-88' 134'-194'
22"'-90"' 139"'-198"'

Inter-H-L (h 5-CL 126)* 219-214' 133"-126"'

Inter-H-H (h 11, h 14)* 225-233" 228-236"

Inter-H-H (CH3 C5-C10)** 348-361"

*At least three inter-chain disulfide bridges are not present, an average of 6 cysteinyl being conjugated each via a thioether bond to a drug linker.

*Au moins trois ponts disulfures inter-chaînes ne sont pas présents, 6 cystéinyl en moyenne étant chacun conjugué via une liaison thioéther à un linker-principe actif.

*Al menos tres puentes disulfuro inter-catenarios no estan presentes, una media de 6 cisteinil está conjugada a conectores de principio activo.

**variants G1v75 (CH3 C5) and G1v74 (CH3 C10) creating an additional inter-H-H disulfide bond.

**variantes G1v75 (CH3 C5) et G1v74 (CH3 C10) créant une liaison disulfure inter-H-H supplémentaire.

**variantes G1v75 (CH3 C5) y G1v74 (CH3 C10) que crean un enlace disulfuro inter-H-H adicional.

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal

Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)

H VH Q1: 1, 1"

L VL Q1: 1'"

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

H CH2 N84.4: 296, 304"

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

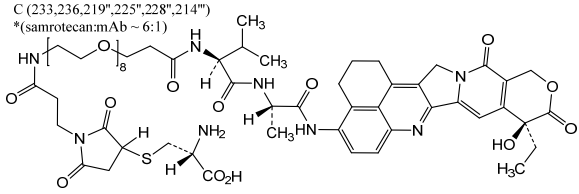
C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal

H CHS K2: 446, 454"

Modified residues / résidus modifiés /restos modificados*

C (233,236,219",225",228",214"')

*(samrotecan:mAb ~ 6:1)



tisorimcovateinum #

tisorimcovatein — severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), omicron lineage XBB.1 (Gisaid: EPI_ISL_14917761) spike (S) glycoprotein fragment (1-1191), stable prefusion conformation variant (H^{664}>P, R^{665}>G, R^{666}>S, R^{668}>S, A^{875}>P, F^{800}>P, A^{882}>P, A^{925}>P, K^{969}>P, V^{970}>P) fused to the enterobacteria phage T4 fibritin foldon domain fragment (458-484, 1192-1218 in the current sequence), trimer, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

tisorimcovatéine — coronavirus 2 du syndrome respiratoire aigu sévère (SRAS-CoV-2), fragment de la glycoprotéine de spicule (S) (1-1191) de la lignée omicron XBB.1 (Gisaid: EPI_ISL_14917761), variant de conformation stabilisée par préfusion (H^{664}>P, R^{665}>G, R^{666}>S, R^{668}>S, A^{875}>P, F^{800}>P, A^{882}>P, A^{925}>P, K^{969}>P, V^{970}>P) fusionné au fragment du domaine foldon de la fibritine de l'entérobactérie du phage T4 (458-484, 1192-1218 dans la séquence actuelle), trimère, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

tisorimcovateína — síndrome respiratorio agudo grave coronavirus 2 (SARS-CoV-2), linaje XBB.1 de ómicron (Gisaid: EPI_ISL_14917761) fragment de la glicoproteína de espícula (S) (1-1191), variante de conformación de prefusión estable (H^{664}>P, R^{665}>G, R^{666}>S, R^{668}>S, A^{875}>P, F^{800}>P, A^{882}>P, A^{925}>P, K^{969}>P, V^{970}>P) fusionada al fragmento del dominio plegable de fibritina del fago T4 de enterobacterias (458-484, 1192-1218 en la secuencia actual), trímero, producido en células ováricas de hámster Chino (CHO), glicoforma alfa

Monomer sequence / Séquence du monomère / Secuencia del monómero

```
QCVNLITRTQ SYTNSFTRGV YYPDKVFRSS VLHSTQDLFL PFFSNVTWFH    50
AIHVSGTNGT KRFDNPALPF NDGVYFASTE KSNIIRGWIF GTTLDSKTQS   100
LLIVNNATNV VIKVCEFQFC NDPFLDVYQK NNKSWMESEF RVYSSANNCT   150
FEYVSQPFLM DLEGKEGNFK NLREFVFKNI DGYFKIYSKH TPINLERDLP   200
QGFSALEPLV DLPIGINITR FQTLLALHRS YLTPVDSSSG WTAGAAAYYV   250
GYLQPRTFLL KYNENGTITD AVDCALDPLS ETKCTLKSFT VEKGIYQTSN   300
FRVQPTESIV RFPNITNLCP FHEVFNATTF ASVYAWNRKR ISNCVADYSV   350
IYNFAPFFAF KCYGVSPTKL NDLCFTNVYA DSFVIRGNEV SQIAPGQTGN   400
IADYNYKLPD DFTGCVIAWN SNKLDSKPSG NYNYLYRLFR KSKLKPFERD   450
ISTEIYQAGN KPCNGVAGSN CYSPLQSYGF RPTYGVGHQP YRVVVLSFEL   500
LHAPATVCGP KKSTNLVKNK CVNFNFNGLT GTGVLTESNK KFLPFQQFGR   550
DIADTTDAVR DPQTLEILDI TPCSFGGVSV ITPGTNTSNQ VAVLYQGVNC   600
TEVPVAIHAD QLTPTWRVYS TGSNVFQTRA GCLIGAEYVN NSYECDIPIG   650
AGICASYQTQ TKSPGSASSV ASQSIIAYTM SLGAENSVAY SNNSIAIPTN   700
FTISVTTEIL PVSMTKTSVD CTMYICGDST ECSNLLLQYG SFCTQLKRAL   750
TGIAVEQDKN TQEVFAQVKQ IYKTPPIKYF GGFNFSQILP DPSKPSKRSP   800
IEDLLFNKVT LADAGFIKQY GDCLGDIAAR DLICAQKFNG LTVLPPLLTD   850
EMIAQYTSAL LAGTITSGWT FGAGPALQIP FPMQMAYRFN GIGVTQNVLY   900
ENQKLIANQF NSAIGKIQDS LSSTPSALGK LQDVVNHNAQ ALNTLVKQLS   950
SKFGAISSVL NDILSRLDPP EAEVQIDRLI TGRLQSLQTY VTQQLIRAAE  1000
IRASANLAAT KMSECVLGQS KRVDFCGKGY HLMSFPQSAP HGVVFLHVTY  1050
VPAQEKNFTT APAICHDGKA HFPREGVFVS NGTHWFVTQR NFYEPQIITT  1100
DNTFVSGNCD VVIGIVNNTV YDPLQPELDS FKEELDKYFK NHTSPDVDLG  1150
DISGINASVV NIQKEIDRLN EVAKNLNESL IDLQELGKYE QGYIPEAPRD  1200
GQAYVRKDGE WVLLSTFL                                     1218
```

Mutation / Mutation / Mutación
H664>P, R665>G, R666>S, R668>S, F800>P, A875>P, A882>P, A925>P, K969>P, V970>P

Foldon domain / Foldon domaine / Foldon dominio
GYIPEAPRDG QAYVRKDGEW VLLSTFL 1192-1218

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-chain: 2-120, 115-149, 274-284, 319-344, 362-415, 374-508, 463-471, 521-573,
600-632, 645-654, 721-743, 726-732, 824-834, 1015-1026, 1065-1109
2'-120', 115'-149', 274'-284', 319'-344', 362'-415', 374'-508', 463'-471', 521'-573',
600'-632', 645'-654', 721'-743', 726'-732', 824'-834', 1015'-1026', 1065'-1109'
2"-120", 115"-149", 274"-284", 319"-344", 362"-415", 374"-508", 463"-471", 521"-573",
600"-632", 645"-654", 721"-743", 726"-732", 824"-834", 1015"-1026", 1065"-1109"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
N44, N58, N106, N132, N148, N217, N265, N314, N326, N586, N599, N640, N692, N700,
N784, N1057, N1081, N1117, N1141, N1156, N1177

N44', N58', N106', N132', N148', N217', N265', N314', N326', N586', N599', N640', N692', N700',
N784', N1057', N1081', N1117', N1141', N1156', N1177'

N44", N58", N106", N132", N148", N217", N265", N314", N326", N586", N599", N640", N692", N700",
N784", N1057", N1081", N1117", N1141", N1156", N1177"

O-glycosylation sites / Sites de O-glycosylation / Posiciones de O-glicosilación
T306, S308, T306', S308', T306", S308"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
Q1, Q1', Q1" >pyroglutamyl (pE, 5-oxoprolyl)

trastuzumabum envedotinum #

trastuzumab envedotin

immunoglobulin G1-kappa, anti-[*Homo sapiens* ERBB2 (receptor tyrosine-protein kinase erbB-2, epidermal growth factor receptor 2, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], humanized monoclonal antibody, conjugated at glutaminyl residues to monomethylauristatin E (MMAE), with a ratio of 1 to 2, via a cleavable linker;
H-gamma1 heavy chain humanized (1-450) [VH (*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 CH1 K120, CH3 E12, M14 (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 L-kappa light chain humanized (1'-214') [V-KAPPA (*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')]; dimer (229-229'':232-232'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa; substituted at the side chain nitrogen atom of L-glutaminyl residues 298 and 298'' with a radical group consisting of (6*S*,9*S*)-1-amino-6-({4-[(5*S*,8*S*,11*S*,12*R*)-11-[(2*S*)-butan-2-yl]-12-(2-{(2*S*)-2-[(1*R*,2*R*)-3-{[(1*S*,2*R*)-1-hydroxy-1-phenylpropan-2-yl]amino}-1-methoxy-2-methyl-3-oxopropyl]pyrrolidin-1-yl}-2-oxoethyl)-4,10-dimethyl-3,6,9-trioxo-5,8-di(propan-2-yl)-2,13-dioxa-4,7,10-triazatetradecyl]phenyl}carbamoyl)-1,8,11-trioxo-9-(propan-2-yl)-13,16,19-trioxa-2,7,10-triazahenicosan-21-yl (*envedotin*)

trastuzumab envédotine

immunoglobuline G1-kappa, anti-[*Homo sapiens* ERBB2 (récepteur tyrosine-protéine kinase erbB-2, récepteur 2 du facteur de croissance épidermique, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], anticorps monoclonal humanisé, conjugué, par des résidus glutaminyle, au monométhylauristatine E (MMAE), via un linker clivable avec un rapport de 1 pour 2;
chaîne lourde H-gamma1 humanisée (1-450) [VH (*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 CH1 K120, CH3 E12, M14 (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 L-kappa humanisée (1'-214') [V-KAPPA (*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')]; dimère (229-229'':232-232'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa; substitué sur l'atome d'azote de la chaîne latérale des résidus L-glutaminyle 298 et 298'' avec un groupement radical (6*S*,9*S*)-1-amino-6-({4-[(5*S*,8*S*,11*S*,12*R*)-11-[(2*S*)-butan-2-yl]-12-(2-{(2*S*)-2-[(1*R*,2*R*)-3-{[(1*S*,2*R*)-1-hydroxy-1-phénylpropan-2-yl]amino}-1-méthoxy-2-méthyl-3-oxopropyl]pyrrolidin-1-yl}-2-oxoéthyl)-4,10-diméthyl-3,6,9-trioxo-5,8-di(propan-2-yl)-2,13-dioxa-4,7,10-triazatétradécyl]phényl}carbamoyl)-1,8,11-trioxo-9-(propan-2-yl)-13,16,19-trioxa-2,7,10-triazahénicosan-21-yle (*envédotine*)

trastuzumab envedotina

inmunoglobulina G1-kappa, anti-[*Homo sapiens* ERBB2 (receptor tirosina-proteína kinasa erbB-2, receptor 2 del factor de crecimiento epidérmico, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], anticuerpo monoclonal humanizado, conjugado, por los residuos glutaminil, a la monometilauristatina E (MMAE) a través de un enlace escindible, con una proporción de uno a dos;

cadena pesada H-gamma1 humanizada(1-450) [VH (*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 CH1 K120, CH3 E12, M14 (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 L-kappa humanizada (1'-214') [V-KAPPA (*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')]; dímero (229-229":232-232")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa; sustituido en el átomo de nitrógeno de la cadena lateral de los residuos de L-glutaminilo 298 y 298" con un grupo radical (6*S*,9*S*)-1-amino-6-({4-[(5*S*,8*S*,11*S*, 12*R*)-11- [(2*S*)-butan-2-il]-12-(2-{(2*S*)-2-[(1*R*,2*R*)-3-{[(1*S*,2*R*)-1-fenil-1-hidroxipropan-2 -il]amino}-1-metoxi-2-metil-3-oxopropil]pirrolidin-1-il}-2-oxoetil)-4,10-dimetil-3,6,9-trioxo-5,8-di(propan-2-il)-2,13-dioxa-4,7,10-triazatetradecil]fenil}carbamoil)-1,8,11-trioxo-9-(propan-2-il)-13,16,19- trioxa-2,7,10-triazhenicosan-21-il (*envedotina*)

Heavy chain / Chaîne lourde / Cadena pesada

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

Light chain / Chaîne légère / Cadena ligera

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

Post-translational modifications

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

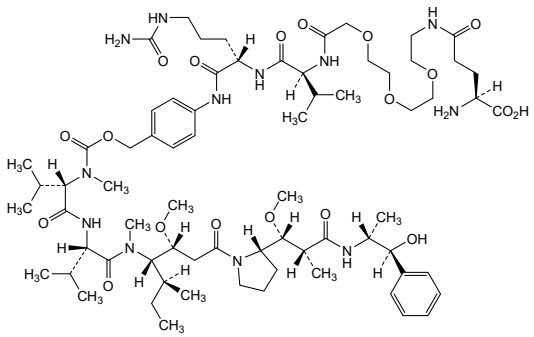
Intra-H (C23-C104) 22-96 147-203 264-324 370-428
22"-96" 147"-203" 264"-324" 370"-428"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194'"
Inter-H-L (h 5-CL 126) 223-214' 223"-214'"
Inter-H-H (h 11, h 14) 229-229" 232-232"

Specific drug attachment site / Site spécifique de fixation / Sitio específico de unión
H CH2 Q84.2: 298, 298"

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"

Modified residues / résidus modifiés / restos modificados*
Q (298, 298")
*(envedotin:mAb ~ 2:1)



trosunilimabum #

trosunilimab	immunoglobulin G1-kappa, anti-[*Homo sapiens* integrin ITGA4_ITGB7 (integrin alpha4 (CD49d)_beta7, integrin α4β7, lymphocyte Peyer's patch adhesion molecule 1, LPAM-1)]; gamma1 heavy chain (1-442) [VH (*Homo sapiens* IGHV1-69*11 (79.2%) -(IGHD) -IGHJ3*01 (92.3%) M123>T (107), CDR-IMGT [8.8.5] (26-33.51-58.97-101)) (1-112) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (209) (113-210), hinge 1-15 (211-225), CH2 (226-335), CH3 E12 (351), M14 (353) (336-440), CHS (441-442)) (113-442)], (215-214')-disulfide with kappa light chain (1'-214') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV14-100*01 (85.3%) -IGKJ1*01 (91.7%) L124>V (104)/*Homo sapiens* IGKV1-33*01 (80.0%) -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 (221-221'':224-224'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa
trosunilimab	immunoglobuline G1-kappa, anti-[*Homo sapiens* intégrine ITGA4_ITGB7 (intégrine alpha4 (CD49d)_bêta7, intégrine α4β7, récepteur d'adressage spécifique des plaques de Peyer, LPAM-1)]; chaîne lourde gamma1 (1-442) [VH (*Homo sapiens* IGHV1-69*11 (79.2%) -(IGHD) -IGHJ3*01 (92.3%) M123>T (107), CDR-IMGT [8.8.5] (26-33.51-58.97-101)) (1-112) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (209) (113-210), charnière 1-15 (211-225), CH2 (226-335), CH3 E12 (351), M14 (353) (336-440), CHS (441-442)) (113-442)], (215-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV14-100*01 (85.3%) -IGKJ1*01 (91.7%) L124>V (104)/*Homo sapiens* IGKV1-33*01 (80.0%) -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 (221-221'':224-224'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa
trosunilimab	inmunoglobulina G1-kappa, anti-[*Homo sapiens* integrina ITGA4_ITGB7 (integrina alfa4 (CD49d)_beta7, integrina α4β7, receptor específico de las placas de Peyer, LPAM-1)]; cadena pesada gamma1 (1-442) [VH (*Homo sapiens* IGHV1-69*11 (79.2%) -(IGHD) -IGHJ3*01 (92.3%) M123>T (107), CDR-IMGT [8.8.5] (26-33.51-58.97-101)) (1-112) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (209) (113-210), bisagra 1-15 (211-225), CH2 (226-335), CH3 E12 (351), M14 (353) (336-440), CHS (441-442)) (113-442)], (215-214')-disulfure con la cadena ligera kappa (1'-214') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV14-100*01 (85.3%) -IGKJ1*01 (91.7%) L124>V (104)/*Homo sapiens* IGKV1-33*01 (80.0%) -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 (221-221'':224-224'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVQSGAE VKKPGSSVKV SCKASGFNIK NTYMHWVRQA PGQGLEWIGR  50
IDPAKGHTEY APKFLGRVTI TADESTNTAY MELSSLRSED TAVYYCYYVD 100
VWGQGTTVTV SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT 150
VSWNSGALTS GVHTFPAVLQ SSGLYSLSSV VTVPSSSLGT QTYICNVNHK 200
PSNTKVDKKV EPKSCDKTHT CPPCPAPELL GGPSVFLFPP KPKDTLMISR 250
TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ YNSTYRVVSV 300
LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR 350
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF 400
LYSKLTVDKS RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GK          442
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Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCHASQDIS DNIGWLQQKP GKSFKLLIYH  50
GTNLEDGVPS RFSGSGSGTD YTLTISSLQP EDFATYYCVQ YAQFPWTFGG 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) 22-96 139-195 256-316 362-420
22"-96" 139"-195" 256"-316" 362"-420"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194'"
Inter-H-L (h 5-CL 126) 215-214' 215"-214'"
Inter-H-H (h 11, h 14) 221-221" 224-224"

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

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2: 442, 442"

ucalolictidum

ucalolictide — L-lysyl-L-phenylalanyl-L-alanyl-L-lysyl-L-phenylalanyl-L-alanyl-L-lysyl-L-lysyl-L-phenylalanyl-L-alanyl-L-lysyl-L-phenylalanyl-L-alanyl-L-lysyl-L-lysyl-L-phenylalanyl-L-alanyl-L-lysyl-L-glutaminyl-L-histidyl-L-tryptophyl-L-seryl-L-tyrosylglycyl-L-leucyl-L-arginyl-L-prolylglycine

ucalolictide — L-lysyl-L-phénylalanyl-L-alanyl-L-lysyl-L-phénylalanyl-L-alanyl-L-lysyl-L-lysyl-L-phénylalanyl-L-alanyl-L-lysyl-L-phénylalanyl-L-alanyl-L-lysyl-L-lysyl-L-phénylalanyl-L-alanyl-L-lysyl-L-glutaminyl-L-histidyl-L-tryptophyl-L-séryl-L-tyrosylglycyl-L-leucyl-L-arginyl-L-prolylglycine

ucalolictida — L-lisil-L-fenilalanil-L-alanil-L-lisil-L-fenilalanil-L-alanil-L-lisil-L-lisil-L-fenilalanil-L-alanil-L-lisil-L-fenilalanil-L-alanil-L-lisil-L-lisil-L-fenilalanil-L-alanil-L-lisil-L-glutaminil-L-histidil-L-triptofil-L-seril-L-tirosilglicil-L-leucil-L-arginil-L-prolilglicina

$C_{163}H_{243}N_{43}O_{32}$

KFAKFAKKFA KFAKKFAKQH WSYGLRPG 28

ulintoclaxum pegondrimerum

ulintoclax pegondrimer — α-(diphenylmethyl)-ω^{2}-dotriacontakis{2-[(2-{2-[{2-[(3*R*,11*R*)-1^{4}-chloro-3-hydroxy-6,8,8-trioxo-9^{3}-(trifluoromethanesulfonyl)-8λ^{6},13-dithia-7,10-diaza-4(4,1)-piperidina-1,14(1),2(1,2),5,9(1,4)-pentabenzenatetradecaphan-11-yl]ethyl}(methyl)amino]ethoxy}-2-oxoethyl)(methyl)amino]acetamido}-ω^{6}-dotriacontakis{2-[α-methylpoly(oxyethylene)-ω-oxy]acetamido}-*dendro*^{G6}-{azanediyl[(2*S*)-1-oxohexane-1,2,6-triyl)]})

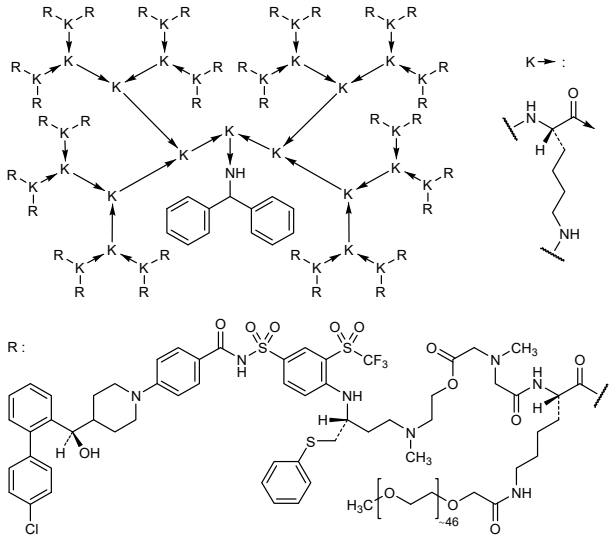
ulintoclax pégondrimère

α-(diphénylméthyl)-ω^{2}-dotriacontakis{2-[(2-{2-[{2-[(3*R*,11*R*)-1^{4}-chloro-3-hydroxy-6,8,8-trioxo-9^{3}-(trifluorométhanesulfonyl)-8λ^{6},13-dithia-7,10-diaza-4(4,1)-pipéridina-1,14(1),2(1,2),5,9(1,4)-pentabenzénatétradécaphan-11-yl]éthyl}(méthyl)amino]éthoxy}-2-oxoéthyl)(méthyl)amino]acétamido}-ω^{6}-dotriacontakis{2-[α-méthylpoly(oxyéthylène)-ω-oxy]acétamido}-*dendro*^{G6}-{azanediyl[(2*S*)-1-oxohexane-1,2,6-triyle)]})

ulintoclax pegondrímero

α-(difenilmetil)-ω^{2}-dotriacontakis{2-[(2-{2-[{2-[(3*R*,11*R*)-1^{4}-cloro-3-hidroxi-6,8,8-trioxo-9^{3}-(trifluorometanosulfonil)-8λ^{6},13-ditia-7,10-diaza-4(4,1)-piperidina-1,14(1),2(1,2),5,9(1,4)-pentabencenatetradecafan-11-il]etil}(metil)amino]etoxi}-2-oxoetil)(metil)amino]acetamido}-ω^{6}-dotriacontakis{2-[α-metilpoli(oxietileno)-ω-oxi]acetamido}-*dendro*^{G6}-{azanodiil[(2*S*)-1-oxohexano-1,2,6-triilo)]})

$C_{2087}H_{2593}Cl_{32}F_{96}N_{287}O_{415}S_{96}(C_2H_4O)_{32n}$



umikibartum #

umikibart

immunoglobulin G4-kappa, anti-[*Homo sapiens* HGF (hepatocyte growth factor, scatter factor, SF, hepatopoeitin A)], humanized monoclonal antibody;
H-gamma4 heavy chain humanized (1-443) [VH (*Homo sapiens* IGHV3-23*04 (89.8%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.8.9] (26-33.51-58.97-105)) (1-116)-*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, G4v5 h P10, G4v3 CH2 E1.2 (CH1 (117-214), hinge 1-12 S10>P (224) (215-226), CH2 L92 (305), L1.2>E (231) (227-336), CH3 (337-441), CHS (442-443)) (117-443)], (130-215')-disulfide with L-kappa light chain humanized (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-13*02 (94.3%) -IGKJ1*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'-115')];dimer (222-222'':225-225'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-DG44, glycoform alfa

umikibart

immunoglobuline G4-kappa, anti-[*Homo sapiens* HGF (facteur de croissance de l'hépatocyte, facteur dispersant, SF, hépatopoïétine A)], anticorps monoclonal humanisé;
chaîne lourde H-gamma4 humanisée (1-443) [VH (*Homo sapiens* IGHV3-23*04 (89.8%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.8.9] (26-33.51-58.97-105)) (1-116)-*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, G4v5 h P10, G4v3 CH2 E1.2 (CH1 (117-214), charnière 1-12 S10>P (224) (215-226), CH2 L92 (305), L1.2>E (231) (227-336), CH3 (337-441), CHS (442-443)) (117-443)], (130-215')-disulfure avec la chaîne légère L-kappa humanisée (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-13*02 (94.3%) -IGKJ1*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'-115')]; dimère (222-222":225-225")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-DG44, glycoforme alfa

umikibart

immunoglobulina G4-kappa, anti-[*Homo sapiens* HGF (factor de crecimiento del hepatocito, factor dispersante, SF, hepatopoyetina A)], anticuerpo monoclonal humanizado;
cadena pesada H-gamma4 humanizada (1-443) [VH (*Homo sapiens* IGHV3-23*04 (89.8%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.8.9] (26-33.51-58.97-105)) (1-116)-*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, G4v5 h P10, G4v3 CH2 E1.2 (CH1 (117-214), bisagra 1-12 S10>P (224) (215-226), CH2 L92 (305), L1.2>E (231) (227-336), CH3 (337-441), CHS (442-443)) (117-443)], (130-215')-disulfuro con la cadena ligera L-kappa humanizada (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-13*02 (94.3%) -IGKJ1*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'-115')]; dímero (222-222":225-225")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-DG44, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada : H-gamma4 (H, H") anti-HGF

```
EVQLVESGGG LVQPGGSLRL SCAASGFTFS TYYMSWVRQA PGKGLEWVAY  50
IGTSSGTTYY ADSVKGRFTI SRDGSKNTLY LQMNSLRAED TAVYYCARGL 100
GRINLWGQGT LVTVSSASTK GPSVFPLAPC SRSTSESTAA LGCLVKDYFP 150
EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVVTVPSS SLGTKTYTCN 200
VDHKPSNTKV DKRVESKYGP PCPPCPAPEF EGGPSVFLFP PKPKDTLMIS 250
RTPEVTCVVV DVSQEDPEVQ FNWYVDGVEV HNAKTKPREE QFNSTYRVVS 300
VLTVLHQDWL NGKEYKCKVS NKGLPSSIEK TISKAKGQPR EPQVYTLPPS 350
QEEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT PPVLDSDGSF 400
FLYSRLTVDK SRWQEGNVFS CSVMHEALHN HYTQKSLSLS LGK        443
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Light chain / Chaîne légère / Cadena ligera : L-kappa (L', L'") anti-HGF

```
DIQMTQSPSS LSASVGDRVT ITCRASQGIS NILAWYQQKP GKAPKLLIYG  50
ASNLESGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQS GYYSRGATFG 100
QGTKVEIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK 150
VDNALQSGNS QESVTEQDSK DSTYSLSSTL TLSKADYEKH KVYACEVTHQ 200
GLSSPVTKSF NRGEC                                       215
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 143-199 257-317 363-421
22"-96" 143"-199" 257"-317" 363"-421"
Intra-L (C23-C104) 23'-88' 135'-195'
23'"-88'" 135'"-195'"
Inter-H-L (CH1 10-CL 126) 130-215' 130"-215'"
Inter-H-H (h 8, h 11) 222-222" 225-225"

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

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2: 443, 443"

uzatresgenum autoleucelum #

uzatresgene autoleucel

autologous CD3+ enriched T lymphocytes obtained from peripheral blood mononuclear cells (PBMCs) by apheresis. The cells are transduced with a self-inactivating, non-replicating lentiviral vector encoding an enhanced-affinity T cell receptor (TCR) targeting the HLA-A*02:01-restricted MAGE-A4 peptide (GVYDGREHTV) alongside the CD8 alpha (CD8α) co-receptor. The expressed transgene comprises the coding sequence for the CD8α co-receptor, separated by a foot-and-mouth disease virus 2A self-cleaving peptide sequence from the coding sequence of the MAGE-A4 T-cell receptor alpha and beta chains that are separated from each other by a *porcine teschovirus-1* 2A self-cleaving peptide sequence, under control of the human elongation factor 1 alpha (EF-1α) promoter. The construct is flanked by 5' and 3' long terminal repeats (LTRs) and also contains a tRNA primer binding site, a ψ packaging signal, a truncated *gag*, a Rev response element (RRE) and a central polypurine tract (cPPT) sequence 5' to the transgene, and a polypurine tract (PPT) 3' to the transgene. The vector is pseudotyped with the vesicular stomatitis virus (VSV) G envelope glycoprotein.
The CD3+ T lymphocytes are purified and activated using anti-CD3/anti-CD28 monoclonal antibody coated magnetic beads. The cells are then cultured in media containing interleukin 2 (IL-2), human AB serum and a protein kinase B (AKT inhibitor). The cells are CD3+ (> 80%), express the high affinity MAGE-A4 specific TCR and CD8α co-receptor (CD8α +TCR+; >16%) and are cytotoxic to MAGE-A4 expressing tumor cells

uzatresgène autoleucel

lymphocytes T autologues enrichis en CD3+ obtenus par aphérèse à partir de cellules mononucléaires de sang périphérique (PBMC). Les cellules sont transduites avec un vecteur lentiviral auto-inactivant et non répliquant codant un récepteur des lymphocytes T (RCT) à affinité amplifiée ciblant le peptide MAGE-A4 (GVYDGREHTV) restreint au HLA-A*02:01 ainsi que le corécepteur CD8 alpha (CD8α). Le transgène comprend la séquence codante du corécepteur CD8α, séparée par une séquence codante du peptide auto-clivant 2A du virus de la fièvre aphteuse, de la séquence codante des chaînes alpha et bêta du récepteur des lymphocytes T MAGE-A4 qui sont séparés l'une de l'autre par une séquence codant un peptide auto-clivant 2A du *teschovirus-1 porcin*, sous le contrôle du promoteur du facteur d'élongation 1 alpha (EF-1α) humain. La construction est flanquée de longues répétitions terminales (LTR) en 5' et 3' et contient également un site de liaison d'une amorce d'ARNt, un signal d'encapsidation ψ, une séquence *gag* tronquée, un élément de réponse Rev (RRE) et une séquence du tractus polypurine central (cPPT) en 5' du transgène, et un tractus polypurine (PPT) en 3' du transgène. Le vecteur est pseudotypé avec la glycoprotéine d'enveloppe G du virus de la stomatite vésiculaire (VSV).
Les lymphocytes T CD3+ sont purifiés et activés à l'aide de billes magnétiques recouvertes d'anticorps monoclonaux anti-CD3/anti-CD28. Les cellules sont ensuite cultivées dans un milieu contenant de l'interleukine 2 (IL-2), du sérum AB humain et un inhibiteur de la protéine kinase B (inhibitrice de l'AKT). Les cellules sont CD3+ (>80%), expriment le RCT de haute affinité spécifique du MAGE-A4 et le corécepteur CD8α (CD8α +TCR+; >16%) et sont cytotoxiques pour les cellules tumorales exprimant le MAGE-A4.

uzatresgén autoleucel

linfocitos T CD3+ enriquecidos autólogos, obtenidos a partir de células mononucleares de sangre periférica (PBMCs) mediante aféresis. Las células se transducen con un vector lentiviral, no replicativo y auto inactivante que codifica para un receptor de linfocitos T (TCR) con afinidad aumentada dirigido al péptido MAGE-A4 restringido por HLA-A*02:01 (GVYDGREHTV) junto al correceptor CD8 alfa (CD8α). El transgén contiene la secuencia codificante del correceptor CD8αseparada por una secuencia codificante del péptido de autoexcisión 2A del virus de la fiebre aftosa de la secuencia codificante de las cadenas alfa y beta del receptor de linfocitos T MAGE-A4 que están separadas entre sí por una secuencia codificante de un péptido de autoexcisión 2A del *teschovirus porcino*, bajo el control del promotor del factor de elongación 1 alpha (EF-1α) humano. El constructo está flanqueado por repeticiones terminales largas (LTRs) en 5' y 3' y también contiene un sitio de unión del tRNA cebador. una señal de empaquetamiento ψ, un *gag* truncado, un elemento de respuesta Rev (RRE) y una secuencia de tracto de poli-purina central (cPPT) en 5' del transgén, y un tracto de poli-purina (PPT) en 3' del transgén. El vector está seudotipado con la glicoproteína G de la envuelta del virus de la estomatitis vesicular (VSV). Los linfocitos T CD3+ se purifican y se activan usando bolas magnéticas forradas con anticuerpos monoclonales anti-CD3/anti-CD28. A continuación las células se cultivan en medio que contiene interleuquina 2 (IL-2), suero humano AB y una proteína quinasa B (inhibidor AKT). Las células son CD3+ (> 80%), expresan el TCR específico de MAGE-A4 de alta afinidad y el correceptor CD8α (CD8α +TCR+; >16%) y son citotóxicas frente a células tumorales que expresan MAGE-A4

varegacestatum

varegacestat

(2*R*,3*S*)-*N*^{1}-[(3*S*)-5-(3-fluorophenyl)-9-methyl-2-oxo-2,3-dihydro-1*H*-1,4-benzodiazepin-3-yl]-2,3-bis(3,3,3-trifluoropropyl)butanediamide

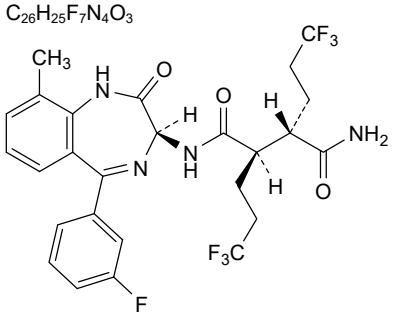
varégacestat

(2*R*,3*S*)-*N*^{1}-[(3*S*)-5-(3-fluorophényl)-9-méthyl-2-oxo-2,3-dihydro-1*H*-1,4-benzodiazépin-3-yl]-2,3-bis(3,3,3-trifluoropropyl)butanediamide

varegacestat

(2*R*,3*S*)-*N*^{1}-[(3*S*)-5-(3-fluorofenil)-9-metil-2-oxo-2,3-dihidro-1*H*-1,4-benzodiazepin-3-il]-2,3-bis(3,3,3-trifluoropropil)butanodiamida

$C_{26}H_{25}F_7N_4O_3$



vebanvibartum #

vebanvibart

immunoglobulin G1-kappa, anti-[severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) spike (S) protein, receptor binding domain (RBD)], *Homo sapiens* monoclonal antibody;

	H-gamma1 heavy chain *Homo sapiens* (1-455) [VH (*Homo sapiens* IGHV1-69*01 (88.8%) -(IGHD) -IGHJ4*01 (85.7%) S128>A (125), CDR-IMGT [8.8.18] (26-33.51-58.97-114)) (1-125) -*Homo sapiens* IGHG1*01, G1m17,1, CH1 K120, CH3 D12, L14, G1v21 CH2 Y15.1, T16, E18 (CH1 K120 (222) (126-223), hinge 1-15 (224-238), CH2 M15.1>Y (260), S16>T (262), T18>E (264) (239-348), CH3 D12 (364), L14 (366) (349-453), CHS (454-455)) (126-455)], (228-215')-disulfide with L-kappa light chain *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (95.8%) -IGKJ2*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 (234-234'':237-237'')-bisdisulfide, produced in a cell line from Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, glycoform alfa
vébanvibart	immunoglobuline G1-kappa, anti-[domaine de liaison au récepteur (RBD) de la glycoprotéine spike (S) du coronavirus 2 du syndrome respiratoire aigu sévère (SARS-CoV-2)], anticorps monoclonal *Homo sapiens*; chaîne lourde H-gamma1 *Homo sapiens* (1-455) [VH (*Homo sapiens* IGHV1-69*01 (88.8%) -(IGHD) -IGHJ4*01 (85.7%) S128>A (125), CDR-IMGT [8.8.18] (26-33.51-58.97-114)) (1-125) -*Homo sapiens* IGHG1*01, G1m17,1, CH1 K120, CH3 D12, L14, G1v21 CH2 Y15.1, T16, E18 (CH1 K120 (222) (126-223), charnière 1-15 (224-238), CH2 M15.1>Y (260), S16>T (262), T18>E (264) (239-348), CH3 D12 (364), L14 (366) (349-453), CHS (454-455)) (126-455)], (228-215')-disulfure avec la chaîne légère L-kappa *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (95.8%) -IGKJ2*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 (234-234'':237-237'')-bisdisulfure, produit dans une lignée cellulaire des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1, glycoforme alfa
vebanvibart	inmunoglobulina G1-kappa, anti-[dominio de unión al receptor (RBD) de la glicoproteína de espícula (S) del coronavirus 2 del síndrome respiratorio agudo severo (SARS-CoV-2)], anticuerpo monoclonal *Homo sapiens*; cadena pesada H-gamma1 *Homo sapiens* (1-455) [VH (*Homo sapiens* IGHV1-69*01 (88.8%) -(IGHD) -IGHJ4*01 (85.7%) S128>A (125), CDR-IMGT [8.8.18] (26-33.51-58.97-114)) (1-125) -*Homo sapiens* IGHG1*01, G1m17,1, CH1 K120, CH3 D12, L14, G1v21 CH2 Y15.1, T16, E18 (CH1 K120 (222) (126-223), bisagra 1-15 (224-238), CH2 M15.1>Y (260), S16>T (262), T18>E (264) (239-348), CH3 D12 (364), L14 (366) (349-453), CHS (454-455)) (126-455)], (228-215')-disulfuro con la cadena ligera L-kappa *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (95.8%) -IGKJ2*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 (234-234'':237-237'')-bisdisulfuro, producido en una línea celular de las células ováricas de hámster chino (CHO), línea celular derivada de CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGSSVKV SCKASGGTFR SHVISWVRQA PGQGLEWMGG  50
FIPLFGTTIY AQAFQGRVMI SADESTSTAY MELSSLRSED TAVYFCARLF 100
PNGDPNSPED GFDIWGQGTL VTVSAASTKG PSVFPLAPSS KSTSGGTAAL 150
GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL SSVVTVPSSS 200
LGTQTYICNV NHKPSNTKVD KKVEPKSCDK THTCPPCPAP ELLGGPSVFL 250
FPPKPKDTLY ITREPEVTCV VVDVSHEDPE VKFNWYVDGV EVHNAKTKPR 300
EEQYNSTYRV VSVLTVLHQD WLNGKEYKCK VSNKALPAPI EKTISKAKGQ 350
PREPQVYTLP PSRDELTKNQ VSLTCLVKGF YPSDIAVEWE SNGQPENNYK 400
TTPPVLDSDG SFFLYSKLTV DKSRWQQGNV FSCSVMHEAL HNHYTQKSLS 450
LSPGK                                                   455
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCQASQDIG NYLNWYQQKP GKAPKLLIYD  50
ASHLETGVPS RFSGSGSGTD FTFTISSLQP EDIATYYCQR YDDLPSYTFG 100
QGTKVEIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK 150
VDNALQSGNS QESVTEQDSK DSTYSLSSTL TLSKADYEKH KVYACEVTHQ 200
GLSSPVTKSF NRGEC                                        215
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 152-208 269-329 375-433
22"-96" 152"-208" 269"-329" 375"-433"
Intra-L (C23-C104) 23'-88' 135'-195'
23'"-88'" 135'"-195'"
Inter-H-L (h 5-CL 126) 228-215' 228"-215'"
Inter-H-H (h 11, h 14) 234-234" 237-237"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)
H VH Q1: 1, 1"

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

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2: 455, 455"

velaglucerasum beta

velaglucerase beta	human lysosomal acid glucosylceramidase (EC 3.2.1.45, beta-glucosylceramidase 1 (beta-GC), beta-glucocerebrosidase), produced in Chinese hamster ovary (CHO) K1 cells, glycoform beta
vélaglucérase bêta	glucosylcéramidase acide lysosomale humaine (EC 3.2.1.45, bêta-glucosylcéramidase 1 (bêta-GC), bêta-glucocérébrosidase), produite dans des cellules ovariennes K1 de hamster chinois (CHO), glycoforme bêta
velaglucerasa beta	glucosilceramidasa ácida humana lisosomal (EC 3.2.1.45, beta-glucosilceramidasa 1 (beta-GC), beta-glucocerebrosidasa), producido en las células ováricas de hámster chino (CHO), glicoforma beta

Sequence / Séquence / Secuencia

```
ARPCIPKSFG YSSVVCVCNA TYCDSFDPPT FPALGTFSRY ESTRSGRRME   50
LSMGPIQANH TGTGLLLTLQ PEQKFQKVKG FGGAMTDAAA LNILALSPPA  100
QNLLLKSYFS EEGIGYNIIR VPMASCDFSI RTYTYADTPD DFQLHNFSLP  150
EEDTKLKIPL IHRALQLAQR PVSLLASPWT SPTWLKTNGA VNGKGSLKGQ  200
PGDIYHQTWA RYFVKFLDAY AEHKLQFWAV TAENEPSAGL LSGYPFQCLG  250
FTPEHQRDFI ARDLGPTLAN STHHNVRLLM LDDQRLLLPH WAKVVLTDPE  300
AAKYVHGIAV HWYLDFLAPA KATLGETHRL FPNTMLFASE ACVGSKFWEQ  350
SVRLGSWDRG MQYSHSIITN LLYHVVGWTD WNLALNPEGG PNWVRNFVDS  400
PIIVDITKDT FYKQPMFYHL GHFSKFIPEG SQRVGLVASQ KNDLDAVALM  450
HPDGSAVVVV LNRSSKDVPL TIKDPAVGFL ETISPGYSIH TYLWRRQ     497
```

Post-translation modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
4-16, 18-23

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
19, 59, 146, 270, 462 (mannose-5 glycan dominant)

vezocolmitidum

vezocolmitide — L-prolyl-L-prolylglycyl-L-prolyl-L-prolylglycyl-L-prolyl-L-prolylglycyl-L-prolyl-L-prolylglycyl-L-prolyl-L-prolylglycyl-L-prolyl-L-prolylglycyl-L-prolyl-L-prolylglycine

vézocolmitide — L-prolyl-L-prolylglycyl-L-prolyl-L-prolylglycyl-L-prolyl-L-prolylglycyl-L-prolyl-L-prolylglycyl-L-prolyl-L-prolylglycyl-L-prolyl-L-prolylglycyl-L-prolyl-L-prolylglycine

vezocolmitida — L-prolil-L-prolilglicil-L-prolil-L-prolilglicil-L-prolil-L-prolilglicil-L-prolil-L-prolilglicil-L-prolil-L-prolilglicil-L-prolil-L-prolilglicil-L-prolil-L-prolilglicina

$C_{84}H_{121}N_{21}O_{22}$

PPGPPGPPGP PGPPGPPGPP G 21

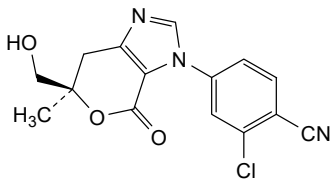
vicadrostatum

vicadrostat — 2-chloro-4-[(6*R*)-6-(hydroxymethyl)-6-methyl-4-oxo-6,7-dihydropyrano[3,4-*d*]imidazol-3(4*H*)-yl]benzonitrile

vicadrostat — 2-chloro-4-[(6*R*)-6-(hydroxyméthyl)-6-méthyl-4-oxo-6,7-dihydropyrano[3,4-*d*]imidazol-3(4*H*)-yl]benzonitrile

vicadrostat — 2-cloro-4-[(6*R*)-6-(hidroximetil)-6-metil-4-oxo-6,7-dihidropirano[3,4-*d*]imidazol-3(4*H*)-il]benzonitrilo

$C_{15}H_{12}ClN_3O_3$



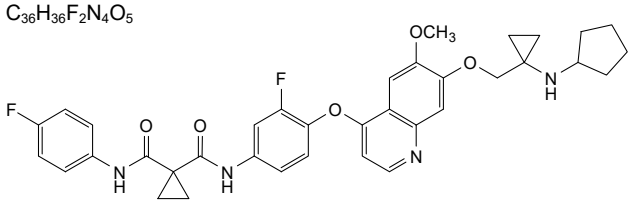
vilzemetkibum

vilzemetkib — N^1-[1^2-fluoro-3^6-methoxy-2,4-dioxa-7-aza-3(4,7)-quinolina-1(1)-benzena-8(1)-cyclopentana-6(1,1)-cyclopropanaoctaphan-1^4-yl]-N'^1-(4-fluorophenyl)cyclopropane-1,1-dicarboxamide

vilzémetkib — N^1-[1^2-fluoro-3^6-méthoxy-2,4-dioxa-7-aza-3(4,7)-quinoléina-1(1)-benzéna-8(1)-cyclopentana-6(1,1)-cyclopropanaoctaphan-1^4-yl]-N'^1-(4-fluorophényl)cyclopropane-1,1-dicarboxamide

vilzemetkib — N^1-(4-fluorofenil)-N'^1-[1^2-fluoro-3^6-metoxi-2,4-dioxa-7-aza-3(4,7)-quinoleína-1(1)-bencena-8(1)-ciclopentana-6(1,1)-ciclopropanaoctafan-1^4-il]ciclopropano-1,1-dicarboxamida

$C_{36}H_{36}F_2N_4O_5$



vislarafuspum alfa #

vislarafusp alfa — human signal regulatory protein alpha (SIRPα) fragment, anti-(human CD47, integrin associated protein (IAP)), fused via a $(G_4S)_3$ peptide linker to the N-terminus of both light chains of a humanized immunoglobulin G1-kappa anti-(human epidermal growth factor receptor 2), glycoform alfa; gamma 1 heavy chain (1-450) [VH (*Homo sapiens* IGHV3-66*01 -(IGHD) - IGHJ4*01, CDR-Kabat [5.17.11] (31-35.50-66.99-109)) (1-120) -*Homo sapiens* IGHG1*03 (CH1 (121-218), hinge (219-233), CH2 S^{301}>A, E^{336}>A, K^{337}>A (234-343), CH3 (344-448), CHS (449-450)) (121-450)], (223-354')-disulfide with human signal regulatory protein alpha (SIRP alpha natural variant V2 extracellular D1 domain, SIRP alpha V2D1) fragment (1-125), comprising the first two extracellular loops of the D1 domain, engineered variant (N^{80}>A), anti-(human CD47, integrin associated protein (IAP)) fused via a $(G_4S)_3$ peptide linker (126-140) to kappa light chain (141'-354') [V-KAPPA (*Homo sapiens* IGKV1-39*01 -IGKJ1*01, CDR-Kabat [11.7.9] (164'-174'.190'-196'.229'-237')) (141'-247') -*Homo sapiens* IGKC*01 (248'-354')]; dimer (229-229'':232-232'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa

vislarafusp alfa — fragment de la protéine humaine de régulation du signal alpha (SIRPα) anti-(CD47 humain, protéine associée à l'intégrine (IAP)), fusionné via un peptide liant $(G_4S)_3$ à l'extrémité N-terminale des deux chaînes légères d'une immunoglobuline G1-kappa humanisée anti-(récepteur 2 du facteur de croissance épidermique humain), glycoforme alfa;
chaîne lourde gamma 1 (1-450) [VH (*Homo sapiens* IGHV3-66*01 -(IGHD) - IGHJ4*01, CDR-Kabat [5.17.11] (31-35. 50-66. 99-109)) (1-120) -*Homo sapiens* IGHG1*03 (CH1 (121-218), charnière (219-233), CH2 S^{301}>A, E^{336}>A, K^{337}>A (234-343), CH3 (344-448), CHS (449-450)) (121-450)], (223-354')-disulfure avec un fragment (1-125) de la protéine humaine de régulation du signal alpha (SIRP alpha, variante naturelle V2 du domaine extracellulaire D1, SIRP alpha V2D1), comprenant les deux premières boucles extracellulaires du domaine D1, variante construite (N^{80}>A), anti-(CD47 humain, protéine associée à l'intégrine (IAP)) fusionné via un peptide liant $(G_4S)_3$ (126-140) à la chaîne légère kappa (141'-354') [V-KAPPA (*Homo sapiens* IGKV1-39*01 -IGKJ1*01, CDR-Kabat [11. 7.9] (164'-174'.190'-196'.229'-237')) (141'-247') -*Homo sapiens* IGKC*01 (248'-354')]; dimère (229-229'':232-232'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa

vislarafusp alfa — fragmento de proteína reguladora de señal alfa (SIRPα) humana, anti-(CD47 humana, integrina asociada a proteína (IAP)), fusionada a través de un enlace peptídico $(G_4S)_3$ al terminal N de ambas cadenas ligeras de inmunoglobulina G1-kappa humanizada anti-(receptor 2 del factor de crecimiento epidérmico humano), glicoforma alfa;
cadena pesada gamma 1 (1-450) [VH (*Homo sapiens* IGHV3-66*01 -(IGHD) - IGHJ4*01, CDR-Kabat [5.17.11] (31-35. 50-66. 99-109)) (1-120) -*Homo sapiens* IGHG1*03 (CH1 (121-218), bisagra (219-233), CH2 S^{301}>A, E^{336}>A, K^{337}>A (234-343), CH3 (344-448), CHS (449-450)) (121-450)], (223-354')-disulfuro con proteína reguladora de señales alfa humana (SIRP alpha, variante natural V2 extracelular dominio D1, SIRP alpha V2D1) fragmento (1-125), que comprende los dos primeros loops estracelulareds de dominio D1, variante diseñada (N^{80}>A), anti-(CD47 humana, integrina asociada a proteína (IAP)) fusionada a través de un enlace peptídico $(G_4S)_3$ (126-140) a la cadena ligera kappa (141'-354') [V-KAPPA (*Homo sapiens* IGKV1-39*01 -IGKJ1*01, CDR-Kabat [11.7.9] (164'-174'.190'-196'.229'-237')) (141'-247') -*Homo sapiens* IGKC*01 (248'-354')]; dímero (229-229'':232-232'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, glicoforma alfa

Sequence / Séquence / Secuencia
IgG1 heavy chain

```
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 NTKVDKRVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP  250
KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  300
ATYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIAATIS KAKGQPREPQ  350
VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV  400
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK  450
```

SIRPα IgG1 light chain

```
EEELQVIQPD KSVSVAAGES AILHCTVTSL IPVGPIQWFR GAGPARELIY   50
NQKEGHFPRV TTVSESTKRE NMDFSISISA ITPADAGTYY CVKFRKGSPD  100
TEFKSGAGTE LSVRAKPSAP VVSGPGGGGS GGGGSGGGGS DIQMTQSPSS  150
LSASVGDRVT ITCRASQDVN TAVAWYQQKP GKAPKLLIYS ASFLYSGVPS  200
RFSGSRSGTD FTLTISSLQP EDFATYYCQQ HYTTPPTFGQ GTKVEIKRTV  250
AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ  300
ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG LSSPVTKSFN  350
RGEC                                                    354
```

Natural variant / Variante naturelle / Variante natural
SIRPα: L^{14}>S, T^{20}>S, T^{22}>I, R^{24}>H, A^{27}>V, G^{45}>A, D^{65}>E, L^{66}>S, N^{70}>E, R^{77}>S, G^{79}>S, D^{100}>del, V^{102}>T^{101}

Mutations / Mutations / Mutaciónes
IgG1 heavy chain: S^{301},$S^{301''}$>**A**, E^{336},$E^{336''}$>**A**, K^{337},$K^{337''}$>**A**
SIRPα IgG1 light chain: $N^{80'}$,$N^{80''}$>**A**

Peptide linker / Peptide liant / Péptido de unión
SIRPα IgG1 light chain: ^{126}*GGGGSGGGGSGGGGS*^{140}

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra heavy chain: 22-96, 147-203, 264-324, 370-428,
22"-96", 147"-203", 264"-324", 370-428"
Intra SIRPα light chain: 25'-91', 163'-228', 274'-334'; 25'"-91'", 163'"-228'", 274'"-334'"
Inter heavy chain-SIRPα light chain: 223-354', 223"-354'"
Inter heavy chain: 229-229", 232-232"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
IgG1 heavy chain: 300, 300"

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

vixticibartum #

vixticibart — immunoglobulin G4-kappa, anti-[*Homo sapiens* NPR1 (natriuretic peptide receptor 1, natriuretic peptide receptor A, NPRA, atrionatriuretic peptide receptor A, ANPRA, guanylate cyclase A, GUCY2A)], *Homo sapiens* monoclonal antibody, agonist;
H-gamma4 heavy chain *Homo sapiens*(1-451) [VH (*Homo sapiens* IGHV1-2*02 (91.8%) -(IGHD) -IGHJ6*01 (100%), CDR-IMGT [8.8.17] (26-33.51-58.97-113)) (1-124)-*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, G4v5 h P10 (CH1 (125-222), hinge 1-12 S10>P (232) (223-234), CH2 L92 (313) (235-344), CH3 (345-449), CHS (450-451)) (125-451)], (138-213')-disulfide with L-kappa light chain *Homo sapiens* (1'-213') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (94.7%) -IGKJ5*02 (100%), CDR-IMGT [6.3.8] (27'-32'.50'-52'.89'-96')) (1'-106') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (152'), V101 (190') (107'-113')]; dimer (230-230":233-233")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa

vixticibart — immunoglobuline G4-kappa, anti-[*Homo sapiens* NPR1 (récepteur 1 du peptide natriurétique, récepteur A du peptide natriurétique, NPRA, récepteur A du peptide atrionatriurétique, ANPRA, guanylate cyclase A, GUCY2A)], anticorps monoclonal *Homo sapiens,* agoniste;

chaîne lourde H-gamma4 *Homo sapiens* (1-451) [VH (*Homo sapiens* IGHV1-2*02 (91.8%) -(IGHD) -IGHJ6*01 (100%), CDR-IMGT [8.8.17] (26-33.51-58.97-113)) (1-124)-*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, G4v5 h P10 (CH1 (125-222), charnière 1-12 S10>P (232) (223-234), CH2 L92 (313) (235-344), CH3 (345-449), CHS (450-451)) (125-451)], (138-213')-disulfure avec la chaîne légère L-kappa *Homo sapiens* (1'-213') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (94.7%) -IGKJ5*02 (100%), CDR-IMGT [6.3.8] (27'-32'.50'-52'.89'-96')) (1'-106') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (152'), V101 (190') (107'-113')]; dimère (230-230":233-233")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa

vixticibart

inmunoglobulina G4-kappa, anti-[*Homo sapiens* NPR1 (receptor 1 del péptido natriurético, receptor A del péptido natriurético, NPRA, receptor A del péptido atrionatriurético, ANPRA, guanilato ciclasa A, GUCY2A)], anticuerpo monoclonal *Homo sapiens*, agonista;
cadaena pesada H-gamma4 *Homo sapiens* (1-451) [VH (*Homo sapiens* IGHV1-2*02 (91.8%) -(IGHD) -IGHJ6*01 (100%), CDR-IMGT [8.8.17] (26-33.51-58.97-113)) (1-124)-*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, G4v5 h P10 (CH1 (125-222), bisagra 1-12 S10>P (232) (223-234), CH2 L92 (313) (235-344), CH3 (345-449), CHS (450-451)) (125-451)], (138-213')-disulfuro con la cadena ligera L-kappa *Homo sapiens* (1'-213') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (94.7%) -IGKJ5*02 (100%), CDR-IMGT [6.3.8] (27'-32'.50'-52'.89'-96')) (1'-106') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (152'), V101 (190') (107'-113')]; 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 : H-gamma4 (H, H") anti-NPR1

```
QVQLVQSGAE VKKPGASVTV SCKASGYTFT DYYMHWVRQA PGQGLEWMGW  50
IKPNSGGTNS AQRFQGRITM TWDTSISTAY MELSRLRSDD TAVYYCSRGG 100
PVMNYYYYYG 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 : L-kappa (L', L'") anti-NPR1

```
NIQMTQSPSS LSASVGDRVT ITCRASQSID SYLNWYQQKP GKAPKLLIYV  50
ASSLQSGVPS RFSGSGSGKD FTLTISSLQP EDFATYYCQQ SYSIPTFGQG 100
TRLEIKRTVA APSVFIFPPS DEQLKSGTAS VVCLLNNFYP REAKVQWKVD 150
NALQSGNSQE SVTEQDSKDS TYSLSSTLTL SKADYEKHKV YACEVTHQGL 200
SSPVTKSFNR GEC                                          213
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 151-207 265-325 371-429
22"-96" 151"-207" 265"-325" 371"-429"
Intra-L (C23-C104) 23'-88' 133'-193'
23'"-88'" 133'"-193'"
Inter-H-L (CH1 10-CL 126) 138-213' 138"-213'"
Inter-H-H (h 8, h 11) 230-230" 233-233"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)
H VH Q1: 1, 1"

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"

volenrelaxinum #

volenrelaxin

immunoglobulin single chain VH, anti-[*Homo sapiens* ALB (albumin, human serum albumin, HSA)], fused via peptide linkers with relaxin 2 *Homo sapiens* chains B and A;
Ig single chain VH humanized [*Homo sapiens* IGHV3-23*01 -(IGHD) -IGHJ4*01 (CDR-Kabat [5.17.17] (31-35.50-66.99-115)] (1-126), fused via peptide linker $(G_4Q)_5$ (127-151) to des-Asp[1]-relaxin 2 chain B *Homo sapiens* (2-29, 152-179 in the current sequence) fused via peptide linker $G_3SG_2SG_3$ (180-189) to relaxin 2 chain A *Homo sapiens* (1-24, 190-213 in the current sequence), monomer (22-96:161-200:173-213:199-204)-tetrakisdisulfide, produced in Chinese hamster ovary (CHO) cells, non-glycosylated

volenrelaxine

immunoglobuline monocaténaire domaine variable (VH), anti-[*Homo sapiens* ALB (albumine, sérum-albumine humaine, SAH)], fusionnée à l'aide de coupleurs peptidiques avec les chaînes B et A de la relaxine 2 d'*Homo sapiens*;
Ig monocaténaire VH humanisée [*Homo sapiens* IGHV3-23*01 -(IGHD) -IGHJ4*01 (CDR-Kabat [5.17.17] (31-35.50-66.99-115)] (1-126), fusionnée à l'aide du coupleur peptidique $(G_4Q)_5$ (127-151) à la chaîne B de la dès-Asp[1]-relaxine 2 d'*Homo sapiens* (2-29, 152-179 dans la séquence actuelle) fusionnée à l'aide du coupleur peptidique $G_3SG_2SG_3$ (180-189) à la chaîne A de la relaxine 2 *Homo sapiens* (1-24, 190-213 dans la séquence actuelle), monomère (22-96:161-200:173-213:199-204)-tétrakisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), non glycosylé

volenrelaxina

inmunoglobulina cadena única VH, anti-[*Homo sapiens* ALB (albúmina, albúmina sérica humana, ASH)], fusionada mediante conectores peptidicos con las cadenas B y A de la relaxina 2 de *Homo sapiens*;
Ig cadena única humanizada [*Homo sapiens* IGHV3-23*01 -(IGHD) -IGHJ4*01 (CDR-Kabat [5.17.17] (31-35.50-66.99-115)] (1-126), fusionada a través del conector peptídico $(G_4Q)_5$ (127-151) con la cadena B de la des-Asp[1]-relaxina 2 de *Homo sapiens* (2-29, 152-179 en la secuencia actual) fusionado a través del conector peptídico $G_3SG_2SG_3$ (180-189) con la cadena A de la relaxina 2 de *Homo sapiens* (1-24, 190-213 en la secuencia actual), monómero (22-96:161-200:173-213:199-204)-tetrakisdisulfuro, producido en células de ovario de hámster chino (CHO), no glicosilado

$C_{941}H_{1475}N_{281}O_{295}S_{11}$

Sequence / Séquence / Secuencia

```
EVQLLESGGG LVQPGGSLRL SCAASGRYID ETAVAWFRQA PGKGREFVAG   50
IGGGVDITYY ADSVKGRFTI SRDNSKNTLY LQMNSLRPED TAVYYCAARP  100
GRPLITSKVA DLYPYWGQGT LVTVSSGGGG QGGGGQGGGG QGGGGQGGGG  150
QSWMEEVIKL CGRELVRAQI AICGMSTWSG GGSGGSGGGQ LYSALANKCC  200
HVGCTKRSLA RFC                                          213
```

Peptide linkers / Peptides liants / Péptidos de unión

^{127}GGGGQGGGGQGGGGQGGGGQGGGGQ^{151}, ^{180}GGGSGGSGGG^{189}

Post-translational modifications

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

22-96, 161-200, 173-213, 199-204

Glycosylation site / Site de glycosylation / Posición de glicosilación

none / aucun / ninguna

zaltenibartum #

zaltenibart	immunoglobulin G4-kappa, anti-[*Homo sapiens* MASP3 (mannan-binding lectin-associated serine protease-3)]; H-gamma4 heavy chain (1-440) [VH Musmus/Homsap (*Mus musculus* IGHV1-9*01 (79.6%) -(IGHD) -IGHJ3*01 (90.9%) A128>S (113)/*Homo sapiens* IGHV1-46*01 (79.6%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.8.6] (26-33.51-58.97-102)) (1-113)-*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, G4v5 h P10, G4v24 CH3 L107, S114 (CH1 (114-211), hinge 1-12 S10>P (221) (212-223), CH2 L92 (302) (224-333), CH3 M107>L (421), N114>S (427) (334-438), CHS (439-440)) (114-440)], (127-219')-disulfide with L-kappa light chain (1'-219') [V-KAPPA (*Homo sapiens* IGKV4-1*01 (91.1%) -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 (219-219'':222-222'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-DG44, glycoform alfa
zalténibart	immunoglobuline G4-kappa, anti-[*Homo sapiens* MASP3 (sérine protéase 3 associée à la lectine liant le mannane)]; chaîne lourde H-gamma4 (1-440) [VH Musmus/Homsap (*Mus musculus* IGHV1-9*01 (79.6%) -(IGHD) -IGHJ3*01 (90.9%) A128>S (113)/*Homo sapiens* IGHV1-46*01 (79.6%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.8.6] (26-33.51-58.97-102)) (1-113)-*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, G4v5 h P10, G4v24 CH3 L107, S114 (CH1 (114-211), charnière 1-12 S10>P (221) (212-223), CH2 L92 (302) (224-333), CH3 M107>L (421), N114>S (427) (334-438), CHS (439-440)) (114-440)], (127-219')-disulfure avec la chaîne légère L-kappa (1'-219') [V-KAPPA (*Homo sapiens* IGKV4-1*01 (91.1%) -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 (219-219'':222-222'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-DG44, glycoforme alfa
zaltenibart	inmunoglobulina G4-kappa, anti-[*Homo sapiens* MASP3 (serina proteasa 3 associada a la lectina de unión al manano)]; cadena pesada H-gamma4 (1-440) [VH Musmus/Homsap (*Mus musculus* IGHV1-9*01 (79.6%) -(IGHD) -IGHJ3*01 (90.9%) A128>S (113)/*Homo sapiens* IGHV1-46*01 (79.6%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.8.6] (26-33.51-58.97-102)) (1-113)-*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, G4v5 h P10, G4v24 CH3 L107, S114 (CH1 (114-211), bisagra 1-12 S10>P (221) (212-223), CH2 L92 (302) (224-333), CH3 M107>L (421), N114>S (427) (334-438), CHS (439-440)) (114-440)], (127-219')-disulfuro con la cadena ligera L-kappa (1'-219') [V-KAPPA (*Homo sapiens* IGKV4-1*01 (91.1%) -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 (219-219'':222-222'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-DG44, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada : H-gamma4 (H, H") anti-MASP3

```
QVQLVQSGAE VKKPGASVKV SCKASGYTFT GKWIEWVRQA PGQGLEWIGE  50
ILPGTGSTNY NEKFKGRATF TADSSTSTAY MELSSLRSED TAVYYCLRSE 100
DVWGQGTLVT VSSASTKGPS VFPLAPCSRS TSESTAALGC LVKDYFPEPV 150
TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG TKTYTCNVDH 200
KPSNTKVDKR VESKYGPPCP PCPAPEFLGG PSVFLFPPKP KDTLMISRTP 250
EVTCVVVDVS QEDPEVQFNW YVDGVEVHNA KTKPREEQFN STYRVVSVLT 300
VLHQDWLNGK EYKCKVSNKG LPSSIEKTIS KAKGQPREPQ VYTLPPSQEE 350
MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY 400
SRLTVDKSRW QEGNVFSCSV LHEALHSHYT QKSLSLSLGK             440
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Light chain / Chaîne légère / Cadena ligera : L-kappa (L', L'") anti-MASP3

```
DIVMTQSPDS LAVSLGERAT INCKSSQSLL ASRTRKNYLA WYQQKPGQPP  50
KLLIYWASTR ESGVPDRFSG SGSGTDFTLT ISSLQAEDVA VYYCKQSYNI 100
PTFGQGTKVE 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) 22-96 140-196 254-314 360-418
22"-96" 140"-196" 254"-314" 360"-418"
Intra-L (C23-C104) 23'-94' 139'-199'
23'"-94'" 139'"-199'"
Inter-H-L (CH1 10-CL 126) 127-219' 127"-219'"
Inter-H-H (h 8, h 11) 219-219" 222-222"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)
H VH Q1: 1, 1"

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

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2: 440, 440"

zamzetoclaxum

zamzetoclax

N-{(1^3*S*,3^1*R*,3^2*R*,4*S*,5*E*,8*S*,10*S*)-6'-chloro-4-methoxy-8-methyl-10,12-dioxo-3',4'-dihydro-1^2*H*,1^4*H*,2'*H*-spiro[10λ^6-thia-11-aza-1(5,7)-[1,5]benzoxazepina-3(1,2)-cyclobutanacyclododecaphane-5,10-diene-1^3,1'-naphthalen]-10-yl}-3-methoxy-1-methyl-1*H*-pyrazole-4-carboxamide

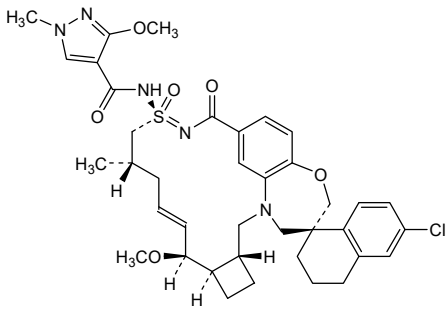
zamzétoclax

N-{(1^3*S*,3^1*R*,3^2*R*,4*S*,5*E*,8*S*,10*S*)-6'-chloro-4-méthoxy-8-méthyl-10,12-dioxo-3',4'-dihydro-1^2*H*,1^4*H*,2'*H*-spiro[10λ^6-thia-11-aza-1(5,7)-[1,5]benzoxazépina-3(1,2)-cyclobutanacyclododécaphane-5,10-diène-1^3,1'-naphtalén]-10-yl}-3-méthoxy-1-méthyl-1*H*-pyrazole-4-carboxamide

zamzetoclax

N-{(1^3*S*,3^1*R*,3^2*R*,4*S*,5*E*,8*S*,10*S*)-6'-cloro-8-metil-4-metoxi-10,12-dioxo-3',4'-dihidro-1^2*H*,1^4*H*,2'*H*-espiro[10λ^6-tia-11-aza-1(5,7)-[1,5]benzoxazepina-3(1,2)-ciclobutanaciclododecafano-5,10-dieno-1^3,1'-naftalen]-10-il}-3-metoxi-1-metil-1*H*-pirazol-4-carboxamida

$C_{38}H_{46}ClN_5O_6S$



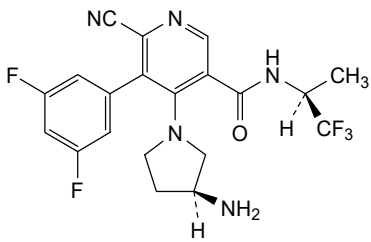
zavolosotinum

zavolosotine — 4-[(3*S*)-3-aminopyrrolidin-1-yl]-6-cyano-5-(3,5-difluorophenyl)-*N*-[(2*S*)-1,1,1-trifluoropropan-2-yl]pyridine-3-carboxamide

zavolosotine — 4-[(3*S*)-3-aminopyrrolidin-1-yl]-6-cyano-5-(3,5-difluorophényl)-*N*-[(2*S*)-1,1,1-trifluoropropan-2-yl]pyridine-3-carboxamide

zavolosotina — 4-[(3*S*)-3-aminopirrolidin-1-il]-6-ciano-5-(3,5-difluorofenil)-*N*-[(2*S*)-1,1,1-trifluoropropan-2-il]piridina-3-carboxamida

$C_{20}H_{18}F_5N_5O$



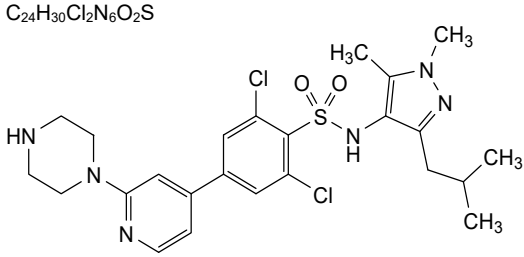
zelenirstatum

zelenirstat — 2,6-dichloro-*N*-[1,5-dimethyl-3-(2-methylpropyl)-1*H*-pyrazol-4-yl]-4-[2-(piperazin-1-yl)pyridin-4-yl]benzene-1-sulfonamide

zélénirstat — 2,6-dichloro-*N*-[1,5-diméthyl-3-(2-méthylpropyl)-1*H*-pyrazol-4-yl]-4-[2-(pipérazin-1-yl)pyridin-4-yl]benzène-1-sulfonamide

zelenirstat — 2,6-dicloro-*N*-[1,5-dimetil-3-(2-metilpropil)-1*H*-pirazol-4-il]-4-[2-(piperazin-1-il)piridin-4-il]benceno-1-sulfonamida

$C_{24}H_{30}Cl_2N_6O_2S$



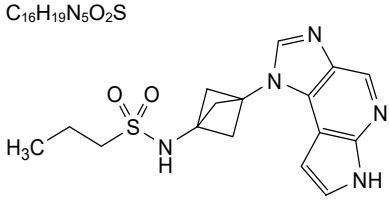
zemprocitinibum

zemprocitinib — *N*-[3-(imidazo[4,5-*d*]pyrrolo[2,3-*b*]pyridin-1(6*H*)-yl)bicyclo[1.1.1]pentan-1-yl]propane-1-sulfonamide

zemprocitinib — *N*-[3-(imidazo[4,5-*d*]pyrrolo[2,3-*b*]pyridin-1(6*H*)-yl)bicyclo[1.1.1]pentan-1-yl]propane-1-sulfonamide

zemprocitinib — *N*-[3-(imidazo[4,5-*d*]pirrolo[2,3-*b*]piridin-1(6*H*)-il)biciclo[1.1.1]pentan-1-il]propano-1-sulfonamida

$C_{16}H_{19}N_5O_2S$



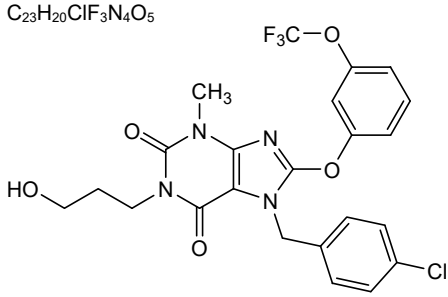
zerencotrepum

zerencotrep — 7-[(4-chlorophenyl)methyl]-1-(3-hydroxypropyl)-3-methyl-8-[3-(trifluoromethoxy)phenoxy]-3,7-dihydro-1*H*-purine-2,6-dione

zérencotrep — 7-[(4-chlorophényl)méthyl]-1-(3-hydroxypropyl)-3-méthyl-8-[3-(trifluorométhoxy)phénoxy]-3,7-dihydro-1*H*-purine-2,6-dione

zerencotrep — 7-[(4-clorofenil)metil]-1-(3-hidroxipropil)-3-metil-8-[3-(trifluorometoxi)fenoxi]-3,7-dihidro-1*H*-purina-2,6-diona

$C_{23}H_{20}ClF_3N_4O_5$



zifogaptidum

zifogaptide — N^2-(6-{5-[(3a*S*,4*S*,6a*R*)-hexahydro-2-oxo-1*H*-thieno[3,4-*d*]imidazol-4-yl]pentanamido}hexanoyl)-L-arginyl-L-glutaminyl-L-prolyl-L-lysyl-L-isoleucyl-L-tryptophyl-L-phenylalanyl-L-prolyl-L-asparaginyl-L-arginyl-L-arginyl-L-lysyl-L-prolyl-L-tryptophyl-L-lysyl-L-lysyl-L-arginyl-L-prolyl-L-arginyl-L-prolyl-L-α-aspartyl-L-α-aspartyl-L-leucyl-L-α-glutamyl-L-isoleucine

zifogaptide — N^2-(6-{5-[(3a*S*,4*S*,6a*R*)-hexahydro-2-oxo-1*H*-thiéno[3,4-*d*]imidazol-4-yl]pentanamido}hexanoyl)-L-arginyl-L-glutaminyl-L-prolyl-L-lysyl-L-isoleucyl-L-tryptophyl-L-phénylalanyl-L-prolyl-L-asparaginyl-L-arginyl-L-arginyl-L-lysyl-L-prolyl-L-tryptophyl-L-lysyl-L-lysyl-L-arginyl-L-prolyl-L-arginyl-L-prolyl-L-α-aspartyl-L-α-aspartyl-L-leucyl-L-α-glutamyl-L-isoleucine

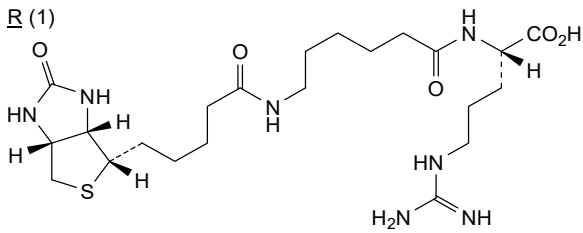
zifogaptida — N^2-(6-{5-[(3a*S*,4*S*,6a*R*)-2-oxohexahidro-1*H*-tieno[3,4-*d*]imidazol-4-il]pentanamido}hexanoil)-L-arginil-L-glutaminil-L-prolil-L-lisil-L-isoleucil-L-triptofil-L-fenilalanil-L-prolil-L-asparaginil-L-arginil-L-arginil-L-lisil-L-prolil-L-triptofil-L-lisil-L-lisil-L-arginil-L-prolil-L-arginil-L-prolil-L-α-aspartil-L-α-aspartil-L-leucil-L-α-glutamil-L-isoleucina

$C_{166}H_{263}N_{51}O_{37}S$

RQPKIWFPNR RKPWKKRPRP DDLEI 25

Modified residue / Résidu modifié / Resto modificado

R (1)



zirconium (^{89}Zr) girentuximabum senvedoxamum #

zirconium (^{89}Zr) girentuximab senvedoxam

immunoglobulin G1-kappa, anti-[*Homo sapiens* carbonic anhydrase 9 (CA9, carbonic anhydrase IX, CAIX, MN, G250)], chimeric monoclonal antibody; conjugated on L-lysine residues to zirconium (^{89}Zr) radiolabelled *senvedoxam*, with an average ratio of 1 to 1.5;
H-gamma1 heavy chain chimeric (1-449) [VH (*Mus musculus* IGHV5-6-2*01 (94.9%) -(IGHD) -IGHJ4*01 (88.2%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (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 L-kappa light chain chimeric (1'-214') [V-KAPPA (*Mus musculus* IGKV6-13*01 (93.7%) -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 (228-228":231-231")-bisdisulfide, produced in the mouse myeloma cell line P3x63Ag8.653, glycoform alfa; substituted at the N^6 nitrogen atoms of an average of 1.5 lysine residues, among which 449, with 3,14,25-trihydroxy-2,10,13,21,24,32-hexaoxo-3,9,14,20,25,31-hexaazapentatriacontan-35-oyl (*senvedoxam*) groups and converted to (^{89}Zr) zirconium (4+) chelate complex salts

zirconium (^{89}Zr) girentuximab senvédoxam

immunoglobuline G1-kappa, anti-[*Homo sapiens* anhydrase carbonique 9 (CA9, anhydrase carbonique IX, CAIX, MN, G250)], anticorps monoclonal chimérique; conjugué sur les résidus L-lysine au *senvédoxam* radiomarqué au zirconium (^{89}Zr), avec un ratio moyen de 1 à 1,5;
chaîne lourde H-gamma1 chimérique (1-449) [VH (*Mus musculus* IGHV5-6-2*01 (94.9%) -(IGHD) -IGHJ4*01 (88.2%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (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 L-kappa chimérique (1'-214') [V-KAPPA (*Mus musculus* IGKV6-13*01 (93.7%) -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 (228-228":231-231")- bisdisulfure, produit dans la lignée cellulaire de myélome de souris P3x63Ag8.653, glycoforme alfa; substitué en N^6 sur une moyenne de 1,5 de résidus lysine, parmi lesquels celui en position 449, avec des groupes 3,14,25-trihydroxy-2,10,13,21,24,32-hexaoxo-3,9,14,20,25,31-hexaazapentatriacontan-35-oyle (*senvédoxam*) et convertis en sels complexes de chélate de (^{89}Zr) zirconium (4+)

zirconio (^{89}Zr) girentuximab senvedoxam

inmunoglobulina G1-kappa, anti-[*Homo sapiens* anhidrasa carbónica 9 (CA9, anhidrasa carbónica IX, CAIX, MN, G250)], anticuerpo monoclonal quimérico; conjugado en los restos L-lisina al *senvedoxam* radiomarcado con zirconio (^{89}Zr), con un promedio de 1 a 1,5;
cadena pesada H-gamma1 quimérica (1-449) [VH (*Mus musculus* IGHV5-6-2*01 (94.9%) -(IGHD) -IGHJ4*01 (88.2%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (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')- disulfureo con la cadena ligera L-kappa quimérica (1'-214') [V-KAPPA (*Mus musculus* IGKV6-13*01 (93.7%) -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 (228-228":231-231")-bisdisulfuro, producido en la línea celular de mieloma de ratón P3x63Ag8.653, forma glicosilada alfa; sustituido en los N^6 de 1,5 restos lysina, por término medio, incluido el de la posición 449, con grupos 3,14,25-trihidroxi-2,10,13,21,24,32-hexaoxo-3,9,14,20,25,31-hexaazapentatriacontan-35-oilo (*senvedoxam*) y convertido en sales complejas de quelato de zirconio (^{89}Zr) (4+)

Heavy chain / Chaîne lourde / Cadena pesada

```
DVKLVESGGG LVKLGGSLKL SCAASGFTFS NYYMSWVRQT PEKRLELVAA  50
INSDGGITYY LDTVKGRFTI SRDNAKNTLY LQMSSLKSED TALFYCARHR 100
SGYFSMDYWG QGTSVTVSSA 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
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Light chain / Chaîne légère / Cadena ligera

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DIVMTQSQRF MSTTVGDRVS ITCKASQNVV SAVAWYQQKP GQSPKLLIYS  50
ASNRYTGVPD RFTGSGSGTD FTLTISNMQS EDLADFFCQQ YSNYPWTFGG 100
GTKLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Post-translational modifications

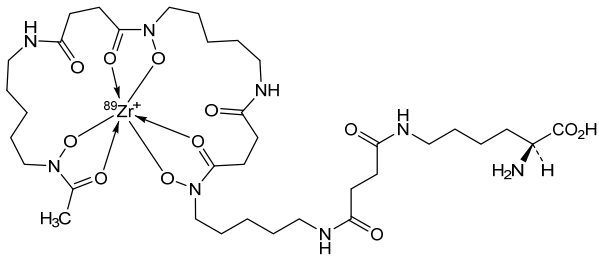
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

Intra-H (C23-C104) 22-96 146-202 263-323 369-427
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"

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

Potential modified residues / résidus modifiés potentiels / restos modificados potenciales*
K (449, 449")
*(*senvedoxam*:mAb ~ 1.5:1)



zodasiranum
zodasiran

all-P-ambo-3'-*O*-[({(1*s*,4*s*)-4-[(3*S*,8*S*)-17-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]-3,8-bis[(2-{2-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]ethoxy}ethyl)carbamoyl]-6,11-dioxo-15-oxa-2,7,12-triazaheptadecan-1-oyl]cyclohexyl}oxy)(sulfanyl)phosphoryl]-1'-de(6-amino-9*H*-purin-9-yl)-2'-deoxy-*P*-thioadenylyl-(5'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-deoxy-2'-fluorouridylyl-(3'→5')-2'-deoxy-2'-fluoroadenylyl-(3'→5')-2'-deoxy-2'-fluorouridylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methyl-*P*-thioadenylyl-(3'→3')-1'-de(6-amino-9*H*-purin-9-yl)-2'-deoxyadenosine

duplex with *all-P-ambo*-2'-*O*-methyl-*P*-thiocytidylyl-(5'→3')-2'-deoxy-2'-fluoroguanylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-deoxy-2'-fluoroguanylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-deoxy-2'-fluorouridylyl-(5'→3')-2'-*O*-methylguanylyl-(5'→3')-2'-deoxy-2'-fluorouridylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-deoxy-2'-fluorouridylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-deoxy-2'-fluoroadenylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-deoxy-2'-fluorocytidylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-deoxy-2'-fluoroadenylyl-(5'→3')-2'-*O*-methylguanylyl-(5'→3')-2'-deoxy-2'-fluoro-*P*-thiouridylyl-(5'→3')-2'-*O*-methyl-*P*-thiocytidylyl-(5'→3')-2'-deoxy-2'-fluoro-*P*-thioadenylyl-(5'→3')-2'-*O*-methyluridine

zodasiran

tout-P-ambo-3′-*O*-[({(1*s*,4*s*)-4-[(3*S*,8*S*)-17-[(2-acétamido-2-désoxy-β-D-galactopyranosyl)oxy]-3,8-bis[(2-{2-[(2-acétamido-2-désoxy-β-D-galactopyranosyl)oxy]éthoxy}éthyl)carbamoyl]-6,11-dioxo-15-oxa-2,7,12-triazaheptadécan-1-oyl]cyclohexyl}oxy)(sulfanyl)phosphoryl]-1'-dés(6-amino-9*H*-purin-9-yl)-2'-désoxy-*P*-thioadénylyl-(5'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyladenylyl-(3'→5')-2'-*O*-méthyladenylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-désoxy-2'-fluorouridylyl-(3'→5')-2'-désoxy-2'-fluoroadénylyl-(3'→5')-2'-désoxy-2'-fluorouridylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthyl-*P*-thioadénylyl-(3'→3')-1'-dés(6-amino-9*H*-purin-9-yl)-2'-désoxyadénosine
duplex avec *tout-P-ambo*-2'-*O*-méthyl-*P*-thiocytidylyl-(5'→3')-2'-désoxy-2'-fluoroguanylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-désoxy-2'-fluoroguanylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-désoxy-2'-fluorouridylyl-(5'→3')-2'-*O*-méthylguanylyl-(5'→3')-2'-désoxy-2'-fluorouridylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-désoxy-2'-fluorouridylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-désoxy-2'-fluoroadénylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-désoxy-2'-fluorocytidylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-désoxy-2'-fluoroadénylyl-(5'→3')-2'-*O*-méthylguanylyl-(5'→3')-2'-désoxy-2'-fluoro-*P*-thiouridylyl-(5'→3')-2'-*O*-méthyl-*P*-thiocytidylyl-(5'→3')-2'-désoxy-2'-fluoro-*P*-thioadénylyl-(5'→3')-2'-*O*-méthyluridine

zodasirán

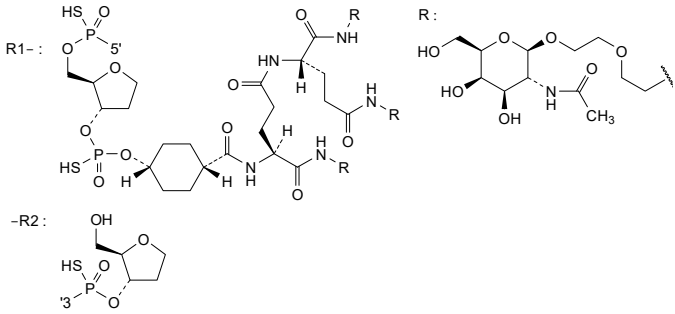
todo-P-ambo-3′-*O*-[({(1*s*,4*s*)-4-[(3*S*,8*S*)-17-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]-3,8-bis[(2-{2-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]etoxi}etil)carbamoil]-6,11-dioxo-15-oxa-2,7,12-triazaheptadecan-1-oil]ciclohexil}oxi)(sulfanil)fosforil]-1'-des(6-amino-9*H*-purin-9-il)-2'-desoxi-*P*-tioadenilil-(5'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-desoxi-2'-fluorouridilil-(3'→5')-2'-desoxi-2'-fluoroadenilil-(3'→5')-2'-desoxi-2'-fluorouridilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metil-*P*-tioadenilil-(3'→3')-1'-des(6-amino-9*H*-purin-9-il)-2'-desoxiadenosina
dúplex con *todo-P-ambo*-2'-*O*-metil-*P*-tiocitidilil-(5'→3')-2'-desoxi-2'-fluoroguanilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-desoxi-2'-fluoroguanilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-desoxi-2'-fluorouridilil-(5'→3')-2'-*O*-metilguanilil-(5'→3')-2'-desoxi-2'-fluorouridilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-desoxi-2'-fluorouridilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-desoxi-2'-fluoroadenilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-desoxi-2'-fluorocitidilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-desoxi-2'-fluoroadenilil-(5'→3')-2'-*O*-metilguanilil-(5'→3')-2'-desoxi-2'-fluoro-*P*-tiouridilil-(5'→3')-2'-*O*-metil-*P*-tiocitidilil-(5'→3')-2'-desoxi-2'-fluoro-*P*-tioadenilil-(5'→3')-2'-*O*-metiluridina

$C_{491}H_{646}F_{13}N_{162}O_{309}P_{43}S_7$

(3'-5')R1–*G*–*C*–*U*–*C*–*A*–*A*–*C*–*A*–U–A–U–*U*–*U*–*G*–*A*–*U*–*C*–*A*–*G*–*U*–*A*–R2

(5'-3')*C*=G–*A*–G–*U*–U–*G*–U–*A*–U–*A*–A–*A*–C–*U*–A–*G*–U=*C*=A=*U*

N : A,C,G,U
N : 2'-*O*-methyl-N / 2'-*O*-méthyl-N / 2'-*O*-metil-N
N : 2'-deoxy-2'-fluoro-N / 2'-désoxy-2'-fluoro-N / 2'-desoxi-2'-fluoro-N
– : –PO(OH)– = : –PO(SH)–



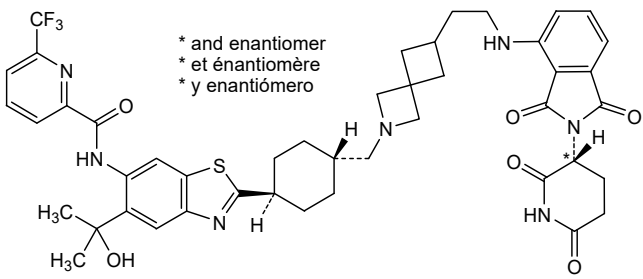
zomiradomidum

zomiradomide — *rac-N*-[2[1],2[4]-*trans*-(9[3]*R*)-1[5]-(2-hydroxypropan-2-yl)-8[1],8[3],9[2],9[6]-tetraoxo-8[1],8[3]-dihydro-4[2],7-diaza-1(2)-[1,3]benzothiazola-8(4,2)-isoindola-9(3)-piperidina-4(2,6)-spiro[3.3]heptana-2(1,4)-cyclohexananonaphan-1[6]-yl]-6-(trifluoromethyl)pyridine-2-carboxamide

zomiradomide — *rac-N*-[2[1],2[4]-*trans*-(9[3]*R*)-1[5]-(2-hydroxypropan-2-yl)-8[1],8[3],9[2],9[6]-tétraoxo-8[1],8[3]-dihydro-4[2],7-diaza-1(2)-[1,3]benzothiazola-8(4,2)-isoindola-9(3)-pipéridina-4(2,6)-spiro[3.3]heptana-2(1,4)-cyclohexananonaphan-1[6]-yl]-6-(trifluorométhyl)pyridine-2-carboxamide

zomiradomida — *rac-N*-[2[1],2[4]-*trans*-(9[3]*R*)-1[5]-(2-hidroxipropan-2-il)-8[1],8[3],9[2],9[6]-tetraoxo-8[1],8[3]-dihidro-4[2],7-diaza-1(2)-[1,3]benzotiazola-8(4,2)-isoindola-9(3)-piperidina-4(2,6)-espiro[3.3]heptana-2(1,4)-ciclohexananonafan-1[6]-il]-6-(trifluorometil)piridina-2-carboxamida

$C_{45}H_{48}F_3N_7O_6S$



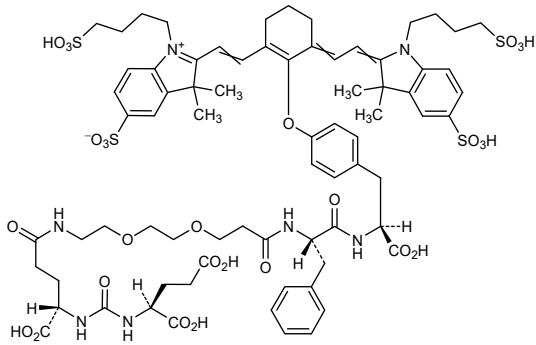
zopapogenum imadenovecum #

zopapogene imadenovec	replication-deficient gorilla adenovirus vector (strain GC46) encoding human papillomavirus (HPV) type 6 and type 11 antigens comprising 11 epitopes derived from regions of the E2, E4, E6, and E7 proteins under control of a human cytomegalovirus (CMV) promoter and terminated with a 3' untranslated region and a simian virus 40 (SV40) polyadenylation signal
zopapogène imadénovec	vecteur d'adénovirus de gorille à réplication déficiente (souche GC46) codant les antigènes des papillomavirus humains (HPV) de type 6 et de type 11 comprenant 11 épitopes dérivés des régions des protéines E2, E4, E6 et E7 sous le contrôle d'un promoteur du cytomégalovirus (CMV) humain et se terminant par un signal de polyadénylation du virus simien (SV40)
zopapogén imadenovec	vector de adenovirus de gorila deficiente en replicación (cepa GC46) que codifica los antígenos tipo 6 y tipo 11 del virus del papiloma humano (VPH) que contienen 11 epítopos derivados de regiones de las proteínas E2, E4, E6 y E7 bajo el control de un promotor del citomegalovirus (CMV) humano y se termina con una señal de poliadenilación del virus simio 40 (SV40)

zopocianinum

zopocianine	*N*-{[(1*S*)-1,3-dicarboxypropyl]carbamoyl}-L-γ-glutamyl-3-[2-(2-aminoethoxy)ethoxy]propanoyl-L-phenylalanyl-*O*-[(6Ξ)-2-{(1Ξ)-2-[3,3-dimethyl-1-(4-sulfobutyl)-5-sulfonato-3*H*-indol-1-ium-2-yl]ethen-1-yl}-6-{(2Ξ)-2-[3,3-dimethyl-5-sulfo-1-(4-sulfobutyl)-1,3-dihydro-2*H*-indol-2-ylidene]ethylidene}cyclohex-1-en-1-yl]-L-tyrosine
zopocianine	*N*-{[(1*S*)-1,3-dicarboxypropyl]carbamoyl}-L-γ-glutamyl-3-[2-(2-aminoéthoxy)éthoxy]propanoyl-L-phénylalanyl-*O*-[(6Ξ)-2-{(1Ξ)-2-[3,3-dimethyl-1-(4-sulfobutyl)-5-sulfonato-3*H*-indol-1-ium-2-yl]éthén-1-yl}-6-{(2Ξ)-2-[3,3-diméthyl-5-sulfo-1-(4-sulfobutyl)-1,3-dihydro-2*H*-indol-2-ylidène]éthylidène}cyclohex-1-én-1-yl]-L-tyrosine
zopocianina	*N*-{[(1*S*)-1,3-dicarboxipropil]carbamoil}-L-γ-glutamil-3-[2-(2-aminoetoxi)etoxi]propanoil-L-fenilalanil-*O*-[(6Ξ)-2-{(1Ξ)-2-[3,3-dimetil-1-(4-sulfobutil)-5-sulfonato-3*H*-indol-1-io-2-il]eten-1-il}-6-{(2Ξ)-2-[3,3-dimetil-5-sulfo-1-(4-sulfobutil)-1,3-dihidro-2*H*-indol-2-ilideno]etilideno}ciclohex-1-en-1-il]-L-tirosina

$C_{74}H_{93}N_7O_{27}S_4$



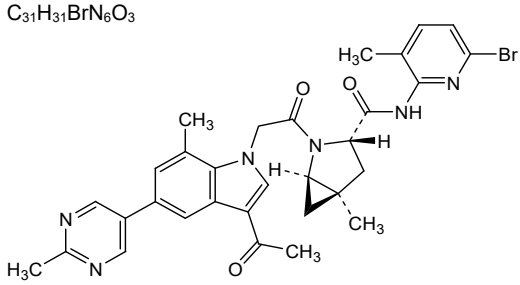
zoracopanum

zoracopan (1*R*,3*S*,5*R*)-2-{[3-acetyl-7-methyl-5-(2-methylpyrimidin-5-yl)-1*H*-indol-1-yl]acetyl}-*N*-(6-bromo-3-methylpyridin-2-yl)-5-methyl-2-azabicyclo[3.1.0]hexane-3-carboxamide

zoracopan (1*R*,3*S*,5*R*)-2-{[3-acétyl-7-méthyl-5-(2-méthylpyrimidin-5-yl)-1*H*-indol-1-yl]acétyl}-*N*-(6-bromo-3-méthylpyridin-2-yl)-5-méthyl-2-azabicyclo[3.1.0]hexane-3-carboxamide

zoracopán (1*R*,3*S*,5*R*)-2-{[3-acetil-7-metil-5-(2-metilpirimidin-5-il)-1*H*-indol-1-il]acetil}-*N*-(6-bromo-3-metilpiridin-2-il)-5-metil-2-azabiciclo[3.1.0]hexano-3-carboxamida

$C_{31}H_{31}BrN_6O_3$



zubotamigum #

zubotamig immunoglobulin (H-gamma1_L-kappa)_(H-gamma1_L-lambda2), anti-[*Homo sapiens* VTCN1 (V-set domain containing T cell activation inhibitor 1, B7 family member H4, B7H4, B7-H4) and anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], bispecific; H-gamma1 heavy chain anti-VTCN1(1-446) [VH (*Homo sapiens* IGHV4-34*01 (95.9%) -(IGHD) -IGHJ5*01 (100%), CDR-IMGT [8.7.11] (26-33.51-57.96-106)) (1-117)-*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v41 CH2 F1.3, E1.2, G1v66 CH2 A27, G1v82-2 CH3 R88 (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 K2>del (446)) (118-446)], (220-214')-disulfide with L-kappa light chain(1'-214') [V-KAPPA (*Homo sapiens* IGKV1-17*01 (98.9%) -IGKJ1*01 (90.9%) K123>T (103'), 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')];

	H-gamma1 heavy chain anti-CD3E(1"-454") [VH Musmus/Homsap (*Mus musculus* IGHV10-1*02 (93.9%) -(IGHD) -IGHJ3*01 (93.3%) A128>S (125")/*Homo sapiens* IGHV3-72*01 (81.0%) -(IGHD) -IGHJ6*01 (90.9%) T123>L (120"), CDR-IMGT [8.10.16] (26"-33".51"-60".99"-114")) (1"-125")-*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v41 CH2 F1.3, E1.2, G1v66 CH2 A27, G1v82-1 CH3 L85.1 (CH1 R120 (222") (126"-223"), hinge 1-15 (224"-238"), CH2 L1.3>F (242"), L1.2>E (243"), D27>A (273") (239"-348"), CH3 E12 (364"), M14 (366"), F85.1>L (413") (349"-453"), CHS K2>del (454")) (126"-454")], (228"-214"')-disulfide with L-lambda2 light chain (1"'-215"') [V-LAMBDA Musmus/Homsap (*Mus musculus* IGLV1*01 (83.3%) -IGLJ1*01 (100%)/*Homo sapiens* IGLV8-61*01 (70.8%) -IGLJ3*02 (100%), CDR-IMGT [9.3.9] (26"'-34"'.52"'-54"'.91"'"-99"') (1"'-109"') -*Homo sapiens* IGLC2*01 (100%) (110"'-215"')]; dimer (226-234":229-237")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1SV, glycoform alfa
zubotamig	immunoglobuline (H-gamma1_L-kappa)_(H-gamma1_L-lambda2), anti-[*Homo sapiens* VTCN1 (inhibiteur 1 de l'activation des cellules T contenant un domaine V-like, membre H4 de la famille B7, B7-H4, B7H4)] et anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], bispécifique; chaîne lourde H-gamma1 anti-VTCN1(1-446) [VH (*Homo sapiens* IGHV4-34*01 (95.9%) -(IGHD) -IGHJ5*01 (100%), CDR-IMGT [8.7.11] (26-33.51-57.96-106)) (1-117)-*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v41 CH2 F1.3, E1.2, G1v66 CH2 A27, G1v82-2 CH3 R88 (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 K2>del (446)) (118-446)], (220-214')-disulfure avec la chaîne légère L-kappa (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-17*01 (98.9%) -IGKJ1*01 (90.9%) K123>T (103'), 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 H-gamma1 anti-CD3E(1"-454") [VH Musmus/Homsap (*Mus musculus* IGHV10-1*02 (93.9%) -(IGHD) -IGHJ3*01 (93.3%) A128>S (125")/*Homo sapiens* IGHV3-72*01 (81.0%) -(IGHD) -IGHJ6*01 (90.9%) T123>L (120"), CDR-IMGT [8.10.16] (26"-33".51"-60".99"-114")) (1"-125")-*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v41 CH2 F1.3, E1.2, G1v66 CH2 A27, G1v82-1 CH3 L85.1 (CH1 R120 (222") (126"-223"), charnière 1-15 (224"-238"), CH2 L1.3>F (242"), L1.2>E (243"), D27>A (273") (239"-348"), CH3 E12 (364"), M14 (366"), F85.1>L (413") (349"-453"), CHS K2>del (454")) (126"-454")], (228"-214"')-disulfure avec la chaîne légère

	L-lambda2 (1'''-215''') [V-LAMBDA Musmus/Homsap (*Mus musculus* IGLV1*01 (83.3%) -IGLJ1*01 (100%)/*Homo sapiens* IGLV8-61*01 (70.8%) -IGLJ3*02 (100%), CDR-IMGT [9.3.9] (26'''-34'''.52'''-54'''.91'''-99''') (1'''-109''') -*Homo sapiens* IGLC2*01 (100%) (110'''-215''')]; dimère (226-234'':229-237'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1SV, glycoforme alfa
zubotamig	inmunoglobulina (H-gamma1_L-kappa)_(H-gamma1_L-lambda2), anti-[*Homo sapiens* VTCN1 (inhibidor 1 de la activiación de las células T que contienen un dominio V-like, miembro H4 de la familia B7, B7-H4, B7H4)] y anti-[*Homo sapiens* CD3E (CD3 épsilon, Leu-4)], biespecífico; cadena pesada H-gamma1 anti-VTCN1(1-446) [VH (*Homo sapiens* IGHV4-34*01 (95.9%) -(IGHD) -IGHJ5*01 (100%), CDR-IMGT [8.7.11] (26-33.51-57.96-106)) (1-117)-*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v41 CH2 F1.3, E1.2, G1v66 CH2 A27, G1v82-2 CH3 R88 (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 K2>del (446)) (118-446)], (220-214')-disulfuro con la cadena ligera L-kappa (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-17*01 (98.9%) -IGKJ1*01 (90.9%) K123>T (103'), 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 H-gamma1 anti-CD3E(1''-454'') [VH Musmus/Homsap (*Mus musculus* IGHV10-1*02 (93.9%) -(IGHD) -IGHJ3*01 (93.3%) A128>S (125'')/*Homo sapiens* IGHV3-72*01 (81.0%) -(IGHD) -IGHJ6*01 (90.9%) T123>L (120''), CDR-IMGT [8.10.16] (26''-33''.51''-60''.99''-114'')) (1''-125'')-*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v41 CH2 F1.3, E1.2, G1v66 CH2 A27, G1v82-1 CH3 L85.1 (CH1 R120 (222'') (126''-223''), bisagra 1-15 (224''-238''), CH2 L1.3>F (242''), L1.2>E (243''), D27>A (273'') (239''-348''), CH3 E12 (364''), M14 (366''), F85.1>L (413'') (349''-453''), CHS K2>del (454'')) (126''-454'')], (228''-214''')-disulfuro con la cadena ligera L-lambda2 (1'''-215''') [V-LAMBDA Musmus/Homsap (*Mus musculus* IGLV1*01 (83.3%) -IGLJ1*01 (100%)/*Homo sapiens* IGLV8-61*01 (70.8%) -IGLJ3*02 (100%), CDR-IMGT [9.3.9] (26'''-34'''.52'''-54'''.91'''-99''') (1'''-109''') -*Homo sapiens* IGLC2*01 (100%) (110'''-215''')]; dímero (226-234'':229-237'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1SV, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada : H-gamma1 (H) anti-VTCN1

```
QVQLQQWGAG LLKPSETLSL TCAVYGGSFS GYYWSWIRQP PGKGLEWIGE  50
ISHSGSTNYN PSLKSRVTIS IDTSKNQFSL KLTSVTAADT AVFYCARGLF 100
NWNFDSWGQG 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
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Light chain / Chaîne légère / Cadena ligera : L-kappa (L') anti-VTCN1

```
DIQMTQSPSS LSASVGDRVT ITCRASQGIR NDLGWYQQKP GKAPKRLIYG  50
ASSLQSGVPS RFSGSGSGTE FTLTISSLQP EDFATYYCLQ HNSYPRTFGQ 100
GTTVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Heavy chain / Chaîne lourde / Cadena pesada : H-gamma1 (H'') anti-CD3E

```
EVKLVESGGG LVQPGGSLRL SCAASGFTFN TYAMNWVRQA PGKGLEWVAR  50
IRSKYNNYAT YYADSVKDRF TISRDDSKSS LYLQMNNLKT EDTAMYYCVR 100
GGNFGNSYVS WFAYWGQGTL VTVSSASTKG PSVFPLAPSS KSTSGGTAAL 150
GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL SSVVTVPSSS 200
LGTQTYICNV NHKPSNTKVD KRVEPKSCDK THTCPPCPAP EFEGGPSVFL 250
FPPKPKDTLM ISRTPEVTCV VVAVSHEDPE VKFNWYVDGV EVHNAKTKPR 300
EEQYNSTYRV VSVLTVLHQD WLNGKEYKCK VSNKALPAPI EKTISKAKGQ 350
PREPQVYTLP PSREEMTKNQ VSLTCLVKGF YPSDIAVEWE SNGQPENNYK 400
TTPPVLDSDG SFLLYSKLTV DKSRWQQGNV FSCSVMHEAL HNHYTQKSLS 450
LSPG                                                   454
```

Light chain / Chaîne légère / Cadena ligera : L-lambda2 (L''') anti-CD3E

```
QAVVTQEPSF SVSPGGTVTL TCRSSTGAVT TSNYANWVQQ TPGQAFRGLI  50
GGTNKRAPGV PARFSGSLIG DKAALTITGA QADDESIYFC ALWYSNLWVF 100
GGGTKLTVLG QPKAAPSVTL FPPSSEELQA NKATLVCLIS DFYPGAVTVA 150
WKADSSPVKA GVETTTPSKQ SNNKYAASSY LSLTPEQWKS HRSYSCQVTH 200
EGSTVEKTVA PTECS                                       215
```

Post-translational modifications

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

Intra-H (C23-C104) 22-95 144-200 261-321 367-425
22''-98'' 152''-208'' 269''-329'' 375''-433''
Intra-L (C23-C104) 23'-88' 134'-194'
22'''-90''' 137'''-196'''
Inter-H-L (h 5-CL 126) 220-214' 228''-214'''
Inter-H-H (h 11, h 14) 226-234'' 229-237''

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)
H VH Q1: 1
L VL V-LAMBDA Q1: 1'''

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4: 297, 305''
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

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

Recommended International Nonproprietary Names (Rec. INN): List 31
Dénominations communes internationales recommandées (DCI Rec.): Liste 31
Denominaciones Comunes Internacionales Recomendadas (DCI Rec.): Lista 31
(WHO Drug Information, Vol. 5, No. 3, 1991)

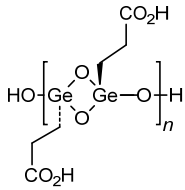
p.11 **propagermanium**

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

α-hydroxy-ω-hydropoly{[*trans*-2,4-bis(2-carboxyethyl)-1,3,2,4-dioxadigermetane-2,4-diyl]oxy}

α-hydroxy-ω-hydropoly{[*trans*-2,4-bis(2-carboxyéthyl)-1,3,2,4-dioxadigermétane-2,4-diyl]oxy}

α-hidroxi-ω-hidropoli{[*trans*-2,4-bis(2-carboxietil)-1,3,2,4-dioxadigermetano-2,4-diil]oxi}



Recommended International Non Proprietary Names (Rec. INN): List 82
Dénominations communes internationales recommandées (DCI Rec.): Liste 82
Denominaciones Comunes Internacionales Recomendadas (DCI Rec.): Lista 82
(WHO Drug Information, Vol. 33, No. 3, 2019)

p.686-687 **teclistamabum #**

teclistamab — *replace the chemical name by the following one*
téclistamab — *remplacer la description par la suivante*
teclistamab — *sustitúyase el nombre químico por el siguiente*

immunoglobulin G4-lambda, anti-[*Homo sapiens* TNFRSF17 (TNF receptor superfamily member 17, tumor necrosis factor receptor superfamily, member 17, B cell maturation antigen, BCMA, BCM, TNFRSF13A, CD269)] and anti-[*Homo sapiens* CD3 epsilon (CD3E, Leu-4)], monoclonal antibody, bispecific;
gamma4 heavy chain anti-TNFRSF17 (1-448) [VH (*Homo sapiens* IGHV4-39*01 (97.0%) -(IGHD) -IGHJ4*01 (100%)) [10.7.13] (1-121) -*Homo sapiens* IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10, G4v4 CH2 A1.3, A1.2 (CH1 (122-219), hinge S10>P (229) (220-231), CH2 L92 (310), **F**1.3>A (235), L1.2>A (236) (232-341), CH3 (342-446), CHS (447-448)) (122-448)], (135-213')-disulfide with lambda light chain anti-TNFRSF17 (1'-214') [V-LAMBDA (*Homo sapiens* IGLV3-21*02 (96.9%) -IGLJ2*01 (100.0%)) [6.3.11] (1'-108') -*Homo sapiens* IGLC2*01 (99.1%) A43>G (152) (109'-214')];

gamma4 heavy chain anti-CD3E (1''-452'') [VH (*Mus musculus* IGHV10-1*02 (89.8%) -(IGHD) -IGHJ3*01 (93.3%)/*Homo sapiens*

IGHV3-72*01 (88.0%) -(IGHD) -IGHJ6*01 (90.9%)) [8.10.16] (1''-125'') -*Homo sapiens* IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10, G4v4 CH2 A1.3, A1.2, G4v10 CH3 F85.1, K88 (CH1 (126-223), hinge S10>P (233) (224-235), CH2 L92 (314), **F**1.3>A (239), L1.2**>A** (240) (236-345), CH3 F85.1>L (410), R88>K (414) (346-450), CHS (451-452)) (126''-452'')], (139''-214''')-disulfide with lambda light chain anti-CD3 (1'''-215''') [V-LAMBDA (*Homo sapiens* IGLV7-43*01 (81.9%) -IGLJ3*02 (100%)) [9.3.9] (1'''-109''') -*Homo sapiens* IGLC2*01 (100%) (110'''-215''')]; dimer (**227-231'':230-234''**)-bisdisulfide

immunoglobuline G4-lambda, anti-[*Homo sapiens* TNFRSF17 (membre 17 de la superfamille des récepteurs du TNF, membre 17 de la superfamille des récepteurs du facteur de nécrose tumorale, antigène de maturation de cellule B, BCMA, BCM, TNFRSF13A, CD269)] et anti-[*Homo sapiens* CD3 epsilon (CD3E, Leu-4)], anticorps monoclonal, bispécifique;
chaîne lourde gamma4 anti-TNFRSF17(1-448) [VH (*Homo sapiens* IGHV4-39*01 (97.0%) -(IGHD) -IGHJ4*01 (100%)) [10.7.13] (1-121) -*Homo sapiens* IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10, G4v4 CH2 A1.3, A1.2 (CH1 (122-219), charnière S10>P (229) (220-231), CH2 L92 (310), **F**1.3>A (235), L1.2**>A** (236) (232-341), CH3 (342-446), CHS (447-448)) (122-448)], (135-213')-disulfure avec la chaîne légère lambda anti-TNFRSF17 (1'-214') [V-LAMBDA (*Homo sapiens* IGLV3-21*02 (96.9%) -IGLJ2*01 (100.0%)) [6.3.11] (1'-108') -*Homo sapiens* IGLC2*01 (99.1%) A43>G (152) (109'-214')];
chaîne lourde gamma4 anti-CD3E (1''-452'') [VH (*Mus musculus* IGHV10-1*02 (89.8%) -(IGHD) -IGHJ3*01 (93.3%)/*Homo sapiens* IGHV3-72*01 (88.0%) -(IGHD) -IGHJ6*01 (90.9%)) [8.10.16] (1''-125'') -*Homo sapiens* IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10, G4v4 CH2 A1.3, A1.2, G4v10 CH3 F85.1, K88 (CH1 (126-223), charnière S10>P (233) (224-235), CH2 L92 (314), **F**1.3>A (239), L1.2**>A** (240) (236-345), CH3 F85.1>L (410), R88>K (414) (346-450), CHS (451-452)) (126''-452'')], (139''-214''')-disulfure avec la chaîne légère lambda anti-CD3 (1'''-215''') [V-LAMBDA (*Homo sapiens* IGLV7-43*01 (81.9%) -IGLJ3*02 (100%)) [9.3.9] (1'''-109''') -*Homo sapiens* IGLC2*01 (100%) (110'''-215''')];
dimère (227-231'':230-234'')-bisdisulfure

inmunoglobulina G4-lambda, anti-[*Homo sapiens* TNFRSF17 (miembro 17 de la superfamilia de los receptores del TNF, miembro 17 de la superfamilia de los receptores del factor de necrosis tumoral, antígeno de maduración de la célula B, BCMA, BCM, TNFRSF13A, CD269)] y anti-[*Homo sapiens CD3 épsilon (CD3E, Leu-4)*], anticuerpo monoclonal, biespecífico;
cadena pesada gamma4 anti-TNFRSF17(1-448) [VH (*Homo sapiens* IGHV4-39*01 (97.0%) -(IGHD) -IGHJ4*01 (100%)) [10.7.13] (1-121) -*Homo sapiens* IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10, G4v4 CH2 A1.3, A1.2 (CH1 (122-219), bisagra S10>P (229) (220-231), CH2 L92 (310), **F**1.3>A (235), L1.2**>A** (236) (232-341), CH3 (342-446), CHS (447-448)) (122-448)], (135-213')-disulfuro con la cadena ligera lambda anti- TNFRSF17 (1'-214') [V-LAMBDA (*Homo sapiens* IGLV3-21*02 (96.9%) -IGLJ2*01 (100.0%)) [6.3.11] (1'-108') -*Homo sapiens* IGLC2*01 (99.1%) A43>G (152) (109'-214')];
cadena pesada gamma4 anti-CD3E (1''-452'') [VH (*Mus musculus* IGHV10-1*02 (89.8%) -(IGHD) -IGHJ3*01 (93.3%)/*Homo sapiens* IGHV3-72*01 (88.0%) -(IGHD) -IGHJ6*01 (90.9%)) [8.10.16] (1''-125'') -*Homo sapiens* IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10, G4v4 CH2 A1.3, A1.2, G4v10 CH3 F85.1, K88 (CH1 (126-223),

bisagra S10>P (233) (224-235), CH2 L92 (314), **F**1.3>A (239), L1.2**>A** (240) (236-345), CH3 F85.1>L (410), R88>K (414) (346-450), CHS (451-452)) (126''-452'')], (139''-214''')-disulfuro con la cadena ligera lambda anti-CD3 (1'''-215''') [V-LAMBDA (*Homo sapiens* IGLV7-43*01 (81.9%) -IGLJ3*02 (100%)) [9.3.9] (1'''-109''') -*Homo sapiens* IGLC2*01 (100%) (110'''-215''')]; dímero (227-231'':230-234'')-bisdisulfuro

Recommended International Non Proprietary Names (Rec. INN): List 88
Dénominations communes internationales recommandées (DCI Rec.): Liste 88
Denominaciones Comunes Internacionales Recomendadas (DCI Rec.): Lista 88
(WHO Drug Information, Vol. 36, No. 3, 2022)

p.858-859 **visugromabum #**
visugromab *replace the description by the following one*
visugromab *remplacer la description par la suivante*
visugromab *sustitúyase la descripción por la siguiente*

immunoglobulin G4-kappa, anti-[*Homo sapiens* GDF15 (growth differentiation factor 15, PLAB, MIC-1, PDF, MIC1, NAG-1, PTGFB)], monoclonal antibody;
gamma4 heavy chain (1-444) [VH (*Homo sapiens* IGHV2-5*02 (92.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [10.7.10] (26-35.53-59.98-107)) (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 K2>del (444)) (119-444)], (**132**-214')-disulfide with kappa light chain (1'-214') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV6-15*01 (82.1%) -IGKJ2*01 (100%)/*Homo sapiens* IGKV1-9*01 (76.8%) -IGKJ2*01 (91.7%) Q120>G (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 (224-224'':227-227'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1SV lacking the glutamine synthetase (GS-KO) gene, glycoform alfa

immunoglobuline G4-kappa, anti-[*Homo sapiens* GDF15 (facteur 15 de croissance et de différenciation, PLAB, MIC-1, PDF, MIC1, NAG-1, PTGFB)], anticorps monoclonal;
chaîne lourde gamma4 (1-444) [VH (*Homo sapiens* IGHV2-5*02 (92.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [10.7.10] (26-35.53-59.98-107)) (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 K2>del (444)) (119-444)], (**132**-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV6-15*01 (82.1%) -IGKJ2*01 (100%)/*Homo sapiens* IGKV1-9*01 (76.8%) -IGKJ2*01 (91.7%) Q120>G (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 (224-224'':227-227'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1SV ne présentant pas le gène de la glutamine synthétase (GS-KO), glycoforme alfa

inmunoglobulina G4-kappa, anti-[*Homo sapiens* GDF15 (factor 15 de crecimiento y de diferenciación, PLAB, MIC-1, PDF, MIC1, NAG-1, PTGFB)], anticuerpo monoclonal;
cadena pesada gamma4 (1-444) [VH (*Homo sapiens* IGHV2-5*02 (92.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [10.7.10] (26-35.53-59.98-107)) (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 K2>del (444)) (119-444)], (**132**-214')-disulfuro con la cadena ligera kappa (1'-214') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV6-15*01 (82.1%) -IGKJ2*01 (100%)/*Homo sapiens* IGKV1-9*01

(76.8%) -IGKJ2*01 (91.7%) Q120>G (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 (224-224":227-227")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1SV en ausencia del gen glutamina sintetasa (GS-KO), forma glicosilada alfa

Recommended International Non Proprietary Names (Rec. INN): List 91
Dénominations communes internationales recommandées (DCI Rec.): Liste 91
Denominaciones Comunes Internacionales Recomendadas (DCI Rec.): Lista 91
(WHO Drug Information, Vol. 38, No. 1, 2024)

p.5 **alisvetcelum**
-6 alisvetcel *replace the description by the following one*
alisvetcel *remplacer la description par la suivante*
alisvetcel *sustitúyase la descripción por la siguiente*

EN, lines 10-12 The final cells have a cobblestone morphology, express cellular surface markers CD90 (≥95%) and **CD44** (≥85%) and are negative for MHC class II expression (≤2%).

FR, lignes 11-14 Les cellules finales ont une morphologie en forme de pavé, expriment les marqueurs de surface cellulaire CD90 (≥95%) et **CD44** (≥85%) et sont négatives pour l'expression du CMH de classe II (≤2%).

ES, líneas 11-13 Las células finales tienen una morfología de empedrado, expresan los marcadores de superficie CD90 (≥95%) y **CD44** (≥85%) y son negativas para MHC de clase II (≤2%).

p. 80 **latovetcelum**
-81 latovetcel *replace the description by the following one*
latovetcel *remplacer la description par la suivante*
latovetcel *sustitúyase la descripción por la siguiente*

equine **xenogeneic** mesenchymal stem/stromal cells (MSCs) isolated from peripheral blood mononuclear cells (PBMCs) collected from donor horses. The MSCs are selected for by growing the PBMCs in media containing fetal bovine serum (FBS) and dexamethasone and then further expanded in media containing FBS. The final cells are characterized by their ~~stretched~~ spindle shaped morphology, and by expression of the cellular surface markers CD90 (≥95%) and **CD44** (≥85%) and absence of MHC class II expression (≤2%). The cells secrete prostaglandin E2 (PGE2) and interleukin 6 (IL-6) and can decrease proliferation (>85%) in a mixed lymphocyte reaction assay with concanavalin A (ConA)-stimulated canine PMBCs

cellules souches/stromales mésenchymateuses (CSM) **xénogéniques** équines isolées à partir de cellules mononucléaires de sang périphérique (PBMC) prélevées sur des chevaux donneurs. Les CSM sont sélectionnées en cultivant les PBMC dans un milieu contenant du sérum bovin fœtal (FBS) et de la dexaméthasone, puis en les développant dans un milieu contenant du FBS.
Les cellules finales sont caractérisées par leur morphologie fusiforme ~~étirée~~ et par l'expression des marqueurs de surface cellulaire CD90 (≥95%) et **CD44** (≥85%) et l'absence d'expression du CMH de classe II (≤2%). Les cellules sécrètent de la prostaglandine E2 (PGE2) et de l'interleukine 6 (IL-6) et peuvent diminuer la prolifération (>85%) dans un test de réaction lymphocytaire mixte avec des PMBC canins stimulés par la concanavaline A (ConA)

células madre/estromales mesenquimales (MSC) equinas, **xenogénicas**, aisladas de células mononucleares de sangre periférica (PBMCs) recogida de caballos donantes. Las MSCs se seleccionan mediante crecimiento de las PBMCs en medio que contiene suero bovino fetal (FBS) y dexametasona, y después se expanden en medio que contiene FBS.
Las células finales se caracterizan por su morfología en forma de huso ~~estirado~~ y por la expresión de los marcadores de superficie CD90 (≥95%) y **CD44** (≥85%) y ausencia de expresión de MHC de clase II (≤2%). Las células secretan prostaglandina E2 (PGE2) e interleuquina 6 (IL-6) y pueden disminuir la proliferación (>85%) en un ensayo de reacción cruzada de linfocitos con PBMCs caninos estimulados con concanavalina A (Con-A)

p.122-124

rapirosiranum
rapirosiran
rapirosiran
rapirosirán

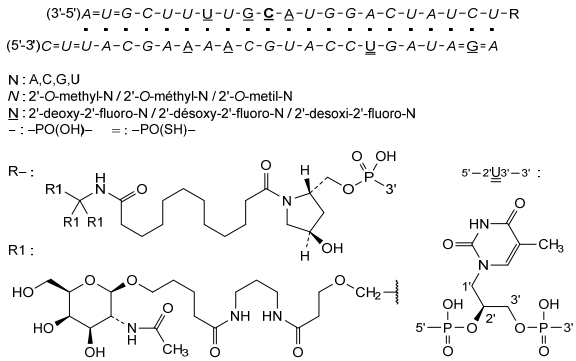
replace the chemical name and structure by the following ones
remplacer le nom chimique et la structure par les suivants
sustitúyase el nombre químico y la estructura por los siguientes

[(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-oxopropyl}methyl)-5,11,18-trioxo-14-oxa-6,10,17-triazanonacosan-29-oyl)-4-hydroxypyrrolidin-2-yl]methyl hydrogen *all-P-ambo*-2'-*O*-methyl-P-thioadenylyl-(3'→5')-2'-*O*-methyl-*P*-thiouridylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-deoxy-2'-fluorouridylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-deoxy-2'-fluoroguanylyl-(3'→5')-**2'-désoxy-2'-fluorocytidylyl**-(3'→5')-2'-deoxy-2'-fluoroadenylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyluridylate duplex with *all-P-ambo*-2'-*O*-methyl-*P*-thiocytidylyl-(5'→3')-2'-*O*-methyl-*P*-thiouridylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-*O*-methylguanylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-deoxy-2'-fluoroadenylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-deoxy-2'-fluoroadenylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-*O*-methylguanylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→2')-1-de-β-D-ribofuranosyl-1-[(2S)-2,3-dihydroxypropyl]-5-methyluridylyl-(3'→3')-2'-*O*-methylguanylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-*O*-methyl-*P*-thioadenylyl-(5'→3')-2'-deoxy-2'-fluoro-P-thioguanylyl-(5'→3')-2'-*O*-methyladenosine

tout-P-ambo-2'-*O*-méthyl-*P*-thioadénylyl-(3'→5')-2'-*O*-méthyl-*P*-thiouridylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-désoxy-2'-fluorouridylyl-(3'→5')-2'-*O*-méthyluridylyl-(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*-méthylguanylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-hydrogéno-2'-*O*-méthyluridylate 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-oxopropyl}méthyl)-5,11,18-trioxo-14-oxa-6,10,17-triazanonacosan-29-oyl)-4-

hydroxypyrrolidin-2-yl]méthyle
duplex avec *tout-P-ambo*-2'-*O*-méthyl-*P*-thiocytidylyl-(5'→3')-2'-*O*-méthyl-*P*-thiouridylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-*O*-méthylguanylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-désoxy-2'-fluoroadénylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-désoxy-2'-fluoroadénylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-*O*-méthylguanylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→2')-1-dé-β-D-ribofuranosyl-1-[(2*S*)-2,3-dihydroxypropyl]-5-méthyluridylyl-(3'→3')-2'-*O*-méthylguanylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-*O*-méthyl-*P*-thioadénylyl-(5'→3')-2'-désoxy-2'-fluoro-*P*-thioguanylyl-(5'→3')-2'-*O*-méthyladénosine

todo-P-ambo-2'-*O*-metil-*P*-tioadenilil-(3'→5')-2'-*O*-metil-*P*-tiouridilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-desoxi-2'-fluorouridilil-(3'→5')-2'-*O*-metiluridilil-(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*-metilguanilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-hidrógeno-2'-*O*-metiluridilato 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-oxopropil}metil)-5,11,18-trioxo-14-oxa-6,10,17-triazanonacosan-29-oil)-4-hidroxipirrolidin-2-il]metilo
dúplex con *todo-P-ambo*-2'-*O*-metil-*P*-tiocitidilil-(5'→3')-2'-*O*-metil-*P*-tiouridilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-*O*-metilguanill-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-desoxi-2'-fluoroadenilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-desoxi-2'-fluoroadenilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-*O*-metilguanilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-*O*-metilcitidilil-(5'→2')-1-des-β-D-ribofuranosil-1-[(2*S*)-2,3-dihidroxipropil]-5-metiluridilil-(3'→3')-2'-*O*-metilguanilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-*O*-metil-*P*-tioadenilil-(5'→3')-2'-desoxi-2'-fluoro-*P*-tioguanilil-(5'→3')-2'-*O*-metiladenosina



p.160-161 **tesrivetcelum**

tesrivetcel	*replace the description by the following one*
tesrivetcel	*remplacer la description par la suivante*
tesrivetcel	*sustitúyase la descripción por la siguiente*

EN, lines 9-12 The final cells are characterized by their stretched spindle shaped morphology, and by expression of the cellular surface

markers CD90 (≥95%) and **CD44** (≥85%) and absence of MHC class II expression (≤2%).

FR, lignes 11-14 — Les cellules finales sont caractérisées par leur morphologie fusiforme étirée, et par l'expression des marqueurs de surface cellulaire CD90 (≥95%) et **CD44** (≥85%) et l'absence d'expression du CMH de classe II (≤2%).

ES, líneas 11-14 — Las células finales se caracterizan por su morfología en forma de huso estirado y por la expresión de los marcadores de superficie CD90 (≥95%) y **CD44** (≥85%) y ausencia de expresión de MHC de clase II (≤2%).

p.206 **zapomeranum #**

zapomeran	*Please note that the MedNet file has been updated*
zapoméran	*Veuillez noter que le fichier MedNet a été mis à jour*
zapomerán	*Tenga en cuenta que se ha actualizado el archivo MedNet*

p.208 **elriterceptum #**

elritercept	*amend the structure as follows*
elritercept	*corriger la structure comme suit*
elritercept	*modificar la estructura de la siguiente manera*
at O-glycosylation sites only	O-glycosylation sites / Sites de O-glycosylation / Posiciones de O-glicosilación S97, S97', T108, T108', S109, S109', **T115, T115', T117, T117'**

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.