International Nonproprietary Names for Pharmaceutical Substances (INN)

RECOMMENDED International Nonproprietary Names: List 94

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 94

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 94

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*

abazistobartum #

abazistobart	immunoglobulin G4-kappa, anti-[*Homo sapiens* PDCD1 (programmed cell death 1, PD-1, PD1, CD279)], chimeric and humanized monoclonal antibody; H-gamma4 heavy chain chimeric (1-444) [VH Musmus/Homsap (*Mus musculus* IGHV5-9*02 (85.6%) -(IGHD) -IGHJ1*01 (86.7%) A120>Q (109), T123>L (112)/*Homo sapiens* IGHV3-23*04 (84.5%) -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, 12-G4v5 h P10 (CH1 (118-215), hinge 1-12 S10>P (225) (216-227), CH2 L92 (306) (228-337), CH3 (338-442), CHS (443-444)) (118-444)], (131-214')-disulfide with L-kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-11*01 (85.3%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dimer (223-223'':226-226'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, lacking the glutamine synthetase (GS-KO) gene, glycoform alfa
abazistobart	immunoglobuline G4-kappa, anti-[*Homo sapiens* PDCD1 (protéine 1 de mort cellulaire programmée, PD-1, PD1, CD279)], anticorps monoclonal chimérique et humanisé; chaîne lourde H-gamma4 chimérique (1-444) [VH Musmus/Homsap (*Mus musculus* IGHV5-9*02 (85.6%) -(IGHD) -IGHJ1*01 (86.7%) A120>Q (109), T123>L (112)/*Homo sapiens* IGHV3-23*04 (84.5%) -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92,12-G4v5 h P10 (CH1 (118-215), charnière 1-12 S10>P (225) (216-227), CH2 L92 (306) (228-337), CH3 (338-442), CHS (443-444)) (118-444)], (131-214')-disulfure avec la chaîne légère L-kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-11*01 (85.3%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dimère (223-223'':226-226'')-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
abazistobart	inmunoglobulina G4-kappa, anti-[*Homo sapiens* PDCD1 (proteína 1 de muerte celular programada, PD-1, PD1, CD279)], anticuerpo monoclonal quimérico y humanizado;

cadena pesada H-gamma4 quimérica (1-444) [VH Musmus/Homsap (*Mus musculus* IGHV5-9*02 (85.6%) -(IGHD) -IGHJ1*01 (86.7%) A120>Q (109), T123>L (112)/*Homo sapiens* IGHV3-23*04 (84.5%) -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92,12-G4v5 h P10 (CH1 (118-215), bisagra 1-12 S10>P (225) (216-227), CH2 L92 (306) (228-337), CH3 (338-442), CHS (443-444)) (118-444)], (131-214')-disulfuro con la cadena ligera L-kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-11*01 (85.3%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dímero (223-223'':226-226'')-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

```
EVKLVESGGG LVQPGGSLRL SCAASGFAFS SYDMSWVRQA PGKRLEWVAT  50
ISGGGRYTYY PDTVKGRFTI SRDNAKNSHY LQMNSLRAED TAVYFCASPY 100
GGYFDVWGQG TLVTVSSAST KGPSVFPLAP CSRSTSESTA ALGCLVKDYF 150
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTKTYTC 200
NVDHKPSNTK VDKRVESKYG PPCPPCPAPE FLGGPSVFLF PPKPKDTLMI 250
SRTPEVTCVV VDVSQEDPEV QFNWYVDGVE VHNAKTKPRE EQFNSTYRVV 300
SVLTVLHQDW LNGKEYKCKV SNKGLPSSIE KTISKAKGQP REPQVYTLPP 350
SQEEMTKNQV SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS 400
FFLYSRLTVD KSRWQEGNVF SCSVMHEALH NHYTQKSLSL SLGK        444
```

Light chain / Chaîne légère / Cadena ligera

```
EIVLTQSPAT LSLSPGERAT LSCRASQSIS NFLHWYQQKP GQAPRLLIKY  50
ASQSISGIPA RFSGSGSGTD FTLTISSLEP EDFAVYFCQQ SNSWPHTFGQ 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	258-318	364-422
	22''-96''	144''-200''	258''-318''	364''-422''
Intra-L (C23-C104)	23'-88'	134'-194'		
	23'''-88'''	134'''-194'''		
Inter-H-L (CH1 10-CL 126)	131-214'	131''-214'''		
Inter-H-H (h 8, h 11)	223-223''	226-226''		

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4: 294, 294''
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: 444, 444''

acinterferonum alfa

acinterferon alfa — human interferon α-14 (IFN-α-14, IFNA14, interferon α-H, interferon λ2-H), [N^{10}>G, N^{11}>S, R^{12}>K, M^{18}>L, R^{22}>G, R^{23}>K, P^{26}>L, M^{60}>L, M^{61}>I, N^{72}>E, T^{80}>G, E^{83}>D, Y^{86}>R, I^{87}>T, F^{90}>Y, Q^{91}>R, M^{93}>L, V^{100}>M, I^{101}>M, E^{114}>A, A^{146}>V, R^{164}>G]-variant, non-glycosylated, produced by *Escherichia coli*

acinterféron alfa — interféron α-14 humain (IFN-α-14, IFNA14, interféron α-H, interféron λ2-H), [N^{10}>G, N^{11}>S, R^{12}>K, M^{18}>L, R^{22}>G, R^{23}>K, P^{26}>L, M^{60}>L, M^{61}>I, N^{72}>E, T^{80}>G, E^{83}>D, Y^{86}>R, I^{87}>T, F^{90}>Y, Q^{91}>R, M^{93}>L, V^{100}>M, I^{101}>M, E^{114}>A, A^{146}>V, R^{164}>G]-variant, non-glycosylé, produit par *Escherichia coli*

acinterferón alfa — interferón α-14 humano (IFN-α-14, IFNA14, interferón α-H, interferón λ2-H), [N^{10}>G, N^{11}>S, R^{12}>K, M^{18}>L, R^{22}>G, R^{23}>K, P^{26}>L, M^{60}>L, M^{61}>I, N^{72}>E, T^{80}>G, E^{83}>D, Y^{86}>R, I^{87}>T, F^{90}>Y, Q^{91}>R, M^{93}>L, V^{100}>M, I^{101}>M, E^{114}>A, A^{146}>V, R^{164}>G]-variante, no glicosilado, producido por *Escherichia coli*

Sequence / Séquence / Secuencia

```
CNLSQTHSLG SKRTLMLLAQ MGKISLFSCL KDRHDFEFPQ EEFDGNQFQK    50
AQAISVLHEL IQQTFNLFST KESSAAWDEG LLDKFRTELY RQLNDLEACM   100
MQEVGVEETP LMNADSILAV KKYFQRITLY LMEKKYSPCA WEVVRVEIMR   150
SLSFSTNLQK RLRGKD                                        166
```

Mutations / Mutations / Mutaciónes

N^{10}>**G**, N^{11}>**S**, R^{12}>**K**, M^{18}>**L**, R^{22}>**G**, R^{23}>**K**, P^{26}>**L**, M^{60}>**L**, M^{61}>**I**, N^{72}>**E**, T^{80}>**G**, E^{83}>**D**, Y^{86}>**R**, I^{87}>**T**, F^{90}>**Y**, Q^{91}>**R**, M^{93}>**L**, V^{100}>**M**, I^{101}>**M**, E^{114}>**A**, A^{146}>**V**, R^{164}>**G**

Post-translational modifications

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

1-99 29-139

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

none / aucun / ninguna

actinium (^{225}Ac) zadavotidum guraxetanum

actinium (^{225}Ac) zadavotide guraxetan

hydrogen (*N*-{(4*R*)-4-carboxylato-κ*O*-4-[4,7,10-tris(carboxylato-κ*O*-methyl)-1,4,7,10-tetraazacyclododecan-1-yl-κ^4*N*^{1},*N*^{4},*N*^{7},*N*^{10}]butanoyl}-3-iodo-D-tyrosyl-D-phenylalanyl-*N*^{6}-{8-[*N*^{2}-(L-glutamocarbonyl)-*N*^{6}-L-lysino]-8-oxooctanoyl}-D-lysine)(^{225}Ac)actinate(1−)

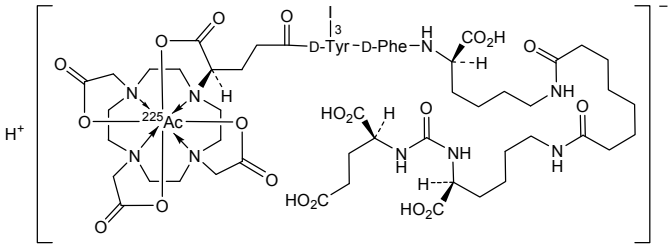
actinium (^{225}Ac) zadavotide guraxétan

hydrogéno(*N*-{(4*R*)-4-carboxylato-κ*O*-4-[4,7,10-tris(carboxylato-κ*O*-méthyl)-1,4,7,10-tétraazacyclododécan-1-yl-κ^4*N*^{1},*N*^{4},*N*^{7},*N*^{10}]butanoyl}-3-iodo-D-tyrosyl-D-phénylalanyl-*N*^{6}-{8-[*N*^{2}-(L-glutamocarbonyl)-*N*^{6}-L-lysino]-8-oxooctanoyl}-D-lysine)(^{225}Ac)actinate(1−)

actinio (^{225}Ac) zadavotida guraxetán

hidrógeno(*N*-{(4*R*)-4-carboxilato-κ*O*-4-[4,7,10-tris(carboxilato-κ*O*-metil)-1,4,7,10-tetraazaciclododecan-1-il-κ^4*N*^{1},*N*^{4},*N*^{7},*N*^{10}]butanoil}-3-iodo-D-tirosil-D-fenilalanil-*N*^{6}-{8-[*N*^{2}-(L-glutamocarbonil)-*N*^{6}-L-lisino]-8-oxooctanoil}-D-lisina)(^{225}Ac)actinato(1−)

$C_{63}H_{89}{}^{225}AcIN_{11}O_{23}$



adezkibartum #

adezkibart — immunoglobulin G1-lambda2, anti-[*Homo sapiens* FLT3LG (fms related receptor tyrosine kinase 3 ligand)], *Homo sapiens* monoclonal antibody;
H-gamma1 heavy chain *Homo sapiens* (1-449) [VH (*Homo sapiens* IGHV1-69*11 (89.7%) -(IGHD) -IGHJ5*01 (90.9%) L123>T (114), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, 6-G1v39 CH2 F1.3, E1.2, S116 (CH1 R120 (216) (120-217), hinge 1-15 (218-232), CH2 L1.3>F (236), L1.2>E (237), P116>S (333) (233-342), CH3 E12 (358), M14 (360) (343-447), CHS (448-449)) (120-449)], (222-216')-disulfide with L-lambda2 light chain *Homo sapiens* (1'-217') [V-LAMBDA (*Homo sapiens* IGLV6-57*01 (93.7%) -IGLJ2*01 (100%), CDR-IMGT [8.3.10] (26'-33'.51'-53'.92'-101')) (1'-111') -*Homo sapiens* IGLC2*01 (100%) (C-LAMBDA2) (112'-217')]; dimer (228-228'':231-231'')-bisdisulfide, produced in a cell line from Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, glycoform alfa

adezkibart — immunoglobuline G1-lambda2, anti-[*Homo sapiens* FLT3LG (ligand du récepteur tyrosine kinase 3 apparenté au fms)], anticorps monoclonal *Homo sapiens*;
chaîne lourde H-gamma1 *Homo sapiens* (1-449) [VH (*Homo sapiens* IGHV1-69*11 (89.7%) -(IGHD) -IGHJ5*01 (90.9%) L123>T (114), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, 6-G1v39 CH2 F1.3, E1.2, S116 (CH1 R120 (216) (120-217), charnière 1-15 (218-232), CH2 L1.3>F (236), L1.2>E (237), P116>S (333) (233-342), CH3 E12 (358), M14 (360) (343-447), CHS (448-449)) (120-449)], (222-216')-disulfure avec la chaîne légère L-lambda2 *Homo sapiens* (1'-217') [V-LAMBDA (*Homo sapiens* IGLV6-57*01 (93.7%) -IGLJ2*01 (100%), CDR-IMGT [8.3.10] (26'-33'.51'-53'.92'-101')) (1'-111') -*Homo sapiens* IGLC2*01 (100%) (C-LAMBDA2) (112'-217')]; dimère (228-228'':231-231'')-bisdisulfure, produit dans une lignée cellulaire des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1, glycoforme alfa

adezkibart — inmunoglobulina G1-lambda2, anti-[*Homo sapiens* FLT3LG (ligando del receptor tirosina kinasa 3 acoplado al fms)], anticuerpo monoclonal *Homo sapiens*;
cadena pesada H-gamma1 *Homo sapiens* (1-449) [VH (*Homo sapiens* IGHV1-69*11 (89.7%) -(IGHD) -IGHJ5*01 (90.9%) L123>T (114), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, 6-G1v39 CH2 F1.3, E1.2, S116 (CH1 R120 (216) (120-217), bisagra 1-15 (218-232), CH2 L1.3>F (236), L1.2>E (237), P116>S (333) (233-342), CH3 E12 (358), M14 (360) (343-447), CHS (448-449)) (120-449)], (222-216')-disulfuro con la cadena ligeraL-lambda2 *Homo sapiens* (1'-217') [V-LAMBDA (*Homo sapiens* IGLV6-57*01 (93.7%) -IGLJ2*01 (100%), CDR-IMGT [8.3.10] (26'-33'.51'-53'.92'-101')) (1'-111') -*Homo sapiens* IGLC2*01 (100%) (C-LAMBDA2) (112'-217')]; dímero (228-228'':231-231'')-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

```
QVQLVQSGAE VKKPGSSVKV SCKASGGTFS SYALSWVRQA PGQGLEWMGT  50
RPPTSRTASY AQKFQGRVTI TVDESTSTGY MELSSLRSED TAVYYCASND 100
FVYGSYRFWG QGTTVTVSSA STKGPSVFPL APSSKSTSGG TAALGCLVKD 150
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY 200
ICNVNHKPSN TKVDKRVEPK SCDKTHTCPP CPAPEFEGGP SVFLFPPKPK 250
DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS 300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PASIEKTISK AKGQPREPQV 350
YTLPPSREEM TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL 400
DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK  449
```

Light chain / Chaîne légère / Cadena ligera

```
NFMLTQPHSV SESPGKTVTI SCTRTSGNIA GYFVQWYQQR PGSSPTTVIY  50
EDYQRPSGVP DRFSGSIDSS SNSASLTISG LKTEDEADYY CQSYDDYRRA 100
AFGGGTKLTV LGQPKAAPSV TLFPPSSEEL QANKATLVCL ISDFYPGAVT 150
VAWKADSSPV KAGVETTTPS KQSNNKYAAS SYLSLTPEQW KSHRSYSCQV 200
THEGSTVEKT VAPTECS                                     217
```

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) 22'-91' 139'-198'
22'"-91'" 139'"-198'"

Inter-H-L (h 5-CL 126) 222-216' 222"-216'"

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

N-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: 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"

adimanebartum #

adimanebart

immunoglobulin G1-lambda2, anti-[*Homo sapiens* MUSK (muscle associated receptor tyrosine kinase)], humanized monoclonal antibody, agonist;
H-gamma1 heavy chain humanized (1-450) [VH (*Homo sapiens* IGHV3-23*01 (93.9%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1-121) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, 6-G1v14 CH2 A1.3, A1.2 (CH1 K120 (218) (122-219), hinge 1-15 (220-234), CH2 L1.3>A (238), L1.2>A (239) (235-344), CH3 D12 (360), L14 (362) (345-449), CHS K2>del (450)) (122-450)], (224-217')-disulfide with L-lambda2 light chain humanized (1'-218') [V-LAMBDA (*Homo sapiens* IGLV8-61*01 (89.7%) -IGLJ2*01 (100%), CDR-IMGT [9.3.12] (26'-34'.52'-54'.91'-102')) (1'-112') -*Homo sapiens* IGLC2*01 (100%) (C-LAMBDA2) (113'-218')]; dimer (230-230":233-233")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, lacking the glutamine synthetase (GS-KO) gene, glycoform alfa

adimanebart

immunoglobuline G1-lambda2, anti-[*Homo sapiens* MUSK (récepteur tyrosine kinase associée aux muscles)], anticorps monoclonal humanisé, agoniste;
chaîne lourde H-gamma1 humanisée (1-450) [VH (*Homo sapiens* IGHV3-23*01 (93.9%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1-121) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, 6-G1v14 CH2 A1.3, A1.2 (CH1 K120 (218) (122-219), charnière 1-15 (220-234), CH2 L1.3>A (238), L1.2>A (239) (235-344), CH3 D12 (360), L14 (362) (345-449), CHS K2>del (450)) (122-450)], (224-217')-disulfure avec la chaîne légère L-lambda2 humanisée (1'-218') [V-LAMBDA (*Homo sapiens* IGLV8-61*01 (89.7%) -IGLJ2*01 (100%), CDR-IMGT [9.3.12] (26'-34'.52'-54'.91'-102')) (1'-112') -*Homo sapiens* IGLC2*01 (100%) (C-LAMBDA2) (113'-218')]; dimère (230-230":233-233")-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

adimanebart

inmunoglobulina G1-lambda2, anti-[*Homo sapiens* MUSK (receptor tirosina kinasa asociada a los músculos)], anticuerpo monoclonal humanizado, agonista;
cadena pesada H-gamma1 humanizada (1-450) [VH (*Homo sapiens* IGHV3-23*01 (93.9%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1-121) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, 6-G1v14 CH2 A1.3, A1.2 (CH1 K120 (218) (122-219), bisagra 1-15 (220-234), CH2 L1.3>A (238), L1.2>A (239) (235-344), CH3 D12 (360), L14 (362) (345-449), CHS K2>del (450)) (122-450)], (224-217')-disulfuro con la cadena ligera L-lambda2 humanizada (1'-218') [V-LAMBDA (*Homo sapiens* IGLV8-61*01 (89.7%) -IGLJ2*01 (100%), CDR-IMGT [9.3.12] (26'-34'.52'-54'.91'-102')) (1'-112') -*Homo sapiens* IGLC2*01 (100%) (C-LAMBDA2) (113'-218')]; dímero (230-230":233-233")-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

```
EVQLLESGGG LVQPGGSLRL SCAASGFTFS DYGMSWVRQA PGKGLEWVSA  50
IPWSGGSTYY KESVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKRS 100
GRIAFGALDA WGQGTLVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200
TYICNVNHKP SNTKVDKKVE PKSCDKTHTC PPCPAPEAAG GPSVFLFPPK 250
PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY 300
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP 350
QVYTLPPSRD ELTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP 400
VLDSDGSFFL YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG 450
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Light chain / Chaîne légère / Cadena ligera

```
QTVVTQEPSF SVSPGGTVTL TCGLSSGSVT SSNYPDWYQQ TPGQAPRTLI  50
YSTDSRHSGV PDRFSGSILG NKAALTITGA QADDESDYYC GLYSYSGSKN 100
YVFGGGTKLT VLGQPKAAPS VTLFPPSSEE LQANKATLVC LISDFYPGAV 150
TVAWKADSSP VKAGVETTTP SKQSNNKYAA SSYLSLTPEQ WKSHRSYSCQ 200
VTHEGSTVEK TVAPTECS                                    218
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 148-204 265-325 371-429
22"-96" 148"-204" 265"-325" 371"-429"
Intra-L (C23-C104) 22'-90' 140'-199'
22'"-90'" 140'"-199'"
Inter-H-L (h 5-CL 126) 224-217' 224"-217'"
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)
L VL V-LAMBDA 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

agazisiranum

agazisiran

O-[(2*R*,3*S*)-2-(hydroxymethyl)oxolan-3-yl] hydrogen *all-P-ambo*-3'-*O*-(2-{[(1-{17-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]-3,6,9,12,15-pentaoxaheptadecan-1-yl}-1*H*-1,2,3-triazol-4-yl)methyl]amino}-2-oxoethyl)-2'-*O*-(2-{bis[(1-{17-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]-3,6,9,12,15-pentaoxaheptadecan-1-yl}-1*H*-1,2,3-triazol-4-yl)methyl]amino}-2-oxoethyl)-*P*-thiouridylyl-(5'→5')-2'-*O*-methyl-*P*-thioguanylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-deoxy-2'-fluorouridylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-deoxy-2'-fluoroadenylyl-(3'→5')-2'-deoxy-2'-fluorouridylyl-(3'→5')-2'-deoxy-2'-fluorocytidylyl-(3'→5')-2'-deoxy-2'-fluorouridylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylguanylyl-(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*-methyl-*P*-thiouridylyl-(3'→5')-2'-*O*-methyl-*P*-thio-3'-adenylate
duplex with *all-P-ambo*-2'-*O*-methyl-*P*-thiocytidylyl-(5'→3')-2'-*O*-methyl-*P*-thiocytidylyl-(5'→3')-2'-deoxy-2'-fluorouridylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-deoxy-2'-fluorocytidylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-deoxy-2'-fluorouridylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-deoxy-2'-fluoroadenylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-deoxy-2'-fluoroadenylyl-(5'→3')-2'-*O*-methylguanylyl-(5'→3')-2'-deoxy-2'-fluoroadenylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-deoxy-2'-fluorocytidylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-deoxy-2'-fluoroadenylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-deoxy-2'-fluoroadenylyl-(5'→3')-2'-*O*-methyl-*P*-thioguanylyl-(5'→3')-2'-deoxy-2'-fluoro-*P*-thioadenylyl-(5'→3')-2'-*O*-methyluridine

agazisiran

tout-P-ambo-3'-*O*-(2-{[(1-{17-[(2-acétamido-2-désoxy-β-D-galactopyranosyl)oxy]-3,6,9,12,15-pentaoxaheptadécan-1-yl}-1H-1,2,3-triazol-4-yl)méthyl]amino}-2-oxoéthyl)-2'-*O*-(2-{bis[(1-{17-[(2-acétamido-2-désoxy-β-D-galactopyranosyl)oxy]-3,6,9,12,15-pentaoxaheptadécan-1-yl}-1H-1,2,3-triazol-4-yl)méthyl]amino}-2-oxoéthyl)-*P*-thiouridylyl-(5'→5')-2'-*O*-méthyl-*P*-thioguanylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-désoxy-2'-fluorouridylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-désoxy-2'-fluoroadénylyl-(3'→5')-2'-désoxy-2'-fluorouridylyl-(3'→5')-2'-désoxy-2'-fluorocytidylyl-(3'→5')-2'-désoxy-2'-fluorouridylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyl-*P*-thiouridylyl-(3'→5')-hydrogéno-2'-*O*-méthyl-*P*-thio-3'-adénylate de *O*-[(2*R*,3*S*)-2-(hydroxyméthyl)oxolan-3-yle]
duplex avec *tout-P-ambo*-2'-*O*-méthyl-*P*-thiocytidylyl-(5'→3')-2'-*O*-méthyl-*P*-thiocytidylyl-(5'→3')-2'-désoxy-2'-fluorouridylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-désoxy-2'-fluorocytidylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-désoxy-2'-fluorouridylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-désoxy-2'-fluoroadénylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-désoxy-2'-fluoroadénylyl-(5'→3')-2'-*O*-méthylguanylyl-(5'→3')-2'-désoxy-2'-fluoroadénylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-désoxy-2'-fluorocytidylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-désoxy-2'-fluoroadénylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-désoxy-2'-fluoroadénylyl-(5'→3')-2'-*O*-méthyl-*P*-thioguanylyl-(5'→3')-2'-désoxy-2'-fluoro-*P*-thioadénylyl-(5'→3')-2'-*O*-méthyluridine

agazisirán

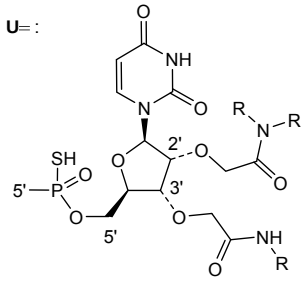
todo-P-ambo-3'-*O*-(2-{[(1-{17-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]-3,6,9,12,15-pentaoxaheptadecan-1-il}-1H-1,2,3-triazol-4-il)metil]amino}-2-oxoetil)-2'-*O*-(2-{bis[(1-{17-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]-3,6,9,12,15-pentaoxaheptadecan-1-il}-1H-1,2,3-triazol-4-il)metil]amino}-2-oxoetil)-*P*-tiouridilil-(5'→5')-2'-*O*-metil-*P*-tioguanilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-desoxi-2'-fluorouridilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-desoxi-2'-fluoroadenilil-(3'→5')-2'-desoxi-2'-fluorouridilil-(3'→5')-2'-desoxi-2'-fluorocitidilil-(3'→5')-2'-desoxi-2'-fluorouridilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metil-*P*-tiouridilil-(3'→5')-hidrógeno-2'-*O*-metil-*P*-tio-3'-adenilato de *O*-[(2*R*,3*S*)-2-(hidroximetil)oxolan-3-ilo]
dúplex con *todo-P-ambo*-2'-*O*-metil-*P*-tiocitidilil-(5'→3')-2'-*O*-metil-*P*-tiocitidilil-(5'→3')-2'-desoxi-2'-fluorouridilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-desoxi-2'-fluorocitidilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-desoxi-2'-fluorouridilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-desoxi-2'-fluoroadenilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-desoxi-2'-fluoroadenilil-(5'→3')-2'-*O*-metilguanilil-(5'→3')-2'-desoxi-2'-fluoroadenilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-desoxi-2'-fluorocitidilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-desoxi-2'-fluoroadenilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-desoxi-2'-fluoroadenilil-(5'→3')-2'-*O*-metil-*P*-tioguanilil-(5'→3')-2'-desoxi-2'-fluoro-*P*-tioadenilil-(5'→3')-2'-*O*-metiluridina

$C_{534}H_{706}F_{15}N_{179}O_{329}P_{44}S_8$

(3'-5')**U**=*G*-*G*-*A*-*A*-*G*-*G*-*G*-*A*-U-*U*-A-U-C-U-*G*-*G*-*G*-*A*-*U*-*G*-*U*-*C*-*U*=*A*=R_1
(5'-3')*C*=*C*=U-*U*-C-*C*-U-*A*-A-*U*-A-*G*-A-*C*-C-*U*-A-*C*-A-*G*=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)-

U= :



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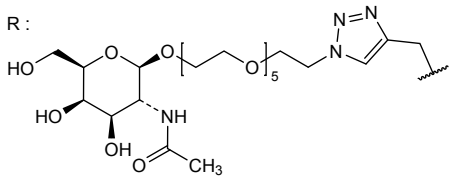
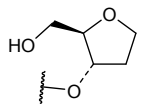


R1 :



alixorextonum

alixorexton

N-[7,10-*cis*-(4*S*,4a*R*)-17-oxo-1,2,3,4,4a,5,7,8,9,10,16,17-dodecahydro-7,10-ethanopyrido[1,2-*d*][1,7,4]benzodioxaazacyclotridecin-4-yl]methanesulfonamide

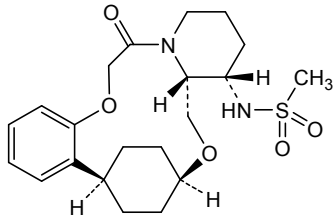
alixorexton

N-[7,10-*cis*-(4*S*,4a*R*)-17-oxo-1,2,3,4,4a,5,7,8,9,10,16,17-dodécahydro-7,10-éthanopyrido[1,2-*d*][1,7,4]benzodioxaazacyclotridécin-4-yl]méthanesulfonamide

alixorextón

N-[7,10-*cis*-(4*S*,4a*R*)-17-oxo-1,2,3,4,4a,5,7,8,9,10,16,17-dodecahidro-7,10-etanopirido[1,2-*d*][1,7,4]benzodioxaazaciclotridecin-4-il]metanosulfonamida

$C_{21}H_{30}N_2O_5S$



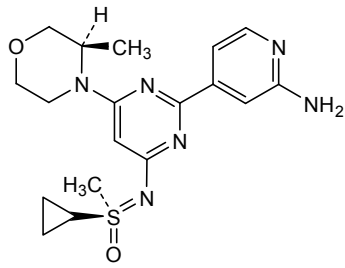
alnodesertibum

alnodesertib (*S*)-({2-(2-aminopyridin-4-yl)-6-[(3*R*)-3-methylmorpholin-4-yl]pyrimidin-4-yl}imino)(cyclopropyl)(methyl)-λ^6-sulfanone

alnodésertib (*S*)-({2-(2-aminopyridin-4-yl)-6-[(3*R*)-3-méthylmorpholin-4-yl]pyrimidin-4-yl}imino)(cyclopropyl)(méthyl)-λ^6-sulfanone

alnodesertib (*S*)-({2-(2-aminopiridin-4-il)-6-[(3*R*)-3-metilmorfolin-4-il]pirimidin-4-il}imino)(ciclopropil)(metil)-λ^6-sulfanona

$C_{18}H_{24}N_6O_2S$



amdokitugum #

amdokitug immunoglobulin G1-kappa, anti-[*Homo sapiens* IL17A (Interleukin 17A, IL-17)], monoclonal antibody; H-gamma1 heavy chain (1-445) [VH (*Homo sapiens* IGHV3-23*04 (89.8%) -(IGHD) -IGHJ5*01 (100%), CDR-IMGT [8.7.9] (26-33.51-57.96-104)) (1-115) -*Homo sapiens* IGHG1*03v (100%) G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K(212) (116-213), hinge 1-15 (214-228), CH2 (229-338), CH3 E12 (354), M14 (356) (339-443), CHS (444-445)) (116-445)], (218-214')-disulfide with L-kappa light chain (1'-214') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV13-85*01 (87.4%) -IGKJ4*01 (100%)/*Homo sapiens* IGKV1-NL1*01 (87.4%) -IGKJ2*02 (90.9%) Q120>S (100'), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dimer (224-224": 227-227")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, lacking the glutamine synthetase (GS-KO) gene, glycoform alfa

amdokitug

immunoglobuline G1-kappa, anti-[*Homo sapiens* IL17A (interleukine 17A, IL-17)], anticorps monoclonal;
chaîne lourde H-gamma1 (1-445) [VH (*Homo sapiens* IGHV3-23*04 (89.8%) -(IGHD) -IGHJ5*01 (100%), CDR-IMGT [8.7.9] (26-33.51-57.96-104)) (1-115) -*Homo sapiens* IGHG1*03v (100%) G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (212) (116-213), charnière 1-15 (214-228), CH2 (229-338), CH3 E12 (354), M14 (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* IGKV13-85*01 (87.4%) -IGKJ4*01 (100%)/*Homo sapiens* IGKV1-NL1*01 (87.4%) -IGKJ2*02 (90.9%) Q120>S (100'), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dimère (224-224''': 227-227''')-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

amdokitug

inmunoglobulina G1-kappa, anti-[*Homo sapiens* IL17A (interleukina 17A, IL-17)], anticuerpo monoclonal;
cadena pesada H-gamma1 (1-445) [VH (*Homo sapiens* IGHV3-23*04 (89.8%) -(IGHD) -IGHJ5*01 (100%), CDR-IMGT [8.7.9] (26-33.51-57.96-104)) (1-115) -*Homo sapiens* IGHG1*03v (100%) G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (212) (116-213), bisagra 1-15 (214-228), CH2 (229-338), CH3 E12 (354), M14 (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* IGKV13-85*01 (87.4%) -IGKJ4*01 (100%)/*Homo sapiens* IGKV1-NL1*01 (87.4%) -IGKJ2*02 (90.9%) Q120>S (100'), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dímero (224-224''': 227-227''')-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

```
EVQLVESGGG LVQPGGSLRL SCAASGFTFS SFDMSWGRQA PGKRLEWVAF  50
MSSGGSTYYP DSVKGRFTIS RDNSKNTLYL QMNSLRAEDT AVYYCARGER 100
YGSYWGQGTL VTVSSASTKG PSVFPLAPSS KSTSGGTAAL GCLVKDYFPE 150
PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL SSVVTVPSSS LGTQTYICNV 200
NHKPSNTKVD KKVEPKSCDK THTCPPCPAP ELLGGPSVFL FPPKPKDTLM 250
ISRTPEVTCV VVDVSHEDPE VKFNWYVDGV EVHNAKTKPR EEQYNSTYRV 300
VSVLTVLHQD WLNGKEYKCK VSNKALPAPI EKTISKAKGQ PREPQVYTLP 350
PSREEMTKNQ VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG 400
SFFLYSKLTV DKSRWQQGNV FSCSVMHEAL HNHYTQKSLS LSPGK       445
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Light chain / Chaîne légère / Cadena ligera

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DIQMTQSPSS LSASVGDRVT ITCKASDHIN NWLAWYQQKP GKAPKLLISG  50
ATSLETGVPS RFSGSGSGTD YTLTISSLQP EDFATYYCQQ YWSTPFTFGS 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) 22-95 142-198 259-319 365-423
22''-95'' 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''

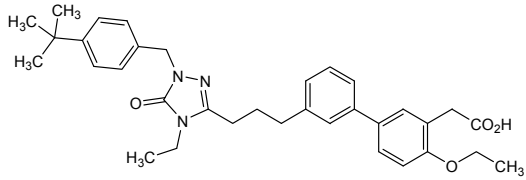
amezalpatum

amezalpat — [8^4-*tert*-butyl-1^4-ethoxy-6^4-ethyl-6^5-oxo-6^4,6^5-dihydro-6(3,1)-[1,2,4]triazola-1,8(1),2(1,3)-tribenzenaoctaphan-1^3-yl]acetic acid

amézalpat — acide [8^4-*tert*-butyl-1^4-éthoxy-6^4-éthyl-6^5-oxo-6^4,6^5-dihydro-6(3,1)-[1,2,4]triazola-1,8(1),2(1,3)-tribenzénaoctaphan-13-yl]acétique

amezalpat — ácido [8^4-*terc*-butil-6^4-etil-1^4-etoxi-6^5-oxo-6^4,6^5-dihidro-6(3,1)-[1,2,4]triazola-1,8(1),2(1,3)-tribencenaoctafan-1^3-il]acético

$C_{34}H_{41}N_3O_4$



amrecibartum #

amrecibart — immunoglobulin G4-kappa, anti-[*Homo sapiens* F11 (coagulation factor 11, coagulation factor XI, FXI, plasma thromboplastin antecedent, PTA)], *Homo sapiens* monoclonal antibody;
H-gamma4 heavy chain *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV3-23*03 (91.8%) -(IGHD) -IGHJ3*02 (100%), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, 12-G4v5 h P10 (CH1 (124-221), hinge 1-12 S10>P (231) (222-233), CH2 L92 (312) (234-343), CH3 (344-448), CHS (449-450)) (124-450)], (137-215')-disulfide with L-kappa light chain *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (100%) -IGKJ5*01 (100%), CDR-IMGT [6.3.10] (27'-32'.50'-52'.89'-98')) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (154'), V101 (192')) (109'-215')]; dimer (229-229'':232-232'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa

amrécibart — immunoglobuline G4-kappa, anti-[*Homo sapiens* F11 (facteur de coagulation 11, facteur de coagulation XI, FXI, antécédent de la thromboplastine plasmatique, PTA)], anticorps monoclonal *Homo sapiens*;
chaîne lourde H-gamma4 *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV3-23*03 (91.8%) -(IGHD) -IGHJ3*02 (100%), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, 12-G4v5 h P10 (CH1 (124-221), charnière 1-12 S10>P (231) (222-233), CH2 L92 (312) (234-343), CH3 (344-448), CHS (449-450)) (124-450)], (137-215')-disulfure avec la chaîne légère L-kappa

Homo sapiens (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (100%) -IGKJ5*01 (100%), CDR-IMGT [6.3.10] (27'-32'.50'-52'.89'-98')) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (154'), V101 (192')) (109'-215')]; dimère (229-229":232-232")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa

amrecibart — inmunoglobulina G4-kappa, anti-[*Homo sapiens* F11 (factor de coagulación 11, factor de coagulación XI, FXI, antecedente de la tromboplastina plasmática PTA)], anticuerpo monoclonal *Homo sapiens*; cadena pesada H-gamma4 *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV3-23*03 (91.8%) -(IGHD) -IGHJ3*02 (100%), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, 12-G4v5 h P10 (CH1 (124-221), bisagra 1-12 S10>P (231) (222-233), CH2 L92 (312) (234-343), CH3 (344-448), CHS (449-450)) (124-450)], (137-215')-disulfuro con la cadena ligera L-kappa *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (100%) -IGKJ5*01 (100%), CDR-IMGT [6.3.10] (27'-32'.50'-52'.89'-98')) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (154'), V101 (192')) (109'-215')]; dímero (229-229":232-232")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAASGFTFS NYAMNWVRQA PGKGLDWVSF  50
IRSGGDTTYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVH 100
PYTWDYGDAF DIWGQGTMVT VSSASTKGPS VFPLAPCSRS TSESTAALGC 150
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG 200
TKTYTCNVDH KPSNTKVDKR VESKYGPPCP PCPAPEFLGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS QEDPEVQFNW YVDGVEVHNA KTKPREEQFN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKG LPSSIEKTIS KAKGQPREPQ 350
VYTLPPSQEE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SRLTVDKSRW QEGNVFSCSV MHEALHNHYT QKSLSLSLGK 450
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Light chain / Chaîne légère / Cadena ligera

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DIQMTQSPSS LSASVGDRVT ITCRASQSIS SYLNWYQQKP GKAPKLLIYA  50
ASSLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ SYSTPPITFG 100
QGTRLEIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK 150
VDNALQSGNS QESVTEQDSK DSTYSLSSTL TLSKADYEKH KVYACEVTHQ 200
GLSSPVTKSF NRGEC                                       215
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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	264-324	370-428
	22"-96"	150"-206"	264"-324"	370"-428"
Intra-L (C23-C104)	23'-88'	135'-195'		
	23'"-88'"	135'"-195'"		
Inter-H-L (CH1 10-CL 126)	137-215'	137"-215'"		
Inter-H-H (h 8, h 11)	229-229"	232-232"		

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

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

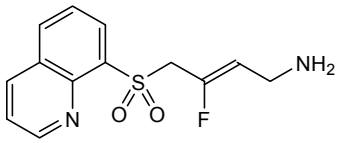
amsulostatum

amsulostat — (2*Z*)-3-fluoro-4-(quinolin-8-ylsulfonyl)but-2-en-1-amine

amsulostat — (2*Z*)-3-fluoro-4-(quinolin-8-ylsulfonyl)but-2-én-1-amine

amsulostat — (2*Z*)-3-fluoro-4-(quinolin-8-ilsulfonil)but-2-en-1-amina

$C_{13}H_{13}FN_2O_2S$



anbenitamabum repodatecanum #

anbenitamab repodatecan

immunoglobulin G1-kappa, anti-[*Homo sapiens* ERBB2 (epidermal growth factor receptor 2, receptor tyrosine protein kinase erbB-2, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], humanized monoclonal antibody, bispecific biparatopic, tetravalent, conjugated at O-4 of the four terminal GlcNAc groups of the two branched glycans to a *repodatecan* group, consisting of a cleavable linker and a camptothecin derivative;
H-gamma1 heavy chain anti-ERBB2 domain II humanized (1-449) [VH (*Homo sapiens* IGHV3-66*01 (78.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, 14-G1v32 CH3 W22 (knob), 18-G1v82-4 CH3 A88(CH1 K120 (216) (120-217), hinge 1-15 (218-232), CH2 (233-342), CH3 D12 (358), L14 (360), T22>W (368), K88>A (411) (343-447), CHS (448-449)) (120-449)], (222-214')-disulfide with L-kappa light chain anti-ERBB2 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, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')];
H-gamma1 heavy chain anti-ERBB2 domain IV 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*01, G1m17,1 CH1 K120, CH3 D12, L14, 14-G1v33 CH3 S22, A24, V86(hole), 18-G1v82-3 CH3 K85.1 (CH1 K120 (217'') (121''-218''), hinge 1-15 (219''-233''), CH2 (234''-343''), CH3 D12 (359), L14 (361) T22>S (369''), L24>A (371''), F85.1>K (408''), Y86>V (410'') (344''-448''), CHS (449''-450'')) (121''-450'')], (223''-214''')-disulfide with L-kappa light chain anti-ERBB2 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, V101 (C-KAPPA A45.1 (153'''), V101 (191''')) (108'''-214''')]; dimer (228-229'':231-232'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa, substituted at O-4 of the four distal 2-acetamido-2-deoxy-β-D-glucopyranosyl groups of the two glycans at N-4 of the asparaginyl residues 299 and 300'' with 2-(2-{8-[(10*S*)-10-benzyl-1-{[(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]amino}-1,6,9,12,15,18,34-heptaoxo-3,21,24,27,30-pentaoxa-5,8,11,14,17,33-hexaazaheptatriacontan-37-oyl]-8,9-dihydro-1(*or* 3)*H*-dibenzo[*b*,*f*][1,2,3]triazolo[4,5-*d*]azocin-1(*or* 3)-yl}acetamido)-2-deoxy-β-D-galactopyranosyl (*repodatecan*) groups (introduced by enzymatic glycosylation with 2-(2-azidoacetamido)-2-deoxy-D-galactopyranose and subsequent reaction of the azido groups with the specific click reagent), resulting in a drug/antibody ratio of ~3.8 on average

anbénitamab répodatécan	immunoglobuline G1-kappa, anti-[*Homo sapiens* ERBB2 (récepteur 2 du facteur de croissance épidermique, récepteur tyrosine-protéine kinase erbB2, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], anticorps monoclonal humanisé, bispécifique biparatopique, tétravalent, conjugué en O-4 des quatre groupes terminaux GlcNAc des deux glycanes ramifiés à un groupe *répodatécan*, constitué d'un lieur clivable et d'un dérivé de camptothécine; chaîne lourde H-gamma1 anti-ERBB2 domaine II humanisée (1-449) [VH (*Homo sapiens* IGHV3-66*01 (78.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, 14-G1v32 CH3 W22 (knob), 18-G1v82-4 CH3 A88 (CH1 K120 (216) (120-217), charnière 1-15 (218-232), CH2 (233-342), CH3 D12 (358), L14 (360), T22>W (368), K88>A (411) (343-447), CHS (448-449)) (120-449)], (222-214')-disulfure avec la chaîne légère L-kappa anti-ERBB2 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, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; chaîne lourde H-gamma1 anti-ERBB2 domaine IV 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*01, G1m17,1 CH1 K120, CH3 D12, L14, 14-G1v33 CH3 S22, A24, V86 (hole), 18-G1v82-3 CH3 K85.1 (CH1 K120 (217'') (121''-218''), charnière 1-15 (219''-233''), CH2 (234''-343''), CH3 D12 (359), L14 (361) T22>S (369''), L24>A (371''), F85.1>K (408''), Y86>V (410'') (344''-448''), CHS (449''-450'')) (121''-450'')], (223''-214''')-disulfure avec la chaîne légère L-kappa anti-ERBB2 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, V101 (C-KAPPA A45.1 (153'''), V101 (191''')) (108'''-214''')]; dimère (228-229'':231-232'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa, substitué en O-4 des quatre groupes distaux 2-acétamido-2-désoxy-β-D-glucopyranosyle des deux glycanes en N-4 des résidus asparaginyle 299 et 300'' par des groupes 2-(2-{8-[(10*S*)-10-benzyl-1-{[(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]amino}-1,6,9,12,15,18,34-heptaoxo-3,21,24,27,30-pentaoxa-5,8,11,14,17,33-hexaazaheptatriacontan-37-oyl]-8,9-dihydro-1(*ou* 3)*H*-dibenzo[*b*,*f*][1,2,3]triazolo[4,5-*d*]azocin-1(*ou* 3)-yl}acétamido)-2-désoxy-β-D-galactopyranosyle (*répodatécan*) (introduits par glycosylation enzymatique avec le 2-(2-azidoacétamido)-2-désoxy-D-galactopyranose et réaction ultérieure des groupes azido avec le réactif click spécifique), ce qui donne un rapport médicament/anticorps d'environ 3,8 en moyenne

anbenitamab repodatecán	inmunoglobulina G1-kappa, anti-[*Homo sapiens* ERBB2 (receptor 2 del factor de crecimiento epidérmico, receptor tirosina-proteína kinasa erbB2, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], anticuerpo monoclonal humanizado, biparatópico biespecífico, tetravalente, conjugado en O-4 de los cuatro grupos GlcNAc terminales de los dos glicanos ramificados con un grupo *repodatecán*, que consta de un conector escindible y un derivado de camptotecina; cadena pesada H-gamma1 anti-ERBB2 dominio II humanizada (1-449) [VH (*Homo sapiens* IGHV3-66*01 (78.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.12] (26-33.51-58.97-108) (1-119) -*Homo sapiens* IGHG1*01, G1m7,1, CH1 K120, CH3 D12, L14, 14-G1v32 CH3 W22 (knob), 18-G1v82-4 CH3 A88 (CH1 K120 (216) (120-217), bisagra 1-15 (218-232), CH2 (233-342), CH3 D12 (358), L14 (360), T22>W (368), K88>A (411) (343-447), CHS (448-449)) (120-449)], (222-214')-disulfuro con la cadena ligera L-kappa anti-ERBB2 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, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; cadena pesada H-gamma1 anti-ERBB2 domnio IV 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*01, G1m7,1, CH1 K120, CH3 D12, L14, 14-G1v33 CH3 S22, A24, V86 (hole), 18-G1v82-3 CH3 K85.1 (CH1 K120 (217'') (121''-218''), bisagra 1-15 (219''-233''), CH2 (234''-343''), CH3 D12 (359), L14 (361) T22>S (369''), L24>A (371''), F85.1>K (408''), Y86>V (410'') (344''-448''), CHS (449''-450'')) (121''-450'')], (223''-214''')-disulfuro con la cadena ligera L-kappa anti-ERBB2 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, V101 (C-KAPPA A45.1 (153'''), V101 (191''') (108'''-214''')]; dímero (228-229'':231-232'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa, sustituido en O-4 de los cuatro grupos distales 2-acetamido-2-desoxi-β-D-glucopiranosilo de los dos glicanos en N-4 de los residuos de asparaginilo 299 y 300'' con grupos 2-(2-{8-[(10*S*)-10-bencil-1-{[(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]amino}-1,6,9,12,15,18,34-heptaoxo-3,21,24,27,30-pentaoxa-5,8,11,14,17,33-hexaazaheptatriacontan-37-oil]-8,9-dihidro-1(*o* 3)*H*-dibenzo[*b*,*f*][1,2,3]triazolo[4,5-*d*]azocin-1(*o* 3)-il}acetamido)-2-desoxi-β-D-galactopiranosilo (*repodatecán*) (introducidos por glicosilación enzimática con 2-(2-azidoacetamido)-2-desoxi-D-galactopiranosa y posterior reacción de los grupos azido con el reactivo clic específico), lo que da como resultado una relación fármaco/anticuerpo de ~3,8 en promedio

Heavy chain / Chaîne lourde / Cadena pesada : H-gamma1 anti-ERBB2 domain II (knob) (H)

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EVQLVESGGG LVQPGGSLRL SCAASGFTFT DYTMDWVRQA PGKGLEWVAD  50
VNPNSGGSIY NQRFKGRFTL SVDRSKNTLY LQMNSLRAED TAVYYCARNL 100
GPSFYFDYWG QGTLVTVSSA STKGPSVFPL APSSKSTSGG TAALGCLVKD 150
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY 200
ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP CPAPELLGGP SVFLFPPKPK 250
DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS 300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV 350
YTLPPSRDEL TKNQVSLWCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL 400
DSDGSFFLYS ALTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK  449
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Heavy chain / Chaîne lourde / Cadena pesada : H-gamma1 anti-ERBB2 domain IV (hole) (H")

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

Light chain / Chaîne légère / Cadena ligera : L-kappa anti-ERBB2 (L', L'")

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

Post-translational modifications

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

Intra-H (C23-C104) 22-96 146-202 263-323 369-427
22"-96" 147"-203" 264"-324" 370"-428"

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

Inter-H-L (h 5-CL 126) 222-214' 223"-214'"

Inter-H-H (h 11, h 14) 228-229" 231-232"

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

H CH2 N84.4: 299, 300"

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

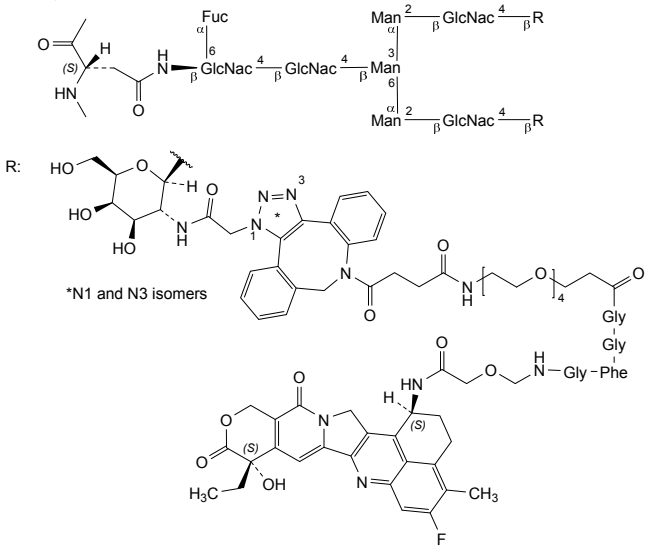
C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal

H CHS K2: 449, 450"

Modified distal βdGlcNAc groups / Groupes βdGlcNAc distaux modifiés / Grupos βdGlcNAc distales modificados

*(*repodatecan*:mAb ~ 3.8:1)

Asn299, Asn300":



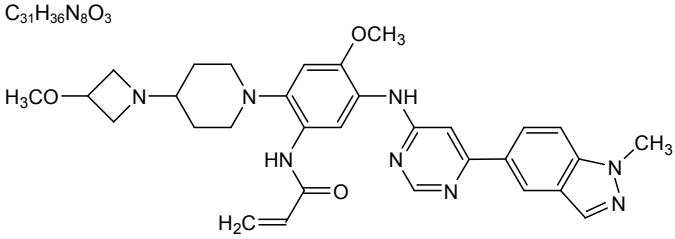
andamertinibum

andamertinib — *N*-(4-methoxy-2-[4-(3-methoxyazetidin-1-yl)piperidin-1-yl]-5-{[6-(1-methyl-1*H*-indazol-5-yl)pyrimidin-4-yl]amino}phenyl)prop-2-enamide

andamertinib — *N*-(4-méthoxy-2-[4-(3-méthoxyazétidin-1-yl)pipéridin-1-yl]-5-{[6-(1-méthyl-1*H*-indazol-5-yl)pyrimidin-4-yl]amino}phényl)prop-2-énamide

andamertinib — *N*-(5-{[6-(1-metil-1*H*-indazol-5-il)pirimidin-4-il]amino}-4-metoxi-2-[4-(3-metoxiazetidin-1-il)piperidin-1-il]fenil)prop-2-enamida

$C_{31}H_{36}N_8O_3$



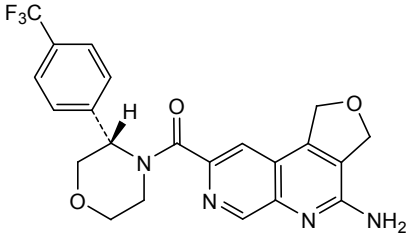
anvumetostatum

anvumetostat — (4-amino-1,3-dihydrofuro[3,4-*c*][1,7]naphthyridin-8-yl){(3*S*)-3-[4-(trifluoromethyl)phenyl]morpholin-4-yl}methanone

anvumétostat — (4-amino-1,3-dihydrofuro[3,4-*c*][1,7]naphtyridin-8-yl){(3*S*)-3-[4-(trifluorométhyl)phényl]morpholin-4-yl}méthanone

anvumetostat — (4-amino-1,3-dihidrofuro[3,4-*c*][1,7]naftiridin-8-il){(3*S*)-3-[4-(trifluorometil)fenil]morfolin-4-il}metanona

$C_{22}H_{19}F_3N_4O_3$



anzutresgenum autoleucelum #

anzutresgene autoleucel

autologous CD4+/CD8+ enriched T lymphocytes transduced with a self-inactivating, non-replicating lentiviral vector encoding a T cell receptor (TCR) specific for the preferentially expressed antigen in melanoma (PRAME). The TCR transgene consists of a TCRα and a TCRβ chain separated by a self-cleaving ribosome skipping sequence derived from porcine teschovirus (P2A) under the control of a murine stem cell virus (MSCV) promoter and a Woodchuck hepatitis virus post-transcriptional response element (WPRE). The viral vector backbone also comprises a packaging signal ψ (psi), residual *gag* sequence, a Rev response element (RRE), a central polypurine tract/central termination sequence (cPPT/CTS) and is flanked by 5' and 3' long terminal repeats (LTRs). The vector is pseudotyped with vesicular stomatitis virus 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 a lentiviral vector and expanded in growth media containing human AB serum, IL-7 and IL-15. The cell suspension consists of CD3+ T lymphocytes (≥90%) of which >20% of the CD3+CD8+ cells express the PRAME-specific TCR. The transduced T lymphocytes release interferon gamma (IFN-γ) by co-culture with PRAME-expressing tumor cells *in vitro*

anzutresgène autoleucel

lymphocytes T autologues enrichis en CD4+/CD8+ transduits avec un vecteur lentiviral auto-inactivant et non réplicatif codant un récepteur de lymphocytes T (TCR) spécifique de l'antigène préférentiellement exprimé dans le mélanome (PRAME). Le transgène TCR est constitué d'une chaîne TCRα et d'une chaîne TCRβ séparées par une séquence auto-clivante de saut de ribosomes dérivée du teschovirus porcin (P2A), sous le contrôle d'un promoteur du virus des cellules souches murines (MSCV) et d'un élément de réponse post-transcriptionnelle du virus de l'hépatite de la marmotte (WPRE). Le squelette du vecteur viral comprend également un signal d'empaquetage ψ (psi), une séquence *gag* résiduelle, un élément de réponse Rev (RRE), un tractus polypurine central/une séquence de terminaison centrale (cPPT/CTS) et, il est flanqué de répétitions terminales longues (LTRs) en 5' et en 3'. Le vecteur est pseudotypé 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 activation 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 un vecteur lentiviral et expansées dans un milieu de croissance contenant du sérum AB humain, de l'IL-7 et de l'IL-15. La suspension cellulaire est constituée de lymphocytes T CD3+ (≥90%) dont >20% des cellules CD3+CD8+ expriment le TCR spécifique de PRAME. Les lymphocytes T transduits libèrent de l'interféron gamma (IFN-γ) par co-culture avec des cellules tumorales exprimant PRAME *in vitro*

anzutresgén autoleucel

linfocitos T CD4+/CD8+ autólogos enriquecidos, transducidos con un vector lentiviral auto-inactivante, no replicativo, que codifica un receptor de células T (TCR) específico del antígeno preferentemente expresado en melanoma (PRAME). El transgén del TCR consiste en una cadena TCRα y una cadena TCRβ separadas por una secuencia de auto-escisión de salto ribosómico derivada del teschovirus porcino (P2A) bajo el control de un promotor del virus de células madre murino (MSCV) y un elemento regulador post-transcripcional del virus de la hepatitis de la marmota (WPRE). El esqueleto del vector viral también consta de una señal de empaquetamiento ψ (psi), una secuencia residual *gag*, un elemento de respuesta Rev (RRE), una secuencia de tracto de poli-purina central/terminación central (cPPT/CTS), y está flanqueado por repeticiones terminales largas (LTRs) en 5' y 3'. El vector está seudotipado con la glicoproteína G del virus de la estomatitis vesicular (VSV).
El material de leucoaféresis se enriquece en 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 15 (IL-15). Las células después se transducen con el vector lentiviral y se expanden más en medio de crecimiento que contiene suero AB humano, IL-7 e IL-15. La suspensión celular consiste en linfocitos T CD3+ (≥90%) de los cuales >20% de las células CD3+CD8+ expresan el TCR específico de PRAME. Los linfocitos T transducidos liberan interferón gamma (IFN-γ) mediante co-cultivo *in vitro* con células tumorales que expresan PRAME

apazunersenum

apazunersen

all-P-ambo-2'-*O*,4'-*C*-methylene-*P*-thioadenylyl-(3'→5')-2'-*O*,4'-*C*-methylene-*P*-thioguanylyl-(3'→5')-2'-*O*,4'-*C*-methylene-*P*-thioadenylyl-(3'→5')-2'-deoxy-*P*-thioadenylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-deoxy-*P*-thioguanylyl-(3'→5')-2'-deoxy-*P*-thioguanylyl-(3'→5')-2'-deoxy-*P*-thiocytidylyl-(3'→5')-2'-deoxy-*P*-thioadenylyl-(3'→5')-2'-deoxy-*P*-thiocytidylyl-(3'→5')-2'-deoxy-*P*-thioadenylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-deoxy-*P*-thiocytidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-5-methyl-2'-*O*,4'-*C*-methylene-*P*-thiocytidylyl-(3'→5')-5-methyl-2'-*O*,4'-*C*-methylene-*P*-thiouridylyl-(3'→5')-5-methyl-2'-*O*,4'-*C*-methylene-*P*-thiouridylyl-(3'→5')-2'-*O*,4'-*C*-methyleneguanosine

apazunersen

tout-P-ambo-2'-*O*,4'-*C*-méthylène-*P*-thioadénylyl-(3'→5')-2'-*O*,4'-*C*-méthylène-*P*-thioguanylyl-(3'→5')-2'-*O*,4'-*C*-méthylène-*P*-thioadénylyl-(3'→5')-2'-désoxy-*P*-thioadénylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-désoxy-*P*-thioguanylyl-(3'→5')-2'-désoxy-*P*-thioguanylyl-(3'→5')-2'-désoxy-*P*-thiocytidylyl-(3'→5')-2'-désoxy-*P*-thioadénylyl-(3'→5')-2'-désoxy-*P*-thiocytidylyl-(3'→5')-2'-désoxy-*P*-thioadénylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-désoxy-*P*-thiocytidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-5-méthyl-2'-*O*,4'-*C*-méthylène-*P*-thiocytidylyl-(3'→5')-5-méthyl-2'-*O*,4'-*C*-méthylène-*P*-thiouridylyl-(3'→5')-5-méthyl-2'-*O*,4'-*C*-méthylène-*P*-thiouridylyl-(3'→5')-2'-*O*,4'-*C*-méthylèneguanosine

apazunersén

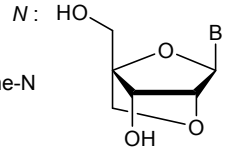
todo-P-ambo-2'-*O*,4'-*C*-metileno-*P*-tioadenilil-(3'→5')-2'-*O*,4'-*C*-metileno-*P*-tioguanilil-(3'→5')-2'-*O*,4'-*C*-metileno-*P*-tioadenilil-(3'→5')-2'-desoxi-*P*-tioadenilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2'-desoxi-*P*-tioguanilil-(3'→5')-2'-desoxi-*P*-tioguanilil-(3'→5')-2'-desoxi-*P*-tiocitidilil-(3'→5')-2'-desoxi-*P*-tioadenilil-(3'→5')-2'-desoxi-*P*-tiocitidilil-(3'→5')-2'-desoxi-*P*-tioadenilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2'-desoxi-*P*-tiocitidilil-(3'→5')-*P*-tiotimidilil-(3'→5')-5-metil-2'-*O*,4'-*C*-metileno-*P*-tiocitidilil-(3'→5')-5-metil-2'-*O*,4'-*C*-metileno-*P*-tiouridilil-(3'→5')-5-metil-2'-*O*,4'-*C*-metileno-*P*-tiouridilil-(3'→5')-2'-*O*,4'-*C*-metilenoguanosina

$C_{184}H_{224}N_{67}O_{96}P_{17}S_{17}$

(3'-5')*A*=*G*=*A*=dA=dT=dG=dG=dC=dA=dC=dA=dT=dC=dT=<u>*C*</u>=<u>*U*</u>=<u>*U*</u>=*G*

N : nucleoside / nucléoside / nucleósido
B : nucleobase / nucléobase / nucleobase
dN : 2'-deoxy-N / 2'-désoxy-N / 2'-desoxi-N
N : 2'-*O*,4'-*C*-methylene-N / 2'-*O*,4'-*C*-méthylène-N / 2'-*O*,4'-*C*-metileno-N
<u>N</u> : 5-methyl-N / 5-méthyl-N / 5-metil-N
= : -PO(SH)-

N :



arumakimigum #

arumakimig

immunoglobulin (H-gamma1_L-lambda2)_(H-gamma1_L-kappa), anti-[*Homo sapiens* IL18 (interleukin 18, IL-18, interferon gamma-inducing factor, IGIF, interleukin-1 gamma, IL-1G, IL1F4)] and anti-[*Homo sapiens* IL1B (interleukin 1 beta, IL-1B, 1L1F2)], *Homo sapiens* monoclonal antibody, bispecific, bivalent;
H-gamma1 heavy chain anti-IL18 *Homo sapiens* (1-449) [VH (*Homo sapiens* IGHV1-69*01 (91.8%) -(IGHD) -IGHJ5*01 (92.9%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, 6-G1-v14 CH2 A1.3, A1.2, 14-G1v74 CH3 C10, 14-G1v32 CH3 W22 (knob) (CH1 R120 (216) (120-217), hinge 1-15 (218-232), CH2 L1.3>A (236), L1.2>A (237) (233-342), CH3 S10>C (356), E12 (358), M14 (360), T22>W (368) (343-447), CHS (448-449)) (120-449)], (222-215')-

	disulfide with L-lambda2 light chain anti-IL18 *Homo sapiens* (1'-216') [V-Lambda (*Homo sapiens* IGLV1-40*01 (88.3%) -IGLJ2*01 (100%), CDR-IMGT [8.3.11] (26'-33'.51'-53'.90'-100')) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (C-LAMBDA2) (111'-216')]; H-gamma1 heavy chain anti-IL1B *Homo sapiens* (1''-448'') [VH (*Homo sapiens* IGHV3-30-5*03 (93.9%) -(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, 6-G1v14 CH2 A1.3, A1.2, 14-G1v75 CH3 C5, 14-G1v33 CH3S22, A24, V86 (hole) (CH1 R120 (215'') (119''-216''), hinge 1-15 (217''-231''), CH2 L1.3>A (235''), L1.2>A (236'') (232''-341''), CH3 Y5>C (350''), E12 (357''), M14 (359''), T22>S (367''), L24>A (369''), Y86>V (408'') (342''-446''), CHS (447''-448'')) (119''-448'')], (221''-214''')-disulfide with L-kappa light chain anti-IL1B *Homo sapiens* (1'-214''') [V-Kappa (*Homo sapiens* IGKV6-21*01 (98.9%) -IGKJ3*01 (100%), CDR-IMGT [6.3.9] (27'''-32'''.50'''-52'''.89'''-97''')) (1'''-107''') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153''')), V101 (191''')) (108'''-214''')]; dimer (228-227'':231-230'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa
arumakimig	immunoglobuline (H-gamma1_L-lambda2)_(H-gamma1_L-kappa), anti-[*Homo sapiens* IL18 (interleukine 18, IL-18, facteur inducteur d'interferon gamma, IGIF, interleukine-1 gamma, IL-1G, IL1F4)] et anti-[*Homo sapiens* IL1B (interleukine 1 bêta, IL-1B, 1L1F2)], anticorps monoclonal *Homo sapiens,* bispécifique, bivalent; chaîne lourde H-gamma1 anti-IL18 *Homo sapiens* (1-449) [VH (*Homo sapiens* IGHV1-69*01 (91.8%) -(IGHD) -IGHJ5*01 (92.9%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, 6-G1v14 CH2 A1.3, A1.2, 14-G1v74 CH3 C10, 14-G1v32 CH3 W22 (knob) (CH1 R120 (216) (120-217), charnière 1-15 (218-232), CH2 L1.3>A (236), L1.2>A (237) (233-342), CH3 S10>C (356), E12 (358), M14 (360), T22>W (368) (343-447), CHS (448-449)) (120-449)], (222-215')-disulfure avec la chaîne légère L-lambda2 anti-IL18 *Homo sapiens* (1'-216') [V-Lambda (*Homo sapiens* IGLV1-40*01 (88.3%) -IGLJ2*01 (100%), CDR-IMGT [8.3.11] (26'-33'.51'-53'.90'-100')) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (C-LAMBDA2) (111'-216')]; chaîne lourde H-gamma1 anti-IL1B *Homo sapiens* (1''-448'') [VH (*Homo sapiens* IGHV3-30-5*03 (93.9%) -(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, 6-G1v14 CH2 A1.3, A1.2, 14-G1v75 CH3 C5, 14-G1v33 CH3S22, A24, V86 (hole) (CH1 R120 (215'') (119''-216''), charnière 1-15 (217''-231''), CH2 L1.3>A (235''), L1.2>A (236'') (232''-341''), CH3 Y5>C (350''), E12 (357''), M14 (359''), T22>S (367''), L24>A (369''), Y86>V (408'') (342''-446''), CHS (447''-448'')) (119''-448'')], (221''-

	214'")-disulfure avec la chaîne légère L-kappa anti-IL1B *Homo sapiens* (1'-214'") [V-Kappa (*Homo sapiens* IGKV6-21*01 (98.9%) -IGKJ3*01 (100%), CDR-IMGT [6.3.9] (27'"-32'".50'"-52'".89'"-97'")) (1'"-107'") -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'"), V101 (191'")) (108'"-214'")]; dimère (228-227":231-230")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa
arumakimig	inmunoglobulina (H-gamma1_L-lambda2)_(H-gamma1_L-kappa), anti-[*Homo sapiens* IL18 (interleukina 18, IL-18, factor inductor del interferón gamma, IGIF, interleukina-1 gamma, IL-1G, IL1F4)] y anti-[*Homo sapiens* IL1B (interleukina 1 beta, IL-1B, 1L1F2)], anticuerpo monoclonal *Homo sapiens,* biespecífico, bivalente; cadena pesada H-gamma1 anti-IL18 *Homo sapiens* (1-449) [VH (*Homo sapiens* IGHV1-69*01 (91.8%) -(IGHD) -IGHJ5*01 (92.9%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, 6-G1v14 CH2 A1.3, A1.2, 14-G1v74 CH3 C10, 14-G1v32 CH3 W22 (knob) (CH1 R120 (216) (120-217), bisagra 1-15 (218-232), CH2 L1.3>A (236), L1.2>A (237) (233-342), CH3 S10>C (356), E12 (358), M14 (360), T22>W (368) (343-447), CHS (448-449)) (120-449)], (222-215')-disulfuro con la cadena ligera L-lambda2 anti-IL18 *Homo sapiens* (1'-216') [V-Lambda (*Homo sapiens* IGLV1-40*01 (88.3%) -IGLJ2*01 (100%), CDR-IMGT [8.3.11] (26'-33'.51'-53'.90'-100')) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (C-LAMBDA2) (111'-216')]; cadena pesada H-gamma1 anti-IL1B *Homo sapiens* (1''-448'') [VH (*Homo sapiens* IGHV3-30-5*03 (93.9%) -(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, 6-G1v14 CH2 A1.3, A1.2, 14-G1v75 CH3 C5, 14-G1v33 CH3S22, A24, V86 (hole) (CH1 R120 (215'') (119''-216''), bisagra 1-15 (217''-231''), CH2 L1.3>A (235''), L1.2>A (236'') (232''-341''), CH3 Y5>C (350''), E12 (357''), M14 (359''), T22>S (367''), L24>A (369''), Y86>V (408'') (342''-446''), CHS (447''-448'')) (119''-448'')], (221''-214''')-disulfuro con la cadena ligera L-kappa anti-IL1B *Homo sapiens* (1'-214''') [V-Kappa (*Homo sapiens* IGKV6-21*01 (98.9%) -IGKJ3*01 (100%), CDR-IMGT [6.3.9] (27'"-32'".50'"-52'".89'"-97'")) (1'"-107'") -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'"), V101 (191'")) (108'"-214'")]; dímero (228-227":231-230")-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 anti-IL18 (knob) (H)

```
EVQLVQSGAE VKKPGSSVKV SCKASGGTFK SYAISWVRQA PGQGLEWMGN  50
IIPMTGQTYY AQKFQGRVTI TADESTSTAY MELSSLRSED TAVYYCARAA 100
YHPLVFDNWG QGTLVTVSSA STKGPSVFPL APSSKSTSGG TAALGCLVKD 150
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY 200
ICNVNHKPSN TKVDKRVEPK SCDKTHTCPP CPAPEAAGGP SVFLFPPKPK 250
DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS 300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV 350
YTLPPCREEM TKNQVSLWCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL 400
DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK  449
```

Light chain / Chaîne légère / Cadena ligera: L-lambda anti-IL18 (L')

```
DIVLTQPPSV SGAPGQRVTI SCSGSSSNIG NHYVNWYQQL PGTAPKLLIY  50
RNNHRPSGVP DRFSGSKSGT SASLAITGLQ SEDEADYYCQ SWDYSGFSTV 100
FGGGTKLTVL GQPKAAPSVT LFPPSSEELQ ANKATLVCLI SDFYPGAVTV 150
AWKADSSPVK AGVETTTPSK QSNNKYAASS YLSLTPEQWK SHRSYSCQVT 200
HEGSTVEKTV APTECS                                     216
```

Heavy chain / Chaîne lourde / Cadena pesada: H-gamma1 anti-IL1B (hole) (H")

```
QVQLVESGGG VVQPGRSLRL SCAASGFTFS VYGMNWVRQA PGKGLEWVAI  50
IWYDGDNQYY ADSVKGRFTI SRDNSKNTLY LQMNGLRAED TAVYYCARDL 100
RTGPFDYWGQ GTLVTVSSAS TKGPSVFPLA PSSKSTSGGT AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTQTYI 200
CNVNHKPSNT KVDKRVEPKS CDKTHTCPPC PAPEAAGGPS VFLFPPKPKD 250
TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNST 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVC 350
TLPPSREEMT KNQVSLSCAV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD 400
SDGSFFLVSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPGK   448
```

Light chain / Chaîne légère / Cadena ligera: L-kappa anti-IL1B (L'")

```
EIVLTQSPDF QSVTPKEKVT ITCRASQSIG SSLHWYQQKP DQSPKLLIKY  50
ASQSFSGVPS RFSGSGSGTD FTLTINSLEA EDAAAYYCHQ SSSLPFTFGP 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) 22-96 146-202 263-323 369-427
22"-96" 145"-201" 262"-322" 368"-426"
Intra-L (C23-C104) 22'-89' 138'-197'
23'"-88'" 134'"-194'"
Inter-H-L (h 5-CL 126) 222-215' 221"-214'"
Inter-H-H (h 11, h 14) 228-227" 231-230"
Inter-H-H (CH3 C10-C5)* 356-350"
*variants 14-G1v74 (H CH3 C10) and 14-G1v75 (H" CH3 C5) creating an additional inter-H-H disulfide bond.

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: 299, 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: 449, 448"

astepatidum

astepatide

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-leucyl-L-leucyl-L-α-glutamyl-*N*^{6}-(*N*^{6}-{*N*^{6}-[*N*-(17-carboxyheptadecanoyl)-L-γ-glutamyl]-L-lysyl}-L-lysyl)-L-lysyl-L-glutaminyl-L-alanyl-L-alanyl-L-arginyl-L-α-glutamyl-L-phenylalanyl-L-isoleucyl-L-α-glutamyl-L-tryptophyl-L-leucyl-L-leucyl-L-alanylglycylglycyl-L-prolyl-L-seryl-L-serylglycyl-L-alanyl-L-prolyl-L-prolyl-L-prolyl-L-serine

astépatide

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-leucyl-L-leucyl-L-α-glutamyl-*N*^{6}-(*N*^{6}-{*N*^{6}-[*N*-(17-carboxyheptadécanoyl)-L-γ-glutamyl]-L-lysyl}-L-lysyl)-L-lysyl-L-glutaminyl-L-alanyl-L-alanyl-L-arginyl-L-α-glutamyl-L-phénylalanyl-L-isoleucyl-L-α-glutamyl-L-tryptophyl-L-leucyl-L-leucyl-L-alanylglycylglycyl-L-prolyl-L-séryl-L-sérylglycyl-L-alanyl-L-prolyl-L-prolyl-L-prolyl-L-sérine

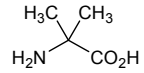
astepatida

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-leucil-L-leucil-L-α-glutamil-N^6-(N^6-{N^6-[*N*-(17-carboxiheptadecanoil)-L-γ-glutamil]-L-lisil}-L-lisil)-L-lisil-L-glutaminil-L-alanil-L-alanil-L-arginil-L-α-glutamil-L-fenilalanil-L-isoleucil-L-α-glutamil-L-triptofil-L-leucil-L-leucil-L-alanilglicilglicil-L-prolil-L-seril-L-serilglicil-L-alanil-L-prolil-L-prolil-L-prolil-L-serina

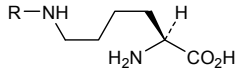
$C_{226}H_{348}N_{50}O_{68}$

YAEGTFTSDY SILLEKQAAR EFIEWLLAGG PSSGAPPPS 39

Modified residues / Résidus modifiés / Restos modificados

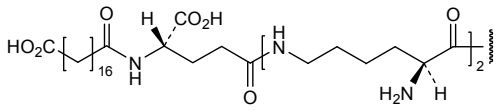


A (2)
2-methyl-Ala, Aib



K (16)
N^6-R-L-Lys

R:



atebimetinibum

atebimetinib

4-[(dimethylamino)methyl]-3-({2-fluoro-3-[(methylsulfamoyl)amino]phenyl}methyl)-2-oxo-2*H*-1-benzopyran-7-yl dimethylcarbamate

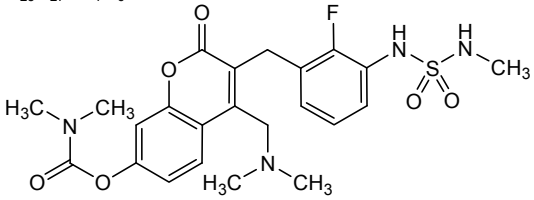
atébimétinib

diméthylcarbamate de 4-[(diméthylamino)méthyl]-3-({2-fluoro-3-[(méthylsulfamoyl)amino]phényl}méthyl)-2-oxo-2*H*-1-benzopyran-7-yle

atebimetinib

dimetilcarbamato de 4-[(dimetilamino)metil]-3-({2-fluoro-3-[(metilsulfamoil)amino]fenil}metil)-2-oxo-2*H*-1-benzopiran-7-ilo

$C_{23}H_{27}FN_4O_6S$



avicursenum

avicursen

all-P-ambo-2'-*O*-(2-methoxyethyl)-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyl-*P*-thiouridylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-*P*-thioguanylyl-(3'→5')-2'-deoxy-*P*-thioadenylyl-(3'→5')-2'-deoxy-*P*-thioguanylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-deoxy-5-methyl-*P*-thiocytidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-deoxy-*P*-thioguanylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(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)-*P*-thioadenylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyl-*P*-thiouridylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyl-*P*-thiouridylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyluridine

avicursen — *tout-P-ambo*-2'-*O*-(2-méthoxyéthyl)-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthyl-*P*-thiouridylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-*P*-thioguanylyl-(3'→5')-2'-désoxy-*P*-thioadénylyl-(3'→5')-2'-désoxy-*P*-thioguanylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-désoxy-5-méthyl-*P*-thiocytidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-désoxy-*P*-thioguanylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(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)-*P*-thioadénylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthyl-*P*-thiouridylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthyl-*P*-thiouridylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthyluridine

avicursén — *todo-P-ambo*-5-metil-2'-*O*-(2-metoxietil)-*P*-tiocitidilil-(3'→5')-5-metil-2'-*O*-(2-metoxietil)-*P*-tiouridilil-(3'→5')-2'-*O*-(2-metoxietil)-*P*-tioguanilil-(3'→5')-2'-desoxi-*P*-tioadenilil-(3'→5')-2'-desoxi-*P*-tioguanilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2'-desoxi-5-metil-*P*-tiocitidilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2'-desoxi-*P*-tioguanilil-(3'→5')-*P*-tiotimidilil-(3'→5')-*P*-tiotimidilil-(3'→5')-*P*-tiotimidilil-(3'→5')-5-metil-2'-*O*-(2-metoxietil)-*P*-tiouridilil-(3'→5')-5-metil-2'-*O*-(2-metoxietil)-*P*-tiocitidilil-(3'→5')-5-metil-2'-*O*-(2-metoxietil)-*P*-tiocitidilil-(3'→5')-2'-*O*-(2-metoxietil)-*P*-tioadenilil-(3'→5')-5-metil-2'-*O*-(2-metoxietil)-*P*-tiouridilil-(3'→5')-5-metil-2'-*O*-(2-metoxietil)-*P*-tiouridilil-(3'→5')-5-metil-2'-*O*-(2-metoxietil)-*P*-tiocitidilil-(3'→5')-5-metil-2'-*O*-(2-metoxietil)uridina

$C_{233}H_{327}N_{60}O_{129}P_{19}S_{19}$

m^5Cmoe=m^5Umoe=Gmoe=dA=dG=dT=m^5C_d=dT=dG=dT=dT=dT=m^5Umoe=m^5Cmoe=m^5Cmoe=Amoe=m^5Umoe=m^5Umoe=m^5Cmoe=m^5Umoe

N : nucleoside / nucléoside / nucleósido
m^5N : 5-methyl-N / 5-méthyl-N / 5-metil-N
dN & N_d : 2'-deoxy-N / 2'-désoxy-N / 2'-desoxi-N
Nmoe : 2'-*O*-methoxyethyl-N / 2'-*O*-méthoxyéthyl-N / 2'-*O*-metoxietil-N

= : -PO(SH)-

balekafuspum alfa #

balekafusp alfa — humanized immunoglobulin G1-kappa, anti-[human interleukin-2 (IL-2, T-cell growth factor, TCGF)] with an engineered kappa light chain, where a circular permuted form of human interleukin-2 is inserted within CDR-L1 between Y^{31} (Kabat L.27D) and D^{34} (Kabat L.30), Q^{32}>del (Kabat L.28), G^{33}>del (Kabat L.29) through ^{32}GGG^{34} and ^{167}GGGG^{170} linkers; gamma 1 heavy chain (1-451) [VH (*Homo sapiens* IGHV5-51*01 -(IGHD) -IGHJ3*01, CDR-Kabat [5.17.12] (31-35.50-66.99-110)) (1-121) -*Homo sapiens* IGHG1*03 (CH1 (122-219), hinge (220-234), CH2 N>^{301}A (235-344), CH3 (345-449), CHS (450-451)) (122-451)], (224-355')-disulfide with partial kappa light chain fused to a circular permuted form of human interleukin-2 (1'-355') [partial V-KAPPA (*Homo sapiens* IGKV1-39*01, CDR-Kabat [8] (partial CDR-L1: Kabat L.24-L.27D) (24'-31')) (1'-31')] fused via peptide linker $^{32'}$GGG$^{34'}$ to human interleukin-2 (IL-2, T-cell growth factor (TCGF)) in a permuted form (C-terminal fragment 77-133 (35'-91' in the current sequence) fused to the N-terminal fragment 2-76 (92'-166'

	in the current sequence)), variant (^{125}C>S$^{83'}$), fused via peptide linker $^{167'}$GGGG$^{170'}$ to a partial kappa light chain [V-KAPPA (*Homo sapiens* IGKV1-39*01 -IGKJ4*01, CDR-Kabat [5.7.9] (partial CDR-L1: Kabat L.30-L.34) (171'-175'.191'-197'.230'-238')) (171'-248') -*Homo sapiens* IGKC*01 (249'-355')]; dimer (230-230'':233-233'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa
balékafusp alfa	immunoglobuline humanisée G1-kappa, anti-[interleukine-2 humaine (IL-2, facteur de croissance des lymphocytes T (FCLT)], avec une chaîne légère kappa recombinée, dans laquelle une forme circulaire permutée d'interleukine-2 humaine est insérée dans le CDR-L1 entre Y^{31} (Kabat L.27D) et D^{34} (Kabat L.30), Q^{32}>dél (Kabat L.28), G^{33}>dél (Kabat L.29) jusqu'aux coupleurs ^{32}GGG34 et ^{167}GGGG^{170}; chaîne lourde gamma 1 (1-451) [VH (*Homo sapiens* IGHV5-51*01 -(IGHD) -IGHJ3*01, CDR-Kabat [5.17.12] (31-35.50-66.99-110)) (1-121) -*Homo sapiens* IGHG1*03 (CH1 (122-219), charnière (220-234), CH2 N>^{301}A (235-344), CH3 (345-449), CHS (450-451)) (122-451)], (224-355')-disulfure avec la chaîne légère partielle, fusionnée avec une forme circulaire permutée de l'interleukine-2 humaine (1'-355') [V-KAPPA partielle (*Homo sapiens* IGKV1-39*01, CDR-Kabat [8] (CDR-L1 partiel: Kabat L.24-L.27D) (24'-31')) (1'-31')] fusionnée à l'aide d'un coupleur peptidique $^{32'}$GGG$^{34'}$ au fragment de l'interleukine-2 humaine (IL-2, facteur de croissance des lymphocytes T (FCLT)), dans sa forme permutée (fragment C-terminal 77-133 (35'-91' dans la séquence en cours) fusionné au fragment N-terminal 2-76 (92'-166' de la séquence en cours)), variante (^{125}C>S$^{83'}$), fusionné à l'aide du coupleur peptidique $^{167'}$GGGG$^{170'}$ à la chaîne légère kappa partielle [V-KAPPA (*Homo sapiens* IGKV1-39*01 -IGKJ4*01, CDR-Kabat [5.7.9] (CDR-L1 partiel: Kabat L.30-L.34) (171'-175'.191'-197'.230'-238') (171'-248') -*Homo sapiens* IGKC*01 (249'-355')]; dimère (230-230'':233-233'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa
balekafusp alfa	inmunoglobulina humanizada G1-kappa, anti-[interleukina-2 humana (IL-2, factor de crecimiento de células T, TCGF)] con una cadena ligera kappa manipulada, donde una forma circular permutada de una interleukina-2 human se insera en CDR-L1 entre Y^{31} (Kabat L.27D) y D^{34} (Kabat L.30), Q^{32}>del (Kabat L.28), G^{33}>del (Kabat L.29) a través de enlaces ^{32}GGG^{34} y ^{167}GGGG^{170}; cadena pesada gamma 1(1-451) [VH (*Homo sapiens* IGHV5-51*01 -(IGHD) -IGHJ3*01, CDR-Kabat [5.17.12] (31-35.50-66.99-110)) (1-121) -*Homo sapiens* IGHG1*03 (CH1 (122-219), bisagra (220-234), CH2 N>^{301}A (235-344), CH3 (345-449), CHS (450-451)) (122-451)], (224-355')-disulfuro con una cadena ligera kappa parcial fusionada a una forma permutada circular de interleukina-2 humana (1'-355') [parcial V-KAPPA (*Homo sapiens* IGKV1-39*01, CDR-Kabat [8] (parcial CDR-L1: Kabat L.24-L.27D) (24'-31')) (1'-31')] fusionada a través de un enlace peptídico $^{32'}$GGG$^{34'}$ a una interleukina-2 humana (IL-2, factor de crecimiento de células T (TCGF)) en una forma permutada (C-terminal fragmento 77-133 (35'-91' en la secuencia actual) fusionada al fragmento N-terminal 2-76 (92'-166' en la secuencia actual)), variante (^{125}C>S$^{83'}$), fusionada a través de enlace peptídico $^{167'}$GGGG$^{170'}$ a una cadena ligera kappa parcial [V-KAPPA (*Homo sapiens* IGKV1-39*01 -IGKJ4*01, CDR-Kabat [5.7.9] (parcial CDR-L1: Kabat L.30-L.34) (171'-175'.191'-197'.230'-238')) (171'-248') -*Homo sapiens* IGKC*01 (249'-355')]; dímero (230-230'':233-233'')-bisdisulfuro, producido en células ováricas de hamster Chino (CHO), línea celular CHO-K1, glicoforma alfa

Sequence / Séquence / Secuencia
IgG1 heavy chain

```
EVQLVQSGAE VKKPGESLKI SCKGSGYAFT NYLIEWVRQM PGKGLEWMGV   50
INPGSGGTNY NEKFKGQVTI SADKSISTAY LQWSSLKASD TAMYYCARWR  100
GEGYYAYFDV WGQGTTVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV  150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ  200
TYICNVNHKP SNTKVDKRVE PKSCDKTHTC PPCPAPELLG GPSVFLFPPK  250
PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY  300
ASTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP  350
QVYTLPPSRE EMTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP  400
VLDSDGSFFL YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG  450
K                                                       451
```

IgG1 light chain-permuted IL-2

```
AIRLTQSPSS FSASTGDRVT ITCKASQSVD YGGGNFHLRP RDLISNINVI   50
VLELKGSETT FMCEYADETA TIVEFLNRWI TFSQSIISTL TPTSSSTKKT  100
QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  150
EELKPLEEVL NLAQSKGGGG DSYMNWYQQK PGKAPKLLIY AASNLESGVP  200
SRFSGSGSGT DFTLTISSLQ SEDFATYYCQ QSNEDPYTFG GGTKVEIKRT  250
VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK VDNALQSGNS  300
QESVTEQDSK DSTYSLSSTL TLSKADYEKH KVYACEVTHQ GLSSPVTKSF  350
NRGEC                                                   355
```

Mutations / Mutations / Mutaciónes
N^{301}>A, $^{125'}C$>S$^{83'}$

Peptide linker / Peptide liant / Péptido de unión
$^{32'}GGG^{34'}$, $^{167'}GGGG^{170'}$

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra IgG1 heavy chain: 22-96, 148-204, 265-325, 371-429,
22"-96", 148"-204", 265"-325", 371"-429"
Intra IgG1 light chain-IL-2: 23'-229', 63'-148', 275'-335', 23'"-229'", 63'"-148'", 275'"-335'"
Inter IgG1 heavy chain-light chain-IL-2: 224-355', 224"-355'"
Inter IgG1 heavy chain-heavy chain: 230-230", 233-233"

O-glycosylation sites / Sites de O-glycosylation / Posiciones de O-glicosilación
T93', T93'"

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
IgG1 heavy chain: 451, 451"

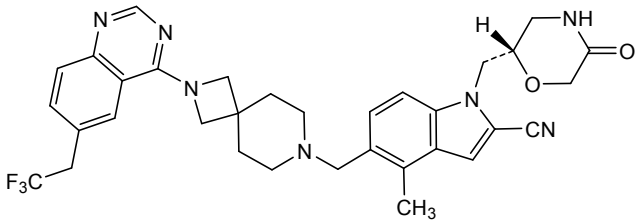
balomenibum

balomenib — 4-methyl-1-{[(2*S*)-5-oxomorpholin-2-yl]methyl}-5-({2-[6-(2,2,2-trifluoroethyl)quinazolin-4-yl]-2,7-diazaspiro[3.5]nonan-7-yl}methyl)-1*H*-indole-2-carbonitrile

baloménib — 4-méthyl-1-{[(2S)-5-oxomorpholin-2-yl]méthyl}-5-({2-[6-(2,2,2-trifluoroéthyl)quinazolin-4-yl]-2,7-diazaspiro[3.5]nonan-7-yl}méthyl)-1*H*-indole-2-carbonitrile

balomenib — 4-metil-1-{[(2S)-5-oxomorfolin-2-il]metil}-5-({2-[6-(2,2,2-trifluoroetil)quinazolin-4-il]-2,7-diazaespiro[3.5]nonan-7-il}metil)-1*H*-indol-2-carbonitrilo

$C_{33}H_{34}F_3N_7O_2$



baloncibartum #

baloncibart	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; H-gamma4 heavy chain *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV3-23*04 (89.6%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, 12-G4v5 h P10 (CH1 (121-218), hinge 1-12 S10>P (228) (219-230), CH2 L92 (309) (231-340), CH3 (341-445), CHS (446-447)) (121-447)], (134-214')-disulfide with L-kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-6*01 (93.7%) -IGKJ3*01 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-07') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dimer (226-226'':229-229'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa
baloncibart	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*; chaîne lourde H-gamma4 *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV3-23*04 (89.6%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, 12-G4v5 h P10 (CH1 (121-218), charnière 1-12 S10>P (228) (219-230), CH2 L92 (309) (231-340), CH3 (341-445), CHS (446-447)) (121-447)], (134-214')-disulfure avec la chaîne légère L-kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-6*01 (93.7%) -IGKJ3*01 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-07') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dimère (226-226'':229-229'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa
baloncibart	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*; cadena pesada H-gamma4 *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV3-23*04 (89.6%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, 12-G4v5 h P10 (CH1 (121-218), bisagra 1-12 S10>P (228) (219-230), CH2 L92 (309) (231-340), CH3 (341-445), CHS (446-447)) (121-447)], (134-214')-disulfuro con la cadena ligera L-kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-6*01 (93.7%) -IGKJ3*01 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-07') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dímero (226-226'':229-229'')-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 SCAASGFSFV SYVMGWVRQA PGKGLEWVSS  50
ISGSLTNTYY ADPVKGRFTI SRDNSKNTLY LQMNSLRAED TAAYYCVTYD 100
ILTGHLFDYW GQGTLVTVSS ASTKGPSVFP LAPCSRSTSE STAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTKT 200
YTCNVDHKPS NTKVDKRVES KYGPPCPPCP APEFLGGPSV FLFPPKPKDT 250
LMISRTPEVT CVVVDVSQED PEVQFNWYVD GVEVHNAKTK PREEQFNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKGLPS SIEKTISKAK GQPREPQVYT 350
LPPSQEEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS 400
DGSFFLYSRL TVDKSRWQEG NVFSCSVMHE ALHNHYTQKS LSLSLGK    447
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Light chain / Chaîne légère / Cadena ligera

```
AIQMTQSPSS LSASVGDRVT ITCRSSQGIR NDFGWYQQKP GKAPKLLIYA  50
ASRLQSGVPS RFSGSGSGTD FTLTINNLQP EDFATYYCLQ DYTYPFTFGP 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) 22-96 147-203 261-321 367-425
22"-96" 147"-203" 261"-321" 367"-425"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194'"
Inter-H-L (CH1 10-CL 126) 134-214' 134"-214'"
Inter-H-H (h 8, h 11) 226-226" 229-229"

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

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

baluretgenum parvecum

baluretgene parvec	recombinant non-replicating adeno-associated virus serotype 5 (rAAV5) vector encoding human photoreceptor-specific nuclear hormone receptor subfamily 2, group E member 3 (NR2E3) under control of the CAG promoter (CMV enhancer / chicken beta-actin (CBA) promoter / chimeric intron) and a simian virus 40 (SV40) polyadenylation signal; flanked by AAV2 inverted terminal repeats
baluretgène parvec	vecteur recombinant de virus adéno-associé non réplicatif de sérotype 5 (rAAV5) codant le membre 3 du groupe E de la sous-famille 2 de récepteurs d'hormones nucléaires spécifiques aux photorécepteurs humains (NR2E3), sous le contrôle du promoteur CAG (amplificateur du CMV / promoteur de la bêta-actine de poulet (CBA) / intron chimérique), et un signal de polyadénylation du virus simien 40 (SV40); flanqué des répétitions terminales inversées AAV2
baluretgén parvec	vector de virus adenoasociado del serotipo 5, recombinante (rAAV5), no replicativo, que codifica el miembro 3 del grupo E de la subfamilia 2 del receptor nuclear de hormona específico de fotorreceptores (NR2E3) humano bajo el control del promotor CAG (potenciador de CMV / promotor de la beta actina de pollo (CBA) / intrón quimérico) y una señal de poliadenilación del virus simio 40 (SV40); flanqueado por las repeticiones terminales invertidas del AAV2

becondogrelum

becondogrel	methyl (*S*)-(2-chlorophenyl)[(7a*S*)-2-oxo-2,6,7,7a-tetrahydrothieno[3,2-*c*]pyridin-5(4*H*)-yl]acetate

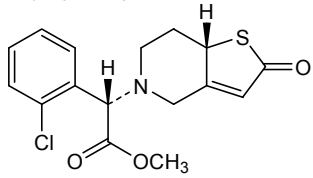
bécondogrel

(*S*)-(2-chlorophényl)[(7a*S*)-2-oxo-2,6,7,7a-tétrahydrothiéno[3,2-*c*]pyridin-5(4*H*)-yl]acétate de méthyle

becondogrel

(*S*)-(2-clorofenil)[(7a*S*)-2-oxo-2,6,7,7a-tetrahidrotieno[3,2-*c*]piridin-5(4*H*)-il]acetato de metilo

$C_{16}H_{16}ClNO_3S$



besufetamigum #

besufetamig

immunoglobulin (H-gamma1_L-kappa)_(H-gamma1_L-kappa), anti-[*Homo sapiens* PDCD1 (programmed cell death 1, PD-1, PD1, CD279)] and anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], *Homo sapiens* monoclonal antibody, bispecific;
H-gamma1 heavy chain anti-PDCD1 *Homo sapiens* (1-456) [VH (*Homo sapiens* IGHV7-4-1*02 (90.8%) -(IGHD) -IGHJ3*01 (92.3%) M123>T (122), CDR-IMGT [8.8.20] (26-33.51-58.97-116)) (1-127) -*Homo sapiens* IGHG1*03 G1m3, nG1m1 CH1 R120, CH3 E12, M14, 6-G1v59-1 CH2 G1.2, R1.1, 14-G1v72 CH3 D7, E24 (CH1 R120 (224) (128-225), hinge 1-15 (226-240), CH2 L1.2>G (245), G1.1>R (246) (241-350), CH3 L7>D (361), E12 (366), M14 (368), L24>E (378) (351-455), CHS K2>del (456)) (128-456)], (230-214')-disulfide with common L-kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*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, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')];
H-gamma1 heavy chain anti-CD3E *Homo sapiens* (1''-447'') [VH (*Homo sapiens* IGHV3-30-5*03 (88.8%) -(IGHD) -IGHJ5*02 (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, 6-G1v59-1 CH2 G1.2, R1.1, 14-G1v73 CH3 K7, K22 (CH1 R120 (215) (119''-216''), hinge 1-15 (217'', 231''), CH2 L1.2>G (236''), G1.1>R (237'') (232''-341''), CH3 L7>K (352''), E12 (357''), M14 (359''), T22>K (367'') (342''-446''), CHS K2>del (447'')) (119''-447'')], (221''-214''')-disulfide with common L-kappa light chain *Homo sapiens* (1'''-214''') [V-KAPPA (*Homo sapiens* IGKV1-39*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, V101 (C-KAPPA A45.1 (153'''), V101 (191''')) (108'''-214''')]; dimer (236-227'':239-230'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-DG44, glycoform alfa

bésufétamig	immunoglobuline (H-gamma1_L-kappa)_(H-gamma1_L-kappa), anti-[*Homo sapiens* PDCD1 (protéine 1 de mort cellulaire programmée, PD-1, PD1, CD279)] et anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], anticorps monoclonal *Homo sapiens*, bispécifique; chaîne lourde H-gamma1 anti-PDCD1 *Homo sapiens* (1-456) [VH (*Homo sapiens* IGHV7-4-1*02 (90.8%) -(IGHD) -IGHJ3*01 (92.3%) M123>T (122), CDR-IMGT [8.8.20] (26-33.51-58.97-116)) (1-127) -*Homo sapiens* IGHG1*03 G1m3, nG1m1 CH1 R120, CH3 E12, M14, 6-G1v59-1 CH2 G1.2, R1.1, 14-G1v72 CH3 D7, E24 (CH1 R120 (224) (128-225), charnière 1-15 (226-240), CH2 L1.2>G (245), G1.1>R (246) (241-350), CH3 L7>D (361), E12 (366), M14 (368), L24>E (378) (351-455), CHS K2>del (456)) (128-456)], (230-214')-disulfure avec la chaîne légère commune L-kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*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, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; chaîne lourde H-gamma1 anti-CD3E *Homo sapiens* (1''-447'') [VH (*Homo sapiens* IGHV3-30-5*03 (88.8%) -(IGHD) -IGHJ5*02 (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, 6-G1v59-1 CH2 G1.2, R1.1, 14-G1v73 CH3 K7, K22 (CH1 R120 (215) (119''-216''), charnière 1-15 (217'', 231''), CH2 L1.2>G (236''), G1.1>R (237'') (232''-341''), CH3 L7>K (352''), E12 (357''), M14 (359''), T22>K (367'') (342''-446''), CHS K2>del (447'')) (119''-447'')], (221''-214''')-disulfure avec la chaîne légère commune L-kappa *Homo sapiens* (1'''-214''') [V-KAPPA (*Homo sapiens* IGKV1-39*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, V101 (C-KAPPA A45.1 (153'''), V101 (191''')) (108'''-214''')]; dimère (236-227'': 239-230'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-DG44, glycoforme alfa
besufetamig	inmunoglobulina (H-gamma1_L-kappa)_(H-gamma1_L-kappa), anti-[*Homo sapiens* PDCD1 (proteína 1 de muerte celular programada, PD-1, PD1, CD279)] y anti-[*Homo sapiens* CD3E (CD3 épsilon, Leu-4)], anticuerpo monoclonal *Homo sapiens*, biespecífico; cadena pesada H-gamma1 anti-PDCD1 *Homo sapiens* (1-456) [VH (*Homo sapiens* IGHV7-4-1*02 (90.8%) -(IGHD) -IGHJ3*01 (92.3%) M123>T (122), CDR-IMGT [8.8.20] (26-33.51-58.97-116)) (1-127) -*Homo sapiens* IGHG1*03 G1m3, nG1m1 CH1 R120, CH3 E12, M14, 6-G1v59-1 CH2 G1.2, R1.1, 14-G1v72 CH3 D7, E24 (CH1 R120 (224) (128-225), bisagra 1-15 (226-240), CH2 L1.2>G (245), G1.1>R (246) (241-350), CH3 L7>D (361), E12 (366), M14 (368), L24>E (378) (351-455), CHS K2>del (456)) (128-456)], (230-214')-disulfuro con la cadena ligera común L-kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*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, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; cadena pesada H-gamma1 anti-CD3E *Homo sapiens* (1''-447'') [VH (*Homo sapiens* IGHV3-30-5*03 (88.8%) -(IGHD) -IGHJ5*02 (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, 6-G1v59-1 CH2 G1.2, R1.1, 14-G1v73 CH3 K7, K22 (CH1 R120 (215) (119''-216''), bisagra 1-15 (217'', 231''), CH2 L1.2>G (236''), G1.1>R (237'') (232''-341''), CH3 L7>K (352''), E12 (357''), M14 (359''), T22>K (367'') (342''-446''), CHS K2>del (447'')) (119''-447'')], (221''-214''')-disulfuro con la cadena ligera común L-kappa *Homo sapiens* (1'''-214''') [V-KAPPA (*Homo sapiens* IGKV1-39*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, V101 (C-KAPPA A45.1 (153'''), V101 (191''')) (108'''-214''')]; dímero (236-227'': 239-230'')-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 anti-PDCD1 (H)

```
QVQLVQSGSE LKQPGASVKV SCKASGYTFT HYALHWLRQA PGQGLEWMGW  50
LNTNTENPTF AQGFTGRFVF SLDTSVTTAY LQISSLKAED TAVYYCARGD 100
MVVPTTIWNY YHFMDVWGQG TTVTVSSAST KGPSVFPLAP SSKSTSGGTA 150
ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS 200
SSLGTQTYIC NVNHKPSNTK VDKRVEPKSC DKTHTCPPCP APELGRGPSV 250
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK 300
PREEQYNSTY RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK 350
GQPREPQVYT DPPSREEMTK NQVSLTCEVK GFYPSDIAVE WESNGQPENN 400
YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS 450
LSLSPG                                               456
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Heavy chain / Chaîne lourde / Cadena pesada: H-gamma1 anti-CD3E (H")

```
QVQLVQSGGG VVQPGRSLRL SCVASGFTFS SYGMHWVRQA PGKGLEWVAQ  50
IWYNARKQEY SDSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCTRGT 100
GYNWFDPWGQ GTLVTVSSAS TKGPSVFPLA PSSKSTSGGT AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTQTYI 200
CNVNHKPSNT KVDKRVEPKS CDKTHTCPPC PAPELGRGPS VFLFPPKPKD 250
TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNST 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY 350
TKPPSREEMT KNQVSLKCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD 400
SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPG    447
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Light chain / Chaîne légère / Cadena ligera: L-kappa common (L', L'")

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

Post-translational modifications

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

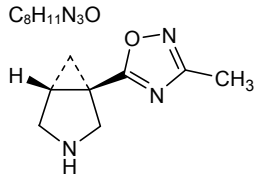
Intra-H (C23-C104) 22-96 154-210 271-331 377-435
22"-96" 145"-201" 262"-322" 368"-426"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194'"
Intra-H-L (h 5-CL 126) 230-214' 221"-214'"
Inter-H-H (h 11, h 14) 236-227" 239-230"

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: 307, 298"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

betovumelinum

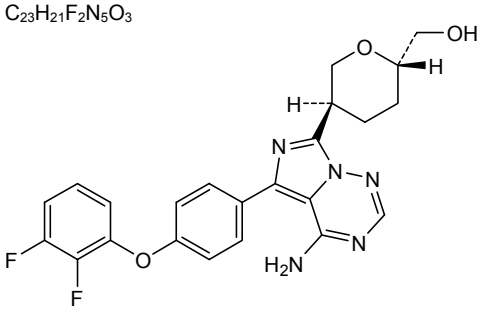
betovumeline	(1*R*,5*R*)-1-(3-methyl-1,2,4-oxadiazol-5-yl)-3-azabicyclo[3.1.0]hexane
bétovuméline	(1*R*,5*R*)-1-(3-méthyl-1,2,4-oxadiazol-5-yl)-3-azabicyclo[3.1.0]hexane
betovumelina	(1*R*,5*R*)-1-(3-metil-1,2,4-oxadiazol-5-il)-3-azabiciclo[3.1.0]hexano



birelentinibum

birelentinib	[(2*S*,5*S*)-5-{4-amino-5-[4-(2,3-difluorophenoxy)phenyl]imidazo[5,1-*f*][1,2,4]triazin-7-yl}oxan-2-yl]methanol
birélentinib	[(2*S*,5*S*)-5-{4-amino-5-[4-(2,3-difluorophénoxy)phényl]imidazo[5,1-*f*][1,2,4]triazin-7-yl}oxan-2-yl]méthanol
birelentinib	[(2*S*,5*S*)-5-{4-amino-5-[4-(2,3-difluorofenoxi)fenil]imidazo[5,1-*f*][1,2,4]triazin-7-il}oxan-2-il]metanol

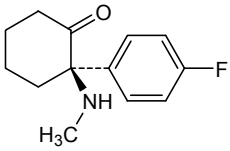
$C_{23}H_{21}F_2N_5O_3$



blixeprodilum

blixeprodil	(2*R*)-2-(4-fluorophenyl)-2-(methylamino)cyclohexan-1-one
blixéprodil	(2*R*)-2-(4-fluorophényl)-2-(méthylamino)cyclohexan-1-one
blixeprodil	(2*R*)-2-(4-fluorofenil)-2-(metilamino)ciclohexan-1-ona

$C_{13}H_{16}FNO$



bocunebartum #

bocunebart	immunoglobulin G1-kappa, anti-[*Homo sapiens* ADCYAP1 (adenylate cyclase-activating polypeptide 1, pituitary adenylate cyclase-activating polypeptide, PACAP)], humanized monoclonal antibody; H-gamma1 heavy chain humanized (1-442) [VH (*Homo sapiens* IGHV3-66*01 (81.4%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.7.6] (26-33.51-57.96-101)) (1-112) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, 8-G1v29 CH2 A84.4 (CH1 R120>K (209) (113-210), hinge 1-15 (211-225), CH2 N84.4>A (292) (226-335), CH3 E12 (351), M14 (353) (336-440), CHS (441-442)) (113-442)], (215-216')-disulfide with L-kappa light

	chain humanized (1'-216') [V-KAPPA (*Homo sapiens* IGKV1-5*01 (85.4%) -IGKJ1*01 (90.0%) Q120>G (102'), CDR-IMGT [7.3.10] (27'-33'.51'-53'.90'-99')) (1'-109') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (155'), V101 (193')) (110'-216')]; dimer (221-221":224-224")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-DG44, non-glycosylated
bocunebart	immunoglobuline G1-kappa, anti-[*Homo sapiens* ADCYAP1 (polypeptide 1 activant l'adénylate cyclase, polypeptide activant l'adénylate cyclase pituitaire, PACAP)], anticorps monoclonal humanisé; chaîne lourde H-gamma1 humanisée (1-442) [VH (*Homo sapiens* IGHV3-66*01 (81.4%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.7.6] (26-33.51-57.96-101)) (1-112) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, 8-G1v29 CH2 A84.4 (CH1 R120>K (209) (113-210), charnière 1-15 (211-225), CH2 N84.4>A (292) (226-335), CH3 E12 (351), M14 (353) (336-440), CHS (441-442)) (113-442)], (215-216')-disulfure avec la chaîne légère L-kappa humanisée (1'-216') [V-KAPPA (*Homo sapiens* IGKV1-5*01 (85.4%) -IGKJ1*01 (90.0%) Q120>G (102'), CDR-IMGT [7.3.10] (27'-33'.51'-53'.90'-99')) (1'-109') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (155'), V101 (193')) (110'-216')]; dimère (221-221":224-224")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-DG44, non-glycosylé
bocunebart	inmunoglobulina G1-kappa, anti-[*Homo sapiens* ADCYAP1 (polipéptido 1 activador de la adenilato ciclasa, polipéptido activador de la adenilato ciclasa pituitaria, PACAP)], anticuerpo monoclonal humanizado; cadena pesada H-gamma1 humanizada (1-442) [VH (*Homo sapiens* IGHV3-66*01 (81.4%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.7.6] (26-33.51-57.96-101)) (1-112) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, 8-G1v29 CH2 A84.4 (CH1 R120>K (209) (113-210), bisagra 1-15 (211-225), CH2 N84.4>A (292) (226-335), CH3 E12 (351), M14 (353) (336-440), CHS (441-442)) (113-442)], (215-216')-disulfuro con la cadena ligera L-kappa humanizada (1'-216') [V-KAPPA (*Homo sapiens* IGKV1-5*01 (85.4%) -IGKJ1*01 (90.0%) Q120>G (102'), CDR-IMGT [7.3.10] (27'-33'.51'-53'.90'-99')) (1'-109') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (155'), V101 (193')) (110'-216')]; dímero (221-221":224-224")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-DG44, no glicosilado

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAASGIDLN SYYMTWVRQA PGKGLEWIGF  50
IDAGGDAYYA SWAKGRFTIS RDNSKNTVYL QMNSLRAEDT AVYFCARDLD 100
LWGQGTLVTV SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT 150
VSWNSGALTS GVHTFPAVLQ SSGLYSLSSV VTVPSSSLGT QTYICNVNHK 200
PSNTKVDKKV EPKSCDKTHT CPPCPAPELL GGPSVFLFPP KPKDTLMISR 250
TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ YASTYRVVSV 300
LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR 350
EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF 400
LYSKLTVDKS RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GK          442
```

Light chain / Chaîne légère / Cadena ligera

```
DIQLTQSPST LSASVGDRVT ITCQSSESVY GNYLAWFQQK PGKAPKFLIY  50
EASKLESGVP SRFSGSGSGT EFTLTISSLQ PDDFATYYCA GGDISEGVAF 100
GGGTKVEIKR 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) 22-95 139-195 256-316 362-420
22"-95" 139"-195" 256"-316" 362"-420"
Intra-L (C23-C104) 23'-89' 136'-196'
23'"-89'" 136'"-196'"
Inter-H-L (h 5-CL 126) 215-216' 215"-216'"
Inter-H-H (h 11, h 14) 221-221" 224-224"

No N-glycosylation sites / pas de sites de N-glycosylation / ningùm posición de N-glycosilación
H CH2 N84.4>A (8-G1v29): 292, 292"

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

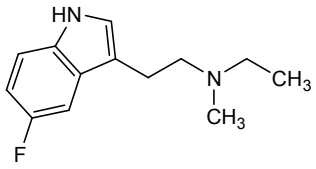
bretisilocinum

bretisilocin — *N*-ethyl-2-(5-fluoro-1*H*-indol-3-yl)-*N*-methylethan-1-amine

brétisilocine — *N*-éthyl-2-(5-fluoro-1*H*-indol-3-yl)-*N*-méthyléthan-1-amine

bretisilocina — *N*-etil-2-(5-fluoro-1*H*-indol-3-il)-*N*-metiletan-1-amina

$C_{13}H_{17}FN_2$



cemivameranum

cemivameran — messenger RNA (mRNA), 5'-capped, encoding a full-length, codon-optimised pre-fusion stabilised conformation variant (K982P and V983P) of the SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2) spike (S) glycoprotein (Omicron KP.2 variant; GISAID: EPI_ISL_18912216), flanked by 5' and 3' untranslated regions and a 3' polyadenylation (polyA) tail; contains N^1-methylpseudouridine instead of uridine (*all*-U>m$^1\Psi$)

cémivaméran — ARN messager (ARNm), coiffé en 5', codant une variante de conformation stabilisée de préfusion, de longueur complète, optimisée par codon (K982P et V983P) de la glycoprotéine du spicule (S) du SRAS-CoV-2 (coronavirus 2 du syndrome respiratoire aigu sévère) (variant Omicron KP.2; GISAID: EPI_ISL_18912216), flanqué en 5' et 3' de régions non traduites et d'une queue de polyadénylation (polyA) en 3'; contient de la N^1-méthylpseudouridine en lieu de l'uridine (*tout*-U>m$^1\Psi$)

cemivamerán — ARN mensajero (ARNm), protegido en 5', que codifica, con codones optimizados, para la secuencia completa de una variante estabilizada en conformación pre-fusión (K982P y V983P) de la glicoproteína de la espícula (S) del SRAS-Cov-2 (coronavirus 2 del síndrome respiratorio agudo severo) (variante Omicron KP.2; GISAID: EPI_ISL_18912216), flanqueada por regiones sin traducir 5' y 3' y una cola de poliadenilación (poliA) en 3'; contiene N^1-metilpseudouridina en lugar de uridina (*todo*-U>$m^1\Psi$)

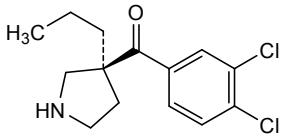
cendifensinum

cendifensine — (3,4-dichlorophenyl)[(3*S*)-3-propylpyrrolidin-3-yl]methanone

cendifensine — (3,4-dichlorophényl)[(3*S*)-3-propylpyrrolidin-3-yl]méthanone

cendifensina — (3,4-diclorofenil)[(3*S*)-3-propilpirrolidin-3-il]metanona

$C_{14}H_{17}Cl_2NO$



cenvacibartum #

cenvacibart — immunoglobulin G4-kappa, anti-[*Homo sapiens* F11 (coagulation factor 11, coagulation factor XI, FXI, plasma thromboplastin antecedent, PTA)], *Homo sapiens* monoclonal antibody;
H-gamma4 heavy chain *Homo sapiens* (1-445) [VH (*Homo sapiens* IGHV3-11*01 (91.7%) -(IGHD) -IGHJ3*02 (100%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, 12-G4v5 h P10 (CH1 (119-216), hinge 1-12 S10>P (226) (217-228), CH2 L92 (307) (229-338), CH3 (339-443), CHS (444-445)) (119-445)], (132-214')-disulfide with L-kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (95.8%) -IGKJ2*02 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA 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

cenvacibart — immunoglobuline G4-kappa, anti-[*Homo sapiens* F11 (facteur de coagulation 11, facteur de coagulation XI, FXI, antécédent de la thromboplastine plasmatique, PTA)], anticorps monoclonal *Homo sapiens*;
chaîne lourde H-gamma4 *Homo sapiens* (1-445) [VH (*Homo sapiens* IGHV3-11*01 (91.7%) -(IGHD) -IGHJ3*02 (100%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, 12-G4v5 h P10 (CH1 (119-216), charnière 1-12 S10>P (226) (217-228), CH2 L92 (307) (229-338), CH3 (339-443), CHS (444-445)) (119-445)], (132-214')-disulfure avec la chaîne légère L-kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (95.8%) -IGKJ2*02 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA 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

cenvacibart

inmunoglobulina G4-kappa, anti-[*Homo sapiens* F11 (factor de coagulación 11, factor de coagulación XI, FXI, antecedente de la tromboplastina plasmática, PTA)], anticuerpo monoclonal *Homo sapiens*;
cadena pesada H-gamma4 *Homo sapiens* (1-445) [VH (*Homo sapiens* IGHV3-11*01 (91.7%) -(IGHD) -IGHJ3*02 (100%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, 12-G4v5 h P10 (CH1 (119-216), bisagra 1-12 S10>P (226) (217-228), CH2 L92 (307) (229-338), CH3 (339-443), CHS (444-445)) (119-445)], (132-214')-disulfuro con la cadena ligera L-kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (95.8%) -IGKJ2*02 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA 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

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVESGGG LVKPGGSLRL SCAASGFTFS DYSMNWIRQA PGKGLEWISY  50
ISFSGNSIYY ADSVKGRFTI SRDNAKNSLY LQMNSLRVED TAIYYCTSRD 100
WGYAFDIWGQ GTMVTVSSAS TKGPSVFPLA PCSRSTSEST AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTKTYT 200
CNVDHKPSNT KVDKRVESKY GPPCPPCPAP EFLGGPSVFL FPPKPKDTLM 250
ISRTPEVTCV VVDVSQEDPE VQFNWYVDGV EVHNAKTKPR EEQFNSTYRV 300
VSVLTVLHQD WLNGKEYKCK VSNKGLPSSI EKTISKAKGQ PREPQVYTLP 350
PSQEEMTKNQ VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG 400
SFFLYSRLTV DKSRWQEGNV FSCSVMHEAL HNHYTQKSLS LSLGK      445
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Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSF LSASLGDRVT ITCQASQDIS NYLNWYQVKP GKAPKLLIYD  50
ASNLETGVPS RFSGSGSGTD FTFTISSLQP EDIATYFCQQ YDNLPYIFGQ 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) 22-96 145-201 259-319 365-423
22"-96" 145"-201" 259"-319" 365"-423"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194'"
Inter-H-L (CH1 10-CL 126) 132-214' 132"-214'"
Inter-H-H (h 8, h 11) 224-224" 227-227"

N-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: 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"

cenzestotugum #

cenzestotug

immunoglobulin G1-kappa, anti-[*Homo sapiens* TNFRSF4 (tumor necrosis factor receptor (TNFR) superfamily member 4, OX40, CD134)], monoclonal antibody;
H-gamma1 heavy chain (1-443) [VH Musmus/Homsap (*Mus musculus* IGHV2-2*01 (80.4%) -(IGHD) -IGHJ4*01 (91.7%) S123>L (108)/*Homo sapiens* IGHV3-30-5*03 (76.5%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.7.7] (26-33.51-57.96-102)) (1-113) -*Homo sapiens* IGHG1*03v (100%) G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (210) (114-211), hinge 1-15 (212-226), CH2 (227-336), CH3 E12 (352), M14 (354) (337-441), CHS (442-443)) (114-443)], (216-214')-disulfide with L-kappa

	light chain (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (87.4%) -IGKJ4*01 (81.8%) V124>L (104'), I126>V (106'), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dimer (222-222'':225-225'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa
cenzestotug	immunoglobuline G1-kappa, anti-[*Homo sapiens* TNFRSF4 (membre 4 de la superfamille des récepteurs des facteurs de nécrose tumorale (TNFR), OX40, CD134)], anticorps monoclonal; chaîne lourde H-gamma1 (1-443) [VH Musmus/Homsap (*Mus musculus* IGHV2-2*01 (80.4%) -(IGHD) -IGHJ4*01 (91.7%) S123>L (108)/*Homo sapiens* IGHV3-30-5*03 (76.5%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.7.7] (26-33.51-57.96-102)) (1-113) -*Homo sapiens* IGHG1*03v (100%) G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (210) (114-211), charnière 1-15 (212-226), CH2 (227-336), CH3 E12 (352), M14 (354) (337-441), CHS (442-443)) (114-443)], (216-214')-disulfure avec la chaîne légère L-kappa (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (87.4%) -IGKJ4*01 (81.8%) V124>L (104'), I126>V (106'), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dimère (222-222'':225-225'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa
cenzestotug	inmunoglobulina G1-kappa, anti-[*Homo sapiens* TNFRSF4 (miembro 4 de la superfamilia de los receptores de los factores de necrosis tumoral (TNFR), OX40, CD134)], anticuerpo monoclonal; cadena pesada H-gamma1 (1-443) [VH Musmus/Homsap (*Mus musculus* IGHV2-2*01 (80.4%) -(IGHD) -IGHJ4*01 (91.7%) S123>L (108)/*Homo sapiens* IGHV3-30-5*03 (76.5%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.7.7] (26-33.51-57.96-102)) (1-113) -*Homo sapiens* IGHG1*03v (100%) G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (210) (114-211), bisagra 1-15 (212-226), CH2 (227-336), CH3 E12 (352), M14 (354) (337-441), CHS (442-443)) (114-443)], (216-214')-disulfuro con la cadena ligera L-kappa (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (87.4%) -IGKJ4*01 (81.8%) V124>L (104'), I126>V (106'), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dímero (222-222'':225-225'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVESGGG VVQPGRSLRI SCAVSGFSLT SYGVLWVRQA PGKGLEWLGV  50
IWSGGSTDYN AAFISRLTIS RDNSKSTVYF QMNSLRAEDT AVYYCAREEF 100
GYWGQGTLVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC LVKDYFPEPV 150
TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG TQTYICNVNH 200
KPSNTKVDKK VEPKSCDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS 250
RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYNSTYRVVS 300
VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR EPQVYTLPPS 350
REEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT PPVLDSDGSF 400
FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLS PGK         443
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Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCRASQDIN NYLNWYQQKP GGAVKLLIYY  50
TSRLHTGVPS RFSGSGSGTD FTLTISSLQP EDIATYYCQQ TNTLPWTFGG 100
GTKLEVKRTV 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) 22-95 140-196 257-317 363-421
22"-95" 140"-196" 257"-317" 363"-421"

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

Inter-H-L (h 5-CL 126) 216-214' 216"-214'"

Inter-H-H (h 11, h 14) 222-222" 225-225"

N-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"

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"

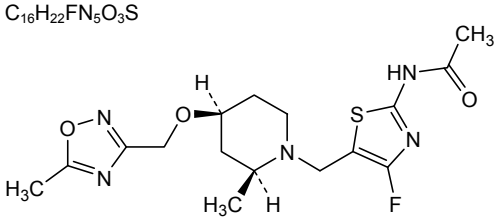
ceperognastatum

ceperognastat — *N*-[4-fluoro-5-({(2*S*,4*S*)-2-methyl-4-[(5-methyl-1,2,4-oxadiazol-3-yl)methoxy]piperidin-1-yl}methyl)-1,3-thiazol-2-yl]acetamide

cépérognastat — *N*-[4-fluoro-5-({(2*S*,4*S*)-2-méthyl-4-[(5-méthyl-1,2,4-oxadiazol-3-yl)méthoxy]pipéridin-1-yl}méthyl)-1,3-thiazol-2-yl]acétamide

ceperognastat — *N*-[4-fluoro-5-({(2*S*,4*S*)-2-metil-4-[(5-metil-1,2,4-oxadiazol-3-il)metoxi]piperidin-1-il}metil)-1,3-tiazol-2-il]acetamida

$C_{16}H_{22}FN_5O_3S$



ciltistotugum

ciltistotug — immunoglobulin G2-kappa, anti-[*Homo sapiens* CD40 (TNFRSF5, tumor necrosis factor receptor (TNFR) superfamily member 5, p50)], monoclonal antibody;
H-gamma2 heavy chain (1-441) [VH Musmus/Homsap (*Mus musculus* IGHV1-47-14*01 (84.7%) -(IGHD) -IGHJ2*01 (100%)/*Homo sapiens* IGHV1-2*02 (79.6%) -(IGHD) -IGHJ6*01 (90.9%) V124>L (111), CDR-IMGT [8.8.8] (26-33.51-58.97-104)) (1-115) -*Homo sapiens* IGHG2*01 G2m.. (100%) CH2 V45.1 (CH1 (116-213), hinge 1-12 (214-225), CH2 V45.1 (276) (226-334), CH3 (335-439), CHS (440-441)) (116-441)], (129-219')-disulfide with L-kappa light chain (1'-219') [V-KAPPA

	Musmus/Homsap (*Mus musculus* IGKV1-110*01 (88.0%) -IGKJ1*01 (91.7%) L124>V (109')/*Homo sapiens* IGKV2-30*02 (88.0%) -IGKJ4*01 (100%), CDR-IMGT [11.3.9] (27'-37'.55'-57'.94'-102')) (1'-112') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (158'), V101 (196')) (113'-219')]; dimer (217-217'':218-218'':221-221'':224-224'')-tetrakisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa
ciltistotug	immunoglobuline G2-kappa, anti-[*Homo sapiens*CD40 (TNFRSF5, membre 5 de la superfamille des récepteurs des facteurs de nécrose tumorale (TNFR), p50)], anticorps monoclonal; chaîne lourde H-gamma2 (1-441) [VH Musmus/Homsap (*Mus musculus* IGHV1-47-14*01 (84.7%) -(IGHD) -IGHJ2*01 (100%)/*Homo sapiens* IGHV1-2*02 (79.6%) -(IGHD) -IGHJ6*01 (90.9%) V124>L (111), CDR-IMGT [8.8.8] (26-33.51-58.97-104)) (1-115) -*Homo sapiens* IGHG2*01 G2m.. (100%) CH2 V45.1 (CH1 (116-213), charnière 1-12 (214-225), CH2 V45.1 (276) (226-334), CH3 (335-439), CHS (440-441)) (116-441)], (129-219')-disulfure avec la chaîne légère kappa (1'-219') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV1-110*01 (88.0%) -IGKJ1*01 (91.7%) L124>V (109')/*Homo sapiens* IGKV2-30*02 (88.0%) -IGKJ4*01 (100%), CDR-IMGT [11.3.9] (27'-37'.55'-57'.94'-102')) (1'-112') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (158'), V101 (196')) (113'-219')]; dimère (217-217'':218-218'':221-221'':224-224'')-tétrakisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa
ciltistotug	inmunoglobulina G2-kappa, anti-[*Homo sapiens* CD40 (TNFRSF5, miembro 5 de la superfamilia de los receptores de los factores de necrosis tumoral (TNFR), p50)], anticuerpo monoclonal; cadena pesada H-gamma2 (1-441) [VH Musmus/Homsap (*Mus musculus* IGHV1-47-14*01 (84.7%) -(IGHD) -IGHJ2*01 (100%)/*Homo sapiens* IGHV1-2*02 (79.6%) -(IGHD) -IGHJ6*01 (90.9%) V124>L (111), CDR-IMGT [8.8.8] (26-33.51-58.97-104)) (1-115) -*Homo sapiens* IGHG2*01 G2m.. (100%) CH2 V45.1 (CH1 (116-213), bisagra 1-12 (214-225), CH2 V45.1 (276) (226-334), CH3 (335-439), CHS (440-441)) (116-441)], (129-219')-disulfuro con la cadena ligera kappa (1'-219') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV1-110*01 (88.0%) -IGKJ1*01 (91.7%) L124>V (109')/*Homo sapiens* IGKV2-30*02 (88.0%) -IGKJ4*01 (100%), CDR-IMGT [11.3.9] (27'-37'.55'-57'.94'-102')) (1'-112') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (158'), V101 (196')) (113'-219')]; dímero (217-217'':218-218'':221-221'':224-224'')-tetrakisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGASVKL SCKASGYTFI SYYIYWVKQA PGQGLEWIGG  50
INPRNGGTNF NEKFKSRATL TVDTSISTAY MELSRLRSED TAVYYCTRHG 100
NGVYWGQGTT LTVSSASTKG PSVFPLAPCS RSTSESTAAL GCLVKDYFPE 150
PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL SSVVTVPSSN FGTQTYTCNV 200
DHKPSNTKVD KTVERKCCVE CPPCPAPPVA GPSVFLFPPK PKDTLMISRT 250
PEVTCVVVDV SHEDPEVQFN WYVDGVEVHN AKTKPREEQF NSTFRVVSVL 300
TVVHQDWLNG KEYKCKVSNK GLPAPIEKTI SKTKGQPREP QVYTLPPSRE 350
EMTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP MLDSDGSFFL 400
YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG K          441
```

Light chain / Chaîne légère / Cadena ligera

```
DVVMTQSPLS LPVTLGQPAS ISCRSSQSLL HSNGNTYLHW YQQRPGQSPN  50
HLIYQVSNRF SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YFCSQTTHVP 100
WTFGGGTKVE IKRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK 150
VQWKVDNALQ SGNSQESVTE QDSKDSTYSL SSTLTLSKAD YEKHKVYACE 200
VTHQGLSSPV TKSFNRGEC                                   219
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 142-198 255-315 361-419
22"-96" 142"-198" 255"-315" 361"-419"
Intra-L (C23-C104) 23'-93' 139'-199'
23'"-93'" 139'"-199'"
Inter-H-L (CH1 10-CL 126) 129-219' 129"-219'"
Inter-H-H (h 4, h 5, h 8, h11) 217-217" 218-218" 221-221" 224-224"

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: 291, 291"
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: 441, 441"

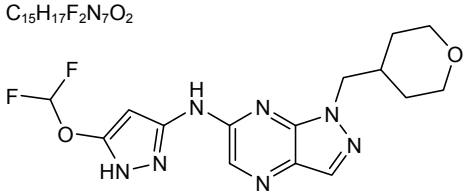
cirtociclibum

cirtociclib — *N*-[5-(difluoromethoxy)-1*H*-pyrazol-3-yl]-1-[(oxan-4-yl)methyl]-1*H*-pyrazolo[3,4-*b*]pyrazin-6-amine

cirtociclib — *N*-[5-(difluorométhoxy)-1*H*-pyrazol-3-yl]-1-[(oxan-4-yl)méthyl]-1*H*-pyrazolo[3,4-*b*]pyrazin-6-amine

cirtociclib — *N*-[5-(difluorometoxi)-1*H*-pirazol-3-il]-1-[(oxan-4-il)metil]-1*H*-pirazolo[3,4-*b*]pirazin-6-amina

$C_{15}H_{17}F_2N_7O_2$



claseprubartum

claseprubart — immunoglobulin G4-kappa, anti-[*Homo sapiens* C1S (complement C1s)], *Homo sapiens* monoclonal antibody; H-gamma4 heavy chain *Homo sapiens* (1-443) [VH (*Homo sapiens* IGHV3-11*01 (96.9%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, 12-G4v5 h P10, 6-G4v3 CH2 E1.2, 9-G4v21 CH2 Y15.1, T16, E18 (CH1 (118-215), hinge 1-12 S10>P (225) (216-227), CH2 L1.2>E (232), M15.1>Y (249), S16>T (251), T18>E (253), L92 (306) (228-337), CH3 (338-442), CHS K2>del (443)) (118-

	443)], (131-214')-disulfide with L-kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (95.8%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dimer (223-223'':226-226'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa
claséprubart	immunoglobuline G4-kappa, anti-[*Homo sapiens* C1S (complément C1s)], anticorps monoclonal *Homo sapiens*; chaîne lourde H-gamma4 *Homo sapiens* (1-443) [VH (*Homo sapiens* IGHV3-11*01 (96.9%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, 12-G4v5 h P10, 6-G4v3 CH2 E1.2, 9-G4v21 CH2 Y15.1, T16, E18 (CH1 (118-215), charnière 1-12 S10>P (225) (216-227), CH2 L1.2>E (232), M15.1>Y (249), S16>T (251), T18>E (253), L92 (306) (228-337), CH3 (338-442), CHS K2>del (443)) (118-443)], (131-214')-disulfure avec la chaîne légère L-kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (95.8%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dimère (223-223'':226-226'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa
claseprubart	inmunoglobulina G4-kappa, anti-[*Homo sapiens* C1S (complemento C1s)], anticuerpo monoclonal *Homo sapiens*; cadena pesada H-gamma4 *Homo sapiens* (1-443) [VH (*Homo sapiens* IGHV3-11*01 (96.9%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, 12-G4v5 h P10, 6-G4v3 CH2 E1.2, 9-G4v21 CH2 Y15.1, T16, E18 (CH1 (118-215), bisagra 1-12 S10>P (225) (216-227), CH2 L1.2>E (232), M15.1>Y (249), S16>T (251), T18>E (253), L92 (306) (228-337), CH3 (338-442), CHS K2>del (443)) (118-443)], (131-214')-disulfuro con la cadena ligera L-kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (95.8%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dímero (223-223'':226-226'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVKPGGSLRL SCAASGFTFS DYYMSWIRQA PGKGLEWVSY  50
ISRSGSTKYY ADSVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARDE 100
NYALDWWGQG TLVTVSSAST KGPSVFPLAP CSRSTSESTA ALGCLVKDYF 150
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTKTYTC 200
NVDHKPSNTK VDKRVESKYG PPCPPCPAPE FEGGPSVFLF PPKPKDTLYI 250
TREPEVTCVV VDVSQEDPEV QFNWYVDGVE VHNAKTKPRE EQFNSTYRVV 300
SVLTVLHQDW LNGKEYKCKV SNKGLPSSIE KTISKAKGQP REPQVYTLPP 350
SQEEMTKNQV SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS 400
FFLYSRLTVD KSRWQEGNVF SCSVMHEALH NHYTQKSLSL SLG         443
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCQASQDIS NYLNWYQQKP GKAPKLLIYD  50
ASNLETGVPS RFSGSGSGTD FTFTISSLQP EDIATYYCQH YEDYPLTFGG 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

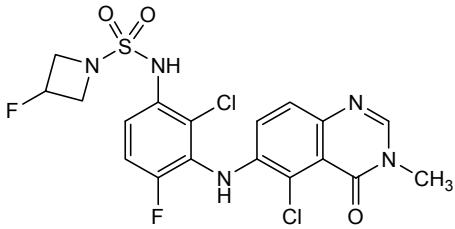
Intra-H (C23-C104)	22-96	144-200	258-318	364-422
	22"-96"	144"-200"	258"-318"	364"-422"
Intra-L (C23-C104)	23'-88'	134'-194'		
	23'"-88'"	134'"-194'"		
Inter-H-L (CH1 10-CL 126)	131-214'	131"-214'"		
Inter-H-H (h 8, h 11)	223-223"	226-226"		

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

claturafenibum

claturafenib	*N*-{2-chloro-3-[(5-chloro-3-methyl-4-oxo-3,4-dihydroquinazolin-6-yl)amino]-4-fluorophenyl}-3-fluoroazetidine-1-sulfonamide
claturafénib	*N*-{2-chloro-3-[(5-chloro-3-méthyl-4-oxo-3,4-dihydroquinazolin-6-yl)amino]-4-fluorophényl}-3-fluoroazétidine-1-sulfonamide
claturafenib	*N*-{2-cloro-3-[(5-cloro-3-metil-4-oxo-3,4-dihidroquinazolin-6-il)amino]-4-fluorofenil}-3-fluoroazetidina-1-sulfonamida

$C_{18}H_{15}Cl_2F_2N_5O_3S$



cliramitugum

cliramitug	immunoglobulin G1-kappa, anti-[*Homo sapiens* TTR (transthyretin) amyloid], *Homo sapiens* monoclonal antibody; H-gamma1 heavy chain *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV4-39*01 (87.9%) -(IGHD) -IGHJ3*02 (100%), CDR-IMGT [10.7.12](26-35.53-59.98-109)) (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* IGKV1-39*01 (92.6%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dimer (229-229":232-232")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa

cliramitug

immunoglobuline G1-kappa, anti-[*Homo sapiens* TTR (transthyrétine) amyloïde], anticorps monoclonal *Homo sapiens*;
chaîne lourde H-gamma1 *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV4-39*01 (87.9%) -(IGHD) -IGHJ3*02 (100%), CDR-IMGT [10.7.12] (26-35.53-59.98-109)) (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* IGKV1-39*01 (92.6%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dimère (229-229'':232-232'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa

cliramitug

inmunoglobulina G1-kappa, anti-[*Homo sapiens* TTR (transtiretina) amieloide], anticuerpo monoclonal *Homo sapiens*;
cadena pesada H-gamma1 *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV4-39*01 (87.9%) -(IGHD) -IGHJ3*02 (100%), CDR-IMGT [10.7.12] (26-35.53-59.98-109)) (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 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* IGKV1-39*01 (92.6%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dímero (229-229'':232-232'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QLQLQESGPG LVKPSETLSL TCSVSGGSII SRSSYWGWIR QPPGKGLEWI  50
GGIYHSGNTY DNPSLKSRLT MSVDTSKNQF SLNLRSVTAA DTAVYYCARI 100
VPGGDAFDIW 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 QKSLSLSPGK 450
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT IACRASQSVG TYLNWYQQKR GKAPKLLIFA  50
ASSLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ SYSSPPTFGQ 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-97 147-203 264-324 370-428
22''-97'' 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''

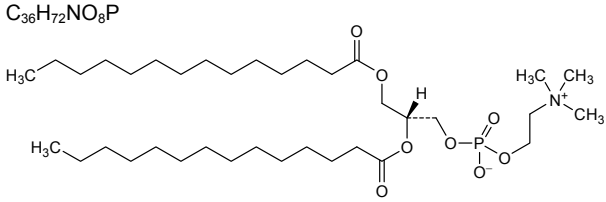
colfoscerili miristas

colfosceril miristate — (2*R*)-2,3-bis(tetradecanoyloxy)propyl 2-(trimethylazaniumyl)ethyl phosphate

miristate de colfoscéril — phosphate de (2*R*)-2,3-bis(tétradécanoyloxy)propyle et de 2-(triméthylazaniumyl)éthyle

miristato de colfoscerilo — fosfato de (2*R*)-2,3-bis(tetradecanoiloxi)propilo y 2-(trimetilazanioil)etilo

$C_{36}H_{72}NO_8P$



colulintidum

colulintide — *N*$^{2.1}$-acetyl-*N*$^{6.11}$-[(22*S*)-22,42-dicarboxy-10,19,24-trioxo-3,6,12,15-tetraoxa-9,18,23-triazadotetracontan-1-oyl]calcitonin [*Anguilla japonica* (Japanese eel)], [C^{1}>A, N^{3}>H, C^{7}>A, Q^{14}>2MeAla, Q^{20}>E, T^{21}>D, G^{30}>E, T^{31}>S]-variant; *N*-acetyl-L-alanyl-L-seryl-L-histidyl-L-leucyl-L-seryl-L-threonyl-L-alanyl-L-valyl-L-leucylglycyl-N^{6}-({[N-(19-carboxynonadecanoyl)-L-γ-glutamyl]amino}-10-oxo-3,6,12,15-tetraoxa-9-azaheptadecanoic-1-oyl)-L-lysyl-L-leucyl-L-seryl-2-methylalanyl-L-α-glutamyl-L-leucyl-L-histidyl-L-lysyl-L-leucyl-L-α-glutamyl-L-α-aspartyl-L-tyrosyl-L-prolyl-L-arginyl-L-threonyl-L-α-aspartyl-L-valylglycyl-L-alanyl-L-α-glutamyl-L-seryl-L-prolylamide

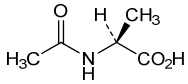
colulintide — *N*$^{2.1}$-acétyl-*N*$^{6.11}$-[(22*S*)-22,42-dicarboxy-10,19,24-trioxo-3,6,12,15-tétraoxa-9,18,23-triazadotétracontan-1-oyl]calcitonine [*Anguilla japonica* (anguille du Japon)], variant [C^{1}>A, N^{3}>H, C^{7}>A, Q^{14}>2MeAla, Q^{20}>E, T^{21}>D, G^{30}>E, T^{31}>S]; *N*-acétyl-L-alanyl-L-séryl-L-histidyl-L-leucyl-L-séryl-L-thréonyl-L-alanyl-L-valyl-L-leucylglycyl-*N*^{6}-({[*N*-(19-carboxynonadécanoyl)-L-γ-glutamyl]amino}-10-oxo-3,6,12,15-tétraoxa-9-azaheptadécanoïc-1-oyl)-L-lysyl-L-leucyl-L-séryl-2-méthylalanyl-L-α-glutamyl-L-leucyl-L-histidyl-L-lysyl-L-leucyl-L-α-glutamyl-L-α-aspartyl-L-tyrosyl-L-prolyl-L-arginyl-L-thréonyl-L-α-aspartyl-L-valylglycyl-L-alanyl-L-α-glutamyl-L-séryl-L-prolylamide

colulintida — *N*$^{2.1}$-acetil-*N*$^{6.11}$-[(22*S*)-22,42-dicarboxi-10,19,24-trioxo-3,6,12,15-tetraoxa-9,18,23-triazadotetracontan-1-oil]calcitonina (*Anguilla japonica*), variante [C^{1}>A, N^{3}>H, C^{7}>A, Q^{14}>2MeAla, Q^{20}>E, T^{21}>D, G^{30}>E, T^{31}>S]; *N*-acetil-L-alanil-L-seril-L-histidil-L-leucil-L-seril-L-treonil-L-alanil-L-valil-L-leucilglicil-*N*^{6}-({[*N*-(19-carboxinonadecanoil)-L-γ-glutamil]amino}-10-oxo-3,6,12,15-tetraoxa-9-azaheptadecanoic-1-oil)-L-lisil-L-leucil-L-seril-2-metilalanil-L-α-glutamil-L-leucil-L-histidil-L-lisil-L-leucil-L-α-glutamil-L-α-aspartil-L-tirosil-L-prolil-L-arginil-L-treonil-L-α-aspartil-L-valilglicil-L-alanil-L-α-glutamil-L-seril-L-prolilamida

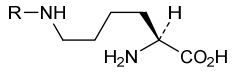
$C_{188}H_{309}N_{45}O_{62}$

ASHLSTAVLG KLSAELHKLE DYPRTDVGAE SP 32

Modified residues / Résidus modifiés / Restos modificados

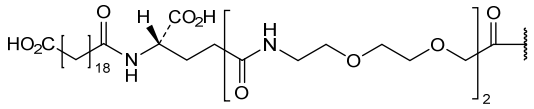


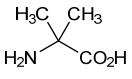
A (1)
N-Ac-L-Ala



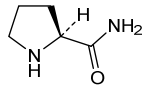
K (11)
N^{ε}-R-L-Lys

R:





A (14)
2-methyl-Ala, Aib



P (32)
L-Pro-NH_2

corabotasum #

corabotase

botulinum neurotoxin type A (BoNT/A, botA) [*Clostridium botulinum* strain Hall (ATCC 3502, NCTC 13319)], heavy chain fragment (HC 1-424), fused to botulinum neurotoxin type B (BoNT/B, botB) (*Clostridium botulinum* strain Okra), heavy chain, C-terminal fragment (HC 419-850, 425-856 in the final protein), variant (E^{750}>M^{756}, S^{758}>Y^{764}), (6-429')-disulfide with botulinum neurotoxin type A (BoNT/A, botA) [*Clostridium botulinum* strain Hall (ATCC 3502, NCTC 13319)], des-Met^0-light chain (LC 1'-437') (EC:3.4.24.69), produced by *Escherichia coli*

corabotase

neurotoxine botulique de type A (BoNT/A, botA) [*Clostridium botulinum*, souche Hall (ATCC 3502, NCTC 13319)], chaîne lourde, fragment (HC 1-424), fusionné à la neurotoxine botulique de type B (BoNT/B, botB) (*Clostridium botulinum*, souche Okra), chaîne lourde, fragment C-terminal (HC 419-850, 425-856 dans la protéine finale), variant (E^{750}>M^{756}, S^{758}>Y^{764}), (6-429')-disulfure avec neurotoxine botulique de type A (BoNT/A, botA) [*Clostridium botulinum*, souche Hall (ATCC 3502, NCTC 13319)], chaîne légère dés-Met^0 (LC 1'-437') (EC:3.4.24.69), produite par *Escherichia coli*

corabotasa

neurotoxina botulínica tipo A (BoNT/A, botA) [*Clostridium botulinum* cepa Hall (ATCC 3502, NCTC 13319)], cadena pesada, fragmento (HC 1-424), fusionada a neurotoxina botulínica tipo B (BoNT/B, botB) (*Clostridium botulinum* cepa Okra), cadena pesada, fragmento C-terminal (HC 419-850, 425-856 en la proteína final), variante (E^{750}>M^{756}, S^{758}>Y^{764}), (6-429')-disulfuro con neurotoxina botulínica tipo A (BoNT/A, botA) [*Clostridium botulinum* cepa Hall (ATCC 3502, NCTC 13319)], cadena ligera des-Met^0 (LC 1'-437') (EC:3.4.24.69), producida por *Escherichia coli*

Sequence / Séquence / Secuencia
Heavy chain / Chaîne lourde / Cadena pesada: **BoNT/A** + BoNT/B

```
ALNDLCIKVN NWDLFFSPSE DNFTNDLNKG EEITSDTNIE AAEENISLDL    50
IQQYYLTFNF DNEPENISIE NLSSDIIGQL ELMPNIERFP NGKKYELDKY   100
TMFHYLRAQE FEHGKSRIAL TNSVNEALLN PSRVYTFFSS DYVKKVNKAT   150
EAAMFLGWVE QLVYDFTDET SEVSTTDKIA DITIIIPYIG PALNIGNMLY   200
KDDFVGALIF SGAVILLEFI PEIAIPVLGT FALVSYIANK VLTVQTIDNA   250
LSKRNEKWDE VYKYIVTNWL AKVNTQIDLI RKKMKEALEN QAEATKAIIN   300
YQYNQYTEEE KNNINFNIDD LSSKLNESIN KAMININKFL NQCSVSYLMN   350
SMIPYGVKRL EDFDASLKDA LLKYIYDNRG TLIGQVDRLK DKVNNTLSTD   400
IPFQLSKYVD NQRLLSTFTE YIKNILNNII LNLRYKDNNL IDLSGYGAKV   450
EVYDGVELND KNQFKLTSSA NSKIRVTQNQ NIIFNSVFLD FSVSFWIRIP   500
KYKNDGIQNY IHNEYTIINC MKNNSGWKIS IRGNRIIWTL IDINGKTKSV   550
FFEYNIREDI SEYINRWFFV TITNNLNNAK IYINGKLESN TDIKDIREVI   600
ANGEIIFKLD GDIDRTQFIW MKYFSIFNTE LSQSNIEERY KIQSYSEYLK   650
DFWGNPLMYN KEYYMFNAGN KNSYIKLKKD SPVGEILTRS KYNQNSKYIN   700
YRDLYIGEKF IIRRKSNSQS INDDIVRKED YIYLDFFNLN QEWRVYTYKY   750
FKKEEMKLFL APIYDSDEFY NTIQIKEYDE QPTYSCQLLF KKDEESTDEI   800
GLIGIHRFYE SGIVFEEYKD YFCISKWYLK EVKRKPYNLK LGCNWQFIPK   850
DEGWTE                                                   856
```

Light chain / Chaîne légère / Cadena ligera: BoNT/A

```
PFVNKQFNYK DPVNGVDIAY IKIPNAGQMQ PVKAFKIHNK IWVIPERDTF    50
TNPEEGDLNP PPEAKQVPVS YYDSTYLSTD NEKDNYLKGV TKLFERIYST   100
DLGRMLLTSI VRGIPFWGGS TIDTELKVID TNCINVIQPD GSYRSEELNL   150
VIIGPSADII QFECKSFGHE VLNLTRNGYG STQYIRFSPD FTFGFEESLE   200
VDTNPLLGAG KFATDPAVTL AHELIHAGHR LYGIAINPNR VFKVNTNAYY   250
EMSGLEVSFE ELRTFGGHDA KFIDSLQENE FRLYYYNKFK DIASTLNKAK   300
SIVGTTASLQ YMKNVFKEKY LLSEDTSGKF SVDKLKFDKL YKMLTEIYTE   350
DNFVKFFKVL NRKTYLNFDK AVFKINIVPK VNYTIYDGFN LRNTNLAANF   400
NGQNTEINNM NFTKLKNFTG LFEFYKLLCV RGIITSK                 437
```

Mutations / Mutations / Mutaciónes
BoNT/B C-terminal fragment: E^{750}>**M**^{756}, S^{758}>**Y**^{764}

Post-translational modifications
Disulfide bridge location / Position du pont disulfure / Posición del puente disulfuro
6-429'

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

crusekitugum #
crusekitug

immunoglobulin G1-kappa, anti-[*Homo sapiens* IL17A (interleukin 17A, IL-17A)], humanized monoclonal antibody;
H-gamma1 heavy chain humanized (1-450) [VH (*Homo sapiens* IGHV4-4*08 (79.4%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.7.14] (26-33.51-57.96-109)) (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)], (223-217')-disulfide with L-kappa light chain humanized (1'-217') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (89.2%) -IGKJ4*01 (91.7%), CDR-IMGT [6.3.12] (27'-32'.50'-52'.89'-100')) (1'-110') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (156'), V101 (194')) (111'-217')]; dimer (229-229":232-232")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-S, glycoform alfa

crusékitug

immunoglobuline G1-kappa, anti-[*Homo sapiens* IL17A (interleukine 17A, IL-17A)], anticorps monoclonal humanisé; chaîne lourde H-gamma1 humanisée (1-450) [VH (*Homo sapiens* IGHV4-4*08 (79.4%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.7.14] (26-33.51-57.96-109)) (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)], (223-217')-disulfure avec la chaîne légère L-kappa humanisée (1'-218') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (89.2%) -IGKJ4*01 (91.7%), CDR-IMGT [6.3.12] (27'-32'.50'-52'.89'-100')) (1'-110') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (156'), V101 (194')) (111'-217')]; dimère (229-229":232-232")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-S, glycoforme alfa

crusekitug

inmunoglobulina G1-kappa, anti-[*Homo sapiens* IL17A (interleukina 17A, IL-17A)], anticuerpo monoclonal humanizado; cadena pesada H-gamma1 humanizada (1-450) [VH (*Homo sapiens* IGHV4-4*08 (79.4%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.7.14] (26-33.51-57.96-109)) (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)], (223-217')-disulfuro con la cadena ligera L-kappa humanizada (1'-218') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (89.2%) -IGKJ4*01 (91.7%), CDR-IMGT [6.3.12] (27'-32'.50'-52'.89'-100')) (1'-110') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (156'), V101 (194')) (111'-217')]; dímero (229-229":232-232")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-S, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLQESGPG LVKPSETLSL TCTVSGIDLS LFYMSWIRQP PGKGLEWIGT  50
IHEVASSYYA SWAKGRVTIS KDTSKNQFSL KLSSVTAADT AVYYCARETY 100
SSRYPYPNIW 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
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS VSASVGDRVT ITCQASQNIG GSLAWYQQKP GKAPKLLIYG  50
ASSLASGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQS YNTISTYGLA 100
FGGGTKVEIK RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ 150
WKVDNALQSG NSQESVTEQD SKDSTYSLSS TLTLSKADYE KHKVYACEVT 200
HQGLSSPVTK SFNRGEC                                     217
```

Post-translational modifications

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-95 147-203 264-324 370-428
22"-95" 147"-203" 264"-324" 370"-428"
Intra-L (C23-C104) 23'-88' 137'-197'
23'"-88'" 137'"-197'"
Inter-H-L (h 5-CL 126) 223-217' 223"-217'"
Inter-H-H (h 11, h 14) 229-229" 232-232"

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

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

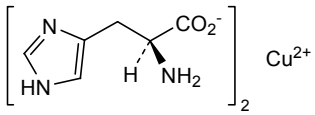
cupri histidinas

copper histidinate — di(L-histidinato)copper

histidinate de cuivre — di(L-histidinato)cuivre

histidinato de cobre — di(L-histidinato)cobre

$C_{12}H_{16}CuN_6O_4$



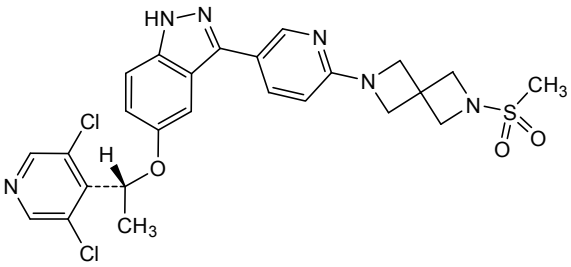
dabogratinibum

dabogratinib — [6-(5-{5-[(1*R*)-1-(3,5-dichloropyridin-4-yl)ethoxy]-1*H*-indazol-3-yl}pyridin-2-yl)-2,6-diazaspiro[3.3]heptan-2-yl](methyl)-λ^6-sulfanedione

dabogratinib — [6-(5-{5-[(1*R*)-1-(3,5-dichloropyridin-4-yl)éthoxy]-1*H*-indazol-3-yl}pyridin-2-yl)-2,6-diazaspiro[3.3]heptan-2-yl](méthyl)- λ^6-sulfanedione

dabogratinib — [6-(5-{5-[(1*R*)-1-(3,5-dicloropiridin-4-il)etoxi]-1*H*-indazol-3-il}piridin-2-il)-2,6-diazaespiro[3.3]heptan-2-il](metil)-λ^6-sulfanodiona

$C_{25}H_{24}Cl_2N_6O_3S$



dalidnetugum #

dalidnetug — immunoglobulin G1-kappa, anti-[*Homo sapiens* APP (amyloid beta, A4 precursor protein, Abeta)], humanized monoclonal antibody; H-gamma1 heavy chain humanized (1-449) [VH (*Homo sapiens* IGHV3-23*03 (87.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1*03v (100%) G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (216) (120-217), hinge 1-15 (218-232), CH2 (233-342), CH3 E12 (358), M14 (360) (343-447), CHS (448-449)) (120-449)], (222-219')-disulfide with L-kappa light chain humanized (1'-219') [V-KAPPA (*Homo sapiens* IGKV2-30*02 (85.0%) -IGKJ1*01 (90.9%), CDR-IMGT [11.3.9] (27'-37'.55'-57'.94'-102')) (1'-112') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (158'), V101 (196')) (113'-219')]; dimer (228-228":231-231")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-S, glycoform alfa

dalidnetug — immunoglobuline G1-kappa, anti-[*Homo sapiens* APP (amyloïde bêta, protéine précurseur A4, Abêta)]; anticorps monoclonal humanisé;

chaîne lourde H-gamma1 humanisée (1-449) [VH (*Homo sapiens* IGHV3-23*03 (87.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1*03v (100%) G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (216) (120-217), charnière 1-15 (218-232), CH2 (233-342), CH3 E12 (358), M14 (360) (343-447), CHS (448-449)) (120-449)], (222-219')-disulfure avec la chaîne légère L-kappa humanisée (1'-219') [V-KAPPA (*Homo sapiens* IGKV2-30*02 (85.0%) -IGKJ1*01 (90.9%), CDR-IMGT [11.3.9] (27'-37'.55'-57'.94'-102')) (1'-112') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (158'), V101 (196')) (113'-219')]; dimère (228-228'':231-231'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-S, glycoforme alfa

dalidnetug

inmunoglobulina G1-kappa, anti-[*Homo sapiens* APP (amieloide beta, proteína precursor A4, Abeta)]; anticuerpo monoclonal humanizado; cadena pesada H-gamma1 humanizada (1-449) [VH (*Homo sapiens* IGHV3-23*03 (87.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1*03v (100%) G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14(CH1 R120>K (216) (120-217), bisagra 1-15 (218-232), CH2 (233-342), CH3 E12 (358), M14 (360) (343-447), CHS (448-449)) (120-449)], (222-219')-disulfuro con la cadena ligera L-kappa humanizada (1'-219') [V-KAPPA (*Homo sapiens* IGKV2-30*02 (85.0%) -IGKJ1*01 (90.9%), CDR-IMGT [11.3.9] (27'-37'.55'-57'.94'-102')) (1'-112') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (158'), V101 (196')) (113'-219')]; dímero (228-228'':231-231'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-S, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLLESGGG LVQPGGSLRL SCAASGFTFS NYGMSWVRQA PGKGLEWVAS  50
IRSGSGRTYY SDNVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVRYD 100
HYSGSSDYWG 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
YTLPPSREEM TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL 400
DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK  449
```

Light chain / Chaîne légère / Cadena ligera

```
DVVMTQSPLS LPVTLGEPAS ISCKSSQSLL DYDGKTYLNW LLQKPGQSPQ  50
RLIYRVTNRD TGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCWQGTHFP 100
RSFGQGTKVE IKRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK 150
VQWKVDNALQ SGNSQESVTE QDSKDSTYSL SSTLTLSKAD YEKHKVYACE 200
VTHQGLSSPV TKSFNRGEC                                   219
```

Post-translational modifications

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

Intra-H (C23-C104) 22-96 146-202 263-323 369-427
22''-96'' 146''-202'' 263''-323'' 369''-427''
Intra-L (C23-C104) 23'-93' 139'-199'
23'''-93''' 139'''-199'''
Inter-H-L (h 5-CL 126) 222-219' 222''-219'''
Inter-H-H (h 11, h 14) 228-228'' 231-231''

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

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

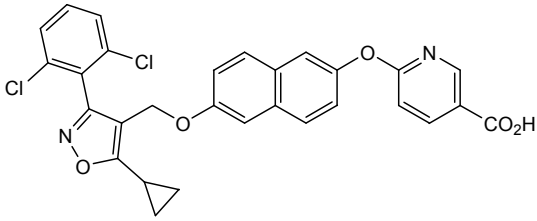
danifexorum

danifexor — 1^2,1^6-dichloro-2^5-cyclopropyl-4,6-dioxa-7(2)-pyridina-2(3,4)-[1,2]oxazola-5(2,6)-naphthalena-1(1)-benzenaheptaphane-7^5-carboxylic acid

danifexor — acide 1^2,1^6-dichloro-2^5-cyclopropyl-4,6-dioxa-7(2)-pyridina-2(3,4)-[1,2]oxazola-5(2,6)-naphtaléna-1(1)-benzénaheptaphane-7^5-carboxylique

danifexor — ácido 2^5-ciclopropil-1^2,1^6-dicloro-4,6-dioxa-7(2)-piridina-2(3,4)-[1,2]oxazola-5(2,6)-naftalena-1(1)-bencenaheptafano-7^5-carboxílico

$C_{29}H_{20}Cl_2N_2O_5$



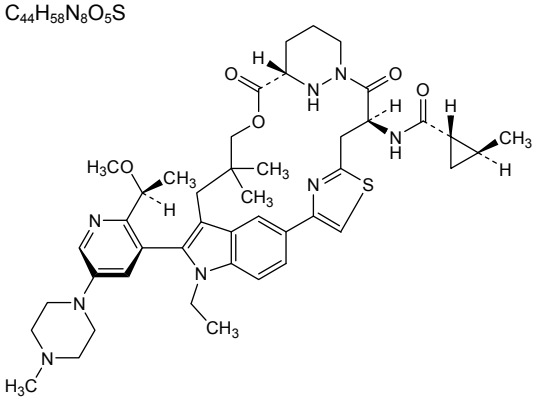
daraxonrasibum

daraxonrasib — (1*S*,2*S*)-*N*-[(1^2*M*,4*S*,6^3*S*)-1^1-ethyl-1^2-{2-[(1*S*)-1-methoxyethyl]-5-(4-methylpiperazin-1-yl)pyridin-3-yl}-10,10-dimethyl-5,7-dioxo-1^1*H*-8-oxa-1(5,3)-indola-6(1,3)-[1,2]diazinana-2(4,2)-[1,3]thiazolacycloundecaphan-4-yl]-2-methylcyclopropane-1-carboxamide

daraxonrasib — (1*S*,2*S*)-*N*-[(1^2*M*,4*S*,6^3*S*)-1^1-éthyl-1^2-{2-[(1*S*)-1-méthoxyéthyl]-5-(4-méthylpipérazin-1-yl)pyridin-3-yl}-10,10-diméthyl-5,7-dioxo-1^1*H*-8-oxa-1(5,3)-indola-6(1,3)-[1,2]diazinana-2(4,2)-[1,3]thiazolacycloundécaphan-4-yl]-2-méthylcyclopropane-1-carboxamide

daraxonrasib — (1*S*,2*S*)-*N*-[(1^2*M*,4*S*,6^6*S*)-1^1-etil-10,10-dimetil-1^2-{5-(4-metilpiperazin-1-il)-2-[(1*S*)-1-metoxietil]piridin-3-il}-5,7-dioxo-1^1*H*-8-oxa-1(5,3)-indola-6(2,6)-[1,2]diazinana-2(4,2)-[1,3]tiazolaciclоundecafan-4-il]-2-metilciclopropano-1-carboxamida

$C_{44}H_{58}N_8O_5S$



daretabartum #

daretabart

immunoglobulin G1-kappa, anti-[*Homo sapiens* GD2 (disialoganglioside GD2)], monoclonal antibody;
H-gamma1 heavy chain (1-443) [VH Musmus/Homsap (*Mus musculus* IGHV1-42*04 (86.5%) -(IGHD) -IGHJ4*01 (71.4%) Q120>T (105), G121>Q (106), T122>G (107) /*Homo sapiens* IGHV1-46*01 (71.9%) -(IGHD) -IGHJ5*01 (75.0%) Q120>T (105), G121>Q (106), T122>G (107), L123>S (108), CDR-IMGT [8.8.6] (26-33.51-58.97-102)) (1-113) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, 5-G1v20 CH2 A105 (CH1 R120 (210) (114-211), hinge 1-15 (212-226), CH2 K105>A (318) (227-336), CH3 E12 (352), M14 (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 (94.0%) -IGKJ5*01 (100%)/*Homo sapiens* IGKV2D-29*02 (82.0%) -IGKJ2*01 (81.8%) Q120>A (106'), I126>L (112'), CDR-IMGT [11.3.10] (27'-37'.55'-57'.94'-103')) (1'-113') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (159'), V101 (197')) (114'-220')];
dimer (222-222'':225-225'')-bisdisulfide, produced in YB2/0 cell line, glycoform alfa

darétabart

immunoglobuline G1-kappa, anti-[*Homo sapiens* GD2 (disialoganglioside GD2)], anticorps monoclonal;
chaîne lourde H-gamma1 (1-443) [VH Musmus/Homsap (*Mus musculus* IGHV1-42*04 (86.5%) -(IGHD) -IGHJ4*01 (71.4%) Q120>T (105), G121>Q (106), T122>G (107) /*Homo sapiens* IGHV1-46*01 (71.9%) -(IGHD) -IGHJ5*01 (75.0%) Q120>T (105), G121>Q (106), T122>G (107), L123>S (108), CDR-IMGT [8.8.6] (26-33.51-58.97-102)) (1-113) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, 5-G1v20 CH2 A105 (CH1 R120 (210) (114-211), charnière 1-15 (212-226), CH2 K105>A (318) (227-336), CH3 E12 (352), M14 (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 (94.0%) -IGKJ5*01 (100%)/*Homo sapiens* IGKV2D-29*02 (82.0%) -IGKJ2*01 (81.8%) Q120>A (106'), I126>L (112'), CDR-IMGT [11.3.10] (27'-37'.55'-57'.94'-103')) (1'-113') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (159'), V101 (197')) (114'-220')]; dimère (222-222'':225-225'')-bisdisulfure, produit dans la lignée cellulaire YB2/0, glycoforme alfa

daretabart

inmunoglobulina G1-kappa, anti-[*Homo sapiens* GD2 (disialogangliósido GD2)], anticuerpo monoclonal;
cadena pesada H-gamma1 (1-443) [VH Musmus/Homsap (*Mus musculus* IGHV1-42*04 (86.5%) -(IGHD) -IGHJ4*01 (71.4%) Q120>T (105), G121>Q (106), T122>G (107) /*Homo sapiens* IGHV1-46*01 (71.9%) -(IGHD) -IGHJ5*01 (75.0%) Q120>T (105), G121>Q (106), T122>G (107), L123>S (108), CDR-IMGT [8.8.6] (26-33.51-58.97-102)) (1-113) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, 5-G1v20 CH2 A105 (CH1 R120 (210) (114-211), bisagra 1-15 (212-226), CH2 K105>A (318) (227-336), CH3 E12 (352), M14 (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 (94.0%) -IGKJ5*01 (100%)/*Homo sapiens* IGKV2D-29*02 (82.0%) -IGKJ2*01 (81.8%) Q120>A (106'), I126>L (112'), CDR-IMGT [11.3.10] (27'-37'.55'-57'.94'-103')) (1'-113') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (159'), V101 (197')) (114'-220')]; dímero (222-222'':225-225'')-bisdisulfuro, producido en la línea celular YB2/0, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVQSGAE VEKPGASVKI SCKASGSSFT GYNMNWVRQN IGKSLEWIGA  50
IDPYYGGTSY NQKFKGRATL TVDKSTSTAY MHLKSLRSED TAVYYCVSGM 100
EYWGTQGSVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC LVKDYFPEPV 150
TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG TQTYICNVNH 200
KPSNTKVDKR VEPKSCDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS 250
RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYNSTYRVVS 300
VLTVLHQDWL NGKEYKCAVS NKALPAPIEK TISKAKGQPR EPQVYTLPPS 350
REEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT PPVLDSDGSF 400
FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLS PGK         443
```

Light chain / Chaîne légère / Cadena ligera

```
DVVMTQTPLS LPVTPGEPAS ISCRSSQSLV HRNGNTYLHW YLQKPGQSPK  50
LLIHKVSNRF SGVPDRFSGS GSGTDFTLKI SRVEAEDLGV YFCSQSTHVP 100
PLTFGAGTKL ELKRTVAAPS VFIFPPSDEQ LKSGTASVVC LLNNFYPREA 150
KVQWKVDNAL QSGNSQESVT EQDSKDSTYS LSSTLTLSKA DYEKHKVYAC 200
EVTHQGLSSP VTKSFNRGEC                                  220
```

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

H CH2 N84.4: 293, 293"

Mainly (>40%) afucosylated complex bi-antennary YB2/0-type glycans / glycanes de type YB2/0 bi-antennaires complexes principalement (>40%) afucosylés / glicanos de tipo YB2/0 biantenarios complejos principalmente (>40%) afucosilados

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

H CHS K2: 443, 443"

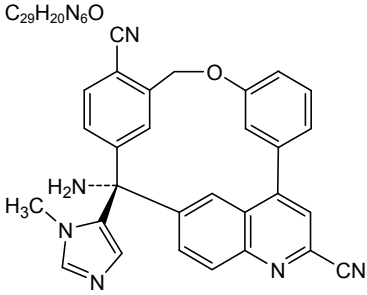
darlifarnibum

darlifarnib — (3*S*)-3-amino-3-(1-methyl-1*H*-imidazol-5-yl)-6-oxa-2(4,6)-quinolina-1,4(1,3)-dibenzenacyclohexaphane-2^2,4^4-dicarbonitrile

darlifarnib — (3*S*)-3-amino-3-(1-méthyl-1*H*-imidazol-5-yl)-6-oxa-2(4,6)-quinoléina-1,4(1,3)-dibenzénacyclohexaphane-2^2,4^4-dicarbonitrile

darlifarnib — (3*S*)-3-amino-3-(1-metil-1*H*-imidazol-5-il)-6-oxa-2(4,6)-quinoleína-1,4(1,3)-dibencenaciclohexafano-2^2,4^4-dicarbonitrilo

$C_{29}H_{20}N_6O$



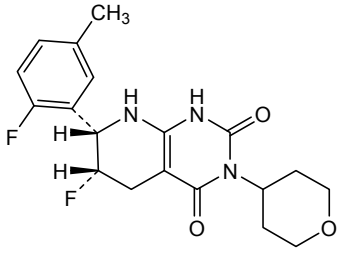
delocamtenum

delocamten — (6*S*,7*S*)-6-fluoro-7-(2-fluoro-5-methylphenyl)-3-(oxan-4-yl)-5,6,7,8-tetrahydropyrido[2,3-*d*]pyrimidine-2,4(1*H*,3*H*)-dione

délocamten — (6*S*,7*S*)-6-fluoro-7-(2-fluoro-5-méthylphényl)-3-(oxan-4-yl)-5,6,7,8-tétrahydropyrido[2,3-*d*]pyrimidine-2,4(1*H*,3*H*)-dione

delocamtén — (6*S*,7*S*)-6-fluoro-7-(2-fluoro-5-metilfenil)-3-(oxan-4-il)-5,6,7,8-tetrahidropirido[2,3-*d*]pirimidina-2,4(1*H*,3*H*)-diona

$C_{19}H_{21}F_2N_3O_3$



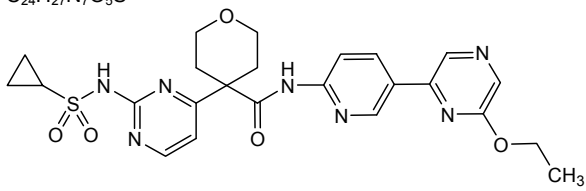
dencatistatum

dencatistat — 4-[2-(cyclopropanesulfonamido)pyrimidin-4-yl]-*N*-[5-(6-ethoxypyrazin-2-yl)pyridin-2-yl]oxane-4-carboxamide

dencatistat — 4-[2-(cyclopropanesulfonamido)pyrimidin-4-yl]-*N*-[5-(6-éthoxypyrazin-2-yl)pyridin-2-yl]oxane-4-carboxamide

dencatistat — 4-[2-(ciclopropanosulfonamido)pirimidin-4-il]-*N*-[5-(6-etoxipirazin-2-il)piridin-2-il]oxano-4-carboxamida

$C_{24}H_{27}N_7O_5S$



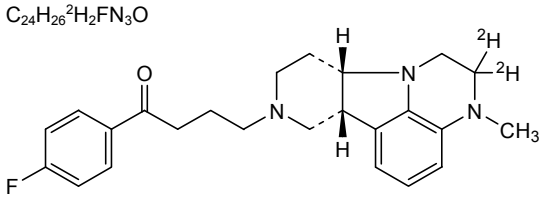
deulumateperonum

deulumateperone — 1-(4-fluorophenyl)-4-[(6b*R*,10a*S*)-3-methyl-2,3,6b,9,10,10a-(2-^{2}H)hexahydro(2-^{2}H)-1*H*-pyrido[3',4':4,5]pyrrolo[1,2,3-*de*]quinoxalin-8(7*H*)-yl]butan-1-one

deulumatépérone — 1-(4-fluorophényl)-4-[(6b*R*,10a*S*)-3-méthyl-2,3,6b,9,10,10a-(2-^{2}H)hexahydro(2-^{2}H)-1*H*-pyrido[3',4':4,5]pyrrolo[1,2,3-*de*]quinoxalin-8(7*H*)-yl]butan-1-one

deulumateperona — 1-(4-fluorofenil)-4-[(6b*R*,10a*S*)-3-metil-2,3,6b,9,10,10a-(2-^{2}H)hexahidro(2-^{2}H)-1*H*-pirido[3',4':4,5]pirrolo[1,2,3-*de*]quinoxalin-8(7*H*)-il]butan-1-ona

$C_{24}H_{26}{}^2H_2FN_3O$



diranersenum

diranersen — *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)-*P*-thioguanylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyl-*P*-thiouridylyl-(3'→5')-2'- *O*-(2-methoxyethyl) -5-methyl-

P-thiouridylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-deoxy-5-methyl-*P*-thiocytidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-deoxy-*P*-thioadenylyl-(3'→5')-2'-deoxy-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-deoxy-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-*P*-thioadenylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methylcytidylyl-(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-methyluridine

diranersen

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

diranersén

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)-*P*-tioguanilil-(3'→5')-5-metil-2'-*O*-(2-metoxietil)-*P*-tiouridilil-(3'→5')-5-metil-2'-*O*-(2-metoxietil)-*P*-tiouridilil-(3'→5')-*P*-tiotimidilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2'-desoxi-5-metil-*P*-tiocitidilil-(3'→5')-*P*-tiotimidilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2'-desoxi-*P*-tioadenilil-(3'→5')-2'-desoxi-5-metil-*P*-tiocitidilil-(3'→5')-2'-desoxi-5-metil-*P*-tiocitidilil-(3'→5')-2'-*O*-(2-metoxietil)-*P*-tioadenilil-(3'→5')-5-metil-2'-*O*-(2-metoxietil)citidilil-(3'→5')-5-metil-2'-*O*-(2-metoxietil)-*P*-tiocitidilil-(3'→5')-5-metil-2'-*O*-(2-metoxietil)-*P*-tiocitidilil-(3'→5')-5-metil-2'-*O*-(2-metoxietil)uridina

$C_{210}H_{300}N_{53}O_{116}P_{17}S_{15}$

(3'-5')*C*=*C*–G=*U*=*U*=dT=dT=d*C*=dT=dT=dA=d*C*=d*C*=A=*C*–*C*=*C*=*U*

N : nucleoside / nucléoside / nucleósido
dN : 2'-deoxy-N / 2'-désoxy-N / 2'-desoxi-N
N : 5-methyl-N / 5-méthyl-N / 5-metil-N
N : 2'-*O*-(2-methoxyethyl)-N / 2'-*O*-(2-méthoxyéthyl)-N / 2'-*O*-(metoxietil)-N
- : -PO(OH)- = : -PO(SH)-

dirozalkibum

dirozalkib

5-chloro-N^2-[7-methyl-8-(piperidin-4-yl)-2,3-dihydro-1,4-benzodioxin-5-yl]-N^4-[2-(propane-2-sulfonyl)phenyl]pyrimidine-2,4-diamine

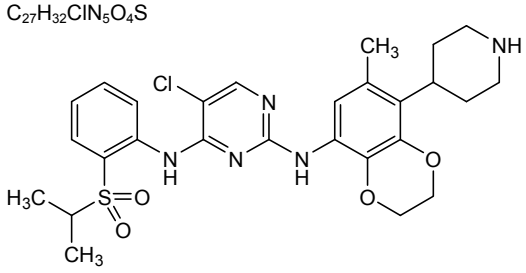
dirozalkib

5-chloro-N^2-[7-méthyl-8-(pipéridin-4-yl)-2,3-dihydro-1,4-benzodioxin-5-yl]-N^4-[2-(propane-2-sulfonyl)phényl]pyrimidine-2,4-diamine

dirozalkib

5-cloro-N^2-[7-metil-8-(piperidin-4-il)-2,3-dihidro-1,4-benzodioxin-5-il]-N^4-[2-(propano-2-sulfonil)fenil]pirimidina-2,4-diamina

$C_{27}H_{32}ClN_5O_4S$



efclarofuspum alfa #

efclarofusp alfa	human vascular endothelial growth factor receptor 1 (VEGFR1, vascular permeability factor receptor, Fms-like tyrosine kinase 1, FLT1, tyrosine-protein kinase receptor FLT, tyrosine-protein kinase FRT, EC:2.7.10.1), fragment 103-206 (containing the Ig-like C2-type domain 2) (1-104), fused to human vascular endothelial growth factor receptor 2 (VEGFR2, fetal liver kinase 1, FLK1, protein-tyrosine kinase receptor flk-1, kinase insert domain receptor, KDR, CD309, EC:2.7.10.1), fragment 208-308 (containing the Ig-like C2-type domain 3) (105-205), fused to an immunoglobulin G1 (IgG1) Fc fragment (h-CH2-CH3-CHS domains) (206-431) [*Homo sapiens* IGHG1*01 (hinge (206-215), CH2 (216-325), CH3 (326-430), CHS K^{432}>del (431-431))] fused via the peptide linker $(G_4S)_3$ (432-446) to disintegrin rhodostomin [*Calloselasma rhodostoma* (Malayan pit viper, *Agkistrodon rhodostoma*)] (447-514), [S^{39}>K^{485}, R^{40}>K^{486}, G^{42}>R^{488}, K^{43}>T^{489}, R^{46}>A^{492}, I^{47}>R^{493}, P^{48}>G^{494}, M^{52}>N^{498}]-variant; dimer (211-211':214-214')-bisdisulfide; produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1; glycoform alfa
efclarofusp alfa	récepteur 1 du facteur de croissance endothélial vasculaire humain (VEGFR1, récepteur du facteur de perméabilité vasculaire, tyrosine kinase 1 de type Fms, FLT1, récepteur tyrosine-protéine kinase FLT, tyrosine-protéine kinase FRT, EC:2.7.10.1), fragment 103-206 (contenant le domaine 2 de type Ig de type C2) (1-104), fusionné au récepteur 2 du facteur de croissance endothélial vasculaire humain (VEGFR2, kinase hépatique 1 fœtale, FLK1, récepteur protéine-tyrosine kinase flk-1, récepteur du domaine d'insertion de kinase, KDR, CD309, EC:2.7.10.1), fragment 208-308 (contenant le domaine 3 de type C2 de type Ig) (105-205), fusionné à un fragment Fc d'immunoglobuline G1 (IgG1) (domaines h-CH2-CH3-CHS) (206-431) [*Homo sapiens* IGHG1*01 (charnière (206-215), CH2 (216-325), CH3 (326-430), CHS K^{432}>del (431-431))] fusionné via le coupleur peptidique $(G_4S)_3$ (432-446) à la désintégrine rhodostomine [*Calloselasma rhodostoma* (vipère malaise, *Agkistrodon rhodostoma*)] (447-514), variant [S^{39}>K^{485}, R^{40}>K^{486}, G^{42}>R^{488}, K^{43}>T^{489}, R^{46}>A^{492}, I^{47}>R^{493}, P^{48}>G^{494}, M^{52}>N^{498}]; dimère (211-211':214-214')-bisdisulfure; produit dans des cellules d'ovaire de hamster chinois (CHO), lignée cellulaire CHO-K1; glycoforme alfa
efclarofusp alfa	receptor 1 del factor de crecimiento endotelial vascular humano (VEGFR1, receptor del factor de permeabilidad vascular, tirosina quinasa 1 similar a Fms, FLT1, receptor de tirosina-proteína quinasa FLT, tirosina-proteína quinasa FRT, EC:2.7.10.1), fragmento 103-206 (que contiene el dominio 2 tipo C2 similar a Ig) (1-104), fusionado al receptor 2 del factor de crecimiento endotelial vascular humano (VEGFR2, quinasa 1 de hígado fetal, FLK1, receptor de proteína tirosina quinasa flk-1, receptor de dominio de inserción de quinasa, KDR, CD309, EC:2.7.10.1), fragmento 208-308 (que contiene el dominio 3 tipo C2 similar a Ig) (105-205), fusionado a un fragmento Fc de inmunoglobulina G1 (IgG1) (dominios h-CH2-CH3-CHS) (206-431) [*Homo sapiens* IGHG1*01 (bisagra (206-215), CH2 (216-325), CH3 (326-430), CHS K^{432}>del (431-431))] fusionado mediante el enlazador peptídico $(G_4S)_3$ (432-446) a la desintegrina rodostomina [*Calloselasma rhodostoma* (víbora malaya, *Agkistrodon rhodostoma*)] (447-514), variante [S^{39}>K^{485}, R^{40}>K^{486}, G^{42}>R^{488}, K^{43}>T^{489}, R^{46}>A^{492}, I^{47}>R^{493}, P^{48}>G^{494}, M^{52}>N^{498}]; dímero (211-211':214-214')-bisdisulfuro; producido en células ováricas de hámster chino (CHO), línea celular CHO-K1; forma glicosilada alfa

Sequence / Séquence / Secuencia

```
SDTGRPFVEM YSEIPEIIHM TEGRELVIPC RVTSPNITVT LKKFPLDTLI   50
PDGKRIIWDS RKGFIISNAT YKEIGLLTCE ATVNGHLYKT NYLTHRQTNT  100
IIDVVLSPSH GIELSVGEKL VLNCTARTEL NVGIDFNWEY PSSKHQHKKL  150
VNRDLKTQSG SEMKKFLSTL TIDGVTRSDQ GLYTCAASSG LMTKKNSTFV  200
RVHEKDKTHT CPPCPAPELL GGPSVFLFPP KPKDTLMISR TPEVTCVVVD  250
VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ YNSTYRVVSV LTVLHQDWLN  300
GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR DELTKNQVSL  350
TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS  400
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GGGGGSGGGG SGGGGSGKEC  450
DCSSPENPCC DAATCKLRPG AQCGEGLCCE QCKFKKARTI CARGRGDNPD  500
DRCTGQSADC PRYH                                         514
```

Mutations / Mutations / Mutaciónes

disintegrin: S^{39}>**K**^{485}, R^{40}>**K**^{486}, G^{42}>**R**^{488}, K^{43}>**T**^{489}, R^{46}>**A**^{492}, I^{47}>**R**^{493}, P^{48}>**G**^{494}, M^{52}>**N**^{498}

Peptide linker / Peptide liant / Péptido de unión

^{432}*GGGGSGGGG SGGGGS*^{446}

Post-translational modifications

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

VEGFR1 IgC2 domain 2: 30-79 30'-79' VEGFR2 IgC2 domain 3: 124-185 124'-185'

IgG1 Fc: 246-306 352-410 246'-306' 352'-410' inter-IgG1 Fc: 211-211' 214-214'

disintegrin: 450-465 452-460 459-482 473-479 478-503 491-510 450'-465' 452'-460' 459'-482' 473'-479' 478'-503' 491'-510'

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

VEGFR1 IgC2 domain 2: N36, N68, N36', N68'

VEGFR2 IgC2 domain 3: N123, N196, N123', N196'; IgG1 Fc: N282, N282'

efitazanamivirum alfa

efitazanamivir alfa

Fc fragment of human immunoglobulin G1 (1-247) [*Homo sapiens* IGHG1*01(CH1 final 15 residues (1-15), hinge (16-30), CH2 M^{52}>Y, S^{54}>T, T^{56}>E (31-140), CH3 (141-245), CHS (246-247))], dimer (26-26':29-29')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa; substituted on an average of 4 to 5 L-lysine residues at N^6 with radical group 1-{4-[(23*R*,24*R*)-23-[(2*R*,3*R*,4*S*)-3-acetamido-4-(carbamimidoylamino)-6-carboxy-3,4-dihydro-2*H*-pyran-2-yl]-14-(2-{2-[({(1*R*,2*R*)-1-[(2*R*,3*R*,4*S*)-3-acetamido-4-(carbamimidoylamino)-6-carboxy-3,4-dihydro-2*H*-pyran-2-yl]-2,3-dihydroxypropoxy}carbonyl)(methyl)amino]ethoxy}ethyl)-24,25-dihydroxy-20-methyl-21-oxo-2,5,8,11,17,22-hexaoxa-14,20-diazapentacosan-1-yl]-1*H*-1,2,3-triazol-1-yl}-3,6,9,12-tetraoxapentadecan-15-oyl

éfitazanamivir alfa

fragment Fc d'immunoglobuline humaine G1 (1-247) [*Homo sapiens* IGHG1*01(15 résidus finaux CH1 (1-15), charnière (16-30), CH2 M^{52}>Y, S^{54}>T, T^{56}>E (31-140), CH3 (141-245), CHS (246-247))], dimère (26-26':29-29')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa; substitué en N^6 de 4 à 5 résidus L-lysine en moyenne avec le groupe 1-(4-{(23*R*,24*R*)-14-(2-{2-[({(1*R*,2*R*)-1-[(2*R*,3*R*,4*S*)-3-acétamido-4-carbamimidamido-6-carboxy-3,4-dihydro-2*H*-pyran-2-yl]-2,3-dihydroxypropoxy}carbonyl)(méthyl)amino]éthoxy}éthyl)-23-[(2*R*,3*R*,4*S*)-3-acétamido-4-(carbamimidoylamino)-6-carboxy-3,4-dihydro-2*H*-pyran-2-yl]-24,25-dihydroxy-20-méthyl-21-oxo-2,5,8,11,17,22-hexaoxa-14,20-diazapentacosan-1-yl}-1*H*-1,2,3-triazol-1-yl)-15-oxo-3,6,9,12-tétraoxapentadécan-15-yle

efitazanamivir alfa

fragmento Fc de inmunoglobulina humana G1 (1-247) [*Homo sapiens* IGHG1*01(15 residuos finales CH1 (1-15), bisagra (16-30), CH2 M^{52}>Y, S^{54}>T, T^{56}>E (31-140), CH3 (141-245), CHS (246-247))], dímero (26-26':29-29')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, forma glicosilada alfa; sustituido en N^6 de 4 a 5 residuos L-lisina por término medio con el grupo 1-(4-{(23*R*,24*R*)-14-(2-{2-[({(1*R*,2*R*)-1-[(2*R*,3*R*,4*S*)-3-acetamido-4-carbamimidamido-6-carboxi-3,4-dihidro-2*H*-piran-2-il]-2,3-dihidroxipropoxi}carbonil)(metil)amino]etoxi}etil)-23-[(2*R*,3*R*,4*S*)-3-acetamido-4-(carbamimidoilamino)-6-carboxi-3,4-dihidro-2*H*-piran-2-il]-24,25-dihidroxi-20-metil-21-oxo-2,5,8,11,17,22-hexaoxa-14,20-diazapentacosan-1-il}-1*H*-1,2,3-triazol-1-il)-15-oxo-3,6,9,12-tetraoxapentadecan-15-ilo

Monomer sequence / Séquence du monomère / Secuencia del monómero

```
NVNHKPSNTK  VDKKVEPKSS  DKTHTCPPCP  APELLGGPSV  FLFPPKPKDT 50
LYITREPEVT  CVVVDVSHED  PEVKFNWYVD  GVEVHNAKTK  PREEQYNSTY 100
RVVSVLTVLH  QDWLNGKEYK  CKVSNKALPA  PIEKTISKAK  GQPREPQVYT 150
LPPSRDELTK  NQVSLTCLVK  GFYPSDIAVE  WESNGQPENN  YKTTPPVLDS 200
DGSFFLYSKL  TVDKSRWQQG  NVFSCSVMHE  ALHNHYTQKS  LSLSPGK    247
```

Post-translational modifications

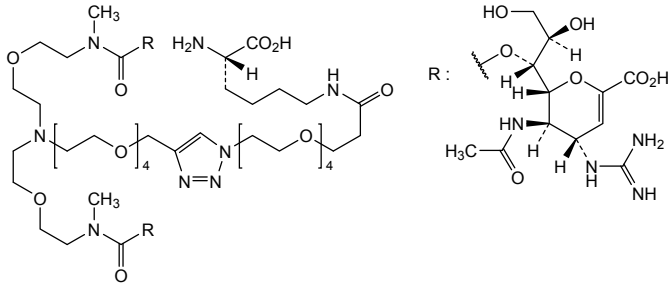
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

Intra 61-121 167-225
61'-121' 167'-225'
Inter 26-26' 29-29'

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
97, 97'

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS: 247, 247"

Potential modified residues / résidus modifiés potentiels / restos modificados potenciales*
K
*(*zanamivir*:protein ~ 9:1)



efranarelaxinum alfa #

efranarelaxin alfa

human immunoglobulin G1 (IgG1) Fc fragment (h-CH2-CH3-CHS domains) (1-226) [Homo sapiens IGHG1*03 (hinge (1-10), CH2 L^{14}>F, L^{15}>E, P^{111}>S (11-120), CH3 S^{134}>C, T^{146}>W (121-225), CHS K^{227}>del (226))] fused via peptide linker $(G_4S)_3G_5S$ (227-247) to the chain A of human relaxin H2 (RLN2) (1-24, 248-271 in the actual sequence), heterodimer (6-6':9-9':134-129':258-257':271-269')-pentakisdisulfide with human immunoglobulin G1 (IgG1) Fc fragment (h-CH2-CH3-CHS domains) (1'-226') [Homo sapiens IGHG1*03 (hinge (1'-10'), CH2 $L^{14'}$>F, $L^{15'}$>E, $P^{111'}$>S (11'-120'), CH3 $Y^{129'}$>C, $T^{146'}$>S, $L^{148'}$>A, $Y^{187'}$>V (121'-225'), CHS $K^{227'}$>del (226'))] fused via peptide linker $(G_4S)_3G_5S$ (227'-247') to the des-Asp^1-chain B of human relaxin H2 (RLN2) (2-29, 248'-275' in the actual sequence), produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa

efranarélaxine alfa

fragment Fc de l'immunoglobuline G1 humaine (1-226) [*Homo sapiens* IGHG1*03 (charnière (1-10), CH2 L^{14}>F, L^{15}>E, P^{111}>S (11-120), CH3 S^{134}>C, T^{146}>W (121-225), CHS K^{227}>del (226))] fusionné via un coupleur peptidique $(G_4S)_3G_5S$ (227-247) à la chaîne A de la relaxine H2 (RLN2) humaine (1-24, 248-271 dans la sequence actuelle), hétérodimère (6-6':9-9':134-129':258-257':271-269')-pentakisdisulfure avec fragment Fc de l'immunoglobuline G1 humaine (1'-226') [*Homo sapiens* IGHG1*03 (charnière (1'-10'), CH2 $L^{14'}$>F, $L^{15'}$>E, $P^{111'}$>S (11'-120'), CH3 $Y^{129'}$>C, $T^{146'}$>S, $L^{148'}$>A, $Y^{187'}$>V (121'-225'), CHS $K^{227'}$>del (226'))] fusionné via un coupleur peptidique $(G_4S)_3G_5S$ (227'-247') à la dés-Asp^1-chaîne B de la relaxine H2 (RLN2) humaine (2-29, 248'-275' dans la sequence actuelle), produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa

efranarelaxina alfa

fragmento Fc de la inmunoglobulina G1 humana (1-226) [*Homo sapiens* IGHG1*03 (bisagra (1-10), CH2 L^{14}>F, L^{15}>E, P^{111}>S (11-120), CH3 S^{134}>C, T^{146}>W (121-225), CHS K^{227}>del (226))] fusionado mediante el enlazador peptídico $(G_4S)_3G_5S$ (227-247) a la cadena A de la relaxina H2 (RLN2) humana (1-24, 248-271 en la secuencia actual), heterodímero (6-6':9-9':134-129':258-257':271-269')-pentakisdisulfuro con fragmento Fc de la inmunoglobulina G1 humana (1'-226') [*Homo sapiens* IGHG1*03 (bisagra (1'-10'), CH2 $L^{14'}$>F, $L^{15'}$>E, $P^{111'}$>S (11'-120'), CH3 $Y^{129'}$>C, $T^{146'}$>S, $L^{148'}$>A, $Y^{187'}$>V (121'-225'), CHS $K^{227'}$>del (226'))] fusionado mediante el enlazador peptídico $(G_4S)_3G_5S$ (227'-247') a la des-Asp^1-cadena B de la relaxina H2 (RLN2) humana (2-29, 248'-275' en la secuencia actual), producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, glicoforma alfa

Sequences / Séquences / Secuencias

Fc-$(G_4S)_3G_5S$-RLN2 A

```
DKTHTCPPCP APEFEGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED   50
PEVKFNWYVD GVEVHNAKTK PREEQYNSTY RVVSVLTVLH QDWLNGKEYK  100
CKVSNKALPA SIEKTISKAK GQPREPQVYT LPPCREEMTK NQVSLWCLVK  150
GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG  200
NVFSCSVMHE ALHNHYTQKS LSLSPGGGGG SGGGGSGGGG SGGGGGSQLY  250
SALANKCCHV GCTKRSLARF C                                 271
```

Fc-$(G_4S)_3G_5S$-RLN2 B

```
DKTHTCPPCP APEFEGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED   50
PEVKFNWYVD GVEVHNAKTK PREEQYNSTY RVVSVLTVLH QDWLNGKEYK  100
CKVSNKALPA SIEKTISKAK GQPREPQVCT LPPSREEMTK NQVSLSCAVK  150
GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLVSKL TVDKSRWQQG  200
NVFSCSVMHE ALHNHYTQKS LSLSPGGGGG SGGGGSGGGG SGGGGGSSWM  250
EEVIKLCGRE LVRAQIAICG MSTWS                             275
```

Mutations / Mutations / Mutaciónes

L^{14}>**F**, L^{15}>**E**, P^{111}>**S**, S^{134}>**C**, T146>**W**;
L14'>**F**, L15'>**E**, $P^{111'}$>**S**, $Y^{129'}$>**C**, $T^{146'}$>**S**, $L^{148'}$>**A**, $Y^{187'}$>**V**

Peptide linkers / Peptides liants / Péptidos de unión

^{227}*GGGGSGGGGS GGGGSGGGGG S*^{247} (1-21);
$^{227'}$*GGGGSGGGGS GGGGSGGGGG S*$^{247'}$ (1-21)

Post-translational modifications

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

intra-Fc: 41-101 147-205 intra-RLN2 A: 257-261
41'-101' 147'-205'
inter-Fc-Fc': 6-6' 9-9' 134-129' inter-RLN2 A-B: 258-257' 271-269'

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

N77, N77'

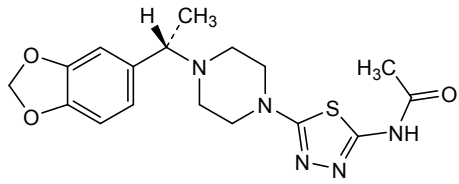
egalognastatum

egalognastat — *N*-(5-{4-[(1*S*)-1-(2*H*-1,3-benzodioxol-5-yl)ethyl]piperazin-1-yl}-1,3,4-thiadiazol-2-yl)acetamide

égalognastat — *N*-(5-{4-[(1*S*)-1-(2*H*-1,3-benzodioxol-5-yl)éthyl]pipérazin-1-yl}-1,3,4-thiadiazol-2-yl)acétamide

egalognastat — *N*-(5-{4-[(1*S*)-1-(2*H*-1,3-benzodioxol-5-il)etil]piperazin-1-il}-1,3,4-tiadiazol-2-il)acetamida

$C_{17}H_{21}N_5O_3S$



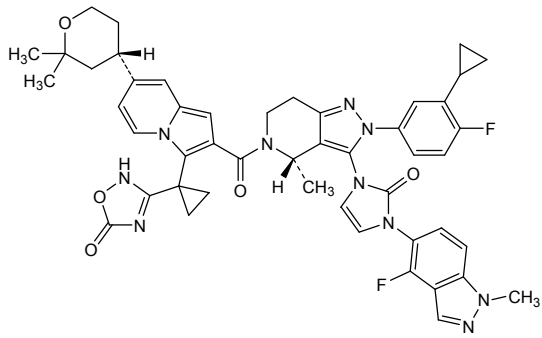
elecoglipronum

elecoglipron — (3^4*S*)-3^2-(3-cyclopropyl-4-fluorophenyl)-5^7-[(4*S*)-2,2-dimethyloxan-4-yl]-1^4-fluoro-1^1,3^4-dimethyl-3^2,3^4,3^6,3^7-tetrahydro-1^1*H*,2^2*H*-3(3,5)-pyrazolo[4,3-*c*]pyridina-1(5)-indazola-5(2,3)-indolizina-7(3)-[1,2,4]oxadiazola-2(1,3)-imidazola-6(1,1)-ciclopropanaheptaphane-2^2,4,7^5(7^2*H*)-trione

élécoglipron — (3^4*S*)-3^2-(3-cyclopropyl-4-fluorophényl)-5^7-[(4*S*)-2,2-diméthyloxan-4-yl]-1^4-fluoro-1^1,3^4-diméthyl-3^2,3^4,3^6,3^7-tétrahydro-1^1*H*,2^2*H*-3(3,5)-pyrazolo[4,3-*c*]pyridina-1(5)-indazola-5(2,3)-indolizina-7(3)-[1,2,4]oxadiazola-2(1,3)-imidazola-6(1,1)-ciclopropanaheptaphane-2^2,4,7^5(7^2*H*)-trione

elecogliprón — (3^4*S*)-3^2-(3-ciclopropil-4-fluorofenil)-5^7-[(4*S*)-2,2-dimetiloxan-4-il]-1^4-fluoro-1^1,3^4-dimetil-3^2,3^4,3^6,3^7-tetrahidro-1^1*H*,2^2*H*-3(3,5)-pirazolo[4,3-*c*]piridina-1(5)-indazola-5(2,3)-indolizina-7(3)-[1,2,4]oxadiazola-2(1,3)-imidazola-6(1,1)-ciclopropanaheptafano-2^2,4,7^5(7^2*H*)-triona

$C_{48}H_{46}F_2N_{10}O_5$



elegrobartum #

elegrobart — immunoglobulin G1-kappa, anti-[*Homo sapiens* IGF1R (insulin-like growth factor 1 receptor, IGF1-R, IGF-1R, CD221)], monoclonal antibody;
H-gamma1 heavy chain (1-453) [VH Musmus/Homsap (*Mus musculus* IGHV1-69-5*01 (92.9%) -(IGHD) -IGHJ1*01 (93.8%) A120>Q (116)/*Homo sapiens* IGHV1-46*01 (77.6%) C104>F (96) -(IGHD) -IGHJ6*01 (100%), CDR-IMGT [8.8.17] (26-33.51-58.97-113)) (1-124) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, 9-G1v21 CH2 Y15.1, T16, E18 (CH1 K120 (221) (125-222), hinge 1-15 (223-237), CH2 M15.1>Y (259), S16>T (261), T18>E (263) (238-347), CH3 D12 (363), L14 (365) (348-452), CHS K2>del (453)) (125-453)], (227-219')-disulfide with L-kappa light chain (1'-219') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV1-117*01 (93.0%) -IGKJ1*02 (100%)/*Homo sapiens* IGKV2-30*02 (81.0%) -IGKJ4*01 (90.9%) V124>L (109'), CDR-IMGT [11.3.9] (27'-37'.55'-57'.94'-102')) (1'-112') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (158'), V101 (196')) (113'-219')]; dimer (233-233'':236-236'')-bisdisulfide, produced in a cell line from Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, glycoform alfa

élégrobart — immunoglobuline G1-kappa, anti-[*Homo sapiens* IGF1R (récepteur du facteur de croissance insuline-like 1, IGF1-R, IGF-1R, CD221)], anticorps monoclonal;
chaîne lourde H-gamma1 (1-453) [VH Musmus/Homsap (*Mus musculus* IGHV1-69-5*01 (92.9%) -(IGHD) -IGHJ1*01 (93.8%) A120>Q (116)/*Homo sapiens* IGHV1-46*01 (77.6%) C104>F (96) -(IGHD) -IGHJ5*04 (100%), CDR-IMGT [8.8.17] (26-33.51-58.97-113)) (1-124) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, 9-G1v21 CH2 Y15.1, T16, E18 (CH1 K120 (221) (125-222), charnière 1-15 (223-237), CH2 M15.1>Y (259), S16>T (261), T18>E (263) (238-347), CH3 D12 (363), L14 (365) (348-452), CHS K2>del (453)) (125-453)], (227-219')-disulfure avec la chaîne légère L-kappa (1'-219') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV1-117*01 (93.0%) -IGKJ1*02 (100%)/*Homo sapiens* IGKV2-30*02 (81.0%) -IGKJ4*01 (90.9%) V124>L (109'), CDR-IMGT [11.3.9] (27'-37'.55'-57'.94'-102')) (1'-112') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (158'), V101 (196')) (113'-219')]; dimère (233-233'':236-236'')-bisdisulfure, produit dans une lignée cellulaire des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1, glycoforme alfa

elegrobart — inmunoglobulina G1-kappa, anti-[*Homo sapiens* IGF1R (receptor 1 del factor de crecimiento similar a la insulina, IGF1-R, IGF-1R, CD221)], anticuerpo monoclonal;
cadena pesada H-gamma1 (1-453) [VH Musmus/Homsap (*Mus musculus* IGHV1-69-5*01 (92.9%) -(IGHD) -IGHJ1*01 (93.8%) A120>Q (116)/*Homo sapiens* IGHV1-46*01 (77.6%) C104>F (96) -(IGHD) -IGHJ5*04 (100%), CDR-IMGT [8.8.17] (26-33.51-58.97-113)) (1-124) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, 9-G1v21 CH2 Y15.1, T16, E18 (CH1 K120 (221) (125-222), bisagra 1-15 (223-237), CH2 M15.1>Y (259), S16>T (261), T18>E (263) (238-347), CH3 D12 (363), L14 (365) (348-452), CHS K2>del (453)) (125-453)], (227-219')-disulfuro con la cadena ligera L-kappa (1'-219') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV1-117*01 (93.0%) -IGKJ1*02 (100%)/*Homo sapiens* IGKV2-30*02 (81.0%) -IGKJ4*01 (90.9%) V124>L (109'), CDR-IMGT [11.3.9] (27'-37'.55'-57'.94'-102')) (1'-112') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (158'), V101 (196')) (113'-219')]; dímero (233-233'':236-236'')-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

```
QVQLVQSGAE VVKPGASVKL SCKASGYTFT SYWMHWVKQR PGQGLEWIGE  50
INPSNGRTNY NQKFQGKATL TVDKSSSTAY MQLSSLTSED SAVYYFARGR 100
PDYYGSSKWY FDVWGQGTTV TVSSASTKGP SVFPLAPSSK STSGGTAALG 150
CLVKDYFPEP VTVSWNSGAL TSGVHTFPAV LQSSGLYSLS SVVTVPSSSL 200
GTQTYICNVN HKPSNTKVDK KVEPKSCDKT HTCPPCPAPE LLGGPSVFLF 250
PPKPKDTLYI TREPEVTCVV VDVSHEDPEV KFNWYVDGVE VHNAKTKPRE 300
EQYNSTYRVV SVLTVLHQDW LNGKEYKCKV SNKALPAPIE KTISKAKGQP 350
REPQVYTLPP SRDELTKNQV SLTCLVKGFY PSDIAVEWES NGQPENNYKT 400
TPPVLDSDGS FFLYSKLTVD KSRWQQGNVF SCSVMHEALH NHYTQKSLSL 450
SPG                                                     453
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Light chain / Chaîne légère / Cadena ligera

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DVVMTQTPLS LPVSLGDPAS ISCRSSQSIV HSNVNTYLEW YLQKPGQSPR  50
LLIYKVSNRF SGVPDRFSGS GAGTDFTLRI SRVEAEDLGI YYCFQGSHVP 100
PTFGGGTKLE 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 * 151-207 268-328 374-432
22" * 151"-207" 268"-328" 374"-432"

Intra-L (C23-C104) 23'-93' 139'-199'
23'"-93'" 139'"-199'"

Inter-H-L (h 5-CL 126) 227-219' 227"-219'"

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

* Free sulfhydryl owing to the amino acid change C104>F (96, 96").

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

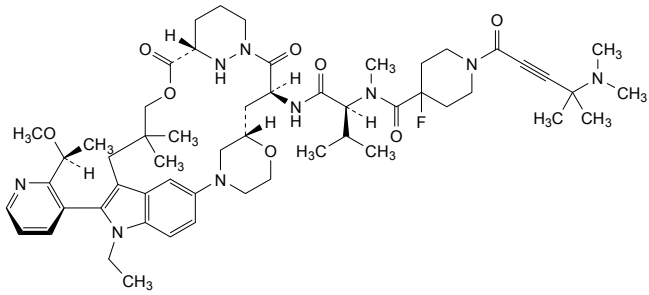
H CH2 N84.4: 304, 304"

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

elironrasibum

elironrasib	1-[4-(dimethylamino)-4-methylpent-2-ynoyl]-*N*-[(2*S*)-1-{[(1^2*M*,2^2*S*,4*S*,6^3*S*)-1^1-ethyl-1^2-{2-[(1*S*)-1-methoxyethyl]pyridin-3-yl}-10,10-dimethyl-5,7-dioxo-1^1*H*-8-oxa-1(5,3)-indola-2(4,2)-morpholina-6(1,3)-[1,2]diazinanacycloundecaphan-4-yl]amino}-3-methyl-1-oxobutan-2-yl]-4-fluoro-*N*-methylpiperidine-4-carboxamide
élironrasib	1-[4-(diméthylamino)-4-méthylpent-2-ynoyl]-*N*-[(2*S*)-1-{[(1^2*M*,2^2*S*,4*S*,6^3*S*)-1^1-éthyl-1^2-{2-[(1*S*)-1-méthoxyéthyl]pyridin-3-yl}-10,10-diméthyl-5,7-dioxo-1^1*H*-8-oxa-1(5,3)-indola-2(4,2)-morpholina-6(1,3)-[1,2]diazinanacycloundécaphan-4-yl]amino}-3-méthyl-1-oxobutan-2-yl]-4-fluoro-*N*-méthylpipéridine-4-carboxamide
elironrasib	1-[4-(dimetilamino)-4-metilpent-2-inoil]-*N*-[(2*S*)-1-{[(1^2*M*,2^2*S*,4*S*,6^6*S*)-1^1-etil-10,10-dimetil-1^2-{2-[(1*S*)-1-metoxietil]piridin-3-il}-5,7-dioxo-1^1*H*-8-oxa-1(5,3)-indola-2(4,2)-morfolina-6(2,6)-[1,2]diazinanacicloundecafan-4-il]amino}-3-metil-1-oxobutan-2-il]-4-fluoro-*N*-metilpiperidina-4-carboxamida

$C_{55}H_{78}FN_9O_8$



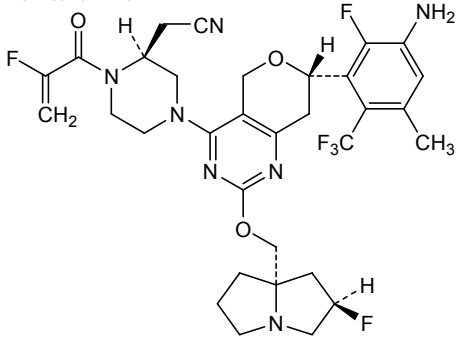
elisrasibum

elisrasib [(2*S*)-4-[(7*S*)-7-[3-amino-2-fluoro-5-methyl-6-(trifluoromethyl)phenyl]-2-{[(2*R*,7a*S*)-2-fluorotetrahydro-1*H*-pyrrolizin-7a(5*H*)-yl]methoxy}-7,8-dihydro-5*H*-pyrano[4,3-*d*]pyrimidin-4-yl]-1-(2-fluoroprop-2-enoyl)piperazin-2-yl]acetonitrile

élisrasib [(2*S*)-4-[(7*S*)-7-[3-amino-2-fluoro-5-méthyl-6-(trifluorométhyl)phényl]-2-{[(2*R*,7a*S*)-2-fluorotétrahydro-1*H*-pyrrolizin-7a(5*H*)-yl]méthoxy}-7,8-dihydro-5*H*-pyrano[4,3-*d*]pyrimidin-4-yl]-1-(2-fluoroprop-2-énoyl)pipérazin-2-yl]acétonitrile

elisrasib [(2*S*)-4-[(7*S*)-7-[3-amino-2-fluoro-5-metil-6-(trifluorometil)fenil]-2-{[(2*R*,7a*S*)-2-fluorotetrahidro-1*H*-pirrolizin-7a(5*H*)-il]metoxi}-7,8-dihidro-5*H*-pirano[4,3-*d*]pirimidin-4-il]-1-(2-fluoroprop-2-enoil)piperazin-2-il]acetonitrilo

$C_{32}H_{35}F_6N_7O_3$



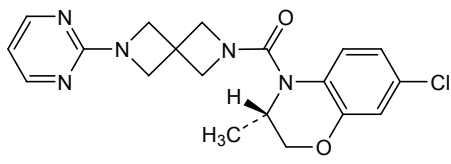
elsovaptanum

elsovaptan [(3*S*)-7-chloro-3-methyl-2,3-dihydro-4*H*-1,4-benzoxazin-4-yl][6-(pyrimidin-2-yl)-2,6-diazaspiro[3.3]heptan-2-yl]methanone

elsovaptan [(3*S*)-7-chloro-3-méthyl-2,3-dihydro-4*H*-1,4-benzoxazin-4-yl][6-(pyrimidin-2-yl)-2,6-diazaspiro[3.3]heptan-2-yl]méthanone

elsovaptán [(3*S*)-7-cloro-3-metil-2,3-dihidro-4*H*-1,4-benzoxazin-4-il][6-(pirimidin-2-il)-2,6-diazaespiro[3.3]heptan-2-il]metanona

$C_{19}H_{20}ClN_5O_2$



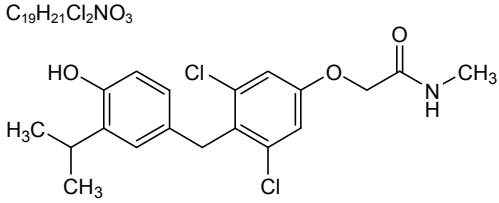
elunetiromum

elunetirom — 2-(3,5-dichloro-4-{[4-hydroxy-3-(propan-2-yl)phenyl]methyl}phenoxy)-*N*-methylacetamide

élunétirom — 2-(3,5-dichloro-4-{[4-hydroxy-3-(propan-2-yl)phényl]méthyl}phénoxy)-*N*-méthylacétamide

elunetirom — 2-(3,5-dicloro-4-{[4-hidroxi-3-(propan-2-il)fenil]metil}fenoxi)-*N*-metilacetamida

$C_{19}H_{21}Cl_2NO_3$



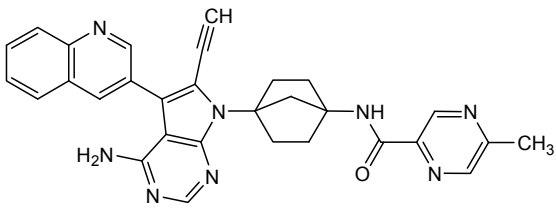
emupertinibum

emupertinib — *N*-{4-[4-amino-6-ethynyl-5-(quinolin-3-yl)-7*H*-pyrrolo[2,3-*d*]pyrimidin-7-yl]bicyclo[2.2.1]heptan-1-yl}-5-methylpyrazine-2-carboxamide

émupertinib — *N*-{4-[4-amino-6-éthynyl-5-(quinoléin-3-yl)-7*H*-pyrrolo[2,3-*d*]pyrimidin-7-yl]bicyclo[2.2.1]heptan-1-yl}-5-méthylpyrazine-2-carboxamide

emupertinib — *N*-{4-[4-amino-6-etinil-5-(quinolein-3-il)-7*H*-pirrolo[2,3-*d*]pirimidin-7-il]biciclo[2.2.1]heptan-1-il}-5-metilpirazina-2-carboxamida

$C_{30}H_{26}N_8O$



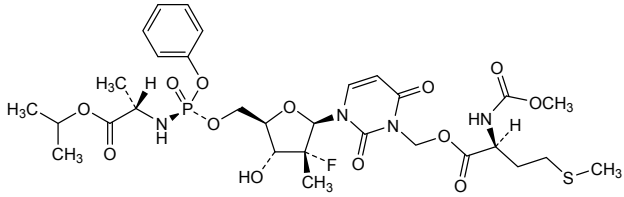
encofosbuvirum

encofosbuvir — propan-2-yl *N*-[(*P*$^{5'}$*S*,2'*R*)-2'-deoxy-2'-fluoro-3-({[*N*-(methoxycarbonyl)-L-methionyl]oxy}methyl)-2'-methyl-*O*^{P}-phenyl-5'-uridylyl]-L-alaninate

encofosbuvir — *N*-[(*P*$^{5'}$*S*,2'*R*)-2'-désoxy-2'-fluoro-3-({[*N*-(méthoxycarbonyl)-L-méthionyl]oxy}méthyl)-2'-méthyl-*O*^{P}-phényl-5'-uridylyl]-L-alaninate de propan-2-yle

encofosbuvir — *N*-[(*P*$^{5'}$*S*,2'*R*)-2'-desoxi-*O*^{P}-fenil-2'-fluoro-2'-metil-3-({[*N*-(metoxicarbonil)-L-metionil]oxi}metil)-5'-uridilil]-L-alaninato de propan-2-ilo

$C_{30}H_{42}FN_4O_{13}PS$



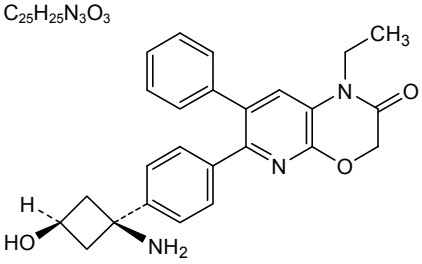
engasertibum

engasertib — 6-{4-[(1*S*,3*S*)-1-amino-3-hydroxycyclobutyl]phenyl}-1-ethyl-7-phenyl-1*H*-pyrido[2,3-*b*][1,4]oxazin-2(3*H*)-one

engasertib — 6-{4-[(1*S*,3*S*)-1-amino-3-hydroxycyclobutyl]phényl}-1-éthyl-7-phényl-1*H*-pyrido[2,3-*b*][1,4]oxazin-2(3*H*)-one

engasertib — 6-{4-[(1*S*,3*S*)-1-amino-3-hidroxiciclobutil]fenil}-1-etil-7-fenil-1*H*-pirido[2,3-*b*][1,4]oxazin-2(3*H*)-ona

$C_{25}H_{25}N_3O_3$



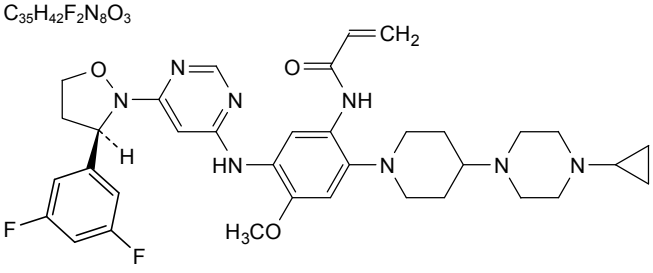
enozertinibum

enozertinib — *N*-[(7^{3}*R*)-8^{3},8^{5}-difluoro-4^{5}-methoxy-5-aza-6(4,6)-pyrimidina-2(1,4)-piperazina-3(4,1)-piperidina-7(2,3)-[1,2]oxazolidina-4(1,4),8(1)-dibenzena-1(1)-cyclopropanaoctaphan-4^{2}-yl]prop-2-enamide

énozertinib — *N*-[(7^{3}*R*)-8^{3},8^{5}-difluoro-4^{5}-méthoxy-5-aza-6(4,6)-pyrimidina-2(1,4)-pipérazina-3(4,1)-pipéridina-7(2,3)-[1,2]oxazolidina-4(1,4),8(1)-dibenzéna-1(1)-cyclopropanaoctaphan-4^{2}-yl]prop-2-énamide

enozertinib — *N*-[(7^{3}*R*)-8^{3},8^{5}-difluoro-4^{5}-metoxi-5-aza-6(4,6)-pirimidina-2(1,4)-piperazina-3(4,1)-piperidina-7(2,3)-[1,2]oxazolidina-4(1,4),8(1)-dibencena-1(1)-ciclopropanaoctafan-4^{2}-il]prop-2-enamida

$C_{35}H_{42}F_2N_8O_3$



enzelkitugum #

enzelkitug	immunoglobulin G1-kappa, anti-[*Homo sapiens* CCR8 (C-C motif chemokine receptor 8, CKR-L1, CDw198) N-terminus], humanized monoclonal antibody; H-gamma1 heavy chain humanized (1-449) [VH (*Homo sapiens* IGHV3-23*01 (81.6%) -(IGHD) -IGHJ3*02 (91.7%) M123>T (114), CDR-IMGT [8.7.13] (26-33.51-57.96-108)) (1-119) -*Homo sapiens* IGHG1*03v (100%) G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (216) (120-217), hinge 1-15 (218-232), CH2 (233-342), CH3 E12 (358), M14 (360) (343-447), CHS (448-449)) (120-449)], (222-218')-disulfide with L-kappa light chain humanized (1'-218') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (87.8%) -IGKJ4*01 (100%), CDR-IMGT [6.3.13] (27'-32'.50'-52'.89'-101')) (1'-111') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (157'), V101 (195')) (112'-218')]; dimer (228-228'':231-231'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa
enzelkitug	immunoglobuline G1-kappa, anti-[*Homo sapiens* CCR8 (récepteur 8 de chimiokine C-C motif, CKR-L1, CDw198) N-terminus], anticorps monoclonal humanisé; chaîne lourde H-gamma1 humanisée (1-449) [VH (*Homo sapiens* IGHV3-23*01 (81.6%) -(IGHD) -IGHJ3*02 (91.7%) M123>T (114), CDR-IMGT [8.7.13] (26-33.51-57.96-108)) (1-119) -*Homo sapiens* IGHG1*03v (100%) G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (216) (120-217), charnière 1-15 (218-232), CH2 (233-342), CH3 E12 (358), M14 (360) (343-447), CHS (448-449)) (120-449)], (222-218')-disulfure avec la chaîne légère L-kappa humanisée (1'-218') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (87.8%) -IGKJ4*01 (100%), CDR-IMGT [6.3.13] (27'-32'.50'-52'.89'-101')) (1'-111') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (157'), V101 (195')) (112'-218')]; dimère (228-228'':231-231'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa
enzelkitug	inmunoglobulina G1-kappa, anti-[*Homo sapiens* CCR8 (receptor 8 de quimiocina C-C motivo, CKR-L1, CDw198) N-terminus], anticuerpo monoclonal humanizado; cadena pesada H-gamma1 humanizada (1-449) [VH (*Homo sapiens* IGHV3-23*01 (81.6%) -(IGHD) -IGHJ3*02 (91.7%) M123>T (114), CDR-IMGT [8.7.13] (26-33.51-57.96-108)) (1-119) -*Homo sapiens* IGHG1*03v (100%) G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (216) (120-217), bisagra 1-15 (218-232), CH2 (233-342), CH3 E12 (358), M14 (360) (343-447), CHS (448-449)) (120-449)], (222-218')-disulfuro con la cadena ligera L-kappa humanizada (1'-218') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (87.8%) -IGKJ4*01 (100%), CDR-IMGT [6.3.13] (27'-32'.50'-52'.89'-101')) (1'-111') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (157'), V101 (195')) (112'-218')]; 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

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EVQLLESGGG LVQPGGSLRL SCAASGIDLS TYAMGWVRQA PGKGLEWVGL  50
IHRSGRTYYA TWAKGRFTIS KDSSKNTLYL QMNSLRAEDT AVYYCTRSYP 100
DYSATASIWG QGTTVTVSSA STKGPSVFPL APSSKSTSGG TAALGCLVKD 150
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY 200
ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP CPAPELLGGP SVFLFPPKPK 250
DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS 300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV 350
YTLPPSREEM TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL 400
DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK  449
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Light chain / Chaîne légère / Cadena ligera

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DIQVTQSPSS LSASVGDRVT ITCQASENIA NALAWYQQKP GKPPKFLIYG  50
ASNLASGVPS RFSGSGSGTD FTFTISSLQP EDIATYYCQQ AYYGNSFVEG 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) 22-95 146-202 263-323 369-427
22''-95'' 146''-202'' 263''-323'' 369''-427''
Intra-L (C23-C104) 23'-88' 138'-198'
23'''-88''' 138'''-198'''
Inter-H-L (h 5-CL 126) 222-218' 222''-218'''
Inter-H-H (h 11, h 14) 228-228'' 231-231''

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4: 299, 299''
Low fucosylated (<15%) complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes faiblement fucosylés (<15%) / glicanos de tipo CHO biantenarios complejos bajo fucosilados (<15 %)

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

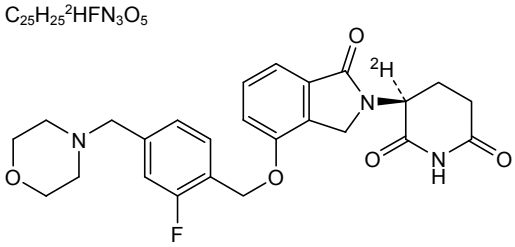
epaldeudomidum

epaldeudomide — (1^3*S*)-5^2-fluoro(1^3-^{2}H)-3-oxa-2(2,4)-isoindola-7(4)-morpholina-1(3)-piperidina-5(1,4)-benzenaheptaphane-1^2,1^6,2^1(2^3*H*)-trione

épaldeudomide — (1^3*S*)-5^2-fluoro(1^3-^{2}H)-3-oxa-2(2,4)-isoindola-7(4)-morpholina-1(3)-pipéridina-5(1,4)-benzénaheptaphane-1^2,1^6,2^1(2^3*H*)-trione

epaldeudomida — (1^3*S*)-5^2-fluoro(1^3-^{2}H)-3-oxa-2(2,4)-isoindola-7(4)-morfolina-1(3)-piperidina-5(1,4)-bencenaheptafano-1^2,1^6,2^1(2^3*H*)-triona

$C_{25}H_{25}{}^2HFN_3O_5$



etuptamigum

etuptamig — immunoglobulin L-kappa-H-gamma1_L-lambda-H-gamma1, anti-[*Homo sapiens* NCR3LG1 (natural killer cell cytotoxicity receptor 3 ligand 1, B7 homolog 6, B7-H6)] and anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], monoclonal antibody, bispecific;
fused chain L-kappa-H-gamma1 anti-NCR3LG1 (1-698) (knob) [L-kappa anti-NCR3LG1 (1-214) [V-KAPPA (*Homo sapiens* IGKV1-16*01 (85.3%) -IGKJ2*01 (90.9%) Q120>A (100), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1-107)-*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')] -38-mer(tetraglycylseryl-bis(EGKSSGSGSESKST)-

	tetraglycylseryl) linker (215-252) -[H-gamma-1 heavy chain anti-NCR3LG1 (253-698) [VH (*Homo sapiens* IGHV1-46*01 (81.6%) -(IGHD) -IGHJ5*01 (92.3%), CDR-IMGT [8.8.10] (278-285.303-310.349-358)) (253-369)-*Homo sapiens* IGHG1*03, G1m3, nG1m1, CH1 R120, CH3 E12, M14,6-G1v14 CH2 A1.3, A1.2, 14-G1v32 CH3 W22 (knob) (CH1 R120 (466) (370-467), hinge 1-15 (468-482), CH2 L1.3>A (486), L1.2>A (487) (483-592), CH3 E12 (608), M14 (610), T22>W (618) (593-697), CHS K2>del (698)) (370-698)]]; fused chain L-lambda6-H-gamma1 anti-CD3E (1-707) (hole) [L-lambda6 anti-CD3E (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%) (C-LAMBDA6) (110'-215')] -38-mer (tetraglycylseryl-bis(EGKSSGSGSESKST)-tetraglycylseryl) linker (216'-253') -[H-gamma-1 anti-CD3E (254'-707') [VH Musmus/Homsap (*Mus musculus* IGHV10-1*04 (93.0%) -(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, 6-G1v14 CH2 A1.3, A1.2,14-G1v33 CH3 S22, A24, V86 (hole), 10-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 (668'), H115>R (696'), Y116>F (697') (602'-706'), CHS K2>del (707')) (379'-707')]]; dimer (478-487':481-490')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa
étuptamig	immunoglobuline L-kappa-H-gamma1_L-lambda-H-gamma1, anti-[*Homo sapiens* NCR3LG1 (ligand 1 du récepteur 3 de la cytotoxicité des cellules tueuses naturelles, B7 homologue 6, B7-H6)] et anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], anticorps monoclonal, bispécifique; chaîne fusionnée L-kappa-H-gamma1 anti-NCR3LG1 (1-698) (knob) [L-kappa anti-NCR3LG1 (1-214) [V-KAPPA (*Homo sapiens* IGKV1-16*01 (85.3%) -IGKJ2*01 (90.9%) Q120>A (100), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1-107)-*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')] -38-mer(GGGGS tétraglycylséryl-bis(EGKSSGSGSESKST)-tétraglycylséryl) linker (215-252) -[H-gamma1 anti-NCR3LG1 (253-698) [VH (*Homo sapiens* IGHV1-46*01 (81.6%) -(IGHD) -IGHJ5*01 (92.3%), CDR-IMGT [8.8.10] (278-285.303-310.349-358)) (253-369)-*Homo sapiens* IGHG1*03, G1m3, nG1m1, CH1 R120, CH3 E12, M14,6-G1v14 CH2 A1.3, A1.2, 14-G1v32 CH3 W22 (knob) (CH1 R120 (466) (370-467), charnière 1-15 (468-482), CH2 L1.3>A (486), L1.2>A (487) (483-592), CH3 E12 (608), M14 (610), T22>W (618) (593-697), CHS K2>del (698)) (370-698)]];

	chaîne fusionnée L-lambda6-H-gamma1 anti-CD3E (1-707) (hole) [L-lambda6 anti-CD3E (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%) (C-LAMBDA6) (110'-215')] -38-mer (GGGGS tétraglycylséryl-bis(EGKSSGSGSESKST)-tétraglycylséryl) linker (216'-253') -[H-gamma1 anti-CD3E (254'-707') [VH Musmus/Homsap (*Mus musculus* IGHV10-1*04 (93.0%) -(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, 6-G1v14 CH2 A1.3, A1.2,14-G1v33 CH3 S22, A24, V86 (hole), 10-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 (668'), H115>R (696'), Y116>F (697') (602'-706'), CHS K2>del (707')) (379'-707')]]; dimère (478-487':481-490')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa
etuptamig	inmunoglobulina L-kappa-H-gamma1_L-lambda-H-gamma1, anti-[*Homo sapiens* NCR3LG1 (ligando 1 del receptor 3 de la citotoxicidad de las células asesinas naturales, B7 homólogo 6, B7-H6)] y anti-[*Homo sapiens* CD3E (CD3 épsilon, Leu-4)], anticuerpo monoclonal, biespecífico; cadena fusionada L-kappa-H-gamma1 anti-NCR3LG1 (1-698) (knob) [L-kappa anti-NCR3LG1 (1-214) [V-KAPPA (*Homo sapiens* IGKV1-16*01 (85.3%) -IGKJ2*01 (90.9%) Q120>A (100), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1-107)-*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')] -38-mer(GGGGS tetraglicilseril-bis(EGKSSGSGSESKST)-tetraglicilseril) enlace (215-252) -[H-gamma1 anti-NCR3LG1 (253-698) [VH (*Homo sapiens* IGHV1-46*01 (81.6%) -(IGHD) -IGHJ5*01 (92.3%), CDR-IMGT [8.8.10] (278-285.303-310.349-358)) (253-369)-*Homo sapiens* IGHG1*03, G1m3, nG1m1, CH1 R120, CH3 E12, M14,6-G1v14 CH2 A1.3, A1.2, 14-G1v32 CH3 W22 (knob) (CH1 R120 (466) (370-467), bisagra 1-15 (468-482), CH2 L1.3>A (486), L1.2>A (487) (483-592), CH3 E12 (608), M14 (610), T22>W (618) (593-697), CHS K2>del (698)) (370-698)]]; cadena fusionada L-lambda6-H-gamma1 anti-CD3E (1-707) (hole) [L-lambda6 anti-CD3E (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%) (C-LAMBDA6) (110'-215')] -38-mer (GGGGS tetraglicilseril-bis(EGKSSGSGSESKST)-tetraglicilseril) enlace (216'-253') -[H-gamma1 anti-CD3E (254'-707') [VH Musmus/Homsap (*Mus musculus* IGHV10-1*04 (93.0%) -(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, 6-G1v14 CH2 A1.3, A1.2,14-G1v33 CH3 S22, A24, V86 (hole), 10-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 (668'), H115>R (696'), Y116>F (697') (602'-706'), CHS K2>del (707'))

(379'-707')]]; dímero (478-487':481-490')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, forma glicosilada alfa

Fused chain / Chaîne fusionnée / Cadena fusionada:
L-kappa-H-gamma1 (L-H) anti-NCR3LG1 (knob)

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DIQMTQSPSS LSASVGDRVT ITCKASQNVG KYVAWYQQKP GKAPKSLIYS  50
ASNRYDGVPS RFSGSGSGTD FTLTISSLQP EDFATYFCQQ YISYPLTFGA 100
GTKLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGECGGGGSE GKSSGSGSES KSTEGKSSGS GSESKSTGGG 250
GSQVQLVQSG AEVKKPGASV KVSCKASGYT FTNYWMNWMK QAPGQGLEWI 300
GGIYLNGDST DYNEKFKGKV TMTVDTSTST VYMELSSLRS EDTAVYYCTR 350
RGDYFGDFWG QGTLVTVSSA STKGPSVFPL APSSKSTSGG TAALGCLVKD 400
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY 450
ICNVNHKPSN TKVDKRVEPK SCDKTHTCPP CPAPEAAGGP SVFLFPPKPK 500
DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS 550
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV 600
YTLPPSREEM TKNQVSLWCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL 650
DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPG   698
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Fused chain / Chaîne fusionnée / Cadena fusionada:
L-lambda6-H-gamma1 (L'-H') anti-CD3E (hole)

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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
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Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
L-H Intra-L (C23-C104) 23-88 134-194
(knob) Intra-H (C23-C104) 274-348 396-452 513-573 619-677
Intra-(L-H) (h 5-CL 126) 472-214
L'-H' Intra-L' (C23-C104) 22'-90' 137'-196'
(hole) Intra-H ' (C23-C104) 275'-351' 405'-461' 522'-582' 628'-686'
Intra-(L'-H') (h 5-CL 126) 481'-214'
Inter-(L-H)-(L'-H') (h 11, h 14) 478-487' 481-490'

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4: 549, 558"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

exerenibartum #

exerenibart — immunoglobulin G4-kappa, anti-[*Homo sapiens* TMPRSS6 (transmembrane serine protease 6, matriptase-2, MT2)], *Homo sapiens* monoclonal antibody;
H-gamma4 heavy chain *Homo sapiens* (1-451) [VH (*Homo sapiens* IGHV3-23*04 (95.9%) -(IGHD) -IGHJ1*01 (90.9%) L123>T (119), CDR-IMGT [8.8.17] (26-33.51-58.97-113)) (1-124) -*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, 12-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)], (138-214')-disulfide with L-kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*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, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dimer (230-230":233-233")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa

exérénibart — immunoglobuline G4-kappa, anti-[*Homo sapiens* TMPRSS6 (sérine protéase transmembranaire 6, matriptase-2, MT2)], anticorps monoclonal *Homo sapiens*;

chaîne lourde H-gamma4 *Homo sapiens* (1-451) [VH (*Homo sapiens* IGHV3-23*04 (95.9%) -(IGHD) -IGHJ1*01 (90.9%) L123>T (119), CDR-IMGT [8.8.17] (26-33.51-58.97-113)) (1-124) -*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, 12-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)], (138-214')-disulfure avec la chaîne légère L-kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*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, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dimère (230-230'':233-233'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa

exerenibart

inmunoglobulina G4-kappa, anti-[*Homo sapiens* TMPRSS6 (serina proteasa transmembranaria 6, matriptasa-2, MT2)], anticuerpo monoclonal *Homo sapiens*;
cadena pesada H-gamma4 *Homo sapiens* (1-451) [VH (*Homo sapiens* IGHV3-23*04 (95.9%) -(IGHD) -IGHJ1*01 (90.9%) L123>T (119), CDR-IMGT [8.8.17] (26-33.51-58.97-113)) (1-124) -*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, 12-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)], (138-214')-disulfuro con la cadena ligera L-kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*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, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; 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

```
EVQLVESGGG LVQPGGSLRL SCAASGFTFS SYAMTWVRQA PGKGLEWVSA  50
ISGSDTSTYY ADSVKGRFTI SRDNSKNTLF LQMNSLRAED TAVYYCAKHQ 100
DYDFSYYYSA MDVWGQGTTV TVSSASTKGP SVFPLAPCSR STSESTAALG 150
CLVKDYFPEP VTVSWNSGAL TSGVHTFPAV LQSSGLYSLS SVVTVPSSSL 200
GTKTYTCNVD HKPSNTKVDK RVESKYGPPC PPCPAPEFLG GPSVFLFPPK 250
PKDTLMISRT PEVTCVVVDV SQEDPEVQFN WYVDGVEVHN AKTKPREEQF 300
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK GLPSSIEKTI SKAKGQPREP 350
QVYTLPPSQE EMTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP 400
VLDSDGSFFL YSRLTVDKSR WQEGNVFSCS VMHEALHNHY TQKSLSLSLG 450
K                                                       451
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVI ITCRASQDFN SWLAWYQQKP GKAPKLLIYA  50
ASSLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ TDSFPFTFGP 100
GTKVDIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 151-207 265-325 371-429
22"-96" 151"-207" 265"-325" 371"-429"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194'"
Inter-H-L (CH1 10-CL 126) 138-214' 138"-214'"
Inter-H-H (h 8, h 11) 230-230" 233-233"

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

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

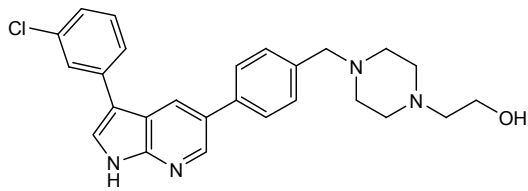
famlasertibum

famlasertib — 2-[4-({4-[3-(3-chlorophenyl)-1*H*-pyrrolo[2,3-*b*]pyridin-5-yl]phenyl}methyl)piperazin-1-yl]ethan-1-ol

famlasertib — 2-[4-({4-[3-(3-chlorophényl)-1*H*-pyrrolo[2,3-*b*]pyridin-5-yl]phényl}méthyl)pipérazin-1-yl]éthan-1-ol

famlasertib — 2-[4-({4-[3-(3-clorofenil)-1*H*-pirrolo[2,3-*b*]piridin-5-il]fenil}metil)piperazin-1-il]etan-1-ol

$C_{26}H_{27}ClN_4O$



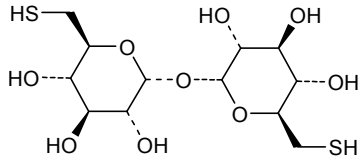
fexlamosum

fexlamose — 6-thio-α-D-glucopyranosyl 6-thio-α-D-glucopyranoside; 6,6'-dithiotrehalose

fexlamose — 6-thio-α-D-glucopyranoside de 6-thio-α-D-glucopyranosyle; 6,6'-dithiotréhalose

fexlamosa — 6-tio-α-D-glucopiranósido de 6-tio-α-D-glucopiranosilo; 6,6'-ditiotrehalosa

$C_{12}H_{22}O_9S_2$



firsekibartum #

firsekibart — immunoglobulin G4-lambda2, anti-[*Homo sapiens* IL1B (interleukin 1 beta, IL-1B, 1L1F2)], *Homo sapiens* monoclonal antibody;
H-gamma4 heavy chain *Homo sapiens* (1-455) [VH (*Homo sapiens* IGHV3-49*05 (94.0%) -(IGHD) -IGHJ6*01 (94.4%), CDR-IMGT [8.10.19] (26-33.51-60.99-117)) (1-128) -*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, 12-G4v5 h P10 (CH1 (129-226), hinge 1-12 S10>P (236) (227-238), CH2 L92 (317) (239-348), CH3 (349-453), CHS (454-455)) (129-455)], (142-211')-disulfide with L-lambda2 light chain *Homo sapiens* (1'-212') [V-LAMBDA (*Homo sapiens* IGLV3-1*01 (96.8%) -IGLJ2*01 (100%), CDR-IMGT [6.3.9] (26'-31'.49'-51'.88'-96')) (1'-106') -*Homo sapiens* IGLC2*01 (100%) (C-LAMBDA2) (107'-212')]; dimer (234-234":237-237")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa

firsékibart

immunoglobuline G4-lambda2, anti-[*Homo sapiens* IL1B (interleukine 1 bêta, IL-1B, 1L1F2)], anticorps monoclonal *Homo sapiens*; chaîne lourde H-gamma4 *Homo sapiens* (1-455) [VH (*Homo sapiens* IGHV3-49*05 (94.0%) -(IGHD) -IGHJ6*01 (94.4%), CDR-IMGT [8.10.19] (26-33.51-60.99-117)) (1-128) -*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, 12-G4v5 h P10 (CH1 (129-226), charnière 1-12 S10>P (236) (227-238), CH2 L92 (317) (239-348), CH3 (349-453), CHS (454-455)) (129-455)], (142-211')-disulfure avec la chaîne légère L-lambda2 *Homo sapiens* (1'-212') [V-LAMBDA (*Homo sapiens* IGLV3-1*01 (96.8%) -IGLJ2*01 (100%), CDR-IMGT [6.3.9] (26'-31'.49'-51'.88'-96')) (1'-106') -*Homo sapiens* IGLC2*01 (100%) (C-LAMBDA2) (107'-212')]; dimère (234-234":237-237")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa

firsekibart

inmunoglobulina G4-lambda2, anti-[*Homo sapiens* IL1B (interleukina 1 beta, IL-1B, 1L1F2)], anticuerpo monoclonal *Homo sapiens*; cadena pesada H-gamma4 *Homo sapiens* (1-455) [VH (*Homo sapiens* IGHV3-49*05 (94.0%) -(IGHD) -IGHJ6*01 (94.4%), CDR-IMGT [8.10.19] (26-33.51-60.99-117)) (1-128) -*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, 12-G4v5 h P10 (CH1 (129-226), bisagra 1-12 S10>P (236) (227-238), CH2 L92 (317) (239-348), CH3 (349-453), CHS (454-455)) (129-455)], (142-211')-disulfuro con la cadena ligera L-lambda2 *Homo sapiens* (1'-212') [V-LAMBDA (*Homo sapiens* IGLV3-1*01 (96.8%) -IGLJ2*01 (100%), CDR-IMGT [6.3.9] (26'-31'.49'-51'.88'-96')) (1'-106') -*Homo sapiens* IGLC2*01 (100%) (C-LAMBDA2) (107'-212')]; dímero (234-234":237-237")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVKPGRSLRL SCTGSGFTFG DYALNWFRQA PGMGLEWVGF  50
IRGKAYGGTT EYAASVKGRF TISRDDSKSI AYLQMNSLKT EDTAVYYCNR 100
EVEYCRSSEN YCYGMDVWGQ GTTVTVSSAS TKGPSVFPLA PCSRSTSEST 150
AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP 200
SSSLGTKTYT CNVDHKPSNT KVDKRVESKY GPPCPPCPAP EFLGGPSVFL 250
FPPKPKDTLM ISRTPEVTCV VVDVSQEDPE VQFNWYVDGV EVHNAKTKPR 300
EEQFNSTYRV VSVLTVLHQD WLNGKEYKCK VSNKGLPSSI EKTISKAKGQ 350
PREPQVYTLP PSQEEMTKNQ VSLTCLVKGF YPSDIAVEWE SNGQPENNYK 400
TTPPVLDSDG SFFLYSRLTV DKSRWQEGNV FSCSVMHEAL HNHYTQKSLS 450
LSLGK                                                   455
```

Light chain / Chaîne légère / Cadena ligera

```
SYELTQPPSV SVSPGQTASI TCSGDKLGDK FACWYQQKPG QSPVLVIYQD  50
TKRPSGIPER FSGSNSGNTA TLTISGTQAM DEADYYCQAW DSNTVVFGGG 100
TKLTVLGQPK AAPSVTLFPP SSEELQANKA TLVCLISDFY PGAVTVAWKA 150
DSSPVKAGVE TTTPSKQSNN KYAASSYLSL TPEQWKSHRS YSCQVTHEGS 200
TVEKTVAPTE CS                                          212
```

Post-translational modifications

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

Intra-H (C23-C104)	22-98	105-112	155-211	269-329	375-433
	22"-98"	105"-112"	155"-211"	269"-329"	375"-433"
Intra-L (C23-C104)	22'-87'	134'-193'			
	22'"-87'"	134'"-193'"			
Inter-H-L (CH1 10-CL 126)	142-211'	142"-211'"			
Inter-H-H (h 8, h 11)	234-234"	237-237"			

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

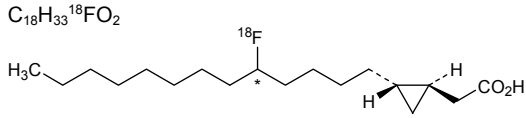
C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2: 455, 455"

florcicaperum (^{18}F)

florcicaper (^{18}F) — *rac*-{(1*R*,2*S*)-2-[(5*RS*)-5-(^{18}F)fluorotridecyl]cyclopropyl}acetic acid

florcicaper (^{18}F) — acide *rac*-{(1*R*,2*S*)-2-[(5*RS*)-5-(^{18}F)fluorotridécyl]cyclopropyl}acétique

florcicapero (^{18}F) — ácido *rac*-{(1*R*,2*S*)-2-[(5*RS*)-5-(^{18}F)fluorotridecil]ciclopropil}acético



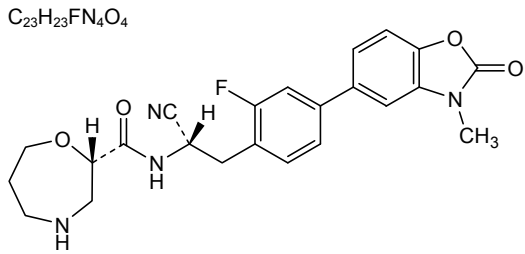
its epimer at C* and their enantiomers
son épimère en C* et leurs énantiomères
su epímero al C* y sus enantiómeros

florensocatibum

florensocatib — (2*S*)-*N*-{(1*S*)-1-cyano-2-[2-fluoro-4-(3-methyl-2-oxo-2,3-dihydro-1,3-benzoxazol-5-yl)phenyl]ethyl}-1,4-oxazepane-2-carboxamide

florensocatib — (2*S*)-*N*-{(1*S*)-1-cyano-2-[2-fluoro-4-(3-méthyl-2-oxo-2,3-dihydro-1,3-benzoxazol-5-yl)phényl]éthyl}-1,4-oxazépane-2-carboxamide

florensocatib — (2*S*)-*N*-{(1*S*)-1-ciano-2-[2-fluoro-4-(3-metil-2-oxo-2,3-dihidro-1,3-benzoxazol-5-il)fenil]etil}-1,4-oxazepano-2-carboxamida



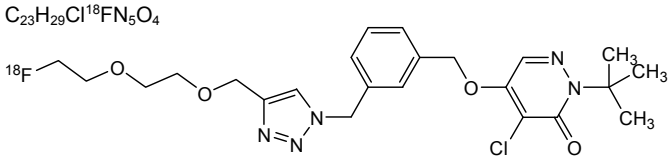
flormotridazum (18F)

flormotridaz (18F) — 2-*tert*-butyl-4-chloro-5-[(3-{[4-({2-[2-(^{18}F)fluoroethoxy]ethoxy}methyl)-1*H*-1,2,3-triazol-1-yl]methyl}phenyl)methoxy]pyridazin-3(2*H*)-one

flormotridaz (18F) — 2-*tert*-butyl-4-chloro-5-[(3-{[4-({2-[2-(^{18}F)fluoroéthoxy]éthoxy}méthyl)-1*H*-1,2,3-triazol-1-yl]méthyl}phényl)méthoxy]pyridazin-3(2*H*)-one

flormotridaz (18F) — 2-*terc*-butil-4-cloro-5-[(3-{[4-({2-[2-(^{18}F)fluoroetoxi]etoxi}metil)-1*H*-1,2,3-triazol-1-il]metil}fenil)metoxi]piridazin-3(2*H*)-ona

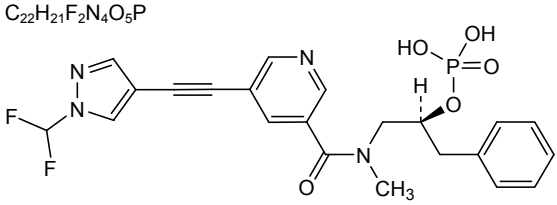
$C_{23}H_{29}Cl^{18}FN_5O_4$



fosizensertibum

fosizensertib	(2*S*)-1-(5-{[1-(difluoromethyl)-1*H*-pyrazol-4-yl]ethynyl}-*N*-methylpyridine-3-carboxamido)-3-phenylpropan-2-yl dihydrogen phosphate
fosizensertib	dihydrogénophosphate de (2*S*)-1-(5-{[1-(difluorométhyl)-1*H*-pyrazol-4-yl]éthynyl}-*N*-méthylpyridine-3-carboxamido)-3-phénylpropan-2-yle
fosizensertib	dihidrógenofosfato de (2*S*)-1-(5-{[1-(difluorometil)-1*H*-pirazol-4-il]etinil}-*N*-metilpiridina-3-carboxamido)-3-fenilpropan-2-ilo

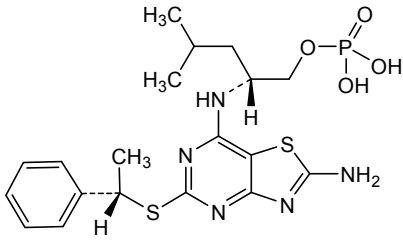
$C_{22}H_{21}F_2N_4O_5P$



fosrugocrixanum

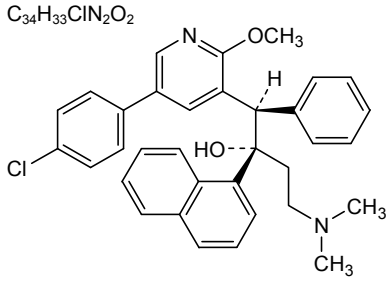
fosrugocrixan	(2*R*)-2-[(2-amino-5-{[(1*S*)-1-phenylethyl]sulfanyl}[1,3]thiazolo[4,5-*d*]pyrimidin-7-yl)amino]-4-methylpentyl dihydrogen phosphate
fosrugocrixan	dihydrogénophosphate de (2*R*)-2-[(2-amino-5-{[(1*S*)-1-phényléthyl]sulfanyl}[1,3]thiazolo[4,5-*d*]pyrimidin-7-yl)amino]-4-méthylpentyle
fosrugocrixán	dihidrógenofosfato de (2*R*)-2-[(2-amino-5-{[(1*S*)-1-feniletil]sulfanil}[1,3]tiazolo[4,5-*d*]pirimidin-7-il)amino]-4-metilpentilo

$C_{19}H_{26}N_5O_4PS_2$



fudapirinum

fudapirine	(1*R*,2*S*)-1-[5-(4-chlorophenyl)-2-methoxypyridin-3-yl]-4-(dimethylamino)-2-(naphthalen-1-yl)-1-phenylbutan-2-ol
fudapirine	(1*R*,2*S*)-1-[5-(4-chlorophényl)-2-méthoxypyridin-3-yl]-4-(diméthylamino)-2-(naphtalén-1-yl)-1-phénylbutan-2-ol
fudapirina	(1*R*,2*S*)-1-[5-(4-clorofenil)-2-metoxipiridin-3-il]-4-(dimetilamino)-1-fenil-2-(naftalen-1-il)butan-2-ol



fulipiftidum

fulipiftide

pigment epithelium-derived factor *(Homo sapiens)* (PEDF, cell proliferation-inducing gene 35 protein, PIG-35, EPC-1, serpin F1), $N^{2.1}$-acetyl-(74-102)-peptide (1-29)-29-amide;
N-acetyl-L-seryl-L-leucylglycyl-L-alanyl-L-α-glutamyl-L-glutaminyl-L-arginyl-L-threonyl-L-α-glutamyl-L-seryl-L-isoleucyl-L-isoleucyl-L-histidyl-L-arginyl-L-alanyl-L-leucyl-L-tyrosyl-L-tyrosyl-L-α-aspartyl-L-leucyl-L-isoleucyl-L-seryl-L-seryl-L-prolyl-L-α-aspartyl-L-isoleucyl-L-histidylglycyl-L-threoninamide

fulipiftide

facteur dérivé de l'épithélium pigmentaire *(Homo sapiens)* (PEDF, protéine du gène 35 induisant la prolifération cellulaire, PIG-35, EPC-1, serpine F1), $N^{2.1}$-acétyl-(74-102)-peptide (1-29)-29-amide;
N-acétyl-L-séryl-L-leucylglycyl-L-alanyl-L-α-glutamyl-L-glutaminyl-L-arginyl-L-thréonyl-L-α-glutamyl-L-séryl-L-isoleucyl-L-isoleucyl-L-histidyl-L-arginyl-L-alanyl-L-leucyl-L-tyrosyl-L-tyrosyl-L-α-aspartyl-L-leucyl-L-isoleucyl-L-séryl-L-séryl-L-prolyl-L-α-aspartyl-L-isoleucyl-L-histidylglycyl-L-thréoninamide

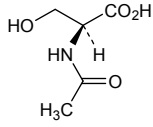
fulipiftida

factor derivado del epitelio pigmentario *(Homo sapiens)* (PEDF, proteína del gen 35 inductor de proliferación celular, PIG-35, EPC-1, serpina F1), $N^{2.1}$-acetil-(74-102)-péptido (1-29)-29-amida;
N-acetil-L-seril-L-leucilglicil-L-alanil-L-α-glutamil-L-glutaminil-L-arginil-L-treonil-L-α-glutamil-L-seril-L-isoleucil-L-isoleucil-L-histidil-L-arginil-L-alanil-L-leucil-L-tirosil-L-tirosil-L-α-aspartil-L-leucil-L-isoleucil-L-seril-L-seril-L-prolil-L-α-aspartil-L-isoleucil-L-histidilglicil-L-treoninamida

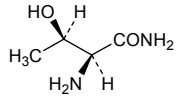
$C_{144}H_{227}N_{41}O_{47}$

SLGAEQRTES IIHRALYYDL ISSPDIHGT 29

Modified residues / Résidus modifiés / Restos modificados



S (1)
N-Ac-L-Ser



T (29)
L-Thr-NH_2

futermestotugum #

futermestotug	immunoglobulin G1-kappa, anti-[*Homo sapiens* CTLA4 (cytotoxic T-lymphocyte associated protein 4, CTLA-4, CD152)], humanized monoclonal antibody; H-gamma1 heavy chain humanized (1-452) [VH (*Homo sapiens* IGHV3-23*04 (90.8%) -(IGHD) -IGHJ4*01 (80.0%) S128>A (122), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens* IGHG1*03v (100%) G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (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 humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-9*01 (85.3%) -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, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dimer (231-231'':234-234'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa
futermestotug	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 (1-452) [VH (*Homo sapiens* IGHV3-23*04 (90.8%) -(IGHD) -IGHJ4*01 (80.0%) S128>A (122), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens* IGHG1*03v (100%) G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (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 humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-9*01 (85.3%) -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, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dimère (231-231'':234-234'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa
futermestotug	inmunoglobulina G1-kappa, anti-[*Homo sapiens* CTLA4 (proteína 4 asociada a los linfocitos T citotóxicos, CTLA-4, CD152)], anticuerpo monoclonal humanizado; cadena pesada H-gamma1 humanizada (1-452) [VH (*Homo sapiens* IGHV3-23*04 (90.8%) -(IGHD) -IGHJ4*01 (80.0%) S128>A (122), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens* IGHG1*03v (100%) G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (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 humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-9*01 (85.3%) -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, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dímero (231-231'':234-234'')-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 SYTMSWVRQA PGKGLEWVAT  50
ISRGGGYTSY PDSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARED 100
YGSSYVHWFA YWGQGTLVTV SAASTKGPSV 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 EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP 400
PVLDSDGSFF LYSKLTVDKS RWQQGNVFSC SVMHEALHNH YTQKSLSLSP 450
GK                                                      452
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSF LSASVGDRVT ITCRAGENIY SYLAWYQQKP GKAPKLLIYN  50
ARTLAEGVPS RFSGSGSGTE FTLTISSLQP EDFATYYCQH HYGSPRTFGG 100
GTKLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Post-translational modifications

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

Intra-H (C23-C104) 22-96 149-205 266-326 372-430
22"-96" 149"-205" 266"-326" 372"-430"
Intra-L (C23-C104) 23'-88' 134'-194'
23'"-88'" 134'"-194'"
Inter-H-L (h 5-CL 126) 225-214' 225"-214'"
Inter-H-H (h 11, h 14) 231-231" 234-234"

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

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

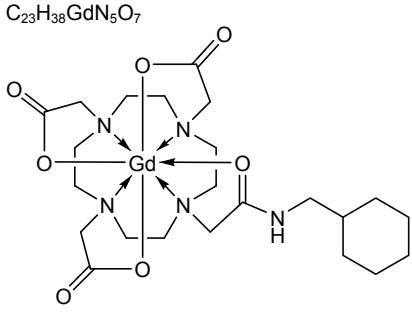
gadosircoclamidum

gadosircoclamide — [2,2',2"-(10-{2-[(cyclohexylmethyl)amino]-2-oxo-κ*O*-ethyl}-1,4,7,10-tetraazacyclododecane-1,4,7-triyl-κ^4*N*^{1},*N*^{4},*N*^{7},*N*^{10})tri(acetato-κ*O*)]gadolinium

gadosircoclamide — [2,2',2"-(10-{2-[(cyclohexylméthyl)amino]-2-oxo-κ*O*-éthyl}-1,4,7,10-tétraazacyclododécane-1,4,7-triyl-κ^4*N*^{1},*N*^{4},*N*^{7},*N*^{10})tri(acétato-κ*O*)]gadolinium

gadosircoclamida — [2,2',2"-(10-{2-[(ciclohexilmetil)amino]-2-oxo-κ*O*-etil}-1,4,7,10-tetraazaciclododecano-1,4,7-triil-κ^4*N*^{1},*N*^{4},*N*^{7},*N*^{10})tri(acetato-κ*O*)]gadolinio

$C_{23}H_{38}GdN_5O_7$



garetatugum

garetatug — immunoglobulin G1-kappa, anti-[*Homo sapiens* CLDN18 (claudin 18, claudin-18, surfactant associated protein J, SFTPJ) isoform 2], humanized monoclonal antibody;

	H-gamma1 heavy chain humanized (1-448) [VH (*Homo sapiens* IGHV1-3*01 (87.8%) -(IGHD) - IGHJ4*01 (92.9%) L123>T (113), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (215) (119-216), hinge 1-15 (217-231), CH2 (232-341), CH3 D12 (357), L14 (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 (90.1%) -IGKJ2*02 (100%), CDR-IMGT [12.3.9] (27'-38'.56'-58'.95'-103')) (1'-113') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (159'), V101 (197')) (114'-220')]; dimer (227-227'':230-230'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa
garétatug	immunoglobuline G1-kappa, anti-[*Homo sapiens* CLDN18 (claudine 18, claudine-18, protéine J associée au surfactant, SFTPJ) isoforme 2], anticorps monoclonal humanisé; chaîne lourde H-gamma1 humanisée (1-448) [VH (*Homo sapiens* IGHV1-3*01 (87.8%) -(IGHD) - IGHJ4*01 (92.9%) L123>T (113), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (215) (119-216), charnière 1-15 (217-231), CH2 (232-341), CH3 D12 (357), L14 (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 (90.1%) - IGKJ2*02 (100%), CDR-IMGT [12.3.9] (27'-38'.56'-58'.95'-103')) (1'-113') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA 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-K1, glycoforme alfa
garetatug	inmunoglobulina G1-kappa, anti-[*Homo sapiens* CLDN18 (claudina 18, claudina-18, proteína J asociada al surfactante, SFTPJ) isoforma 2], anticuerpo monoclonal humanizado; cadena pesada H-gamma1 humanizada (1-448) [VH (*Homo sapiens* IGHV1-3*01 (87.8%) -(IGHD) - IGHJ4*01 (92.9%) L123>T (113), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (215) (119-216), bisagra 1-15 (217-231), CH2 (232-341), CH3 D12 (357), L14 (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 (90.1%) - IGKJ2*02 (100%), CDR-IMGT [12.3.9] (27'-38'.56'-58'.95'-103')) (1'-113') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA 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-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVQSGAE VKKPGASVKV SCKASGYTFT SYWMHWVRQA PGQRLEWMGM  50
IHPNSGSTNY NEKFKGRVTI TRDTSASTAY MELSSLRSED TAVYYCARLK 100
TGNSFDYWGQ 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
TLPPSRDELT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD 400
SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPGK   448
```

Light chain / Chaîne légère / Cadena ligera

```
DIVLTQSPDS LAVSLGERAT INCKSSQSLL NSGNQKNYLT WYQQKPGQPP  50
KLLIYWASTR ESGVPDRFSG SGSGTDFTLT ISSLQAEDVA VYYCQNAYTY 100
PFTFGQGTKL 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-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"

garetatugum rezetecanum #

garetatug rezetecan

immunoglobulin G1-kappa, anti-[*Homo sapiens* CLDN18 (claudin 18, claudin-18, surfactant associated protein J, SFTPJ) isoform 2], humanized monoclonal antibody; conjugated on an average of four cysteinyl residues to *rezetecan*, comprising a linker and a camptothecin derivative (*exatecan*); H-gamma1 heavy chain humanized (1-448) [VH (*Homo sapiens* IGHV1-3*01 (87.8%) -(IGHD) -IGHJ4*01 (92.9%) L123>T (113), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (215) (119-216), hinge 1-15 (217-231), CH2 (232-341), CH3 D12 (357), L14 (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 (90.1%) -IGKJ2*02 (100%), CDR-IMGT [12.3.9] (27'-38'.56'-58'.95'-103')) (1'-113') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (159'), V101 (197')) (114'-220')]; dimer (227-227":230-230")-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 220', 220'", 221, 221", 227, 227", 230 and 230" with (3*RS*)-1-[(2*R*,10*S*)-10-benzyl-2-cyclopropyl-1-{[(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]amino}-1,6,9,12,15,18-hexaoxo-3-oxa-5,8,11,14,17-pentaazatricosan-23-yl]-2,5-dioxopyrrolidin-3-yl (*rezetecan*) groups

garétatug rézétecan

immunoglobuline G1-kappa, anti-[*Homo sapiens* CLDN18 (claudine 18, claudine-18, protéine J associée au surfactant, SFTPJ) isoforme 2], anticorps monoclonal humanisé, conjuguée par quatre résidus cystéinyles en moyenne au *rézétécan*, comprenant un linker et un dérivé de la camptothécine (*exatécan*);

	chaîne lourde H-gamma1 humanisée (1-448) [VH (*Homo sapiens* IGHV1-3*01 (87.8%) -(IGHD) -IGHJ4*01 (92.9%) L123>T (113), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (215) (119-216), charnière 1-15 (217-231), CH2 (232-341), CH3 D12 (357), L14 (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 (90.1%) -IGKJ2*02 (100%), CDR-IMGT [12.3.9] (27'-38'.56'-58'.95'-103')) (1'-113') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA 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-K1, glycoforme alfa; substitué, sur les atomes de soufre de quatre résidus L-cystéinyle en moyenne parmi 220', 220''', 221, 221'', 227, 227'', 230 et 230'', avec des groupes (3*RS*)-1-[(2*R*,10*S*)-10-benzyl-2-cyclopropyl-1-{[(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]amino}-1,6,9,12,15,18-hexaoxo-3-oxa-5,8,11,14,17-pentaazatricosan-23-yl]-2,5-dioxopyrrolidin-3-yle (*rézétécan*)
garetatug rezetecán	inmunoglobulina G1-kappa, anti-[*Homo sapiens* CLDN18 (claudina 18, claudina-18, proteína J asociada al surfactante, SFTPJ) isoforma 2], anticuerpo monoclonal humanizado, conjugado, por cuatro residuos de cisteinilo, por término medio a *rezetecán*, que comprende un enlace y un derivado de la camptotecina (*exatecán*); cadena pesada H-gamma1 humanizada (1-448) [VH (*Homo sapiens* IGHV1-3*01 (87.8%) -(IGHD) -IGHJ4*01 (92.9%) L123>T (113), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (215) (119-216), bisagra 1-15 (217-231), CH2 (232-341), CH3 D12 (357), L14 (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 (90.1%) -IGKJ2*02 (100%), CDR-IMGT [12.3.9] (27'-38'.56'-58'.95'-103')) (1'-113') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA 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-K1, forma glicosilada alfa; sustituido, en los átomos de azufre de cuatro residuos de L-cisteinilo en promedio de 220', 220''', 221, 221'', 227, 227'', 230 y 230'', con grupos (3*RS*)-1-[(2*R*,10*S*)-10-bencil-2-ciclopropil-1-{[(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]amino}-1,6,9,12,15,18-hexaoxo-3-oxa-5,8,11,14,17-pentaazatricosan-23-il]-2,5-dioxopirrolidin-3-ilo (*rezetecán*)

Heavy chain / Chaîne lourde / Cadena pesada (H, H'')

```
EVQLVQSGAE VKKPGASVKV SCKASGYTFT SYWMHWVRQA PGQRLEWMGM  50
IHPNSGSTNY NEKFKGRVTI TRDTSASTAY MELSSLRSED TAVYYCARLK 100
TGNSFDYWGQ 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
TLPPSRDELT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD 400
SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPGK   448
```

Light chain / Chaîne légère / Cadena ligera (L', L''')

```
DIVLTQSPDS LAVSLGERAT INCKSSQSLL NSGNQKNYLT WYQQKPGQPP  50
KLLIYWASTR ESGVPDRFSG SGSGTDFTLT ISSLQAEDVA VYYCQNAYTY 100
PFTFGQGTKL 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''

*Three or four of the four inter-chain disulfide bridges are not present, an average of 4 (3.5-4.5) cysteinyl being conjugated each via a thioether bond to a drug linker.

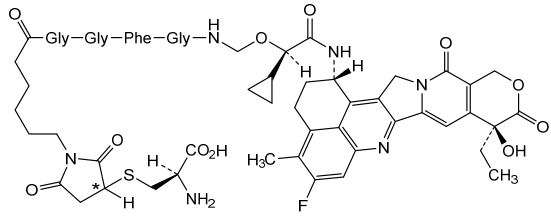
*Trois ou quatre des quatre ponts disulfures inter-chaînes ne sont pas présents, 4 (3.5-4.5) cystéinyl en moyenne étant chacun conjugué via une liaison thioéther à un linker-principe actif.

*Tres or cuatro de los cuatro puentes disulfuro inter-catenarios no estan presentes, una media de 4 (3.5-4.5) cisteinil está conjugada a conectores de principio activo.

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''

Modified residues / Résidus modifiés / Restos modificados*
C (221, 227, 230, 220', 221'', 227'', 230'', 220''')
*(*rezetecan*:mAb ~ 4:1)



gatuzosiranum
gatuzosiran

all-P-ambo-[(2*R*,3*S*)-2-(hydroxymethyl)oxolan-3-yl] hydrogen 5'-*O*-({[(2*R*,3*S*)-3-({[(*cis*-4-{(3*S*,8*S*)-17-[(2-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]hydroxyphosphorothioyl}oxy)oxolan-2-yl]methoxy}hydroxyphosphorothioyl)-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methylguanylyl-(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'-deoxy-2'-fluoroguanylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-deoxy-2'-fluorocytidylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-deoxy-2'-fluoroguanylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methyladenylyl-

(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyl-*P*-thio-3'-adenylate
duplex with *all-P-ambo* 2'-*O*-methyl-*P*-thioguanylyl-(5'→3')-2'-deoxy-2'-fluorocytidylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-deoxy-2'-fluorouridylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-deoxy-2'-fluorocytidylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-deoxy-2'-fluorouridylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-deoxy-2'-fluoroadenylyl-(5'→3')-2'-*O*-methylguanylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-deoxy-2'-fluorouridylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-deoxy-2'-fluoro-*P*-thiouridylyl-(5'→3')-2'-*O*-methyl-*P*-thioadenylyl-(5'→3')-2'-deoxy-2'-fluoro-*P*-thiocytidylyl-(5'→3')-2'-*O*-methyluridine

gatuzosiran

tout-P-ambo-5'-*O*-({[(2*R*,3*S*)-3-({[(*cis*-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]hydroxyphosphorothioyl}oxy)oxolan-2-yl]méthoxy}hydroxyphosphorothioyl)-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthylguanylyl-(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'-désoxy-2'-fluoroguanylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-désoxy-2'-fluorocytidylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-désoxy-2'-fluoroguanylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-hydrogéno-2'-*O*-méthyl-*P*-thio-3'-adénylate de[(2*R*,3*S*)-2-(hydroxyméthyl)oxolan-3-yle]
duplex avec *tout-P-ambo*-2'-*O*-méthyl-*P*-thioguanylyl-(5'→3')-2'-désoxy-2'-fluorocytidylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-désoxy-2'-fluorouridylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-désoxy-2'-fluorocytidylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-désoxy-2'-fluorouridylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-désoxy-2'-fluoroadénylyl-(5'→3')-2'-*O*-méthylguanylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-désoxy-2'-fluorouridylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-désoxy-2'-fluoro-*P*-thiouridylyl-(5'→3')-2'-*O*-méthyl-*P*-thioadénylyl-(5'→3')-2'-désoxy-2'-fluoro-*P*-thiocytidylyl-(5'→3')-2'-*O*-méthyluridine

gatuzosirán

todo-P-ambo-5'-*O*-({[(2*R*,3*S*)-3-({[(*cis*-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]hidroxifosforotioil}oxi)oxolan-2-il]metoxi}hidroxifosforotioil)-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metilguanilil-(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*-metiladenilil-(3'→5')-2'-desoxi-2'-fluoroguanilil-(3'→5')-2'-*O*-

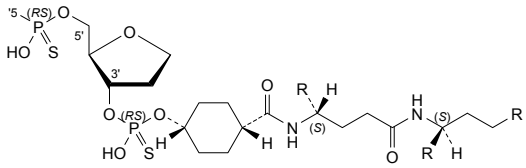
metiluridilil-(3'→5')-2'-desoxi-2'-fluorocitidilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-desoxi-2'-fluoroguanilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-hidrógeno-2'-*O*-metil-*P*-tio-3'-adenilato de *O*-[(2*R*,3*S*)-2-(hidroximetil)oxolan-3-ilo]
dúplex con *todo-P-ambo*-2'-*O*-metil-*P*-tioguanilil-(5'→3')-2'-desoxi-2'-fluoroocitidilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-desoxi-2'-fluorouridilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-desoxi-2'-fluorocitidilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-desoxi-2'-fluorouridilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-desoxi-2'-fluoroadenilil-(5'→3')-2'-*O*-metilguanilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-desoxi-2'-fluorouridilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-desoxi-2'-fluoro-*P*-tiouridilil-(5'→3')-2'-*O*-metil-*P*-tioadenilil-(5'→3')-2'-desoxi-2'-fluoro-*P*-tiocitidilil-(5'→3')-2'-*O*-metiluridina

$C_{493}H_{653}F_{11}N_{163}O_{311}P_{43}S_7$

(3'-5')R1−*C*−*G*−*U*−*A*−*A*−*G*−*A*−*A*−G−*U*−C−*U*−G−*A*−*U*−*A*−*G*−*A*−*U*−*G*−*A*−R2
(5'-3')*G*=C−*A*−U−*U*−C−*U*−U−*C*−A−*G*−*A*−*C*−*U*−*A*−U−*C*−U=*A*=C=*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)-

R1 :



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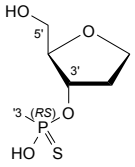
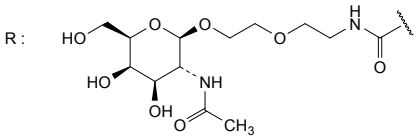


R :



getacatetidum

getacatetide — *N*-acetyl-D-tyrosylglycyl-D-arginyl-D-lysyl-D-lysyl-D-arginyl-D-arginyl-D-glutaminyl-D-arginyl-D-arginyl-D-arginylglycyl-D-lysyl-D-threonyl-D-leucyl-D-arginyl-D-valyl-D-alanyl-D-lysyl-D-alanyl-D-isoleucyl-D-tyrosyl-D-lysyl-D-arginyl-D-tyrosyl-D-isoleucyl-D-isoglutamine

gétacatétide — *N*-acétyl-D-tyrosylglycyl-D-arginyl-D-lysyl-D-lysyl-D-arginyl-D-arginyl-D-glutaminyl-D-arginyl-D-arginyl-D-arginylglycyl-D-lysyl-D-thréonyl-D-leucyl-D-arginyl-D-valyl-D-alanyl-D-lysyl-D-alanyl-D-isoleucyl-D-tyrosyl-D-lysyl-D-arginyl-D-tyrosyl-D-isoleucyl-D-isoglutamine

getacatetida — *N*-acetil-D-tirosilglicil-D-arginil-D-lisil-D-lisil-D-arginil-D-arginil-D-glutaminil-D-arginil-D-arginil-D-arginilglicil-D-lisil-D-treonil-D-leucil-D-arginil-D-valil-D-alanil-D-lisil-D-alanil-D-isoleucil-D-tirosil-D-lisil-D-arginil-D-tirosil-D-isoleucil-D-isoglutamina

$C_{154}H_{268}N_{58}O_{35}$

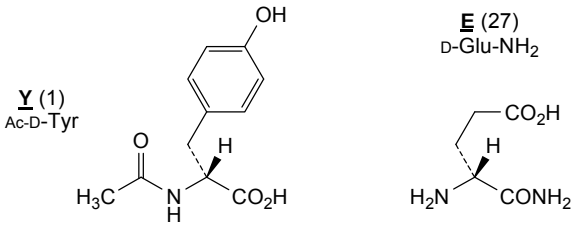
YGRKKRRQRR RGKTLRVAKA IYKRYIE 27

Configuration / Configuration / Configuracion

All-D / *Tout*-D / *Todo*-D

X (1-27)
D-Xaa

Modified residues / Résidus modifiés / Restos modificados



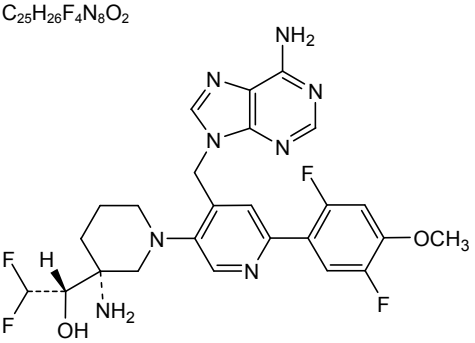
gintemetostatum

gintemetostat — (1*S*)-1-[(3*R*)-3-amino-4'-[(6-amino-9*H*-purin-9-yl)methyl]-6'-(2,5-difluoro-4-methoxyphenyl)-3,4,5,6-tetrahydro-2*H*-[1,3'-bipyridin]-3-yl]-2,2-difluoroethan-1-ol

gintémétostat — (1*S*)-1-[(3*R*)-3-amino-4'-[(6-amino-9*H*-purin-9-yl)méthyl]-6'-(2,5-difluoro-4-méthoxyphényl)-3,4,5,6-tétrahydro-2*H*-[1,3'-bipyridin]-3-yl]-2,2-difluoroéthan-1-ol

gintemetostat — (1*S*)-1-[(3*R*)-3-amino-4'-[(6-amino-9*H*-purin-9-il)metil]-6'-(2,5-difluoro-4-metoxifenil)-3,4,5,6-tetrahidro-2*H*-[1,3'-bipiridin]-3-il]-2,2-difluoroetan-1-ol

$C_{25}H_{26}F_4N_8O_2$



girocovateinum #

girocovatein — severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), omicron lineage JN.1 (Gisaid: EPI_ISL_18872762) spike (S) glycoprotein receptor binding domain (RBD) fragment (303-520, 1-218 in the current sequence), variant ($K^{520}>G^{218}$) fused to severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), omicron lineage JN.1 spike (S) glycoprotein receptor binding domain (RBD) fragment (303-520, 219-436 in the current sequence), single-chain homodimer, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa

girocovatéine

fragment du domaine de liaison au récepteur (RBD) de la glycoprotéine du spicule (S) du coronavirus 2 du syndrome respiratoire aigu sévère (SRAS-CoV-2), lignée omicron JN.1 (Gisaid: EPI_ISL_18872762) (303-520, 1-218 dans la séquence en cours), variant ($K^{520}>G^{218}$), fusionné au fragment du domaine de liaison au récepteur de la glycoprotéine du spicule (S) du coronavirus 2 du syndrome respiratoire aigu sévère (SRAS-CoV-2), lignée omicron JN.1 (303-520, 219-436 dans la séquence en cours), homodimère monocaténaire, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1 glycoforme alfa

girocovateína

fragmento del dominio de unión al receptor (RBD) de la glicoproteína de espícula (S) del coronavirus 2 del síndrome respiratorio agudo severo (SRAS-CoV-2), linaje ómicron JN.1 (Gisaid: EPI_ISL_18872762) (303-520, 1-218 en la secuencia actual), variante ($K^{520}>G^{218}$), fusionado al fragmento del dominio de unión al receptor (RBD) de la glicoproteína de espícula (S) del coronavirus 2 del síndrome respiratorio agudo severo (SRAS-CoV-2), linaje ómicron JN.1 (303-520, 219-436 en la secuencia actual), homodímero de cadena única, producido en células ováricas de hámster Chino (CHO), línea celular CHO-K1, glicoforma alfa

Sequence / Séquence / Secuencia

RVQPTESIVR FPNVTNLCPF HEVFNATRFA SVYAWNRTRI SNCVADYSVL 50
YNFAPFFAFK CYGVSPTKLN DLCFTNVYAD SFVIKGNEVS QIAPGQTGNI 100
ADYNYKLPDD FTGCVIAWNS NKLDSKHSGN YDYWYRSFRK SKLKPFERDI 150
STEIYQAGNK PCKGKGPNCY FPLQSYGFRP TYGVGHQPYR VVVLSFELLH 200
APATVCGPKK STNLVKNGRV QPTESIVRFP NVTNLCPFHE VFNATRFASV 250
YAWNRTRISN CVADYSVLYN FAPFFAFKCY GVSPTKLNDL CFTNVYADSF 300
VIKGNEVSQI APGQTGNIAD YNYKLPDDFT GCVIAWNSNK LDSKHSGNYD 350
YWYRSFRKSK LKPFERDIST EIYQAGNKPC KGKGPNCYFP LQSYGFRPTY 400
GVGHQPYRVV VLSFELLHAP ATVCGPKKST NLVKNK 436

Mutation / Mutation / Mutación
$K^{520}>\underline{\mathbf{G}}^{218}$

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-chain: 18-43, 61-114, 73-206, 162-169, 236-261, 279-332, 291-424, 380-387

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
N13, N25; N231, N243

O-glycosylation sites / Sites de O-glycosylation / Posiciones de O-glicosilación
T5, T223

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
436

givopegsomatropinum

givopegsomatropin

human somatotropin (growth hormone, GH), conjugated to a two-arm polyethylene glycol carrier molecule; produced by *Escherichia coli*, mono-substituted at the N-terminus (F1) or at $N^{6.Lys}$ of either K38, K140, K145 or K158 with one N^{2},N^{6}-bis{[α-methylpoly(oxyethylene)-ω-oxy]carbonyl}-L-lysyl group (~40 kDa)

givopegsomatropine

somatotropine humaine (hormone de croissance, GH), conjuguée à une molécule porteuse de polyéthylène glycol à deux bras; produite par *Escherichia coli*, mono-substituée à l'extrémité N-terminale (F1) ou en $N^{6.Lys}$ de K38, K140, K145 ou K158 par un groupe N^{2},N^{6}-bis{[α-méthylpoly(oxyéthylène)-ω-oxy]carbonyl}-L-lysyle (~40 kDa)

givopegsomatropina

somatotropina humana (hormona de crecimiento, GH), conjugada con una molécula portadora con dos brazos de polietelenglicol; producida por *Escherichia coli*, mono-sustituida en el extremo N-terminal (F1) o en $N^{6\text{-Lys}}$ de K38, K140, K145 o K158 con un grupo N^2,N^6-bis{[α-metilpoli(oxietileno)-ω-oxi]carbonil}-L-lisilo (~40 kDa)

Sequence / Séquence / Secuencia

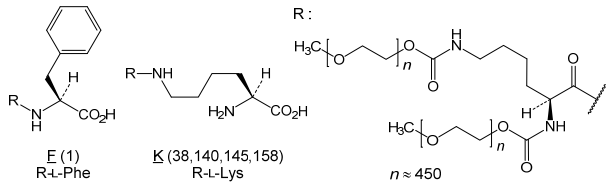
```
FPTIPLSRLF DNAMLRAHRL HQLAFDTYQE FEEAYIPKEQ KYSFLQNPQT    50
SLCFSESIPT PSNREETQQK SNLELLRISL LLIQSWLEPV QFLRSVFANS   100
LVYGASDSNV YDLLKDLEEG IQTLMGRLED GSPRTGQIFK QTYSKFDTNS   150
HNDDALLKNY GLLYCFRKDM DKVETFLRIV QCRSVEGSCG F            191
```

Post-translational modifications

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
53-165 182-189

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
none / aucun / ninguna

Potential modified residues / Résidus modifiés potentiels / restos modificados potenciales
F1, K38, K140, K145, or K158



gozanertinibum

gozanertinib

(2*E*)-4-(dimethylamino)-*N*-[3-(4-{[(1*S*)-2-hydroxy-1-phenylethyl]amino}-6-phenylfuro[2,3-*d*]pyrimidin-5-yl)phenyl]but-2-enamide

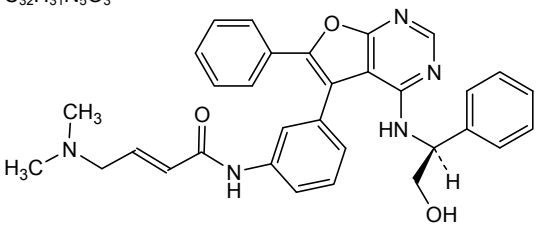
gozanertinib

(2*E*)-4-(diméthylamino)-*N*-[3-(4-{[(1*S*)-2-hydroxy-1-phényléthyl]amino}-6-phénylfuro[2,3-*d*]pyrimidin-5-yl)phényl]but-2-énamide

gozanertinib

(2*E*)-4-(dimetilamino)-*N*-[3-(6-fenil-4-{[(1*S*)-1-fenil-2-hidroxietil]amino}furo[2,3-*d*]pirimidin-5-il)fenil]but-2-enamida

$C_{32}H_{31}N_5O_3$



ibramvibartum #

ibramvibart

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* (1-454) [VH (*Homo sapiens* IGHV3-21*07 (88.8%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.8.17] (26-33.51-58.97-113)) (1-124) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, 9-G1v78 CH3 L107 A114 (CH1 R120 (221) (125-222), hinge 1-15 (223-237), CH2 (238-347), CH3 E12 (363), M14 (365), M107>L (435), N114>A (441) (348-452), CHS (453-454)) (125-454)], (227-217')-disulfide with L-lambda2 light chain *Homo sapiens* (1'-218') [V-LAMBDA (*Homo sapiens* IGLV1-40*01 (92.8%) -IGLJ1*01 (91.7%), CDR-IMGT [9.3.12] (26'-34'.52'-54'.91'-102')) (1'-112') -*Homo sapiens* IGLC2*01 (100%) (C-LAMBDA2) (113'-218')]; dimer (233-233'':236-236'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa
ibramvibart	immunoglobuline G1-kappa, anti-[domaine de liaison au récepteur (RBD) de la glycoprotéine spike (S) du coronavirus 2 du syndrome respiratoire aigu sévère (SRAS-CoV-2)], anticorps monoclonal *Homo sapiens*; chaîne lourde H-gamma1 *Homo sapiens* (1-454) [VH (*Homo sapiens* IGHV3-21*07 (88.8%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.8.17] (26-33.51-58.97-113)) (1-124) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, 9-G1v78 CH3 L107 A114 (CH1 R120 (221) (125-222), charnière 1-15 (223-237), CH2 (238-347), CH3 E12 (363), M14 (365), M107>L (435), N114>A (441) (348-452), CHS (453-454)) (125-454)], (227-217')-disulfure avec la chaîne légère L-lambda2 *Homo sapiens* (1'-218') [V-LAMBDA (*Homo sapiens* IGLV1-40*01 (92.8%) -IGLJ1*01 (91.7%), CDR-IMGT [9.3.12] (26'-34'.52'-54'.91'-102')) (1'-112') -*Homo sapiens* IGLC2*01 (100%) (C-LAMBDA2) (113'-218')]; dimère (233-233'':236-236'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa
ibramvibart	immunoglobulina G1-kappa, anti-[dominio de unión al receptor (RBD) de la glicoproteína spike (S) del coronavirus 2 (humano) del síndrome respiratorio agudo severo (SRAS-CoV-2)], anticuerpo monoclonal *Homo sapiens*; cadena pesada H-gamma1 *Homo sapiens* (1-454) [VH (*Homo sapiens* IGHV3-21*07 (88.8%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.8.17] (26-33.51-58.97-113)) (1-124) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, 9-G1v78 CH3 L107 A114 (CH1 R120 (221) (125-222), bisagra 1-15 (223-237), CH2 (238-347), CH3 E12 (363), M14 (365), M107>L (435), N114>A (441) (348-452), CHS (453-454)) (125-454)], (227-217')-disulfuro con la cadena ligera L-lambda2 *Homo sapiens* (1'-218') [V-LAMBDA (*Homo sapiens* IGLV1-40*01 (92.8%) -IGLJ1*01 (91.7%), CDR-IMGT [9.3.12] (26'-34'.52'-54'.91'-102')) (1'-112') -*Homo sapiens* IGLC2*01 (100%) (C-LAMBDA2) (113'-218')]; dímero (233-233'':236-236'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVKPGGSLRL SCAASGFEFG SYEMNWVRQA PGKGLEWVSS  50
ISEDGYTTYY PDSLKGRFTI SRDSAKNSLY LQMNSLRADD TAVYYCARDF 100
GGDTNWAGTG FTYWGQGTLV TVSSASTKGP SVFPLAPSSK STSGGTAALG 150
CLVKDYFPEP VTVSWNSGAL TSGVHTFPAV LQSSGLYSLS SVVTVPSSSL 200
GTQTYICNVN HKPSNTKVDK RVEPKSCDKT HTCPPCPAPE LLGGPSVFLF 250
PPKPKDTLMI SRTPEVTCVV VDVSHEDPEV KFNWYVDGVE VHNAKTKPRE 300
EQYNSTYRVV SVLTVLHQDW LNGKEYKCKV SNKALPAPIE KTISKAKGQP 350
REPQVYTLPP SREEMTKNQV SLTCLVKGFY PSDIAVEWES NGQPENNYKT 400
TPPVLDSDGS FFLYSKLTVD KSRWQQGNVF SCSVLHEALH AHYTQKSLSL 450
SPGK                                                    454
```

Light chain / Chaîne légère / Cadena ligera

```
QSVLTQPPSV SGAPGQRITI SCEGSSSNIG AGYDVHWYQQ LPGTAPKLLI  50
YGSSVRNYGV PDRFSGSKSG TSASLAITGL QAEDEADYYC QSYDSDLGIL 100
YTFGTGTKVT VLGQPKAAPS VTLFPPSSEE LQANKATLVC LISDFYPGAV 150
TVAWKADSSP VKAGVETTTP SKQSNNKYAA SSYLSLTPEQ WKSHRSYSCQ 200
VTHEGSTVEK TVAPTECS                                    218
```

Post-translational modifications

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 151-207 268-328 374-432
22''-96'' 151''-207'' 268''-328'' 374''-432''
Intra-L (C23-C104) 22'-90' 140'-199'
22'''-90''' 140'''-199'''
Inter-H-L (h 5-CL 126) 227-217' 227''-217'''
Inter-H-H (h 11, h 14) 233-233'' 236-236''

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: 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''

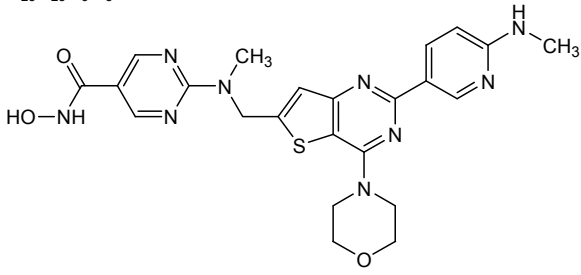
ifupinostatum

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

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

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

$C_{23}H_{25}N_9O_3S$



imapextidum

imapextide

glucagon-like peptide 1(15-35) [human GLP-1(15-35)] (1-21 in the real sequence), [G^{22}>E^{8}, A^{25}>V^{11}, K^{26}>R^{12}, K^{34}>R^{20}]-variant, fused to the C-terminal (30-39)-peptide of exendin-4 (*Heloderma suspectum*) (22-31), substituted at the N-atom of the L-α-aspartyl residue 1 with a 17-carboxyheptadecanoyl group;
N-(17-carboxyheptadecanoyl)-L-α-aspartyl-L-valyl-L-seryl-L-seryl-L-tyrosyl-L-leucyl-L-α-glutamyl-L-α-glutamyl-L-glutaminyl-L-alanyl-L-valyl-L-arginyl-L-α-glutamyl-L-phenylalanyl-L-isoleucyl-L-alanyl-L-tryptophyl-L-leucyl-L-valyl-L-arginylglycylglycyl-L-prolyl-L-seryl-L-serylglycyl-L-alanyl-L-prolyl-L-prolyl-L-prolyl-L-serine

imapextide

peptide similaire au glucagon de type 1(15-35) [GLP-1(15-35) humain] (1-21 dans la séquence réelle), variante [G^{22}>E^{8}, A^{25}>V^{11}, K^{26}>R^{12}, K^{34}>R^{20}], fusionné au (30-39)-peptide C-terminal d'exendine-4 (*Heloderma suspectum*) (22-31), substitué en l'atome N du résidu L-α-aspartyle 1 par un groupe 17-carboxyheptadécanoyle;
N-(17-carboxyheptadécanoyl)-L-α-aspartyl-L-valyl-L-séryl-L-séryl-L-tyrosyl-L-leucyl-L-α-glutamyl-L-α-glutamyl-L-glutaminyl-L-alanyl-L-valyl-L-arginyl-L-α-glutamyl-L-phénylalanyl-L-isoleucyl-L-alanyl-L-tryptophyl-L-leucyl-L-valyl-L-arginylglycylglycyl-L-prolyl-L-séryl-L-sérylglycyl-L-alanyl-L-prolyl-L-prolyl-L-prolyl-L-sérine

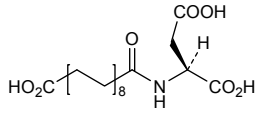
imapextida

péptido similar al glucagón tipo 1(15-35) [GLP-1(15-35) humano] (1-21 en la secuencia real), variante [G^{22}>E^{8}, A^{25}>V^{11}, K^{26}>R^{12}, K^{34}>R^{20}], fusionado al (30-39)-péptido C-terminal de exendina-4 (*Heloderma suspectum*) (22-31), sustituido en el átomo de N del residuo L-α-aspartilo con un grupo 17-carboxiheptadecanoilo;
N-(17-carboxiheptadecanoil)-L-α-aspartil-L-valil-L-seril-L-seril-L-tyrosil-L-leucil-L-α-glutamil-L-α-glutamil-L-glutaminil-L-alanil-L-valil-L-arginil-L-α-glutamil-L-fenilalanil-L-isoleucil-L-alanil-L-triptofil-L-leucil-L-valil-L-arginilglicilglicil-L-prolil-L-seril-L-serilglicil-L-alanil-L-prolil-L-prolil-L-prolil-L-serina

$C_{166}H_{257}N_{39}O_{50}$

DVSSYLEEQA VREFIAWLVR GGPSSGAPPP S 31

Modified residue / Résidu modifié / Resto modificado



D (1)
N-(HO$_2$C-[CH$_2$]$_{16}$-CO)-L-Asp

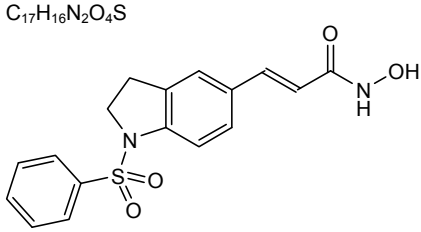
imofinostatum

imofinostat (2*E*)-3-[1-(benzenesulfonyl)-2,3-dihydro-1*H*-indol-5-yl]-*N*-hydroxyprop-2-enamide

imofinostat (2*E*)-3-[1-(benzènesulfonyl)-2,3-dihydro-1*H*-indol-5-yl]-*N*-hydroxyprop-2-énamide

imofinostat (2*E*)-3-[1-(bencenosulfonil)-2,3-dihidro-1*H*-indol-5-il]-*N*-hidroxiprop-2-enamida

$C_{17}H_{16}N_2O_4S$



infliximabum beta #

infliximab beta immunoglobulin G1-kappa, anti-[*Homo sapiens* TNF (tumor necrosis factor, TNF superfamily member 2, TNFSF2, TNF-alpha, TNFA)], chimeric monoclonal antibody;
H-gamma1 heavy chain chimeric (1-450) [VH (*Mus musculus* IGHV6-6*02 (89.0%) -(IGHD) -IGHJ2*01 (92.9%), CDR-IMGT [8.10.11] (26-33.51-60.99-109)) (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)], (223-214')-disulfide with L-kappa light chain chimeric (1'-214') [V-KAPPA (*Mus musculus* IGKV5-48*01 (93.7%) -IGKJ4*01 (83.3%) K123>N (103'), I126>V (106'), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dimer (229-229'':232-232'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-S, glycoform alfa

infliximab bêta immunoglobuline G1-kappa, anti-[*Homo sapiens* TNF (facteur de nécrose tumorale, membre 2 de la superfamille du TNF, TNFSF2, TNF-alpha, TNFA)], anticorps monoclonal chimérique;
chaîne lourde H-gamma1 chimérique (1-450) [VH (*Mus musculus* IGHV6-6*02 (89.0%) -(IGHD) -IGHJ2*01 (92.9%), CDR-IMGT [8.10.11] (26-33.51-60.99-109)) (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)], (223-214')-disulfure avec la chaîne légère L-kappa chimérique (1'-214') [V-KAPPA (*Mus musculus* IGKV5-48*01 (93.7%) -IGKJ4*01 (83.3%) K123>N (103'), I126>V (106'), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dimère (229-229'':232-232'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-S, glycoforme alfa

infliximab beta

inmunoglobulina G1-kappa, anti-[*Homo sapiens* TNF (factor de necrosis tumoral, miembro 2 de la superfamilia del TNF, TNFSF2, TNF-alfa, TNFA)], anticuerpo monoclonal quimérico;
cadena pesada H-gamma1 quimérica (1-450) [VH (*Mus musculus* IGHV6-6*02 (89.0%) -(IGHD) -IGHJ2*01 (92.9%), CDR-IMGT [8.10.11] (26-33.51-60.99-109)) (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)], (223-214')-disulfuro con la cadena ligera L-kappa quimérica (1'-214') [V-KAPPA (*Mus musculus* IGKV5-48*01 (93.7%) -IGKJ4*01 (83.3%) K123>N (103'), I126>V (106'), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dímero (229-229'':232-232'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-S, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVKLEESGGG LVQPGGSMKL SCVASGFIFS NHWMNWVRQS PEKGLEWVAE  50
IRSKSINSAT HYAESVKGRF TISRDDSKSA VYLQMTDLRT EDTGVYYCSR 100
NYYGSTYDYW GQGTTLTVSS 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
```

Light chain / Chaîne légère / Cadena ligera

```
DILLTQSPAI LSVSPGERVS FSCRASQFVG SSIHWYQQRT NGSPRLLIKY  50
ASESMSGIPS RFSGSGSGTD FTLSINTVES EDIADYYCQQ SHSWPFTFGS 100
GTNLEVKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-98 147-203 264-324 370-428
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''
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''

inidascaminum

inidascamine

(2*R*,3*S*)-2-amino-3-hydroxy-3-(pyridin-4-yl)-1-(pyrrolidin-1-yl)propan-1-one

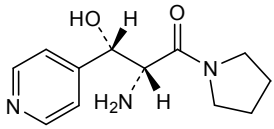
inidascamine

(2*R*,3*S*)-2-amino-3-hydroxy-3-(pyridin-4-yl)-1-(pyrrolidin-1-yl)propan-1-one

inidascamina

(2*R*,3*S*)-2-amino-3-hidroxi-3-(piridin-4-il)-1-(pirrolidin-1-il)propan-1-ona

$C_{12}H_{17}N_3O_2$



inlecitugum #

inlecitug	immunoglobulin G1-kappa, anti-[*Homo sapiens* KDR (kinase insert domain receptor, vascular endothelial growth factor receptor 2, VEGFR2, VEGF-R2, FLK1, CD309)], chimeric monoclonal antibody; H-gamma1 heavy chain chimeric (1-447) [VH (*Mus musculus* IGHV14-4*02 (91.8%) -(IGHD) -IGHJ4*01 (91.7%) S123>T (112), 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 (446-447)) (118-447)], (220-213')-disulfide with L-kappa light chain chimeric (1'-213') [V-KAPPA (*Mus musculus* IGKV4-57*01 (98.9%) -IGKJ4*01 (100%), CDR-IMGT [5.3.9] (27'-31'.49'-51'.88'-96')) (1'-106') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (152'), V101 (190')) (107'-213')]; dimer (226-226'':229-229'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-DG44, glycoform alfa
inlécitug	immunoglobuline G1-kappa, anti-[*Homo sapiens* KDR (récepteur à domaine insert kinase, récepteur 2 du facteur de croissance endothélial vasculaire, VEGFR2, VEGF-R2, FLK1, CD309)], anticorps monoclonal chimérique; chaîne lourde H-gamma1 chimérique (1-447) [VH (*Mus musculus* IGHV14-4*02 (91.8%) -(IGHD) -IGHJ4*01 (91.7%) S123>T (112), 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 (446-447)) (118-447)], (220-213')-disulfure avec la chaîne légère L-kappa chimérique (1'-213') [V-KAPPA (*Mus musculus* IGKV4-57*01 (98.9%) -IGKJ4*01 (100%), CDR-IMGT [5.3.9] (27'-31'.49'-51'.88'-96')) (1'-106') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (152'), V101 (190')) (107'-213')]; dimère (226-226'':229-229'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-DG44, glycoforme alfa
inlecitug	inmunoglobulina G1-kappa, anti-[*Homo sapiens* KDR (receptor de dominio kinasa de inserción, receptor 2 del factor de crecimiento endotelial vascular, VEGFR2, VEGF-R2, FLK1, CD309)], anticuerpo monoclonal quimérico; cadena pesada H-gamma1 quimérica (1-447) [VH (*Mus musculus* IGHV14-4*02 (91.8%) -(IGHD) -IGHJ4*01 (91.7%) S123>T (112), 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 (446-447)) (118-447)], (220-213')-disulfuro con la cadena ligera L-kappa quimérica (1'-213') [V-KAPPA (*Mus musculus* IGKV4-57*01 (98.9%) -IGKJ4*01 (100%), CDR-IMGT [5.3.9] (27'-31'.49'-51'.88'-96')) (1'-106') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (152'), V101 (190')) (107'-213')]; 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

```
QVKLQQSGAE LVGSGASVKL SCTTSGFNIK DFYMHWVKQR PEQGLEWIGW  50
IDPENGDSDY APKFQGKATM TADSSSNTAY LQLSSLTSED TAVYYCNAYY 100
GDYEGYWGQG TTVTVSSAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF 150
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC 200
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT 250
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT 350
LPPSRDELTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS 400
DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPGK    447
```

Light chain / Chaîne légère / Cadena ligera

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DIELTQSPAI MSASPGEKVT ITCSASSSVS YMHWFQQKPG TSPKLWIYST  50
SNLASGVPAR FSGSGSGTSY SLTISRMEAE DAATYYCQQR SSYPFTFGSG 100
TKLEIKRTVA APSVFIFPPS DEQLKSGTAS VVCLLNNFYP REAKVQWKVD 150
NALQSGNSQE SVTEQDSKDS TYSLSSTLTL SKADYEKHKV YACEVTHQGL 200
SSPVTKSFNR GEC                                         213
```

Post-translational modifications

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 144-200 261-321 367-425
22"-96" 144"-200" 261"-321" 367"-425"
Intra-L (C23-C104) 23'-87' 133'-193'
23'"-87'" 133'"-193'"
Inter-H-L (h 5-CL 126) 220-213' 220"-213'"
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"

ipanumeranum #

ipanumeran

messenger RNA (mRNA), 5'[1,2-[m^7G_m-(5'→5')-p-[P(R)]-s^p-p-G]]-capped, encoding codon-optimised human claudin-6 (CLDN6), flanked by 5' and 3' untranslated regions (UTRs), followed by a 3' polyadenylation (polyA) tail. The 5' UTR is derived from the human alpha-globin gene and contains an optimised Kozak sequence; the synthetic 3' UTR is a combination of two elements derived from the amino-terminal enhancer of split (AES) mRNA and the mitochondrial encoded 12S ribosomal RNA. The polyA tail consists of 30 adenosine residues followed by a 10-nucleotide linker sequence and another 70 adenosine residues

ipanuméran

ARN messager (ARNm), coiffé en 5'[1,2-[m^7G_m-(5'→5')-p-[P(R)]-s^p-p-G]], codant, avec des codons optimisés, la claudine-6 humaine (CLDN6), flanqué des régions non traduites (UTRs) en 5' et en 3' et suivie d'une queue de polyadénylation (polyA) en 3'. La région UTR en 5' est dérivée du gène de l'alpha-globine humaine et contient une séquence Kozak optimisée; la région UTR en 3' synthétique est une combinaison de deux éléments dérivés de l'ARNm de l'amplificateur amino-terminal divisé (AES) et de l'ARN ribosomique 12S codé par les mitochondries. La queue polyA se compose de 30 résidus d'adénosine, suivis d'une séquence de liaison de 10 nucléotides et de 70 autres résidus d'adénosine

ipanumerán

ARN mensajero (ARNm), protegido con la caperuza 5'[1,2-[m^7G_m-(5'→5')-p-[P(R)]-s^p-p-G]], que codifica, con codones optimizados, claudina-6 (CLDN6) humana, flanqueado

por regiones sin traducir (UTRs) 5' y 3' seguido de una cola de poliadenilación (poliA) en 3'. La 5' UTR deriva del gen de la alfa-globina humana y contiene una secuencia Kozak optimizada; la 3' UTR sintética es una combinación de dos elementos derivados del ARNm del potenciador amino-terminal de división (AES) y el ARN ribosómico 12S codificado en la mitocondria. El poliA consta de 30 residuos de adenosina seguidos de una secuencia enlazadora de 10 nucleótidos y otros 70 residuos de adenosina

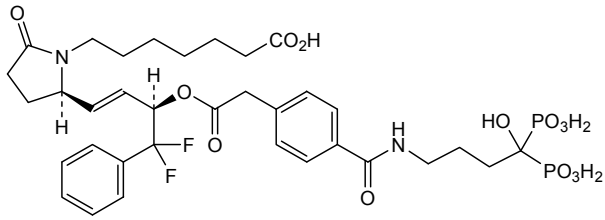
irodanoprostum

irodanoprost — 7-[(2*R*)-2-{(1*E*,3*R*)-4,4-difluoro-3-[({4-[(4-hydroxy-4,4-diphosphonobutyl)carbamoyl]phenyl}acetyl)oxy]-4-phenylbut-1-en-1-yl}-5-oxopyrrolidin-1-yl]heptanoic acid

irodanoprost — acide 7-[(2*R*)-2-{(1*E*,3*R*)-4,4-difluoro-3-[({4-[(4-hydroxy-4,4-diphosphonobutyl)carbamoyl]phényl}acétyl)oxy]-4-phénylbut-1-én-1-yl}-5-oxopyrrolidin-1-yl]heptanoïque

irodanoprost — ácido 7-[(2*R*)-2-{(1*E*,3*R*)-3-[({4-[(4,4-difosfono-4-hidroxibutil)carbamoil]fenil}acetil)oxi]-4-fenil-4,4-difluorobut-1-en-1-il}-5-oxopirrolidin-1-il]heptanoico

$C_{34}H_{44}F_2N_2O_{13}P_2$



isuventatugum #

isuventatug — immunoglobulin G1-kappa, anti-[*Homo sapiens* MICA (MIC-A, MH1-like A) and *Homo sapiens* MICB (MIC-B, MH1-like B)], monoclonal antibody;
H-gamma1 heavy chain (1-450) [VH (*Homo sapiens* IGHV3-11*01 (93.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1-121) -*Homo sapiens* IGHG1*03v (100%) 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 K2>del (450)) (122-450)], (224-219')-disulfide with L-kappa light chain (1'-219') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV2-137*01 (90.0%) -IGKJ4*01 (91.7%) S120>P (105')/*Homo sapiens* IGKV2-28*01 (86.0%) -IGKJ2*02 (90.9%) Q120>P (105'), CDR-IMGT [11.3.9] (27'-37'.55'-57'.94-102')) (1'-112') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (158'), V101 (196')) (113'-219')]; dimer (230-230":233-233")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-DG44, glycoform alfa

isuventatug — immunoglobuline G1-kappa, anti-[*Homo sapiens* MICA (MIC-A, MH1-like A) et *Homo sapiens* MICB (MIC-B, MH1-like B)], anticorps monoclonal;

chaîne lourde H-gamma1 (1-450) [VH (*Homo sapiens* IGHV3-11*01 (93.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1-121) -*Homo sapiens* IGHG1*03v (100%) 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 K2>del (450)) (122-450)], (224-219')-disulfure avec la chaîne légère L-kappa (1'-219') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV2-137*01 (90.0%) -IGKJ4*01 (91.7%) S120>P (105')/*Homo sapiens* IGKV2-28*01 (86.0%) -IGKJ2*02 (90.9%) Q120>P (105'), CDR-IMGT [11.3.9] (27'-37'.55'-57'.94-102')) (1'-112') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (158'), V101 (196')) (113'-219')]; dimère (230-230'':233-233'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-DG44, glycoforme alfa

isuventatug

inmunoglobulina G1-kappa, anti-[*Homo sapiens* MICA (MIC-A, MH1-like A) y *Homo sapiens* MICB (MIC-B, MH1-like B)], anticuerpo monoclonal; cadena pesada H-gamma1 (1-450) [VH (*Homo sapiens* IGHV3-11*01 (93.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1-121) -*Homo sapiens* IGHG1*03v (100%) 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 K2>del (450)) (122-450)], (224-219')-disulfuro con la cadena ligera L-kappa (1'-219') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV2-137*01 (90.0%) -IGKJ4*01 (91.7%) S120>P (105')/*Homo sapiens* IGKV2-28*01 (86.0%) -IGKJ2*02 (90.9%) Q120>P (105'), CDR-IMGT [11.3.9] (27'-37'.55'-57'.94-102')) (1'-112') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (158'), V101 (196')) (113'-219')]; dímero (230-230'':233-233'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-DG44, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVESGGG LVKPGGSLRL SCAASGFTFS NYAMSWIRQA PGKGLEWVSY  50
ISPGGDYIYY ADSVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCTTDR 100
RHYGSYAMDY WGQGTLVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200
TYICNVNHKP SNTKVDKKVE PKSCDKTHTC PPCPAPELLG GPSVFLFPPK 250
PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY 300
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP 350
QVYTLPPSRE EMTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP 400
VLDSDGSFFL YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG 450
```

Light chain / Chaîne légère / Cadena ligera

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

Post-translational modifications

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

Intra-H (C23-C104) 22-96 148-204 265-325 371-429
22''-96'' 148''-204'' 265''-325'' 371''-429''
Intra-L (C23-C104) 23'-93' 139'-199'
23'''-93''' 139'''-199'''
Inter-H-L (h 5-CL 126) 224-219' 224''-219'''
Inter-H-H (h 11, h 14) 230-230'' 233-233''

N-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

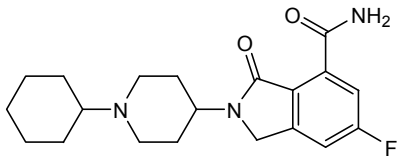
itareparibum

itareparib — 2-(1-cyclohexylpiperidin-4-yl)-6-fluoro-3-oxo-2,3-dihydro-1*H*-isoindole-4-carboxamide

itaréparib — 2-(1-cyclohexylpipéridin-4-yl)-6-fluoro-3-oxo-2,3-dihydro-1*H*-isoindole-4-carboxamide

itareparib — 2-(1-ciclohexilpiperidin-4-il)-6-fluoro-3-oxo-2,3-dihidro-1*H*-isoindol-4-carboxamida

$C_{20}H_{26}FN_3O_2$



ixotatugum #

ixotatug — immunoglobulin G1-kappa, anti-[*Homo sapiens* CLDN6 (claudin 6, claudin-6)], monoclonal antibody; H-gamma1 heavy chain (1-447) [VH Musmus/Homsap (*Mus musculus* IGHV6-3*01 (88.8%) -(IGHD) -IGHJ2*01 (90.9%) T123>L (112)/*Homo sapiens* IGHV3-23*03 (82.7%) -(IGHD) -IGHJ5*01 (91.7%) V124>L (113), CDR-IMGT [8.10.8] (26-33.51-60.99-106)) (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 (446-447)) (118-447)], (220-214')-disulfide with L-kappa light chain (1'-214') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV12-44*01 (83.2%) -IGKJ1*01 (91.7%) G120>Q (100')/*Homo sapiens* IGKV1-39*01 (83.2%) -IGKJ2*02 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dimer (226-226":229-229")-bisdisulfide, produced in a cell line from Chinese hamster ovary (CHO) cells, derived from the cell line CHO-S, glycoform alfa

ixotatug — immunoglobuline G1-kappa, anti-[*Homo sapiens* CLDN6 (claudine 6, claudine-6)], anticorps monoclonal; chaîne lourde H-gamma1 (1-447) [VH Musmus/Homsap (*Mus musculus* IGHV6-3*01 (88.8%) -(IGHD) -IGHJ2*01 (90.9%) T123>L (112)/*Homo sapiens* IGHV3-23*03 (82.7%) -(IGHD) -IGHJ5*01 (91.7%) V124>L (113), CDR-IMGT [8.10.8] (26-33.51-60.99-106)) (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 (446-447)) (118-447)], (220-214')-disulfure avec la chaîne légère L-kappa (1'-218') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV12-44*01 (83.2%) -IGKJ1*01 (91.7%) G120>Q (100')/*Homo sapiens* IGKV1-39*01 (83.2%) -IGKJ2*02 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dimère (226-226":229-229")-bisdisulfure, produit dans une lignée cellulaire des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-S, glycoforme alfa

ixotatug

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CLDN6 (claudina 6, claudina-6)], anticuerpo monoclonal;
cadena pesada H-gamma1 (1-447) [VH Musmus/Homsap (*Mus musculus* IGHV6-3*01 (88.8%) -(IGHD) -IGHJ2*01 (90.9%) T123>L (112)/*Homo sapiens* IGHV3-23*03 (82.7%) -(IGHD) -IGHJ5*01 (91.7%) V124>L (113), CDR-IMGT [8.10.8] (26-33.51-60.99-106)) (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 (446-447)) (118-447)], (220-214')-disulfuro con la cadena ligera L-kappa (1'-218') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV12-44*01 (83.2%) -IGKJ1*01 (91.7%) G120>Q (100')/*Homo sapiens* IGKV1-39*01 (83.2%) -IGKJ2*02 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dímero (226-226":229-229")-bisdisulfuro, producido en una línea celular de las células ováricas de hámster chino (CHO), línea celular derivada de CHO-S, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLLESGGG LVQPGGSMRL SCAASGFTFS NYWMNWVRQA PGKGLEWVAQ  50
IRLKSDNYAT HYADSVKGRF TISRDDSKNT VYLQMNSLRA EDTGVYYCND 100
GPPSGSWGQG TLLTVSSAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF 150
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC 200
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT 250
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT 350
LPPSRDELTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS 400
DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPGK    447
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCRISENIY SYLAWYQQKP GKAPKLLVYN  50
AKILVEGVPS RFSGSGSGTD FTLTISSLQP EDFGTYYCQH HYTVPWTFGQ 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) 22-98 144-200 261-321 367-425
22"-98" 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-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"

ixotatugum vedotinum #

ixotatug vedotin

immunoglobulin G1-kappa, anti-[*Homo sapiens* CLDN6 (claudin 6, claudin-6)], monoclonal antibody, conjugated on an average of four cysteinyl residues to *vedotin*, comprising a cleavable linker and monomethylauristatin E (MMAE);
H-gamma1 heavy chain (1-447) [VH Musmus/Homsap (*Mus musculus* IGHV6-3*01 (88.8%) -(IGHD) -IGHJ2*01 (90.9%) T123>L (112)/*Homo sapiens* IGHV3-23*03 (82.7%) -(IGHD) -IGHJ5*01 (91.7%) V124>L (113), CDR-IMGT [8.10.8] (26-33.51-60.99-106)) (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 (446-447)) (118-447)], (220-214')-disulfide with L-kappa light chain (1'-214') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV12-44*01 (83.2%) -IGKJ1*01 (91.7%) G120>Q (100')/*Homo sapiens* IGKV1-39*01 (83.2%) -IGKJ2*02 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dimer (226-226":229-229")-bisdisulfide, produced in a cell line from Chinese hamster ovary

(CHO) cells, derived from the cell line CHO-S, glycoform alfa; substituted at the sulfur atoms of an average of four L-cysteinyl residues among 220, 226, 229, 214', 220'', 226'', 229'' and 214''' with (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*) groups

ixotatug védotine

immunoglobuline G1-kappa, anti-[*Homo sapiens* CLDN6 (claudine 6, claudine-6)], anticorps monoclonal, conjugué par quatre résidus cystéinyle en moyenne à la *védotine*, comprenant un linker clivable et monométhylauristatine E (MMAE);
chaîne lourde H-gamma1 (1-447) [VH Musmus/Homsap (*Mus musculus* IGHV6-3*01 (88.8%) -(IGHD) -IGHJ2*01 (90.9%) T123>L (112)/*Homo sapiens* IGHV3-23*03 (82.7%) -(IGHD) -IGHJ5*01 (91.7%) V124>L (113), CDR-IMGT [8.10.8] (26-33.51-60.99-106)) (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 (446-447)) (118-447)], (220-214')-disulfure avec la chaîne légère L-kappa (1'-218') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV12-44*01 (83.2%) -IGKJ1*01 (91.7%) G120>Q (100')/*Homo sapiens* IGKV1-39*01 (83.2%) -IGKJ2*02 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dimère (226-226'':229-229'')-bisdisulfure, produit dans une lignée cellulaire des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-S, glycoforme alfa; substitué sur l'atome de soufre de quatre résidus L-cystéinyle en moyenne parmi 220, 226, 229, 214', 220'', 226'', 229'' et 214''' avec des groupes (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*)

ixotatug vedotina

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CLDN6 (claudina 6, claudina-6)], anticuerpo monoclonal, conjugado en una media de cuatro residuos cisteinilo a la *vedotina*, que comprende un enlace escindible y monometilauristatina E (MMAE);
cadena pesada H-gamma1 (1-447) [VH Musmus/Homsap (*Mus musculus* IGHV6-3*01 (88.8%) -(IGHD) -IGHJ2*01 (90.9%) T123>L (112)/*Homo sapiens* IGHV3-23*03 (82.7%) -(IGHD) -IGHJ5*01 (91.7%) V124>L (113), CDR-IMGT [8.10.8] (26-33.51-60.99-106)) (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 (446-447)) (118-447)], (220-214')-disulfuro con la cadena ligera L-kappa (1'-218') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV12-44*01 (83.2%) -IGKJ1*01 (91.7%) G120>Q (100')/*Homo sapiens* IGKV1-39*01 (83.2%) -IGKJ2*02 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dímero (226-226'':229-229'')-bisdisulfuro, producido en una línea celular de las células ováricas de hámster chino (CHO), línea celular derivada de CHO-S, forma glicosilada alfa; sustituido en el átomo de azufre de cuatro residuos L-cisteinilo en promedio entre 220, 226, 229, 214', 220'', 226'', 229'' y 214''' con grupos

(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-fenil-1-hidroxipropan-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 (H, H")

```
EVQLLESGGG LVQPGGSMRL SCAASGFTFS NYWMNWVRQA PGKGLEWVAQ  50
IRLKSDNYAT HYADSVKGRF TISRDDSKNT VYLQMNSLRA EDTGVYYCND 100
GPPSGSWGQG TLLTVSSAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF 150
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC 200
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT 250
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT 350
LPPSRDELTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS 400
DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPGK    447
```

Light chain / Chaîne légère / Cadena ligera (L', L"')

```
DIQMTQSPSS LSASVGDRVT ITCRISENIY SYLAWYQQKP GKAPKLLVYN  50
AKILVEGVPS RFSGSGSGTD FTLTISSLQP EDFGTYYCQH HYTVPWTFGQ 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) 22-98 144-200 261-321 367-425
22"-98" 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"

*Two or three 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.

*Deux ou trois 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.

*Dos o tres 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: 297, 297"

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

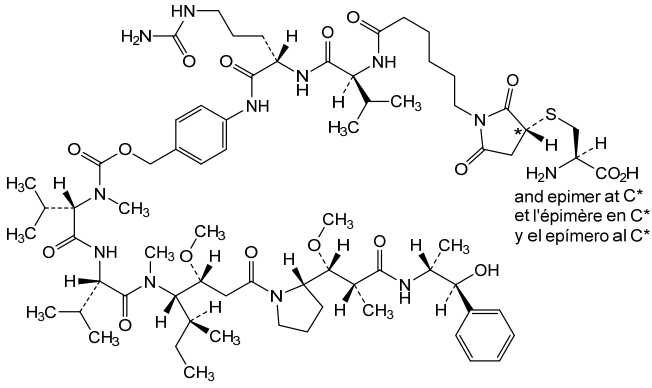
C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal

H CHS K2: 447, 447"

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

C (220, 226, 229, 214', 220", 226", 229", 214"')

*(*vedotin*:mAb ~ 4:1)



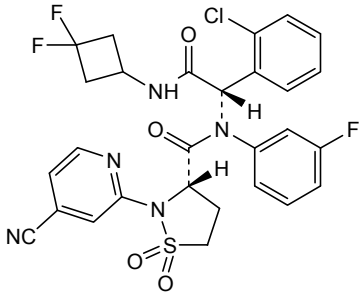
lanisidenibum

lanisidenib (3*S*)-*N*-{(1*S*)-1-(2-chlorophenyl)-2-[(3,3-difluorocyclobutyl)amino]-2-oxoethyl}-2-(4-cyanopyridin-2-yl)-*N*-(3-fluorophenyl)-1,1-dioxo-1λ^6,2-thiazolidine-3-carboxamide

lanisidénib (3*S*)-*N*-{(1*S*)-1-(2-chlorophenyl)-2-[(3,3-difluorocyclobutyl)amino]-2-oxoethyl}-2-(4-cyanopyridin-2-yl)-*N*-(3-fluorophenyl)-1,1-dioxo-1λ^6,2-thiazolidine-3-carboxamide

lanisidenib (3*S*)-*N*-{(1*S*)-1-(2-chlorophenyl)-2-[(3,3-difluorocyclobutyl)amino]-2-oxoethyl}-2-(4-cyanopyridin-2-yl)-*N*-(3-fluorophenyl)-1,1-dioxo-1λ^6,2-thiazolidine-3-carboxamide

$C_{28}H_{23}ClF_3N_5O_4S$



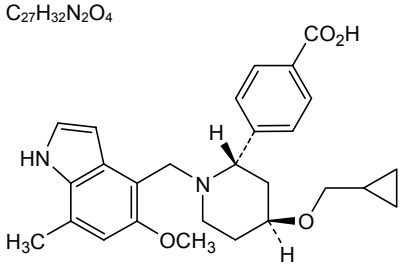
lanoracopanum

lanoracopan 4-{(2*S*,4*S*)-4-(cyclopropylmethoxy)-1-[(5-methoxy-7-methyl-1*H*-indol-4-yl)methyl]piperidin-2-yl}benzoic acid

lanoracopan acide 4-{(2*S*,4*S*)-4-(cyclopropylméthoxy)-1-[(5-méthoxy-7-méthyl-1*H*-indol-4-yl)méthyl]pipéridin-2-yl}benzoïque

lanoracopán ácido 4-{(2*S*,4*S*)-4-(ciclopropilmetoxi)-1-[(7-metil-5-metoxi-1*H*-indol-4-il)metil]piperidin-2-il}benzoico

$C_{27}H_{32}N_2O_4$



laporolimusum

laporolimus (1*R*,2*R*,4*S*)-4-{(2*R*)-2-[(3*S*,6*R*,7*E*,9*R*,10*R*,12*R*,14*S*,15*E*,17*E*,19*E*,21*S*,23*S*,26*R*,27*R*,34a*S*)-9,27-dihydroxy-10,21-dimethoxy-6,8,12,14,20,26-hexamethyl-1,5,11,28,29-pentaoxo-1,4,5,6,9,10,11,12,13,14,21,22,23,24,25,26,27,28,29,31,32,33,34,34a-tetracosahydro-3*H*-23,27-epoxypyrido[2,1-*c*][1,4]oxaazacyclohentriacontin-3-yl]propyl}-2-methoxycyclohexyl cyclohexanecarboxylate

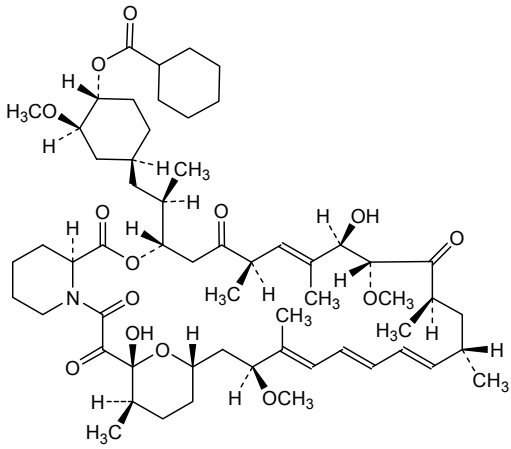
laporolimus

cyclohexanecarboxylate de (1*R*,2*R*,4*S*)-4-{(2*R*)-2-[(3*S*,6*R*,7*E*,9*R*,10*R*,12*R*,14*S*,15*E*,17*E*,19*E*,21*S*,23*S*,26*R*,27*R*,34a*S*)-9,27-dihydroxy-10,21-diméthoxy-6,8,12,14,20,26-hexaméthyl-1,5,11,28,29-pentaoxo-1,4,5,6,9,10,11,12,13,14,21,22,23,24,25,26,27,28,29,31,32,33,34,34a-tétracosahydro-3*H*-23,27-époxypyrido[2,1-*c*][1,4]oxaazacyclohentriacontin-3-yl]propyl}-2-méthoxycyclohexyle

laporólimus

ciclohexanocarboxilato de (1*R*,2*R*,4*S*)-4-{(2*R*)-2-[(3*S*,6*R*,7*E*,9*R*,10*R*,12*R*,14*S*,15*E*,17*E*,19*E*,21*S*,23*S*,26*R*,27*R*,34a*S*)-9,27-dihidroxi-6,8,12,14,20,26-hexametil-10,21-dimetoxi-1,5,11,28,29-pentaoxo-1,4,5,6,9,10,11,12,13,14,21,22,23,24,25,26,27,28,29,31,32,33,34,34a-tetracosahidro-3*H*-23,27-epoxipirido[2,1-*c*][1,4]oxaazaciclohentriacontin-3-il]propil}-2-metoxiciclohexilo

$C_{58}H_{89}NO_{14}$



laromestrocelum

laromestrocel

allogeneic mesenchymal stromal cells (MSC) derived from bone marrow of healthy human donors. The cells are expanded in media containing fetal bovine serum. The cells are positive (≥95%) for the mesenchymal stromal cell surface markers CD73, CD90, CD105, and are negative (≤5%) for CD34 and negative (≤2%) for markers CD11b, CD19, CD45, and HLA class II histocompatibility antigen gamma chain (HLA-DR). The cells secrete immunomodulatory factors including the interleukin 1 receptor antagonist (IL-1RA), interleukin 4 (IL-4), IL-7, IL-8, IL- 10, IL-13, and granulocyte colony stimulating factor (G-CSF) upon stimulation. In absence of exogenous stimulation, the MSCs also secrete vascular endothelial growth factor A (VEGF-A) and tissue inhibitor of metalloproteinases 2 (TIMP-2). The secreted TIMP-2 is able to inhibit matrix metalloprotease-14 (MMP-14) activity in an *in vitro* assay

laromestrocel

cellules stromales mésenchymateuses (CSM) allogéniques dérivées de la moelle osseuse de donneurs humains sains. Les cellules sont expansées dans un milieu contenant du sérum bovin fœtal. Les cellules sont positives (≥95%) pour les marqueurs de surface des cellules stromales

mésenchymateuses CD73, CD90, CD105, et sont négatives (≤5%) pour CD34 et négatives (≤2%) pour les marqueurs CD11b, CD19, CD45 et la chaîne gamma de l'antigène d'histocompatibilité (HLA) de classe II (HLA-DR). Les cellules sécrètent des facteurs immunomodulateurs, notamment l'antagoniste du récepteur de l'interleukine 1 (IL-1RA), l'interleukine 4 (IL-4), l'IL-7, l'IL-8, l'IL-10, l'IL-13 et le facteur de stimulation des colonies de granulocytes (G-CSF), lors de la stimulation. En l'absence de stimulation exogène, les CSM sécrètent également le facteur de croissance endothélial vasculaire A (VEGF-A) et l'inhibiteur tissulaire des métalloprotéinases 2 (TIMP-2). Le TIMP-2 sécrété est capable d'inhiber l'activité de la métalloprotéase matricielle 14 (MMP-14) dans un essai *in vitro*

laromestrocel

células estromales mesenquimales (MSC) alogénicas derivadas de médula ósea de donantes sanos. Las células se expanden en medio que contiene suero bovino fetal. Las células son positivas (≥95%) para los marcadores de superficie de células estromales mesenquimales CD73, CD90, CD105 y son negativas (≤5%) para CD34 y negativas (≤2%) para los marcadores CD11b, CD19, CD45 y la cadena gamma del antígeno de histocompatibilidad HLA de clase II (HLA-DR). Las células secretan factores inmunomoduladores incluyendo el antagonista del receptor de interleuqina 1 (IL-1RA), interleuquina 4 (IL-4), IL-7, IL-8, IL-10, IL-13 y factor estimulador de colonias de granulocitos (G-CSF) tras estimulación. En ausencia de estimulación exógena, las MSC también secretan factor de crecimiento del endotelio vascular A (VEGF-A) e inhibidor tisular de metaloproteinasas 2 (TIMP-2). El TIMP-2 secretado es capaz de inhibir la actividad de la metaloproteinasa de matriz 14 (MMP-14) en un ensayo *in vitro*

larubrilstatum

larubrilstat

(2-{[(5*R*)-6,7-dihydro-5*H*-cyclopenta[*b*]pyridin-5-yl]amino}pyrimidin-5-yl)(8-oxa-2-azaspiro[4.5]decan-2-yl)methanone

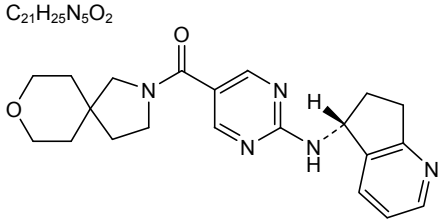
larubrilstat

(2-{[(5*R*)-6,7-dihydro-5*H*-cyclopenta[*b*]pyridin-5-yl]amino}pyrimidin-5-yl)(8-oxa-2-azaspiro[4.5]décan-2-yl)méthanone

larubrilstat

(2-{[(5*R*)-6,7-dihidro-5*H*-ciclopenta[*b*]piridin-5-il]amino}pirimidin-5-il)(8-oxa-2-azaespiro[4.5]decan-2-il)metanona

$C_{21}H_{25}N_5O_2$



lasmotinibum

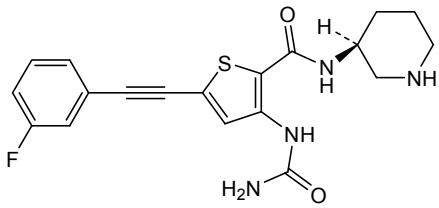
lasmotinib

3-(carbamoylamino)-5-[(3-fluorophenyl)ethynyl]-*N*-[(3*S*)-piperidin-3-yl]thiophene-2-carboxamide

lasmotinib — 3-(carbamoylamino)-5-[(3-fluorophényl)éthynyl]-*N*-[(3*S*)-pipéridin-3-yl]thiophène-2-carboxamide

lasmotinib — 3-(carbamoilamino)-5-[(3-fluorofenil)etinil]-*N*-[(3*S*)-piperidin-3-il]tiofeno-2-carboxamida

$C_{19}H_{19}FN_4O_2S$



lasrekibartum #

lasrekibart — immunoglobulin G1-kappa, anti-[*Homo sapiens* IL5 (interleukin 5, IL-5)], humanized monoclonal antibody;
H-gamma1 heavy chain humanized (1-448) [VH (*Homo sapiens* IGHV3-23*02 (88.7%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, 9-G1v21 CH2 Y15.1, T16, E18 (CH1 K120 (215) (119-216), hinge 1-15 (217-231), CH2 M15.1>Y (253), S16>T (255), T18>E (257) (232-341), CH3 D12 (357), L14 (359) (342-446), CHS (447-448)) (119-448)], (221-214')-disulfide with L-kappa light chain humanized (1'-214')[V-KAPPA (*Homo sapiens* IGKV1-6*01 (84.0%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dimer (227-227":230-230")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa

lasrékibart — immunoglobuline G1-kappa, anti-[*Homo sapiens* IL5 (interleukine 5, IL-5)], anticorps monoclonal humanisé;
chaîne lourde H-gamma1 humanisée (1-448) [VH (*Homo sapiens* IGHV3-23*02 (88.7%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, 9-G1v21 CH2 Y15.1, T16, E18 (CH1 K120 (215) (119-216), charnière 1-15 (217-231), CH2 M15.1>Y (253), S16>T (255), T18>E (257) (232-341), CH3 D12 (357), L14 (359) (342-446), CHS (447-448)) (119-448)], (221-214')-disulfure avec la chaîne légère L-kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-6*01 (84.0%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA 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, glycoforme alfa

lasrekibart — inmunoglobulina G1-kappa, anti-[*Homo sapiens* IL5 (interleukina 5, IL-5)], anticuerpo monoclonal humanizado;
cadena pesada H-gamma1 humanizada (1-448) [VH (*Homo sapiens* IGHV3-23*02 (88.7%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, 9-G1v21 CH2 Y15.1, T16, E18 (CH1 K120 (215) (119-216), bisagra 1-15 (217-231), CH2 M15.1>Y (253), S16>T (255), T18>E (257) (232-341), CH3 D12 (357), L14 (359) (342-446), CHS (447-448)) (119-448)], (221-214')-disulfuro con la cadena ligera L-kappa humanizada (1'-214') [V-

KAPPA (*Homo sapiens* IGKV1-6*01 (84.0%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA 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, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAASGFTFS HYYMAWVRQA PGKGLEWVTS  50
ISYEGDITYY GDSVKGRFTI SRDNSKNTLY LQMNSLRAED TATYYCASQT 100
LRESFDYWGQ GTLVTVSSAS TKGPSVFPLA PSSKSTSGGT AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTQTYI 200
CNVNHKPSNT KVDKKVEPKS CDKTHTCPPC PAPELLGGPS VFLFPPKPKD 250
TLYITREPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNST 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY 350
TLPPSRDELT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD 400
SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPGK   448
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Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS VSASVGDRVT ITCRASQDIA NYLSWYQQKP GKSPKLLIYG  50
TSNLEVGVPS RFSGSRSGTD FTLTISSLQP EDFATYYCLQ DKEFPRTFGG 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 145-201 262-322 368-426
22''-96'' 145''-201'' 262''-322'' 368''-426''
Intra-L (C23-C104) 23'-88' 134'-194'
23'''-88''' 134'''-194'''
Inter-H-L (h 5-CL 126) 221-214' 221''-214'''
Inter-H-H (h 11, h 14) 227-227'' 230-230''

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

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

laventatugum #

laventatug — immunoglobulin G1-kappa, anti-[*Homo sapiens* SLC39A6 (solute carrier family 39 member 6, solute carrier family 39 (metal ion transporter) member 6, solute carrier family 39 (zinc transporter) member 6, LIV-1), ZIP6], humanized monoclonal antibody; H-gamma1 heavy chain humanized (1-450) [VH (*Homo sapiens* IGHV1-69-2*01 (88.5%) -(IGHD) -IGHJ6*05 (81.8%) K120>Q (112), A127>S (119), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (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)], (223-219')-disulfide with L-kappa light chain humanized (1'-219') [V-KAPPA (*Homo sapiens* IGKV2-29*02 (89.0%) -IGKJ2*01 (91.7%) Q120>G (105'), CDR-IMGT [11.3.9] (27'-37'.55'-57'.94'-102')) (1'-112') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (158'), V101 (196')) (113'-219')]; dimer (229-229'':232-232'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-S, glycoform alfa

laventatug — immunoglobuline G1-kappa, anti-[*Homo sapiens* SLC39A6 (membre 6 de la famille 39 des transporteurs de solutés, membre 6 de la famille 39 (transporteur d'ion métal) des transporteurs de solutés, membre 6 de la famille 39 (transporteur du zinc) des transporteurs de solutés, LIV-1, ZIP6)], anticorps monoclonal humanisé; chaîne lourde H-gamma1 humanisée (1-450) [VH (*Homo sapiens* IGHV1-69-2*01 (88.5%) -(IGHD) -IGHJ6*05 (81.8%) K120>Q (112), A127>S (119), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (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)], (223-219')-disulfure avec la chaîne légère L-kappa humanisée (1'-219') [V-KAPPA (*Homo sapiens* IGKV2-29*02 (89.0%) -IGKJ2*01 (91.7%) Q120>G (105'), CDR-IMGT [11.3.9] (27'-37'.55'-57'.94'-102')) (1'-112') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (158'), V101 (196')) (113'-219')]; dimère (229-229":232-232")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-S, glycoforme alfa

laventatug

inmunoglobulina G1-kappa, anti-[*Homo sapiens* SLC39A6 (miembro 6 de la familia 39 de los transportadores de solutos, miembro 6 de la familia 39 (transportador del ión metal) de los transportadores de los solutos, miembro 6 de la familia 39 (transportador del zinc) de los transportadores de solutos, LIV-1, ZIP6)], anticuerpo monoclonal humanizado;
cadena pesada H-gamma1 humanizada (1-450) [VH (*Homo sapiens* IGHV1-69-2*01 (88.5%) -(IGHD) -IGHJ6*05 (81.8%) K120>Q (112), A127>S (119), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (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)], (223-219')-disulfuro con la cadena ligera L-kappa humanizada (1'-219') [V-KAPPA (*Homo sapiens* IGKV2-29*02 (89.0%) -IGKJ2*01 (91.7%) Q120>G (105'), CDR-IMGT [11.3.9] (27'-37'.55'-57'.94'-102')) (1'-112') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (158'), V101 (196')) (113'-219')]; dímero (229-229":232-232")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-S, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada
```
EVQLVQSGAE VKKPGATVKI SCKASGLNIE DYYMHWVQQA PGKGLEWMGW  50
IDPENGDTEY AEKFQGRVTI TADTSTNTAY MELSSLRSED TAVYYCTVHN 100
AHYGTWFAYW GQGTTVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSRDE LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK 450
```

Light chain / Chaîne légère / Cadena ligera
```
DIVMTQTPLS LSVTPGQPAS ISCRSSQTLV RSDGNTYLEW YLQKPGQSPQ  50
LLIYRVSNRF SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCFQGSHVP 100
YTFGGGTKLE IKRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK 150
VQWKVDNALQ SGNSQESVTE QDSKDSTYSL SSTLTLSKAD YEKHKVYACE 200
VTHQGLSSPV TKSFNRGEC                                   219
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 147-203 264-324 370-428
22"-96" 147"-203" 264"-324" 370"-428"
Intra-L (C23-C104) 23'-93' 139'-199'
23'"-93'" 139'"-199'"
Inter-H-L (h 5-CL 126) 223-219' 223"-219'"
Inter-H-H (h 11, h 14) 229-229" 232-232"

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"

laventatugum tivedotinum

laventatug tivedotin

immunoglobulin G1-kappa, anti-[*Homo sapiens* SLC39A6 (solute carrier family 39 member 6, solute carrier family 39 (metal ion transporter) member 6, solute carrier family 39 (zinc transporter) member 6, LIV-1, ZIP6)], humanized monoclonal antibody,

	conjugated on an average of four cysteinyl residues to *tivedotin*, comprising a cleavable monovalent linker and monomethylauristatin E (MMAE); H-gamma1 heavy chain humanized (1-450) [VH (*Homo sapiens* IGHV1-69-2*01 (88.5%) -(IGHD) -IGHJ6*05 (81.8%) K120>Q (112), A127>S (119), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1*01, 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)], (223-219')-disulfide with L-kappa light chain humanized (1'-219') [V-KAPPA (*Homo sapiens* IGKV2-29*02 (89.0%) -IGKJ2*01 (91.7%) Q120>G (105'), CDR-IMGT [11.3.9] (27'-37'.55'-57'.94'-102')) (1'-112') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (158'), V101 (196')) (113'-219')]; dimer (229-229''':232-232'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-S, glycoform alfa; substituted at the sulfur atoms of an average of four L-cysteinyl residues among 223, 229, 232, 219', 223'', 229'', 232'' and 219''' with 2-oxo-2-({L-valyl-N^5-carbamoyl-L-ornithyl[(4-aminophenyl)methoxy]carbonyl-*N*-methyl-L-valyl-L-valyl-(3*R*,4*S*,5*S*)-3-methoxy-5-methyl-4-(methylamino)heptanoyl-(2*R*,3*R*)-*N*-[(1*S*,2*R*)-1-hydroxy-1-phenylpropan-2-yl]-3-methoxy-2-methyl-3-[(2*S*)-pyrrolidin-2-yl]propanamide}-$N^{2.1}$-yl)ethyl (*tivedotin*) groups
laventatug tivédotine	immunoglobuline G1-kappa, anti-[*Homo sapiens* SLC39A6 (membre 6 de la famille 39 des transporteurs de solutés, membre 6 de la famille 39 (transporteur d'ion métal) des transporteurs de solutés, membre 6 de la famille 39 (transporteur du zinc) des transporteurs de solutés, LIV-1, ZIP6)], anticorps monoclonal humanisé; conjugué par quatre résidus cystéinyle en moyenne à la *tivédotine*, comprenant un linker monovalent clivable et monométhylauristatine E (MMAE); chaîne lourde H-gamma1 humanisée (1-450) [VH (*Homo sapiens* IGHV1-69-2*01 (88.5%) -(IGHD) -IGHJ6*05 (81.8%) K120>Q (112), A127>S (119), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1*01, 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)], (223-219')-disulfure avec la chaîne légère L-kappa humanisée (1'-219') [V-KAPPA (*Homo sapiens* IGKV2-29*02 (89.0%) -IGKJ2*01 (91.7%) Q120>G (105'), CDR-IMGT [11.3.9] (27'-37'.55'-57'.94'-102')) (1'-112') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101

	(C-KAPPA A45.1 (158'), V101 (196')) (113'-219')]; dimère (229-229'':232-232'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-S, glycoforme alfa; substitué sur l'atome de soufre de quatre résidus L-cystéinyle en moyenne parmi 223, 229, 232, 219', 223'', 229'', 232'' et 219''' avec des groupes 2-oxo-2-({L-valyl-N^5-carbamoyl-L-ornithyl[(4-aminophényl)méthoxy]carbonyl-*N*-méthyl-L-valyl-L-valyl-(3*R*,4*S*,5*S*)-3-méthoxy-5-méthyl-4-(méthylamino)heptanoyl-(2*R*,3*R*)-*N*-[(1*S*,2*R*)-1-hydroxy-1-phénylpropan-2-yl]-3-méthoxy-2-méthyl-3-[(2*S*)-pyrrolidin-2-yl]propanamide}-$N^{2,1}$-yl)éthyle (*tivédotine*)
laventatug tivedotina	inmunoglobulina G1-kappa, anti-[*Homo sapiens* SLC39A6 (miembro 6 de la familia 39 de los transportadores de solutos, miembro 6 de la familia 39 (transportador del ión metal) de los transportadores de los solutos, miembro 6 de la familia 39 (transportador del zinc) de los transportadores de solutos, LIV-1, ZIP6)], anticuerpo monoclonal humanizado, conjugado en una media de cuatro residuos cisteinilo a la *tivedotina*, que comprende un enlace monovalente escindible y monometilauristatina E (MMAE); cadena pesada H-gamma1 humanizada (1-450) [VH (*Homo sapiens* IGHV1-69-2*01 (88.5%) -(IGHD) -IGHJ6*05 (81.8%) K120>Q (112), A127>S (119), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (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)], (223-219')-disulfuro con la cadena ligera L-kappa humanizada (1'-219') [V-KAPPA (*Homo sapiens* IGKV2-29*02 (89.0%) -IGKJ2*01 (91.7%) Q120>G (105'), CDR-IMGT [11.3.9] (27'-37'.55'-57'.94'-102')) (1'-112') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (158'), V101 (196')) (113'-219')]; dímero (229-229'':232-232'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-S, forma glicosilada alfa, sustituido en el átomo de azufre de 4 residuos L-cisteinilo en promedio entre 223, 229, 232, 219', 223'', 229'', 232'' y 219''' con grupos 2-oxo-2-({L-valil-N^5-carbamoil-L-ornitil[(4-aminofenil)metoxi]carbonil-*N*-metil-L-valil-L-valil-(3*R*,4*S*,5*S*)-5-metil-4-(metilamino)-3-metoxiheptanoil-(2*R*,3*R*)-*N*-[(1*S*,2*R*)-1-fenil-1-hidroxipropan-2-il]-2-metil-3-metoxi-3-[(2*S*)-pirrolidin-2-il]propanamida}-$N^{2,1}$-il)etilo (*tivedotina*)

Heavy chain / Chaîne lourde / Cadena pesada (H, H")

```
EVQLVQSGAE VKKPGATVKI SCKASGLNIE DYYMHWVQQA PGKGLEWMGW  50
IDPENGDTEY AEKFQGRVTI TADTSTNTAY MELSSLRSED TAVYYCTVHN 100
AHYGTWFAYW GQGTTVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSRDE LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK 450
```

Light chain / Chaîne légère / Cadena ligera (L', L'")

```
DIVMTQTPLS LSVTPGQPAS ISCRSSQTLV RSDGNTYLEW YLQKPGQSPQ  50
LLIYRVSNRF SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCFQGSHVP 100
YTFGGGTKLE IKRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK 150
VQWKVDNALQ SGNSQESVTE QDSKDSTYSL SSTLTLSKAD YEKHKVYACE 200
VTHQGLSSPV TKSFNRGEC                                   219
```

Post-translational modifications

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

Intra-H (C23-C104) 22-96 147-203 264-324 370-428
22"-96" 147"-203" 264"-324" 370"-428"

Intra-L (C23-C104) 23'-93' 139'-199'
23'"-93'" 139'"-199'"

Inter-H-L (h 5-CL 126)* 223-219' 223"-219'"

Inter-H-H (h 11, h 14)* 229-229" 232-232"

*Two or three of the four inter-chain disulfide bridges are not present, an average of 4 (3.8) cysteinyl being conjugated each via a thioether bond to a drug linker.

*Deux ou trois des quatre ponts disulfures inter-chaînes ne sont pas présents, 4 (3,8) cystéinyl en moyenne étant chacun conjugué via une liaison thioéther à un linker-principe actif.

*Dos o tres de los cuatro puentes disulfuro inter-catenarios no estan presentes, una media de 4 (3.8) cisteinil está conjugada a conectores de principio activo.

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

H CH2 N84.4: 300, 300"

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

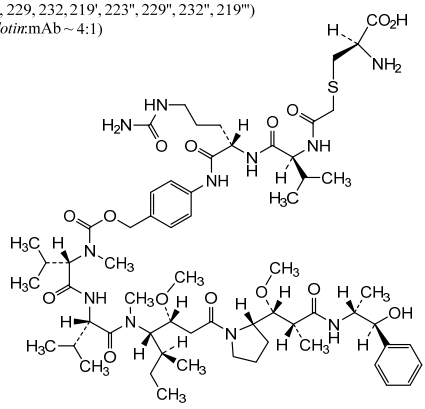
C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal

H CHS K2: 450, 450"

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

C (223, 229, 232, 219', 223", 229", 232", 219'")

*(*tivedotin*:mAb ~ 4:1)



lecankitugum #

lecankitug

immunoglobulin G1-kappa, anti-[*Homo sapiens* IL17A (interleukin 17A, IL-17A) and IL17F (interleukin 17F, IL-17F)], humanized monoclonal antibody;
H-gamma1 heavy chain humanized (1-448) [VH (*Homo sapiens* IGHV1-46*01 (83.7%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens*

	IGHG1*01 (100%) G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (215) (119-216), hinge 1-15 (217-231), CH2 (232-341), CH3 D12 (357), L14 (359) (342-446), CHS (447-448)) (119-448)], (221-219')-disulfide with L-kappa light chain humanized (1'-219') [V-KAPPA (*Homo sapiens* IGKV2D-29*01 (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, V101 (C-KAPPA A45.1 (158'), V101 (196')) (113'-219')]; dimer (227-227'':230-230'')-bisdisulfide, produced in a cell line from Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, glycoform alfa
lécankitug	immunoglobuline G1-kappa, anti-[*Homo sapiens* IL17A (interleukine 17A, IL-17A) et IL17F (interleukine 17F, IL-17F)]; anticorps monoclonal humanisé; chaîne lourde H-gamma1 humanisée (1-448) [VH (*Homo sapiens* IGHV1-46*01 (83.7%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (215) (119-216), charnière 1-15 (217-231), CH2 (232-341), CH3 D12 (357), L14 (359) (342-446), CHS (447-448)) (119-448)], (221-219')-disulfure avec la chaîne légère L-kappa humanisée (1'-219') [V-KAPPA (*Homo sapiens* IGKV2D-29*01 (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, V101 (C-KAPPA A45.1 (158'), V101 (196')) (113'-219')]; dimère (227-227'':230-230'')-bisdisulfure, produit dans une lignée cellulaire des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1, glycoforme alfa
lecankitug	inmunoglobulina G1-kappa, anti-[*Homo sapiens* IL17A (interleukina 17A, IL-17A) y IL17F (interleukina 17F, IL-17F)]; anticuerpo monoclonal humanizado; cadena pesada H-gamma1 humanizada (1-448) [VH (*Homo sapiens* IGHV1-46*01 (83.7%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG1*01 (100%) G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (215) (119-216), bisagra 1-15 (217-231), CH2 (232-341), CH3 D12 (357), L14 (359) (342-446), CHS (447-448)) (119-448)], (221-219')-disulfuro con la cadena ligera L-kappa humanizada (1'-219') [V-KAPPA (*Homo sapiens* IGKV2D-29*01 (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, V101 (C-KAPPA A45.1 (158'), V101 (196')) (113'-219')]; dímero (227-227'':230-230'')-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

```
QFQLVQSGAE VKKPGASVKV SCKASGYTFT DYNLNWVRQA PGKGLEWMGV  50
IHPDYGTTSY NQKFKDRVTM TVDTSTSTVY MELSSLRSED TAVYYCVRYD 100
YGDAMDYWGQ GTLVTVSSAS TKGPSVFPLA PSSKSTSGGT AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTQTYI 200
CNVNHKPSNT KVDKKVEPKS CDKTHTCPPC PAPELLGGPS VFLFPPKPKD 250
TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNST 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY 350
TLPPSRDELT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD 400
SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPGK   448
```

Light chain / Chaîne légère / Cadena ligera

```
DIVMTQSPLS LSVTPGQPAS ISCRSSQSLV HSNGNTYLHW YLQKPGQPPQ  50
LLIYKVSNRF SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCSQSTHVP 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) 22-96 145-201 262-322 368-426
22"-96" 145"-201" 262"-322" 368"-426"
Intra-L (C23-C104) 23'-93' 139'-199'
23'"-93'" 139'"-199'"
Inter-H-L (h 5-CL 126) 221-219' 221"-219'"
Inter-H-H (h 11, h 14) 227-227"' 230-230"

N-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"

ledostomigum #

ledostomig

immunoglobulin (H-gamma1-scFvhk_L-kappa) dimer, anti-[*Homo sapiens* NT5E (5'-nucleotidase ecto, 5'-nucleotidase, NT5, eN, eNT, NTE, CALJA, CD73)] and anti-[*Homo sapiens* PDCD1 (programmed cell death 1, PD-1, PD1, CD279)], monoclonal antibody, bispecific, tetravalent;
H-gamma1 heavy chain anti-NT5E fused to a scFvhk anti-PDCD1 (1-717) [H-gamma1 heavy chain anti-NT5E (1-451) [VH Musmus/Homsap (*Mus musculus* IGHV1-42-1*01 (82.7%) -(IGHD) -IGHJ2*01 (100%)/*Homo sapiens* IGHV1-46*01 (81.6%) -(IGHD) -IGHJ4*01 (86.7%) L123>T (116), V124>L (117), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1-121)-*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, 6-G1v14-1 CH2 A1.3, A1.2, A1(CH1 K120 (218) (122-219), hinge 1-15 (220-234), CH2 L1.3>A (238), L1.2>A (239), G1>A (241) (235-344), CH3 D12 (360), L14 (362) (345-449), CHS (450-451)) (122-451)] -20-mer tetrakis(tetraglycyl-seryl) linker (452-471) -scFvhk anti-PDCD1 (472-717) [VH (*Homo sapiens* IGHV3-23*04 (88.7%) -(IGHD) -IGHJ6*01 (90.9%) T123>L (584), CDR-IMGT [8.8.11] (497-504.522-529.568-578)) (472-589) -20-mer tetrakis(tetraglycyl-seryl) linker (590-609) -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 (709), I126>L (715), CDR-IMGT [6.3.9] (636-641.659-661.698-706)) (610-717)]]; (224-220')-disulfide with L-kappa light chain anti-NT5E humanized (1'-220') [V-KAPPA (*Homo sapiens* IGKV4-1*01 (89.1%) -IGKJ2*01 (91.7%) Q120>G (106'), CDR-IMGT [12.3.9] (27'-38'.56'-58'.95'-103')) (1'-113') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (159'), V101 (197')) (114'-220')]; dimer (230-230":233-233")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

lédostomig	immunoglobuline (H-gamma1-scFvhk_L-kappa) dimère, anti-[*Homo sapiens* NT5E (5'-nucléotidase ecto, 5'-nucléotidase, NT5, eN, eNT, NTE, CALJA, CD73)] et anti-[*Homo sapiens* PDCD1 (protéine 1 de mort cellulaire programmée, PD-1, PD1, CD279)], anticorps monoclonal, bispécifique, tétravalent; chaîne lourde H-gamma1 anti-NT5E fusionnée à un scFvhk anti-PDCD1 (1-717) [chaîne lourde H-gamma1 anti-NT5E (1-451) [VH Musmus/Homsap (*Mus musculus* IGHV1-42-1*01 (82.7%) -(IGHD) -IGHJ2*01 (100%)/*Homo sapiens* IGHV1-46*01 (81.6%) -(IGHD) -IGHJ4*01 (86.7%) L123>T (116), V124>L (117), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1-121)-*Homo sapiens* IGHG1*01 G1m17,1 CH1 K120, CH3 D12, L14, 6-G1v14-1 CH2 A1.3, A1.2, A1(CH1 K120 (218) (122-219), charnière 1-15 (220-234), CH2 L1.3>A (238), L1.2>A (239), G1>A (241) (235-344), CH3 D12 (360), L14 (362) (345-449), CHS (450-451)) (122-451)] -20-mer tétrakis(tétraglycyl-séryl) linker (452-471) -scFvhk anti-PDCD1 (472-717) [VH (*Homo sapiens* IGHV3-23*04 (88.7%) -(IGHD) -IGHJ6*01 (90.9%) T123>L (584), CDR-IMGT [8.8.11] (497-504.522-529.568-578)) (472-589) -20-mer tétrakis(tétraglycyl-séryl) linker (590-609) -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 (709), I126>L (715), CDR-IMGT [6.3.9] (636-641.659-661.698-706)) (610-717)]]; (224-220')-disulfure avec la chaîne légère L-kappa anti-NT5E humanisée (1'-220') [V-KAPPA (*Homo sapiens* IGKV4-1*01 (89.1%) -IGKJ2*01 (91.7%) Q120>G (106'), CDR-IMGT [12.3.9] (27'-38'.56'-58'.95'-103')) (1'-113') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (159'), V101 (197')) (114'-220')]; dimère (230-230'':233-233'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa
ledostomig	inmunoglobulina (H-gamma1-scFvhk_L-kappa) dímero, anti-[*Homo sapiens* NT5E (5'-nucleotidasa ecto, 5'-nucleotidasa, NT5, eN, eNT, NTE, CALJA, CD73)] y anti-[*Homo sapiens* PDCD1 (proteína 1 de muerte celular programada, PD-1, PD1, CD279)], anticuerpo monoclonal, biespecífico, tetravalente; cadena pesada H-gamma1 anti-NT5E fusionada con un scFvhk anti-PDCD1 (1-717) [cadena pesada H-gamma1 anti-NT5E (1-451) [VH Musmus/Homsap (*Mus musculus* IGHV1-42-1*01 (82.7%) -(IGHD) -IGHJ2*01 (100%)/*Homo sapiens* IGHV1-46*01 (81.6%) -(IGHD) -IGHJ4*01 (86.7%) L123>T (116), V124>L (117), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1-121)-*Homo sapiens* IGHG1*01 G1m17,1 CH1 K120, CH3 D12, L14, 6-G1v14-1 CH2 A1.3, A1.2, A1(CH1 K120 (218) (122-219), bisagra 1-15 (220-234), CH2 L1.3>A (238), L1.2>A (239), G1>A (241) (235-344), CH3 D12 (360), L14 (362) (345-449), CHS (450-451)) (122-451)] -20-mer tetrakis(tetraglicil-seril) enlace (452-471) -scFvhk anti-PDCD1 (472-717) [VH (*Homo sapiens* IGHV3-23*04 (88.7%) -(IGHD) -IGHJ6*01 (90.9%) T123>L (584), CDR-IMGT [8.8.11] (497-504.522-529.568-578)) (472-589) -20-mer tetrakis(tetraglicil-seril) enlace (590-609) -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 (709), I126>L (715), CDR-IMGT [6.3.9] (636-641.659-661.698-706)) (610-717)]]; (224-220')-disulfuro com la cadena ligera L-kappa anti-NT5E humanizada (1'-220') [V-KAPPA (*Homo sapiens* IGKV4-1*01 (89.1%) -IGKJ2*01 (91.7%) Q120>G (106'), CDR-IMGT [12.3.9] (27'-38'.56'-58'.95'-103')) (1'-113') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (159'), V101 (197')) (114'-220')]; dímero (230-230'':233-233'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada: fused H-gamma1 anti-NT5E -scFvhk anti-PDCD1 (H, H'')

```
QVQLVQSGAE VVKPGASVKV SCKASGYSFT GYTMNWVRQA PGQNLEWIGL  50
INPYNAGTSY NQKFQGKVTL TVDKSTSTAY MELSSLRSED TAVYYCARSE 100
YRYGGDYFDY WGQGTTLTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200
TYICNVNHKP SNTKVDKKVE PKSCDKTHTC PPCPAPEAAG APSVFLFPPK 250
PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY 300
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP 350
QVYTLPPSRD ELTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP 400
VLDSDGSFFL YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG 450
KGGGGSGGGG SGGGGSGGGG SEVQLVESGG GLVQPGGSLR LSCAASGFAF 500
SSYDMSWVRQ APGKGLDWVA TISGGGRYTY YPDSVKGRFT ISRDNSKNNL 550
YLQMNSLRAE DTALYYCANR YGEAWFAYWG QGTLVTVSSG GGGSGGGGSG 600
GGGSGGGGSD IQMTQSPSSM SASVGDRVTF TCRASQDINT YLSWFQQKPG 650
KSPKTLIYRA NRLVSGVPSR FSGSGSGQDY TLTISSLQPE DMATYYCLQY 700
DEFPLTFGAG TKLELKR                                     717
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Light chain / Chaîne légère / Cadena ligera: L-kappa anti-NT5E (L', L''')

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DIVMTQSPSS LAVSVGERVT ISCKSSQSLL NSSNQKNYLA WYQQKPGQAP  50
KLLIYFASTR ESGVPDRFSG SGSGTDFTLT ISSLQAEDVA VYYCQQHYDT 100
PYTFGGGTKL 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) 22-96 148-204 265-325 371-429
22''-96'' 148''-204'' 265''-325'' 371''-429''
493-567 632-697
493''-567'' 632''-697''

Intra-L (C23-C104) 23'-94' 140'-200'
23'''-94''' 140'''-200'''

Intra-H-L (h 5-CL 126) 224-220' 224''-220'''

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.

lerepmeranum

lerepmeran — messenger RNA (mRNA), 5'(m^7G-(5'→5')-ppp-Gm)-capped, encoding codon-optimised human propionyl-CoA carboxylase subunit alpha (PCCA), flanked by 5' and 3' untranslated regions (UTRs), followed by a 3' polyadenylation (polyA) tail and concluded by a 5-nucleotide *Xba*I scar. The 3' UTR contains three microRNA-142 (miR-142) binding sites. Contains N^1-methylpseudouridine instead of uridine (*all*-U>$m^1\Psi$)

lérepméran — ARN messager (ARNm), coiffé en 5'(m^7G-(5'→5')-ppp-Gm), codant, avec des codons optimisés, la sous-unité alpha de la propionyl-CoA carboxylase humaine (PCCA), flanqué des régions non traduites (UTRs) en 5' et 3', suivie d'une queue de polyadénylation (polyA) en 3' et conclue par une cicatrice *Xba*I de 5 nucléotides. Le 3' UTR contient trois sites de liaison du microARN-142 (miR-142). Contient de la N^1-méthylpseudouridine au lieu de l'uridine (*tout*-U>$m^1\Psi$)

lerepmerán — ARN mensajero (ARNm), protegido con la caperuza 5'(m^7G-(5'→5')-ppp-Gm), que codifica, con codones optimizados, la subunidad alfa de la propionil-CoA carboxilasa (PCCA), flanqueado por regiones sin traducir (UTRs) 5' y 3', seguido de una cola de poliadenilación (poliA) en 3' y concluido con una cicatriz *Xba*I de 5 nucleótidos. La 3' UTR contiene tres sitios de unión del microARN-142 (miR-142). Contiene N^1-metilpseudouridina en lugar de uridina (*todo*-U>$m^1\Psi$)

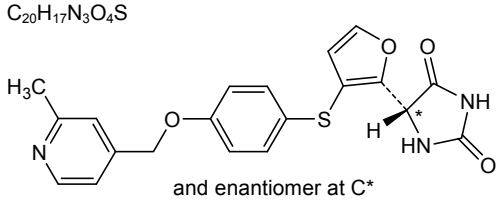
linvemastatum

linvemastat — *rac*-(1^4*R*)-7^2-methyl-5-oxa-3-thia-7(4)-pyridina-1(4)-imidazolidina-2(2,3)-furana-4(1,4)-benzenaheptaphane-1^2,1^5-dione

linvémastat — *rac*-(1^4*R*)-7^2-méthyl-5-oxa-3-thia-7(4)-pyridina-1(4)-imidazolidina-2(2,3)-furana-4(1,4)-benzénaheptaphane-1^2,1^5-dione

linvemastat — *rac*-(1^4*R*)-7^2-metil-5-oxa-3-tia-7(4)-piridina-1(4)-imidazolidina-2(2,3)-furana-4(1,4)-bencenaheptafano-1^2,1^5-diona

$C_{20}H_{17}N_3O_4S$



and enantiomer at C*
et énantiomère at C*
y enantiómero at C*

liraltagenum autoleucelum #

liraltagene autoleucel — autologous CD4+/CD8+ enriched T lymphocytes derived from leukapheresis material, transduced with a non-replicating murine stem cell virus (MSCV)-derived gamma retroviral vector, encoding codon-optimised follicle-stimulating hormone (FSH) (subunits FSHβ and CGα, linked by a glycine/serine spacer), preceded by the FSHβ signal peptide, and fused to a CD8α hinge and transmembrane domain, a 4-1BB co-stimulatory domain and a CD3ζ signalling domain, under control of the Moloney murine leukemia virus (MMLV) LTR promoter. The vector also has long terminal repeats (LTRs) derived from MSCV and an extended packaging signal (Ψ+) derived from MMLV and has a splice acceptor sequence immediately upstream of the start codon. A Kozak sequence precedes the transgene. The leukapheresis material is enriched for the CD4+/CD8+ lymphocyte fraction by immunoselection prior to activation with anti-CD3 and interleukin 2 (IL-2). The cells are then transduced with the retroviral vector and expanded in growth media containing anti-CD3 and IL-2. The cell suspension consists of T lymphocytes (≥90% CD3+; ≤0.5% CD14+, ≤0.08% CD19+, ≤5% CD3-CD56+, ≤0.55% CD3-CD33+), with ≥10% of the T lymphocytes expressing the transgene. The transduced T lymphocytes demonstrate cytotoxicity against follicle-stimulating hormone receptor (FSHR)-expressing cells

liraltagène autoleucel — lymphocytes T autologues enrichis en CD4+/CD8+, dérivés de matériel de leucaphérèse, transduits avec un vecteur rétroviral gamma dérivé du virus des cellules souches murines (MSCV), non réplicatif, codant l'hormone folliculo-stimulante (FSH) à codons optimisés (sous-unités FSHβ et CGα, liées par un espaceur glycine/sérine), précédé du peptide signal FSHβ, et fusionné à un domaine charnière et un

	domaine transmembranaire CD8α, un domaine co-stimulateur 4-1BB et un domaine de signalisation CD3ζ, sous le contrôle du promoteur LTR du virus de la leucémie murine Moloney (MMLV). Le vecteur possède de répétitions terminales longues (LTRs) dérivées du MSCV et un signal d'encapsidation (Ψ+) dérivé du MMLV et possède une séquence accepteur d'épissage immédiatement en amont du codon d'initiation. Une séquence Kozak précède le transgène. Le matériel de leucaphérèse est enrichi en fraction de lymphocytes CD4+/CD8+ par immunosélection avant l'activation avec de l'anti-CD3 et de l'interleukine 2 (IL-2). Les cellules sont ensuite transduites avec le vecteur rétroviral et expansées dans un milieu de croissance contenant de l'anti-CD3 et de l'IL-2. La suspension cellulaire est constituée de lymphocytes T (≥90% CD3+; ≤0,5% CD14+, ≤0,08% CD19+, ≤5% CD3-CD56+, ≤0,55% CD3-CD33+), avec ≥10% des lymphocytes T exprimant le transgène. Les lymphocytes T transduits démontrent une cytotoxicité contre les cellules exprimant le récepteur de l'hormone folliculo-stimulante (FSHR)
liraltagén autoleucel	linfocitos T CD4+/CD8+ enriquecidos autólogos derivados de material de leucoaféresis, transducidos con un vector gamma retroviral derivado del virus de células madre murino (MSCV), no replicativo, que codifica, con codones optimizados, la hormona estimuladora del folículo (FSH) (subunidades FSHβ an CGα, unidas mediante un espaciador glicina/serina), precedido por el péptido señal de FSHβ y fusionado a un dominio bisagra y transmembrana de CD8α, un dominio coestimulador de 4-1BB y un dominio de señalización de CD3ζ, bajo el control del promotor LTR del virus de la leucemia murina de Moloney (MMLV). El vector tiene repeticiónes terminales largas (LTRs) derivadas del MSCV y una señal empaquetadora (Ψ+) derivada del MMLV y tiene una secuencia aceptora del procesamiento inmediatamente antes del codón de iniciación. Una secuencia Kozack precede al transgén. El material de leucoaféresis se enriquece para la fracción de linfocitos CD4+/CD8+ mediante inmunoselección antes de la activación con anti-CD3 e interleuquina 2 (IL-2). Las células después se transducen con el vector retroviral y se expanden en medio que contiene anti-CD3 e IL-2. La suspensión celular consiste en linfocitos T (≥90% CD3+; ≤0.5% CD14+, ≤0.08% CD19+, ≤5% CD3-CD56+, ≤0.55% CD3-CD33+), con ≥10% de los linfocitos T que expresan el transgén. Los linfocitos T transducidos muestran actividad citotóxica frente a células que expresan el receptor de la hormona estimuladora del folículo (FSHR)

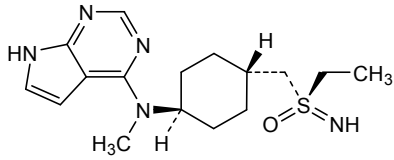
lirucitinibum
lirucitinib

(*R*)-ethyl(imino)({*trans*-4-[methyl(7*H*-pyrrolo[2,3-*d*]pyrimidin-4-yl)amino]cyclohexyl}methyl)-λ^6-sulfanone

lirucitinib (*R*)-éthyl(imino)({*trans*-4-[méthyl(7*H*-pyrrolo[2,3-*d*]pyrimidin-4-yl)amino]cyclohexyl}méthyl)-λ^6-sulfanone

lirucitinib (*R*)-etil(imino)({*trans*-4-[metil(7*H*-pirrolo[2,3-*d*]pirimidin-4-il)amino]ciclohexil}metil)-λ^6-sulfanona

$C_{16}H_{25}N_5OS$



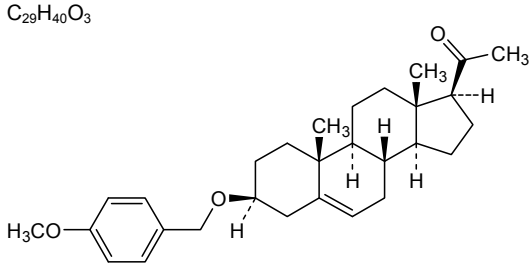
lixosiconum

lixosicone 3β-[(4-methoxyphenyl)methoxy]pregn-5-en-20-one

lixosicone 3β-[(4-méthoxyphényl)méthoxy]prégn-5-én-20-one

lixosicona 3β-[(4-metoxifenil)metoxi]pregn-5-en-20-ona

$C_{29}H_{40}O_3$



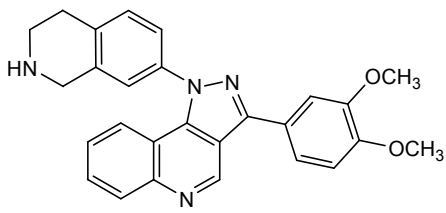
lomonitinibum

lomonitinib 3-(3,4-dimethoxyphenyl)-1-(1,2,3,4-tetrahydroisoquinolin-7-yl)-1*H*-pyrazolo[4,3-*c*]quinoline

lomonitinib 3-(3,4-diméthoxyphényl)-1-(1,2,3,4-tétrahydroisoquinoléin-7-yl)-1*H*-pyrazolo[4,3-*c*]quinoléine

lomonitinib 3-(3,4-dimetoxifenil)-1-(1,2,3,4-tetrahidroisoquinolein-7-il)-1*H*-pirazolo[4,3-*c*]quinoleína

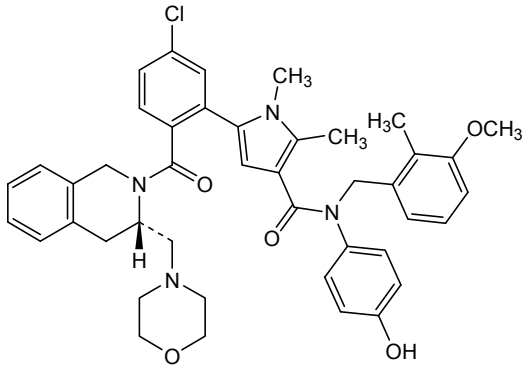
$C_{27}H_{24}N_4O_2$



Ionitoclaxum

Ionitoclax	5-(5-chloro-2-{(3*S*)-3-[(morpholin-4-yl)methyl]-3,4-dihydroisoquinoline-2(1*H*)-carbonyl}phenyl)-*N*-(4-hydroxyphenyl)-*N*-[(3-methoxy-2-methylphenyl)methyl]-1,2-dimethyl-1*H*-pyrrole-3-carboxamide
Ionitoclax	5-(5-chloro-2-{(3*S*)-3-[(morpholin-4-yl)méthyl]-3,4-dihydroisoquinoléine-2(1*H*)-carbonyl}phényl)-*N*-(4-hydroxyphényl)-*N*-[(3-méthoxy-2-méthylphényl)méthyl]-1,2-diméthyl-1*H*-pyrrole-3-carboxamide
Ionitoclax	5-(5-cloro-2-{(3*S*)-3-[(morfolin-4-il)metil]-3,4-dihidroisoquinoleína-2(1*H*)-carbonil}fenil)-*N*-(4-hidroxifenil)-1,2-dimetil-*N*-[(2-metil-3-metoxifenil)metil]-1*H*-pirrol-3-carboxamida

$C_{43}H_{45}ClN_4O_5$



Iumekefamidum

Iumekefamide	L-tyrosyl-D-arginyl-L-phenylalanylglycinamide
Iuméképamide	L-tyrosyl-D-arginyl-L-phénylalanylglycinamide
Iumekefamida	L-tirosil-D-arginil-L-fenilalanilglicinamida

$C_{26}H_{36}N_8O_5$

H—Tyr—D-Arg—Phe—Gly—NH_2

Iunsotogenum parvecum #

Iunsotogene parvec	two recombinant, non-replicating adeno-associated virus serotype 1 (rAAV1) vectors containing the 5' and 3' portions, respectively, of the DNA sequence coding for wild-type human otoferlin (OTOF) protein isoform e. The 5' vector contains exons 1-18 and 20-21 of the

	OTOF gene based on the consensus genome numbering, under expression control of the hair cell-specific myosin 15 (Myo15) promoter, followed by a splice donor and alkaline phosphatase homology region 3' to the transgene. The 3' vector contains the alkaline phosphatase homology region and a splice acceptor, followed by exons 22-46 and exon 48 of the OTOF gene, and is terminated by a bovine somatotropin growth hormone polyadenylation sequence. Both vectors are flanked by AAV2 inverted terminal repeats
lunsotogène parvec	deux vecteurs recombinants de virus adéno-associés de sérotype 1 (rAAV1), non réplicatifs, contenant respectivement les parties 5' et 3' de la séquence d'ADN codant pour l'isoforme e de la protéine otoferline (OTOF) humaine sauvage. Le vecteur 5' contient les exons 1-18 et 20-21 du gène OTOF, selon la numérotation consensuelle du génome sous le contrôle de l'expression du promoteur de la myosine 15 (Myo15) spécifique des cellules ciliées, suivis d'un donneur d'épissage et d'une région d'homologie de la phosphatase alcaline 3' du transgène. Le vecteur 3' contient la région d'homologie de la phosphatase alcaline et un accepteur d'épissage, suivi des exons 22-46 et 48 du gène OTOF et se termine par une séquence de polyadénylation de l'hormone de croissance somatotropine bovine. Les deux vecteurs sont flanqués des répétitions terminales inversées de l'AAV2
lunsotogén parvec	dos vectores de virus adenoasociado del serotipo 1, recombinantes (rAAV1), no replicativos, que contienen las porciones 5' y 3', respectivamente, de la secuencia de ADN que codifica la isoforma e de la proteína otoferlina (OTOF) humana de tipo silvestre. El vector 5' contiene los exones 1-18 y 20-21 del gen de OTOF según la numeración consensuada del genoma bajo el control de expresión del promotor de la miosina 15 (Myio15) específica de células ciliadas, seguido de un dador del procesamiento y una región de homología de la fosfatasa alcalina 3' del transgén. El vector 3' contiene la región de homología de la fosfatasa alcalina y un aceptor de procesamiento, seguido de los exones 22-46 y 48 del gen de OTOF y se termina por una secuencia de poliadenilación de la hormona de crecimiento somatotropina bovina. Ambos vectores están flanqueados por las repeticiones terminales invertidas del AAV2

macupatidum

macupatide	L-tyrosyl-2-methylalanyl-L-α-glutamylglycyl-L-threonyl-L-phenylalanyl-L-isoleucyl-L-seryl-L-α-aspartyl-L-tyrosyl-L-seryl-L-isoleucyl-2-methyl-L-leucyl-L-leucyl-L-α-aspartyl-L-lysyl-N^6-(17-{[*N* -(19-carboxynonadecanoyl)- L-γ-glutamyl]amino}-10-oxo-3,6,12,15-tetraoxa-9-azaheptadecan-1-oyl)-L-lysyl-L-histidyl-L-glutaminyl-2-methylalanyl-L-α-aspartyl-L-phenylalanyl-L-valyl-L-α-glutamyl-3-(pyridine-4-yl)-L-alanyl-L-leucyl-L-leucyl-L-α-glutamyl-L-alanylglycyl-L-prolyl-L-seryl-L-serylglycyl-L-alanyl-L-prolyl-L-prolyl-L-prolyl- L-serinamide

macupatide

L-tyrosyl-2-méthylalanyl-L-α-glutamylglycyl-L-thréonyl-L-phénylalanyl-L-isoleucyl-L-séryl-L-α-aspartyl-L-tyrosyl-L-séryl-L-isoleucyl-2-méthyl-L-leucyl-L-leucyl-L-α-aspartyl-L-lysyl-*N*^{6}-(17-{[*N*-(19-carboxynonadécanoyl)- L-γ-glutamyl]amino}-10-oxo-3,6,12,15-tétraoxa-9-azaheptadécan-1-oyl)-L-lysyl-L-histidyl-L-glutaminyl-2-méthylalanyl-L-α-aspartyl-L-phénylalanyl-L-valyl-L-α-glutamyl-3-(pyridine-4-yl)-L-alanyl-L-leucyl-L-leucyl-L-α-glutamyl-L-alanylglycyl-L-prolyl-L-séryl-L-sérylglycyl-L-alanyl-L-prolyl-L-prolyl-L-prolyl- L-sérinamide

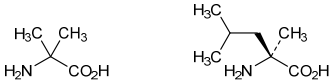
macupatida

L-tirosil-2-metilalanil-L-α-glutamlglicil-L-treonil-L-fenilalanil-L-isoleucil-L-seril-L-α-aspartil-L-tirosil-L-seril-L-isoleucil-2-metil-L-leucil-L-leucil-L-α-aspartil-L-lisil-*N*^{6}-(17-{[*N*-(19-carboxinonadecanoil)- L-γ-glutamil]amino}-10-oxo-3,6,12,15-tetraoxa-9-azaheptadecan-1-oil)-L-lisil-L-histidil-L-glutaminil-2-metilalanil-L-α-aspartil-L-fenilalanil-L-valil-L-α-glutamil-3-(piridina-4-il)-L-alanil-L-leucil-L-leucil-L-α-glutamil-L-alanilglicil-L-prolil-L-seril-L-serilglicil-L-alanil-L-prolil-L-prolil-L-prolil- L-serinamide

$C_{232}H_{357}N_{49}O_{72}$

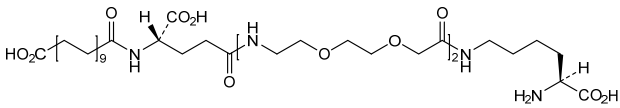
YAEGTFISDY SILLDKKHQA DFVEXLLEAG PSSGAPPPS 39

Modified residues / Résidus modifiés / Restos modificados

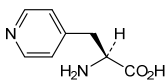


A (2, 20)
2-Me-L-Ala

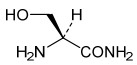
L (13)
2-Me-L-Leu



K (17)
N^6-(HO$_2$C-[CH$_2$]$_{18}$-CO-L-Glu-[NH-CH$_2$-CH$_2$-O-CH$_2$-CH$_2$-O-CH$_2$-CO]$_2$)-L-Lys



X (25)
pyridin-4-yl-L-Ala



S (39)
L-Ser-NH$_2$

marlotamigum #

marlotamig

immunoglobulin G4-kappa, anti-[*Homo sapiens* EGFR (epidermal growth factor receptor, receptor tyrosine-protein kinase erbB-1, ERBB1, HER1, HER-1, ERBB)] and anti-[*Homo sapiens* CD28 (T cell specific surface glycoprotein CD28, TP44)], *Homo sapiens* monoclonal antibody, bispecific, bivalent;
H-gamma4 heavy chain anti-EGFR *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV4-59*01 (92.8%) -(IGHD) -IGHJ3*01 (92.3%) M123>T (116), CDR-IMGT [8.7.15] (26-33.51-57.96-110)) (1-121)-*Homo sapiens* IGHG4*01, G4v5 h P10,nG4m(a) CH2 L92, G4v7 CH2 delE1.4, P1.3, V1.2, A1.1 (CH1 (122-219), hinge 1-12 S10>P (229) (220-231), CH2 E1.4>del, F1.3>P (234), L1.2>V (235), G1.1>A (236), L92 (312) (232-340), CH3 (341-445), CHS (446-447)) (122-447)], (135-215')-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')]; H-gamma4 heavy chain anti-CD28 *Homo sapiens* (1"-448") [VH (*Homo sapiens* IGHV4-59*01 (96.9%) -(IGHD) -IGHJ6*01 (100%), CDR-IMGT [8.7.16] (26"-33".51"-57".96"-111")) (1"-122")-*Homo sapiens* IGHG4*01, G4v5 h P10,nG4m(a) CH2 L92, G4v7 CH2 delE1.4, P1.3, V1.2, A1.1, G4v8 CH3 R115, F116, P125 (CH1 (123"-220"), hinge 1-12 S10>P (230") (221"-232"), CH2 E1.4>del, F1.3>P (235"), L1.2>V (236"), G1.1>A (237"), L92 (310") (233"-341"), CH3 H115>R (436"), Y116>F (437"), L125>P (446") (342"-446"), CHS (447"-448")) (123"-448")], (136"-215"')-disulfide with L-kappa light chain *Homo sapiens* common (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 (227-228":230-231")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-DG44, glycoform alfa

marlotamig

immunoglobuline G4-kappa, anti-[*Homo sapiens* EGFR (récepteur du facteur de croissance épidermique, récepteur tyrosine-protéine kinase erbB-1, ERBB1, HER1, HER-1, ERBB)] et anti-[*Homo sapiens* CD28 (glycoprotéine de surface CD28 spécifique des cellules T, TP44)], anticorps monoclonal *Homo sapiens,* bispécifique, bivalent;
chaîne lourde H-gamma4 anti-EGFR *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV4-59*01 (92.8%) -(IGHD) -IGHJ3*01 (92.3%) M123>T (116), CDR-IMGT [8.7.15] (26-33.51-57.96-110)) (1-121)-*Homo sapiens* IGHG4*01, G4v5 h P10,nG4m(a) CH2 L92, G4v7 CH2 delE1.4, P1.3, V1.2, A1.1 (CH1 (122-219), charnière 1-12 S10>P (229) (220-231), CH2 E1.4>del, F1.3>P (234), L1.2>V (235), G1.1>A (236), L92 (312) (232-340), CH3 (341-445), CHS (446-447)) (122-447)], (135-215')-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')];
chaîne lourde H-gamma4 anti-CD28 *Homo sapiens* (1"-448") [VH (*Homo sapiens* IGHV4-59*01 (96.9%) -(IGHD) -IGHJ6*01 (100%), CDR-IMGT [8.7.16] (26"-33".51"-57".96"-111")) (1"-122")-*Homo sapiens* IGHG4*01, G4v5 h P10,nG4m(a) CH2 L92, G4v7 CH2 delE1.4, P1.3, V1.2, A1.1, G4v8 CH3 R115, F116, P125 (CH1 (123"-220"), charnière 1-12 S10>P (230") (221"-232"), CH2 E1.4>del, F1.3>P (235"), L1.2>V (236"), G1.1>A (237"), L92 (310") (233"-341"), CH3 H115>R (436"), Y116>F (437"), L125>P (446") (342"-446"), CHS (447"-448")) (123"-448")], (136"-215"')-disulfure avec la chaîne légère L-kappa *Homo sapiens* commune (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 (227-228":230-231")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-DG44, glycoforme alfa

marlotamig

inmunoglobulina G4-kappa, anti-[*Homo sapiens* EGFR (receptor del factor de crecimiento epidérmico, receptor tirosina-proteína kinasa erbB-1, ERBB1, HER1, HER-1, ERBB)] y anti-[*Homo sapiens* CD28 (glicoproteína de superficie CD28 específica de las células T, TP44)], anticuerpo monoclonal *Homo sapiens,* biespecífico, bivalente;
cadena pesada H-gamma4 anti-EGFR *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV4-59*01 (92.8%) -(IGHD) -IGHJ3*01 (92.3%) M123>T (116), CDR-IMGT [8.7.15] (26-33.51-57.96-110)) (1-121)-*Homo sapiens* IGHG4*01, G4v5 h P10,nG4m(a) CH2 L92, G4v7 CH2 delE1.4, P1.3, V1.2, A1.1 (CH1 (122-219), bisagra 1-12 S10>P (229) (220-231), CH2 E1.4>del, F1.3>P (234), L1.2>V (235), G1.1>A (236), L92 (312) (232-340), CH3 (341-445), CHS (446-447)) (122-447)], (135-215')-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')];
cadena pesada H-gamma4 anti-CD28 *Homo sapiens* (1"-448") [VH (*Homo sapiens* IGHV4-59*01 (96.9%) -(IGHD) -IGHJ6*01 (100%), CDR-IMGT [8.7.16] (26"-33".51"-57".96"-111")) (1"-122")-*Homo sapiens* IGHG4*01, G4v5 h P10,nG4m(a) CH2 L92, G4v7 CH2 delE1.4, P1.3, V1.2, A1.1, G4v8 CH3 R115, F116, P125 (CH1 (123"-220"), bisagra 1-12 S10>P (230") (221"-232"), CH2 E1.4>del, F1.3>P (235"), L1.2>V (236"), G1.1>A (237"), L92 (310") (233"-341"), CH3 H115>R (436"), Y116>F (437"), L125>P (446") (342"-446"), CHS (447"-448")) (123"-448")], (136"-215"')-disulfuro con la cadena ligera L-kappa *Homo sapiens* común (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 (227-228":230-231")-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) anti-EGFR

```
QVQLQESGPG LVKPSETLSL TCTVSGDSII TFYWSWIRQP PGRGLEWIGY  50
IYYSGITNYN PSLKSRVTIS VDTSKNQVSL KLSSVTAADT AVYYCARVSE 100
DSYFHYGMDV WGQGTTVTVS SASTKGPSVF PLAPCSRSTS ESTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTK 200
TYTCNVDHKP SNTKVDKRVE SKYGPPCPPC PAPPVAGPSV FLFPPKPKDT 250
LMISRTPEVT CVVVDVSQED PEVQFNWYVD GVEVHNAKTK PREEQFNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKGLPS SIEKTISKAK GQPREPQVYT 350
LPPSQEEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS 400
DGSFFLYSRL TVDKSRWQEG NVFSCSVMHE ALHNHYTQKS LSLSLGK    447
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Heavy chain / Chaîne lourde / Cadena pesada : H-gamma4 (H") anti-CD28

```
QVQLQESGPG LVKPSETLSL TCTVSGGSIS SYYWSWIRQP PGKGLEWIGY  50
IYYSGITHYN PSLKSRVTIS VDTSKIQFSL KLSSVTAADT AVYYCARWGV 100
RRDYYYYGMD VWGQGTTVTV SSASTKGPSV FPLAPCSRST SESTAALGCL 150
VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ SSGLYSLSSV VTVPSSSLGT 200
KTYTCNVDHK PSNTKVDKRV ESKYGPPCPP CPAPPVAGPS 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
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Light chain / Chaîne légère / Cadena ligera : L-kappa (L', L"') common

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

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-95 148-204 261-321 367-425
22"-95" 149"-205" 262"-322" 368"-426"
Intra-L (C23-C104) 23'-89' 135'-195'
23"'-89"' 135"'-195"'
Inter-H-L (CH1 10-CL 126) 135-215' 136"-215"'
Inter-H-H (h 8, h 11) 227-228" 230-231"

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, 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: 447, 448"

marpinersenum

marpinersen

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

marpinersen

tout-P-ambo-2'-*O*-(2-méthoxyéthyl)-5-méthyl-*P*-thiouridylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)guanylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)guanylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)adénylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthyluridylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthyluridylyl-(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'-désoxy-*P*-thioadénylyl-(3'→5')-2'-désoxy-5-méthyl-*P*-thiocytidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthylcytidylyl-(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)adénosine

marpinersén

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

$C_{230}H_{319}N_{62}O_{132}P_{19}S_{13}$

(3'-5')*U*=G-G-A-*U*-*U*-d*C*=dT=dG=dT=dA=d*C*=dT=dT=dT=dT=*C*-*U*=*C*=A

N : nucleoside / nucléoside / nucleósido
dN : 2'-deoxy-N / 2'-désoxy-N / 2'-desoxi-N
N : 5-methyl-N / 5-méthyl-N / 5-metil-N
N : 2'-*O*-(2-methoxyethyl)-N / 2'-*O*-(2-méthoxyéthyl)-N / 2'-*O*-(metoxietil)-N
- : -PO(OH)- = : -PO(SH)-

mazisotinum

mazisotine

(1*R*,5*S*,6*r*)-*N*-{2-methyl-1-[(3-methylpyridin-2-yl)oxy]propan-2-yl}-3-azabicyclo[3.1.0]hexane-6-carboxamide

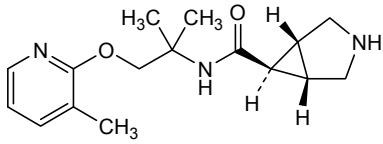
mazisotine

(1*R*,5*S*,6*r*)-*N*-{2-méthyl-1-[(3-méthylpyridin-2-yl)oxy]propan-2-yl}-3-azabicyclo[3.1.0]hexane-6-carboxamide

mazisotina

(1*R*,5*S*,6*r*)-*N*-{2-metil-1-[(3-metilpiridin-2-il)oxi]propan-2-il}-3-azabiciclo[3.1.0]hexano-6-carboxamida

$C_{16}H_{23}N_3O_2$



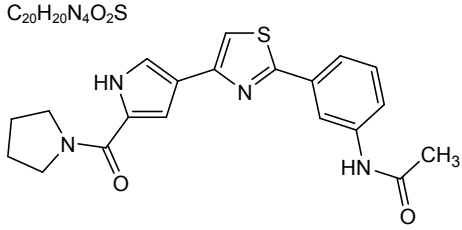
milpecitinibum

milpecitinib — *N*-(3-{4-[5-(pyrrolidine-1-carbonyl)-1*H*-pyrrol-3-yl]-1,3-thiazol-2-yl}phenyl)acetamide

milpécitinib — *N*-(3-{4-[5-(pyrrolidine-1-carbonyl)-1*H*-pyrrol-3-yl]-1,3-thiazol-2-yl}phényl)acétamide

milpecitinib — *N*-(3-{4-[5-(pirrolidina-1-carbonil)-1*H*-pirrol-3-il]-1,3-tiazol-2-il}fenil)acetamida

$C_{20}H_{20}N_4O_2S$



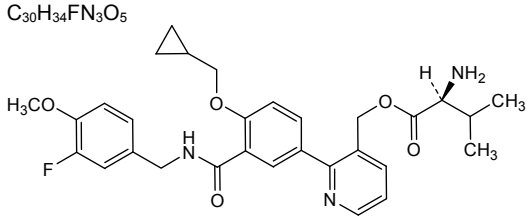
mirivadelgatum

mirivadelgat — {2-[4-(cyclopropylmethoxy)-3-{[(3-fluoro-4-methoxyphenyl)methyl]carbamoyl}phenyl]pyridin-3-yl}methyl L-valinate

mirivadelgat — L-valinate de {2-[4-(cyclopropylméthoxy)-3-{[(3-fluoro-4-méthoxyphényl)méthyl]carbamoyl}phényl]pyridin-3-yl}méthyle

mirivadelgat — L-valinato de {2-[4-(ciclopropilmetoxi)-3-{[(3-fluoro-4-metoxifenil)metil]carbamoil}fenil]piridin-3-il}metilo

$C_{30}H_{34}FN_3O_5$



mivocabtagenum autoleucelum #

mivocabtagene autoleucel — autologous CD4+/CD8+ enriched T lymphocytes derived from leukapheresis material, transduced with a self-inactivating, non-replicating lentiviral vector encoding a CD19 targeting chimeric antigen receptor (CAR) comprising a CD8 alpha (CD8α) signal peptide, a single-chain variable fragment (scFv) derived from the human anti-CD19 monoclonal antibody clone 47G4, a CD8α hinge and transmembrane domain, a

	CD28 cytoplasmic co-stimulatory domain, and a CD3-zeta (CD3ζ) signaling domain, under control of the murine stem cell virus 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 /central termination sequence (CTS) and an optimised Woodchuck hepatitis virus posttranscriptional regulatory element. The vector is 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 human serum, 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 (>80%), with greater than 10% of the T lymphocytes expressing the CAR-CD19 transgene. The transduced T lymphocytes demonstrate cytotoxicity against CD19-expressing cells and secrete interferon gamma (IFN-γ) and interleukin 2 (IL-2)
mivocabtagène autoleucel	lymphocytes T autologues enrichis en CD4+/CD8+ dérivés de matériel obtenu par leucaphérèse, transduits avec un vecteur lentiviral auto-inactivant et non réplicatif codant un récepteur antigénique chimérique (RAC) ciblant CD19, comprenant un peptide signal CD8 alpha (CD8α), un fragment variable à chaîne unique (scFv) dérivé du clone 47G4 d'anticorps monoclonal anti-CD19 humain, un domaine charnière et transmembranaire CD8α, un domaine co-stimulateur cytoplasmique CD28 et un domaine de signalisation CD3-zêta (CD3ζ), sous le contrôle du promoteur du virus des cellules souches murines. La construction est flanquée de répétitions terminales longues (LTRs) en 5' et en 3' et contient également un signal d'empaquetage Ψ, un élément de réponse Rev (RRE), une séquence de tractus polypurine central (cPPT)/séquence de terminaison centrale (CTS) et un élément de régulation post-transcriptionnel optimisé du virus de l'hépatite de la marmotte. Le vecteur est pseudotypé 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 activation avec des agonistes CD3 et CD28 dans un milieu de croissance contenant du sérum humain, de l'interleukine 7 (IL-7) et de l'interleukine 5 (IL-5). Les cellules sont ensuite transduites avec le vecteur lentiviral et expansées dans un milieu de croissance contenant de l'interleukine 7 (IL-7) et de l'interleukine 5 (IL-5). La suspension cellulaire est constituée de lymphocytes T (>80%), avec plus de 10% des lymphocytes T exprimant le transgène CAR-CD19. Les lymphocytes T transduits démontrent une cytotoxicité contre les cellules exprimant CD19 et sécrètent de l'interféron gamma (IFN-γ) et de l'interleukine 2 (IL-2)
mivocabtagén autoleucel	linfocitos T CD4+/CD8+ autólogos enriquecidos, derivados de material de leucoaféresis, transducidos con un vector lentiviral auto inactivante, no replicativo, que codifica un receptor de antígenos quimérico (CAR) dirigido a CD19, que consta de un péptido señal de CD8 alfa (CD8α), un fragmento variable de cadena sencilla (scFv) derivado del anticuerpo monoclonal anti-CD19 clon 47G4, un dominio bisagra y transmembrana de CD8α,

un dominio coestimulador citoplásmico de CD28 y un dominio de señalización de CD3-zeta (CD3ζ), bajo el control del promotor del virus de células madre murino. 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 poli-purina (cPPT) central/terminación central (CTS) y un elemento regulador post-transcripcional del virus de la hepatitis de la marmota (WPRE) optimizado. El vector está seudotipado con la glicoproteína G del virus de la estomatitis vesicular (VSV).
El material de leucoaféresis se enriquece en linfocitos T CD4+ y CD8+ mediante inmunoselección positiva antes de la activación con agonistas de CD3 y CD28 en medio de crecimiento que contiene suero humano, interleuquina 7 (IL-7) e interleuquina 5 (IL-5). Las células se transducen a continuación con el vector lentiviral y se expanden en medio de crecimiento que contiene interleuquina 7 (IL-7) e interleuquina 5 (IL-5). La suspensión celular consiste en linfocitos T (≥80%) con más del 10% de los linfocitos T que expresan el transgén del CAR-CD19. Los linfocitos T transducidos muestran citotoxicidad frente a células que expresan CD19 y secretan interferón gamma (IFN-γ) e interleuquina 2 (IL-2)

moflerafuspum alfa #

moflerafusp alfa

human signal regulatory protein alpha (SIRPα) variant V2 D1 domain, (SIRPα V2D1) fragment 30-154 (1-125 in the actual sequence, comprising the first two extracellular loops of the D1 domain) variant (N^{110}>A^{80}) fused via peptide linker ^{126}GGGGSGGGGSGGGGS^{140} to the gamma 1 heavy chain of anti-(human programmed cell death 1 ligand 1 (PD-L1, programmed death ligand 1, PDCD1 ligand 1, B7 homolog 1, B7-H1, CD274)) (141-591) [VH (*Homo sapiens* IGHV1-46*01 -(IGHD) -IGHJ4*01, CDR-Kabat [5.17.12] (171-175.190-206.239-250)) (141-261) -*Homo sapiens* IGHG1*03 (CH1 (262-359), hinge (360-374), CH2 S^{442}>A, E^{477}>A, K^{478}>A (375-484), CH3 (485-589), CHS (590-591)) (262-591)], (364-214')-disulfide with kappa light chain anti-(human programmed cell death 1 ligand 1 (PD-L1, programmed death ligand 1, PDCD1 ligand 1, B7 homolog 1, B7-H1, CD274)) (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 -IGKJ1*01, CDR-Kabat [11.7.9] (24'-34'.50'-56'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (108'-214')]; dimer (370-370'':373-373'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa

moflérafusp alfa

protéine régulatrice de signal alpha (SIRPα) humaine variant V2 domaine D1 (SIRPα V2D1) fragment 30-154 (1-125 dans la séquence réelle, comprenant les deux premières boucles extracellulaires du domaine D1), variant (N^{110}>A^{80}) fusionné, via un coupleur peptidique ^{126}GGGGSGGGGSGGGGS^{140}, à la chaîne lourde gamma 1 de l'anti-(ligand 1 de mort cellulaire programmée 1 humaine (PD-L1, ligand de mort programmée 1, ligand 1 PDCD1, homologue 1 B7, B7-H1, CD274)) (141-591) [VH (*Homo sapiens* IGHV1-46*01 -(IGHD) -IGHJ4*01, CDR-Kabat [5.17.12] (171-175.190-206.239-250)) (141-261) -*Homo sapiens* IGHG1*03 (CH1 (262-359), charnière (360-374), CH2 S^{442}>A, E^{477}>A, K^{478}>A (375-484), CH3 (485-589), CHS (590-591)) (262-591)], (364-214')-disulfure avec la chaîne légère

kappa anti-(ligand 1 de mort cellulaire programmée 1 humaine (PD-L1, ligand de mort programmée 1, ligand 1 PDCD1, homologue B7 1, B7-H1, CD274)) (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 -IGKJ1*01, CDR-Kabat [11.7.9] (24'-34'.50'-56'.89'-97')) (1'- 107') -*Homo sapiens* IGKC*01 (108'-214')]; dimère (370-370'':373-373'')-bisdisulfure, produit dans les cellules d'ovaire de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa

moflerafusp alfa

proteína reguladora de señales alfa humana (SIRPα) variante V2 dominio D1 (SIRPα V2D1) fragmento 30-154 (1-125 en la secuencia real, que comprende los dos primeros bucles extracelulares del dominio D1) variante (N110>A80) fusionado mediante un enlazador peptídico ^{126}GGGGSGGGGSGGGGS^{140} a la cadena pesada gamma 1 de anti-(ligando 1 de muerte celular programada 1 humana (PD-L1, ligando 1 de muerte programada, ligando 1 de PDCD1, homólogo 1 de B7, B7-H1, CD274)) (141-591) [VH (*Homo sapiens* IGHV1-46*01 -(IGHD) -IGHJ4*01, CDR-Kabat [5.17.12] (171-175.190-206.239-250)) (141-261) -*Homo sapiens* IGHG1*03 (CH1 (262-359)), bisagra (360-374), CH2 S^{442}>A, E^{477}>A, K^{478}>A (375-484), CH3 (485-589), CHS (590-591)) (262-591)], (364-214')-disulfuro con cadena ligera kappa anti-(ligando 1 de muerte celular programada 1 humana (PD-L1, ligando 1 de muerte programada, ligando 1 de PDCD1, homólogo 1 de B7, B7-H1, CD274)) (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 -IGKJ1*01, CDR-Kabat [11.7.9] (24'-34'.50'-56'.89'-97')) (1'- 107') -*Homo sapiens* IGKC*01 (108'-214')]; dímero (370-370'':373-373'')-bisdisulfuro, producido en células de ovario 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 VVSGPGGGGS GGGGSGGGGS QVQLVQSGAE  150
VKKPGASVKV SCKASGYTFT SNWMHWVRQA PGQGLEWMGM IHPNSGSSNY  200
NEKFKSRVTM TRDTSTSTVY MELSSLRSED TAVYYCARSY YGSSPYYFDY  250
WGQGTLVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV KDYFPEPVTV  300
SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ TYICNVNHKP  350
SNTKVDKRVE PKSCDKTHTC PPCPAPELLG GPSVFLFPPK PKDTLMISRT  400
PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY NATYRVVSVL  450
TVLHQDWLNG KEYKCKVSNK ALPAPIAATI SKAKGQPREP QVYTLPPSRE  500
EMTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP VLDSDGSFFL  550
YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG K           591
```

IgG1 light chain

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

Mutations / Mutations / Mutaciónes
SIRPα - IgG1 heavy chain: N^{110}>**A**^{80}, S^{442}>**A**, E^{477}>**A**, K^{478}>**A**

Peptide linker / Coupleur peptidique / Enlazador peptídico
^{126}*GGGGSGGGGSGGGGS*^{140}

Post-translation modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra SIRPα-IgG1 heavy chain: 25-91, 162-236, 288-344, 405-465, 511-569,
25''-91'', 162''-236'', 288''-344'', 405''-465'', 511''-569''
Intra IgG1 light chain: 23'-88', 134'-194', 23'''-88''', 134'''-194'''
Inter IgG1 light chain - SIRPα-IgG1 heavy chain: 214'-364, 214'''-364''
Inter SIRPα-IgG1 heavy chain: 370-370'', 373-373''

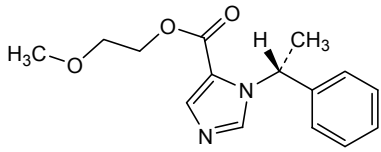
N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
SIRPα-IgG1 heavy chain: 441, 441''

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
SIRPα-IgG1 heavy chain: K591, K591''

moxetomidatum

moxetomidate	2-methoxyethyl 1-[(1*R*)-1-phenylethyl]-1*H*-imidazole-5-carboxylate
moxétomidate	1-[(1*R*)-1-phényléthyl]-1*H*-imidazole-5-carboxylate de 2-méthoxyéthyle
moxetomidato	1-[(1*R*)-1-feniletil]-1*H*-imidazol-5-carboxilato de 2-metoxietilo

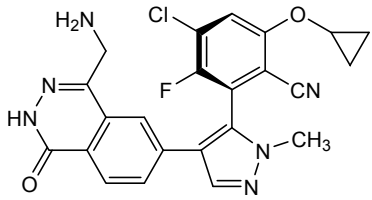
$C_{15}H_{18}N_2O_3$



navlimetostatum

navlimetostat	(2*M*)-2-{4-[4-(aminomethyl)-1-oxo-1,2-dihydrophthalazin-6-yl]-1-methyl-1*H*-pyrazol-5-yl}-4-chloro-6-(cyclopropyloxy)-3-fluorobenzonitrile
navlimétostat	(2*M*)-2-{4-[4-(aminométhyl)-1-oxo-1,2-dihydrophtalazin-6-yl]-1-méthyl-1*H*-pyrazol-5-yl}-4-chloro-6-(cyclopropyloxy)-3-fluorobenzonitrile
navlimetostat	(2*M*)-2-{4-[4-(aminometil)-1-oxo-1,2-dihidroftalazin-6-il]-1-metil-1*H*-pirazol-5-il}-4-cloro-6-(ciclopropiloxi)-3-fluorobenzonitrilo

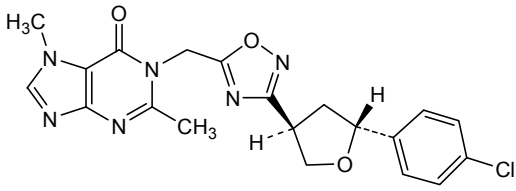
$C_{23}H_{18}ClFN_6O_2$



nedizantrepum

nedizantrep	1-({3-[(3*R*,5*R*)-5-(4-chlorophenyl)oxolan-3-yl]-1,2,4-oxadiazol-5-yl}methyl)-2,7-dimethyl-1,7-dihydro-6*H*-purin-6-one
nédizantrep	1-({3-[(3*R*,5*R*)-5-(4-chlorophényl)oxolan-3-yl]-1,2,4-oxadiazol-5-yl}méthyl)-2,7-diméthyl-1,7-dihydro-6*H*-purin-6-one
nedizantrep	1-({3-[(3*R*,5*R*)-5-(4-clorofenil)oxolan-3-il]-1,2,4-oxadiazol-5-il}metil)-2,7-dimetil-1,7-dihidro-6*H*-purin-6-ona

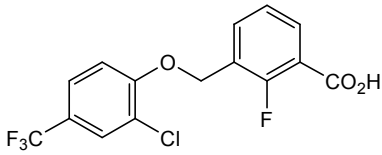
$C_{20}H_{19}ClN_6O_3$



nelremagpranum

nelremagpran	3-{[2-chloro-4-(trifluoromethyl)phenoxy]methyl}-2-fluorobenzoic acid
nelrémagpran	acide 3-{[2-chloro-4-(trifluorométhyl)phénoxy]méthyl}-2-fluorobenzoïque
nelremagprán	ácido 3-{[2-cloro-4-(trifluorometil)fenoxi]metil}-2-fluorobenzoico

$C_{15}H_9ClF_4O_3$



nesfrotamigum #

nesfrotamig	immunoglobulin (H-gamma1-scFvlh_L-kappa) dimer, anti-[*Homo sapiens* ERBB2 (receptor tyrosine-protein kinase erbB-2, epidermal growth factor receptor 2, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)] and anti-[*Homo sapiens* TNFRSF9 (TNF receptor superfamily member 9, 4-1BB, T cell antigen ILA, CD137)], humanized and *Homo sapiens* monoclonal antibody; bispecific, tetravalent; H-gamma1 heavy chain anti-ERBB2 fused to a scFvlh anti-TNFRSF9 (1-719) [H-gamma1 heavy chain anti-ERBB2 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 (100%) 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)] -18-mer nonakis(glycyl-seryl) linker (451-468) -scFvlh anti-TNFRSF9 *Homo sapiens* (469-719), 11-scFv-v2 C120 (VL)-C49 (VH) [V-LAMBDA (*Homo sapiens* IGLV1-47*02 (91.8%) -IGLJ2*01 (90.9%) VL G120>C (571), CDR-IMGT [8.3.11] (493-501.519-521.558-568)) (469-578) -20-mer tetrakis(tetraglycyl-seryl) linker (579-598) -VH (*Homo sapiens* IGHV3-23*01 (93.9%) -IGHD -IGHJ4*01 (100%) VH G49>C (642), CDR-IMGT [8.8.14] (624-631.649-656.695-708)) (599-719)]]; (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, V101 (C-KAPPA 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-K1, lacking the glutamine synthetase (GS-KO) gene, glycoform alfa

nesfrotamig	immunoglobuline (H-gamma1-scFvlh_L-kappa) dimère, 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)] et anti-[*Homo sapiens* TNFRSF9 (membre 9 de la superfamille des récepteurs du TNF, 4-1BB, antigène ILA des cellules T, CD137)], anticorps monoclonal humanisé et *Homo sapiens*; bispécifique, tétravalent; chaîne lourde H-gamma1 anti-ERBB2 fusionnée à un scFvlh anti-TNFRSF9 (1-719) [H-gamma1 chaîne lourde anti-ERBB2 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 (100%) 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)] -18-mer nonakis(glycyl-séryl) linker (451-468) -scFvlh anti-TNFRSF9 *Homo sapiens* (469-719), 11-scFv-v2 C120 (VL)-C49 (VH) [V-LAMBDA (*Homo sapiens* IGLV1-47*02 (91.8%) -IGLJ2*01 (90.9%) VL G120>C (571), CDR-IMGT [8.3.11] (493-501.519-521.558-568)) (469-578) -20-mer tétrakis(tétraglycyl-séryl) linker (579-598) -VH (*Homo sapiens* IGHV3-23*01 (93.9%) -IGHD -IGHJ4*01 (100%) VH G49>C (642), CDR-IMGT [8.8.14] (624-631.649-656.695-708)) (599-719)]]; (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, V101 (C-KAPPA 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-K1, ne présentant pas le gène de la glutamine synthétase (GS-KO), glycoforme alfa
nesfrotamig	inmunoglobulina (H-gamma1-scFvlh_L-kappa) dímero, 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)] y anti-[*Homo sapiens* TNFRSF9 (miembro 9 de la superfamilia de los receptores del TNF, 4-1BB, antígeno ILA de las células, CD137)], anticuerpo monoclonal humanizado y *Homo sapiens*; biespecífico, tetravalente; cadena pesada H-gamma1 anti-ERBB2 fusionada con un scFvlh anti-TNFRSF9 (1-719) [H-gamma1 cadena pesada anti-ERBB2 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 (100%) 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)] -18-mer nonakis(glicil-seril) enlace (451-468) -scFvlh anti-TNFRSF9 *Homo sapiens* (469-719), 11-scFv-v2 C120 (VL)-C49 (VH) [V-LAMBDA (*Homo sapiens* IGLV1-47*02 (91.8%) -IGLJ2*01 (90.9%) VL G120>C (571), CDR-IMGT [8.3.11] (493-501.519-521.558-568)) (469-578) -20-mer tetrakis(tetraglicil-seril)

enlace(579-598) -VH (*Homo sapiens* IGHV3-23*01 (93.9%) -IGHD -IGHJ4*01 (100%) VH G49>C (642), CDR-IMGT [8.8.14] (624-631.649-656.695-708)) (599-719)]]; (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, V101 (C-KAPPA 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-K1, en ausencia del gen glutamina sintetasa (GS-KO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada: fused H-gamma1 anti-ERBB2 -scFvlh anti-TNFRSF9 (H, H'')

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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
GSGSGSGSGS GSGSGSGSQS VLTQPPSASG TPGQRVTISC SGSSSNIGNN 500
YVTWYQQLPG TAPKLLIYAD SHRPSGVPDR FSGSKSGTSA SLAISGLRSE 550
DEADYYCATW DYSLSGYVFG CGTKLTVLGG GGSGGGGSGG GGSGGGGSEV 600
QLLESGGGLV QPGGSLRLSC AASGFTFSSY DMSWVRQAPG KCLEWVSWIS 650
YSGGSIYYAD SVKGRFTISR DNSKNTLYLQ MNSLRAEDTA VYYCARDAQR 700
NSMREFDYWG QGTLVTVSS                                   719
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Light chain / Chaîne légère / Cadena ligera: L-kappa (L', L'")

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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
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Post-translational modifications

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

Intra-H (C23-C104) 22-96 147-203 264-324 370-428
22"-96" 147"-203" 264"-324" 370"-428"
490-557 620-694
490"-557" 620"-694"

Intra-H scFv C120 (VL)-C49 (VH)* 571-642
571"-642"

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"

*engineered additional disulfide bond C120 (VL)-C49 (VH) to stabilize the scFv (variant 11-scFv-v2).

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

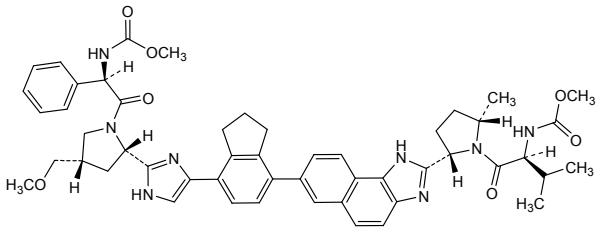
H CH2 N84.4: 300, 300"

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

netanasvirum

netanasvir	methyl {(2*S*)-1-[(1^{2}*S*,1^{5}*S*,5^{2}*S*,5^{4}*S*,7*R*)-7-[(methoxycarbonyl)amino]-5^{4}-(methoxymethyl)-1^{5}-methyl-6-oxo-3^{2},3^{3}-dihydro-2^{1}*H*,3^{1}*H*,4^{1}*H*-2(2,7)-naphtho[1,2-*d*]imidazola-4(4,2)-imidazola-1(2),5(2,1)-dipyrrolidina-3(4,7)-indena-8(1)-benzenaoctaphan-1^{1}-yl]-3-methyl-1-oxobutan-2-yl}carbamate
nétanasvir	{(2*S*)-1-[(1^{2}*S*,1^{5}*S*,5^{2}*S*,5^{4}*S*,7*R*)-7-[(méthoxycarbonyl)amino]-5^{4}-(méthoxyméthyl)-1^{5}-méthyl-6-oxo-3^{2},3^{3}-dihydro-2^{1}*H*,3^{1}*H*,4^{1}*H*-2(2,7)-naphto[1,2-*d*]imidazola-4(4,2)-imidazola-1(2),5(2,1)-dipyrrolidina-3(4,7)-indéna-8(1)-benzénaoctaphan-1^{1}-yl]-3-méthyl-1-oxobutan-2-yl}carbamate de méthyle
netanasvir	{(2*S*)-3-metil-1-[(1^{2}*S*,1^{5}*S*,5^{2}*S*,5^{4}*S*,7*R*)-1^{5}-metil-7-[(metoxicarbonil)amino]-5^{4}-(metoximetil)-6-oxo-3^{2},3^{3}-dihidro-2^{1}*H*,3^{1}*H*,4^{1}*H*-2(2,7)-nafto[1,2-*d*]imidazola-4(4,2)-imidazola-1(2),5(2,1)-dipirrolidina-3(4,7)-indena-8(1)-bencenaoctafan-1^{1}-il]-1-oxobutan-2-il}carbamato de metilo

$C_{51}H_{58}N_8O_7$



nivudirsenum

nivudirsen — *all-P-ambo*-5'-*O*-(1,10-dihydroxy-1-oxo-2,5,8-trioxa-1λ^5-phosphadecan-1-yl)-2'-*O*,4'-*C*-methylene-*P*-thioguanylyl-(3'→5')-2'-*O*,4'-*C*-methylene-*P*-thioguanylyl-(3'→5')-2'-*O*-methyl-*P*-thiouridylyl-(3'→5')-2'-*O*-methyl-*P*-thioadenylyl-(3'→5')-2'-*O*-methyl-*P*-thioadenylyl-(3'→5')-2'-*O*,4'-*C*-methylene-*P*-thioguanylyl-(3'→5')-2'-*O*-methyl-*P*-thiouridylyl-(3'→5')-2'-*O*-methyl-*P*-thiouridylyl-(3'→5')-2'-*O*,5-dimethyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-methyl-*P*-thiouridylyl-(3'→5')-2'-*O*-methyl-*P*-thioguanylyl-(3'→5')-2'-*O*-methyl-*P*-thiouridylyl-(3'→5')-2'-*O*,5-dimethyl-*P*-thiocytidylyl-(3'→5')-2'-*O*,5-dimethyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-methyl-*P*-thioadenylyl-(3'→5')-2'-*O*-methyl-*P*-thioadenylyl-(3'→5')-2'-*O*-methyl-*P*-thioguanylyl-(3'→5')-5-methyl-2'-*O*,4'-*C*-methylenecytidine

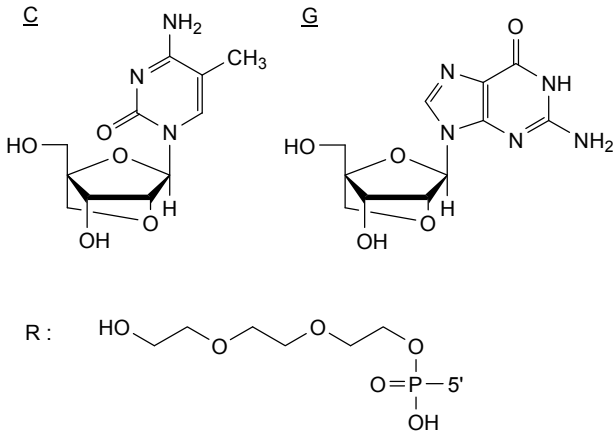
nivudirsen — *tout-P-ambo*-5'-*O*-(1,10-dihydroxy-1-oxo-2,5,8-trioxa-1λ^5-phosphadécan-1-yl)-2'-*O*,4'-*C*-méthylène-*P*-thioguanylyl-(3'→5')-2'-*O*,4'-*C*-méthylène-*P*-thioguanylyl-(3'→5')-2'-*O*-méthyl-*P*-thiouridylyl-(3'→5')-2'-*O*-méthyl-*P*-thioadénylyl-(3'→5')-2'-*O*-méthyl-*P*-thioadénylyl-(3'→5')-2'-*O*,4'-*C*-méthylène-*P*-thioguanylyl-(3'→5')-2'-*O*-méthyl-*P*-thiouridylyl-(3'→5')-2'-*O*-méthyl-*P*-thiouridylyl-(3'→5')-2'-*O*,5-diméthyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-méthyl-*P*-thiouridylyl-(3'→5')-2'-*O*-méthyl-*P*-thioguanylyl-(3'→5')-2'-*O*-méthyl-*P*-thiouridylyl-(3'→5')-2'-*O*,5-diméthyl-*P*-thiocytidylyl-(3'→5')-2'-*O*,5-diméthyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-méthyl-*P*-thioadénylyl-(3'→5')-2'-*O*-méthyl-*P*-thioadénylyl-(3'→5')-2'-*O*-méthyl-*P*-thioguanylyl-(3'→5')-5-méthyl-2'-*O*,4'-*C*-méthylènecytidine

nivudirsén — *todo-P-ambo*-5'-*O*-(1,10-dihidroxi-1-oxo-2,5,8-trioxa-1λ^5-fosfadecan-1-il)-2'-*O*,4'-*C*-metileno-*P*-tioguanilil-(3'→5')-2'-*O*,4'-*C*-metileno-*P*-tioguanilil-(3'→5')-2'-*O*-metil-*P*-tiouridilil-(3'→5')-2'-*O*-metil-*P*-tioadenilil-(3'→5')-2'-*O*-metil-*P*-tioadenilil-(3'→5')-2'-*O*,4'-*C*-metileno-*P*-tioguanilil-(3'→5')-2'-*O*-metil-*P*-tiouridilil-(3'→5')-2'-*O*-metil-*P*-tiouridilil-(3'→5')-2'-*O*,5-dimetil-*P*-tiocitidilil-(3'→5')-2'-*O*-metil-*P*-tiouridilil-(3'→5')-2'-*O*-metil-*P*-tioguanilil-(3'→5')-2'-*O*-metil-*P*-tiouridilil-(3'→5')-2'-*O*,5-dimetil-*P*-tiocitidilil-(3'→5')-2'-*O*,5-dimetil-*P*-tiocitidilil-(3'→5')-2'-*O*-metil-*P*-tioadenilil-(3'→5')-2'-*O*-metil-*P*-tioadenilil-(3'→5')-2'-*O*-metil-*P*-tioguanilil-(3'→5')-5-metil-2'-*O*,4'-*C*-metilenocitidina

$C_{199}H_{261}N_{67}O_{114}P_{18}S_{17}$

R-G=G=U=A=A=G=U=U=m^{5}C=U=G=U=m^{5}C=m^{5}C=A=A=G=C

N: 2'-*O*-methyl-N / 2'-*O*-méthyl-N / 2'-*O*-metil-N
m^{5}N : 5-methyl-N / 5-méthyl-N / 5-metil-N
- : -PO(OH)- = : -PO(SH)-



nufaleucelum

nufaleucel — human culture expanded activated autologous tumour-infiltrating lymphocytes (TIL), isolated from non-small cell lung cancer. The cells are mechanically isolated from resected tumour biopsies and culture-expanded using a two-step protocol consisting of a pre rapid expansion phase (Pre-REP) and a rapid expansion phase (REP) in serum-free media containing interleukin 2 (IL-2). During the REP, the cells are activated and expanded by culture on colloidal polymeric nanomatrix conjugated to humanized CD3 and CD28 agonists in media containing IL-2 in the absence of allogeneic irradiated feeder cells. The T lymphocytes (>80%) are a heterogeneous mixture of CD4+ and CD8+ T lymphocytes, predominantly with effector memory, central memory and effector cell subsets, and a low level of CD45+CD3-CD56+ natural killer (NK) cells (<10%). The T-lymphocytes demonstrate IFN-γ release (>1.0 fg/cell) after CD3/CD28 bead stimulation

nufaleucel — lymphocytes infiltrant la tumeur (LIT) autologues humains, activés et expansés en culture, isolés à partir du cancer du poumon non à petites cellules. Les cellules sont isolées mécaniquement à partir de biopsies tumorales réséquées et expansées en culture à l'aide d'un protocole en deux étapes comprenant une phase de pré-expansion rapide (Pre-REP) et une phase d'expansion rapide (REP) dans un milieu sans sérum contenant de l'interleukine 2 (IL-2). Au cours du REP, les cellules sont activées et expansées par culture sur nanomatrice polymère colloïdale conjuguée à des agonistes CD3 et CD28 humanisés, dans un milieu contenant de l'IL-2, en l'absence de cellules nourricières allogéniques irradiées. Les lymphocytes T (>80%) sont un mélange hétérogène de lymphocytes T CD4+ et

CD8+, avec principalement des sous-types de cellules effectrices à mémoire, de mémoire centrale et de cellules effectrices, et d'un faible niveau de cellules tueuses naturelles (NK) CD45+CD3-CD56+ (<10%). Les lymphocytes T démontrent une libération d'IFN-γ (>1.0 fg/cellule) après stimulation par billes CD3/CD28

nufaleucel — linfocitos infiltrantes de tumor (TIL) humanos autólogos activados y expandidos en cultivo, aislados de cáncer de pulmón de células no microcíticas. Las células se aíslan mecánicamente de biopsias de tumor resecado y se expanden en cultivo usando un protocolo de dos etapas que consiste en una pre fase de expansión rápida (Pre-REP) y una fase de expansión rápida (REP) en medio sin suero que contiene interleuquina 2 (IL-2). Durante la REP, las células se activan y expanden mediante cultivo en una nanomatriz polimérica coloidal conjugada con agonistas humanizados de CD3 y CD28 en medio que contiene IL-2 en ausencia de células alimentadoras irradiadas alogénicas. Los linfocitos T (>80%) son una mezcla heterogénea de linfocitos T CD4+ y CD8+, predominantemente con subtipos de células de memoria efectora, memoria central y efectoras, y un bajo nivel (<10%) de células natural killer (NK) CD45+CD3-CD56+. Los linfocitos T muestran liberación de IFN-γ (>1.0 fg/célula) tras la estimulación con bolas CD3/CD28

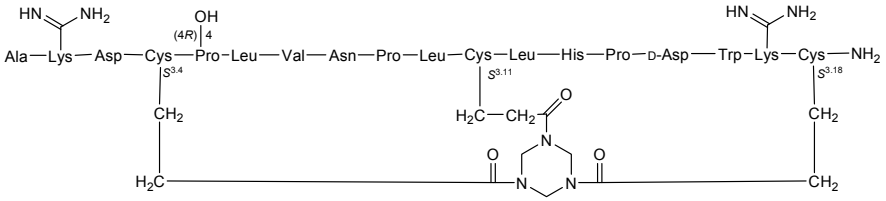
nuzefatidum

nuzefatide — *S*$^{3.4}$,*S*$^{3.11}$,*S*$^{3.18}$-[(1,3,5-triazinane-1,3,5-triyl)tris(3-oxopropane-3,1-diyl)][L-alanyl-*N*^{6}-carbamimidoyl-L-lysyl-L-α-aspartyl-L-cysteinyl-(4*R*)-4-hydroxy-L-prolyl-L-leucyl-L-valyl-L-asparaginyl-L-prolyl-L-leucyl-L-cysteinyl-L-leucyl-L-histidyl-L-prolyl-D-α-aspartyl-L-tryptophyl-*N*^{6}-carbamimidoyl-L-lysyl-L-cysteinamide]

nuzéfatide — *S*$^{3.4}$,*S*$^{3.11}$,*S*$^{3.18}$-[(1,3,5-triazinane-1,3,5-triyl)tris(3-oxopropane-3,1-diyl)][L-alanyl-*N*^{6}-carbamimidoyl-L-lysyl-L-α-aspartyl-L-cystéinyl-(4*R*)-4-hydroxy-L-prolyl-L-leucyl-L-valyl-L-asparaginyl-L-prolyl-L-leucyl-L-cystéinyl-L-leucyl-L-histidyl-L-prolyl-D-α-aspartyl-L-tryptophyl-*N*^{6}-carbamimidoyl-L-lysyl-L-cystéinamide]

nuzefatida — *S*$^{3.4}$,*S*$^{3.11}$,*S*$^{3.18}$-[(1,3,5-triazinano-1,3,5-triil)tris(3-oxopropano-3,1-diil)][L-alanil-*N*^{6}-carbamimidoil-L-lisil-L-α-aspartil-L-cysteinil-(4*R*)-4-hidroxi-L-prolil-L-leucil-L-valil-L-asparaginil-L-prolil-L-leucil-L-cisteinil-L-leucil-L-histidil-L-prolil-D-α-aspartil-L-triptofil-*N*^{6}-carbamimidoil-L-lisil-L-cisteinamida]

$C_{105}H_{162}N_{32}O_{27}S_3$



nuzefatidum pevedotinum

nuzefatide pevedotin

S$^{3.15}$,*S*$^{3.22}$,*S*$^{3.29}$-[(1,3,5-triazinane-1,3,5-triyl)tris(3-oxopropane-3,1-diyl)]{*N*-[5-oxo-5-({L-valyl-*N*^{5}-carbamoyl-L-ornithyl[(4-aminophenyl)methoxy]carbonyl-*N*-methyl-L-valyl-L-valyl-(3*R*,4*S*,5*S*)-3-methoxy-5-methyl-4-(methylamino)heptanoyl-(2*R*,3*R*)-*N*-[(1*S*,2*R*)-1-hydroxy-1-phenylpropan-2-yl]-3-methoxy-2-methyl-3-[(2*S*)-pyrrolidin-2-yl]propanamide}-*N*$^{2.1}$-yl)pentanoyl]-β-alanyldecakis(*N*-methylglycyl)-L-alanyl-*N*^{6}-carbamimidoyl-L-lysyl-L-α-aspartyl-L-cysteinyl-(4*R*)-4-hydroxy-L-prolyl-L-leucyl-L-valyl-L-asparaginyl-L-prolyl-L-leucyl-L-cysteinyl-L-leucyl-L-histidyl-L-prolyl-D-α-aspartyl-L-tryptophyl-*N*^{6}-carbamimidoyl-L-lysyl-L-cysteinamide}

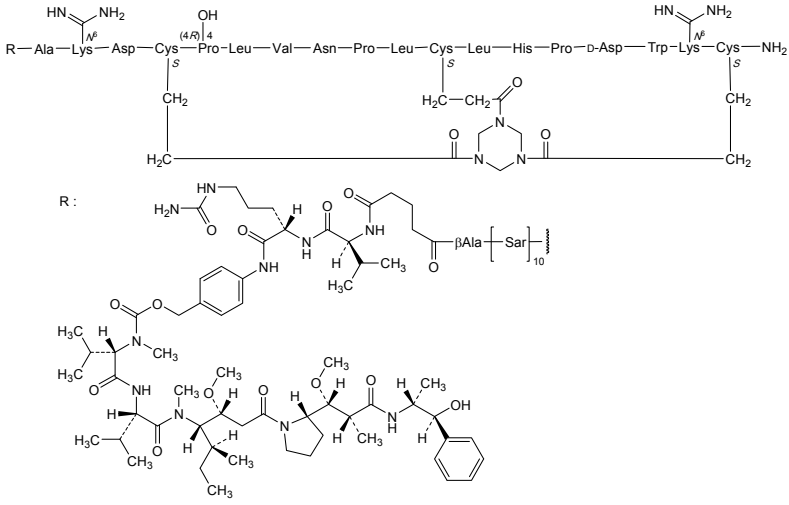
nuzéfatide pévédotine

S$^{3.15}$,*S*$^{3.22}$,*S*$^{3.29}$-[(1,3,5-triazinane-1,3,5-triyl)tris(3-oxopropane-3,1-diyl)]{*N*-[5-oxo-5-({L-valyl-*N*^{5}-carbamoyl-L-ornithyl[(4-aminophényl)méthoxy]carbonyl-*N*-méthyl-L-valyl-L-valyl-(3*R*,4*S*,5*S*)-3-méthoxy-5-méthyl-4-(méthylamino)heptanoyl-(2*R*,3*R*)-*N*-[(1*S*,2*R*)-1-hydroxy-1-phénylpropan-2-yl]-3-méthoxy-2-méthyl-3-[(2*S*)-pyrrolidin-2-yl]propanamide}-*N*$^{2.1}$-yl)pentanoyl]-β-alanyldécakis(*N*-méthylglycyl)-L-alanyl-*N*^{6}-carbamimidoyl-L-lysyl-L-α-aspartyl-L-cystéinyl-(4*R*)-4-hydroxy-L-prolyl-L-leucyl-L-valyl-L-asparaginyl-L-prolyl-L-leucyl-L-cystéinyl-L-leucyl-L-histidyl-L-prolyl-D-α-aspartyl-L-tryptophyl-*N*^{6}-carbamimidoyl-L-lysyl-L-cystéinamide}

nuzefatida pevedotina

S$^{3.15}$,*S*$^{3.22}$,*S*$^{3.29}$-[(1,3,5-triazinane-1,3,5-triil)tris(3-oxopropane-3,1-diil)]{*N*-[5-oxo-5-({L-valil-*N*^{5}-carbamoil-L-ornitil[(4-aminofenil)metoxi]carbonil-*N*-metil-L-valil-L-valil-(3*R*,4*S*,5*S*)-5-metil-4-(metilamino)-3-metoxiheptanoil-(2*R*,3*R*)-*N*-[(1*S*,2*R*)-1-fenil-1-hidroxipropan-2-il]-2-metil-3-metoxi-3-[(2*S*)-pirrolidin-2-il]propanamida}-*N*$^{2.1}$-il)pentanoil]-β-alanildecakis(*N*-metilglicil)-L-alanil-*N*^{6}-carbamimidoil-L-lisil-L-α-aspartil-L-cisteinil-(4*R*)-4-hidroxi-L-prolil-L-leucil-L-valil-L-asparaginil-L-prolil-L-leucil-L-cisteinil-L-leucil-L-histidil-L-prolil-D-α-aspartil-L-triptofil-*N*^{6}-carbamimidoil-L-lisil-L-cisteinamida}

$C_{201}H_{315}N_{53}O_{52}S_3$



obudanersenum

obudanersen

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

obudanersen

tout-P-ambo-2'-*O*-(2-méthoxyéthyl)-*P*-thioadénylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthylcytidylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthylcytidylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)adénylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthyluridylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-désoxy-*P*-thioguanylyl-(3'→5')-2'-désoxy-*P*-thioadénylyl-(3'→5')-2'-désoxy-5-méthyl-*P*-thiocytidylyl-(3'→5')-2'-désoxy-5-méthyl-*P*-thiocytidylyl-(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)-5-méthyluridylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-*P*-thioadénylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-*P*-thioguanylyl-(3'→5')-2'-*O*-(2-méthoxyéthyl)-5-méthylcytidine

obudanersén

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

$C_{230}H_{321}N_{64}O_{129}P_{19}S_{13}$

(3'-5') A=*C*–*C*–A–*U*–dT=dT=dT=dG=dA=d*C*=d*C*=dT=dT=d*C*=*U*–*U*–A=G=*C*

N : nucleoside / nucléoside / nucleósido
dN : 2'-deoxy-N / 2'-désoxy-N / 2'-desoxi-N
N : 5-methyl-N / 5-méthyl-N / 5-metil-N
N : 2'-*O*-(2-methoxyethyl)-N / 2'-*O*-(2-méthoxyéthyl)-N / 2'-*O*-(metoxietil)-N
- : -PO(OH)- = : -PO(SH)-

olisutrigini bromidum

olisutrigine bromide

(2*R*)-2-{2-[*N*-(2,3-dihydro-1*H*-inden-2-yl)-2-methylanilino]ethyl}-1,1-dimethylpiperidin-1-ium bromide

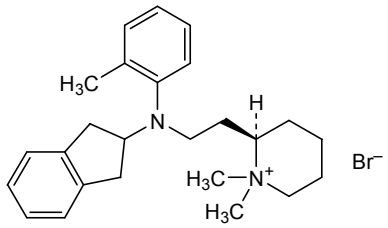
bromure d'olisutrigine

bromure de (2*R*)-2-{2-[*N*-(2,3-dihydro-1*H*-indén-2-yl)-2-méthylanilino]éthyl}-1,1-diméthylpipéridin-1-ium

bromuro de olisutrigina

bromuro de (2*R*)-2-{2-[*N*-(2,3-dihidro-1*H*-inden-2-il)-2-metilanilino]etil}-1,1-dimetilpiperidin-1-io

$C_{25}H_{35}BrN_2$



olmocabtagenum autoleucelum #

olmocabtagene autoleucel — autologous CD4+/CD8+ enriched T lymphocytes obtained by leukapheresis, transduced with a self-inactivating, non-replicating gamma Moloney murine leukemia virus (MMLV) vector encoding a chimeric antigen receptor (CAR) targeting claudin 6 (CLDN6), composed of a human IgG heavy chain signal peptide, a single chain variable fragment (scFv; IMAB206-C46S), a CD8 hinge and transmembrane domain, and a 4-1BB co-stimulatory and CD3ζ intracellular signalling domain, under control of the elongation factor 1 alpha short (EFS) promoter. The vector also contains an MMLV psi-region, an enlarged MMLV psi+ packaging region, a Kozak sequence, and a truncated version of the post-transcriptional regulatory element of the Woodchuck hepatitis virus (WPRE); flanked by 5' and 3' MMLV wildtype long terminal repeats (LTRs). The vector is pseudotyped with gibbon ape leukemia virus (GALV) 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 retroviral vector. The cells are then expanded in media with interleukin 15 (IL-15) and interleukin 7 (IL-7). The T lymphocytes (≥80%; with ≤20% CD3-cells) are positive for the transgene (≥10% CAR positive) and secrete interferon gamma in response to CLDN6 expressing target cells

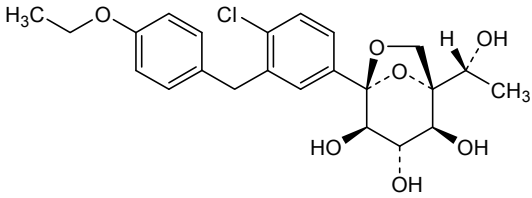
olmocabtagène autoleucel — lymphocytes T autologues enrichis en CD4+/CD8+ obtenus par leucaphérèse, transduits avec un vecteur du virus de la leucémie murine gamma de Moloney (MMLV) auto-inactivant et non réplicatif codant pour un récepteur antigénique chimérique (RAC) ciblant claudine 6 (CLDN6) composé d'un peptide signal de chaîne lourde d'IgG humaine, d'un fragment variable à chaîne unique (scFv; IMAB206-C46S), d'un domaine charnière et transmembranaire CD8 et de domaines de co-stimulation 4-1BB et de signalisation intracellulaire CD3ζ, sous le contrôle du promoteur facteur d'élongation 1 alpha court (EFS). Le vecteur contient également une région ψ de MMLV, une région d'emballage ψ+ élargie de MMLV, une séquence Kozak et une version tronquée de l'élément régulateur post-transcriptionnel du virus de l'hépatite de la marmotte (WPRE); flanqué de répétitions terminales longues (LTRs) de MMLV de type sauvage en 5' et en 3'. Le vecteur est pseudotypé avec la protéine d'enveloppe du virus de la leucémie du singe gibbon (GALV).
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 rétroviral. Les cellules sont ensuite éxpansées dans un milieu contenant de

	l'interleukine 15 (IL-15) et de l'interleukine 7 (IL-7). Les lymphocytes T (≥80%; avec ≤20% de cellules CD3-) sont positifs pour le transgène (≥10% RAC positifs) et sécrètent de l'interféron gamma en réponse aux cellules cibles exprimant CLDN6
olmocabtagén autoleucel	linfocitos T CD4+/CD8+ autólogos enriquecidos, obtenidos por leucoaféresis, transducidos con un vector del virus gamma de la leucemia de Moloney murino (MMLV) auto-inactivante, no replicativo, que codifica un receptor de antígenos quimérico (CAR) anti-claudina 6 (CLDN6), compuesto por un péptido señal de la cadena pesada de la IgG humana, un fragmento variable de cadena sencilla (scFv; IMAB206-C46S), un dominio bisagra y transmembrana de CD8, y dominios intracelulares coestimulador de 4-1BB y señalización de CD3ζ, bajo el control del promotor corto del factor de elongación 1 alfa (EFS). El vector también contiene una región psi de MMLV, una región alargada de empaquetamiento psi+ de MMLV, una secuencia Kozak y una versión truncada del elemento regulador post-transcripcionaldel virus de la hepatitis de la marmota (WPRE); flanqueado por repeticiones terminales largas (LTRs) de tipo salvaje del MMLV en 5' y 3'. El vector está seudotipado con la proteína de la envuelta del virus de la leucemia del Gibón (GALV). El material de leucoaféresis se enriquece en linfocitos T CD4+/CD8+ mediante inmunoselección positiva, se activa con agonistas de CD3 y CD28 y se transduce con el vector retroviral. Las células se expanden después en medio con interleuquina 15 (IL-15) e interleuquina 7 (IL-7). Los linfocitos T (≥80%; con ≤20% de células CD3-) son positivos para el transgén (≥10% CAR positivos) y secretan interferón gamma en respuesta a células diana que expresan CLDN6

oloriglíflozinum

oloriglíflozin	1-*C*-{4-chloro-3-[(4-ethoxyphenyl)methyl]phenyl}-1-*O*,5-*C*-methylene-D-*glycero*-α-D-*gluco*-heptopyranose
oloriglíflozine	1-*C*-{4-chloro-3-[(4-éthoxyphényl)méthyl]phényl}-1-*O*,5-*C*-méthylène-D-*glycéro*-α-D-*gluco*-heptopyranose
oloriglíflozina	1-*C*-{4-cloro-3-[(4-etoxifenil)metil]fenil}-1-*O*,5-*C*-metileno-D-*glicero*-α-D-*gluco*-heptopiranosa

$C_{23}H_{27}ClO_7$



ompekimigum #
ompekimig

immunoglobulin (L-kappa-H-gamma1(_L-VH-G1(CH1-h))_L-kappa)_(H-gamma1_L-kappa), anti-[*Homo sapiens* IL4 (interleukin 4, IL-4)], anti-[*Homo sapiens* IL13 (interleukin 13, IL-13)] and anti-[*Homo sapiens* IL33 (interleukin 33, IL-33)], monoclonal antibody, trispecific, trivalent;
fused L-kappa-H-gamma1 chain anti-IL13 and anti-IL4 (1-674) [L-kappa anti-IL13 (1-218) [V-KAPPA (*Homo sapiens* IGKV1-39*01 (82.8%) -IGKJ4*01 (100%), CDR-IMGT [10.3.9] (27-36.54-56.93-101)) (1-111) -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (157), V101 (195)) (112-218)] -5-mer (tetraglycyl-seryl) linker (219-223) -H-gamma1 heavy chain anti-IL4 (224-674) [VH (*Homo sapiens* IGHV2-5*08 (87.0%) -(IGHD) -IGHJ3*01 (92.9%) M123>T (339), CDR-IMGT [10.7.13] (249-258.276-282.321-333)) (224-344) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, CH1 K120, CH3 E12, M14, 6-G1v14-1 CH2 A1.3, A1.2, A1, 9-G1v24 CH3 L107, S114, 14-G1v99-1 hinge E6, CH3 E24 (CH1 R120>K (441) (345-442), hinge 1-15 D6>E (448) (443-457), CH2 L1.3>A (461), L1.2>A (462), G1>A (464) (458-567), CH3 E12 (583), M14 (585), L24>E (595), M107>L (655), N114>S (661) (568-672), CHS (673-674)) (345-674)]]; (218-221')-disulfide with L-VH-G1(CH1-h) light chain anti-IL13 (1'-221')[VH (*Homo sapiens* IGHV3-21*07 (91.8%) -IGHD -IGHJ1*01 (100%), CDR-IMGT [8.7.12] (26'-33'.51'-57'.96'-107')) (1'-118') -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, CH1 K120 (CH1 R120>K (215') (119'-216'), hinge 1-5 (217'-221')) (119'-221')]; (447-218"')-disulfide with L-kappa light chain anti-IL4 (1"'-218"') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (87.9%) -IGKJ4*01 (100%), CDR-IMGT [10.3.9] (27"'-36"'.54"'-56"'.93"'-101"')) (1"'-111"') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (157"'), V101 (195"')) (112"'-218"')];
H-gamma1 heavy chain anti-IL33 (1"-451") [VH (*Homo sapiens* IGHV3-7*01 (89.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.14] (26"-33".51"-58".97"-110")) (1"-121") -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, 6-G1v14-1 CH2 A1.3, A1.2, A1, 9-G1v24 CH3 L107, S114, 14-G1v99-2 hinge R6, CH3 R88 (CH1 R120>K (218") (122"-219"), hinge 1-15 D6>R (225") (220"-234"), CH2 L1.3>A (238"), L1.2>A (239"), G1>A (241") (235"- 344"), CH3 E12 (360"), M14 (362"), K88>R (413"), M107>L (432"), N114>S (438") (345"-449"), CHS (450"-451")) (122"-451")], (224"-213"")-disulfide with L-kappa light chain anti-IL33 (1""-213"") [V-KAPPA (*Homo sapiens* IGKV1-6*01 (88.8%) -IGKJ4*01 (90.9%), CDR-IMGT [6.3.8] (27""-32"".50""-52"".89""-96"")) (1""-106"") -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (152""), V101 (190"")) (107""- 213"")]; dimer (453-230":456-233")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1SV lacking the glutamine synthetase (GS-KO) gene, glycoform alfa

ompékimig	immunoglobuline (L-kappa-H-gamma1(_L-VH-G1(CH1-h))_L-kappa)_(H-gamma1_L-kappa), anti-[*Homo sapiens* IL4 (interleukine 4, IL-4)], anti-[*Homo sapiens* IL13 (interleukine 13, IL-13)] et anti-[*Homo sapiens* IL33 (interleukine 33, IL-33)], anticorps monoclonal, trispécifique, trivalent; chaîne fusionnée L-kappa-H-gamma1 anti-IL13 et anti-IL4 (1-674) [L-kappa anti-IL13 (1-218) [V-KAPPA (*Homo sapiens* IGKV1-39*01 (82.8%) -IGKJ4*01 (100%), CDR-IMGT [10.3.9] (27-36.54-56.93-101)) (1-111) -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (157), V101 (195)) (112-218)] -5-mer (tétraglycyl-séryl) linker (219-223) -chaîne lourde H-gamma1 anti-IL4 (224-674) [VH (*Homo sapiens* IGHV2-5*08 (87.0%) -(IGHD) -IGHJ3*01 (92.9%) M123>T (339), CDR-IMGT [10.7.13] (249-258.276-282.321-333)) (224-344) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, CH1 K120, CH3 E12, M14, 6-G1v14-1 CH2 A1.3, A1.2, A1, 9-G1v24 CH3 L107, S114, 14-G1v99-1 charnière E6, CH3 E24 (CH1 R120>K (441) (345-442), charnière 1-15 D6>E (448) (443-457), CH2 L1.3>A (461), L1.2>A (462), G1>A (464) (458-567), CH3 E12 (583), M14 (585), L24>E (595), M107>L (655), N114>S (661) (568-672), CHS (673-674)) (345-674)]]; (218-221')-disulfure avec la chaîne légère L-VH-G1(CH1-h) anti-IL13 (1'-221') [VH (*Homo sapiens* IGHV3-21*07 (91.8%) -IGHD -IGHJ1*01 (100%), CDR-IMGT [8.7.12] (26'-33'.51'-57'.96'-107')) (1'-118') -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, CH1 K120 (CH1 R120>K (215') (119'-216'), charnière 1-5 (217'-221')) (119'-221')]; (447-218'")-disulfure avec la chaîne légère L-kappa anti-IL4 (1'"-218'") [V-KAPPA (*Homo sapiens* IGKV1-39*01 (87.9%) -IGKJ4*01 (100%), CDR-IMGT [10.3.9] (27'"-36'".54'"-56'".93'"-101'")) (1'"-111'") -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (157'"), V101 (195'")) (112'"-218'")]; chaîne lourde H-gamma1 anti-IL33 (1"-451") [VH (*Homo sapiens* IGHV3-7*01 (89.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.14] (26"-33".51"-58".97"-110")) (1"-121") -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, 6-G1v14-1 CH2 A1.3, A1.2, A1, 9-G1v24 CH3 L107, S114, 14-G1v99-2 charnière R6, CH3 R88(CH1 R120>K (218") (122"-219"), charnière 1-15 D6>R (225") (220"-234"), CH2 L1.3>A (238"), L1.2>A (239"), G1>A (241") (235"- 344"), CH3 E12 (360"), M14 (362"), K88>R (413"), M107>L (432"), N114>S (438") (345"-449"), CHS (450"-451")) (122"-451")], (224"-213"")-disulfure avec la chaîne légère L-kappa anti-IL33 (1""-213"") [V-KAPPA (*Homo sapiens* IGKV1-6*01 (88.8%) -IGKJ4*01 (90.9%), CDR-IMGT [6.3.8] (27""-32"".50""-52"".89""-96"")) (1""-106"") -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (152""), V101 (190"")) (107""- 213"")]; dimère (453-230":456-233")-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

ompekimig	inmunoglobulina (L-kappa-H-gamma1(_L-VH-G1(CH1-h))_L-kappa)_(H-gamma1_L-kappa), anti-[*Homo sapiens* IL4 (interleukina 4, IL-4)], anti-[*Homo sapiens* IL13 (interleukina 13, IL-13)] y anti-[*Homo sapiens* IL33 (interleukina 33, IL-33)], anticuerpo monoclonal, triespecífico, trivalente; cadena fusionada L-kappa-H-gamma1 anti-IL13 y anti-IL4 (1-674) [L-kappa anti-IL13 (1-218) [V-KAPPA (*Homo sapiens* IGKV1-39*01 (82.8%) -IGKJ4*01 (100%), CDR-IMGT [10.3.9] (27-36.54-56.93-101)) (1-111) -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (157), V101 (195)) (112-218)] -5-mer (tetraglicil-seril) enlace (219-223) -cadena pesada H-gamma1 anti-IL4 (224-674) [VH (*Homo sapiens* IGHV2-5*08 (87.0%) -(IGHD) -IGHJ3*01 (92.9%) M123>T (339), CDR-IMGT [10.7.13] (249-258.276-282.321-333)) (224-344) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, CH1 K120, CH3 E12, M14, 6-G1v14-1 CH2 A1.3, A1.2, A1, 9-G1v24 CH3 L107, S114, 14-G1v99-1 bisagra E6, CH3 E24 (CH1 R120>K (441) (345-442), bisagra 1-15 D6>E (448) (443-457), CH2 L1.3>A (461), L1.2>A (462), G1>A (464) (458-567), CH3 E12 (583), M14 (585), L24>E (595), M107>L (655), N114>S (661) (568-672), CHS (673-674)) (345-674)]]; (218-221')-disulfuro con la cadena ligera L-VH-G1(CH1-h) anti-IL13 (1'-221') [VH (*Homo sapiens* IGHV3-21*07 (91.8%) -IGHD -IGHJ1*01 (100%), CDR-IMGT [8.7.12] (26'-33'.51'-57'.96'-107')) (1'-118') -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, CH1 K120 (CH1 R120>K (215') (119'-216'), bisagra 1-5 (217'-221')) (119'-221')]; (447-218'")-disulfuro con la cadena ligera L-kappa anti-IL4 (1'"-218'") [V-KAPPA (*Homo sapiens* IGKV1-39*01 (87.9%) -IGKJ4*01 (100%), CDR-IMGT [10.3.9] (27'"-36'".54'"-56'".93'"-101'")) (1'"-111'") -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (157'"), V101 (195'")) (112'"-218'")]; cadena pesada H-gamma1 anti-IL33 (1"-451") [VH (*Homo sapiens* IGHV3-7*01 (89.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.14] (26"-33".51"-58".97"-110")) (1"-121") -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, 6-G1v14-1 CH2 A1.3, A1.2, A1, 9-G1v24 CH3 L107, S114, 14-G1v99-2 bisagra R6, CH3 R88 (CH1 R120>K (218") (122"-219"), bisagra 1-15 D6>R (225") (220"-234"), CH2 L1.3>A (238"), L1.2>A (239"), G1>A (241") (235"- 344"), CH3 E12 (360"), M14 (362"), K88>R (413"), M107>L (432"), N114>S (438") (345"-449"), CHS (450"-451")) (122"-451")], (224"-213"")-disulfuro con la cadena ligera L-kappa anti-IL33 (1""-213"") [V-KAPPA (*Homo sapiens* IGKV1-6*01 (88.8%) -IGKJ4*01 (90.9%), CDR-IMGT [6.3.8] (27""-32"".50""-52"".89""-96"")) (1""-106"") -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (152""), V101 (190"")) (107""- 213"")]; dímero (453-230":456-233")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1SV en ausencia del gen de la glutamina sintetasa (GS-KO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada: fused L-kappa-H-gamma1 anti-IL13 and anti-IL4 (H)

```
DIQMTQSPSS LSASVGDRVT ITCKASESVD HFGWSLVHWY QQKPGKAPKL  50
LIYRASNLES GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSNEDPW 100
TFGGGTKVEI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL NNFYPREAKV 150
QWKVDNALQS GNSQESVTEQ DSKDSTYSLS STLTLSKADY EKHKVYACEV 200
THQGLSSPVT KSFNRGECGG GGSEVTLRES GPALVKPTQT LTLTCTFSGF 250
SLSNFGEGLS WIRQPPGKGL EWLAHIYWDD DKRYNPSLKS RLTISKDTSR 300
NQVVLTMTNM DPVDTATYYC ARRETVFYWY FDVWGQGTTV TVSSASTKGP 350
SVFPLAPSSK STSGGTAALG CLVKDYFPEP VTVSWNSGAL TSGVHTFPAV 400
LQSSGLYSLS SVVTVPSSSL GTQTYICNVN HKPSNTKVDK KVEPKSCEKT 450
HTCPPCPAPE AAGAPSVFLF PPKPKDTLMI SRTPEVTCVV VDVSHEDPEV 500
KFNWYVDGVE VHNAKTKPRE EQYNSTYRVV SVLTVLHQDW LNGKEYKCKV 550
SNKALPAPIE KTISKAKGQP REPQVYTLPP SREEMTKNQV SLTCEVKGFY 600
PSDIAVEWES NGQPENNYKT TPPVLDSDGS FFLYSKLTVD KSRWQQGNVF 650
SCSVLHEALH SHYTQKSLSL SPGK                              674
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Light chain / Chaîne légère / Cadena ligera: L-VH-G1(CH1-h) anti-IL13 (L')

```
EVQLVESGGG LVQPGGSLRL SCAASGFTFS SYAMSWVRQA PGKGLEWVAS  50
ISSGDTTYYP DSVKGRFTIS RDNAKNSLYL QMNSLRAEDT AVYYCARNEG 100
YYFGLTLWGQ GTLVTVSSAS TKGPSVFPLA PSSKSTSGGT AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTQTYI 200
CNVNHKPSNT KVDKKVEPKS C                                221
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Light chain / Chaîne légère / Cadena ligera: L-kappa anti-IL4 (L''')

```
DIQMTQSPSS LSASVGDRVT ITCRASQSVD EEGDSYMNWY QQKPGKAPKL  50
LIYAASNLES GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSNKDPP 100
TFGGGTKVEI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL NNFYPREAKV 150
QWKVDNALQS GNSQESVTEQ DSKDSTYSLS STLTLSKADY EKHKVYACEV 200
THQGLSSPVT KSFNRGEC                                    218
```

Heavy chain / Chaîne lourde / Cadena pesada: H-gamma1 anti-IL33 (H'')

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EVQLVESGGG LVQPGGSLRL SCAASGFTFS SYWMYWVRQA PGKGLEWVAA  50
ITPNAGEDYY PESVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARGQ 100
YYYTKYSLGY WGQGTLVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200
TYICNVNHKP SNTKVDKKVE PKSCRKTHTC PPCPAPEAAG APSVFLFPPK 250
PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY 300
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP 350
QVYTLPPSRE EMTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP 400
VLDSDGSFFL YSRLTVDKSR WQQGNVFSCS VLHEALHSHY TQKSLSLSPG 450
K                                                      451
```

Light chain / Chaîne légère / Cadena ligera: L-kappa anti-IL33 (L'''')

```
DIQMTQSPSS LSASVGDRVT ITCRASQPIH NHLDWYQQKP GKAPKLLIYF  50
GKNLQEGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCFQ YKKGWSFGGG 100
TKVEIKRTVA APSVFIFPPS DEQLKSGTAS VVCLLNNFYP REAKVQWKVD 150
NALQSGNSQE SVTEQDSKDS TYSLSSTLTL SKADYEKHKV YACEVTHQGL 200
SSPVTKSFNR GEC                                         213
```

Post-translational modifications

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

Intra-H (C23-C104) 23-92 138-198 245-320 371-427 488-548 594-652
22''-96'' 148''-204'' 265''-325'' 371''-429''

Intra-L (C23-C104) 22'-95' 145'-201'
23'''-92''' 138'''-198'''
23''''-88'''' 133''''-193''''

Inter-H-L' (CL 126-h 5)* 218-221'

Inter-H-L''' (h 5-CL 126) 447-218''' 224''-213''''

Inter-H-H (h 11, h 14) 453-230'' 456-233''

*crosslink / lien croisé / enlace cruzado

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4: 524, 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: 674, 451''

ontunisertibum

ontunisertib *N*-[(2,6-difluorophenyl)methyl]-2-[3-(6-methylpyridin-2-yl)-4-(quinolin-4-yl)-1*H*-pyrazol-1-yl]acetamide

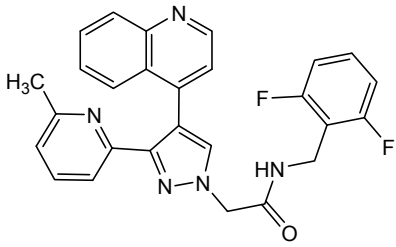
ontunisertib

N-[(2,6-difluorophényl)méthyl]-2-[3-(6-méthylpyridin-2-yl)-4-(quinoléin-4-yl)-1*H*-pyrazol-1-yl]acétamide

ontunisertib

N-[(2,6-difluorofenil)metil]-2-[3-(6-metilpiridin-2-il)-4-(quinolein-4-il)-1*H*-pirazol-1-il]acetamida

$C_{27}H_{21}F_2N_5O$



onvuzosiranum

onvuzosiran

O-[(2*R*,3*S*)-2-(hydroxymethyl)oxolan-3-yl] hydrogen *all-P-ambo*-3'-*O*-(2-{[(1-{17-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]-3,6,9,12,15-pentaoxaheptadecan-1-yl}-1*H*-1,2,3-triazol-4-yl)methyl]amino}-2-oxoethyl)-2'-*O*-(2-{bis[(1-{17-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]-3,6,9,12,15-pentaoxaheptadecan-1-yl}-1*H*-1,2,3-triazol-4-yl)methyl]amino}-2-oxoethyl)-*P*-thiocytidylyl-(5'→5')-2'-*O*-methyl-*P*-thiouridylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-deoxy-2'-fluorocytidylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-deoxy-2'-fluorocytidylyl-(3'→5')-2'-deoxy-2'-fluorocytidylyl-(3'→5')-2'-deoxy-2'-fluorouridylyl-(3'→5')-2'-deoxy-2'-fluorouridylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-methyl-*P*-thio-3'-adenylate
duplex with *all-P-ambo*-2'-*O*-methyl-*P*-thiouridylyl-(5'→3')-2'-*O*-methyl-*P*-thioguanylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-deoxy-2'-fluoroguanylyl-(5'→3')-2'-*O*-methylguanylyl-(5'→3')-2'-deoxy-2'-fluorouridylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-deoxy-2'-fluorocytidylyl-(5'→3')-2'-*O*-methylguanylyl-(5'→3')-2'-deoxy-2'-fluoroadenylyl-(5'→3')-2'-*O*-methylguanylyl-(5'→3')-2'-deoxy-2'-fluoroguanylyl-(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'-fluorouridylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-deoxy-2'-fluoroadenylyl-(5'→3')-2'-*O*-methyl-*P*-thiouridylyl-(5'→3')-2'-deoxy-2'-fluoro-*P*-thioguanylyl-(5'→3')-2'-*O*-methyluridine

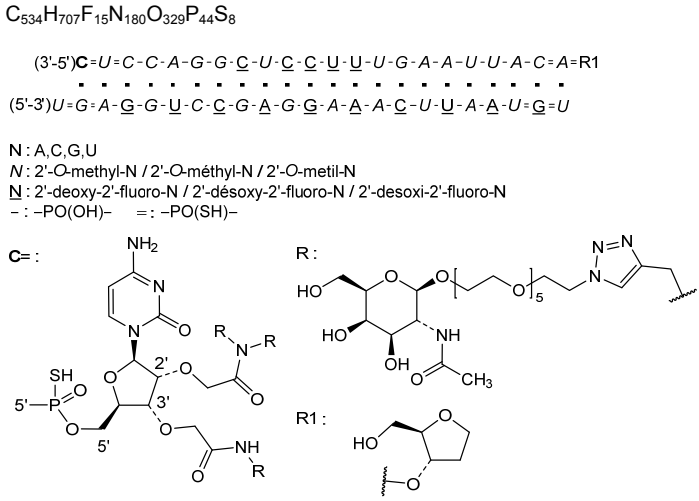
onvuzosiran

tout-P-ambo-3'-*O*-(2-{[(1-{17-[(2-acétamido-2-désoxy-β-D-galactopyranosyl)oxy]-3,6,9,12,15-pentaoxaheptadécan-1-yl}-1*H*-1,2,3-triazol-4-yl)méthyl]amino}-2-oxoéthyl)-2'-*O*-(2-{bis[(1-{17-[(2-acétamido-2-désoxy-β-D-galactopyranosyl)oxy]-3,6,9,12,15-pentaoxaheptadécan-1-yl}-1*H*-1,2,3-triazol-4-yl)méthyl]amino}-2-oxoéthyl)-*P*-thiocytidylyl-(5'→5')-2'-*O*-méthyl-*P*-thiouridylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-

méthylguanylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-désoxy-2'-fluorocytidylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-désoxy-2'-fluorocytidylyl-(3'→5')-2'-désoxy-2'-fluorocytidylyl-(3'→5')-2'-désoxy-2'-fluorouridylyl-(3'→5')-2'-désoxy-2'-fluorouridylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthyl-*P*-thiocytidylyl-(3'→5')-hydrogéno-2'-*O*-méthyl-*P*-thio-3'-adénylate de *O*-[(2*R*,3*S*)-2-(hydroxyméthyl)oxolan-3-yle]
duplex avec *tout-P-ambo*-2'-*O*-méthyl-*P*-thiouridylyl-(5'→3')-2'-*O*-méthyl-*P*-thioguanylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-désoxy-2'-fluoroguanylyl-(5'→3')-2'-*O*-méthylguanylyl-(5'→3')-2'-désoxy-2'-fluorouridylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-désoxy-2'-fluorocytidylyl-(5'→3')-2'-*O*-méthylguanylyl-(5'→3')-2'-désoxy-2'-fluoroadénylyl-(5'→3')-2'-*O*-méthylguanylyl-(5'→3')-2'-désoxy-2'-fluoroguanylyl-(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'-fluorouridylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-désoxy-2'-fluoroadénylyl-(5'→3')-2'-*O*-méthyl-*P*-thiouridylyl-(5'→3')-2'-désoxy-2'-fluoro-*P*-thioguanylyl-(5'→3')-2'-*O*-méthyluridine

onvuzosirán

todo-P-ambo-3'-*O*-(2-{[(1-{17-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]-3,6,9,12,15-pentaoxaheptadecan-1-il}-1*H*-1,2,3-triazol-4-il)metil]amino}-2-oxoetil)-2'-*O*-(2-{bis[(1-{17-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]-3,6,9,12,15-pentaoxaheptadecan-1-il}-1*H*-1,2,3-triazol-4-il)metil]amino}-2-oxoetil)-*P*-tiocitidilil-(5'→5')-2'-*O*-metil-*P*-tiouridilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-desoxi-2'-fluorocitidilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-desoxi-2'-fluorocitidilil-(3'→5')-2'-desoxi-2'-fluorocitidilil-(3'→5')-2'-desoxi-2'-fluorouridilil-(3'→5')-2'-desoxi-2'-fluorouridilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metil-*P*-tiocitidilil-(3'→5')-hidrógeno-2'-*O*-metil-*P*-tio-3'-adenilato de *O*-[(2*R*,3*S*)-2-(hidroximetil)oxolan-3-ilo]
dúplex con *todo-P-ambo*-2'-*O*-metil-*P*-tiouridilil-(5'→3')-2'-*O*-metil-*P*-tioguanilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-desoxi-2'-fluoroguanilil-(5'→3')-2'-*O*-metilguanilil-(5'→3')-2'-desoxi-2'-fluorouridilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-desoxi-2'-fluorocitidilil-(5'→3')-2'-*O*-metilguanilil-(5'→3')-2'-desoxi-2'-fluoroadenilil-(5'→3')-2'-*O*-metilguanilil-(5'→3')-2'-desoxi-2'-fluoroguanilil-(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'-fluorouridilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-desoxi-2'-fluoroadenilil-(5'→3')-2'-*O*-metil-*P*-tiouridilil-(5'→3')-2'-desoxi-2'-fluoro-*P*-tioguanilil-(5'→3')-2'-*O*-metiluridina



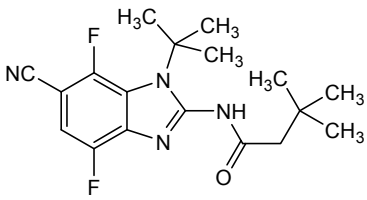
onzemipgenum parvecum #

onzemipgene parvec	recombinant non-replicating adeno-associated virus serotype 2 (rAAV2) vector, encoding a truncated soluble form of human CD59 (sCD59, membrane-independent human CD59) under control of the CAG promoter (cytomegalovirus (CMV) enhancer / chicken beta-actin (CBA) promoter / rabbit beta-globin acceptor containing chimeric intron) and a rabbit beta-globin polyadenylation signal
onzémipgène parvec	vecteur recombinant du virus adéno-associé non réplicatif de sérotype 2 (rAAV2) codant une forme tronquée soluble du CD59 humain (sCD59, CD59 humain indépendant de la membrane) sous le contrôle du promoteur CAG (amplificateur du cytomégalovirus (CMV) / promoteur de la bêta-actine de poulet (CBA) / intron chimérique contenant l'accepteur de la bêta-globine de lapin), et un signal de polyadénylation de bêta-globine de lapin
onzemipgén parvec	vector de virus adenoasociado del serotipo 2, recombinante (rAAV2), no replicativo, que codifica una forma truncada soluble de CD59 humano (sCD59, CD59 humano independiente de membrana) bajo el control de un promotor CAG (potenciador de citomegalovirus (CMV) / promotor de beta actina de pollo (CBA) / intrón quimérico que contiene el aceptor de la beta globina de conejo) y una señal de poliadenilación de la beta globina de conejo

opakalimum

opakalim	*N*-(1-*tert*-butyl-6-cyano-4,7-difluoro-1*H*-1,3-benzimidazol-2-yl)-3,3-dimethylbutanamide
opakalim	*N*-(1-*tert*-butyl-6-cyano-4,7-difluoro-1*H*-1,3-benzimidazol-2-yl)-3,3-diméthylbutanamide
opakalim	*N*-(1-*terc*-butil-6-ciano-4,7-difluoro-1*H*-1,3-bencimidazol-2-il)-3,3-dimetilbutanamida

$C_{18}H_{22}F_2N_4O$



opamtistomigum #

opamtistomig

immunoglobulin (H-gamma1-scFvhl_L-kappa) dimer, anti-[*Homo sapiens* CD274 (programmed cell death 1 ligand 1, PDL1, PD-L1, B7 homolog 1, B7H1, B7-H1, PDCD1LG1)] and anti-[*Homo sapiens* TNFRSF9 (TNF receptor superfamily member 9, 4-1BB, T cell antigen ILA, CD137)], humanized and *Homo sapiens* monoclonal antibody, tetravalent, bispecific;
H-gamma1 heavy chain anti-CD274 fused to a scFvhl anti-TNFRSF9 (1-714) [H-gamma1 heavy chain anti-CD274 humanized (1-449) [VH (*Homo sapiens* IGHV4-30-4*09 (87.8%) -(IGHD) -IGHJ4*01 (93.3%) L123>T (114), CDR-IMGT [8.7.13] (26-33.51-57.96-108)) (1-119)-*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, 6-G1v14-4 CH2 A1.3, A1.2, A114, 1-G1v66 CH2 A27 (CH1 K120 (216) (120-217), hinge 1-15 (218-232), CH2 L1.3>A (236), L1.2>A (237), D27>A (267), P114>A (331) (233-342), CH3 D12 (358), L14 (360) (343-447), CHS (448-449)) (120-449)] -15-mer tris(tetraglycyl-seryl) linker (450-464) -scFvhl anti-TNFRSF9 *Homo sapiens* (465-714), C49 (VH)-C120 (VL) 11-scFv-v1 [VH (*Homo sapiens* IGHV3-30*01 (92.9%) -IGHD -IGHJ6*03 (95.0%) G49>C (508), CDR-IMGT [8.8.17] (490-497.515-522.561-577)) (465-588) -15-mer tris(glycyl-tetraseryl) linker (589-603) -V-LAMBDA (*Homo sapiens* IGLV2-14*01 (91.9%) -IGLJ7*01 (90.9%) G120>C (707), CDR-IMGT [9.3.11] (629-637.655-657.694-704)) (604-714)]]; (222-214')-disulfide with L-kappa light chain anti-CD274 humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-16*01 (84.2%) -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 (228-228":231-231")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa

opamtistomig

immunoglobuline (H-gamma1-scFvhl_L-kappa) dimère, anti-[*Homo sapiens* CD274 (ligand 1 de mort cellulaire programmée 1, PDL1, PD-L1, B7 homologue 1, B7H1, B7-H1, PDCD1LG1)] et anti-[*Homo sapiens* TNFRSF9 (membre 9 de la superfamille des récepteurs du TNF, 4-1BB, antigène ILA des cellules T, CD137)], anticorps monoclonal humanisé et *Homo sapiens*, tétravalent, bispécifique;
chaîne lourde H-gamma1 anti-CD274 fusionnée à un scFvhl anti-TNFRSF9 (1-714) [chaîne lourde H-gamma1 anti-CD274 humanisée (1-449) [VH (*Homo sapiens* IGHV4-30-4*09 (87.8%) -(IGHD) -IGHJ4*01 (93.3%) L123>T (114), CDR-IMGT [8.7.13] (26-33.51-57.96-108)) (1-119)-*Homo sapiens* IGHG1*01,

	G1m17,1 CH1 K120, CH3 D12, L14, 6-G1v14-4 CH2 A1.3, A1.2, A114, 1-G1v66 CH2 A27 (CH1 K120 (216) (120-217), charnière 1-15 (218-232), CH2 L1.3>A (236), L1.2>A (237), D27>A (267), P114>A (331) (233-342), CH3 D12 (358), L14 (360) (343-447), CHS (448-449)) (120-449)] -15-mer tris(tétraglycyl-séryl) linker (450-464) -scFvhl anti-TNFRSF9 *Homo sapiens* (465-714), C49 (VH)-C120 (VL) 11-scFv-v1 [VH (*Homo sapiens* IGHV3-30*01 (92.9%) -IGHD -IGHJ6*03 (95.0%) G49>C (508), CDR-IMGT [8.8.17] (490-497.515-522.561-577)) (465-588) -15-mer tris(glycyl-tétraséryl) linker (589-603) -V-LAMBDA (*Homo sapiens* IGLV2-14*01 (91.9%) -IGLJ7*01 (90.9%) G120>C (707), CDR-IMGT [9.3.11] (629-637.655-657.694-704)) (604-714)]]; (222-214')-disulfure avec la chaîne légère L-kappa anti-CD274 humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-16*01 (84.2%) -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 (228-228'':231-231'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa
opamtistomig	inmunoglobulina (H-gamma1-scFvhl_L-kappa) dímero, anti-[*Homo sapiens* CD274 (ligando 1 de muerte celular programada 1, PDL1, PD-L1, B7 homólogo 1, B7H1, B7-H1, PDCD1LG1)] y anti-[*Homo sapiens* TNFRSF9 (miembro 9 de la superfamilia de los receptores del TNF, 4-1BB, antígeno ILA de las células T, CD137)], anticuerpo monoclonal humanizado y *Homo sapiens*, tetravalente, biespecífico; cadena pesada H-gamma1 anti-CD274 fusionada con un scFvhl anti-TNFRSF9 (1-714) [cadena pesada H-gamma1 anti-CD274 humanizada (1-449) [VH (*Homo sapiens* IGHV4-30-4*09 (87.8%) -(IGHD) -IGHJ4*01 (93.3%) L123>T (114), CDR-IMGT [8.7.13] (26-33.51-57.96-108)) (1-119)-*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, 6-G1v14-4 CH2 A1.3, A1.2, A114, 1-G1v66 CH2 A27 (CH1 K120 (216) (120-217), bisagra 1-15 (218-232), CH2 L1.3>A (236), L1.2>A (237), D27>A (267), P114>A (331) (233-342), CH3 D12 (358), L14 (360) (343-447), CHS (448-449)) (120-449)] -15-mer tris(tetraglicil-seril) enlace (450-464) -scFvhl anti-TNFRSF9 *Homo sapiens* (465-714), C49 (VH)-C120 (VL) 11-scFv-v1 [VH (*Homo sapiens* IGHV3-30*01 (92.9%) -IGHD -IGHJ6*03 (95.0%) G49>C (508), CDR-IMGT [8.8.17] (490-497.515-522.561-577)) (465-588) -15-mer tris(glicil-tetraseril) enlace (589-603) -V-LAMBDA (*Homo sapiens* IGLV2-14*01 (91.9%) -IGLJ7*01 (90.9%) G120>C (707), CDR-IMGT [9.3.11] (629-637.655-657.694-704)) (604-714)]]; (222-214')-disulfuro con la cadena ligera L-kappa anti-CD274 humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-16*01 (84.2%) -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 (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: fused H-gamma1 anti-CD274 -scFvhl anti-TNFRSF9 (H, H")

```
EVQLQESGPG LVKPSQTLSL TCTVSGDSFS SGYWNWIRQH PGKGLEYIGY  50
VSYTGSTYYI PSLKSRVTIS RDTSKNQFSL KLSSVTAADT AVYYCAGYRD 100
WLHGYFDYWG QGTTVTVSSA STKGPSVFPL APSSKSTSGG TAALGCLVKD 150
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY 200
ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP CPAPEAAGGP SVFLFPPKPK 250
DTLMISRTPE VTCVVVAVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS 300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL AAPIEKTISK AKGQPREPQV 350
YTLPPSRDEL TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL 400
DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGKG 450
GGGSGGGGSG GGGSQVQLQE SGGGLVQPGG SLRLSCAVSG FTFSSYAMHW 500
VRQAPGKCLE WVAVISYDGS KKWYADSVKG RFTISRDNSK NTLYLQMNSL 550
RAEDTAVYYC ARNQGSGSYL YYYYMDVWGK GTTVTVSSGS SSSGSSSSGS 600
SSSQSALTQP RSVSGSPGQS VTISCTGTSS DVGGYNYVSW YQQLPGKAPK 650
VIIYEVSNRP SGVSNRFSGS KSGNTASLTI SGVQSEDEAD YYCSSYTSSS 700
TFYVFGCGTQ LTVL                                        714
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Light chain / Chaîne légère / Cadena ligera: L-kappa anti-CD274 (L', L'")

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DIQMTQSPSS LSASVGDRVT ITCKASQNVM DNVAWYQQKP GKAPKRLIYS  50
ASYRFSGVPS RFSGSGSGTE FTLTISSLQP EDFATYYCQQ YNGYPLTFGQ 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) 22-95 146-202 263-323 369-427
22"-95" 146"-202" 263"-323" 369"-427"
486-560 625-693
486"-560" 625"-693"

Intra-H scFv C49 (VH)-C120 (VL)* 508-707
508"-707"

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"

*engineered additional disulfide bond C49 (VH)-C120 (VL) to stabilize the scFv (variant 11-scFv-v1).

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.

oturkibartum #

oturkibart — 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 (1-444) [VH (*Homo sapiens* IGHV3-66*01 (83.5%) -(IGHD) -IGHJ2*01 (85.7%) R120>Q (109), CDR-IMGT [8.7.11] (26-33.51-57.96-106)) (1-117) -*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, 12-G4v5 h P10 (CH1 (118-215), hinge 1-12 S10>P (225) (216-227), CH2 L92 (306) (228-337), CH3 (338-442), CHS (443-444)) (118-444)], (131-217')-disulfide with L-kappa light chain humanized (1'-217') [V-KAPPA (*Homo sapiens* IGKV1-27*01 (84.4%) -IGKJ2*02 (90.0%) L124>V (107'), CDR-IMGT [8.3.10] (27'-34'.52'-54'.91'-100')) (1'-110') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (156'), V101 (194')) (111'-217')]; dimer (223-223":226-226")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-S, glycoform alfa

oturkibart — 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 (1-444) [VH (*Homo sapiens* IGHV3-66*01 (83.5%) -(IGHD) -IGHJ2*01 (85.7%) R120>Q (109), CDR-IMGT [8.7.11] (26-33.51-57.96-106)) (1-117) -*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, 12-G4v5 h P10(CH1 (118-215), charnière 1-12 S10>P (225) (216-227), CH2 L92 (306) (228-337), CH3 (338-442), CHS (443-444)) (118-444)], (131-217')-disulfure avec

la chaîne légère L-kappa humanisée (1'-217') [V-KAPPA (*Homo sapiens* IGKV1-27*01 (84.4%) -IGKJ2*02 (90.0%) L124>V (107'), CDR-IMGT [8.3.10] (27'-34'.52'-54'.91'-100')) (1'-110') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (156'), V101 (194')) (111'-217')]; dimère (223-223'':226-226'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-S, glycoforme alfa

oturkibart

inmunoglobulina G4-kappa, anti-[*Homo sapiens* IL4R (receptor de la interleukina, IL4RA, IL-4RA, receptor de la interleukina 13, CD124)], anticuerpo monoclonal humanizado*;*
cadena pesada H-gamma4 humanizada (1-444) [VH (*Homo sapiens* IGHV3-66*01 (83.5%) -(IGHD) -IGHJ2*01 (85.7%) R120>Q (109), CDR-IMGT [8.7.11] (26-33.51-57.96-106)) (1-117) -*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, 12-G4v5 h P10 (CH1 (118-215), bisagra 1-12 S10>P (225) (216-227), CH2 L92 (306) (228-337), CH3 (338-442), CHS (443-444)) (118-444)], (131-217')-disulfuro con la cadena ligera L-kappa humanizada *(*1'-217') [V-KAPPA (*Homo sapiens* IGKV1-27*01 (84.4%) -IGKJ2*02 (90.0%) L124>V (107'), CDR-IMGT [8.3.10] (27'-34'.52'-54'.91'-100')) (1'-110') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (156'), V101 (194')) (111'-217')]; dímero (223-223'':226-226'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-S, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAASGIDLR TNSMSWVRQA PGKGLEWVGI  50
IGSSGYMDYA SWAKGRFTIS RDNSKNTLYL QMNSLRAEDT AVYYCARHGD 100
SSSFALWGQG TLVTVSSAST KGPSVFPLAP CSRSTSESTA ALGCLVKDYF 150
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTKTYTC 200
NVDHKPSNTK VDKRVESKYG PPCPPCPAPE FLGGPSVFLF PPKPKDTLMI 250
SRTPEVTCVV VDVSQEDPEV QFNWYVDGVE VHNAKTKPRE EQFNSTYRVV 300
SVLTVLHQDW LNGKEYKCKV SNKGLPSSIE KTISKAKGQP REPQVYTLPP 350
SQEEMTKNQV SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS 400
FFLYSRLTVD KSRWQEGNVF SCSVMHEALH NHYTQKSLSL SLGK       444
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Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCRASESVY KNNRLSWYQQ KPGKAPKLLI  50
YEASKVASGV PSRFSGSGSG TDFTLTISSL QPEDFATYYC AGAYRGNIYP 100
FGQGTKVEIK RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ 150
WKVDNALQSG NSQESVTEQD SKDSTYSLSS TLTLSKADYE KHKVYACEVT 200
HQGLSSPVTK SFNRGEC                                     217
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-95 144-200 258-318 364-422
22''-95'' 144''-200'' 258''-318'' 364''-422''
Intra-L (C23-C104) 23'-90' 137'-197'
23'''-90''' 137'''-197'''
Inter-H-L (CH1 10-CL 126) 131-217' 131''-217'''
Inter-H-H (h 8, h 11) 223-223'' 226-226''

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

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2: 444, 444''

ozisiranum

ozisiran

(2*RS*)-3-(1,23-bis[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]-14-{5-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]pentanoyl}-5,19-dioxo-6,10,14,18-tetraazatricosan-10-yl)-2-hydroxy-3-oxopropyl hydrogen *all-P-ambo*-2'-*O*-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-deoxy-2'-fluoroguanylyl-(3'→5')-2'-deoxy-2'-fluoroguanylyl-(3'→5')-2'-deoxy-2'-fluorocytidylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methyladenylyl-(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*-methyladenylyl-(3'→5')-2'-*O*-methyl-3'-adenylate,
duplex with *all-P-ambo*-2'-*O*-methyl-*P*-thiouridylyl-(5'→3')-2'-*O*-methyl-*P*-thiouridylyl-(5'→3')-2'-*O*-methylguanylyl-(5'→3')-2'-*O*-methylguanylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-deoxy-2'-fluoroadenylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-deoxy-2'-fluorouridylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-*O*-methylguanylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-*O*-methylguanylyl-(5'→3')-2'-deoxy-2'-fluoroadenylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-*O*-methylguanylyl-(5'→3')-2'-*O*-methyl-*P*-thiouridylyl-(5'→3')-2'-deoxy-2'-fluoro-*P*-thiouridylyl-(5'→3')-(5'*E*)-2'-*O*-methyl-5',$C^{5'}$-didehydro-$O^{5'}$-carba-5'-uridylic acid

ozisiran

tout-P-ambo-2'-*O*-méthyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-méthyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-désoxy-2'-fluoroguanylyl-(3'→5')-2'-désoxy-2'-fluoroguanylyl-(3'→5')-2'-désoxy-2'-fluorocytidylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthyladénylyl-(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*-méthyladénylyl-(3'→5')-hydrogéno-2'-*O*-méthyl-3'-adénylate de (2*RS*)-3-(1,23-bis[(2-acétamido-2-désoxy-β-D-galactopyranosyl)oxy]-14-{5-[(2-acétamido-2-désoxy-β-D-galactopyranosyl)oxy]pentanoyl}-5,19-dioxo-6,10,14,18-tétraazatricosan-10-yl)-2-hydroxy-3-oxopropyle,
duplex avec acide *tout-P-ambo*-2'-*O*-méthyl-*P*-thiouridylyl-(5'→3')-2'-*O*-méthyl-*P*-thiouridylyl-(5'→3')-2'-*O*-méthylguanylyl-(5'→3')-2'-*O*-méthylguanylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-désoxy-2'-fluoroadénylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-désoxy-2'-fluorouridylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-*O*-méthylguanylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-*O*-méthylguanylyl-(5'→3')-2'-désoxy-2'-fluoroadénylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-*O*-méthylguanylyl-(5'→3')-2'-*O*-méthyl-*P*-thiouridylyl-(5'→3')-2'-désoxy-2'-fluoro-*P*-thiouridylyl-(5'→3')-(5'*E*)-2'-*O*-méthyl-5',$C^{5'}$-didéhydro-$O^{5'}$-carba-5'-uridylique

ozisirán

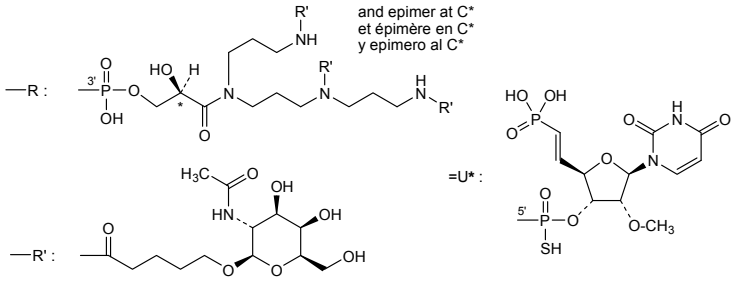
todo-P-ambo-2'-*O*-metil-*P*-tiocitidilil-(3'→5')-2'-*O*-metil-*P*-tiocitidilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-desoxi-2'-fluoroguanilil-(3'→5')-2'-desoxi-2'-fluoroguanilil-(3'→5')-2'-desoxi-2'-fluorocitidilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metiladenilil-(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*-metiladenilil-(3'→5')-hidrógeno-2'-*O*-metil-3'-adenilato de (2*RS*)-3-(1,23-bis[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]-14-{5-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]pentanoil}-5,19-dioxo-6,10,14,18-tetraazatricosan-10-il)-2-hidroxi-3-oxopropilo,
duplex con ácido *todo-P-ambo*-2'-*O*-metil-*P*-tiouridilil-(5'→3')-2'-*O*-metil-*P*-tiouridilil-(5'→3')-2'-*O*-metilguanilil-(5'→3')-2'-*O*-metilguanilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-desoxi-2'-fluoroadenilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-desoxi-2'-fluorouridilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-*O*-metilguanilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-*O*-metilguanilil-(5'→3')-2'-desoxi-2'-fluoroadenilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-*O*-metilguanilil-(5'→3')-2'-*O*-metil-*P*-tiouridilil-(5'→3')-2'-desoxi-2'-fluoro-*P*-tiouridilil-(5'→3')-(5'*E*)-2'-*O*-metil-5',$C^{5'}$-didehidro-$O^{5'}$-carba-5'-uridílico

$C_{464}H_{619}F_7N_{152}O_{293}P_{40}S_6$

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

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



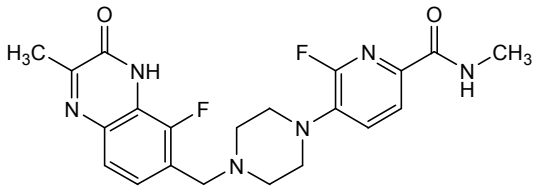
palacaparibum

palacaparib — 6-fluoro-5-{4-[(5-fluoro-2-methyl-3-oxo-3,4-dihydroquinoxalin-6-yl)methyl]piperazin-1-yl}-*N*-methylpyridine-2-carboxamide

palacaparib — 6-fluoro-5-{4-[(5-fluoro-2-méthyl-3-oxo-3,4-dihydroquinoxalin-6-yl)méthyl]pipérazin-1-yl}-*N*-méthylpyridine-2-carboxamide

palacaparib — 6-fluoro-5-{4-[(5-fluoro-2-metil-3-oxo-3,4-dihidroquinoxalin-6-il)metil]piperazin-1-il}-*N*-metilpiridina-2-carboxamida

$C_{21}H_{22}F_2N_6O_2$



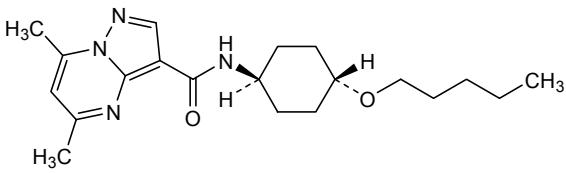
pariceractum

pariceract — 5,7-dimethyl-*N*-[*trans*-4-(pentyloxy)cyclohexyl]pyrazolo[1,5-*a*]pyrimidine-3-carboxamide

paricéract — 5,7-diméthyl-*N*-[*trans*-4-(pentyloxy)cyclohexyl]pyrazolo[1,5-*a*]pyrimidine-3-carboxamide

pariceract — 5,7-dimetil-*N*-[*trans*-4-(pentiloxi)ciclohexil]pirazolo[1,5-*a*]pirimidina-3-carboxamida

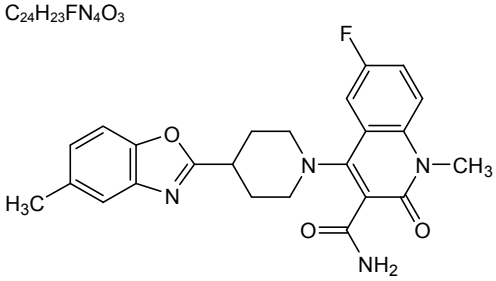
$C_{20}H_{30}N_4O_2$



pasodacigibum

pasodacigib	6-fluoro-1-methyl-4-[4-(5-methyl-1,3-benzoxazol-2-yl)piperidin-1-yl]-2-oxo-1,2-dihydroquinoline-3-carboxamide
pasodacigib	6-fluoro-1-méthyl-4-[4-(5-méthyl-1,3-benzoxazol-2-yl)piperidin-1-yl]-2-oxo-1,2-dihydroquinoléine-3-carboxamide
pasodacigib	6-fluoro-1-metil-4-[4-(5-metil-1,3-benzoxazol-2-il)piperidin-1-il]-2-oxo-1,2-dihidroquinoleina-3-carboxamida

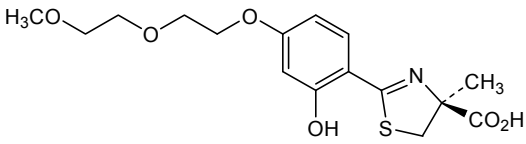
$C_{24}H_{23}FN_4O_3$



petadeferitrinum

petadeferitrin	(4*S*)-2-{2-hydroxy-4-[2-(2-methoxyethoxy)ethoxy]phenyl}-4-methyl-4,5-dihydro-1,3-thiazole-4-carboxylic acid
pétadéféritrine	acide (4*S*)-2-{2-hydroxy-4-[2-(2-méthoxyéthoxy)éthoxy]phényl}-4-méthyl-4,5-dihydro-1,3-thiazole-4-carboxylique
petadeferitrina	ácido (4*S*)-2-{2-hidroxi-4-[2-(2-metoxietoxi)etoxi]fenil}-4-metil-4,5-dihidro-1,3-tiazol-4-carboxílico

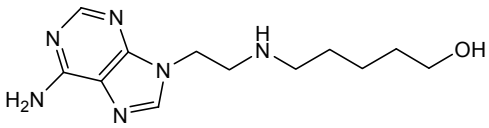
$C_{16}H_{21}NO_6S$



peturadolum

peturadol	5-{[2-(6-amino-9*H*-purin-9-yl)ethyl]amino}pentan-1-ol
péturadol	5-{[2-(6-amino-9*H*-purin-9-yl)éthyl]amino}pentan-1-ol
peturadol	5-{[2-(6-amino-9*H*-purin-9-il)etil]amino}pentan-1-ol

$C_{12}H_{20}N_6O$



pezatresgenum leucelum #

pezatresgene leucel	allogeneic T lymphocytes derived from peripheral blood mononuclear cells (PBMCs) of a haploidentical hematopoietic cell transplantation (HCT) donor that is negative for the HA-1 genotype and/or negative for HLA A*02, engineered by transposon/transposase-mediated gene delivery to express a T cell

receptor (TCR) that is specific for a 9-amino acid peptide (VLHDDLLEA) termed HA-1 derived from the Rho GTPase-activating protein 45 (ARHGAP45) and presented on HLA-A*02:01. The TCR comprises α and β subunits separated by a P2A self-cleaving peptide. The transgene also encodes a codon-optimised CD8 co-receptor consisting of α and β chains separated by a P2A self-cleaving peptide, with the CD8 co-receptor separated from the TCR by an additional P2A self-cleaving peptide. Each P2A sequence is preceded by a furin cleavage site. A 16 amino acid epitope encoding a portion of human CD34 is incorporated into the N-terminus of the CD8α chain. The transgene is under the control of a murine stem cell virus (MSCV) promoter, a Woodchuck hepatitis virus post-transcriptional response element and a simian virus 40 (SV40) polyadenylation (polyA) signal.
The transposase (Armyworm transposase) is introduced in form of an mRNA that comprises an anti-reverse cap analogue, a *Xenopus* globin 5' untranslated region (UTR), a Kozak sequence, the transposase open reading frame, and a *Xenopus* globin 3' UTR. The transgene is introduced via a nanoplasmid DNA vector and contains inverted terminal repeats (ITRs).
The leukapheresis material is electroporated with mRNA transposase as well as the nanoplasmid transposon followed by activation with CD2, CD3 and CD28 agonists. The cells are then grown in serum free media supplemented with interleukin 2 (IL-2), interleukin 7 (IL-7) and interleukin 15 (IL-15). The T lymphocytes (≥95%) are positive for the transgene (≥80% TCR+) and release interferon- gamma (IFN-γ) in response to co-culture with THP-1 cells that express the HA-1 target peptide

pézatresgène leucel

lymphocytes T allogéniques dérivés de cellules mononucléaires du sang périphérique (CMSP) d'un donneur haploidentiques de greffe de cellules hématopoïétiques (GCH) qui sont ngatifs pour le génotype HA-1 et/ou négatifs pour HLA A*02, modifiés par un système de délivrance de gènes par transposon/transposase pour exprimer un récepteur de lymphocytes T (TCR) spécifique d'un peptide de 9 acides aminés (VLHDDLLEA) appelé HA-1, dérivé de la protéine activatrice Rho GTPase 45 (ARHGAP45) et présenté sur HLA-A*02:01. Le TCR comprend des sous-unités α et β, séparées par un peptide auto-clivant P2A. Le transgène code également avec des codons optimisés un co-récepteur CD8, constitué de chaînes α et β, séparées par un peptide auto-clivant P2A, le co-récepteur CD8 étant séparé du TCR par un autre peptide auto-clivant P2A. Chaque séquence P2A est précédée d'un site de clivage de la furine. Un épitope de 16 acides aminés codant une partie du CD34 humain est incorporé à l'extrémité N-terminale de la chaîne CD8α. Le transgène est sous le contrôle d'un promoteur du virus des cellules souches murines (MSCV), d'un élément de réponse post-transcriptionnelle du virus de l'hépatite de la marmotte et d'un signal de polyadénylation (polyA) du virus simien 40 (SV40).
La transposase (transposase de la chenille légionnaire) est introduite sous la forme d'un ARNm qui comprend un analogue de la coiffe anti-inverse, une région 5' non traduite (UTR) de la globine de *Xenopus*, une séquence de Kozak, le cadre de lecture ouvert de la transposase et une région 3' UTR de la globine de *Xenopus*. Le transgène est introduit via l'ADN nanoplasmidique et contient des répétitions terminales inversées (RTI).
Le matériel de leucaphérèse est électroporé avec l'ARNm de la transposase ainsi que le transposon nanoplasmidique, suivie d'une activation avec des agonistes CD2, CD3 et CD28. Les cellules sont ensuite cultivées dans un milieu sans sérum, supplémenté en

	interleukine 2 (IL-2), d'interleukine 7 (IL-7) et d'interleukine 15 (IL-15). Les lymphocytes T (≥95%) sont positifs au transgène (≥80%+) et libèrent de l'interféron gamma (IFN-γ) en réponse à une co-culture avec des cellules THP-1 qui expriment le peptide cible HA-1
pezatresgén leucel	linfocitos T alogénicos derivados de células mononucleares de sangre periférica (PBMCs) de un donante de transplante de células hematopoyéticas (HCT) haploidéntico que es negativo para el genotipo HA-1 y/o negativo para HLA A*02, manipulados mediante un sistema de entrega genética mediado por transposón/transposasa para expresar el receptor de células T (TCR) que es específico para un péptido de 9 amino ácidos (VLHDDLLEA) llamado HA-1, derivado de la proteína activadora de GTPasa Rho 45 (ARHGAP45) y presentado en HLA-A*02:01. El TCR consta de subunidades α y β separadas por un péptido de auto-escisión P2A. El transgén también codifica, con codones optimizados, un correceptor CD8 que contiene cadenas α y β separadas por un péptido de auto-escisión P2A, con el correceptor CD8 separado del TCR por otro péptido de auto-escisión P2A. Cada secuencia P2A está precedida por un sitio de escisión de furina. En la zona N-terminal de la cadena CD8α se incorpora un epítopo de 16 amino ácidos que codifica una porción del CD34 humano. El transgén está bajo el control de un promotor del virus de células madre murino (MSCV), un elemento de respuesta post-transcripcional del virus de la hepatitis de la marmota (WPRE) y una señal de poliadenilación (poliA) del virus simio 40 (SV40). La transposasa (transposasa de gusano soldado) se introduce en forma de un ARNm que contiene un análogo de caperuza anti-reverso, una región sin traducir (UTR) en 5' de la globina de *Xenopus*, una secuencia Kozak, el marco de lectura abierto de la transposasa, y una UTR en 3' de la globina de *Xenopus*. El transgén se introduce mediante un nanoplásmido de ADN y contiene repeticiones terminales invertidas (ITRs). El material de leucoaféresis se electropora con el ARNm de la transposasa así como el nanoplásmido del transposónseguido de activación con agonistas de CD2, CD3 y CD28. Las células se crecen después en medio sin suero suplementado con interleuquina 2 (IL-2), interleuquina-7 (IL-7) e interleuquina 15 (IL-15). Los linfocitos T (≥95%) son positivos para el transgén (≥80% TCR+) y liberan interferón gamma (IFN-γ) en respuesta al co-cultivo con células diana THP-1 que expresan el péptido diana HA-1

pivodisgenum parvecum #

pivodisgene parvec	recombinant, non-replicating adeno-associated virus serotype 8 (rAAV8) vector, encoding a codon-optimised miniaturised version of human dystrophin (microdystrophin variant ABD1-H1-R1-R2-R3-H3-R24-H4-CR-CT194), under control of a synthetic muscle-specific promoter (SPc5-12) and a small synthetic polyadenylation signal; flanked by AAV2 inverted terminal repeats. The expressed microdystrophin variant contains the actin-binding domain 1 (ABD1), four rod domains (R1-3, R24), three hinge domains (H1, H3, H4) and a cysteine rich (CR) domain; it also features the proximal portion of the C-terminal domain, amino acids 3361-3554 (CT194)
pivodisgène parvec	vecteur recombinant de virus adéno-associé de sérotype 8 (rAAV8), non réplicatif, codant une version miniaturisée, optimisée en codons, de la dystrophine humaine (variante de microdystrophine ABD1-H1-R1-R2-R3-H3-R24-H4-CR-CT194),

	sous le contrôle d'un promoteur synthétique spécifique du muscle (SPc5-12) et d'un petit signal synthétique de polyadénylation; flanqué des répétitions terminales inversées AAV2. Le variant de microdystrophine exprimé contient le domaine de liaison à l'actine 1 (ABD1), quatre domaines en bâtonnets (R1-3, R24), trois domaines charnières (H1, H3, H4), et un domaine riche en cystéine (CR); il contient également la partie proximale du domaine C-terminal, acides aminés 3361-3554 (CT194)
pivodisgén parvec	vector de virus adenoasociado del serotipo 8, recombinante (rAAV8), no replicativo, que codifica, con codones optimizados, una versión miniaturizada de la distrofina humana (microdistrofina variante ABD1-H1-R1-R2-R3-H3-R24-H4-CR-CT194), bajo el control de un promotor sintético específico de musculo (SPc5-12) y una pequeña señal de poliadenilación sintética; flanqueado por las repeticiones terminales invertidas del AAV2. La variante de microdistrofina expresada contiene el dominio 1 de unión a actina (ABD1), cuatro dominios rod (R1-3, R24), tres dominios bisagra (H1, H3, H4) y un dominio rico en cisteína (CR); también presenta la porción proximal del domino C-terminal, amino ácidos 3361-3554 (CT194)

plencifgenum parvecum #

plencifgene parvec	recombinant, non-replicating adeno-associated virus (AAV) vector (with capsid variant A101) encoding codon-optimised human cystic fibrosis transmembrane conductance regulator (CFTR) with the regulatory domain deleted (CFTRΔR), under control of a 173bp cytomegalovirus (CMV173) minimal promoter and a short synthetic polyadenylation signal; flanked by AAV2 inverted terminal repeats. The variant A101 capsid is a chimera consisting primarily of serotype AAV1 but also including amino acids from serotypes AAV2, AAV4, AAV6 and AAV9
plencifgène parvec	vecteur de virus adéno-associé (AAV) recombinant, non réplicatif (avec variante de capside A101) codant un régulateur humain de conductance transmembranaire de la mucoviscidose (CFTR), optimisé en codons, avec le domaine régulateur supprimé (CFTRΔR), sous le contrôle d'un promoteur minimal de cytomégalovirus de 173 paires de bases (CMV173), et un court signal de polyadénylation synthétique; flanqué des répétitions terminales inversées AAV2. La capside variante A101 est une chimère, constituée principalement du sérotype AAV1, mais comprenant également des acides aminés des sérotypes AAV2, AAV4, AAV6 et AAV9
plencifgén parvec	vector de virus adenoasociado (AAV) recombinante, no replicativo (con la variante de cápside A101), que codifica, con codones optimizados, el regulador de la conductancia de transmembrana de la fibrosis quística (CFTR) humano con el domino regulador delecionado (CFTRΔR), bajo el control de un promotor mínimo de 173 bp del citomegalovirus (CMV173) y una señal sintética corta de poliadenilación; flanqueado por las repeticiones terminales invertidas de AAV2. La variante de cápside A101 es una quimera que consta primariamente del serotipo AAV1 pero también incluye amino ácidos de los serotipos AAV2, AAV4, AAV6 y AAV9

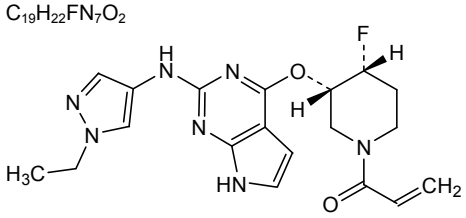
plodicitinibum

plodicitinib — 1-[(3*S*,4*R*)-3-({2-[(1-ethyl-1*H*-pyrazol-4-yl)amino]-7*H*-pyrrolo[2,3-*d*]pyrimidin-4-yl}oxy)-4-fluoropiperidin-1-yl]prop-2-en-1-one

plodicitinib — 1-[(3*S*,4*R*)-3-({2-[(1-éthyl-1*H*-pyrazol-4-yl)amino]-7*H*-pyrrolo[2,3-*d*]pyrimidin-4-yl}oxy)-4-fluoropipéridin-1-yl]prop-2-én-1-one

plodicitinib — 1-[(3*S*,4*R*)-3-({2-[(1-etil-1*H*-pirazol-4-il)amino]-7*H*-pirrolo[2,3-*d*]pirimidin-4-il}oxi)-4-fluoropiperidin-1-il]prop-2-en-1-ona

$C_{19}H_{22}FN_7O_2$



plozalizumabum plevistinagum #

plozalizumab plevistinag — immunoglobulin G1-kappa, anti-[*Homo sapiens* CCR2 (chemokine (C-C motif) receptor 2, C-C chemokine receptor 2, CC-CKR-2, CKR-2, monocyte chemoattractant protein 1 receptor, MCP-1-R, CD192)], humanized monoclonal antibody, conjugated, on an average of 3.8-4.4 cysteinyl residues, to *dazostinag* (a STING agonist) via a cleavable linker;
H-gamma1 heavy chain humanized (1-447) [VH (*Homo sapiens* IGHV3-73*01 (86.9%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.10.8] (26-33.51-60.99-106)) (1-117) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, 6-G1v3-1 A1.2, A1 (CH1 K120 (214) (118-215), hinge 1-15 (216-230), CH2 L1.2>A (235), G1>A (237) (231-340), CH3 D12 (356), L14 (358) (341-445), CHS (446-447)) (118-447)], (220-219')-disulfide with L-kappa light chain humanized (1'-219') [V-KAPPA (*Homo sapiens* IGKV2-30*02 (90.0%) -IGKJ5*01 (100%), CDR-IMGT [11.3.9] (27'-37'.55'-57'.94'-102')) (1'-112') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (158'), V101 (196')) (113'-219')]; dimer (226-226":229-229")-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 four L-cysteinyl residues on average among 220, 226, 229, 219', 220", 226", 229" and 219"' with (3*RS*)-1-[(28*S*)-28-{[(2*S*)-1-{[(2*S*)-1-{4-[({[(2-{cyclo[(*P*$^{3'}$*R*)-2'-deoxy-2'-fluoro-*P*-thioadenylyl-(3'→5')-(*P*$^{2'}$*R*)-7-fluoro-7-carba-*P*-thioinosinylyl-(2'→5')]-*N*$^{6.1}$-carbonyl}phenyl)methyl](methyl)carbamoyl}oxy)methyl]anilino}-1-oxopropan-2-yl]amino}-3-methyl-1-oxobutan-2-yl]carbamoyl}-26-oxo-2,5,8,11,14,17,20,23-octaoxa-27-azadotriacontan-32-yl]-2,5-dioxopyrrolidin-3-yl (*plevistinag*) groups

plozalizumab plévistinag — immunoglobuline G1-kappa, anti-[*Homo sapiens* CCR2 (récepteur 2 de chimiokine (C-C motif), récepteur 2 de chimiokine C-C, CC-CKR-2, CKR-2, récepteur de la protéine 1 chimio-attractive du monocyte, MCP-1-R, CD192)], anticorps monoclonal humanisé; conjugué, sur 4,1 (3,8-4,4) cystéinyl en moyenne, via un linker maléimide-peg-val-ala-PAB clivable, à un agoniste synthétique de STING1 (stimulateur de la réponse à l'interféron cGAMP interacteur 1), conjugué sur une moyenne de 3,8 à 4,4 résidus cystéinyle au *dazostinag* (un agoniste du STING) via un linker clivable;

	chaîne lourde H-gamma1 humanisée (1-447) [VH (*Homo sapiens* IGHV3-73*01 (86.9%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.10.8] (26-33.51-60.99-106)) (1-117) -*Homo sapiens* IGHG1*01 G1m17,1 CH1 K120, CH3 D12, L14, 6-G1v3-1 A1.2, A1 (CH1 K120 (214) (118-215), charnière 1-15 (216-230), CH2 L1.2>A (235), G1>A (237) (231-340), CH3 D12 (356), L14 (358) (341-445), CHS (446-447)) (118-447)], (220-219')-disulfure avec la chaîne légère L-kappa humanisée (1'-219') [V-KAPPA (*Homo sapiens* IGKV2-30*02 (90.0%) -IGKJ5*01 (100%), CDR-IMGT [11.3.9] (27'-37'.55'-57'.94'-102')) (1'-112') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (158'), V101 (196')) (113'-219')]; dimère (226-226":229-229")-bisdisulfure, produit dans une lignée cellulaire des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1, glycoforme alfa, substitué sur les atomes de soufre de 4 résidus L-cystéinyle en moyenne parmi 220, 226, 229, 219', 220", 226", 229" et 219"' avec des groupes (3*RS*)-1-[(28*S*)-28-{[(2*S*)-1-{[(2*S*)-1-{4-[({[(2-{cyclo[(*P*$^{3'}$*R*)-2'-désoxy-2'-fluoro-*P*-thioadénylyl-(3'→5')-(*P*$^{2'}$*R*)-7-fluoro-7-carba-*P*-thioinosinylyl-(2'→5')]-*N*$^{6.1}$-carbonyl}phényl)méthyl](méthyl)carbamoyl}oxy)méthyl]anilino}-1-oxopropan-2-yl]amino}-3-méthyl-1-oxobutan-2-yl]carbamoyl}-26-oxo-2,5,8,11,14,17,20,23-octaoxa-27-azadotriacontan-32-yl]-2,5-dioxopyrrolidin-3-yle (*plévistinag*)
plozalizumab plevistinag	inmunoglobulina G1-kappa, anti-[*Homo sapiens* CCR2 (receptor 2 de quimiokina (C-C motif), receptor 2 de quimiokina C-C, CC-CKR-2, CKR-2, receptor de la proteína 1 quimioatrayente de monocitos, MCP-1-R, CD192)], anticuerpo monoclonal humanizado, conjugado, en un promedio de 3,8-4,4 residuos de cisteinilo, al *dazostinag* (un agonista del STING), a través de un enlace escindible; cadena pesada gamma1 humanizada (1-447) [VH (*Homo sapiens* IGHV3-73*01 (86.90%) -(IGHD)-IGHJ1*01 (100%), CDR-IMGT [8.10.8] (26-33.51-60.99-106)) (1-117) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, 6-G1v3-1 A1.2, A1 (CH1 K120 (214) (118-215), bisagra 1-15 (216-230), CH2 L1.2>A (235), G1>A (237) (231-340), CH3 D12 (356), L14 (358) (341-445), CHS (446-447)) (118-447)], (220-219')-disulfuro con la cadena ligera L-kappa humanizada (1'-219') [V-KAPPA (*Homo sapiens* IGKV2-30*02 (90.0%) -IGKJ5*01 (100%), CDR-IMGT [11.3.9] (27'-37'.55'-57'.94'-102')) (1'-112') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (158'), V101 (196'))(113'-219')]; dímero (226-226":229-229")-bisdisulfuro, producido en una línea celular de las células ováricas de hámster chino (CHO), línea celular derivada de CHO-K1, forma glicosilada alfa, substituido en los átomo de azufre de 4 residuos L-cisteinilo por término medio entre 220, 226, 229, 219', 220", 226", 229" y 219"' con grupos (3*RS*)-1-[(28*S*)-28-{[(2*S*)-1-{[(2*S*)-1-{4-[({[(2-{ciclo[(*P*$^{3'}$*R*)-2'-desoxi-2'-fluoro-*P*-tioadenilil-(3'→5')-(*P*$^{2'}$*R*)-7-fluoro-7-carba-*P*-tioinosinilil-(2'→5')]-*N*$^{6.1}$-carbonil}fenil)metil](metil)carbamoil}oxi)metil]anilino}-1-oxopropan-2-il]amino}-3-metil-1-oxobutan-2-il]carbamoil}-26-oxo-2,5,8,11,14,17,20,23-octaoxa-27-azadotriacontan-32-il]-2,5-dioxopirrolidin-3-ilo (*plevistinag*)

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVKPGGSLRL SCAASGFTFS AYAMNWVRQA PGKGLEWVGR  50
IRTKNNNYAT YYADSVKDRF TISRDDSKNT LYLQMNSLKT EDTAVYYCTT 100
FYGNGVWGQG TLVTVSSAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF 150
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC 200
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELAGAPSV FLFPPKPKDT 250
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT 350
LPPSRDELTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS 400
DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPGK    447
```

Light chain / Chaîne légère / Cadena ligera

```
DVVMTQSPLS LPVTLGQPAS ISCKSSQSLL DSDGKTFLNW FQQRPGQSPR  50
RLIYLVSKLD SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCWQGTHFP 100
YTFGQGTRLE 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

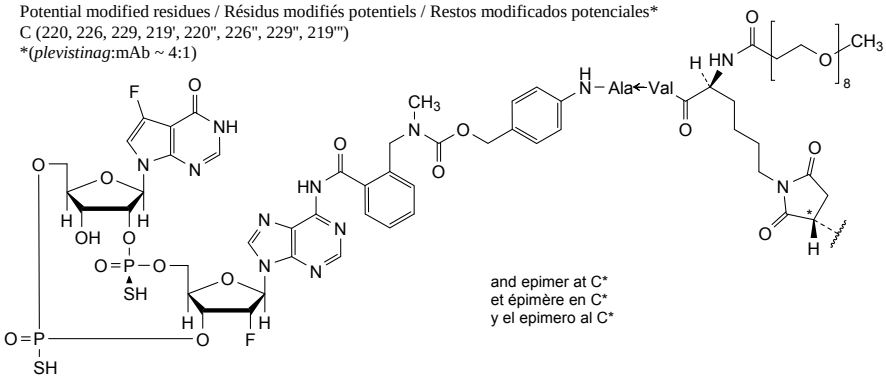
Intra-H (C23-C104) 22-98 144-200 261-321 367-425
22"-98" 144"-200" 261"-321" 367"-425"
Intra-L (C23-C104) 23'-93' 139'-199'
23'"-93'" 139'"-199'"
Inter-H-L (h 5-CL 126)* 220-219' 220"-219'"
Inter-H-H (h 11, h 14)* 226-226" 229-229"

*The four inter-chain disulfide bridges are not present, an average of 4.1 (3.8-4.4) cysteinyl being conjugated, each via two thioether bonds, to a drug linker.
*Les quatre ponts disulfures inter-chaînes ne sont pas présents, de 4.1 (3.8-4.4) cystéinyl en moyenne étant chacune conjuguée, via deux liaisons thioéther, à un linker-principe actif.
*Los cuatro puentes disulfuro inter-catenarios no estan presentes, una media de 4.1 (3.8-4.4) cisteinil está conjugada, a través de dos enlaces tioéter, con un principio activo.

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"

Potential modified residues / Résidus modifiés potentiels / Restos modificados potenciales*
C (220, 226, 229, 219', 220", 226", 229", 219'")
*(*plevistinag*:mAb ~ 4:1)



potravitugum #

potravitug immunoglobulin G1-kappa, anti-[BK polyomavirus (BKV) (betapolyomavirus hominis) major capsid protein VP1], *Homo sapiens* monoclonal antibody;

	H-gamma1 heavy chain *Homo sapiens* (1-451) [VH (*Homo sapiens* IGHV4-34*01 (87.5%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.7.15] (26-33.51-57.96-110)) (1-121) -*Homo sapiens* IGHG1*03v (100%) 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)], (224-215')-disulfide with L-kappa light chain *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (95.8%) -IGKJ3*01 (91.7%), CDR-IMGT [7.3.9] (27'-33'.51'-53'.90'-98')) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (154'), V101 (192')) (109'- 215')]; dimer (230-230":233-233")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, lacking the glutamine synthetase (GS-KO) gene, glycoform alfa
potravitug	immunoglobuline G1-kappa, anti-[protéine majeure VP1 de la capside du polyomavirus BK (BKV) (betapolyomavirus hominis)], anticorps monoclonal *Homo sapiens*; chaîne lourde H-gamma1 *Homo sapiens* (1-451) [VH (*Homo sapiens* IGHV4-34*01 (87.5%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.7.15] (26-33.51-57.96-110)) (1-121) -*Homo sapiens* IGHG1*03v (100%) 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)], (224-215')-disulfure avec la chaîne légère L-kappa *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (95.8%) -IGKJ3*01 (91.7%), CDR-IMGT [7.3.9] (27'-33'.51'-53'.90'-98')) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (154'), V101 (192')) (109'- 215')]; dimère (230-230":233-233")-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
potravitug	inmunoglobulina G1-kappa, anti-[proteína importante VP1 de la cápside del poliomavirus BK (BKV) (betapoliomavirus hominis)], anticuerpo monoclonal *Homo sapiens*; cadena pesada H-gamma1 *Homo sapiens* (1-451) [VH (*Homo sapiens* IGHV4-34*01 (87.5%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.7.15] (26-33.51-57.96-110)) (1-121) -*Homo sapiens* IGHG1*03v (100%) 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)], (224-215')-disulfuro con la cadena ligera L-kappa *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (95.8%) -IGKJ3*01 (91.7%), CDR-IMGT [7.3.9] (27'-33'.51'-53'.90'-98')) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (154'), V101 (192')) (109'- 215')]; dímero (230-230":233-233")-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

```
QVQLQQWGAG LLKPSETLSL TCAVYRGSFS AYYWTWFRQP PGKGLEWIGE  50
INHRGYTNYN PSLRGRVSIS VDTSKKQFSL KLRSVNAADT AVYYCATLRS 100
TSGWHDYFDY WGQGTLVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200
TYICNVNHKP SNTKVDKKVE PKSCDKTHTC PPCPAPELLG GPSVFLFPPK 250
PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY 300
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP 350
QVYTLPPSRE EMTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP 400
VLDSDGSFFL YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG 450
K                                                       451
```

Light chain / Chaîne légère / Cadena ligera

```
EIVLTQSPGT LSLSPGERAT LSCRASQSVS SSYLAWYQQT PGQAPRLLIY  50
GASSRATGIP DRFSGSGSGT DFTLTISRLE PEDFVVYFCL QYGSSPLTFG 100
PGTKVDIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK 150
VDNALQSGNS QESVTEQDSK DSTYSLSSTL TLSKADYEKH KVYACEVTHQ 200
GLSSPVTKSF NRGEC                                       215
```

Post-translational modifications

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

Intra-H (C23-C104) 22-95 148-204 265-325 371-429
22"-95" 148"-204" 265"-325" 371"-429"
Intra-L (C23-C104) 23'-89' 135'-195'
23'"-89'" 135'"-195'"
Inter-H-L (h 5-CL 126) 224-215' 224"-215'"
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

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

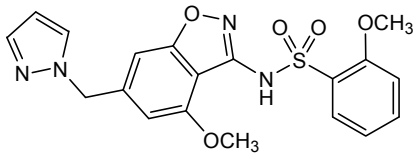
prifetrastatum

prifetrastat — 2-methoxy-*N*-{4-methoxy-6-[(1*H*-pyrazol-1-yl)methyl]-1,2-benzoxazol-3-yl}benzene-1-sulfonamide

prifétrastat — 2-méthoxy-*N*-{4-méthoxy-6-[(1*H*-pyrazol-1-yl)méthyl]-1,2-benzoxazol-3-yl}benzène-1-sulfonamide

prifetrastat — 2-metoxi-*N*-{4-metoxi-6-[(1*H*-pirazol-1-il)metil]-1,2-benzoxazol-3-il}benceno-1-sulfonamida

$C_{19}H_{18}N_4O_5S$

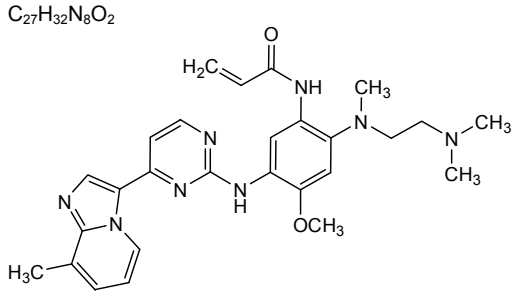


pruvonertinibum

pruvonertinib — *N*-(2-{[2-(dimethylamino)ethyl](methyl)amino}-4-methoxy-5-{[4-(8-methylimidazo[1,2-*a*]pyridin-3-yl)pyrimidin-2-yl]amino}phenyl)prop-2-enamide

pruvonertinib — *N*-(2-{[2-(diméthylamino)éthyl](méthyl)amino}-4-méthoxy-5-{[4-(8-méthylimidazo[1,2-*a*]pyridin-3-yl)pyrimidin-2-yl]amino}phényl)prop-2-énamide

pruvonertinib — *N*-(2-{[2-(dimetilamino)etil](metil)amino}-5-{[4-(8-metilimidazo[1,2-*a*]piridin-3-il)pirimidin-2-il]amino}-4-metoxifenil)prop-2-enamida



puliretgenum parvecum #

puliretgene parvec — recombinant non-replicating adeno-associated virus serotype 8 (rAAV8) vector encoding human cytochrome P450 family 4, subfamily V member 2 (CYP4V2) under control of a cytomegalovirus (CMV) immediate-early enhancer, chicken β-actin promoter and synthetic intron, and a bovine somatotropin polyadenylation signal; flanked by AAV2 inverted terminal repeats

puliretgène parvec — vecteur recombinant de virus adéno-associé non réplicatif de sérotype 8 (rAAV8) codant le membre 2 de la sous-famille V, famille 4 du cytochrome P450 humain (CYP4V2), sous le contrôle d'un amplificateur précoce immédiat du cytomégalovirus (CMV), d'un promoteur de β-actine de poulet et d'un intron synthétique, ainsi que d'un signal de polyadénylation de la somatotropine bovine; flanqué des répétitions terminales inversées AAV2

puliretgén parvec — vector de virus adenoasociado del serotipo 8, recombinante (rAAV8), no replicativo, que codifica el miembro 2 de la subfamilia V, familia 4 del citocromo P450 (CYP4V2) bajo el control de un potenciador inmediato-temprano de citomegalovirus (CMV), promotor de la β-actina de pollo y un intrón sintético, y una señal de poliadenilación de la somatotropina bovina; flanqueado por las repeticiones terminales invertidas del AAV2

pumitamigum #

pumitamig — immunoglobulin (H-gamma1-VH_L-kappa) dimer, anti-[*Homo sapiens* VEGFA (vascular endothelial growth factor A, VEGF-A, VEGF)] 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, tetravalent;
H-gamma1 heavy chain anti-VEGFA fused to a VH anti-CD274 (1-578) [H-gamma1 heavy chain anti-VEGFA humanized (1-452) [VH (*Homo sapiens* IGHV3-30*02 (76.8%) -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [8.9.16] (26-33.51-59.97-112)) (1-123)-*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, 6-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 K2>del (452)) (124-452)] -11-mer bis(tetraglycyl-seryl)-glycyl linker (453-463) -VH anti-CD274 humanized (*Homo sapiens* IGHV3-74*01 (88.8%) -(IGHD) -IGHJ3*01 (90.0%) W113>K (568), M118>Q (573), CDR-IMGT [8.8.8] (489-496.514-521.560-567)) (464-578)]; (226-214')-disulfide with L-kappa light chain humanized

	(1'-214') [V-KAPPA (*Homo sapiens* IGKV1-16*01 (88.4%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dimer (232-232":235-235")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-S, glycoform alfa
pumitamig	immunoglobuline (H-gamma1-VH_L-kappa) dimère, anti-[*Homo sapiens* VEGFA facteur de croissance A de l'endothélium vasculaire, VEGF-A, VEGF)] et anti-[*Homo sapiens* CD274 (ligand 1 de la protéine 1 de mort cellulaire programmée, PDL1, PD-L1, homologue B7.1, PDCD1LG1)], anticorps monoclonal humanisé, bispécifique, tétravalent; chaîne lourde H-gamma1 anti-VEGFA fusionnée à un VH anti-CD274 (1-578) [chaine lourde H-gamma1 anti-VEGFA humanisée (1-452) [VH (*Homo sapiens* IGHV3-30*02 (76.8%) -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [8.9.16] (26-33.51-59.97-112)) (1-123)-*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, 6-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 K2>del (452)) (124-452)] -11-mer bis(tétraglycyl-séryl)-glycyl linker (453-463) -VH anti-CD274 humanisée (*Homo sapiens* IGHV3-74*01 (88.8%) -(IGHD) -IGHJ3*01 (90.0%) W113>K (568), M118>Q (573), CDR-IMGT [8.8.8] (489-496.514-521.560-567)) (464-578)]; (226-214')-disulfure avec la chaîne légère L-kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-16*01 (88.4%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dimère (232-232":235-235")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-S, glycoforme alfa
pumitamig	inmunoglobulina (H-gamma1-VH_L-kappa) dímero, anti-[*Homo sapiens* VEGFA factor de crecimiento A del endotelio vascular, VEGF-A, VEGF)] y anti-[*Homo sapiens* CD274 (ligando 1 de la proteína 1 de muerte celular programada, PDL1, PD-L1, homólogo B7.1, PDCD1LG1)], anticuerpo monoclonal humanizado, biespecífico, tetravalente; cadena pesada H-gamma1 anti-VEGFA fusionada con un VH anti-CD274 (1-578) [cadena pesada H-gamma1 anti-VEGFA humanizada (1-452) [VH (*Homo sapiens* IGHV3-30*02 (76.8%) -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [8.9.16] (26-33.51-59.97-112)) (1-123)-*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, 6-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 K2>del (452)) (124-452)] -11-mer bis(tetraglicil-seril)-glicil enlace (453-463) -VH anti-CD274 humanizada (*Homo sapiens* IGHV3-74*01 (88.8%) -(IGHD) -IGHJ3*01 (90.0%) W113>K (568), M118>Q (573), CDR-IMGT [8.8.8] (489-496.514-521.560-567)) (464-578)]; (226-214')-disulfuro con la cadena ligera L-kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-16*01 (88.4%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dímero (232-232":235-235")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-S, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada:
H-gamma1 anti-VEGFA fused to VH anti-CD274 (H, H")

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EVQLVESGGG LVQPGGSLRL SCAASGYTFT NYGMNWVRQA PGKGLEWVGW  50
INTYTGEPTY AADFKRRFTF SLDTSKSTAY LQMNSLRAED TAVYYCAKYP 100
HYYGSSHWYF DVWGQGTLVT 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
PGGGGGSGGG GSGEVQLQES GGGLVQPGGS LRLSCAASGF TFSSYWMYWL 500
RQAPGKGLEW VSSINSDSSS TYYRDSVKGR FTISRDNAKN TLYLQMNSLK 550
SEDTAVYYCA KDPGGYAKGQ GTQVTVSS                         578
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Light chain / Chaîne légère / Cadena ligera: L-kappa : anti-VEGFA (L', L"')

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DIQMTQSPSS LSASVGDRVT ITCSASQDIS NYLNWYQQKP GKAPKVLIYF  50
TSSLHSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YSTVPWTFGQ 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                       214
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Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 150-206 267-327 373-431 485-559
22"-96" 150"-206" 267"-327" 373"-431" 485"-559"
Intra-L (C23-C104) 23'-88' 134'-194'
23"'-88"' 134"'-194"'
Intra-H-L (h 5-CL 126) 226-214' 226"-214"'
Inter-H-H (h 11, h 14) 232-232" 235-235"

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

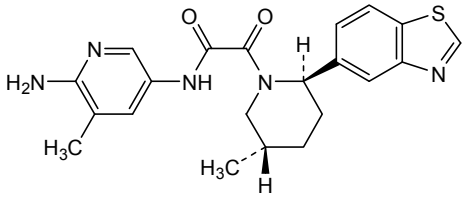
ralometostatum

ralometostat — *N*-(6-amino-5-methylpyridin-3-yl)-2-[(2*R*,5*S*)-2-(1,3-benzothiazol -5-yl)-5-methylpiperidin-1-yl]-2-oxoacetamide

ralométostat — *N*-(6-amino-5-méthylpyridin-3-yl)-2-[(2*R*,5*S*)-2-(1,3-benzothiazol-5-yl)-5-methylpiperidin-1-yl]-2-oxoacetamide

ralometostat — *N*-(6-amino-5-metilpiridin-3-il)-2-[(2*R*,5*S*)-2-(1,3-benzotiazol-5-il)-5-metilpiperidin-1-il]-2-oxoacetamida

$C_{21}H_{23}N_5O_2S$



ramantamigum

ramantamig — immunoglobulin (H-gamma1-scFvkh_L-lambda2)_scFvkh-G1(h-CH2-CH3), anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], anti-[*Homo sapiens* GPRC5D (G protein-coupled receptor class C group 5 member D)] and anti-[*Homo sapiens* TNFRSF17 (tumor necrosis factor (TNF) receptor superfamily member 17, B cell maturation antigen, BCMA, TNFRSF13A, CD269)], *Homo sapiens* monoclonal antibody; trispecific, trivalent;
H-gamma1 heavy chain anti-CD3E fused to a scFvkh anti-GPRC5D (1-721) [H-gamma1 heavy chain anti-CD3E *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV6-1*01 (88.1%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [10.9.10] (26-35.53-61.100-109)) (1-120)-*Homo sapiens*

IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, 6-G1v14-67 CH2 A1.3, A1.2, S27, 14-G1v33 CH3 S22, A24, V86 (hole), 10-G1v83 CH3 R115, F116 (CH1 R120>K (217) (121-218), hinge 1-15 (219-233), CH2 L1.3>A (237), L1.2>A (238), D27>S (268) (234-343), CH3 E12 (359), M14 (361), T22>S (369), L24>A (371), Y86>V (410), H115>R (438), Y116>F (439) (344-448), CHS (449-450)) (121-450)] -20-mer tetrakis(tetraglycyl-seryl) linker (451-470) -scFvkh anti-GPRC5D *Homo sapiens* (471-721) [V-KAPPA (*Homo sapiens* IGKV2-24*01 (99.0%) -IGKJ2*02 (100%), CDR-IMGT [11.3.9] (497-507.525-527.564-572)) (471-582) -20-mer (GGSEGKSSGSGSESKSTGGS) linker (583-602) -VH (*Homo sapiens* IGHV2-26*04 (93.9%) -IGHD -IGHJ6*01 (100%), CDR-IMGT [10.7.11] (628-637.655-661.700-710)) (603-721)]]; (223-215')-disulfide with L-lambda2 light chain anti-CD3E *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV2-23*02 (84.8%) -IGLJ2*01 (90.9%), CDR-IMGT [9.3.10] (26'-34'.52'-54'.91'-100')) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (C-LAMBDA2) (111'-216')];
fused heavy chain scFvkh-G1(h-CH2-CH3) anti-TNFRSF17 *Homo sapiens* (1''-484'') [scFvkh anti-TNFRSF17 *Homo sapiens* (1''-252'') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (94.8%) -IGKJ2*01 (100%), CDR-IMGT [7.3.10] (27''-33''.51''-53''.90''-99'')) (1''-109'') -20-mer (GGSEGKSSGSGSESKSTGGS) linker (110''-129'') -[VH (*Homo sapiens* IGHV3-23*01 (100%) -(IGHD) -IGHJ6*01 (94.4%), CDR-IMGT [8.8.16] (155''-162''.180''-187''.226''-241'')) (130''-252'')] -*Homo sapiens* IGHG1*03v h-CH2-CH3-CHS, nG1m1 CH3 E12, M14, 6-G1v14-67 CH2 A1.3, A1.2, S27, 14-G1v32 CH3 W22 (knob), 15-G1v37 hinge S5 [(hinge 1-15 C5>S(257'') (253''-267''), CH2 L1.3>A (271''), L1.2>A (272''), D27>S (302'') (268''-377''), CH3 E12 (393''), M14 (395''), T22>W (403'') (378''-482''), CHS (483''-484'')) (253''-484'')]]; dimer (229-263'': 232-266'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

ramantamig

immunoglobuline (H-gamma1-scFvkh_L-lambda2)_ scFvkh-G1(h-CH2-CH3), anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], anti-[*Homo sapiens* GPRC5D (membre D du groupe 5 de la classe C des récepteurs couplés aux protéines G)] and anti-[*Homo sapiens* TNFRSF17 (membre 17 de la superfamille des récepteurs du facteur de nécrose tumorale (TNF), antigène de maturation de cellule B, BCMA, TNFRSF13A, CD269)], anticorps monoclonal *Homo sapiens*; trispécifique, trivalent;
chaîne lourde H-gamma1 anti-CD3E fusionnée à un scFvkh anti-GPRC5D (1-721) [H-gamma1 heavy chain anti-CD3E *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV6-1*01 (88.1%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [10.9.10] (26-35.53-61.100-109)) (1-120)-*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, 6-G1v14-67 CH2 A1.3, A1.2, S27, 14-G1v33 CH3 S22, A24, V86 (hole), 10-G1v83 CH3 R115, F116 (CH1 R120>K (217) (121-218), charnière 1-15 (219-233), CH2 L1.3>A (237), L1.2>A (238), D27>S (268) (234-343), CH3 E12 (359), M14 (361), T22>S (369), L24>A (371), Y86>V (410), H115>R (438), Y116>F (439) (344-448), CHS (449-450)) (121-450)] -20-mer tétrakis(tétraglycyl-séryl) linker (451-470) -scFvkh anti-GPRC5D *Homo sapiens* (471-721) [V-KAPPA (*Homo sapiens* IGKV2-24*01 (99.0%) -IGKJ2*02 (100%), CDR-IMGT [11.3.9] (497-507.525-527.564-572)) (471-582) -20-mer (GGSEGKSSGSGSESKSTGGS) linker (583-602) -VH (*Homo sapiens* IGHV2-26*04 (93.9%) -IGHD -IGHJ6*01 (100%), CDR-IMGT [10.7.11] (628-637.655-661.700-710)) (603-721)]]; (223-215')-disulfure avec la chaîne légère L-lambda2 anti-CD3E *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV2-23*02 (84.8%) -IGLJ2*01 (90.9%), CDR-IMGT [9.3.10] (26'-34'.52'-54'.91'-100')) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (C-LAMBDA2) (111'-216')];

	chaîne lourde fusionnée scFvkh-G1(h-CH2-CH3) anti-TNFRSF17 *Homo sapiens* (1''-484'') [scFvkh anti-TNFRSF17 *Homo sapiens* (1''-252'') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (94.8%) -IGKJ2*01 (100%), CDR-IMGT [7.3.10] (27''-33''.51''-53''.90''-99'')) (1''-109'') -20-mer (GGSEGKSSGSGSESKSTGGS) linker (110''-129'') -[VH (*Homo sapiens* IGHV3-23*01 (100%) -(IGHD) -IGHJ6*01 (94.4%), CDR-IMGT [8.8.16] (155''-162''.180''-187''.226''-241'')) (130''-252'')] -*Homo sapiens* IGHG1*03v h-CH2-CH3-CHS, nG1m1 CH3 E12, M14, 6-G1v14-67 CH2 A1.3, A1.2, S27, 14-G1v32 CH3 W22 (knob), 15-G1v37 charnière S5 [(charnière 1-15 C5>S(257'') (253''-267''), CH2 L1.3>A (271''), L1.2>A (272''), D27>S (302'') (268''-377''), CH3 E12 (393''), M14 (395''), T22>W (403'') (378''-482''), CHS (483''-484'')) (253''-484'')]]; dimère (229-263'': 232-266'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa
ramantamig	inmunoglobulina (H-gamma1-scFvkh_L-lambda2)_ scFvkh-G1(h-CH2-CH3), anti-[*Homo sapiens* CD3E (CD3 épsilon, Leu-4)], anti-[*Homo sapiens* GPRC5D (miembro D del grupo 5 de la clase C de los receptores acoplados a proteínas G)] y anti-[*Homo sapiens* TNFRSF17 (miembro 17 de la superfamilia de los receptores del factor de necrosis tumoral (TNF), antígeno de maduración de célula B, BCMA, TNFRSF13A, CD269)], anticuerpo monoclonal *Homo sapiens*; triespecífico, trivalente; cadena pesada H-gamma1 anti-CD3E fusionada con un scFvkh anti-GPRC5D (1-721) [H-gamma1 cadena pesada anti-CD3E *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV6-1*01 (88.1%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [10.9.10] (26-35.53-61.100-109)) (1-120)-*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, 6-G1v14-67 CH2 A1.3, A1.2, S27, 14-G1v33 CH3 S22, A24, V86 (hole), 10-G1v83 CH3 R115, F116 (CH1 R120>K (217) (121-218), bisagra 1-15 (219-233), CH2 L1.3>A (237), L1.2>A (238), D27>S (268) (234-343), CH3 E12 (359), M14 (361), T22>S (369), L24>A (371), Y86>V (410), H115>R (438), Y116>F (439) (344-448), CHS (449-450)) (121-450)] -20-mer tetrakis(tetraglicil-seril) enlace (451-470) -scFvkh anti-GPRC5D *Homo sapiens* (471-721) [V-KAPPA (*Homo sapiens* IGKV2-24*01 (99.0%) -IGKJ2*02 (100%), CDR-IMGT [11.3.9] (497-507.525-527.564-572)) (471-582) -20-mer (GGSEGKSSGSGSESKSTGGS) enlace (583-602) -VH (*Homo sapiens* IGHV2-26*04 (93.9%) -IGHD -IGHJ6*01 (100%), CDR-IMGT [10.7.11] (628-637.655-661.700-710)) (603-721)]]; (223-215')-disulfuro con la cadena ligera L-lambda2 anti-CD3E *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV2-23*02 (84.8%) -IGLJ2*01 (90.9%), CDR-IMGT [9.3.10] (26'-34'.52'-54'.91'-100')) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (C-LAMBDA2) (111'-216')]; cadena pesada fusionada scFvkh-G1(h-CH2-CH3) anti-TNFRSF17 *Homo sapiens* (1''-484'') [scFvkh anti-TNFRSF17 *Homo sapiens* (1''-252'') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (94.8%) -IGKJ2*01 (100%), CDR-IMGT [7.3.10] (27''-33''.51''-53''.90''-99'')) (1''-109'') -20-mer (GGSEGKSSGSGSESKSTGGS) enlace (110''-129'') -[VH (*Homo sapiens* IGHV3-23*01 (100%) -(IGHD) -IGHJ6*01 (94.4%), CDR-IMGT [8.8.16] (155''-162''.180''-187''.226''-241'')) (130''-252'')] -*Homo sapiens* IGHG1*03v h-CH2-CH3-CHS, nG1m1 CH3 E12, M14, 6-G1v14-67 CH2 A1.3, A1.2, S27, 14-G1v32 CH3 W22 (knob), 15-G1v37 bisagra S5 [(bisagra 1-15 C5>S(257'') (253''-267''), CH2 L1.3>A (271''), L1.2>A (272''), D27>S (302'') (268''-377''), CH3 E12 (393''), M14 (395''), T22>W (403'') (378''-482''), CHS (483''-484'')) (253''-484'')]]; dímero (229-263'': 232-266'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada: fused H-gamma1 anti-CD3E -scFvkh anti-GPRC5D (H) (hole)

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QVQLQQSGPR LVRPSQTLSL TCAISGDSVF NNNAAWSWIR QSPSRGLEWL  50
GRTYYRSKWL YDYAVSVKSR ITVNPDTSRN QFTLQLNSVT PEDTALYYCA 100
RGYSSSFDYW GQGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPEAAGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVSVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSREE MTKNQVSLSC AVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLV SKLTVDKSRW QQGNVFSCSV MHEALHNRFT QKSLSLSPGK 450
GGGGSGGGGS GGGGSGGGGS DIVMTQTPLS SPVTLGQPAS ISCRSSQSLV 500
HSDGNTYLSW LQQRPGQPPR LLIYKISNRF FGVPDRFSGS GAGTDFTLKI 550
SRVEAEDVGV YYCMQATQFP HTFGQGTKLE IKGGSEGKSS GSGSESKSTG 600
GSQVTLKESG PVLVKPTETL TLTCTVSGFS LTNIRMSVSW IRQPPGKALE 650
WLAHIFSNDE KSYSTSLKSR LTISRDTSKS QVVLTLTNVD PVDTATYYCA 700
RMRLPYGMDV WGQGTTVTVS S                                 721
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Light chain / Chaîne légère / Cadena ligera: L-kappa anti-CD3E (L')

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QSALTQPASV SGSPGQSITI SCTGTSSNIG TYKFVSWYQQ HPDKAPKVLL  50
YEVSKRPSGV SSRFSGSKSG NTASLTISGL QAEDQADYHC VSYAGSGTLL 100
FGGGTKLTVL GQPKAAPSVT LFPPSSEELQ ANKATLVCLI SDFYPGAVTV 150
AWKADSSPVK AGVETTTPSK QSNNKYAASS YLSLTPEQWK SHRSYSCQVT 200
HEGSTVEKTV APTECS                                      216
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Heavy chain / Chaîne lourde / Cadena pesada: fused scFvkh anti-TNFRSF17 -G1(h-CH2-CH3) (H") (knob)

```
EIVLTQSPGT LSLSPGERAT LSCRASQSIS SSFLTWYQQK PGQAPRLLIY  50
GASSRATGIP DRFSGGGSGT DFTLTISRLE PEDFAVYYCQ HYGSSPMYTF 100
GQGTKLEIKG GSEGKSSGSG SESKSTGGSE VQLLESGGGL VQPGGSLRLS 150
CAASGFTFSS YAMSWVRQAP GKGLEWVSAI SGSGGSTYYA DSVKGRFTIS 200
RDNSKNTLYL QMNSLRAEDT AVYYCAKDEG YSSGHYYGMD VWGQGTTVTV 250
SSEPKSSDKT HTCPPCPAPE AAGGPSVFLF PPKPKDTLMI SRTPEVTCVV 300
VSVSHEDPEV KFNWYVDGVE VHNAKTKPRE EQYNSTYRVV SVLTVLHQDW 350
LNGKEYKCKV SNKALPAPIE KTISKAKGQP REPQVYTLPP SREEMTKNQV 400
SLWCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS FFLYSKLTVD 450
KSRWQQGNVF SCSVMHEALH NHYTQKSLSL SPGK                  484
```

Post-translational modifications

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-99 147-203 264-324 370-428 493-563 624-699 23"-89" 151"-225" 298"-358" 404"-462"
Intra-L (C23-C104) 22'-90' 138'-197'
Intra-H-L (h 5-CL 126) 223-215'
Inter-H-H (h 11, h 14) 229-263" 232-266"

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: 300, 334"
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: 484"

ranicabtagenum autoleucelum

ranicabtagene autoleucel

autologous T lymphocytes obtained from peripheral blood mononuclear cells by leukapheresis, transduced with a non-replicating gamma-retroviral vector, encoding a chimeric antigen receptor targeting CD19, comprising a CD8α signal peptide, an anti-CD19 single chain variable fragment (scFv) (derived from clone FMC63), a CD8α hinge, a CD28 transmembrane region, an intracellular CD28 co-stimulatory and a CD3ζ signalling domain. The construct is flanked by 5' and 3' long terminal repeats (LTRs), derived from the myeloproliferative sarcoma virus (MPSV) and the murine embryonic stem cell virus (MESV), which contain a 5' LTR promoter and 3' LTR termination sequence. The vector also contains a psi packaging signal and is pseudotyped with gibbon ape

	leukemia virus (GALV) Env glycoprotein. The leukapheresis material is enriched for CD3+ T lymphocytes by positive immunoselection, prior to activation with CD3 and CD28 agonists. The cells are then transduced with the retroviral vector and expanded in media containing interleukin 2 (IL-2). The T lymphocytes (≥90%) are positive for the transgene (≥20% CAR positive), express CD107a (≥20%) and demonstrate cytotoxicity towards CD19 expressing cells
ranicabtagène autoleucel	lymphocytes T autologues obtenus à partir de cellules mononucléaires du sang périphérique par leucaphérèse, transduits avec un vecteur gamma-rétroviral non réplicatif, codant un récepteur antigénique chimérique ciblant CD19, comprenant un peptide signal CD8α, un fragment variable à chaîne unique anti-CD19 (scFv) (dérivé du clone FMC63), une charnière CD8α, une région transmembranaire CD28, un domaine intracellulaire de co-stimulation CD28 et un domaine de signalisation CD3ζ. La construction est flanquée de répétitions terminales longues (LTRs) en 5' et en 3', dérivées du virus du sarcome myéloprolifératif (MPSV) et du virus des cellules souches embryonnaires murines (MESV), qui contiennent un promoteur LTR en 5', et une séquence de terminaison LTR en 3'. Le vecteur contient également un signal d'emballage ψ et est pseudotypé avec la glycoprotéine Env du virus de la leucémie du singe gibbon (GALV). Le matériel de leucaphérèse est enrichi en lymphocytes T CD3+ par immunosélection positive, avant activation avec des agonistes CD3 et CD28. Les cellules sont ensuite transduites avec le vecteur rétroviral et expansées dans un milieu contenant de l'interleukine 2 (IL-2). Les lymphocytes T (≥90%) sont positifs pour le transgène (≥20% RAC positifs), expriment CD107a (≥20%) et présentent une cytotoxicité envers les cellules exprimant CD19
ranicabtagén autoleucel	linfocitos T autólogos obtenidos de células mononucleares de sangre periférica por leucoaféresis, transducidos con un vector gamma retroviral, no replicativo, que codifica un receptor de antígenos quimérico dirigido a CD19, que consta de un péptido señal de CD8α, un fragmento variable de cadena sencilla (scFv) anti-CD19 (derivado del clon FMC63), una bisagra de CD8α, una región transmembrana de CD28, un dominio intracelular coestimulador de CD28 y un dominio de señalización de CD3ζ. El constructo está flanqueado por repeticiones terminales largas (LTRs) en 5' y 3', derivadas del virus del sarcoma mieloproliferativo (MPSV) y del virus de células madre embrionarias murino (MESV), que contienen un promotor 5' LTR y una secuencia de terminación 3' LTR. El vector también contiene una señal de empaquetamiento psi y está seudotipado con la glicoproteína Env del virus de la leucemia del Gibón (GALV). El material de leucoaféresis se enriquece en linfocitos T CD3+ mediante inmunoselección antes de la activación con agonistas de CD3 y CD28. Las células se transducen a continuación con el vector retroviral y se expanden en medio que contiene interleuquina 2 (IL-2). Los linfocitos T (≥90%) son positivos para el transgén (≥20% CAR positivos), expresan CD107a (≥20%) y muestran citotoxicidad frente células que expresan CD19

rapaprutugum #

rapaprutug	immunoglobulin G1-kappa, anti-[*Homo sapiens* KARS1 (lysyl-tRNA synthetase 1)], *Homo sapiens* monoclonal antibody; H-gamma1 heavy chain *Homo sapiens* (1-446) [VH (*Homo sapiens* IGHV3-23*01 (92.9%) -(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 (445-446)) (117-446)], (219-217')-disulfide with V-lambda-C-kappa light chain *Homo sapiens* (1'-217') [V-LAMBDA (*Homo sapiens* IGLV1-47*02 (88.5%) -IGLJ2*01 (100%), CDR-IMGT [8.3.11] (26'-33'.51'-53'.90'-100')) (1'-110') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (156'), V101 (194')) (111'-217')]; dimer (225-225":228-228")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, lacking the glutamine synthetase (GS-KO) gene, glycoform alfa
rapaprutug	immunoglobuline G1-kappa, anti-[*Homo sapiens* KARS1 (lysyl-ARNt synthétase 1)], anticorps monoclonal *Homo sapiens*; chaîne lourde H-gamma1 *Homo sapiens* (1-446) [VH (*Homo sapiens* IGHV3-23*01 (92.9%) -(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 (445-446)) (117-446)], (219-217')-disulfure avec la chaîne légère V-lambda-C-kappa *Homo sapiens* (1'-217') [V-LAMBDA (*Homo sapiens* IGLV1-47*02 (88.5%) -IGLJ2*01 (100%), CDR-IMGT [8.3.11] (26'-33'.51'-53'.90'-100')) (1'-110') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (156'), V101 (194')) (111'-217')]; dimère (225-225":228-228")-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
rapaprutug	inmunoglobulina G1-kappa, anti-[*Homo sapiens* KARS1 (lisil-ARNt sintetasa 1)], anticuerpo monoclonal *Homo sapiens*; cadena pesada H-gamma1 *Homo sapiens* (1-446) [VH (*Homo sapiens* IGHV3-23*01 (92.9%) -(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 (445-446)) (117-446)], (219-217')-disulfuro con la cadena ligera V-lambda-C-kappa *Homo sapiens* (1'-217') [V-LAMBDA (*Homo sapiens* IGLV1-47*02 (88.5%) -IGLJ2*01 (100%), CDR-IMGT [8.3.11] (26'-33'.51'-53'.90'-100')) (1'-110') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (156'), V101 (194')) (111'-217')]; dímero (225-225":228-228")-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 (H, H'') H-gamma1

```
EVQLLESGGG LVQPGGSLRL SCAASGFTFS SYDMSWVRQA PGKGLEWVSA  50
ISPYSGRIYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARMA 100
LDFDYWGQGT LVTVSSASTK GPSVFPLAPS SKSTSGGTAA LGCLVKDYFP 150
EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVVTVPSS SLGTQTYICN 200
VNHKPSNTKV DKKVEPKSCD KTHTCPPCPA PELLGGPSVF LFPPKPKDTL 250
MISRTPEVTC VVVDVSHEDP EVKFNWYVDG VEVHNAKTKP REEQYNSTYR 300
VVSVLTVLHQ DWLNGKEYKC KVSNKALPAP IEKTISKAKG QPREPQVYTL 350
PPSRDELTKN QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD 400
GSFFLYSKLT VDKSRWQQGN VFSCSVMHEA LHNHYTQKSL SLSPGK     446
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Light chain / Chaîne légère / Cadena ligera (L', L''') V-lambda-C-kappa

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QSVLTQPPSA SGTPGQRVTI SCTGSSSNIG SNYVTWYQQL PGTAPKLLIY  50
DNSNRPSGVP DRFSGSKSGT SASLAISGLQ SEDEADYYCS SFSDELGAYV 100
FGGGTKLTVL RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ 150
WKVDNALQSG NSQESVTEQD SKDSTYSLSS TLTLSKADYE KHKVYACEVT 200
HQGLSSPVTK SFNRGEC                                     217
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 143-199 260-320 366-424
22''-96'' 143''-199'' 260''-320'' 366''-424''
Intra-L (C23-C104) 22'-89' 137'-197'
22'''-89''' 137'''-197'''
Inter-H-L (h 5-CL 126) 219-217' 219''-217'''
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)
L VL V-LAMBDA Q1: 1', 1'''

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

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

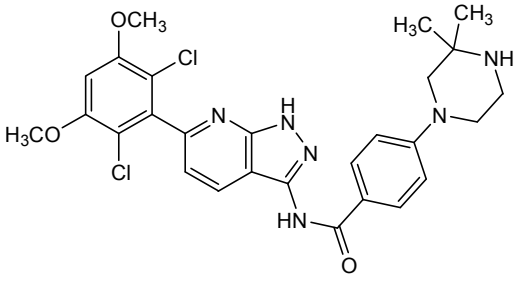
ratangratinibum

ratangratinib — *N*-[6-(2,6-dichloro-3,5-dimethoxyphenyl)-1*H*-pyrazolo[3,4-*b*]pyridin-3-yl]-4-(3,3-dimethylpiperazin-1-yl)benzamide

ratangratinib — *N*-[6-(2,6-dichloro-3,5-diméthoxyphényl)-1*H*-pyrazolo[3,4-*b*]pyridin-3-yl]-4-(3,3-diméthylpipérazin-1-yl)benzamide

ratangratinib — *N*-[6-(2,6-dicloro-3,5-dimetoxifenil)-1*H*-pirazolo[3,4-*b*]piridin-3-il]-4-(3,3-dimetilpiperazin-1-il)benzamida

$C_{27}H_{28}Cl_2N_6O_3$



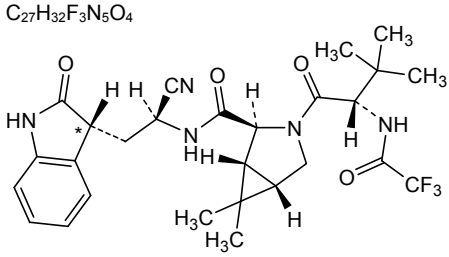
ratutrelvirum

ratutrelvir — (1*R*,2*S*,5*S*)-*N*-{(1*S*)-1-cyano-2-[(3*RS*)-2-oxo-2,3-dihydro-1*H*-indol-3-yl]ethyl}-3-[(2*S*)-3,3-dimethyl-2-(2,2,2-trifluoroacetamido)butanoyl]-6,6-dimethyl-3-azabicyclo[3.1.0]hexane-2-carboxamide

ratutrelvir (1*R*,2*S*,5*S*)-*N*-{(1*S*)-1-cyano-2-[(3*RS*)-2-oxo-2,3-dihydro-1*H*-indol-3-yl])éthyl}-3-[(2*S*)-3,3-diméthyl-2-(2,2,2-trifluoroacétamido)butanoyl]-6,6-diméthyl-3-azabicyclo[3.1.0]hexane-2-carboxamide

ratutrelvir (1*R*,2*S*,5*S*)-*N*-{(1*S*)-1-ciano-2-[(3*RS*)-2-oxo-2,3-dihidro-1*H*-indol-3-il])etil}-3-[(2*S*)-3,3-dimetil-2-(2,2,2-trifluoroacetamido)butanoil]-6,6-dimetil-3-azabiciclo[3.1.0]hexano-2-carboxamida

$C_{27}H_{32}F_3N_5O_4$



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

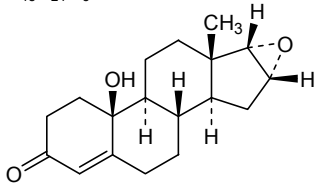
refisolonum

refisolone 10-hydroxy-16α,17α-epoxyestr-4-en-3-one

réfisolone 10-hydroxy-16α,17α-époxyestr-4-én-3-one

refisolona 10-hidroxi-16α,17α-epoxiestr-4-en-3-ona

$C_{18}H_{24}O_3$



retavibartum #

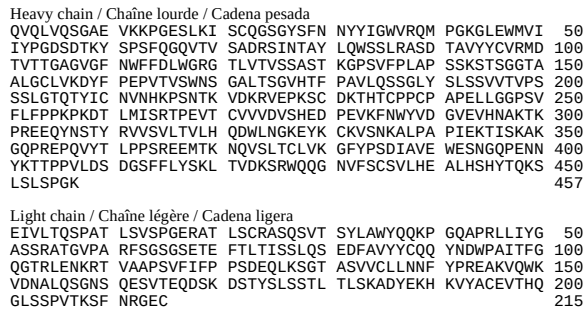
retavibart immunoglobulin G1-kappa, anti-[human respiratory syncytial virus (RSV) fusion glycoprotein F], *Homo sapiens* monoclonal antibody; H-gamma1 heavy chain *Homo sapiens* (1-457) [VH (*Homo sapiens* IGHV5-51*01 (86.7%) -(IGHD) -IGHJ2*01 (93.8%), CDR-IMGT [8.8.20] (26-33.51-58.97-116)) (1-127) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, 9-G1v24 CH3 L107, S114 (CH1 R120 (224) (128-225), hinge 1-15 (226-240), CH2 (241-350), CH3 E12 (366), M14 (368), M107>L (438), N114>S (444) (351-455), CHS (456-457)) (128-457)], (230-215')-disulfide with L-kappa light chain *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-15*01 (92.6%) -IGKJ5*01 (91.7%) I126>N (107'), CDR-IMGT [6.3.10] (27'-32'.50'-52'.89'-98'))(1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (154'), V101 (192')) (109'-215')]; dimer (236-236'':239-239'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa

rétavibart immunoglobuline G1-kappa, anti-[glycoprotéine de fusion F du virus respiratoire syncytial (VRS) humain], anticorps monoclonal *Homo sapiens*;
chaîne lourde H-gamma1 *Homo sapiens* (1-457) [VH (*Homo sapiens* IGHV5-51*01 (86.7%) -(IGHD) -IGHJ2*01 (93.8%), CDR-IMGT [8.8.20] (26-33.51-58.97-116)) (1-127) -*Homo sapiens*

IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, 9-G1v24 CH3 L107, S114 (CH1 R120 (224) (128-225), charnière 1-15 (226-240), CH2 (241-350), CH3 E12 (366), M14 (368), M107>L (438), N114>S (444) (351-455), CHS (456-457)) (128-457)], (230-215')-disulfure avec la chaîne légère L-kappa *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-15*01 (92.6%) -IGKJ5*01 (91.7%) I126>N (107'), CDR-IMGT [6.3.10] (27'-32'.50'-52'.89'-98')) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (154'), V101 (192')) (109'-215')]; dimère (236-236'':239-239'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa

retavibart

inmunoglobulina G1-kappa, anti-[glicoproteína de fusión F del virus respiratorio sincitial (VRS) humano], anticuerpo monoclonal *Homo sapiens*;
cadena pesada H-gamma1 *Homo sapiens* (1-457) [VH (*Homo sapiens* IGHV5-51*01 (86.7%) -(IGHD) -IGHJ2*01 (93.8%), CDR-IMGT [8.8.20] (26-33.51-58.97-116)) (1-127) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, 9-G1v24 CH3 L107, S114 (CH1 R120 (224) (128-225), bisagra 1-15 (226-240), CH2 (241-350), CH3 E12 (366), M14 (368), M107>L (438), N114>S (444) (351-455), CHS (456-457)) (128-457)], (230-215')-disulfuro con la cadena ligera L-kappa *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV3-15*01 (92.6%) -IGKJ5*01 (91.7%) I126>N (107'), CDR-IMGT [6.3.10] (27'-32'.50'-52'.89'-98')) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (154'), V101 (192')) (109'-215')]; dímero (236-236'':239-239'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, forma glicosilada alfa



Heavy chain / Chaîne lourde / Cadena pesada

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QVQLVQSGAE VKKPGESLKI SCQGSGYSFN NYYIGWVRQM PGKGLEWMVI  50
IYPGDSDTKY SPSFQGQVTV SADRSINTAY LQWSSLRASD TAVYYCVRMD 100
TVTTGAGVGF NWFFDLWGRG TLVTVSSAST KGPSVFPLAP SSKSTSGGTA 150
ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS 200
SSLGTQTYIC NVNHKPSNTK VDKRVEPKSC DKTHTCPPCP APELLGGPSV 250
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK 300
PREEQYNSTY RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK 350
GQPREPQVYT LPPSREEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN 400
YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG NVFSCSVLHE ALHSHYTQKS 450
LSLSPGK                                               457
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Light chain / Chaîne légère / Cadena ligera

```
EIVLTQSPAT LSVSPGERAT LSCRASQSVT SYLAWYQQKP GQAPRLLIYG  50
ASSRATGVPA RFSGSGSETE FTLTISSLQS EDFAVYYCQQ YNDWPAITFG 100
QGTRLENKRT 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) 22-96 154-210 271-331 377-435
22"-96" 154"-210" 271"-331" 377"-435"
Intra-L (C23-C104) 23'-88' 135'-195'
23'"-88'" 135'"-195'"
Inter-H-L (h 5-CL 126) 230-215' 230"-215'"
Inter-H-H (h 11, h 14) 236-236" 239-239"

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 N84.4:307, 307"
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 K2:457, 457"

retogateinum #

retogatein — $N^{2.1}$-acetyl-[des-N-terminal methionyl]-glutamate decarboxylase 2 (*Homo sapiens*) (GAD2, 65 kDa glutamic acid decarboxylase, glutamate decarboxylase 65 kDa isoform, GAD65, EC:4.1.1.15), produced in *Spodoptera frugiperda* insect cells (cell line Sf9)

rétogatéine — $N^{2.1}$-acétyl-[des-méthionyle N-terminal]-glutamate décarboxylase 2 (*Homo sapiens*) (GAD2, 65 kDa acide glutamique décarboxylase, glutamate décarboxylase isoforme 65 kDa, GAD65, EC:4.1.1.15), produite par cellules d'insectes *Spodoptera frugiperda* (ligne cellulaire Sf9)

retogateína — $N^{2.1}$-acetil-[des-metionilo N-terminal]-glutamato decarboxilasa 2 (*Homo sapiens*) (GAD2, 65 kDa ácido glutamico decarboxilasa, glutamato decarboxylasa isoforma 65 kDa, GAD65, EC:4.1.1.15), producido en células de insecto *Spodoptera frugiperda* (línea celular Sf9)

Sequence / Séquence / Secuencia

```
ASPGSGFWSF GSEDGSGDSE NPGTARAWCQ VAQKFTGGIG NKLCALLYGD    50
AEKPAESGGS QPPRAAARKA ACACDQKPCS CSKVDVNYAF LHATDLLPAC   100
DGERPTLAFL QDVMNILLQY VVKSFDRSTK VIDFHYPNEL LQEYNWELAD   150
QPQNLEEILM HCQTTLKYAI KTGHPRYFNQ LSTGLDMVGL AADWLTSTAN   200
TNMFTYEIAP VFVLLEYVTL KKMREIIGWP GGSGDGIFSP GGAISNMYAM   250
MIARFKMFPE VKEKGMAALP RLIAFTSEHS HFSLKKGAAA LGIGTDSVIL   300
IKCDERGKMI PSDLERRILE AKQKGFVPFL VSATAGTTVY GAFDPLLAVA   350
DICKKYKIWM HVDAAWGGGL LMSRKHKWKL SGVERANSVT WNPHKMMGVP   400
LQCSALLVRE EGLMQNCNQM HASYLFQQDK HYDLSYDTGD KALQCGRHVD   450
VFKLWLMWRA KGTTGFEAHV DKCLELAEYL YNIIKNREGY EMVFDGKPQH   500
TNVCFWYIPP SLRTLEDNEE RMSRLSKVAP VIKARMMEYG TTMVSYQPLG   550
DKVNFFRMVI SNPAATHQDI DFLIEEIERL GQDL                    584
```

Post-translational modifications

Removal of N-terminal methionyl
M^0>del

Disulfide bridge location / Position du pont disulfure / Posición del puente disulfuro
162-303 (rarely 162-403 or 303-403)

N-Acetylation site / Site de N-acétylation / Posición de N-acetilación
A1 = *N*-acetyl-L-alanyl

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
none / aucun / ninguna

K^{395} = N^6-(pyridoxal phosphate)-Lys

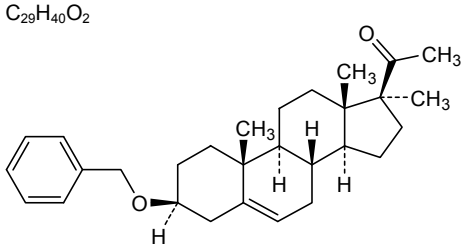
rezosiconum

rezosicone — 3β-(benzyloxy)-17-methylpregn-5-en-20-one

rézosicone — 3β-(benzyloxy)-17-méthylprégn-5-én-20-one

rezosicona — 3β-(benciloxi)-17-metilpregn-5-en-20-ona

$C_{29}H_{40}O_2$



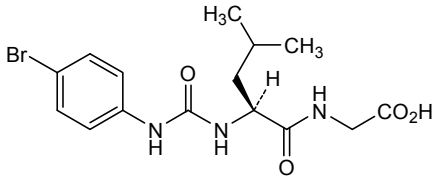
rezuforimodum

rezuforimod — *N*-[(4-bromophenyl)carbamoyl]-L-leucylglycine

rézuforimod — *N*-[(4-bromophényl)carbamoyl]-L-leucylglycine

rezuforimod — *N*-[(4-bromofenil)carbamoil]-L-leucilglicina

$C_{15}H_{20}BrN_3O_4$



ricefidasum

ricefidase — L-methionyl (1)-IgG endopeptidase (immunoglobulin G-degrading endopeptidase) of *Streptococcus equi* subsp. *zooepidemicus* strain H70 (ideE, ideZ), fragment 19-315 (2-298 in the actual sequence); produced by *Escherichia coli*; non-glycosylated

ricéfidase — L-méthionyl (1)-IgG endopeptidase (endopeptidase qui dégrade l'immunoglobuline G, Ide) de *Streptococcus equi* subsp. *zooepidemicus* souche H70 (ideE, ideZ), fragment 19-315 (2-298 dans la séquence actuelle); produite par *Escherichia coli*; non-glycosylée

ricefidasa — L-metionil (1)-IgG endopeptidasa (endopeptidasa que degrada la inmunoglobulina G) de *Streptococcus equi* subsp. *zooepidemicus* cepa H70 (ideE, ideZ), fragmento 19-315 (2-298 en la secuencia actual); producida por *Escherichia coli*; no glicosilada

Sequence / Séquence / Secuencia

```
MITSVWTKGV TPLTPEQFRY NNEDVIHAPY LAHQGWYDIT KAFDGKDNLL    50
CGAATAGNML HWWFDQNKTE IEAYLSKHPD KQKIIFNNQE LFDLKAAIDT   100
KDSQTNSQLF NYFRDKAFPN LSARQLGVMP DLVLDMFING YYLNVFKTQS   150
TDVNRPYQDK DKRGGIFDAV FTRGDQTTLL TARHDLKNKG LNDISTIIKQ   200
ELTEGRALAL SHTYANVSIS HVINLWGADF NAEGNLEAIY VTDSDANASI   250
GMKKYFVGIN AHGHVAISAK KIEGENIGAQ VLGLFTLSSG KDIWQKLS     298
```

Mutation / Mutation / Mutación

$Q^{18}>\underline{\mathbf{M}}^{1}$

Post-translational modifications

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

none / aucune / ninguna

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

none / aucun / ninguna

rinvaterceptum

rinvatercept — glycyl (1)-chimeric N-terminal (1-108)-peptide (2-109) combined from the sequences of the extracellular domains of the human activin type 2A and 2B receptors (ACTR-2A/B, ACVR2A/B, activin receptor type IIA/B, ACTR-IIA/B, EC:2.7.11.30), fused via a G_3 peptide linker (110-112) to an immunoglobulin G1 (IgG1) Fc fragment (h-CH2-CH3-CHS domains) (113-339) [*Homo sapiens* IGHG1*01 (hinge (113-

122), CH2 (123-232), CH3 (233-337), CHS (338-339))], dimer (118-118':121-121')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells; glycoform alfa

rinvatercept — glycyl (1)-(1-108)-peptide N-terminal chimérique (2-109) combiné à partir des séquences des domaines extracellulaires des récepteurs d'activine de types 2A et 2B humains (ACTR-2A/B, ACVR2A/B, récepteur d'activine de type IIA/B, ACTR-IIA/B, EC:2.7.11.30), fusionné, via un coupleur peptidique G_3 (110-112), à un fragment Fc de l'immunoglobuline G1 (IgG1) (domaines h-CH2-CH3-CHS) (113-339) [*Homo sapiens* IGHG1*01 (charnière (113-122), CH2 (123-232), CH3 (233-337), CHS (338-339))], dimère (118-118',121-121')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO); glycoforme alfa

rinvatercept — glicil (1)-(1-108)-péptido N-terminal quimérico (2-109) combinado a partir de las secuencias de los dominios extracelulares de los receptores de activina de tipos 2A y 2B humanos (ACTR-2A/B, ACVR2A /B, receptor de activina tipo IIA/B, ACTR-IIA/B, EC:2.7.11.30), fusionado mediante un enlazador peptídico G_3 (110-112) a un fragmento Fc de la inmunoglobulina G1 (IgG1) (dominios h-CH2-CH3-CHS) (113-339) [*Homo sapiens* IGHG1*01 (bisagra (113-122)), CH2 (123-232), CH3 (233-337), CHS (338-339))]; dímero (118-118',121-121')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO); glicoforma alfa

Sequence / Séquence / Secuencia

```
GAILGRSETQ ECIYYNANWE LERTNQSGLE RCEGEQDKRL HCYASWRNSS    50
GTIEIVKQGC WLDDFNCYDR TDCVEKKDSP QVYFCCCEGN MCNEKFSYFP   100
EMEVTQPTSG GGDKTHTCPP CPAPELLGGP SVFLFPPKPK DTLMISRTPE   150
VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS TYRVVSVLTV   200
LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV YTLPPSRDEL   250
TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS   300
KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK              339
```

Chimeric peptide / Peptide chimérique / Péptido quimérico
ACTR-2A: ***1-10***, ***53-64***, ***66-80***, ***82-109***
ACTR-2B: 11-52, 65, 81

Peptide linker / Peptide liant / Péptido de unión
$^{110}GGG^{112}$

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
ActRIIA/B: 12-42 32-60 67-86 73-85 87-92 IgG1 Fc: 153-213 259-317
12'-42' 32'-60' 67'-86' 73'-85' 87'-92' 153'-213' 259'-317'
inter-IgG1 Fc: 118-118' 121-121'

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
ActRIIA/B: N25, N48, N25', N48'; IgG1 Fc: N189, N189'

O-glycosylation sites / Sites de O-glycosylation / Posiciones de O-glicosilación
IgG1 Fc: T115, S131, T115', S131'

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
K339, K339'

ristoglogenum autogetemcelum

ristoglogene autogetemcel — autologous CD34+ hematopoietic stem and progenitor cells (HSPCs) obtained from peripheral blood by leukapheresis, genetically modified *ex vivo* by electroporation of a guide RNA

(gRNA) that targets the two γ-globin gene (*HBG1* and *HBG2*) promotors and a messenger RNA (mRNA) that encodes the adenine base editor 8.8 (ABE8.8). When introduced into CD34+ cells by electroporation the gRNA binds to the translated ABE8.8 protein, which targets the promoter regions of *HBG1* and *HBG2*, resulting in adenine to inosine modifications which subsequently leads to an A to G change.
The ABE8.8 mRNA is composed of three parts: (i) an impaired form of the *Streptococcus pyogenes* CRISPR-associated nuclease Cas9, referred to as Cas9 D10A nickase (nCas9-D10A), (ii) an *Escherichia coli* derived TadA deaminase that catalyses the adenosine to inosine conversion within a small activity window along the exposed, single-stranded DNA (ssDNA) formed within the R-loop, (iii) a C-terminal nuclear localization signal (NLS).
The cell suspension is enriched for CD34+ cells using magnetic bead separation. Following electroporation, the cells are cultured in media containing thrombopoietin, Fms-related tyrosine kinase 3 ligand (Flt3L), and stem cell factor (SCF). The substance consists of cells with ≥85% CD45+ and ≥75% CD34+ purity and ≥75% on-target editing.

ristoglogène autogétemcel — cellules souches et progénitrices hématopoïétiques (CSPH) autologues CD34+, obtenues à partir de sang périphérique par leucaphérèse, génétiquement modifiées *ex vivo* par électroporation d'un ARN guide (ARNg) ciblant les deux promoteurs du gène de la γ-globine (*HBG1* et *HBG2*) et un ARN messager (ARNm) qui code l'éditeur de bases d'adénine 8.8 (ABE8.8). Lorsqu'il est introduit dans les cellules CD34+ par électroporation, l'ARNg se lie à la protéine ABE8.8 traduite, qui cible les régions promotrices de *HBG1* et *HBG2*, entraînant des modifications de l'adénine en inosine, qui conduisent ensuite à un changement A>G.
L'ARNm ABE8.8 est composé de trois parties: (i) une forme altérée de la nucléase Cas9 associée à CRISPR de *Streptococcus pyogenes*, appelée Cas9 D10A nickase (nCas9-D10A); (ii) une désaminase TadA dérivée d'*Escherichia coli* qui catalyse la conversion de l'adénosine en inosine, dans une petite fenêtre d'activité le long de l'ADN simple brin (ADNsb) exposé formé dans la boucle R; (iii) un signal de localisation nucléaire C-terminal (SLN).
La suspension cellulaire est enrichie en cellules CD34+ par séparation des billes magnétiques. Après l'électroporation, les cellules sont cultivées dans un milieu contenant de la thrombopoïétine, du ligand de la tyrosine kinase 3 lié au Fms (Flt3L) et du facteur de cellules souches (FCS). La substance est constituée de cellules avec une pureté ≥85% CD45+ et ≥75% CD34+ et une édition sur cible ≥75%.

ristoglogén autogetemcel — células madre y progenitoras hematopoyéticas (HSPC) CD34+ autólogas, obtenidas de sangre periférica mediante leucoaféresis, modificadas genéticamente *ex vivo* mediante electroporación de un ARN guía (ARNg) dirigido a los promotores de los dos genes de la γ-globina (*HBG1* y *HBG2*) y un ARN mensajero (ARNm) que codifica el editor de bases de adenina 8.8 (ABE8.8). Cuando se introduce en las células CD34+ mediante electroporación, el ARNg se une a la proteína ABE8.8 traducida, la cual se dirige a las regiones promotoras de *HBG1* y *HBG2*, resultando en modificaciones de adenina a inosina que posteriormente conduce a un cambio de A a G.
El ARNm de ABE8.8 está compuesto por tres partes: (i) una forma dañada de la nucleasa Cas9 asociada a CRISPR de

Streptococcus pyogenes, referida como nicasa Cas9 D10A (nCas9-D10A), (ii) una deaminasa TadA derivada de *Escherichia coli* que cataliza la conversión de adenosina a inosina en una pequeña ventana de actividad a lo largo del ADN de cadena sencilla (ssADN) que se forma dentro del bucle R, (iii) una señal de localización nuclear (NLS) C-terminal.
La suspensión celular se enriquece en células CD34+ mediante separación con bolas magnéticas. Tras la electroporación, las células se cultivan en medio que contiene trombopoyetina, ligando de tirosina quinasa 3 similar a Fms (Flt3L) y factor de células madre (SCF). La substancia consta de células con una pureza de ≥85% CD45+ y ≥75% CD34+ y ≥75% de edición en el sitio diana

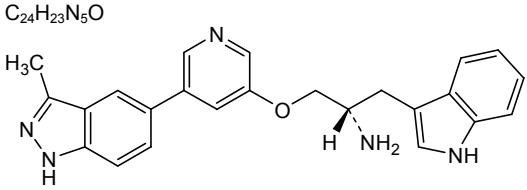
rizavasertibum

rizavasertib — (2*S*)-1-(1*H*-indol-3-yl)-3-{[5-(3-methyl-1*H*-indazol-5-yl)pyridin-3-yl]oxy}propan-2-amine

rizavasertib — (2*S*)-1-(1*H*-indol-3-yl)-3-{[5-(3-méthyl-1*H*-indazol-5-yl)pyridin-3-yl]oxy}propan-2-amine

rizavasertib — (2*S*)-1-(1*H*-indol-3-il)-3-{[5-(3-metil-1*H*-indazol-5-il)piridin-3-il]oxi}propan-2-amina

$C_{24}H_{23}N_5O$



riztunitidum

riztunitide — D-tyrosyl-D-valyl-D-α-aspartyl-D-lysyl-D-arginine

riztunitide — D-tyrosyl-D-valyl-D-α-aspartyl-D-lysyl-D-arginine

riztunitida — D-tirosil-D-valil-D-α-aspartil-D-lisil-D-arginina

$C_{30}H_{49}N_9O_9$

D-Tyr—D-Val—D-Asp—D-Lys—D-Arg

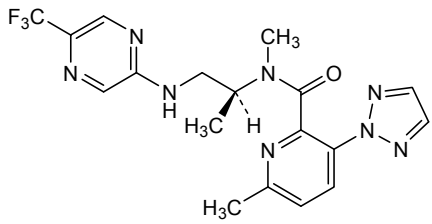
rocavorexantum

rocavorexant — *N*,6-dimethyl-3-(2*H*-1,2,3-triazol-2-yl)-*N*-[(2*S*)-1-{[5-(trifluoromethyl)pyrazin-2-yl]amino}propan-2-yl]pyridine-2-carboxamide

rocavorexant — *N*,6-diméthyl-3-(2*H*-1,2,3-triazol-2-yl)-*N*-[(2*S*)-1-{[5-(trifluorométhyl)pyrazin-2-yl]amino}propan-2-yl]pyridine-2-carboxamide

rocavorexant — *N*,6-dimetil-3-(2*H*-1,2,3-triazol-2-il)-*N*-[(2*S*)-1-{[5-(trifluorometil)pirazin-2-il]amino}propan-2-il]piridina-2-carboxamida

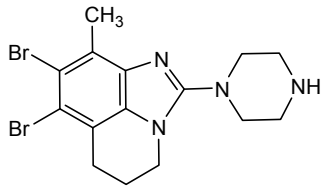
$C_{18}H_{19}F_3N_8O$



romaciclibum

romaciclib	7,8-dibromo-9-methyl-2-(piperazin-1-yl)-5,6-dihydro-4*H*-imidazo[4,5,1-*ij*]quinoline
romaciclib	7,8-dibromo-9-méthyl-2-(pipérazin-1-yl)-5,6-dihydro-4*H*-imidazo[4,5,1-*ij*]quinoléine
romaciclib	7,8-dibromo-9-metil-2-(piperazin-1-il)-5,6-dihidro-4*H*-imidazo[4,5,1-*ij*]quinoleína

$C_{15}H_{18}Br_2N_4$



rondecabtagenum autoleucelum #

rondecabtagene autoleucel

autologous T lymphocytes obtained by leukapheresis enriched for the cell surface marker CD62L (also known as L-selectin) transduced with a self-inactivating non-replicating lentiviral vector encoding a tandem chimeric antigen receptor (CAR) targeting both CD20and CD19 [comprising a single chain variable fragment (scFvs) derived from the antibody clone Leu16 fused via flexible linkers to a scFvs derived from clone FMC63]. The transgene has a murine immunoglobulin kappa (mIgK) leader sequence and also comprises an IgG4 hinge, a CD28 transmembrane, and the intracellular 4-1BB co-stimulatory and CD3ζ signaling domains and is under control of the elongation factor 1 alpha (EF-1α) promoter and the Woodchuck hepatitis virus post-transcriptional regulatory element (WPRE) modified to eliminate the X-protein open reading frame. The vector genome also contains a human immunodeficiency virus (HIV) packaging signal, a Rev response element (RRE), central polypurine tract and central termination sequence (cPPT/CTS) and is flanked by 5' and 3' long terminal repeats (LTRs). The vector is pseudotyped with vesicular stomatitis virus (VSV) G glycoprotein. The leukapheresis material is enriched for CD62L expressing T lymphocytes by positive immunoselection and cultured in media containing interleukin 2 (IL-2) and interleukin 15 (IL-15). The lymphocytes are

	activated by CD3 and CD28 agonists and transduced with the lentiviral vector followed by culture in media containing IL-2 and IL-15. The T lymphocytes (≥80%) are predominantly composed of naïve and central memory rich T lymphocyte subsets as measured by expression of CD62L and CD45RA surface markers, and positive for the transgene (≥10% CAR positive) with few (<5%) CD19 expressing B lymphocytes. The cells exhibit cytotoxicity and secrete interferon gamma in response to CD19 and CD20 expressing tumour cell lines
rondécabtagène autoleucel	lymphocytes T autologues obtenus par leucaphérèse, enrichis pour le marqueur de surface cellulaire CD62L (également connu sous le nom de L-sélectine) transduits avec un vecteur lentiviral non réplicatif auto-inactivant, codant un récepteur antigénique chimérique (RAC) en tandem ciblant à la fois CD20 et CD19 [comprenant un fragment variable à chaîne unique (scFvs) dérivé du clone d'anticorps Leu16 fusionné, via des coupleurs flexibles, à un scFvs dérivé du clone FMC63]. Le transgène possède une séquence de tête de l'immunoglobuline kappa murine (mIgK), et comprend également une charnière IgG4, un domain transmembranaire CD28 et les domaines intracellulaires de costimulation 4-1BB et de signalisation CD3ζ, et est sous le contrôle du promoteur du facteur d'élongation 1 alpha (EF-1α), et de l'élément régulateur post-transcriptionnel du virus de l'hépatite de la marmotte (WPRE), modifié pour éliminer le cadre de lecture ouvert de la protéine X. Le génome du vecteur contient également un signal d'empaquetage du virus de l'immunodéficience humaine (VIH), un élément de réponse Rev (RRE), une séquence de tractus polypurine central et de terminaison centrale (cPPT/CTS), et est flanqué de longues répétitions terminales (LTRs) en 5' et en 3'. Le vecteur est pseudotypé avec la glycoprotéine G du virus de la stomatite vésiculaire (VSV). Le matériel de leucaphérèse est enrichi en lymphocytes T exprimant CD62L, par immunosélection positive, et cultivé dans un milieu contenant de l'interleukine 2 (IL-2) et de l'interleukine 15 (IL-15). Les lymphocytes sont activés par les agonistes CD3 et CD28 et transduits avec le vecteur lentiviral suivi d'une culture dans un milieu contenant de l'IL-2 et de l'IL-15. Les lymphocytes T (≥80%) sont principalement composés de lymphocytes T riches en sous-types naïfs et mémoire centrale, mesurés par l'expression des marqueurs de surface CD62L et CD45RA, et positifs pour le transgène (≥10% RAC positifs) avec peu (<5%) de lymphocytes B exprimant CD19. Les cellules présentent une cytotoxicité et sécrètent de l'interféron gamma en réponse aux lignées de cellules tumorales exprimant CD19 et CD20
rondecabtagén autoleucel	linfocitos T autólogos obtenidos por leucoaféresis, enriquecidos para el marcador de superficie CD62L (también conocido como L-selectina), transducidos con un vector lentiviral auto inactivante, no replicativo, que codifica un tándem de receptores de antígenos

quiméricos (CAR) dirigidos a CD20 y CD19 [consta de un fragmento variable de cadena sencilla (scFv) derivado del clon del anticuerpo Leu16 fusionado mediante enlaces flexibles a un scFv derivado del clon FMC63]. El transgén tiene una secuencia líder de la inmunoglobulina kappa murina (mIgK) y también consta de un dominio bisagra de IgG4, un dominio transmembrana de CD28, y los dominios intracelulares coestimulador de 4-1BB y de señalización de CD3ζ, y está bajo el control del promotor del factor de elongación 1 alfa (EF-1α) y el elemento regulador post-transcripcional del virus de la hepatitis de la marmota (WPRE) modificado para eliminar el marco de lectura abierto de la proteína X. El genoma del vector también contiene una señal de empaquetamiento del virus de la inmunodeficiencia humana (VIH), un elemento de respuesta Rev (RRE), una secuencia de tracto de poli-purina/terminación central (cPPT/CTS) y está flanqueado por repeticiones terminales largas (LTRs) en 5' y 3'. El vector está seudotipado con la glicoproteína G del virus de la estomatitis vesicular (VSV).
El material de leucoaféresis se enriquece en linfocitos T que expresan CD62L mediante inmunoselección positiva y se cultiva en medio que contiene interleuquina 2 (IL-2) e interleuquina 15 (IL-15). Los linfocitos se activan con agonistas de CD3 y CD28 y se transducen con el vector lentiviral seguido de cultivo en medio que contiene IL-2 e IL-15. Los linfocitos T (≥80%) están compuestos predominantemente por linfocitos T ricos en los subtipos naïve y memoria central, medido por la expresión de los marcadores de superficie CD62L y CD45RA, y positivos para el transgén (≥10% CAR positivos) con pocos (<5%) linfocitos B que expresan CD19. Las células muestran citotoxicidad y secretan interferón gamma en respuesta a líneas celulares tumorales que expresan CD19 y CD20

rubravameranum #
rubravameran

self-amplifying messenger RNA (mRNA), 5'-capped, encoding Venezuelan equine encephalitis virus (VEEV; strain TC-83) RNA-dependent RNA polymerase complex (VEEV non-structural proteins 1-4 [nsP1, nsP2, nsP3 and nsP4]) and a codon-optimised receptor binding domain (RBD) of the SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2) spike (S) glycoprotein (Omicron XBB.1.5 variant derived from GenBank ID: OQ054680.1; amino acids 323-527), preceded by the SARS-CoV-2 signal peptide and fused to an H1N1 influenza virus hemagglutinin transmembrane domain and a universal (pan) HLA DR-binding epitope (PADRE), flanked by VEEV 5' and 3' untranslated regions (UTRs) and terminated with a 3' polyadenylation (polyA) tail; contains 5-methylcytosine instead of cytosine (*all*-C>5mC). Generation of the SARS-CoV-2 RBD mRNA is under control of the VEEV subgenomic promoter

rubravaméran	ARN messager auto-amplifiant (ARNm), avec une coiffe en 5', codant pour le complexe d'ARN polymérase ARN-dépendante (protéines non structurales 1-4 [nsP1, nsP2, nsP3 et nsP4]) du virus de l'encéphalite équine vénézuélienne (VEEV; souche TC-83) et un domaine de liaison au récepteur (RBD), optimisé pour les codons, de la glycoprotéine du spicule (S) (variante Omicron XBB.1.5 dérivée de GenBank ID: OQ054680.1; acides aminés 323 à 527), du SRAS-CoV-2 (coronavirus 2 du syndrome respiratoire aigu sévère), précédée du peptide signal du SRAS-CoV-2 et fusionnée à un domaine transmembranaire d'hémagglutinine du virus de la grippe H1N1, et à un épitope universel (pan) de liaison au HLA DR (PADRE), flanqué des régions non traduites de VEEV (UTRs) en 3' et 5' et terminées par une queue de polyadénylation (polyA) en 3'; contient de la 5-méthylcytosine au lieu de la cytosine (*tout*-C>5mC). La génération de l'ARNm du SRAS-CoV-2 RBD est sous le contrôle du promoteur subgénomique du VEEV
rubravamerán	ARN mensajero (ARNm) auto amplificante, protegido mediante caperuza en 5', que codifica el complejo de ARN polimerasa dependiente de ARN (proteínas no estructurales 1-4 de VEEV [nsP1, nsP2, nsP3 y nsP4]) del virus de la encefalitis equina venezolana (VEEV; cepa TC-83) y un dominio de unión al receptor con codones optimizados (RBD) de la glicoproteína de la espícula (S) (variante Omicron XBB.1.5 derivada de GenBank ID: OQ054680.1; aminoácidos 323-527) del SRAS-CoV-2 (coronavirus 2 del síndrome respiratorio agudo severo), precedido por el péptido señal del SRAS-CoV-2 y fusionado a un dominio transmembrana de la hemaglutinina del virus de la gripe H1N1 y un epítopo universal (pan) de unión a HLA DR (PADRE), flanqueado por regiones no traducidas (UTRs) 5' y 3' de VEEV y terminado con una cola de poliadenilación 3' (poliA); contiene 5-metilcitosina en lugar de citosina (*todos*-C>5 mC). La generación del ARNm de RBD del SRAS-CoV-2 está bajo el control del promotor subgenómico de VEEV

rugecitidum

rugecitide	neuregulin 4 (NRG4) (*Homo sapiens*), fragment 1-50, [^{1}MPTD^{4}>^{1}GGGGSG^{6}, V^{25}>Q^{27}, E^{47}>K^{49}]-variant (1-52), not glycosylated
rugécitide	neuréguline 4 (NRG4) (*Homo sapiens*), fragment 1-50, variant ^{1}MPTD^{4}>^{1}GGGGSG^{6}, V^{25}>Q^{27}, E^{47}>K^{49}] (1-52), non glycosylé
rugecitida	neuregulina 4 (NRG4) (*Homo sapiens*), fragmento 1-50, variante [^{1}MPTD^{4}>^{1}GGGGSG^{6}, V^{25}>Q^{27}, E^{47}>K^{49}] (1-52), no glicosilado

$C_{238}H_{355}N_{67}O_{72}S_6$

Sequence / Séquence / Secuencia

```
GGGGSGHEEP CGPSHKSFCL NGGLCYQIPT IPSPFCRCVE NYTGARCEKV 50
FL                                                      52
```

Post-translational modifications

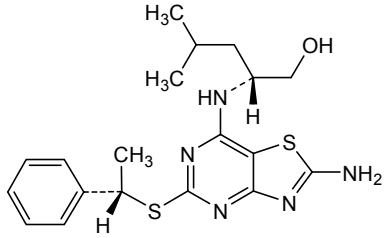
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
11-25, 19-36, 38-47

rugocrixanum

rugocrixan	(2*R*)-2-[(2-amino-5-{[(1*S*)-1-phenylethyl]sulfanyl}[1,3]thiazolo[4,5-*d*]pyrimidin-7-yl)amino]-4-methylpentan-1-ol
rugocrixan	(2*R*)-2-[(2-amino-5-{[(1*S*)-1-phényléthyl]sulfanyl}[1,3]thiazolo[4,5-*d*]pyrimidin-7-yl)amino]-4-méthylpentan-1-ol

rugocrixán (2*R*)-2-[(2-amino-5-{[(1*S*)-1-feniletil]sulfanil}[1,3]tiazolo[4,5-*d*]pirimidin-7-il)amino]-4-metilpentan-1-ol

$C_{19}H_{25}N_5OS_2$



runitresgenum leucelum #

runitresgene leucel allogeneic T lymphocytes derived from peripheral blood mononuclear cells (PBMCs) of a haploidentical hematopoietic cell transplantation (HCT) donor that is negative for the HA-2 genotype and/or negative for HLA A*02, engineered by transposon/transposase-mediated gene delivery to express a T cell receptor (TCR) that is specific for a 9-amino acid peptide (YIGEVLVSV) termed HA-2, derived from myosin 1G (MYO1G) and presented on HLA-A*02:01. The TCR comprises α and β subunits separated by a P2A self-cleaving peptide. The transgene also encodes a codon-optimised CD8 co-receptor consisting of α and β chains separated by a P2A self-cleaving peptide, with the CD8 co-receptor separated from the TCR by an additional P2A self-cleaving peptide. Each P2A sequence is preceded by a furin cleavage site. A 16 amino acid epitope encoding a portion of human CD34 is incorporated into the N-terminus of the CD8α chain. The transgene is under the control of a murine stem cell virus (MSCV) promoter, a Woodchuck hepatitis virus post-transcriptional response element and a simian virus 40 (SV40) polyadenylation (polyA) signal.
The transposase (Armyworm transposase) is introduced in form of an mRNA that comprises an anti-reverse cap analogue, a *Xenopus* globin 5' untranslated region (UTR), a Kozak sequence, the transposase open reading frame, and a *Xenopus* globin 3' UTR. The transgene is introduced via a nanoplasmid DNA and contains inverted terminal repeats (ITRs). The leukapheresis material is electroporated with mRNA transposase as well as the nanoplasmid transposon followed by activation with CD2, CD3 and CD28 agonists. The cells are grown in serum free media supplemented with interleukin 2 (IL-2), interleukin 7 (IL-7) and interleukin-15 (IL-15). The T lymphocytes (≥95%) are positive for the transgene (≥80% TCR+), and release interferon -gamma (IFN-γ) in response to co-culture with THP-1 cells that express the HA-2 target peptide

runitresgène leucel lymphocytes T allogéniques dérivés de cellules mononucléaires du sang périphérique (CMSP) d'un donneur haploidentiques de greffe de cellules hématopoïétiques (GCH) qui sont négatifs pour le génotype HA-2 et/ou négatifs pour HLA A*02, modifiés par un système de délivrance de gènes par transposon/transposase, pour exprimer un récepteur de lymphocytes T (TCR) spécifique d'un peptide de 9 acides aminés (YIGEVLVSV) appelé HA-2, dérivé de la myosine 1G (MYO1G) et présenté sur HLA-A*02:01. Le TCR comprend des sous-unités α et β, séparées par un peptide auto-clivant P2A. Le transgène code également avec des codons optimisés un co-récepteur CD8 constitué de chaînes α et β séparées par un peptide auto-clivant P2A, le co-récepteur CD8 étant séparé du TCR par un autre peptide auto-clivant P2A. Chaque séquence P2A est précédée d'un site de clivage de la furine. Un épitope de 16 acides aminés codant pour une

	partie du CD34 humain est incorporé à l'extrémité N-terminale de la chaîne CD8α. Le transgène est sous le contrôle d'un promoteur du virus des cellules souches murines (MSCV), d'un élément de réponse post-transcriptionnelle du virus de l'hépatite de la marmotte et d'un signal de polyadénylation (polyA) du virus simien 40 (SV40). La transposase (transposase de la chenille légionnaire) est introduite sous la forme d'un ARNm qui comprend un analogue de la coiffe anti-inverse, une région 5' non traduite (UTR) de la globine de *Xenopus*, une séquence Kozak, le cadre de lecture ouvert de la transposase et une région 3' UTR de la globine de *Xenopus*. Le transgène est introduit via un vecteur d'ADN nanoplasmidique et contient des répétitions terminales inversées (RTI). Le matériel de leucaphérèse est électroporé avec l'ARNm de la transposase ainsi que le transposon nanoplasmidique, suivi d'une activation avec des agonistes CD2, CD3 et CD28. Les cellules sont cultivées dans un milieu sans sérum supplémenté en interleukine 2 (IL-2), interleukine 7 (IL-7) et interleukine 15 (IL-15). Les lymphocytes T (≥95%) sont positifs pour le transgène (≥80% TCR+) et libèrent de l'interféron gamma (IFN-γ) en réponse à une co-culture avec des cellules THP-1 qui expriment le peptide cible HA-2
runitresgén leucel	linfocitos T alogénicos derivados de células mononucleares de sangre periférica (PBMCs) de un donante de transplante de células hematopoyéticas (HCT) haploidéntico que es negativo para el genotipo HA-2 y/o negativo para HLA A*02, manipulados mediante un sistema de entrega genética mediado por transposón/transposasa para expresar el receptor de células T (TCR) que es específico para un péptido de 9 amino ácidos (YIGEVLVSV) llamado HA-2, derivado de la miosina 1G (MYO1G) y presentado en HLA-A*02:01. El TCR consta de subunidades α y β separadas por un péptido de auto-escisión P2A. El transgén también codifica, con codones optimizados, un correceptor CD8 que contiene cadenas α y β separadas por un péptido de auto-escisión P2A, con el correceptor CD8 separado del TCR por un otro péptido de auto-escisión P2A. Cada secuencia P2A está precedida por un sitio de escisión de furina. En la zona N-terminal de la cadena CD8α se incorpora un epítopo de 16 amino ácidos que codifica una porción del CD34 humano. El transgén está bajo el control de un promotor del virus de células madre murino (MSCV), un elemento de respuesta post-transcripcional del virus de la hepatitis de la marmota (WPRE) y una señal de poliadenilación (poliA) del virus simio 40 (SV40). La transposasa (transposasa de gusano soldado) se introduce en forma de un ARNm que contiene un análogo de caperuza anti-reverso, una región sin traducir (UTR) en 5' de la globina de *Xenopus*, una secuencia Kozak, el marco de lectura abierto de la transposasa, y una UTR en 3' de la globina de *Xenopus*. El transgén se introduce mediante un nanoplásmido de ADN y contiene repeticiones terminales invertidas (ITRs).

ruzaltatugum #

ruzaltatug	immunoglobulin G1-kappa, anti-[*Homo sapiens* ERBB3 (receptor tyrosine-protein kinase erbB-3, HER3)], *Homo sapiens* monoclonal antibody; H-gamma1 heavy chain *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV3-9*01 (97.0%) -(IGHD) -IGHJ4*01 (92.9%), 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 (446-447)) (118-447)], (220-215')-disulfide with L-kappa light chain *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (87.4%) -IGKJ2*04 (90.9%) L124>V (105'), CDR-IMGT [6.3.10] (27'-32'.50'-52'.89'-98')) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (154'), V101 (192')) (109'-215')]; dimer (226-226'':229-229'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa
ruzaltatug	immunoglobuline G1-kappa, anti-[*Homo sapiens* ERBB3 (récepteur tyrosine-protéine kinase erbB-3, HER3)], anticorps monoclonal *Homo sapiens*; chaîne lourde H-gamma1 *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV3-9*01 (97.0%) -(IGHD) -IGHJ4*01 (92.9%), 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 (446-447)) (118-447)], (220-215')-disulfure avec la chaîne légère L-kappa *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (87.4%) -IGKJ2*04 (90.9%) L124>V (105'), CDR-IMGT [6.3.10] (27'-32'.50'-52'.89'-98')) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA 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-K1, glycoforme alfa
ruzaltatug	inmunoglobulina G1-kappa, anti-[*Homo sapiens* ERBB3 (receptor tirosina-proteína kinasa erbB-3, HER3)], anticuerpo monoclonal *Homo sapiens*; cadena pesada H-gamma1 *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV3-9*01 (97.0%) -(IGHD) -IGHJ4*01 (92.9%), 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 (446-447)) (118-447)], (220-215')-disulfuro con la cadena ligera L-kappa *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (87.4%) -IGKJ2*04 (90.9%) L124>V (105'), CDR-IMGT [6.3.10] (27'-32'.50'-52'.89'-98')) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA 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-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGGG LVQPGRSLRL SCAASGFTFD DYAMHWVRQA PGKGLEWVSG  50
ISWNSGSIGY ADSVKGRFTI SRDNAKNSLY LQMNSLRAED TALYYCAKEG 100
LPGLDYWGQG TLVTVSSAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF 150
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC 200
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT 250
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT 350
LPPSRDELTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS 400
DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPGK    447
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Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASIGDRAT ITCRASQHVG TYLNWYQQKP GKTPKLLISG  50
AANLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ SYNTPPFSFG 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) 22-96 144-200 261-321 367-425
22"-96" 144"-200" 261"-321" 367"-425"
Intra-L (C23-C104) 23'-88' 135'-195'
23'"-88'" 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-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"

ruzaltatugum rezetecanum

ruzaltatug rezetecan

immunoglobulin G1-kappa, anti-[*Homo sapiens* ERBB3 (receptor tyrosin-protein kinase erbB-3, HER3)], *Homo sapiens* monoclonal antibody,conjugated on an average of four cysteinyl residues to *rezetecan*, comprising a linker and a camptothecin derivative (*exatecan*);
H-gamma1 heavy chain *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV3-9*01 (97.0%) -(IGHD) -IGHJ4*01 (92.9%), 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 (446-447)) (118-447)], (220-215')-disulfide with L-kappa light chain *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (87.4%) -IGKJ2*04 (90.9%) L124>V (105'), CDR-IMGT [6.3.10] (27'-32'.50'-52'.89'-98')) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (154'), V101 (192')) (109'-215')]; dimer (226-226":229-229")-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 215', 215'", 220, 220", 226, 226", 229 and 229" with (3*RS*)-1-[(2*R*,10*S*)-10-benzyl-2-cyclopropyl-1-{[(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]amino}-1,6,9,12,15,18-hexaoxo-3-oxa-5,8,11,14,17-pentaazatricosan-23-yl]-2,5-dioxopyrrolidin-3-yl (*rezetecan*) groups

ruzaltatug rézétécan	immunoglobuline G1-kappa, anti-[*Homo sapiens* ERBB3 (récepteur tyrosine-protéine kinase erbB-3, HER3)], anticorps monoclonal *Homo sapiens*, conjuguée par quatre résidus cystéinyles en moyenne au *rézétécan*, comprenant un linker et un dérivé de la camptothécine (*exatécan*); chaîne lourde H-gamma1 *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV3-9*01 (97.0%) -(IGHD) -IGHJ4*01 (92.9%), 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 (446-447)) (118-447)], (220-215')-disulfure avec la chaîne légère L-kappa *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (87.4%) -IGKJ2*04 (90.9%) L124>V (105'), CDR-IMGT [6.3.10] (27'-32'.50'-52'.89'-98')) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA 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-K1, glycoforme alfa; substitué, sur les atomes de soufre de quatre résidus L-cystéinyle en moyenne parmi 215', 215''', 220, 220'', 226, 226'', 229 et 229'', avec des groupes (3*RS*)-1-[(2*R*,10*S*)-10-benzyl-2-cyclopropyl-1-{[(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]amino}-1,6,9,12,15,18-hexaoxo-3-oxa-5,8,11,14,17-pentaazatricosan-23-yl]-2,5-dioxopyrrolidin-3-yle (*rézétécan*)
ruzaltatug rezetecán	inmunoglobulina G1-kappa, anti-[*Homo sapiens* ERBB3 (receptor tirosina-proteína kinasa erbB-3, HER3)], anticuerpo monoclonal *Homo sapiens*, conjugado, por cuatro residuos de cisteinilo, por término medio a *rezetecán*, que comprende un enlace y un derivado de la camptotecina (*exatecán*); cadena pesada H-gamma1 *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV3-9*01 (97.0%) -(IGHD) -IGHJ4*01 (92.9%), 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 (446-447)) (118-447)], (220-215')-disulfuro con la cadena ligera L-kappa *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (87.4%) -IGKJ2*04 (90.9%) L124>V (105'), CDR-IMGT [6.3.10] (27'-32'.50'-52'.89'-98')) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA 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-K1, forma glicosilada alfa; sustituido, en los átomos de azufre de cuatro residuos de L-cisteinilo en promedio de 215', 215''', 220, 220'', 226, 226'', 229 y 229'', con grupos (3*RS*)-1-[(2*R*,10*S*)-10-bencil-2-ciclopropil-1-{[(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]amino}-1,6,9,12,15,18-hexaoxo-3-oxa-5,8,11,14,17-pentaazatricosan-23-il]-2,5-dioxopirrolidin-3-ilo (*rezetecán*)

Heavy chain / Chaîne lourde / Cadena pesada (H, H")

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QVQLVQSGGG LVQPGRSLRL SCAASGFTFD DYAMHWVRQA PGKGLEWVSG  50
ISWNSGSIGY ADSVKGRFTI SRDNAKNSLY LQMNSLRAED TALYYCAKEG 100
LPGLDYWGQG TLVTVSSAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF 150
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC 200
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT 250
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT 350
LPPSRDELTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS 400
DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPGK    447
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Light chain / Chaîne légère / Cadena ligera (L', L'")

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DIQMTQSPSS LSASIGDRAT ITCRASQHVG TYLNWYQQKP GKTPKLLISG  50
AANLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ SYNTPPFSFG 100
QGTKVEIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK 150
VDNALQSGNS QESVTEQDSK DSTYSLSSTL TLSKADYEKH KVYACEVTHQ 200
GLSSPVTKSF NRGEC                                       215
```

Post-translational modifications

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

Intra-H (C23-C104) 22-96 144-200 261-321 367-425
22"-96" 144"-200" 261"-321" 367"-425"

Intra-L (C23-C104) 23'-88' 135'-195'
23'"-88'" 135'"-195'"

Inter-H-L (h 5-CL 126)* 220-215' 220"-215'"

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

*Two or three 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.

*Deux ou trois 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.

*Dos o tres 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: 297, 297"

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

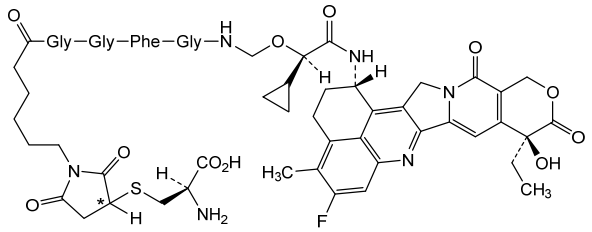
C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal

H CHS K2: 447, 447"

Modified residues / Résidus modifiés / Restos modificados*

C (215', 215'", 220, 220", 226, 226", 229, 229")

*(*rezetecan*:mAb ~ 4:1)



sasineprocelum

sasineprocel

autologous dopaminergic neuron precursor cells (DANPCs) derived from human induced pluripotent stem cells (iPSCs). The iPSCs are derived from patient skin fibroblasts that are expanded and reprogrammed by a non-integrating method with plasmid vectors expressing octamer-binding transcription factor 3/4 (OCT-3/4), SOX2, Krueppel-like factor 4 (KLF4), and L-Myc.
The cells are expanded on recombinant laminin and frozen as intermediates to be then thawed, expanded, dissociated with a

	proteolytic and collagenolytic enzyme mixture and initially seeded in medium supplemented with Rho-associated protein kinase (ROCK). Differentiation into dopaminergic precursor cells is then performed in neurobasal medium supplemented with serum replacement containing a transforming growth factor-β (TGFβ)/activin-Nodal signaling inhibitor, a bone morphogenetic protein (BMP) inhibitor, a glycogen synthase kinase (GSK) 3 inhibitor, a Sonic hedgehog (Shh) signaling activator and a γ-secretase inhibitor, as well as recombinant brain-derived neurotrophic factor (BDNF), glial cell-line-derived neurotrophic factor (GDNF), transforming growth factor β3 (TGFβ3) and Sonic hedgehog (Shh). The differentiated and mature DANPCs are then harvested, washed, and cryopreserved. The final cell population expresses forkhead box protein A2 (FoxA2; >80%) as characteristic factor of dopaminergic neurons, with a minor (<5%) cell population expressing paired box protein (PAX6). Uncommitted iPSCs are absent or present at low level (<0.1%; octamer-binding transcription factor 3/4 (OCT-3/4) and vertnin (VRTN))
sasinéprocel	cellules précurseures de neurones dopaminergiques autologues (DANPCs) dérivées de cellules souches pluripotentes induites humaines (CSPi). Les CSPi sont dérivées de fibroblastes cutanés de patients, qui sont expansés et reprogrammés par une méthode non intégrative avec des vecteurs plasmidiques exprimant le facteur de transcription 3/4 de liaison à l'octamère (OCT-3/4), SOX2, le facteur 4 de type Krueppel (KLF4), et L-Myc. Les cellules sont expansées sur de la laminine recombinante et congelées comme intermédiaires pour être ensuite décongelées, expansées, dissociées avec un mélange d'enzymes protéolytiques et collagénolytiques, et initialement ensemencées dans un milieu supplémenté en protéine kinase associée à Rho (ROCK). La différenciation en cellules précurseures dopaminergiques est ensuite réalisée dans un milieu neurobasal complété par un substitut de sérum contenant un inhibiteur de la signalisation du facteur de croissance transformant β (TGFβ)/activine-Nodal, un inhibiteur de la protéine morphogénétique osseuse (PMO), un inhibiteur de la glycogène synthase kinase (GSK) 3, un activateur de signalisation Sonic hedgehog (Shh) et un inhibiteur de la γ-sécrétase, ainsi que le facteur neurotrophique dérivé du cerveau (BDNF) recombinant, le facteur neurotrophe dérivé de la glie (GDNF), le facteur de croissance transformant β3 (TGFβ3) et Sonic hedgehog (Shh). Les DANPCs différenciées et matures sont ensuite récoltées, lavées et cryoconservées. La population cellulaire finale exprime la protéine A2 de la boîte forkhead (FoxA2; >80%) comme facteur caractéristique des neurones dopaminergiques, avec une population cellulaire mineure (<5%) exprimant la protéine paired box 6 (PAX6). Les CSPi non engagées sont absentes ou présentes à un faible niveau (<0,1%; facteur 3/4 de transcription de liaison à l'octamère (OCT-3/4) et la vertnine (VRTN))
sasineprocel	células precursoras de neuronas dopaminérgicas (DANPCs) autólogas derivadas de células madre pluripotentes inducidas (iPSCs) humanas. Las iPSCs se derivan a partir de fibroblastos de la piel del paciente que son expandidos y reprogramados mediante un método no integrativo con vectores plasmídicos que expresan el factor 3/4 de trascripción de unión a octámero (OCT-3/4), SOX2, factor similar a Krueppel 4 (KLF4) y L-Myc. Las células se expanden en laminina recombinante y se congelan como intermediarios para ser después descongeladas, expandidas, disociadas con una mezcla de enzimas proteolíticas y

colagenolíticas y sembradas inicialmente en medio suplementado con proteína quinasa asociada a Rho (ROCK). La diferenciación a células precursoras dopaminérgicas se realiza en medio neurobasal suplementado con substituto de suero que contiene un inhibidor de la señalización del factor de crecimiento transformante β (TGFβ)/activina-Nodal, un inhibidor de la proteína morfogenética del hueso (BMP), un inhibidor de la glicogén sintasa quinasa (GSK) 3, un activador de señalización Sonic hedghog (Shh) y un inhibidor de la γ-secretasa, así como factor neurotrófico derivado de cerebro (BDNF) recombinante, factor neurotrófico derivado de línea celular de la glia (GDNF), factor de crecimiento transformante β3 (TGFβ3) y Sonic hedgehog (Shh). Las DANPCs diferenciadas y maduras se cosechan a continuación, se lavan y se criopreservan.
La población celular final expresa la proteína A2 de caja forkhead (FoxA2; >80%) como factor característico de neuronas dopaminérgicas, con una población celular menor (<5%) que expresa la proteína paired box 6 (PAX6). Las iPSCs sin diferenciar están ausentes o a bajo nivel (<0.1%; factor 3/4 de transcripción de unión a octámero (OCT-3/4) y vertnina (VRTN))

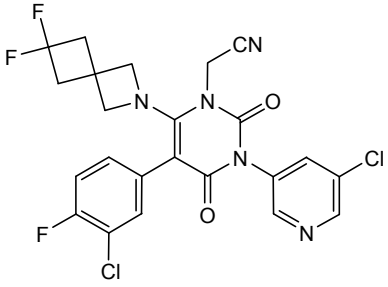
secutrelvirum

secutrelvir — [5-(3-chloro-4-fluorophenyl)-3-(5-chloropyridin-3-yl)-6-(6,6-difluoro-2-azaspiro[3.3]heptan-2-yl)-2,4-dioxo-3,4-dihydropyrimidin-1(2*H*)-yl]acetonitrile

sécutrelvir — [5-(3-chloro-4-fluorophényl)-3-(5-chloropyridin-3-yl)-6-(6,6-difluoro-2-azaspiro[3.3]heptan-2-yl)-2,4-dioxo-3,4-dihydropyrimidin-1(2*H*)-yl]acétonitrile

secutrelvir — [5-(3-cloro-4-fluorofenil)-3-(5-cloropiridin-3-il)-6-(6,6-difluoro-2-azaespiro[3.3]heptan-2-il)-2,4-dioxo-3,4-dihidropirimidin-1(2*H*)-il]acetonitrilo

$C_{23}H_{16}Cl_2F_3N_5O_2$



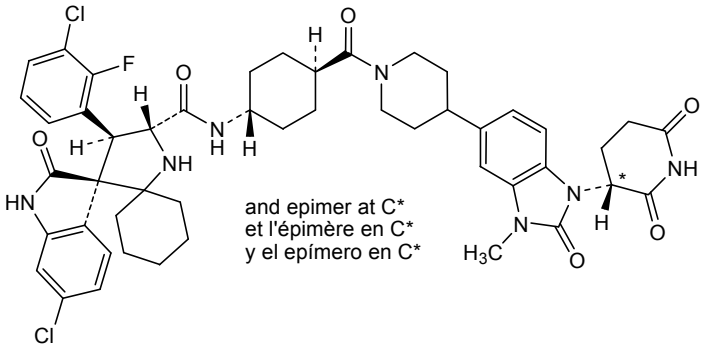
seldegamadlinum

seldegamadlin — (3'*R*,4'*S*,5'*R*)-6''-chloro-4'-(3-chloro-2-fluorophenyl)-*N*-[*trans*-4-(4-{1-[(3*RS*)-2,6-dioxopiperidin-3-yl]-3-methyl-2-oxo-2,3-dihydro-1*H*-1,3-benzimidazol-5-yl}piperidine-1-carbonyl)cyclohexyl]-2''-oxo-1'',2''-dihydrodispiro[cyclohexane-1,2'-pyrrolidine-3',3''-indole]-5'-carboxamide

seldégamadline — (3'*R*,4'*S*,5'*R*)-6''-chloro-4'-(3-chloro-2-fluorophényl)-*N*-[*trans*-4-(4-{1-[(3*RS*)-2,6-dioxopipéridin-3-yl]-3-méthyl-2-oxo-2,3-dihydro-1*H*-1,3-benzimidazol-5-yl}pipéridine-1-carbonyl)cyclohexyl]-2''-oxo-1'',2''-dihydrodispiro[cyclohexane-1,2'-pyrrolidine-3',3''-indole]-5'-carboxamide

seldegamadlina (3'*R*,4'*S*,5'*R*)-6''-cloro-4'-(3-cloro-2-fluorofenil)-*N*-[*trans*-4-(4-{1-[(3*RS*)-2,6-dioxopiperidin-3-il]-3-metil-2-oxo-2,3-dihidro-1*H*-1,3-benzimidazol-5-il}piperidina-1-carbonil)ciclohexil]-2''-oxo-1'',2''-dihidrodiespiro[ciclohexano-1,2'-pirrolidina-3',3''-indol]-5'-carboxamida

$C_{48}H_{52}Cl_2FN_7O_6$



sersacabtagenum autoleucelum #

sersacabtagene autoleucel

autologous CD4+/CD8+ enriched T lymphocytes obtained from peripheral blood lymphocytes by leukapheresis, transduced with a self-inactivating lentiviral vector encoding a humanized chimeric antigen receptor (CAR) targeting CD20 that includes a CD8α signalling peptide, an anti-CD20 single chain variable fragment (scFv) derived from human monoclonal IgG1 kappa antibody *ofatumumab*, an IgG4 hinge region, CD8 transmembrane region, and an intracellular 4-1BB co-stimulatory and CD3ζ signalling domain under control of the elongation factor 1 alpha (EF-1α) promoter and a Woodchuck hepatitis virus posttranscriptional regulatory element (WPRE). The vector also contains an HIV-1 packaging signal (Ψ), *gag*, Rev response element (RRE), central polypurine tract and central termination sequence (cPPT/CTS), is flanked by 5' and 3' long terminal repeats (LTRs) and is pseudotyped by the vesicular stomatitis virus (VSV) G glycoprotein. The leukapheresis material is enriched for CD4+/CD8+ T lymphocytes by positive immunoselection, activated by CD3 and CD28 agonists and transduced with the lentiviral vector. The cells are then expanded in media with serum replacement and interleukin 2 (IL-2). The T lymphocytes (≥90% CD3+; ≤1% CD19+ or CD20+) are positive for the transgene (≥10% CAR positive) and secrete interferon gamma in response to co-culture with CD20-expressing tumour cell lines.

sersacabtagéne autoleucel

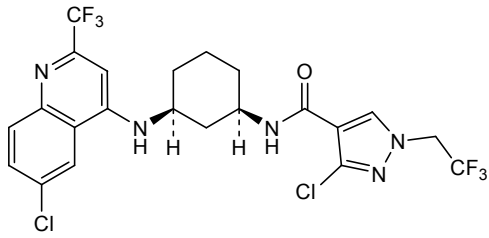
lymphocytes T autologues enrichis en CD4+/CD8+ obtenus à partir de lymphocytes du sang périphérique par leucaphérèse, transduits avec un vecteur lentiviral auto-inactivant codant un récepteur antigénique chimérique humanisé (RAC) ciblant CD20, qui comprend un peptide de signalisation CD8α, un fragment variable à chaîne unique anti-CD20 (scFv) dérivé de l'anticorps monoclonal IgG1 kappa humain *ofatumumab*, d'une région charnière IgG4, d'une région transmembranaire CD8 et d'un domaine intracellulaire de co-stimulation 4-1BB et de signalisation CD3ζ, sous le contrôle du promoteur du facteur d'élongation 1 alpha (EF-1α) et d'un élément régulateur post-transcriptionnel du virus de l'hépatite de la marmotte (WPRE). Le vecteur contient également un signal d'empaquetage du VIH-1 (Ψ), *gag*, un élément de réponse Rev (RRE), un tractus polypurine central et une séquence de terminaison centrale

	(cPPT/CTS), est flanqué de répétitions terminales longues (LTRs) en 5' et en 3' et est pseudotypé par la glycoprotéine G du virus de la stomatite vésiculaire (VSV). Le matériel de leucaphérèse est enrichi en lymphocytes T CD4+/CD8+ par immunosélection positive, activés par les agonistes CD3 et CD28 et transduits avec le vecteur lentiviral. Les cellules sont ensuite expansées dans un milieu avec remplacement de sérum et interleukine 2 (IL-2). Les lymphocytes T (≥90% CD3+; ≤1% CD19+ ou CD20+) sont positifs au transgène (≥10% RAC positif) et sécrètent de l'interféron gamma en réponse à une co-culture avec des lignées de cellules tumorales exprimant CD20
sersacabtagén autoleucel	linfocitos T CD4+/CD8+ autólogos enriquecidos obtenidos de linfocitos de sangre periférica por leucoaféresis, transducidos con un vector lentiviral auto inactivante, que codifica un receptor de antígenos quimérico (CAR) humanizado dirigido a CD20 que incluye un péptido señal de CD8α, un fragmento variable de cadena sencilla (scFv) anti-CD20 derivado del anticuerpo monoclonal humano IgG1 kappa *ofatumumab*, una región bisagra de IgG4, una región transmembrana de CD8, 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) y un elemento regulador post-transcripcional del virus de la hepatitis de la marmota (WPRE). El vector también contiene una señal de empaquetamiento de HIV-1 (ψ), *gag*, un elemento de respuesta Rev (RRE), una secuencia de tracto de poli-purina/terminación central (cPPT/CTS), está flanqueado por repeticiones terminales largas (LTRs) en 5' y 3' y está seudotipado con la glicoproteína G 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 lentiviral. Las células se expanden después en medio con substituto de suero e interleuquina 2 (IL-2). Los linfocitos T (≥90% CD3+; ≤1% CD19+ o CD20+) son positivos para el transgén (≥10% positivos para el CAR) y secretan interferón gamma en respuesta al co-cultivo con líneas celulares tumorales que expresan CD20

setomagpranum

setomagpran	3-chloro-*N*-[(1*R*,3*S*)-3-{[6-chloro-2-(trifluoromethyl)quinolin-4-yl]amino}cyclohexyl]-1-(2,2,2-trifluoroethyl)-1*H*-pyrazole-4-carboxamide
sétomagpran	3-chloro-*N*-[(1*R*,3*S*)-3-{[6-chloro-2-(trifluorométhyl)quinoléin-4-yl]amino}cyclohexyl]-1-(2,2,2-trifluoroéthyl)-1*H*-pyrazole-4-carboxamide
setomagprán	3-cloro-*N*-[(1*R*,3*S*)-3-{[6-cloro-2-(trifluorometil)quinolein-4-il]amino}ciclohexil]-1-(2,2,2-trifluoroetil)-1*H*-pirazol-4-carboxamida

$C_{22}H_{19}Cl_2F_6N_5O$



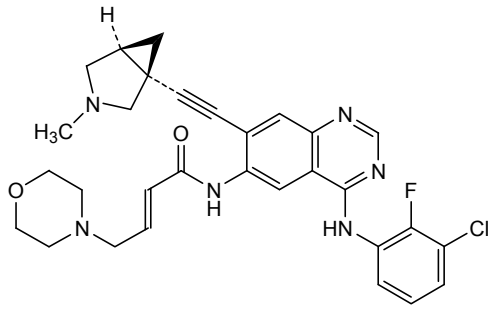
silevertinibum

silevertinib — (2*E*)-*N*-[4-(3-chloro-2-fluoroanilino)-7-{[(1*R*,5*S*)-3-methyl-3-azabicyclo[3.1.0]hexan-1-yl]ethynyl}quinazolin-6-yl]-4-(morpholin-4-yl)but-2-enamide

silévertinib — (2*E*)-*N*-[4-(3-chloro-2-fluoroanilino)-7-{[(1*R*,5*S*)-3-méthyl-3-azabicyclo[3.1.0]hexan-1-yl]éthynyl}quinazolin-6-yl]-4-(morpholin-4-yl)but-2-énamide

silevertinib — (2*E*)-*N*-[4-(3-cloro-2-fluoroanilino)-7-{[(1*R*,5*S*)-3-metil-3-azabiciclo[3.1.0]hexan-1-il]etinil}quinazolin-6-il]-4-(morfolin-4-il)but-2-enamida

$C_{30}H_{30}ClFN_6O_2$



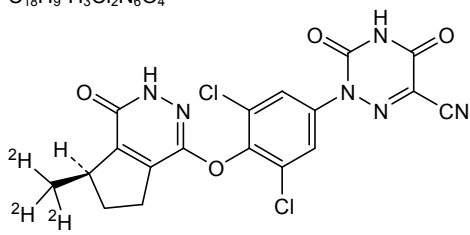
simedeutiromum

simedeutirom — 2-(3,5-dichloro-4-{[(7*R*)-7-($^2H_3$)methyl-1-oxo-2,5,6,7-tetrahydro-1*H*-cyclopenta[*d*]pyridazin-4-yl]oxy}phenyl)-3,5-dioxo-2,3,4,5-tetrahydro-1,2,4-triazine-6-carbonitrile

simédeutirom — 2-(3,5-dichloro-4-{[(7*R*)-7-($^2H_3$)méthyl-1-oxo-2,5,6,7-tétrahydro-1*H*-cyclopenta[*d*]pyridazin-4-yl]oxy}phényl)-3,5-dioxo-2,3,4,5-tétrahydro-1,2,4-triazine-6-carbonitrile

simedeutirom — 2-(3,5-dicloro-4-{[(7*R*)-7-($^2H_3$)metil-1-oxo-2,5,6,7-tetrahidro-1*H*-ciclopenta[*d*]piridazin-4-il]oxi}fenil)-3,5-dioxo-2,3,4,5-tetrahidro-1,2,4-triazina-6-carbonitrilo

$C_{18}H_9{}^2H_3Cl_2N_6O_4$



sitmutolimodum

sitmutolimod — *all-P-ambo*-(3'→5')-*P*-thiothymidylyl-(3'→5')-2′-deoxy-*P*-thiocytidylyl-(3'→5')-2′-deoxy-*P*-thioguanylyl-(3'→5')-2′-deoxy-*P*-thiocytidylyl-(3'→5')-2′-deoxy-*P*-thioguanylyl-(3'→5')-2′-deoxy-*P*-thioadenylyl-(3'→5')-2′-deoxy-*P*-thioadenylyl-(3'→5')-2′-deoxy-*P*-thiocytidylyl-(3'→5')-2′-deoxy-*P*-thioguanylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2′-deoxy-*P*-thiocytidylyl-(3'→5')-2′-deoxy-*P*-thioguanylyl-(3'→5')-2′-deoxy-*P*-thiocytidylyl-(3'→5')-2′-deoxy-*P*-thioguanylyl-(3'→5')-2′-deoxy-*P*-thiocytidylyl-(3'→5')-2′-deoxy-*P*-thioguanylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2′-deoxy-*P*-thioadenylyl-(3'→5')-2′-deoxy-*P*-thiocytidylyl-(3'→5')-2′-deoxy-*P*-thioguanylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2′-deoxy-*P*-thioadenylyl-(3'→5')-2′-deoxy-*P*-thiocytidylyl-(3'→5')-2′-deoxy-*P*-thioguanylyl-(3'→5')-2′-deoxy-*P*-thiocytidylyl-(3'→5')-2′-deoxy-*P*-thioguanylyl

sitmutolimod — *tout-P-ambo*-(3'→5')-*P*-thiothymidylyl-(3'→5')-2′-désoxy-*P*-thiocytidylyl-(3'→5')-2′-désoxy-*P*-thioguanylyl-(3'→5')-2′-désoxy-*P*-thiocytidylyl-(3'→5')-2′-désoxy-*P*-thioguanylyl-(3'→5')-2′-désoxy-*P*-thioadénylyl-(3'→5')-2′-désoxy-*P*-thioadénylyl-(3'→5')-2′-désoxy-*P*-thiocytidylyl-(3'→5')-2′-désoxy-*P*-thioguanylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2′-désoxy-*P*-thiocytidylyl-(3'→5')-2′-désoxy-*P*-thioguanylyl-(3'→5')-2′-désoxy-*P*-thiocytidylyl-(3'→5')-2′-désoxy-*P*-thiocytidylyl-(3'→5')-2′-désoxy-*P*-thioguanylyl-(3'→5')-2′-désoxy-*P*-thioguanylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2′-désoxy-*P*-thioadénylyl-(3'→5')-2′-désoxy-*P*-thiocytidylyl-(3'→5')-2′-désoxy-*P*-thioguanylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2′-désoxy-*P*-thioadénylyl-(3'→5')-2′-désoxy-*P*-thiocytidylyl-(3'→5')-2′-désoxy-*P*-thioguanylyl-(3'→5')-2′-désoxy-*P*-thiocytidylyl-(3'→5')-2′-désoxy-*P*-thioguanylyl

sitmutolimod — *todo-P-ambo*-(3'→5')-*P*-tiotimidilil-(3'→5')-2′-desoxi-*P*-tiocitidilil-(3'→5')-2′-desoxi-*P*-tioguanilil-(3'→5')-2′-desoxi-*P*-tiocitidilil-(3'→5')-2′-desoxi-*P*-tioguanilil-(3'→5')-2′-desoxi-*P*-tioadenilil-(3'→5')-2′-desoxi-*P*-tioadenilil-(3'→5')-2′-desoxi-*P*-tiocitidilil-(3'→5')-2′-desoxi-*P*-tioguanilil-(3'→5')-*P*-tiotimidilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2′-desoxi-*P*-tiocitidilil-(3'→5')-2′-desoxi-*P*-tioguanilil-(3'→5')-2′-desoxi-*P*-tiocitidilil-(3'→5')-2′-desoxi-*P*-tioguanilil-(3'→5')-2′-desoxi-*P*-tiocitidilil-(3'→5')-2′-desoxi-*P*-tioguanilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2′-desoxi-*P*-tioadenilil-(3'→5')-2′-desoxi-*P*-tiocitidilil-(3'→5')-2′-desoxi-*P*-tioguanilil-(3'→5')-*P*-tiotimidilil-(3'→5')-2′-desoxi-*P*-tioadenilil-(3'→5')-2′-desoxi-*P*-tiocitidilil-(3'→5')-2′-desoxi-*P*-tioguanilil-(3'→5')-2′-desoxi-*P*-tiocitidilil-(3'→5')-2′-desoxi-*P*-tioguanilil-(3'→5')-2′-desoxi-*P*-tioguanilil

$C_{280}H_{354}N_{110}O_{145}P_{28}S_{28}$

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

N : nucleoside / nucléoside / nucleósido
dN : 2'-deoxy-N / 2'-désoxy-N / 2'-desoxi-N
= : –PO(SH)–

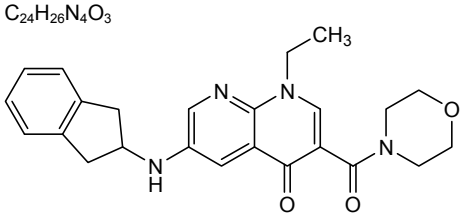
soclenicantum

soclenicant — 6-[(2,3-dihydro-1*H*-inden-2-yl)amino]-1-ethyl-3-(morpholine-4-carbonyl)-1,8-naphthyridin-4(1*H*)-one

soclénicant — 6-[(2,3-dihydro-1*H*-indén-2-yl)amino]-1-éthyl-3-(morpholine-4-carbonyl)-1,8-naphtyridin-4(1*H*)-one

soclenicant — 6-[(2,3-dihidro-1*H*-inden-2-il)amino]-1-etil-3-(morfolina-4-carbonil)-1,8-naftiridin-4(1*H*)-ona

$C_{24}H_{26}N_4O_3$



soficabtagenum geleucelum #

soficabtagene geleucel

allogeneic CD4+ and CD8+ T lymphocytes derived from leukapheresis material of healthy donors, genetically modified using CRISPR/Cas9 gene editing to knockout the expression of endogenous CD7 and TRAC using guide RNAs (gRNAs), followed by transduction with a self-inactivating, non-replicating lentivirus vector encoding an anti-CD7 chimeric antigen receptor (CAR) comprising a CD8 leader sequence, anti-CD7 single-chain variable fragment (scFv) (clone TH69), CD8 hinge, CD28 transmembrane domain, 4-1BB co-stimulatory domain and CD3ζ intracellular signalling domain, under control of the elongation factor 1 alpha (EF-1α) promoter. The transgene also encodes a truncated human CD34 extracellular domain separated from the CAR by a 2A peptide derived from porcine teschovirus-1. The CRISPR/Cas9 and gRNAs are introduced as a ribonucleoprotein (RNP) complex by electroporation. The lentivirus vector is flanked by 5' and 3' LTRs and also contains a viral packaging sequence ψ, partial *gag*, a Rev response element (RRE), a central polypurine tract/central termination sequence (cPPT/CTS) and a synthetic identification (ID) sequence. The vector is pseudotyped with VSV G envelope 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 gene-edited and then transduced with the lentiviral vector and expanded in growth media containing human AB serum, IL-7, and IL-15. The cell suspension consists of T lymphocytes (≥98.0% CD45+, ≤1.0% CD7+, ≤8.0% CD3+) with greater than 30% of the T lymphocytes expressing the CAR transgene and >70% (CD7) and >85% (TRAC) on-target gene editing. The transduced T lymphocytes demonstrate cytotoxicity against CD7+ T-lymphoblastic target cells

soficabtagène géleucel	lymphocytes T allogéniques CD4+ et CD8+ dérivés de matériel de leucaphérèse de donneurs sains, génétiquement modifiés à l'aide de l'édition génique CRISPR/Cas9 pour éliminer l'expression endogènes de CD7 et TRAC à l'aide d'ARN guides (ARNg), suivis d'une transduction avec un vecteur lentiviral auto-inactivant et non réplicatif codant pour un récepteur antigénique chimérique (RAC) anti-CD7 comprenant une séquence de tête CD8, un fragment variable à chaîne unique (scFv) anti-CD7 (clone TH69), une charnière CD8, un domaine transmembranaire CD28, un domaine co-stimulateur 4-1BB et un domaine de signalisation intracellulaire CD3ζ, sous le contrôle du promoteur du facteur d'élongation 1 alpha (EF-1α). Le transgène code également pour un domaine extracellulaire tronqué du CD34 humain séparé du RAC par un peptide 2A dérivé du teschovirus-1 porcin. Le CRISPR/Cas9 et les ARNg sont introduits sous forme de complexe ribonucléoprotéique (RNP) par électroporation. Le vecteur lentiviral est flanqué de longues répétitions terminales en 5' et en 3' et contient également une séquence d'empaquetage virale ψ, une partie de gène *gag*, un élément de réponse Rev (RRE), une séquence centrale de tractus polypurine/terminaison centrale (cPPT/CTS) et une identification synthétique (ID). Le vecteur est pseudotypé avec la glycoprotéine G d'enveloppe du virus de la stomatite vésiculaire (VSV). Le matériel de leucaphérèse est enrichi en lymphocytes T CD4+ et CD8+ par immunosélection positive, avant activation 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 modifiées génétiquement, puis transduites avec le vecteur lentiviral et expansées dans un milieu de croissance contenant du sérum AB humain, de l'IL-7 et de l'IL-15. La suspension cellulaire est constituée de lymphocytes T (≥98.0% CD45+, ≤1.0% CD7+, ≤8.0% CD3+) avec plus de 30% de lymphocytes T exprimant le transgène RAC, et >70% (CD7) et >85% (TRAC) d'édition de gènes sur cible. Les lymphocytes T transduits démontrent une cytotoxicité contre les cellules cibles lymphoblastiques T CD7+
soficabtagén geleucel	linfocitos T CD4+ y CD8+ alogénicos derivados de material de leucoaféresis de donantes sanos, modificados genéticamente usando edición génica con CRISPR/Cas9 para eliminar la expresión de CD7 y TRAC endógenos usando ARNs guía (ARNg), seguido de transducción con un vector lentiviral auto-inactivante, no replicativo que codifica un receptor de antígenos quimérico (CAR) anti-CD7 que consta de una secuencia líder de CD8, un fragmento variable de cadena sencilla (scFv) anti-CD7 (clon TH69), bisagra de CD8, un dominio transmembrana de CD28, un dominio coestimulador de 4-1BB y un dominio de señalización intracelular de CD3ζ, bajo el control del promotor del factor de elongación 1 alfa (EF-1α). El transgén también codifica un dominio extracelular

truncado de CD34 humano separado del CAR por un péptido 2A derivado del teschovirus porcino 1. El CRISP/Cas9 y los ARNg se introducen como un complejo de ribonucleoproteína (RNP) mediante electroporación. El vector lentiviral está flanqueado por repeticiones terminales largas (LTRs) en 5' y 3' y también contiene una secuencia de empaquetamiento viral ψ, un *gag* parcial, un elemento de respuesta Rev (RRE), una secuencia de tracto de poli-purina/terminación central (cPPT/CTS) y una secuencia de identificación (ID) sintética. El vector está seudotipado con la glicoproteína G de la envuelta de VSV.
El material de leucoaféresis se enriquece en 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 15 (IL-15). Las células se editan genéticamente y después se transducen con el vector lentiviral y se expanden en medio de crecimiento que contiene suero AB humano, IL-7 e IL-15. La suspensión celular consiste en linfocitos T (≥98.0% CD45+, ≤1.0% CD7+, ≤8.0% CD3+) con más del 30% de los linfocitos T que expresan el transgén del CAR y con ≥70% (CD7) y >85% (TRAC) de edición génica dirigida. Los linfocitos transducidos muestran citotoxicidad frente a células T linfoblásticas diana CD7+

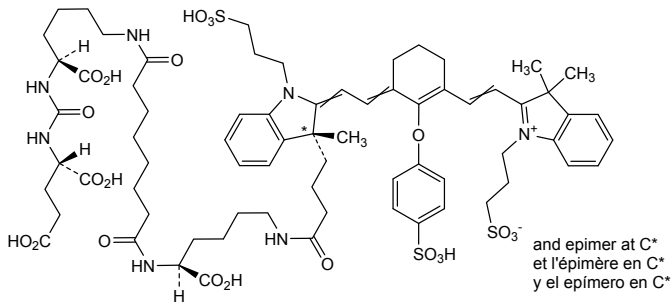
sonzivotidum filricianinum

sonzivotide filricianine — 3-(3,3-dimethyl-2-{(Ξ)-2-[(3Ξ)-3-[(2Ξ)-2-{(3*RS*)-3-methyl-1-(3-sulfopropyl)-3-[(3*S*,7*S*,22*S*)-1,3,7,22-tetracarboxy-5,13,20,28-tetraoxo-4,6,12,21,27-pentaazahentriacontan-31-yl]-1,3-dihydro-2*H*-indol-2-ylidene}ethylidene]-2-(4-sulfophenoxy)cyclohex-1-en-1-yl]ethen-1-yl}-3*H*-indol-1-ium-1-yl)propane-1-sulfonate

sonzivotide filricianine — 3-(3,3-diméthyl-2-{(Ξ)-2-[(3Ξ)-3-[(2Ξ)-2-{(3*RS*)-3-méthyl-1-(3-sulfopropyl)-3-[(3*S*,7*S*,22*S*)-1,3,7,22-tétracarboxy-5,13,20,28-tétraoxo-4,6,12,21,27-pentaazahéntriacontan-31-yl]-1,3-dihydro-2*H*-indol-2-ylidène}éthylidène]-2-(4-sulfophénoxy)cyclohex-1-én-1-yl]éthén-1-yl}-3*H*-indol-1-ium-1-yl)propane-1-sulfonate

sonzivotida filricianina — 3-(3,3-dimetil-2-{(Ξ)-2-[(3Ξ)-3-[(2Ξ)-2-{(3*RS*)-3-metil-1-(3-sulfopropil)-3-[(3*S*,7*S*,22*S*)-1,3,7,22-tetracarboxi-5,13,20,28-tetraoxo-4,6,12,21,27-pentaazahentriacontan-31-il]-1,3-dihidro-2*H*-indol-2-ilideno}etilideno]-2-(4-sulfofenoxi)ciclohex-1-en-1-il]eten-1-il}-3*H*-indol-1-io-1-il)propano-1-sulfonato

$C_{71}H_{95}N_7O_{22}S_3$



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

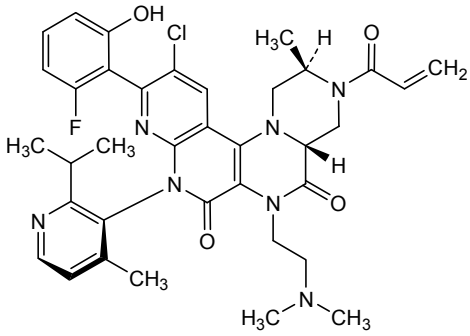
sosimerasibum

sosimerasib — (2*R*,4a*R*,8*M*)-11-chloro-6-[2-(dimethylamino)ethyl]-10-(2-fluoro-6-hydroxyphenyl)-2-methyl-8-[4-methyl-2-(propan-2-yl)pyridin-3-yl]-3-(prop-2-enoyl)-2,3,4,4a,6,8-hexahydro-1*H*-pyrazino[1',2':4,5]pyrazino[2,3-*c*][1,8]naphthyridine-5,7-dione

sosimérasib — (2*R*,4a*R*,8*M*)-11-chloro-6-[2-(diméthylamino)éthyl]-10-(2-fluoro-6-hydroxyphényl)-2-méthyl-8-[4-méthyl-2-(propan-2-yl)pyridin-3-yl]-3-(prop-2-énoyl)-2,3,4,4a,6,8-hexahydro-1*H*-pyrazino[1',2':4,5]pyrazino[2,3-*c*][1,8]naphtyridine-5,7-dione

sosimerasib — (2*R*,4a*R*,8*M*)-11-cloro-6-[2-(dimetilamino)etil]-10-(2-fluoro-6-hidroxifenil)-2-metil-8-[4-metil-2-(propan-2-il)piridin-3-il]-3-(prop-2-enoil)-2,3,4,4a,6,8-hexahidro-1*H*-pirazino[1',2':4,5]pirazino[2,3-*c*][1,8]naftiridina-5,7-diona

$C_{36}H_{39}ClFN_7O_4$



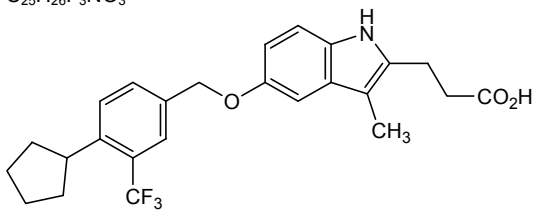
sumonerimodum

sumonerimod — 3-(5-{[4-cyclopentyl-3-(trifluoromethyl)phenyl]methoxy}-3-methyl-1*H*-indol-2-yl)propanoic acid

sumonérimod — acide 3-(5-{[4-cyclopentyl-3-(trifluorométhyl)phényl]méthoxy}-3-méthyl-1*H*-indol-2-yl)propanoïque

sumonerimod — ácido 3-(5-{[4-ciclopentil-3-(trifluorometil)fenil]metoxi}-3-metil-1*H*-indol-2-il)propanoico

$C_{25}H_{26}F_3NO_3$



suraxavirum marboxilum

suraxavir marboxil — ({(12'a*R*)-12'-[(11*S*)-7,8-difluoro-6,11-dihydrodibenzo[*b*,*e*]thiepin-11-yl]-6',8'-dioxo-6',8',12',12'a-tetrahydro-1'*H*,4'*H*-spiro[cyclopropane-1,3'-[1,4]oxazino[3,4-*c*]pyrido[2,1-*f*][1,2,4]triazin]-7'-yl}oxy)methyl methyl carbonate

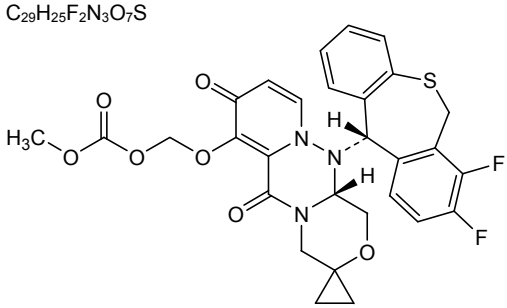
suraxavir marboxil

carbonate de ({(12'a*R*)-12'-[(11*S*)-7,8-difluoro-6,11-dihydrodibenzo[*b*,*e*]thiépin-11-yl]-6',8'-dioxo-6',8',12',12'a-tétrahydro-1'*H*,4'*H*-spiro[cyclopropane-1,3'-[1,4]oxazino[3,4-*c*]pyrido[2,1-*f*][1,2,4]triazin]-7'-yl}oxy)méthyle et de méthyle

suraxavir marboxilo

carbonato de ({(12'a*R*)-12'-[(11*S*)-7,8-difluoro-6,11-dihidrodibenzo[*b*,*e*]tiepin-11-il]-6',8'-dioxo-6',8',12',12'a-tetrahidro-1'*H*,4'*H*-espiro[ciclopropano-1,3'-[1,4]oxazino[3,4-*c*]pirido[2,1-*f*][1,2,4]triazin]-7'-il}oxi)metilo y metilo

$C_{29}H_{25}F_2N_3O_7S$



suvonstobartum #

suvonstobart

immunoglobulin G1-kappa, anti-[*Homo sapiens* CD24 (signal transducer CD24)], monoclonal antibody; H-gamma1 heavy chain (1-447) [VH Musmus/Homsap (*Mus musculus* IGHV3-1*02 (98.0%) -(IGHD) -IGHJ4*01 (87.5%) G121>R (110)/*Homo sapiens* IGHV4-30-4*09 (74.5%) -(IGHD) -IGHJ4*01 (78.6%) G121>R (110), L123>S (112), CDR-IMGT [9.7.10] (26-34.52-58.97-106)) (1-117) -*Homo sapiens* IGHG1*03,G1m3, nG1m1 CH1 R120, CH3 E12, M14, 2-G1v6 CH2 A85.4, A118, A119 (CH1 R120 (214) (118-215), hinge 1-15 (216-230), CH2 S85.4>A (298), E118>A (333), K119>A (334) (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-220')-disulfide with L-kappa light chain (1'-220') [V-KAPPA (*Homo sapiens* IGKV1-27*01 (82.3%) -IGKJ4*01 (91.7%) I126>L (112'), CDR-IMGT [12.3.9] (27'-38'.56'-58'.95'-103')) (1'-113') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (159'), V101 (197')) (114'-220')]; dimer (226-226'':229-229'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa

suvonstobart

immunoglobuline G1-kappa, anti-[*Homo sapiens* CD24 (transducteur de signal CD24)], anticorps monoclonal; chaîne lourde H-gamma1 (1-447) [VH Musmus/Homsap (*Mus musculus* IGHV3-1*02 (98.0%) -(IGHD) -IGHJ4*01 (87.5%) G121>R (110)/*Homo sapiens* IGHV4-30-4*09 (74.5%) -(IGHD) -IGHJ4*01 (78.6%) G121>R (110), L123>S (112), CDR-IMGT [9.7.10] (26-34.52-58.97-106)) (1-117) -*Homo sapiens* IGHG1*03,G1m3, nG1m1 CH1 R120, CH3 E12, M14, 2-G1v6 CH2 A85.4, A118, A119 (CH1 R120 (214) (118-215), charnière 1-15 (216-230), CH2 S85.4>A (298), E118>A (333), K119>A (334) (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447))

(118-447)], (220-220')-disulfure avec la chaîne légère L-kappa (1'-220') [V-KAPPA (*Homo sapiens* IGKV1-27*01 (82.3%) -IGKJ4*01 (91.7%) I126>L (112'), CDR-IMGT [12.3.9] (27'-38'.56'-58'.95'-103')) (1'-113') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (159'), V101 (197')) (114'-220')]; dimère (226-226'':229-229'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa

suvonstobart — inmunoglobulina G1-kappa, anti-[*Homo sapiens* CD24 (transductor de señal CD24)], anticuerpo monoclonal;
cadena pesada H-gamma1 (1-447) [VH Musmus/Homsap (*Mus musculus* IGHV3-1*02 (98.0%) -(IGHD) -IGHJ4*01 (87.5%) G121>R (110)/*Homo sapiens* IGHV4-30-4*09 (74.5%) -(IGHD) -IGHJ4*01 (78.6%) G121>R (110), L123>S (112), CDR-IMGT [9.7.10] (26-34.52-58.97-106)) (1-117) -*Homo sapiens* IGHG1*03,G1m3, nG1m1 CH1 R120, CH3 E12, M14, 2-G1v6 CH2 A85.4, A118, A119 (CH1 R120 (214) (118-215), bisagra 1-15 (216-230), CH2 S85.4>A (298), E118>A (333), K119>A (334) (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-220')-disulfuro con la cadena ligera L-kappa (1'-220') [V-KAPPA (*Homo sapiens* IGKV1-27*01 (82.3%) -IGKJ4*01 (91.7%) I126>L (112'), CDR-IMGT [12.3.9] (27'-38'.56'-58'.95'-103')) (1'-113') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (159'), V101 (197')) (114'-220')]; dímero (226-226'':229-229'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
DVQLQESGPD LVKPSQSLSL TCTVTGYSIT SGYSWHWIRQ FPGNKLEWMG  50
YIHYSGSTKY NPSLKSRISI TRDTSKNQFF LQLNSVTTED TATYFCARGA 100
DYALDYWGQR TSVTVSSAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF 150
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC 200
NVNHKPSNTK VDKRVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT 250
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNATY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIAATISKAK GQPREPQVYT 350
LPPSREEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS 400
DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPGK    447
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Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCKSSQSLL YSSNQKNYLA WYQQKPGKAP  50
KLLIYWASTR ESGVPSRFSG SGSGTDFTLT ISSLQPEDFA TYYCQQNFIY 100
PLTFGGGTKV 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) 22-96 144-200 261-321 367-425
22''-96'' 144''-200'' 261''-321'' 367''-425''
Intra-L (C23-C104) 23'-94' 140'-200'
23'''-94''' 140'''-200'''
Inter-H-L (h 5-CL 126) 220-220' 220''-220'''
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''

tagovameranum #

tagovameran	self-amplifying messenger RNA (mRNA), 5'-capped, encoding codon-optimised Venezuelan equine encephalitis virus (VEEV) RNA-dependent RNA polymerase complex (VEEV proteins nsP1, nsP2, nsP3 and nsP4) and a full-length codon-optimised pre-fusion stabilised conformation variant (K981P and V982P) of the SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2) spike (S) glycoprotein BA.4/BA.5 variant (derived from GenBank ID: UVX18152) containing furin cleavage-inactivating mutations (R677G, R678S and R680S), flanked by 5' and 3' untranslated regions and a 3' polyadenylation (poly(A) tail; generation of capped S glycoprotein mRNA is under control of a VEEV subgenomic promoter
tagovaméran	ARN messager (ARNm) auto-amplifiant, avec une coiffe en 5', codant l'ARN polymérase dépendante de l'ARN du virus de l'encéphalite équine vénézuélienne (VEEV) optimisé par codon (protéines nsP1, nsP2, nsP3 et nsP4 de VEEV) et une variante de conformation stabilisée de préfusion (K981P et V982P), de séquence complète, optimisée par codon, de la glycoprotéine du spicule (S) du SRAS-CoV-2 (coronavirus 2 du syndrome respiratoire aigu sévère) variant BA.4/BA.5 (dérivé de la base de données GenBank ID: UVX18152), contenant des mutations inactivant le clivage par la furine (R677G, R678S et R680S), flanqué en 5' et 3' par des régions non traduites et une queue de polyadénylation (polyA) en 3'; la génération de l'ARNm de la glycoprotéine S coiffée est sous le contrôle du promoteur subgénomique de VEEV
tagovamerán	ARN mensajero (ARNm) auto amplificante, protegido en 5', que codifica, con codones optimizados, para una ARN polimerasa dependiente de ARN del virus de la encefalitis equina venezolana (VEEV) (proteínas nsP1, nsP2, nsP3 y nsP4 de VEEV) y para una secuencia completa, con codones optimizados, de una variante estabilizada en conformación pre-fusión (K981P y V982P) de la glicoproteína de la espícula (S) del SRAS-CoV-2 (coronavirus 2 del síndrome respiratorio agudo severo) variante BA.4/BA.5 (derivada de GenBank ID: UVX18152) que contiene mutaciones inactivantes de la rotura por furina (R677G, R678S y R680S), flanqueado por regiones sin traducir 5' y 3' y una cola de poliadenilación (poliA) en 3'; la generación del ARNm protegido de la glicoproteína S está bajo el control del promotor subgenómico de VEEV

talicabtagene autoleucelum #

talicabtagene autoleucel	autologous peripheral blood mononuclear cells (PBMCs) obtained by leukapheresis enriched for CD3+ T lymphocytes, transduced with a self-inactivating non-replicating lentiviral vector encoding a chimeric antigen receptor (CAR) targeting CD19, comprising a CD8α leader sequence, a humanised anti-CD19 single chain variable fragment (scFv; derived from the FMC63 antibody), human CD8α hinge and transmembrane domain, human 4-1BB co-stimulatory domain and human CD3ζ signalling domain, under control of the elongation factor-1 alpha (EF-1α) promoter. The vector genome also contains an HIV-1 packaging signal (ψ), a Rev response element (RRE), a central polypurine tract (cPPT)/central termination sequence (CTS) and is flanked by 5' and 3' long terminal repeats (LTRs). The vector is pseudotyped with vesicular stomatitis virus (VSV) G glycoprotein.

	The leukapheresis material is enriched for CD3+ T lymphocytes by positive immunoselection, activated by CD3 and CD28 agonists and transduced with the lentiviral vector. The cells are then expanded in media supplemented with human AB serum and interleukin 2 (IL-2). The T lymphocytes (≥95%) are positive for the transgene (≥15% CAR positive) and are cytotoxic (≥50%) when co-cultured with CD19 expressing tumour cell lines
talicabtagène autoleucel	cellules mononucléaires du sang périphérique (PBMC) autologues, obtenues par leucaphérèse et enrichies en lymphocytes T CD3+, transduites avec un vecteur lentiviral non réplicatif auto-inactivant codant un récepteur antigénique chimérique (RAC) ciblant CD19, comprenant une séquence de tête CD8α, un fragment variable à chaîne unique anti-CD19 humanisé (scFv; dérivé de l'anticorps FMC63), un domaine charnière et un domain transmembranaire CD8α humain, un domaine co-stimulateur 4-1BB humain et un domaine de signalisation CD3ζ humain, sous le contrôle du promoteur du facteur d'élongation 1 alpha (EF-1α). Le génome du vecteur contient également un signal d'emballage du VIH-1 (ψ), un élément de réponse Rev (RRE), un tractus polypurine central (cPPT)/séquence de terminaison centrale (CTS), et est flanqué de répétitions terminales longues (LTRs) en 5' et en 3'. Le vecteur est pseudotypé avec la glycoprotéine G du virus de la stomatite vésiculaire (VSV). Le matériel de leucaphérèse est enrichi en lymphocytes T CD3+ par immunosélection positive, activé par des agonistes CD3 et CD28 et transduit avec le vecteur lentiviral. Les cellules sont ensuite éxpansées dans un milieu supplémenté de sérum AB humain et d'interleukine 2 (IL-2). Les lymphocytes T (≥95%) sont positifs pour le transgène (≥15% RAC positifs), et sont cytotoxiques (≥50%) lorsqu'ils sont co-cultivés avec des lignées cellulaires tumorales exprimant CD19
talicabtagén autoleucel	células monucleares de sangre periférica (PBMCs) autólogas obtenidas por leucoaféresis, enriquecidas en linfocitos T CD3+, transducidas con un vector lentiviral auto-inactivante, no replicativo, que codifica un receptor de antígenos quimérico (CAR) dirigido a CD19, que consta de una secuencia líder de CD8α, un fragmento variable de cadena sencilla anti-CD19 humanizado (scFv; derivado del anticuerpo FMC63), un dominio bisagra y transmembrana de CD8α, un dominio coestimulador de 4-1BB humano y un dominio de señalización de CD3ζ humano, bajo el control del promotor del factor de elongación 1 alfa (EF-1α). El genoma del vector también contiene una señal de empaquetamiento del HIV-1 (ψ), un elemento de respuesta Rev (RRE) y una secuencia de tracto de poli-purina central (cPPT)/terminación central (CTS), y está flanqueado por repeticiones terminales largas (LTRs) en 5' y 3'. El vector está seudotipado con la glicoproteína G del virus de la estomatitis vesicular (VSV). El material de leucoaféresis se enriquece en linfocitos T CD3+ mediante inmunoselección positiva, se activa con agonistas de CD3 y CD28 y se transduce con el vector lentiviral. Las células se expanden después en medio suplementado con suero AB humano e interleuquina 2 (IL-2). Los linfocitos T (≥95%) son positivos para el transgén (≥15% CAR positivos) y son citotóxicos (≥50%) cuando se co-cultivan con líneas de células tumorales que expresan CD19

tanruprubartum #

tanruprubart	immunoglobulin G4-kappa, anti-[*Homo sapiens* C1q (complement C1q)], monoclonal antibody; H-gamma4 heavy chain (1-448) [VH Musmus/Homsap (*Mus musculus* IGHV1-64*01 (82.5%) -(IGHD) -IGHJ4*01 (92.9%) S123>T (116)/*Homo sapiens* IGHV1-46*01 (79.4%) -(IGHD) -IGHJ6*01 (92.9%), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1-121) -*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, 12-G4v5 h P10, 6-G4v3 CH2 E1.2 (CH1 (122-219), hinge 1-12 S10>P (229) (220-231), CH2 L1.2>E (236), L92 (310) (232-341), CH3 (342-446), CHS (447-448)) (122-448)], (135-214')-disulfide with L-kappa light chain (1'-214') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV16-104*01 (89.5%) -IGKJ2*03 (90.9%) S120>Q (100')/*Homo sapiens* IGKV1-9*03 (80.9%) -IGKJ2*01 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dimer (227-227'':230-230'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1SV, lacking the glutamine synthetase (GS-KO) gene, glycoform alfa
tanruprubart	immunoglobuline G4-kappa, anti-[*Homo sapiens* C1q (complément C1q)], anticorps monoclonal; chaîne lourde H-gamma4 (1-448) [VH Musmus/Homsap (*Mus musculus* IGHV1-64*01 (82.5%) -(IGHD) -IGHJ4*01 (92.9%) S123>T (116)/*Homo sapiens* IGHV1-46*01 (79.4%) -(IGHD) -IGHJ6*01 (92.9%), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1-121) -*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, 12-G4v5 h P10, 6-G4v3 CH2 E1.2 (CH1 (122-219), charnière 1-12 S10>P (229) (220-231), CH2 L1.2>E (236), L92 (310) (232-341), CH3 (342-446), CHS (447-448)) (122-448)], (135-214')-disulfure avec la chaîne légère L-kappa (1'-214') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV16-104*01 (89.5%) -IGKJ2*03 (90.9%) S120>Q (100')/*Homo sapiens* IGKV1-9*03 (80.9%) -IGKJ2*01 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dimère (227-227'':230-230'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1SV, ne présentant pas le gène de la glutamine synthétase (GS-KO), glycoforme alfa
tanruprubart	inmunoglobulina G4-kappa, anti-[*Homo sapiens* C1q (complemento C1q)], anticuerpo monoclonal; cadena pesada H-gamma4 (1-448) [VH Musmus/Homsap (*Mus musculus* IGHV1-64*01 (82.5%) -(IGHD) -IGHJ4*01 (92.9%) S123>T (116)/*Homo sapiens* IGHV1-46*01 (79.4%) -(IGHD) -IGHJ6*01 (92.9%), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1-121) -*Homo sapiens* IGHG4*01, *nG4m(a)* CH2 L92, 12-G4v5 h P10, 6-G4v3 CH2 E1.2 (CH1 (122-219), bisagra 1-12 S10>P (229) (220-231), CH2 L1.2>E (236), L92 (310) (232-341), CH3 (342-446), CHS (447-448)) (122-448)], (135-214')-disulfuro con la cadena ligera L-kappa (1'-214') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV16-104*01 (89.5%) -IGKJ2*03 (90.9%) S120>Q (100')/*Homo sapiens* IGKV1-9*03 (80.9%) -IGKJ2*01 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dímero (227-227'':230-230'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular derivada de CHO-K1SV, en ausencia del gen glutamina sintetasa (GS-KO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE LKKPGASVKV SCKSSGYHFT SYWMHWVKQA PGQGLEWIGV  50
IHPNSGSINY NEKFESRVTI TVDKSTSTAY MELSSLRSED TAVYYCAGER 100
DSTEVLPMDY WGQGTTVTVS SASTKGPSVF PLAPCSRSTS ESTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTK 200
TYTCNVDHKP SNTKVDKRVE SKYGPPCPPC PAPEFEGGPS VFLFPPKPKD 250
TLMISRTPEV TCVVVDVSQE DPEVQFNWYV DGVEVHNAKT KPREEQFNST 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKGLP SSIEKTISKA KGQPREPQVY 350
TLPPSQEEMT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD 400
SDGSFFLYSR LTVDKSRWQE GNVFSCSVMH EALHNHYTQK SLSLSLGK   448
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Light chain / Chaîne légère / Cadena ligera

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DVQITQSPSS LSASLGERAT INCRASKSIN KYLAWYQQKP GKAPKLLIYS  50
GSTLQSGIPA RFSGSGSGTD FTLTISSLEP EDFAMYYCQQ HNEYPLTFGQ 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) 22-96 148-204 262-322 368-426
22''-96'' 148''-204'' 262''-322'' 368''-426''
Intra-L (C23-C104) 23'-88' 134'-194'
23'''-88''' 134'''-194'''
Inter-H-L (CH1 10-CL 126) 135-214' 135''-214'''
Inter-H-H (h 8, h 11) 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''

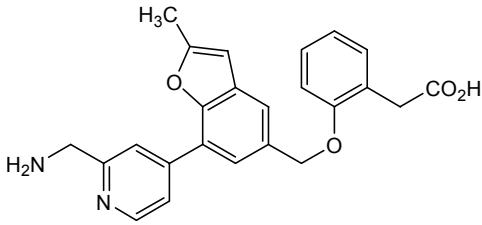
tarvicopanum

tarvicopan — [2-({7-[2-(aminomethyl)pyridin-4-yl]-2-methyl-1-benzofuran-5-yl}methoxy)phenyl]acetic acid

tarvicopan — acide [2-({7-[2-(aminométhyl)pyridin-4-yl]-2-méthyl-1-benzofuran-5-yl}méthoxy)phényl]acétique

tarvicopán — ácido [2-({7-[2-(aminometil)piridin-4-il]-2-metil-1-benzofuran-5-il}metoxi)fenil]acético

$C_{24}H_{22}N_2O_4$



technetium (^{99m}Tc) gleceparinum natricum

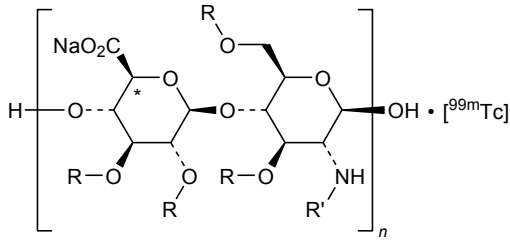
technetium (^{99m}Tc) gleceparin sodium — sodium salt of heparin with a degree of sulfatation of about 2.7 per disaccharide unit, fractionated to a product containing ≥50% of molecules with mass >20 kDa, radiolabeled with (^{99m}Tc)technetium

technétium (^{99m}Tc) glécéparine sodique

sel de sodium d'héparine avec une degré de sulfatation d'environ 2,7 par unité disaccharidique, fractionné en un produit contenant ≥50% de molécules de masse >20 kDa, radiomarqué avec du (^{99m}Tc)technétium

tecnecio (^{99m}Tc) gleceparina sódica

sal sódica de heparina con un grado de sulfatación de aproximadamente 2,7 por unidad disacarídica, fraccionada hasta obtener un producto que contenga ≥50% de moléculas con masa >20 kDa, radiomarcado con (^{99m}Tc)tecnecio



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N-(2-aminopyrimidin-5-yl)-*N*'-[(1*R*)-1-(5,7-difluoro-3-methyl-1-benzofuran-2-yl)-2,2,2-trifluoroethyl]urea

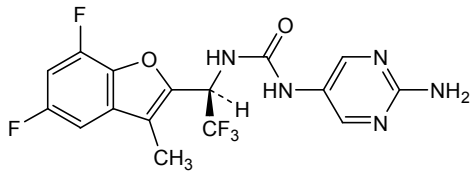
tersolisib

N-(2-aminopyrimidin-5-yl)-*N*'-[(1*R*)-1-(5,7-difluoro-3-méthyl-1-benzofuran-2-yl)-2,2,2-trifluoroéthyl]urée

tersolisib

N-(2-aminopirimidin-5-il)-*N*'-[(1*R*)-1-(5,7-difluoro-3-metil-1-benzofuran-2-il)-2,2,2-trifluoroetil]urea

$C_{16}H_{12}F_5N_5O_2$



tetrandrinum

tetrandrine

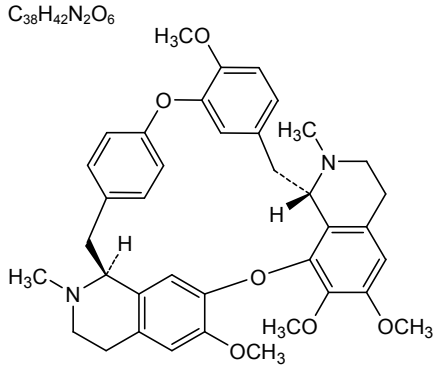
(1^1*S*,3^1*S*)-1^6,3^6,3^7,5^4-tetramethoxy-1^2,3^2-dimethyl-1^1,1^2,1^3,1^4,3^1,3^2,3^3,3^4-octahydro-2,6-dioxa-1(7,1),3(8,1)-diisoquinolina-5(1,3),7(1,4)-dibenzenacyclooctaphane;
6,6',7,12-tetramethoxy-2,2'-dimethyl-1-*epi*-berbaman

tétrandrine

(1^1*S*,3^1*S*)-1^6,3^6,3^7,5^4-tétraméthoxy-1^2,3^2-diméthyl-1^1,1^2,1^3,1^4,3^1,3^2,3^3,3^4-octahydro-2,6-dioxa-1(7,1),3(8,1)-diisoquinoléina-5(1,3),7(1,4)-dibenzénacyclooctaphane;
6,6',7,12-tétraméthoxy-2,2'-diméthyl-1-*épi*-berbamane

tetrandrina

(1^1*S*,3^1*S*)-1^2,3^2-dimetil-1^6,3^6,3^7,5^4-tetrametoxi-1^1,1^2,1^3,1^4,3^1,3^2,3^3,3^4-octahidro-2,6-dioxa-1(7,1),3(8,1)-diisoquinoleina-5(1,3),7(1,4)-dibencenaciclooctafano;
2,2'-dimetil-6,6',7,12-tetrametoxi-1-*epi*-berbamano



tezusomantum

tezusomant

N-(15-carboxypentadecanoyl)-L-γ-glutamyl-L-γ-glutamyl-N^6-{$N^{6.2}$,$C^{1.7}$-anhydro-$S^{N.1}$,$C^{3.13}$-cyclo[4-carboxy-*N*-(sulfanylacetyl)-L-phenylalanyl-N^2-methyl-L-lysyl-L-valyl-L-valyl-L-seryl-L-asparaginyl-1-(carboxymethyl)-L-tryptophyl-4-carboxy-L-phenylalanyl-L-lysyl-5-hydroxy-L-tryptophyl-2-methylalanyl-L-valyl-L-alanyl]}-L-lysinamide

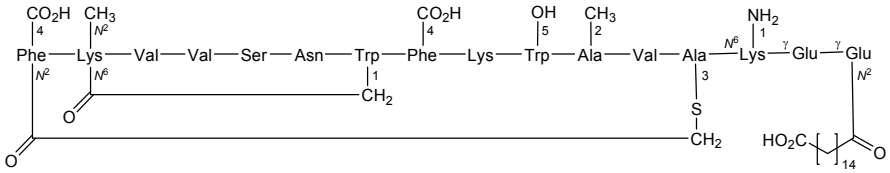
tézusomant

N-(15-carboxypentadécanoyl)-L-γ-glutamyl-L-γ-glutamyl-N^6-{$N^{6.2}$,$C^{1.7}$-anhydro-$S^{N.1}$,$C^{3.13}$-cyclo[4-carboxy-*N*-(sulfanylacétyl)-L-phénylalanyl-N^2-méthyl-L-lysyl-L-valyl-L-valyl-L-séryl-L-asparaginyl-1-(carboxyméthyl)-L-tryptophyl-4-carboxy-L-phénylalanyl-L-lysyl-5-hydroxy-L-tryptophyl-2-méthylalanyl-L-valyl-L-alanyl]}-L-lysinamide

tezusomant

N-(15-carboxipentadecanoil)-L-γ-glutamil-L-γ-glutamil-N^6-{$N^{6.2}$,$C^{1.7}$-anhidro-$S^{N.1}$,$C^{3.13}$-ciclo[4-carboxi-*N*-(sulfanilacetil)-L-fenilalanil-N^2-metil-L-lisil-L-valil-L-valil-L-seril-L-asparaginil-1-(carboximetil)-L-triptofil-4-carboxi-L-fenilalanil-L-lisil-5-hidroxi-L-triptofil-2-metilalanil-L-valil-L-alanil]}-L-lisinamida

$C_{120}H_{171}N_{23}O_{32}S$



tilrekimigum #

tilrekimig

immunoglobulin (L-kappa-H-gamma1 (_L-VH-G1(CH1-h))_L-kappa)_(H-gamma1_L-lambda2), anti-[*Homo sapiens* IL4 (interleukin 4, IL-4)], anti-[*Homo sapiens* IL13 (interleukin 13, IL-13)] and anti-[*Homo sapiens* TSLP (thymic stromal lymphopoietin)], humanized and *Homo sapiens* monoclonal antibody, trispecific, trivalent;

	fused L-kappa-H-gamma1 heavy chain anti-IL13 and anti-IL4 (1-674) [L-kappa anti-IL13 humanized (1-218) [V-KAPPA (*Homo sapiens* IGKV1-39*01 (82.8%) - IGKJ4*01 (100%), CDR-IMGT [10.3.9] (27-36.54-56.93-101)) (1-111) -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (157), V101 (195)) (112-218)]-5-mer (tetraglycyl-seryl) linker (219-223) - H-gamma1 heavy chain anti-IL4 *Homo sapiens* (224-674) [VH (*Homo sapiens* IGHV2-5*08 (87.0%) -(IGHD) -IGHJ3*01 (92.9%) M123>T (339), CDR-IMGT [10.7.13] (249-258.276-282.321-333)) (224-344) - *Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, CH1 K120, CH3 E12, M14, 6-G1v14-1 CH2 A1.3, A1.2, A1, 9-G1v24 CH3 L107, S114, 14-G1v99-1 hinge E6, CH3 E24 (CH1 R120>K (441) (345-442), hinge 1-15 D6>E (448) (443-457), CH2 L1.3>A (461), L1.2>A (462), G1>A (464) (458-567), CH3 E12 (583), M14 (585), L24>E (595), M107>L (655), N114>S (661) (568-672), CHS (673-674)) (345-674)]]; (218-221')-disulfide with L-VH-G1(CH1-h) light chain anti-IL13 humanized (1'-221') [VH (*Homo sapiens* IGHV3-21*07 (91.8%) -IGHD -IGHJ1*01 (100%), CDR-IMGT [8.7.12] (26'-33'.51'-57'.96'-107')) (1'-118') -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, CH1 K120 (CH1 R120>K (215') (119'-216'), hinge 1-5 (217'-221')) (119'-221')]; (447-218'")-disulfide with L-kappa light chain *Homo sapiens* anti-IL4 *Homo sapiens* (1'"-218'") [V-KAPPA (*Homo sapiens* IGKV1-39*01 (87.9%) - IGKJ4*01 (100%), CDR-IMGT [10.3.9] (27'"-36'".54'"-56'".93'"-101'")) (1'"-111'") -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (157'"), V101 (195'")) (112'"-218'")]; H-gamma1 heavy chain anti-TSLP *Homo sapiens* (1"-452") [VH (*Homo sapiens* IGHV3-33*01 (95.9%) - (IGHD) -IGHJ3*02 (93.8%), 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, 6-G1v14-1 CH2 A1.3, A1.2, A1, 9-G1v24 CH3 L107, S114, 14-G1v99-2 hinge R6, CH3 R88 (CH1 R120>K (219") (123"-220"), hinge 1-15 D6>R (226") (221"-235"), CH2 L1.3>A (239"), L1.2>A (240"), G1>A (242") (236"- 345"), CH3 E12 (361"), M14 (363"), K88>R (414"), M107>L (433"), N114>S (439") (346"-450"), CHS (451"-452")) (123"-452")], (225"-213"")-disulfide with L-lambda2 light chain anti-TSLP *Homo sapiens* (1""-214"") [V-LAMBDA (*Homo sapiens* IGLV3-21*02 (94.8%) -IGLJ2*01 (100%), CDR-IMGT [6.3.11] (26""-31"".49""-51"".88""-98"")) (1""-108"") - *Homo sapiens* IGLC2*01 (100%) (C-LAMBDA2) (109""-214"")]; dimer (453-231":456-234")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1SV lacking the glutamine synthetase (GS-KO) gene, glycoform alfa
tilrékimig	immunoglobuline (L-kappa-H-gamma1 (_L-VH-G1(CH1-h))_L-kappa)_(H-gamma1_L-lambda2), anti-[*Homo sapiens* IL4 (interleukine 4, IL-4)], anti-[*Homo sapiens* IL13 (interleukine 13, IL-13)] et anti-[*Homo sapiens* TSLP (lymphopoïétine stromale thymique)], anticorps monoclonal humanisé et *Homo sapiens* trispécifique, trivalent;

	chaîne fusionnée L-kappa-H-gamma1 anti-IL13 et anti-IL4 (1-674) [L-kappa anti-IL13 humanisée (1-218) [V-KAPPA (*Homo sapiens* IGKV1-39*01 (82.8%) -IGKJ4*01 (100%), CDR-IMGT [10.3.9] (27-36.54-56.93-101)) (1-111) -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (157), V101 (195)) (112-218)] -5-mer (tétraglycyl-séryl) linker (219-223) -chaîne lourde H-gamma1 anti-IL4 *Homo sapiens* (224-674) [VH (*Homo sapiens* IGHV2-5*08 (87.0%) -(IGHD) -IGHJ3*01 (92.9%) M123>T (339), CDR-IMGT [10.7.13] (249-258.276-282.321-333)) (224-344) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, CH1 K120, CH3 E12, M14, 6-G1v14-1 CH2 A1.3, A1.2, A1, 9-G1v24 CH3 L107, S114, 14-G1v99-1 hinge E6, CH3 E24 (CH1 R120>K (441) (345-442), charnière 1-15 D6>E (448) (443-457), CH2 L1.3>A (461), L1.2>A (462), G1>A (464) (458-567), CH3 E12 (583), M14 (585), L24>E (595), M107>L (655), N114>S (661) (568-672), CHS (673-674)) (345-674)]]; (218-221')-disulfure avec la chaîne légère L-VH-G1(CH1-h) anti-IL13 humanisée (1'-221')[VH (*Homo sapiens* IGHV3-21*07 (91.8%) -IGHD -IGHJ1*01 (100%), CDR-IMGT [8.7.12] (26'-33'.51'-57'.96'-107')) (1'-118') -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, CH1 K120 (CH1 R120>K (215') (119'-216'), charnière 1-5 (217'-221')) (119'-221')]; (447-218"")-disulfure avec la chaîne légère L-kappa anti-IL4 *Homo sapiens* (1""-218"") [V-KAPPA (*Homo sapiens* IGKV1-39*01 (87.9%) -IGKJ4*01 (100%), CDR-IMGT [10.3.9] (27""-36"".54""-56"".93""-101"")) (1""-111"") -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (157""), V101 (195"")) (112""-218"")]; chaîne lourde H-gamma1 anti-TSLP *Homo sapiens* (1"-452") [VH (*Homo sapiens* IGHV3-33*01 (95.9%) -(IGHD) -IGHJ3*02 (93.8%), 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, 6-G1v14-1 CH2 A1.3, A1.2, A1, 9-G1v24 CH3 L107, S114, 14-G1v99-2 hinge R6, CH3 R88 (CH1 R120>K (219") (123"-220"), charnière 1-15 D6>R (226") (221"-235"), CH2 L1.3>A (239"), L1.2>A (240"), G1>A (242") (236"- 345"), CH3 E12 (361"), M14 (363"), K88>R (414"), M107>L (433"), N114>S (439") (346"-450"), CHS (451"-452")) (123"-452")], (225"-213"")-disulfure avec la chaîne légère L-lambda2 anti-TSLP *Homo sapiens* (1""-214"") [V-LAMBDA (*Homo sapiens* IGLV3-21*02 (94.8%) -IGLJ2*01 (100%), CDR-IMGT [6.3.11] (26""-31"".49""-51"".88""-98"")) (1""-108"") -*Homo sapiens* IGLC2*01 (100%) (C-LAMBDA2) (109""-214"")]; dimère (453-231":456-234")-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
tilrekimig	inmunoglobulina (L-kappa-H-gamma1 (_L-VH-G1(CH1-h))_L-kappa)_(H-gamma1_L-lambda2), anti-[*Homo sapiens* IL4 (interleukina 4, IL-4)], anti-[*Homo sapiens* IL13 (interleukina 13, IL-13)] y anti-[*Homo sapiens* TSLP (linfopoyetina estromal tímica)],

anticuerpo monoclonal humanizado y *Homo sapiens* triespecífico, trivalente;
cadena fusionada L-kappa-H-gamma1 anti-IL13 anti-IL4 (1-674) [L-kappa anti-IL13 humanizada (1-218) [V-KAPPA (*Homo sapiens* IGKV1-39*01 (82.8%) - IGKJ4*01 (100%), CDR-IMGT [10.3.9] (27-36.54-56.93-101)) (1-111) -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (157), V101 (195)) (112-218)] -5-mer (tetraglicil-seril) enlace (219-223) - cadena pesada H-gamma1 anti-IL4 *Homo sapiens* (224-674) [VH (*Homo sapiens* IGHV2-5*08 (87.0%) - (IGHD) -IGHJ3*01 (92.9%) M123>T (339), CDR-IMGT [10.7.13] (249-258.276-282.321-333)) (224-344) - *Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, CH1 K120, CH3 E12, M14, 6-G1v14-1 CH2 A1.3, A1.2, A1, 9-G1v24 CH3 L107, S114, 14-G1v99-1 bisagra E6, CH3 E24 (CH1 R120>K (441) (345-442), bisagra 1-15 D6>E (448) (443-457), CH2 L1.3>A (461), L1.2>A (462), G1>A (464) (458-567), CH3 E12 (583), M14 (585), L24>E (595), M107>L (655), N114>S (661) (568-672), CHS (673-674)) (345-674)]]; (218-221')-disulfuro con la cadena ligera L-VH-G1(CH1-h) anti-IL13 humanizada (1'-221')[VH (*Homo sapiens* IGHV3-21*07 (91.8%) -IGHD -IGHJ1*01 (100%), CDR-IMGT [8.7.12] (26'-33'.51'-57'.96'-107')) (1'-118') -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, CH1 K120 (CH1 R120>K (215') (119'-216'), bisagra 1-5 (217'-221')) (119'-221')]; (447-218''')-disulfuro con la cadena ligera L-kappa anti-IL4 *Homo sapiens* (1'''-218''') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (87.9%) -IGKJ4*01 (100%), CDR-IMGT [10.3.9] (27'''-36'''.54'''-56'''.93'''-101''')) (1'''-111''') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (157'''), V101 (195''')) (112'''-218''')];
cadena pesada H-gamma1 anti-TSLP *Homo sapiens* (1''-452'') [VH (*Homo sapiens* IGHV3-33*01 (95.9%) - (IGHD) -IGHJ3*02 (93.8%), 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, 6-G1v14-1 CH2 A1.3, A1.2, A1, 9-G1v24 CH3 L107, S114, 14-G1v99-2 bisagra R6, CH3 R88 (CH1 R120>K (219'') (123''-220''), bisagra 1-15 D6>R (226'') (221''-235''), CH2 L1.3>A (239''), L1.2>A (240''), G1>A (242'') (236''- 345''), CH3 E12 (361''), M14 (363''), K88>R (414''), M107>L (433''), N114>S (439'') (346''-450''), CHS (451''-452'')) (123''-452'')], (225''-213'''')-disulfuro con la cadena ligera L-lambda2 anti-TSLP *Homo sapiens* (1''''-214'''') [V-LAMBDA (*Homo sapiens* IGLV3-21*02 (94.8%) -IGLJ2*01 (100%), CDR-IMGT [6.3.11] (26''''-31''''.49''''-51''''.88''''-98'''')) (1''''-108'''') -*Homo sapiens* IGLC2*01 (100%) (C-LAMBDA2) (109''''-214'''')]; dímero (453-231'':456-234'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1SV en ausencia del gen de la glutamina sintetasa (GS-KO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada: fused L-kappa-H-gamma1 anti-IL13 and anti-IL4 (H)

```
DIQMTQSPSS LSASVGDRVT ITCKASESVD HFGWSLVHWY QQKPGKAPKL  50
LIYRASNLES GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSNEDPW 100
TFGGGTKVEI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL NNFYPREAKV 150
QWKVDNALQS GNSQESVTEQ DSKDSTYSLS STLTLSKADY EKHKVYACEV 200
THQGLSSPVT KSFNRGECGG GGSEVTLRES GPALVKPTQT LTLTCTFSGF 250
SLSNFGEGLS WIRQPPGKGL EWLAHIYWDD DKRYNPSLKS RLTISKDTSR 300
NQVVLTMTNM DPVDTATYYC ARRETVFYWY FDVWGQGTTV TVSSASTKGP 350
SVFPLAPSSK STSGGTAALG CLVKDYFPEP VTVSWNSGAL TSGVHTFPAV 400
LQSSGLYSLS SVVTVPSSSL GTQTYICNVN HKPSNTKVDK KVEPKSCEKT 450
HTCPPCPAPE AAGAPSVFLF PPKPKDTLMI SRTPEVTCVV VDVSHEDPEV 500
KFNWYVDGVE VHNAKTKPRE EQYNSTYRVV SVLTVLHQDW LNGKEYKCKV 550
SNKALPAPIE KTISKAKGQP REPQVYTLPP SREEMTKNQV SLTCEVKGFY 600
PSDIAVEWES NGQPENNYKT TPPVLDSDGS FFLYSKLTVD KSRWQQGNVF 650
SCSVLHEALH SHYTQKSLSL SPGK                              674
```

Light chain / Chaîne légère / Cadena ligera: L-VH-G1(CH1-h) anti-IL13 (L')

```
EVQLVESGGG LVQPGGSLRL SCAASGFTFS SYAMSWVRQA PGKGLEWVAS  50
ISSGDTTYYP DSVKGRFTIS RDNAKNSLYL QMNSLRAEDT AVYYCARNEG 100
YYFGLTLWGQ GTLVTVSSAS TKGPSVFPLA PSSKSTSGGT AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTQTYI 200
CNVNHKPSNT KVDKKVEPKS C                                221
```

Light chain / Chaîne légère / Cadena ligera: L-kappa anti-IL4 (L''')

```
DIQMTQSPSS LSASVGDRVT ITCRASQSVD EEGDSYMNWY QQKPGKAPKL  50
LIYAASNLES GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSNKDPP 100
TFGGGTKVEI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL NNFYPREAKV 150
QWKVDNALQS GNSQESVTEQ DSKDSTYSLS STLTLSKADY EKHKVYACEV 200
THQGLSSPVT KSFNRGEC                                    218
```

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

```
QMQLVESGGG VVQPGRSLRL SCAASGFTFR TYGMHWVRQA PGKGLEWVAV  50
IWYDGSNKHY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARAP 100
QWYLVHEAFD IWGQGTMVTV SSASTKGPSV FPLAPSSKST SGGTAALGCL 150
VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ SSGLYSLSSV VTVPSSSLGT 200
QTYICNVNHK PSNTKVDKKV EPKSCRKTHT CPPCPAPEAA GAPSVFLFPP 250
KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE 350
PQVYTLPPSR EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP 400
PVLDSDGSFF LYSRLTVDKS RWQQGNVFSC SVLHEALHSH YTQKSLSLSP 450
GK                                                     452
```

Light chain / Chaîne légère / Cadena ligera: L-lambda2 anti-TSLP (L'''')

```
SYVLTQPPSV SVAPGQTARI TCGGNNLGSK SVHWYQQKPG QAPVLVVYDD  50
KDRPSWIPER FSGSNSGNTA TLTISRGEAG DEADYYCQVW DSKSDHVVFG 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) 23-92 138-198 245-320 371-427 488-548 594-652
22''-96'' 149''-205'' 266''-326'' 372''-430''

Intra-L (C23-C104) 22'-95' 145'-201'
23'''-92''' 138'''-198'''
22''''-87'''' 136''''-195''''

Inter-H-L' (CL 126-h 5)* 218-221'

Inter-H-L (h 5-CL 126) 447-218''' 225''-213''''

Inter-H-H (h 11, h 14) 453-231'' 456-234''

*crosslink / lien croisé / enlace cruzado

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: 524, 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: 674, 452''

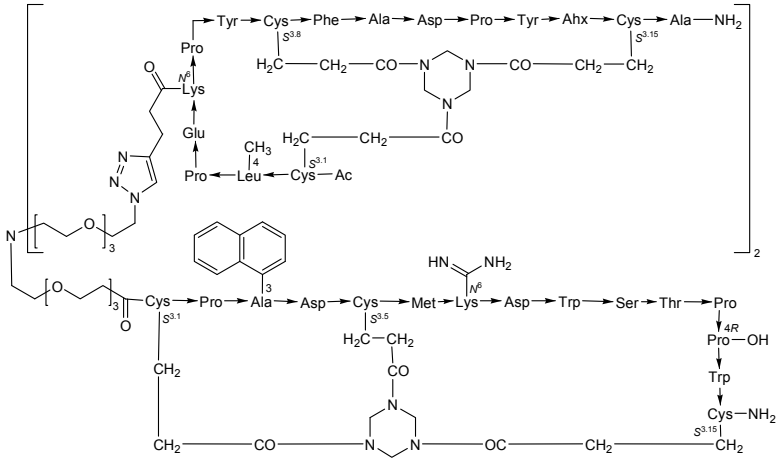
tivinectidum

tivinectide $N^{6.5},N^{6.5'}$-({12-[2-(2-{2-[3-oxo-3-({$S^{3.1}$,$S^{3.5}$,$S^{3.15}$-[(1,3,5-triazinane-1,3,5-triyl)tris(3-oxopropane-3,1-diyl)][L-cysteinyl-L-prolyl-3-(naphthalen-1-yl)-L-alanyl-L-α-aspartyl-L-cysteinyl-L-methionyl-N^6-carbamimidoyl-L-lysyl-L-α-aspartyl-L-tryptophyl-L-seryl-L-threonyl-L-prolyl-(4*R*)-4-hydroxy-L-prolyl-L-tryptophyl-L-cysteinamide]}-$N^{2.1}$-yl)propoxy]ethoxy}ethoxy)ethyl]-3,6,9,15,18,21-hexaoxa-12-azatricosane-1,23-diyl}bis[1*H*-1,2,3-triazole-1,4-diyl(1-oxopropane-3,1-diyl)])bis{$S^{3.1}$,$S^{3.8}$,$S^{3.15}$-[(1,3,5-triazinane-1,3,5-triyl)tris(3-oxopropane-3,1-diyl)][*N*-acetyl-L-cysteinyl-4-methyl-L-leucyl-L-prolyl-L-α-glutamyl-L-lysyl-L-prolyl-L-tyrosyl-L-cysteinyl-L-phenylalanyl-L-alanyl-L-α-aspartyl-L-prolyl-L-tyrosyl-(2*S*)-2-aminohexanoyl-L-cysteinyl-L-alaninamide]}

tivinectide $N^{6.5},N^{6.5'}$-({12-[2-(2-{2-[3-oxo-3-({$S^{3.1}$,$S^{3.5}$,$S^{3.15}$-[(1,3,5-triazinane-1,3,5-triyl)tris(3-oxopropane-3,1-diyl)][-L-cystéinyl-L-prolyl-3-(naphtalén-1-yl)-L-alanyl-L-α-aspartyl-L-cystéinyl-L-méthionyl-N^6-carbamimidoyl-L-lysyl-L-α-aspartyl-L-tryptophyl-L-séryl-L-thréonyl-L-prolyl-(4*R*)-4-hydroxy-L-prolyl-L-tryptophyl-L-cystéinamide]}-$N^{2.1}$-yl)propoxy]éthoxy}éthoxy)éthyl]-3,6,9,15,18,21-hexaoxa-12-azatricosane-1,23-diyl}bis[1*H*-1,2,3-triazole-1,4-diyl(1-oxopropane-3,1-diyl)])bis{$S^{3.1}$,$S^{3.8}$,$S^{3.15}$-[(1,3,5-triazinane-1,3,5-triyl)tris(3-oxopropane-3,1-diyl)][*N*-acétyl-L-cystéinyl-4-méthyl-L-leucyl-L-prolyl-L-α-glutamyl-L-lysyl-L-prolyl-L-tyrosyl-L-cystéinyl-L-phénylalanyl-L-alanyl-L-α-aspartyl-L-prolyl-L-tyrosyl-(2*S*)-2-aminohexanoyl-L-cystéinyl-L-alaninamide]}

tivinectida $N^{6.5},N^{6.5'}$-({12-[2-(2-{2-[3-oxo-3-({$S^{3.1}$,$S^{3.5}$,$S^{3.15}$-[(1,3,5-triazinano-1,3,5-triil)tris(3-oxopropano-3,1-diil)][-L-cisteinil-L-prolil-3-(naftalen-1-il)-L-alanil-L-α-aspartil-L-cisteinil-L-metionil-N^6-carbamimidoil-L-lisil-L-α-aspartil-L-triptofil-L-seril-L-treonil-L-prolil-(4*R*)-4-hidroxi-L-prolil-L-triptofil-L-cisteinamida]}-$N^{2.1}$-il)propoxi]etoxi}etoxi)etil]-3,6,9,15,18,21-hexaoxa-12-azatricosano-1,23-diil}bis[1*H*-1,2,3-triazolo-1,4-diil(1-oxopropano-3,1-diil)])bis{$S^{3.1}$,$S^{3.8}$,$S^{3.15}$-[(1,3,5-triazinano-1,3,5-triil)tris(3-oxopropano-3,1-diil)][*N*-acetil-L-cisteinil-4-metil-L-leucil-L-prolil-L-α-glutamil-L-lisil-L-prolil-L-tirosil-L-cisteinil-L-fenilalanil-L-alanil-L-α-aspartil-L-prolil-L-tirosil-(2*S*)-2-aminohexanoil-L-cisteinil-L-alaninamida]}

$C_{331}H_{467}N_{73}O_{89}S_{10}$



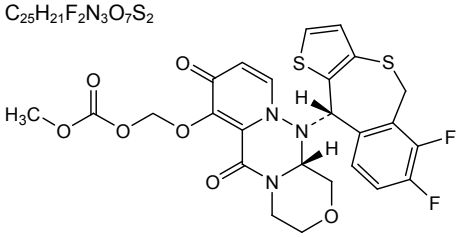
tivoxavirum marboxilum

tivoxavir marboxil ({(12a*R*)-12-[(10*S*)-6,7-difluoro-5,10-dihydrothieno[3,2-*c*][2]benzothiepin-10-yl]-6,8-dioxo-3,4,6,8,12,12a-hexahydro-1*H*-[1,4]oxazino[3,4-*c*]pyrido[2,1-*f*][1,2,4]triazin-7-yl}oxy)methyl methyl carbonate

tivoxavir marboxil carbonate de ({(12a*R*)-12-[(10*S*)-6,7-difluoro-5,10-dihydrothiéno[3,2-*c*][2]benzothiépin-10-yl]-6,8-dioxo-3,4,6,8,12,12a-hexahydro-1*H*-[1,4]oxazino[3,4-*c*]pyrido[2,1-*f*][1,2,4]triazin-7-yl}oxy)méthyle et de méthyle

tivoxavir marboxilo carbonato de ({(12a*R*)-12-[(10*S*)-6,7-difluoro-5,10-dihidrotieno[3,2-*c*][2]benzotiepin-10-il]-6,8-dioxo-3,4,6,8,12,12a-hexahidro-1*H*-[1,4]oxazino[3,4-*c*]pirido[2,1-*f*][1,2,4]triazin-7-il}oxi)metilo y metilo

$C_{25}H_{21}F_2N_3O_7S_2$



tixentamigum #

tixentamig immunoglobulin (H-gamma1_L-kappa)_scFvhh-G1(h-CH2-CH3), anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)] and anti-[*Homo sapiens* CLDN18 (claudin 18, claudin-18, surfactant associated protein J, SFTPJ) isoform 2], monoclonal antibody, bispecific, trivalent;
H-gamma1 heavy chain anti-CD3E (1-455) [VH (*Homo sapiens* IGHV3-73*01 (92.0%) -(IGHD) -IGHJ6*01 (90.9%) T123>L (120), CDR-IMGT [8.10.16] (26-33.51-60.99-114))(1-125) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, 6-G1v14-1 CH2 A1.3, A1.2, A1, 14-G1v32 CH3 W22 (knob), 14-G1v74 CH3 C10 (CH1 R120>K (222) (126-223), hinge 1-15 (224-238), CH2 L1.3>A (242), L1.2>A (243), G1>A (245) (239-348), CH3 S10>C (362), E12 (364), M14 (366), T22>W (374) (349-453), CHS (454-455)) (126-455)], (228-214')-disulfide with L-lambda2 light chain anti-CD3E (1'-215') [V-LAMBDA Musmus/Homsap (*Mus musculus* IGLV1*01 (81.2%) -IGLJ1*01 (100%)/*Homo sapiens* IGLV7-46*02 (80.0%) -IGLJ3*02 (100%), CDR-IMGT [9.3.9] (26'-34'.52'-54'.91'-99')) (1'-109') -*Homo sapiens* IGLC2*01 (100%) (C-LAMBDA2) (110'-215')];
scFvhh-G1(h-CH2-CH3) heavy chain anti-CLDN18 (1"-491") [VH (*Homo sapiens* IGHV3-74*03 (94.9%) -(IGHD) -IGHJ1*01 (90.0%) W118>R (111"), L124>T (116"), CDR-IMGT [8.8.14] (26"-33".51"-58".97"-110")) (1"-121") -15-mer tris(tetraglycyl-seryl) linker (122"-136") -VH (*Homo sapiens* IGHV3-74*03 (94.9%) -IGHD -IGHJ1*01 (90.0%) W118>R (247"), L124>T (252"), CDR-IMGT [8.8.14] (162"-169".187"-194".233"-246")) (137"-257") -2-mer alanyl-seryl linker (258"-259") -*Homo sapiens* IGHG1*03v h-CH2-CH3-CHS, G1m3>G1m17, nG1m1 CH3 E12, M14, 15-G1v37 hinge S5, 6-G1v14-1 CH2 A1.3, A1.2, A1, 14-G1v33 CH3 S22, A24, V86 (hole), 14-G1v75 CH3 C5 (hinge 1-15 C5>S (264") (260"-274"), CH2 L1.3>A (278), L1.2>A (279), G1>A (281) (275"-384"), CH3 Y5>C (393"), E12 (400), M14 (402), T22>S (410"), L24>A (412"), Y86>V (451") (385"-489"), CHS (490"-491")) (260"-491")]; dimer (234-270":237-273")-bisdisulfide, produced in a cell line from Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, glycoform alfa

tixentamig immunoglobuline (H-gamma1_L-kappa)_scFvhh-G1(h-CH2-CH3), anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)] and anti-[*Homo sapiens*

	CLDN18 (claudine 18, claudine-18, protéine J associée au surfactant, SFTPJ) isoforme 2], anticorps monoclonal, bispécifique, trivalent; chaîne lourde H-gamma1 anti-CD3E (1-455) [VH (*Homo sapiens* IGHV3-73*01 (92.0%) -(IGHD) -IGHJ6*01 (90.9%) T123>L (120), CDR-IMGT [8.10.16] (26-33.51-60.99-114)) (1-125) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, 6-G1v14-1 CH2 A1.3, A1.2, A1, 14-G1v32 CH3 W22 (knob), 14-G1v74 CH3 C10 (CH1 R120>K (222) (126-223), charnière 1-15 (224-238), CH2 L1.3>A (242), L1.2>A (243), G1>A (245) (239-348), CH3 S10>C (362), E12 (364), M14 (366), T22>W (374) (349-453), CHS (454-455)) (126-455)], (228-214')-bisdisulfure avec la chaine légère L-lambda2 anti-CD3E (1'-215') [V-LAMBDA Musmus/Homsap (*Mus musculus* IGLV1*01 (81.2%) -IGLJ1*01 (100%)/*Homo sapiens* IGLV7-46*02 (80.0%) -IGLJ3*02 (100%), CDR-IMGT [9.3.9] (26'-34'.52'-54'.91'-99')) (1'-109') -*Homo sapiens* IGLC2*01 (100%) (C-LAMBDA2) (110'-215')]; chaîne lourde scFvhh-G1(h-CH2-CH3) anti-CLDN18 (1"-491") [VH (*Homo sapiens* IGHV3-74*03 (94.9%) -(IGHD) -IGHJ1*01 (90.0%) W118>R (111"), L124>T (116"), CDR-IMGT [8.8.14] (26"-33".51"-58".97"-110")) (1"-121") -15-mer tris(tétraglycyl-séryl) linker (122"-136") -VH (*Homo sapiens* IGHV3-74*03 (94.9%) -IGHD -IGHJ1*01 (90.0%) W118>R (247"), L124>T (252"), CDR-IMGT [8.8.14] (162"-169".187"-194".233"-246")) (137"-257") -2-mer alanyl-séryl linker (258"-259") -*Homo sapiens* IGHG1*03v h-CH2-CH3-CHS, G1m3>G1m17, nG1m1 CH3 E12, M14, 15-G1v37 charnière S5, 6-G1v14-1 CH2 A1.3, A1.2, A1, 14-G1v33 CH3 S22, A24, V86 (hole), 14-G1v75 CH3 C5 (charnière 1-15 C5>S (264") (260"-274"), CH2 L1.3>A (278), L1.2>A (279), G1>A (281) (275"-384"), CH3 Y5>C (393"), E12 (400), M14 (402), T22>S (410"), L24>A (412"), Y86>V (451") (385"-489"), CHS (490"-491")) (260"-491")]; dimère (234-270":237-273")-bisdisulfure, produit dans une lignée cellulaire des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1, glycoforme alfa
tixentamig	inmunoglobulina (H-gamma1_L-kappa)_scFvhh-G1(h-CH2-CH3), anti-[*Homo sapiens* CD3E (CD3 épsilon, Leu-4)] y anti-[*Homo sapiens* CLDN18 (claudina 18, claudina-18, proteína J asociada a los surfactantes, SFTPJ) isoforma 2], anticuerpo monoclonal, biespecífico, trivalente; cadena pesada H-gamma1 anti-CD3E (1-455) [VH (*Homo sapiens* IGHV3-73*01 (92.0%) -(IGHD) -IGHJ6*01 (90.9%) T123>L (120), CDR-IMGT [8.10.16] (26-33.51-60.99-114)) (1-125) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, 6-G1v14-1 CH2 A1.3, A1.2, A1, 14-G1v32 CH3 W22 (knob), 14-G1v74 CH3 C10 (CH1 R120>K (222) (126-223), bisagra 1-15 (224-238), CH2 L1.3>A (242), L1.2>A (243), G1>A (245) (239-348), CH3 S10>C (362), E12 (364), M14 (366), T22>W (374) (349-453), CHS (454-455)) (126-455)], (228-214')-bisdisulfuro con la cadena ligera L-lambda2 anti-CD3E (1'-215') [V-LAMBDA Musmus/Homsap (*Mus musculus* IGLV1*01 (81.2%) -IGLJ1*01 (100%)/*Homo sapiens* IGLV7-46*02 (80.0%) -IGLJ3*02 (100%), CDR-IMGT [9.3.9] (26'-34'.52'-54'.91'-99')) (1'-109') -*Homo sapiens* IGLC2*01 (100%) (C-LAMBDA2) (110'-215')]; cadena pesada scFvhh-G1(h-CH2-CH3) anti-CLDN18 (1"-491") [VH (*Homo sapiens* IGHV3-74*03 (94.9%) -(IGHD) -IGHJ1*01 (90.0%) W118>R (111"), L124>T (116"), CDR-IMGT [8.8.14] (26"-33".51"-58".97"-110")) (1"-121") -15-mer tris(tetraglicil-seril) enlace (122"-136") -VH (*Homo sapiens* IGHV3-74*03 (94.9%) -IGHD -IGHJ1*01 (90.0%) W118>R (247"), L124>T (252"), CDR-IMGT [8.8.14] (162"-169".187"-194".233"-246")) (137"-257") -2-mer alanyl-séryl linker (258"-259") -*Homo sapiens* IGHG1*03v h-CH2-CH3-CHS, G1m3>G1m17, nG1m1 CH3 E12, M14, 15-G1v37 bisagra S5, 6-G1v14-1 CH2 A1.3, A1.2, A1, 14-G1v33 CH3 S22, A24, V86 (hole), 14-G1v75 CH3 C5 (bisagra 1-15

C5>S (264") (260"-274"), CH2 L1.3>A (278), L1.2>A (279), G1>A (281) (275"-384"), CH3 Y5>C (393"), E12 (400), M14 (402), T22>S (410"), L24>A (412"), Y86>V (451") (385"-489"), CHS (490"-491")) (260"-491")]; dímero (234-270":237-273")-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 anti-CD3E (knob) (H)

```
EVQLVESGGG LVQPGGSLKL SCAASGFTFS TYAMNWVRQA SGKGLEWVGR  50
IRSKYNNYAT YYADSVKDRF TISRDDSKNT AYLQMNSLKT EDTAVYYCTR 100
HGNFGNSYVS WFAYWGQGTL VTVSSASTKG PSVFPLAPSS KSTSGGTAAL 150
GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL SSVVTVPSSS 200
LGTQTYICNV NHKPSNTKVD KKVEPKSCDK THTCPPCPAP EAAGAPSVFL 250
FPPKPKDTLM ISRTPEVTCV VVDVSHEDPE VKFNWYVDGV EVHNAKTKPR 300
EEQYNSTYRV VSVLTVLHQD WLNGKEYKCK VSNKALPAPI EKTISKAKGQ 350
PREPQVYTLP PCREEMTKNQ VSLWCLVKGF YPSDIAVEWE SNGQPENNYK 400
TTPPVLDSDG SFFLYSKLTV DKSRWQQGNV FSCSVMHEAL HNHYTQKSLS 450
LSPGK                                                  455
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Light chain / Chaîne légère / Cadena ligera : L-lambda2 anti-CD3E (L')

```
QAVVTQEPSL TVSPGGTVTL TCRSSTGAVT TSNYANWVQQ KPGQAPRGLI  50
GGTNKRAPWT PARFSGSLLG DKAALTLLGA QPEDEAEYFC ALWYSNLWVF 100
GGGTKLTVLG QPKAAPSVTL FPPSSEELQA NKATLVCLIS DFYPGAVTVA 150
WKADSSPVKA GVETTTPSKQ SNNKYAASSY LSLTPEQWKS HRSYSCQVTH 200
EGSTVEKTVA PTECS                                       215
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Heavy chain / Chaîne lourde / Cadena pesada : scFvhh-G1(h-CH2-CH3) anti-CLDN18 (hole) (H")

```
EVQLVESGGG LVQPGGSLRL SCAASGFTFS SYWMHWVRQV PGKGLVWVSR  50
ISSDASRTIY ADSVKGRFTI SRDNAKNTLY LQMNSLRAED TAVYYCARGE 100
DHDILTGYPI RGQGTTVTVS SGGGGSGGGG SGGGGSEVQL VESGGGLVQP 150
GGSLRLSCAA SGFTFSSYWM HWVRQVPGKG LVWVSRISSD ASRTIYADSV 200
KGRFTISRDN AKNTLYLQMN SLRAEDTAVY YCARGEDHDI LTGYPIRGQG 250
TTVTVSSASE PKSSDKTHTC PPCPAPEAAG APSVFLFPPK PKDTLMISRT 300
PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY NSTYRVVSVL 350
TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP QVCTLPPSRE 400
EMTKNQVSLS CAVKGFYPSD IAVEWESNGQ PENNYKTTPP VLDSDGSFFL 450
VSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG K          491
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Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-98 152-208 269-329 375-433
22"-96" 158"-232" 305"-365" 411"-469"
Intra-L (C23-C104) 22'-90' 137'-196'
Inter-H-L (h 5-CL 126) 228-214'
Inter-H-H (h 11, h 14) 234-270" 237-273"
Inter-H-H (CH3 C10-C5)* 362-393"
*variants 14-G1v74 (H CH3 C10) and 14-G1v75 (H" CH3 C5) creating an additional inter-H-H disulfide bond.

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'

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4: 305, 341"
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, 491"

tixestobartum #
tixestobart

immunoglobulin G1-lambda2, anti-[*Homo sapiens* CD27 (TNFRSF7, tumor necrosis factor receptor (TNFR) superfamily member 7)], *Homo sapiens* monoclonal antibody;

	H-gamma1 heavy chain *Homo sapiens* (1-445) [VH (*Homo sapiens* IGHV7-4-1*02 (91.8%) -(IGHD) - IGHJ4*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, 6-G1v4-2 CH2 R114, 10-G1v98 CH3 R1 (CH1 R120 (213) (117-214), hinge 1-15 (215-229), CH2 P114>R (328) (230-339), CH3 E1>R (344), E12 (355), M14 (357) (340-444), CHS K2>del (445)) (117-445)], (219-215')-disulfide with L-lambda2 light chain *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV2-14*03 (94.7%) - IGLJ3*02 (100%), CDR-IMGT [9.3.10] (26'-34'.52'-54'.91'-100')) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (C-LAMBDA2) (111'-216')]; dimer (225-225":228-228")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa
tixestobart	immunoglobuline G1-lambda2, anti-[*Homo sapiens* CD27 (TNFRSF7, membre 7 de la superfamille des récepteurs du facteur de nécrose tumorale (TNFR))], anticorps monoclonal *Homo sapiens*; chaîne lourde H-gamma1 *Homo sapiens* (1-445) [VH (*Homo sapiens* IGHV7-4-1*02 (91.8%) -(IGHD) - IGHJ4*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, 6-G1v4-2 CH2 R114, 10-G1v98 CH3 R1 (CH1 R120 (213) (117-214), charnière 1-15 (215-229), CH2 P114>R (328) (230-339), CH3 E1>R (344), E12 (355), M14 (357) (340-444), CHS K2>del (445)) (117-445)], (219-215')-disulfure avec la chaîne légère L-lambda2 *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV2-14*03 (94.7%) -IGLJ3*02 (100%), CDR-IMGT [9.3.10] (26'-34'.52'-54'.91'-100')) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (C-LAMBDA2) (111'-216')]; dimère (225-225":228-228")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa
tixestobart	inmunoglobulina G1-lambda2, anti-[*Homo sapiens* CD27 (TNFRSF7, miembro 7 de la superfamilia de los receptores del factor de necrosis tumoral (TNFR))], anticuerpo monoclonal *Homo sapiens*; cadena pesada H-gamma1 *Homo sapiens* (1-445) [VH (*Homo sapiens* IGHV7-4-1*02 (91.8%) -(IGHD) - IGHJ4*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, 6-G1v4-2 CH2 R114, 10-G1v98 CH3 R1 (CH1 R120 (213) (117-214), bisagra 1-15 (215-229), CH2 P114>R (328) (230-339), CH3 E1>R (344), E12 (355), M14 (357) (340-444), CHS K2>del (445)) (117-445)], (219-215')-disulfuro con la cadena ligera L-lambda2 *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV2-14*03 (94.7%) -IGLJ3*02 (100%), CDR-IMGT [9.3.10] (26'-34'.52'-54'.91'-100')) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (C-LAMBDA2) (111'-216')]; dímero (225-225":228-228")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLMQSGSE LKKPGASVKV SCRASGYTFT TYAMNWVRQA PGQGPEWMGW  50
INTNTGNPTY AQGFTGRFVF SLDTTVTTTY LQISSLKAED TAVYFCAREA 100
GSFDYWGQGT 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 KVSNKALRAP IEKTISKAKG QPRRPQVYTL 350
PPSREEMTKN QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD 400
GSFFLYSKLT VDKSRWQQGN VFSCSVMHEA LHNHYTQKSL SLSPG      445
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Light chain / Chaîne légère / Cadena ligera

```
QSALTQPASV SGSPGQSITI SCTGTSSDVY YYNYVSWYQQ HPGRAPKLVI  50
YDVSNRPSGV SNRFSGSKSG NTASLTISGL RAEDEADYYC SSYTVNRVWV 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) 22-96 143-199 260-320 366-424
22"-96" 143"-199" 260"-320" 366"-424"
Intra-L (C23-C104) 22'-90' 138'-197'
22'"-90'" 138'"-197'"
Inter-H-L (h 5-CL 126) 219-215' 219"-215'"
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"
L VL V-LAMBDA 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

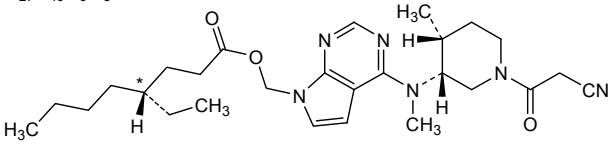
tofacitinibum etocomilum

tofacitinib etocomil — (4-{[(3*R*,4*R*)-1-(cyanoacetyl)-4-methylpiperidin-3-yl](methyl)amino}-7*H*-pyrrolo[2,3-*d*]pyrimidin-7-yl)methyl (4*RS*)-4-ethyloctanoate

tofacitinib étocomil — (4*RS*)-4-éthyloctanoate de (4-{[(3*R*,4*R*)-1-(cyanoacétyl)-4-méthylpipéridin-3-yl](méthyl)amino}-7*H*-pyrrolo[2,3-*d*]pyrimidin-7-yl)méthyle

tofacitinib etocomilo — (4*RS*)-4-etiloctanoato de (4-{[(3*R*,4*R*)-1-(cianoacetil)-4-metilpiperidin-3-il](metil)amino}-7*H*-pirrolo[2,3-*d*]pirimidin-7-il)metilo

$C_{27}H_{40}N_6O_3$



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

torvutatugum

torvutatug — 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* (1-449) [VH (*Homo sapiens* IGHV6-1*01 (98.0%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [10.9.9] (26-35.53-61.100-108)) (1-119) -*Homo sapiens* IGHG1*03 (100%) G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (216) (120-217), hinge 1-15 (218-232), CH2 (233-342), CH3 E12 (358), M14 (360) (343-447), CHS (448-449)) (120-449)], (222-215')-disulfide with L-kappa light chain *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-5*03 (98.9%) -IGKJ4*01 (100%), CDR-IMGT [6.3.10] (27'-32'.50'-52'.89'-98')) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (154'), V101 (192')) (109'-215')]; dimer (228-228'':231-231'')-bisdisulfide, produced in a cell line from Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, glycoform alfa
torvutatug	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* (1-449) [VH (*Homo sapiens* IGHV6-1*01 (98.0%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [10.9.9] (26-35.53-61.100-108)) (1-119) -*Homo sapiens* IGHG1*03 (100%) G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (216) (120-217), charnière 1-15 (218-232), CH2 (233-342), CH3 E12 (358), M14 (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* IGKV1-5*03 (98.9%) -IGKJ4*01 (100%), CDR-IMGT [6.3.10] (27'-32'.50'-52'.89'-98')) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (154'), V101 (192')) (109'-215')]; dimère (228-228'':231-231'')-bisdisulfure, produit dans une lignée cellulaire des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1, glycoforme alfa
torvutatug	inmunoglobulina G1-kappa, anti-[*Homo sapiens* FOLR1 (receptor 1 del folato, receptor alfa del folato, FR-alfa, proteína adulta fijadora de folato, FBP, antígeno MOv18 asociado a los tumores ováricos)], anticuerpo monoclonal *Homo sapiens*; cadena pesada H-gamma1 *Homo sapiens* (1-449) [VH (*Homo sapiens* IGHV6-1*01 (98.0%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [10.9.9] (26-35.53-61.100-108)) (1-119) -*Homo sapiens* IGHG1*03 (100%) G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (216) (120-217), bisagra 1-15 (218-232), CH2 (233-342), CH3 E12 (358), M14 (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* IGKV1-5*03 (98.9%) -IGKJ4*01 (100%), CDR-IMGT [6.3.10] (27'-32'.50'-52'.89'-98')) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (154'), V101 (192')) (109'-215')]; dímero (228-228'':231-231'')-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

```
LVQLQQSGPG LVKPSQTLSL TCAISGDSVS SDSATWNWIR QSPSRGLEWL  50
GRTYYRSKWY NDYAVSVKSR ITINPDTSKN QFSLQLNSVT PEDTAVYYCA 100
RGVGSFDYWG QGTLVTVSSA STKGPSVFPL APSSKSTSGG TAALGCLVKD 150
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY 200
ICNVNHKPSN TKVDKRVEPK SCDKTHTCPP CPAPELLGGP SVFLFPPKPK 250
DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS 300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV 350
YTLPPSREEM TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL 400
DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK  449
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPST LSASVGDRVT ITCRASQSIS SWLAWYQQKP GKAPKLLIYK  50
ASGLESGVPS RFSGSGSGTE FTLTISSLQP DDFATYYCQQ YNSYSQLTFG 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) 22-99 146-202 263-323 369-427
22"-99" 146"-202" 263"-323" 369"-427"
Intra-L (C23-C104) 23'-88' 135'-195'
23'"-88'" 135'"-195'"
Inter-H-L (h 5-CL 126) 222-215' 222"-215'"
Inter-H-H (h 11, h 14) 228-228" 231-231"

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

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

torvutatugum samrotecanum

torvutatug samrotecan	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 eight cysteinyl residues to *samrotecan*, comprising a linker and a camptothecin derivative (*exatecan*); H-gamma1 heavy chain *Homo sapiens* (1-449) [VH (*Homo sapiens* IGHV6-1*01 (98.0%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [10.9.9] (26-35.53-61.100-108)) (1-119) -*Homo sapiens* IGHG1*03 (100%) G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (216) (120-217), hinge 1-15 (218-232), CH2 (233-342), CH3 E12 (358), M14 (360) (343-447), CHS (448-449)) (120-449)], (222-215')-disulfide with L-kappa light chain *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-5*03 (98.9%) -IGKJ4*01 (100%), CDR-IMGT [6.3.10] (27'-32'.50'-52'.89'-98')) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (154'), V101 (192')) (109'-215')]; dimer (228-228":231-231")-bisdisulfide, produced in a cell line from Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, glycoform alfa; substituted at the eight sulfur atoms of L-cysteinyl residues 222, 228, 231, 215', 222", 228", 231" and 215'" with (3*RS*)-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*) groups
torvutatug samrotécan	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 par huit résidus cystéinyle au *samrotécan*, comprenant un linker et un dérivé de la camptothécine (*exatécan*);

	chaîne lourde H-gamma1 *Homo sapiens* (1-449) [VH (*Homo sapiens* IGHV6-1*01 (98.0%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [10.9.9] (26-35.53-61.100-108)) (1-119) -*Homo sapiens* IGHG1*03 (100%) G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (216) (120-217), charnière 1-15 (218-232), CH2 (233-342), CH3 E12 (358), M14 (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* IGKV1-5*03 (98.9%) -IGKJ4*01 (100%), CDR-IMGT [6.3.10] (27'-32'.50'-52'.89'-98')) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (154'), V101 (192')) (109'-215')]; dimère (228-228'':231-231'')-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 222, 228, 231, 215', 222'', 228'', 231'' et 215''' avec des groupes (3*RS*)-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*)
torvutatug samrotecán	inmunoglobulina G1-kappa, anti-[*Homo sapiens* FOLR1 (receptor 1 del folato, receptor alfa del folato, FR-alfa, proteína adulta fijadora de folato, FBP, antígeno MOv18 asociado a los tumores ováricos)], anticuerpo monoclonal *Homo sapiens*, conjugué par ocho résidus cystéinyle au *samrotécan*, que comprende un enlace y un derivado de la camptotecina (*exatecán*); cadena pesada H-gamma1 *Homo sapiens* (1-449) [VH (*Homo sapiens* IGHV6-1*01 (98.0%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [10.9.9] (26-35.53-61.100-108)) (1-119) -*Homo sapiens* IGHG1*03 (100%) G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (216) (120-217), bisagra 1-15 (218-232), CH2 (233-342), CH3 E12 (358), M14 (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* IGKV1-5*03 (98.9%) -IGKJ4*01 (100%), CDR-IMGT [6.3.10] (27'-32'.50'-52'.89'-98')) (1'-108') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (154'), V101 (192')) (109'-215')]; dímero (228-228'':231-231'')-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 el átomo de azufre de los residuos L-cisteinilo 222, 228, 231, 215', 222'', 228'', 231'' y 215'' con grupos (3*RS*)-1-[(2*S*,5*S*)-1-{[(9*S*)-9-etil-9-hidroxi-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-4-il]amino}-2-metil-1,4,7,35-tetraoxo-5-(propan-2-il)-10,13,16,19,22,25,28,31-octaoxa-3,6,34-triazaheptatriacontan-37-il]-2,5-dioxopirrolidin-3-ilo (*samrotecán*)

Heavy chain / Chaîne lourde / Cadena pesada (H, H'')

```
LVQLQQSGPG LVKPSQTLSL TCAISGDSVS SDSATWNWIR QSPSRGLEWL  50
GRTYYRSKWY NDYAVSVKSR ITINPDTSKN QFSLQLNSVT PEDTAVYYCA 100
RGVGSFDYWG QGTLVTVSSA STKGPSVFPL APSSKSTSGG TAALGCLVKD 150
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY 200
ICNVNHKPSN TKVDKRVEPK SCDKTHTCPP CPAPELLGGP SVFLFPPKPK 250
DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS 300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV 350
YTLPPSREEM TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL 400
DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK  449
```

Light chain / Chaîne légère / Cadena ligera (L', L''')

```
DIQMTQSPST LSASVGDRVT ITCRASQSIS SWLAWYQQKP GKAPKLLIYK  50
ASGLESGVPS RFSGSGSGTE FTLTISSLQP DDFATYYCQQ YNSYSQLTFG 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) 22-99 146-202 263-323 369-427
22''-99'' 146''-202'' 263''-323'' 369''-427''

Intra-L (C23-C104) 23'-88' 135'-195'
23'''-88''' 135'''-195'''

Inter-H-L (h 5-CL 126)* 222-215' 222''-215'''

Inter-H-H (h 11, h 14)* 228-228'' 231-231''

*The inter-chain disulfide bridges are not present, the 8 cysteinyl being conjugated each via a thioether bond to a drug linker.

*Les ponts disulfures inter-chaînes ne sont pas présents, les 8 cystéinyl étant chacun conjugué via une liaison thioéther à un linker-principe actif.

*Los puentes disulfuro entre cadenas no están presentes, cada uno de los 8 cisteinil está conjugada a través de un enlace tioéter a un linker-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

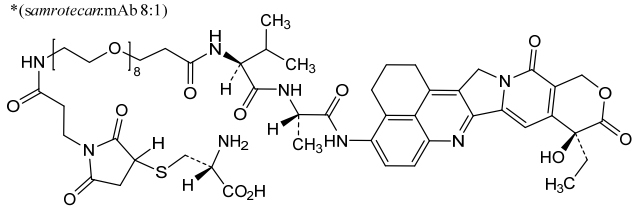
C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal

H CHS K2: 449, 449''

Modified residues / Résidus modifiés / Restos modificados*

C (222, 228, 231, 215', 222'', 228'', 231'', 215''')

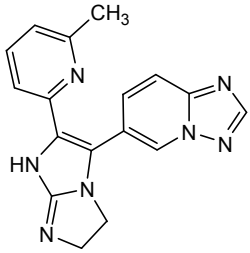
*(*samrotecan*:mAb 8:1)



tosposertibum

tosposertib	6-[2-(6-methylpyridin-2-yl)-5,6-dihydro-1*H*-imidazo[1,2-*a*]imidazol-3-yl][1,2,4]triazolo[1,5-*a*]pyridine
tosposertib	6-[2-(6-méthylpyridin-2-yl)-5,6-dihydro-1*H*-imidazo[1,2-a]imidazol-3-yl][1,2,4]triazolo[1,5-a]pyridine
tosposertib	6-[2-(6-metilpiridin-2-il)-5,6-dihidro-1*H*-imidazo[1,2-a]imidazol-3-il][1,2,4]triazolo[1,5-a]piridina

$C_{17}H_{15}N_7$



trovostobartum #

trovostobart — immunoglobulin G1-kappa, anti-[*Homo sapiens* VSIR (V-set immunoregulatory receptor, B7H5, B7-H5, PDCD1 homolog, PD-1H, stress induced secreted protein 1, SISP1, V-domain Ig suppressor of T cell activation, VISTA)], *Homo sapiens* monoclonal antibody;
H-gamma1 heavy chain *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV4-59*01 (99.0%) -(IGHD) -IGHJ3*02 (93.3%) T125>I (114), CDR-IMGT [8.7.11] (26-33.51-57.96-106)) (1-117) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, 9-G1v21 CH2 Y15.1, T16, E18 (CH1 K120 (214) (118-215), hinge 1-15 (216-230), CH2 M15.1>Y (252), S16>T (254), T18>E (256) (231-340), CH3 D12 (356), L14 (358) (341-445), CHS (446-447)) (118-447)], (220-214')-disulfide with L-kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-11*01 (96.8%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dimer (226-226'':229-229'')-bisdisulfide, produced in a cell line derived from Chinese hamster ovary (CHO) cells, glycoform alfa

trovostobart — immunoglobuline G1-kappa, anti-[*Homo sapiens* VSIR (récepteur immunorégulateur du V-set, B7H5, B7-H5, homologue du PDCD1, PD-1H, protéine 1 secrétée induite par le stress, SISP1, suppresseur d'activation de cellule T du V-set Ig, VISTA)], anticorps monoclonal *Homo sapiens*; chaîne lourde H-gamma1 *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV4-59*01 (99.0%) -(IGHD) -IGHJ3*02 (93.3%) T125>I (114), CDR-IMGT [8.7.11] (26-33.51-57.96-106)) (1-117) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, 9-G1v21 CH2 Y15.1, T16, E18 (CH1 K120 (214) (118-215), charnière 1-15 (216-230), CH2 M15.1>Y (252), S16>T (254), T18>E (256) (231-340), CH3 D12 (356), L14 (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* IGKV3-11*01 (96.8%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dimère (226-226'':229-229'')-bisdisulfure, produit dans une lignée cellulaire dérivant des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

trovostobart

inmunoglobulina G1-kappa, anti-[*Homo sapiens* VSIR (receptor inmunoregulador del V-set, B7H5, B7-H5, homólogo del PDCD1, PD-1H, proteína 1 secretada inducida por el estrés, SISP1, supresor de activación de célula T del V-set Ig, VISTA)], anticuerpo monoclonal *Homo sapiens*;
cadena pesada H-gamma1 *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV4-59*01 (99.0%) -(IGHD) -IGHJ3*02 (93.3%) T125>I (114), CDR-IMGT [8.7.11] (26-33.51-57.96-106)) (1-117) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, 9-G1v21 CH2 Y15.1, T16, E18 (CH1 K120 (214) (118-215), bisagra 1-15 (216-230), CH2 M15.1>Y (252), S16>T (254), T18>E (256) (231-340), CH3 D12 (356), L14 (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* IGKV3-11*01 (96.8%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dímero (226-226":229-229")-bisdisulfuro, producido en una línea celular derivada de las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLQESGPG LVKPSETLSL TCTVSGGSIS SYYWSWIRQP PGKGLEWIGY  50
IYYSGSTNYN PSLKSRVTIS VDTSKSQFSL KLSSVTAADT AVYYCARDIP 100
AFAFDIWGQG TMVIVSSAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF 150
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC 200
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT 250
LYITREPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT 350
LPPSRDELTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS 400
DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPGK    447
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Light chain / Chaîne légère / Cadena ligera

```
EIVLTQSPAT LSLSPGERAT LSCRASQSVS YYLAWYQQKP GQAPRLLIYD  50
AFNRATGIPA RFSGSGSGTD FTLTISSLEP EDFAVYYCQQ RINWPLTFGG 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) 22-95 144-200 261-321 367-425
22"-95" 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"

ubavitinibum

ubavitinib

N-(4-{[5-fluoro-7-(2-methoxyethoxy)quinazolin-4-yl]amino}phenyl)-2-[4-(propan-2-yl)-1*H*-1,2,3-triazol-1-yl]acetamide

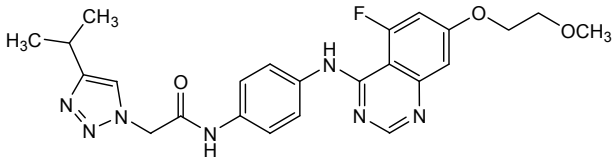
ubavitinib

N-(4-{[5-fluoro-7-(2-methoxyethoxy)quinazolin-4-yl]amino}phenyl)-2-[4-(propan-2-yl)-1*H*-1,2,3-triazol-1-yl]acetamide

ubavitinib

N-(4-{[5-fluoro-7-(2-metoxietoxi)quinazolin-4-il]amino}fenil)-2-[4-(propan-2-il)-1*H*-1,2,3-triazol-1-il]acetamida

$C_{24}H_{26}FN_7O_3$



ubletamigum #

ubletamig

immunoglobulin (H-gamma4_L-kappa)_(H-gamma4_L-kappa), anti-[*Homo sapiens* MUC16 (mucin 16, MUC-16, cancer antigen 125, CA125)] and anti-[*Homo sapiens* CD28 (T cell specific surface glycoprotein CD28, TP44)], *Homo sapiens* monoclonal antibody, bispecific, bivalent;
H-gamma4 heavy chain anti-MUC16 *Homo sapiens* (1-455) [VH (*Homo sapiens* IGHV3-49*04 (93.9%) -(IGHD) -IGHJ6*04 (90.0%) K120>R (121), CDR-IMGT [8.10.20] (26-33.51-60.99-118)) (1-129)-*Homo sapiens* IGHG4*01 nG4m(a) CH2 L92, 12-G4v5 h P10, 6-G4v7 CH2 delE1.4, P1.3, V1.2, A1.1 (CH1 (130-227), hinge 1-12 S10>P (237) (228-239), CH2 E1.4>del, F1.3>P (242), L1.2>V (243), G1.1>A (244), L92 (318) (240-348), CH3 (349-453), CHS (454-455)) (130-455)], (143-215')-disulfide with common 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, V101 (C-KAPPA A45.1 (154'), V101 (192')) (109'-215')];
H-gamma4 heavy chain anti-CD28 *Homo sapiens* (1"-448") [VH (*Homo sapiens* IGHV4-59*01 (96.9%) -(IGHD) -IGHJ6*01 (100%), CDR-IMGT [8.7.16] (26"-33".51"-57".96"-111")) (1"-122")-*Homo sapiens* IGHG4*01 nG4m(a) CH2 L92, 12-G4v5 h P10, 6-G4v7 CH2 delE1.4, P1.3, V1.2, A1.1, 10-G4v8 CH3 R115, F116, P125 (CH1 (123"-220"), hinge 1-12 S10>P (230") (221"-232"), CH2 E1.4>del, F1.3>P (235"), L1.2>V (236"), G1.1>A (237"), L92 (311") (233"-341"), CH3 H115>R (436"), Y116>F (437"), L125>P (446") (342"-446"), CHS (447"-448")) (123"-448")], (136"-215"')-disulfide with common 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, V101 (C-KAPPA A45.1 (154"'), V101 (192"')) (109"'-215"')]; dimer (235-228": 238-231")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa

ublétamig

immunoglobuline (H-gamma4_L-kappa)_(H-gamma4_L-kappa), anti-[*Homo sapiens* MUC16 (mucine 16, MUC-16, antigène de cancer 125, CA125)] et anti-[*Homo sapiens* CD28 (glycoprotéine de surface CD28 spécifique des cellules T, TP44)], anticorps monoclonal *Homo sapiens,* bispécifique, bivalent;
chaîne lourde H-gamma4 anti-MUC16 *Homo sapiens* (1-455) [VH (*Homo sapiens* IGHV3-49*04 (93.9%) -(IGHD) -IGHJ6*04 (90.0%) K120>R (121), CDR-IMGT [8.10.20] (26-33.51-60.99-118)) (1-129)-*Homo sapiens* IGHG4*01 nG4m(a) CH2 L92, 12-G4v5 h P10, 6-G4v7 CH2 delE1.4, P1.3, V1.2, A1.1 (CH1 (130-227), charnière 1-12 S10>P (237) (228-239), CH2 E1.4>del, F1.3>P (242), L1.2>V (243), G1.1>A (244), L92 (318) (240-348), CH3 (349-453), CHS (454-455)) (130-455)], (143-215')-disulfure avec

	la chaîne légère L-kappa commune *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, V101 (C-KAPPA A45.1 (154'), V101 (192')) (109'-215')]; chaîne lourde H-gamma4 anti-CD28 *Homo sapiens* (1"-448") [VH (*Homo sapiens* IGHV4-59*01 (96.9%) -(IGHD) -IGHJ6*01 (100%), CDR-IMGT [8.7.16] (26"-33".51"-57".96"-111")) (1"-122")-*Homo sapiens* IGHG4*01 nG4m(a) CH2 L92, 12-G4v5 h P10, 6-G4v7 CH2 delE1.4, P1.3, V1.2, A1.1,10-G4v8 CH3 R115, F116, P125 (CH1 (123"-220"), charnière 1-12 S10>P (230") (221"-232"), CH2 E1.4>del, F1.3>P (235"), L1.2>V (236"), G1.1>A (237"), L92 (311") (233"-341"), CH3 H115>R (436"), Y116>F (437"), L125>P (446") (342"-446"), CHS (447"-448")) (123"-448")], (136"-215"')-disulfure avec la chaîne légère L-kappa commune *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, V101 (C-KAPPA A45.1 (154"'), V101 (192"')) (109"'-215"')]; dimère (235-228": 238-231")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa
ubletamig	inmunoglobulina (H-gamma4_L-kappa)_(H-gamma4_L-kappa), anti-[*Homo sapiens* MUC16 (mucina 16, MUC-16, antígeno de cáncer 125, CA125)] y anti-[*Homo sapiens* CD28 (glicoproteína de superficie CD28 específico de las células T, TP44)], anticuerpo monoclonal *Homo sapiens,* biespecífico, bivalente; cadena pesada H-gamma4 anti-MUC16 *Homo sapiens* (1-455) [VH (*Homo sapiens* IGHV3-49*04 (93.9%) -(IGHD) -IGHJ6*04 (90.0%) K120>R (121), CDR-IMGT [8.10.20] (26-33.51-60.99-118)) (1-129)-*Homo sapiens* IGHG4*01 nG4m(a) CH2 L92, 12-G4v5 h P10, 6-G4v7 CH2 delE1.4, P1.3, V1.2, A1.1 (CH1 (130-227), bisagra 1-12 S10>P (237) (228-239), CH2 E1.4>del, F1.3>P (242), L1.2>V (243), G1.1>A (244), L92 (318) (240-348), CH3 (349-453), CHS (454-455)) (130-455)], (143-215')-disulfuro con la cadena ligera L-kappa común *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, V101 (C-KAPPA A45.1 (154'), V101 (192')) (109'-215')]; cadena pesada H-gamma4 anti-CD28 *Homo sapiens* (1"-448") [VH (*Homo sapiens* IGHV4-59*01 (96.9%) -(IGHD) -IGHJ6*01 (100%), CDR-IMGT [8.7.16] (26"-33".51"-57".96"-111")) (1"-122")-*Homo sapiens* IGHG4*01 nG4m(a) CH2 L92, 12-G4v5 h P10, 6-G4v7 CH2 delE1.4, P1.3, V1.2, A1.1,10-G4v8 CH3 R115, F116, P125 (CH1 (123"-220"), bisagra 1-12 S10>P (230") (221"-232"), CH2 E1.4>del, F1.3>P (235"), L1.2>V (236"), G1.1>A (237"), L92 (311") (233"-341"), CH3 H115>R (436"), Y116>F (437"), L125>P (446") (342"-446"), CHS (447"-448")) (123"-448")], (136"-215"')-disulfuro con la cadena ligera L-kappa común *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, V101 (C-KAPPA A45.1 (154"'), V101 (192"')) (109"'-215"')]; dímero (235-228": 238-231")-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 anti-MUC16 (H)

```
EVQLVESGGG LEQPGRSLRL SCTASGFAFG DHTMSWVRQA PGKGLEWVGF  50
IRSRAYGGTT EYAASVKGRF TISRDDSKSI AYLQMDSLKT EDTAVYYCTS 100
GGYDSSLHYY YYYHGMDVWG RGTTVTVSSA STKGPSVFPL APCSRSTSES 150
TAALGCLVKD YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV 200
PSSSLGTKTY TCNVDHKPSN TKVDKRVESK YGPPCPPCPA PPVAGPSVFL 250
FPPKPKDTLM ISRTPEVTCV VVDVSQEDPE VQFNWYVDGV EVHNAKTKPR 300
EEQFNSTYRV VSVLTVLHQD WLNGKEYKCK VSNKGLPSSI EKTISKAKGQ 350
PREPQVYTLP PSQEEMTKNQ VSLTCLVKGF YPSDIAVEWE SNGQPENNYK 400
TTPPVLDSDG SFFLYSRLTV DKSRWQEGNV FSCSVMHEAL HNHYTQKSLS 450
LSLGK                                                   455
```

Heavy chain / Chaîne lourde / Cadena pesada: H-gamma4 anti-CD28 (H")

```
QVQLQESGPG LVKPSETLSL TCTVSGGSIS SYYWSWIRQP PGKGLEWIGY  50
IYYSGITHYN PSLKSRVTIS VDTSKIQFSL KLSSVTAADT AVYYCARWGV 100
RRDYYYYGMD VWGQGTTVTV SSASTKGPSV FPLAPCSRST SESTAALGCL 150
VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ SSGLYSLSSV VTVPSSSLGT 200
KTYTCNVDHK PSNTKVDKRV ESKYGPPCPP CPAPPVAGPS 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 common (L', L'")

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

Post-translational modifications

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

Intra-H (C23-C104)	22-98	156-212	269-329	375-433
	22"-95"	149"-205"	262"-322"	368"-426"
Intra-L (C23-C104)	23'-89'	135'-195'		
	23'"-89'"	135'"-195'"		
Inter-H-L (CH1 10-CL 126)	143-215'	136"-215'"		
Inter-H-H (h 8, h 11)	235-228"	238-231"		

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"

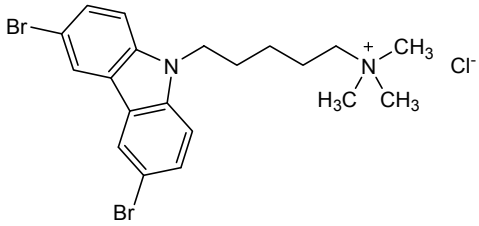
N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4: 305, 298"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2: 455, 448"

utenpanii chloridum

utenpanium chloride	5-(3,6-dibromo-9*H*-carbazol-9-yl)-*N*,*N*,*N*-trimethylpentan-1-aminium chloride
chlorure d'utenpanium	chlorure de 5-(3,6-dibromo-9*H*-carbazol-9-yl)-*N*,*N*,*N*-triméthylpentan-1-aminium
cloruro de utenpanio	cloruro de 5-(3,6-dibromo-9*H*-carbazol-9-il)-*N*,*N*,*N*-trimetilpentan-1-aminio

$C_{20}H_{25}Br_2ClN_2$



vecantoxatugum #

vecantoxatug	immunoglobulin G1-kappa, anti-[*Clostridium tetani* tetanus toxin (TeNT, neurotoxin)], humanized monoclonal antibody; H-gamma1 heavy chain humanized (1-445) [VH (*Homo sapiens* IGHV1-69*02 (81.4%) -(IGHD) - IGHJ4*01 (85.7%) L123>M (110), CDR-IMGT [8.8.8] (26-33.51-58.97-104)) (1-115) -*Homo sapiens* IGHG1*03 (100%) G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (212) (116-213), hinge 1-15 (214-228), CH2 (229-338), CH3 E12 (354), M14 (356) (339-443), CHS (444-445)) (116-445)], (218-214')-disulfide with L-kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-NL1*01 (86.3%) - IGKJ2*01 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dimer (224-224'': 227-227'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa
vécantoxatug	immunoglobuline G1-kappa, anti-[*Clostridium tetani* toxine tétanique (TeNt, neurotoxine)], anticorps monoclonal humanisé; chaîne lourde H-gamma1 humanisée (1-445) [VH (*Homo sapiens* IGHV1-69*02 (81.4%) -(IGHD) - IGHJ4*01 (85.7%) L123>M (110), CDR-IMGT [8.8.8] (26-33.51-58.97-104)) (1-115) -*Homo sapiens* IGHG1*03 (100%) G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (212) (116-213), charnière 1-15 (214-228), CH2 (229-338), CH3 E12 (354), M14 (356) (339-443), CHS (444-445)) (116-445)], (218-214')-disulfure avec la chaîne légère L-kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-NL1*01 (86.3%) -IGKJ2*01 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dimère (224-224'': 227-227'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa
vecantoxatug	inmunoglobulina G1-kappa, anti-[*Clostridium tetani* toxina tetánica (TeNt, neurotoxina)], anticuerpo monoclonal humanizado; cadena pesada H-gamma1 humanizada (1-445) [VH (*Homo sapiens* IGHV1-69*02 (81.4%) -(IGHD) - IGHJ4*01 (85.7%) L123>M (110), CDR-IMGT [8.8.8] (26-33.51-58.97-104)) (1-115) -*Homo sapiens* IGHG1*03 (100%) G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (212) (116-213), bisagra 1-15 (214-228), CH2 (229-338), CH3 E12 (354), M14 (356) (339-443), CHS (444-445)) (116-445)], (218-214')-disulfuro con la cadena ligera L-kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-NL1*01 (86.3%) -IGKJ2*01 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (100%) Km3 A45.1, V101 (C-KAPPA A45.1 (153'), V101 (191')) (108'-214')]; dímero (224-224'': 227-227'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada
```
QVQLVQSGAE VKKPGSSVKV SCKASGYTFT SYWIYWVRQA PGQGLEWIGE  50
INPTNAFANY NEKFKTKATI TVDKSTSTAY MELSSLRSED TAVYYCAIHF 100
RFPYWGQGTM VTVSSASTKG PSVFPLAPSS KSTSGGTAAL GCLVKDYFPE 150
PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL SSVVTVPSSS LGTQTYICNV 200
NHKPSNTKVD KRVEPKSCDK THTCPPCPAP ELLGGPSVFL FPPKPKDTLM 250
ISRTPEVTCV VVDVSHEDPE VKFNWYVDGV EVHNAKTKPR EEQYNSTYRV 300
VSVLTVLHQD WLNGKEYKCK VSNKALPAPI EKTISKAKGQ PREPQVYTLP 350
PSREEMTKNQ VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG 400
SFFLYSKLTV DKSRWQQGNV FSCSVMHEAL HNHYTQKSLS LSPGK      445
```

Light chain / Chaîne légère / Cadena ligera
```
DIQMTQSPSS LSASVGDRVT ITCRASQDIG SSLTWLQQKP GKAPKRLIYA  50
TSSLDSGVPS RFSGSGSGTD YTLTISSLQP EDFATYYCLQ YASSPYTFGQ 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) 22-96 142-198 259-319 365-423
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-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: 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''

velaprumigum#

velaprumig immunoglobulin scFvkh-L-VH-G1(CH1-h)_scFvkh-L-kappa, anti-[*Homo sapiens* CD40LG (CD40 ligand, CD40L, tumor necrosis factor ligand superfamily member 5, TNFSF5, tumor necrosis factor related activation protein, TRAP, CD154)] and anti-[*Homo sapiens* ALB (albumin, human serum albumin, HSA)], monoclonal antibody, bispecific, trivalent;
fused scFvkh-L-VH-G1(CH1-h) chain anti-CD40LG and anti-ALB (1-483) [scFvkh anti-CD40LG (1-245) [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV3-7*01 (87.9%) -IGKJ1*02 (100%)/*Homo sapiens* IGKV3-11*01 (75.5%) -IGKJ4*01 (90.9%) V124>L (108), CDR-IMGT [10.3.9] (27-36.54-56.93-101)) (1-112) -15-mer tris(tetraglycyl-seryl) linker (113-127) -VH Musmus/Homsap (*Mus musculus* IGHV1-47-14*01 (88.8%) -(IGHD) -IGHJ3*01 (90.9%) A128>S (245)/*Homo sapiens* IGHV1-46*01 (76.5%) -IGHD -IGHJ1*01 (100%), CDR-IMGT [8.8.11] (153-160.178-185.224-234)) (128-245)] -15-mer tris(tetraglycyl-seryl) linker (246-260) -VH-G1(CH1-h) anti-ALB (261-483) [VH anti-ALB (*Homo sapiens* IGHV3-21*01 (90.8%) -IGHD -IGHJ4*01 (92.9%), CDR-IMGT [8.8.13] (286-293.311-318.357-369)) (261-380) -*Homo sapiens* IGHG1*01 CH1-h, G1m17,1 CH1 K120, 10-G1v100-1 CH1 E16, 15-G1v37 h S5 (CH1 G16>E (400), K120 (477) (381-478), hinge 1-5 C5>S (483) (479-483)) (381-483)]];
fused scFvkh-L-KAPPA chain anti-CD40LG and anti-ALB (1'-478') [scFvkh anti-CD40LG (1'-245') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV3-7*01 (87.9%) -IGKJ1*02 (100%)/*Homo sapiens* IGKV3-11*01 (75.5%) -IGKJ4*01 (90.9%) V124>L (108'), CDR-IMGT [10.3.9] (27'-36'.54'-56'.93'-101')) (1'-112') -15-mer tris(tetraglycyl-seryl) linker (113'-127') -VH Musmus/Homsap (*Mus musculus* IGHV1-47-14*01 (88.8%) -(IGHD) -IGHJ3*01 (90.9%) A128>S (245')/*Homo sapiens* IGHV1-46*01 (76.5%) -IGHD -IGHJ1*01 (100%), CDR-IMGT [8.8.11] (153'-160'.178'-185'.224'-234')) (128'-245')]-18-mer (GSTSGSGKPGSGEGSTKG) linker (246'-263') -L-KAPPA anti-ALB (264'-478') [V-KAPPA anti-ALB (*Homo sapiens* IGKV3-15*01 (85.7%) -IGKJ2*01 (90.9%) K123>Q (367'), CDR-IMGT [6.3.10] (290'-295'.313'-315'.352'-361')) (264'-371') -

Homo sapiens IGKC*01, Km3 A45.1, V101, 15-KCv36 S126 (C-KAPPA A45.1 (417'), V101 (455'), C226>S (478')) (372'-478')]], produced in Chinese hamster ovary (CHO) cells, cell line CHO-DG44, non-glycosylated

vélaprumig immunoglobuline scFvkh-L-VH-G1(CH1-h)_scFvkh-L-kappa, anti-[*Homo sapiens* CD40LG (CD40 ligand, CD40L, membre 5 de la superfamille des ligands facteurs de nécrose tumorale, TNFSF5, protéine d'activation apparentée au facteur de nécrose tumorale, TRAP, CD154)] et anti-[*Homo sapiens* ALB (albumine, sérum albumine humaine, SAH)], anticorps monoclonal, bispecific, trivalent;
chaîne fusionnée scFvkh-L-VH-G1(CH1-h) anti-CD40LG et anti-ALB (1-483) [scFvkh anti-CD40LG (1-245) [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV3-7*01 (87.9%) -IGKJ1*02 (100%)/*Homo sapiens* IGKV3-11*01 (75.5%) -IGKJ4*01 (90.9%) V124>L (108), CDR-IMGT [10.3.9] (27-36.54-56.93-101)) (1-112) -15-mer tris(tétraglycyl-séryl) linker (113-127) -VH Musmus/Homsap (*Mus musculus* IGHV1-47-14*01 (88.8%) -(IGHD) -IGHJ3*01 (90.9%) A128>S (245)/*Homo sapiens* IGHV1-46*01 (76.5%) -IGHD -IGHJ1*01 (100%), CDR-IMGT [8.8.11] (153-160.178-185.224-234)) (128-245)] -15-mer tris(tétraglycyl-séryl) linker (246-260) -[VH-G1(CH1-h) anti-ALB (261-483) [VH anti-ALB (*Homo sapiens* IGHV3-21*01 (90.8%) -IGHD -IGHJ4*01 (92.9%), CDR-IMGT [8.8.13] (286-293.311-318.357-369)) (261-380)] -*Homo sapiens* IGHG1*01 CH1-h, G1m17,1 CH1 K120, 10-G1v100-1 CH1 E16, 15-G1v37 h S5 [(CH1 G16>E (400), K120 (477) (381-478), hinge 1-5 C5>S (483) (479-483)) (381-483)]];
chaîne fusionnée scFvkh-L-KAPPA anti-CD40LG et anti-ALB (1'-478') [scFvkh anti-CD40LG (1'-245') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV3-7*01 (87.9%) -IGKJ1*02 (100%)/*Homo sapiens* IGKV3-11*01 (75.5%) -IGKJ4*01 (90.9%) V124>L (108'), CDR-IMGT [10.3.9] (27'-36'.54'-56'.93'-101')) (1'-112') -15-mer tris(tétraglycyl-séryl) linker (113'-127') -VH Musmus/Homsap (*Mus musculus* IGHV1-47-14*01 (88.8%) -(IGHD) -IGHJ3*01 (90.9%) A128>S (245')/*Homo sapiens* IGHV1-46*01 (76.5%) -IGHD -IGHJ1*01 (100%), CDR-IMGT [8.8.11] (153'-160'.178'-185'.224'-234')) (128'-245')] -18-mer (GSTSGSGKPGSGEGSTKG) linker (246'-263') -L-KAPPA anti-ALB (264'-478') [V-KAPPA anti-ALB (*Homo sapiens* IGKV3-15*01 (85.7%) -IGKJ2*01 (90.9%) K123>Q (367'), CDR-IMGT [6.3.10] (290'-295'.313'-315'.352'-361')) (264'-371') -*Homo sapiens* IGKC*01, Km3 A45.1, V101, 15-KCv36 S126 (C-KAPPA A45.1 (417'), V101 (455'), C226>S (478')) (372'-478')]], produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-DG44, non-glycosylé

velaprumig inmunoglobulina scFvkh-L-VH-G1(CH1-h) scFvkh-L-kappa, anti-[*Homo sapiens* CD40LG (CD40 ligando, CD40L, miembro 5 de la superfamilia de los ligandos factores de necrosis tumoral, TNFSF5, proteína de activación asociada al factor de necrosis tumoral, TRAP, CD154)] y anti-[*Homo sapiens* ALB (albúmina, albumina sérica humana, SAH)], anticuerpo monoclonal, bispecífico, trivalente;
cadena fusionada scFvkh-L-VH-G1(CH1-h) anti-CD40LG y anti-ALB (1-483) [scFvkh anti-CD40LG (1-245) [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV3-7*01 (87.9%) -IGKJ1*02 (100%)/*Homo sapiens* IGKV3-11*01 (75.5%) -IGKJ4*01 (90.9%) V124>L (108), CDR-IMGT [10.3.9] (27-36.54-56.93-101)) (1-112) -15-mer tris(tetraglicil-seril) enlace(113-127) -VH Musmus/Homsap (*Mus musculus* IGHV1-47-14*01 (88.8%) -(IGHD) -IGHJ3*01 (90.9%) A128>S (245)/*Homo sapiens* IGHV1-46*01 (76.5%) -IGHD -IGHJ1*01 (100%), CDR-IMGT [8.8.11] (153-160.178-185.224-234)) (128-245)] -15-mer tris(tetraglicil-seril) enlace (246-260) -[VH-G1(CH1-h) anti-ALB (261-483) [VH anti-ALB (*Homo sapiens* IGHV3-21*01 (90.8%) -IGHD -IGHJ4*01 (92.9%), CDR-IMGT [8.8.13] (286-293.311-318.357-369)) (261-380)] -*Homo sapiens* IGHG1*01 CH1-h, G1m17,1 CH1 K120, 10-G1v100-1 CH1 E16, 15-G1v37 h S5 [(CH1 G16>E (400), K120 (477) (381-478), bisagra 1-5 C5>S (483) (479-483)) (381-483)]];
cadena fusionada scFvkh-L-KAPPA anti-CD40LG y anti-ALB (1'-478') [scFvkh anti-CD40LG (1'-245') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV3-7*01 (87.9%) -IGKJ1*02 (100%)/*Homo sapiens* IGKV3-11*01 (75.5%) -IGKJ4*01

(90.9%) V124>L (108'), CDR-IMGT [10.3.9] (27'-36'.54'-56'.93'-101')) (1'-112') -15-mer tris(tetraglicil-seril) enlace (113'-127') -VH Musmus/Homsap (*Mus musculus* IGHV1-47-14*01 (88.8%) -(IGHD) -IGHJ3*01 (90.9%) A128>S (245')/*Homo sapiens* IGHV1-46*01 (76.5%) -IGHD -IGHJ1*01 (100%), CDR-IMGT [8.8.11] (153'-160'.178'-185'.224'-234')) (128'-245')] -18-mer (GSTSGSGKPGSGEGSTKG) enlace (246'-263') -L-KAPPA anti-ALB (264'-478') [V-KAPPA anti-ALB (*Homo sapiens* IGKV3-15*01 (85.7%) -IGKJ2*01 (90.9%) K123>Q (367'), CDR-IMGT [6.3.10] (290'-295'.313'-315'.352'-361')) (264'-371') -*Homo sapiens* IGKC*01, Km3 A45.1, V101, 15-KCv36 S126 (C-KAPPA A45.1 (417'), V101 (455'), C226>S (478')) (372'-478')]], producido en las células ováricas de hámster chino (CHO), línea celular CHO-DG44, no glicosilado

Heavy chain / Chaîne lourde / Cadena pesada: fused scFvkh
anti-CD40LG -L-VH-G1(CH1-h) anti-ALB (H)

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DIVLTQSPAT LSVSPGERAT ISCRASQRVS SSTYSYMHWY QQKPGQPPKL  50
LIKYASNLES GVPARFSGSG SGTDFTLTIS SVEPEDFATY YCQHSWEIPP 100
TFGGGTKLEI KRGGGGSGGG GSGGGGSQVQ LVQSGAEVVK PGASVKLSCK 150
ASGYIFTSYY MYWVKQAPGQ GLEWIGEINP SNGDTNFNEK FKSKATLTVD 200
KSASTAYMEL SSLRSEDTAV YYCTRSDGRN DMDSWGQGTL VTVSSGGGGS 250
GGGGSGGGGS QVQLVQSGGG PVKPGGSLRL SCAASGFMFR AYSMNWVRQA 300
PGKGLEWVSS ISSSGRYIHY ADSVKGRFTI SRDNAKNSLY LQMNSLRAED 350
TAVYYCARET VMAGKALDYW GQGTLVTVSS ASTKGPSVFP LAPSSKSTSE 400
GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT 450
VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSS                   483
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Heavy chain / Chaîne lourde / Cadena pesada: fused scFvkh
anti-CD40LG -L-kappa anti-ALB (H')

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DIVLTQSPAT LSVSPGERAT ISCRASQRVS SSTYSYMHWY QQKPGQPPKL  50
LIKYASNLES GVPARFSGSG SGTDFTLTIS SVEPEDFATY YCQHSWEIPP 100
TFGGGTKLEI KRGGGGSGGG GSGGGGSQVQ LVQSGAEVVK PGASVKLSCK 150
ASGYIFTSYY MYWVKQAPGQ GLEWIGEINP SNGDTNFNEK FKSKATLTVD 200
KSASTAYMEL SSLRSEDTAV YYCTRSDGRN DMDSWGQGTL VTVSSGSTSG 250
SGKPGSGEGS TKGDIVLTQS PGTLSLSPGE TATLSCRASQ SVGSNLAWYQ 300
QKPGQAPRLL IYGASTGATG VPARFSGSRS GTDFTLTITS LQPEDFATYY 350
CQQYYSFLAK TFGQGTQLEI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL 400
NNFYPREAKV QWKVDNALQS GNSQESVTEQ DSKDSTYSLS NTLTLSKADY 450
EKHKVYACEV THQGLSSPVT KSFNRGES                         478
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Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 23-92 149-223 282-356 407-463
Intra-H' (C23-C104) 23'-92' 149'-223' 286'-351' 398'-458'

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

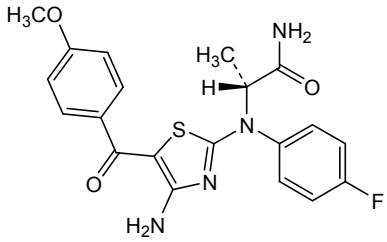
veludacigibum

veludacigib (2*R*)-2-{*N*-[4-amino-5-(4-methoxybenzoyl)-1,3-thiazol-2-yl]-4-fluoroanilino}propanamide

véludacigib (2*R*)-2-{*N*-[4-amino-5-(4-méthoxybenzoyl)-1,3-thiazol-2-yl]-4-fluoroanilino}propanamide

veludacigib (2*R*)-2-{*N*-[4-amino-5-(4-metoxibenzoil)-1,3-tiazol-2-il]-4-fluoroanilino}propanamida

$C_{20}H_{19}FN_4O_3S$



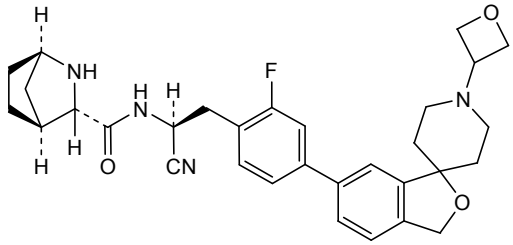
verducatibum

verducatib — (1*R*,3*S*,4*S*)-*N*-[(1*S*)-1-cyano-2-{2-fluoro-4-[1'-(oxetan-3-yl)-3*H*-spiro[[2]benzofuran-1,4'-piperidin]-6-yl]phenyl}ethyl]-2-azabicyclo[2.2.1]heptane-3-carboxamide

verducatib — (1*R*,3*S*,4*S*)-*N*-[(1*S*)-1-cyano-2-{2-fluoro-4-[1'-(oxétan-3-yl)-3*H*-spiro[[2]benzofurane-1,4'-pipéridin]-6-yl]phényl}éthyl]-2-azabicyclo[2.2.1]heptane-3-carboxamide

verducatib — (1*R*,3*S*,4*S*)-*N*-[(1*S*)-1-ciano-2-{2-fluoro-4-[1'-(oxetan-3-il)-3*H*-espiro[[2]benzofurano-1,4'-piperidin]-6-il]fenil}etil]-2-azabiciclo[2.2.1]heptano-3-carboxamida

$C_{31}H_{35}FN_4O_3$



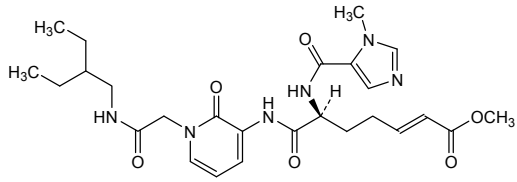
vilagletistatum

vilagletistat — methyl (2*E*,6*S*)-7-[(1-{2-[(2-ethylbutyl)amino]-2-oxoethyl}-2-oxo-1,2-dihydropyridin-3-yl)amino]-6-(1-methyl-1*H*-imidazole-5-carboxamido)-7-oxohept-2-enoate

vilaglétistat — (2*E*,6*S*)-7-[(1-{2-[(2-éthylbutyl)amino]-2-oxoéthyl}-2-oxo-1,2-dihydropyridin-3-yl)amino]-6-(1-méthyl-1*H*-imidazole-5-carboxamido)-7-oxohept-2-énoate de méthyle

vilagletistat — (2*E*,6*S*)-7-[(1-{2-[(2-etilbutil)amino]-2-oxoetil}-2-oxo-1,2-dihidropiridin-3-il)amino]-6-(1-metil-1*H*-imidazol-5-carboxamido)-7-oxohept-2-enoato de metilo

$C_{26}H_{36}N_6O_6$



vopimetostatum

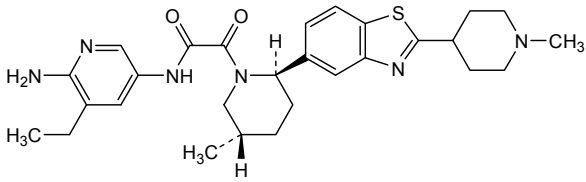
vopimetostat — *N*-(6-amino-5-ethylpyridin-3-yl)-2-{(2*R*,5*S*)-5-methyl-2-[2-(1-methylpiperidin-4-yl)-1,3-benzothiazol-5-yl]piperidin-1-yl}-2-oxoacetamide

vopimétostat — *N*-(6-amino-5-éthylpyridin-3-yl)-2-{(2*R*,5*S*)-5-méthyl-2-[2-(1-méthylpipéridin-4-yl)-1,3-benzothiazol-5-yl]pipéridin-1-yl}-2-oxoacétamide

vopimetostat

N-(6-amino-5-etilpiridin-3-il)-2-{(2*R*,5*S*)-5-metil-2-[2-(1-metilpiperidin-4-il)-1,3-benzotiazol-5-il]piperidin-1-il}-2-oxoacetamida

$C_{28}H_{36}N_6O_2S$



vortosiranum

vortosiran

(2*RS*)-3-(1,23-bis[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]-14-{5-[(2-acetamido-2-deoxy-β-D-galactopyranosyl)oxy]pentanoyl}-5,19-dioxo-6,10,14,18-tetraazatricosan-10-yl)-2-hydroxy-3-oxopropyl hydrogen *all-P-ambo*-2'-*O*-methyl-*P*-thioguanylyl-(3'→5')-2'-*O*-methyl-*P*-thiouridylyl-(3'→5')-2'-*O*-methyladenylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methylguanylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-deoxy-2'-fluoroguanylyl-(3'→5')-2'-deoxy-2'-fluoroguanylyl-(3'→5')-2'-deoxy-2'-fluoroadenylyl-(3'→5')-2'-*O*-methylcytidylyl-(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'-*O*-methyluridylyl-(3'→5')-2'-*O*-methylcytidylyl-(3'→5')-2'-*O*-methyluridylyl-(3'→5')-2'-*O*-methyl-3'-guanylate
duplex with *all-P-ambo*-2'-*O*-methyl-*P*-thiouridylyl-(5'→3')-2'-*O*-methyl-*P*-thiouridylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-deoxy-2'-fluoroguanylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-deoxy-2'-fluoroadenylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-*O*-methyluridylyl-(5'→3')-2'-*O*-methylguanylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-*O*-methylcytidylyl-(5'→3')-2'-deoxy-2'-fluorouridylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-*O*-methyladenylyl-(5'→3')-2'-*O*-methyl-*P*-thioguanylyl-(5'→3')-2'-deoxy-2'-fluoro-*P*-thioadenylyl-(5'→3')-cytidine

vortosiran

(2*RS*)-3-(1,23-bis[(2-acétamido-2-désoxy-β-D-galactopyranosyl)oxy]-14-{5-[(2-acétamido-2-désoxy-β-D-galactopyranosyl)oxy]pentanoyl}-5,19-dioxo-6,10,14,18-tétraazatricosan-10-yl)-2-hydroxy-3-oxopropyle hydrogène *tout-P-ambo*-2'-*O*-méthyl-*P*-thioguanylyl-(3'→5')-2'-*O*-méthyl-*P*-thiouridylyl-(3'→5')-2'-*O*-méthyladénylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthylguanylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-désoxy-2'-fluoroguanylyl-(3'→5')-2'-désoxy-2'-fluoroguanylyl-(3'→5')-2'-désoxy-2'-fluoroadénylyl-(3'→5')-2'-*O*-méthylcytidylyl-(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'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthylcytidylyl-(3'→5')-2'-*O*-méthyluridylyl-(3'→5')-2'-*O*-méthyl-3'-guanylate
duplex avec *tout-P-ambo*-2'-*O*-méthyl-*P*-thiouridylyl-(5'→3')-2'-*O*-méthyl-*P*-thiouridylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-*O*-méthyluridylyl-(5'→3')-2'-désoxy-2'-fluoroguanylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-désoxy-2'-fluoroadénylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-*O*-

méthylcytidylyl-(5'→3')-2'-*O*-méhyluridylyl-(5'→3')-2'-*O*-méthylguanylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-*O*-méthylcytidylyl-(5'→3')-2'-*O*-méhylcytidylyl-(5'→3')-2'-désoxy-2'-fluorouridylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-*O*-méthyladénylyl-(5'→3')-2'-*O*-méthyl-*P*-thioguanylyl-(5'→3')-2'-désoxy-2'-fluoro-*P*-thioadénylyl-(5'→3')-cytidine

vortosirán

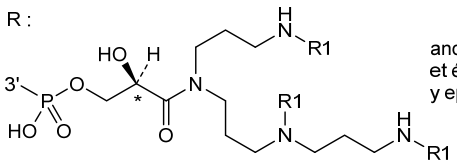
(2*RS*)-3-(1,23-bis[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]-14-{5-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]pentanoil}-5,19-dioxo-6,10,14,18-tetraazatricosan-10-il)-2-hidroxi-3-oxopropil hidrógeno *todo-P-ambo*-2'-*O*-metil-*P*-tioguanilil-(3'→5')-2'-*O*-metil-*P*-tiouridilil-(3'→5')-2'-*O*-metiladenilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metilguanilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-desoxi-2'-fluoroguanilil-(3'→5')-2'-desoxi-2'-fluoroguanilil-(3'→5')-2'-desoxi-2'-fluoroadenilil-(3'→5')-2'-*O*-metilcitidilil-(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'-*O*-metiluridilil-(3'→5')-2'-*O*-metilcitidilil-(3'→5')-2'-*O*-metiluridilil-(3'→5')-2'-*O*-metil-3'-guanilato
dúplex con *todo-P-ambo*-2'-*O*-metil-*P*-tiouridilil-(5'→3')-2'-*O*-metil-*P*-tiouridilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-desoxi-2'-fluoroguanilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-desoxi-2'-fluoroadenilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-*O*-metiluridilil-(5'→3')-2'-*O*-metilguanilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-*O*-metilcitidilil-(5'→3')-2'-desoxi-2'-fluorouridyilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-*O*-metiladenilil-(5'→3')-2'-*O*-metil-*P*-tioguanilil-(5'→3')-2'-desoxi-2'-fluoro-*P*-tioadenilil-(5'→3')-citidina

$C_{463}H_{620}F_7N_{154}O_{291}P_{39}S_6$

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

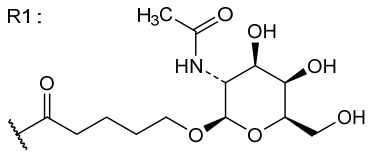
N : A,C,G,U
N : 2'-*O*-methyl-N / 2'-*O*-méthyl-N / 2'-*O*-metil-N
N : 2'-deoxy-2'-fluoro-N / 2'-désoxy-2'-fluoro-N / 2'-desoxi-2'-fluoro-N
− : −PO(OH)− = : −PO(SH)−

R :



and epimer at C*
et épimère en C*
y epimero al C*

R1 :



xeruborbactamum isoboxilum

xeruborbactam isoboxil

[(2-methylpropanoyl)oxy]methyl (1a*R*,7b*S*)-5-fluoro-2-hydroxy-1,1a,2,7b-tetrahydrocyclopropa[*c*][1,2]benzoxaborinine-4-carboxylate

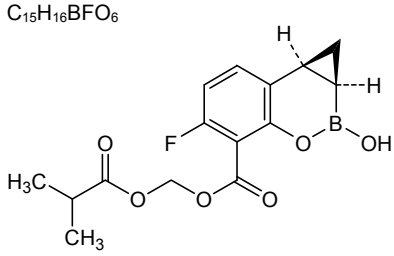
xéruborbactam isoboxil

(1a*R*,7b*S*)-5-fluoro-2-hydroxy-1,1a,2,7b-tétrahydrocyclopropa[*c*][1,2]benzoxaborinine-4-carboxylate de [(2-méthylpropanoyl)oxy]méthyle

xeruborbactam isoboxilo

(1a*R*,7b*S*)-5-fluoro-2-hidroxi-1,1a,2,7b-tetrahidrociclopropa[*c*][1,2]benzoxaborinina-4-carboxilato de [(2-metilpropanoil)oxi]metilo

$C_{15}H_{16}BFO_6$



zaladenantum

zaladenant

{5-amino-8-[2-methyl-6-(trifluoromethyl)pyridin-4-yl]-7-phenyl[1,2,4]triazolo[1,5-*c*]pyrimidin-2-yl}methanol

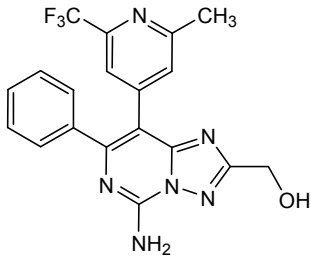
zaladénant

{5-amino-8-[2-méthyl-6-(trifluorométhyl)pyridin-4-yl]-7-phényl[1,2,4]triazolo[1,5-*c*]pyrimidin-2-yl}méthanol

zaladenant

{5-amino-7-fenil-8-[2-metil-6-(trifluorometil)piridin-4-il][1,2,4]triazolo[1,5-*c*]pirimidin-2-il}metanol

$C_{19}H_{15}F_3N_6O$



zalsupindolum

zalsupindole

(2*R*)-1-(5-methoxy-1*H*-indol-1-yl)-*N*,*N*-dimethylpropan-2-amine

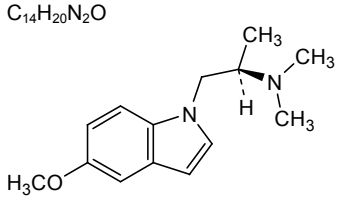
zalsupindole

(2*R*)-1-(5-méthoxy-1*H*-indol-1-yl)-*N*,*N*-diméthylpropan-2-amine

zalsupindol

(2*R*)-*N*,*N*-dimetil-1-(5-metoxi-1*H*-indol-1-il)propan-2-amina

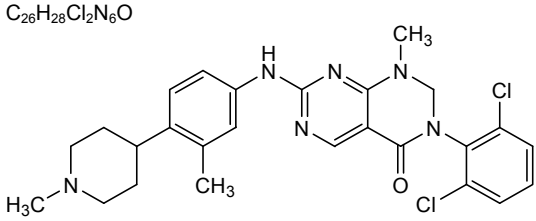
$C_{14}H_{20}N_2O$



zedoresertibum

zedoresertib	3-(2,6-dichlorophenyl)-1-methyl-7-[3-methyl-4-(1-methylpiperidin-4-yl)anilino]-2,3-dihydropyrimido[4,5-*d*]pyrimidin-4(1*H*)-one
zédorésertib	3-(2,6-dichlorophényl)-1-méthyl-7-[3-méthyl-4-(1-méthylpipéridin-4-yl)anilino]-2,3-dihydropyrimido[4,5-*d*]pyrimidin-4(1*H*)-one
zedoresertib	3-(2,6-diclorofenil)-1-metil-7-[3-metil-4-(1-metilpiperidin-4-il)anilino]-2,3-dihidropirimido[4,5-*d*]pirimidin-4(1*H*)-ona

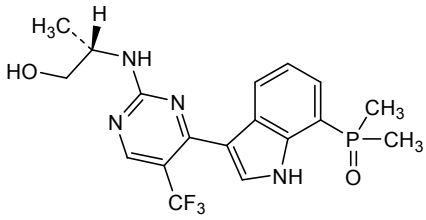
$C_{26}H_{28}Cl_2N_6O$



zeltociclibum

zeltociclib	{3-[2-{[(2*S*)-1-hydroxypropan-2-yl]amino}-5-(trifluoromethyl)pyrimidin-4-yl]-1*H*-indol-7-yl}di(methyl)-λ^5-phosphanone
zeltociclib	{3-[2-{[(2*S*)-1-hydroxypropan-2-yl]amino}-5-(trifluorométhyl)pyrimidin-4-yl]-1*H*-indol-7-yl}di(méthyl)-λ^5-phosphanone
zeltociclib	{3-[2-{[(2*S*)-1-hidroxipropan-2-il]amino}-5-(trifluorometil)pirimidin-4-il]-1*H*-indol-7-il}di(metil)-λ^5-fosfanona

$C_{18}H_{20}F_3N_4O_2P$



zemocimigum

zemocimig	immunoglobulin (H-gamma4_L-kappa)_(H-gamma4_L-lambda2), anti-[*Homo sapiens* F9a (coagulation factor F9, coagulation factor IX, hemophilia B) activated] and anti-[*Homo sapiens* F10 (coagulation factor 10, coagulation factor X)], humanized and *Homo sapiens* monoclonal antibody, bispecific, bivalent;

	H-gamma4 heavy chain anti-F9a humanized (1-447) [VH (*Homo sapiens* IGHV3-23*04 (87.8%) -(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, 12-G4v5 h P10, 17-G4v57-1 CH1 K84.2, 18-G4v11 CH1 Q100, CH2 Y84.3, 14-G4v12-1 CH3 K12, 12-G4v6 CH3 K88, 9-G4v78 L107, A114, 10-G4v89 CH3 R118, E120 (CH1 Q84.2>K (180), K100>Q (201) (123-220), hinge 1-12 S10>P (230) (221-232), CH2 F84.3>Y (298), L92 (311) (233-342), CH3 E12>K (358), R88>K (411), M107>L (430), N114>A (436), Q118>R (440), S120>E (442) (343-447)) (123-447)], (136-214')-disulfide with L-kappa light chain anti-F9a *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3D-11*02 (84.4%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (98.1%) Km3 A45.1, V101 KCv57-1 E20, E90 (C-KAPPA S20>E (131'), A45.1 (153'), T90>E (180), V101 (191')) (108'-214')]; H-gamma4 heavy chain anti-F10 humanized (1''-444'') [VH (*Homo sapiens* IGHV1-2*06 (74.5%) -(IGHD) -IGHJ4*01 (80.0%) Q120>E (111''), CDR-IMGT [8.8.12] (26''-33''.51''-58''.97''-108'')) (1''-119'')-*Homo sapiens* IGHG4*01, nG4m(a) CH2 L92, 12-G4v5 h P10, 17-G4v57-2 CH1 E26, K84.2, 18-G4v11 CH1 Q100, CH2 Y84.3, 12-G4v6 CH3 K88, 9-G4v78 L107, A114, 10-G4v89 CH3 R118, E120, 14-G4v13 CH3 E119 (CH1 K26>E (149''), Q84.2>E (177''), K100>Q (198'') (120''-217''), hinge 1-12 S10>P (227'') (218''-229''), CH2 F84.3>Y (295''), L92 (308'') (230''-339''), CH3 R88>K (408''), M107>L (427''), N114>A (433''), Q118>R (437''), K119>E (438''), S120>E (439'') (340''-444'')) (120''-444'')], (133''-212''')-disulfide with L-lambda2 light chain anti-F10 *Homo sapiens* (1'''-213''') [V-LAMBDA (*Homo sapiens* IGLV3-9*01 (78.7%) -IGLJ2*01 (81.8%) L124>V (104'''), L127>V (107'''), CDR-IMGT [6.3.10] (26'''-31'''.49'''-51'''.88'''-97''')) (1'''-107''') -*Homo sapiens* IGLC2*01 (98.1%) LC2v57-2 K20, K90 (C-LAMBDA2 T20>K (132'''), S90>K (180''')) (108'''-213''')]; dimer (228-225'': 231-228'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-DXB11, glycoform alfa
zémocimig	immunoglobuline (H-gamma4_L-kappa)_(H-gamma4_L-lambda2), anti-[*Homo sapiens* F9a (facteur de coagulation F9, facteur de coagulation IX, hémophilie B) activé] et anti-[*Homo sapiens* F10 (facteur de coagulation 10, facteur de coagulation X)], anticorps monoclonal humanisé et *Homo sapiens,* bispécifique, bivalent; chaîne lourde H-gamma4 anti-F9a humanisée (1-447) [VH (*Homo sapiens* IGHV3-23*04 (87.8%) -(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, 12-G4v5 h P10, 17-G4v57-1 CH1 K84.2, 18-G4v11 CH1 Q100, CH2 Y84.3, 14-G4v12-1 CH3 K12, 12-G4v6 CH3 K88, 9-G4v78 L107, A114, 10-G4v89 CH3 R118, E120 (CH1 Q84.2>K (180), K100>Q (201) (123-220), charnière 1-12 S10>P (230) (221-232), CH2 F84.3>Y (298), L92 (311) (233-342), CH3 E12>K (358), R88>K (411), M107>L (430), N114>A (436), Q118>R (440), S120>E (442) (343-447)) (123-447)], (136-214')-disulfure avec la chaîne légère L-kappa anti-F9a *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3D-11*02 (84.4%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (98.1%) Km3 A45.1, V101 KCv57-1 E20, E90 (C-KAPPA S20>E (131'), A45.1 (153'), T90>E (180), V101 (191')) (108'-214')];

	chaîne lourde H-gamma4 anti-F10 humanisée (1''-444'') [VH (*Homo sapiens* IGHV1-2*06 (74.5%) -(IGHD) -IGHJ4*01 (80.0%) Q120>E (111''), CDR-IMGT [8.8.12] (26''-33''.51''-58''.97''-108'')) (1''-119'')-*Homo sapiens* IGHG4*01, nG4m(a) CH2 L92, 12-G4v5 h P10, 17-G4v57-2 CH1 E26, K84.2, 18-G4v11 CH1 Q100, CH2 Y84.3, 12-G4v6 CH3 K88, 9-G4v78 CH3 L107, A114, 10-G4v89 CH3 R118, E120, 14-G4v13 CH3 E119 (CH1 K26>E (149''), Q84.2>E (177''), K100>Q (198'') (120''-217''), charnière 1-12 S10>P (227'') (218''-229''), CH2 F84.3>Y (295''), L92 (308'') (230''-339''), CH3 R88>K (408''), M107>L (427''), N114>A (433''), Q118>R (437''), K119>E (438''), S120>E (439'') (340''-444'')) (120''-444'')], (133''-212''')-disulfure avec la chaîne légère L-lambda2 anti-F10 *Homo sapiens* (1''-213''') [V-LAMBDA (*Homo sapiens* IGLV3-9*01 (78.7%) -IGLJ2*01 (81.8%) L124>V (104'''), L127>V (107'''), CDR-IMGT [6.3.10] (26'''-31'''.49'''-51'''.88'''-97''')) (1'''-107''') - *Homo sapiens* IGLC2*01 (98.1%) LC2v57-2 K20, K90 (C-LAMBDA2 T20>K (132'''), S90>K (180''')) (108'''-213''')]; dimère (228-225'': 231-228'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-DXB11, glycoforme alfa
zemocimig	inmunoglobulina (H-gamma4_L-kappa)_(H-gamma4_L-lambda2), anti-[*Homo sapiens* F9a (factor de coagulación F9, factor de coagulación IX, hemofilia B) activado] y anti-[*Homo sapiens* F10 (factor de coagulación 10, factor de coagulación X)], anticuerpo monoclonal humanizado y *Homo sapiens,* bispecífico, bivalente; cadena pesada H-gamma4 anti-F9a humanizada (1-447) [VH (*Homo sapiens* IGHV3-23*04 (87.8%) -(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, 12-G4v5 h P10, 17-G4v57-1 CH1 K84.2, 18-G4v11 CH1 Q100, CH2 Y84.3, 14-G4v12-1 CH3 K12, 12-G4v6 CH3 K88, 9-G4v78 L107, A114, 10-G4v89 CH3 R118, E120 (CH1 Q84.2>K (180), K100>Q (201) (123-220), bisagra 1-12 S10>P (230) (221-232), CH2 F84.3>Y (298), L92 (311) (233-342), CH3 E12>K (358), R88>K (411), M107>L (430), N114>A (436), Q118>R (440), S120>E (442) (343-447)) (123-447)], (136-214')-disulfuro con la cadena ligera L-kappa anti-F9a *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3D-11*02 (84.4%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27'-32'.50'-52'.89'-97')) (1'-107') -*Homo sapiens* IGKC*01 (98.1%) Km3 A45.1, V101 KCv57-1 E20, E90 (C-KAPPA S20>E (131'), A45.1 (153'), T90>E (180), V101 (191')) (108'-214')]; cadena pesada H-gamma4 anti-F10 humanizada (1''-444'') [VH (*Homo sapiens* IGHV1-2*06 (74.5%) -(IGHD) -IGHJ4*01 (80.0%) Q120>E (111''), CDR-IMGT [8.8.12] (26''-33''.51''-58''.97''-108'')) (1''-119'')-*Homo sapiens* IGHG4*01, nG4m(a) CH2 L92, 12-G4v5 h P10, 17-G4v57-2 CH1 E26, K84.2, 18-G4v11 CH1 Q100, CH2 Y84.3, 12-G4v6 CH3 K88, 9-G4v78 CH3 L107, A114, 10-G4v89 CH3 R118, E120, 14-G4v13 CH3 E119 (CH1 K26>E (149''), Q84.2>E (177''), K100>Q (198'') (120''-217''), bisagra 1-12 S10>P (227'') (218''-229''), CH2 F84.3>Y (295''), L92 (308'') (230''-339''), CH3 R88>K (408''), M107>L (427''), N114>A (433''), Q118>R (437''), K119>E (438''), S120>E (439'') (340''-444'')) (120''-444'')], (133''-212''')-disulfuro con la cadena ligera L-lambda2 anti-F10 *Homo sapiens* (1''-213''') [V-LAMBDA (*Homo sapiens* IGLV3-9*01 (78.7%) -IGLJ2*01 (81.8%) L124>V (104'''), L127>V (107'''), CDR-IMGT [6.3.10] (26'''-31'''.49'''-51'''.88'''-97''')) (1'''-107''') -

Homo sapiens IGLC2*01 (98.1%) LC2v57-2 K20, K90 (C-LAMBDA2 T20>K (132'"), S90>K (180'")) (108'"-213'")]; dímero (228-225": 231-228")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-DXB11, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada: H-gamma4 anti-F9a (H)

```
QVQLVESGGG LVQPGGSLRL SCAASGFTFS YYDIQWVRQA PGKGLEWVSS    50
ISPSGQSTYY RREVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARRT   100
GREEGGWIFD YWGQGTLVTV SSASTKGPSV FPLAPCSRST SESTAALGCL   150
VKDYFPEPVT VSWNSGALTS GVHTFPAVLK SSGLYSLSSV VTVPSSSLGT   200
QTYTCNVDHK PSNTKVDKRV ESKYGPPCPP CPAPEFLGGP SVFLFPPKPK   250
DTLMISRTPE VTCVVVDVSQ EDPEVQFNWY VDGVEVHNAK TKPREEQYNS   300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKGL PSSIEKTISK AKGQPREPQV   350
YTLPPSQKEM TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL   400
DSDGSFFLYS KLTVDKSRWQ EGNVFSCSVL HEALHAHYTR KELSLSP      447
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Light chain / Chaîne légère / Cadena ligera: L-kappa anti-F9a (L')

```
EIVLTQSPAT LSVSPGERAT LSCRASRSVR RELAWYQQKP GQAPELLIYG    50
ASTRETGIPA RFSGSGSGTD FTLTINSLEA EDAATYYCQQ YRDPPGTFGG   100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA EVVCLLNNFY PREAKVQWKV   150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLE LSKADYEKHK VYACEVTHQG   200
LSSPVTKSFN RGEC                                          214
```

Heavy chain / Chaîne lourde / Cadena pesada: H-gamma4 anti-F10 (H")

```
QVQLVQSGSE LKKPGASVKV SCKASGYTFT QNNMDWVRQA PGQGLEWMGD    50
INTRSGGVIY NEEFQDRLIM TVDKSTDTAY MELSSLRSED TATYHCARRK   100
SYGYYLDVWG EGTLVTVSSA STKGPSVFPL APCSRSTSES TAALGCLVED   150
YFPEPVTVSW NSGALTSGVH TFPAVLESSG LYSLSSVVTV PSSSLGTQTY   200
TCNVDHKPSN TKVDKRVESK YGPPCPPCPA PEFLGGPSVF LFPPKPKDTL   250
MISRTPEVTC VVVDVSQEDP EVQFNWYVDG VEVHNAKTKP REEQYNSTYR   300
VVSVLTVLHQ DWLNGKEYKC KVSNKGLPSS IEKTISKAKG QPREPQVYTL   350
PPSQEEMTKN QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD   400
GSFFLYSKLT VDKSRWQEGN VFSCSVLHEA LHAHYTREEL SLSP          444
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Light chain / Chaîne légère / Cadena ligera: L-lambda anti-F10 (L'")

```
SYVLTQPVSV SVALGQTATI TCEGEQIGSK EVHWYHQRPG QAPILVMFRD    50
ARRPSGIPER LSGSNSGNTA SLTISGAEAG DEGDYYCQVW DSSSYTVFGG   100
GTKVTVVGQP KAAPSVTLFP PSSEELQANK AKLVCLISDF YPGAVTVAWK   150
ADSSPVKAGV ETTTPSKQSN NKYAASSYLK LTPEQWKSHR SYSCQVTHEG   200
STVEKTVAPT ECS                                           213
```

Post-translational modifications

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

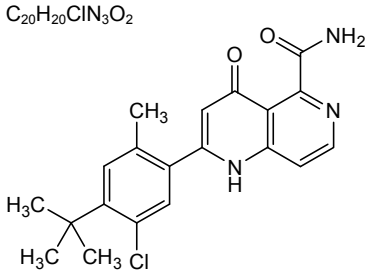
Intra-H (C23-C104) 22-96 149-205 263-323 369-427
22"-96" 146"-202" 260"-320" 366"-424"
Intra-L (C23-C104) 23'-88' 134'-194'
22'"-87'" 135'"-194'"
Inter-H-L (CH1 10-CL 126) 136-214' 133"-212'"
Inter-H-H (h 8, h 11) 228-225" 231-228"

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: 299, 296"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

zilvetriginum

zilvetrigine	2-(4-*tert*-butyl-5-chloro-2-methylphenyl)-4-oxo-1,4-dihydro-1,6-naphthyridine-5-carboxamide
zilvétrigine	2-(4-*tert*-butyl-5-chloro-2-méthylphényl)-4-oxo-1,4-dihydro-1,6-naphtyridine-5-carboxamide
zilvetrigina	2-(4-*terc*-butil-5-cloro-2-metilfenil)-4-oxo-1,4-dihidro-1,6-naftiridina-5-carboxamida



zolacabtagenum autoleucelum #

zolacabtagene autoleucel	autologous CD4+ and CD8+ T lymphocytes obtained by leukapheresis and transduced with a self-inactivating, non-replicating lentiviral vector encoding (i) a CD19 specific chimeric antigen receptor (CAR) and (ii) truncated human epidermal growth factor receptor (EGFRt) separated from the CAR by a T2A self-cleaving peptide, under control of a chimeric promoter composed of the elongation factor 1 alpha (EF-1α) promoter/R region of the human T cell leukaemia virus 1 (HTLV-1 R) and a Woodchuck hepatitis virus posttranscriptional regulatory element (WPRE). The CD19-specific CAR transgene consists of a single-chain variable fragment (scFv) derived from a CD19-specific monoclonal antibody (FMC63), an IgG4 hinge region, a CD28 transmembrane domain, and the intracellular CD137 (4-1BB) co-stimulatory and CD3ζ signalling domains. Both transgenes, the CD19-specific CAR and the EGFRt, are preceded by human granulocyte-macrophage colony-stimulating factor receptor alpha (GMCSFR-alpha) signal peptide sequence. The vector genome also contains a psi packaging signal, a splice donor, partial *gag*, Rev response element (RRE), a DNA FLAP, and a splice acceptor. The vector is flanked by 5' and 3' long terminal repeats (LTRs) and is pseudotyped by vesicular stomatitis virus (VSV) G glycoprotein. The leukapheresis material is sorted to co-select the CD4+ and CD8+ T lymphocytes by positive immunoselection prior to activation with CD3 and CD28 agonists in growth media containing interleukin 2 (IL-2), interleukin 7 (IL-7) and interleukin 15 (IL-15). The mixed CD4+/CD8+ cells are then transduced with the lentiviral vector and minimally expanded in growth media containing IL-2, IL-7 and IL-15. The cell suspension consists of CD4+ and CD8+ lymphocytes that are ≥80% CD3+ and contain ≥10% CD3+CAR+ cells. The transduced T lymphocytes release interferon gamma (IFN-γ) by co-culture with target cells *in vitro*
zolacabtagène autoleucel	lymphocytes T autologues CD4+ et CD8+ obtenus par leucaphérèse et transduits avec un vecteur lentiviral auto-inactivant et non réplicatif codant (i) un récepteur antigénique chimérique (RAC) spécifique de CD19 et (ii) un récepteur du facteur de croissance épidermique humain tronqué (EGFRt) séparé du RAC par un peptide auto-clivant T2A, sous le contrôle d'un promoteur chimérique composé du facteur d'élongation 1-alpha (EF1-α) promoteur/région R du virus T-lymphotrope humain 1 (HTLV-1 R) et d'un élément régulateur post-transcriptionnel du virus de l'hépatite Woodchuck (WPRE). Le transgène RAC spécifique de CD19 est constitué d'un fragment variable à chaîne unique (scFv) dérivé d'un anticorps monoclonal spécifique de CD19 (FMC63), d'une région charnière IgG4, d'un domaine transmembranaire CD28 et les domaines

	intracellulaires de co-stimulation CD137 (4-1BB), et de signalisation CD3ζ. Les deux transgènes, le RAC spécifiques de CD19 et le EGFRt, sont précédés d'une séquence de peptide signal du récepteur alpha du facteur de stimulation des colonies de granulocytes-macrophages humains (GMCSFR-alpha). Le génome du vecteur contient également un signal d'empaquetage psi, un donneur d'épissage, une partie du gène *gag*, un élément de réponse Rev (RRE), un volet d'ADN, et un accepteur d'épissage. Le vecteur est flanqué de répétitions terminales longues (LTRs) en 5' et 3' et est pseudotypé par la glycoprotéine G du virus de la stomatite vésiculaire (VSV). Le matériel de leucaphérèse est trié pour co-sélectionner les lymphocytes T CD4+ et CD8+ par immunosélection positive avant activation avec les agonistes CD3 et CD28 dans un milieu de croissance contenant de l'interleukine 2 (IL-2), de l'interleukine 7 (IL-7) et de l'interleukine 15 (IL -15). Le mélange de cellules CD4+/CD8+ est ensuite transduit avec le vecteur lentiviral et expansées de façon minimale dans un milieu de croissance contenant de l'IL-2, de l'IL-7 et de l'IL-15. La suspension cellulaire est constituée de lymphocytes CD4+ et CD8+ qui sont ≥80% CD3+ et contiennent ≥10% de cellules CD3+RAC+. Les lymphocytes T transduits libèrent de l'interféron gamma (IFN-γ) par co-culture avec des cellules cibles *in vitro*
zolacabtagén autoleucel	linfocitos T CD4+ y CD8+ autólogos obtenidos por leucoaféresis y transducidos con un vector lentiviral auto inactivante, no replicativo que codifica (i) un receptor de antígenos quimérico (CAR) específico de CD19 y (ii) un receptor truncado del factor de crecimiento epidérmico (EGFRt) humano separado del CAR por un péptido de auto-escisión T2A, bajo el control de un promotor quimérico compuesto del factor de elongación 1-alfa (EF1-α) promotor/región R del virus linfotrópico T humano 1 (HTLV-1 R) y un elemento regulador post-transcripcional del virus de la hepatitis de la marmota (WPRE). El transgén CAR específico de CD19 consiste en un fragmento variable de cadena sencilla (scFv) derivado de un anticuerpo monoclonal específico de CD19 (FMC63), una región bisagra de IgG4, un domino transmembrana de CD28 y los dominios intracelulares coestimulador de CD137 (4-1BB) y de señalización de CD3ζ. Ambos transgenes, el CAR específico de CD19 y el EGFRt, están precedidos por una secuencia de péptido señal del receptor alfa del factor estimulador de colonias de granulocitos-macrófagos (GMCSFR-alfa) humano. El genoma del vector también contiene una secuencia de empaquetamiento psi, un donante de procesamiento, un *gag* parcial, un elemento de respuesta Rev (RRE), una solapa de ADN, y un aceptor de procesamiento. El vector está flanqueado por repeticiones terminales largas (LTRs) en 5' y 3' y está seudotipado con la glicoproteína G del virus de la estomatitis vesicular (VSV). El material de leucoaféresis es clasificado para la co-selección de 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 2 (IL-2), interleuquina 7 (IL-7) e interleuquina 15 (IL-15). La mezcla de células CD4+/CD8+ después se transducen con el vector lentiviral y se expanden mínimamente en medio de crecimiento que contiene IL-2, IL-7 e IL-15. La suspensión celular consiste en linfocitos T CD4+ y CD8+ que son ≥80% CD3+ y contien ≥10% de células CD3+CAR+. Los linfocitos T transducidos liberan interferón gamma (IFN-γ) mediante co-cultivo con células diana *in vitro*

zoldonrasibum

zoldonrasib

(2*S*)-2-cyclopentyl-2-{(5*S*)-7-[(2*R*,3*R*)-3-cyclopropyl-1-methylaziridine-2-carbonyl]-2,7-diazaspiro[4.4]nonan-2-yl}-*N*-[(1^{2}*M*,2^{2}*S*,4*S*,6^{3}*S*)-1^{2}-{5-(4-cyclopropylpiperazin-1-yl)-2-[(1*S*)-1-methoxyethyl]pyridin-3-yl}-10,10-dimethyl-5,7-dioxo-1^{1}-(2,2,2-trifluoroethyl)-1^{1}*H*-8-oxa-1(5,3)-indola-2(4,2)-morpholina-6(1,3)-[1,2]diazinanacycloundecaphan-4-yl]acetamide

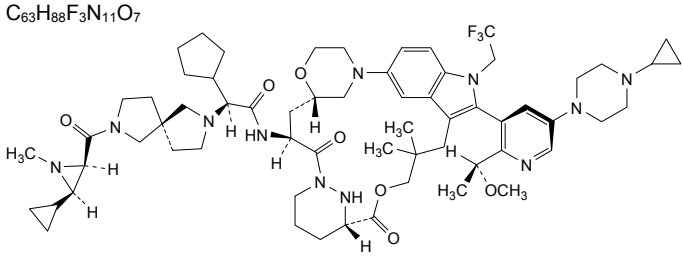
zoldonrasib

(2*S*)-2-cyclopentyl-2-{(5*S*)-7-[(2*R*,3*R*)-3-cyclopropyl-1-méthylaziridine-2-carbonyl]-2,7-diazaspiro[4.4]nonan-2-yl}-*N*-[(1^{2}*M*,2^{2}*S*,4*S*,6^{3}*S*)-1^{2}-{5-(4-cyclopropylpipérazin-1-yl)-2-[(1*S*)-1-méthoxyéthyl]pyridin-3-yl}-10,10-diméthyl-5,7-dioxo-1^{1}-(2,2,2-trifluoroéthyl)-1^{1}*H*-8-oxa-1(5,3)-indola-2(4,2)-morpholina-6(1,3)-[1,2]diazinanacycloundécaphan-4-yl]acétamide

zoldonrasib

(2*S*)-2-ciclopentil-2-{(5*S*)-7-[(2*R*,3*R*)-3-ciclopropil-1-metilaziridina-2-carbonil]-2,7-diazaspiro[4.4]nonan-2-il}-*N*-[(1^{2}*M*,2^{2}*S*,4*S*,6^{3}*S*)-1^{2}-{5-(4-ciclopropilpiperazin-1-il)-2-[(1*S*)-1-metoxietil]piridin-3-il}-10,10-dimetil-5,7-dioxo-1^{1}-(2,2,2-trifluoroetil)-1^{1}*H*-8-oxa-1(5,3)-indola-2(4,2)-morfolina-6(1,3)-[1,2]diazinanacicloundecafan-4-il]acetamida

$C_{63}H_{88}F_3N_{11}O_7$



zoninterferonum alfa-2b #

zoninterferon alfa-2b

immunoglobulin single-chain VH domain (1-115), anti-(human albumin (ALB, human serum albumin, HSA)) [*Homo sapiens* IGHV3-23*04 -(IGHD) -IGHJ1*01, (CDR-Kabat [5.17.6] (31-35.50-66.99-104))], fused via the protease-cleavable peptide linker SGGPALFKSSFPPGS (116-130) with human interferon α-2 (IFN-α-2, interferon α-A, LeIF A, IFNA2, IFNA2A, IFNA2B) (131-295) and via the same linker (296-310) with another identical immunoglobulin single chain VH domain (311-425), anti-(human albumin (ALB, human serum albumin, HSA)) [*Homo sapiens* IGHV3-23*04 -(IGHD) -IGHJ1*01, (CDR-Kabat [5.17.6] (341-345.360-376.409-414))], produced by a cell line derived from human embryonic kidney (HEK293) cells; glycoform alfa

zoninterféron alfa-2b

domaine VH monocaténaire d'immunoglobuline (1-115), anti-(albumine humaine (ALB, sérum-albumine humaine, SAH)) [*Homo sapiens* IGHV3-23*04 -(IGHD) -IGHJ1*01, (CDR-Kabat [5.17.6] (31-35.50-66.99-104))], fusionné via le coupleur peptidique SGGPALFKSSFPPGS clivable par les protéases (116-130) avec l'interféron α-2 humain (IFN-α-2, interféron α-A, LeIF A, IFNA2, IFNA2A, IFNA2B) (131-295) et via le même coupleur peptidique (296-310) avec un autre domaine VH monocaténaire d'immunoglobuline identique (311-425), anti-(albumine humaine (ALB, sérum albumine humaine, SAH)) [*Homo sapiens* IGHV3-23*04 -(IGHD) -IGHJ1*01, (CDR-Kabat [5.17.6] (341-345.360-376.409-414))], produite par une lignée cellulaire dérivée de cellules rénales embryonnaires humaines (HEK293); glycoforme alfa

zoninterferón alfa-2b

dominio VH monocatenario de inmunoglobulina (1-115), anti-[albúmina humana (ALB, albúmina sérica humana, ASH)] [*Homo sapiens* IGHV3-23*04 -(IGHD) -IGHJ1*01, (CDR-Kabat [5.17.6] (31-35.50-66.99-104))], fusionado mediante el conector peptídico SGGPALFKSSFPPGS escindible por proteasa (116-130) con interferón α-2 humano (IFN-α-2, interferón α-A, LeIF A, IFNA2, IFNA2A, IFNA2B) (131-295) y a través del mismo conector (296-310) con otro dominio VH monocatenario de inmunoglobulina idéntico (311-425), anti-(albúmina humana (ALB, albúmina sérica humana, ASH) [*Homo sapiens* IGHV3-23*04 -(IGHD) -IGHJ1*01, (CDR-Kabat [5.17.6] (341-345.360-376.409-414))], producido por una línea celular derivada de células renales embrionarias humanas (HEK293); glicoforma alfa

Sequence / Séquence / Secuencia

```
EVQLVESGGG LVQPGNSLRL SCAASGFTFS KFGMSWVRQA PGKGLEWVSS    50
ISGSGRDTLY AESVKGRFTI SRDNAKTTLY LQMNSLRPED TAVYYCTIGG   100
SLSVSSQGTL VTVSSSGGPA LFKSSFPPGS CDLPQTHSLG SRRTLMLLAQ   150
MRRISLFSCL KDRHDFGFPQ EEFGNQFQKA ETIPVLHEMI QQIFNLFSTK   200
DSSAAWDETL LDKFYTELYQ QLNDLEACVI QGVGVTETPL MKEDSILAVR   250
KYFQRITLYL KEKKYSPCAW EVVRAEIMRS FSLSTNLQES LRSKESGGPA   300
LFKSSFPPGS EVQLVESGGG LVQPGNSLRL SCAASGFTFS KFGMSWVRQA   350
PGKGLEWVSS ISGSGRDTLY AESVKGRFTI SRDNAKTTLY LQMNSLRPED   400
TAVYYCTIGG SLSVSSQGTL VTVSS                              425
```

Peptide linkers / Coupleurs peptidiques / Enlazadores peptídicos
^{116}SGGPALFKSS FPPGS^{130} (1-15)
^{296}SGGPALFKSS FPPGS^{310} (1-15)

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
intra-VH 1: 22-96
intra-IFNA2: 131-228, 159-268
intra-VH 2: 332-406

O-Glycosylation site / Site de O-glycosylation / Posición de O-glicosilación
T236 (predicted), T216 (uncertain), T238 (uncertain)

zovaglutidum

zovaglutide

glucagon-like peptide 1(7-37) [human GLP-1(7-37)] (1-31), (A^{8}>2-MeAla^{2}, G^{22}>E^{16}, K^{34}>R^{28}, R^{36}>G^{30})-variant, fused to the artificial 40-peptide $(GAQP)^{9}$GQKP (32-71), substituted at N^{6} of each of the two lysyl residues 20 and 70 with a (22*S*)-22,40-dicarboxy-10,19,24-trioxo-3,6,12,15-tetraoxa-9,18,23-triazatetracontan-1-oyl group

zovaglutide

peptide similaire au glucagon de type 1(7-37) [GLP-1(7-37) humain] (1-31), variant (A^{8}>2-MeAla^{2}, G22>E16, K^{34}>R^{28}, R^{36}>G^{30}), fusionné au 40-peptide artificiel $(GAQP)^{9}$GQKP (32-71), substitué en N^{6} de chacun des deux résidus lysyles 20 et 70 par un groupe (22*S*)-22,40-dicarboxy-10,19,24-trioxo-3,6,12,15-tétraoxa-9,18,23-triazatétracontan-1-oyle

zovaglutida

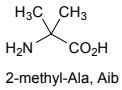
péptido similar al glucagón tipo 1(7-37) [GLP-1(7-37) humano] (1-31), variante (A^{8}>2-MeAla^{2}, G^{22}>E^{16}, K^{34}>R^{28}, R^{36}>G^{30}), fusionado a un 40-péptido artificial $(GAQP)^{9}$GQKP (32-71), sustituido en N^{6} de cada uno de los dos residuos lisilo 20 y 70 con un grupo (22*S*)-22,40-dicarboxi-10,19,24-trioxo-3,6,12,15-tetraoxa-9,18,23-triazatetracontan-1-oilo

$C_{374}H_{584}N_{96}O_{123}$

```
HXEGTFTSDV SSYLEEQAAK EFIAWLVRGG GGAQPGAQPG AQPGAQPGAQ 50
PGAQPGAQPG AQPGAQPGQK P                                71
```

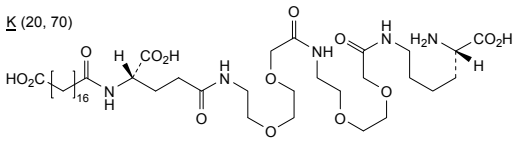
Modified residues / Résidus modifiés / Restos modificados

X (2)



2-methyl-Ala, Aib

K (20, 70)



Electronic structure available on MedNet: https://extranet.who.int/soinn/
Structure électronique disponible sur MedNet: https://extranet.who.int/soinn/
Estructura electrónica disponible en MedNet: https://extranet.who.int/soinn/

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

Recommended International Nonproprietary Names (Rec. INN): List 39
Dénominations communes internationales recommandées (DCI Rec.): Liste 39
Denominaciones Comunes Internacionales Recomendadas (DCI Rec.): Lista 39
(WHO Drug Information, Vol. 12, No. 1, 1998)

p.47 **infliximabum #**

infliximab *insert the following sequence*
infliximab *insérer la séquence suivante*
infliximab *insertese la siguiente secuencia*

Sequence

Heavy chain / Chaîne lourde / Cadena pesada

```
EVKLEESGGG LVQPGGSMKL SCVASGFIFS NHWMNWVRQS PEKGLEWVAE  50
IRSKSINSAT HYAESVKGRF TISRDDSKSA VYLQMTDLRT EDTGVYYCSR 100
NYYGSTYDYW GQGTTLTVSS 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
```

Light chain / Chaîne légère / Cadena ligera

```
DILLTQSPAI LSVSPGERVS FSCRASQFVG SSIHWYQQRT NGSPRLLIKY  50
ASESMSGIPS RFSGSGSGTD FTLSINTVES EDIADYYCQQ SHSWPFTFGS 100
GTNLEVKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

p.54 **rituximabum #**

rituximab *insert the following sequence*
rituximab *insérer la séquence suivante*
rituximab *insertese la siguiente secuencia*

Sequence

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLQQPGAE LVKPGASVKM SCKASGYTFT SYNMHWVKQT PGRGLEWIGA  50
IYPGNGDTSY NQKFKGKATL TADKSSSTAY MQLSSLTSED SAVYYCARST 100
YYGGDWYFNV WGAGTTVTVS AASTKGPSVF PLAPSSKSTS GGTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200
TYICNVNHKP SNTKVDKKAE PKSCDKTHTC PPCPAPELLG GPSVFLFPPK 250
PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY 300
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP 350
QVYTLPPSRD ELTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP 400
VLDSDGSFFL YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG 450
K                                                       451
```

Light chain / Chaîne légère / Cadena ligera

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

Recommended International Nonproprietary Names (Rec. INN): List 40
Dénominations communes internationales recommandées (DCI Rec.): Liste 40
Denominaciones Comunes Internacionales Recomendadas (DCI Rec.): Lista 40
(WHO Drug Information, Vol. 12, No. 2, 1998)

p.207 **daclizumabum #**

daclizumab	*insert the following sequence*
daclizumab	*insérer la séquence suivante*
daclizumab	*insertese la siguiente secuencia*

Sequence:
Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGSSVKV SCKASGYTFT SYRMHWVRQA PGQGLEWIGY  50
INPSTGYTEY NQKFKDKATI TADESTNTAY MELSSLRSED TAVYYCARGG 100
GVFDYWGQGT LVTVSSASTK GPSVFPLAPS SKSTSGGTAA LGCLVKDYFP 150
EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVVTVPSS SLGTQTYICN 200
VNHKPSNTKV DKKVEPKSCD KTHTCPPCPA PELLGGPSVF LFPPKPKDTL 250
MISRTPEVTC VVVDVSHEDP EVKFNWYVDG VEVHNAKTKP REEQYNSTYR 300
VVSVLTVLHQ DWLNGKEYKC KVSNKALPAP IEKTISKAKG QPREPQVYTL 350
PPSRDELTKN QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD 400
GSFFLYSKLT VDKSRWQQGN VFSCSVMHEA LHNHYTQKSL SLSPGK     446
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPST LSASVGDRVT ITCSASSSIS YMHWYQQKPG KAPKLLIYTT  50
SNLASGVPAR FSGSGSGTEF TLTISSLQPD DFATYYCHQR STYPLTFGQG 100
TKVEVKRTVA APSVFIFPPS DEQLKSGTAS VVCLLNNFYP REAKVQWKVD 150
NALQSGNSQE SVTEQDSKDS TYSLSSTLTL SKADYEKHKV YACEVTHQGL 200
SSPVTKSFNR GEC                                         213
```

p.203 **trastuzumabum #**

trastuzumab	*insert the following sequence*
trastuzumab	*insérer la séquence suivante*
trastuzumab	*insertese la siguiente secuencia*

Sequence
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
```

Recommended International Nonproprietary Names (Rec. INN): List 44
Dénominations communes internationales recommandées (DCI Rec.): Liste 44
Denominaciones Comunes Internacionales Recomendadas (DCI Rec.): Lista 44
(WHO Drug Information, Vol. 14, No. 3, 2000)

p.188 **cetuximabum #**

cetuximab	*insert the following sequence*
cétuximab	*insérer la séquence suivante*
cetuximab	*insertese la siguiente secuencia*

Sequence
Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLKQSGPG LVQPSQSLSI TCTVSGFSLT NYGVHWVRQS PGKGLEWLGV  50
IWSGGNTDYN TPFTSRLSIN KDNSKSQVFF KMNSLQSNDT AIYYCARALT 100
YYDYEFAYWG QGTLVTVSAA STKGPSVFPL APSSKSTSGG TAALGCLVKD 150
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY 200
ICNVNHKPSN TKVDKRVEPK SCDKTHTCPP CPAPELLGGP SVFLFPPKPK 250
DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS 300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV 350
YTLPPSREEM TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL 400
DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK  449
```

Light chain / Chaîne légère / Cadena ligera

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

Recommended International Nonproprietary Names (Rec. INN): List 45
Dénominations communes internationales recommandées (DCI Rec.): Liste 45
Denominaciones Comunes Internacionales Recomendadas (DCI Rec.): Lista 45
(WHO Drug Information, Vol. 15, No. 1, 2001)

p.32 **alemtuzumabum #**

alemtuzumab	*insert the following sequence*
alemtuzumab	*insérer la séquence suivante*
alemtuzumab	*insertese la siguiente secuencia*

Sequence
Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLQESGPG LVRPSQTLSL TCTVSGFTFT DFYMNWVRQP PGRGLEWIGF  50
IRDKAKGYTT EYNPSVKGRV TMLVDTSKNQ FSLRLSSVTA ADTAVYYCAR 100
EGHTAAPFDY WGQGSLVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200
TYICNVNHKP SNTKVDKKVE PKSCDKTHTC PPCPAPELLG GPSVFLFPPK 250
PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY 300
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP 350
QVYTLPPSRD ELTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP 400
VLDSDGSFFL YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG 450
K                                                       451
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCKASQNID KYLNWYQQKP GKAPKLLIYN  50
TNNLQTGVPS RFSGSGSGTD FTFTISSLQP EDIATYYCLQ HISRPRTFGQ 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                         214
```

p.55 **adalimumabum #**

adalimumab	*insert the following sequence*
adalimumab	*insérer la séquence suivante*
adalimumab	*insertese la siguiente secuencia*

Sequence:
Heavy chain / Chaîne lourde / Cadena pesada

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

Light chain / Chaîne légère / Cadena ligera

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

Recommended International Nonproprietary Names (Rec. INN): List 46
Dénominations communes internationales recommandées (DCI Rec.): Liste 46
Denominaciones Comunes Internacionales Recomendadas (DCI Rec.): Lista 46
(WHO Drug Information, Vol. 15, No. 3-4, 2001)

p.205 **omalizumabum #**

omalizumab	*insert the following sequence*
omalizumab	*insérer la séquence suivante*
omalizumab	*insertese la siguiente secuencia*

Sequence
Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAVSGYSIT SGYSWNWIRQ APGKGLEWVA  50
SITYDGSTNY NPSVKGRITI SRDDSKNTFY LQMNSLRAED TAVYYCARGS 100
HYFGHWHFAV WGQGTLVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200
TYICNVNHKP SNTKVDKKVE PKSCDKTHTC PPCPAPELLG GPSVFLFPPK 250
PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY 300
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP 350
QVYTLPPSRE EMTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP 400
VLDSDGSFFL YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG 450
K                                                       451
```

Light chain / Chaîne légère / Cadena ligera

```
DIQLTQSPSS LSASVGDRVT ITCRASQSVD YDGDSYMNWY QQKPGKAPKL  50
LIYAASYLES GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YCQQSHEDPY 100
TFGQGTKVEI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL NNFYPREAKV 150
QWKVDNALQS GNSQESVTEQ DSKDSTYSLS STLTLSKADY EKHKVYACEV 200
THQGLSSPVT KSFNRGEC                                    218
```

Recommended International Nonproprietary Names (Rec. INN): List 48
Dénominations communes internationales recommandées (DCI Rec.): Liste 48
Denominaciones Comunes Internacionales Recomendadas (DCI Rec.): Lista 48
(WHO Drug Information, Vol. 16, No. 3, 2002)

p.266 **bevacizumabum #**

bevacizumab	*insert the following sequence*
bévacizumab	*insérer la séquence suivante*
bevacizumab	*insertese la siguiente secuencia*

Sequence

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAASGYTFT NYGMNWVRQA PGKGLEWVGW  50
INTYTGEPTY AADFKRRFTF SLDTSKSTAY LQMNSLRAED TAVYYCAKYP 100
HYYGSSHWYF DVWGQGTLVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC 150
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG 200
TQTYICNVNH KPSNTKVDKK VEPKSCDKTH TCPPCPAPEL LGGPSVFLFP 250
PKPKDTLMIS RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE 300
QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR 350
EPQVYTLPPS REEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT 400
PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLS 450
PGK                                                     453
```

Light chain / Chaîne légère / Cadena ligera

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

Recommended International Nonproprietary Names (Rec. INN): List 51
Dénominations communes internationales recommandées (DCI Rec.): Liste 51
Denominaciones Comunes Internacionales Recomendadas (DCI Rec.): Lista 51
(WHO Drug Information, Vol. 18, No. 1, 2004)

p. 85 **belimumabum #**

belimumab	*insert the following sequence*
bélimumab	*insérer la séquence suivante*
belimumab	*insertese la siguiente secuencia*

Sequence

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLQQSGAE VKKPGSSVRV SCKASGGTFN NNAINWVRQA PGQGLEWMGG  50
IIPMFGTAKY SQNFQGRVAI TADESTGTAS MELSSLRSED TAVYYCARSR 100
DLLLFPHHAL SPWGRGTMVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC 150
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG 200
TQTYICNVNH KPSNTKVDKK VEPKSCDKTH TCPPCPAPEL LGGPSVFLFP 250
PKPKDTLMIS RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE 300
QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR 350
EPQVYTLPPS RDELTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT 400
PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLS 450
PGK                                                     453
```

Light chain / Chaîne légère / Cadena ligera

```
SSELTQDPAV SVALGQTVRV TCQGDSLRSY YASWYQQKPG QAPVLVIYGK  50
NNRPSGIPDR FSGSSSGNTA SLTITGAQAE DEADYYCSSR DSSGNHWVFG 100
GGTELTVLGQ PKAAPSVTLF PPSSEELQAN KATLVCLISD FYPGAVTVAW 150
KADSSPVKAG VETTTPSKQS NNKYAASSYL SLTPEQWKSH RSYSCQVTHE 200
GSTVEKTVAP TECS                                        214
```

p.102 **pertuzumabum #**

pertuzumab	*insert the following sequence*
pertuzumab	*insérer la séquence suivante*
pertuzumab	*insertese la siguiente secuencia*

Sequence
Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAASGFTFT DYTMDWVRQA PGKGLEWVAD  50
VNPNSGGSIY NQRFKGRFTL SVDRSKNTLY LQMNSLRAED TAVYYCARNL 100
GPSFYFDYWG QGTLVTVSSA STKGPSVFPL APSSKSTSGG TAALGCLVKD 150
YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY 200
ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP CPAPELLGGP SVFLFPPKPK 250
DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS 300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV 350
YTLPPSREEM TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL 400
DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK  449
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS SASVGDRVTI TCKASQDVSI GVAWYQQKPG KAPKLLIYSA  50
SYRYTGVPSR FSGSGSGTDF TLTISSLQPE DFATYYCQQY YIYPYTFGQG 100
TKVEIKRTVA APSVFIFPPS DEQLKSGTAS VVCLLNNFYP REAKVQWKVD 150
NALQSGNSQE SVTEQDSKDS TYSLSSTLTL SKADYEKHKV YACEVTHQGL 200
SSPVTKSFNR GEC                                          213
```

Recommended International Nonproprietary Names (Rec. INN): List 52
Dénominations communes internationales recommandées (DCI Rec.): Liste 52
Denominaciones Comunes Internacionales Recomendadas (DCI Rec.): Lista 52
(WHO Drug Information, Vol. 18, No. 3, 2004)

p.259 **ranibizumabum #**

ranibizumab	*insert the following sequence*
ranibizumab	*insérer la séquence suivante*
ranibizumab	*insertese la siguiente secuencia*

Sequence
Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAASGYDFT HYGMNWVRQA PGKGLEWVGW  50
INTYTGEPTY AADFKRRFTF SLDTSKSTAY LQMNSLRAED TAVYYCAKYP 100
YYYGTSHWYF DVWGQGTLVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC 150
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG 200
TQTYICNVNH KPSNTKVDKK VEPKSCDKTH L                      231
```

Light chain / Chaîne légère / Cadena ligera

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

p.261 **tadekinigum alfa #**

tadekinig alfa	*replace the chemical name and sequence by the following ones*
tadékinig alfa	*remplacer la séquence par la suivante*
tadekinig alfa	*sustitúyase la secuencia por la siguiente*

extracellular part of the human Interleukin-18-binding protein (IL-18BP)

Sequence / Séquence / Secuencia

```
TPVSQTTTAA TASVRSTKDP CPSQPPVFPA AKQCPALEVT WPEVEVPLNG  50
TLSLSCVACS RFPNFSILYW LGNGSFIEHL PGRLWEGSTS RERGSTGTQL 100
CKALVLEQLT PALHSTNFSC VLVDPEQVVQ RHVVLAQLWA GLRATLPPTQ 150
EALPSSHSSP QQQG                                        164
```

p.2662 **tocilizumabum #**

tocilizumab	*insert the following sequence*
tocilizumab	*insérer la séquence suivante*
tocilizumab	*insertese la siguiente secuencia*

Sequence
Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLQESGPG LVRPSQTLSL TCTVSGYSIT SDHAWSWVRQ PPGRGLEWIG  50
YISYSGITTY NPSLKSRVTM LRDTSKNQFS LRLSSVTAAD TAVYYCARSL 100
ARTTAMDYWG QGSLVTVSSA 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 KSLSLSPG   448
```

Light chain / Chaîne légère / Cadena ligera

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

Recommended International Nonproprietary Names (Prop. INN): List 53
Dénominations communes internationales recommandées (DCI Rec.): Liste 53
Denominaciones Comunes Internacionales Recomendadas (DCI Rec.): Lista 53
(WHO Drug Information, Vol. 19, No. 1, 2005)

p.80 **golimumabum #**

golimumab	*insert the following sequence*
golimumab	*insérer la séquence suivante*
golimumab	*insertese la siguiente secuencia*

Sequence
Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVESGGG VVQPGRSLRL SCAASGFIFS SYAMHWVRQA PGNGLEWVAF  50
MSYDGSNKKY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARDR 100
GIAAGGNYYY YGMDVWGQGT TVTVSSASTK GPSVFPLAPS SKSTSGGTAA 150
LGCLVKDYFP EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVVTVPSS 200
SLGTQTYICN VNHKPSNTKV DKKVEPKSCD KTHTCPPCPA PELLGGPSVF 250
LFPPKPKDTL MISRTPEVTC VVVDVSHEDP EVKFNWYVDG VEVHNAKTKP 300
REEQYNSTYR VVSVLTVLHQ DWLNGKEYKC KVSNKALPAP IEKTISKAKG 350
QPREPQVYTL PPSRDELTKN QVSLTCLVKG FYPSDIAVEW ESNGQPENNY 400
KTTPPVLDSD GSFFLYSKLT VDKSRWQQGN VFSCSVMHEA LHNHYTQKSL 450
SLSPGK                                                 456
```

Light chain / Chaîne légère / Cadena ligera

```
EIVLTQSPAT LSLSPGERAT LSCRASQSVY SYLAWYQQKP GQAPRLLIYD  50
ASNRATGIPA RFSGSGSGTD FTLTISSLEP EDFAVYYCQQ RSNWPPFTFG 100
PGTKVDIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK 150
VDNALQSGNS QESVTEQDSK DSTYSLSSTL TLSKADYEKH KVYACEVTHQ 200
GLSSPVTKSF NRGEC                                       215
```

Recommended International Nonproprietary Names (Rec. INN): List 55
Dénominations communes internationales recommandées (DCI Rec.): Liste 55
Denominaciones Comunes Internacionales Recomendadas (DCI Rec.): Lista 55
(WHO Drug Information, Vol. 20, No. 1, 2006)

p.46 **ofatumumabum #**

ofatumumab	*insert the following structure*
ofatumumab	*insérer la structure suivante*
ofatumumab	*insertese la siguiente estructura*

Sequence
Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGRSLRL SCAASGFTFN DYAMHWVRQA PGKGLEWVST  50
ISWNSGSIGY ADSVKGRFTI SRDNAKKSLY LQMNSLRAED TALYYCAKDI 100
QYGNYYYGMD 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
```

Light chain / Chaîne légère / Cadena ligera

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

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H 22-96 149-205 266-326 372-430
22''-96'' 149''-205'' 266''-326'' 372''-430''
Intra-L 23'-88' 134'-194'
23'''-88''' 134'''-194'''
Inter-H-L 225-214' 225''-214'''
Inter-H-H 231-231'' 234-234''

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
302, 302''

Recommended International Nonproprietary Names (Rec. INN): List 59
Dénominations communes internationales recommandées (DCI Rec.): Liste 59
Denominaciones Comunes Internacionales Recomendadas (DCI Rec.): Lista 59
(WHO Drug Information, Vol. 22, No. 1, 2008)

p.74 **certolizumabum pegolum #**

certolizumab pegol	*insert the following sequence*
certolizumab pégol	*insérer la séquence suivante*
certolizumab pegol	*insertese la siguiente secuencia*

Sequence

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAASGYVFT DYGMNWVRQA PGKGLEWMGW  50
INTYIGEPIY ADSVKGRFTF SLDTSKSTAY LQMNSLRAED TAVYYCARGY 100
RSYAMDYWGQ GTLVTVSSAS TKGPSVFPLA PSSKSTSGGT AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTQTYI 200
CNVNHKPSNT KVDKKVEPKS CDKTHTCAA                       229
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCKASQNVG TNVAWYQQKP GKAPKALIYS  50
ASFLYSGVPY RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YNIYPLTFGQ 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                       214
```

Recommended International Nonproprietary Names (Rec. INN): List 79
Dénominations communes internationales recommandées (DCI Rec.): Liste 79
Denominaciones Comunes Internacionales Recomendadas (DCI Rec.): Lista 79
(WHO Drug Information, Vol. 32, No. 1, 2018)

p.148 **pegdarbepoetinum beta #**

pegdarbepoetin beta	*replace the structure by the following one*
pegdarbépoétine bêta	*remplacer la structure par la suivante*
pegdarbepoetina beta	*sustitúyase la estructura por la siguiente*

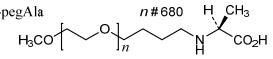
Sequence / Séquence / Secuencia

```
APPRLICDSR VLERYLLEAK EAENITTGCN ETCSLNENIT VPDTKVNFYA  50
WKRMEVGQQA VEVWQGLALL SEAVLRGQAL LVNSSQVNET LQLHVDKAVS 100
GLRSLTTLLR ALGAQKEAIS PPDAASAAPL RTITADTFRK LFRVYSNFLR 150
GKLKLYTGEA CRTGD                                       165
```

Disulfide bridge location / Position du pont disulfure / Posición del puente disulfuro
7-161 29-33

Modified residue / Résidu modifié / Resto modificado

A (1) = *N*-pegAla *n* ≈ 680



Glycosylation site (N, S) / Site de glycosylation (N, S) / Posición de glicosilatión (N, S)
Asn-24 Asn-30 Asn-38 **Asn-83** Asn-88 Ser-126

p.157 **rezafungini acetas**

rezafungin acetate	*replace the chemical name by the following one*
acétate de rézafungine	*remplacer le nom chimique par le suivant*
acetato de rezafungina	*sustitúyase el nombre químico por el siguiente*

N$^{5.1}$,6-anhydro[(4*R*,5*R*)-4-hydroxy-***N*^{2}**-[3^{4}-(pentyloxy)[1^{1},2^{1}:2^{4},3^{1}-terphenyl]-1^{4}-**carbonyl**]-5-[2-(trimethylazaniumyl)**ethoxy**]-L-ornithyl-L-threonyl-*trans*-4-hydroxy-L-prolyl-(4*S*)-4-hydroxy-4-(4-hydroxyphenyl)-L-threonyl-L-threonyl-(3*S*,4S)-3-hydroxy-4-methyl-L-proline] acetate

acétate de *N*$^{5.1}$,6-anhydro[(4*R*,5*R*)-4-hydroxy-***N*^{2}**-[3^{4}-(pentyloxy)[1^{1},2^{1}:2^{4},3^{1}-terphényl]-1^{4}-**carbonyl**]-5-[2-(triméthylazaniumyl)**éthoxy**]-L-ornithyl-L-thréonyl-*trans*-4-hydroxy-L-prolyl-(4*S*)-4-hydroxy-4-(4-hydroxyphényl)-L-thréonyl-L-thréonyl-(3*S*,4S)-3-hydroxy-4-méthyl-L-proline]

acetato de *N*$^{5.1}$,6-anhidro[(4*R*,5*R*)-4-hidroxi-***N*^{2}**-[3^{4}-(pentiloxi)[1^{1},2^{1}:2^{4},3^{1}-terfenil]-1^{4}-**carbonil**]-5-[2-

(trimetilazaniumil)**etoxi**]-L-ornitil-L-treonil-*trans*-4-hidroxi-L-prolil-(4*S*)-4-hidroxi-4-(4-hidroxifenil)-L-treonil-L-treonil-(3*S*,4S)-3-hidroxi-4-metil-L-prolina]

Recommended International Nonproprietary Names (Rec. INN): List 84
Dénominations communes internationales recommandées (DCI Rec.): Liste 84
Denominaciones Comunes Internacionales Recomendadas (DCI Rec.): Lista 84
(WHO Drug Information, Vol. 34, No. 3, 2020)

p.696 **belzupacapum sarotalocanum #**

-697 belzupacap sarotalocan *replace the chemical name and sequence by the following ones*

belzupacap sarotalocan *remplacer le nom chimique et la séquence par les suivants*

belzupacap sarotalocán *sustitúyase el nombre químico y la secuencia por los siguientes*

a modified human papillomavirus (HPV) type 16-derived empty nanoparticle, 55 nm in diameter conjugated to approximately 200 molecules of a phthalocyanine-based photosensitizer (*sarotalocan* group). Each nanoparticle is comprised of 72 capsomeres, made of 5 molecules of modified viral capsid protein L1 [~~P^{78}>R, T^{176}>N,~~ D^{273}>T, N^{285}>T, S^{288}>N, ~~T^{353}>P, T^{389}>S~~] and one molecule of viral capsid protein L2;
human papilloma virus type 16 (HPV16) capsid, a spherical shell of 72 self-assembling pentagonal $(L1)_5(L2)_1$ capsomere units comprising the recombinant viral capsid proteins L1 ([~~P^{78}>R, T^{176}>N,~~ D^{273}>T, N^{285}>T, S^{288}>N, ~~T^{353}>P, T^{389}>S~~]-modified) and L2, conjugated to approximately 200 *sarotalocan* groups (near infrared absorbing dye) at N^6 of lysine residues; produced by human embryonic kidney 293 (HEK293) cells

nanoparticule vide dérivée du virus du papillomavirus humain 16 (HPV) modifié, 55 nm de diamètre, conjuguée à approximativement 200 molécules d'un photosensibilisant à base de **phtalocyanine** (groupe *sarotalocan*). Chaque particule est composée de 72 capsomères, faits de 5 molécules de protéine de capside virale L1 modifiée [~~P^{78}>R, T^{176}>N,~~ D^{273}>T, N^{285}>T, S^{288}>N, ~~T^{353}>P, T^{389}>S~~] et d'une molécule de protéine de capside virale L2;
capside du virus du papillomavirus humain 16 (HPV16), une coquille sphérique de 72 unités de capsomère pentagonal $(L1)_5(L2)_1$ s'auto-assemblant comprenant les protéines recombinantes de capside virale L1 ([~~P^{78}>R, T^{176}>N,~~ D^{273}>T, N^{285}>T, S^{288}>N, ~~T^{353}>P, T^{389}>S~~]-modifiée) et L2, conjuguées à environ 200 groupes *sarotalocan* (colorant absorbant les proches infrarouges) en N^6 des résidus lysine; produite par des cellules rénales embryonnaires humaines (HEK293)

nanopartícula vacía derivada del virus del papilomavirus humano 16 (HPV) modificado, 55nm de diámetro, conjugado con aproximadamente 200 moléculas de un fotosensibilizante a base de ftalocianina (grupo *sarotalocán*). Cada partícula se compone de 72 capsómeros, hechos de 5 moléculas de proteína de cápside viral L1 modificada [~~P^{78}>R, T^{176}>N,~~ D^{273}>T, N^{285}>T, S^{288}>N, ~~T^{353}>P, T^{389}>S~~] y de una molécula de proteína de cápside viral L2;
cápside del virus del papilomavirus humano 16 (HPV16), una cavidad esférica de 72 unidades de capsómero pentagonal $(L1)_5(L2)_1$ que se autoensamblan abarcando las proteínas recombinantes de cápside viral L1 ([~~P^{78}>R, T^{176}>N,~~ D^{273}>T, N^{285}>T, S^{288}>N, ~~T^{353}>P, T^{389}>S~~]-modificada) y L2, conjugadas

aproximadamente a 200 grupos *sarotalocán* (colorante absorbente infrarrojo cercano) en N^6 de los residuos de lisina; producido por las células renales embrionarias humanas (HEK293)

Sequence / Séquence / Secuencia
major capsid protein L1:

```
MSLWLPSEAT VYLPPVPVSK VVSTDEYVAR TNIYYHAGTS RLLAVGHPYF   50
PIKKPNNNKI LVPKVSGLQY RVFRIHLPDP NKFGFPDTSF YNPDTQRLVW  100
ACVGVEVGRG QPLGVGISGH PLLNKLDDTE NASAYAANAG VDNRECISMD  150
YKQTQLCLIG CKPPIGEHWG KGSPCTNVAV NPGDCPPLEL INTVIQDGDM  200
VDTGFGAMDF TTLQANKSEV PLDICTSICK YPDYIKMVSE PYGDSLFFYL  250
RREQMFVRHL FNRAGAVGEN VPTDLYIKGS GSTATLANSN YFPTPSGSMV  300
TSDAQIFNKP YWLQRAQGHN NGICWGNQLF VTVVDTTRST NMSLCAAIST  350
SETTYKNTNF KEYLRHGEEY DLQFIFQLCK ITLTADVMTY IHSMNSTILE  400
DWNFGLQPPP GGTLEDTYRF VTSQAIACQK HTPPAPKEDP LKKYTFWEVN  450
LKEKFSADLD QFPLGRKFLL QAGLKAKPKF TLGKRKATPT TSSTSTTAKR  500
KKRKL                                                   505
```

cyclic pentamer (175-428',175'-428",175"-428"',175"'-428"",175""-428)-disulfide, with further intermolecular disulfide bridges of unknown position linking the 72 pentamers together

minor capsid protein L2:

```
MRHKRSAKRT KRASATQLYK TCKQAGTCPP DIIPKVEGKT IAEQILQYGS   50
MGVFFGGLGI GTGSGTGGRT GYIPLGTRPP TATDTLAPVR PPLTVDPVGP  100
SDPSIVSLVE ETSFIDAGAP TSVPSIPPDV SGFSITTSTD TTPAILDINN  150
TVTTVTTHNN PTFTDPSVLQ PPTPAETGGH FTLSSSTIST HNYEEIPMDT  200
FIVSTNPNTV TSSTPIPGSR PVARLGLYSR TTQQVKVVDP AFVTTPTKLI  250
TYDNPAYEGI DVDNTLYFSS NDNSINIAPD PDFLDIVALH RPALTSRRTG  300
IRYSRIGNKQ TLRTRSGKSI GAKVHYYYDL STIDPAEEIE LQTITPSTYT  350
TTSHAASPTS INNGLYDIYA DDFITDTSTT PVPSVPSTSL SGYIPANTTI  400
PFGGAYNIPL VSGPDIPINI TDQAPSLIPI VPGSPQYTII ADAGDFYLHP  450
SYYMLRKRRK RLPYFFSDVS LAA                               473
```

intramolecular disulfide bridge: 22-28

Glycosylation sites / Sites de glycosylation / Posiciones de glicosilación
None / aucune / ninguna

Recommended International Nonproprietary Names (Rec. INN): List 90
Dénominations communes internationales recommandées (DCI Rec.): Liste 90
Denominaciones Comunes Internacionales Recomendadas (DCI Rec.): Lista 90
(WHO Drug Information, Vol. 37, No. 3, 2023)

p.786 **maridebartum #**
maridebart
maridébart
maridebart

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

immunoglobulin G1-kappa , anti-[*Homo sapiens* GIPR (gastric inhibitory polypeptide receptor)], *Homo sapiens* monoclonal antibody;
gamma1 heavy chain *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV3-33*01 (92.9%) -(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, G1v64 CH2 C36, G1v54-30 CH2 C83, G84.4, C85 (CH1 R120>K (217) (121-218), hinge 1-15 (219-233), CH2 E36>C (275), R83>C (295), N84.4>G (300), V85>C (305) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-15*01 (97.9%) -IGKJ4*01 (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')]; dimer (229-229":232-232")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, **non-glycosylated**

immunoglobuline G1-kappa, anti-[*Homo sapiens* GIPR (récepteur du polypeptide inhibiteur gastrique)], anticorps monoclonal *Homo sapiens*;

chaîne lourde gamma1 *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV3-33*01 (92.9%) -(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, G1v64 CH2 C36, G1v54-30 CH2 C83, G84.4, C85 (CH1 R120>K (217) (121-218), charnière 1-15 (219-233), CH2 E36>C (275), R83>C (295), N84.4>G (300), V85>C (305) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-15*01 (97.9%) -IGKJ4*01 (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')]; dimère (229-229'':232-232'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), **non-glycosylé**

inmunoglobulina G1-kappa, anti-[*Homo sapiens* GIPR (receptor del polipéptido inhibidor gástrico)], anticuerpo monoclonal *Homo sapiens*;
cadena pesada gamma1 *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV3-33*01 (92.9%) -(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, G1v64 CH2 C36, G1v54-30 CH2 C83, G84.4, C85 (CH1 R120>K (217) (121-218), bisagra 1-15 (219-233), CH2 E36>C (275), R83>C (295), N84.4>G (300), V85>C (305) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-15*01 (97.9%) -IGKJ4*01 (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')]; dímero (229-229'':232-232'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), **no glicosilado**

p.787-788

maridebartum cafraglutidum #
maridebart cafraglutide *replace the chemical name by the following one*
maridébart cafraglutide *remplacer le nom chimique par le suivant*
maridebart cafraglutida *sustitúyase el nombre químico por el siguiente*

immunoglobulin G1-kappa , anti-[*Homo sapiens* GIPR (gastric inhibitory polypeptide receptor)], *Homo sapiens* monoclonal antibody; conjugated with two identical glucagon-like peptide 1 (GLP-1) analogues;
gamma1 heavy chain *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV3-33*01 (92.9%) -(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, G1v64 CH2 C36, G1v54-30 CH2 C83, G84.4, C85 (CH1 R120>K (217) (121-218), hinge 1-15 (219-233), CH2 E36>C (275), R83>C (295), N84.4>G (300), V85>C (305) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-15*01 (97.9%) -IGKJ4*01 (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')]; dimer (229-229'':232-232'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, **non-glycosylated**; 275,275''-bis(thioether) conjugated to a glucagon-like peptide 1 (GLP-1) analogue (GCG (glucagon) 98-126, GLP-1 7-35 A8>methylalanine (2), V16>Y (10), G22>E (16)), via a fused 18-mer linker (diglycyl-tris(tetraglycyl-seryl)-lysinamide

immunoglobuline G1-kappa, anti-[*Homo sapiens* GIPR (récepteur du polypeptide inhibiteur gastrique)], anticorps monoclonal *Homo sapiens*; conjugué avec deux peptides identiques analogues du peptide-1 similaire au glucagon(GLP-1);
chaîne lourde gamma1 *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV3-33*01 (92.9%) -(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, G1v64 CH2 C36, G1v54-30 CH2 C83, G84.4, C85 (CH1 R120>K (217) (121-218), charnière 1-15 (219-233), CH2 E36>C (275), R83>C (295), N84.4>G (300), V85>C (305) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-15*01 (97.9%) -IGKJ4*01 (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')]; dimère (229-229":232-232")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), **non-glycosylé**; 275,275"-bis(thioéther) conjugué à un analogue du glucagon-like peptide 1 (GLP-1)(GCG (glucagon) 98-126, GLP-1 7-35 A8>méthylalanine (2), V16>Y (10), G22>E (16)), via un linker fusionné de 18-mer (diglycyl-tris(tétraglycyl-séryl)-lysinamide)

inmunoglobulina G1-kappa, anti-[*Homo sapiens* GIPR (receptor del polipéptido inhibidor gástrico)], anticuerpo monoclonal *Homo sapiens*; conjugado con dos péptidos idénticos análogos del péptido tipo glucagón 1 (GLP-1);
cadena pesada gamma1 *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV3-33*01 (92.9%) -(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, G1v64 CH2 C36, G1v54-30 CH2 C83, G84.4, C85 (CH1 R120>K (217) (121-218), bisagra 1-15 (219-233), CH2 E36>C (275), R83>C (295), N84.4>G (300), V85>C (305) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-15*01 (97.9%) -IGKJ4*01 (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')]; dímero (229-229":232-232")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), **no glicosilado**; 275,275"-bis(tioéter) conjugado con un análogo del péptido de tipo glucagón 1 (GLP-1)(GCG (glucagón) 98-126, GLP-1 7-35 A8>metilalanina (2), V16>Y (10), G22>E (16)), a través de un enlace fusionado de 18-mer (diglicil-tris(tetraglicil-seril)-lisinamida)

Recommended International Nonproprietary Names (Rec. INN): List 92
Dénominations communes internationales recommandées (DCI Rec.): Liste 92
Denominaciones Comunes Internacionales Recomendadas (DCI Rec.): Lista 92
(WHO Drug Information, Vol. 38, No. 3, 2024)

p.792 **setidegrasibum**

setidegrasib
sétidegrasib
setidegrasib

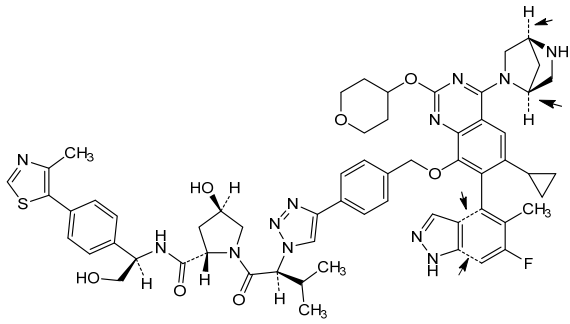
replace the chemical name and structure by the following ones
remplacer le nom chimique et la structure par les suivants
sustitúyase el nombre químico y la estructura por los siguientes

(**1^{4}*M***,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

(**1^4*M*,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

(**1^4*M*,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



Recommended International Nonproprietary Names (Rec. INN): List 93
Dénominations communes internationales recommandées (DCI Rec.): Liste 93
Denominaciones Comunes Internacionales Recomendadas (DCI Rec.): Lista 93
(WHO Drug Information, Vol. 39, No. 1, 2025)

p.292 **tabirafuspum alfa #**

tabirafusp alfa	*replace the structure by the following one*
tabirafusp alfa	*remplacer la structure par la suivante*
tabirafusp alfa	*sustitúyase la estructura por la siguiente*

Disulfide bridges location

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra VEGFR1/2-heavy chain: 30-79, 124-185, 237-311, 361-417, 478-538, 584-642
30''-79'', 124''-185'', 237''-311'', 361''-417'', 478''-538'', 584''-642''
Intra kappa light chain: 23'-87', 133'-193', 23'''-87''', 133'''-193'''
Inter VEGFR1/2-heavy chain: 443-443'', 446-446''
Inter heavy chain-light chain: 437-213', **437''-213'''**

p.295 **tabirafuspum alfa tedromerum #**

tabirafusp alfa tedromer	*replace the structure by the following one*
tabirafusp alfa tédromère	*remplacer la structure par la suivante*
tabirafusp alfa tedrómero	*sustitúyase la estructura por la siguiente*

Disulfide bridges location

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra VEGFR1/2-heavy chain: 30-79, 124-185, 237-311, 361-417, 478-538, 584-642
30''-79'', 124''-185'', 237''-311'', 361''-417'', 478''-538'', 584''-642''
Intra kappa light chain: 23'-87', 133'-193', 23'''-87''', 133'''-193'''
Inter VEGFR1/2-heavy chain: 443-443'', 446-446''
Inter heavy chain-light chain: 437-213', **437''-213'''**

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.