

International Nonproprietary Names for Pharmaceutical Substances (INN)

RECOMMENDED International Nonproprietary Names: List 90

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 90

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 90

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); Resolución 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

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immunoglobulin chain VH-V-kappa-VH'-V-lambda homodimer, anti-[*Homo sapiens* FCGR3A (Fc gamma receptor IIIa, CD16a)] and anti-[*Homo sapiens* TNFRSF8 (TNF receptor superfamily member 8, CD30)], monoclonal antibody *Homo sapiens* and *Mus musculus* VH-V-kappa-VH'-V-lambda chain non covalent head to tail homodimer, bispecific, tetravalent; IG chain VH-V-kappa-VH'-V-lambda *Homo sapiens* and *Mus musculus* (1-483) [anti-FCGR3A VH (*Homo sapiens*IGHV1-46*01 (98.0%) -(IGHD) -IGHJ5*01 (92.3%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -9-mer tris(bisglycyl-seryl) linker (121-129) -anti-TNFRSF8 V-KAPPA (*Mus musculus* IGKV6-15*01 (93.7%) -(IGHD) -IGKJ1*02 (90.0%) K127>N (236), CDR-IMGT [6.3.9] (156-161.179-181.218-226)) (130-236) -9-mer tris(bisglycyl-seryl) linker (237-245) -anti-TNFRSF8 VH' (*Mus musculus* IGHV1-4*01 (87.8%) -(IGHD) -IGHJ3*01 (86.7%) L123>T (363), A128>S (368), CDR-IMGT [8.8.16] (271-278.296-303.342-357)) (246-368) -9-mer tris(bisglycyl-seryl) linker (369-377) -anti-FCGR3A V-LAMBDA (*Homo sapiens* IGLV3-9*01 (83.7%) -(IGHD) -IGLJ2*01 (91.7%), CDR-IMGT [6.3.9] (403-408.426-428.465-473)) (378-483)]; homodimer head to tail non covalent, produced in Chinese hamster ovary (CHO) cells, cell line CHO-DG44, glycoform alfa

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immunoglobuline chaîne VH-V-kappa-VH'-V-lambda homodimère, anti-[*Homo sapiens* FCGR3A (Fc gamma récepteur IIIa, CD16a)] et anti-[*Homo sapiens* TNFRSF8 (membre 8 de la superfamille des récepteurs du TNF, CD30)], anticorps monoclonal chaîne *Homo sapiens* et *Mus musculus* VH-V-kappa-VH'-V-lambda homodimère tête-bêche non covalent, bispécifique, tétravalent; IG chaîne VH-V-kappa-VH'-V-lambda *Homo sapiens* and *Mus musculus* (1-483) [anti-FCGR3A VH (*Homo sapiens*IGHV1-46*01 (98.0%) -(IGHD) -IGHJ5*01 (92.3%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -9-mer tris(bisglycyl-séryl) linker (121-129) -anti-TNFRSF8 V-KAPPA (*Mus musculus* IGKV6-15*01 (93.7%) -(IGHD) -IGKJ1*02 (90.0%) K127>N (236), CDR-IMGT [6.3.9] (156-161.179-181.218-226)) (130-236) -9-mer tris(bisglycyl-séryl) linker (237-245) -anti-TNFRSF8 VH' (*Mus musculus* IGHV1-4*01 (87.8%) -(IGHD) -IGHJ3*01 (86.7%) L123>T (363), A128>S (368), CDR-IMGT [8.8.16] (271-278.296-303.342-357)) (246-368) -9-mer tris(bisglycyl-séryl) linker (369-377) -anti-FCGR3A V-LAMBDA (*Homo sapiens* IGLV3-9*01 (83.7%) -(IGHD) -IGLJ2*01 (91.7%), CDR-IMGT [6.3.9] (403-408.426-428.465-473)) (378-483)]; homodimère tête-bêche non covalent, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-DG44, glycoforme alfa

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inmunoglobulina VH-V-kappa-VH'-V-lambda homodímero, anti-[*Homo sapiens* FCGR3A (Fc gamma receptor IIIa, CD16a)] y anti-[*Homo sapiens* TNFRSF8 (miembro 8 de la superfamilia de los receptores del TNF, CD30)], anticuerpo monoclonal *Homo sapiens* y *Mus musculus* VH-V-kappa-VH'-V-lambda homodímero de cabeza a cola no covalente, biespecífico, tetravalente; IG cadena VH-V-kappa-VH'-V-lambda *Homo sapiens* and *Mus musculus* (1-483) [anti-FCGR3A VH (*Homo sapiens* IGHV1-46*01 (98.0%) -(IGHD) -IGHJ5*01 (92.3%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -9-mer tris(bisglicil-seril) enlace (121-129) -anti-TNFRSF8 V-KAPPA (*Mus musculus* IGKV6-15*01 (93.7%) -(IGHD) -IGKJ1*02 (90.0%) K127>N (236), CDR-IMGT [6.3.9] (156-161.179-181.218-226)) (130-236) -9-mer tris(bisglicil-seril) enlace (237-245) -anti-TNFRSF8 VH' (*Mus musculus* IGHV1-4*01 (87.8%) -(IGHD) -IGHJ3*01 (86.7%) L123>T (363), A128>S (368), CDR-IMGT [8.8.16] (271-278.296-303.342-357)) (246-368) -9-mer tris(bisglicil-seril) enlace (369-377) -anti-FCGR3A V-LAMBDA (*Homo sapiens* IGLV3-9*01 (83.7%) -(IGHD) -IGLJ2*01 (91.7%), CDR-IMGT [6.3.9] (403-408.426-428.465-473)) (378-483)]; homodímero de dabez a cola no covalente, producido en las células ováricas de hámster chino (CHO), línea celular CHO-DG44, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

QVQLVQSGAE VKKPGESLKV SCKASGYTFT SYMHVWRQA PGQGLEWMMGI 50
 INPSGGSTSY AQKFQGRVTM TRDTSTSTVY MELSSLRSED TAVYYCARGS 100
 AYYDFADYW GQGTLVTVSS GSGSGSGGSD IVMTQSPKFM STSVGRDRTV 150
 TCKASQNVGT NVAWFQKQKPG QSPKVLIIYA SYRYSVDPDR FTGSGSGTDF 200
 TLTISMVQSE DLAEYFCQQY HTYPLTFGGG TKLEINGGSG GSGGSQVQLQ 250
 QSGAELARPQ ASVKMSCKAS GYFTFTYTIH WVRQRPQHD L EWIGYINPSS 300
 GYSDYNQNFK GKTTLTADKS SNTAYMQLNS LTSSESAVY CARRADYGNV 350
 EYTFAYWQ G TTVTVSSGG SGGSGGSSYV LTQPSSVVA PGQTATISCG 400
 GHNIGSKNVH WYQQRPGQSP VLVIYQDNKR PSGIPERFSG SNSGNATLTL 450
 ISGTQAMDEA DYQCQWWDNY SVLFGGGTKL TVL 483

Post-translational modifications

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

Intra chain (C23-C104) 22-96 152-217 267-341 399-464
 22'-96' 152'-217' 267'-341' 399'-464'

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-oxoprolylo)
 VH Q1: 1, 1'

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

VH Y112.2
 350, 350' (12-20% Glycosylated / 12-20% Glycosylé / 12-20% Glicosilado)
 (Hex1HexNAc1NeuAc1 (<13%), Hex1HexNAc1 (<5%), Hex1HexNAc1NeuAc2 (<3%), HexNAc1 (<0.1%))

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

V-LAMBDA N109: 469, 469' (Not glycosylated / Non glycosylé / No glicosilado)

aderamastatum

aderamastat

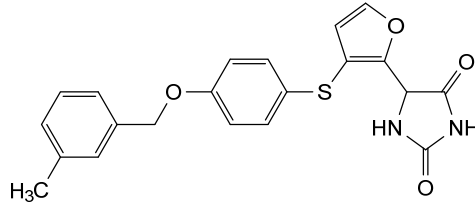
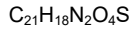
(1⁴Ξ)-7³-methyl-5-oxa-3-thia-1(4)-imidazolidina-2(2,3)-furana-4(1,4),7(1)-dibzenaheptaphane-1²,1⁵-dione

adéramastat

(1⁴Ξ)-7³-méthyl-5-oxa-3-thia-1(4)-imidazolidina-2(2,3)-furana-4(1,4),7(1)-dibzenaheptaphane-1²,1⁵-dione

aderamastat

(1⁴Ξ)-7³-metil-5-oxa-3-tia-1(4)-imidazolidina-2(2,3)-furana-4(1,4),7(1)-dibencenaheptafano-1²,1⁵-diona



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adrixetinib

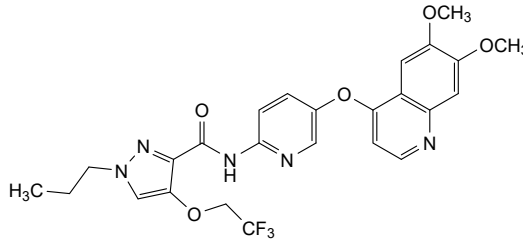
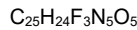
N-{5-[(6,7-dimethoxyquinolin-4-yl)oxy]pyridin-2-yl}-1-propyl-4-(2,2,2-trifluoroethoxy)-1*H*-pyrazole-3-carboxamide

adrixétinib

N-{5-[(6,7-diméthoxyquinoléin-4-yl)oxy]pyridin-2-yl}-1-propyl-4-(2,2,2-trifluoroéthoxy)-1*H*-pyrazole-3-carboxamide

adrixetinib

N-{5-[(6,7-dimetoxyquinolein-4-il)oxi]piridin-2-il}-1-propil-4-(2,2,2-trifluoroetoxy)-1*H*-pirazolo-3-carboxamida



alemtuzumabum beta #

alemtuzumab beta

immunoglobulin G1-kappa , anti-[*Homo sapiens* CD52 (CD52 antigen, CAMPATH-1 antigen, CDW52)], humanized monoclonal antibody;
 gamma1 heavy chain humanized (1-451) [VH (*Homo sapiens* IGHV4-30-4*01 (73.5%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.10.12] (26-33.51-60.99-110)) (1-121) -*Homo sapiens* IGHG1*01 (100%), G1m17,1, CH1 K120, CH3 D12, L14 (CH1 K120 (218) (122-219), hinge 1-15 (220-234), CH2 (235-344), CH3 D12 (360), L14 (362) (345-449), CHS (450-451)) (122-451)], (224-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (86.3%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dimer (230-230":233-233")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

alemtuzumab bêta

immunoglobuline G1-kappa, anti-[*Homo sapiens* CD52 (antigène CD52, antigène CAMPATH-1, CDW52)], anticorps monoclonal humanisé;
 chaîne lourde gamma1 humanisée (1-451) [VH (*Homo sapiens* IGHV4-30-4*01 (73.5%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.10.12] (26-33.51-60.99-110)) (1-121) -*Homo sapiens* IGHG1*01 (100%), G1m17,1, CH1 K120, CH3 D12, L14 (CH1 K120 (218) (122-219), charnière 1-15 (220-234), CH2 (235-344), CH3 D12 (360), L14 (362) (345-449), CHS (450-451)) (122-451)], (224-214')-disulfure avec la chaîne légère kappa humanisée (1'-214')

[V-KAPPA (*Homo sapiens* IGKV1-33*01 (86.3%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dimère (230-230":233-233")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

alemtuzumab beta

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CD52 (antígeno CD52, cadena CAMPATH-1, CDW52)], anticuerpo monoclonal humanizado; cadena pesada gamma1 humanizada (1-451) [VH (*Homo sapiens* IGHV4-30-4*01 (73.5%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.10.12] (26-33.51-60.99-110)) (1-121) -*Homo sapiens* IGHG1*01 (100%), G1m17,1, CH1 K120, CH3 D12, L14 (CH1 K120 (218) (122-219), bisagra 1-15 (220-234), CH2 (235-344), CH3 D12 (360), L14 (362) (345-449), CHS (450-451)) (122-451)], (224-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (86.3%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dímero (230-230":233-233")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

QVQLQESGPG LVRFSQTLSL TCTVSGFTFT DFYMNWVRQP PGRGLEWIGF 50
 IRDKAKGYTT EYNFSVKGRV TMLVDTSKNQ FSLRLSSVTA ADTAVYYCAR 100
 EGHTAAPFDY WQQGSLVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150
 KDYFPEPEVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200
 TYICNVNHKP SNTKVDKVE PKSCDKHTC PPCPAPELLG GPSVFLFPPK 250
 PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY 300
 NSTYRVVSVL TVLHQDWLNG KEYCKVSNK ALPAPIEKTI SKAKGQPREP 350
 QVYTLPPSRD ELTKNQVSLT CLVKGFYPSD IAEWEWSNGQ PENNYKTPP 400
 VLDSDDGSFFL YSKLTVDKSR WQQGNVFCSS VMHEALHNYH TQKSLSLSPG 450
 K 451

Light chain / Chaîne légère / Cadena ligera

DIQMTQSPSS LSASVGRDVT ITCKASQNIID KYLNWYQQKPK GKAPKLLIYN 50
 TNNLQTVGVPV RFGSGSGGTD FTFTISLQPD EDIATYYCLO HISRPRTFGQ 100
 GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNFFY PREAKVQWVK 150
 DNALQSGNSQ ESVTEQDSKD STYLSSTLT LSKADYKHK VYACEVTHQG 200
 LSSPVTKSFN RGEK 214

Post-translational modifications

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

Intra-H (C23-C104) 22-98 148-204 265-325 371-429
 22"-98" 148"-204" 265"-325" 371"-429"

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

Inter-H-L (h 5-CL 126) 224-214' 224"-214"

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

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal

Q > pyroglutamylyl (pE, 5-oxopropyl) / pyroglutamyle (pE, 5-oxopropyle) / piroglutamilo (pE, 5-oxopropilo)
 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 biantenaricos complejos fucosilados

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

H CHS K2: 451, 451"

alintegimodum

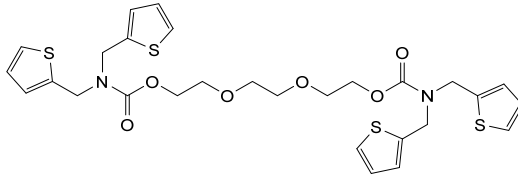
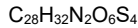
alintegimod

[ethane-1,2-diylbis(oxyethane-2,1-diyl)] bis[bis[(thiophen-2-yl)methyl]carbamate]

alintégimod

bis[bis[(thiophén-2-yl)méthyl]carbamate] d'[éthane-1,2-diylbis(oxyéthane-2,1-diyle)]

alintegimod bis[bis[(tiofen-2-il)metil]carbamato] de [etano-1,2-diilbis(oxietano-2,1-diilo)]



alsecovateinum #

alsecovatein severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) spike (S) glycoprotein (S glycoprotein, UniProt P0DTC2, strain Wuhan-Hu-1) (1-1260), stable prefusion conformation variant (R⁶⁶⁹>Q, R⁶⁷⁰>Q, R⁶⁷²>Q, K⁹⁷³>P, V⁹⁷⁴>P), trimer, produced in *Spodoptera frugiperda* (Sf9) insect cells, glycoform alfa

alsécovateína glycoprotéine du spicule (S) du coronavirus 2 du syndrome respiratoire aigu sévère (SARS-CoV-2) (glycoprotéine S, UniProt P0DTC2, souche Wuhan-Hu-1) (1-1260), variant de conformation stable par pré-fusion (R⁶⁶⁹>Q, R⁶⁷⁰>Q, R⁶⁷²>Q, K⁹⁷³>P, V⁹⁷⁴>P), trimère, produit dans des cellules d'insecte *Spodoptera frugiperda* (Sf9), glycoforme alfa

alsecovateína glicoproteína de la espícula (S) del coronavirus 2 del síndrome respiratorio severo agudo (SARS-CoV-2) (glicoproteína S, UniProt P0DTC2, cepa Wuhan-Hu-1) (1-1260), variante de conformación de prefusión estable (R⁶⁶⁹>Q, R⁶⁷⁰>Q, R⁶⁷²>Q, K⁹⁷³>P, V⁹⁷⁴>P), trímero, producido en células de insecto de *Spodoptera frugiperda* (Sf9), glicofoma alfa

Monomer sequence / Séquence du monomère / Secuencia del monómero

QCVNLIHTRTQ	LFPAYTNSFT	RGVYYPDKVF	RSSVLHSTQD	LFLPFFSNVT	50
WFHAIHVSQT	NGTKRFDNEV	LPFNDGVYFA	STKSNIIIRG	WIFGTTLDSK	100
TQSLLLVWNA	TNVVIKVCEP	QFCNDPFLGV	YHKNKNSWM	ESEFRVYSSA	150
NNCTFEYVSQ	PFLMDLEGRQ	GNFRNLRFEV	FKNIDGYFKI	YSKHTPINLV	200
RDLFQGFSAI	EPLVDLPIGI	NITRFQTLIA	LHRSYLTFGD	SSSGWTAGAA	250
AYYVGLQPR	FFLLKYENSG	TITDAVDCAL	DPLSEKCTL	KSFTVEKGIY	300
QTSNFRVQPT	ESIVRFPNIT	NLCPFGEVEF	ATRFASVYAW	NRKRISNCVA	350
DYSVLVNSAS	FSTFKCYGVS	PTKLNDLCFT	NVIADSFVIR	GDEVQRVAPG	400
QTGKIADYNY	KLPDDFTGCV	IAWNSNLDLS	KVGGVNYVLY	RLFRKSNLKP	450
FERDITSTEIY	QAGSTPCNGV	EGFNCYFPLQ	SYGFQPTNGV	GYQPYRVVVL	500
SPELLHAPAT	VCGPKKSTNL	VKNKCVNMFN	NGLTGTGVLV	ESNKKFLPFP	550
QFGRDIADTT	DAVRDPQMLE	ILLDITPCSEF	GVSVITPGTN	TSNQVAVLYQ	600
DVNCTEVPVA	IHADQLTFTW	RVYSTGSMVF	QTRAGCLIGA	EHVNSNYECD	650
IPIGAGICAS	YQTQNSPFGQ	AGSVAQSII	AYTMSLGAEN	SVAYSNNNSIA	700
IPTNFTISVT	TEILPVSMTK	TSVDCMTYIC	GDSTECSNLL	LQYGSFCTQL	750
NRALTGIAVE	QDKNTQEVFA	QVKQIYKTFP	IKDFGGFNFS	QILPDPSPKPS	800
KRSFIEDLLP	NKVTLADAGF	IKQYGDCLGD	IAARDLICAQ	KFNGLTVLFP	850
LLTDEMIAQY	TSALLAGTIT	SGWTFGAGAA	LQIPFAMQMA	YRFNGIGVTV	900
NVLYENQKLI	ANQFNSAIGK	IQDLSLSTAS	ALGKLDQVNV	QNAQALNTLV	950
KQLSSNFGAI	SSVLNDILSR	LDPEAEVQI	DRLLTGRLLS	LQTYVYVQQLI	1000
RAAEIRASAN	LAATRMESEV	LGGQSRVDFC	GKGYHLSMFP	QSAHPGVVFL	1050
HVTYVPAQEK	NFTTAPAICH	DGKAHFDFEG	VFVSNGTWFF	VTQRNFYEPQ	1100
IITVTDNTEV	GNCDVIVIGV	NNTVYDFLQP	ELDSFKLEED	KYFKNHTSPD	1150
VDLGDISGIN	ASVNNIQKEI	DRLNEVAKNL	NESLIDLQEL	GKYEQYKWF	1200
WYIWLGFIAQ	LIAIVMTIIM	LCCMTSCCCS	LKGCCSCGSC	CKFDEDDSEP	1250
VLKGVKRLHYT					1260

Mutation / Mutation / Mutación
R⁶⁶⁹>Q, R⁶⁷⁰>Q, R⁶⁷²>Q, K⁹⁷³>P, V⁹⁷⁴>P

Post-translational modifications
Disulfide location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-chain: 2-123, 118-153, 278-288, 323-348, 366-419, 378-512, 467-475, 525-577, 604-636, 649-658, 725-747, 730-736, 827-838, 1019-1030, 1069-1113

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
N48, N61, N109, N136, N152, N221, N269, N318, N330, N590, N603, N644, N788, N1061, N1085, N1121, N1145, N1160

O-glycosylation / O-glycosylation / O-glicosilación
O-glycosylation is experimentally confirmed with uncertainty on precise Ser and Thr glycosylated residues

andusomeranum #

andusomeran

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 variant XBB.1.5; based upon GISAID: EPI_ISL_15948646) further optimized by two additional stop codons, flanked by an artificial 5' untranslated region (UTR) and a 3' UTR derived from the human alpha globin gene (HBA1) modified to contain an identification and ratio (IDR) sequence to enable identification and relative ratio determination of individual RNA components in a multivalent mRNA vaccine, and terminated by a 3' polyadenylation (polyA) tail; contains N^1 -methylpseudouridine instead of uridine (*all-U>m¹Ψ*)

andusomérán

ARN messenger (ARNm), protégé d'une coiffe en 5', codant la séquence entière aux codons optimisés d'un variant de conformation stabilisée avant fusion (K982P et V983P) de la glycoprotéine de spicule (S) du SARS-CoV-2 (coronavirus 2 du syndrome respiratoire aigu sévère) (variant Omicron XBB.1.5; d'après GISAID: EPI_ISL_15948646) dont l'optimisation a été renforcée par l'addition de deux codons stop supplémentaires, flanquée d'une région non traduite (UTR) artificielle en 5' et d'une UTR en 3' dérivée du gène de l'alpha-globine humaine (HBA1) modifiée pour contenir une séquence d'identification et de ratio (IDR) afin de permettre l'identification et la détermination du ratio relatif de chaque composant d'ARN dans un vaccin ARNm multivalent, et terminée par une queue polyadénylation (polyA) en 3'; contient de la N^1 -méthylpseudouridine en lieu de l'uridine (*tout-U>m¹Ψ*)

andusomerán

ARN mensajero (ARNm), protegido en 5', que codifica, para la secuencia completa con codones optimizados, de una variante (K982P y V983P) estabilizada en la conformación pre-fusión de la glicoproteína de la espícula (S) del SARS-Cov-2 (coronavirus 2 del síndrome respiratorio agudo severo) (variante XBB.1.5 de Omicron; basado en GISAID: EPI_ISL_15948646), optimizada mediante dos codones de terminación adicionales, flanqueado por una región artificial no traducida (UTR) en 5' y una 3' UTR derivada del gen de la alfa globina humana (HBA1), modificada para que contenga una secuencia de identificación y ratio (IDR) para permitir la identificación y la determinación del ratio relativo de los componentes individuales de ARN en una vacuna de ARNm multivalente, y terminado por una cola poliadenilación (poliA) en 3'; contiene N^1 -metilpseudouridina en lugar de uridina (*todo-U>m¹Ψ*)

anitocabtagenum autoleucelum #

anitocabtagene autoleucel

autologous T lymphocytes obtained from peripheral blood mononuclear cells by leukapheresis, transduced with a self-inactivating, non-replicating lentiviral vector encoding a chimeric antigen receptor (CAR) comprising a three-helix bundle D domain polypeptide (DDpp) targeting human B-cell maturation antigen (BCMA). The expressed transgene comprises a chymotrypsinogen B leader sequence, the anti-BCMA binding domain, a CD8 α hinge and transmembrane domain, and a 4-1BB (CD137) and CD3 ζ signalling domain, under control of the elongation factor 1 alpha (EF1 α) promoter. The construct is flanked by 5' and 3' long terminal repeats (LTRs) and also

contains a ψ packaging signal, a central polypurine tract (cPPT) sequence and a Woodchuck hepatitis virus posttranscriptional regulatory element (WPRE). 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. The cells are then activated by CD3 and CD28 agonists and transduced with the lentiviral vector. The cells are further culture expanded in growth media containing interleukin 2 (IL-2) and human AB serum. The cell suspension consists of T lymphocytes (>83%), with greater than 10% of the T lymphocytes expressing the CAR-BCMA transgene. The transduced T lymphocytes demonstrate cytotoxicity against BCMA-expressing cells and secrete interferon gamma (IFN- γ) and IL-2

anitocabtagène autoleucel

lymphocytes T autologues obtenus à partir de cellules mononucléaires de sang périphérique par leucaphérèse, transduits avec un vecteur lentiviral auto-inactivant et non répliquant codant un récepteur antigénique chimérique (CAR) comprenant un polypeptide à domaine D regroupant trois hélices (DDpp) ciblant l'antigène de maturation des cellules B humaines (BCMA). Le transgène exprimé comprend une séquence de tête du chymotrypsinogène B, le domaine de liaison anti-BCMA, un domaine charnière et transmembranaire CD8 α , et un domaine de signalisation 4-1BB (CD137) et CD3 ζ , sous le contrôle du promoteur du facteur d'élongation 1 alpha (EF1 α). La construction est flanquée de répétitions longues terminales (LTR) en 5' et 3' et contient également un signal d'encapsulation ψ , une séquence de tractus polypurine central (cPPT) et un élément régulateur post-transcriptionnel (WPRE) du virus de l'hépatite de Woodchuck. 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. Les cellules sont ensuite activées par des agonistes CD3 et CD28 et transduites avec le vecteur lentiviral. Les cellules sont ensuite mises en culture dans un milieu de croissance contenant de l'interleukine 2 (IL-2) et du sérum AB humain. La suspension cellulaire est composée de lymphocytes T (>83%), avec plus de 10% des lymphocytes T exprimant le transgène CAR-BCMA. Les lymphocytes T transduits font preuve de cytotoxicité contre les cellules exprimant le BCMA et sécrètent de l'interféron gamma (IFN- γ) et IL-2

anitocabtagén autoleucel

linfocitos T autólogos obtenidos de células mononucleares de sangre periférica mediante leucoaféresis, transducidos con un vector lentiviral auto inactivante, no replicativo, que codifica para un receptor de antígenos quimérico (CAR) que contiene el dominio D de un polipéptido con un paquete de tres hélices (DDpp) dirigido al antígeno de maduración de células B (BCMA) humano. El transgén expresado contiene una secuencia líder de quimotripsinógeno B, el dominio de unión anti-BCMA, un domino bisagra y transmembrana de CD8 α , y un dominio de señalización 4-1BB (CD137) y CD3 ζ , bajo el control del promotor del factor de elongación 1 alfa (EF1 α). El constructo está flanqueado por repeticiones terminales largas (LTRs) en 5' y 3' y también contiene una señal de empaquetamiento ψ , una secuencia de tracto de polipurina central (cPPT) y un elemento regulador post-transcripcional del virus de la hepatitis de la marmota (WPRE). El vector está seudotipado con la glicoproteína G del virus de la estomatitis vesicular (VSV). El material de leucoaféresis se enriquece para linfocitos T CD4+ y CD8+ mediante inmunoselección positiva. Las células se activan

después mediante agonistas de CD3 y CD28 y se transducen con el vector lentiviral. Las células se expanden más en cultivo con medio de crecimiento que contiene interleuquina 2 (IL-2) y suero AB humano. La suspensión celular consiste en linfocitos T (>83%) con más del 10% de los linfocitos T que expresan el transgén del CAR-BCMA. Los linfocitos T transducidos demuestran citotoxicidad frente a células que expresan BCMA y secretan interferon gamma (IFN- γ) e IL-2

anpocoginum #

anpocogin

Ancylostoma canium nematode anticoagulant protein c2, variant (C-terminal P⁸⁵ added), produced in *Pichia pastoris*

anpocogine

protéine anticoagulante c2 du nématode *Ancylostoma canium*, variant (ajout de P⁸⁵ en C-terminal), produite chez *Pichia pastoris*

anpocogina

Ancylostoma canium proteína c2 anticoagulante de nematodo, variante (C-terminal P⁸⁵ añadida), producida por *Pichia pastoris*

Sequence / Séquence / Secuencia

KATM^QCGENE KYDSCGSKEC DKKCKYDGV EEDDEEFNVP CLVRVCHQDC 50
VCEEGFYRNK DDKCVSAEDC ELDNMDFIYP GTRNP 85

Mutation / Mutation / Mutación

P85 >added

Post-translational modifications

Disulfide bridge locations / Position des ponts disulfure / Posiciones de los puentes disulfuro
6-50, 15-46, 20-41, 24-70, 52-64

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

avibactam tomilopilum

avibactam tomilopil

ethyl 3-[[[[(1*R*,2*S*,5*R*)-2-carbamoyl-7-oxo-1,6-diazabicyclo[3.2.1]octan-6-yl]oxy]sulfonyl]oxy]-2,2-dimethylpropanoate

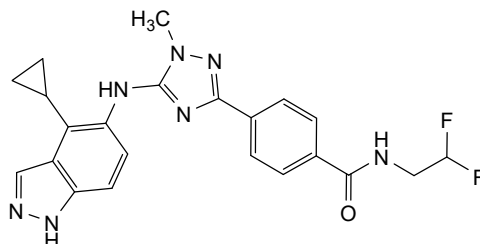
avibactam tomilopil

3-[[[[(1*R*,2*S*,5*R*)-2-carbamoyl-7-oxo-1,6-diazabicyclo[3.2.1]octan-6-yl]oxy]sulfonyl]oxy]-2,2-diméthylpropanoate d'éthyle

avibactam tomilopil

3-[[[[(1*R*,2*S*,5*R*)-2-carbamoiil-7-oxo-1,6-diazabicyclo[3.2.1]octan-6-yl]oxi]sulfonyl]oxi]-2,2-dimetilpropanoato de etilo

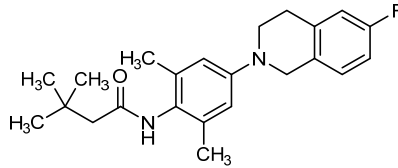
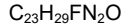
C₁₄H₂₃N₃O₈S

**azetukalnerum**

azetukalner

N-[4-(6-fluoro-3,4-dihydroisoquinolin-2(1*H*)-yl)-2,6-dimethylphenyl]-3,3-dimethylbutanamide

- azétukalner *N*-[4-(6-fluoro-3,4-dihydroisoquinoléin-2(1*H*)-yl)-2,6-diméthylphényl]-3,3-diméthylbutanamide
- azetukalner *N*-[4-(6-fluoro-3,4-dihydroisoquinolein-2(1*H*)-il)-2,6-dimetilfenil]-3,3-dimetilbutanamida



basiliximabum sarotalocanum #

- basiliximab sarotalocan immunoglobulin G1-kappa , anti-[*Homo sapiens* IL2RA (interleukin 2 receptor subunit alpha; IL-2RA, TAC, p55, CD25)], chimeric monoclonal antibody conjugated to IRDye 700DX (IR700) near-infrared photosensitizing dye; gamma1 heavy chain chimeric (1-447) [VH (*Mus musculus* IGHV1-5*01 (92.9%) -(IGHD) -IGHJ2*01 (93.3%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (214) (118-215), hinge 1-15 (216-230), CH2 (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-211')-disulfide with kappa light chain chimeric (1'-211') [V-KAPPA (*Mus musculus* IGKV4-70*01 (98.9%) -IGKJ1*01 (100%), CDR-IMGT [11.3.10] (27-31.49-51.88-94)) (1'-104') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (150), V101 (188) (105'-211')]; dimer (226-226":229-229")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, glycoform alfa; conjugated on an average of 2 or 3 lysyl to photosensitizing dye IRDye 700DX
- basiliximab sarotalocan immunoglobuline G1-kappa, anti-[*Homo sapiens* IL2RA (sous-unité alpha du récepteur de l'interleukine 2; IL-2RA, TAC, p55, CD25)]; anticorps monoclonal chimérique; conjugué au photosensibilisateur proche de l'infrarouge IRDye 700DX (IR700); chaîne lourde gamma1 chimérique (1-447) [VH (*Mus musculus* IGHV1-5*01 (92.9%) -(IGHD) -IGHJ2*01 (93.3%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (214) (118-215), charnière 1-15 (216-230), CH2 (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-211')-disulfure avec la chaîne légère kappa chimérique (1'-211') [V-KAPPA (*Mus musculus* IGKV2-24*01 (90.0%) -IGKJ2*01 (100%), CDR-IMGT [11.3.10] (27-37.55-57.94-103)) (1'-113') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (150), V101 (188) (105'-211')]; dimère (226-226":229-229")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1, glycoforme alfa; conjugué sur 2 ou 3 lysyl en moyenne au photosensibilisateur IRDye 700DX
- basiliximab sarotalocán inmunoglobulina G1-kappa, anti-[*Homo sapiens* IL2RA (subunidad alfa del receptor de la interleukina 2; IL-2RA, TAC, p55, CD25)]; anticuerpo monoclonal quimérico; conjugado con fotosensibilizante de infrarrojo cercano IRDye 700DX (IR700);

cadena pesada gamma1 quimérica (1-447) [VH (*Mus musculus* IGHV1-5*01 (92.9%) - (IGHD) - IGHJ2*01 (93.3%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (214) (118-215), bisagra 1-15 (216-230), CH2 (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-211')-disulfuro con la cadena ligera kappa quimérica (1'-211') [V-KAPPA (*Mus musculus* IGKV2-24*01 (90.0%) - IGKJ2*01 (100%), CDR-IMGT [11.3.10] (27-37.55-57.94-103)) (1'-113') - *Homo sapiens* IGKC*01 (100%), Km3 A45.1 (150), V101 (188) (105'-211')]; dímero (226-226":229-229")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular derivada de CHO-K1, forma glicosilada alfa; conjugada en 2 o 3 restos lisil por término medio con fotosensibilizante IRDye 700DX

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLQQSGTV LARPGASVKM SCKASGYSFT RYWMHWIKQR PGQGLEWIGA 50
IYPGNSDTSY NQKFEKGAKL TAVTSASTAY MELSSLTHED SAVVYCSRDY 100
GYPDFFGQG TLLTVSSAST KGPSVFPPLAP SSKSTSGGTA ALGCLVKDYF 150
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC 200
NVNHHKPSNTK VDKRVEPKSC DKHTCTPCPC APELLGGPSV FLFPPKPKDT 250
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALFA PIEKTSKAK GQPREPQVYT 350
LPPSRREEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTPFPVLDS 400
DGSFFLYSKL TVDKSRWQQG NWFSCSVME ALHNHYTQKS LSLSPGK 447
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Light chain / Chaîne légère / Cadena ligera

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QIVLTQSPAI MSASPGKEVT MTCASASSIS YMQWYQQKPG TSPKRWIYDT 50
SKLASGVPAR FSGSGSGTSY SLTISSEAE DAATYCHQR SSYTFGGGTK 100
LEIKRTVAAP SVFIFPPSDE QLKSGTASV CLLNFPYPRE AKVQWKVDNA 150
LQSGNSQESV TEQDSKSTY SLSSSTLTLSK ADYKHKVYA CEVTHQGLSS 200
PVTKSFRNGE C 211
```

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" 131"-191"
 23"-87" 131"-191"

Inter-H-L (h 5-CL 126) 220-211" 220"-211"

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

N-terminal glutaminy cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal

Q > pyroglutamyl (pE, 5-oxopropyl) / pyroglutamide (pE, 5-oxopropyle) / piroglutamilo (pE, 5-oxoprolilo)

L VL Q1: 1, 1"

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

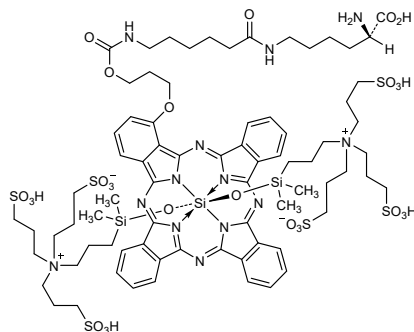
H CH2 N84.4: 297, 297"

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



benmelstobartum #
benmelstobart

immunoglobulin G1- kappa, anti-*Homo sapiens* CD274 (programmed cell death 1 ligand 1, PDL1, PD-L1, B7 homolog 1, B7H1, B7-H1, PDCD1LG1)], humanized monoclonal antibody;
gamma1 heavy chain humanized (1-446) [VH (*Homo sapiens*IGHV2-5*01 (78.6%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.7.10] (26-33.51-57.96-105)) (1-116) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, G1v66 CH2 A27 (CH1 K120 (213) (117-214), hinge 1-15 (215-229), CH2 D27>A (264) (230-339), CH3 D12 (355), L14 (357) (340-444), CHS (445-446)) (117-446)], (219-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (82.1%) -IGKJ2*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dimer (225-225":228-228")-bisdisulfide

benmelstobart

immunoglobuline G1-kappa, anti-[*Homo sapiens* CD274 (ligand 1 de mort cellulaire programmée 1, PDL1, PD-L1, B7 homologue 1, B7H1, B7-H1, PDCD1LG1)], anticorps monoclonal humanisé;
chaîne lourde gamma1 humanisée (1-446) [VH (*Homo sapiens*IGHV2-5*01 (78.6%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.7.10] (26-33.51-57.96-105)) (1-116) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, G1v66 CH2 A27 (CH1 K120 (213) (117-214), charnière 1-15 (215-229), CH2 D27>A (264) (230-339), CH3 D12 (355), L14 (357) (340-444), CHS (445-446)) (117-446)], (219-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (82.1%) -IGKJ2*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dimère (225-225":228-228")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO)-S, glycoforme alfa

benmelstobart

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CD274 (ligando 1 de muerte celular programada 1, PDL1, PD-L1, B7 homólogo 1, B7H1, B7-H1, PDCD1LG1)], anticuerpo monoclonal humanizado;
cadena pesada gamma1 humanizada (1-446) [VH (*Homo sapiens*IGHV2-5*01 (78.6%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.7.10] (26-33.51-57.96-105)) (1-116) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, G1v66 CH2 A27 (CH1 K120 (213) (117-214), bisagra 1-15 (215-229), CH2 D27>A (264) (230-339), CH3 D12 (355), L14 (357) (340-444), CHS (445-446)) (117-446)],(219-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (82.1%) -IGKJ2*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dímero (225-225":228-228")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO)-S, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada
 QITLKESGPT LVKPTQTLTL TCTVSGFSLs TYGVHWIRQP PGKALEWLGV 50
 IWRGVTTDYN AAFMSRLTIT KDNSKNQVVL TMNNMDPVDI ATYYCARLGF 100
 YAMDYWGQGT LVTVSSASTK GPSVFPLAPS SKSTSGGTAA LGCLVKDYFP 150
 EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVVTVPSS SLGTQTYICN 200
 VNHKPSNTKV DKKVEPKSCD KHTCPCPCA PELLGGPSVF LFPPKPKDTL 250
 MISRTPEVTC VVVAVSHEDF EVKFNWYVDG VEVHNAKTKP REEQYNSTYR 300
 VVSVLTVLHQ DWLNGKEYKC KVSNKALPAP IEKTIKSKARG QPREPQVYTL 350
 PPSRDELTKN QVSLTCLVKG FYPSDIAVEW ESNQGPENNY KTTPPVLDSD 400
 GSFFLYSLTL VDKSRWQQGN VFSCSVMHEA LHNHYTKQSL SLSPGK 446

Light chain / Chaîne légère / Cadena ligera
 DIQMTQSPSS LSASVGRDVT ITCKASQSVS NDVAWYQQKPK GKAPKLLIYY 50
 AANRYTGVDP RFGSGYGTD FTFITISLQP EDIATYFCQQ DYTSPTYFGQ 100
 GTKLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
 DNALQSGNSQ ESVTEQDSKD STYLSLSTLT LSKADYEKHK VYACEVTHQG 200
 LSSPVTKSFN RGEK 214

Post-translational modifications
 Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
 Intra-H (C23-C104) 22-95 143-199 260-320 366-424
 22"-95" 143"-199" 260"-320" 366"-424"
 Intra-L (C23-C104) 23"-88" 134"-194"
 23"-88" 134"-194"
 Inter-H-L (h 5-CL 126) 219-214' 219"-214"
 Inter-H-H (h 11, h 14) 225-225" 228-228"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
 Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamide (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprofilo)
 H V H Q 1:1, 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"

berahyaluronidasum alfa #
 berahyaluronidase alfa

human hyaluronidase isozyme-5 (HYAL5, sperm adhesion molecule 1, SPAM1, hyaluronidase PH-20, EC:3.2.1.35) fragment (3-433, 1-431 in the current sequence) engineered variant with the structural domain replaced by the corresponding region of human hyaluronidase isozyme-1 (HYAL1) (³⁰⁶TLSIMRSMKSCLLDDNYMETI³²²>³⁰⁴SWENTRTKESCQAIKEYMDTT³²⁴), produced in Chinese hamster ovary (CHO) cells, cell line DG44, glycoform alfa

bérahyaluronidase alfa

variant modifié d'un fragment (3-433, 1-431 dans la séquence actuelle) de l'isozyme-5 de la hyaluronidase humaine (HYAL5, molécule d'adhésion des spermatozoïdes 1, SPAM1, hyaluronidase PH-20, EC:3.2.1.35) dont le domaine structural a été remplacé par la région correspondante de l'isozyme-1 de la hyaluronidase humaine (HYAL1) (³⁰⁶TLSIMRSMKSCLLDDNYMETI³²²>³⁰⁴SWENTRTKESCQAIKEYMDTT³²⁴), produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire DG44, glycoforme alfa

berahialuronidasa alfa

hialuronidasa humana isoenzima-5 (HYAL5, molécula de adhesión de esperma 1, SPAM1, hialuronidasa PH-20, EC:3.2.1.35) fragmento (3-433, 1-431 en la secuencia actual) variante diseñada con el dominio estructural reemplazado por la región correspondiente a la hialuronidasa humana isoenzima-1 (HYAL1) (³⁰⁶TLSIMRSMKSCLLDDNYMETI³²²>

³⁰⁴SWENTRTKESCQAIKEYMDTT³²⁴), producida en células ováricas de hámster Chino (CHO), línea celular DG44, forma glicosilada alfa

Sequence / Séquence / Secuencia

FRAP FVIPNV PFLWAWNAPS EFCLGKFDEP LMSLFSFIG SPRINATGGQ	50
VTIFYVDRLG YYPYIDSITG VTVNGGIPQK ISLQDHLDKA KKDITFYMPV	100
DNLGMAVIDW EEWRTWARN WPKPDVYKNR SIELVQQQNV QLSLATEATEK	150
AKQEFKAGK DFLVETIKLG KLLRPNHLWG YYLFPDCYNH HYKPKGYNGS	200
CFNVEIKRND DLSWLWNEST ALYPSIYLNT QQSPVAATLY VNRVREAIR	250
VSKI PDAKSP LPVFAYTRIV FTDQVLKFLS QDELVYTFGE TVALGASGIV	300
IWGSWENTRT KESCQAIKEY MDTTLNPHYII NVTLAARMCS QVLCQEQGVF	350
IRKNWNSSDY LHLNPDNFAT QLEKGGKFTV RGKPTLELDLE QFSEKFCVCS	400
YSTLSCKEKA DVKDTDAVDV CIADGVCIDA F	431

Post-translational modifications

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
23-314, 187-201, 339-350, 344-398, 400-406, 421-427

Glycosylation sites / Sites de glycosylation / Posiciones de glicosilación

N45, N129, N198, N217, N331, N356 (3 to 6 glycans per N-glycosylation site)

Deamidation sites / Sites de désamidation / Posiciones de desamidación

N74, Q84, N120, N139, N189, Q391 (for residues Q341/Q345/Q347 and N354/N364/N367 the specific deamidation site could not be determined due to close proximity among these residues)

besvatresgenum autoleucelum #
besvatresgene autoleucel

autologous T lymphocytes obtained from peripheral blood lymphocytes by leukapheresis transduced with a self-inactivating, non-replicating lentiviral vector encoding an affinity-enhanced cancer testis antigen (NY-ESO-1^{c259}) specific T-cell receptor (TCR) and co-expressing the CD8α chain of the CD8 co-receptor. The TCR is based on *letetresgene autoleucel* and specifically recognises a peptide (SLLMWITQC), which is shared by the cancer antigens NY-ESO-1 (CTAG1B) and LAGE-1a (CTAG2) presented on human leukocyte antigen HLA-A*02. The expressed transgene comprises CD8α joined by the foot-and-mouth disease virus ribosome skipping sequence (F2A) to the TCRα chain, joined by the porcine teschovirus-1 ribosome skipping sequence (P2A) to the TCR β chain and is under control of the elongation factor 1 alpha (EF1α) promoter. The construct is flanked by long terminal repeats (LTR) that have a deletion in the U3 part of the LTR, and also contains a ψ packaging signal, Rev response element (RRE), central polypurine tract (cPPT) and a central termination sequence (CTS). The vector is pseudotyped with 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 initially in media supplemented with AB serum and interleukin 2 (IL-2), and then in media supplemented with only IL-2. The T lymphocytes (≥95%) are positive for the transgene (≥10% CAR positive), and are cytotoxic to T2 cells loaded with the target peptide

besvatresgène autoleucel

lymphocytes T autologues obtenus à partir de lymphocytes de sang périphérique par leucaphérese, transduits avec un vecteur lentiviral auto-inactivant et non répliquant codant un récepteur de cellules T (TCR) spécifique d'un antigène du cancer du testicule à affinité renforcée (NY-ESO-1c259) et co-exprimant la chaîne CD8α du corécepteur CD8. Le TCR est basé sur le *lététresgène autoleucel* et reconnaît spécifiquement

un peptide (SLLMWITQC), qui est partagé par les antigènes de cancer NY-ESO-1 (CTAG1B) et LAGE-1a (CTAG2) présentés sur l'antigène de leucocyte humain HLA-A*02. Le transgène exprimé comprend le CD8α lié par la séquence de saut (skipping) du ribosome du virus de la fièvre aphteuse (F2A) à la chaîne TCRα, lié par la séquence de saut (skipping) du ribosome du teschovirus-1 porcin (P2A) à la chaîne TCR β et est sous le contrôle du promoteur du facteur d'élongation 1 alpha (EF1α). La construction est flanquée de longues répétitions terminales (LTR) qui présentent une délétion dans la partie U3 de la LTR, et contient également un signal d'encapsidation ψ, un élément de réponse Rev (RRE), un tractus polypurine central (cPPT) et une séquence de terminaison centrale (CTS). 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/CD8 par immunosélection positive, activé par des agonistes CD3 et CD28 et transduit avec le vecteur lentiviral. Les cellules sont ensuite développées dans un premier temps dans un milieu complété par du sérum AB et de l'interleukine 2 (IL-2), puis dans un milieu complété uniquement par de l'IL-2. Les lymphocytes T (≥95%) sont positifs pour le transgène (≥10% CAR positif), et sont cytotoxiques pour les cellules T2 chargées avec le peptide cible

besvatresgén autoleucel

linfocitos T autólogos obtenidos de linfocitos de sangre periférica mediante leucoaféresis, transducidos con un vector lentiviral auto inactivante, no replicativo, que codifica para un receptor de linfocitos T (TCR) con afinidad aumentada, específico del antígeno de cáncer de testículo (NY-ESO-1^{c259}) y que coexpresa la cadena CD8α del correceptor CD8. El TCR está basado en *letetresgén autoleucel* y reconoce específicamente un péptido (SLLMWITQC), compartido por los antígenos de cáncer NY-ESO-1 (CTAG1B) y LAGE-1a (CTAG2), presentado en el antígeno común leucocitario HLA-A*02. El transgén expresado contiene CD8α unido, mediante la secuencia de salto ribosómico del virus de la fiebre aftosa (F2A), a la cadena TCRα, unida, mediante la secuencia de salto ribosómico del teschovirus 1 porcino (P2A), a la cadena TCRβ y está bajo el control del promotor del factor de elongación 1 alfa (EF1α). El constructo está flanqueado por repeticiones terminales largas (LTR) que tienen una delección en la parte U3 del LTR, y también contiene una señal de empaquetamiento ψ, un elemento de respuesta Rev (RRE), una secuencia de tracto de polipurina central (cPPT) y una secuencia de terminación central (CTS). El vector está seudotipado con la glicoproteína G del virus de la estomatitis vesicular (VSV). El material de leucoaféresis se enriquece para linfocitos T CD4/CD8 mediante inmunoselección positiva, se activa mediante agonistas de CD3 y CD28 y se transduce con el vector lentiviral. Las células son después expandidas inicialmente en medio suplementado con suero AB e interleuquina 2 (IL-2), y después en medio suplementado sólo con IL-2. Los linfocitos T (≥95%) son positivos para el transgén (≥10% positivos para el CAR) y son citotóxicos frente a células T2 cargadas con el péptido diana

bevacizumabum gamma

bevacizumab gamma

immunoglobulin G1-kappa, anti-[*Homo sapiens* VEGFA (vascular endothelial growth factor A, VEGF-A, VEGF)], humanized monoclonal antibody; gamma1 heavy chain humanized (1-453) [VH (*Homo sapiens* IGHV3-30*02 (76.8%) -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (220) (124-221), hinge 1-15 (222-236), CH2 (237-346), CH3 E12 (362), M14 (364) (347-451), CHS (452-453)) (124-453)], (226-214')-disulfide with kappa light chain 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 (153), V101 (191) (108'-214')]; dimer (232-232":235-235")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

bévacizumab gamma

immunoglobuline G1-kappa, anti-[*Homo sapiens* VEGF (facteur de croissance A de l'endothélium vasculaire, VEGF-A, VEGF)], anticorps monoclonal humanisé; chaîne lourde gamma1 humanisée (1-453) [VH (*Homo sapiens* IGHV3-30*02 (76.8%) -(IGHD) - IGHJ4*01 (93.3%), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (220) (124-221), charnière 1-15 (222-236), CH2 (237-346), CH3 E12 (362), M14 (364) (347-451), CHS (452-453)) (124-453)], (226-214')-disulfure avec la chaîne légère kappa 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 (153), V101 (191) (108'-214')]; dimère (232-232":235-235")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

bevacizumab gamma

immunoglobulina G1-kappa, anti-[*Homo sapiens* VEGF (factor de crecimiento A del endotelio vascular, VEGF-A, VEGF)], anticuerpo monoclonal humanizado; cadena pesada gamma1 humanizada (1-453) [VH (*Homo sapiens* IGHV3-30*02 (76.8%) -(IGHD) - IGHJ4*01 (93.3%), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (220) (124-221), bisagra 1-15 (222-236), CH2 (237-346), CH3 E12 (362), M14 (364) (347-451), CHS (452-453)) (124-453)], (226-214')-disulfuro con la cadena ligera 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 (153), V101 (191) (108'-214')]; dímero (232-232":235-235")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

EVQLVESGGG LVQPGGSLRL SCAASGYTFT NYGMNWRQA PGKLEWVWG 50
 INTYTGPEPT AADFKRRFTF SLDTSKSTAY LQMNSLRAED TAVVYCAKYP 100
 HYYGSSHWYF DVWQQTGLVT VSSASTKGPS VFLAPSSKS TSGGTAAALG 150
 LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLS VVTVPSSSLG 200
 TQTYICNVNH KPSNTKVDKK VEPKSCDKTH TCPPCPAPEL LGGPSVFLPF 250
 PKPKDTLMIS RTPVETCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE 300
 QYNSTYRVVS VLTVLHQDWL NGKEYKCKV NKALPAPIEK TISKAKGQPR 350
 EPQVYTLPPS REEMTKNQVS LTCLVKGFPY SDIAVEWESN GQFENNYKTT 400
 PVLDSGGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSL 450
 PGK 453

Light chain / Chaîne légère / Cadena ligera

DIQMTQSPSS LSASVGDRTV ITCSASQDIS NYLNWYQQK GKAPKVLIIYF 50
 TSSLHSGVPS RFGSGSGSDT PTLTISSLQP EDFATYYCQQ YSTVPWTFGQ 100
 GTKVEIKRTV AAPSVEIFPP SDEQLKSGTA SVVCLLNIFY PREAKVQWKV 150
 DNALQSGNSQ ESVTEQDSKD STYLSLSTLT LSKADYKHK VYACEVTHQG 200
 LSSPVTKSNF RGEK 214

Post-translational modifications

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

Intra-H (C23-C104) 22"-96" 150"-206" 267"-327" 373"-431"

22"-96" 150"-206" 267"-327" 373"-431"

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

23"-88" 134"-194"

Inter-H-L (h 5-CL126) 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 (sum of G0F, G1F, G2F >14%) and afucosylated (sum of G0, G1, G2 >5%)

complex bi-antennary CHO-type glycans without sialylation / glycanes fucosylés (somme

de G0F, G1F, G2F >14%) et afucosylés (somme of G0, G1, G2 >5%) de type CHO bi-antennaires

complexes sans sialylation / glicanos fucosilados (suma de G0F, G1F, G2F >14%) y afucosilados

(suma de G0, G1, G2 >5%) de tipo CHO biantennarios complejos sin sialilación

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

H CHS K2: 453, 453"

bevonescéinum

bevonescéin

*N*²-(3',6'-dihydroxy-3-oxo-3*H*-spiro[[2]benzofuran-1,9'-xanthene]-5-carbonyl)-L-glutaminy-L-valyl-L-prolyl-L-tryptophyl-L-α-glutamyl-L-α-glutamyl-L-prolyl-L-tyrosyl-L-tyrosyl-L-valyl-L-valyl-L-lysyl-L-lysyl-L-seryl-L-serylglycylglycinamide

bévonescéine

*N*²-(3',6'-dihydroxy-3-oxo-3*H*-spiro[[2]benzofuran-1,9'-xanthène]-5-carbonyl)-L-glutaminy-L-valyl-L-prolyl-L-tryptophyl-L-α-glutamyl-L-α-glutamyl-L-prolyl-L-tyrosyl-L-tyrosyl-L-valyl-L-valyl-L-lysyl-L-lysyl-L-séryl-L-sérylglycylglycinamide

bevonescéina

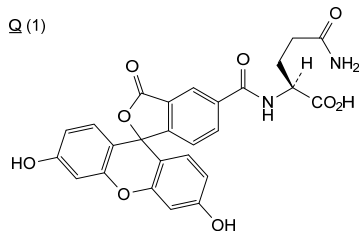
*N*²-(3',6'-dihidroxi-3-oxo-3*H*-spiro[[2]benzofuran-1,9'-xanteno]-5-carbonil)-L-glutamín-L-valil-L-prolil-L-triptofil-L-α-glutamil-L-α-glutamil-L-prolil-L-tirosil-L-tirosil-L-valil-L-valil-L-lisil-L-lisil-L-seril-L-serilglicilglicinamida

C₁₁₂H₁₄₄N₂₂O₃₂

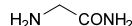
QVPWEEPYV VKKSSGG 17

Modified residues / Résidus modifiés / Restos modificados

Q (1)



G (17)



bidoleucelum

bidoleucel

allogeneic invariant natural killer T cells (iNKT), isolated from peripheral blood leukapheresis of HLA-A2 positive donors. The iNKT cells are enriched using antibody-specific positive selection, and expanded through a two-step stimulation procedure, initially by co-culture with irradiated peripheral blood mononuclear cells (PBMCs) derived from the same donor and alpha-galactosylceramide (αGalCer), and then by co-culture with αGalCer-pulsed irradiated PBMCs, each in media containing human AB serum and interleukin 2 (IL-2). The final cell substance is >99% iNKTs (CD3 and invariant T cell receptor α chain positive) and are in an activated state (CD25 and CD69 positive). The cells can induce dose-dependent target cell killing of glycolipid-presenting tumour cell lines

bidoleucel

cellules T tueuses naturelles invariantes allogéniques (iNKT), isolées à partir de la leucaphérese de sang périphérique de donneurs HLA-A2 positifs. Les cellules iNKT sont enrichies à l'aide d'une sélection positive spécifique à un anticorps, et amplifiées par une procédure de stimulation en deux étapes, d'abord par co-culture avec des cellules mononucléaires irradiées du sang périphérique (PBMC) provenant du même donneur et de l'alpha-galactosylcéramide (αGalCer), puis par co-culture avec des PBMC irradiées pulsées par αGalCer, chacune dans un milieu contenant du sérum AB humain et de l'interleukine 2 (IL-2). La substance cellulaire finale est composée à >99% de iNKTs (CD3 et chaîne α invariante du récepteur des cellules T) et sont dans un état activé (CD25 et CD69 positifs). Les cellules peuvent induire une destruction dose-dépendante des cellules cibles des lignées de cellules tumorales présentant des glycolipides

bidoleucel

células T natural killer invariantes (iNKT) alogénicas, aisladas de leucoaféresis de sangre periférica de donantes HLA-A2 positivos. Las células iNKT se enriquecen usando selección positiva específica de anticuerpo y se expanden a través de un procedimiento de estimulación en dos pasos, inicialmente por cocultivo con células mononucleares de sangre periférica (PBMCs) irradiadas derivadas del mismo donante y galactosilceramide alfa (αGalCer), y después mediante cocultivo con PBMCs irradiadas pulsadas con αGalCer, ambos en medio que contiene suero AB e interleuquina 2 (IL-2). La substancia celular final es >99% iNKTs (CD3 y cadena invariante α del receptor de linfocitos T) y están en un estado activado (positivas para CD25 y CD69). Las células pueden inducir, de forma dependiente de dosis, la muerte de líneas celulares tumorales que presentan glicolípidos

boditrectinibum

boditrectinib

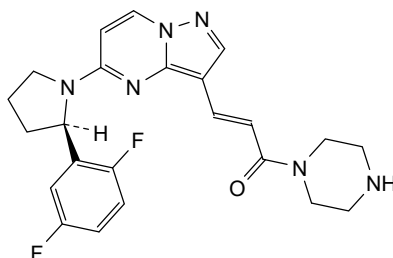
(2E)-3-{5-[(2R)-2-(2,5-difluorophenyl)pyrrolidin-1-yl]pyrazolo[1,5-a]pyrimidin-3-yl}-1-(piperazin-1-yl)prop-2-en-1-one

boditrectinib

(2E)-3-{5-[(2R)-2-(2,5-difluorophényl)pyrrolidin-1-yl]pyrazolo[1,5-a]pyrimidin-3-yl}-1-(pipérazin-1-yl)prop-2-én-1-one

bodontrectinib

(2E)-3-[5-[(2R)-2-(2,5-difluorophenyl)pyrrolidin-1-yl]pirazolo[1,5-a]pirimidin-3-yl]-1-(piperazin-1-yl)prop-2-en-1-ona

C₂₃H₂₄F₂N₆O**brenetafuspum #**

brenetafusp

humanized immunoglobulin anti-(human T-cell surface glycoprotein CD3 epsilon chain) single chain variable fragment (scFv) (1-253) containing the light chain variable (VL) region (1-107), the linker ¹⁰⁸GGGGSGGGGSGGGGSGGGGSGGGG¹³¹ and the heavy chain variable (VH) region (132-253) fused via the peptide linker ²⁵⁴GGGGS²⁵⁸ to a human T-cell receptor beta chain anti-(human HLA-A2 antigen complex with preferentially expressed antigen in melanoma (PRAME) protein) fragment (259-502 in the current sequence) engineered variant (S⁴²⁹>C, C⁴⁴⁷>A, N⁴⁶¹>D), disulfide bridged to a human T cell receptor alpha chain anti-(human HLA-A2 antigen complex with preferentially expressed antigen in melanoma (PRAME) protein) fragment (1-201), engineered variant (T¹⁶³>C), non-glycosylated, produced in *Escherichia coli*;

humanized monoclonal scFv antibody fusion with human T-cell receptor; CDR source: *Mus musculus*; antigen: human T-cell surface glycoprotein CD3 epsilon chain, T-cell surface antigen T3/Leu-4 epsilon chain, CD3e (CD3E); type: Fv-kappa scFv; light chain class: kappa; LV germline: *Homo sapiens* IGKV1-NL1*01; LJ germline: *Homo sapiens* IGKJ1*01; VL: 1-107; CDR Kabat L1: RASQDIRNYLN (24-34); CDR Kabat L2: YTSRLES (50-56); CDR Kabat L3: QQGNTLPWT (89-97); linker: 108-131; HV germline: *Homo sapiens* IGHV3-23*04; HJ germline: *Homo sapiens* IGHJ4*01; VH: 132-253; CDR Kabat H1: GYTMN (162-166); CDR Kabat H2: LINPYKGVSTYNQKFKD (181-197); CDR Kabat H3: SGYYGDSDWYFDV (230-242); linker: 254-258; fusion protein: 259-372; T-cell receptor beta chain (CB) variable domain [TRBV19*01-TRBJ2-7*01]; fusion protein: 373-502 (S429C C447A N461D); T-cell receptor beta chain constant domain [TRBC2*01]; mutation: S429C (disulfide with CA); mutation: C447A (removed disulfide); mutation: N461D (natural variant); fusion protein: 1-115; T-cell receptor alpha chain (CA) variable domain [TRAV26.1*01-TRAJ15*02]; fusion protein: 116-201 (T163C); T-cell receptor alpha chain constant domain [TRAC*01]; mutation: T163C (disulfide with CB)

brénétafusp

fragment variable à chaîne unique (scFv) de l'immunoglobuline humanisée anti-(chaîne epsilon de la glycoprotéine de surface des lymphocytes T humains CD3) (1-253,) contenant la région variable (VL) de la chaîne légère (1-107), la liaison ¹⁰⁸GGGGSGGGGSGGGGSGGGGSGGGG¹³¹ et la région variable (VH) de la chaîne lourde (132-253) fusionnées via la liaison peptidique ²⁵⁴GGGGS²⁵⁸ à un fragment (259-502 dans la séquence actuelle) de la chaîne bêta du récepteur des lymphocytes T

humains anti-(complexe antigénique HLA-A2 humain avec l'antigène préférentiellement exprimé dans le mélanome (PRAME), variant modifié (S⁴²⁹>C, C⁴⁴⁷>A, N⁴⁶¹>D), disulfure ponté à un fragment (1-201) de la chaîne alpha du récepteur des lymphocytes T humains anti-(complexe antigénique HLA-A2 humain avec l'antigène préférentiellement exprimé dans le mélanome (PRAME)), variant modifié (T¹⁶³>C), non glycosylé, produite chez *Escherichia coli*;

fusion d'un anticorps monoclonal scFv humanisé avec le récepteur des lymphocytes T humains; source CDR: *Mus musculus*; antigène: chaîne epsilon de la glycoprotéine de surface des lymphocytes T humains CD3, antigène T3 de surface des cellules T /Leu-4 chaîne epsilon, CD3e (CD3E); type: Fv-kappa scFv; classe de la chaîne légère: kappa; LV lignée germinale: *Homo sapiens* IGKV1-NL1*01; LJ lignée germinale: *Homo sapiens* IGKJ1*01; VL: 1-107; CDR Kabat L1: RASQDIRNYLN (24-34); CDR Kabat L2: YTSRLES (50-56); CDR Kabat L3: QQGNTLPWT (89-97); liaison: 108-131; HV lignée germinale: *Homo sapiens* IGHV3-23*04; HJ lignée germinale: *Homo sapiens* IGHJ4*01; VH: 132-253; CDR Kabat H1: GYTMN (162-166); CDR Kabat H2: LINPYKGVSTYNQKFKD (181-197); CDR Kabat H3: SGYYGSDSDWYFDV (230-242); liaison: 254-258; protéine de fusion: 259-372; domaine variable de la chaîne bêta (CB) du récepteur des lymphocytes T [TRBV19*01-TRBJ2-7*01]; protéine de fusion: 373-502 (S429C C447A N461D); domaine constant de la chaîne bêta du récepteur des lymphocytes T [TRBC2*01]; mutation: S429C (disulfure avec CA); mutation: C447A (disulfure supprimé); mutation: N461D (variant naturel); protéine de fusion: 1-115; domaine variable de la chaîne alpha (CA) du récepteur des lymphocytes T [TRAV26.1*01-TRAJ15*02]; protéine de fusion: 116-201 (T163C); domaine constant de la chaîne alpha du récepteur des lymphocytes T [TRAC*01]; mutation: T163C (disulfure avec CB)

brenetafusp inmunoglobulina humanizada anti-(cadena épsilon CD3 de glicoproteína de superficie de linfocitos T humanos) fragmento variable de cadena única (scFv) (1-253), conteniendo la cadena ligera variable (VL) región (1-107) el enlace ¹⁰⁸GGGGSGGGGSGGGGSGGGGSGGGGS¹³¹ y la cadena pesada variable (VH) región (132-253) fusionado a través del enlace peptídico ²⁵⁴GGGS²⁵⁸ a una cadena beta del receptor de linfocitos T humanos anti-(complejo antígeno humano HLA-A2 con antígeno expresado preferentemente en melanoma (PRAME)) fragmento (259-502 en la secuencia actual) variante diseñada (S⁴²⁹>C, C⁴⁴⁷>A, N⁴⁶¹>D), unido por puente disulfuro a una cadena alfa del receptor de linfocitos T humanos anti-(complejo antígeno humano HLA-A2 con antígeno expresado preferentemente en melanoma (PRAME)) fragmento (1-201), variante diseñada (T¹⁶³>C), no glicosilada, producida en *Escherichia coli*; anticuerpo monoclonal scFv de fusión con receptor de linfocitos T humanos; fuente CDR: *Mus musculus*; antígeno: cadena épsilon CD3 de glicoproteína de superficie de linfocitos T humanos, cadena épsilon de antígeno de superficie de células T T3/Leu-4, CD3e (CD3E); tipo: Fv-kappa scFv; clase cadena ligera: kappa; línea germinal LV: *Homo sapiens* IGKV1-NL1*01; línea germinal LJ: *Homo sapiens* IGKJ1*01; VL: 1-107; CDR Kabat L1: RASQDIRNYLN (24-34); CDR Kabat L2: YTSRLES (50-56); CDR Kabat L3: QQGNTLPWT (89-97); enlace: 108-131; línea germinal HV: *Homo sapiens* IGHV3-23*04; línea germinal HJ: *Homo sapiens* IGHJ4*01; VH: 132-253; CDR Kabat H1: GYTMN (162-166); CDR Kabat H2: LINPYKGVSTYNQKFKD (181-197); CDR Kabat H3: SGYYGSDSDWYFDV (230-242); enlace: 254-258; proteína de fusión: 259-372; dominio variable de la cadena beta (CB) del receptor de linfocitos T [TRBV19*01-TRBJ2-7*01]; proteína de fusión proteína: 373-502 (S429C C447A N461D); dominio constante de la cadena beta del receptor de linfocitos T [TRBC2*01]; mutación: S429C (disulfuro con CA); mutación: C447A (disulfuro eliminado); mutación: N461D (variante natural); proteína de fusión: 1-115; dominio variable de la cadena alfa (CA) del receptor de linfocitos T [TRAV26.1*01-TRAJ15*02]; proteína de fusión: 116-201 (T163C); dominio constante de la cadena alfa del receptor de linfocitos T [TRAC*01]; mutación: T163C (disulfuro con CB)

Sequence / Séquence / Secuencia

ScFv-T cell receptor beta chain

AIQMTQSPSS LSASVGDVRT ITCRASQDIR NYLNWYQKPK GKAPKLLIYY 50
 TSRLESGVPS RFGSGSGTD YTLTISSLQP EDFATYYCQQ GNTLPWTFGQ 100
 GTKVEIKGGG GSGGGSGGGG GSGGGSGGGG SEVQLVESGG GLVQPPGSLR 150
 LSCAASGYSF TGYTMNWVRQ APKGLEWVA LINPYKGVST YNQKEDRFT 200
 ISVDKSKNTA YLQMNSLRAE DTAVYVCARS GYYGSDWYF DVWGGQLT 250
 VSSGGGSDG GITQSPKYLK RKEGQNVTLK CEQNLNHDAM YWYRQDPGQG 300
 LRLIYYSQIM GDEQKGDIAE GYSVSRKKE SFPLTVTSAQ KNPTAFYLCA 350
 SSWWTGGASP IRFGPGTRLT VTEDLKNVFP PEVAVFEPSE AEISHTQKAT 400
 LVCLATGFYP DHVELSWWVN GKEVHSGVCT DPQPLKEQPA LNSRYALSS 450
 RLRVSATFWQ DPRNHFRQV QFYGLSENDE WTQDRAKPV TQIVSAEAWGR 500
 AD 502

T-cell receptor alpha chain

GDAKTTQPNL MESNEEEPVH LPCNHSTISG TDYIHWYRQL PSQGPEYVIH 50
 GLTSNVNRM ASLAIADRK SSTLILHRAT LRDAVYVYCI LILGHSRLNG 100
 YIATFGKTK LSVIPNIQNP DPVYQLRDS KSSDKSVCLF TDFDSQTNVS 150
 QSKSDVYIT DKCVLDMRSM DFKNSAVAW SNKSDFACAN AFNNSIIPED 200
 T 201

Peptide linkers / Peptides liants / Péptidos de unión

GGGGSGGGSGGGSGGGSGGGG 108-131, GGGG 254-258

Mutation / Mutation / Mutación

T-Cell Receptor beta chain: S429>C, C447>A, N461>D

T-Cell Receptor alpha chain: T163>C

Post-translational modifications

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

Intra-scFv: 23-88, 153-227

Intra-TCR beta chain: 281-349, 403-468

Intra-TCR alpha chain: 23'-89', 138'-188'

Inter-TCR alpha chain - TCR beta chain: 163'-429

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

none

brigimadlinum

brigimadlin

(3S,3'S,3a'S,10a'S)-6-chloro-3'-(3-chloro-2-fluorophenyl)-1'-(cyclopropylmethyl)-6'-methyl-2-oxo-1,2,3',3'a,10',10'a-hexahydro-1'H-spiro[indole-3,2'-pyrrolo[2',3':4,5]pyrrolo[1,2-b]indazole]-7'-carboxylic acid

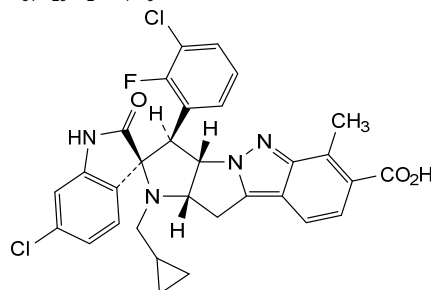
brigimadline

acide (3S,3'S,3a'S,10a'S)-6-chloro-3'-(3-chloro-2-fluorophényl)-1'-(cyclopropylméthyl)-6'-méthyl-2-oxo-1,2,3',3'a,10',10'a-hexahydro-1'H-spiro[indole-3,2'-pyrrolo[2',3':4,5]pyrrolo[1,2-b]indazole]-7'-carboxylique

brigimadlina

ácido (3S,3'S,3a'S,10a'S)-6-cloro-3'-(3-cloro-2-fluorofenil)-1'-(ciclopropilmetil)-6'-metil-2-oxo-1,2,3',3'a,10',10'a-hexahidro-1'H-spiro[indol-3,2'-pirrolo[2',3':4,5]pirrolo[1,2-b]indazol]-7'-carboxílico

C₃₁H₂₅Cl₂FN₄O₃



canrivitugum

canrivitug

immunoglobulin G1- lambda, anti-[*Homo sapiens* severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) spike (S) protein, receptor binding domain (RBD)], *Homo sapiens* monoclonal antibody; gamma1 heavy chain *Homo sapiens* (1-451) [VH (*Homo sapiens*IGHV4-59*11 (97.9%) -(IGHD) -IGHJ5*02 (93.8%), CDR-IMGT [8.7.15] (26-33.51-57.96-110)) (1-121) -*Homo sapiens*IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (218) (122-219), hinge 1-15 (220-234), CH2 (235-344), CH3 D12 (360), L14 (362) (345-449), CHS (450-451)) (122-451)], (224-217')-disulfide with lambda light chain *Homo sapiens* (1'-218') [V- LAMBDA (*Homo sapiens*IGLV1-40*01 (94.9%) -IGLJ1*01 (100%), CDR-IMGT [9.3.12] (26-34.52-54.91-102)) (1'-112') -*Homo sapiens*IGLC2*01 (100%) (113'-218')]; dimer (230-230":233-233")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

canrivitug

immunoglobuline G1-lambda, anti-[domaine de liaison au récepteur (RBD) de la glycoprotéine spike (S) du coronavirus 2 du syndrome respiratoire aigu sévère (SARS-CoV-2)], anticorps monoclonal *Homo sapiens*; chaîne lourde gamma1 *Homo sapiens* (1-451) [VH (*Homo sapiens*IGHV4-59*11 (97.9%) -(IGHD) -IGHJ5*02 (93.8%), CDR-IMGT [8.7.15] (26-33.51-57.96-110)) (1-121) -*Homo sapiens*IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (218) (122-219), charnière 1-15 (220-234), CH2 (235-344), CH3 D12 (360), L14 (362) (345-449), CHS (450-451)) (122-451)], (224-217')-disulfure avec la chaîne légère lambda *Homo sapiens* (1'-218') [V-LAMBDA (*Homo sapiens*IGLV1-40*01 (94.9%) -IGLJ1*01 (100%), CDR-IMGT [9.3.12] (26-34.52-54.91-102)) (1'-112') -*Homo sapiens*IGLC2*01 (100%) (113'-218')]; dimère (230-230":233-233")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

canrivitug

immunoglobulina G1-lambda, anti-[dominio de unión al receptor (RBD) de la glicoproteína spike (S) del coronavirus 2 del síndrome respiratorio agudo severo (SARS-CoV-2)], anticuerpo monoclonal *Homo sapiens*; cadena pesada gamma1 *Homo sapiens* (1-451) [VH (*Homo sapiens*IGHV4-59*11 (97.9%) -(IGHD) -IGHJ5*02 (93.8%), CDR-IMGT [8.7.15] (26-33.51-57.96-110)) (1-121) -*Homo sapiens*IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (218) (122-219), bisagra 1-15 (220-234), CH2 (235-344), CH3 D12 (360), L14 (362) (345-449), CHS (450-451)) (122-451)], (224-217')-disulfuro con la cadena ligera lambda *Homo sapiens* (1'-218') [V-LAMBDA (*Homo sapiens*IGLV1-40*01 (94.9%) -IGLJ1*01 (100%), CDR-IMGT [9.3.12] (26-34.52-54.91-102)) (1'-112') -*Homo sapiens*IGLC2*01 (100%) (113'-218')]; dímero (230-230":233-233")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

QVLTQESGPG	LVPKSETLSL	TCTVSGGSIS	SHYWSWIRQP	PGKLEWIGY	50
IYYSGSSNNY	PSLKSRTVIS	VDTSKNQFSL	KLNSVTAADT	AVVYCARHYD	100
ILTGFDWFDP	WQGGTLVTVS	SASTKGPVSF	PLAPSSKSTS	GGTAALGLCLV	150
KDYFPEFVTV	SWNSGALTSQ	VHTFPAVLQS	SGLYSLSSVV	TVPSSSLGTQ	200
TYICNVNHPK	SNTKVDKKVE	PKSCDKTHTC	PPCPAPELLG	GPSVFLFPFK	250
PKDTLMSRT	PEVTCVVVDV	SHEDPEVKFN	WYVDGVEVHN	AKTKPREEQY	300
NSTYRVVSVL	TVLHQDMLNG	KEYKCKVSNK	ALPAPIEKTI	SKARGQPREP	350
QVYTLPPSRD	ELTKNQVSLT	CLVKGFPYPS	IAVWESNGQ	PENNYKTTFP	400
VLDSGDGFLL	YSKLTVDKSR	WQQGNVFSCS	VMHEALHNHY	TQKSLSLSPG	450
K					451

Light chain / Chaîne légère / Cadena ligera

QSVLTQPPSV	SGAPGQRVTI	SCTGSSSNIG	THYDVHWYQQ	LPGTAPKLLI	50
YGNNSNRPSG	PDRFSGSKSG	TSASLAITGL	QAEDEADYIC	QSFNDSLTPA	100
YVFGTGKTVT	VLGQPKAAPS	VTLFPPSSSE	LQANKATLVC	LISDFYPGAV	150
TVAWKADSSP	VKAGVETTFP	SKQSNKYAA	SSYLSLTPEQ	WKSHRYSYSC	200
VTHEGSTVEK	TVAPTECS				218

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)	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-oxoproliolo)

H VH Q1: 1, 1"
L VL 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 biantenaricos complejos fucosilados

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

H CHS K2: 451, 451"

cemavafuspum #
cemavafusp

enterobacteria phage H19B L-methionyl-Shiga-like toxin 1 subunit A1 (SLT-1 subunit A1, SLT-1a1, verotoxin 1 subunit A1, verocytotoxin 1 subunit A1, EC:3.2.2.22) (2-252), variant (S⁴⁵>I⁴⁶, V⁵⁴>I⁵⁵, R⁵⁵>L⁵⁶, I⁵⁷>F⁵⁸, P⁵⁹>F⁶⁰, E⁶⁰>T⁶¹, E⁶¹>L⁶², G¹¹⁰>A¹¹¹, R¹⁸⁸>A¹⁸⁹, C²⁴²>S²⁴³, R²⁴⁸>A²⁴⁹, R²⁵¹>A²⁵²) fused via the peptide linker ²⁵³EFPKPSTPPGSSGGAP²⁶⁸ to an anti-(human programmed cell death 1 ligand 1 (PD-L1, CD274)) murine immunoglobulin single chain variable fragment (scFv) (269-501) containing the heavy chain variable region (VH) region (269-390), a ³⁹¹G³⁹⁵ peptide linker and the light chain variable region (VL) region (396-501) fused via peptide linker ⁵⁰²HHAA⁵⁰⁵ to an HLA-A*02 immunodominant MHC class I restricted epitope derived from human cytomegalovirus (CMV) pp65 (UL83) protein (506-514), disulfide bridged dimer, produced in *Escherichia coli*;

human scFv dimer monoclonal antibody fusion with human SLTA and MHC-I antigen; antigen: human programmed cell death 1 ligand 1, PD-L1, programmed death ligand 1, PDCD1 ligand 1, B7 homolog 1, B7-H1 (CD274); fusion protein (Shiga-like toxin 1, *Escherichia coli* subunit A1): 1-251 (ins1M T46I V55I R56L I58F P60F E61T E62L G111A R189A C243S R249A, R252A); linker: 252-268; type: Fv-heavy scFv; VH: 269-390; HV germline: *Homo sapiens* IGHV1-2*02; HJ germline: *Homo sapiens* IGHJ4*01; CDR Kabat H1: EYTMH (299-303); CDR Kabat H2: GINPNNGGTYWYNQKFKG (318-334); CDR Kabat H3: PYYGSGREDYFDY (367-379); linker: 391-395; Type: Fv-kappa scFv; light chain class: kappa; LV germline: *Homo sapiens* IGKV1-39*01; LJ germline: *Homo sapiens* IGKJ2*01; VL: 396-501; CDR Kabat L1: SASSSVSYMY (419-428); CDR Kabat L2: LTSNLAS (444-450); CDR Kabat L3: QQWSSNPPT (483-491); Linker: 502-505; fusion protein: 506-514 (major histocompatibility complex I HLA-A*02-restricted epitope, derived from human cytomegalovirus viral tegument protein UL83/pp65)

- cémavafusp sous-unité A1 de la toxine 1 du phage H19B d'entérobactéries de type L-méthionyl-Shiga (SLT-1 sous-unité A1, SLT-1a1, vérotoxine 1 sous-unité A1, vérocitotoxine 1 sous-unité A1, EC:3.2.2.22) (2-252), variant (S^{S45>I46}, V^{54>I55}, R^{55>L56}, I^{57>F58}, P^{59>F60}, E^{60>T61}, E^{61>L62}, G^{110>A111}, R^{188>A189}, C^{242>S243}, R^{248>A249}, R^{251>A252}) fusionnée via la liaison peptidique ²⁵³EFPKPSTPPGSSGGAP²⁶⁸ à un anti-(ligand 1 humain de mort cellulaire programmée 1 (PD-L1, CD274)) d'immunoglobuline murine au fragment variable à chaîne unique (scFv) (269-501) contenant la région (269-390) de la région variable de la chaîne lourde (VH), la liaison peptidique ³⁹¹GGGS³⁹⁵ et la région (396-501) de la région variable de la chaîne légère (VL) fusionnée via la liaison peptidique ⁵⁰²HHAA⁵⁰⁵ à un épitope restreint du CMH de classe I immunodominant HLA-A*02 dérivé de la protéine (506-514) pp65 (UL83) du cytomégalovirus humain (CMV), homodimère à pont disulfure, produit chez *Escherichia coli*;
fusion d'un anticorps monoclonal humain scFv dimère avec l'antigène humain SLTA et MHC-I; antigène: ligand 1 humain de mort cellulaire programmée 1, PD-L1, ligand de mort programmée 1, PDCD1 ligand 1, homologue 1 de B7, B7-H1 (CD274); protéine de fusion (toxine 1 de type Shiga, sous-unité A1 d'*Escherichia coli*): 1-251 (ins1M T46I V55I R56L I58F P60F E61T E62L G111A R189A C243S R249A, R252A); liaison: 252-268; type: Fv-lourde scFv; VH: 269-390; HV lignée germinale: *Homo sapiens* IGHV1-2*02; HJ lignée germinale: *Homo sapiens* IGHJ4*01; CDR Kabat H1: EYTMH (299-303); CDR Kabat H2: GINPNNGGTWYNQKFKG (318-334); CDR Kabat H3: PYYYSREDYFDY (367-379); liaison: 391-395; Type: Fv-kappa scFv; classe de la chaîne légère: kappa; LV lignée germinale: *Homo sapiens* IGKV1-39*01; LJ lignée germinale: *Homo sapiens* IGKJ2*01; VL: 396-501; CDR Kabat L1: SASSSVSYMY (419-428); CDR Kabat L2: LTSNLAS (444-450); CDR Kabat L3: QQWSSNPPT (483-491); liaison: 502-505; protéine de fusion: 506-514 (épitope restreint au complexe majeur d'histocompatibilité I HLA-A*02, dérivé de la protéine tégumentale virale UL83/pp65 du cytomégalovirus humain)
- cemavafusp enterobacteria fago H19B L-metionil-Shiga-like toxina 1 subunidad A1 (SLT-1 subunidad A1, SLT-1a1, verotoxina 1 subunidad A1, verocitotoxina 1 subunidad A1, EC:3.2.2.22) (2-252), variante (S^{45>I46}, V^{54>I55}, R^{55>L56}, I^{57>F58}, P^{59>F60}, E^{60>T61}, E^{61>L62}, G^{110>A111}, R^{188>A189}, C^{242>S243}, R^{248>A249}, R^{251>A252}) fusionada a través del enlace peptídico ²⁵³EFPKPSTPPGSSGGAP²⁶⁸ a un anti-(ligando 1 de muerte celular programada humana 1 (PD-L1, CD274)) fragmento variable de cadena única de inmunoglobulina murina (scFv) (269-501) que contiene la región variable de cadena pesada (VH) región (269-390), un enlace peptídico ³⁹¹GGGS³⁹⁵ y la región variable de cadena ligera (VL) región (396-501) fusionado a través de un enlace peptídico ⁵⁰²HHAA⁵⁰⁵ a un epítipo HLA-A*02 restringido inmunodominante MHC de clase I derivado del citomegalovirus humano (CMV) pp65 (UL83) proteína (506-514), homodímero con puente disulfuro, producido en *Escherichia coli*;
anticuerpo monoclonal humano con dímero scFv de fusión con SLTA humano y antígeno MHC-I; antígeno: ligando 1 de muerte celular programada humana, PD-L1, ligando 1 de muerte programada, ligando 1 PDCD1, B7 homólogo 1, B7-H1 (CD274); proteína de fusión (toxina 1 de tipo Shiga, subunidad A1 de *Escherichia coli*): 1-251 (ins1M T46I V55I R56L I58F P60F E61T E62L G111A R189A C243S R249A, R252A); enlace: 252-268; type: Fv-pesado scFv; VH: 269-390; línea germinal HV: *Homo sapiens* IGHV1-2*02; línea germinal HJ: *Homo sapiens* IGHJ4*01; CDR Kabat H1: EYTMH (299-303); CDR Kabat H2: GINPNNGGTWYNQKFKG (318-334); CDR Kabat H3: PYYYSREDYFDY (367-379); enlace: 391-395; tipo: Fv-kappa scFv; cadena ligera: chain class: kappa; LV Germline: *Homo sapiens* IGKV1-39*01; LJ germline: *Homo sapiens* IGKJ2*01; VL: 396-501; CDR Kabat L1: SASSSVSYMY (419-428); CDR Kabat L2: LTSNLAS (444-450); CDR Kabat L3: QQWSSNPPT (483-491); enlace: 502-505; proteína de fusión: 506-514 (epítipo restringido del complejo de histocompatibilidad mayor I HLA-A*02, derivado de la proteína del tegumento viral de citomegalovirus humano UL83/pp65)

Sequence / Séquence / Secuencia

MKEFTLD~~F~~ST AKTYVDSLNV IRSAIGTPLQ TISSGGTSLL MIDSGI~~G~~DNL 50
 FAVD~~I~~L~~G~~F~~D~~F~~E~~ TLGRFNNLRL IVERN~~N~~LYVT GFVNRTNNVF YRFADEFSHVT 100
 FPGTTAVTLS ADSSYTTLQR VAGISRTGMQ INRHSLTTSY LDLMSHSGTS 150
 LTQSVARAML R~~F~~VTVTAEAL RFRQIQRGFR TTLDDLSC~~A~~S YVMTAEDVDL 200
 TLN~~W~~GR~~L~~SSV LPDYHGQDSV RVGRISFGSI NAILGSVALI LNS~~H~~H~~H~~A~~S~~AV 250
A~~A~~~~E~~F~~F~~K~~P~~S~~T~~P PGSSGGAFEV QLQQSGPELV KPGASVKISC KTSGYTFTEY 300
 TMHWVKQRHG K~~S~~LEWIGGIN PNNGGTWYNQ KFKGKATLTV DKSSSTAYME 350
 LRSLTSEDSA VYFCARPYYY GSREDYFDYW GQGTTLTVSS GGGGSDIQMT 400
 QSPSSLSASV GDRVTITCSA SSSVS~~Y~~MYWY QQKPRSSPKP WIYLTSLNLS 450
 GVPARFSGSG SGTYSYLTIS SMEAEDAATY YCQQWSSNPP TFGGGTKLEL 500
KHHAANLVPM VATV 514

Mutation / Mutación / Mutación

N-L-methionyl added (M¹), S⁴⁵>I⁴⁶, V⁵⁴>I⁵⁵, R⁵⁵>L⁵⁶, I⁵⁷>E⁵⁸, P⁵⁹>F⁶⁰, E⁶⁰>T⁶¹, E⁶¹>I⁶²,
 G¹¹⁰>A¹¹¹, R¹⁸⁸>A¹⁸⁹, C²⁴²>S²⁴³, R²⁴⁸>A²⁴⁹, R²⁵¹>A²⁵²

Peptide linkers / Peptides liants / Péptidos de unión

EFPKPSTPPGSSGGAP 253-268; GGGS 391-395, HHAA 502-505

Post-translational modifications

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

Intra VH: 290-364, 290'-364'

Intra VL: 418-482, 418'-482'

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

none

cemsidomidum

cemsidomide

(3S)-3-(6-[[4-(morpholin-4-ylmethyl)phenyl]methyl]-2-oxobenz[*cd*]indol-1(2*H*)-yl]piperidine-2,6-dione

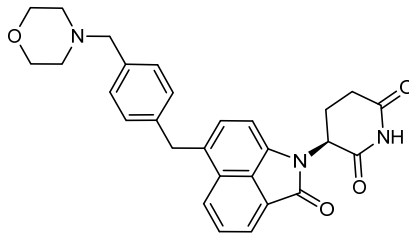
cemsidomide

(3S)-3-(6-[[4-(morpholin-4-ylméthyl)phényl]méthyl]-2-oxobenz[*cd*]indol-1(2*H*)-yl]pipéridine-2,6-dione

cemsidomida

(3S)-3-(6-[[4-(morfolin-4-ilmetil)fenil]metil]-2-oxobenz[*cd*]indol-1(2*H*)-yl]piperidina-2,6-diona

C₂₈H₂₇N₃O₄



crisugabalinum

crisugabalin

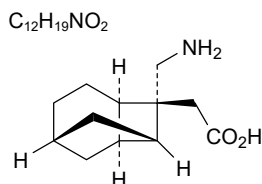
[(1*S*,2*S*,3*R*,6*S*,8*S*)-2-(aminomethyl)tricyclo[4.2.1.0^{3,8}]nonan-2-yl]acetic acid

crisugabalin

acide [(1*S*,2*S*,3*R*,6*S*,8*S*)-2-(aminométhyl)tricyclo[4.2.1.0^{3,8}]nonan-2-yl]acétique

crisugabalina

ácido [(1*S*,2*S*,3*R*,6*S*,8*S*)-2-(aminométil)triciclo[4.2.1.0^{3,8}]nonan-2-il]acético



daniluromerum

daniluromer

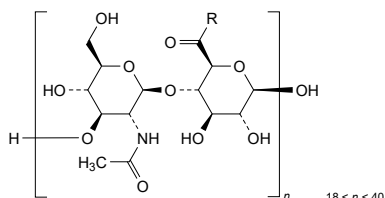
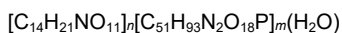
hyaluronic acid, degraded, partially amidated with (2*R*)-3-[[2-aminoethoxy](hydroxy)phosphoryl]oxy}propane-1,2-diyl di(hexadecanoate)

daniluromère

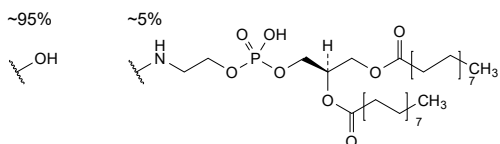
acide hyaluronique, dégradé, partiellement amidifié par le di(hexadécanoate) de (2*R*)-3-[[2-aminoéthoxy](hydroxy)phosphoryl]oxy}propane-1,2-diyle

danilurómero

ácido hialurónico, degradado, parcialmente amidificado por (2*R*)-3-[[2-aminoetoxi](hidroxi)fosforil]oxi}propano-1,2-diilo di(hexadecanoato)



R :



darizmetinibum

darizmetinib

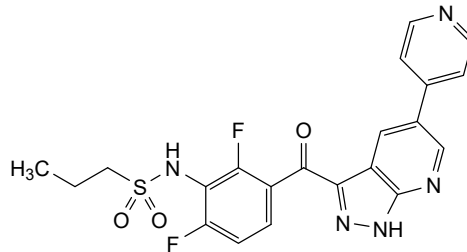
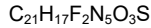
N-{2,6-difluoro-3-[5-(pyridin-4-yl)-1*H*-pyrazolo[3,4-*b*]pyridine-3-carbonyl]phenyl}propane-1-sulfonamide

darizmétinib

N-{2,6-difluoro-3-[5-(pyridin-4-yl)-1*H*-pyrazolo[3,4-*b*]pyridine-3-carbonyl]phényl}propane-1-sulfonamide

darizmetinib

N-{2,6-difluoro-3-[5-(piridin-4-il)-1*H*-pirazolo[3,4-*b*]piridina-3-carbonil]fenil}propano-1-sulfonamida



davutamigum #
davutamig

immunoglobulin G4-kappa, anti-MET (met proto-oncogene, hepatocyte growth factor (HGF) receptor, HGFR, scatter factor (SF) receptor, HGF/SF receptor, receptor tyrosine-protein kinase c-met, papillary renal cell carcinoma 2, RCCP2)], *Homo sapiens* monoclonal antibody, biparatopic (targeting two different non-overlapping epitopes on MET);

gamma4 heavy chain anti-MET *Homo sapiens* (1-448) [VH (*Homo sapiens* IGHV3-9*01 (94.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1-121) -*Homo sapiens* IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (122-219), hinge 1-12 S10>P (229) (220-231), CH2 L92 (310) (232-341), CH3 (342-446), CHS (447-448)) (122-448)], (135-215')-disulfide with kappa light chain anti-MET *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 (154), V101 (192) (109'-215')];

gamma4 heavy chain anti-MET *Homo sapiens* (1"-444") [VH (*Homo sapiens* IGHV3-53*04 (90.6%) -(IGHD) -IGHJ3*02 (93.8%), CDR-IMGT [8.7.11] (26-33.51-57.96-106)) (1"-117") -*Homo sapiens* IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10, G4v8 R115, F116, P125 (CH1 (118"-215"), hinge 1-12 S10>P (225) (216"-227"), CH2 L92 (306) (228"-337"), CH3 H115>R (432), Y116>F (433), L125>P (442) (338"-442"), CHS (443"-444")) (118"-444")], (131"-215""-disulfide with kappa light chain anti-MET *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 (154), V101 (192) (109""-215"")); dimer (227-223":230-226")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

davutamig

immunoglobuline G4-kappa, anti-MET (proto-oncogène met, récepteur du facteur de croissance hépatocytaire, HGFR, récepteur du facteur de dispersion (SF), récepteur de l'HGF/SF, récepteur protéine-tyrosine kinase c-met, carcinome papillaire à cellules rénales 2, RCCP2)], anticorps monoclonal *Homo sapiens*, biparatopique (ciblant deux épitopes différents non chevauchants sur MET);

chaîne lourde gamma4 anti-MET *Homo sapiens* (1-448) [VH (*Homo sapiens* IGHV3-9*01 (94.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1-121) - *Homo sapiens* IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (122-219), charnière 1-12 S10>P (229) (220-231), CH2 L92 (310) (232-341), CH3 (342-446), CHS (447-448)) (122-448)], (135-215')-disulfure avec la chaîne légère kappa anti-MET *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 (154), V101 (192) (109'-215')];

chaîne lourde gamma4 anti-MET *Homo sapiens* (1"-444") [VH (*Homo sapiens* IGHV3-53*04 (90.6%) -(IGHD) -IGHJ3*02 (93.8%), CDR-IMGT [8.7.11] (26-33.51-57.96-106)) (1"-117") - *Homo sapiens* IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10, G4v8 R115, F116, P125 (CH1 (118"-215")), charnière 1-12 S10>P (225) (216"-227"), CH2 L92 (306) (228"-337"), CH3 H115>R (432), Y116>F (433), L125>P (442) (338"-442"), CHS (443"-444")) (118"-444"), (131"-215")-disulfure avec la chaîne légère kappa anti-MET *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 (154), V101 (192) (109""-215"""); dimère (227-223":230-226")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

davutamig

immunoglobulina G4-kappa, anti-MET (proto-oncogen met, receptor del factor de crecimiento hepatocitario, HGFR, receptor del factor de dispersión (SF), receptor del HGF/SF, receptor proteína-tirosina kinasa c-met, carcinoma papilar con células renales 2, RCCP2)], anticuerpo monoclonal *Homo sapiens*, biparatópico (apuntando dos epítomos diferentes no superpuestos sobre MET);

cadena pesada gamma4 anti-MET *Homo sapiens* (1-448) [VH (*Homo sapiens* IGHV3-9*01 (94.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1-121) - *Homo sapiens* IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (122-219), bisagra 1-12 S10>P (229) (220-231), CH2 L92 (310) (232-341), CH3 (342-446), CHS (447-448)) (122-448)], (135-215')-disulfuro con la cadena ligera kappa anti-MET *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 (154), V101 (192) (109'-215')];

cadena pesada gamma4 anti-MET *Homo sapiens* (1"-444") [VH (*Homo sapiens* IGHV3-53*04 (90.6%) -(IGHD) -IGHJ3*02 (93.8%), CDR-IMGT [8.7.11](26-33.51-57.96-106)) (1"-117") - *Homo sapiens* IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10, G4v8 R115, F116, P125 (CH1 (118"-215")), bisagra 1-12 S10>P (225) (216"-227"), CH2 L92 (306) (228"-337"), CH3 H115>R (432), Y116>F (433), L125>P (442) (338"-442"), CHS (443"-444")) (118"-444"), (131"-215")-disulfuro con la cadena ligera kappa anti-MET *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 (154), V101 (192) (109""-215"""); dímero (227-223":230-226")-bisdisulfuro, producido en las células ováricas de hamster chino (CHO), forma glicosilada alfa

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

EVQLVESGGG LVQPGETSLRL SCAASGFTFD DYAMHWVRQA PGKGLEWVSG 50
 ITWNSYNIDY ADSVKGRFTI SRDNAKNSLY LQMNSLRAED TALYYCAKDD 100
 DYSNYVYFDY WQQGTLVTVS SASTKGPSVF PLAPCSRSTS ESTAALGCLV 150
 KDYFPEPVTV SWNSGALTSV VHTFPAVLQS SGLYSLSSVV TVPSSSLGTK 200
 TYTCNVDHKP SNTKVDKRVV SKYGPPCPPE PAPEFLGGPS VFLEPPKPKD 250
 TLMISRTPV TCVVVDVSQE DPEVQFNWYV DGVEVHNAKT KPREEQFNST 300
 YRVSVLTVL HQDWLNGKEY KCKVSNKGLP SSIKRTISKA KGQPREPQVY 350
 TLPPSQEEMT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTFPVLD 400
 SDGSFFLYSR LTVDKSRWQE GNVFSCSVMH EALHNHYTQK SLSLSLGLK 448

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

EVQLVESGGG LVQPGGSLRL SCAASGFIVT TNYMTWLRQA PGKGLEWVSL 50
 IYSSGHTYYA DSVKGRFTIS RHNSKNTLYL QMDSLRAEDT AVYVCASAFR 100
 ADVFDIWGQG TMVTVSSAST KGPSVFLPLAP CSRSTSESTA ALGCLVKDYF 150
 PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVTVVPS SSLGTRKTYTC 200
 NVDHKKPSNTK VDKRVESKYG PPCPPCPAPE FLGGPSVFLF PPKPKDTLMI 250
 SRTPEVTCVV VDVSDQEDPEV QFNWYVDGVE VHNAKTKPRE EQFNSTYRVV 300
 SVLTVLHQDW LNGKEYKCKV SNKGLPSSIE KTISKAKGQP REPQVYTLPP 350
 SQEEMTKNQV SLTCLVKGFI PSDIAVEWES NGQFENNYKT TFPVLDSDGS 400
 FFLYSRLTVD KSRWQEGNVF SCSVMHEALH NRFTQKSLSL SPGK 444

Light chain / Chaîne légère / Cadena ligera: anti-MET (L, L')

DIQMTQSPSS LSASVGRVIT ITCRASQSIIS SYLNWYQQKPK GKAPKLLIYA 50
 ASSLQSGVPS RFSGSGSGTD FTLLTISLQPE EDFATYICQQ SYSTPPITFG 100
 QGTRLEIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQNK 150
 VDNALQSGNS QESVTEQDSK DSTYSLSTL TSKADYEKH KKYACEVTHQ 200
 GLSSPVTKSF NRGEC 215

Post-translational modifications

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

Intra-H (C23-C104) 22-96 148-204 262-322 368-426
 22"-95" 144"-200" 258"-318" 364"-422"

Intra-L (C23-C104) 23"-88" 135"-195"
 23""-88"" 135""-195""

Inter-H-L (CH1 10-CL 126) 135-215' 131"-215"

Inter-H-H (h 8, h 11) 227-223* 230-226*

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

H CH2 N84.4: 298, 294"

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

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

H CHS K2: 448, 444"

dazostinagum

dazostinag

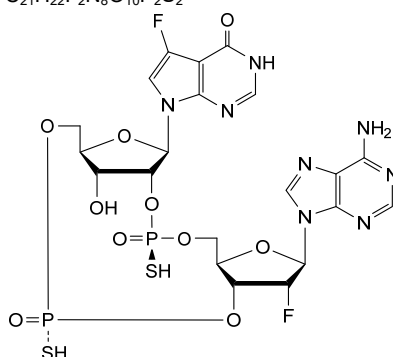
cyclo[(*P*³*R*)-2'-deoxy-2'-fluoro-*P*-thioadenylyl-(3'→5')-(*P*²*R*)-7-fluoro-*P*-thio-7-deazainosinyl-(2'→5')]

dazostinag

cyclo[(*P*³*R*)-2'-désoxy-2'-fluoro-*P*-thioadénylyl-(3'→5')-(*P*²*R*)-7-fluoro-*P*-thio-7-désazainosinyl-(2'→5')]

dazostinag

ciclo[(*P*³*R*)-2'-desoxi-2'-fluoro-*P*-tioadenilil-(3'→5')-(*P*²*R*)-7-fluoro-*P*-tio-7-desazainosinil-(2'→5')]

C₂₁H₂₂F₂N₈O₁₀P₂S₂

dazukibartum #
dazukibart

immunoglobulin G1- kappa, anti-[*Homo sapiens* IFNB1 (interferon beta)], humanized monoclonal antibody; gamma1 heavy chain humanized (1-448) [VH (*Homo sapiens* IGHV1-69*11 (84.7%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, G1v14-1 CH2 A1.3, A1.2, A1 (CH1 K120 (216) (120-217), hinge 1-15 (218-232), CH2 L1.3>A (236), L1.2>A (237), G1>A (239) (233-342), CH3 E12 (358), M14 (360) (343-447), CHS K2>del (448)) (120-448)], (222-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-16*01 (87.8%) -IGKJ4*01 (91.7%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (228-228":231-231")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from CHO-K1 cell line, lacking the glutamine synthetase (GS-KO) gene, glycoform alfa

dazukibart

immunoglobuline G1-kappa, anti-[*Homo sapiens* IFNB1 (interféron bêta)], anticorps monoclonal humanisé; chaîne lourde gamma1 humanisée (1-448) [VH (*Homo sapiens* IGHV1-69*11 (84.7%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, G1v14-1 CH2 A1.3, A1.2, A1 (CH1 K120 (216) (120-217), charnière 1-15 (218-232), CH2 L1.3>A (236), L1.2>A (237), G1>A (239) (233-342), CH3 E12 (358), M14 (360) (343-447), CHS K2>del (448)) (120-448)], (222-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-16*01 (87.8%) -IGKJ4*01 (91.7%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (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

dazukibart

inmunoglobulina G1-kappa, anti-[*Homo sapiens* IFNB1 (interferón beta)], anticuerpo monoclonal humanizado; cadena pesada gamma1 humanizada (1-448) [VH (*Homo sapiens* IGHV1-69*11 (84.7%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14, G1v14-1 CH2 A1.3, A1.2, A1 (CH1 K120 (216) (120-217), bisagra 1-15 (218-232), CH2 L1.3>A (236), L1.2>A (237), G1>A (239) (233-342), CH3 E12 (358), M14 (360) (343-447), CHS K2>del (448)) (120-448)], (222-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-16*01 (87.8%) -IGKJ4*01 (91.7%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (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

QVQLVQSGAE	VKKPGSSVKV	SCKASGYTFS	RYWMHWVRQA	PGQGLEWMGH	50
IDPSSDSTYY	NQKFKGRVTI	TADESTSTAY	MELSSLRSED	TAVYYCARWD	100
YGNLLFEYWG	QGTTLVTVSSA	STKGPSVFPL	APSSKSTSGG	TAALGCLVKD	150
YFPEPVTVSW	NSGALTSVGH	TTPAVLQSSG	LYSLSSVTVV	PSSSLGTQTY	200
ICNVNHKPSN	TKVDKVEPK	SCDKTHTCPP	CPAPEAAGAP	SFLLFPKPKK	250
DILMISRTP	VTCVVDVSH	EDPEVKFNWY	VDGVEVHNAK	TKPREEQYNS	300
TYRVVSVLTV	LHQDWLNGKE	YKCKVSNKAL	PAPIEKTISK	AKGQPREPQV	350
YTLPPSREEM	TKNQVSLTCL	VKGFYPSDIA	VEVESNGQPE	NNYKTTTPVL	400
DSDGSFFFLYS	KLTVDKSRWQ	QGNVFSCSVM	HEALHNHYTQ	KSLSLSPG	448

Light chain / Chaîne légère / Cadena ligera

DIQMTQSPSS	LSASVGDRTV	ITCRTSQDIG	NYLNWYQQKP	GKAFKLLIYS	50
TSRLHSGVPS	RFGSGSGTD	FTLTISSLQP	EDFATYYCQQ	GIILPITFGG	100
GTKVEIKRTV	AAPSVFIFPP	SDEQLKSGTA	SVVCLLNNFY	PREAKVQWVK	150
DNALQSGNSQ	ESVTEQDSK	STYLSLSTLT	LSKADYEKHK	VYACEVTHQG	200
LSPFVTKSFN	RGEC				214

Post-translational modifications

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

Intra-H (C23-C104) 22'-96' 146'-202' 263'-323' 369'-427'
22''-96'' 146''-202'' 263''-323'' 369''-427''

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

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

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

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal

Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamide (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprofilo)

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 biantennarios complejos fucosilados.

debamestrocelum

debamestrocel

autologous bone marrow-derived mesenchymal stromal cells (MSC) differentiated to secrete high levels of neurotrophic factors (NTF). The MSCs are isolated from the bone marrow aspirate and cultured in xeno-free growth medium containing 10% platelet lysate. To induce MSC differentiation, the cells are cultured in serum-free media supplemented with dibutyl cyclic AMP (dbcAMP), human basic fibroblast growth factor (bFGF), human platelet derived growth factor (PDGF-AA), and human heregulin- β 1. The cells express mesenchymal progenitor cell marker cluster of differentiation 73 (CD73), CD90, and CD105 (>90%) and secrete high levels of NTF (glial cell line-derived neurotrophic factor (GDNF), brain derived neurotrophic factor (BDNF), vascular endothelial growth factor (VEGF) and hepatocyte growth factor (HGF)), having VEGF (≥ 7000 pg/ 10^6 cells) as the most representative

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cellules stromales mésenchymateuses (MSC) autologues dérivées de la moelle osseuse, différenciées pour sécréter des niveaux élevés de facteurs neurotrophiques (NTF). Les MSC sont isolées à partir d'une aspiration de moelle osseuse et cultivées dans un milieu de croissance non-xéno contenant 10% de lysat de plaquettes. Pour induire la différenciation des MSC, les cellules sont cultivées dans un milieu sans sérum complété par de l'AMP cyclique dibutyryle (dbcAMP), du facteur de croissance basique des fibroblastes humain (bFGF), du facteur de croissance dérivé des plaquettes humaines (PDGF-AA) et de l'héréguline β 1 humaine.

Les cellules expriment les marqueurs des classes de différenciation 73 (CD73) de cellules progénitrices mésenchymateuses, CD90 et CD105 (>90%) et sécrètent des niveaux élevés de NTF (facteur neurotrophique dérivé de la lignée de cellules gliales (GDNF), facteur neurotrophique dérivé du cerveau (BDNF), facteur de croissance endothéliale vasculaire (VEGF) et facteur de croissance des hépatocytes (HGF)), le VEGF (≥ 7000 pg/10⁶ cellules) étant le plus représentatif

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células mesenquimales estromales (MSC) autólogas, derivadas de médula ósea, diferenciadas para secretar niveles altos de factores neurotróficos (NFT). Las MSCs se aíslan del aspirado de médula ósea y se cultivan en medio de crecimiento sin componentes xenogénicos que contiene 10% de lisado plaquetario. Para inducir la diferenciación de las MSC, las células se cultivan en medio sin suero suplementado con dibutilil AMP cíclico (dbcAMP), factor de crecimiento de fibroblastos básico (bFGF) humano, factor de crecimiento derivado de plaquetas humano (PDGF-AA) y heregulina β 1 humana. Las células expresan marcadores de células mesenquimales progenitoras grupo de diferenciación 73 (CD73), CD90 y CD105 (>90%) y secretan niveles altos de NTF (factor neurotrófico derivado de la línea de células gliales (GDNF), factor neurotrófico derivado de cerebro (BDNF), factor de crecimiento del endotelio vascular (VEGF) y factor de crecimiento de hepatocitos (HGF)), teniendo al VEGF (≥ 7000 pg/10⁶ células) como el más representativo

detalimogenum voraplasmidum #

detalimogene voraplasmid

DNA plasmid encoding codon-optimized human interleukin-12 (IL-12) subunits p40 (β) and p35 (α) joined by a ten amino acid linker sequence (VPGVG)₂, under control of a cytomegalovirus (CMV) enhancer-promoter and a bovine growth hormone (bGH) polyadenylation signal, plus two retinoic acid-inducible gene I (RIG-I) agonists (non-protein coding double-stranded RNA eRNA11a and adenovirus VA RNAI) under control of RNA Pol-III promoters. The plasmid also contains an origin of replication, a human T-cell leukemia virus type 1 (HTLV-1) R region, and a β -globin intron

détalimogène voraplasme

plasmide d'ADN codant les sous-unités p40 (β) et p35 (α) de l'interleukine-12 (IL-12) humaine aux codons optimisés et réunies par une séquence de liaison de dix acides aminés (VPGVG)₂, sous le contrôle d'un amplificateur-promoteur du cytomégalovirus (CMV) et d'un signal de polyadénylation de l'hormone de croissance bovine (bGH), plus deux agonistes du gène I inducible par l'acide rétinoïque (RIG-I) (ARN eRNA11a double brin non codant des protéines et le RNAI de l'adénovirus VA) sous le contrôle de promoteurs RNA Pol-III. Le plasmide contient également une origine de répllication, une région R du virus de la leucémie humaine à lymphocytes T de type 1 (HTLV-1) et un intron de la β -globine

detalimogén voraplásmido

plásmido de ADN que codifica, con codones optimizados, para las subunidades p40 (β) y p35 (α) de la interleuquina-12 (IL-12) humana unida a una secuencia de unión de diez amino ácidos (VPGVG)₂, bajo el control de un potenciador-promotor de citomegalovirus (CMV) y una señal de poliadenilación de la

hormona de crecimiento bovina (bGH), más dos agonistas del gen inducible por ácido retinoico I (RIG-I) (ARN no codificante de doble cadena eRNA11a y VA RNAI de adenovirus) bajo el control de promotores de ARN pol-III. El plásmido también contiene un origen de la replicación, una región R del virus de la leucemia de linfocitos T humano tipo 1 (HTLV-1) y un intrón de la β-globina

deupirfenidonum

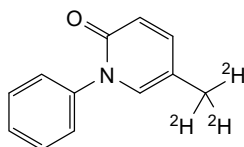
deupirfenidone

5-(²H₃)methyl-1-phenylpyridin-2(1*H*)-one

deupirfénidone

5-(²H₃)méthyl-1-phénylpyridin-2(1*H*)-one

deupirfenidona

5-(²H₃)metil-1-fenilpiridin-2(1*H*)-onaC₁₂H₈²H₃NO**dibutepinephrinum**

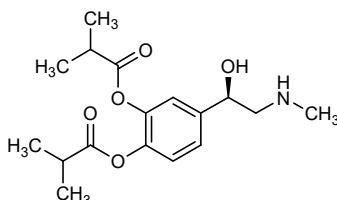
dibutepinephrine

4-[(1*R*)-1-hydroxy-2-(methylamino)ethyl]-1,2-phenylene bis(2-methylpropanoate)

dibutépinéphrine

bis(2-méthylpropanoate) de 4-[(1*R*)-1-hydroxy-2-(méthylamino)éthyl]-1,2-phénylène

dibutepinefrina

bis(2-metilpropanoato) de 4-[(1*R*)-1-hidroxi-2-(metilamino)etil]-1,2-fenilenoC₁₇H₂₅NO₅**durcabtagemum autoleucelum #**

durcabtogene autoleucel

autologous T lymphocytes obtained from peripheral blood mononuclear cells by leukapheresis, transduced with a self-inactivating, non-replicating lentiviral vector encoding a chimeric antigen receptor (CAR) targeting human B cell maturation antigen (BCMA). The expressed transgene comprises a CD8α leader sequence, an anti-BCMA single chain variable fragment (scFv), a CD8α hinge and transmembrane domain, and a 4-1BB (CD137) and CD3ζ signalling domain, under control of the human elongation factor 1α (EF-1α) promoter. The construct is flanked by 5' and 3' long terminal repeats (LTRs) and also contains a ψ packaging signal, a truncated *gag*, a Rev response element

	<p>(RRE), a central polypurine tract (cPPT) sequence and a synthetic ID tag sequence. The leukapheresis material is enriched for CD4+ and CD8+ T lymphocytes by positive immunoselection, activated by CD3 and CD28 agonists and transduced with the lentiviral vector in serum-free media containing interleukin 2 (IL-2). Without further cell propagation <i>in vitro</i>, the T lymphocytes are washed, formulated for infusion, and cryopreserved. The T lymphocytes phenotype very closely resembles that of the initial leukapheresis material. The cell suspension consists of T lymphocytes ($\geq 80\%$; $\leq 1\%$ B cells), with a minimum of 4.0% of the T lymphocytes expressing the CAR-BCMA transgene. The T lymphocytes secrete interferon gamma (IFN-γ) and IL-2 following co-culture with BCMA-expressing cells</p>
durcabtagène autoleucel	<p>lymphocytes T autologues obtenus à partir de cellules mononucléaires de sang périphérique par leucaphérèse, transduits avec un vecteur lentiviral auto-inactivant et non répliquant codant un récepteur antigénique chimérique (CAR) ciblant l'antigène de maturation des cellules B humaines (BCMA). Le transgène exprimé comprend une séquence de tête CD8α, un fragment variable à chaîne unique (scFv) anti-BCMA, un domaine charnière et transmembranaire CD8α, et un domaine de signalisation 4-1BB (CD137) et CD3ζ, sous le contrôle du promoteur du facteur d'élongation 1α (EF-1α) humain. La construction est flanquée de répétitions longues terminales (LTR) en 5' et 3' et contient également un signal d'encapsulation ψ, un <i>gag</i> tronqué, un élément de réponse Rev (RRE), une séquence de tractus polypurine central (cPPT) et une séquence synthétique avec étiquette d'identification. Le matériel de leucaphérèse est enrichi en lymphocytes T CD4+ et CD8+ par immunosélection positive, activé par des agonistes CD3 et CD28 et transduit avec le vecteur lentiviral dans un milieu sans sérum contenant de l'interleukine 2 (IL-2). Sans propagation cellulaire supplémentaire <i>in vitro</i>, les lymphocytes T sont lavés, formulés pour la perfusion et cryoconservés. Le phénotype des cellules T ressemble beaucoup à celui du matériel de leucaphérèse initial. La suspension cellulaire est constituée de lymphocytes T ($\geq 80\%$; $\leq 1\%$ de cellules B), avec un minimum de 4.0 % des lymphocytes T exprimant le transgène CAR-BCMA. Les lymphocytes T sécrètent de l'interféron gamma (IFN- γ) et IL-2 suite à la coculture avec des cellules exprimant BCMA</p>
durcabtagén autoleucel	<p>linfocitos T autólogos obtenidos de células mononucleares de sangre periférica mediante leucoaféresis, transducidos con un vector lentiviral auto inactivante, no replicativo, que codifica para un receptor de antígenos quimérico (CAR) dirigido al antígeno de maduración de células B (BCMA). El transgén expresado contiene una secuencia líder de CD8α, un fragmento variable de cadena sencilla (scFv) anti-BCMA, un dominio bisagra y transmembrana de CD8α, y un dominio de señalización 4-1BB (CD137) y CD3ζ, bajo el control del promotor del factor de elongación 1 alfa (EF1α). El constructo está flanqueado por repeticiones terminales largas (LTRs) en 5' y 3' y también contiene una señal de empaquetamiento ψ, un <i>gag</i> truncado, un elemento de respuesta Rev (RRE), una secuencia de tracto de polipurina central (cPPT) y una secuencia etiqueta ID sintética. El material de leucoaféresis se enriquece para linfocitos T CD4+ y CD8+ mediante inmunoselección positiva, se activa mediante agonistas de CD3 y CD28 y se transduce con el vector lentiviral en medio sin suero que contiene interleuquina 2 (IL-2). Sin más propagación <i>in vitro</i>, los linfocitos T se lavan, se formulan para infusión y se</p>

criopreservan. El fenotipo de los linfocitos T se parece mucho al del material de leucoaféresis inicial. La suspensión celular consiste en linfocitos T ($\geq 80\%$; $\leq 1\%$ de linfocitos B), con un mínimo del 4.0% de linfocitos T que expresan el transgén CAR-BCMA. Los linfocitos T secretan interferón gamma (IFN- γ) e IL-2 tras el cocultivo con células que expresan BCMA

duvakitugum

duvakitug

immunoglobulin G1-lambda, anti-[*Homo sapiens* TNFSF15 (tumor necrosis factor (TNF) superfamily member 15, vascular endothelial cell growth inhibitor, VEGI, TNF superfamily ligand TL1A)], *Homo sapiens* monoclonal antibody;
gamma1 heavy chain *Homo sapiens* (1-448) [VH (*Homo sapiens* IGHV1-8*01 (92.9%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119)-*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (216) (120-217), hinge 1-15 (218-232), CH2 (233-342), CH3 D12 (358), L14 (360) (343-447), CHS K2>del (448)) (120-448)], (222-215')-disulfide with lambda light chain *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV1-40*01 (85.7%) -IGLJ2*01 (90.9%), CDR-IMGT [9.3.10] (26-34.52-54.91-100)) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')]; dimer (228-228":231-231")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1SV, glycoform alfa

duvakitug

immunoglobuline G1-lambda, anti-[*Homo sapiens* TNFSF15 (membre 15 de la superfamille du facteur de nécrose tumorale (TNF), inhibiteur de la croissance des cellules endothéliales vasculaires, VEGI, ligand TL1A de la superfamille du TNF)], anticorps monoclonal *Homo sapiens*;
chaîne lourde gamma1 *Homo sapiens* (1-448) [VH (*Homo sapiens* IGHV1-8*01 (92.9%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119)-*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (216) (120-217), charnière 1-15 (218-232), CH2 (233-342), CH3 D12 (358), L14 (360) (343-447), CHS K2>del (448)) (120-448)], (222-215')-disulfure avec la chaîne légère lambda *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV1-40*01 (85.7%) -IGLJ2*01 (90.9%), CDR-IMGT [9.3.10] (26-34.52-54.91-100)) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')]; dimère (228-228":231-231")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1SV, glycoforme alfa

duvakitug

inmunoglobulina G1-lambda, anti-[*Homo sapiens* TNFSF15 (miembro 15 de la superfamilia del factor de necrosis tumoral (TNF), inhibidor del crecimiento de las células endoteliales vasculares, VEGI, ligando TL1A de la superfamilia del TNF)], anticuerpo monoclonal *Homo sapiens*;
cadena pesada gamma1 *Homo sapiens* (1-448) [VH (*Homo sapiens* IGHV1-8*01 (92.9%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119)-*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14(CH1 K120 (216) (120-217), bisagra 1-15 (218-232), CH2 (233-342), CH3 D12 (358), L14 (360) (343-447), CHS K2>del (448)) (120-448)], (222-215')-disulfuro con la cadena ligera lambda *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV1-40*01 (85.7%) -IGLJ2*01 (90.9%), CDR-IMGT [9.3.10] (26-34.52-54.91-100)) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')]; dímero (228-228":231-231")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1SV, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada
 QVQLVQSGAE VKKPGASVKV SCKASGYTFT SYDINWVRQA PGQGLEWMGW 50
 LNPNSGYTGY AQKPFQGRVTM TADRSTSTAY MELSSLRSED TAVYYCAREV 100
 PETAAAFYEWG QGTLVTVSSA STKGPSVFPPL APSSKSTSGG TAALGCLVKD 150
 YFPEPVTWVW NSGALTSQVH TFPVAVLQSSG LYSLSVTVV PSSSLGTQTY 200
 ICNVNHHKPSN TKVDKKEVEPK SCDKHTHTCPP CPAPPELLGGP SVFLFPPKPK 250
 DTLMISRTP E VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKFREEQYNS 300
 TYRVVSVLTV LHQDNLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV 350
 YTLPPSRDEL TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTTPEVL 400
 DSDGSEFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPG 448

Light chain / Chaîne légère / Cadena ligera
 QSVLTQPPSV SGAPGQRVTI SCTSSSSSDIG AGLGVHVVYQQ LPGTAPKLLI 50
 EGYYNRPSPGV PDRFSGSKSG TSASLTITGL LPEDEGDYIC QSWDGTLSAL 100
 FGGGKTLTVL GQPKAAPSVT LFPSPSEELQ 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) 22-96 146-202 263-323 369-427
 22"-96" 146"-202" 263"-323" 369"-427"
 Intra-L (C23-C104) 22"-90" 138"-197"
 22"-90" 138"-197"
 Inter-H-L (h 5-CL 126) 222-215' 222"-215"
 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"
 L VL 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 biantenaricos complejos fucosilados

ederimotidum
 ederimotide

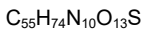
[R126>Y]-human Wilms tumor protein (WT33)-(126-134)-peptide;
 L-tyrosyl-L-methionyl-L-phenylalanyl-L-prolyl-L-asparaginyl-L-alanyl-L-prolyl-L-tyrosyl-L-leucine

édérimotide

[R126>Y]-protéine humaine de la tumeur de Wilms (WT33)-(126-134)-peptide;
 L-tyrosyl-L-méthionyl-L-phénylalanyl-L-prolyl-L-asparaginyl-L-alanyl-L-prolyl-L-tyrosyl-L-leucine

ederimotida

[R126>Y]-proteína humana del tumor de Wilms (WT33)-(126-134)-péptido;
 L-tirosil-L-metionil-L-fenilalanil-L-prolil-L-asparaginil-L-alanyl-L-prolil-L-tirosil-L-leucina



H – Tyr – Met – Phe – Pro – Asn – Ala – Pro – Tyr – Leu – OH

efbalropendekinum alfa #
 efbalropendekin alfa

human interleukin-15 (IL-15) fragment (1-114) variant (D³⁰>N, E⁶⁴>Q, N⁶⁵>D) fused via peptide linker ¹¹⁵GGGG¹¹⁹ to a human immunoglobulin G1 C-terminal Fc fragment (120-350) variant, [*Homo sapiens* IGHG1*03; hinge: 120-134 (C124S); CH2: 135-243 (E137P, L138V, L139A, G139-140del, S170K, Q198E) whereby E137P, L138V, L139A, G139-140del matches

	<p>IGHG2*02); CH3: 244-348 (L271D, K273S, N287D, Q321E, N324D, M331L, N337S); CHS: 349-350], disulfide bridge with human interleukin-15 receptor subunit alpha fragment (1-65) fused via the ⁶⁶GGGGS⁷⁰ peptide linker to a human immunoglobulin G1 Fc fragment (71-301) variant [<i>Homo sapiens</i> IGHG1*03; Hinge: 71-85 C75S]; CH2: 86-194 (E88P, L89V, L90A, G90-91del, S121K); CH3: 195-299 (E211Q, S218K, M282L, N288S); CHS: 300-301], disulfide bridged heterodimer, produced in Chinese hamster ovary (CHO-M) cells, glycoform alfa</p>
<p>efbalropendékine alfa</p>	<p>variant (D³⁰>N, E⁶⁴>Q, N⁶⁵>D) du fragment (1-114) de l'interleukine-15 (IL-15) humaine fusionné via la liaison peptidique ¹¹⁵GGGGS¹¹⁹ à un variant du fragment Fc C-terminal de l'immunoglobuline G1 humaine (120-350), [<i>Homo sapiens</i> IGHG1*03; charnière: 120-134 (C124S); CH2: 135-243 (E137P, L138V, L139A, G139-140del, S170K, Q198E par lequel E137P, L138V, L139A, G139-140del correspond à IGHG2*02); CH3: 244-348 (L271D, K273S, N287D, Q321E, N324D, M331L, N337S); CHS: 349-350], pont disulfure avec le fragment alpha de la sous-unité du récepteur de l'interleukine-15 humaine (1-65) fusionné via la liaison peptidique ⁶⁶GGGGS⁷⁰ à un variant du fragment Fc de l'immunoglobuline G1 humaine (71-301) [<i>Homo sapiens</i> IGHG1*03; charnière: 71-85 (C75S); CH2 : 86-194 (E88P, L89V, L90A, G90-91del, S121K); CH3: 195-299 (E211Q, S218K, M282L, N288S); CHS: 300-301], hétérodimère à pont disulfure, produit dans des cellules ovariennes de hamster chinois (CHO-M), glycoforme alfa</p>
<p>efbalropendekina alfa</p>	<p>interleukina-15 humana (IL-15) fragmento (1-114) variante (D³⁰>N, E⁶⁴>Q, N⁶⁵>D) fusionado a través del enlace peptídico ¹¹⁵GGGGS¹¹⁹ al fragment Fc de una inmunoglobulina humana terminal G1 C (120-350) variante, [<i>Homo sapiens</i> IGHG1*03; bisagra: 120-134 (C124S); CH2: 135-243 (E137P, L138V, L139A, G139-140del, S170K, Q198E por lo cual E137P, L138V, L139A, G139-140del se corresponde con IGHG2*02); CH3: 244-348 (L271D, K273S, N287D, Q321E, N324D, M331L, N337S); CHS: 349-350], puente disulfuro con el fragment de la subunidad alfa del receptor de la interleukina-15 humana (1-65) fusionado a través del enlace peptídico ⁶⁶GGGGS⁷⁰ al fragment Fc de la inmunoglobulina humana G1 (71-301) variante [<i>Homo sapiens</i> IGHG1*03; bisagra: 71-85 (C75S); CH2: 86-194 (E88P, L89V, L90A, G90-91del, S121K); CH3: 195-299 (E211Q, S218K, M282L, N288S); CHS: 300-301], heterodímero con puente disulfuro, prodido en células ováricas de hámster Chino (CHO-M), forma glicosilada alfa</p>

Sequence / Séquence / Secuencia

IL15-Fc:
NWVNVISDLK KIEDLIQSMH IDATLYTES_N VHPSCVKVTAM KCFLELQVIT 50
SLESGDASIH DTVQ_DLIILA NNSLSSNGVN TESSGCKECEE LEEKNIKEFL 100
QSFVHIVQMF INTS^{GGGGS}E PKSS_DDKTHTC PPCPAP^{PVA}G PSVFLFPPKP 150
 KDTLMISRTP EVTCVVVDV_K HEDPEVKFNW YVDGVEVHNA KTKPREE_EYN 200
 STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 250
 VYTLPPSREE MTKNQVSLTCLT **DV_SGFYPSDI AVEWES_DGQP ENNYKTTTPV** 300
 LQSDSGSFFLY SKLTVDKSRW **E_QGD_VVFSCSV L_LHEALH_SHYT QKSLSLSPGK** 350

IL15R-Fc:
ITCPPPMSVE HADIWVKSYS LYSRERYICN SGFKRKAGTS SLTECVLNKA 50
TNVAHWTTPS LKCIR^{GGGGS} EPKS_DDKTHT CPPCPAP^{PVA} GPSVFLFPPK 100
 PKDTLMISRTP EVTCVVVDV **K_HEDPEVKFNW WYVDGVEVHNA AKTKPREEQY** 150
 NSTYRVVSVL TVLHQDWLNGK KEYKCKVSNK ALPAPIEKTI SKAKGQPREPQ 200
 QVYTLPPSREE **Q_MMTKNQV_KLT CLVKGFPYPSD IAVEWESNGQ PENNYKTTTPP** 250
 VLDSGSGSFFL YSKLTVDKSR **W_QQGNV_FSCSV V_LHEALH_SHYT TQKSLSLSPG** 300
 K 301

Peptide linkers / Peptides liants / Péptidos de unión

IL15-IgG1Fc: GGGGS 115-119
 IL15R-IgG1Fc: GGGGS 66-70

Mutation / Mutation / Mutación

IL-15: D³⁰>N, E⁶⁴>Q, N⁶⁵>D
 IL15-Fc: C¹²⁴>S, E¹³⁷>P, L¹³⁸>Y, L¹³⁹>A, G¹³⁹⁻¹⁴⁰>del, S¹⁷⁰>K, Q¹⁹⁸>E, L²⁷¹>D, K²⁷³>S, N²⁸⁷>D, Q³²¹>E, N³²⁴>D, M³³¹>L, N³³⁷>S
 IL15R-Fc: C⁷⁵>S, E⁸⁸>P, L⁸⁹>Y, L⁹⁰>A, G⁹⁰⁻⁹¹>del, S¹²¹>K, E²¹¹>Q, S²¹⁸>K, M²⁸²>L, N²⁸⁸>S

Post-translational modifications

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
 Intra-chain IL15-IgG1 Fc: 35-85, 42 - 88, 164 - 224, 270 - 328
 Intra-chain IL15R-IgG1Fc: 3'-45', 29'-63', 115'-175', 221'-279'
 Inter-chain: IL15Fc-IL15Rfc: 130-81', 133-84'

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

IL15-IgG1Fc: N71, N79, N112, N200
 IL15R-IgG1Fc: N151'

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

IL15R-IgG1Fc: T2'

efzimfotatum alfa #
 efzimfotase alfa

human alkaline phosphatase, tissue-nonspecific isozyme (AP-TNAP, TNS-ALP, EC:3.1.3.1) soluble fragment (1-491), variant (E¹⁰⁸>M, N²¹³>Q, N²⁸⁶>Q) fused to a human immunoglobulin G4 heavy chain constant region fragment (492-714) [*Homo sapiens* IGHG4*01; hinge: 492-498 (ERKCC 491-492del, P492V, P493E, S496P (matches IGHG2*02)); CH2: 499-607 (E501P, F502V, L503A, G503-504del (matches IGHG2*02)); CH3: 608-712; CHS: 713-714], fused to a deca-aspartate peptide (⁷¹⁵DDDDDDDDDD⁷²⁴), disulfide bridged dimer, produced in Chinese hamster ovary (CHO) cells, cell line K1SV, glycoform alfa

efzimfotase alfa

fragment soluble (1-491) de l'isozyme humaine de la phosphatase alcaline non spécifique des tissus (AP-TNAP, TNS-ALP, EC:3.1.3.1), variant (E¹⁰⁸>M, N²¹³>Q, N²⁸⁶>Q) fusionné à un fragment de la région constante de la chaîne lourde de l'immunoglobuline G4 humaine (492-

714) [*Homo sapiens* IGHG4*01; charnière: 492-498 (ERKCC 491-492del, P492V, P493E, S496P (correspond à IGHG2*02)); CH2: 499-607 (E501P, F502V, L503A, G503-504del (correspond à IGHG2*02)); CH3: 608-712; CHS: 713-714], fusionné à un peptide déca-aspartate (⁷¹⁵DDDDDDDDDD⁷²⁴), dimère à pont disulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire K1SV, glycoforme alfa

efzimofotasa alfa

fosfatasa humana alcalina isoenzima tisular no específica (AP-TNAP, TNS-ALP, EC:3.1.3.1) fragmento soluble (1-491), variante (E¹⁰⁸>M, N²¹³>Q, N²⁸⁶>Q) fusionada a una cadena pesada de la inmunoglobulina humana G4 fragmento de la región constante (492-714) [*Homo sapiens* IGHG4*01; bisagra: 492-498 (ERKCC 491-492del, P492V, P493E, S496P (corresponde IGHG2*02)); CH2: 499-607 (E501P, F502V, L503A, G503-504del (corresponde IGHG2*02)); CH3: 608-712; CHS: 713-714], fusionada a un péptido deca-aspartato (⁷¹⁵DDDDDDDDDD⁷²⁴), dímero con puente disulfuro, producida en células ováricas de hámster Chino (CHO), línea celular K1SV, forma glicosilada alfa

Sequence / Séquence / Secuencia

LVPEKEKDPK	YWRDQAQETL	KYALELQKLN	TNVAKNVIMF	LGDMGMVSTV	50
TAARILKQQL	HHNPGGEETRL	EMDKFPFVAL	SKTYNTNAQV	PDSAGTATAY	100
LCGVKANMST	VGVSAAATERS	RCNTTQGNFV	TSILRWAKDA	GKSVGIVTTT	150
RVNHATPSAA	YAHSAADRWDY	SDNEMPPEAL	SQGCKDIAYQ	LMHNIRDIDV	200
IMGGGRKMYI	PKQKT DVEYE	SDEKARGTRL	DGLDLVDTWK	SFKPRYKSHH	250
FIWNRTELLT	LDPHNVDYLL	GLFEPGDMQY	ELNRRQVTDV	SLSEMVVVAI	300
QILRKNPKGF	FLLVEGGRID	HGHHEGKAKQ	ALHEAVEMDR	AIGQAGSLTS	350
SEDTLTVVTA	DHSHVFTFGG	YTPRGNSIFG	LAPMLSDTDK	KPFTAILLYGN	400
GPGYKVVGGE	RENVSMVDYA	HNNYQAQSAV	PLRHETHGGE	DVAVFSKQPM	450
AHLLHGVHEQ	NYVPHVMAYA	ACIGANLGHC	APASSAGSLA	AVECPCPPAP	500
PVAGPSVFLF	PPKPKDTLMI	SRTPEVTCVV	VDSQEDPEV	QFNWYVDGVE	550
VHNAKTKPRE	EQFNSTYRVV	SVLTVLHQDV	LNGKEYKCKV	SNKGLPSIE	600
KTISKAKQGP	REPQVYTLPP	SQEMTKNQV	SLTCLVKGFY	PSDIAVEWES	650
NGQPNNYKT	TPPVLDSDGS	FFLYSRLTVD	KSRWQEGNVF	SCSVMHEALH	700
NHYTQKSLSL	SLGKDDDDDD	DDDD			724

Mutation / Mutation / Mutación

E108>M, N213>Q, N286>Q

Post-translational modifications

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

Intra-chain: 122-184, 472-480, 528-588, 634-692

122'-184', 472'-480', 528'-588', 634'-692'

Inter-chain: 494-494', 497-497'

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

N123, N254, N413, N564, N123', N254', N413', N564'

Potential O-glycosylation sites / Sites de O-glycosylation potentielle / Posiciones de

O-glicosilación potencial

S484, S485, S488, or S506 (one site only)

elenestinium

elenestininib

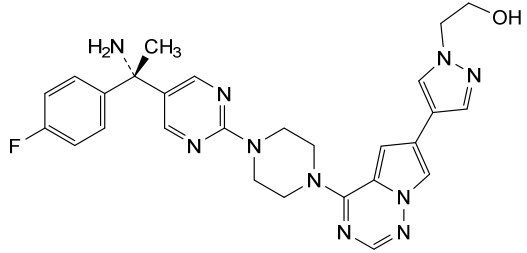
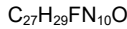
2-{4-[4-(4-{5-[(1S)-1-amino-1-(4-fluorophenyl)ethyl]pyrimidin-2-yl}piperazin-1-yl)pyrrolo[2,1-f][1,2,4]triazin-6-yl]-1H-pyrazol-1-yl}ethan-1-ol

élénestininib

2-{4-[4-(4-{5-[(1S)-1-amino-1-(4-fluorophényl)éthyl]pyrimidin-2-yl}pipérazin-1-yl)pyrrolo[2,1-f][1,2,4]triazin-6-yl]-1H-pyrazol-1-yl}éthan-1-ol

elenestininib

2-{4-[4-(4-{5-[(1S)-1-amino-1-(4-fluorofenil)etil]pirimidin-2-il}piperazin-1-il)pirrolo[2,1-f][1,2,4]triazin-6-il]-1H-pirazol-1-il}etan-1-ol



elriterceptum #
elritercept

human activin receptor type 2-A (activin receptor type IIA, ACTR-IIA) extracellular domain (ECD) fragment (1-109) engineered variant (F¹⁵>Y, ²¹KD²²>LE, P³¹>R, Y³³>E, D³⁵>E, R⁴⁰>L, F⁴³>Y, K⁴⁷>R, Q⁵⁸>K, I⁶⁵>F, ⁷⁶KKDS⁷⁹>TEEN, E⁸¹>Q) fused via the peptide linker ¹¹⁰GGG¹¹² to a human immunoglobulin G1 heavy chain fragment C-terminal Fc fragment (113-338), [*Homo sapiens* IGHG1*01; hinge: 113-122 (EPKSC 112-113del); CH2: 123-232; CH3: 233-337; CHS: 338-338 (K339del)]; disulfide bridged dimer, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

elritercept

variant modifié du fragment (1-109) du domaine extracellulaire (ECD) du récepteur de l'activine humaine de type 2-A (récepteur de l'activine de type IIA, ACTR-IIA) (F¹⁵>Y, ²¹KD²²>LE, P³¹>R, Y³³>E, D³⁵>E, R⁴⁰>L, F⁴³>Y, K⁴⁷>R, Q⁵⁸>K, I⁶⁵>F, ⁷⁶KKDS⁷⁹>TEEN, E⁸¹>Q) fusionné via la liaison peptidique ¹¹⁰GGG¹¹² à un fragment Fc en C-terminal de la chaîne lourde de l'immunoglobuline G1 humaine (113-338), [*Homo sapiens* IGHG1*01; charnière: 113-122 (EPKSC 112-113del); CH2: 123-232 ; CH3: 233-337; CHS: 338-338 (K339del)]; dimère à pont disulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

elritercept

receptor humano de la activina de tipo 2-A (receptor de la activina tipo IIA, ACTR-IIA) dominio extracelular (ECD) fragmento (1-109) variante diseñada (F¹⁵>Y, ²¹KD²²>LE, P³¹>R, Y³³>E, D³⁵>E, R⁴⁰>L, F⁴³>Y, K⁴⁷>R, Q⁵⁸>K, I⁶⁵>F, ⁷⁶KKDS⁷⁹>TEEN, E⁸¹>Q) fusionada a través de un enlace peptídico ¹¹⁰GGG¹¹² a la cadena pesada de la inmunoglobulina humana G1 fragmento C-terminal Fc fragmento (113-338), [*Homo sapiens* IGHG1*01; bisagra: 113-122 (EPKSC 112-113del); CH2: 123-232; CH3: 233-337; CHS: 338-338 (K339del)]; dímero con puente disulfuro, producido en células ováricas de hámster Chino (CHO), forma glicosilada alfa

Sequence / Séquence / Secuencia
 GAILGRSETQ ECLFY~~N~~ANWE ~~L~~E~~R~~T~~N~~Q~~T~~GVE ~~R~~C~~E~~~~C~~E~~K~~D~~K~~R~~L~~ HC~~Y~~ATW~~R~~NIS 50
 GSIEIVK~~K~~GC WLDD~~F~~NCYDR TDCVE~~T~~E~~E~~N~~P~~ Q~~V~~YFCCEGN MCNEKFSYFP 100
 EMEVTQPTSG ~~G~~GDKTHTCPP CPAPELLGGP SVFLFPKPK DTLMISRTPE 150
 VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS TYRVVSVLTV 200
 LHQDNLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV YTLPPSRDEL 250
 TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTTPVL DSDGSFFLYS 300
 KLTVDKSRWQ QGNVFSCSVM HEALHNYHTQ KSLSLSPG 338

Peptide linker / Peptides liant / Péptido de unión
 GGG 110-112

Mutation / Mutation / Mutación
 F¹⁵>Y, ²¹KD²²>LE, P³¹>R, Y³³>E, D³⁵>E, R⁴⁰>L, F⁴³>Y, K⁴⁷>R, Q⁵⁸>K, I⁶⁵>E,
⁷⁶KKDS⁷⁹>TEEN, E⁸¹>Q

Post-translational modifications
 Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
 Intra-chain 12 - 42, 32 - 60, 67 - 86, 73 - 85, 87 - 92, 153 - 213, 259 - 317
 12'-42', 32'-60', 67'-86', 73'-85', 87'-92', 153'-213', 259'-317'
 Inter-chain 118-118', 121-121'

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
 N25, N48, N189, N25', N48', N189'

O-glycosylation sites / Sites de O-glycosylation / Posiciones de O-glicosilación
 S97, S97'

emzeltrectinibum

emzeltrectinib

2-amino-5-[(2R,4S)-2-(2,5-difluorophenyl)-4-fluoropyrrolidin-1-yl]-pyrazolo[1,5-a]pyrimidine-3-carboxamide

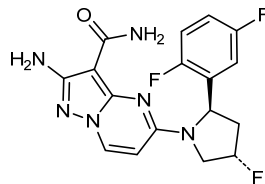
emzeltrectinib

2-amino-5-[(2R,4S)-2-(2,5-difluorophényl)-4-fluoropyrrolidin-1-yl]-pyrazolo[1,5-a]pyrimidine-3-carboxamide

emzeltrectinib

2-amino-5-[(2R,4S)-2-(2,5-difluorofenil)-4-fluoropirrolidin-1-il]-pirazolo[1,5-a]pirimidina-3-carboxamida

C₁₇H₁₅F₃N₆O



enlicitidi chloridum

enlicitide chloride

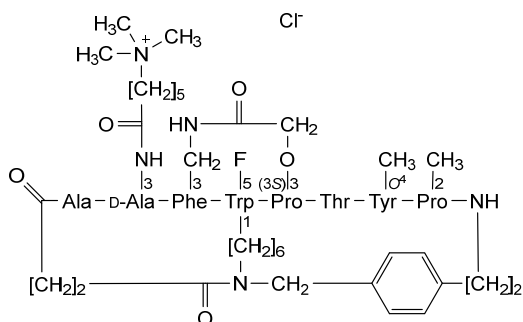
1,4:3,5:4,8-trianhydro[L-alanyl-3-[6-(trimethylazaniumyl)hexanamido]-D-alanyl-3-(aminomethyl)-L-phenylalanyl-1-{6-[[4-(2-aminoethyl)phenyl]methyl]}(3-carboxypropanoyl)amino]hexyl]-5-fluoro-L-tryptophyl-(3S)-3-(carboxymethoxy)-L-prolyl-L-threonyl-O-methyl-L-tyrosyl-2-methyl-L-proline] chloride

chlorure d'enlicitide

chlorure de 1,4:3,5:4,8-trianhydro[L-alanyl-3-[6-(triméthylazaniumyl)hexanamido]-D-alanyl-3-(aminométhy)-L-phénylalanyl-1-{6-[[4-(2-aminoéthyl)phényl]méthyl]}(3-carboxypropanoyl)amino]hexyl]-5-fluoro-L-tryptophyl-(3S)-3-(carboxyméthoxy)-L-prolyl-L-thréonyl-O-méthyl-L-tyrosyl-2-méthyl-L-proline]

cloruro de enlicitida

cloruro de 1,4:3,5:4,8-trianhidro[L-alanil-3-[6-(trimetilazaniumil)hexanamido]-D-alanil-3-(aminometil)-L-fenilalanil-1-{6-[[4-(2-aminoetil)fenil]metil]}(3-carboxipropanoil)amino]hexil]-5-fluoro-L-triptofil-(3S)-3-(carboximetoxi)-L-prolil-L-treonil-O-metil-L-tirosil-2-metil-L-prolina]

C₈₂H₁₁₀ClFN₁₄O₁₅**enlicovateinum #**

enlicovatein

severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) spike (S) glycoprotein (UniProt P0DTC2, strain Wuhan-Hu-1) fragment (3-1260, 1-1258 in the current sequence), stable prefusion conformation variant (R⁶⁶⁹>G⁶⁶⁷, R⁶⁷⁰>S⁶⁶⁸, R⁶⁷²>S⁶⁷⁰, K⁹⁷³>P⁹⁷¹, V⁹⁷⁴>P⁹⁷²) fused to a C-terminal hexahistidine tag (1259-1264), trimer, produced in *Trichoplusia ni* (derivative of TnT4) insect cells, glycoform alfa

enlicovateïne

fragment (3-1260, 1-1258 dans la séquence actuelle) de la glycoprotéine du spicule (S) du coronavirus 2 du syndrome respiratoire aigu sévère (UniProt P0DTC2, souche Wuhan-Hu-1), variant de conformation stable par pré-fusion (R⁶⁶⁹>G⁶⁶⁷, R⁶⁷⁰>S⁶⁶⁸, R⁶⁷²>S⁶⁷⁰, K⁹⁷³>P⁹⁷¹, V⁹⁷⁴>P⁹⁷²) fusionné à une étiquette hexahistidine en C-terminal (1259-1264), trimère, produit dans des cellules d'insecte *Trichoplusia ni* (derivant de TnT4), glycoforme alfa

enlicovateína

glicoproteína de la espícula (S) del coronavirus 2 del síndrome respiratorio severo agudo (SARS-CoV-2) (UniProt P0DTC2, cepa Wuhan-Hu-1) fragmento (3-1260, 1-1258 en la secuencia actual), variante de conformación de prefusión estable (R⁶⁶⁹>G⁶⁶⁷, R⁶⁷⁰>S⁶⁶⁸, R⁶⁷²>S⁶⁷⁰, K⁹⁷³>P⁹⁷¹, V⁹⁷⁴>P⁹⁷²) fusionada a la etiqueta de hexahistidina del terminal C (1259-1264), trímero, producido en células de insectos de *Trichoplusia ni* (derivada de TnT4), glicoforma alfa

Monomer sequence / Séquence du monomère / Secuencia del monómero

VNLTTRTQLP	PAYTNSFTRG	VYYPDKVFRS	SVLHSTQDLF	LPFPSNVTFW	50
HAIHVSGTNG	TKRFDNPVLP	FNDGVYFAST	EKSNIIRGWI	FGTTLDSKTQ	100
SLLVNNAATN	VVIKVCFEFQ	CNDPFLGVVY	HKNKNSWMS	EFRVYSSANN	150
CTFEYVSQPF	LMDLGKQGN	FKNLREFVFK	NIDGYFKIYS	KHTPINLVRD	200
LPQGFSALEP	LVDLPIGINI	TRFQTLALH	RSYLTPGDSS	SGWTAGAAAY	250
YVGYLQPRTF	LLKYNENGTI	TDAVDCALDP	LSETKCTLKS	FTVEKGIYQT	300
SNFRVQPTES	IVRFPNITNL	CPFGEVFNAT	RFASVYAWNR	KRISNCVADY	350
SVLYNSASF	TFKCYGVSP	KLNDLCFTNV	YADSFVIRGD	EVQRAPQGT	400
GKIADYNYKL	PDDFTGCVIA	WNSNNLDSKV	GNYNLYLRL	FRKSNLKFPE	450
RDISTEIYQA	GSTPCNGVEG	FNCYFPLQSY	GFQPTNGVGY	QPYRVVVLFS	500
ELLHAPATVC	GPKKSTNLVK	NKCVNENFNG	LTGTGVLTES	NKKFLPFQGF	550
GRDIADTTDA	VRDPQTLEIL	DITPCSFQGV	SVITPGTNTS	NQAVVLYQDV	600
NCTEVPVAIH	ADQLTPTWRV	YSTGNSVFNQ	RAGCLIGAETH	VNNSYECCIP	650
IGAGICASYQ	TQTNSP GSAS	SVASQSIIAY	TMSLGAENSV	AYSNNIAIP	700
TNFTISVTTE	ILPVSMTKTS	VDCTMYICGD	STECSNLLLQ	YGSFCTQLNR	750
ALTGIAVEQD	KNTQEVFAQV	KQIYKTPPIK	DFGGFNFSQI	LPDPSKPSKR	800
SFIEDLLFNK	VTLADAGFIK	QYGDCLDGIA	ARDLICAQKF	NGLTVLPELL	850
TDEMIQAQYTS	ALLAGTITSG	WTFGAGAAALQ	IPFAMQMAYR	FNGIGVTQNV	900
LYENQKLIAN	QFNSAIGKIQ	DSLSTASAL	GKLDQVVNQN	AQALNTLVKQ	950
LSSNFGAISS	VLNDILSRLD	PE AEVQIDR	LITGRLQSLQ	TYVTQQLIRA	1000
AEIRASANLA	ATKMECVLQ	QSKRVDFCGK	GYHLMSPQOS	APHGVVFLHV	1050
TYVPAQEKNF	TTAPAICHGD	KAHFPREGVF	VSNGTHWFVT	QRNFVEPQII	1100
TTDNTFVSGN	CDVVIGIVNN	TVYDPLQPEL	DSFKELDKY	FKNHTSPDVD	1150
LGDISGINAS	VVNIQKEIDR	LNEVAKNLNE	SLIDLQELGK	YEQYIKWPWY	1200
IWLGFIAGLI	AIWVMTIMLC	CMTSCCSCLK	GCCSCGSCCK	FDEDDSEPLV	1250
KGVKLHYT HH	HHHH				1264

Mutation / Mutation / Mutación
R⁶⁶⁶->G⁶⁶⁷, R⁶⁷⁰->S⁶⁶⁸, R⁶⁷²->S⁶⁷⁰, K⁹⁷³->P⁹⁷¹, V⁹⁷⁴->P⁹⁷²

Hexahistidine tag / Marqueur hexahistidine / Etiqueta de hexahistidina
HHHHHHH 1259-1264

Post-translational modifications

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-chain: 116-151, 276-286, 321-346, 364-417, 376-510, 465-473, 523-575, 602-634, 647-656, 723-745, 728-734, 825-836, 1017-1028, 1067-1111

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
N2, N46, N59, N107, N134, N150, N219, N267, N316, N328, N588, N601, N642, N694, N702, N786, N1059, N1083, N1119, N1143, N1158, N1179

O-glycosylation sites / Sites de O-glycosylation / Posiciones de O-glicosilación (predicted)
T308, S310, T661, T663

enlonstobartum #
enlonstobart

immunoglobulin G4-kappa, anti-[*Homo sapiens* PDCD1 (programmed cell death 1, PD1, PD-1, CD279)], *Homo sapiens* monoclonal antibody;
gamma4 heavy chain *Homo sapiens* (1-440) [VH (*Homo sapiens* IGHV3-33*01 (92.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.6] (26-33.51-58.97-102)) (1-113) -*Homo sapiens* IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (114-211), hinge 1-12 S10>P (221) (212-223), CH2 L92 (302) (224-333), CH3 (334-438), CHS (439-440)) (114-440)], (127-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-11*01 (97.9%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (219-219":222-222")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

enlonstobart

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

chaîne lourde gamma4 *Homo sapiens* (1-440) [VH (*Homo sapiens* IGHV3-33*01 (92.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.6] (26-33.51-58.97-102)) (1-113) -*Homo sapiens* IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (114-211), charnière 1-12 S10>P (221) (212-223), CH2 L92 (302) (224-333), CH3 (334-438), CHS (439-440)) (114-440)], (127-214')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-11*01 (97.9%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (219-219":222-222")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

enlonstobart

inmunoglobulina G4-kappa, anti-[*Homo sapiens* PDCD1 (proteína 1 de muerte celular programada, PD-1, PD1, CD279)], anticuerpo monoclonal *Homo sapiens*;

cadena pesada gamma4 *Homo sapiens* (1-440) [VH (*Homo sapiens* IGHV3-33*01 (92.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.6] (26-33.51-58.97-102)) (1-113) -*Homo sapiens* IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (114-211), bisagra 1-12 S10>P (221) (212-223), CH2 L92 (302) (224-333), CH3 (334-438), CHS (439-440)) (114-440)], (127-214')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-11*01 (97.9%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (219-219":222-222")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

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QVQLVESGGG VVQPGRSLRL TCKASGLTFS SSGMHWVRQA PGKGLEWVAV 50
IWYDGSKRYI ADSVKGRFTI SRDNSKNTLF LQMNSLRAED TAVYYCATNN 100
DYWGQGTLVLT VSSASTKGPS VFPLAPCSRS TSESTAALGC LVKDYFPEPV 150
TVSWNSGALT SGVHTFPAVL QSSGLYLSLS VVTVPSSSLG KTKYTCNVDH 200
KPSNTKVDKR VESKYGPFCP PCPAPEFLGG PSVFLFPPKP KDTLMISRTP 250
EVTCCVVVDVS QEDPEVQFNW YVDGVEVHNA KTKPREEQFN STYRVVSVLT 300
VLHQDWLNGK EYKCKVSNKG LPSSIEKTI S KAKGQPREPQ VYTLPPSQEE 350
MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTTPV LDSGDSFFLY 400
SRLTVDKSRW QEGNVFSCSV MHEALHNHYT QKSLSLSLGK 440
    
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Light chain / Chaîne légère / Cadena ligera

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EIVLTQSPAT LSLSPGERAT LSCRASQSVS SYLAWYQQKP GQAPRLLIYT 50
ASNRAATGIPA RFSGSGSGTD FTLTISSLEP EDFAVYYCQQ YSNWPRTFGQ 100
GTKVEIKRTV AAPSVFIAPP SDEQLKSGTA SVVCLLNIFY PREAKVQNKV 150
DNALQSGNSQ ESVTEQDSKD STYLSLSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEK 214
    
```

Post-translational modifications

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

Intra-H (C23-C104) 22-96 140-196 254-314 360-418
 22"-96" 140"-196" 254"-314" 360"-418"
 Intra-L (C23-C104) 23'-88' 134'-194'
 23'''-88''' 134'''-194'''
 Inter-H-L (CH1 10-CL 126) 127-214' 127"-214"
 Inter-H-H (h 8, h 11) 219-219" 222-222"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutamínilo N-terminal

Q > pyroglutamyl (pE, 5-oxoprollyl) / pyroglutamyle (pE, 5-oxoprollyle) / piroglutamilo (pE, 5-oxoprolilo)
 H VH Q1: 1, 1"

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

H CH2 N84.4: 290, 290"

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

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

H CHS K2: 440, 440"

ersodetugum #
ersodetug

immunoglobulin G2-kappa, anti-[*Homo sapiens* INSR (insulin receptor)], *Homo sapiens* monoclonal antibody, allosteric;
gamma2 heavy chain *Homo sapiens* (1-444) [VH (*Homo sapiens* IGHV3-20*01 (98.0%) -(IGHD) - IGHJ6*01 (93.8%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG2*02 (100%), G2m23 CH2 M45.1 (CH1 (119-216), hinge 1-12 (217-228), CH2 M45.1 (279) (229-337), CH3 (338-442), CHS (443-444)) (119-444)], (132-219')-disulfide with kappa light chain humanized (1'-219') [V-KAPPA (*Homo sapiens* IGKV2-30*01 (93.0%) -IGKJ2*01 (100%), CDR-IMGT [11.3.9] (27-37.55-57.94-102)) (1'-112') -*Homo sapiens* IGKC*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dimer (220-220":221-221":224-224":227-227")-tetrakisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, glycoform alfa

ersodétug

immunoglobuline G2-kappa, anti-[*Homo sapiens* INSR (récepteur de l'insuline)], anticorps monoclonal *Homo sapiens*, allostérique;
chaîne lourde gamma2 *Homo sapiens* (1-444) [VH (*Homo sapiens* IGHV3-20*01 (98.0%) -(IGHD) - IGHJ6*01 (93.8%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG2*02 (100%), G2m23 CH2 M45.1 (CH1 (119-216), charnière 1-12 (217-228), CH2 M45.1 (279) (229-337), CH3 (338-442), CHS (443-444)) (119-444)], (132-219')-disulfure avec la chaîne légère kappa humanisée (1'-219') [V-KAPPA (*Homo sapiens* IGKV2-30*01 (93.0%) -IGKJ2*01 (100%), CDR-IMGT [11.3.9] (27-37.55-57.94-102)) (1'-112') -*Homo sapiens* IGKC*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dimère (220-220":221-221":224-224":227-227")- tétrakisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1, glycoforme alfa

ersodetug

immunoglobulina G2-kappa, anti-[*Homo sapiens* INSR (receptor de la insulina)], anticuerpo monoclonal *Homo sapiens*, alostérico;
cadena pesada gamma2 *Homo sapiens* (1-444) [VH (*Homo sapiens* IGHV3-20*01 (98.0%) -(IGHD) - IGHJ6*01 (93.8%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG2*02 (100%), G2m23 CH2 M45.1 (CH1 (119-216), bisagra 1-12 (217-228), CH2 M45.1 (279) (229-337), CH3 (338-442), CHS (443-444)) (119-444)], (132-219')-disulfuro con la cadena ligera kappa humanizada (1'-219') [V-KAPPA (*Homo sapiens* IGKV2-30*01 (93.0%) -IGKJ2*01 (100%), CDR-IMGT [11.3.9] (27-37.55-57.94-102)) (1'-112') -*Homo sapiens* IGKC*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dímero (220-220":221-221":224-224":227-227")-tetrakisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular derivada de CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

EVQLVETGGG VVQFGRSLRL SCAASGFTFS SYAMHWVRQA FGKGLEWVAV 50
 ISYDGSNKYY ADSVKRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARHE 100
 WGFMDVWQQ GTTVTVSSAS TRGFSVFPLA PCSRSTSEST AALGLVKDY 150
 FPEFVTVSWN SGALTSQVHT FPAVLOSSGL YSLSSVVTY SSNEGTQTYT 200
 CNVDHKFSNT KVDKTVKRC CVECPCPCAP PVAGPSVLEF PFKKDTIMI 250
 SRTPEVTCVV VDVSHEDPEV QFNWYVDGME VHNAKTKFRE EQFNSTFRV 300
 SVLTVVHQDW LNKGYKCKV SNKGLPAPIE KTISKTKGQP REPQVYTLFP 350
 SREEMTRNQV SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPLDSDGS 400
 FFYLSKLTVD KSRWQQGNVF SCSVMHEALH NHYTQKSLSL SPGK 444

Light chain / Chaîne légère / Cadena ligera

DVVMTQSPSL LSVTLGQPAS ISCRSSLSLV YGDENTYLNW FQRRPGQSPR 50
 RLLYKVSDRD SGVPDRFSGS GSGTDFTLKI SRVEADAVGV YFCMQGTHWP 100
 YTFGQGTKLE IKRTVAAPSV FIFPPSDEQL KSGTASVCL LNNFYPREAK 150
 VQWKVDNALQ SGNSQESVTE QDSKDYSL SSSLTSLSKAD YEKHKVYACE 200
 VTHQGLSSPV TKSFNREGC 219

Post-translational modifications

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

Intra-H (C23-C104) 22-96 145-201 258-318 364-422

22"-96" 145"-201" 258"-318" 364"-422"

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

23"-93" 139"-199"

Inter-H-L (CH1 10-CL 126) 132-219" 132"-219"

Inter-H-H (h 4, h 5, h 8, h11) 220-220" 221-221" 224-224" 227-227"

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

H CH2N84.4:294, 294"

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

H CHS K2: 444, 444"

erzotabartum #

erzotabart

immunoglobulin G1-kappa , anti-[*Homo sapiens* CD38 (ADP-ribose cyclase 1, cyclic ADP-ribose hydrolase 1, cADPr hydrolase 1, cADPR1)], *Homo sapiens* monoclonal antibody; gamma1 heavy chain *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV1-69*04 (93.8%) -(IGHD) -IGHJ3*02 (93.8%), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1-121)-*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120 CH3 E12, M14, IGHG1v34 CH3 G109 (CH1 R120 (218) (122-219), hinge 1-15 (220-234), CH2 (235-344), CH3 E12 (360), M14 (362), E109>G (434) (345-449), CHS K2>del (450)) (122-450)], (224-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1D-16*01 (98.9%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (230-230":233-233")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

erzotabart

immunoglobuline G1-kappa, anti-[*Homo sapiens* CD38 (ADP-ribose cyclase 1, ADP cyclique-ribose hydrolase 1, cADPr hydrolase 1, cADPR1)], anticorps monoclonal *Homo sapiens*; chaîne lourde gamma1 *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV1-69*04 (93.8%) -(IGHD) - IGHJ3*02 (93.8%), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1-121) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120 CH3 E12, M14, IGHG1v34 CH3 G109 (CH1 R120 (218) (122-219), charnière 1-15 (220-234), CH2 (235-344), CH3 E12 (360), M14 (362), E109>G (434) (345-449), CHS K2>del (450)) (122-450)], (224-214')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1D-16*01 (98.9%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (230-230":233-233")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

erzotabart

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CD38 (ADP-ribosil ciclasa 1, ADP ciclico-ribosa hidrolasa 1, cADPr hidrolasa 1, cADPR1)], anticuerpo monoclonal *Homo sapiens*; cadena pesada gamma1 *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV1-69*04 (93.8%) -(IGHD) - IGHJ3*02 (93.8%), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1-121) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120 CH3 E12, M14, IGHG1v34 CH3 G109 (CH1 R120 (218) (122-219), bisagra 1-15 (220-234), CH2 (235-344), CH3 E12 (360), M14 (362), E109>G (434) (345-449), CHS K2>del (450)) (122-450)], (224-214')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1D-16*01 (98.9%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97))(1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (230-230":233-233")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

QVQLVQSGAE VKKPGSSVKV SCKAFGGTFS SYAISWVRQA PGQGLEWMGR 50
 IIRFLGIANY AQKFPQGRVTL IADKSTNTAY MELSLRSED TAVYYCAGEP 100
 GERDPAVDI WGGGTMVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150
 KDYFPEPVTV SWNSGALTSV VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200
 TYICNVNHPK SNTKVDKRVE PKSCDKHTHC PPCPAPELLG GPSVFLFPPK 250
 PKDITLMSRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY 300
 NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP 350
 QVYTLPPSRE EMTKNQVSLT CLVKGFPYPSD IAVEWESNGQ PENNYKTTTP 400
 VLDSDSGSFFL YSKLTVDKSR WQQGNVFCVS VMHGALHNHY TQKSLSLSPG 450

Light chain / Chaîne légère / Cadena ligera

DIQMTQSPSS LSASVGDRTV ITCRASQGIT SWLAWYQQKPK EKAPKSLIYA 50
 ASSLQSGVPS RFSGSGSGTD FTLTISLSLPQ EDFATYYCQQ YNSYPLTFGG 100
 GTRVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNIFY PREAKVQWVK 150
 DNALQSGNSQ ESVTEQDSKD STYLSLSTLT LSKADYEKHK VYACEVTHQG 200
 LSSPVTKSFN RGECC 214

Post-translational modifications

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

Intra-H (C23-C104) 22-96 148-204 265-325 371-429
 22"-96" 148"-204" 265"-325" 371"-429"

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

Inter-H-L (h 5-CL 126) 224-214' 224"-214"

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

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal

Q > pyroglutamyl (pE, 5-oxopropyl) / pyroglutamyle (pE, 5-oxopropyle) / 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

esonadogenum imvoparvovecum

esonadogene imvoparvovec

recombinant, non-replicating adeno-associated virus serotype 2 (AAV2) vector encoding codon-optimised human NADH dehydrogenase subunit 4 (also known as NADH-ubiquinone oxidoreductase chain 4; MTND4, NADH4, ND4) preceded by a Kozak sequence and a mitochondrial targeting sequence from human heme A: farnesyltransferase cytochrome C oxidase assembly factor (also known as protoheme IX farnesyltransferase, mitochondrial; gene COX10), under control of a human cytomegalovirus enhancer/promoter plus a Macacine herpesvirus-3 chimeric intron, followed with a COX10 gene 3'-untranslated region (UTR), and terminated by a simian virus 40 (SV40) polyadenylation signal, and flanked by AAV2 inverted terminal repeats (ITRs)

ésonadogène imvoparvec

vecteur recombinant et non répliquant du virus adéno-associé de sérotype 2 (AAV2) codant la sous-unité 4 de la NADH déshydrogénase humaine aux codons optimisés (également connue sous le nom de chaîne 4 de la NADH-ubiquinone oxydoréductase; MTND4, NADH4, ND4) précédée d'une séquence Kozak et d'un hème A humain: facteur d'assemblage de la farnésyltransférase cytochrome C oxydase (également connu sous le nom de farnésyltransférase protohème IX, mitochondriale; gène COX10) ciblant les mitochondries, sous le contrôle d'un amplificateur/promoteur du cytomégalovirus humain plus d'un intron chimérique de l'herpèsvirus-3 Macacine, suivi d'une région 3' non traduite (UTR) du gène COX10, et terminé par un signal de polyadénylation du virus simien 40 (SV40), et flanqué de répétitions terminales inversées (ITR) de l'AAV2

esonadogén imvoparvec

vector de virus adenoasociado recombinante del serotipo 2 (AAV2), no replicativo, que codifica, con codones optimizados, para la subunidad 4 de la NADH deshidrogenasa humana (también conocida como cadena 4 de la NADH-ubiquinona oxidorreductasa; MTND4, NADH4, ND4) precedida por una secuencia Kozak y un hemo A humano: factor de ensamblaje de citocromo C oxidasa de farnesiltransferasa (también conocido como protohemo IX farnesiltransferasa, mitocondrial; gen COX10), bajo el control de un potenciador/promotor del citomegalovirus humano más un intrón quimérico del herpesvirus-3 Macacine, seguido de una región no traducida (UTR) en 3' del gen COX10, y terminado con una señal de poliadenilación del virus simio 40 (SV40) y flanqueado por repeticiones terminales invertidas (ITRs) del AAV2

etimumotidum

etimumotide

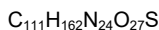
L-phenylalanyl-L-methionyl-L-threonyl-L-tyrosyl-L-tryptophyl-L-histidyl-L-leucyl-L-leucyl-L-asparaginyll-alanyl-L-phenylalanyl-L-threonyl-L-valyl-L-threonyl-L-valyl-L-prolyl-L-lysyl-L-α-aspartyl-L-leucine

étimumotide

L-phénylalanyl-L-méthionyl-L-thréonyl-L-tyrosyl-L-tryptophyl-L-histidyl-L-leucyl-L-leucyl-L-asparaginyll-alanyl-L-phénylalanyl-L-thréonyl-L-valyl-L-thréonyl-L-valyl-L-prolyl-L-lysyl-L-α-aspartyl-L-leucine

etimumotida

L-fenilalanil-L-metionil-L-treonil-L-tirosil-L-triptofil-L-histidil-L-leucil-L-leucil-L-asparaginil-L-alanil-L-fenilalanil-L-treonil-L-valil-L-treonil-L-valil-L-prolil-L-lisil-L-α-aspartil-L-leucina



FMTYWHLINA FTVTVPKDL 20

eurestobartum

eurestobart

immunoglobulin G1-kappa, anti-[*Homo sapiens* ENTPD1 (ectonucleoside triphosphate diphosphohydrolase 1, CD39)], humanized monoclonal antibody;
 gamma1 heavy chain humanized (1-453) [VH (*Homo sapiens* IGHV1-3*01 (80.4%) -(IGHD) -IGHJ3*01 (92.3%), CDR-IMGT [8.8.16] (26-33.51-58.97-112))] (1-123) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, CH1 K120, CH3 E12, M14, G1v14 CH2 A1.3, A1.2 (CH1 R120>K (220) (124-221), hinge 1-15 (222-236), CH2 L1.3>A (240), L1.2>A (241) (237-346), CH3 E12 (362), M14 (364) (347-451), CHS (452-453)) (124-453)], (226-213')-disulfide with kappa light chain humanized (1'-213') [V-KAPPA (*Homo sapiens* IGKV3-11*01 (82.1%) -IGKJ2*02 (100%), CDR-IMGT [5.3.9] (27-31.49-51.88-96))] (1'-106') -*Homo sapiens* IGKC*01 (100%), Km3, A45.1 (152), V101 (190) (107'-213'); dimer (232-232":235-235")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1 lacking the glutamine synthetase (GS-KO) gene, glycoform alfa

eurestobart

immunoglobuline G1-kappa, anti-[*Homo sapiens* ENTPD1 (ectonucleoside triphosphate diphosphohydrolase 1, CD39)], anticorps monoclonal humanisé;
 chaîne lourde gamma1 humanisée (1-453) [VH (*Homo sapiens* IGHV1-3*01 (80.4%) -(IGHD) -IGHJ3*01 (92.3%), CDR-IMGT [8.8.16] (26-33.51-58.97-112))] (1-123) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, CH1 K120, CH3 E12, M14, G1v14 CH2 A1.3, A1.2 (CH1 R120>K (220) (124-221), charnière 1-15 (222-236), CH2 L1.3>A (240), L1.2>A (241) (237-346), CH3 E12 (362), M14 (364) (347-451), CHS (452-453)) (124-453)], (226-213')-disulfure avec la chaîne légère kappa humanisée (1'-213') [V-KAPPA (*Homo sapiens* IGKV3-11*01 (82.1%) -IGKJ2*02 (100%), CDR-IMGT [5.3.9] (27-31.49-51.88-96))] (1'-106') -*Homo sapiens* IGKC*01 (100%), Km3, A45.1 (152), V101 (190) (107'-213'); dimère (232-232":235-235")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1 ne présentant pas le gène de la glutamine synthétase (GS-KO), glycoforme alfa

eurestobart

inmunoglobulina G1-kappa, anti-[*Homo sapiens* ENTPD1 (ectonucleosido trifosfato difosfohidrolasa 1, CD39)], anticuerpo monoclonal humanizado;
 cadena pesada gamma1 humanizada (1-453) [VH (*Homo sapiens* IGHV1-3*01 (80.4%) -(IGHD) -IGHJ3*01 (92.3%), CDR-IMGT [8.8.16] (26-33.51-58.97-112))] (1-123) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, CH1 K120, CH3 E12, M14, G1v14 CH2 A1.3, A1.2 (CH1 R120>K (220) (124-221), bisagra 1-15 (222-236), CH2 L1.3>A (240), L1.2>A (241) (237-346), CH3 E12 (362), M14 (364) (347-451), CHS (452-453)) (124-453)], (226-213')-disulfuro con la cadena ligera kappa humanizada (1'-213') [V-KAPPA (*Homo sapiens* IGKV3-11*01 (82.1%) -IGKJ2*02 (100%), CDR-IMGT [5.3.9] (27-31.49-51.88-96))] (1'-106') -*Homo sapiens* IGKC*01 (100%), Km3, A45.1 (152), V101 (190) (107'-213'); dímero (232-232":235-235")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1 en ausencia del gen glutamina sintetasa (GS-KO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

QVQLVQSGAE VKKPGASVKV SCKASGYNLK DTFLHWVRQA PGQGLEWMGR 50
 IDPAQGNIKY DPKFQGRVTI TADTSANTAY MELISLRSED TAVYYCANS 100
 YYYGSGYRIF DWVGGQTGTVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC 150
 LVKDYFFPEPV TVSWNSGALT SGVHTFFPAVL QSSGLYLSLS VVTFVSSSLG 200
 TQTYICNVNH KPSNTKVDKK VEPKSCDKTH TCPPCPAPEA AGGSPVFLFP 250
 FPKPKDTLMIS RTPPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE 300
 QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR 350
 EPQVYTLPPS REEMTKNQVS LTCLVKGFPY SDIAVEWESN GQFENNYKTT 400
 PPFVDSDDGSF FLYSKLTVDK SRWQQGNVFS CSMVHEALHN HYTQKSLSL 450
 PGK 453

Light chain / Chaîne légère / Cadena ligera

QIVLTQSPAT LSLSPGERAT LSCSAFSSVN YMHYQQKPG QAPRLLIYTT 50
 SNLASGIPTR FSGSGSGTSY TLTISLSEPE DFAVYYCQQR STYPFTFGQG 100
 TKLEIKRTVA APSVFIFFPS DEQLKSGTAS VVCLLNFPY REAKVQWKVD 150
 NALQSGNSQE SVTEQDSKDS TYSLSSLTLL 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) 22-96 150-206 267-327 373-431
 22"-96" 150"-206" 267"-327" 373"-431"
 Intra-L (C23-C104) 23'-87' 133'-193'
 23"-87" 133"-193"
 Inter-H-L (h 5-CL 126) 226-213" 226"-213"
 Inter-H-H (h 11, h 14) 232-232" 235-235"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal

Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyl (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)
 H VH Q1: 1, 1"
 L VL Q1: 1', 1"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
 H CH2 N84.4: 303, 303"

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

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

falbikitungum #
 falbikitung

immunoglobulin G1-kappa , anti-[*Homo sapiens* LIF (LIF interleukin 6 family cytokine, leukemia inhibitory factor)], humanized monoclonal antibody;
 gamma1 heavy chain humanized (1-448) [VH (*Homo sapiens* IGHV3-15*07 (86.9%) -(IGHD) -IGHJ1*01 (90.9%), CDR-IMGT [8.10.9] (26-33.51-60.99-107))(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 kappa light chain humanized (1'-220') [V-KAPPA (*Homo sapiens* IGKV2-24*01 (90.0%) -IGKJ2*01 (100%), CDR-IMGT [11.3.10] (27-37.55-57.94-103)) (1'-113') -*Homo sapiens* IGKC*01 (100%), Km3, A45.1 (159), V101 (197) (114'-220')]; dimer (227-227":230-230")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, glycoform alfa

falbikitung

immunoglobuline G1-kappa, anti-[*Homo sapiens* LIF (cytokine LIF de la famille 6 des interleukines, facteur inhibiteur de la leucémie)]; anticorps monoclonal humanisé;

chaîne lourde gamma1 humanisée (1-448) [VH (*Homo sapiens* IGHV3-15*07 (86.9%) -(IGHD) -IGHJ1*01 (90.9%), CDR-IMGT [8.10.9] (26-33.51-60.99-107)) (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 kappa humanisée (1'-220') [V-KAPPA (*Homo sapiens* IGKV2-24*01 (90.0%) -IGKJ2*01 (100%), CDR-IMGT [11.3.10] (27-37.55-57.94-103)) (1'-113') -*Homo sapiens* IGKC*01 (100%), Km3, A45.1 (159), V101 (197) (114'-220')]; dimère (227-227":230-230")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1, glycoforme alfa

falbikitug

immunoglobulina G1-kappa, anti-[*Homo sapiens* LIF (citoquina LIF de la familia 6 de las interleukinas, factor inhibidor de la leucemia)]; anticuerpo monoclonal humanizado;

cadena pesada gamma1 humanizada (1-448) [VH (*Homo sapiens* IGHV3-15*07 (86.9%) -(IGHD) -IGHJ1*01 (90.9%), CDR-IMGT [8.10.9] (26-33.51-60.99-107)) (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 kappa humanizada (1'-220') [V-KAPPA (*Homo sapiens* IGKV2-24*01 (90.0%) -IGKJ2*01 (100%), CDR-IMGT [11.3.10] (27-37.55-57.94-103)) (1'-113') -*Homo sapiens* IGKC*01 (100%), Km3, A45.1 (159), V101 (197) (114'-220')]; dímero (227-227":230-230")-bisdisulfuro, producido en las células ováricas de hamster chino (CHO), línea celular derivada de CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```

QVQLQESGGG LVKPGGSLRL SCAASGFTFS HAWMHVVRQA PGKGLEWVQG 50
IKAKSDDYAT YYAESVKGRF TISRDDSKNT LYLQMNLSLKT EDTAVYYCTC 100
WEWDLDFWQG GTMVTVSSAS TKGPSVFLA PSSKSTSGGT AALGCLVKDY 150
FPEPVTVSWN SGALTSVGHV FPAVLQSSGL YLSLSSVTVV SSSLGTQTYI 200
CNYNHKPSNT KVDKKVEPKS CDKTHTCPPC PAPELLGGPS VFLFPPKPKD 250
TLMISRTPEV TCVVVDVSHS DPEVKFNWYV DGVEVHNAKT KPREEQYNST 300
YRVVSVLTVL HQDNLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY 350
TLPPSRDELK KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTTPVLD 400
SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNYHTQK SLSLSPGK 448

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Light chain / Chaîne légère / Cadena ligera

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DIVMTQTPLS SPVTLGQPAS ISCRSSQSLL DSDGHTYLNW LQQRPGQPPR 50
LLIYSVSNLE SGVPRDFSGS GAGTDFTLKI SRVEAEDVGV YYCMQATHAP 100
PYTFGQGTGL EIKRTVAAPS VFIFPPSDEQ LKSGTASVVC LLNMFYPREA 150
KVQWKVDNAL QSGNSQESVT EQDSKSTYS LSSLTLLSKA DYEKHKVYAC 200
EVTHQGLSSP VTKSFNRGEC 220

```

Post-translational modifications

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

Intra-H (C23-C104) 22-98 145-201 262-322 368-426
22"-98" 145"-201" 262"-322" 368"-426"

Intra-L (C23-C104) 23'-93' 140'-200'
23"'-93" 140"-200"

Inter-H-L (h 5-CL 126) 221-220' 221"-220"

Inter-H-H (h 11, h 14) 227-227" 230-230"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal

Q > pyroglutamyl (pE, 5-oxopropyl) / pyroglutamyle (pE, 5-oxopropyle) / piroglutamilo (pE, 5-oxopropilo)

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 biantenaricos complejos fucosilados

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

H CHSK2: 448, 448"

fazamorexantum

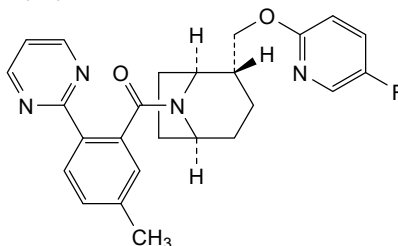
fazamorexant

(4¹S,4²R,4⁵S)-7⁵-fluoro-2⁴-methyl-6-oxa-4⁸-aza-1(2)-pyrimidina-7(2)-pyridina-4(8,2)-bicyclo[3.2.1]octana-2(1,2)-benzenaheptaphan-3-one

fazamorexant

(4¹S,4²R,4⁵S)-7⁵-fluoro-2⁴-méthyl-6-oxa-4⁸-aza-1(2)-pyrimidina-7(2)-pyridina-4(8,2)-bicyclo[3.2.1]octana-2(1,2)-benzénaheptaphan-3-one

fazamorexant

(4¹S,4²R,4⁵S)-7⁵-fluoro-2⁴-metil-6-oxa-4⁸-aza-1(2)-pirimidina-7(2)-piridina-4(8,2)-biciclo[3.2.1]octana-2(1,2)-benzenaheptafan-3-onaC₂₅H₂₅FN₄O₂**faznolutamidum**

faznolutamide

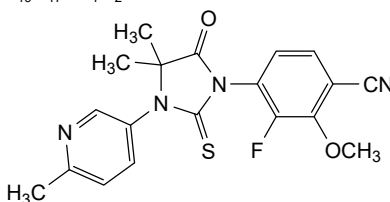
4-[4,4-dimethyl-3-(6-methylpyridin-3-yl)-5-oxo-2-sulfanylidenedimidazolidin-1-yl]-3-fluoro-2-methoxybenzonitrile

faznolutamide

4-[4,4-diméthyl-3-(6-méthylpyridin-3-yl)-5-oxo-2-sulfanylidènimidazolidin-1-yl]-3-fluoro-2-méthoxybenzonitrile

faznolutamida

4-[4,4-dimetil-3-(6-metilpiridin-3-il)-5-oxo-2-sulfanilidenimidazolidin-1-il]-3-fluoro-2-metoxibenzonitrilo

C₁₉H₁₇FN₄O₂S**ficonalkibum**

ficonalkib

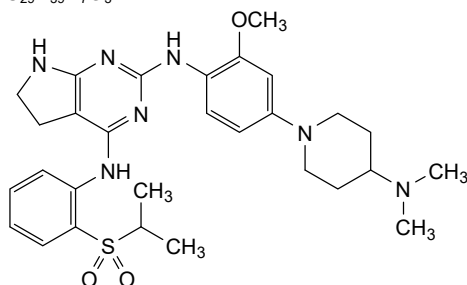
*N*²-{4-[4-(dimethylamino)piperidin-1-yl]-2-methoxyphenyl}-*N*⁴-[2-(propane-2-sulfonyl)phenyl]-6,7-dihydro-5*H*-pyrrolo[2,3-*d*]pyrimidine-2,4-diamine

ficonalkib

*N*²-{4-[4-(diméthylamino)pipéridin-1-yl]-2-méthoxyphényl}-*N*⁴-[2-(propane-2-sulfonyl)phényl]-6,7-dihydro-5*H*-pyrrolo[2,3-*d*]pyrimidine-2,4-diamine

ficonalkib

*N*²-{4-[4-(dimetilamino)piperidin-1-il]-2-metoxifenil}-*N*⁴-[2-(propano-2-sulfonyl)fenil]-6,7-dihidro-5*H*-pirrolo[2,3-*d*]pirimidina-2,4-diamina

C₂₉H₃₉N₇O₃S**firastotugum #**

firastotug

immunoglobulin G1- kappa, anti-[*Homo sapiens* CTLA4 (cytotoxic T-lymphocyte associated protein 4, CTLA-4, CD152)], monoclonal antibody;

gamma1 heavy chain (1-446) [VH (*Homo sapiens*IGHV3-7*01 (77.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [9.7.9] (26-34.52-58.97-105)) (1-116) -*Homo sapiens*IGHG1*01 (100%), G1m17,1 CH1 K120, 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)], (219-215')-disulfide with kappa light chain (1'-215') [V-KAPPA (*Homo sapiens*IGKV1-13*02 (85.3%) -IGKJ1*01 (100%), CDR-IMGT [7.3.9](27-33.51-53.90-98)) (1'-108') -*Homo sapiens*IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')]; dimer (225-225'':228-228'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa

firastotug

immunoglobuline G1-kappa, anti-[*Homo sapiens* CTLA4 (protéine 4 associée aux lymphocytes T cytotoxiques, CTLA-4, CD152)], anticorps monoclonal;

chaîne lourde gamma1 (1-446) [VH (*Homo sapiens*IGHV3-7*01 (77.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [9.7.9] (26-34.52-58.97-105)) (1-116) -*Homo sapiens*IGHG1*01 (100%), G1m17,1 CH1 K120, 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)], (219-215')-disulfure avec la chaîne légère kappa (1'-215') [V-KAPPA (*Homo sapiens*IGKV1-13*02 (85.3%) -IGKJ1*01 (100%), CDR-IMGT [7.3.9] (27-33.51-53.90-98)) (1'-108') -*Homo sapiens*IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')]; dimère (225-225'':228-228'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa

firastotug

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CTLA4 (proteína 4 asociada a los linfocitos T citotóxicos, CTLA-4, CD152)], anticuerpo monoclonal;

cadena pesada gamma1 (1-446) [VH (*Homo sapiens*IGHV3-7*01 (77.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [9.7.9] (26-34.52-58.97-105)) (1-116) -*Homo sapiens*IGHG1*01 (100%), G1m17,1 CH1 K120, 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)], (219-215')-disulfuro con la cadena ligera kappa (1'-215') [V-KAPPA (*Homo sapiens*IGKV1-13*02 (85.3%) -IGKJ1*01 (100%), CDR-IMGT [7.3.9] (27-33.51-53.90-98)) (1'-108') -*Homo sapiens*IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')]; dímero (225-225'':228-228'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

EVQLVESGGG	LVQPGGSLRL	SCAASGYSIS	SGYHWSWIRQ	APGKGLEWLA	50
RIDWDDDKYY	STSLKSRLLTI	SRDNSKNTLY	LQLNSLRAED	TAVYYCARSY	100
VYFDYWGQGT	LVTVSSASTK	GPSVFPPLAPS	SKSTSGGTAA	LGCLVKDYFP	150
EPVTVSWNSG	ALTSVGHVTFP	AVLQSSGLYS	LSSVTVVPSS	SLGTQYIYCN	200
VNHKPSNTKV	DKKVEPKSCD	KTHTCPPCPA	PELLGGPSVF	LFPKPKDITL	250
MISRTPEVTC	VVVDVSHEDP	EVKFNWYVDG	VEVHNAKTKP	REEQYNSTYR	300
VVSVLTVLHQ	DWLNKEYKVC	KVSNKALPAP	IEKTIKAKG	QPREPQVYTL	350
PFSRDELTKN	QVSLTCLVKG	FYPSDIAVEW	ESNGQFPENY	KTTTPVLDSD	400
GSFFLYSKLT	VDKSRWQQGN	VFSCSVMHEA	LHNHYTQKSL	SLSPGK	446

Light chain / Chaîne légère / Cadena ligera

DIQLTQSPSS	LSASVGDVRT	ITCRASQSVR	GRFLAWYQQK	PGKAPKLLIY	50
DASNRATGIP	SRFSGSGSGT	DFTLTISSLQ	PEDFATYYCQ	QSSSWPPTFG	100
QGTKVEIKRT	VAAPSVEIFP	PSDEQLKSGT	ASVVCLLNNF	YPREAKVQWK	150
VDNALQSGNS	QESVTEQDSK	DSTYLSLSTL	TLSKADYEKH	KVYACEVTHQ	200
GLSSFPVKSF	NRGEC				215

Post-translational modifications

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

Intra-H (C23-C104) 22-96 143-199 260-320 366-424
 22"-96" 143"-199" 260"-320" 366"-424"

Intra-L (C23-C104) 23'-89' 135'-195'
 23"'-89'" 135"'-195'"

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

Inter-H-H (h 11, h 14) 225-225" 228-228"

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

H CH2 N84.4: 296, 296"

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

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

H CHS K2: 446, 446"

flizaseritibum

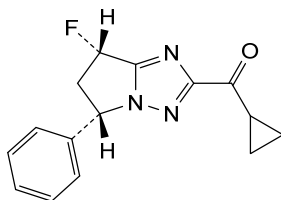
flizaseritib

cyclopropyl[(5*S*,7*S*)-7-fluoro-5-phenyl-6,7-dihydro-5*H*-pyrrolo[1,2-*b*][1,2,4]triazol-2-yl]methanone

flizaseritib

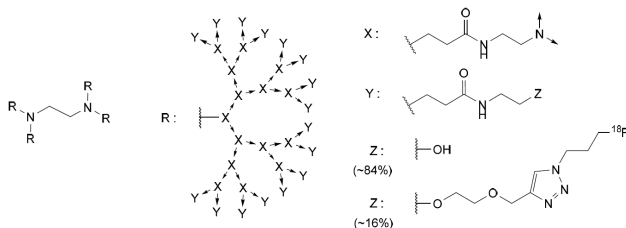
cyclopropyl[(5*S*,7*S*)-7-fluoro-5-phényl-6,7-dihydro-5*H*-pyrrolo[1,2-*b*][1,2,4]triazol-2-yl]méthanone

flizaseritib

ciclopropil[(5*S*,7*S*)-7-fluoro-5-fenil-6,7-dihidro-5*H*-pirrolo[1,2-*b*][1,2,4]triazol-2-il]metanonaC₁₅H₁₄FN₃O**flurimedrimerum (¹⁸F)**flurimedrimer (¹⁸F)

2-({1-[3-(¹⁸F)fluoropropyl]-1*H*-1,2,3-triazol-4-yl]methoxy)ethyl ether with about 16 % of hydroxyl end groups of α,α',α'',α'''-(ethane-1,2-diyl)dinitrilo)tetrakis(ω-hexadecakis{3-[(2-hydroxyethyl)amino]-3-oxopropyl}-*dendro*^{G4}-[(3-oxopropane-1,3-diyl)azanediylethylenenitrilo]), a regular 4-dendron poly(amidoamine)-type dendrimer

- flurimédrimère (^{18}F) éther 2-({1-[3-(^{18}F)fluoropropyl]-1*H*-1,2,3-triazol-4-yl)méthoxy}éthyl) avec approximativement 16 % de groupes terminaux hydroxyles d' $\alpha, \alpha', \alpha'', \alpha'''$ -{éthane-1,2-diyl dinitrilo}tétrakis(ω -hexadécakis{3-[(2-hydroxyéthyl)amino]-3-oxopropyl]-*dendro*^{G4}[(3-oxopropane-1,3-diyl)azanediyléthylénitrilo]}, un dendrimère régulier de type 4-dendron poly(amidoamine)
- flurimedrímero (^{18}F) éter 2-({1-[3-(^{18}F)fluoropropil]-1*H*-1,2,3-triazol-4-il]metoxi)etilico con aproximadamente 16% de los grupos terminados hidroxilos de $\alpha, \alpha', \alpha'', \alpha'''$ -(etano-1,2-diildinitrilo)tetrakis(ω -hexadecakis{3-[(2-hidroxietil)amino]-3-oxopropil]-*dendro*^{G4}[(3-oxopropano-1,3-diil)azanodiiililenonitrilo]}, uno dendrímero regular de tipo 4-dendron poly(amidoamina)

**foslevcromakalimum**

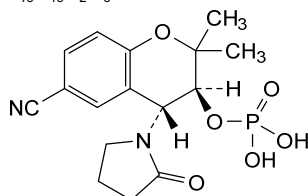
foslevcromakalim

(3*S*,4*R*)-6-cyano-2,2-diméthyl-4-(2-oxopyrrolidin-1-yl)-3,4-dihydro-2*H*-1-benzopyran-3-yl dihydrogen phosphate

foslevcromakalim

dihydrogénophosphate de (3*S*,4*R*)-6-cyano-2,2-diméthyl-4-(2-oxopyrrolidin-1-yl)-3,4-dihydro-2*H*-1-benzopyran-3-yle

foslevcromakalim

dihidrogenofosfato de (3*S*,4*R*)-6-ciano-2,2-dimetil-4-(2-oxopirrolidin-1-il)-3,4-dihidro-2*H*-1-benzopirano-3-ilo $\text{C}_{16}\text{H}_{19}\text{N}_2\text{O}_6\text{P}$ **fulzerasibum**

fulzerasib

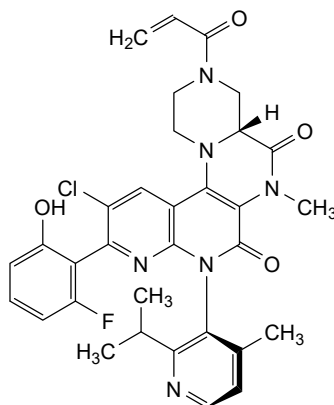
(4*aR*,8*M*)-11-chloro-10-(2-fluoro-6-hydroxyphényl)-6-méthyl-8-[2-(propan-2-yl)-4-méthylpyridin-3-yl]-3-prop-2-énoyl-2,3,4,4*a*,6,8-hexahydro-1*H*-pyrazino[1',2':4,5]pyrazino[2,3-*c*][1,8]naphthyridine-5,7-dione

fulzérasib

(4*aR*,8*M*)-11-chloro-10-(2-fluoro-6-hydroxyphényl)-6-méthyl-8-[2-(propan-2-yl)-4-méthylpyridin-3-yl]-3-prop-2-énoyl-2,3,4,4*a*,6,8-hexahydro-1*H*-pyrazino[1',2':4,5]pyrazino[2,3-*c*][1,8]naphthyridine-5,7-dione

fulzerasib

(4*aR*,8*M*)-11-cloro-10-(2-fluoro-6-hidroxifenil)-6-metil-8-[2-(propan-2-il)-4-metilpiridin-3-il]-3-prop-2-enoil-2,3,4,4*a*,6,8-hexahidro-1*H*-pirazino[1',2':4,5]pirazino[2,3-*c*][1,8]naftiridina-5,7-diona

 $C_{32}H_{30}ClFN_6O_4$
gallium (⁶⁸Ga) rofapitidum tetraxetanumgallium (⁶⁸Ga) rofapitide tetraxetan

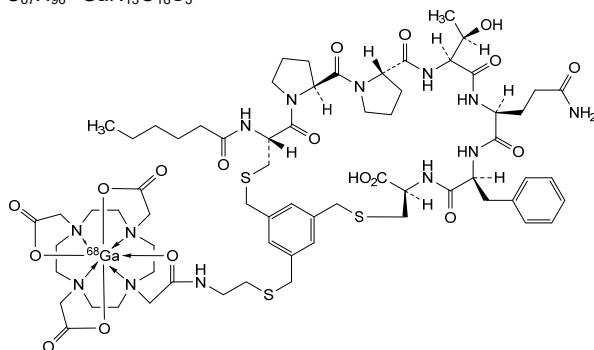
[2,2',2''-{10-[2-(oxo-κO)-2-[[2-(((1²S,3²S,5R,13R,16S,19S,22S))-19-(3-amino-3-oxopropyl)-16-benzyl-13-carboxy-5-hexanamido-22-[(1R)-1-hydroxyethyl]-2,4,15,18,21,24-hexaoxo-7,11-dithia-14,17,20,23-tetraaza-1(1,2),3(2,1)-dipyrrolidina-9(1,3)-benzenacyclotetracosaphan-9⁵-yl)methyl)sulfanyl]ethyl]amino}ethyl]-1,4,7,10-tetraazacyclododecane-1,4,7-triyl-κ⁴N¹,N⁴,N⁷,N¹⁰}tri(acetato-κO)](⁶⁸Ga)gallium

gallium (⁶⁸Ga) rofapitide tétraxétan

[2,2',2''-{10-[2-(oxo-κO)-2-[[2-(((1²S,3²S,5R,13R,16S,19S,22S))-19-(3-amino-3-oxopropyl)-16-benzyl-13-carboxy-5-hexanamido-22-[(1R)-1-hydroxyéthyl]-2,4,15,18,21,24-hexaoxo-7,11-dithia-14,17,20,23-tétraza-1(1,2),3(2,1)-dipyrrolidina-9(1,3)-benzénacyclotétracosaphan-9⁵-yl)méthyl)sulfanyl]éthyl]amino}éthyl]-1,4,7,10-tétrazacyclododécane-1,4,7-triyl-κ⁴N¹,N⁴,N⁷,N¹⁰}tri(acétato-κO)](⁶⁸Ga)gallium

galio (⁶⁸Ga) rofapitida tetraxetán

[2,2',2''-{10-[2-(oxo-κO)-2-[[2-(((1²S,3²S,5R,13R,16S,19S,22S))-19-(3-amino-3-oxopropil)-16-bencil-13-carboxi-5-hexanamido-22-[(1R)-1-hidroxietyl]-2,4,15,18,21,24-hexaoxo-7,11-ditia-14,17,20,23-tetraaza-1(1,2),3(2,1)-dipirrolidina-9(1,3)-bencenacicotetracosafan-9⁵-il]metil)sulfanil]etil]amino}etil]-1,4,7,10-tetraazaciclododecano-1,4,7-triyl-κ⁴N¹,N⁴,N⁷,N¹⁰}tri(acetato-κO)](⁶⁸Ga)galio

**ganfaborolum**

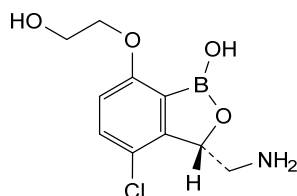
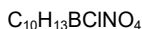
ganfeborole

(3*S*)-3-(aminomethyl)-4-chloro-7-(2-hydroxyethoxy)-2,1-benzoxaborol-1(3*H*)-ol

ganfèborole

(3*S*)-3-(aminométhyl)-4-chloro-7-(2-hydroxyéthoxy)-2,1-benzoxaborol-1(3*H*)-ol

ganfeborol

(3*S*)-3-(aminometil)-4-cloro-7-(2-hidroxietoksi)-2,1-benzoxaborol-1(3*H*)-ol**gemlapodectum**

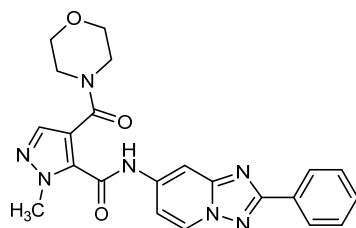
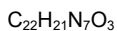
gemlapodect

1-methyl-4-[(morpholin-4-yl)carbonyl]-*N*-(2-phenyl[1,2,4]triazolo[1,5-*a*]pyridin-7-yl)-1*H*-pyrazole-5-carboxamide

gemlapodect

1-méthyl-4-[(morpholin-4-yl)carbonyl]-*N*-(2-phényl[1,2,4]triazolo[1,5-*a*]pyridin-7-yl)-1*H*-pyrazole-5-carboxamide

gemlapodect

1-metil-4-[(morfolin-4-il)carbonyl]-*N*-(2-fenil[1,2,4]triazolo[1,5-*a*]piridin-7-il)-1*H*-pirazolo-5-carboxamida

gotistobartum #
gotistobart

immunoglobulin G1-kappa , anti-[*Homo sapiens* CTLA4 (cytotoxic T-lymphocyte-associated protein 4, CTLA-4, CD152)], humanized monoclonal antibody; gamma1 heavy chain humanized (1-454) [VH (*Homo sapiens* IGHV4-59*01 (86.6%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.7.19] (26-33.51-57.96-114)) (1-125) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120 CH3 D12, L14, G1v6CH2 A85.4, A118, A119, G1v21 CH2 Y15.1, T16, E18 (CH1 K120 (222) (126-223), hinge 1-15 (224-238), CH2 M15.1>Y (260), S16>T (262), T18>E (264), S85.4>A (306), E118>A (341), K119>A (342) (239-348), CH3 D12 (364), L14 (366) (349-453), CHS K2>del (454)) (126-454)], (228-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-NL1*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 (234-234":237-237")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

gotistobart

immunoglobuline G1-kappa, anti-[*Homo sapiens* CTLA4 (protéine 4 associée aux lymphocytes T cytotoxiques, CTLA-4, CD152)], anticorps monoclonal humanisé; chaîne lourde gamma1 humanisée (1-454) [VH (*Homo sapiens* IGHV4-59*01 (86.6%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.7.19] (26-33.51-57.96-114)) (1-125) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120 CH3 D12, L14, G1v6 CH2 A85.4, A118, A119, G1v21 CH2 Y15.1, T16, E18 (CH1 K120 (222) (126-223), hinge 1-15 (224-238), CH2 M15.1>Y (260), S16>T (262), T18>E (264), S85.4>A (306), E118>A (341), K119>A (342) (239-348), CH3 D12 (364), L14 (366) (349-453), CHS K2>del (454)) (126-454)], (228-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-NL1*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 (234-234":237-237")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

gotistobart

immunoglobulina G1-kappa, anti-[*Homo sapiens* CTLA4 (proteína 4 asociada a los linfocitos T citotóxicos, CTLA-4, CD152)], anticuerpo monoclonal humanizado; cadena pesada gamma1 humanizada (1-454) [VH (*Homo sapiens* IGHV4-59*01 (86.6%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.7.19] (26-33.51-57.96-114)) (1-125) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120 CH3 D12, L14, G1v6 CH2 A85.4, A118, A119, G1v21 CH2 Y15.1, T16, E18 (CH1 K120 (222) (126-223), bisagra 1-15 (224-238), CH2 M15.1>Y (260), S16>T (262), T18>E (264), S85.4>A (306), E118>A (341), K119>A (342) (239-348), CH3 D12 (364), L14 (366) (349-453), CHS K2>del (454)) (126-454)], (228-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-NL1*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 (234-234":237-237")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

QVQLQESGPG LVKPSETLSL TCTVSGFSLT SYGLSWIRQP PGKGLEWIGY 50
 IWYDGNNTNFH SPLKSRVTIS VDTSKNQFSL KLSSVTAADT AVYYCAKTEG 100
 HYYGSNYGY ALDYWGQGTLL VTVSSASTKG PSVFPLAPSS KSTSSGTAAL 150
 GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL SSVVTVPSSS 200
 LGTQTYICNV NHPKSNKVD KKVPEKSCDK THTCPCCPAP ELLGGSFVFL 250
 FPPKPKDTLY ITRPEVTCV VVDVSHEDPE VKNWYVDGV EVHNAKTKPR 300
 EEQYNATYRV VSVLTVLHQD WLNKEYKCK VSNKALPAPI AATISKAKGQ 350
 PREPQVYTLF PSRDELTKNQ VSLTCLVKGK YPSDIAVEWE SNGQPENNYK 400
 TTPPVLDSDG SFFLYSKLTW DKSRWQQGNV FSCVMHEAL HNHYTEKSL 450
 LSPG 454

Light chain / Chaîne légère / Cadena ligera

DIQMTQSPSS LSASVGRVIT ITCRASENIY SNLAWYQQKQ GKAPKLLLYA 50
 ATNLQDGVPS RFSGSGSGTD YTLTISSLQP EDFATYFCQH LWGTPYTFGQ 100
 GTKLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PRAKVKQWKV 150
 DNALQSGNSQ ESVTEQDSK STYLSLSTLT LSKADYKHKH VYACEVTHQG 200
 LSSPVTKSFN RGEK 214

Post-translational modifications

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

Intra-H (C23-C104) 22-95 152-208 269-329 375-433
 22"-95" 152"-208" 269"-329" 375"-433"

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

Inter-H-L (h 5-CL 126) 228-214' 228"-214"

Inter-H-H (h 11, h 14) 234-234" 237-237"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal

Q > pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprolilo)
 H VH Q1: 1, 1"

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

H CH2 N84.4: 305, 305"

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

gulgafafuspum alfa

gulgafafusp alfa

humanized immunoglobulin G2-kappa, anti-(human glucagon-like peptide 1 receptor, GLP1R) (heavy chain 1-451, variant S³⁸²>A) fused at the N-terminus of each light chain (53-266) via the peptide linker ³⁰GSGSATGGSGSGASSGSGSATGS⁵² to a glucagon-like peptide-1 (GLP-1) fragment (7-35, 1-29 in the current sequence), variant (A²>G), disulfide bridged dimer, produced in Chinese hamster ovary (CHO) cells, glycoform alfa; humanized monoclonal antibody fusion with human Glucagon-like peptide 1 (GLP1); type: IgG2-kappa; antigen: human glucagon-like peptide 1 receptor, GLP-1 receptor, GLP-1-R, GLP-1R (GLP1R); CDR source: *Mus musculus* (humanized by Kabat CDR grafting); heavy chain class: gamma2; heavy chain length: 451; HV germline: *Homo sapiens* IGHV3-33*01; HJ germline: *Homo sapiens* IGHJ6*01; HC germline: *Homo sapiens* IGHG2*01; VH: 1-125; CH1: 126-223; hinge: 224-235; CH2: 236-344; CH3: 345-449 (S382A, non-functional mutation); CHS: 450-451; CDR Kabat H1: SYGMH (31-35); CDR Kabat H2: VIWYDGSNKYYADSVKG (50-66); CDR Kabat H3: GGGSGSYRYYYGLDV (99-114); fusion protein: 1-29 (human 7-35 glucagon-like peptide-1); linker: 30-52; light chain class: kappa; light chain length: 266; LV germline: *Homo sapiens* IGKV1-12*01; LJ germline: *Homo sapiens* IGKJ1*01; LC germline: *Homo sapiens* IGKC*01; VL: 53-159; CL: 160-266; CDR Kabat L1: RASQNINLLA (76-86); CDR Kabat L2: TASSLQS (102-108); CDR Kabat L3: QQAHRFPPT (141-149)

gulgafafusp alfa

immunoglobuline humanisée G2-kappa, anti-(récepteur humain du peptide 1 de type glucagon, GLP1R) (chaîne lourde 1-451, variant S³⁸²>A) fusionnée à l'extrémité N-terminale de chaque chaîne légère (53-266) via la liaison peptidique ³⁰GSGSATGGSGSGASSGSGSATGS⁵² à un fragment du peptide-1 de type glucagon (GLP-1) (7-35, 1-29 dans la séquence actuelle), variant (A²>G), dimère à pont disulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa;

fusion d'un anticorps monoclonal humanisé avec le peptide 1 de type glucagon (GLP1) humain; type: IgG2-kappa; antigène: récepteur humain du peptide 1 de type glucagon récepteur GLP-1, GLP-1-R, GLP-1R (GLP1R); source CDR: *Mus musculus* (humanisé par greffe de CDR Kabat); classe de chaîne lourde: gamma2; longueur de la chaîne lourde: 451; HV lignée germinale: *Homo sapiens* IGHV3-33*01; HJ lignée germinale: *Homo sapiens* IGHJ6*01; HC lignée germinale: *Homo sapiens* IGHG2*01; VH: 1-125; CH1: 126-223; charnière: 224-235; CH2: 236-344; CH3: 345-449 (S382A, mutation non fonctionnelle); CHS: 450-451; CDR Kabat H1: SYGMH (31-35); CDR Kabat H2: VIWYDGSNKYYADSVKG (50-66); CDR Kabat H3: GGGSGSYRYYYGLDV (99-114); protéine de fusion: 1-29 (peptide-1 de type glucagon humain 7-35); liaison: 30-52; classe de chaîne légère: kappa; longueur de chaîne légère: 266; LV lignée germinale: *Homo sapiens* IGKV1-12*01; LJ lignée germinale: *Homo sapiens* IGKJ1*01; LC lignée germinale: *Homo sapiens* IGKC*01; VL: 53-159; CL: 160-266; CDR Kabat L1: RASQNINLLA (76-86); CDR Kabat L2: TASSLQS (102-108); CDR Kabat L3: QQAHRFPPT (141-149)

gulgafafusp alfa

immunoglobulina humana G2-kappa, anti-(receptor del péptido 1 similar al glucagón humano, GLP1R) (cadena pesada 1-451, variante S³⁸²>A) fusionada al N-terminal de cada cadena ligera (53-266) a través del enlace peptídico ³⁰GSGSATGGSGSGASSGSGSATGS⁵² al receptor del péptido 1 similar al glucagón humano (GLP-1) fragmento (7-35, 1-29 en la secuencia actual), variante (A²>G), dímero con puente disulfuro, producido en células ováricas de hámster Chino (CHO), forma glicosilada alfa;

anticuerpo monoclonal humanizado de fusión con receptor del péptido 1 similar al glucagón (GLP1); tipo: IgG2-kappa; antígeno: receptor del péptido 1 similar al glucagón, receptor GLP-1, GLP-1-R, GLP-1R (GLP1R); fuente CDR: *Mus musculus* (humanizado por injerto de CDR de Kabat); clase cadena pesada: gamma2; longitud cadena pesada: 451; línea germinal HV: *Homo sapiens* IGHV3-33*01; línea germinal HJ: *Homo sapiens* IGHJ6*01; línea germinal HC: *Homo sapiens* IGHG2*01; VH: 1-125; CH1: 126-223; bisagra: 224-235; CH2: 236-344; CH3: 345-449 (S382A, mutación no funcional); CHS: 450-451; CDR Kabat H1: SYGMH (31-35); CDR Kabat H2: VIWYDGSNKYYADSVKG (50-66); CDR Kabat H3: GGGSGSYRYYYGLDV (99-114); proteína de fusión: 1-29 (péptido 1 similar al glucagón humano 7-35); enlace: 30-52; clase de cadena ligera: kappa; longitud de cadena ligera: 266; línea germinal LV: *Homo sapiens* IGKV1-12*01; línea germinal LJ: *Homo sapiens* IGKJ1*01; línea germinal LC: *Homo sapiens* IGKC*01; VL: 53-159; CL: 160-266; CDR Kabat L1: RASQNINLLA (76-86); CDR Kabat L2: TASSLQS (102-108); CDR Kabat L3: QQAHRFPPT (141-149)

Sequence / Séquence / Secuencia

Heavy chain / Chaîne lourde / Cadena pesada

QVQLVESGGG VVQPGRSLRL SCAASGFTLS SYGMHWVRQA PGKGLEWVAV 50
 IWYDGSNKYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARGG 100
 GSGSYRYYY GLDVWGQGT VTVSSASTKG PSVFLAPCS RSTSESTAAL 150
 GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL SSVVTVPSNN 200
 FGTQTYTCNV DHKPSNTRVD KTVRKKCCVE CPFCPPVVA GPSVFLFPPK 250
 PKDTLMSRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQF 300
 NSTFRVSVL TVVHQDWLNG KEYKCKVSNK GLPAPIEKTI SKTKGQPREP 350
 QVYTLPPSRE EMTKNQVSLT CLVKGFPYSD IAVENESNGQ PENNYKTPFP 400
 MLDSDGSEFFL YSKLTVDKSR WQQGNVFPSC VMHEALHNNH TQKSLSLSPG 450
 K 451

Light chains / Chaînes légères / Cadenas ligeras: GLP-1- IgG2 kappa

HGE~~G~~TFTSDV SSYLEGQAAK EFIAWLKVG *SGSATGGSGS GASSGSGSAT* 50
*GS*AIQMTQSP SSVSASIGDR VTITCRASQN INNLLAWYQQ KPGKAPKLLI 100
 YTASLQSEV PSRFSGSGSG TDFTLTISSL QPEDFAIYCC QQAHRFPPTF 150
 QGTGKVEIRR TWAAPSVFIF PPSDEQLKSG TASVUCLLNN FYPREAKVQQ 200
 KVDNALQSGN SQESVTEQDS KDSTYLSLST LTLKADYER HKVYACEVTH 250
 QGLSSPVTKS FNRGEC 266

Mutation / Mutation / Mutación

S382, S382"[>]**A**, A2', A2"[>]**G**

Peptide linker / Peptides liant / Péptido de unión

SGSATGGSGASSGSGSATGS 30-52

Post-translational modifications

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

Intra-H 22 - 96, 152 - 208, 265 - 325, 371 - 429
 22"-96", 152"-208", 265"-325", 371"-429"

Intra-L 75"-140", 186"-246"
 75"-140"', 186"-246''

Inter-H-L 139-266', 139"-266''

Inter-H-H 227-227", 228-228", 231-231", 234-234"

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

N301, N301"

N-terminal glutaminy cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutamínilo N-terminal

H VH Q1 > pyroglutamyl (pE, 5-oxoprolyl): 1, 1"

gumelutamidum

gumelutamide

2-chloro-4-(4-[[5-(2-hydroxypropan-2-yl)pyridin-2-yl]amino]-5,8-dihydropyrido[3,4-*d*]pyrimidin-7(6*H*)-yl]benzonitrile

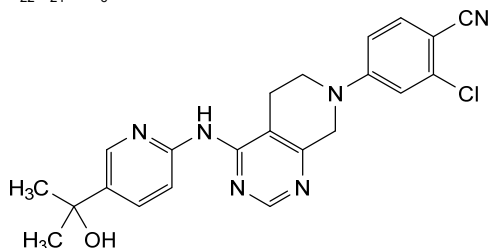
gumélutamide

2-chloro-4-(4-[[5-(2-hydroxypropan-2-yl)pyridin-2-yl]amino]-5,8-dihydropyrido[3,4-*d*]pyrimidin-7(6*H*)-yl]benzonitrile

gumelutamida

2-cloro-4-(4-[[5-(2-hidroxiopropan-2-il)piridin-2-il]amino]-5,8-dihidropirido[3,4-*d*]pirimidin-7(6*H*)-il]benzonitrilo

C₂₂H₂₁ClN₆O



hypericinum

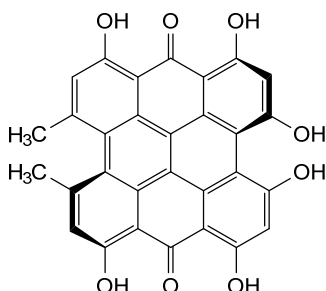
hypericin

rac-(3*aM*,10*aM*)-1,3,4,6,8,13-hexahydroxy-10,11-dimethylphenanthro[1,10,9,8-*opqra*]perylene-7,14-dione

hypéricine

rac-(3*aM*,10*aM*)-1,3,4,6,8,13-hexahydroxy-10,11-diméthylphénanthro[1,10,9,8-*opqra*]pérylène-7,14-dione

hipericina

rac-(3*aM*,10*aM*)-1,3,4,6,8,13-hexahidroxi-10,11-dimetilfenantro[1,10,9,8-*opqra*]perileno-7,14-diona $C_{30}H_{16}O_8$ and enantiomer
et énantiomère
y enantiómero**ifebentinibum**

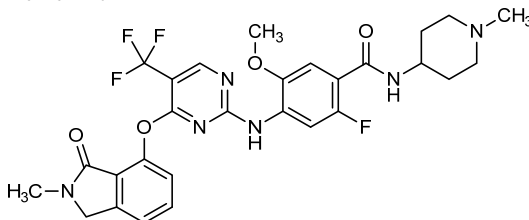
ifebentinib

2-fluoro-5-methoxy-4-({4-[(2-methyl-3-oxo-2,3-dihydro-1*H*-isoindol-4-yl)oxy]-5-(trifluoromethyl)pyrimidin-2-yl}amino)-*N*-(1-methylpiperidin-4-yl)benzamide

ifébentinib

2-fluoro-5-méthoxy-4-({4-[(2-méthyl-3-oxo-2,3-dihydro-1*H*-isoindol-4-yl)oxy]-5-(trifluorométhyl)pyrimidin-2-yl}amino)-*N*-(1-méthylpipéridin-4-yl)benzamide

ifebentinib

2-fluoro-5-metoxi-4-({4-[(2-metil-3-oxo-2,3-dihidro-1*H*-isoindol-4-il)oxi]-5-(trifluorometil)pirimidin-2-il}amino)-*N*-(1-metilpiperidin-4-il)benzamide $C_{28}H_{28}F_4N_6O_4$ **iluzanebartum #**

iluzanebart

immunoglobulin G1- kappa, anti-[*Homo sapiens* TREM2 (triggering receptor expressed on myeloid cells 2)], *Homo sapiens* monoclonal antibody, agonist;
 gamma1 heavy chain *Homo sapiens* (1-451) [VH (*Homo sapiens* IGHV5-51*01 (96.9%) -(IGHD) -IGHJ1*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, G1v54-30 CH2 C83, G84.4, C85 (CH1 R120>K (218) (122-219), hinge 1-15 (220-234), CH2 R83>C (296), N84.4>G (301), V85>C (306) (235-344), CH3 E12 (360), M14 (362) (345-449), CHS (450-451)) (122-451)], (224-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-15*01 (94.7%) -IGKJ1*01 (90.9%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%) (108'-214')]; dimer (230-230''-233-233'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

iluzanebart immunoglobuline G1-kappa, anti-[*Homo sapiens* TREM2 (récepteur déclenchant exprimé sur les cellules myéloïdes 2)], anticorps monoclonal *Homo sapiens*, agoniste; chaîne lourde gamma1 *Homo sapiens* (1-451) [VH (*Homo sapiens* IGHV5-51*01 (96.9%) -(IGHD) - IGHJ1*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, G1v54-30 CH2 C83, G84.4, C85 (CH1 R120>K (218) (122-219), charnière 1-15 (220-234), CH2 R83>C (296), N84.4>G (301), V85>C (306)(235-344), CH3 E12 (360), M14 (362) (345-449), CHS (450-451)) (122-451)], (224-214')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-15*01 (94.7%) - IGKJ1*01 (90.9%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%) (108'-214')]; dimère (230-230":233-233")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

iluzanebart inmunoglobulina G1-kappa, anti-[*Homo sapiens* TREM2 (receptor desencadenante expresado sobre las células mieloides 2)], anticuerpo monoclonal *Homo sapiens*, agonista; cadena pesada gamma1 *Homo sapiens* (1-451) [VH (*Homo sapiens* IGHV5-51*01 (96.9%) -(IGHD) - IGHJ1*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, G1v54-30 CH2 C83, G84.4, C85 (CH1 R120>K (218) (122-219), bisagra 1-15 (220-234), CH2 R83>C (296), N84.4>G (301), V85>C (306)(235-344), CH3 E12 (360), M14 (362) (345-449), CHS (450-451)) (122-451)], (224-214')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-15*01 (94.7%) -IGKJ1*01 (90.9%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%) (108'-214')]; dímero (230-230":233-233")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada
 EVQLVQSGAE VPKPGESLKI SCKGSGVSFT SYWIGWVRQM PGKGLEWNGI 50
 IYPGDADARY SPSFQGGVTI SADKSIStAY LQWSSLKASD TAMYFCARRR 100
 QGIFGDALDF WQGGTLVTVS SASTKGPSVF PLAPSSKTS GGTAALGCLV 150
 KDYFPEPVTV SWNSGALTSV VHTFPAVLGS SGLYLSLSSVV TTPSSSLGTQ 200
 TYICNVNHKP SNTKVDKKVE PKSCDKTHTC PFCPAPELLG GPSVFLFPFK 250
 PKDTLMI SRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPCREEQY 300
 GSTYRCVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP 350
 QVYTLPPSRE EMTKNQVSLT CLVKGFPYPSD IAVEWESNGQ PENNYKTTTFF 400
 VLDSDDGSFPL YSKLTVDKSR WQQGNVFSCS VMHEALHNNHY TQKSLSLSPG 450
 K 451

Light chain / Chaîne légère / Cadena ligera
 EIVMTQSPAT LSVSPGERAT LSCRASQSVS SNLAWFQQKP CQAPRLLLYG 50
 ASTRATGIPA RFSGSGSGTE FTLTISLSLPQ EDFAVYICLQ DNNFPPFTGQ 100
 GTKVDIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNIFY PREAKVQWKV 150
 DNALQSGNSQ ESVTEQDSKD STYLSLSTLT LSKADYEKHK VYACEVTHQG 200
 LSSPVTKSPN RGEC 214

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

No N-glycosylation sites / pas de sites de N-glycosylation / ningun posición de N-glicosilación
 H CH2 N84.4-G (G1v30): 301, 301"

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

imsamotidum

imsamotide

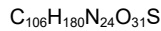
L- α -aspartyl-L-threonyl-L-leucyl-L-leucyl-L-lysyl-L-alanyl-L-leucyl-L-leucyl-L- α -glutamyl-L-isoleucyl-L-alanyl-L-seryl-L-cysteinyl-L-leucyl-L- α -glutamyl-L-lysyl-L-alanyl-L-leucyl-L-glutaminy-L-valyl-L-phenylalanine

imsamotide

L- α -aspartyl-L-thréonyl-L-leucyl-L-leucyl-L-lysyl-L-alanyl-L-leucyl-L-leucyl-L- α -glutamyl-L-isoleucyl-L-alanyl-L-séryl-L-cystéinyl-L-leucyl-L- α -glutamyl-L-lysyl-L-alanyl-L-leucyl-L-glutaminy-L-valyl-L-phénylalanine

imsamotida

L- α -aspartil-L-treonil-L-leucil-L-leucil-L-lisil-L-alanil-L-leucil-L-leucil-L- α -glutamil-L-isoleucil-L-alanil-L-seril-L-cisteinil-L-leucil-L- α -glutamil-L-lisil-L-alanil-L-leucil-L-glutaminil-L-valil-L-fenilalanina



DTLLKALLEI ASCLEKALQV F 21

inaticabtagenum autoleucelum #

inaticabtagene autoleucel

autologous T lymphocytes obtained from peripheral blood mononuclear cells by leukapheresis, transduced with a self-inactivating, non-replicating lentiviral vector, encoding a chimeric antigen receptor targeting CD19. The expressed transgene comprises a CD8 α leader sequence, an anti-CD19 single chain variable fragment (scFv) derived from clone HI19a, a CD8 α hinge and transmembrane region, and a 4-1BB and CD3 ζ signalling domain and is under control of the elongation factor 1 alpha (EF1 α) promoter. The construct is flanked by 5' and 3' long terminal repeats (LTRs) and also contains a ψ packaging signal, parts of the *gag* and *env* genes, a Rev response element (RRE), a central polypurine tract (cPPT) sequence, a Kozak sequence, and a Woodchuck hepatitis virus posttranscriptional regulatory element (WPRE). The vector is pseudotyped with vesicular stomatitis virus (VSV) G glycoprotein. The leukapheresis material is enriched for CD4/CD8 T lymphocytes by positive immunoselection, activated by CD3 and CD28 magnetic beads and transduced with the vector. The cells are then expanded in media supplemented with serum replacement and interleukin 2 (IL-2). The T lymphocytes ($\geq 90\%$) are positive for the transgene ($\geq 15\%$ CAR positive), secrete interferon gamma, and demonstrate cytotoxicity against CD19 expressing cells

inaticabtagène autoleucel

lymphocytes T autologues obtenus à partir de cellules mononucléaires de sang périphérique par leucaphérese, transduits avec un vecteur lentiviral auto-inactif et non répliquant, codant un récepteur antigénique chimérique ciblant CD19. Le transgène exprimé comprend une séquence leader CD8 α , un fragment variable à chaîne unique (scFv) anti-CD19 dérivé du clone HI19a, une charnière CD8 α et une région transmembranaire, ainsi qu'un domaine de signalisation 4-1BB et CD3 ζ et est sous le contrôle du promoteur du facteur d'élongation 1 alpha (EF1 α). La construction est flanquée de répétitions longues terminales (LTR) en 5' et 3' et contient également un signal d'encapsidation ψ , des parties des gènes *gag* et *env*, un élément de réponse Rev (RRE), une séquence du tractus polypurine central (cPPT), une séquence Kozak et un

élément de régulation post-transcriptionnel du virus de l'hépatite de Woodchuck (WPRE). Le vecteur est pseudotypé avec la glycoprotéine G du virus de la stomatite vésiculaire (VSV). Le matériel de leucaphérese est enrichi en lymphocytes T CD4/CD8 par immunosélection positive, activé par des billes magnétiques CD3 et CD28 et transduit avec le vecteur. Les cellules sont ensuite développées dans un milieu complétement par du sérum de remplacement et de l'interleukine 2 (IL-2). Les lymphocytes T ($\geq 90\%$) sont positifs pour le transgène ($\geq 15\%$ CAR positif), sécrètent de l'interféron gamma et démontrent une cytotoxicité contre les cellules exprimant le CD19

inaticabtagén autoleucel

linfocitos T autólogos obtenidos de células mononucleares de sangre periférica mediante leucoaféresis, transducidos con un vector lentiviral auto inactivante, no replicativo, que codifica para un receptor de antígenos quimérico dirigido a CD19. El transgén expresado contiene una secuencia líder de CD8 α , un fragmento variable de cadena sencilla (scFv) anti-CD19 derivado del clon HI19a, una región bisagra y transmembrana de CD8 α , y un dominio de señalización 4-1BB y CD3 ζ , y está bajo el control del promotor del factor de elongación 1 alfa (EF1 α). El constructo está flanqueado por repeticiones terminales largas (LTRs) en 5' y 3' y también contiene una señal de empaquetamiento ψ , partes de los genes *gag* y *env*, un elemento de respuesta Rev (RRE), una secuencia de tracto de polipurina central (cPPT), una secuencia Kozak y un elemento regulador post-transcripcional del virus de la hepatitis de la marmota (WPRE). El vector está seudotipado con la glicoproteína G del virus de la estomatitis vesicular (VSV). El material de leucoaféresis se enriquece para linfocitos T CD4/CD8 mediante inmunoselección positiva, se activa mediante bolas magnéticas de CD3 y CD28 y se transduce con el vector. Las células son después expandidas en medio suplementado con sustituto de suero e interleuquina 2 (IL-2). Los linfocitos T ($\geq 90\%$) son positivos para el transgén ($\geq 15\%$ CAR positivas), secretan interferón gamma y demuestran citotoxicidad contra células que expresan CD19

inpegsomatropinum #
inpegsomatropin

recombinant human somatotropin (growth hormone, GH), conjugated to a multi-arm polyethylene glycol carrier molecule; somatotropin (human), produced by *Pichia pastoris*, non-glycosylated, N-terminal or $N^{6\text{-Lys}}$ mono-substituted with one (2-[ω -methoxypoly(oxyethylene)- α -yl]-N-{2-[ω -methoxypoly(oxyethylene)- α -yl]ethyl}acetamido)acetyl group (~40 kDa)

inpegsomatropine

somatotropine humaine recombinante (hormone de croissance, GH), conjuguée à une molécule transporteur multi-bras de polyéthylène glycol; somatotropine (humaine), produite par *Pichia pastoris*, non glycosylée, mono-substituée à l'extrémité N-terminale ou en $N^{6\text{-Lys}}$ par un groupe (2-[ω -méthoxypoly(oxyéthylène)- α -yl]-N-{2-[ω -méthoxypoly(oxyéthylène)- α -yl]éthyl}acétamido)acétyle (~40 kDa)

inpegsomatropina

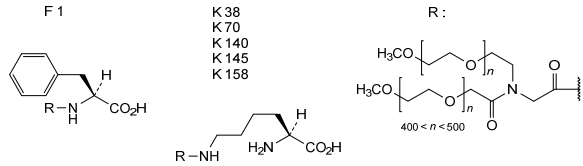
somatotropina humana recombinante (hormona de crecimiento, GH), conjugada con una molécula transportadora multi-brazo de polietileno glicol; somatotropina (humana), producida por *Pichia pastoris*, no glicosilada, mono-sustituída con el extremo N-terminal o con N⁶.Lys por un grupo (2-[ω-metoxipoli(oxietileno)-α-il]-N-{2-[ω-metoxipoli(oxietileno)-α-il]etil}acetamido)acetil (~40 kDa)

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EPTIPLSRFL DNAMLRRAHRL HQLAFDITYQE FEEAYIPKEQ KYSFLQNPQT 50
SLCFSESIST PSNREETQOK SNLELLRLSL LLIQSWLEPV QFLRSVFANS 100
LVYGASDSNV YDLLKDLEEG IQTLMGRLED GSPRTGQIFK QTYSKPDTNS 150
HNDDALLKNY GLLYCFRKDM DKVETFLRIV QCRSVEGSCG F 191
    
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Disulfide bridges location / Positions des ponts disulfure / Posiciones de los puentes disulfuro
53-165 182-189

Potential modified residues / Résidus modifiés potentiels / restos modificados potenciales



izumerogantum

izumerogant

4-{4-[3-(2-chloro-6-fluorophenyl)-4-(pyrimidin-2-yl)-1,2-oxazol-5-yl]-5-(trifluoromethyl)-1H-pyrazol-1-yl]-2-methylbutan-2-ol

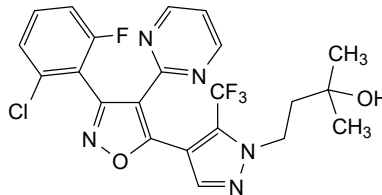
izumérogant

4-{4-[3-(2-chloro-6-fluorophényl)-4-(pyrimidin-2-yl)-1,2-oxazol-5-yl]-5-(trifluorométhy)-1H-pyrazol-1-yl]-2-méthylbutan-2-ol

izumerogant

4-{4-[3-(2-cloro-6-fluorofenil)-4-(pirimidin-2-il)-1,2-oxazol-5-il]-5-(trifluorometil)-1H-pirazol-1-il]-2-metilbutan-2-ol

C₂₂H₁₈ClF₄N₅O₂



labafenogenum marselecobacum #

labafenogene marselecobac

recombinant live *Escherichia coli* strain Nissle 1917 (EcN) bacteria, genetically engineered as follows:

- Insertion across the genome of four copies of a modified phenylalanine ammonia lyase (mPAL) gene from *Photobacterium laumondii* subsp. *laumondii* with mutations S92G, H133M, I167K, L432I, V470A under control of the LacI repressor/P_{tac} inducible promoter.
- Insertion of one extra copy of the endogenous high affinity phenylalanine specific permease (PheP), under control of the LacI repressor/P_{tac} inducible promoter.
- Insertion of the gene L-amino acid deaminase (LAAD), derived from *Proteus mirabilis*, under control of the endogenous AraC transcriptional regulator/P_{BAD} inducible promoter.

- d) Deletion of the *dapA* gene, which renders bacteria cells auxotrophic unless supplemented with diaminopimelate (DAP) exogenously.
e) Deletion of its endogenous prophage Φ .
- labafénogène marsélécobac bactérie recombinante vivante *Escherichia coli* souche Nissle 1917 (EcN), génétiquement modifiée comme suit:
a) Insertion dans le génome de quatre copies d'un gène de phénylalanine ammoniac lyase (mPAL) modifié de *Photorhabdus laumondii* subsp. *laumondii* avec les mutations S92G, H133M, I167K, L432I, V470A sous le contrôle du répresseur Lacl /promoteur inducible P_{tac} .
b) Insertion d'une copie supplémentaire de la perméase spécifique de la phénylalanine endogène à haute affinité (PheP), sous le contrôle du répresseur Lacl /promoteur inducible P_{tac} .
c) Insertion du gène L-aminoacide désaminase (LAAD), dérivé de *Proteus mirabilis*, sous le contrôle du régulateur de transcription endogène AraC /promoteur inducible P_{BAD} .
d) La délétion du gène *dapA*, qui rend les cellules bactériennes auxotrophes à moins d'être complémentées par du diaminopimélate (DAP) de manière exogène.
e) Suppression de son prophage endogène Φ .
- labafenogén marselecobac bacteria recombinante viva *Escherichia coli* cepa Nissle 1917 (EcN), modificada genéticamente como sigue:
a) Inserción a lo largo del genoma de cuatro copias de un gen modificado de fenilalanina amonio liasa (mPAL) de *Photorhabdus laumondii* subesp. *laumondii* con mutaciones S92G, H133M, I167K, L432I, V470A bajo el control del represor Lacl /promotor inducible P_{tac} .
b) Inserción de una copia extra de la permeasa de alta afinidad endógena específica de fenilalanina (PheP), bajo el control del represor Lacl /promotor inducible P_{tac} .
c) Inserción el gen de la L-amino ácido deaminasa (LAAD), derivado de *Proteus mirabilis*, bajo el control del regulador transcripcional endógeno AraC /promotor inducible P_{BAD} .
d) Deleción del gen *dapA*, que produce células de bacteria auxotróficas salvo que se las suplemente exógenamente con diaminopimelato (DAP).
e) Deleción de su profago endógeno Φ .
- lafuvitugum #
lafuvitug immunoglobulin G1-kappa , anti-[HIV-1 (human immunodeficiency virus type 1) gp120 envelope glycoprotein, CD4-binding site)], *Homo sapiens* monoclonal antibody; gamma1 heavy chain *Homo sapiens* (1-453) [VH (*Homo sapiens*IGHV1-2*02 (62.7%) -(IGHD)-IGHJ3*01 (85.7%), CDR-IMGT [8.8.12] (26-33.51-58.101-112), FR3 insertion D84.1, F84.2, D85.2, T85.1 (77-80)) (1-123) -*Homo sapiens*IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (220) (124-221), hinge 1-15 (222-236), CH2 (237-346), CH3 D12 (362), L14 (364) (347-451), CHS (452-453)) (124-453)], (226-206')-disulfide with kappa light chain *Homo sapiens* (1'-206') [V-KAPPA (*Homo sapiens*IGKV1-33*01 (72.8%) -IGKJ5*01 (41,6%) del(F118, G119, Q120) 92^93, E125>D (97), I126>L (98), CDR-IMGT [2.3.8] (27-28.46-48.85-92)) (1'-99') -*Homo sapiens*IGKC*01 (100%), Km3 A45.1 (145), V101 (183) (100'-206')]; dimer (232-232":235-235")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHOK1SV, glycoform alfa

lafuvitug immunoglobuline G1-kappa, anti-[site de liaison au CD4 de la protéine d'enveloppe gp120 du virus de l'immunodéficience humaine de type 1 (HIV-1)], anticorps monoclonal *Homo sapiens*; chaîne lourde gamma1 *Homo sapiens* (1-453) [VH (*Homo sapiens* IGHV1-2*02 (62.7%) -(IGHD)-IGHJ3*01 (85.7%), CDR-IMGT [8.8.12] (26-33.51-58.101-112), FR3 insertion D84.1, F84.2, D85.2, T85.1 (77-80)) (1-123) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (220) (124-221), charnière 1-15 (222-236), CH2 (237-346), CH3 D12 (362), L14 (364) (347-451), CHS (452-453)) (124-453)], (226-206')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-206') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (72.8%) -IGKJ5*01 (41,6%) del(F118, G119, Q120) 92^93, E125>D (97), I126>L (98) , CDR-IMGT [2.3.8] (27-28.46-48.85-92)) (1'-99') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (145), V101 (183) (100'-206')]; dimère (232-232":235-235')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHOK1SV, glycoforme alfa

lafuvitug inmunoglobulina G1-kappa, anti-[lugar de unión al CD4 de la proteína de recubrimiento gp120 del virus de la inmunodeficiencia humana de tipo 1 (HIV-1)], anticuerpo monoclonal *Homo sapiens*; cadena pesada gamma1 *Homo sapiens* (1-453) [VH (*Homo sapiens* IGHV1-2*02 (62.7%) -(IGHD)-IGHJ3*01 (85.7%), CDR-IMGT [8.8.12] (26-33.51-58.101-112), FR3 inserción D84.1, F84.2, D85.2, T85.1 (77-80)) (1-123) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14(CH1 K120 (220) (124-221), bisagra 1-15 (222-236), CH2 (237-346), CH3 D12 (362), L14 (364) (347-451), CHS (452-453)) (124-453)], (226-206')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-206') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (72.8%) -IGKJ5*01 (41,6%) del(F118, G119, Q120) 92^93, E125>D (97), I126>L (98), CDR-IMGT [2.3.8] (27-28.46-48.85-92)) (1'-99') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (145), V101 (183) (100'-206')]; dímero (232-232":235-235')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHOK1SV, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada
 QVQLLQSGAA VTKPGASVRV SCEASGYNIR DYFIHWRRQA PGQGLQWGWG 50
 INPKTGGPNN PRQFGGRVSL TRHASWDFDT FSYFDLKLAL RSDDTAVVFC 100
 ARQRSDWDF DVMGSGTQVT VSSASTKGPS VFELAPSSKS TGGDTAALGC 150
 LVKDYFPEFV TVSNMGALD GSHFFPAVL QSGSLSLSS VVTVPSSLG 200
 TQTYICNNH KPSNTKVDKK VEPKSCDKTH TCPPCPAPEL LGGSPVFLFP 250
 PKPKDLMIS RTPEVTCVVV DVSHEDEPK FNVYVDGVEV HNAKTKPREE 300
 QYNSTRVRS VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR 350
 EPOVYTLPPS RDELTKNQVS LTCLQGGEYP SDIAVENESN GQPENNYKTT 400
 PFLVDSGDSF FLYSKLTVDK SRWQGVNFS CSMVHEALHN HYTKLSLSLS 450
 PGK 453

Light chain / Chaîne légère / Cadena ligera
 DIQMTQSPSS LSASVGDVIT ITQANGYLN WYQQRGKAP KLLIYDGSKL 50
 ERGVPSRFSS RRWQGEYNLT INNLPEDIA TYFCQVYEFV VPGTRLDLKR 100
 TVAAPSVEIF PPSDEQLKSG TASVVCLLNN FYPREAKVQW KVDNALQSGN 150
 SQESVTEQDS KDSTYLSLST LTLKADYEK HKVYACEVTH QGLSSPVTKS 200
 FNRGEC 206

Post-translational modifications
 Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
 Intra-H (C23-C104) 22-100 150-206 267-327 373-431
 22-100 150-206 267-327 373-431"
 Intra-L (C23-C104) 23-84 126-186
 23-84 126-186"
 Inter-H-L (h5-CL 126) 226-206 226-206"
 Inter-H-H (h 11, h 14) 232-232 235-235"

N-terminal glutaminy cyclization / Cyclisation du glutaminy N-terminal/ Ciclación del glutaminilo N-terminal
 Q> pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamyle (pE, 5-oxoprolyle) / piroglutamilo (pE, 5-oxoprofilo)
 HVH Q1:1, 1"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
 H CH2 N84.4: 303, 303"
 Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantennarios complejos fucosilados
 V-KAPPA N88: 68, 68"

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

laricovateinum #

laricovatein

severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) alpha lineage B.1.1.7 (Gisaid: EPI_ISL_764238) spike (S) glycoprotein fragment (1-1192), stable prefusion conformation variant (R⁶⁶⁶G, R⁶⁶⁷>S, R⁶⁶⁹>S, F⁸⁰¹>P, A⁸⁷⁶>P, A⁸⁸³>P, A⁹²⁶>P, K⁹⁷⁰>P, V⁹⁷¹>P) fused to the enterobacteria phage T4 fibrin foldon domain fragment (458-484, 1193-1219 in the current sequence), trimer, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

laricovatéine

fragment de la glycoprotéine du spicule (S) (1-1192) du coronavirus 2 du syndrome respiratoire aigu sévère (SARS-CoV-2), lignée alpha B.1.1.7 (Gisaid: EPI_ISL_764238), variante de conformation stable par pré-fusion (R⁶⁶⁶G, R⁶⁶⁷>S, R⁶⁶⁹>S, F⁸⁰¹>P, A⁸⁷⁶>P, A⁸⁸³>P, A⁹²⁶>P, K⁹⁷⁰>P, V⁹⁷¹>P) fusionné au fragment du domaine foldon de la fibratine de phage T4 d'entérobactéries (458-484, 1193-1219 dans la séquence actuelle), trimère, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

laricovateína

fragmento de la glicoproteína de la espícula (S) (1-1192) del coronavirus 2 del síndrome respiratorio severo agudo (SARS-CoV-2) linaje alfa B.1.1.7 (Gisaid: EPI_ISL_764238), variante de conformación de prefusión estable (R⁶⁶⁶G, R⁶⁶⁷>S, R⁶⁶⁹>S, F⁸⁰¹>P, A⁸⁷⁶>P, A⁸⁸³>P, A⁹²⁶>P, K⁹⁷⁰>P, V⁹⁷¹>P) fusionada al fragmento de dominio de foldón de fibratina del fago T4 de enterobacterias (458-484, 1193-1219 en la secuencia actual), trímero, producido en células ováricas de hámster Chino (CHO), glicoforma alfa

Monomer sequence / Séquence du monomère / Secuencia del monómero

QCVNLTTRTQ LPPAYTNSFT RGVVYPDKVF RSSVLHSTQD LFLPFFSNVT	50
WFHAISGTNG TKRFDFNPVLP FNDGYYFAST EKSNIIRGWI FGTTLDLSTQ	100
SLLIIVNNATN VVIKVCFFQF CNDPFLGVYH KNNKSWMESE FRVYSSANNC	150
TFEYVVSQPFLL MDLEGGKQGNF KNLREFVFRN IDGYFKIYSK HTPINLVRDL	200
PQGFSALEPL VDLFIGINIT RFQTLALHR SYLTPGDSSS GWTAGAAAYY	250
VGYLQPRFTFL LKYNENGTIT DAVDCALDEL SETKCTLKSF TVEKGIYQTS	300
NFRVQPTESEI VRFNITNLCL PFGVEFNATR FASYAMNRK RINSCVADYS	350
VLYNSASFST FKCYGVSPTK LNDLCTFNIV ADSFVIRGDE VRQIAPGQTG	400
KIADINYKLP DDFTCGVLAW NSNNDLSKYG GNYNYLYRLF RKSNNLKFPER	450
DISTEYIQAQ STPCNGVEGF NCFYFPLQSYG FQPTYGVGYQ PYRVVLSFE	500
LLHAPATVCG PKKSTNLVKN KCVNENFNGL TGTGVLTESN KKFLLPQQFG	550
RDIDDDTDAV RDPQTLEILD ITPCSFQGGV VITPGNTSN QVAVLQGVN	600
CTEVPVAIHA DQLTPTWRVY STGSNVFQTR AGCLIGAHEV NNSYECDIPI	650
GAGICASYQT QTNSEGSAS VASQSI IAYT MSLGAENSA VYNSNIAIPI	700
NFTISVTEIE LPVSMTKTSV DCTMYICGDS TECSNLLQY GSPFTQLNRA	750
LTGIAVEQDK NTQEVFAQVK QIYKTPPIKD FGGFNFSQIL PDPSPKSKRS	800
E IEDLLFNKV TLADAGFIKQ YGDCLDGIDAA RDLICAQKFN GLTVLPLLT	850
DEMIQYTSYA LLAGTITSGW TFGGALQI P PEMQAYRF NGIVTQNVL	900
YENQKLIANQ FNSAIGKIQD SLSST E SALG KLQDVVNQNA QALNTLVKQL	950
SSNFGAISSV LNDILARL E P EA ^{EV} IDRL ITGRLOSLQT YVTQQLIRAA	1000
EIRASANLAA TKMSECVLGG SKRVDFCGRG YHLMSFPQSA PHGVVFLHVT	1050
YVPAQEKNEFT TAPAICHDGK AHFPREGVVF SNGTHWFTVQ RNFYEPQIIT	1100
THNTFVSGNC DVVIGIVNNT VYDPLQPELD SFKEELDKYF KNHTSPDVDL	1150
GDISGINASV VNIQKEIDRL NEVARNLNES LIDLQELGKY E QGYI PE APR	1200
<u>DGQAYVRKDG</u> <u>EWVLLSTFL</u>	1219

Mutation / Mutation / Mutación
H⁶⁶⁵>P, R⁶⁶⁶-G, R⁶⁶⁷-S, R⁶⁶⁹-S, F⁸⁰¹>P, A⁸⁷⁶-P, A⁸⁸³-P, A⁹²⁶-P, K⁹⁷⁰-P, V⁹⁷¹-P

Foldon domain / Foldon domaine / Foldon dominio
GYI**PE**APR**DG** QAYVRK**DGEW** VLL**STFL** 1193-1219

Post-translational modifications

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-chain: 2-121, 116-150, 275-285, 320-345, 363-416, 375-509, 464-472, 522-574, 601-633, 646-655, 722-744, 727-733, 824-835, 1016-1027, 1066-1110

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación (predicted)
N4, N48, N59, N107, N133, N149, N218, N266, N315, N327, N587, N600, N641, N693, N701, N785, N1058, N1082, N1118, N1142, N1157, N1178

O-glycosylation sites / Sites de O-glycosylation / Posiciones de O-glicosilación (predicted)
T307, S309

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

lartesertibum

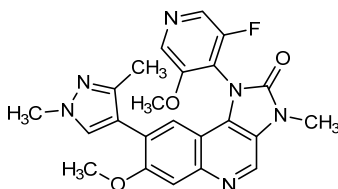
lartesertib

8-(1,3-dimethyl-1*H*-pyrazol-4-yl)-1-(3-fluoro-5-methoxy-pyridin-4-yl)-7-methoxy-3-méthyl-1,3-dihydro-2*H*-imidazo[4,5-*c*]quinolin-2-one

lartésertib

8-(1,3-diméthyl-1*H*-pyrazol-4-yl)-1-(3-fluoro-5-méthoxy-pyridin-4-yl)-7-méthoxy-3-méthyl-1,3-dihydro-2*H*-imidazo[4,5-*c*]quinoléin-2-one

lartesertib

8-(1,3-dimetil-1*H*-pirazol-4-il)-1-(3-fluoro-5-metoxipiridin-4-il)-7-metoksi-3-metil-1,3-dihidro-2*H*-imidazo[4,5-*c*]quinolein-2-ona $C_{23}H_{21}FN_6O_3$ **lenumlostatum**

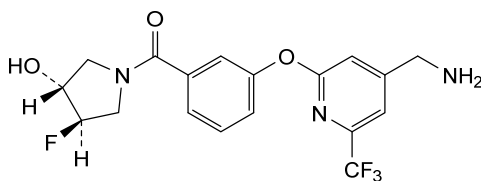
lenumlostat

(3-[[4-(aminométhyl)-6-(trifluorométhyl)pyridin-2-yl]oxy]phényl)[(3*R*,4*R*)-3-fluoro-4-hydroxypyrrolidin-1-yl]méthanone

lénumlostat

(3-[[4-(aminométhyl)-6-(trifluorométhyl)pyridin-2-yl]oxy]phényl)[(3*R*,4*R*)-3-fluoro-4-hydroxypyrrolidin-1-yl]méthanone

lenumlostat

(3-[[4-(aminometil)-6-(trifluorometil)piridin-2-il]oxi]fenil)[(3*R*,4*R*)-3-fluoro-4-hidroxi-pirrolidin-1-il]metanona $C_{18}H_{17}F_4N_3O_3$ **lirafugratinibum**

lirafugratinib

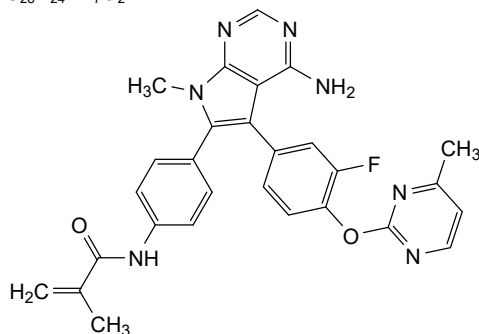
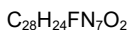
N-[4-(4-amino-5-{3-fluoro-4-[(4-méthylpyrimidin-2-yl)oxy]phényl}-7*H*-pyrrolo[2,3-*d*]pyrimidin-6-yl)phényl]-2-méthylprop-2-énamide

lirafugratinib

N-[4-(4-amino-5-{3-fluoro-4-[(4-méthylpyrimidin-2-yl)oxy]phényl}-7*H*-pyrrolo[2,3-*d*]pyrimidin-6-yl)phényl]-2-méthylprop-2-énamide

lirafugratinib

N-[4-(4-amino-5-{3-fluoro-4-[(4-metilpirimidin-2-il)oxi]fenil}-7-metil-7*H*-pirrolo[2,3-*d*]pirimidin-6-il)fenil]-2-metilprop-2-enamida



lixudebartum #
lixudebart

immunoglobulin G1- kappa, anti-[*Homo sapiens* CLDN1 (claudin-1) conformational epitope of the first extracellular loop (EL1)], humanized monoclonal antibody;
gamma1 heavy chain humanized (1-448) [VH (*Homo sapiens* IGHV3-21*01 (94.9%) -(IGHD) -IGHJ1*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, CH2 IGHG1v39 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 K2>del (448)) (120-448)], (222-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV3-15*01 (84.2%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (228-228'':231-231'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa

lixudébart

immunoglobuline G1-kappa, anti-[*Homo sapiens* CLDN1 (claudine 1) épitope conformationnel de la première boucle extracellulaire (EL1)], anticorps monoclonal humanisé;
chaîne lourde gamma1 humanisée (1-448) [VH (*Homo sapiens* IGHV3-21*01 (94.9%) -(IGHD) -IGHJ1*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, CH2 IGHG1v39 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 K2>del (448)) (120-448)], (222-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-16*01 (87.8%) -IGKJ4*01 (91.7%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (230-230'':233-233'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa

lixudebart

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CLDN1 (claudina 1) epítopo conformacional del primer bucle extracelular (EL1)], anticuerpo monoclonal humanizado; cadena pesada gamma1 humanizada (1-448) [VH (*Homo sapiens* IGHV3-21*01 (94.9%) -(IGHD) - IGHJ1*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, CH2 IGHG1v39 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 K2>del (448)) (120-448)], (222-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-16*01 (87.8%) -IGKJ4*01 (91.7%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (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	LVKPGGSLRL	SCAASGFSFS	SYGMNWRQA	PGKLEWVSS	50
ISPSGSYFYY	ADSVKGRFTI	SRDNAKNSLY	LQMNLSRAED	TAVYYCARLP	100
GFNPPFDHWG	QGTTLTVSSA	STKGPSVFLP	APSSKSTSGG	TAALGCLVKD	150
YFPEFVTVSW	NSGALTSGVH	TFFPAVLQSSG	LYSLSSVTV	PSSSLGTQTY	200
ICNVNHKPSN	TKVDKRVPEK	SCDKTHTCPP	CPAPEFEGGP	SVLFPFKPK	250
DTLMISRTEP	VTCVVDVSH	EDPEVKFNWY	VDGVEVHNAK	TKPREEQYNS	300
TYRVVSVLTV	LHQDNLNGKE	YKCKVSNKAL	PASIEKTIISK	AKGQPREPQV	350
YTLPPSREEM	TKNQVSLTCL	VKGFYPSDIA	VEWESNGQPE	NNYKTTTPVL	400
DSGDGSFLYS	KLTVDKSRWQ	QGNVDFSCVM	HEALHNHYTQ	KSLSLSPG	448

Light chain / Chaîne légère / Cadena ligera

DIQMTQSPAT	LSVSPGERAT	LSCKASQNVG	GNVDWYQWPK	GQAPRLLIYG	50
ASNRVTGIPA	RFRGSGSGTE	FTLTISSLQS	EDFAVYYCLQ	YKNNPWFQ	100
GTKVEIKRTV	AAPSVFIFPP	SDEQLKSGTA	SVVCLLNIFY	PREAKVQWKV	150
DNALQSGNSQ	ESVTEQDSK	STYLSLSTLT	LSKADYEKHK	VYACEVTHQG	200
LSSPVTKSFN	RGEC				214

Post-translational modifications

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

Intra-H (C23-C104)	22-96	146-202	263-323	369-427
	22"-96"	146"-202"	263"-323"	369"-427"

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

Inter-H-L (h 5-CL 126)	222-214'	222"-214"
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Inter-H-H (h 11, h 14)	228-228"	231-231"
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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.

lutetium (¹⁷⁷Lu) edotreotidum

lutetium (¹⁷⁷Lu) edotreotide

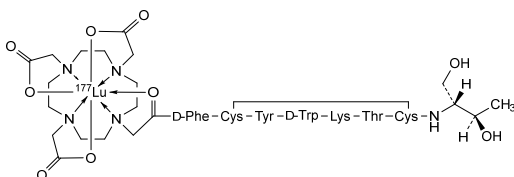
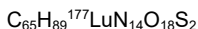
[^{N2}-1-({4,7,10-tris[(carboxilato-κO)methyl]-1,4,7,10-tetraazacyclododecan-1-yl-κ⁴N¹,N⁴,N⁷,N¹⁰)}acetyl-κO)-S^{3,2},S^{3,7}-cyclo(D-phenylalanyl-L-cysteinyl-L-tyrosyl-D-tryptophyl-L-lysyl-L-threonyl-L-cysteinyl-L-threoninol)](¹⁷⁷Lu)lutetium

lutécium (¹⁷⁷Lu) édotréotide

[^{N2}-1-({4,7,10-tris[(carboxilato-κO)méthyl]-1,4,7,10-tétraazacyclododécane-1-yl-κ⁴N¹,N⁴,N⁷,N¹⁰)}acétyl-κO)-S^{3,2},S^{3,7}-cyclo(D-phénylalanyl-L-cystéinyl-L-tyrosyl-D-tryptophyl-L-lysyl-L-thréonyl-L-cystéinyl-L-thréoninol)](¹⁷⁷Lu)lutecium

lutecio (¹⁷⁷Lu) edotreotida

[^{N2}-1-({4,7,10-tris[(carboxilato-κO)metil]-1,4,7,10-tetraazacyclododecan-1-il-κ⁴N¹,N⁴,N⁷,N¹⁰)}acetil-κO)-S^{3,2},S^{3,7}-ciclo(D-fenilalanil-L-cisteinil-L-tirosil-D-triptofil-L-lisil-L-treonil-L-cisteinil-L-treoninol)](¹⁷⁷Lu)lutecio



lutetium (^{177}Lu) rofapitidum tetraacetanum

lutetium (^{177}Lu) rofapitide tetraacetan

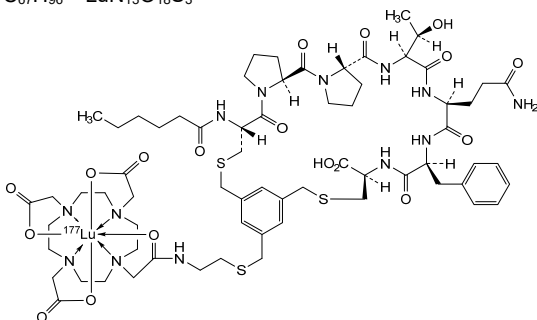
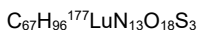
[2,2',2''-{10-[2-(oxo-κO)-2-[[2-(((1²S,3²S,5R,13R,16S,19S,22S)-19-(3-amino-3-oxopropyl)-16-benzyl-13-carboxy-5-hexanamido-22-[(1R)-1-hydroxyethyl]-2,4,15,18,21,24-hexaoxo-7,11-dithia-14,17,20,23-tetraaza-1(1,2),3(2,1)-dipyrrolidina-9(1,3)-benzenacyclotetracosaphan-9⁵-yl)methyl)sulfanyl]ethyl]amino]ethyl]-1,4,7,10-tetraazacyclododecane-1,4,7-triyl-κ⁴N¹,N⁴,N⁷,N¹⁰}]tri(acetato-κO)](^{177}Lu)lutetium

lutécium (^{177}Lu) rofapitide tétraacétan

[2,2',2''-{10-[2-(oxo-κO)-2-[[2-(((1²S,3²S,5R,13R,16S,19S,22S)-19-(3-amino-3-oxopropyl)-16-benzyl-13-carboxy-5-hexanamido-22-[(1R)-1-hydroxyéthyl]-2,4,15,18,21,24-hexaoxo-7,11-dithia-14,17,20,23-tétraaza-1(1,2),3(2,1)-dipyrrolidina-9(1,3)-benzénacyclotétraacosaphan-9⁵-yl)méthyl)sulfanyl]éthyl]amino]éthyl]-1,4,7,10-tétraazacyclododécane-1,4,7-triyl-κ⁴N¹,N⁴,N⁷,N¹⁰}]tri(acétato-κO)](^{177}Lu)lutecium

lutecio (^{177}Lu) rofapitida tetraacetán

[2,2',2''-{10-[2-(oxo-κO)-2-[[2-(((1²S,3²S,5R,13R,16S,19S,22S)-19-(3-amino-3-oxopropil)-16-bencil-13-carboxi-5-hexanamido-22-[(1R)-1-hidroxietyl]-2,4,15,18,21,24-hexaoxo-7,11-ditia-14,17,20,23-tetraaza-1(1,2),3(2,1)-dipirrolidina-9(1,3)-bencenacicotetracosafan-9⁵-il]metil)sulfanil]etil]amino]etil]-1,4,7,10-tetraazaciclododecano-1,4,7-triyl-κ⁴N¹,N⁴,N⁷,N¹⁰}]tri(acetato-κO)](^{177}Lu)lutecio



maridebartum

maridebart

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")-bisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

maridébart

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), glycoforme alfa

maridebart

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), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

VQQLVESGGG VVQPGKSLRL SCAASGFTFS NYGMHWVRQA PGEGLEWVAA 50
 IWFDAADKYY ADAVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARDQ 100
 AIFGVVVDYW GQGLTIVTSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
 DYFPEPVTVS WNSGALTSV HTFFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
 YICNVNHKPS NTKVDKKEVP KSCDKTHTCP PCPAPPELLGG PSVFLFPPKP 250
 KDTLMIISRTPEVTCVVVDVSDHEDPCKVFENWYVDGVEVHNAKTKPCEEQYQ 300
 STYRCVSLVTLVHQLDNLNGEYKCKVSNKALPAPIEKTIISKAKGQPREPQ 350
 VYTLPPSREE MTKNQVSLTCLVKGFYPSDI AVEWESNGQP ENNYKTTTPV 400
 LDSGDSGFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK 450

Light chain / Chaîne légère / Cadena ligera

EIVMTQSPAT LSVSPGERAT LSCRASQSVS SNLAWYQQKP GQAPRLLIYG 50
 AATRATGIPA RVSGSGSGTE FTLTISLSLQS EDFAVYYCQQ YNNWPLTFGG 100
 GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PRAKAVQWVK 150
 DNALQSGNSQ ESVTEQDSKD STYSLSSLT LSKADYEKHK VYACEVTHQG 200
 LSSPVTKSFN RGECC 214

Post-translational modifications

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

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

Intra-CH2 C83-C85 (G1v54) 295-305 295"-305"

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 glutamínulo N-terminal

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

H VH Q1: 1, 1"

No N-glycosylation sites / pas de sites de N-glycosylation / ningùn posició de N-glicosilació

H CH2 N84.4>G (G1v30): 300, 300"

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

H CHS K2: 450, 450"

maridebartum cafraglutidum

maridebart cafraglutide

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, glycoform alfa; 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)-lysineamide

maridébart cafraglutide

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), glycoforme alfa; 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)-lysineamide)

maridebart cafraglutida

immunoglobulina G1-kappa, anti-[*Homo sapiens* GIPR (receptor del polipéptido inhibitor 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), forma glicosilada alfa; 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)

Heavy chain / Chaîne lourde / Cadena pesada
 QVQLVESGGG VVQPGRSLRL SCAASGFTFS NYGMHWVRQA PGEGLWVAA 50
 IWFDAADKYY ADAVKGRFTI SRDMSKNTLY LQMNSLRAED TAVVYCARDQ 100
 AIFGVVPPDYW GQGTLLVTSS ASTKGPVSFPP LAPSSKSTSG GTAALGCLVK 150
 DYFPEPVTWS WNSGALTSVG HTFFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
 YICNVNHNKPS NTKVDKKVEP KSCDKTHTCP PCPAPPELLGG PSVFLFPPKPT 250
 KDTLMI SRTP EVTCCVVVDVS HEDPCVKFNW YVDGVEVHNA KTKPCEEQYG 300
 STYRCVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
 VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTTPV 400
 LDDSGSFFLY SKLTVDKSRW QQGNVFSQSV MHEALHNHYT QKLSLSLSPGK 450

Light chain / Chaîne légère / Cadena ligera
 EIVMTQSPAT LSVSPGERAT LSCRASQSVS SNLAWYQQKQ GPAPRLLIYG 50
 AATRAATGIPA RVSGSGSGTE FTLTISLSLQS EDFAVYYCQ YNNWPLTFFG 100
 GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
 DNALQSGNSQ ESVTQDQSKD STYLSLSLTL LSKADYEKHK VYACEVTHQG 200
 LSSPVTKSFN RGEC 214

Conjugated peptide / Peptide conjugué / Péptido conjugado
 HXEGTFTSDY SSYLEEQAQK EPIAWLVKGG GGGGSGGGG SGGGSK 47
 X=methylalanine

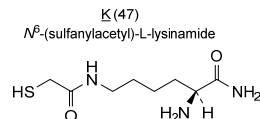
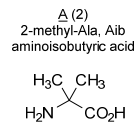
Post-translational modifications
 Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
 Intra-H (C23-C104) 22-96 147-203 264-324 370-428
 22"-96" 147"-203" 264"-324" 370"-428"
 Intra-CH2 C83-C85 (G1v54) 295-305 295"-305"
 Intra-L (C23-C104) 23-88" 134-194"
 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-oxopropyl) / pyroglutamide (pE, 5-oxopropyle) / piroglutamilo (pE, 5-oxopropililo)
 H VH Q1: 1, 1"

No N-glycosylation sites / pas de sites de N-glycosylation / ningùn posició de N-glicosilació
 H CH2 N84.4>G (G1v30): 300, 300"

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

Modified residues / Résidus modifiés / Restos modificados



marlumotidum
 marlumotide

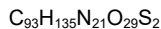
[R126>Y]-human Wilms tumor protein (WT33)-(122-140)-peptide;
 L-serylglycyl-L-glutaminyl-L-alanyl-L-tyrosyl-L-methionyl-L-phenylalanyl-L-prolyl-L-asparaginyll-L-alanyl-L-prolyl-L-tyrosyl-L-leucyl-L-prolyl-L-seryl-L-cysteinyl-L-leucyl-L-α-glutamyl-L-serine

marlumotide

[R126>Y]-protéine humaine de la tumeur de Wilms (WT33)-(122-140)-peptide;
 L-sérylglycyl-L-glutaminyl-L-alanyl-L-tyrosyl-L-méthionyl-L-phénylalanyl-L-prolyl-L-asparaginyll-L-alanyl-L-prolyl-L-tyrosyl-L-leucyl-L-prolyl-L-séryl-L-cystéinyl-L-leucyl-L-α-glutamyl-L-sérine

marlumotida

[R126>Y]-proteína humana del tumor de Wilms (WT33)-(122-140)-péptido;
 L-serilglicil-L-glutaminil-L-alanil-L-tirosil-L-metionil-L-fenilalanil-L-proliil-L-asparaginil-L-alanil-L-proliil-L-tirosil-L-leucil-L-proliil-L-seril-L-cisteinil-L-leucil-L-α-glutamil-L-serina



SGQAYMFPNA PYLPSCLES 19

merigolixum

merigolix

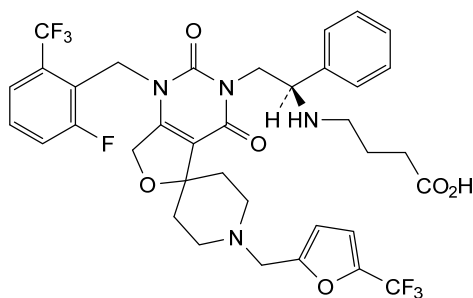
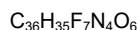
4-[[[(1*R*)-2-(1-[[2-fluoro-6-(trifluoromethyl)phenyl]methyl]-2,4-dioxo-1'-[[5-(trifluoromethyl)furan-2-yl]methyl]-1,2,4,7-tetrahydro-3*H*-spiro[furo[3,4-*d*]pyrimidine-5,4'-piperidin]-3-yl)-1-phenylethyl]amino]butanoic acid

mérigolix

acide 4-[[[(1*R*)-2-(1-[[2-fluoro-6-(trifluorométhy)phényl]méthyl]-2,4-dioxo-1'-[[5-(trifluorométhy)furan-2-yl]méthyl]-1,2,4,7-tétrahydro-3*H*-spiro[furo[3,4-*d*]pyrimidine-5,4'-pipéridin]-3-yl)-1-phényléthyl]amino]butanoïque

merigolix

ácido 4-[[[(1*R*)-2-(1-[[2-fluoro-6-(trifluorometil)fenil]metil]-2,4-dioxo-1'-[[5-(trifluorometil)furan-2-il]metil]-1,2,4,7-tetrahidro-3*H*-spiro[furo[3,4-*d*]pirimidina-5,4'-piperidin]-3-il)-1-feniletil]amino]butanoico



mifanertinibum

mifanertinib

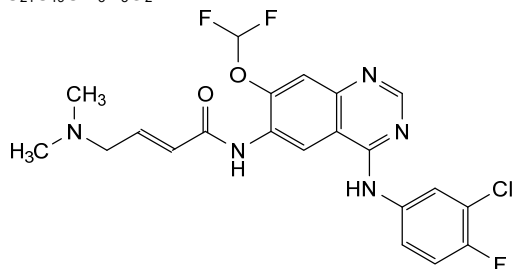
(2*E*)-*N*-[4-(3-chloro-4-fluoroanilino)-7-(difluoromethoxy)quinazolin-6-yl]-4-(dimethylamino)but-2-enamide

mifanertinib

(2*E*)-*N*-[4-(3-cloro-4-fluoroanilino)-7-(difluorométhoxy)quinazolin-6-yl]-4-(diméthylamino)but-2-énamide

mifanertinib

(2*E*)-*N*-[4-(3-cloro-4-fluoroanilino)-7-(difluorometoxi)quinazolin-6-il]-4-(dimetilamino)but-2-enamida



migoprotafibum

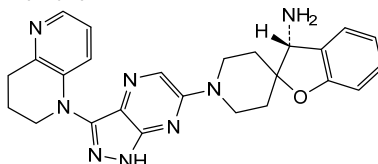
migoprotafib

(3*R*)-1'-[3-(3,4-dihydro-1,5-naphthyridin-1(2*H*)-yl)-1*H*-pyrazolo[3,4-*b*]pyrazin-6-yl]-3*H*-spiro[[1]benzofuran-2,4'-piperidin]-3-amine

migoprotafib

(3*R*)-1'-[3-(3,4-dihydro-1,5-naphthyridin-1(2*H*)-yl)-1*H*-pyrazolo[3,4-*b*]pyrazin-6-yl]-3*H*-spiro[[1]benzofuran-2,4'-pipéridin]-3-amine

migoprotafib

(3*R*)-1'-[3-(3,4-dihydro-1,5-naftiridin-1(2*H*)-il)-1*H*-pirazolo[3,4-*b*]pirazin-6-il]-3*H*-spiro[[1]benzofuran-2,4'-piperidin]-3-aminaC₂₅H₂₆N₈O**mindeudesivirum**

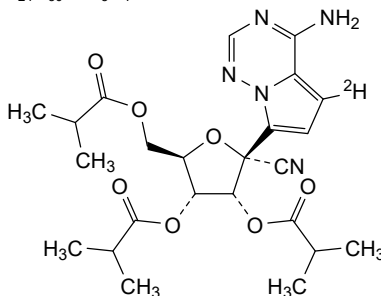
mindeudesivir

(2*R*,3*R*,4*R*,5*R*)-2-(4-amino-(5-²H)pyrrolo[2,1-*f*][1,2,4]triazin-7-yl)-2-cyano-5-[[2-(methylpropanoyl)oxy]methyl]oxolane-3,4-diyl bis(2-methylpropanoate)

mindeudésivir

bis(2-méthylpropanoate) de (2*R*,3*R*,4*R*,5*R*)-2-(4-amino-(5-²H)pyrrolo[2,1-*f*][1,2,4]triazin-7-yl)-2-cyano-5-[[2-méthylpropanoyl]oxy]méthyl]oxolane-3,4-diyle

mindeudesivir

bis(2-metilpropanoato) de (2*R*,3*R*,4*R*,5*R*)-2-(4-amino-(5-²H)pirrolo[2,1-*f*][1,2,4]triazin-7-il)-2-ciano-5-[[2-metilpropanoil]oxi]metil]oxolano-3,4-diiloC₂₄H₃₀²HN₅O₇**monzosertibum**

monzosertib

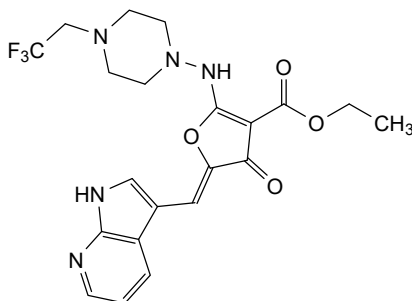
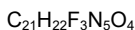
ethyl 5-[(Ξ)-(1*H*-pyrrolo[2,3-*b*]pyridin-3-yl)methylidene]-4-oxo-2-[[4-(2,2,2-trifluoroethyl)piperazin-1-yl]amino]-4,5-dihydrofuran-3-carboxylate

monzosertib

5-[(Ξ)-(1*H*-pyrrolo[2,3-*b*]pyridin-3-yl)méthylidène]-4-oxo-2-[[4-(2,2,2-trifluoroéthyl)pipérazin-1-yl]amino]-4,5-dihydrofurane-3-carboxylate d'éthyle

monzosertib

5-[(Ξ)-(1*H*-pirrolo[2,3-*b*]piridin-3-il)metilideno]-4-oxo-2-[[4-(2,2,2-trifluoroetil)piperazin-1-il]amino]-4,5-dihidrofurano-3-carboxilato de etilo



murcidencelum

murcidencel

autologous dendritic cells (DCs) derived from peripheral blood mononuclear cells (PBMCs) obtained from glioblastoma patients. A sample of the same patients' glioblastoma is also collected, and a tumour lysate prepared. The purified adherent monocytes isolated from PBMCs are initially grown in media containing granulocyte-macrophage colony-stimulating factor (GM-CSF) and interleukin 4 (IL-4) to induce differentiation into dendritic cells, followed by loading of the dendritic cells with the tumour lysate in culture media supplemented with GM-CSF and IL-4. The final cell suspension contains $\geq 60\%$ dendritic cells (MHC Class II+, CD86+; CD14-), with $\leq 40\%$ of the cells in the suspension being other autologous cells, such as T lymphocytes, B lymphocytes, and natural killer cells. The dendritic cells induce T lymphocyte proliferation in a co-stimulation assay

murcidencel

cellules dendritiques (DC) autologues dérivées de cellules mononucléaires de sang périphérique (PBMC) obtenues de patients atteints de glioblastome. Un échantillon du glioblastome de ces mêmes patients est également prélevé et un lysat tumoral est préparé. Les monocytes adhérents purifiés isolés des PBMC sont d'abord cultivés dans un milieu contenant le facteur de stimulation des colonies de granulocytes-macrophages (GM-CSF) et l'interleukine 4 (IL-4) pour induire la différenciation en cellules dendritiques, puis les cellules dendritiques sont chargées avec le lysat tumoral dans un milieu de culture complété en GM-CSF et IL-4. La suspension cellulaire finale contient $\geq 60\%$ de cellules dendritiques (MHC Classe II+, CD86+; CD14-), et $\leq 40\%$ des cellules de la suspension sont d'autres cellules autologues, telles que des lymphocytes T, des lymphocytes B et des cellules tueuses naturelles. Les cellules dendritiques induisent la prolifération des lymphocytes T dans un test de costimulation

murcidencel

células dendríticas (DCs) autólogas derivadas de células mononucleares de sangre periférica (PBMCs) obtenidas de pacientes con glioblastoma. Se recoge también una muestra de glioblastoma del mismo paciente y se prepara un lisado tumoral. Los

monocitos adherentes purificados, aislados de las PBMCs, se crecen inicialmente en medio que contiene factor estimulador de colonias de monocitos-macrófagos (GM-CSF) e interleuquina 4 (IL-4) para inducir la diferenciación en células dendríticas, seguido de la carga de las células dendríticas con el lisado tumoral en medio de cultivo suplementado con GM-CSF e IL-4. La suspensión celular final contiene $\geq 60\%$ de células dendríticas (MHC Clase II+, CD96+, CD14-), con $\leq 40\%$ de otras células autólogas como linfocitos T, linfocitos B y células NK. Las células dendríticas inducen la proliferación de linfocitos T en un ensayo de coestimulación

muvalaplimum

muvalaplín

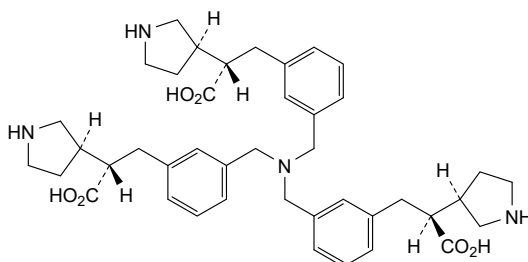
(1³S,2R,10R,11³S)-6-[(3-[(2S)-2-carboxy-2-[(3R)-pirrolidin-3-yl]etil]fenil)metil]-6-aza-1,11(3)-dipirrolidina-4,8(1,3)-dibenzenaundecaphane-2,10-dicarboxylic acid

muvalapline

acide (1³S,2R,10R,11³S)-6-[(3-[(2S)-2-carboxy-2-[(3R)-pirrolidin-3-yl]éthyl]phényl)méthyl]-6-aza-1,11(3)-dipyrrolidina-4,8(1,3)-dibenzénaundécaphane-2,10-dicarboxylique

muvalaplina

ácido (1³S,2R,10R,11³S)-6-[(3-[(2S)-2-carboxi-2-[(3R)-pirrolidin-3-yl]etil]fenil)metil]-6-aza-1,11(3)-dipirrolidina-4,8(1,3)-dibencenaundecafano-2,10-dicarboxílico

C₄₂H₅₄N₄O₆**muzastotugum #**

muzastotug

immunoglobulin G1- kappa, anti-[*Homo sapiens* CTLA4 (cytotoxic T-lymphocyte associated protein 4, CTLA-4, CD152)], monoclonal antibody with cleavable prodomain;

gamma1 heavy chain (1-446) [VH (*Homo sapiens* IGHV3-7*01 (77.8%) - (IGHD) -IGHJ4*01 (100%), CDR-IMGT [9.7.9] (26-34.52-58.97-105)) (1-116) -*Homo sapiens*IGHG1*01 (100%), G1m17,1 CH1 K120, 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)], (219-256')-disulfide with kappa light chain (1'-256') [cleavable prodomain (1'-41') fused to V-KAPPA (*Homo sapiens* IGKV1-13*02 (85.3%) -IGKJ1*01 (100%), CDR-IMGT [7.3.9] (68-74.92-94.131-139)) (42'-149') -*Homo sapiens*IGKC*01 (100%), Km3 A45.1 (195), V101 (233) (150'-256')]; dimer (225-225''-228-228'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa

- muzastotug immunoglobuline G1-kappa, anti-[*Homo sapiens* CTLA4 (protéine 4 associée aux lymphocytes T cytotoxiques, CTLA-4, CD152)], anticorps monoclonal avec prodomaine clivable; chaîne lourde gamma1 (1-446) [VH (*Homo sapiens* IGHV3-7*01 (77.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [9.7.9] (26-34.52-58.97-105)) (1-116) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 (CH1 K120 (213) (117-214), charnière 1-15 (215-229), CH2 (230-339), CH3 D12 (355), L14 (357) (340-444), CHS (445-446)) (117-446)], (219-256')-disulfure avec la chaîne légère kappa (1'-256') [prodomaine clivable (1'-41') fusionné to V-KAPPA (*Homo sapiens* IGKV1-13*02 (85.3%) -IGKJ1*01 (100%), CDR-IMGT [7.3.9] (68-74.92-94.131-139)) (42'-149') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (195), V101 (233) (150'-256')]; dimère (225-225":228-228")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa
- muzastotug inmunoglobulina G1-kappa, anti-[*Homo sapiens* CTLA4 (proteína 4 asociada con los linfocitos T citotóxicos, CTLA-4, CD152)], anticuerpo monoclonal con prodominio escindible; cadena pesada gamma1 (1-446) [VH (*Homo sapiens* IGHV3-7*01 (77.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [9.7.9] (26-34.52-58.97-105)) (1-116) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 (CH1 K120 (213) (117-214), bisagra 1-15 (215-229), CH2 (230-339), CH3 D12 (355), L14 (357) (340-444), CHS (445-446)) (117-446)], (219-256')-disulfuro con la cadena ligera kappa (1'-256') [prodominio escindible (1'-41') fusionado con V-KAPPA (*Homo sapiens* IGKV1-13*02 (85.3%) -IGKJ1*01 (100%), CDR-IMGT [7.3.9] (68-74.92-94.131-139)) (42'-149') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (195), V101 (233) (150'-256')]; dímero (225-225":228-228")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

EVQLVESGGG	LVQPGGSLRL	SCAASGYSIS	SGYHWSWIRQ	APGKGLEWLA	50
RIDWDDDKYY	STSLKSRLLT	SRDNSKNTLY	LQLNSLRAED	TAVYYCARSY	100
VYFDYWGQGT	LVTVSSASTK	GPSVFPLAPS	SKSTSGGTAA	LGCLVKDYFP	150
EPVTVSWNSG	ALTSQVHTFP	AVLQSSGLYS	LSSVTVTPSS	SLGTQTYICN	200
VNHKPSNTKV	DKKVEPKSCD	KHTCPCPCA	PELLGGPSVF	LPFPKPKDTL	250
MISRTEPVTC	VVVVDVSHEDP	EVKFNWYVDG	VEVHNAKTKP	REEQYNSTYR	300
VVSVLTVLHQ	DWLNGKEYKC	KVSNKALPAP	IEKTSKAKG	QPREPQVYTL	350
PPSRDELTKN	QVSLTCLVKG	FYPSDIAVEW	ESNGQPENNY	KTTTTPVLDS	400
GSFPFLYSKLT	VDKSRWQQGN	VFSCSVMHEA	LHNHYTQKSL	SLSPGK	446

Light chain / Chaîne légère / Cadena ligera

EVGSPNPSS	DCVPYYACA	YSGRSAGGGG	TPLGLAGSGG	SDIQLTQSPS	50
SLSASVGNDRV	TITCRASQSV	RGRFLAWYQQ	KPGKAPKLLI	YDASNRAITGI	100
PSRFSGSGSG	TDFTLTISSL	QPEDFATYYC	QQSSSWPPTF	GGGTKVEIKR	150
TVAAPSVFIF	PPSDEQLKSG	TASVVCCLLN	FYPREAKVQW	KVDNALQSGN	200
SQESVTEQDS	KDSTYLSLST	LTLKADYEK	HKVACEVTH	QGLSSPVTKS	250
FNRGEC					256

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) 64'-130" 176"-236"
 64"-130" 176"-236"
 Inter-H-L (h 5-CL 126) 219-256' 219"-256"
 Inter-H-H (h 11, h 14) 225-225" 228-228"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
 H CH2 N84.4: 296, 296"

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

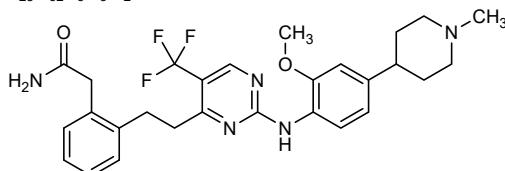
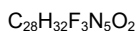
C-terminal lysine clipping / Coupeure de la lysine C-terminale / Recorte de lisina C-terminal
 H CHS K2: 446, 446"

narmafotininibum

narmafotininib 2-{2-[2-[[2-methoxy-4-(1-methylpiperidin-4-yl)phenyl]amino]-5-(trifluoromethyl)pyrimidin-4-yl]ethyl}benzeneacetamide

narmafotininib 2-{2-[2-[[2-méthoxy-4-(1-méthylpipéridin-4-yl)phényl]amino]-5-(trifluorométhyl)pyrimidin-4-yl]éthyl}benzèneacétamide

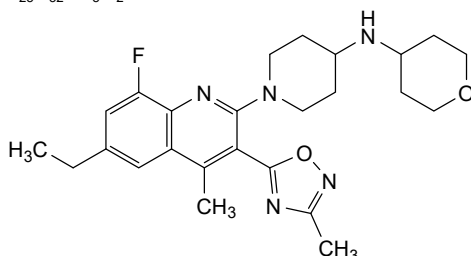
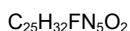
narmafotininib 2-{2-[2-[[2-metoksi-4-(1-metilpiperidin-4-il)fenil]amino]-5-(trifluorometil)pirimidin-4-il]etil}bencenoacetamida

**navacaprantum**

navacaprant 1-[6-ethyl-8-fluoro-4-methyl-3-(3-methyl-1,2,4-oxadiazol-5-yl)quinolin-2-yl]-N-(oxan-4-yl)piperidin-4-amine

navacaprant 1-[6-éthyl-8-fluoro-4-méthyl-3-(3-méthyl-1,2,4-oxadiazol-5-yl)quinoléin-2-yl]-N-(oxan-4-yl)pipéridin-4-amine

navacaprant 1-[6-etil-8-fluoro-4-metil-3-(3-metil-1,2,4-oxadiazol-5-il)quinolein-2-il]-N-(oxan-4-il)piperidin-4-amina

**nebratamigum #**

nebratamig

immunoglobulin scFv-G1-scFv-scFv_L-kappa, anti-[*Homo sapiens* TNFRSF9 (TNF receptor superfamily member 9, 4-1BB, ILA, CD137)], anti-[*Homo sapiens* CD274 (programmed cell death 1 ligand 1, PDL1, PD-L1, B7 homolog 1, B7H1, B7-H1, PDCD1LG1)], anti-[*Homo sapiens* ROR1 (receptor tyrosine kinase like orphan receptor 1)] and anti-[*Homo sapiens* CD3D (CD3 delta) and CD3E (CD3 epsilon, Leu-4) dimer], humanized monoclonal antibody, tetraspecific, octavalent;

scFv-G1-scFv-scFv fused heavy chain humanized (1-1227) [scFv kappa-heavy anti-TNFRSF9 humanized (1-246) [V-KAPPA (*Homo sapiens* IGKV1-12*01 (83.1%) -IGKJ4*01 (100%), CDR-IMGT [6.3.13] (27-32.50-52.89-111)) (1-111)-20-mer tetrakis(tetraglycyl-seryl) linker (112-131) -VH (*Homo sapiens* IGHV3-64*04 (82.1%) - (IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.7.10] (156-163.181-187.226-235)) (132-246)]-10-mer bis(tetraglycyl-seryl) linker (247-256)-gamma-1 heavy chain anti-CD274 humanized (257-700) [VH (*Homo sapiens* IGHV3-23*03 (77.7%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.7.10] (281-288.306-312.351-360)) (257-371) -*Homo*

sapiens IGHG1*01v, G1m17,1>G1m3,1, CH1 R120, CH3 D12, L14, G1v14-1 CH2 A1.3, A1.2, A1, G1v20 CH2 A105 (CH1 K120>R (468) (372-469), hinge 1-15 (470-484), CH2 L1.3>A (488), L1.2>A (489), G1>A (491), K105>A (576) (485-594), CH3 D12 (610), L14 (612) (595-699), CHS K2>del (700)) (372-700)] -10-mer bis(tétraglycyl-séryl) linker (701-710) -scFv heavy-kappa anti-ROR1 humanized (711-965) [VH (*Homo sapiens* IGHV3-23*03 (81.6%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.8.15] (736-743.761-768.807-821)) (711-832) -20-mer tétrakis(tétraglycyl-séryl) linker (833-852) -V-KAPPA (*Homo sapiens* IGKV1-27*01 (88.9%) -(IGHD) -IGKJ4*01 (83.3%), CDR-IMGT [8.3.13] (879-886.904-906.943-955)) (853-965)] -10-mer bis(tétraglycyl-séryl) linker (966-975) -scFv heavy-kappa anti-CD3D-CD3E dimer humanized (976-1227) [VH (*Homo sapiens* IGHV3-66*01 (86.6%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.7.14] (1001-1008.1026-1032.1071-1084)) (976-1095) -20-mer tétrakis(tétraglycyl-séryl) linker (1096-1115) -V-KAPPA (*Homo sapiens* IGKV1-5*01 (90.1%) -IGKJ4*01 (90.9%), CDR-IMGT [6.3.14] (1142-1047.1165-1167.1204-1217)) (1116-1227)]; (474-217')-disulfide with kappa light chain anti-CD274 humanized (1'-217') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (89.7%) -IGKJ4*01 (100%), CDR-IMGT[6.3.12] (27-32.50-52.89-100)) (1'-110') -*Homo sapiens* IGKC*01 (100%), Km3, A45.1 (156), V101 (194) (111'-217')]; dimer (480-480":483-483")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

nébratamig

immunoglobuline scFv-G1-scFv-scFv_L-kappa, anti-[*Homo sapiens* TNFRSF9 (membre 9 de la superfamille des récepteurs du TNF, 4-1BB, ILA, CD137)], anti-[*Homo sapiens* CD274 (ligand 1 de mort programmée 1, PDL1, PD-L1, B7 homologue 1, B7H1, B7-H1, PDCD1LG1)], anti-[*Homo sapiens* ROR1 (récepteur orphelin 1 récepteur tyrosine kinase like)] et anti-[*Homo sapiens* CD3D (CD3 delta) et CD3E (CD3 epsilon, Leu-4) dimère], anticorps monoclonal humanisé, tétraspécifique, octavalent; chaîne lourde fusionnée scFv-G1-scFv-scFv humanisée (1-1227) [scFv kappa-lourde anti-TNFRSF9 humanisé (1-246) [V-KAPPA (*Homo sapiens* IGKV1-12*01 (83.1%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [6.3.13] (27-32.50-52.89-111)) (1-111) -20-mer tétrakis(tétraglycyl-séryl) linker (112-131) -VH (*Homo sapiens* IGHV3-64*04 (82.1%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.7.10] (156-163.181-187.226-235)) (132-246)] -10-mer bis(tétraglycyl-séryl) linker (247-256)-chaîne lourde gamma-1 anti-CD274 humanisée (257-700) [VH (*Homo sapiens* IGHV3-23*03 (77.7%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.7.10] (281-288.306-312.351-360)) (257-371) -*Homo sapiens* IGHG1*01v, G1m17,1>G1m3,1, CH1 R120, CH3 D12, L14, G1v14-1 CH2 A1.3, A1.2, A1, G1v20 CH2 A105 (CH1 K120>R (468) (372-469), charnière 1-15 (470-484), CH2 L1.3>A (488), L1.2>A (489), G1>A (491), K105>A (576) (485-594), CH3 D12 (610), L14 (612) (595-699), CHS K2>del (700)) (372-700)] -10-mer bis(tétraglycyl-séryl) linker (701-710) -scFv lourde-kappa anti-ROR1 humanisé (711-965) [VH (*Homo sapiens* IGHV3-23*03 (81.6%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.8.15] (736-743.761-768.807-821)) (711-832) -20-mer tétrakis(tétraglycyl-séryl) linker (833-852) -V-KAPPA

- (*Homo sapiens* IGKV1-27*01 (88.9%) -(IGHD) -IGKJ4*01 (83.3%), CDR-IMGT [8.3.13] (879-886.904-906.943-955)) (853-965)]-10-mer bis(tetraglicil-séryl) linker (966-975) -scFv lourde-kappa anti-CD3D-CD3E humanisé (976-1227) [VH (*Homo sapiens*IGHV3-66*01 (86.6%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.7.14] (1001-1008.1026-1032.1071-1084)) (976-1095) -20-mer tétrakis(tetraglicil-séryl) linker (1096-1115) -[V-KAPPA (*Homo sapiens* IGKV1-5*01 (90.1%) -(IGHD) -IGKJ4*01 (90.9%), CDR-IMGT [6.3.14] (1142-1047.1165-1167.1204-1217)) (1116-1227)]; (474-217')-disulfure avec la chaîne légère kappa anti-CD274 humanisée (1'-217') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (89.7%) -IGKJ4*01 (100%), CDR-IMGT[6.3.12] (27-32.50-52.89-100)) (1'-110') -*Homo sapiens* IGKC*01 (100%), Km3, A45.1 (156), V101 (194) (111'-217')]; dimère (480-480":483-483")-bisdisulfide, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa
- nebratamig immunoglobulina scFv-G1-scFv-scFv_kappa, anti-[*Homo sapiens* anti-TNFRSF9 (miembro 9 de la superfamilia de los receptores del TNF, 4-1BB, ILA, CD137)], anti-[*Homo sapiens* CD274 (ligando 1 de muerte programada 1, PDL1, PD-L1, B7 homólogo 1, B7H1, B7-H1, PDCD1LG1)], anti-[*Homo sapiens* ROR1 (receptor huérfano 1 receptor tipo tirosina kinasa)] y anti-[*Homo sapiens* anti-CD3D (CD3 delta) y anti-CD3E (CD3 épsilon, Leu-4) dímero], anticuerpo monoclonal humanizado, tetraespecifico, octavalente; cadena pesada fusionada scFv-G1-scFv-scFv humanizada (1-1227) [scFv kappa-pesada anti-TNFRSF9 humanizada (1-246) [V-KAPPA (*Homo sapiens* IGKV1-12*01 (83.1%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [6.3.13] (27-32.50-52.89-111)) (1-111) -20-mer tetrakis(tetraglicil-seril) enlace (112-131) -VH (*Homo sapiens* IGHV3-64*04 (82.1%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.7.10] (156-163.181-187.226-235)) (132-246)] -10-mer bis(tetraglicil-seril) enlace (247-256)-cadena pesada gamma-1 anti-CD274 humanizada (257-700) [VH (*Homo sapiens* IGHV3-23*03 (77.7%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.7.10] (281-288.306-312.351-360)) (257-371) -*Homo sapiens* IGHG1*01v, G1m17,1>G1m3,1, CH1 R120, CH3 D12, L14, G1v14-1 CH2 A1.3, A1.2, A1, G1v20 CH2 A105(CH1 K120>R (468) (372-469), bisagra 1-15 (470-484), CH2 L1.3>A (488), L1.2>A (489), G1>A (491), K105>A (576) (485-594), CH3 D12 (610), L14 (612) (595-699), CHS K2>del (700)) (372-700)] -10-mer bis(tetraglicil-seril) enlace (701-710) -scFv pesada-kappa anti-ROR1 humanizada (711-965) [VH (*Homo sapiens* IGHV3-23*03 (81.6%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.8.15] (736-743.761-768.807-821)) (711-832) -20-mer tetrakis(tetraglicil-seril) enlace (833-852) -V-KAPPA (*Homo sapiens* IGKV1-27*01 (88.9%) -(IGHD) -IGKJ4*01 (83.3%), CDR-IMGT [8.3.13] (879-886.904-906.943-955)) (853-965)]-10-mer bis(tetraglicil-seril) enlace (966-975) -scFv pesada-kappa anti-CD3D-CD3E humanizada (976-1227) [VH (*Homo sapiens* IGHV3-66*01 (86.6%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.7.14] (1001-1008.1026-1032.1071-1084)) (976-1095) -20-mer tetrakis(tetraglicil-seril) enlace (1096-1115) -[V-KAPPA (*Homo sapiens* IGKV1-5*01 (90.1%) -(IGHD) -IGKJ4*01 (90.9%), CDR-IMGT [6.3.14] (1142-1047.1165-1167.1204-1217)) (1116-1227)]; (474-217')-disulfuro com la cadena ligera kappaanti-CD274 humanizada (1'-217') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (89.7%) -IGKJ4*01 (100%), CDR-IMGT [6.3.12] (27-32.50-52.89-100)) (1'-110') -*Homo sapiens* IGKC*01 (100%), Km3, A45.1 (156), V101 (194) (111'-217')]; dímero (480-480":483-483")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada: [scFv (anti-TNFRSF9)-G1 (anti-CD274)-scFv (anti-ROR1)-scFv (anti-CD3D-CD3E)]

DVVMTQSPSS	VSASVGDVRT	ITCQASQNI	TYLSWYQQK	GKAPKLLIYA	50
AANLASGVPS	RFGSGSGT	FTLTISDL	GDAAATYYCQ	TYLGTDTYVGG	100
AFGGGKVEI	KGGGGSGGG	SGGGSGGGG	SRLVSGGGG	LVQPGGSLRL	150
SCTAGFTIS	SYHMQWRQA	PKRGLEYIGT	ISSGGNVYA	SSARGFRFTIS	200
RPSKNTVDL	QMNSLRAEDT	AVYYCARD	YSDFPMWQGT	LVTVSSGGG	250
SGGGGSQSV	ESGGGLVQPG	GSLRLSCTAS	GIDLNTYDMI	WVRQAPGKGL	300
EWVGIITYSG	SRYANWAKG	RFTISKDN	NTVYLQMN	SLRAEDTAVY	350
ARDYMSGSH	WGQGLVTV	SASTKGFV	PLAPSSKST	GGTAALGCLV	400
KDYFPEPVT	SWNSGALTS	VHTFPAVL	QSGLYSLSS	VTVPSSSLGT	450
TYICNVNHP	SNTKVDKRV	EKSCDKT	HTCPCPAPEA	AGAPSVFLFP	500
PKDTLMISRT	PEVTCVVDV	SHEDPEV	KFNWYVDG	VEVHNAKTKPRE	550
NSYRVVSVL	TVLHQDWL	NGKEYKCAV	SNKALPAPIE	KTIKAKGQPRE	600
QVYTLPPSR	DELTKNQV	SLTCLVKGF	YPSDIAVEWES	NGQPENNYKT	650
VLDSDGSG	FFLYSKLTV	DKSRWQQGN	VFSCVMHEAL	HNNHYTQKSL	700
GGGGSGGGG	EVQLLESG	GGGLVQ	PGGSLRSCAAS	GFTISRYHMT	750
PKRGLEWIG	HYVNNDD	TDYASSAKR	GFRFTISRD	NSKNTLQMN	800
TATYFCARL	DVGGGGAY	IGDIWQGL	VTVVSSGGG	SGGGSGGGG	850
GSDIQMTQSP	SSLASVGR	VTITCQSS	QSSVYNNND	LAWYQKPKG	900
LIYYASTLAS	GVPSRFGSG	SGTDFTLT	ISLQPEDVAT	YCYAGGYDT	950
LDYFAPGGT	KVEIKGGGS	GGGSEVQL	VESGGGLV	QPGGSLRL	1000
GFTISTNAMS	WVRQAPGK	GLEWIGVIT	GRDITYYAS	WAKGRFTISR	1050
NTLYLQMN	SLRAEDTAV	YICARDGGS	SAITSNINW	QGGLVTVV	1100
GGGGSGGGG	GGGSDVVM	TQSPSTLS	ASVGDVRT	INCASESIS	1150
YQKPKGKAP	KLLIYEASK	LASGVPSR	FSGSGGTE	FTLTISSLQ	1200
YYCQGYFYFI	SRTYVNSFG	GKVEIK			1227

Light chain / Chaîne légère / Cadena ligera

AYDMTQSPSS	VSASVGDVRT	IKQASEDIY	SFLAWYQQK	GKAPKLLIHS	50
ASLASGVPS	RFGSGSGT	FTLTISLQ	EDFATYYCQ	GYGKNNVDNA	100
FGGGTKVEIK	RTVAAPSVF	I	FPPSDEQLKS	GTASVVCLLN	150
NKVDNALQSG	NSQESVTEQD	SKDSTYS	LSLSTLTL	SKADYERK	200
HQGLSSPVTK	SFNRGEC				217

Post-translational modifications

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

Intra-H (C23-C104)	23-88	152-225	277-350	398-454	515-575
	23"-88"	152"-225"	277"-350"	398"-454"	515"-575"
	621-679	732-806	875-942	997-1070	1138-1203
	621"-679"	732"-806"	875"-942"	997"-1070"	1138"-1203"
Intra-L (C23-C104)	23-88	137-197			
	23"-88"	137"-197"			
Inter-H-L (h 5-CL 126)	474-217	474-217"			
Inter-H-H (h 11, h 14)	480-480	483-483"			

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4: 551, 551"

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

nelistotugum #
nelistotug

immunoglobulin G1-kappa , anti-[*Homo sapiens* CD96 (T cell activation increased late expression, TACTILE, T-cell surface protein tactile)], *Homo sapiens* monoclonal antibody; gamma1 heavy chain *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV1-69*01 (95.9%) -(IGHD)-IGHJ1*01 (90.9%) (L123>T (117), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (219) (123-220), hinge 1-15 (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS (451-452)) (123-452)], (225-213')-disulfide with kappa light chain *Homo sapiens* (1'-213') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (95.7%) -IGKJ4*01 (91.7%), CDR-IMGT [6.3.8] (27-32.50-52.89-96)) (1'-106') -*Homo sapiens* IGKC*01 (100%), Km3, A45.1 (152), V101 (190) (107'-213')]; dimer (231-231":234-234")-bisdisulfide, produced in Chinese Hamster Ovary (CHO) Cell line, glycoform alfa

nélistotug

immunoglobuline G1-kappa, anti-[*Homo sapiens* CD96 (protéine de l'activation des cellules T exprimée tardivement, TACTILE, protéine tactile de la surface des cellules T)];

chaîne lourde gamma1 *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV1-69*01 (95.9%) -(IGHD) -IGHJ1*01 (90.9%) L123>T (117), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (219) (123-220), charnière 1-15 (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS (451-452)) (123-452)], (225-213')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-213') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (95.7%) -IGKJ4*01 (91.7%), CDR-IMGT [6.3.8] (27-32.50-52.89-96)) (1'-106') -*Homo sapiens* IGKC*01 (100%), Km3, A45.1 (152), V101 (190) (107'-213')]; dimère (231-231":234-234")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

nelistotug

immunoglobulina G1-kappa, anti-[*Homo sapiens* CD96 (proteína de la activación de las células T expresadas en etapas tardías, TACTILE, proteína táctil de la superficie de las células T)]; cadena pesada gamma1 *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV1-69*01 (95.9%) -(IGHD) -IGHJ1*01 (90.9%) L123>T (117), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (219) (123-220), bisagra 1-15 (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS (451-452)) (123-452)], (225-213')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-213') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (95.7%) -IGKJ4*01 (91.7%), CDR-IMGT [6.3.8] (27-32.50-52.89-96)) (1'-106') -*Homo sapiens* IGKC*01(100%), Km3, A45.1 (152), V101 (190) (107'-213')]; dímero (231-231":234-234")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

QVQLVQSGAE VKKPGSSVKV SCKASGGTFV EYAISWVRQA PGQGLEWMGG 50
IIPAFGTAQY AOKFQGRVTI TADESTSTAY MELSSLRSED TAVYYCARGA 100
GYYGDKDMD VVWQGTITVT SSASTKGPSV FPLAPSSKST SGGTAAALGCL 150
VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ SSGLYSLSSV VTPVSSSLGT 200
QTYICNVNHK PSNTKVKDKK EPKSCDKTHT CPCCPAPELL GGPSVFLFPP 250
KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDCGEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLW GKEYRCKVSN KALPAPIEKT ISKAKGQPRE 350
PQVYTLPPSR DELTKNQVSL TCLVKGFPYS DIAVEWESNG QPENNYKTPP 400
PVLDSDSGSEFF LYSKLTVDKS RWQQGNVFSC SVMHEALHNN YTQKSLSLSP 450
GK 452

Light chain / Chaîne légère / Cadena ligera

DIQLTQSPSS LSAVGDVRT ITCRASQSI SYLNWYQKPK GKAPKLLIYA 50
ASSLQSGVPS RFGSGSGTD FTLTISLQPF EDFATYYCQQ VLHITPFGGG 100
TKYVEIKRTVA AFSVFIFPPS DEQLKSGTAS VVCLLNFPY REAKVQWQKVD 150
NALQSGNSQE SVTEQDSKDS TYSLSSTLTL SKADYEKHKV YACEVTHQGL 200
SSPVTKSENR GEC 213

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' 133'-193'
23'''-88''' 133'''-193'''

Inter-H-L (h 5-CL 126) 225-213' 225"-213"

Inter-H-H (h 11, h 14) 231-231" 234-234"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal

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

H VH Q1: 1, 1"

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

H CH2 N84.4: 302, 302"

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

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

H CHS K2: 452, 452"

neracorvirum

neracorvir

N-{[2-(2*S*)-1,4-dioxan-2-yl]ethyl}-2-methyl-5,5,11-trioxo-10,11-dihydro-5λ⁶*H*-pyrrolo[1,2-*b*][1,2,5]benzothiadiazepine-8-carboxamide

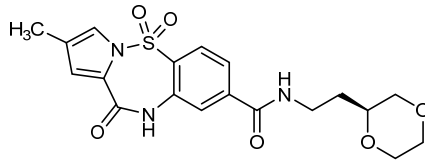
néracorvir

N-{[2-(2*S*)-1,4-dioxan-2-yl]éthyl}-2-méthyl-5,5,11-trioxo-10,11-dihydro-5λ⁶*H*-pyrrolo[1,2-*b*][1,2,5]benzothiadiazépine-8-carboxamide

neracorvir

N-{[2-(2*S*)-1,4-dioxan-2-il]etil}-2-metil-5,5,11-trioxo-10,11-dihidro-5λ⁶*H*-pirrolo[1,2-*b*][1,2,5]benzotiadiazepina-8-carboxamida

C₁₉H₂₁N₃O₆S



nezutatugum #

nezutatug

immunoglobulin G1- kappa, anti-[*Homo sapiens* ERBB3 (receptor tyrosine-protein kinase erbB-3, HER3)], humanized monoclonal antibody; gamma1 heavy chain humanized (1-450) [VH (*Homo sapiens* IGHV4-31*01 (89.9%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [9.7.13] (26-34.52-58.97-109)) (1-120) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, 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 kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (85.3%) -IGKJ2*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (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, glycoform alfa

nézutatug

immunoglobuline G1-kappa, anti-[*Homo sapiens* ERBB3 (récepteur à activité tyrosine kinase erbB-3, HER3)], anticorps monoclonal humanisé; chaîne lourde gamma1 humanisée (1-450) [VH (*Homo sapiens* IGHV4-31*01 (89.9%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [9.7.13] (26-34.52-58.97-109)) (1-120) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, 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')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (85.3%) -IGKJ2*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (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, glycoforme alfa

nezutatug

inmunoglobulina G1-kappa, anti-[*Homo sapiens* ERBB3 (receptor con actividad tirosina kinasa erbB-3, HER3)], anticuerpo monoclonal humanizado;
 cadena pesada gamma1 humanizada (1-450) [VH (*Homo sapiens* IGHV4-31*01 (89.9%) -(IGHD)-IGHJ4*01 (92.9%), CDR-IMGT [9.7.13] (26-34.52-58.97-109)) (1-120) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, 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 kappa humanizada (1'-214'') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (85.3%) -IGKJ2*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107'') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (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, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

QVQLQESGPG LVKPSQTLST TCTVSGYSIT SGYSWHWIRQ HPGKGLEWIG 50
 SIRYSGGTDY NPSLKSIVTI SADTSKNQFS LKLSSVTAAD TAVYYCARMT 100
 TAPWYFFDYW GQGTVTVTSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
 DYFPEPVTVS WNSGALTSV HTPFAVLQSS GLYSLSSVVT VPSSSLGTQT 200
 YICNVNHPFS NTKVDKVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPPK 250
 KDTLIMISRTF EVTCVVDVVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
 STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
 VYTLPPSRDE LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTPPV 400
 LDDSDGFFLY SKLTVDKSRW QQGNVFCVSV MHEALHNHYT QKSLSLSPGK 450

Light chain / Chaîne légère / Cadena ligera

DIQMTQSPSS VSASVGDRTV ITCKASQIVG SNVAWYQQKPK GKAEPLIYS 50
 ASYLYSGVFS RFGSGSGGTD FTLTISLQP EDFATYYCQQ YSSHPLTFGQ 100
 GTKLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQMKV 150
 DNALQSGNSQ ESVTEQDSKDT STYLSLSTLT LSKADYEKHK VYACEVTHQG 200
 LSSPVTKSFN RGECL 214

Post-translational modifications

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

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

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

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

Inter-H-H (h 11, h 14) 229-229'' 232-232''

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal

Q > pyroglutamyl (pE, 5-oxopropyl) / pyroglutamyle (pE, 5-oxopropyle) / piroglutamilo (pE, 5-oxoprolilo)
 H VH Q1: I, I''

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''

nimucitinibum

nimucitinib

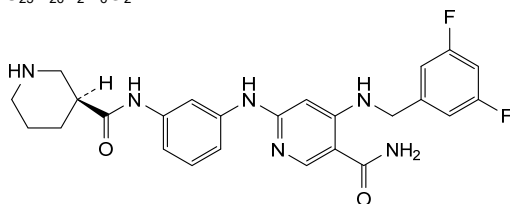
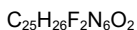
(9³S)-1³,1⁵-difluoro-8-oxo-3,5,7-triaza-4(4,2)-pyridina-9(3)-piperidina-1(1),6(1,3)-dibenzenonaphane-4⁵-carboxamide

nimucitinib

(9³S)-1³,1⁵-difluoro-8-oxo-3,5,7-triaza-4(4,2)-pyridina-9(3)-pipéridina-1(1),6(1,3)-dibenzénanonaphane-4⁵-carboxamide

nimucitinib

(9³S)-1³,1⁵-difluoro-8-oxo-3,5,7-triaza-4(4,2)-piridina-9(3)-piperidina-1(1),6(1,3)-dibencenonafano-4⁵-carboxamida

**nizatidinum**

nizatidinum

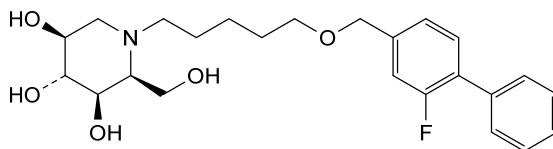
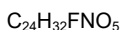
(2*S*,3*R*,4*R*,5*S*)-1-{5-[(2-fluoro-[1,1'-biphenyl]-4-yl)méthoxy]pentyl}-2-(hydroxyméthyl)piperidine-3,4,5-triol

nizatidinum

(2*S*,3*R*,4*R*,5*S*)-1-{5-[(2-fluoro-[1,1'-biphenyl]-4-yl)méthoxy]pentyl}-2-(hydroxyméthyl)piperidine-3,4,5-triol

nizatidinum

(2*S*,3*R*,4*R*,5*S*)-1-{5-[(2-fluoro-[1,1'-biphenyl]-4-yl)méthoxy]pentyl}-2-(hydroxyméthyl)piperidine-3,4,5-triol

**nizatidinum #**

nizatidinum

immunoglobulin G2-kappa, anti-[*Canis lupus familiaris* IL31RA (interleukin 31 receptor A)], caninized monoclonal antibody; gamma2 heavy chain caninized (1-453) [VH (*Canis lupus familiaris*IGHV4-1*01 (77.8%) -(IGHD) -IGHJ4*01 (86.7%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Canis lupus familiaris*IGHG2*02, G2v2 CH2 A1.3, A1.2, G114 (CH1 (120-216), hinge 1-19 (217-235), CH2 M1.3>A (239), L1.2>A (240), P114>G (334) (236-345), CH3 (346-452), CHS K2>del (453)) (120-453)], (134-213')-disulfide with kappa light chain caninized (1'-213') [V-KAPPA (*Canis lupus familiaris*IGKV4-15*01 (76.0%) -IGKJ3*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Canis lupus familiaris*IGKC*01 (100%) (108'-213')]; dimer (231-231''-234-234'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-DG44, glycoform alfa

nizatidinum

immunoglobuline G2-kappa, anti-[*Canis lupus familiaris* IL31RA (récepteur A de l'interleukine 31)], anticorps monoclonal caninisé; chaîne lourde gamma2 caninisée (1-453) [VH (*Canis lupus familiaris*IGHV4-1*01 (77.8%) -(IGHD) -IGHJ4*01 (86.7%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Canis lupus familiaris*IGHG2*02, G2v2 CH2 A1.3, A1.2, G114 (CH1 (120-216), charnière 1-19 (217-235), CH2 M1.3>A (239), L1.2>A (240), P114>G (334) (236-345), CH3 (346-452), CHS K2>del (453)) (120-453)], (134-213')-disulfure avec la chaîne légère kappa caninisée (1'-213') [V-KAPPA (*Canis lupus familiaris*IGKV4-15*01 (76.0%) -IGKJ3*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Canis lupus familiaris*IGKC*01 (100%) (108'-213')]; dimère (231-231''-234-234'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-DG44, glycoforme alfa

nolavetbart

inmunoglobulina G2-kappa, anti-[*Canis lupus familiaris* IL31RA (receptor A de la interleukina 31)], anticuerpo monoclonal caninizado;
 cadena pesada gamma2 caninizada (1-453) [VH (*Canis lupus familiaris* IGHV4-1*01 (77.8%) -(IGHD) -IGHJ4*01 (86.7%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Canis lupus familiaris* IGHG2*02, G2v2 CH2 A1.3, A1.2, G114 (CH1 (120-216), bisagra 1-19 (217-235), CH2 M1.3>A (239), L1.2>A (240), P114>G (334) (236-345), CH3 (346-452), CHS K2>del (453)) (120-453)], (134-213')-disulfuro con la cadena ligera kappa caninizada (1'-213') [V-KAPPA (*Canis lupus familiaris* IGKV4-15*01 (76.0%) -IGKJ3*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Canis lupus familiaris* IGKC*01 (100%) (108'-213')]; dímero (231-231'''-234-234''')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-DG44, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

EVTLQESGPG	LVKPSQTL	SL	TCVASGF	SIK	SSFIHWLR	Q	PGRGLEWIGR	50
IDPAPGATEY	NPAFQGRFSI		TADTAKNQAS	LQLSSMTTED			SAVYCYARYH	100
YAASHFDWAG	QGTLVTVSSA		STTAPSVFPL	APSCGSTSGS			TVALACLVSG	150
YFPEPVTVSW	NSGSLTSGVH		TFPSVLQSSG	LYSLSSMVTV			PSSRWFSETF	200
TCNVAHPAK	TKVDKPKPKR		ENGRVPRPPD	CPKCPAPEAA			GGPSVFIFFP	250
KPKD'TLLIAR	TPEVTCVVVD		LDPEDPEVQI	SWFVDGKQMQ			TAKTQPREEQ	300
FNGTYRVVSV	LPIGHQDWLK		GKQFTCKVNN	KALGSPPIERT			ISKARGQAHQ	350
PSVYVLPFSR	EELSKNTVSL		TCLIKDFFPP	DIDVEWQSNQ			QQEPESKYRT	400
TPPQLDEDS	YFLYSKLSVD		KSRWQRGDTF	ICAVMHEALH			NHYTQESLSH	450
SPG								453

Light chain / Chaîne légère / Cadena ligera

RIVMTQSPGS	LAGSVGESVS		INCKSSQSVT	NDLTWYQQKP			GEAPKVLITY	50
ASQRYTGVPA	RFSGSGYGTD		FTLTINNLQA	EDVGDYFCQQ			DYASPTFGQ	100
GTKLEIKRND	AQPAVYLFQP		SPDQLHTGSA	SVVCLLNSFY			PKDINWKWKV	150
DGVIQDTGIQ	ESVTEQDKDS		TYSLSSTLTM	SSTEYLSHEL			YSCEITHKSL	200
PSTLIKSFQR	SEC							213

Post-translational modifications

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
 Intra-H (C23-C104) 22-96 146-202 266-326 372-432
 22"-96" 146"-202" 266"-326" 372"-432"
 Intra-L (C23-C104) 23'-88" 134'-193"
 23'''-88''' 134'''-193'''
 Inter-H-L (CH1 I1-CL 126) 134-213' 134"-213"
 Inter-H-H (h 15, h 18) 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 biantennarios complejos fucosilados

oberotatumum #
 oberotatum

immunoglobulin G1-kappa, anti-[*Homo sapiens* LY75 (human lymphocyte antigen 75, C-type lectin domain family 13 member B, CLEC13B, DEC-205, CD205)], *Homo sapiens* monoclonal antibody; gamma1 heavy chain *Homo sapiens* (1-448) [VH (*Homo sapiens* IGHV3-15*01 (98.0%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.10.10] (26-33.51-60.99-108)) (1-119) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m 1 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 K2>del (448)) (120-448)], (222-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*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 (153), V101 (191) (108'-214')]; dimer (228-228''-231-231''')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1SV, glycoform alfa

obérotatug immunoglobuline G1-kappa, anti-[*Homo sapiens* LY75 (antigène 75 des lymphocytes humains, membre B de la famille 13 des lectines à domaine de type C, CLEC13B, DEC-205, CD205)], anticorps monoclonal *Homo sapiens*;
chaîne lourde gamma1 *Homo sapiens* (1-448) [VH (*Homo sapiens* IGHV3-15*01 (98.0%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.10.10] (26-33.51-60.99-108)) (1-119) -*Homo sapiens* IGHG1*03v, 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 K2>del (448)) (120-448)], (222-214')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*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 (153), V101 (191) (108'-214')]; dimère (228-228":231-231")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1SV, glycoforme alfa

oberotatug inmunoglobulina G1-kappa, anti-[*Homo sapiens* LY75 (antígeno 75 de los linfocitos humanos, miembro B de la familia 13 de las lectinas con dominio de tipo C, CLEC13B, DEC-205, CD205)], anticuerpo monoclonal *Homo sapiens*;
cadena pesada gamma1 *Homo sapiens* (1-448) [VH humanizado (*Homo sapiens* IGHV3-15*01 (98.0%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.10.10] (26-33.51-60.99-108)) (1-119) -*Homo sapiens* IGHG1*03v, 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 K2>del (448)) (120-448)], (222-214')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*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 (153), V101 (191) (108'-214')]; dímero (228-228":231-231")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular derivada de CHO-K1SV, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada
EVQLVESGGG LVKPGGSLRL SCAASGFTYS NAWMSWRQA PGKGLEWVGR 50
IKSKTDGGT DYAAPVQGRF TISRDDSKNT LYLQMNLSKT EDTAVYYCTI 100
FGVVSFDYWG QGTLVTVSSA STKGPSVFPFL AFSKSTSGG TAALGCLVKD 150
YFPEFVTVSW NSGALTSGVH TFPAVLQSSG LYSLSVVTV PSSSLGTQTY 200
ICNVNHNKPSN TKVDKKVEPK SCDKTHTCP CPAPPELLGGP SVFLFPPKPK 250
DTLMISRTPE VTCVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS 300
TYRVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV 350
YTLPPSREEM TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTTPPV 400
DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPG 448

Light chain / Chaîne légère / Cadena ligera
DVQMTQSPSS LSASVGDRTV ITCRASQGIS DYLSWYQQRG GKAPNLLIYA 50
ASNLRKTVPS RFGSGSGTD FTLTISTLQP EDFATYYCQQ SYRSPWTFGQ 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNIFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYLSSTLT 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) 22-98 146-202 263-323 369-427
22"-98" 146"-202" 263"-323" 369"-427"
Intra-L (C23-C104) 23-88" 134'-194'
23'''-88''' 134'''-194'''
Inter-H-L (h 5-CL 126) 222-214' 222"-214"
Inter-H-H (h 11, h 14) 228-228" 231-231"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4: 299, 299"

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

oberotatugum ravtansinum #

oberotatug ravtansine immunoglobulin G1-kappa, anti-[*Homo sapiens* LY75 (human lymphocyte antigen 75, C-type lectin domain family 13 member B, CLEC13B, DEC-205, CD205)], *Homo sapiens* monoclonal antibody; conjugated to maytansinoid DM4; gamma1 heavy chain *Homo sapiens* (1-448) [VH (*Homo sapiens*IGHV3-15*01 (98.0%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.10.10] (26-33.51-60.99-108)) (1-119) -*Homo sapiens*IGHG1*03v, G1m3>G1m17, nG1m 1 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 K2>del (448)) (120-448)], (222-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens*IGKV1-39*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 (153), V101 (191) (108'-214')]; dimer (228-228":231-231")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1SV, glycoform alfa; conjugated, on an average of 3 to 4 lysyl, to maytansinoid DM4 [*N*²-deacetyl-*N*²-(4-mercapto-4-methyl-1-oxopentyl)-maytansine] via the reducible SPDB linker [*N*-succinimidyl 4-(2-pyridyldithio)butanoate]

For the *ravtansine* part, please refer to the document "*INN for pharmaceutical substances: Names for radicals, groups and others*"

obérotatug ravtansine immunoglobuline G1-kappa, anti-[*Homo sapiens* LY75 (antigène 75 des lymphocytes humains, membre B de la famille 13 des lectines à domaine de type C, CLEC13B, DEC-205, CD205)], anticorps monoclonal *Homo sapiens*; conjugué au maytansinoïde DM4; chaîne lourde gamma1 *Homo sapiens* (1-448) [VH (*Homo sapiens*IGHV3-15*01 (98.0%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.10.10] (26-33.51-60.99-108)) (1-119) -*Homo sapiens*IGHG1*03v, G1m3>G1m17, nG1m 1 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 K2>del (448)) (120-448)], (222-214')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens*IGKV1-39*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 (153), V101 (191) (108'-214')]; dimère (228-228":231-231")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1SV, glycoforme alfa; conjugué, sur 3 ou 4 lysyl en moyenne, au maytansinoïde DM4 [*N*²-déacétyl-*N*²-(4-mercapto-4-méthyl-1-oxopentyl)- maytansine] via le linker SPDB réductible [4-(2-pyridyldithio)butanoate de *N*-succinimidyle]

Pour la partie *ravtansine*, veuillez-vous référer au document "*INN for pharmaceutical substances: Names for radicals, groups and others*"

oberotatug ravtansina inmunoglobulina G1-kappa, anti-[*Homo sapiens* LY75 (antígeno 75 de los linfocitos humanos, miembro B de la familia 13 de las lectinas con dominio tipo C, CLEC13B, DEC-205, CD205)], anticuerpo monoclonal *Homo sapiens*; conjugado con maitansinoide DM4; cadena pesada gamma1 *Homo sapiens* (1-448) [VH humanizado (*Homo sapiens*IGHV3-15*01 (98.0%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.10.10] (26-33.51-60.99-108)) (1-119) -*Homo sapiens*IGHG1*03v, 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 K2>del (448)) (120-448)], (222-214')-disulfuro con la cadena ligera kappa *Homo*

sapiens (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*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 (153), V101 (191) (108'-214')]; dímero (228-228"-231-231")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular derivada de CHO-K1SV, forma glicosilada alf, conjugado, en 3 o 4 restos lisil por término medio, con maitansinoide DM4 [*N*²-deacetil-*N*²-(4-mercapto-4-metil-1-oxopentil)-maitansina] a través del enlace SPDB reducible [4-(2-piridilditio)butanoato de *N*-succinimidilo]

Para la fracción *ravtansine*, se pueda referirse al documento "INN for pharmaceutical substances: Names for radicals, groups and others"

Heavy chain / Chaîne lourde / Cadena pesada

EVQLVESGGG LVKPGGSLRL SCAASGFTYS NAMMSWVRQA PGKLEWVGR 50
 IKSFKDGGT DYAAPVQGRF TISRDDSKNT LYLQMSLKT EDTAVYYCTI 100
 FGVSFDFYWG QGTLIVTVSSA STKGPSVFPPL APSSKSTSGG TAALGCLVKK 150
 YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSVWTV PSSSLGTQTY 200
 ICNVNHRKPSN TKVDRKVEPK SCDKTHTCP CPAPPELLGGP SVFLPPKPK 250
 TLIMLSRTPV VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS 300
 TYRIVSVLTV LHQDNLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV 350
 YTLPPSREEM TKNQVSLTCL VKGFPYPSDIA VEWESNGQPE NNYKTTPEVL 400
 DSDGFFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPG 448

Light chain / Chaîne légère / Cadena ligera

DVQMTQSPSS LSASVGRVIT ITCRASQGIS DYLSWYQQRG GKAPNLLIYA 50
 ASNLKTGVPV RFGSGSGTD FTLTISTLQP EDFATYYCQQ SYRSPWTFEG 100
 GTKVEIKRTV AAPSVEFIFPP SDEQLKSGTA SVVCLLNFFY PREAKVQKVK 150
 DNALQSGNSQ ESVTEQDSKD STYLSLSTLT 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" 146"-202" 263"-323" 369"-427"
 22"-98" 146"-202" 263"-323" 369"-427"

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

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

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

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

H CH2 N84.4: 299, 299"

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

For the *ravtansine* part, please refer to the document "INN for pharmaceutical substances:

Names for radicals, groups and others"

Pour la partie *ravtansine*, veuillez-vous référer au document "INN for pharmaceutical substances:

Names for radicals, groups and others"

Para la fracción *ravtansina*, se ruega referirse al documento "INN for pharmaceutical substances:

Names for radicals, groups and others"

obertamigum #

obertamig

immunoglobulin half IG G1-lambda2/scFv-h-CH2-CH3, anti-[*Homo sapiens* CD3E (CD3 epsilon)] and anti-[*Homo sapiens* HLA-G (class I major histocompatibility (MH1) antigen G, human leucocyte antigen G) C-like domain], *Homo sapiens* monoclonal antibody, bispecific, bivalent; 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, G1v14-67 CH2 A1.3, A1.2, S27, G1v69 V6, Y7, A85.1, V86 (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), T6>V (353), L7>Y (354), F85.1>A (408), Y86>V (410) (344-448), CHS (449-450)) (121-450)], (223-216')-disulfide with lambda light chain anti-CD3E *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV2-23*02 (84.4%) -IGKJ2*01 (90.9%), CDR-IMGT [9.3.10] (26-34.52-54.91-100)) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')];

- IG scFv-h-CH2-CH3 chain single chain, anti-HLA-G *Homo sapiens* (1"-452") [scFv V-kappa-VH anti-HLA-G (1"-258")] [V-KAPPA (*Homo sapiens* IGKV4-1*01 (96.0%) -IGKJ1*01 (100%), CDR-IMGT [12.3.9] (27-38.56-58.95-103)) (1"-113") -20-mer linker (114"-133") -VH (*Homo sapiens* IGHV6-1*01 (99.0%) -IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [10.9.15] (159-168.186-194.233-247)) (134"-258")] -*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1 CH3 E12, M14, G1v37 h S5, G1v14-67 CH2 A1.3, A1.2, S27, G1v68 CH3 V6, L22, L79; W81 (259"-490") [hinge 1-15 C5>S (263) (259"-273"), CH2 L1.3>A (277), L1.2>A (278), D27>S (308) (274"-383"), CH3 T6>V (393), E12 (399), M14 (401), T22>L (409), K79>L (435), T81>W (437) (384"-488"), CHS (489"-490")]; dimer (229-269":232-272")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa
- obertamig immunoglobuline demi-IG G1-lambda2/scFv-h-CH2-CH3, anti-[*Homo sapiens* CD3E (CD3 epsilon)] et anti-[*Homo sapiens* HLA-G (antigène G d'histocompatibilité majeure de classe I (MH1), antigène G leucocytaire humain) domaine C-like], anticorps monoclonal *Homo sapiens*, bispécifique, bivalent; chaîne lourde H-gamma1 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, nG1m1bCH1 K120, CH3 E12, M14, G1v14-67 CH2 A1.3, A1.2, S27, G1v69 V6, Y7, A85.1, V86 (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), T6>V (353), L7>Y (354), F85.1>A (408), Y86>V (410) (344-448), CHS (449-450)) (121-450)], (223-216')-disulfure avec la chaîne légère lambda anti-CD3E *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV2-23*02 (84.4%) -IGKJ2*01 (90.9%), CDR-IMGT [9.3.10] (26-34.52-54.91-100)) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')]; IG scFv-h-CH2-CH3 chaîne unique, anti-HLA-G *Homo sapiens* (1"-452") [scFv V-kappa-VH anti-HLA-G (1"-258")] [V-KAPPA (*Homo sapiens* IGKV4-1*01 (96.0%) -IGKJ1*01 (100%), CDR-IMGT [12.3.9] (27-38.56-58.95-103)) (1"-113") -20-mer linker (114"-133") -VH (*Homo sapiens* IGHV6-1*01 (99.0%) -IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [10.9.15] (159-168.186-194.233-247)) (134"-258")] -*Homo sapiens* IGHG1 h-CH2-CH3, nG1m1 CH3 E12, M14, G1v37 h S5, G1v14-67 CH2 A1.3, A1.2, S27, G1v68 CH3 V6, L22, L79; W81 (259"-490") [charnière 1-15 C5>S (263) (259"-273"), CH2 L1.3>A (277), L1.2>A (278), D27>S (308) (274"-383"), CH3 T6>V (393), E12 (399), M14 (401), T22>L (409), K79>L (435), T81>W (437) (384"-488"), CHS (489"-490")]; dimère (229-269":232-272")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa
- obertamig inmunoglobulina demi-IG G1-lambda2/scFv-h-CH2-CH3, anti-[*Homo sapiens* CD3E (CD3 épsilon)] y anti-[*Homo sapiens* HLA-G (antígeno G de histocompatibilidad de clase I (MH1), antígeno G leucocitario humano de tipo C), anticuerpo monoclonal *Homo sapiens*, biespecifico, bivalente; cadena pesada H-gamma1 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, G1v14-67 CH2 A1.3, A1.2, S27, G1v69 V6, Y7, A85.1, V86 (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), T6>V (353), L7>Y (354), F85.1>A (408), Y86>V (410) (344-448), CHS (449-450)) (121-450)], (223-216')-disulfuro con la cadena ligera lambda anti-CD3E *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV2-23*02 (84.4%) -IGKJ2*01 (90.9%), CDR-IMGT [9.3.10] (26-34.52-54.91-100)) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')];

IG scFv-h-CH2-CH3 cadena única, anti-HLA-G *Homo sapiens* (1"-452") [scFv V-kappa-VH anti-HLA-G (1"-258") [V-KAPPA (*Homo sapiens* IGKV4-1*01 (96.0%) -IGKJ1*01 (100%), CDR-IMGT [12.3.9] (27-38.56-58.95-103)) (1"-113")-20-mer enlace (114"-133") -VH (*Homo sapiens* IGHV6-1*01 (99.0%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [10.9.15] (159-168.186-194.233-247)) (134"-258") -*Homo sapiens* IGHG1 h-CH2-CH3, nG1m1 CH3 E12, M14, G1v37 h S5, G1v14-67 CH2 A1.3, A1.2, S27, G1v68 CH3 V6, L22, L79; W81 (259"-490") [bisagra 1-15 C5>S (263) (259"-273"), CH2 L1.3>A (277), L1.2>A (278), D27>S (308) (274"-383"), CH3 T6>V (393), E12 (399), M14 (401), T22>L (409), K79>L (435), T81>W (437) (384"-488"), CHS (489"-490")]]; dímero (229-269":232-272")-bisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada: anti-CD3E (H)
 QVQLQQSGPR LVRFSQTLSTL TCAISGDSVF NNAAWSWIR QSPSRGLEWL 50
 GRITYRSKWL YDYAVSVKSR ITVNPDTSRN QFTLQLNSVT P EDTALYYCA 100
 RGYSSSFYDW GQGTLVTVSS ASTKQPSVFP LAPSKSTSG GTAALGCLVK 150
 DYFPEPVTVS WNSGALTSKV HTFPAVLQSS GLYSLSVVT VPSSSLGTQT 200
 YICNVNHNKPS NTKVDKVEP KSCDKTHTCP PCPAPAEAGG PSVFLFPPPK 250
 KDTLMI SRTPEVTCVVSVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
 STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
 VYVYPPSREE MTKNQVSLTLC LVKGFYPSDI AVEWESNGQP ENNYKTTTPV 400
 LDSDSGSFALV SKLTVDKSRW QQGNVFSQSV MHEALHNHYT QKSLSLSPGK 450

Light chain / Chaîne légère / Cadena ligera: anti-CD3E (L)
 QVALTQPASV SSGSPGQSITI SCTGTSSNIG TYKFSVWYQQ HPDKAPKVL 50
 YEVSKRPSGV SRSFSGSKSG NTASLTISGL QAEDQADYHC VSYAGSGLL 100
 FGGGKTLTVL GQPKAAPSVT LFPPSSEELQ ANKATLVCLISDFYPGAVTV 150
 AWKADSSPVK AGVETTTPSK QSNNKYAASS YLSLTPEQWK SHRSYSCQVT 200
 HEGSTVEKTV APTCEA 216

Heavy chain / Chaîne lourde / Cadena pesada: anti-HLA-G (H")
 DIVMTQSPDS LAVSLGERAT INCKSSQSVL HSSNNKNYLT WFQKPKGQPP 50
 KLLIYWASTR ESVGPRDFSG SSGSDFTLT ISSLQAEDVA VYCHQYYST 100
 PPTFGQGTKV EIKGGSEKGS SSGSESKST GGSQVQLQQS GPGLVKPST 150
 LSLTCAISGD SVSSNSAAWN WIRQSPSRGL EWLGRYYRS KWNNDYAVSV 200
 KSRITINPDT SKNQISLQLN SVTPEDTAVY YCAGDRRYGI VGLPFAYWGQ 250
 GTLVVVSSEP KSDKHTTCTP PCPAPAEAGG PSVFLFPPPK KDTLMI SRTPE 300
 EVTCVVSVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN STYRVVSVLT 350
 VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VVYLPPSREE 400
 MTKNQVSLLC LVKGFYPSDI AVEWESNGQP ENNYLTWPPV LDSDSGSFFLY 450
 SKLTVDKSRW QQGNVFSQSV MHEALHNHYT QKSLSLSPGK 490

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
 23"-94" 155"-232" 304"-364" 410"-468"
 Intra-L (C23-C104) 22-90" 138"-197"
 Inter-H-L (CHI 10-CL 126) 223-215"
 Inter-H-H (h 8, h 11) 229-269" 232-272"

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

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
 H CH2 N84.4: 300, 340"
 Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantennarios complejos fucosilados.

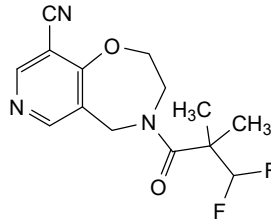
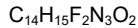
C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
 H CHS K2: 450, 490"

oditrasertibum

oditrasertib 4-(3,3-difluoro-2,2-dimethylpropanoyl)-2,3,4,5-tetrahidropirido[3,4-f][1,4]oxazepine-9-carbonitrile

oditrasertib 4-(3,3-difluoro-2,2-diméthylpropanoïl)-2,3,4,5-tétrahidropirido[3,4-f][1,4]oxazépine-9-carbonitrile

oditrasertib 4-(3,3-difluoro-2,2-dimetilpropanoïl)-2,3,4,5-tetrahidropirido[3,4-f][1,4]oxazepina-9-carbonitrilo



oloctinebartum #
oloctinebart

immunoglobulin G4-kappa, anti-[*Homo sapiens* LGALS3 (galectin 3)], humanized monoclonal antibody; gamma4 heavy chain humanized (1-442) [VH (*Homo sapiens*IGHV1-3*01 (88.7%) -(IGHD) -IGHJ6*01 (93.3%), CDR-IMGT [8.8.9] (26-33.51-58.97-105))] (1-116)-*Homo sapiens*IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (117-214), hinge 1-12 S10>P (224) (215-226), CH2 L92 (305) (227-336), CH3 (337-441), CHS K2>del (442)) (117-442)], (130-219')-disulfide with kappa light chain humanized (1'-219') [V-KAPPA (*Homo sapiens*IGKV2D-29*02 (89.0%) -IGKJ2*01 (100%), CDR-IMGT [11.3.9] (27-37.55-57.94-102))] (1'-112') -*Homo sapiens*IGKC*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; dimer (222-222'':225-225'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

oloctinebart

immunoglobuline G4-kappa, anti-[*Homo sapiens* LGALS3 (galectine 3)], anticorps monoclonal humanisé; chaîne lourde gamma4 humanisée (1-442) [VH (*Homo sapiens*IGHV1-3*01 (88.7%) -(IGHD) -IGHJ6*01 (93.3%), CDR-IMGT [8.8.9] (26-33.51-58.97-105))] (1-116) -*Homo sapiens*IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (117-214), charnière 1-12 S10>P (224) (215-226), CH2 L92 (305) (227-336), CH3 (337-441), CHS K2>del (442)) (117-442)], (130-219')-disulfure avec la chaîne légère kappa humanisée (1'-219') [V-KAPPA (*Homo sapiens*IGKV2D-29*02 (89.0%) -IGKJ2*01 (100%), CDR-IMGT [11.3.9] (27-37.55-57.94-102))] (1'-112') -*Homo sapiens*IGKC*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; dimère (222-222'':225-225'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

oloctinebart

inmunoglobulina G4-kappa, anti-[*Homo sapiens* LGALS3 (galectina 3)], anticuerpo monoclonal humanizado; cadena pesada gamma4 humanizada (1-442) [VH (*Homo sapiens*IGHV1-3*01 (88.7%) -(IGHD) -IGHJ6*01 (93.3%), CDR-IMGT [8.8.9] (26-33.51-58.97-105))] (1-116) -*Homo sapiens*IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (117-214), bisagra 1-12 S10>P (224) (215-226), CH2 L92 (305) (227-336), CH3 (337-441), CHS K2>del (442)) (117-442)], (130-219')-disulfuro com la cadena ligera kappa humanizada (1'-219') [V-KAPPA (*Homo sapiens*IGKV2D-29*02 (89.0%) -IGKJ2*01 (100%), CDR-IMGT [11.3.9] (27-37.55-57.94-102))] (1'-112') -*Homo sapiens*IGKC*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; dímero (222-222'':225-225'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

QVQLVQSGAE VVKPGASVKV SCKASGYSFT NYMHWRQ PGORLEMMGW 50
 IYPGSGNTNY NEKFGQRTI TADTSASTAY MELSLRSED TAVYVCSTAP 100
 GGFDMVQGGT TVTVSSASTK GPSVFLAPC SRSTSESTAA LGCLKVDYFP 150
 EPVTYSWNSG ALTISGVHTFP AVLQSSGLYS LSSVVTVPSS SLGKTYITCN 200
 VDHKPSNTKV DKRVESKYG FCPGPCAPEF LGGFVSFLFP PKPKDTLMIS 250
 RTPEVTCVVV DVSQEDPEVQ FNWYVDGVEV HNAKTKPREE QFNSTYRVVS 300
 VLTVLHQDWL NGKEYKCKVQ NGLPSSIEK TISKAKGQPR EPQVYTLPPS 350
 QEEMTKNQVS LTLCLVKGFYP SDIAVEWESN GQFENNYKTT PPVLDSDGSF 400
 FLYSRLTVDK SRWQEGNVFS CSVMHEALHN HYTKLSLSLG 442

Light chain / Chaîne légère / Cadena ligera

DIVMTQTPLS LSVTPGQPAS ISCKSSKSLD HSDGITYLYW YLQKPGQSPQ 50
 LLIYRMSNLA SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCAQMLEFP 100
 LTFGQGTKLE IKRTVAAPSV FIFPPSDEQL KSGTASVWCL LNNFYPREAK 150
 VQWVKDVALQ SGNISQESVTE QDSKOSTYSL SSTLTLSKAD YEKHKVYACE 200
 VTHQGLSSPV TKSFNREGC 219

Post-translational modifications

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

Intra-H (C23-C104) 22-96 143-199 257-317 363-421
 22"-96" 143"-199" 257"-317" 363"-421"

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

Inter-H-L (CH1 10-CL 126) 130-219" 130"-219"

Inter-H-H (h 8, h 11) 222-222" 225-225"

N-terminal glutaminy cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal

Q> pyroglutamyl (pE, 5-oxoprolyl) / pyroglutamide (pE, 5-oxopropyle) / 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 biantennarios complejos fucosilados.

opnurasibum

opnurasib

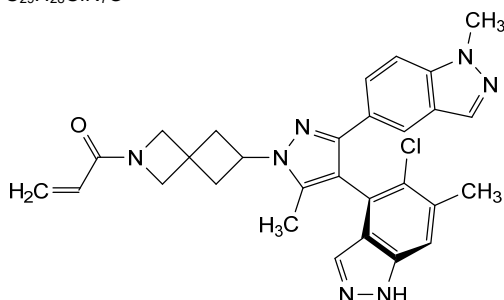
1-{{6-[(4*M*)-4-(5-chloro-6-methyl-1*H*-indazol-4-yl)-5-methyl-3-(1-methyl-1*H*-indazol-5-yl)-1*H*-pyrazol-1-yl]-2-azaspiro[3.3]heptan-2-yl}prop-2-en-1-one

opnurasib

1-{{6-[(4*M*)-4-(5-chloro-6-méthyl-1*H*-indazol-4-yl)-5-méthyl-3-(1-méthyl-1*H*-indazol-5-yl)-1*H*-pyrazol-1-yl]-2-azaspiro[3.3]heptan-2-yl}prop-2-èn-1-one

opnurasib

1-{{6-[(4*M*)-4-(5-cloro-6-metil-1*H*-indazol-4-il)-5-metil-3-(1-metil-1*H*-indazol-5-il)-1*H*-pirazol-1-il]-2-azaspiro[3.3]heptan-2-il}prop-2-en-1-ona

C₂₉H₂₈ClN₇O

orforglipronum

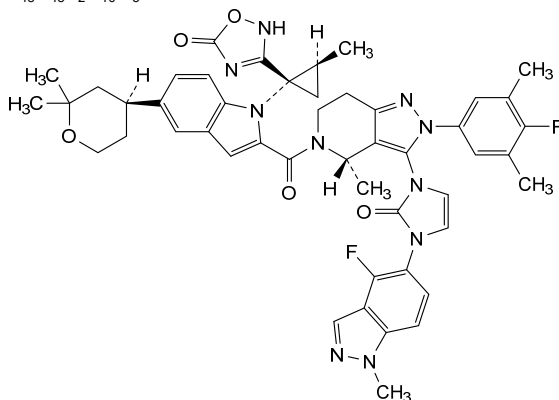
orforglipron

(3⁴*S*,6¹*S*,6²*S*)-5⁵-[(4*S*)-2,2-dimethylloxan-4-yl]-1⁴-fluoro-3²-(4-fluoro-3,5-dimethylphenyl)-1¹,3⁴,6²-trimethyl-3²,3⁴,3⁶,3⁷-tetrahydro-1¹*H*,2²*H*-3(3,5)-pyrazolo[4,3-*c*]pyridina-1(5)-indazola-5(2,1)-indola-7(3)-[1,2,4]oxadiazola-2(1,3)-imidazola-6(1,1)-cyclopropanaheptaphane-2²,4,7²(7²*H*)-trione

orforglipron (3⁴S,6¹S,6²S)-5⁵-[(4S)-2,2-diméthyloxan-4-yl]-1⁴-fluoro-3²-(4-fluoro-3,5-diméthylphényl)-1¹,3⁴,6²-triméthyl-3²,3⁴,3⁶,3⁷-tétrahydro-1¹H,2²H-3(3,5)-pirazolo[4,3-c]pyridina-1(5)-indazola-5(2,1)-indola-7(3)-[1,2,4]oxadiazola-2(1,3)-imidazola-6(1,1)-cyclopropanaheptaphane-2²,4,7⁵(7²H)-trione

orforgliprón (3⁴S,6¹S,6²S)-5⁵-[(4S)-2,2-dimetiloxan-4-il]-1⁴-fluoro-3²-(4-fluoro-3,5-dimetilfenil)-1¹,3⁴,6²-trimetil-3²,3⁴,3⁶,3⁷-tetrahidro-1¹H,2²H-3(3,5)-pirazolo[4,3-c]piridina-1(5)-indazola-5(2,1)-indola-7(3)-[1,2,4]oxadiazola-2(1,3)-imidazola-6(1,1)-ciclopropanaheptafano-2²,4,7⁵(7²H)-triona

C₄₈H₄₈F₂N₁₀O₅



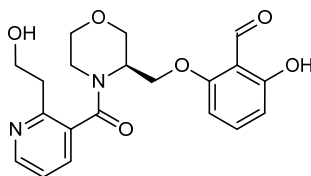
osivelotorum

osivelotor 2-hydroxy-6-[[[(3S)-4-[[2-(2-hydroxyethyl)pyridin-3-yl]carbonyl]morpholin-3-yl]methoxy]benzaldehyde

osivélotor 2-hydroxy-6-[[[(3S)-4-[[2-(2-hydroxyéthyl)pyridin-3-yl]carbonyl]morpholin-3-yl]méthoxy]benzaldehyde

osivelotor 2-hidroxi-6-[[[(3S)-4-[[2-(2-hidroxiétel)piridin-3-il]carbonil]morfolin-3-il]metoxi]benzalhedo

C₂₀H₂₂N₂O₆



ozekibartum

ozekibart

only-heavy-chain immunoglobulin G1, anti-[*Homo sapiens* TNFRSF10B (TNF receptor superfamily member 10B, death receptor 5, DR5, TNF-related apoptosis-inducing ligand TRAIL receptor 2, TRAILR2, TRAIL-R2, TR-2, CD262)], humanized monoclonal antibody, monospecific, tetravalent, agonist; gamma1 heavy chain humanized (1-480) [VH humanized (*Homo sapiens* IGHV3-23*01 (82.5%) -(IGHD) -IGHJ4*01 (91.7%), CDR-IMGT [8.8.16] (26-33,51-58,97-112))] (1-123) -6-mer bis(bisglycyl-seryl linker (124-129) -[VH humanized

(*Homo sapiens* IGHV3-23*01 (82.5%) -(IGHD) -IGHJ4*01 (91.7%), CDR-IMGT [8.8.16] (155-162.180-187.226-241)) (80-252) -4-mer tetraglycyl linker (253-256) -*Homo sapiens* IGHG1*01, h-CH2-CH3, G1m1 CH3 D12, L14, G1v65 CH2 del(E1.4, L1.3, L1.2) (hinge 6-15 (257-266), CH2 (E1.4, L1.3, L1.2)>del 268^269 (267-373), CH3 D12 (389), L14 (391) (374-478), CHS (479-480)) (257-480)]; dimer (262-262":265-265")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

ozékibart

immunoglobuline G1 à chaînes lourdes seulement, anti-[*Homo sapiens* TNFRSF10B (membre 10B de la superfamille des récepteurs du TNF, récepteur de mort 5, DR5, récepteur 2 du ligand TRAIL apparenté au TNF induisant l'apoptose, TRAIL-R2, TR2, CD262)], anticorps monoclonal humanisé, monospécifique, tétravalent, agoniste; chaîne lourde gamma1 humanisée (1-480) [VH humanisé (*Homo sapiens* IGHV3-23*01 (82.5%) -(IGHD) -IGHJ4*01 (91.7%), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -6-mer bis(bisglycyl-séryl linker (124-129) -[VH humanisé (*Homo sapiens* IGHV3-23*01 (82.5%) -(IGHD) -IGHJ4*01 (91.7%), CDR-IMGT [8.8.16] (155-162.180-187.226-241)) (80-252) -4-mer tétraglycyl linker (253-256) -*Homo sapiens* IGHG1*01, h-CH2-CH3, G1m1 CH3 D12, L14, G1v65 CH2 del(E1.4, L1.3, L1.2) (charnière 6-15 (257-266), CH2 (E1.4, L1.3, L1.2)>del 268^269 (267-373), CH3 D12 (389), L14 (391) (374-478), CHS (479-480)) (257-480)]; dimère (262-262":265-265")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

ozekibart

immunoglobulina G1 de cadena pesada única, anti-[*Homo sapiens* TNFRSF10B (miembro 10B de la superfamilia de los receptores del TNF, receptor de muerte 5, DR5, receptor 2 del ligando TRAIL relacionado con TNF que induce la apoptosis, TRAIL-R2, TR2, CD262)], anticuerpo monoclonal humanizado, monospécífico, tetraivalente, agonista; cadena pesada gamma1 humanizada (1-480) [VH humanizado (*Homo sapiens* IGHV3-23*01 (82.5%) -(IGHD) -IGHJ4*01 (91.7%), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -6-mer bis(bisglicil-séryl linker (124-129) -[VH humanizado (*Homo sapiens* IGHV3-23*01 (82.5%) -(IGHD) -IGHJ4*01 (91.7%), CDR-IMGT [8.8.16] (155-162.180-187.226-241)) (80-252) -4-mer tetraglicil enlace (253-256) -*Homo sapiens* IGHG1*01, h-CH2-CH3, G1m1 CH3 D12, L14, G1v65 CH2 del(E1.4, L1.3, L1.2) (bisagra 6-15 (257-266), CH2 (E1.4, L1.3, L1.2)>del 268^269 (267-373), CH3 D12 (389), L14 (391) (374-478), CHS (479-480)) (257-480)]; dímero (262-262":265-265")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

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EVQLLESQGG EVQPGGSLRL SCAASGLTFP NYGMGWRQQA PGKEREFVSA 50
IYWSGGTVVY AESVKGKRFTEI SRDIAKNTLY LQMSSSLRAED TAVVYCAVTEI 100
RGAATQTWKY DYWGQGLTWT VKPGGSGGSE VQLLESQGG E VQPGGSLRLS 150
CAASGLTFPN YGMGWRQAP GKEREFSVAI YWSGGTVVYA ESKGRFTIS 200
RDNIAKNTLYL QMSSSLRAEDT AVVYCAVTIR GAATQTWKYD YWGQGLTWTV 250
KPGGGGDKTH TCPPCPAPGG PSVFLFPPKP KDTLMISRTP EVTCCVVDDVS 300
HEDPEVKFNW YVDGVEVHNA KTKPREEQYN STYRVVSVLT VLHQDQWLNGK 350
EYKCKVSNKA LPAPIEKTTIS KAKGQPREPQ VYTLPPSRDE LTKNQVSLTC 400
LVKGFYPSDI AVEWESNGQP ENNYKTTTPPV LDSDGSFFLY SKLTVDKSRW 450
QQGNVFCSV MHEALHNYT QKSLSLSPGK 480
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Post-translational modifications

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
 Intra-H (C23-C104) 22-96 151-225 294-354 400-458
 22"-96" 151"-225" 294"-354" 400"-458"
 Inter-H-H (h 11, h 14) 262-262" 265-265"

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

H CH2 N84.4: 330, 330"

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

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
 H CHSK2: 480, 480"

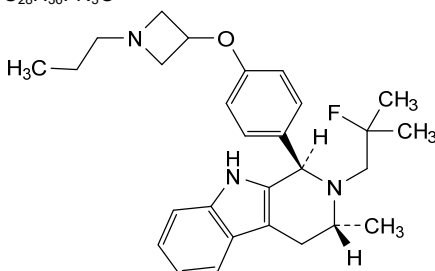
palazestrantum

palazestrant (1*R*,3*R*)-2-(2-fluoro-2-méthylpropyl)-3-méthyl-1-{4-[(1-propylazétidin-3-yl)oxy]phényl}-2,3,4,9-tétrahydro-1*H*-pyrido[3,4-*b*]indole

palazestrant (1*R*,3*R*)-2-(2-fluoro-2-méthylpropyl)-3-méthyl-1-{4-[(1-propylazétidin-3-yl)oxy]phényl}-2,3,4,9-tétrahydro-1*H*-pyrido[3,4-*b*]indole

palazestrant (1*R*,3*R*)-2-(2-fluoro-2-metilpropil)-3-metil-1-{4-[(1-propilazetidín-3-il)oxil]fenil}-2,3,4,9-tetrahidro-1*H*-pirido[3,4-*b*]indol

C₂₈H₃₆FN₃O

**patecibartum #**

patecibart

immunoglobulin G4-kappa, anti-[*Homo sapiens* EDNRA (endothelin receptor type A, ETA, ET-A, ETA-R, ET-AR)], humanized monoclonal antibody;

gamma4 heavy chain humanized (1-446) [VH (*Homo sapiens* IGHV2-5*09 (88.9%) -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [10.7.12] (26-35.53-59.98-109)) (1-120) -*Homo sapiens* IGHG4*01, nG4m(a) CH2 L92,G4v5 h P10, G4v4 CH2 A1.3, A1.2 (CH1 (121-218), hinge 1-12 S10>P (228) (219-230), CH2 F1.3>A (234), L1.2>A (235), L92 (309) (231-340), CH3 (341-445), CHS K2>del (446)) (121-446)], (134-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV6-21*02 (90.5%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (226-226":229-229")-bisdisulfide, produced in Chinese Hamster Ovary (CHO) Cell line, glycoform alfa

patécibart

immunoglobuline G4-kappa, anti-[*Homo sapiens* EDNRA (récepteur de type A de l'endothéline, ETA, ET-A, ETA-R, ET-AR)], anticorps monoclonal humanisé;

chaîne lourde gamma4 humanisée (1-446) [VH (*Homo sapiens* IGHV2-5*09 (88.9%) -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [10.7.12] (26-35.53-59.98-109)) (1-120) -*Homo sapiens* IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10, G4v4 CH2 A1.3, A1.2 (CH1 (121-218), charnière 1-12 S10>P (228) (219-230), CH2 F1.3>A (234), L1.2>A (235), L92 (309) (231-340), CH3 (341-445), CHS K2>del (446)) (121-446)], (134-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV6-21*02 (90.5%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (226-226":229-229")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

patecibart

immunoglobulina G4-kappa, anti-[*Homo sapiens* EDNRA (receptor de tipo A de la endotelina, ETA, ET-A, ETA-R, ET-AR)], anticuerpo monoclonal humanizado;

cadena pesada gamma4 humanizada (1-446) [VH (*Homo sapiens* IGHV2-5*09 (88.9%) -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [10.7.12] (26-35.53-59.98-109)) (1-120) -*Homo sapiens* IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10, G4v4 CH2 A1.3, A1.2 (CH1 (121-218), bisagra 1-12 S10>P (228) (219-230), CH2 F1.3>A (234), L1.2>A (235), L92 (309) (231-340), CH3 (341-445), CHS K2>del (446)) (121-446)], (134-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV6-21*02 (90.5%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (226-226":229-229")-bisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

QVTLKESGPT LVKPTQTLTL TCTFSGFSLT TSGLGVAVIR QPPGKALEWL	50
AHIWSDGDIR YYPALKNRLT ITKDTSKNQV VLTMTNMDPV DTATYYCAHM	100
KDDSLYFDNW GQGTLVTVSS ASTKGPSVFP LAPCSRSTSE STAALGCLVK	150
DYFPEPVTVS WNSGALTSVGV HTFPAVLQSS GLYLSVSVVT VPSSSLGTTK	200
YTCNVDHKPS NTKVDKRVES KYGPPCPPCP APEAAGGPSV FLFPPKPKDT	250
LMISRTP EVT CVVVDVSQED PEVQFNWYVD GVEVHNAKTK PREEQFNSTY	300
RVVSVLTVLH QDWLNGKEYK CKVSNKGLPS SIEKTISKAK GQPREPQVYT	350
LPPSQEEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTTPVLDL	400
DGSFFLYSRL TVDKSRWQEG NVFSCSVME ALHNHYTQKS LLSLSLG	446

Light chain / Chaîne légère / Cadena ligera

EIVLTQSPDF QSVTPKEKVT ITCRASQNIQ TSIHWYQKPK DQYPKLLIKY	50
ASKSISGVPS RFSGSGSGTD FTLLINSLEA EDAATYYCQH SYSPFPTFGQ	100
GTKVETKRTV AAPSVEIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQKWV	150
DNALQSGNSQ ESVTEQDSKD STYLSLSTLT LSKADYEKHK VYACEVTHQG	200
LSSPVTKSFN RGEK	214

Post-translational modifications

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

Intra-H (C23-C104)	22"-97"	147"-203"	261-321	367-425
	22"-97"	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-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutamínilo 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 biantenaricos complejos fucosilados.

pegfosimerum manganeseum

pegfosimer manganese

polymer nanoparticles synthesized from tetramethyl P,P'-[1,7-bis(triethoxysilyl)heptane-4,4-diy]bisphosphonate (~52 molecules per particle on average) by

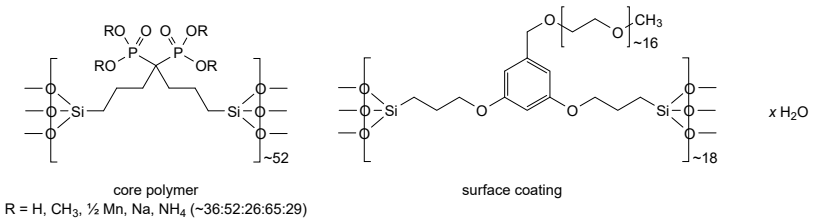
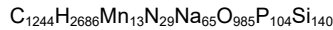
- (i) hydrolysis of the triethoxysilyl groups and ~75% of the dimethyl phosphonate groups and condensation of the resulting bis-silanetriol to a polymeric network with Si-O-Si linkages,
- (ii) coating of the core particles by hydrolysis of α-({3,5-bis[3-(triethoxysilyl)propoxy]phenyl}methyl)-ω-methoxypoly(oxyethylene) (~18 molecules per particle on average) and condensation of the resulting silanetriol groups with surficial silanol groups, and
- (iii) addition of a manganese(2+) salt to form hydrated polymeric ammonium manganese(2+) sodium (≈ 29:13:65) phosphonate complexes

pegfosimère manganèse

nanoparticules polymériques synthétisées à partir de *P,P'*-[1,7-bis(triéthoxysilyl)heptane-4,4-diyl]bisphosphonate de tétraméthyle (~52 molécules par particule en moyenne) par
 (i) hydrolyse des groupes triéthoxysilyle et ~75 % des groupes phosphonate de diméthyle et condensation des groupes silanetriol résultants en un réseau polymérique avec des liaisons Si-O-Si,
 (ii) enrobage de ce noyau de particule par hydrolyse de α -({3,5-bis[3-(triéthoxysilyl)propoxy]phényl)méthyl}- ω -méthoxypoly(oxyéthylène) (~18 molécules par particule en moyenne) et condensation des groupes silanetriol résultants avec des groupes silanol superficiels, et
 (iii) addition d'un sel de manganèse(2+) pour former des complexes de polymères hydratés sous forme de phosphonate d'ammonium et de manganèse(2+) et de sodium (\approx 29:13:65)

pegfosímero manganeso

nanopartículas poliméricas sintetizadas a partir de *P,P'*-[1,7-bis(trietoxisilil)heptano-4,4-diil]bisfosfonato de tetrametilo (~52 moléculas por partícula por término medio) por
 (i) hidrólisis de los grupos trietoxisilil y ~75 % de los grupos fosfonato de dimetilo y condensación de los grupos silanetriol resultantes en una red polimérica con las uniones Si-O-Si,
 (ii) revestimiento de este núcleo de partícula por hidrólisis de α -({3,5-bis[3-(trietoxisilil)propoxi]fenil)metil}- ω -metoxipoli(oxietileno) (~18 moléculas por partícula por término medio) y condensación de los grupos silanetriol resultantes con los grupos silanol superficiales, y
 (iii) adición de una sal de manganeso(2+) para formar los complejos de polímeros hidratados bajo la forma de fosfonato de amonio y de manganeso(2+) y de sodio (\approx 29:13:65)



pegtarazimodum

pegtarazimod

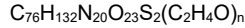
3-{2-[ω -(L-isoleucyl-L-alanyl-L-leucyl-L-isoleucyl-L-leucyl-L- α -glutamyl-L-prolyl-L-isoleucyl-L-cysteinyl-L-cysteinyl-L-glutamyl-L- α -glutamyl-L-arginyl-L-alanyl-L-alanyl-amino)poly(oxyethylene)- α -yl]ethyl}propanoic acid

pegtarazimod

acide 3-{2-[ω -(L-isoleucyl-L-alanyl-L-leucyl-L-isoleucyl-L-leucyl-L- α -glutamyl-L-prolyl-L-isoleucyl-L-cystéinyl-L-cystéinyl-L-glutamyl-L- α -glutamyl-L-arginyl-L-alanyl-L-alanyl-amino)poly(oxyéthylène)- α -yl]éthyl}propanoïque

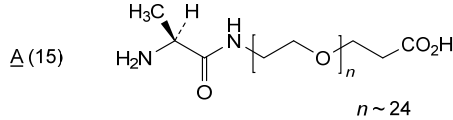
pegтаразимод

ácido 3-{2-[ω-(L-isoleucil-L-alanil-L-leucil-L-isoleucil-L-leucil-L-α-glutamil-L-prolil-L-isoleucil-L-cisteinil-L-cisteinil-L-glutaminil-L-α-glutamil-L-arginil-L-alanil-L-alanilamino)poli(oxietileno)-α-ijetil}propanoico



IALILEPICC QERAA 15

Modified residues / Résidus modifiés / Restos modificados



picankibartum #
picankibart

immunoglobulin G1-kappa , anti-[*Homo sapiens* IL23A (interleukin 23 subunit alpha; IL-23A, IL-23 subunit p19, IL23p19)], humanized monoclonal antibody; gamma1 heavy chain humanized (1-444) [VH (*Homo sapiens* IGHV1-2*02 (93.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.8] (27-32.51-58.97-104)) (1-115) -*Homo sapiens*IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, G1v21 CH2 Y15.1, T16, E18 (CH1 K120 (212) (116-213), hinge 1-15 (214-228), CH2M15.1>Y (250), S16>T (252), T18>E (254) (229-338), CH3 D12 (354), L14 (356) (339-443), CHS K2>del (444)) (116-444)], (218-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (88.4%) -IGKJ2*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dimer (224-224''-227-227'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1SV lacking the glutamine synthetase (GS-KO) gene, glycoform alfa

picankibart

immunoglobuline G1-kappa, anti-[*Homo sapiens* IL23A (interleukine 23 sous-unité alpha, IL-23A, IL-23 sous-unité p19, IL23p19)], anticorps monoclonal humanisé; chaîne lourde gamma1 humanisée (1-444) [VH (*Homo sapiens* IGHV1-2*02 (93.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.8] (26-33.51-58.97-104)) (1-115) -*Homo sapiens*IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, G1v21 CH2 Y15.1, T16, E18 (CH1 K120 (212) (116-213), charnière 1-15 (214-228), CH2 M15.1>Y (250), S16>T (252), T18>E (254) (229-338), CH3 D12 (354), L14 (356) (339-443), CHS K2>del (444)) (116-444)], (218-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (88.4%) -IGKJ2*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dimère (224-224''-227-227'')-bisdisulfure; produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1SV ne présentant pas le gène de la glutamine synthétase (GS-KO), glycoforme alfa

picankibart

inmunoglobulina G1-kappa, anti-[*Homo sapiens* IL23A (interleukina 23 subunidad alfa, IL-23A, IL-23 subunidad p19, IL23p19)], anticuerpo monoclonal humanizado;

cadena pesada gamma1 humanizada (1-444) [VH (*Homo sapiens* IGHV1-2*02 (93.9%) -(IGHD) - IGHJ4*01 (100%), CDR-IMGT [8.8.8] (26-33.51-58.97-104)) (1-115) -*Homo sapiens* IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, G1v21 CH2 Y15.1, T16, E18 (CH1 K120 (212) (116-213), bisagra 1-15 (214-228), CH2 M15.1>Y (250), S16>T (252), T18>E (254) (229-338), CH3 D12 (354), L14 (356) (339-443), CHS K2>del (444)) (116-444)], (218-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (88.4%) -IGKJ2*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dímero (224-224''-227-227''')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1SV en ausencia del gen glutamina sintetasa (GS-KO), glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

QVQLVQSGAE VKKFGASVKV SCKASGYTFT SYLMHWVROA PGQGLEWMGY 50
 INFYNEGTNY AQKFEQGRVTM TRDTSISTAY MELSLRLSDD TAVIYCARNW 100
 DLPYWGQGTLL VTVSSASTKG PSVFFLAPSS KSTSGGTAAL GCLVKDYFPE 150
 PVTVSWNSGA LTSVGHVTFPA VLQSSGLGYL SSVVTVPSSS LGTQTYICNV 200
 NHKPSNTKVD KRVPEKSCDK THTCPPCPAP ELLGGPSVFL FPPKPKDTLY 250
 ITREPEVTCV VVDVSHEDPE VKFNWYVDGV EVHNAKTKPR EEQYNSTYRV 300
 VSVLTVLHQD WLNKKEYKCK VSNKALPAPI EKTISKAKGQ PREPQVYTL 350
 PSRDELTKNQ VSLTCLVKG FYPDSIAVWE SNGQPENNYK TTPPVLDSDG 400
 SFFLYSLKLV DKSRRQQGNV FSCSVMHEAL HNHYTQKSL SLP 444

Light chain / Chaîne légère / Cadena ligera

DIQMTQSPSS LSASVGDRTV ITCRASQSI DYLHWYQQKPK GKAPKLLIKY 50
 ASQMSGVPV RFGSGSGSD FTLTISLQF EDFATYYCQ GHSPFTFGQ 100
 GTKLEIKRTV AAPSIVFIFP SDEQLKSGTA SVVCLLNIFY PREAKVQMKV 150
 DNALQSGNSQ ESVTEQDSKD STYLSLSTLT LSKADYEKHK VYACEVTHQG 200
 LSSPVTKSFN RGE 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-oxopropyl) / pyroglutamyle (pE, 5-oxopropyle) / piroglutamilo (pE, 5-oxopropilo)
 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 biantenarijos complejos fucosilados

pitozinameranum

pitozinameran

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 sub-lineage XBB.1.16; based upon GISAID: EPI_ISL_16835403), flanked by 5' and 3' untranslated regions and a 3' polyadenylation (polyA) tail; contains N¹-methylpseudouridine instead of uridine (*all-U>m¹U*)

pitozinaméran

ARN messenger (ARNm), protégé d'une coiffe en 5', codant la séquence entière aux codons optimisés d'un variant à la conformation stabilisée avant fusion (K982P et V983P) de la glycoprotéine de spicule (S) du SARS-CoV-2 (coronavirus du syndrome respiratoire aigu sévère 2) (sous-lignée Omicron XBB.1.16; d'après GISAID: EPI_ISL_16835403), flanquée de régions non traduites en 5' et 3' et d'une queue polyadénylation (polyA) en 3'; contient de la N¹-méthylpseudouridine au lieu de l'uridine (*tout-U>m¹U*)

pitozinamerán

ARN mensajero (ARNm), protegido en 5', que codifica, para la secuencia completa con codones optimizados, de una variante estabilizada en la conformación pre-fusión (K982P y V983P) de la glicoproteína de la espícula (S) del SARS-Cov-2 (coronavirus 2 del síndrome respiratorio agudo severo) (sublinaje XBB.1.16 de Omicron; basado en GISAID: EPI_ISL_16835403), flanqueado por regiones 5' y 3' no traducidas y una cola poliadenilación (poliA) en 3'; contiene *N*¹-metilpseudouridina en lugar de uridina (*todo-U*>*m*¹Ψ)

plixorafenibum

plixorafenib

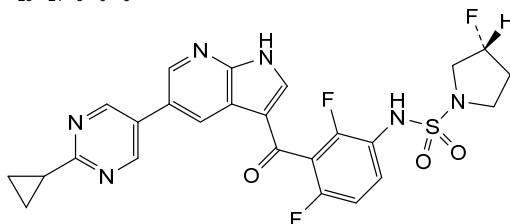
(8^{3R})-5²,5⁶,8³-trifluoro-3¹H-7λ⁶-thia-6-aza-3(5,3)-pyrrolo[2,3-*b*]pyridina-2(2,5)-pyrimidina-8(1)-pyrrolidina-5(1,3)-benzena-1(1)-cyclopropanaoctaphane-4,7,7-trione

plixorafénib

(8^{3R})-5²,5⁶,8³-trifluoro-3¹H-7λ⁶-thia-6-aza-3(5,3)-pyrrolo[2,3-*b*]pyridina-2(2,5)-pyrimidina-8(1)-pyrrolidina-5(1,3)-benzéna-1(1)-cyclopropanaoctaphane-4,7,7-trione

plixorafenib

(8^{3R})-5²,5⁶,8³-trifluoro-3¹H-7λ⁶-tia-6-aza-3(5,3)-pirrolo[2,3-*b*]piridina-2(2,5)-pirimidina-8(1)-pirrolidina-5(1,3)-bencena-1(1)-ciclopropanaoctafano-4,7,7-triona

C₂₅H₂₁F₃N₆O₃S**pocenbrodibum**

pocenbrodib

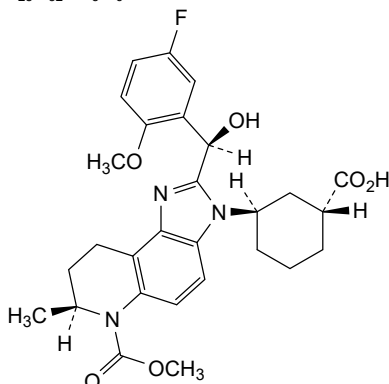
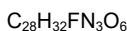
(1*R*,3*R*)-3-((7*S*)-2-[(*R*)-(5-fluoro-2-methoxyphenyl)(hydroxy)methyl]-6-(methoxycarbonyl)-7-methyl-6,7,8,9-tetrahydro-3*H*-imidazo[4,5-*f*]quinolin-3-yl)cyclohexane-1-carboxylic acid

pocenbrodib

ácide (1*R*,3*R*)-3-((7*S*)-2-[(*R*)-(5-fluoro-2-méthoxyphényl)(hydroxy)méthyl]-6-(méthoxycarbonyl)-7-méthyl-6,7,8,9-tétrahydro-3*H*-imidazo[4,5-*f*]quinolin-3-yl)cyclohexane-1-carboxylique

pocenbrodib

ácido (1*R*,3*R*)-3-((7*S*)-2-[(*R*)-(5-fluoro-2-metoxifenil)(hidroxi)metil]-6-(metoxicarbonil)-7-metil-6,7,8,9-tetrahydro-3*H*-imidazo[4,5-*f*]quinolin-3-il)ciclohexano-1-carboxílico

**pralurbactamum**

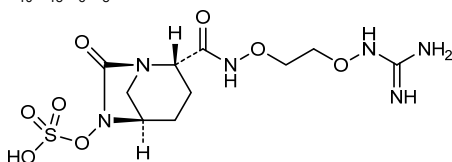
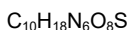
pralurbactam

(1*R*,2*S*,5*R*)-2-[[2-(guanidinoxy)ethoxy]carbamoyl]-7-oxo-1,6-diazabicyclo[3.2.1]octan-6-yl hydrogen sulfate

pralurbactam

hydrogénosulfate de (1*R*,2*S*,5*R*)-2-[[2-[(carbamimidoylamino)oxy]éthoxy]carbamoyl]-7-oxo-1,6-diazabicyclo[3.2.1]octan-6-yle

pralurbactam

hidrogenosulfato de (1*R*,2*S*,5*R*)-2-[[2-[(carbamimidoylamino)oxi]etoxi]carbamoyl]-7-oxo-1,6-diazabicyclo[3.2.1]octan-6-ilo**prizoncabtagemum autoleucelum #**

prizoncabtogene autoleucel

autologous T lymphocytes obtained from peripheral blood lymphocytes by leukapheresis, transduced with a self-inactivating, non-replicating lentiviral vector, encoding a bispecific chimeric antigen receptor targeting CD19 and CD20. The expressed transgene comprises a CD8 α leader sequence, anti-CD19 and anti-CD20 single chain fragment variable (scFv) (derived from FMC-63 and *ofatumumab*, respectively), an IgG4 hinge and a CD28 transmembrane region, a 4-1BB and a CD3 ζ signalling domain, and is under control of the elongation factor 1 alpha (EF1 α) short promoter. The construct is flanked by 5' and 3' long terminal repeats (LTRs) and also contains a ψ packaging signal, a Rev response element (RRE), a central polypurine tract (cPPT) sequence and a mutated Woodchuck hepatitis virus posttranscriptional regulatory element (WPRE). The vector is pseudotyped with vesicular stomatitis virus (VSV) G envelope protein. The leukapheresis material is enriched for CD4/CD8 T lymphocytes by positive

- immunoselection, activated by CD3 and CD28 agonists and transduced with the lentiviral vector. The cells are then expanded in media with serum replacement and interleukin 2 (IL-2). The T lymphocytes ($\geq 95\%$) are positive for the transgene ($\geq 10\%$ CAR positive), and secrete interferon gamma in response to CD19 and CD20 expressing tumour cell lines
- prizloncabtagène autoleucel lymphocytes T autologues obtenus à partir de lymphocytes de sang périphérique par leucaphérèse, transduits avec un vecteur lentiviral auto-inactivant et non répliquant, codant un récepteur antigénique chimérique bispécifique ciblant CD19 et CD20. Le transgène exprimé comprend une séquence de tête CD8 α , un fragment variable à chaîne unique (scFv) anti-CD19 et anti-CD20 (dérivé de FMC-63 et d'*ofatumumab*, respectivement), une charnière IgG4 et une région transmembranaire CD28, un domaine de signalisation 4-1BB et CD3 ζ , et est sous le contrôle du promoteur court du facteur d'élongation 1 alpha (EF1 α). La construction est flanquée de répétitions longues terminales (LTR) en 5' et 3' et contient également un signal d'encapsulation ψ , un élément de réponse Rev (RRE), une séquence du tractus polypurine central (cPPT) et un élément régulateur post-transcriptionnel (WPRE) muté du virus de l'hépatite de Woodchuck. Le vecteur est pseudotypé avec la protéine d'enveloppe G du virus de la stomatite vésiculaire (VSV). Le matériel de leucaphérèse est enrichi en lymphocytes T CD4/CD8 par immunosélection positive, activé par des agonistes CD3 et CD28 et transduit avec le vecteur lentiviral. Les cellules sont ensuite développées dans un milieu avec remplacement du sérum et interleukine 2 (IL-2). Les lymphocytes T ($\geq 95\%$) sont positifs pour le transgène ($\geq 10\%$ CAR positif), et sécrètent de l'interféron gamma en réponse à des lignées de cellules tumorales exprimant CD19 et CD20
- prizloncabtagén autoleucel linfocitos T autólogos obtenidos de linfocitos de sangre periférica mediante leucoaféresis, transducidos con un vector lentiviral auto inactivante, no replicativo, que codifica para un receptor de antígenos quimérico biespecífico dirigido a CD19 y CD20. El transgén expresado contiene una secuencia líder de CD8 α , un fragmento variable de cadena sencilla (scFv) anti-CD19 y otro anti-CD20 (derivados de FMC-63 y *ofatumumab*, respectivamente), una bisagra IgG4 y una región transmembrana de CD28, un dominio de señalización 4-1BB y CD3 ζ , y está bajo el control del promotor corto del factor de elongación 1 alfa (EF1 α). El constructo está flanqueado por repeticiones terminales largas (LTRs) en 5' y 3' y también contiene una señal de empaquetamiento ψ , un elemento de respuesta Rev (RRE), una secuencia de tracto de polipurina central (cPPT) y un elemento regulador post-transcripcional del virus de la hepatitis de la marmota (WPRE) mutado. El vector está seudotipado con la proteína G de la envuelta del virus de la estomatitis vesicular (VSV). El material de leucoaféresis se enriquece para linfocitos T CD4/CD8 mediante inmunoselección positiva, se activa mediante agonistas de CD3 y CD28 y se transduce con el vector lentiviral. Las células son después expandidas en medio con sustituto de suero e interleuquina 2 (IL-2). Los linfocitos T ($\geq 95\%$) son positivos para el transgén ($\geq 10\%$ positivos para el CAR) y secretan interferón gamma en respuesta a líneas de células tumorales que expresan CD19 y CD20

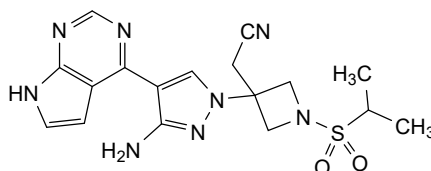
pumecitinibum

pumecitinib {3-[3-amino-4-(7*H*-pyrrolo[2,3-*d*]pyrimidin-4-yl)-1*H*-pyrazol-1-yl]-1-(propane-2-sulfonyl)azetididin-3-yl}acetonitrile

pumécitinib {3-[3-amino-4-(7*H*-pyrrolo[2,3-*d*]pyrimidin-4-yl)-1*H*-pyrazol-1-yl]-1-(propane-2-sulfonyl)azétididin-3-yl}acetonitrile

pumecitinib {3-[3-amino-4-(7*H*-pirrolo[2,3-*d*]pirimidin-4-il)-1*H*-pirazol-1-il]-1-(propano-2-sulfonyl)azetididin-3-il}acetonitrile

C₁₇H₂₀N₈O₂S

**puxitatugum #**

puxitatug

immunoglobulin G1-kappa , anti-[*Homo sapiens* VTCN1(V-set domain containing T cell activation inhibitor 1, B7 family member H4, B7H4, B7-H4)], *Homo sapiens* monoclonal antibody; gamma1 heavy chain *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV4-34*01 (95.9%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.7.11] (26-33.51-57.96-106)) (1-117) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, E12, M14 (CH1 R120 (214) (118-215), hinge 1-15 (216-230), CH2 (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-17*01 (96.8%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dimer (226-226":229-229")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, glycoform alfa

puxitatug

immunoglobuline G1-kappa, anti-[*Homo sapiens* VTCN1 (inhibiteur 1 de l'activation des cellules T contenant un domaine V-set, membre H4 de la famille B7, B7-H4, B7H4)], anticorps monoclonal *Homo sapiens*; chaîne lourde gamma1 *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV4-34*01 (95.9%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.7.11] (26-33.51-57.96-106)) (1-117) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, E12, M14 (CH1 R120 (214) (118-215), charnière 1-15 (216-230), CH2 (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-214')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-17*01 (96.8%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dimère (226-226":229-229")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1, glycoforme alfa

puxitatug

inmunoglobulina G1-kappa, anti-[*Homo sapiens* VTCN1 (inhibidor 1 de la activación de las células T que contiene un dominio V-set, miembro H4 de la familia B7, B7-H4, B7H4)], anticuerpo monoclonal *Homo sapiens*;
 cadena pesada gamma1 *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV4-34*01 (95.9%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.7.11] (26-33.51-57.96-106)) (1-117) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, E12, M14 (CH1 R120 (214) (118-215), bisagra 1-15 (216-230), CH2 (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-214')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-17*01 (96.8%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dímero (226-226''-229-229'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular derivada de CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

QVQLQQWGAG LLKPSETLSL ACTVYGGSF S GYYWNWIRQP PGKGLEWIGE 50
 INHSGSTSYN PSLKSRVTIS VDTSKNQFSL KLSSVTAADT AVYYCARVLY 100
 NWNVDSWGQG TLVTVSSAST KGPSVFPPLAP SSKSTSGGTA ALGCLVKDYF 150
 PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVTVTPS SSLGTQTYIC 200
 NVNHHKPSNTK VDKRVEPKSC DKHTHTCPPCP APELLGGPSV FLFPPKPKDT 250
 LMSIRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300
 RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTIKAK GQPREPQVY 350
 LPPSREEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTTPPVLD 400
 DGSFFLYSKL TVDKSRWQQG NWFSCSVME ALHNHYTQKS LSLSPGK 447

Light chain / Chaîne légère / Cadena ligera

DIQMTQSPSS LSASVGDRTV ITCRASQDIR NDVGWYQQKPK GKAPKRLIYA 50
 ASRLQSGVPS RFGSGSGSTE FTLTISLQPF EDFATYYCQLQ HNSYPRTFGQ 100
 GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWVK 150
 DNALQSGNSQ ESVTEQDSKD STYLSLSTLT LSKADYERHK VYACEVTHGG 200
 LSPSPVTKSFN RGEK 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-oxoprolylo)
 H VH Q1: 1, 1"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
 H VH CDR2 N57: 52, 52"

Deamidation, no glycosylation / déamidation, pas de glycosylation / desamidación, sin 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 biantenaricos complejos fucosilados

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

puxitatugum samrotecanum #

puxitatug samrotecan immunoglobulin G1-kappa , anti-[*Homo sapiens* VTCN1 (V-set domain containing T cell activation inhibitor 1, B7 family member H4, B7H4, B7-H4)], *Homo sapiens* monoclonal antibody; conjugated to a topoisomerase I inhibitor; gamma1 heavy chain *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV4-34*01 (95.9%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.7.11] (26-33.51-57.96-106)) (1-117) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, E12, M14 (CH1 R120 (214) (118-215), hinge 1-15 (216-230), CH2 (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-17*01 (96.8%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dimer (226-226":229-229")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, glycoform alfa; 220, 214', 220", 214"', 226, 226", 229, 229" -octakis (thioether) conjugated with *N*-[31-(3-mercapto-2,5-dioxo-3-pyrrolidinyl)-1,29-dioxo-4,7,10,13,16,19,22,25-octaoxa-28-azahentriacont-1-yl]-*L*-valyl-*N*-[(9*S*)-9-ethyl-2,3,9,10,13,15-hexahydro-9-hydroxy-10,13-dioxo-1*H*,12*H*-benzo[de]pyrano[3',4':6,7]indolizino[1,2-*b*]quinolin-4-yl]-*L*-alaninamide

puxitatug samrotécán immunoglobuline G1-kappa, anti-[*Homo sapiens* VTCN1 (inhibiteur 1 de l'activation des cellules T contenant un domaine V-set, membre H4 de la famille B7, B7-H4, B7H4)], anticorps monoclonal *Homo sapiens*; conjugué à un inhibiteur de la topoisomérase I; chaîne lourde gamma1 *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV4-34*01 (95.9%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.7.11] (26-33.51-57.96-106)) (1-117) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, E12, M14 (CH1 R120 (214) (118-215), charnière 1-15 (216-230), CH2 (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-214')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-17*01 (96.8%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dimère (226-226":229-229")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1, glycoforme alfa; 220, 214', 220", 214"', 226, 226", 229, 229" -octakis (thioéther) conjugué with *N*-[31-(3-mercapto-2,5-dioxo-3-pyrrolidinyl)-1,29-dioxo-4,7,10,13,16,19,22,25-octaoxa-28-azahentriacont-1-yl]-*L*-valyl-*N*-[(9*S*)-9-ethyl-2,3,9,10,13,15-hexahydro-9-hydroxy-10,13-dioxo-1*H*,12*H*-benzo[de]pyrano[3',4':6,7]indolizino[1,2-*b*]quinolin-4-yl]-*L*-alaninamide

puxitatug samrotécán inmunoglobulina G1-kappa, anti-[*Homo sapiens* VTCN1 (inhibidor 1 de la activación de las células T que contiene un dominio V-set, miembro H4 de la familia B7, B7-H4, B7H4)], anticuerpo monoclonal *Homo sapiens*; conjugado con un inhibidor de la topoisomerasa I; cadena pesada gamma1 *Homo sapiens* (1-447) [VH (*Homo sapiens* IGHV4-34*01 (95.9%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.7.11] (26-33.51-57.96-106)) (1-117) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, E12, M14 (CH1 R120 (214) (118-215), bisagra 1-15 (216-230), CH2 (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-214')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-17*01 (96.8%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo*

sapiens IGKC*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214''); dímero (226-226'':229-229'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular derivada de CHO-K1, forma glicosilada alfa; 220, 214', 220'', 214''', 226, 226'', 229, 229'' -octakis (tioéter) conjugado con *N*-[31-(3-mercapto-2,5-dioxo-3-pirrolidinil)-1,29-dioxo-4,7,10,13,16,19,22,25-octaoxa-28-azahentriacont-1-il]-*L*-valil-*N*-[(9*S*)-9-etil-2,3,9,10,13,15-hexahidro-9-hidroxi-10,13-dioxo-1*H*,12*H*-benzo[de]pirano[3',4':6,7]indolizino[1,2-*b*]quinolin-4-il]-*L*-alaninamida

Heavy chain / Chaîne lourde / Cadena pesada

DVQLQQWGAG LLKPSSETLSL ACTVYGGGSFS GYYWNWIRQP PGKGLEWIGE 50
 INHSGSTSYN PSLKSRVTIS VDTSKNQFSL KLSVTAADT AVYYCARVLY 100
 NWNVDSWGGQ TLVTVSSAST KGPSVFLPLAP SSKSTSGGTA ALGCLVKDYF 150
 PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC 200
 NVNHNKPSNTK VDKRVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT 250
 LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300
 RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT 350
 LPPSREEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTFPVLDL 400
 DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPGK 447

Light chain / Chaîne légère / Cadena ligera

DIQMTQSPSS LSASVGRVIT ITCRASQDIR NDVWGYQQKP GKAPKRLIYA 50
 ASRLQSGVPS RFGSGSGSTE FTLTISLQEP EDFATYCYLQ HNSYPTFGQ 100
 PKYVEIKRIV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQMKV 150
 DNALQSGNSQ ESVTEQDSKD STYSLSSLT LSKADYKHK VYACEVTHQG 200
 LSSPVTKSFN RGEK 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''

*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-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal

Q > pyroglutamyl (pE, 5-oxopropyl) / pyroglutamyle (pE, 5-oxopropyle) / piroglutamilo (pE, 5-oxopropilo)
 H VH QI: 1, 1''

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

H VH N57: 52, 52''

Deamidation, no glycosylation / déamidation, pas de glycosylation / desamidación, sin glicosilación

H CH2 N84.4: 297, 297''

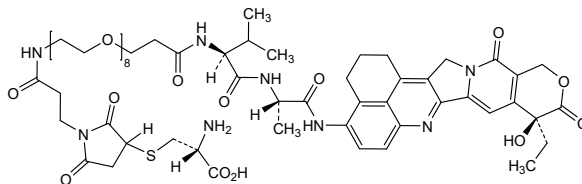
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenaricos complejos fucosilados

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

⊂ (214'',214''',220,220',226,226',229,229'')



quazomotidum

quazomotide

human Wilms tumor protein (WT33)-(427-445)-peptide;
L-arginyl-L-seryl-L- α -aspartyl-L- α -glutamyl-L-leucyl-L-valyl-L-arginyl-
L-histidyl-L-histidyl-L-asparaginyl-L-methionyl-L-histidyl-L-
glutaminyl-L-arginyl-L-asparaginyl-L-methionyl-L-threonyl-L-lysyl-L-
leucine

quazomotide

protéine humaine de la tumeur de Wilms (WT33)-(427-445)-
peptide;
L-arginyl-L-séryl-L- α -aspartyl-L- α -glutamyl-L-leucyl-L-valyl-L-arginyl-
L-histidyl-L-histidyl-L-asparaginyl-L-méthionyl-L-histidyl-L-
glutaminyl-L-arginyl-L-asparaginyl-L-méthionyl-L-thréonyl-L-lysyl-L-
leucine

quazomotida

proteína humana del tumor de Wilms (WT33)-(427-445)-péptido;
L-arginil-L-seril-L- α -aspartil-L- α -glutamil-L-leucil-L-valil-L-arginil-L-
histidil-L-histidil-L-asparaginil-L-metionil-L-histidil-L-glutaminil-L-
arginil-L-asparaginil-L-metionil-L-treonil-L-lisil-L-leucina

$$C_{98}H_{164}N_{38}O_{29}S_2$$

RSDELVRHHN MHQRNMTKL 19

rademikibartum #

rademikibart

immunoglobulin G4-kappa, anti-[*Homo sapiens* IL4R (interleukin 4 receptor, IL4RA, IL-4RA, interleukin 13 receptor, CD124)], *Homo sapiens* monoclonal antibody;
gamma4 heavy chain *Homo sapiens* (1-441) [VH (*Homo sapiens* IGHV3-23*04 (88.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.7.9] (26-33.51-57.96-104)) (1-115) -*Homo sapiens* IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (116-213), hinge 1-12 S10>P (223) (214-225), CH2 L92 (304) (226-335), CH3 (336-440), CHS K2>del (441)) (116-441)], (129-216')-disulfide with kappa light chain *Homo sapiens* (1'-216') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (97.9%) -IGKJ1*01 (100%), CDR-IMGT [7.3.10] (27-33.51-53.90-99)) (1'-109') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (155), V101 (193) (110'-216')]; dimer (221-221":224-224")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

radémikibart

immunoglobuline G4-kappa, anti-[*Homo sapiens* IL4R (récepteur de l'interleukine 4, IL4RA, IL-4RA, récepteur de l'interleukine 13, CD124)], anticorps monoclonal *Homo sapiens*;
chaîne lourde gamma4 *Homo sapiens* (1-441) [VH (*Homo sapiens* IGHV3-23*04 (88.8%) -(IGHD) - IGHJ4*01 (100%), CDR-IMGT [8.7.9] (26-33.51-57.96-104)) (1-115) -*Homo sapiens* IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (116-213), hinge 1-12 S10>P (223) (214-225), CH2 L92 (304) (226-335), CH3 (336-440), CHS K2>del (441)) (116-441)], (129-216')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-216') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (97.9%) -IGKJ1*01 (100%), CDR-IMGT [7.3.10] (27-33.51-53.90-99)) (1'-109') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (155), V101 (193) (110'-216')]; dimère (221-221":224-224")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

rademikibart

immunoglobulina G4-kappa, anti-[*Homo sapiens* IL4R (receptor de la interleukina 4, IL4RA, IL-4RA, receptor de la interleukina, CD124)], anticuerpo monoclonal *Homo sapiens*;

cadena pesada gamma4 *Homo sapiens* (1-441) [VH (*Homo sapiens* IGHV3-23*04 (88.8%) -(IGHD) - IGHJ4*01 (100%), CDR-IMGT [8.7.9] (26-33.51-57.96-104)) (1-115) -*Homo sapiens* IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (116-213), 1-12 bisagra S10>P (223) (214-225), CH2 L92 (304) (226-335), CH3 (336-440), CHS K2>del (441)) (116-441)], (129-216')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-216') [V-KAPPA (*Homo sapiens* IGKV3-20*01 (97.9%) -IGKJ1*01 (100%), CDR-IMGT [7.3.10] (27-33.51-53.90-99)) (1'-109') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (155), V101 (193) (110'-216'')]; dímero (221-221":224-224")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

EVQLVESGGG	LVQPGGSLRL	SCAASGFTFS	RNAMFWVRQA	PGKLEWVSG	50
IGTGGATSYA	DSVKGRFTIS	RDNAKNSLYL	QMNSLRAEDT	AVYVCARGRY	100
YFDYWGGQTL	VTVSSASTKG	PSVFPLAPCS	RSTSESTAAL	GCLVKDYFPE	150
PVTVSWNSGA	LTSGVHTFPA	VLQSSGLYSL	SSVTVTPSSS	LGTKTYTCNV	200
DHKPSNTKVD	KRVESKYGPP	CPPCPAPEFL	GGPSVFLFPP	KPKDTLMISR	250
TPEVTCVVVD	VSQEDPEVQF	NWYVDGVEVH	NAKTKPREEQ	FNSTYRVVSV	300
LTVLHQDWLN	GKEYCKVSN	KGLPSSIEKT	ISKAKGQPRE	PQVYTLPPSQ	350
EEMTKNQVSL	TCLVKGIFYPS	DIAVEWESNG	QPENNYKTP	PVLDSDGSFF	400
LYSRLTVDKS	RWQEGNVFSC	SVMHEALHNN	YTKSLSLSL	G	441

Light chain / Chaîne légère / Cadena ligera

EIVLTQSPGT	LSLSPGERAT	LSCRASQSVS	SSYLAWYQQK	PGQAPRLLIY	50
GASSRATGIP	DRFSGSGSGT	DFTLTISRLE	PEDFAVYYCQ	QYDHSAGWTF	100
GQGTKVEIKR	TVAAPSVFIF	PPSDEQLKSG	TASVVCLLNN	FYPREAKVQW	150
KVDNALQSGN	SQESVTEQDS	KDSTYLSLST	LTLTKADYEK	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"	142"-198"	256"-316"	362"-420"
	22"-95"	142"-198"	256"-316"	362"-420"
Intra-L (C23-C104)	23"-89"	136"-196"		
	23"-89"	136"-196"		
Inter-H-L (CH1 10-CL 126)	129-216'	129"-216"		
Inter-H-H (h 8, h 11)		221-221"	224-224"	

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4: 292, 292"

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

raguneprocelum
raguneprocel

allogenic dopaminergic neural progenitor cells derived from human induced pluripotent stem cells (iPSC). The iPSC cell bank was established from peripheral blood mononuclear cells (PBMCs) isolated from a healthy human donor by episomal reprogramming with plasmid vectors expressing octamer-binding transcription factor 3/4 (OCT-3/4), SOX2, Krueppel-like factor 4 (KLF4), L-Myc, LIN28, tumor suppressor p53 (Tp53), and Epstein-Barr nuclear antigen 1 (EBNA1). The cells were initially cultivated with feeder-free stem cell culture media with interleukin-6 (IL-6), stem cell factor, thrombopoietin, Flt-3 ligand, IL-3, and granulocyte colony-stimulating factor. Following induction, the cells were seeded on plates coated with a truncated form of laminin in the same media. Clones were chosen on the best efficiency for subsequent dopaminergic differentiation.

The iPSCs were differentiated into dopaminergic progenitor cells in media containing a SMAD inhibitor, fibroblast growth factor 8 (FGF8), a Wnt inhibitor and Sonic Hedgehog (SHH). CORIN (atrial natriuretic peptide-converting enzyme)-positive cells were then

isolated by immunoselection, and further cultured under conditions that favour aggregation to promote progenitor spheres. The final cell population expresses the neuron-specific markers forkhead box protein A2 (FoxA2) and neuron-specific class III beta-tubulin (>90%) and are negative for the undifferentiated iPSC markers OCT 3/4 and alkaline phosphatase, tissue-nonspecific isozyme (TRA-2-49). Early neural progenitor cells are not present (no detectable levels of SOX1+ and PAX6+ double positive cells).

ragunéprocel

cellules progénitrices neurales dopaminergiques allogènes dérivées de cellules souches pluripotentes induites (iPSC) humaines. La banque de cellules iPSC a été établie à partir de cellules mononucléaires de sang périphérique (PBMC) isolées d'un donneur humain sain par reprogrammation épisomique avec des vecteurs plasmidiques exprimant le facteur de transcription de liaison à l'octamère 3/4 (OCT-3/4), SOX2, le facteur 4 de type Krueppel (KLF4), L-Myc, LIN28, le suppresseur de tumeur p53 (Tp53) et l'antigène nucléaire 1 d'Epstein-Barr (EBNA1). Les cellules ont été initialement cultivées avec un milieu de culture de cellules souches sans cellules nourricières contenant de l'interleukine-6 (IL-6), du facteur de cellules souches, de la thrombopoïétine, du ligand Flt-3, de l'IL-3 et du facteur de stimulation des colonies de granulocytes. Après induction, les cellules ont été ensemencées sur des plaques recouvertes d'une forme tronquée de laminine dans le même milieu. Les clones ont été choisis en fonction de leur meilleur rendement lors de la différenciation dopaminergique ultérieure.

Les iPSC ont été différenciées en cellules progénitrices dopaminergiques dans des milieux contenant un inhibiteur de SMAD, le facteur de croissance des fibroblastes 8 (FGF8), un inhibiteur de Wnt et Sonic Hedgehog (SHH). Les cellules positives à la CORINE (facteur natriurétique auriculaire-convertisseur d'enzyme) ont ensuite été isolées par immunosélection, puis cultivées dans des conditions qui favorisent l'agrégation pour promouvoir la formation de sphères de progéniteurs. La population cellulaire finale exprime les marqueurs spécifiques des neurones que sont la protéine de la boîte à tête de fourche (forkhead box protein) A2 (FoxA2) et la bêta-tubuline de classe III spécifique des neurones (>90%) et est négative pour les marqueurs des iPSC indifférenciées OCT 3/4 et la phosphatase alcaline et l'isozyme non spécifique des tissus (TRA-2-49). Les cellules progénitrices neurales précoces ne sont pas présentes (aucun niveau détectable de cellules doublement positives SOX1+ et PAX6+).

ragunéprocel

células progenitoras neurales dopaminérgicas alogénicas derivadas de células madre pluripotentes inducidas (iPSCs) humanas. El banco celular de iPSCs se estableció a partir de células mononucleares de sangre periférica (PBMCs) aisladas de un donante humano sano mediante reprogramación episómica con vectores plasmídicos que expresan el factor de transcripción 3/4 de unión a octámero (OCT-3/4), SOX2, el factor similar a Krueppel 4 (KLF4), L-MYC, LIN28, el supresor de tumores p53 (Tp53) y el antígeno nuclear 1 del Epstein-Barr (EBNA1). Las células se cultivaron inicialmente con un medio de cultivo de células madre sin células alimentadoras (feeder) con interleuquina 6 (IL-6), factor de células madre, trombopoyetina, ligando de Flt-3, IL-3 y factor estimulador de colonias de granulocitos. Tras la inducción, las células se sembraron en placas tapizadas con una forma truncada de la laminina en el mismo medio. Los clones se eligieron en base a la mejor eficiencia para la posterior diferenciación dopaminérgica.

Las iPSCs se diferenciaron a células progenitoras dopaminérgicas en un medio que contiene un inhibidor SMAD, factor de crecimiento de fibroblastos 8 (FGF8), un inhibidor de Wnt y Sonic Hedgehog (SHH). Las células positivas para CORIN (enzima convertidora del péptido

natriurético) se aislaron mediante inmunoselección y se cultivaron bajo 3/4 de unión a octámero (OCT-3/4), SOX2, el factor similar a Krueppel condiciones que favorecen la agregación para promover las esferas progenitoras. La población celular final expresa los marcadores específicos de neuronas proteína A2 de la caja de forkhead (FoxA2) y beta-tubulina clase III específica de neuronas (>90%) y son negativas para los marcadores de iPSCs no diferenciadas OCT-3/4 y la fosfatasa alcalina, isocima no específica de tejido (TRA-2-49). No están presentes las células progenitoras neurales tempranas (niveles no detectables de células doble positivas para SOX1+ y PAX6+).

raxtozinameranum

raxtozinameran

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 sub-lineage XBB.1.5; based upon GISAID: EPI_ISL_17157779), flanked by 5' and 3' untranslated regions and a 3' polyadenylation (polyA) tail; contains *N*¹-methylpseudouridine instead of uridine (*all-U*>*m*¹Ψ)

raxtozinaméran

ARN messenger (ARNm), protégé d'une coiffe en 5', codant la séquence entière aux codons optimisés d'un variant à la conformation stabilisée avant fusion (K982P et V983P) de la glycoprotéine de spicule (S) du SARS-CoV-2 (coronavirus du syndrome respiratoire aigu sévère 2) (sous-lignée Omicron XBB.1.5; d'après GISAID: EPI_ISL_17157779), flanquée de régions non traduites en 5' et 3' et d'une queue polyadénylation (polyA) en 3'; contient de la *N*¹-méthylpseudouridine au lieu de l'uridine (*tout-U*>*m*¹Ψ)

raxtozinamerán

ARN mensajero (ARNm), protegido en 5', que codifica, para la secuencia completa con codones optimizados, de una variante estabilizada en la conformación pre-fusión (K982P y V983P) de la glicoproteína de la espícula (S) del SARS-Cov-2 (coronavirus 2 del síndrome respiratorio agudo severo) (sublinaje XBB.1.5 de Omicron; basado en GISAID: EPI_ISL_17157779), flanqueado por regiones 5' y 3' no traducidas y una cola poliadenilación (poliA) en 3'; contiene *N*¹-metilpseudouridina en lugar de uridina (*todo -U*>*m*¹Ψ)

relutriginum

relutrigine

3-(ethoxydifluoromethyl)-6-[5-fluoro-6-(2,2,2-trifluoroethoxy)pyridin-3-yl][1,2,4]triazolo[4,3-*a*]pyrazine

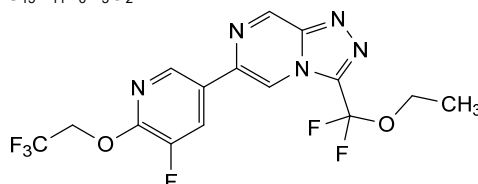
rélutrigine

3-(éthoxydifluorométhyl)-6-[5-fluoro-6-(2,2,2-trifluoroéthoxy)pyridin-3-yl][1,2,4]triazolo[4,3-*a*]pyrazine

relutrigina

3-(etoxidifluorometil)-6-[5-fluoro-6-(2,2,2-trifluoroetoxi)piridin-3-ii][1,2,4]triazolo[4,3-*a*]pirazina

C₁₅H₁₁F₆N₅O₂



remternetugum

remternetug

immunoglobulin G1-kappa , anti-[*Homo sapiens* APP (amyloid beta A4 precursor protein) Abeta42 N3pGlu peptide (N-terminal truncated and pyroglutamate-modified amyloid beta 3-42 peptide)], *Homo sapiens* monoclonal antibody;
 gamma1 heavy chain *Homo sapiens* (1-451) [VH (*Homo sapiens* IGHV3-23*01 (98.0%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (219) (123-220), hinge 1-15 (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS K2>del (451)) (123-451)], (225-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5*03 (93.4%) -IGKJ1*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 (231-231":234-234")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-GSKO, glycoform alfa

remternetug

immunoglobuline G1-kappa, anti-[*Homo sapiens* APP (protéine précurseur A4 amyloïde bêta) Abêta42 N3pGlu peptide (peptide amyloïde bêta 3-42 tronqué, avec un pyroglutamate N-terminal)];
 chaîne lourde gamma1 *Homo sapiens* (1-451) [VH (*Homo sapiens* IGHV3-23*01 (98.0%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (219) (123-220), charnière 1-15 (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS K2>del (451)) (123-451)], (225-214')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5*03 (93.4%) -IGKJ1*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 (231-231":234-234")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-GSKO, glycoforme alfa

remternetug

inmunoglobulina G1-kappa, anti-[*Homo sapiens* APP (proteína precursor A4 amiloide beta) Abeta42 N3pGlu péptido (péptido amiloide beta 3-42 truncado, con un piroglutamato N-terminal)];
 cadena pesada gamma1 *Homo sapiens* (1-451) [VH (*Homo sapiens* IGHV3-23*01 (98.0%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (219) (123-220), bisagra 1-15 (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS K2>del (451)) (123-451)], (225-214')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5*03 (93.4%) -IGKJ1*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 (231-231":234-234")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-GSKO, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

EVQLLESGGG LVQPPGGLRL SCAASGFTFS SYPMWVVRQA PGKGLEWVSA 50
 ISGSGGSTYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAREG 100
 GSGSYNGFD YWGQGLTVTV SSASTKGPSV FPLAPSSKST SGGTAALGCL 150
 VKDYFPEPVT VSWNSGALTS GVHTFFPAVLQ SSGLYSLSSV VTFVSSSLGT 200
 QTYICNVNHK PSNTKVDKVK EPKSCDKTHT CPPCPAPELL GGPSVFLFPP 250
 KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NQYVDGVEVH NAKTKPREEQ 300
 YNSTYRVVSV LTVLHQDWLNL GKEYKCKVSN KALPAPIEKT ISKAKGQPRE 350
 PQVYTLPPSR DELTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTFP 400
 PVLDSGSGFF LYSKLTVDKS RWQQGNVFSV SVMHEALHNN YTQKSLSLSP 450
 G 451

Light chain / Chaîne légère / Cadena ligera

DIQMTQSPST LSASVGRDRTV ITCRASQSLG NWLAWYQQKPK GKAPKLLIYQ 50
 ASTLESQGPS RFGSGSGSTE FTLTISLQF DDFATYYCQH YKGSFVTFGQ 100
 GTKVEIKRIV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY BREAKVQWKV 150
 DNALQSGNSQ ESVTEQDSKD STYSLSTLT LSKADYEKHK VYACEVTHQG 200
 LSSPVTKSFN RGEK 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 biantennarios complejos fucosilados

renvistobartum #
 renvistobart

immunoglobulin G1- kappa, anti-[*Homo sapiens* TIGIT (T cell immunoreceptor with Ig domain and ITIM, V-set Ig member 9, VSIG9, V-set and transmembrane member 3, VSTM3)], *Homo sapiens* monoclonal antibody;
 gamma1 heavy chain *Homo sapiens* (1-459) [VH (*Homo sapiens* IGHV4-61*01 (98.0%) -(IGHD)-IGHJ3*01 (92.3%), CDR-IMGT [10.7.22] (26-35.53-59.98-119)) (1-130) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v43 CH2 A1.3, E1.2, A1, G1v60 S115, S116 (CH1 R120 (227) (131-228), hinge 1-15 (229-243), CH2 L1.3>A (247), L1.2>E (248), G1>A (250), A115>S (343), P116>S (344) (244-353), CH3 E12 (369), M14 (371) (354-458), CHS K2>del (459)) (131-459)], (233-216')-disulfide with kappa light chain *Homo sapiens* (1'-216') [V- KAPPA (*Homo sapiens* IGKV3-11*01 (100%) - IGKJ3*01 (100%), CDR-IMGT [6.3.11] (27-32.50-52.89-99)) (1'-109') - *Homo sapiens* IGKC*01 (100%), Km3 A45.1 (155), V101 (193) (110'-216')]; dimer (239-239":242-242")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1 lacking the glutamine synthetase (GS-KO) gene, glycoform alfa

renvistobart

immunoglobuline G1-kappa, anti-[*Homo sapiens* TIGIT (immunorécepteur des cellules T avec domaines Ig et ITIM, membre 9 de l'Ig V-set, VSIG9, membre 3 de l'Ig V-set et région transmembranaire, VSTM3)], anticorps monoclonal *Homo sapiens*; chaîne lourde gamma1 *Homo sapiens* (1-459) [VH (*Homo sapiens* IGHV4-61*01 (98.0%) -(IGHD)-IGHJ3*01 (92.3%), CDR-IMGT [10.7.22] (26-35.53-59.98-119)) (1-130) -*Homo sapiens* IGHG1*03,

G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v43 CH2 A1.3, E1.2, A1, G1v60 S115, S116 (CH1 R120 (227) (131-228), charnière 1-15 (229-243), CH2 L1.3>A (247), L1.2>E (248), G1>A (250), A115>S (343), P116>S (344) (244-353), CH3 E12 (369), M14 (371) (354-458), CHS K2>del (459)) (131-459)], (233-216')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-216') [V-KAPPA (*Homo sapiens* IGKV3-11*01 (100%) -IGKJ3*01 (100%), CDR-IMGT [6.3.11] (27-32.50-52.89-99)) (1'-109') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (155), V101 (193) (110'-216')]; dimère (239-239':242-242')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1 ne présentant pas le gène de la glutamine synthétase (GS-KO), glycoforme alfa

renvistobart

inmunoglobulina G1-kappa, anti-[*Homo sapiens* TIGIT (immunoreceptor de las células T con dominios Ig e ITIM, miembro 9 de la Ig V-set, VSIG9, miembro 3 de la Ig V-set y región transmembranaria, VSTM3)], anticuerpo monoclonal *Homo sapiens*;
cadena pesada gamma1 *Homo sapiens* (1-459) [VH (*Homo sapiens* IGHV4-61*01 (98.0%) -(IGHD) -IGHJ3*01 (92.3%), CDR-IMGT [10.7.22] (26-35.53-59.98-119)) (1-130) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v43 CH2 A1.3, E1.2, A1, G1v60 S115, S116 (CH1 R120 (227) (131-228), bisagra 1-15 (229-243), CH2 L1.3>A (247), L1.2>E (248), G1>A (250), A115>S (343), P116>S (344) (244-353), CH3 E12 (369), M14 (371) (354-458), CHS K2>del (459)) (131-459)], (233-216')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-216') [V-KAPPA (*Homo sapiens* IGKV3-11*01 (100%) -IGKJ3*01 (100%), CDR-IMGT [6.3.11] (27-32.50-52.89-99)) (1'-109') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (155), V101 (193) (110'-216')]; dímero (239-239':242-242')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, en ausencia del gen glutamina sintetasa (GS-KO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

QVHLQESGPG LVKPSSETLSL TCTVSGGVS SGIYYSWIR QPPGKGLEWI 50
 GYIYSGSTN YNPSLKSRTV ISVDTSKNQF SLKLSVATA DTAVYICARD 100
 YYVSGMYNVV DYYFFGVDVW GQTTVTVSS ASTKGPSVFP LAPSSKSTSG 150
 GTAALGCLVK DYFPEPVTVS WNSGALTSKV HTFFPAVLQSS GLYSLSSVVT 200
 VPSSSLGTTQ YICNVNHKPS NTKVDKRVFP KSCDKHTPC PCPAPAEAGA 250
 PSVFLFPKPK KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA 300
 KTKPREEPQY STYRVVSVLT VLNQDNLNGK EYKCKVSNKA LPSSIEKTIS 350
 KAKGQPREPQ VYFPPSREE MTKNQVSLTCL LVKGFYPSDI AVEWESNGQP 400
 ENNYKTTTTPV LDSGDSFFLY SKLTVDKSRW QQGNVFVCSV MHEALHNHYT 450
 QKLSLSLSPG 459

Light chain / Chaîne légère / Cadena ligera

EIVLTQSPAT LSLSPGERAT LSCRASQSVS SYLAWYQQPK GQAPRLLIYD 50
 ASNRATGIPA RFGSGSGSTD FTLTISLLEP EDFAVYCCQ RSNWPPLETF 100
 GPGTKVDIKR TVAAPSVEFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQW 150
 KVDNALQSGN SQESVTEQDS KDSTYLSLST 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) 22-97 157-213 274-334 380-438
 22"-97" 157"-213" 274"-334" 380"-438"
 Intra-L (C23-C104) 23'-88' 136'-196'
 23"'-88"" 136""-196""

Inter-H-L (h 5-CL 126) 233-216' 233"-216"

Inter-H-H (h 11, h 14) 239-239' 242-242"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del

glutaminilo N-terminal

Q > pyroglutamyl (pE, 5-oxopropyl) / pyroglutamyle (pE, 5-oxopropyle) / piroglutamilo

(pE, 5-oxoprolilo)

H VH Q1: 1, 1"

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

H CH2 N84.4: 310, 310"

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

resencatinibum

resencatinib

6-[[*(2R)*-2-hydroxy-2-methylbut-3-yn-1-yl]oxy]-4-(6-{6-[(6-methoxypyridin-3-yl)methyl]-3,6-diazabicyclo[3.1.1]heptan-3-yl}pyridin-3-yl)pyrazolo[1,5-*a*]pyridine-3-carbonitrile

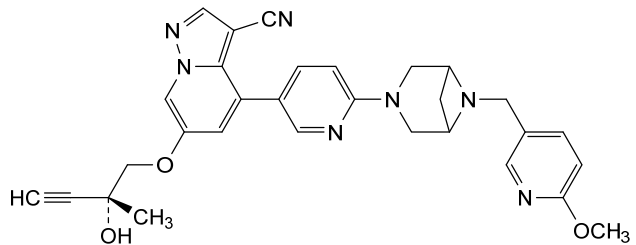
résencatinib

6-[[*(2R)*-2-hydroxy-2-méthylbut-3-yn-1-yl]oxy]-4-(6-{6-[(6-méthoxypyridin-3-yl)méthyl]-3,6-diazabicyclo[3.1.1]heptan-3-yl}pyridin-3-yl)pyrazolo[1,5-*a*]pyridine-3-carbonitrile

resencatinib

6-[[*(2R)*-2-hidroxi-2-metilbut-3-in-1-il]oksi]-4-(6-{6-[(6-metoxipiridin-3-il)metil]-3,6-diazabicyclo[3.1.1]heptan-3-il}piridin-3-il)pirazolo[1,5-*a*]piridina-3-carbonitrilo

C₃₀H₂₉N₇O₃



retatrutidum

retatrutide

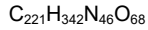
L-tyrosyl-2-methylalanyl-L-glutaminylglycyl-L-threonyl-L-phenylalanyl-L-threonyl-L-seryl-L- α -aspartyl-L-tyrosyl-L-seryl-L-isoleucyl-2-methyl-L-leucyl-L-leucyl-L- α -aspartyl-L-lysyl-N⁶-{2-[2-(2-[[*N*-(19-carboxynonadecanoyl)-L- γ -glutamyl]amino)ethoxy]ethoxy]acetyl}-L-lysyl-L-alanyl-L-glutaminyl-2-methylalanyl-L-alanyl-L-phenylalanyl-L-isoleucyl-L- α -glutamyl-L-tyrosyl-L-leucyl-L-leucyl-L- α -glutamylglycylglycyl-L-prolyl-L-seryl-L-serylglycyl-L-alanyl-L-prolyl-L-prolyl-L-prolyl-L-serinamide

rétatrutide

L-tyrosyl-2-méthylalanyl-L-glutaminylglycyl-L-thréonyl-L-phénylalanyl-L-thréonyl-L-séryl-L- α -aspartyl-L-tyrosyl-L-séryl-L-isoleucyl-2-méthyl-L-leucyl-L-leucyl-L- α -aspartyl-L-lysyl-N⁶-{2-[2-(2-[[*N*-(19-carboxynonadécanoyl)-L- γ -glutamyl]amino)éthoxy]éthoxy]acétyl}-L-lysyl-L-alanyl-L-glutaminyl-2-méthylalanyl-L-alanyl-L-phénylalanyl-L-isoleucyl-L- α -glutamyl-L-tyrosyl-L-leucyl-L-leucyl-L- α -glutamylglycylglycyl-L-prolyl-L-séryl-L-sérylglycyl-L-alanyl-L-prolyl-L-prolyl-L-prolyl-L-sérinamide

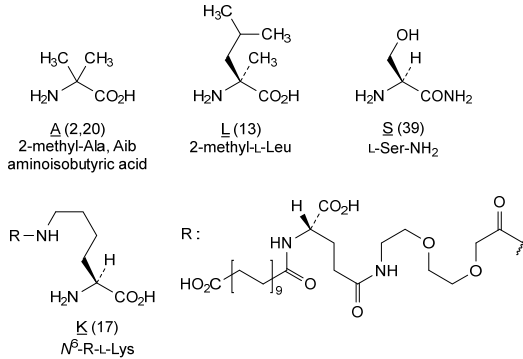
retatrutida

L-tirosil-2-metilalanil-L-glutaminilglicil-L-treonil-L-fenilalanil-L-treonil-L-seril-L- α -aspartil-L-tirosil-L-seril-L-isoleucil-2-metil-L-leucil-L-leucil-L- α -aspartil-L-lisil-N⁶-{2-[2-(2-[[*N*-(19-carboxinonadecanoil)-L- γ -glutamil]amino)etoxi]etoxi]acetil}-L-lisil-L-alanil-L-glutanil-2-metilalanil-L-alanil-L-fenilalanil-L-isoleucil-L- α -glutamil-L-tyrosil-L-leucil-L-leucil-L- α -glutamilglicilglicil-L-prolil-L-seril-L-serilglicil-L-alanil-L-prolil-L-prolil-L-prolil-L-serinamida



YAQGTFTSDY SILLDKKAQA AFIEYLLLEGG PSSGAPPPS 39

Modified residues / Résidus modifiés / Restos modificados



rildinadstrocelum

rildinadstrocel

allogeneic mesenchymal stromal cells (MSC) prepared from subcutaneous adipose tissue of healthy donors, collected by liposuction. The adipose tissue is digested and the released cells placed in culture media containing bovine serum albumin (BSA), fetal bovine serum (FBS), hydrocortisone, recombinant human epidermal growth factor (rh-EGF), recombinant human fibroblast growth factor (rh-FGF), recombinant human transferrin and insulin, heparin and L-alanyl-L-glutamine. The cells are frozen to generate a master cell bank (MCB) at an early passage, and then resuscitated and culture-expanded. The cells express mesenchymal stromal cell marker cluster of differentiation 73 (CD73), CD90, and CD105 (> 80%) and do not express human leukocyte antigen-DR isotype (HLA DR), CD34, CD11b, CD19, and CD45 (<5%). Resting cells are expressing CD274 (PDL1, >2%). The activated cells secrete vascular endothelial growth factor (VEGF) and upregulate expression of indoleamine 2,3-dioxygenase 1 (IDO1) mRNA when activated *in vitro*.

rildinadstrocel

cellules stromales mésenchymateuses (MSC) allogènes préparées à partir du tissu adipeux sous-cutané de donneurs sains, prélevé par liposuction. Le tissu adipeux est digéré et les cellules libérées sont placées dans des milieux de culture contenant de l'albumine de sérum bovin (BSA), du sérum bovin foetal (FBS), de l'hydrocortisone, du facteur de croissance épidermique humain recombinant (rh-EGF), du facteur de croissance des fibroblastes humain recombinant (rh-FGF), de la transferrine humaine recombinante et de l'insuline, de l'héparine et de la L-alanyl-L-glutamine. Les cellules sont congelées pour générer une banque cellulaire primaire (MCB) lors d'un passage précoce, puis ressuscitées et amplifiées en culture. Les cellules expriment les marqueurs de la classe de différenciation 73 (CD73) des cellules stromales mésenchymateuses, CD90 et CD105 (>80%) et n'expriment pas l'antigène leucocytaire humain - isotype DR (HLA DR), CD34, CD11b, CD19 et CD45 (<5%). Les cellules au repos expriment CD274 (PDL1, >2%). Les cellules activées sécrètent le facteur de croissance endothélial vasculaire (VEGF) et régulent à la hausse l'expression de l'ARNm de l'indoleamine 2,3-dioxygénase 1 (IDO1) lorsqu'elles sont activées *in vitro*.

rildinadstrocel	<p>células estromales mesenquimales (MSC) alogénicas preparadas a partir de tejido adiposo subcutáneo de donantes sanos, obtenido por liposucción. El tejido adiposo se digiere y las células liberadas se ponen en medio de cultivo que contiene albúmina sérica bovina (BSA), suero bovino fetal (FBS), hidrocortisona, factor de crecimiento epidérmico humano recombinante (rh-EGF), factor de crecimiento de fibroblastos humano recombinante (rh-FGF), transferrina e insulina humanas recombinantes, heparina y L-alanil-L-glutamina. Las células se congelan para generar un banco de células maestro (MCB) en un pase temprano y después se resucitan y se expanden en cultivo. Las células expresan los marcadores de células estromales mesenquimales, grupo de diferenciación 73 (CD73), CD90 y CD105 (>80%) y no expresan el antígeno común leucocitario - isotipo DR (HLA DR), CD34, CD11b, CD19 y CD45 (<5%). Las células en reposo expresan CD274 (PDL1, >2%). Las células activadas secretan factor de crecimiento del endotelio vascular (VEGF) y aumentan la expresión de ARNm de indoleamina 2,3-dioxigenasa 1 (IDO1) cuando se activan <i>in vitro</i></p>
riliprubartum # riliprubart	<p>immunoglobulin G4-kappa, anti-[<i>Homo sapiens</i> C1S (complement C1s)], chimeric monoclonal antibody; gamma4 heavy chain chimeric (1-446) [VH Musmus/Homsap (<i>Mus musculus</i> IGHV14-3*02 (82.7%) -(IGHD) -IGHJ2*01 (92.9%)/<i>Homo sapiens</i> IGHV1-46*02 (75.5%) -(IGHD) -IGHJ4*01 (92.9%) L123>T (114)), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -<i>Homo sapiens</i> IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10, G4v3 CH2 E1.2, G4v24 CH3 L107, S114 (CH1 (120-217), hinge 1-12 S10>P (227) (218-229), CH2 L1.2>E (234), L92 (308) (230-339), CH3 M107>L (427), N114>S (433) (340-444), CHS (445-446)) (120-446)], (133-218')-disulfide with kappa light chain chimeric (1'-218') [V-KAPPA Musmus/Homsap (<i>Mus musculus</i> IGKV3-4*01 (88.9%) -IGKJ1*01 (91.7%)/ <i>Homo sapiens</i> IGKV4-1*01 (74.3%) -IGKJ4*01 (100%)), CDR-IMGT [10.3.9] (27-36.54-56.93-101)) (1'-111') -<i>Homo sapiens</i> IGKC*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218')]; dimer (225-225":228-228")-bisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa</p>
riliprubart	<p>immunoglobuline G4-kappa, anti-[<i>Homo sapiens</i> C1S (complément C1s)], anticorps monoclonal chimérique; chaîne lourde gamma4 chimérique (1-446) [VH Musmus/Homsap (<i>Mus musculus</i> IGHV14-3*02 (82.7%) -(IGHD) -IGHJ2*01 (92.9%)/<i>Homo sapiens</i> IGHV1-46*02 (75.5%) -(IGHD) -IGHJ4*01 (92.9%) L123>T (114)), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -<i>Homo sapiens</i> IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10, G4v3 CH2 E1.2, G4v24 CH3 L107, S114 (CH1 (120-217), charnière 1-12 S10>P (227) (218-229), CH2 L1.2>E (234), L92 (308) (230-339), CH3 M107>L (427), N114>S (433) (340-444), CHS (445-446)) (120-446)], (133-218')-disulfure avec la chaîne légère kappa chimérique (1'-218') [V-KAPPA Musmus/Homsap (<i>Mus musculus</i> IGKV3-4*01 (88.9%) -IGKJ1*01 (91.7%)/<i>Homo sapiens</i> IGKV4-1*01 (74.3%) -IGKJ4*01 (100%)), CDR-IMGT [10.3.9] (27-36.54-56.93-101)) (1'-111') -<i>Homo sapiens</i> IGKC*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218')]; dimère (225-225":228-228")-bisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa</p>

riliprubart

inmunoglobulina G4-kappa, anti-[*Homo sapiens* C1S (complemento C1s)], anticuerpo monoclonal quimérico; cadena pesada gamma4 quimérica (1-446) [VH Musmus/Homsap (*Mus musculus* IGHV14-3*02 (82.7%) -(IGHD) -IGHJ2*01 (92.9%)/*Homo sapiens* IGHV1-46*02 (75.5%) - (IGHD) -IGHJ4*01 (92.9%) L123>T (114)), CDR-IMGT [8.7.12] (26-33.51-58.97-108)) (1-119)- *Homo sapiens* IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10, G4v3 CH2 E1.2, G4v24 CH3 L107, S114 (CH1 (120-217), bisagra 1-12 S10>P (227) (218-229), CH2 L1.2>E (234), L92 (308) (230-339), CH3 M107>L (427), N114>S (433) (340-444), CHS (445-446)) (120-446)], (133-218')-disulfuro con la cadena ligera kappa quimérica (1'-218') [V-KAPPA Musmus/Homsap (*Mus musculus* IGHV3-4*01 (88.9%) -IGKJ1*01 (91.7%)/*Homo sapiens* IGHV4-1*01 (74.3%) -IGKJ4*01 (100%)), CDR-IMGT [10.3.9] (27-36.54-56.93-101)) (1'-111') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218')]; dímero (225-225":228-228")-bisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

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QVQLVQSGAE VKKPGASVKL SCTASGSENIK DDYIHWVKQA PGQGLEWIGR 50
IDPADGHTKY APKFQVKVTI TADTSTSTAY LELSSLRSED TAVYYCARYG 100
YGREVFDYWG QGTTVTIVSSA STKGPVSFVPL APCSRSTSES TAALGCLVKD 150
YFPEPVTYSW NSGALTSQGVH TFPVAVLQSSG LYSLSSVVTV PSSSLGKTGY 200
TCNVNDHKPSN TKVDDKRVESK YGPPCPPCPA PEFEGGSPSVF LFPKPKDTL 250
MISRTEPEVTC VVVVDSQEDP EVQFNWYVDG VEVHNAKTKP REEQFNSTYR 300
VVSVLTFLHQ DLNNGKEYKC KVSNNKGLPSS LEKTIISKARG QPREPOVYTL 350
PPSQEEMTKN QVSLTCLVKG FYPSDIAVEW ESNQPEPNY KTTPPVLDS 400
GSFFLYSRLT VDKSRWQEGN VFSCSVLHEA LHSHTYQKSL SLSLQK 446

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Light chain / Chaîne légère / Cadena ligera

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DIVLTQSPDS LAVSLGERAT ISCKASQSDV YDGDSYMNY QQKPGQPPKI 50
LIYDASNLDS GIPARFSGSG SGTDFTLTIS SLEPEDFAIY YCQQSNEDPW 100
TFGGGTKEVI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL NNFYPREAKV 150
QWKVDNALQS GNSQESVTEQ DSKDSTYLSL STLTLKADY EKHKVYACEV 200
THQGLSSPVT KSFNRGEC 218

```

Post-translational modifications

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

Intra-H (C23-C104)	22-96	146-202	260-320	366-424
	22"-96"	146"-202"	260"-320"	366"-424"
Intra-L (C23-C104)	23'-92'	138'-198'		
	23'''-92'''	138'''-198'''		

Inter-H-L (CH1 10-CL 126) 133-218' 133"-218"

Inter-H-H (h 8, h 11) 225-225" 228-228"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutamínilo N-terminal

Q > pyroglutamyl (pE, 5-oxopropyl) / pyroglutamyle (pE, 5-oxopropyle) / piroglutamilo (pE, 5-oxoprolilo)
H VH Q1: 1, 1"

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

H CH2 N84.4: 296, 296"

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

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

H CHS K2: 446, 446"

rinvecalinasum alfa #
rinvecalinase alfa

human kallikrein-1 (tissue kallikrein, KLK1, EC:3.4.21.35) mature form, engineered variant (E¹²¹>Q, A¹⁶⁴>V) produced in Chinese hamster ovary (CHO) cells, glycoform alfa

rinvécalinase alfa forme mature de la kallikréine-1 humaine (kallikréine tissulaire, KLK1, EC:3.4.21.35), variant modifié (E¹²¹>Q, A¹⁶⁴>V) produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

rinvocalinasa alfa calicreína-1 humana (calicreína tisular, KLK1, EC:3.4.21.35) forma madura, variante diseñada (E¹²¹>Q, A¹⁶⁴>V) producida en células ováricas de hámster Chino (CHO), forma glicosilada alfa

Sequence / Séquence / Secuencia

```
IVGGWECEQH SQPWQAALYH FSTFQCGGIL VHRQWVLTAA HCISDNYQLW 50
LGRHNLFDDE NTAQFVHVSE SFPHPGFNMS LLENHTRQAD EDYSHDLMLL 100
RLTEPADTIT DAVKVVVELPT QPEVVGSTCL ASGWSIEPE NFSFPDDLQC 150
VDLKILPNDE CKKLVHQKVT DFMLCVGHLE GGDTCVGDG GGPLMCDGVL 200
QGVTSWGYVP CGTPNKPSVA VRVLSYVKWI EDTIAENS 238
```

Mutation / Mutation / Mutación

E121>Q, A164>Y

Post-translational modifications

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
7-150, 7-186, 7-211, 26-42, 129-196, 150-186, 150-211, 161-175, 175-186, 186-211

Glycosylation sites / Sites de glycosylation / Posiciones de glicosilación

N78, N84, N141 (partially glycosylated)

risovalisibum

risovalisib

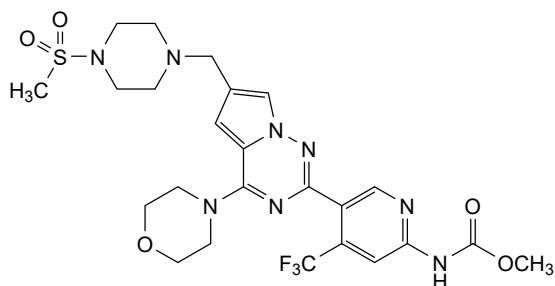
methyl {5-[6-[[4-(methanesulfonyl)piperazin-1-yl]methyl]-4-(morpholin-4-yl)pyrrolo[2,1-f][1,2,4]triazin-2-yl]-4-(trifluoromethyl)pyridine-2-yl}carbamate

risovalisib

{5-[6-[[4-(méthanesulfonyl)pipérazin-1-yl]méthyl]-4-(morpholin-4-yl)pyrrolo[2,1-f][1,2,4]triazin-2-yl]-4-(trifluorométhyl)pyridine-2-yl}carbamate de méthyle

risovalisib

{5-[6-[[4-(metanosulfonil)piperazin-1-il]metil]-4-(morfolin-4-il)pirrolo[2,1-f][1,2,4]triazin-2-il]-4-(trifluorometil)piridina-2-il}carbamato de metilo

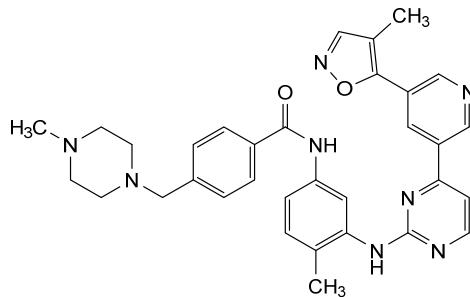
C₂₄H₂₉F₃N₈O₅S

risvodetinibum

risvodetinib

N-[4-methyl-3-({4-[5-(4-methyl-1,2-oxazol-5-yl)pyridin-3-yl]pyrimidin-2-yl}amino)phenyl]-4-[(4-methylpiperazin-1-yl)methyl]benzamide

risvodétinib	<i>N</i> -[4-méthyl-3-({4-[5-(4-méthyl-1,2-oxazol-5-yl)pyridin-3-yl]pyrimidin-2-yl}amino)phényl]-4-[(4-méthylpipérazin-1-yl)méthyl]benzamide
risvodetinib	<i>N</i> -[4-metil-3-({4-[5-(4-metil-1,2-oxazol-5-il)piridin-3-il]pirimidin-2-il}amino)fenil]-4-[(4-metilpipérazin-1-il)metil]benzamide
	C ₃₃ H ₃₄ N ₆ O ₂

**riticovateinum #**

riticovatein

severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) delta lineage B.1.617.2 (Gisaid: EPI_ISL_1999775) spike (S) glycoprotein fragment (1-1193), stable prefusion conformation variant (R⁶⁶⁶>P, R⁶⁶⁷>G, R⁶⁶⁸>S, R⁶⁷⁰>S, F⁸⁰²>P, A⁸⁷⁷>P, A⁸⁸⁴>P, A⁹²⁷>P, K⁹⁷¹>P, V⁹⁷²>P) fused to the enterobacteria phage T4 fibrin foldon domain fragment (458-484, 1194-1220 in the current sequence), trimer, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

riticovatéine

fragment de la glycoprotéine du spicule (S) (1-1193) du coronavirus 2 du syndrome respiratoire aigu sévère (SARS-CoV-2), lignée delta B.1.617.2 (Gisaid: EPI_ISL_1999775), variante de conformation stable par pré-fusion (R⁶⁶⁶>P, R⁶⁶⁷>G, R⁶⁶⁸>S, R⁶⁷⁰>S, F⁸⁰²>P, A⁸⁷⁷>P, A⁸⁸⁴>P, A⁹²⁷>P, K⁹⁷¹>P, V⁹⁷²>P) fusionné au fragment du domaine foldon de la fibratine du phage T4 d'entérobactéries (458-484, 1194-1220 dans la séquence actuelle), trimère, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

riticovateína

fragmento de la glicoproteína de la espícula (S) (1-1193) del coronavirus 2 del síndrome respiratorio severo agudo (SARS-CoV-2) linaje delta B.1.617.2 (Gisaid: EPI_ISL_1999775), variante de conformación de prefusión estable (R⁶⁶⁶>P, R⁶⁶⁷>G, R⁶⁶⁸>S, R⁶⁷⁰>S, F⁸⁰²>P, A⁸⁷⁷>P, A⁸⁸⁴>P, A⁹²⁷>P, K⁹⁷¹>P, V⁹⁷²>P) fusionada al fragmento de dominio de foldón de fibratina del fago T4 de enterobacterias (458-484, 1194-1220 en la secuencia actual), trímero, producido en células ováricas de hámster Chino (CHO), glicofoma alfa

Monomer sequence / Séquence du monomère / Secuencia del monómero

QCVCNLRTRTQ	LPPAYTNSFT	RGVYYPDKVF	RSSVLHSTQD	LFLPFFSNVT	50		
WFHAIHVSQT	NGTKRFDNPV	LPFNDGVYFA	STEKSNIRG	WIFGTTLDSK	100		
TQSLLLVNNNA	TNVVIKVCDF	QFCNDPFLGV	YYHKNNKSWM	ESGVYSANN	150		
CTFEVVSQPF	LMDFLEGKQGN	FKNLREPFVK	NIDGYFKIYS	KHTPINLVRD	200		
LPQGFSALEP	LVDLPIGINI	TRFQTLALH	RSYLTDPGSS	SGWTAGAAAY	250		
YVGYLQPRTF	LLKYNENGTI	TDAVDCLDP	LSETKCTLKS	FTVEKGYIQT	300		
SNFRVQPTES	IVRFFNITNL	CPFGEVFNAT	RFASVYAWNR	KRISNCVADY	350		
SVLYNSASF	TFKCYGVSPT	KLNDLCFTNV	YADSFVIRGD	EVRQIAPGQT	400		
GKIADYNYKL	PDDFTGCVIA	WNSNNLDSKV	GGNYNYRYRL	FRKSNLKPFE	450		
RDISTEIQQA	GSKPCNGVEG	FNCYFPLQSY	GFQPTNGVGY	QPYRVVLSF	500		
ELLHAPQTE	GPKKSTNLVK	NKCVNFNFG	LTGTGVLTES	NKKFLPFQPF	550		
GRDIADTTDA	VRDPQTLLEIL	DITPCSFSGV	SVITPGTNTS	NQVAVLYQGV	600		
NCTEVPVAIH	ADQLTPTWRV	YSTGSNVFQT	RAGCLIGAEH	VNNSYECDIP	650		
IGAGCASYQ	TQTNS	PGSAS	SVASQSI IAY	TMSLGAENSV	AYSNNSTAIP	700	
TNFTISVTE	ILPVSMTKTS	VDCTMYICGD	STECSNLLQ	YGSFCTQLNR	750		
ALTGIAVEQD	KNTQEVFAQV	KQIYKTPPIK	DFGGFNFESI	LPDPSKPSKR	800		
SP	IEDLLFNK	VTLADAGFIK	QYGDCLG DIA	ARDLICAQKF	NGLTVLPLLL	850	
TDEMIAQYTS	ALLAGTITSG	WTFGAG	PALQ	IFP	MQMAYR	FNGIGVTQNV	900
LYENOKLIAN	QFNSAIGKIQ	DSLSST	ESAL	GKLNQVNVQN	AQALNTLVKQ	950	
LSSNFGAISS	VLNDILSRDL	PE	EAEVQIDR	LITGRLQSLQ	TYVTQQILIRA	1000	
AETRASANLA	ATKMSECVLG	QSKRVDFCGK	GYHLSMFPQS	APHGVVFLHW	1050		
TVVPAQEKNF	TTAPAICHGD	KAHFPREGVF	VSNGTWTFVT	QRNFYEPQII	1100		
TDNDTFVSGN	CDVVIQIVNN	TVYDPLQPEL	DSFKEELDKY	FKNHTSPDVD	1150		
LGDISGINAS	VVNIQKEIDR	LNEVAKNLNE	SLIDLQELGK	<u>YEQGYIPEAP</u>	1200		
<u>RDGQAYVRKD</u>	<u>GEWVLLSTFL</u>				1220		

Mutation / Mutation / Mutación
R⁶⁶⁶>P, R⁶⁶⁷>G, R⁶⁶⁸>S, R⁶⁷⁰>S, F⁸⁰²>P, A⁸⁷⁷>P, A⁸⁸⁴>P, A⁹²⁷>P, K⁹⁷¹>P, V⁹⁷²>P

Foldon domain / Foldon domaine / Foldon dominio
GYIPEAPRDG QAYVRKDGEW VLLSTFL 1194-1220

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-chain: 2-123, 118-151, 276-286, 321-346, 364-417, 376-510, 465-473, 523-575, 602-634, 647-656, 723-745, 728-734, 825-836, 1017-1028, 1067-1111

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación (predicted)
N48, N61, N109, N136, N150, N219, N267, N316, N328, N588, N601, N642, N694, N702, N786, N1059, N1083, N1119, N1143, N1158, N1179

O-glycosylation sites / Sites de O-glycosylation / Posiciones de O-glicosilación ((predicted)
T308, S310

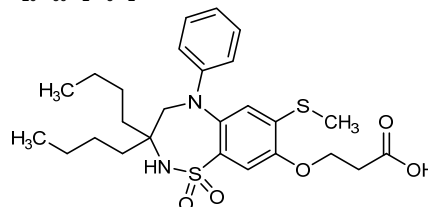
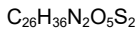
N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutamínilo N-terminal
Q1 >pyroglutamyl (pE, 5-oxopropyl)

ritivixibat

ritivixibat 3-[[3,3-dibutyl-7-(methylsulfanyl)-1,1-dioxo-5-phenyl-2,3,4,5-tetrahydro-1,2,5-benzothiadiazepin-8-yl]oxy]-propanoic acid

ritivixibat acide 3-[[3,3-dibutyl-7-(méthylsulfanyl)-1,1-dioxo-5-phényl-2,3,4,5-tétrahydro-1,2,5-benzothiadiazépin-8-yl]oxy]-propanoïque

ritivixibat ácido 3-[[3,3-dibutil-7-(metilsulfanil)-1,1-dioxo-5-fenil-2,3,4,5-tetrahydro-1,2,5-benzotiadiazepin-8-yl]oxy]-propanoico



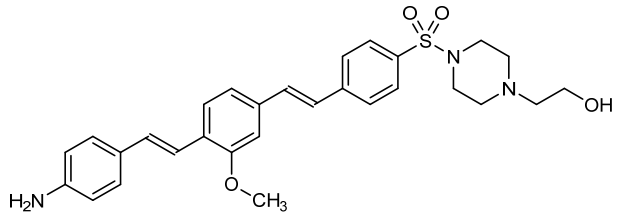
rizedisbenum

rizedisben 2-(9⁴-amino-6³-methoxy-2,2-dioxo-2-thia-1(1)-piperazina-3(1,4),6(1,4),9(1,4)-tribenzenanonaphane-4,7-dien-9⁴-yl)ethanol

rizédisbène 2-(9⁴-amino-6³-méthoxy-2,2-dioxo-2-thia-1(1)-pipérazina-3(1,4),6(1,4),9(1,4)-tribenzenanonaphane-4,7-dién-9⁴-yl)ethanol

rizedisbén 2-(9⁴-amino-6³-metoxi-2,2-dioxo-2-tia-1(1)-piperazina-3(1,4),6(1,4),9(1,4)-tribencenanonafano-4,7-dien-9⁴-il)etanol

C₂₉H₃₃N₃O₄S

**rolistobartum #**

rolistobart

immunoglobulin G4-kappa, anti-[*Homo sapiens* LILRB4 (leukocyte immunoglobulin like receptor B4, ILT3, LIR-5, CD85k)], humanized monoclonal antibody; gamma4 heavy chain humanized (1-449) [VH (*Homo sapiens* IGHV3-7*01 (86.7%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens* IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (123-220), hinge 1-12 S10>P (230) (221-232), CH2 L92 (311) (233-342), CH3 (343-447), CHS (448-449)) (123-449)], (136-218')-disulfide with kappa light chain humanized (1'-218') [V-KAPPA (*Homo sapiens* IGKV1-9*03 (81.6%) -IGKJ2*01 (100%), CDR-IMGT [10.3.9] (27-36.54-56.93-101)) (1'-111') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218')]; dimer (228-228":231-231")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

rolistobart

immunoglobuline G4-kappa, anti-[*Homo sapiens* LILRB4 (récepteur similaire à l'immunoglobuline leucocytaire B4)], anticorps monoclonal humanisé; chaîne lourde gamma4 humanisée (1-449) [VH (*Homo sapiens* IGHV3-7*01 (86.7%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens* IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (123-220), charnière 1-12 S10>P (230) (221-232), CH2 L92 (311) (233-342), CH3 (343-447), CHS (448-449)) (123-449)], (136-218')-disulfure avec la chaîne légère kappa humanisée (1'-218') [V-KAPPA (*Homo sapiens* IGKV1-9*03 (81.6%) -IGKJ2*01 (100%), CDR-IMGT [10.3.9] (27-36.54-56.93-101)) (1'-111') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218')]; dimère (228-228":231-231")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

rolistobart

immunoglobulina G4-kappa, anti-[*Homo sapiens* LILRB4 (receptor B4 immunoglobulina tipo de los leucocitos, ILT3, LIR-5, CD85k)], anticuerpo monoclonal humanizado;

cadena pesada gamma4 humanizada (1-449) [VH (*Homo sapiens* IGHV3-7*01 (86.7%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens* IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (123-220), bisagra 1-12 S10>P (230) (221-232), CH2 L92 (311) (233-342), CH3 (343-447), CHS (448-449)) (123-449)], (136-218')-disulfuro com la cadena ligera kappa humanizada (1'-218') [V-KAPPA (*Homo sapiens* IGHV1-9*03 (81.6%) -IGKJ2*01 (100%), CDR-IMGT [10.3.9] (27-36.54-56.93-101)) (1'-111') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218')]; dímero (228-228":231-231")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

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EVQLVESGGG LVQPGGSLRL SCAASGFTFS NYGMSWVRQA PGKGLEWVAT 50
ISGGGDTYNY PDSVRGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCGRRL 100
WFRSLYYAMD YWGQGLTVTV SSASTKGPSV FPLAPCSRST SESTAALGCL 150
VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ SSGLYSLSSV VIVPSSSLGT 200
KTYTCNVDHK PSNTKVDKRV ESKYGPCCPP CPAPEFLGGP SVFLFPPKPK 250
DTLMSIRTP E VTCVVVDVSO EDPEVQFNWY VDGVEVHNAK TKPREEQFNS 300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKGL PPSIEKTIK AKGQPREPQV 350
YTLPPSQEEM TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTTTPVL 400
DSDGSFFLYS RLTVDKSRWQ EGNVFCSSVM HEALHNHYTQ KSLSLSLGK 449
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Light chain / Chaîne légère / Cadena ligera

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DIQLTQSPSS LSASVGDRTV ITCRASEKVD SFGQSFMHWY QQKPGKAPKL 50
LIYLTSLNLD GVPSPRFSGSG SGTDFTLTIS SLQPEDFATY YCQQNNDPY 100
TFGQGTKLEI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL NNFYPREAKV 150
QWKVDNALQS GNSQESVTEQ DSKDSTYLSL STLTLKADY EKHKVYACEV 200
THQGLSSPVT KSFNRGEC 218
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Post-translational modifications

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

Intra-H (C23-C104) 22-96 149-205 263-323 369-427
22"-96" 149"-205" 263"-323" 369"-427"

Intra-L (C23-C104) 23'-92' 138'-198'
23'''-92''' 138'''-198'''

Inter-H-L (CH1 10-CL 126) 136-218' 136"-218"

Inter-H-H (h 8, h 11) 228-228" 231-231"

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

H CH2N84.4: 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"

rolusafinum

rolusafine

2-(4-ethylphenoxy)-4'-methoxy-3,3'-bipyridine

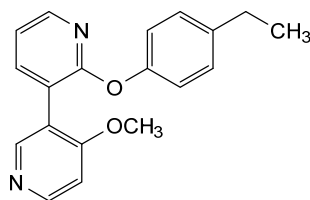
rolusafine

2-(4-éthylphénoxy)-4'-méthoxy-3,3'-bipyridine

rolusafina

2-(4-etilfenoxi)-4'-metoxi-3,3'-bipiridina

C₁₉H₁₈N₂O₂



rovadicitinibum

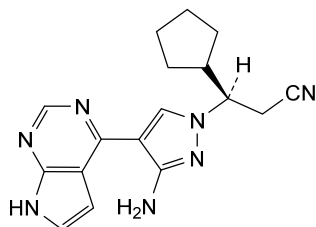
rovadicitinib

(3*R*)-3-[3-amino-4-(7*H*-pyrrolo[2,3-*d*]pyrimidin-4-yl)-1*H*-pyrazol-1-yl]-3-cyclopentylpropanenitrile

rovadicitinib

(3*R*)-3-[3-amino-4-(7*H*-pyrrolo[2,3-*d*]pyrimidin-4-yl)-1*H*-pyrazol-1-yl]-3-cyclopentylpropanenitrile

rovadicitinib

(3*R*)-3-[3-amino-4-(7*H*-pirrolo[2,3-*d*]pirimidin-4-il)-1*H*-pirazol-1-il]-3-ciclopentilpropanenitriloC₁₇H₁₉N₇**sabestomigum #**

sabestomig

immunoglobulin G1-kappa/lambda, anti-[*Homo sapiens* PDCD1 (programmed cell death 1, PD1, PD-1, CD279) and HAVCR2 (hepatitis A virus cellular receptor 2, T cell immunoglobulin and mucin domains family member 3, TIM3, TIM-3, TIMD3, CD366)], humanized and *Homo sapiens* monoclonal antibody, bispecific, bivalent;

gamma1 heavy chain anti-PDCD1 humanized (1-452) [VH humanized (*Homo sapiens*IGHV3-48*01 (92.9%) -(IGHD) -IGHJ4*01 (93.3%) L123>T (117), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens*IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v39 CH2 F1.3, E1.2, S116, G1v33 CH3 S22, A24, V86 (hole) (CH1 R120 (219) (123-220), hinge 1-15 (221-235), CH2 L1.3>F (239), L1.2>E (240), P116>S (336) (236-345), CH3 E12 (361), M14 (363), Y5>C (354), T22>S (371), L24>A (373), Y86>V (412) (346-450), CHS (451-452)) (123-452)], (225-219')-disulfide with kappa light chain anti-PDCD1 humanized (1'-219') [V-KAPPA humanized (*Homo sapiens*IGKV3D-7*01 (81.1%) -IGKJ2*02 (100%), CDR-IMGT [11.3.9] (27-37.55-57.94-102)) (1'-112') -*Homo sapiens*IGKC*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')];

gamma1 heavy chain anti-HAVCR2 *Homo sapiens* (1"-452") [VH (*Homo sapiens*IGHV3-23*01 (99.0%) -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1"-122") -*Homo sapiens*IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v39 CH2 F1.3, E1.2, S116, G1v32 CH3 W22 (knob), G1v58 CH1 C5, h V5 (CH1 F5>C (131), R120 (219) (123"-220"), hinge 1-15 C5>V (225)(221"-235"), CH2 L1.3>F (239), L1.2>E (240), P116>S (336) (236"-345"), CH3 S10>C (359), E12 (361), M14 (363), T22>W (371) (346"-450"), CHS (451"-452")) (123"-452")], (131"-123''')-disulfide with lambda light chain anti-HAVCR2 *Homo sapiens* (1'''-214''') [V-LAMBDA (*Homo sapiens*IGLV3-21*01 (94.8%) -IGKJ2*02 (90.9%), CDR-IMGT [6.3.11] (26-31.49-51.88-98)) (1'''-108''') -*Homo sapiens*IGLC2*01 (98.1%) LC2v58 C10, V126 (S10>C (123), C126>V (213)) (109'''-214''')]; dimer (231-231''':234-234''':354-359''')-trisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CATS, glycoform alfa

- sabestomig immunoglobuline G1-kappa/lambda, anti-[*Homo sapiens* PDCD1 (protéine 1 de mort cellulaire programmée, PD1, PD-1, CD279) et anti-[*Homo sapiens* HAVCR2 (récepteur cellulaire 2 du virus de l'hépatite A, membre 3 de la famille à domaines immunoglobuline et mucine des cellules T, TIM3, TIM-3, TIMD3, CD366)], anticorps monoclonal humanisé et *Homo sapiens*, bispécifique, bivalent; chaîne lourde gamma1 anti-PDCD1 humanisée (1-452) [VH humanisé (*Homo sapiens*IGHV3-48*01 (92.9%) -(IGHD) -IGHJ4*01 (93.3%) L123>T (117), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens*IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v39 CH2 F1.3, E1.2, S116, G1v33 CH3 S22, A24, V86 (hole) (CH1 R120 (219) (123-220), charnière 1-15 (221-235), CH2 L1.3>F (239), L1.2>E (240), P116>S (336) (236-345), CH3 Y5>C (354), E12 (361), M14 (363), T22>S (371), L24>A (373), Y86>V (412) (346-450), CHS (451-452)) (123-452)], (225-219')-disulfure avec la chaîne légère kappa anti-PDCD1 humanisée (1'-219') [V-KAPPA humanisé (*Homo sapiens*IGKV3D-7*01 (81.1%) -IGKJ2*01 (100%), CDR-IMGT [11.3.9] (27-37.55-57.94-102)) (1'-112') -*Homo sapiens*IGKC*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; chaîne lourde gamma1 anti- HAVCR2 *Homo sapiens* (1"-452") [VH (*Homo sapiens*IGHV3-23*01 (99.0%) -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1"-122") -*Homo sapiens*IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v39 CH2 F1.3, E1.2, S116, G1v32 CH3 W22 (knob), G1v58 CH1 C5, h V5 (CH1 F5>C (131), R120 (219) (123"-220"), charnière 1-15 C5>V (225) (221"-235"), CH2 L1.3>F (239), L1.2>E (240), P116>S (336) (236"-345"), CH3 S10>C (359), E12 (361), M14 (363), T22>W (371) (346"-450"), CHS (451"-452")) (123"-452"), (131"-123""-disulfure avec la chaîne légère lambda anti-HAVCR2 *Homo sapiens* (1""-214""") [V-LAMBDA (*Homo sapiens*IGLV3-21*01 (94.8%) -IGKJ2*01 (90.9%), CDR-IMGT [6.3.11] (26-31.49-51.88-98)) (1""-108""") -*Homo sapiens*IGLC2*01 (98.1%) LC2v58 C10, V126 (S10>C (123), C126>V (213)) (109""-214"""); dimère (231-231":234-234":354-359")]-trisdysulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CATS, glycoforme alfa
- sabestomig immunoglobulina G1-kappa/lambda, anti-[*Homo sapiens* PDCD1 (proteína 1 de muerte celular programada, PD1, PD-1, CD279) y anti-[*Homo sapiens* HAVCR2 (receptor celular 2 del virus de la hepatitis A, miembro 3 de la familia con dominios inmunoglobulina y mucina de las células T, TIM3, TIM-3, TIMD3, CD366)], anticuerpo monoclonal humanizado y *Homo sapiens*, biespecífico, bivalente; cadena pesada gamma1 anti-PDCD1 humanizada (1-452) [VH humanizado (*Homo sapiens*IGHV3-48*01 (92.9%) -(IGHD) -IGHJ4*01 (93.3%) L123>T (117), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens*IGHG1*03, G1m3, nG1 m1CH1 R120, CH3 E12, M14, G1v39 CH2 F1.3, E1.2, S116, G1v33 CH3 S22, A24, V86 (hole) (CH1 R120 (219) (123-220), bisagra 1-15 (221-235), CH2 L1.3>F (239), L1.2>E (240), P116>S (336) (236-345), CH3 Y5>C (354), E12 (361), M14 (363), T22>S (371), L24>A (373), Y86>V (412) (346-450), CHS (451-452)) (123-452)], (225-219')-disulfuro con la cadena ligera kappa anti-PDCD1 humanizada (1'-219') [V-KAPPA humanizado (*Homo sapiens*IGKV3D-7*01 (81.1%) -IGKJ2*01 (100%), CDR-IMGT [11.3.9] (27-37.55-57.94-102)) (1'-112') -*Homo sapiens*IGKC*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; cadena pesada gamma1 anti-HAVCR2 *Homo sapiens* (1"-452") [VH (*Homo sapiens*IGHV3-23*01 (99.0%) -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1"-122") -*Homo sapiens*

IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, G1v39 CH2 F1.3, E1.2, S116, G1v32 CH3 W22 (knob), G1v58 CH1 C5, h V5 (CH1 F5>C (131), R120 (219) (123"-220")), bisagra 1-15 C5>V (225) (221"-235"), CH2 L1.3>F (239), L1.2>E (240), P116>S (336) (236"-345"), CH3 S10>C (359), E12 (361), M14 (363), T22>W (371) (346"-450"), CHS (451"-452") (123"-452"), (131"-123")-disulfuro con la cadena ligera lambda anti-HAVCR2 *Homo sapiens* (1"-214") [V-LAMBDA (*Homo sapiens* IGLV3-21*01 (94.8%) -IGKJ2*01 (90.9%), CDR-IMGT [6.3.11] (26-31.49-51.88-98)) (1"-108")]-*Homo sapiens* IGLC2*01 (98.1%) LC2v58 C10, V126 (S10>C (123), C126>V (213)) (109"-214"); dímero (231-231":234-234":354-359")-trisdifuro, producido en las células ováricas de hámster chino (CHO), línea celular CATS, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada: anti-PDCD1 (H)

EVQLVESGGG LVQPGGSLRL SCAASGFTFS DYGMHWVRQA PGKGLEWVAY 50
 ISSGSYTIYS ADSVGRFTI SRDNKNSLY LQMNSLRAED TAVYVCARRA 100
 PMSFYEYDF YWGGQTTVTI SSASTKGPSV FPLAPSSKST SGGTAALGCL 150
 VKDYFPEPVT VSWNSGALTS GVHTFFAVLQ SSGLYSLSSV VTPVSSSLGT 200
 QTYICNVNHK PSNTKVDKRV EPKSCDKTHT CPKCPAPEFE GGPSVFLPEFP 250
 KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NNYVDGVEVH NAKTKPREEQ 300
 YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPASIEKT ISKAKGQPRE 350
 PQVCTLPISR EEMTKNQVSL SCAVKGFPYS DIAVWESNG QPENNYKTTTP 400
 PVLDSGDSGF LVSKLTVDKS RWQQGNVFSC SVMHEALHNN YTKQSLSLSP 450
 GK 452

Light chain / Chaîne légère / Cadena ligera: anti-PDCD1 kappa (L')

QIVLTQSPAT LSLSPGERAT LSCASASSKHT NLYWRSRHYW YQQKPGQAPR 50
 LLLYLTSNRA TGIPARFSGS GSGTDFTLTI SLEPEDEFAV YVCQQWSNP 100
 FTFGQGTKE IKRTVAAPSV FIFPPSDEQL KSGTASVCL LNPFYPREAK 150
 VQWKVDNALQ SGNQSQESVTE QDSKDYSTYL SSTLTLSKAD YEKHKVYACE 200
 VTHQGLSSPV TKSFNRGEC 219

Heavy chain / Chaîne lourde / Cadena pesada: anti-HAVCR2 (H'')

EVQLLESGGG LVQPGGSLRL SCAASGFTFS SYAMSWVRQA PGKGLEWVSA 50
 ISGSGGSTYY ADSVGRFTI SRDNSKNTLY LQMNSLRAED TAVYVCARGS 100
 YGTYYGNYFE YWGGQTLVTI SSASTKGPSV CPLAPSSKST SGGTAALGCL 150
 VKDYFPEPVT VSWNSGALTS GVHTFFAVLQ SSGLYSLSSV VTPVSSSLGT 200
 QTYICNVNHK PSNTKVDKRV EPKSDVKTHT CPKCPAPEFE GGPSVFLPEFP 250
 KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NNYVDGVEVH NAKTKPREEQ 300
 YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPASIEKT ISKAKGQPRE 350
 PQVYTLPPCR EEMTKNQVSL WCLVKGFPYS DIAVWESNG QPENNYKTTTP 400
 PVLDSGDSGF LYSKLTVDKS RWQQGNVFSC SVMHEALHNN YTKQSLSLSP 450
 GK 452

Light chain / Chaîne légère / Cadena ligera: anti-HAVCR2 lambda (L'')

SVVLTQPPSV SVAPGKTARI TCGGDNIGGK SVHWYQQKPG QAPVLVIYYD 50
 SDRPSGIPER FSGNSNGNTA TLTISRVEAG DEADYYCQVL DRRSDHFLFG 100
 GGTKLTVLGQ PKAAPSVTLF PPCSEELQAN KATLVCLISD FYPGAVTVAW 150
 KADSSPVKAG VETITPSKQS NNYAASSYL SLTPEQWKSH RSYSCQVTHE 200
 GSTVEKTVAP TEVS 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'-93' 139'-199'
 22"-87" 136"-195"

Inter-H-L (CH1 10-CL 126) 225-219' (CH1 5-CL 10)* 131"-123"

Inter-H-H (h 8, h 11) 231-231" 234-234" (CH3 5-CH3 10)* 354-359"

*Engineered alternative Inter-H-L (instead of 225"-213") and additional Inter-H-H, owing to 4 amino acid changes to cysteine1.

N-terminal glutaminylation / Cyclisation du glutaminyne N-terminal / Ciclación del glutaminyne N-terminal

Q > pyroglutamyl (pE, 5-oxopropyl) / pyroglutamyl (pE, 5-oxopropyl) / piroglutamino (pE, 5-oxopropilo)

L VLQ1: I, I'

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 biantennarios complejos fucosilados.

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

sabirnetugum

sabirnetug

immunoglobulin G2-kappa, anti-[*Homo sapiens* APP (amyloid beta A4 precursor protein) Abeta42 and Abeta40 soluble non-fibrillar oligomers], humanized monoclonal antibody;
 gamma2 heavy chain humanized (1-443) [VH (*Homo sapiens* IGHV3-48*01 (92.9%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens* IGHG2*01, G2m.. CH2 V45.1 (CH1 (118-215), hinge 1-12 (216-227), CH2 V45.1 (278) (228-336), CH3 (337-441), CHS (442-443)) (118-443)], (131-219')-disulfide with kappa light chain humanized (1'-219') [V-KAPPA (*Homo sapiens* IGKV2-28*01 (89.5%) -IGKJ2*03 (100%), CDR-IMGT [11.3.9] (27-37.55-57.94-102)) (1'-112') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; dimer (219-219":220-220":223-223":226-226")-tetrakisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

sabirnetug

immunoglobuline G2-kappa, anti-[*Homo sapiens* APP (protéine précurseur A4 amyloïde bêta) oligomères solubles non fibrillaires d'Abeta42 et Abeta40], anticorps monoclonal humanisé;
 chaîne lourde gamma2 humanisée (1-443) [VH (*Homo sapiens* IGHV3-48*01 (92.9%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens* IGHG2*01, G2m.. CH2 V45.1 (CH1 (118-215), charnière 1-12 (216-227), CH2 V45.1 (278) (228-336), CH3 (337-441), CHS (442-443)) (118-443)], (131-219')-disulfure avec la chaîne légère kappa humanisée (1'-219') [V-KAPPA (*Homo sapiens* IGKV2-28*01 (89.5%) -IGKJ2*03 (100%), CDR-IMGT [11.3.9] (27-37.55-57.94-102)) (1'-112') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; dimère (219-219":220-220":223-223":226-226")- tétrakisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

sabirnetug

immunoglobulina G2-kappa, anti-[*Homo sapiens* APP (proteína precursor 4 amiloide beta) oligómeros solubles no fibrilares de Abeta42 t Abeta40], anticuerpo monoclonal humanizado;
 cadena pesada gamma2 humanizada (1-443) [VH (*Homo sapiens* IGHV3-48*01 (92.9%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens* IGHG2*01, G2m.. CH2 V45.1 (CH1 (118-215), bisagra 1-12 (216-227), CH2 V45.1 (278) (228-336), CH3 (337-441), CHS (442-443)) (118-443)], (131-219')-disulfuro con la cadena ligera kappa humanizada (1'-219') [V-KAPPA (*Homo sapiens* IGKV2-28*01 (89.5%) -IGKJ2*03 (100%), CDR-IMGT [11.3.9] (27-37.55-57.94-102)) (1'-112') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; dímero (219-219":220-220":223-223":226-226")- tetrakisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

EVQLVESGGG LVQPGGSLRL SCAASGFTFS SFGMHVVRQA PGKGLEWVAY 50
 ISRGSSTIYY ADTVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYVCARGI 100
 TTALDYWGQG TLVTVSSAST KGPSVFPFLAP CSRSTSESTA ALGCLVKDYF 150
 PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SNFGTQTYTC 200
 NVDHKPSNTK VDKTVERKCC VECPPCPAPP VAGPSVFLFP PKPKDTLMIS 250
 RTPVETCVVV DVSHEDPEVQ FNWYVDGVEV HNAKTKPREE QFNSTFRVVS 300
 VLTVVHQDWL NGKEYKCKVS NKGLPAPIEK TISKTKGQPR EPQVYTLPPS 350
 REEMTKNQVS LTCLVKGFYP SDIAVENESN GQPENNYKTT PPMILDSGDSF 400
 FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTKQKLSLSL PGK 443

Light chain / Chaîne légère / Cadena ligera

DVYMTQSPFLS LPVTPGEPAS ISCRSSQSIY HSNGNTYLEW YLQKPGQSPQ 50
 LLIIYKASNRG SGVPPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCFQGSRLG 100
 PSFQGGTKLE IKRTVAAPSV FIFPPSDEQL KSGTASVVCV LNNFYPREAK 150
 VQWVKVDNALQ SGNISQESVTE QDSKDYSTLS SSTITLTKAD YEKHKVYACE 200
 VTHQGLSPV TKSFNREGC 219

Post-translational modifications

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

Intra-H (C23-C104) 22-96 144-200 257-317 363-421
 22"-96" 144"-200" 257"-317" 363"-421"

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

Inter-H-L (CH1 10-CL 126) 131-219" 131"-219"

Inter-H-H (h 4, h 5, h 8, h11) 219-219" 220-220" 223-223" 226-226"

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

H CH2 N84.4: 293, 293"

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

H CHS K2: 443, 443"

saruparibum

saruparib

5-{4-[(7-ethyl-5,6-dihydro-6-oxo-1,5-naphthyridin-3-yl)methyl]piperazin-1-yl}-N-methylpyridine-2-carboxamide

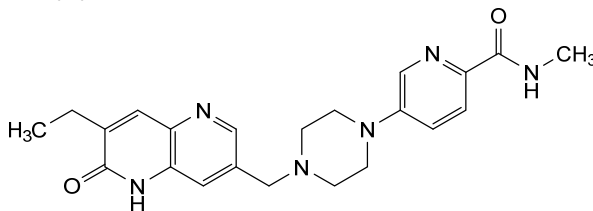
saruparib

5-{4-[(7-éthyl-5,6-dihydro-6-oxo-1,5-naphtyridin-3-yl)méthyl]pipérazin-1-yl}-N-méthylpyridine-2-carboxamide

saruparib

5-{4-[(7-etil-5,6-dihidro-6-oxo-1,5-naftiridin-3-il)metil]piperazin-1-il}-N-metilpiridina-2-carboxamida

C₂₂H₂₆N₆O₂



selvacovateinum

selvacovatein

severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), beta lineage (B.1.351) spike (S) glycoprotein (natural variant K⁴⁰⁴>N⁹⁹, E⁴⁷¹>K¹⁶⁶, N⁴⁸⁸>Y¹⁸³) receptor binding domain (RBD) fragment (306-524, 1-219 in the current sequence), fused to severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), alpha lineage (B.1.1.7) spike (S) glycoprotein (natural variant N⁴⁸⁸>Y⁴⁰²), receptor binding domain (RBD) fragment (306-524, 220-438 in the current sequence), produced in Chinese hamster ovary (CHO)-K1 cells, glycoform alfa

selvacovatéine fragment (306-524, 1-219 dans la séquence actuelle) du domaine de liaison au récepteur (RBD) de la glycoprotéine du spicule (S) du coronavirus 2 du syndrome respiratoire aigu sévère (SARS-CoV-2) de la lignée bêta (B.1.351) (variant naturel (K⁴⁰⁴>N⁹⁹, E⁴⁷¹>K¹⁶⁶, N⁴⁸⁸>Y¹⁸³), fusionné au fragment (306-524, 220-438 dans la séquence actuelle) du domaine de liaison au récepteur (RBD) de la glycoprotéine du spicule (S) du coronavirus 2 du syndrome respiratoire aigu sévère (SARS-CoV-2) de la lignée alpha (B.1.1.7) (variant naturel (N⁴⁸⁸>Y⁴⁰²), produit dans des cellules ovariennes de hamster chinois (CHO)-K1, glycoforme alfa

selvacovateína fragmento del dominio de unión al receptor (RBD) (306-524, 1-219 en la secuencia actual) de la glicoproteína de la espícula (S) del coronavirus 2 del síndrome respiratorio agudo severo (SARS-CoV-2), linaje beta (B.1.351) (variante natural K⁴⁰⁴>N⁹⁹, E⁴⁷¹>K¹⁶⁶, N⁴⁸⁸>Y¹⁸³), fusionado al fragmento del dominio de unión al receptor (RBD) (306-524, 220-438 en la secuencia actual) de la glicoproteína de la espícula (S) del coronavirus 2 del síndrome respiratorio agudo severo (SARS-CoV-2), linaje alfa (B.1.1.7) (variante natural N⁴⁸⁸>Y⁴⁰²), producido en células ováricas de hámster Chino (CHO)-K1, glicoforma alfa

Sequence / Séquence / Secuencia

```
RVQPTEISIVR FPNITNLCPPF GEVFNATRFA SVYAWNRKRI SNCVADYSVL 50
YNSASFSTFK CYGVSPTKLN DLCFTNVYAD SFVIRGDEV R QIAPGQTQNI 100
ADYNYKLPDD FTGCVIAWNS NNLDSKVGGN YNYLYRLEFRK SNLKPFERDI 150
STEIYQAGST PCNGVKGFCN YFPLQSYGFQ PTYGVGYQPY RVVLSFELL 200
HAPATVCGPK KSTNLVKNR VQPTESIVRF PNITNLCPPF EVFNATRFAS 250
VYAWNRKRIS NCVADYSVLY NSASFSTFKC YGVSPTKLNLCFTNVYADS 300
FVIRGDEV RQ IAPGQTGKIA DYNLYRLEFRK TGCVIAWNSN NLDKVGNGNY 350
NYLYRLEFRKS NLKPFERDIS TEIYQAGSTP CNGVEGFNCY FPLQSYGFQPY 400
TYGVGYQPYR VVLSFELLH APATVCGPKK STNLVKNK 438
```

Natural variant / Variante naturelle / Variante natural

K⁴⁰⁴>N⁹⁹, E⁴⁷¹>K¹⁶⁶, N⁴⁸⁸>Y¹⁸³, N⁴⁸⁸>Y⁴⁰²

Post-translational modifications

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
18-43, 61-114, 73-207, 162-70, 237-262, 280-333, 292-426, 381-389

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
N13, N25, N232, N244

O-glycosylation sites / Sites de O-glycosylation / Posiciones de O-glicosilación
T5, T224

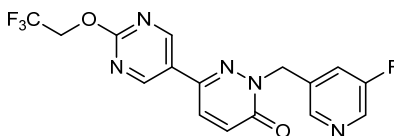
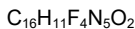
C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
K438

sevasemtenum

sevasemten 2-[(5-fluoropyridin-3-yl)methyl]-6-[2-(2,2,2-trifluoroethoxy)pyrimidin-5-yl]pyridazin-3(2H)-one

sévasemten 2-[(5-fluoropyridin-3-yl)méthyl]-6-[2-(2,2,2-trifluoroéthoxy)pyrimidin-5-yl]pyridazin-3(2H)-one

sevasemtén 2-[(5-fluoropiridin-3-il)metil]-6-[2-(2,2,2-trifluoroetoxi)pirimidin-5-il]piridazin-3(2H)-ona

**sofnobrutinibum**

sofnobrutinib

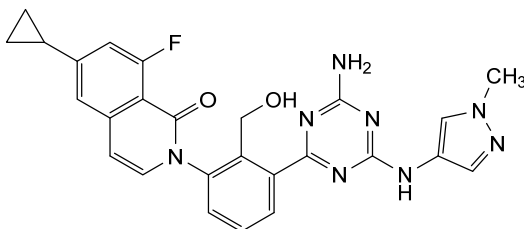
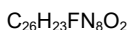
2-[3-{4-amino-6-[(1-méthyl-1*H*-pyrazol-4-yl)amino]-1,3,5-triazin-2-yl}-2-(hydroxyméthyl)phényl]-6-cyclopropyl-8-fluoroisoquinolin-1(2*H*)-one

sofnobrutinib

2-[3-{4-amino-6-[(1-méthyl-1*H*-pyrazol-4-yl)amino]-1,3,5-triazin-2-yl}-2-(hydroxyméthyl)phényl]-6-cyclopropyl-8-fluoroisoquinoléin-1(2*H*)-one

sofnobrutinib

2-[3-{4-amino-6-[(1-méthyl-1*H*-pyrazol-4-yl)amino]-1,3,5-triazin-2-yl}-2-(hydroxyméthyl)phényl]-6-cyclopropyl-8-fluoroisoquinolin-1(2*H*)-one

**sonpirtigenum isteparovecum #**

sonpirtigene isteparovec

recombinant, non-replicating adeno-associated virus serotype 2 (AAV2) vector, encoding a codon-optimized *Chlamydomonas*-derived ambient light-activatable multi-characteristic opsin (MCO) fusion protein with a *Discosoma* red fluorescent bioluminescence reporter (mCherry), under control of the cytomegalovirus (CMV) promoter and human metabotropic glutamate receptor mGluR6 enhancer, terminated with a human growth hormone (hGH) polyadenylation signal, flanked by AAV2 inverted terminal repeats (ITRs)

sonpirtigène istéparovec

vecteur recombinant et non répliquant du virus adéno-associé de sérotype 2 (AAV2), codant une protéine de fusion d'opsine multi-caractéristique (MCO) activable par la lumière ambiante dérivée de *Chlamydomonas* aux codons optimisés avec un rapporteur de bioluminescence fluorescent rouge *Discosoma* (mCherry), sous le contrôle du promoteur du cytomégalo-virus (CMV) et de l'amplificateur mGluR6 du récepteur métabotrope du glutamate humain, terminé par un signal de polyadénylation de l'hormone de croissance humaine (hGH), flanqué de répétitions terminales inversées (ITR) de l'AAV2

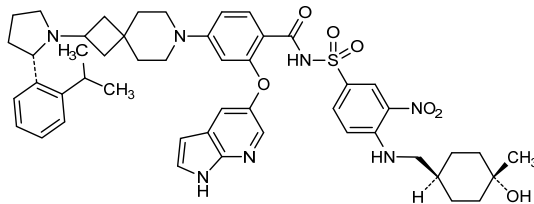
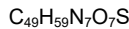
sonpiretigén isteparvovec vector de virus adenoasociado del serotipo 2 (AAV2) recombinante, no replicativo, que codifica, con codones optimizados, una proteína de fusión de la opsina multicaracterística (MCO) activable por luz ambiental derivada de *Chlamydomona* con el reportero de bioluminiscencia fluorescente rojo (mCherry) de *Discosoma*, bajo el control del promotor de citomegalovirus (CMV) y el potenciador del receptor metabotrópico de glutamato humano mGluR6, terminado con una señal de poliadenilación de la hormona de crecimiento humana (hGH), flanqueado por las repeticiones terminales invertidas (ITRs) del AAV2

sonrotocloxum

sonrotoclox *N*-[4-(((1*r*,4*r*)-4-hydroxy-4-methylcyclohexyl)methyl)amino]-3-nitrobenzene-1-sulfonyl]-4-(2-((2*S*)-2-[2-(propan-2-yl)phenyl]pyrrolidin-1-yl)-7-azaspiro[3.5]nonan-7-yl)-2-[(1*H*-pyrrolo[2,3-*b*]pyridin-5-yl)oxy]benzamide

sonrotoclox *N*-[4-(((1*r*,4*r*)-4-hydroxy-4-méthylcyclohexyl)méthyl)amino)-3-nitrobenzène-1-sulfonyl]-4-(2-((2*S*)-2-[2-(propan-2-yl)phényl]pyrrolidin-1-yl)-7-azaspiro[3.5]nonan-7-yl)-2-[(1*H*-pyrrolo[2,3-*b*]pyridin-5-yl)oxy]benzamide

sonrotoclox *N*-[4-(((1*r*,4*r*)-4-hidroxi-4-metilciclohexil)metil)amino)-3-nitrobenzeno-1-sulfonil]-2-[(1*H*-pirrolo[2,3-*b*]piridin-5-il)oxi]-4-(2-((2*S*)-2-[2-(propan-2-il)fenil]pirrolidin-1-il)-7-azaspiro[3.5]nonan-7-il)benzamide



sorimcovateinum #

sorimcovatein severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), omicron lineage B.1.1.529 (Gisaid: EPI_ISL_6640917) spike (S) glycoprotein fragment (1-1192), stable prefusion conformation variant (H⁶⁶⁵>P, R⁶⁶⁶>G, R⁶⁶⁷>S, R⁶⁶⁹>S, F⁸⁰¹>P, A⁸⁷⁶>P, A⁸⁸³>P, A⁹²⁶>P, K⁹⁷⁰>P, V⁹⁷¹>P) fused to the enterobacteria phage T4 fibrin foldon domain fragment (458-484, 1193-1219 in the current sequence), trimer, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

sorimcovatéine fragment de la glycoprotéine du spicule (S) (1-1192) du coronavirus 2 du syndrome respiratoire aigu sévère (SARS-CoV-2), lignée omicron B.1.1.529 (Gisaid: EPI_ISL_6640917), variant de conformation stable par pré-fusion (H⁶⁶⁵>P, R⁶⁶⁶>G, R⁶⁶⁷>S, R⁶⁶⁹>S, F⁸⁰¹>P, A⁸⁷⁶>P, A⁸⁸³>P, A⁹²⁶>P, K⁹⁷⁰>P, V⁹⁷¹>P) fusionné au fragment du domaine foldon de la fibratine du phage T4 d'entérobactéries (458-484, 1193-1219 dans la séquence actuelle), trimère, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

sorimcovateína fragmento de la glicoproteína de la espícula (S) (1-1192) del coronavirus 2 del síndrome respiratorio agudo severo (SARS-CoV-2), linaje omicron B.1.1.529 (Gisaid: EPI_ISL_6640917),

variante de conformación de prefusión estable (H⁶⁶⁵>P, R⁶⁶⁶>G, R⁶⁶⁷>S, R⁶⁶⁹>S, F⁸⁰¹>P, A⁸⁷⁶>P, A⁸⁸³>P, A⁹²⁶>P, K⁹⁷⁰>P, V⁹⁷¹>P) fusionado al fragmento de dominio de foldón de fibrina del fago T4 de enterobacterias (458-484, 1193-1219 en la secuencia actual), trímero, producido en células ováricas de hámster Chino (CHO), glicofoma alfa

Monomer sequence / Séquence du monomère / Secuencia del monómero	
QCVNLTRRTQ LPPAYTNSFT RGVYYPDKVF RSSLVHSTQD LFLPFFSNVT	50
WFHVIGSTNG TKRFDPNPLV FNDGVYFASI EKSNIIRGWI FGTTLDSKQT	100
SLLLVNNTATN VVIKVCPEQF CNDPFLDHKN NKSWMSEPR VYSSANNCTF	150
EYVSQPFLMD LEGKQGNFKN LRFVFKNID GYFKIYSKHT PIIIVREPDL	200
PQGSALQEPV VDLPIGINIT RFQTLALHR SYLTPGDSSS GWTAGAAAYY	250
VGYLQPRTEFL LKYNENGTIT DAVDCALDPL SETKCTLKFS TVEKGIYQTS	300
NFRVQPTESI VRFENITNLC PFDEVFNATR FASVYAMNRK RISNCVADYS	350
VLYNLAPFFT FKYCVGSPTK LNDLCFTNVY ADSFVIRGDE VRQIAPGQTG	400
NIADYNYKLP DDFTCGVIAW NSNKLDSKVS GNYNYLYRLF RKSNLKPFER	450
DISTEIQAG NKPENGVAGF NCFPLRSYS FRPTYGVGHQ PYRVVLSPE	500
LLHAPATVCG PPKSTNLVKN KCVNFENGL KGTGVLTESN KKFLLPQQFG	550
RDIADTDAV RDPQTEILD ITPCSFEGVS VITPGTNTSN QVAVLYQGVN	600
CTEVPVVAIHA DQLTPTWRVY STGSNVFQTR ACGLLGAEYV NNSYECDIPI	650
GAGICASYQT QTKSPGSAAS VASQSI IAYT MSLGAENSA YSNNSIAIPT	700
NFTISVTTTEI LPVSMTKTSV DCTMYICGDS TECSNLLQY GSFCQLKRA	750
LTGIAVEQDK NTQEVFAQVK QIYKTPPIKY FGCNFSQIL PDPSPKRSKRS	800
P IEDLLFNKV TLADAGFIKQ YGDCLGDI AA RDLI CAQKFK GLTVLPPLLT	850
DEMAIQYTS A LLAGITISGW TFGAGPALQI P FMQMA YRF NGIVGTQNVL	900
YENQKLIANQ FNSAIGKIQD SLSST P SALG KLQDVVNHNA QALNTLVKQL	950
SSKFGAISV LNDIFSRLL P P EA EVQIDRL ITGRLQSLQT YVTQQLIRAA	1000
EIRASANLAA TKMSECVLGQ SKRVDFCGKG YHLSMFPQSA PHGVVFLHVT	1050
VYPAQEKNT TAPAICHDGK AHFPREGV FV SNGTHWFVQT RNFVFPQIIT	1100
TDNTFVSGNC DVVIGLVNNT VYDPLQPELD SFKEELDKYF KNHTSPDVDL	1150
GDISGINASV VNIQKEIDRL NEVAKNINES LIDLQELGKY EQGYIPEAPR	1200
<u>DGQAYVRKDG</u> <u>ENVLLSTFL</u>	1219

Mutation / Mutation / Mutación
H⁶⁶⁵>P, R⁶⁶⁶>G, R⁶⁶⁷>S, R⁶⁶⁹>S, F⁸⁰¹>P, A⁸⁷⁶>P, A⁸⁸³>P, A⁹²⁶>P, K⁹⁷⁰>P, V⁹⁷¹>P

Foldon domain / Foldon domaine / Foldon dominio
GYIPEAPRDG QAYVRKDGW VLLSTFL 1193-1219

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-chain: 2-121, 116-148, 275-285, 320-345, 363-416, 375-509, 464-472, 522-574, 601-633, 646-655, 722-744, 727-733, 824-835, 1016-1027, 1066-1110

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación (predicted)
N4, N48, N59, N107, N131, N147, N218, N266, N315, N327, N587, N600, N641, N693, N701, N785, N1058, N1082, N1118, N1142, N1157, N1178

O-glycosylation sites / Sites de O-glycosylation / Posiciones de O-glicosilación (predicted)
T307, S309

N-terminal glutaminylation cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminylo N-terminal
Q1 >pyroglutamyl (pE, 5-oxoprolyl)

sotiburafuspum alfa #
sotiburafusp alfa

humanized vascular endothelial growth factor receptor 1 (VEGFR-1, Fms-like tyrosine kinase 1, FLT-1) extracellular domain fragment (129-228, 1-100 in the current sequence) fused via the peptide linker ¹⁰¹GGSGSGGSGGSGGS¹¹⁵ to the N-terminus of the heavy chain (116-564) of a humanized immunoglobulin G1-kappa anti-(human programmed cell death 1 ligand 1 (PD-L1, CD274) heavy chain variant L³⁵²>A, L³⁵³>A; disulfide bridged dimer, produced in Chinese hamster ovary (CHO) cells, glycoform alfa;
humanized monoclonal antibody fusion with human VEGF receptor type 1; antigen: human programmed cell death 1 ligand 1, PD-L1, programmed death ligand 1, PDCD1 ligand 1, B7 homolog 1, B7-H1 (CD274); CDR Source: *Mus musculus*; chain length: 564; fusion protein: 1-100 (domain 2 of the mature human extracellular domain of vascular endothelial growth factor receptor type-1 (VEGFR-1, VEGFR1) VEGF type 1 receptor); linker: 101-115; type: IgG1-kappa; heavy chain class: gamma1; HV germline: *Homo sapiens* IGHV1-3*01; HJ germline: *Homo sapiens* IGHJ4*01; HC germline:

	<p><i>Homo sapiens</i> IGHG1*03; VH: 116-235; CH1: 236-333; hinge: 334-348; CH2: 349-458 (L352A L353A, reduce FcGammaR and C1q binding); CH3: 459-563; CHS: 564-564 (K565del); CDR Kabat H1: GYTIH (146-150); CDR Kabat H2: WFYPGSGTLKYSEKFQG (165-181); CDR Kabat H3: HGTGTLMAMDY (214-224); light chain class: kappa; light chain length: 219; LV germline: <i>Homo sapiens</i> IGKV2-29*02; LJ germline: <i>Homo sapiens</i> IGKJ2*01; LC germline: <i>Homo sapiens</i> IGKC*01; VL: 1-112; CL: 113-219; CDR Kabat L1: KSSQSLANSYGNTYLS (24-39); CDR Kabat L2: GISNRFS (55-61); CDR Kabat L3: LQGTHQPPT (94-102)</p>
sotiburafusp alfa	<p>fragment du domaine extracellulaire du récepteur 1 du facteur de croissance endothélial vasculaire humanisé (VEGFR-1, tyrosine kinase 1 de type Fms, FLT-1) (129-228, 1-100 dans la séquence actuelle) fusionné via la liaison peptidique¹⁰¹GGSGSGSGSGSGGS¹¹⁵ à l'extrémité N-terminale de la chaîne lourde (116-564) du variant de la chaîne lourde L^{352>A}, L^{353>A} d'une immunoglobuline G1-kappa anti-(ligand 1 humain de mort cellulaire programmée 1 (PD-L1, CD274) humanisée; dimère à pont disulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa; fusion d'un anticorps monoclonal humanisé avec le récepteur humain du VEGF de type 1; antigène: ligand humain 1 de mort cellulaire programmée 1, PD-L1, ligand 1 de mort programmée, ligand 1 de PDCD1, homologue 1 de B7, B7-H1 (CD274); source CDR: <i>Mus musculus</i>; longueur de la chaîne: 564; protéine de fusion: 1-100 (domaine 2 du domaine extracellulaire humain mature du récepteur du facteur de croissance endothélial vasculaire de type 1 (VEGFR-1, VEGFR1) VEGF type 1); liaison: 101-115; type: IgG1-kappa; classe de la chaîne lourde: gamma1; HV lignée germinale: <i>Homo sapiens</i> IGHV1-3*01; HJ lignée germinale: <i>Homo sapiens</i> IGHJ4*01; HC lignée germinale: <i>Homo sapiens</i> IGHG1*03; VH: 116-235; CH1: 236-333; charnière: 334-348; CH2: 349-458 (L352A L353A, réduit la liaison de FcGammaR et C1q); CH3: 459-563; CHS: 564-564 (K565del); CDR Kabat H1: GYTIH (146-150); CDR Kabat H2: WFYPGSGTLKYSEKFQG (165-181); CDR Kabat H3: HGTGTLMAMDY (214-224); classe de la chaîne légère: kappa; longueur de la chaîne légère: 219; LV lignée germinale: <i>Homo sapiens</i> IGKV2-29*02; LJ lignée germinale: <i>Homo sapiens</i> IGKJ2*01; LC lignée germinale: <i>Homo sapiens</i> IGKC*01; VL: 1-112; CL: 113-219; CDR Kabat L1: KSSQSLANSYGNTYLS (24-39); CDR Kabat L2: GISNRFS (55-61); CDR Kabat L3: LQGTHQPPT (94-102)</p>
sotiburafusp alfa	<p>receptor 1 del factor de crecimiento endotelial vascular humanizado (VEGFR-1, tirosina kinasa de tipo Fms, FLT-1) fragmento de dominio extracelular (129-228, 1-100 en la secuencia actual) fusionado a través del enlace peptídico ¹⁰¹GGSGSGSGSGSGGS¹¹⁵ al N-terminal de la cadena pesada (116-564) de la inmunoglobulina humanizada G1-kappa anti-(ligando 1 de muerte celular 1 programada humana 1 (PD-L1, CD274) variante de cadena pesada L^{352>A}, L^{353>A}; dímero con puente disulfuro, producido en células ováricas de hámster Chino (CHO), forma glicosilada alfa; anticuerpo monoclonal humanizado de fusión con receptor VEGF de tipo 1; antígeno: ligando 1 de muerte celular programada humana 1, PD-L1, ligando 1 de muerte programada, PDCD1 ligando 1, B7 homólogo 1, B7-H1 (CD274); fuente CDR: <i>Mus musculus</i>; longitud cadena: 564; proteína de fusión: 1-100 (dominio 2 del dominio extracelular maduro humano del receptor tipo 1 del factor de crecimiento endotelial vascular (VEGFR-1, VEGFR1) receptor VEGF tipo 1); enlace: 101-115; tipo: IgG1-kappa; clase cadena pesada: gamma1; línea germinal HV: <i>Homo sapiens</i> IGHV1-3*01; línea</p>

germinal HC: *Homo sapiens* IGHG1*03; VH: 116-235; CH1: 236-333; bisagra: 334-348; CH2: 349-458 (L352A L353A, unión reducida FcGammaR y C1q); CH3: 459-563; CHS: 564-564 (K565del); CDR Kabat H1: GYTIH (146-150); CDR Kabat H2: WFYPGSGTLKYSEKFQG (165-181); CDR Kabat H3: HGTGTLMAMDY (214-224); clase cadena ligera: kappa; longitud cadena ligera: 219; línea germinal LV: *Homo sapiens* IGKV2-29*02; línea germinal LJ: *Homo sapiens* IGKJ2*01; línea germinal LC: *Homo sapiens* IGKC*01; VL: 1-112; CL: 113-219; CDR Kabat L1: KSSQSLANSYGNTYLS (24-39); CDR Kabat L2: GISNRFS (55-61); CDR Kabat L3: LQGTHQPPT (94-102)

Sequence / Séquence / Secuencia

Heavy chain / Chaîne lourde / Cadena pesada: VEGFR1-IgG1

SDTGRPFVEM YSEIPEIIHM TEGRELVIPC RVTSPNITVT LKKFPLDTLI 50
 PDGKRIIWD S RKGFIISNAT YKEIGLLTCE ATVNGHLYKT NYLTHRQNT 100
 GSGSGSGSGS GSGSQVQLV QSGAEVKKPG ASVKVSKCAS GYAFTGYTIH 150
 WVRQAPGQRL EWMGWFPYPS GTLKYSEKFQ GRVTITRDKS LSTAYMELSS 200
 LRSEDTAVYY CARHGTGTLM AMDYWGGQTL VTVSSASTKG PSVFPFLAPSS 250
 KSTSGGTAAL GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL 300
 SSVVTVPSSS LGTQTYICNV NHKPSNTKVD KRVEPKSCDK THTCPPCPAP 350
 EAAGGSPVFL FPPKPKDTLM ISRTPEVTCV VVDVSHEDPE VKFNWYVDGV 400
 EVHNAKTKPR EEQYNSTYRV VSVLTVLHQD WLNQKEYKCK VSNKALPAPI 450
 EKTISKAKGQ PREPQVYTL PPSREEMTKNQ VSLTCLVKG F YPSDIAVEWE 500
 SNGQPENNYK TTPPVLDSDG SFFLYSKLTV DKSRWQQGNV FSCSVMHEAL 550
 HNHYTQKSL S LSPG 564

Light chains / Chaînes légères / Cadenas ligeras

DVVMTQTPLS LSVTPGQPAS ISCKSSQSLA NSYGNLYLSW YLHKPGQSPQ 50
 LLIYGISNRF SGVPRDFSGS GSGTDFTLKI SRVEAEDVGV YYCLQGTHQP 100
 PTFGQGTKLE IKRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK 150
 VQWKVDNALQ SGNSQESVTE QDSKDYSTYSL SSSLTTLTKAD YEKHKVYACE 200
 VTHQGLSSPV TKSFNRGEC 219

Peptide linker / Peptides liant / Péptido de unión

GGSGSGSGSGSGS 101-115

Mutation / Mutation / Mutación

L352, L352">A, L353, L353">A

Post-translational modifications

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

Intra-VEGFR1 30-79, 30"-79"

Intra-H 137-211, 262-318, 379-439, 485-543
137"-211", 262"-318", 379"-439", 485"-543"

Intra-L 23'-93', 139'-199', 23'''-93'''', 139'''-199'''

Inter-H-L 338-219', 338"-219"

Inter-H-H 344-344", 347-347"

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

VEGFR1-IgG1 heavy chain: N36, N68, N415, N36", N68", N415"

Oxidation sites / Sites de oxidation / Posiciones de oxidación

VEGFR1-HC: M10, M163, M196, M220, M370, M546,
M10", M163", M196", M220", M370", M546"

LC: M4', M4'''

Deamidation sites / Sites de désamidation / Posiciones de desamidación

VEGFR1-HC (succinimide formation): N84, N433, N502, N507, N508,
N84", N433", N502", N507", N508"

LC: N31', N35', N58', N31'''', N35'''', N58'''

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immunoglobulin G1-kappa, anti-[*Homo sapiens* CTLA4 (cytotoxic T-lymphocyte associated protein 4, CTLA-4, CD152)], *Homo sapiens* monoclonal antibody with cleavable prodomain;

gamma1 heavy chain *Homo sapiens* (1-447) [VH (*Homo sapiens*IGHV3-30*01 (94.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens*IGHG1*01v, G1m17,1>G1m3,1 CH1 R120, CH3 D12, L14 (CH1 R120 (215) (119-216), hinge 1-15 (217-231), CH2 (232-341), CH3 D12 (357), L14 (359) (342-446), CHS K2>del (447)) (119-447)], (221-259')-disulfide with kappa light chain *Homo sapiens* (1'-259') [cleavable prodomain (1'-44') fused to V-KAPPA (*Homo sapiens*IGKV3-20*01 (97.9%) -IGKJ1*01 (100%), CDR-IMGT [7.3.9] (71-77.95-97.134-142)) (45'-152') -*Homo sapiens*IGKC*01 (100%), Km3 A45.1 (198), V101 (236) (153'-259')]; dimer (227-227":230-230")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

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immunoglobuline G1-kappa, anti-[*Homo sapiens* CTLA4 (protéine 4 associée aux lymphocytes T cytotoxiques, CTLA-4, CD152)], anticorps monoclonal *Homo sapiens* avec prodomaine clivable;

chaîne lourde gamma1 *Homo sapiens* (1-447) [VH (*Homo sapiens*IGHV3-30*01 (94.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens*IGHG1*01v, G1m17,1>G1m3,1 CH1 R120, CH3 D12, L14 (CH1 R120 (215) (119-216), charnière 1-15 (217-231), CH2 (232-341), CH3 D12 (357), L14 (359) (342-446), CHS K2>del (447)) (119-447)], (221-259')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-259') [prodomaine clivable (1'-44') fusionné to V-KAPPA (*Homo sapiens*IGKV3-20*01 (97.9%) -IGKJ1*01 (100%), CDR-IMGT [7.3.9] (71-77.95-97.134-142)) (45'-152') -*Homo sapiens*IGKC*01 (100%), Km3 A45.1 (198), V101 (236) (153'-259')]; dimère (227-227":230-230")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

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immunoglobulina G1-kappa, anti-[*Homo sapiens* CTLA4 (proteína 4 asociada a los linfocitos T citotóxicos, CTLA-4, CD152)], anticuerpo monoclonal *Homo sapiens* con prodominio escindible;

cadena pesada gamma1 *Homo sapiens* (1-447) [VH (*Homo sapiens*IGHV3-30*01 (94.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens*IGHG1*01v, G1m17,1>G1m3,1 CH1 R120, CH3 D12, L14 (CH1 R120 (215) (119-216), bisagra 1-15 (217-231), CH2 (232-341), CH3 D12 (357), L14 (359) (342-446), CHS K2>del (447)) (119-447)], (221-259')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-259') [prodominio escindible (1'-44') fusionado a V-KAPPA (*Homo sapiens*IGKV3-20*01 (97.9%) -IGKJ1*01 (100%), CDR-IMGT [7.3.9] (71-77.95-97.134-142)) (45'-152') -*Homo sapiens*IGKC*01 (100%), Km3 A45.1 (198), V101 (236) (153'-259')]; dímero (227-227":230-230")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

QVQLVESGGG VVQPGRSRLR SCAASGFTFS SYTMHWVRQA PGKGLEWVTF 50
 ISYDGNKKYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAIYYCARTG 100
 WLGPFDYWGQ GTLVTVSSAS TRGSPVFLA PSSKSTSGGT AALGCLVKDY 150
 FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVTVTP SSSLGTQTYI 200
 CNVNHKPSNT KVKRVEPKS CDKTHTCPPC PAPELLGGPS VFLFPPKPKD 250
 TLMISRTPEV TCVVVDVSHS DPEVKFNMYV DGVEVHNAKT KPREEQYNST 300
 YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY 350
 TLPSPRDEL TKNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTTPPVL 400
 SDGSFFLYSK LTVDKSRWQQ GNVFSCSMH EALNHHTYTK SLSLSPG 447

Light chain / Chaîne légère / Cadena ligera

QQSGSGSRTQ LYGYNLCPYG GSSSGSISL GLLSGRSDNP GGGSEIVLTQ 50
 SPGTLTSLSPG ERATLSCRAS QSVGSSYLAW YQQKPGQAPR LLIYGAFSRA 100
 TGPDRFSGS GSGTDFLTI SRLEPEDFAV YVYQQYVYSSP WTFGQGTQV 150
 IKRTVAAPSV FIFPPSDEQL KSGTASVIVL LNNFYPREAK VQWKVDNALQ 200
 SGNSQESVTE QDSKDYSTLS SPTLTKSKAD YEKHKVYACE VTHQGLSSPV 250
 TKSFNREGC 259

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) 67"-133" 179"-239"
 67"-133" 179"-239"

Inter-H-L (h 5-CL 126) 221-259' 221"-259"

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-oxopropyl) / pyroglutamyle (pE, 5-oxopropyle) / 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 biantennarios complejos fucosilados

stapokibartum #
 stapokibart

immunoglobulin G4-kappa, anti-[*Homo sapiens* IL4R (interleukin 4 receptor, IL4RA, IL-4RA, interleukin 13 receptor, CD124)], humanized monoclonal antibody; gamma4 heavy chain humanized(1-446) [VH (*Homo sapiens* IGHV3-23*03 (92.9%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (120-217), hinge 1-12 S10>P (227) (218-229), CH2 L92 (308) (230-339), CH3 (340-444), CHS (445-446)) (120-446)], (133-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (87.4%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214'')]; dimer (225-225":228-228")-bisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1 lacking the glutamine synthetase (GS-KO) gene, glycoform alfa

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immunoglobuline G4-kappa, anti-[*Homo sapiens* IL-4R (récepteur de l'interleukine 4, IL4RA, IL-4RA, récepteur de l'interleukine 13, CD124)], anticorps monoclonal humanisé; chaîne lourde gamma4 humanisée (1-446) [VH (*Homo sapiens* IGHV3-23*03 (92.9%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (120-217), charnière 1-12 S10>P (227) (218-229), CH2 L92 (308) (230-339), CH3 (340-444), CHS (445-446)) (120-446)], (133-214')-disulfure avec la chaîne légère kappa

humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (87.4%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (225-225":228-228")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1 ne présentant pas le gène de la glutamine synthétase (GS-KO), glycoforme alfa

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immunoglobulina G4-kappa, anti-[*Homo sapiens* IL-4R (receptor de la interleukina 4, IL4RA, IL-4RA, receptor de la interleukina 13, CD124)], anticuerpo monoclonal humanizado; cadena pesada gamma4 humanizada (1-446) [VH (*Homo sapiens*IGHV3-23*03 (92.9%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.8.12] (26-33.51-58.97-108))] (1-119) -*Homo sapiens* IGHG4*01, nG4m(a) CH2 L92, G4v5 h P10 (CH1 (120-217), bisagra 1-12 S10>P (227) (218-229), CH2 L92 (308) (230-339), CH3 (340-444), CHS (445-446)) (120-446)], (133-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (87.4%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (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

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EVQLLESGGG LVQPGGSLRL SCAASGFTFS RYAMSWVRQA PGKGLEWVST 50
ISSGGSYTNV ADSVKGRFTI SRDNVKNLTLY LQMNSLRAED TAVYYCARAT 100
ARATEFAYWG QGTLVTVSSA STKGPSVFFPL APCSRSTSES TAALGCLVKD 150
YFPEPVTVSW NSGALTSGVH TFPVAVLQSSG LYSLSVVTV PSSSLGTRKY 200
TCNVDHKPSN TKVDKRVESK YGPPCPPCA PEFLLGGPSVF LFPPKFKDTL 250
MISRTPVEVTC VVVDVSDQEDP EVQFNWYVDG VEVHNAKTKP REEQFNSTYR 300
VVSVLTVLHQ DWLNGKEYKC KVSNGKLPSS IEKTISKAKG QPREPVYVTL 350
PPSQEEMTKN QVSLTCLVKG FYPSDIAVEW ESNQPEPENNY KTTPPVLDS 400
GSFFLYSRLT VDKSRWQEGN VFSCSVMHEA LHNHYTQKSL SLSLGGK 446
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Light chain / Chaîne légère / Cadena ligera

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DIQMTQSPSS LSASVGDRTV ITCQASQDIS NYLNWYQQKP GKAPKLLIYY 50
TSRLHSGVPS RFSGSGSGTD YTLTISSLQF EDFATYFCQQ GNTLPLTFGG 100
GTVKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY BREAKVQWVK 150
DNALQSGNSQ ESVTEQDSKD STYLSLSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEK 214
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Post-translational modifications

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

Intra-H (C23-C104) 22-96 146-202 260-320 366-424
 22"-96" 146"-202" 260"-320" 366"-424"
 Intra-L (C23-C104) 23"-88" 134"-194"
 23"-88" 134"-194"
 Inter-H-L (CH1 10-CL 126) 133-214' 133"-214"
 Inter-H-H (h 8, h 11) 225-225" 228-228"

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

H CH2 N84.4: 296, 296"

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

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

survodutidum

survodutide

L-histidyl-1-aminocyclobutanoyl-L-glutaminylglycyl-L-threonyl-L-phenylalanyl-L-threonyl-L-seryl-L- α -aspartyl-L-tyrosyl-L-seryl-L-lysyl-L-tyrosyl-L-leucyl-L- α -aspartyl-L- α -glutamyl-L-arginyl-L-alanyl-L-alanyl-L-lysyl-L- α -aspartyl-L-phenylalanyl-L-isoleucyl- N^6 -[N -(17-carboxyheptadecanoyl)-L- γ -glutamylglycyl-L-serylglycyl-L-serylglycylglycyl]-L-lysyl-L-tryptophyl-L-leucyl-L- α -glutamyl-L-seryl-L-alaninamide

survodutide

L-histidyl-1-aminocyclobutanoyl-L-glutaminylglycyl-L-thréonyl-L-phénylalanyl-L-thréonyl-L-séryl-L- α -aspartyl-L-tyrosyl-L-séryl-L-lysyl-L-tyrosyl-L-leucyl-L- α -aspartyl-L- α -glutamyl-L-arginyl-L-alanyl-L-alanyl-L-lysyl-L- α -aspartyl-L-phénylalanyl-L-isoleucyl- N^6 -[N -(17-carboxyheptadécanoyl)-L- γ -glutamylglycyl-L-sérylglycyl-L-sérylglycylglycyl]-L-lysyl-L-tryptophyl-L-leucyl-L- α -glutamyl-L-séryl-L-alaninamide

survodutida

L-histidil-1-aminociclobutanoil-L-glutaminiłglicil-L-treonil-L-fenilalanil-L-treonil-L-seril-L- α -aspartil-L-tirosil-L-seril-L-lisil-L-tirosil-L-leucil-L- α -aspartil-L- α -glutamil-L-arginil-L-alanil-L-alanil-L-lisil-L- α -aspartil-L-fenilalanil-L-isoleucil- N^6 -[N -(17-carboxiheptadecanoil)-L- γ -glutamilglicil-L-serilglicil-L-serilglicilglicil]-L-lisil-L-triptofil-L-leucil-L- α -glutamil-L-seril-L-alaninamida

C₁₉₂H₂₈₉N₄₇O₆₁

Sequence I / Séquence I / Secuencia I

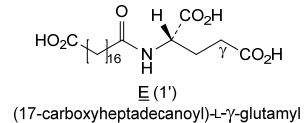
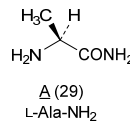
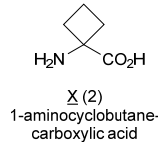
HXQGTFTSDY SKYLDERRAAK DFIKWLESA 29

Sequence II / Séquence II / Secuencia II

EGSGSGG 7'

Amide bridge location / Position du pont amide / Posición del puente amido
7'-24 (Gly⁷-Lys^{6,24})

Modified residues / Résidus modifiés / Restos modificados

**suvemcitugum #**

suvemcitug

immunoglobulin G1-kappa , anti-[*Homo sapiens* VEGFA (vascular endothelial growth factor A, VEGF-A, VEGF)], humanized monoclonal antibody;
gamma1 heavy chain humanized (1-452) [VH (*Homo sapiens*IGHV3-21*01 (74.7%) -(IGHD) -IGHJ2*01 (92.9%), CDR-IMGT [9.8.14] (26-34.52-59.98-111))] (1-122) -*Homo sapiens*IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (219) (123-220), hinge 1-15 (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS (451-452)) (123-452)], (225-219')-disulfide with kappa light chain humanized (1'-219') [V-KAPPA (*Homo sapiens*IGKV1-6*01 (85.4%) -IGKJ4*01 (100%), CDR-IMGT [8.3.12] (27-34.52-54.91-102)) (1'-112')] -*Homo sapiens*IGKC*01 (100%), Km3, A45.1 (158), V101 (196) (113'-219'); dimer (231-231":234-234")-bisdisulfide; produced in Chinese hamster ovary (CHO) cells, cell line CHO-DG44, glycoform alfa

suvemcitug immunoglobuline G1-kappa, anti-[*Homo sapiens* VEGFA facteur de croissance A de l'endothélium vasculaire, VEGF-A, VEGF)]; anticorps monoclonal humanisé chaîne lourde gamma1 humanisée (1-452) [VH (*Homo sapiens* IGHV3-21*01 (74.7%) -(IGHD) -IGHJ2*01 (92.9%), CDR-IMGT [9.8.14] (26-34.52-59.98-111)) (1-122) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (219) (123-220), charnière 1-15 (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS (451-452)) (123-452)], (225-219')-disulfure avec la chaîne légère kappa humanisée (1'-219') [V-KAPPA (*Homo sapiens* IGKV1-6*01 (85.4%) -IGKJ4*01 (100%), CDR-IMGT [8.3.12] (27-34.52-54.91-102))] (1'-112') -*Homo sapiens* IGKC*01 (100%), Km3, A45.1 (158), V101 (196) (113'-219')]; dimère (231-231":234-234")-bisdisulfure; produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-DG44, glycoforme alfa

suvemcitug inmunoglobulina G1-kappa, anti-[*Homo sapiens* VEGFA factor de crecimiento A de la endotelina vascular, VEGF-A, VEGF)]; anticuerpo monoclonal humanizado cadena pesada gamma1 humanizada (1-452) [VH (*Homo sapiens* IGHV3-21*01 (74.7%) -(IGHD) -IGHJ2*01 (92.9%), CDR-IMGT [9.8.14] (26-34.52-59.98-111)) (1-122) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, CH3 D12, L14 (CH1 K120 (219) (123-220), bisagra 1-15 (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS (451-452)) (123-452)], (225-219')-disulfuro con la cadena ligera kappa humanizada (1'-219') [V-KAPPA (*Homo sapiens* IGKV1-6*01 (85.4%) -IGKJ4*01 (100%), CDR-IMGT [8.3.12] (27-34.52-54.91-102))] (1'-112') -*Homo sapiens* IGKC*01 (100%), Km3, A45.1 (158), V101 (196) (113'-219')]; dímero (231-231":234-234")-bisdisulfuro, producido en las células ováricas de hamster chino (CHO), línea celular CHO-DG44, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVKPGGSLRL SCAASGFSPS NNDVMCWVRQ APGKGLEWIG 50
CIMTIDVWTE YANWAKSRFT VSRDSAKNSV YLQMNSLRAE DTAVYFCARD 100
SVGSPILMSFD LWGPGTLVTV SSASTKGPSV FPLAPSSKST SGGTAALGCL 150
VKDYFFPEPVT VSWNSGALTS GVHTFFPAVLQ SSGLYLSLSSV VTFPSSSLGT 200
QTYICNVNHK PSNTKVKDKV EPKSCDKTHT CPPCPAPELL GGPSVFLFPP 250
KPKDTLMIISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLNL GKEYKCKVSN KALPAPIEKT ISKAKGQPRE 350
PQVYTLPPSR DELTKNQVSL TCLVKGFPYS DIAVEWESNG QPENNYKTFP 400
PVLDSGDSFF LYSKLTVDKS RWQQGNVFSC SVMHEALHNN YTQKSLSLSP 450
GK 452
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Light chain / Chaîne légère / Cadena ligera

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DIQMTQSPSS LSASVDRVT INCQASQSIY NNNELSWYQQ KPGKPPKLLI 50
YRASTLASGV PSRFSGSGSG TDFLTITISL QPEDVATYYC GGYKSYSDNG 100
NGFSGGKTVE IKRTVAAPSV FIFPPSDEQL KSGTASVVL LNNFYPREAK 150
VQWKVDNALQ SGNSQESVTE QDSKSTYSLS SSTLTLSKAD YEKHKVYACE 200
VTHQGLSSPV TKSFNREGC 219
```

Post-translational modifications

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

Intra-H (C23-C104) 22-97 149-205 266-326 372-430
 22"-97" 149"-205" 266"-326" 372"-430"

Additional intra-H C40-C55 36-51
 36"-51"

Intra-L (C23-C104) 23'-90' 139'-199'
 23"-90" 139"-199"

Inter-H-L (h 5-CL 126) 225-219' 225"-219"

Inter-H-H (h 11, h 14) 231-231" 234-234"

N-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 biantenares complejos fucosilados

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

suvutresgenum autoleucelum #

suvutresgene autoleucel

autologous T lymphocytes obtained from peripheral blood lymphocytes by leukapheresis, transduced with a self-inactivating, non-replicating lentiviral vector encoding an affinity-enhanced cancer testis antigen (NY-ESO-1^{c259}) specific T-cell receptor (TCR) and co-expressing a dominant-negative transforming growth factor beta (TGF- β) type II cell surface receptor (dnTGF- β RII; truncated non-signalling TGF- β RII). The TCR is based on *letetresgene autoleucel* and specifically recognises a peptide (SLLMWITQC), which is shared by the cancer antigens NY-ESO-1 (CTAG1B) and LAGE-1a (CTAG2) presented on human leukocyte antigen HLA-A*02. The expressed transgene comprises dnTGF- β RII joined by the foot-and-mouth disease virus ribosome skipping sequence (F2A) to the TCR α chain, joined by the porcine teschovirus-1 ribosome skipping sequence (P2A) to the TCR β chain and is under control of the elongation factor 1 alpha (EF1 α) promoter. The construct is flanked by long terminal repeats (LTR) that have a deletion in the U3 part of the LTR, and also contains a ψ packaging signal, Rev response element (RRE), central polypurine tract (cPPT) and a central termination sequence (CTS). The vector is pseudotyped with 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 initially in media supplemented with AB serum and interleukin 2 (IL-2), and then in media supplemented with only IL-2. The T lymphocytes ($\geq 95\%$) are positive for the transgene ($\geq 10\%$ CAR positive), and are cytotoxic to T2 cells loaded with the target peptide

suvutresgène autoleucel

lymphocytes T autologues obtenus à partir de lymphocytes de sang périphérique par leucaphérèse, transduits avec un vecteur lentiviral auto-inactivant et non répliquant codant un récepteur de cellules T (TCR) spécifique de l'antigène du cancer du testicule à affinité renforcée (NY-ESO-1^{c259}) et co-exprimant un récepteur de surface cellulaire dominant-négatif du facteur de croissance transformant bêta (TGF- β) de type II (dnTGF- β RII; TGF- β RII tronqué non signalant). Le TCR est basé sur le *lététresgène autoleucel* et reconnaît spécifiquement un peptide (SLLMWITQC) qui est partagé par les antigènes de cancer NY-ESO-1 (CTAG1B) et LAGE-1a (CTAG2) présentés sur l'antigène leucocytaire humain HLA-A*02. Le transgène exprimé comprend dnTGF- β RII lié par la séquence de saut d'exon du ribosome du virus de la fièvre aphteuse (F2A) à la chaîne TCR α , lié par la séquence de saut d'exon du ribosome du teschovirus-1 de porc (P2A) à la chaîne TCR β et est sous le contrôle du promoteur du facteur d'élongation 1 alpha (EF1 α). La construction est flanquée de longues répétitions terminales (LTR) qui présentent une délétion dans la partie U3 de la LTR, et contient également un signal d'encapsidation ψ , un élément de réponse Rev (RRE), un tractus polypurine central (cPPT) et une séquence de terminaison centrale (CTS). 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/CD8 par immunosélection positive, activé par des agonistes CD3 et CD28 et transduit avec le vecteur lentiviral. Les cellules sont ensuite développées dans un premier temps dans un milieu complété par du sérum AB et

de l'interleukine 2 (IL-2), puis dans un milieu complétement uniquement par de l'IL-2. Les lymphocytes T (≥95%) sont positifs pour le transgène (≥10% CAR positif), et sont cytotoxiques pour les cellules T2 chargées avec le peptide cible

suvutresgén autoleucel

linfocitos T autólogos obtenidos de linfocitos de sangre periférica mediante leucoaféresis, transducidos con un vector lentiviral auto inactivante, no replicativo, que codifica para un receptor de linfocitos T (TCR) con afinidad aumentada, específico para el antígeno de cáncer de testículo (NY-ESO-1^{c259}) y que coexpresa un receptor de superficie celular dominante negativo del factor de crecimiento transformante beta (TGF-β) tipo II (dnTGF-βRII; TGF-βRII truncado, no señalizante). El TCR está basado en *letetresgén autoleucel* y reconoce específicamente un péptido (SLLMWITQC), compartido por los antígenos de cáncer NY-ESO-1 (CTAG1B) y LAGE-1a (CTAG2), presentado en el antígeno común leucocitario HLA-A*02. El transgén expresado contiene dnTGF-βRII unido, mediante la secuencia de salto ribosómico del virus de la fiebre aftosa (F2A), a la cadena TCRα, unida, mediante la secuencia de salto ribosómico del teschovirus 1 porcino (P2A), a la cadena TCRβ y está bajo el control del promotor del factor de elongación 1 alfa (EF1α). El constructo está flanqueado por repeticiones terminales largas (LTR) que tienen una delección en la parte U3 del LTR, y también contiene una señal de empaquetamiento ψ, un elemento de respuesta Rev (RRE), una secuencia de tracto de polipurina central (cPPT) y una secuencia de terminación central (CTS). El vector está seudotipado con la glicoproteína G del virus de la estomatitis vesicular (VSV). El material de leucoaféresis se enriquece para linfocitos T CD4/CD8 mediante inmunoselección positiva, se activa mediante agonistas de CD3 y CD28 y se transduce con el vector lentiviral. Las células son después expandidas inicialmente en medio suplementado con suero AB e interleuquina 2 (IL-2), y después en medio suplementado sólo con IL-2. Los linfocitos T (≥95%) son positivos para el transgén (≥10% positivos para el CAR) y son citotóxicos frente a células T2 cargadas con el péptido diana

suzetriginum

suzetrigine

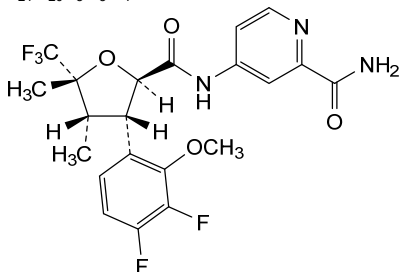
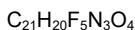
4-[(2R,3S,4S,5R)-3-(3,4-difluoro-2-methoxyphenyl)-4,5-dimethyl-5-(trifluoromethyl)oxolane-2-carboxamido]pyridine-2-carboxamide

suzétrigine

4-[(2R,3S,4S,5R)-3-(3,4-difluoro-2-méthoxyphényl)-4,5-diméthyl-5-(trifluorométhyl)oxolane-2-carboxamido]pyridine-2-carboxamide

suzetrigina

4-[(2R,3S,4S,5R)-3-(3,4-difluoro-2-metoxifenil)-4,5-dimetil-5-(trifluorometil)oxolano-2-carboxamido]piridina-2-carboxamida

**talpirastidum**

talpirastide

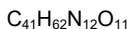
angiotensin-(1-7)-peptide;
L- α -aspartyl-L-arginyl-L-valyl-L-tyrosyl-L-isoleucyl-L-histidyl-L-proline

talpirastide

angiotensine-(1-7)-peptide;
L- α -aspartyl-L-arginyl-L-valyl-L-tyrosyl-L-isoleucyl-L-histidyl-L-proline

talpirastida

angiotensina-(1-7)-péptido;
L- α -aspartil-L-arginil-L-valil-L-tirosil-L-isoleucil-L-histidil-L-prolina



H—Asp—Arg—Val—Tyr—Ile—His—Pro—OH

tamuzimodum

tamuzimod

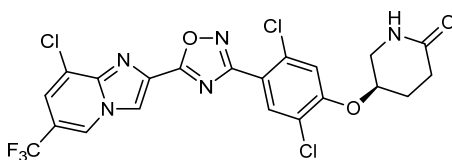
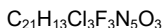
(5*R*)-5-(2,5-dichloro-4-{5-[8-chloro-6-(trifluoromethyl)imidazo[1,2-*a*]pyridin-2-yl]-1,2,4-oxadiazol-3-yl}phenoxy)piperidin-2-one

tamuzimod

(5*R*)-5-(2,5-dichloro-4-{5-[8-chloro-6-(trifluorométhyl)imidazo[1,2-*a*]pyridin-2-yl]-1,2,4-oxadiazol-3-yl}phénoxy)pipéridin-2-one

tamuzimod

(5*R*)-5-(2,5-dicloro-4-{5-[8-cloro-6-(trifluorometil)imidazo[1,2-*a*]piridin-2-il]-1,2,4-oxadiazol-3-il}fenoxi)piperidin-2-ona

**taplucaïnium chloride**

taplucaïnium chloride

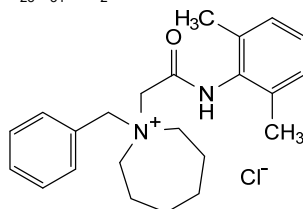
1-benzyl-1-[2-(2,6-dimethylanilino)-2-oxoethyl]azépan-1-ium chloride

chlorure de taplucaïnium

chlorure de 1-benzyl-1-[2-(2,6-diméthylanilino)-2-oxoéthyl]azépan-1-ium

cloruro de taplucainio

cloruro de 1-bencil-1-[2-(2,6-dimetilanilino)-2-oxoetil]azepan-1-ium

C₂₃H₃₁ClN₂Otegoprubartum #
tegoprubart

immunoglobulin G1-kappa, anti-[*Homo sapiens* CD40LG (CD40 ligand, CD40L, tumor necrosis factor ligand superfamily member 5, TNFSF5, tumor necrosis factor related activation protein, TRAP, CD154)], chimeric monoclonal antibody; gamma1 heavy chain chimeric (1-448) [VH Musmus/Homsap (*Mus musculus* IGHV1S81*02 (84.5%) -(IGHD) -IGHJ3*01 (90.9%) A128>S (118)/*Homo sapiens* IGHV1-46*01 (76.5%) -(IGHD) -IGHJ1*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, G1v37 h S5, G1v61 h S11, G1v62 h S14, G1v63 CH2 S2 (CH1 K120 (215) (119-216), hinge 1-15 C5>S (221), C11>S (227), C14>S (230) (217-231), CH2 P2>S (239) (232-341), CH3 D12 (357), L14 (359) (342-446), CHS (447-448)) (119-448)], non covalently paired to the kappa light chain chimeric (1'-218') [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'-111') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218')]; dimer non covalent, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

tégooprubart

immunoglobuline G1-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)], anticorps monoclonal chimérique; chaîne lourde gamma1 chimérique (1-448) [VH Musmus/Homsap (*Mus musculus* IGHV1S81*02 (84.5%) -(IGHD) -IGHJ3*01 (90.9%) A128>S (118)/*Homo sapiens* IGHV1-46*01 (76.5%) -(IGHD) -IGHJ1*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, G1v37 h S5, G1v61 h S11, G1v62 h S14, G1v63 CH2 S2 (CH1 K120 (215) (119-216), charnière 1-15 C5>S (221), C11>S (227), C14>S (230) (217-231), CH2 P2>S (239) (232-341), CH3 D12 (357), L14 (359) (342-446), CHS (447-448)) (119-448)], appariée de manière non covalente à la chaîne légère kappa chimérique (1'-218') [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'-111') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218')]; dimère non covalent, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

tegoprubart

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CD40LG (CD40 ligando, CD40L, miembro 5 de la superfamilia de los ligandos factores de necrosis tumoral, TNFSF5, proteína de activación con el factor de necrosis tumoral, TRAP, CD154)], anticuerpo monoclonal quimérico;
cadena pesada gamma1 quimérica (1-448) [VH Musmus/Homsap (*Mus musculus* IGHV1S81*02 (84.5%) -(IGHD) -IGHJ3*01 (90.9%) A128>S (118)/*Homo sapiens* IGHV1-46*01 (76.5%) -(IGHD) -IGHJ1*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, G1v37 h S5, G1v61 h S11, G1v62 h S14, G1v63 CH2 S2 (CH1 K120 (215) (119-216), bisagra 1-15 C5>S (221), C11>S (227), C14>S (230) (217-231), CH2 P2>S (239) (232-341), CH3 D12 (357), L14 (359) (342-446), CHS (447-448)) (119-448)], manera emparejada no covalente a la cadena ligera kappa quimérica (1'-218') [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'-111') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218')]; dímero no covalente, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

QVQLVQSGAE VVKPGASVKL SCKASGYIFT SYMYWVKQA PGQGLEWIGE 50
INPNSGDTNF NEKFKSKATL TVDKSASTAY MELSSLRSED TAVYYCTRSR 100
GRNDMDSWGQ GTLVTVSSAS TKGPSVFFLA PSSKSTSGGT AALGCLVKDY 150
FPEPVTYISWN SGALTSVGHV FPAVLQSSGL YLSSVVTVV SSSLGTQTYI 200
CNVNHKPSNT KVDKKEPKS SDKTHTSPPS PAPELLGGSS VLFPPKPKD 250
TLMISRTPEV TCVVVDVSHS DPEVKFNWYV DGVEVHNAKT KPREEQYNST 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPVY 350
TLPPSRDELDT KNQVSLTCLV KGFYPSDIAP EWESNGQPEN NYKTTTPVLD 400
SDGSFFLYSK LTVDKSRWQQ GNVFSCVMH EALHNYTQK SLSLSPGK 448

Light chain / Chaîne légère / Cadena ligera

DIVLTQSPAT LSVSPGERAT ISCRASQKRV SSTSVMHWY QQKPGQPKL 50
LTKYASNLDS GVPARFSGSG SGTDFLTITIS SVEPEDFATY YCQHSWEIIP 100
TFGGGTGLEI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL NNFYPREAKV 150
QWKVDNALQS GNSQESVTEQ DSKDSTYSLS STLTLTKADY EKHKVYACEV 200
THQGLSSPVT KSFNRGEC 218

Post-translational modifications

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

Intra-H (C23-C104) 22-96 145-201 262-322 368-426
22"-96" 145"-201" 262"-322" 368"-426"

Intra-L (C23-C104) 23'-92' 138"-198"
23'''-92''' 138'''-198'''

Inter-H-L (h 5-CL 126)* h 5 S (G1v37), CL 126 C h 5" S (G1v37), CL 126" C

Inter-H-H (h 11, h 14)* h 11 S (G1v61), h 14 S (G1v62) h 11" S (G1v61), h 14" S (G1v62)

*No H-L and H-H interchain disulfide bridges

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutamínilo N-terminal

Q > pyroglutamyl (pE, 5-oxopropyl) / pyroglutamyle (pE, 5-oxopropyle) / 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 biantenarijos complejos fucosilados.

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

H CHS K2: 448, 448"

tegrenmeranum #

tegrenmeran

messenger RNA (mRNA), 5'-capped, encoding the codon-optimized receptor binding domain (RBD) of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) spike (S) glycoprotein (Omicron sub-lineages B.1.1.529.4 (BA.4) and B.1.1.529.5 (BA.5); based upon GISAID: EPI_ISL_12607996), with a cysteine 233 to serine substitution, expressed as a fusion protein with the S glycoprotein signal peptide derived from SARS-CoV-2 Wuhan-Hu 1 strain (GenBank: MN908947.3), flanked by 5' and 3' untranslated regions (UTRs) derived from the human β -globin gene and a 3' polyadenylation (polyA) tail; contains 5-methyluridine instead of uridine (*all-U>5-Me-U*) and 5-methylcytidine instead of cytidine (*all-C>5-Me-C*)

tégrenmérán

ARN messenger (ARNm), protégé d'une coiffe en 5', codant le domaine de liaison au récepteur (RBD) aux codons optimisés de la glycoprotéine de spicule (S) du coronavirus 2 du syndrome respiratoire aigu sévère (SARS-CoV-2) (sous-lignes Omicron B.1.1.529.4 (BA.4) et B.1.1.529.5 (BA.5); d'après GISAID: EPI_ISL_12607996), avec substitution de la cystéine 233 par la sérine, exprimé sous la forme d'une protéine de fusion avec le peptide signal de la glycoprotéine S dérivée de la souche SARS-CoV-2 Wuhan-Hu 1 (GenBank: MN908947.3), flanquée des régions non traduites (UTR) en 5' et 3' dérivées du gène de la β -globine humaine et d'une queue de polyadénylation (polyA) en 3'; contient de la 5-méthyluridine en lieu de l'uridine (*tout-U>5-Me-U*) et de la 5-méthylcytidine en lieu de la cytidine (*tout-C>5-Me-C*)

tegrenmerán

ARN mensajero (ARNm), protegido en 5', que codifica, con codones optimizados, para el dominio de unión al receptor (RBD) de la glicoproteína de la espícula (S) del coronavirus 2 del síndrome respiratorio agudo severo (SARS-Cov-2) (sublinajes B.1.1.529.4 (BA.4) y B.1.1.529.5 (BA.5) de Omicron; basado en GISAID: EPI_ISL_12607996), con una substitución de la cisteína 233 a serina, expresado como una proteína de fusión con el péptido señal de la glicoproteína S derivada de la cepa Wuhan-Hu 1 de SARS-Cov-2 (GenBank: MN908947.3), flanqueado por regiones 5' y 3' no traducidas (UTRs) derivadas del gen de la β -globina humana y una cola poliadenilación (poliA) en 3'; contiene 5-metiluridina en lugar de uridina (*todo-U>5-Me-U*) y 5-metilcitudina en lugar de citidina (*todo-C>5-Me-C*)

temtokibartum #

temtokibart

immunoglobulin G1- lambda2, anti-[*Homo sapiens* IL22RA1 interleukin 22 receptor subunit alpha 1, IL22R]], humanized monoclonal antibody;

	<p>gamma1 heavy chain humanized (1-450) [VH (<i>Homo sapiens</i> IGHV3-NL1*01 (89.8%) -(IGHD) -IGHJ5*01 (92.3%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -<i>Homo sapiens</i> IGHG1*01, G1m17,1 CH1 K120, CH3 D12, L14, IGHG1v36 CH2 Q84.4 (CH1 K120 (217) (121-218), hinge 1-15 (219-233), CH2 N84.4>Q (300) (234-343), CH3 D12 (359), L14 (361) (344-448), CHS (449-450)) (121-450)], (223-208')-disulfide with lambda light chain humanized (1'-209') [V-LAMBDA (<i>Homo sapiens</i> IGLV3-9*02 (80.9%) -IGLJ2*01 (100%), CDR-IMGT [2.3.10] (26-27.45-47.84-93)) (1'-103') -<i>Homo sapiens</i> IGLC2*01 (100%) (104'-209')]; dimer (229-229":232-232")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1SV lacking the glutamine synthetase (GS-KO) gene, non-glycosylated</p>
<p>temtokibart</p>	<p>immunoglobuline G1-lambda2, anti-[<i>Homo sapiens</i> IL-22RA1 (sous-unité alpha 1 du récepteur de l'interleukine 22, IL22R)], anticorps monoclonal humanisé;</p> <p>chaîne lourde gamma1 humanisée (1-450) [VH (<i>Homo sapiens</i> IGHV3-NL1*01 (89.8%) -(IGHD) - IGHJ5*01 (92.3%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -<i>Homo sapiens</i> IGHG1*01 G1m17,1 CH1 K120, CH3 D12, L14, IGHG1v36 CH2 Q84.4 (CH1 K120 (217) (121-218), charnière 1-15 (219-233), CH2 N84.4>Q (300) (234-343), CH3 D12 (359), L14 (361) (344-448), CHS (449-450)) (121-450)], (223-208')-disulfure avec la chaîne légère lambda humanisée (1'-209') [V-LAMBDA (<i>Homo sapiens</i> IGLV3-9*02 (80.9%) -IGLJ2*01 (100%), CDR-IMGT [2.3.10] (26-27.45-47.84-93)) (1'-103') -<i>Homo sapiens</i> IGLC2*01 (100%) (104'-209')]; dimère (229-229":232-232")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1SV ne présentant pas le gène de la glutamine synthétase (GS-KO), non-glycosylé</p>
<p>temtokibart</p>	<p>immunoglobulina G1-lambda2, anti-[<i>Homo sapiens</i> IL-22RA1 (subunidad alfa 1 del receptor de la interleukina 22, IL22R)], anticuerpo monoclonal humanizado;</p> <p>cadena pesada gamma1 humanizada (1-450) [VH (<i>Homo sapiens</i> IGHV3-NL1*01 (89.8%) -(IGHD) - IGHJ5*01 (92.3%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -<i>Homo sapiens</i> IGHG1*01 G1m17,1 CH1 K120, CH3 D12, L14, IGHG1v36 CH2 Q84.4 (CH1 K120 (217) (121-218), bisagra 1-15 (219-233), CH2 N84.4>Q (300) (234-343), CH3 D12 (359), L14 (361) (344-448), CHS (449-450)) (121-450)], (223-208')-disulfuro con la cadena ligera lambda humanizada (1'-209') [V-LAMBDA (<i>Homo sapiens</i> IGLV3-9*02 (80.9%) -IGLJ2*01 (100%), CDR-IMGT [2.3.10] (26-27.45-47.84-93)) (1'-103') -<i>Homo sapiens</i> IGLC2*01 (100%) (104'-209')]; dímero (229-229":232-232")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1SV en ausencia del gen glutamina sintetasa (GS-KO), no glicosilado</p>

Heavy chain / Chaîne lourde / Cadena pesada			
QVQLVESGGG	LVQPGGSLRL	SCAASGFTFS	SYDMNWVWVRA PGKGLEWVSS 50
IYNDASNTAY	SDSVKGRFTI	SRDNSKNTLY	LQMNSLRAED TAVIYCAKVG 100
FSGTYYSSEW	GQGTLVTVSS	ASTKGPSVFP	LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS	WNSGALTSKV	HTFPVAVLQSS	GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS	NTKVDKKVEP	KSCDKTHTCP	PCPAPELLGG PSVFLFPPPK 250
KDTLMLISRTF	EVTCTVVVDVS	HEDEPKVFNW	YVDGVEVHNA KTKPREEQY 300
STYRVVSVLT	VLHQDWLNGK	EYKCKVSNKA	LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSRDE	LTKNQVSLTC	LVKGFYPSDI	AVEWESNGQP ENNYKTTTPPV 400
LDSGGSFFLY	SKLTVDKSRW	QQGNVFSCSV	MHEALHNNHYT QKSLSLSPGK 450
Light chain / Chaîne légère / Cadena ligera			
SYELTQPSV	SVALGQTARI	TCQGGYYAHW	YQQKPGQAPV LVIYQGNRRP 50
SGIPERFSGS	GAGNTATLTI	SRAQAEDEAD	YYCQSGSSSS NAVFGGGTKL 100
TVLQGPKAAP	SVTLFPPSSE	ELQANKATLV	CLISDFYPGA VTVAWKADSS 150
PVKAGVETTT	PSKQSNKVA	ASSYLSLTPE	QWKSHRYSYC QVTHEGSTVE 200
KTVAPECS			209

Post-translational modifications

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

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

Intra-L (C23-C104) 22'-83' 131'-190'
 22'''-83''' 131'''-190'''

Inter-H-L (h 5-CL 126) 223-208' 223"-208"

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"

No N-glycosylation sites / pas de sites de N-glycosylation / ningùn posició de N-glicosilació

H CH2 N84.4>Q (G1v36): 300, 300"

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

H CHS K2: 450, 450"

tibrecovateinum #
 tibrecovatein

severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), beta lineage B.1.351 (Gisaid: EPI_ISL_736940) Spike (S) glycoprotein fragment (1-1192), stable prefusion conformation variant (R⁶⁶⁶>G, R⁶⁶⁷>S, R⁶⁶⁹>S, F⁸⁰¹>P, A⁸⁷⁶>P, A⁸⁸³>P, A⁹²⁶>P, K⁹⁷⁰>P, V⁹⁷¹>P) fused to the enterobacteria phage T4 fibrin foldon domain fragment (458-484, 1193-1219 in the current sequence), trimer, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

tibrécovatéine

fragment de la glycoprotéine du spicule (S) (1-1192) du coronavirus 2 du syndrome respiratoire aigu sévère (SARS-CoV-2), lignée bêta B.1.351 (Gisaid: EPI_ISL_736940), variant de conformation stable par pré-fusion (R⁶⁶⁶>G, R⁶⁶⁷>S, R⁶⁶⁹>S, F⁸⁰¹>P, A⁸⁷⁶>P, A⁸⁸³>P, A⁹²⁶>P, K⁹⁷⁰>P, V⁹⁷¹>P) fusionné au fragment du domaine foldon de la fibratine du phage T4 d'entérobactéries (458-484, 1193-1219 dans la séquence actuelle), trimère, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

tibrecovateína

fragmento de la glicoproteína de la espícula (S) (1-1192) del coronavirus 2 del síndrome respiratorio agudo severo (SARS-CoV-2), linaje beta B.1.351 (Gisaid: EPI_ISL_736940), variante de conformación de prefusión estable (R⁶⁶⁶>G, R⁶⁶⁷>S, R⁶⁶⁹>S, F⁸⁰¹>P, A⁸⁷⁶>P, A⁸⁸³>P, A⁹²⁶>P, K⁹⁷⁰>P, V⁹⁷¹>P) fusionado al fragmento de dominio de foldón de fibratina del fago T4 de enterobacterias (458-484, 1193-1219 en la secuencia actual), trímero, producido en células ováricas de hámster Chino (CHO), glicoforma alfa

Monomer sequence / Séquence du monomère / Secuencia del monómero
 QCVNFTTRTQ LPPAYTNSFT RGVYYPDKVF RSSVLHSTQD LFLPFFSNVT 50
 WFHAIHVSQT NGTKRFANPV LPFNDGVYFA STEKSNIRG WIFGTTLDSK 100
 TQSLILVNSA TNVIVKVECF QFCNDPFLGQ YYHKNKSWM ESEFRVYSSA 150
 NNCTFEYVSQ PFLMDLEGKQ GNFKNLREFV FKNIDGYFKI YSKHTPINLV 200
 RGLPQQFSAL EPLVDLPIGI NITRFQTLHI SYLTPGDSST GWTAGAAAYY 250
 VGYLQPTFL LKYNENGTIT DAVDCALDPL SETKCTLKSF TVEKGIYQTS 300
 NFRVQPTESI VRFPNITNLK PFGVEFNATR FASVYANRKR RISNCVADYS 350
 VLYNSASFST FKCYGVSPTK LNDLCFTNVY ADSFVIRGDE VRQIAPGQTG 400
 NIADYNYKLP DDFTCGVIAW NSNNLDSKVG GNYNYLYRLF RKSNLKPFER 450
 DISTEIQAG STPCNGVKGK NCYFPLQSYG FQPTYGVGYQ PYRVVLSFE 500
 LLHAPATVCG PKKSTNLVKN KCVNPNFNGL TGTGVLTESN KKFLLPQQFG 550
 RDIADTTDAV RDPQTEILD ITPCSFVGVS VITPGTNTSN QVAVLYQGVN 600
 CTEVEPVAIHA DQLTPTWRVY STGSNVFQTR AGCLIGAEBV NNSYECDIPI 650
 GAGICASYQT QTNSPGASAS VASQSIAYT MSLGVNSVA YSNNSIAIPT 700
 NFTISVTTTEI LPVSMTRKTSV DCTMYICGDS TECSNLLQY GSFCQLNRA 750
 LTGIAVEQDK NTQEVFAQVK QIYKTPPIKD FGGFNFSQIL PDPSPKSKRS 800
 IEDLLFNKV TLADAGFIKQ YGDCGLDIAA RDLICAQKFN GLTVLPLLT 850
 DEMIAQYTSAL LAGTITSWG TFGAGPALQI PFMQMYRF NGIVTQNVL 900
 YENQKLIANQ FNSAIGIKQD SLSSTPSALG KLQDVVNQNA QALNTLVKQL 950
 SSNFGAIVSS LNDILSRVLD PEAEVQIDRL ITGRQLSLQT YVQQQLIRAA 1000
 EIRASANLAA TKMSECVLGG SKRVDFCGKG YHLMSPQSA PHGVVFLHVT 1050
 YVPAEKNFY TAPAICHDGK AHFPREGVVF SNGTHWEVTO RNFVEPQIT 1100
 TDNTEFVSGNC DVVIGIVNNT VYDPLQPELD SFKEELDKYF KNHTSPDVL 1150
 GDISGINASV VNIQKEIDRL NEVAKNLNES LIDLQELGKY EQGYIPEAPR 1200
 DGQAYVRKDG EWVLLSTFL 1219

Mutation / Mutation / Mutación
 R⁶⁶⁶>G, R⁶⁶⁷>S, R⁶⁶⁹>S, F⁹⁰¹>P, A⁸⁷⁶>P, A⁸⁸³>P, A⁹²⁶>P, K⁹⁷⁰>P, V⁹⁷¹>P

Foldon domain / Foldon domaine / Foldon dominio
 GYIPEAPRDC QAYVRKDGW VLLSTFL 1193-1219

Post-translational modifications
 Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
 Intra-chain: 2-123, 118-153, 275-285, 320-345, 363-416, 375-509, 464-472, 522-574,
 601-633, 646-655, 722-744, 727-733, 824-835, 1016-1027, 1066-1110

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación (predicted)
 N4, N48, N61, N109, N136, N152, N221, N266, N315, N327, N587, N600, N641, N693,
 N701, N785, N1058, N1082, N1118, N1142, N1157, N1178

O-glycosylation sites / Sites de O-glycosylation / Posiciones de O-glicosilación (predicted)
 T307, S309

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

timdarpaceptum #
 timdarpacept

human signal-regulatory protein alpha (SIRPα, tyrosine-protein phosphatase non-receptor type substrate 1) receptor domain 1 fragment (1-133) natural variant V2 (SIRPα V2; L¹⁴>S, T²⁰>S, T²²>I, R²⁴>H, A²⁷>V, G⁴⁵>A, D⁶⁵>E, L⁶⁶>S, N⁷⁰>E, R⁷⁷>S, G⁷⁹>S, D¹⁰⁰>del, V¹⁰²>T¹⁰¹) engineered variant (N⁸⁰>A), fused to a human immunoglobulin G1 C-terminal Fc fragment (134-365) [*Homo sapiens* IGHG1*01; hinge: 134-148; CH2: 149-258; CH3: 259-363; CHS: 364-365]), disulfide bridged dimer, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

timdarpacept

protéine humaine de régulation du signal alpha (SIRPα, substrat 1 de la tyrosine-protéine-phosphatase de type non-récepteur), fragment du domaine 1 du récepteur (1-133) variant modifié (N⁸⁰>A) du variant naturel V2 (SIRPα V2; L¹⁴>S, T²⁰>S, T²²>I, R²⁴>H, A²⁷>V, G⁴⁵>A, D⁶⁵>E, L⁶⁶>S, N⁷⁰>E, R⁷⁷>S, G⁷⁹>S, D¹⁰⁰>del, V¹⁰²>T¹⁰¹), fusionné à un fragment Fc en C-terminal de l'immunoglobuline G1 humaine (134-365) [*Homo sapiens* IGHG1*01; charnière: 134-148; CH2: 149-258; CH3: 259-363; CHS: 364-365]), dimère à pont disulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

timdarpacept

proteína alfa reguladora de la señal humana (SIRP α , sustrato 1 de tipo no receptor de tirosina-proteína fosfatasa), fragmento del dominio receptor 1 (1-133) variante natural V2 (SIRP α V2; L¹⁴>S, T²⁰>S, T²²>I, R²⁴>H, A²⁷>V, G⁴⁵>A, D⁶⁵>E, L⁶⁶>S, N⁷⁰>E, R⁷⁷>S, G⁷⁹>S, D¹⁰⁰>del, V¹⁰²>T¹⁰¹) variante diseñada (N⁸⁰>A), fusionada al fragmento Fc C-terminal de la inmunoglobulina humana G1 (134-365) [*Homo sapiens* IGHG1*01; bisagra: 134-148; CH2: 149-258; CH3: 259-363; CHS: 364-365]], dímero con puente disulfuro, producido en células ováricas de hámster Chino (CHO), forma glicosilada alfa

Sequence / Séquence / Secuencia

```

EEELQVIQPD KSVSVAAAGES ALLHCTVTSL IPVGPQWFR GAGPARELIY 50
NQKEGHFPRV TTVSESTKRE NMDFSISISA ITPADAGTYY CVKFRKGSFD 100
TEFKSGAGTE LSVRAKPSAP VVSGFAARAT PQHEPKSCDK THTCPFCFAP 150
ELGGPSVFL FPPKPKDTLM ISRTEFVTCV VVDVSHEDPE VKFNWYVDGV 200
EVHNAKTKPR EEQYNSTYRV VSVLTVLHQD WLNQKEYKCK VSNKALPAPI 250
EKTISKAKGQ PREPQVYTLF PSRDELTKNQ VSLTCLVKGF YPSDIAVEWE 300
SNGQPENNYK TTPPVLDSDG SFFFLYSKLTV DKSRWQQGNV FSCSVMEHAL 350
HNHYTQKSLK LSPGK 365
    
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Natural variant / Variante naturelle / Variante natural

L¹⁴>S, T²⁰>S, T²²>I, R²⁴>H, A²⁷>V, G⁴⁵>A, D⁶⁵>E, L⁶⁶>S, N⁷⁰>E, R⁷⁷>S, G⁷⁹>S, D¹⁰⁰>del, V¹⁰²>T¹⁰¹

Mutation / Mutation / Mutación

N⁸⁰>A

Post-translational modifications

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

Intra-chain: 25 - 91, 179 - 239, 285 - 343

25'-91', 179'-239', 285'-343'

Inter-chain: 138-138', 144-144', 147-147'

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

N215, N215'

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

H CHS K2: K365, K365'

tinocabtagenm autoleucelum #

tinocabtagene autoleucel

autologous T lymphocytes obtained from peripheral blood lymphocytes by leukapheresis, transduced with a self-inactivating, non-replicating lentiviral vector, encoding a bispecific chimeric antigen receptor targeting CD19 and CD22 (Siglec-2). The expressed transgene comprises a CD8 α leader sequence, an anti-CD19 and anti-CD22 fully human single chain fragment variable (scFv), a CD8 α hinge and transmembrane region, and a 4-1BB and CD3 ζ signalling domain and is under control of the elongation factor 1 alpha (EF1 α) promoter. The construct is flanked by 5' and 3' long terminal repeats (LTRs) and also contains a ψ packaging signal, a Rev response element (RRE), a central polypurine tract (cPPT) sequence and a mutated Woodchuck hepatitis virus posttranscriptional regulatory element (WPRE). The vector is pseudotyped with vesicular stomatitis virus (VSV) G envelope protein. The leukapheresis material is enriched for CD4/CD8 T lymphocytes by positive immunoselection, activated by CD3 and CD28 agonists and transduced with the vector. The cells are then expanded in optimized serum-free cell culture media with serum replacement and interleukin 2 (IL-2). The T lymphocytes ($\geq 90\%$; with $< 5\%$ CD19+/CD22+ B cell impurity) are positive for the transgene ($\geq 10\%$ CAR positive) and secrete interferon gamma (IFN- γ)

tinocabtagène autoleucel

lymphocytes T autologues obtenus à partir de lymphocytes de sang périphérique par leucaphérèse, transduits avec un vecteur lentiviral auto-inactivant et non répliquant, codant un récepteur antigénique chimérique bispécifique ciblant CD19 et CD22 (Siglec-2). Le transgène exprimé comprend une séquence de tête CD8 α , un fragment variable entièrement humain à chaîne unique (scFv) anti-CD19 et anti-CD22, une charnière CD8 α et une région transmembranaire, ainsi qu'un domaine de signalisation 4-1BB et CD3 ζ et est sous le contrôle du promoteur du facteur d'élongation 1 alpha (EF1 α). La construction est flanquée de répétitions longues terminales (LTR) en 5' et 3' et contient également un signal d'encapsidation ψ , un élément de réponse Rev (RRE), une séquence de tractus polypurine central (cPPT) et un élément régulateur post-transcriptionnel (WPRE) muté du virus de l'hépatite de Woodchuck. Le vecteur est pseudotypé avec la protéine d'enveloppe G du virus de la stomatite vésiculaire (VSV). Le matériel de leucaphérèse est enrichi en lymphocytes T CD4/CD8 par immunosélection positive, activé par des agonistes CD3 et CD28 et transduit avec le vecteur. Les cellules sont ensuite amplifiées dans un milieu de culture cellulaire optimisé sans sérum avec remplacement de sérum et interleukine 2 (IL-2). Les lymphocytes T ($\geq 90\%$; avec $< 5\%$ d'impuretés de cellules B CD19+/CD22+) sont positifs pour le transgène ($\geq 10\%$ CAR positif) et sécrètent de l'interféron gamma (IFN- γ).

tinocabtagén autoleucel

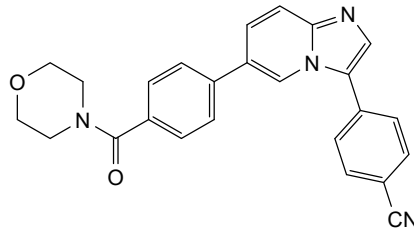
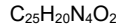
linfocitos T autólogos obtenidos de linfocitos de sangre periférica mediante leucoaféresis, transducidos con un vector lentiviral auto inactivante, no replicativo, que codifica para un receptor de antígenos quimérico biespecífico dirigido a CD19 y CD22 (Siglec-2). El transgén expresado contiene una secuencia líder de CD8 α , un fragmento variable de cadena sencilla (scFv) totalmente humano anti-CD19 y otro anti-CD22, una región bisagra y transmembrana de CD8 α , y un dominio de señalización 4-1BB y CD3 ζ , y está bajo el control del promotor del factor de elongación 1 alfa (EF1 α). El constructo está flanqueado por repeticiones terminales largas (LTRs) en 5' y 3' y también contiene una señal de empaquetamiento ψ , un elemento de respuesta Rev (RRE), una secuencia de tracto de polipurina central (cPPT) y un elemento regulador post-transcripcional del virus de la hepatitis de la marmota (WPRE) mutado. El vector está pseudotipado con la proteína G de la envuelta del virus de la estomatitis vesicular (VSV). El material de leucoaféresis se enriquece para linfocitos T CD4/CD8 mediante inmunoselección positiva, se activa mediante agonistas de CD3 y CD28 y se transduce con el vector. Las células son después expandidas en medio de cultivo celular optimizado sin suero, con sustituto de suero e interleuquina 2 (IL-2). Los linfocitos T ($\geq 90\%$; con $< 5\%$ de impureza de linfocitos B CD19+/CD22+) son positivos para el transgén ($\geq 10\%$ positivos para el CAR) y secretan interferón gamma (IFN- γ).

tinodasertibum

tinodasertib 4-{6-[4-(morpholine-4-carbonyl)phenyl]imidazo[1,2-a]pyridin-3-yl}benzotrile

tinodasertib 4-{6-[4-(morpholine-4-carbonyl)phényl]imidazo[1,2-a]pyridin-3-yl}benzotrile

tinodasertib 4-{6-[4-(morfolina-4-carbonil)fenil]imidazo[1,2-a]piridin-3-il}benzotrilo



tividenofuspum alfa #

tividenofusp alfa

human iduronate 2-sulfatase (IDS, α -L-iduronate sulfate sulfatase, EC:3.1.6.13) pro-protein (1-525), fused via the peptide linker ⁵²⁶GGGGS⁵³⁰ to a human immunoglobulin G1 C-terminal Fc fragment (531-757) variant (L⁵⁴⁴>A, L⁵⁴⁵>A, T⁶⁷⁶>S, L⁶⁷⁸>A, Y⁷¹⁷>V), disulfide bridged to an engineered human immunoglobulin G1 anti-(human type 1 transferrin receptor (TfR1)) C-terminal Fc fragment (1'-227'), variant (L¹⁴>A, L¹⁵>A, T¹⁴⁶>W, N¹⁶⁴>Y, Q¹⁶⁶>T, P¹⁶⁷>E, E¹⁶⁸>W, N¹⁶⁹>A, D¹⁹³>T, S¹⁹⁵>E, R¹⁹⁶>E, N²⁰¹>F), heterodimer, produced in Chinese hamster ovary (CHO) cells, glycoform alfa;

human iduronate 2-sulfatase (IDS, α -L-iduronate sulfate sulfatase, idursulfase, EC:3.1.6.13, UniProt:P22304), pro-protein (1-525), fused via the peptidic linker G₄S (526-530) with a human immunoglobulin G1 hinge-CH2-CH3 Fc fragment [*Homo sapiens* IGHG1*01 (531-757) (hinge (531-540, N-terminal hinge residues EPKSC deleted), CH2 L⁵⁴⁴>A, L⁵⁴⁵>A (541-650), CH3 T⁶⁷⁶>S, L⁶⁷⁸>A, Y⁷¹⁷>V (651-755), CHS (756-757))), (536-6':539-9')-bisdisulfide with a human immunoglobulin G1 hinge-CH2-CH3 Fc fragment [*Homo sapiens* IGHG1*01 (1'-227') (hinge (1-10), CH2 L¹⁴>A, L¹⁵>A (11-120), CH3 T¹⁴⁶>W, N¹⁶⁴>Y, Q¹⁶⁶>T, P¹⁶⁷>E, E¹⁶⁸>W, N¹⁶⁹>A, D¹⁹³>T, S¹⁹⁵>E, R¹⁹⁶>E, N²⁰¹>F) engineered for binding to the human type 1 transferrin receptor (TfR1) (121-225), CHS (226-227))], produced in Chinese hamster ovary (CHO) cells, glycoform alfa

tividénofusp alfa

iduronate 2-sulfatase humaine (IDS, α -L-iduronate sulfate sulfatase, EC:3.1.6. 13) pro-protéine (1-525), fusionnée via la liaison peptidique ⁵²⁶GGGGS⁵³⁰ à une variante du fragment Fc C-terminal de l'immunoglobuline G1 humaine (531-757) (L⁵⁴⁴>A, L⁵⁴⁵>A, T⁶⁷⁶>S, L⁶⁷⁸>A, Y⁷¹⁷>V), attachée par pont disulfure à un fragment Fc C-terminal (1'-227') de l'immunoglobuline G1 humaine modifiée anti-(récepteur de la transferrine de type 1 humaine (TfR1)), variant (L¹⁴>A, L¹⁵>A, T¹⁴⁶>W, N¹⁶⁴>Y, Q¹⁶⁶>T, P¹⁶⁷>E, E¹⁶⁸>W, N¹⁶⁹>A, D¹⁹³>T, S¹⁹⁵>E, R¹⁹⁶>E, N²⁰¹>F), hétérodimère, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa;

tividenufosp alfa

iduronate 2-sulfatase humaine (IDS, α -L-iduronate sulfate sulfatase, idursulfase, EC:3.1.6.13, UniProt:P22304), pro-protéine (1-525), fusionnée via la liaison peptidique G₄S (526-530) avec un fragment charnière-CH2-CH3 (Fc) de l'immunoglobuline G1 humaine [*Homo sapiens* IGHG1*01 (531-757) (charnière (531-540, fragment N-terminal EPKSC supprimé), CH2 L⁵⁴⁴>A, L⁵⁴⁵>A (541-650), CH3 T⁶⁷⁶>S, L⁶⁷⁸>A, Y⁷¹⁷>V (651-755), CHS (756-757))], (536-6':539-9')-bisdisulfide avec un fragment charnière-CH2-CH3 (Fc) de l'immunoglobuline G1 humaine [*Homo sapiens* IGHG1*01 (1'-227') (charnière (1-10), CH2 L¹⁴>A, L¹⁵>A (11-120), CH3 T¹⁴⁶>W, N¹⁶⁴>Y, Q¹⁶⁶>T, P¹⁶⁷>E, E¹⁶⁸>W, N¹⁶⁹>A, D¹⁹³>T, S¹⁹⁵>E, R¹⁹⁶>E, N²⁰¹>F modifiés dans le domaine CH3 pour lier au récepteur de la transferrine de type 1 humaine (TfR1), (121-225), CHS (226-227))], produit dans les cellules ovariennes de hamster chinois (CHO), glycoforme alfa

iduronato 2-sulfatasa humana (IDS, α -L-iduronato sulfato sulfatasa, EC:3.1.6.13) proproteína (1-525), fusionada a través de un enlace peptídico ⁵²⁶GGGGS⁵³⁰ a una inmunoglobulina G1 humana con un fragmento Fc C-terminal (531-757) variante (L⁵⁴⁴>A, L⁵⁴⁵>A, T⁶⁷⁶>S, L⁶⁷⁸>A, Y⁷¹⁷>V), disulfuro unido a una inmunoglobulina humana diseñada G1 anti-(receptor de la transferrina de tipo 1 humano (TfR1)) fragmento Fc C-terminal (1'-227'), variante (L¹⁴>A, L¹⁵>A, T¹⁴⁶>W, N¹⁶⁴>Y, Q¹⁶⁶>T, P¹⁶⁷>E, E¹⁶⁸>W, N¹⁶⁹>A, D¹⁹³>T, S¹⁹⁵>E, R¹⁹⁶>E, N²⁰¹>F), heterodímero, producido en células ováricas de hámster Chino, glicofoma alfa;

iduronato 2-sulfatasa humana (IDS, α -L-iduronato sulfato sulfatasa, idursulfasa, EC:3.1.6.13, UniProt:P22304), proproteína (1-525), fusionada mediante el enlace peptídico G₄S (526-530) con un fragmento bisagra-CH2-CH3 (Fc) de inmunoglobulina G1 humana (531-757), [*Homo sapiens* IGHG1*01 (531-757) (bisagra (531-540, fragmento N-terminal EPKSC suprimido), CH2 L⁵⁴⁴>A, L⁵⁴⁵>A (541-650), CH3 T⁶⁷⁶>S, L⁶⁷⁸>A, Y⁷¹⁷>V (651-755), CHS (756-757))], (536-6':539-9')-bisdisulfuro con un fragmento bisagra-CH2-CH3 (Fc) de inmunoglobulina G1 humana [*Homo sapiens* IGHG1*01 (1'-227') (bisagra (1-10), CH2 L¹⁴>A, L¹⁵>A (11-120), CH3 T¹⁴⁶>W, N¹⁶⁴>Y, Q¹⁶⁶>T, P¹⁶⁷>E, E¹⁶⁸>W, N¹⁶⁹>A, D¹⁹³>T, S¹⁹⁵>E, R¹⁹⁶>E, N²⁰¹>F) diseñados en el dominio CH3 para unirse al receptor de transferrina de tipo 1 humano (TfR1), (121-225), CHS (226-227))], producido en células ováricas de hámster Chino (CHO), glicofoma alfa

Sequences / Séquences / Secuencias

IDS × Fc

SETQANSTTD	ALNVLLIIVD	DLRPSLGCYG	DKLVRSPNID	QLASHSLLFQ	50
NAFAQQAVCA	PSRVSFLTGR	RFDTRLYDF	NSYWRVHAGN	FSTIPQYFKE	100
NGYVTMSVGK	VFHFGISSNH	TDDSPYSWSF	PPYHPSSEKY	ENTKTCRGPD	150
GELHANLLCP	VDVLDVPEGT	LFDKQSTEQA	IQLLEKMKTS	ASPFFLAVGY	200
HKPHIPFRYP	KEFKQKLYPLE	NITLAPDPEV	PDGLPPVAYN	PWMDIRQRED	250
VQALNISVPY	GPIPVDFQRK	IRQSYFASVS	YLDTQVGRLL	SALDDLQLAN	300
STIIAFTSDH	GWALGEHGEW	AKYSNFDVAT	HVPLIFYVPG	RTASLPEAGE	350
KLFPYLDLFPD	SASQLMEPGR	QSMDLVELVS	LFPTLAGLAG	LQVPPRCFVP	400
SFHVLELCREG	KNLLKHFRFR	DLEEDPYLPG	NPRELIAYSQ	YPRPSDIPQW	450
NSDKPSLKDI	KIMGYSIRTI	DYRYTVVWGF	NPDEFANFS	DIHAGELYFV	500
DSDFLQDHNH	YNDSQGGDLF	QLLMPGGGS	DKHTCPCPC	APEAAAGGPSV	550
FLFPPKPKDT	LMISRTPEVT	CVVVDVSHED	PEVKFNWYVD	GVEVHNAKTK	600
PREEQYNSTY	RVVSVLTVLH	QDWLNGKEYK	CKVSNKALPA	PIEKTISKAK	650
GQPREPQVYT	LPPSRDELTK	NQVSLWCLVK	GFYPSDIAVE	WESNGQPENN	700
YKTTTPVLDS	DGSFFLYSKL	TVDKSRWQQG	NVFSCVMHE	ALHNHYTQKS	750
LSLSPGK					757

anti-TfR1 Fc

DKHTCPCPC	APEAAAGGPSV	FLFPPKPKDT	LMISRTPEVT	CVVVDVSHED	50
PEVKFNWYVD	GVEVHNAKTK	PREEQYNSTY	RVVSVLTVLH	QDWLNGKEYK	100
CKVSNKALPA	PIEKTISKAK	GQPREPQVYT	LPPSRDELTK	NQVSLWCLVK	150
GFYPSDIAVE	WESYCTEWAN	YKTTTPVLDS	DGSFFLYSKL	TVTKEEWQQG	200
VFVSCVMHE	ALHNHYTQKS	LSLSPGK			227

Mutation / Mutation / Mutación

L⁵⁴⁴>A, L⁵⁴⁵>A, T⁶⁷⁶>S, L⁶⁷⁸>A, Y⁷¹⁷>Y, L^{14'}>A, L^{15'}>A, T^{146'}>W, N^{164'}>Y, Q^{166'}>T, P^{167'}>E, E^{168'}>W, N^{169'}>A, D^{193'}>T, S^{195'}>E, R^{196'}>E, N^{201'}>E

Peptide linker / Peptide liant / Péptido de unión

526-530 GGGGS

Post-translational modifications

Disulfide bridge locations / Positions de pont disulfure / Posiciones del puentes disulfuro

Intra-chain 146-159, 397-407, 571-631, 677-735

41'-101', 147'-205'

Inter-chain 536-6', 539-9'

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

N6, N90, N300, N488, N512, N607; N77

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

H CHS K2: K757, K227'

Other modification / Autre modification / Otra modificación

C₅₉: Cys → 3-OxoAla (formylGly)

tivumecirnonum

tivumecirnon

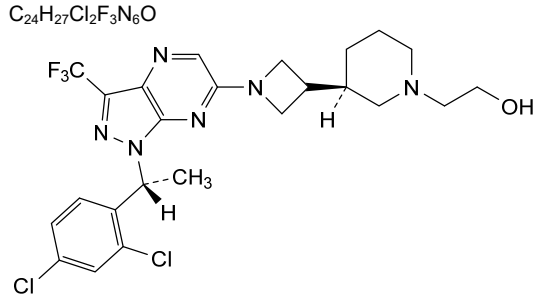
2-[(3R)-3-(1-{1-[(1R)-1-(2,4-dichlorophenyl)ethyl]-3-(trifluoromethyl)-1H-pyrazolo[3,4-b]pyrazin-6-yl}azetidín-3-yl)piperidín-1-yl]éthan-1-ol

tivumécirnon

2-[(3R)-3-(1-{1-[(1R)-1-(2,4-dichlorophényl)éthyl]-3-(trifluorométhy)-1H-pyrazolo[3,4-b]pyrazin-6-yl}azétidín-3-yl)pipéridín-1-yl]éthan-1-ol

tivumecirnon

2-[(3R)-3-(1-{1-[(1R)-1-(2,4-diclorofenil)etil]-3-(trifluorometil)-1H-pirazolo[3,4-b]pirazin-6-il}azetidín-3-il)piperidín-1-il]etan-1-ol

**trabikibartum #**

trabikibart

immunoglobulin G4-kappa, anti-[*Homo sapiens* CSF2RB (colony stimulating factor 2 (granulocyte-macrophage) receptor beta chain, granulocyte-macrophage colony stimulating factor (GM-CSF) receptor beta chain, IL3RB, IL5RB)], *Homo sapiens* monoclonal antibody;

gamma4 heavy chain *Homo sapiens* (1-444) [VH (*Homo sapiens*IGHV3-23*02 (85.7%) -(IGHD) -IGHJ3*02 (100%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens*IGHG4*01, nG4m(a) CH2 L92, 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 kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens*IGKV1-12*01 (100%) -IGKJ5*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens*IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (223-223":226-226")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1SV, glycoform alfa

trabikibart

immunoglobuline G4-kappa, anti-[*Homo sapiens* CSF2RB (chaîne bêta du récepteur du facteur 2 stimulant les colonies (granulocyte-macrophage), chaîne bêta du récepteur du facteur stimulant des colonies de granulocytes et macrophages (GM-CSF), IL3RB, IL5RB)], anticorps monoclonal *Homo sapiens*; chaîne lourde gamma4 *Homo sapiens* (1-444) [VH (*Homo sapiens*IGHV3-23*02 (85.7%) -(IGHD) -IGHJ3*02 (100%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens*IGHG4*01, nG4m(a) CH2 L92, 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 kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens*IGKV1-12*01 (100%) -IGKJ5*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens*IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (223-223":226-226")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1SV, glycoforme alfa

trabikibart

inmunoglobulina G4-kappa, anti-[*Homo sapiens* CSF2RB (cadena beta del receptor del factor 2 estimulante de las colonias (granulocito-macrófago, cadena beta del receptor del factor estimulante de las colonias de granulocitos y macrófagos (GM-CSF), IL3RB, IL5RB)], anticuerpo monoclonal *Homo sapiens*; cadena pesada gamma4 *Homo sapiens* (1-444) [VH (*Homo sapiens* IGHV3-23*02 (85.7%) -(IGHD) -IGHJ3*02 (100%), CDR-IMGT [8.8.10] (26-33.51-58.97-106))] (1-117) -*Homo sapiens* IGHG4*01, nG4m(a) CH2 L92, 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 kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (100%) -IGKJ5*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97))] (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (223-223":226-226")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular derivada de CHO-K1SV, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

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EVQLLESGGG LVQPGGSLRL SCAASGFTFP WYRVHWVRQA PGKGLEWVSS 50
IRSSGGFPFY NYKVKGRFTI SRDNSKNTLY LQMNLSRAED TAVVYCARFY 100
DSFFDIWQQG TMVTVSSAST KGPSVFFLAP CSRSTSESTA ALGCLVKDYF 150
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGKTKYTC 200
NVDHKPSNTK VDKRVESKYG PFCPPCPAPE FLGGPSVLEF PFKPKDTLMI 250
SRTPEVTCVV VDVSQEDPEV QFNWYVDGVE VHNAKTKPRE EQFNSTYRVV 300
SVLTVLHQDV LNKGEYKCKV SNKGLPSSIE KTISKARGQP REPQVYTLPP 350
SQEEMTKNQV SLTCLVKGFY PSDIAVEWES NQGPENNYKT TTPVLDSDGS 400
FFLYSRLTVD KSRWQEGNVF SCSVMHEALH NHYTQKLSLSL SLGK 444
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Light chain / Chaîne légère / Cadena ligera

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DIQMTQSPSS VSASVGDRTV ITCRASQGIS SWLAWYQQKP GKAPKLLIYA 50
ASDLSQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ ANSFPIIFGQ 100
GTRLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNIFY PREAKVQWVK 150
DNALQSGNSQ ESVTEQDSKD STYLSLSTLT LSKADYEKHK VYACEVTHGQ 200
LSSPVTKSFN RGEK 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	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"

trastuzumabum botidotinum #

trastuzumab botidotin

immunoglobulin G1-kappa , anti-[*Homo sapiens* ERBB2 (receptor tyrosine-protein kinase erbB-2, epidermal growth factor receptor 2, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], humanized monoclonal antibody; conjugated to duostatin-5 (Duo-5) via a cleavable linker; gamma1 heavy chain humanized (1-450) [VH (*Homo sapiens* IGHV3-66*01 (81.6%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109))] (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (217) (121-218), hinge 1-15 (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfide with kappa light chain

	<p>humanized (1'-214') [V-KAPPA (<i>Homo sapiens</i> IGKV1-39*01 (86.3%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -<i>Homo sapiens</i> IGKC*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dimer (229-229":232-232")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, glycoform alfa; 188', 188'''- lysine diamide conjugated to duostatin-5 (Duo-5) via a cleavable linker, in a drug-antibody ratio (DAR) of 2</p>
trastuzumab botidotine	<p>immunoglobuline G1-kappa, anti-[<i>Homo sapiens</i> ERBB2 (récepteur tyrosine-protéine kinase erbB-2, récepteur 2 du facteur de croissance épidermique, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], anticorps monoclonal humanisé; conjugué à la duostatine-5 (Duo-5) via un linker clivable;</p> <p>chaîne lourde gamma1 humanisée (1-450) [VH (<i>Homo sapiens</i> IGHV3-66*01 (81.6%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -<i>Homo sapiens</i> IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (217) (121-218), charnière 1-15 (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (<i>Homo sapiens</i> IGKV1-39*01 (86.3%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -<i>Homo sapiens</i> IGKC*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dimère (229-229":232-232")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1, glycoforme alfa; 188', 188'''- lysine diamide conjuguée à la duostatine-5 (Duo-5) via un linker clivable, dans un rapport principe actif-anticorps de 2</p>
trastuzumab botidotina	<p>inmunoglobulina G1-kappa, anti-[<i>Homo sapiens</i> ERBB2 (receptor tirosina-proteína kinasa erbB-2, receptor 2 del factor de crecimiento epidérmico, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], anticuerpo monoclonal humanizado; conjugado con la duostatina-5 (Duo-5) a través de un enlace escindible;</p> <p>cadena pesada gamma1 humanizada (1-450) [VH (<i>Homo sapiens</i> IGHV3-66*01 (81.6%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -<i>Homo sapiens</i> IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (217) (121-218), bisagra 1-15 (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (<i>Homo sapiens</i> IGKV1-39*01 (86.3%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -<i>Homo sapiens</i> IGKC*01 (100%), Km3, A45.1 (153), V101 (191) (108'-214')]; dímero (229-229":232-232")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular derivada de CHO-K1, forma glicosilada alfa; 188', 188'''- lisina diamia conjugada con la duostatina-5 (Duo-5) a través de un enlace escindible, en un ratio de principio activo-anticuerpo de 2</p>

Heavy chain / Chaîne lourde / Cadena pesada
 EVQLVESGGG LVQPGGSLRL SCAASGFNIK DTYIHWVRQA PGKGLEWVAR 50
 IYPTNGYTRY ADSVKGRFTI SADTSKNTAY LQMNSLRAED TAVYYCSRWG 100
 GDGFFYAMDYW GQGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
 DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
 YICNVNHKPS NTKVKDKVEP KSCDKHTHTCP PCPAPELLGG PSVFLFPPKP 250
 KDTLMISRTPEVTCVVVDVSD HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
 STYRVVSVLT VLNQDWSLNGK EYKCKVSNKA LPAPIEKTIIS KARKQPPEQP 350
 VYTLPPSREE MTKNQVSLTLC LVKGFYPSDI AVEWESNGQP ENNYKTPPV 400
 LDSGGSFPLY SKLTVDKSRW QQGNVFSVSV MHEALHNHYT QKSLSLSPGK 450

Light chain / Chaîne légère / Cadena ligera
 DIQMTQSPSS LSASVGRVIT ITCRASQDVN TAVAWYQQKP GKAPKLLIYS 50
 ASFLYSGVPS RFGSGRSGTD FTLTISSLQP EDFATYYCQQ HYTPPTTFGQ 100
 GTVKEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNFFY PREAKVQWVK 150
 DNALQSGNSQ ESVTEQDSKDK STYSLSSLTLL LSKADYEKHK VYACEVTHGQ 200
 LSSPVTKSFN RGEK 214

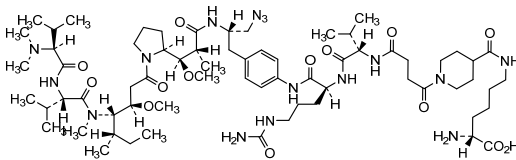
Post-translational modifications
 Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
 Intra-H (C23-C104) 22"-96" 147"-203" 264"-324" 370"-428"
 22"-96" 147"-203" 264"-324" 370"-428"
 Intra-L (C23-C104) 23"-88" 134"-194"
 23"-88" 134"-194"
 Inter-H-L (h 5-CL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

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

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

Modified residues / Résidus modifiés / Restos modificados

K (188', 188")
 N⁶-R-L-Lys



trastuzumab vedotin #
 trastuzumab vedotin

immunoglobulin G1-kappa , anti-[*Homo sapiens* ERBB2 (receptor tyrosine-protein kinase erbB-2, epidermal growth factor receptor 2, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], humanized monoclonal antibody; conjugated to auristatin E; gamma1 heavy chain humanized (1-450) [VH (*Homo sapiens* IGHV3-66*01 (81.6%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (217) (121-218), hinge 1-15 (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (86.3%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (229-229":232-232")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-DG44, glycoform alfa; conjugated, on an average of 3-4 cysteinyl, to monomethylauristatin E (MMAE), via a cleavable maleimidocaproyl-valylcitrullinyl-p-aminobenzyloxycarbonyl (mc-val-cit-PABC) type linker

For the vedotin part, please refer to the document 'INN for pharmaceutical substances: Names for radicals, groups and others'

trastuzumab védotine

immunoglobuline G1-kappa, anti-[*Homo sapiens* ERBB2 (récepteur tyrosine-protéine kinase erbB-2, récepteur 2 du facteur de croissance épidermique, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], anticorps monoclonal humanisé; conjugué à l'auristatine E;

chaîne lourde gamma1 humanisée (1-450) [VH (*Homo sapiens* IGHV3-66*01 (81.6%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (217) (121-218), charnière 1-15 (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (86.3%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (229-229":232-232")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-DG44, glycoforme alfa; conjugué, sur 3-4 résidus cystéinyles en moyenne, à la monométhylauristatine E (MMAE), via un linker clivable de type maléimidocaproil-valylcitrulinylnil-p-aminobenzyloxycarbonyl (mc-val-cit-PABC)

Pour la partie *védotine*, veuillez-vous référer au document 'INN for pharmaceutical substances: Names for radicals, groups and others'

trastuzumab vedotina

immunoglobulina G1-kappa, anti-[*Homo sapiens* ERBB2 (receptor tirosina-proteína kinasa erbB-2, receptor 2 del factor de crecimiento epidérmico, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], anticuerpo monoclonal humanizado; conjugado con la auristatina E;

cadena pesada gamma1 humanizada (1-450) [VH (*Homo sapiens* IGHV3-66*01 (81.6%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 CH1 K120, CH3 E12, M14 (CH1 R120>K (217) (121-218), bisagra 1-15 (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (86.3%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (229-229":232-232")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-DG44, forma glicosilada alfa; conjugado, en 3-4 restos cisteinil por término medio, a la monometilauristatina E (MMAE), a través de un enlace escindible de tipo maléimidocaproil-valilcitrulinylnil-p-aminobenciloxicarbonil (mc-val-cit-PABC)

Para la fracción *vedotina*, se pueda referirse al documento 'INN for pharmaceutical substances: Names for radicals, groups and others'

Heavy chain / Chaîne lourde / Cadena pesada			
EVQLVESGGG	LVQPGGSLRL	SCAASGFNIK	DTYIHWVRQA PGKGLEWVAR 50
IYPTNGYTRY	ADSVKGRFTI	SADTSKNTAY	LQMNSLRAED TAVYICSRWG 100
GDGFYAMDYW	GQGTLVTVSS	ASTKGPSVFP	LAPSSKSTSG GTAALGCLVK 150
DYFPEFVTVS	WNSGALTSKV	HTFPAVLQSS	GLYSLSVVT VPSSSLGTQT 200
YICNVNHKPS	NTKVDKQVEP	KSCDKTHTCP	PCPAPELLGG PSVFLFPPKP 250
KDTLMISRTP	EVTCVVVDVS	HEDPEVKFNW	YVDGVEVHNA KTKPREEQYN 300
STRYVSVLT	VLHQDWLNGK	EYKCKVSNKA	LPAPLEKTIIS KAKGQPREPQ 350
VYTLPPSREE	MTKNQVSLTC	LVKGFYPSDI	AVEWESNGQP ENNYKTTTPV 400
LDSDSGSFFLY	SKLTVDKSRW	QQGNVFSCSV	MHEALHNHYT QKSLSLSPGK 450
Light chain / Chaîne légère / Cadena ligera			
DIQMTQSPSS	LSASVGDRTV	ITCRASQDVN	TAVAWYQQKPK GKAPKLLIYS 50
ASFLYSGVPS	RFSGSRSGTD	FTLTISLQEP	EDFATYYCQQ HYTTPPTFGQ 100
GTKVEIKRVT	AAPSVFIFPP	SDEQLKSGTA	SVVCLLNNFY PREAKVQKWV 150
DNALQSGNSQ	ESVTEQDSKD	STYLSLSTLT	LKADYEKHK VYACEVTHQG 200
LSSPVTKSFN	RGEC		214

Post-translational modifications

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

Intra-H (C23-C104)	22-96	147-203	264-324	370-428
	22"-96"	147"-203"	264"-324"	370"-428"
Intra-L (C23-C104)	23'-88'	134'-194'		
	23"-88"	134"-194"		

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

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

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

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

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

N-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"

For the vedotin part, please refer to the document 'INN for pharmaceutical substances: Names for radicals, groups and others'*.

trovocabtagenum autoleucelum #

trovocabtagene autoleucel

autologous T lymphocytes obtained from peripheral blood mononuclear cells by leukapheresis, transduced with a self-inactivating, non-replicating lentiviral vector encoding a chimeric antigen receptor (CAR) targeting human B cell maturation antigen (BCMA). The expressed transgene comprises a CD8α leader sequence, an anti-BCMA single chain variable fragment (scFv), a CD8α hinge and transmembrane domain, and a 4-1BB (CD137) and CD3ζ signal domain, under control of the human elongation factor 1α (EF-1α) short promoter. The construct is flanked by 5' and 3' long terminal repeats (LTRs) and also contains a ψ packaging signal, a Rev response element (RRE), a central polypurine tract (cPPT) sequence and a mutated Woodchuck hepatitis virus posttranscriptional regulatory element (WPRE). The vector is pseudotyped with vesicular stomatitis virus (VSV) glycoprotein G. The leukapheresis material is enriched for CD4/8+ T lymphocytes by positive immunoselection, activated by CD3 and CD28 agonists and transduced with the lentiviral vector before further culture and expansion in serum free growth media containing interleukin 2 (IL-2). The cell suspension consists of T lymphocytes (>90%; CD3+/CD45+), with ≥10% of the T lymphocytes expressing the CAR-BCMA transgene. The T lymphocytes secrete interferon gamma (IFN-γ) following co-culture with BCMA-expressing cells

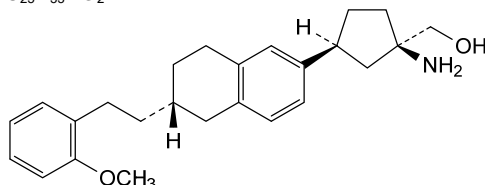
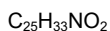
trovocabtagène autoleucel	<p>lymphocytes T autologues obtenus à partir de cellules mononucléaires de sang périphérique par leucaphérèse, transduits avec un vecteur lentiviral auto-inactif et non répliquant codant un récepteur antigénique chimérique (CAR) ciblant l'antigène de maturation des cellules B humaines (BCMA). Le transgène exprimé comprend une séquence de tête CD8α, un fragment variable à chaîne unique (scFv) anti-BCMA, un domaine charnière et transmembranaire CD8α, et un domaine de signalisation 4-1BB (CD137) et CD3ζ, sous le contrôle du promoteur court du facteur d'élongation humain 1α (EF-1α). La construction est flanquée de répétitions longues terminales (LTR) en 5' et 3' et contient également un signal d'encapsulation ψ, un élément de réponse Rev (RRE), une séquence du tractus polypurine central (cPPT) et un élément régulateur post-transcriptionnel (WPPE) muté du virus de l'hépatite de Woodchuck. Le vecteur est pseudotypé avec la glycoprotéine G du virus de la stomatite vésiculaire (VSV). Le matériel de leucaphérèse est enrichi en lymphocytes T CD4/8+ par immunosélection positive, activé par des agonistes CD3 et CD28 et transduit avec le vecteur lentiviral avant une nouvelle culture et une expansion dans un milieu de croissance sans sérum contenant de l'interleukine 2 (IL-2). La suspension cellulaire est composée de lymphocytes T (>90%; CD3+/CD45+), avec \geq10% des lymphocytes T exprimant le transgène CAR-BCMA. Les lymphocytes T sécrètent de l'interféron gamma (IFN- γ) après co-culture avec les cellules exprimant BCMA</p>
trovocabtagén autoleucel	<p>linfocitos T autólogos obtenidos de células mononucleares de sangre periférica mediante leucoaféresis, transducidos con un vector lentiviral auto inactivante, no replicativo, que codifica para un receptor de antígenos quimérico (CAR) dirigido al antígeno de maduración de células B (BCMA). El transgén expresado contiene una secuencia líder de CD8α, un fragmento variable de cadena sencilla (scFv) anti-BCMA, un domino bisagra y transmembrana de CD8α, y un dominio de señalización 4-1BB (CD137) y CD3ζ, bajo el control del promotor corto del factor de elongación 1 alfa (EF1α) humano. El constructo está flanqueado por repeticiones terminales largas (LTRs) en 5' y 3' y también contiene una señal de empaquetamiento ψ, un elemento de respuesta Rev (RRE), una secuencia de tracto de polipurina central (cPPT) y una secuencia y un elemento regulador post-transcripcional del virus de la hepatitis de la marmota (WPPE) mutado. El vector está seudotipado con la glicoproteína G del virus de la estomatitis vesicular (VSV). El material de leucoaféresis se enriquece para linfocitos T CD4/8+ mediante inmunoselección positiva, se activa mediante agonistas de CD3 y CD28 y se transduce con el vector lentiviral antes del cultivo y expansión adicional en medio de crecimiento sin suero que contiene interleuquina 2 (IL-2). La suspensión celular consiste en linfocitos T (>90%; CD3+/CD45+), con \geq10% de linfocitos T que expresan el transgén CAR-BCMA. Los linfocitos T secretan interferón gamma (IFN-γ) tras el cocultivo con células que expresan BCMA</p>

udifitimidum

udifitimidum [(1*R*,3*S*)-1-amino-3-((6*S*)-6-[2-(2-methoxyphenyl)ethyl]-5,6,7,8-tetrahydronaphthalen-2-yl)cyclopentyl]methanol

udifitimidum [(1*R*,3*S*)-1-amino-3-((6*S*)-6-[2-(2-méthoxyphényl)éthyl]-5,6,7,8-tétrahydronaphthalén-2-yl)cyclopentyl]méthanol

udifitimidum [(1*R*,3*S*)-1-amino-3-((6*S*)-6-[2-(2-metoxifenil)etil]-5,6,7,8-tetrahidronaftalén-2-il)ciclopentil]méthanol



umedaptanibum pegolum

umedaptanib pegol

5'-[{{6-[[{(2*RS*)-2,3-bis[ω-methoxypoly(oxyethylene)-α-yl]propoxy}carbonyl]amino]hexanyl}oxy)(hydroxy)phosphoryl]-2'-O-methylguanylyl-(3'→5')-2'-O-methylguanylyl-(3'→5')-2'-O-methylguanylyl-(3'→5')-2'-O-methyladenylyl-(3'→5')-2'-O-methyluridylyl-(3'→5')-2'-O-methyladenylyl-(3'→5')-2'-O-methylcytidylyl-(3'→5')-2'-deoxy-2'-fluorouridylyl-(3'→5')-2'-O-methyladenylyl-(3'→5')-2'-O-methylguanylyl-(3'→5')-2'-O-methylguanylyl-(3'→5')-guanylyl-(3'→5')-2'-O-methylcytidylyl-(3'→5')-2'-O-methyladenylyl-(3'→5')-2'-O-methyluridylyl-(3'→5')-2'-deoxy-2'-fluorouridylyl-(3'→5')-2'-O-methyladenylyl-(3'→5')-2'-O-methyladenylyl-(3'→5')-2'-O-methyluridylyl-(3'→5')-2'-O-methylguanylyl-(3'→5')-2'-deoxy-2'-fluorouridylyl-(3'→5')-2'-O-methyluridylyl-(3'→5')-2'-O-methyladenylyl-(3'→5')-2'-O-methylcytidylyl-(3'→5')-2'-O-methylcytidylyl-(3'→5')-2'-O-methyladenylyl-(3'→5')-guanylyl-(3'→5')-2'-deoxy-2'-fluorouridylyl-(3'→5')-guanylyl-(3'→5')-2'-deoxy-2'-fluorouridylyl-(3'→5')-2'-O-methyladenylyl-(3'→5')-2'-O-methylguanylyl-(3'→5')-2'-O-methyluridylyl-(3'→5')-2'-O-methylcytidylyl-(3'→5')-2'-O-methylcytidylyl-(3'→5')-2'-O-methylcytidylyl-(3'→5')-2'-O-methylcytidylyl-(3'→3')-thymidine

umédaptanib pégol

5'-[{{6-[[{(2*RS*)-2,3-bis[ω-méthoxypoly(oxyéthylène)-α-yl]propoxy}carbonyl]amino]hexanyl}oxy)(hydroxy)phosphoryl]-2'-O-méthylguanylyl-(3'→5')-2'-O-méthylguanylyl-(3'→5')-2'-O-méthylguanylyl-(3'→5')-2'-O-méthyladénylyl-(3'→5')-2'-O-méthyluridylyl-(3'→5')-2'-O-méthyladénylyl-(3'→5')-2'-O-méthylcytidylyl-(3'→5')-2'-désoxy-2'-fluorouridylyl-(3'→5')-2'-O-méthyladénylyl-(3'→5')-2'-O-méthylguanylyl-(3'→5')-2'-O-méthylguanylyl-(3'→5')-guanylyl-(3'→5')-2'-O-méthylcytidylyl-(3'→5')-2'-O-méthyladénylyl-(3'→5')-2'-O-méthyluridylyl-(3'→5')-2'-désoxy-2'-fluorouridylyl-(3'→5')-2'-O-méthyladénylyl-(3'→5')-2'-O-méthyladénylyl-(3'→5')-2'-O-méthyluridylyl-(3'→5')-2'-O-méthylguanylyl-(3'→5')-2'-désoxy-2'-fluorouridylyl-(3'→5')-2'-O-méthyluridylyl-(3'→5')-2'-O-méthyladénylyl-(3'→5')-2'-O-méthylcytidylyl-(3'→5')-2'-O-méthylcytidylyl-(3'→5')-2'-O-méthylcytidylyl-(3'→5')-2'-O-méthylcytidylyl-(3'→5')-2'-O-méthylcytidylyl-(3'→3')-thymidine

Monomer sequence / Séquence du monomère / Secuencia del monómero

QCQNLIIRTRQ	SYTNSFTRGV	YYPDKVFRSS	VLHSTQDLEL	PFSSNVTWFH	50
AISGTNGTKR	FDNPFVLPND	GVPFASTKES	NIIRGWIFGT	TLDSKTQSLL	100
IVNNATNVVI	KVCFQFCND	PFLDVYHKN	NKSWMESEFR	VYSSANCTF	150
EYVSQPFLMD	LEGKQGNFKN	LREFVFKNID	GYPKIYSKHT	PINLGRDLQP	200
GFSALEPLVD	LFIGINITRF	QTLALHRSY	LTPGDDSSGW	TAGAAAAYVG	250
YLQPRTFLLK	YNENGTITDA	VDCALDPLSE	TKCTLKSFTV	EKGIYQTSNF	300
RVQPTEISVR	FPNITNLCPF	DEVFNATRFA	SVYAMNRKRI	SNCVADYSVL	350
YNFAFFFAFK	CYGVSPTKLN	DLCTNVVYAD	SFVIRGNEVS	QIAPGQTGNI	400
ADYNYKLPDD	FTGCVIWNS	NKLDKRVGGN	YNYRYLFRK	SNLKPFPERDI	450
STEIYQAGNK	PCNGVAGVNC	YFPLQSYGFR	PTYGVGHQPY	RVVVLSEFLL	500
HAPATVCGPK	KSTNLVKNKC	VNPNFNLGTG	TGVLTESNKK	FLPFQQFGRD	550
IADTDDAVRD	PQTELELDIT	PCSPGGVSVI	TPGTNTSNQV	AVLYQGVNCT	600
EVVVAIHADQ	LTPTRVYVST	GSNVFQTRAG	CLIGAENVNN	SYECDIPIGA	650
GICASYQTQT	KSHQQAQVSA	SQSI IAYTMS	LGAENSVAYS	NNSIAIPTNF	700
TISVTTTEILP	VSMTKTSVDC	TMVICGDSTE	CSNLLLYQGS	FCTQLKRALT	750
GIAVEQDKNT	QEVFAQVKQI	YKTPPIKYFG	GFNFSQILPD	PSKPSKRSFI	800
EDLLFNKVTL	ADAGFIKQYG	DCLGDIAARD	LICAQKFNGL	TVLPPELLTDE	850
MIAQYTSALL	AGTITSGWTF	GAGAAQIIPF	AMQMAYRFNG	IGVTQNVLYE	900
NQKLIANQFN	SAIGKIQDSL	SSTASALGKL	QDVVHNHQA	LNTLVKQLSS	950
KFGAIISSVLN	DILSRLDPEE	AEVQDRILIT	GRLSQLQTVV	TQQLIRAAEI	1000
RASANLAATK	MSECVLQSK	RVDFPCGKYH	LMSFPQSAPH	GVVFLHVTYV	1050
PAQKKNFTTA	PAICHGDKAH	FPREGVFSVN	GTHWFVTQRN	FYEQIITTD	1100
NTFVSGNCDV	VIGIVNNTVY	DLPQPELDSF	KEELDXYFKN	HTSPDVLDEL	1150
ISGINASVVN	IQKEIDRLNE	VAKNLNESLI	DLQELGKRYE	YIKWFWYIWL	1200
GFIAGLIAIV	MVTIMLCCMT	SCCSCLKGCC	SCGSCKKDFE	DDSEFVLKGV	1250
KLHYT					1255

Mutation / Mutation / Mutación
R⁶⁶⁴-Q, R⁶⁶⁵-Q, R⁶⁶⁷-Q, K⁹⁶⁸-P, V⁹⁶⁹-P

Post-translational modifications

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

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

O-glycosylation sites / Sites de O-glycosylation / Posiciones de O-glicosilación
 O-glycosylation is experimentally confirmed with uncertainty on precise Ser and Thr glycosylated residues

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upleganan

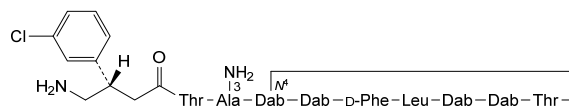
M^{4,3},9-anhidro{N-[(3S)-4-amino-3-(3-chlorophenyl)butanoyl]-L-threonyl-3-amino-L-alanyl-(2S)-2,4-diaminobutanoyl-(2S)-2,4-diaminobutanoyl-D-phenylalanyl-L-leucyl-(2S)-2,4-diaminobutanoyl-(2S)-2,4-diaminobutanoyl-L-threonine}

upléganan

M^{4,3},9-anhidro{N-[(3S)-4-amino-3-(3-chlorophényl)butanoyl]-L-thréonyl-3-amino-L-alanyl-(2S)-2,4-diaminobutanoyl-(2S)-2,4-diaminobutanoyl-D-phénylalanyl-L-leucyl-(2S)-2,4-diaminobutanoyl-(2S)-2,4-diaminobutanoyl-L-thréonine}

upleganán

M^{4,3},9-anhidro{N-[(3S)-4-amino-3-(3-clorofenil)butanoil]-L-treonil-3-amino-L-alanil-(2S)-2,4-diaminobutanoil-(2S)-2,4-diaminobutanoil-D-fenilalanil-L-leucil-(2S)-2,4-diaminobutanoil-(2S)-2,4-diaminobutanoil-L-treonina}



Dab = (2S)-2,4-diaminobutanoic acid
 = acide (2S)-2,4-diaminobutanoïque
 = ácido (2S)-2,4-diaminobutanoico

vabametkibum

vabametkib

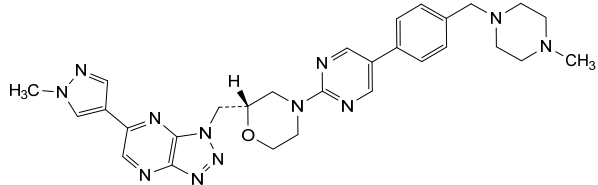
(4²S)-1¹,8⁴-dimethyl-2(6,1)-[1,2,3]triazolo[4,5-*b*]pyrazine-4(2,4)-morpholina-5(2,5)-pyrimidina-8(1)-piperazina-1(4)-pyrazola-6(1,4)-benzenaocéphane

vabametkib

(4²S)-1¹,8⁴-diméthyl-2(6,1)-[1,2,3]triazolo[4,5-*b*]pyrazine-4(2,4)-morpholina-5(2,5)-pyrimidina-8(1)-pipérazina-1(4)-pyrazola-6(1,4)-benzénaocéphane

vabametkib

(4²S)-1¹,8⁴-dimetil-2(6,1)-[1,2,3]triazolo[4,5-*b*]pirazina-4(2,4)-morfolina-5(2,5)-pirimidina-8(1)-piperazina-1(4)-pirazola-6(1,4)-bencenaocetafano

C₂₉H₃₄N₁₂O

vamikibartum

vamikibart

immunoglobulin G2-kappa, anti-[*Homo sapiens* IL6 (interleukin 6)], humanized and chimeric monoclonal antibody; gamma2 heavy chain humanized (1-448) [VH (*Homo sapiens* IGHV1-69*11 (86.7%) -(IGHD) -IGHJ5*02 (90.9%) L123>T (117), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) - *Homo sapiens* IGHG2*01, G2m.. CH2 V45.1, G2v8 CH2 A93 (CH1 (123-220), hinge 1-12 (221-232), CH2 V45.1 (283), H93>A (311) (233-341), CH3 (342-446), CHS (447-448)) (123-448)], (136-218')-disulfide with kappa light chain chimeric (1'-218') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV3-2*01 (79.8%) -IGKJ2*03 (90.9%) S120>Q (104)/*Homo sapiens* IGKV4-1*01 (79.2%) -IGKJ2*01 (100%), CDR-IMGT [10.3.9] (27-36.54-56.93-101)) (1'-111') -*Homo sapiens* IGKC*01, Km3 A45.1 (157), V101 (195) (112'-218')]; dimer (224-224":225-225":228-228":231-231")-tetrakisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1M, glycoform alfa

vamikibart

immunoglobuline G2-kappa, anti-[*Homo sapiens* IL6 (interleukine 6)], anticorps monoclonal humanisé et chimérique; chaîne lourde gamma2 humanisée (1-448) [VH (*Homo sapiens* IGHV1-69*11 (86.7%) -(IGHD) -IGHJ5*02 (90.9%) L123>T (117), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens* IGHG2*01, G2m.. CH2 V45.1, G2v8 CH2 A93 (CH1 (123-220), charnière 1-12 (221-232), CH2 V45.1 (283), H93>A (311) (233-341), CH3 (342-446), CHS (447-448)) (123-448)], (136-218')-disulfure avec la chaîne légère kappa chimérique (1'-218') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV3-2*01 (79.8%) -IGKJ2*03 (90.9%) S120>Q (104)/*Homo sapiens* IGKV4-1*01 (79.2%) -IGKJ2*01 (100%), CDR-IMGT [10.3.9] (27-36.54-56.93-101)) (1'-111') -*Homo sapiens* IGKC*01, Km3 A45.1 (157), V101 (195) (112'-218')]; dimère (224-224":225-225":228-228":231-231")-tétrakisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1M, glycoforme alfa

vamikibart

immunoglobulina G2-kappa, anti-[*Homo sapiens* IL6 (interleukina 6)], anticuerpo monoclonal humanizado y quimérico; cadena pesada gamma2 humanizada (1-448) [VH (*Homo sapiens* IGHV1-69*11 (86.7%) -(IGHD) -IGHJ5*02 (90.9%) L123>T (117), CDR-IMGT [8.8.15] (26-33.51-58.97-111))] (1-122) -*Homo sapiens* IGHG2*01, G2m.. CH2 V45.1, G2v8 CH2 A93 (CH1 (123-220), bisagra 1-12 (221-232), CH2 V45.1 (283), H93>A (311) (233-341), CH3 (342-446), CHS (447-448)) (123-448)], (136-218')-disulfuro con la cadena ligera kappa quimérica (1'-218') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV3-2*01 (79.8%) -IGKJ2*03 (90.9%) S120>Q (104)/*Homo sapiens* IGKV4-1*01 (79.2%) -IGKJ2*01 (100%), CDR-IMGT [10.3.9] (27-36.54-56.93-101))] (1'-111') -*Homo sapiens* IGKC*01, Km3 A45.1 (157), V101 (195) (112'-218')]; dímero (224-224":225-225":228-228":231-231")- tetrakisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1M, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

QVQLVQSGAE VVKPQSSVKV SCKASGYVLP NYLIEWVRQA PQQGLEWMGV 50
 TTPGGGTINY AQRKFGQRTVI TADESTSTAY MELSSLRSED TAVVYCARSR 100
 WDPPLYAYALE YMGQGTITVTV SSASTKGPSV FPLAPCSRST SEBTAALGCL 150
 VKDFPEPEVT VSWNSGALTS GVHTFPAVLQ SSGLYSLSSV VTFVSSNFGT 200
 QTYTCNVHDK PSNTKVDKTV ERKCCVECPF CPAPPVAGPS VFLFFPKFKD 250
 TLMISRTPEV TCVVVDVSH EPEVQFNWYV DGEVHNAKT KFRREQFNST 300
 FRVVSVLTVV AQDWLNGKEY KCKVSNKGLP APIEKTISKT KGQFREPQVY 350
 TLFPSPREMT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTFPMLD 400
 SDGSSFLYSK LTVDKSRWQQ GNVFSCSMH EALHNHYTQK SLSLSPGK 448

Light chain / Chaîne légère / Cadena ligera

DIVMTQSPDS LAVSLGERAT INCREASEVD NYGIPFMNMY QKQFGQPKL 50
 LIYAASNRGS GVPDRFSGSG SGTDFLTITIS SLQAEDVAIV YCQQSEEVPL 100
 TFGQGTKLEI KRTVAAPSVF IFPPSDEQLK SGTASVVCCL NNFYPREAKV 150
 QWKVDNALQS GNSQESVTEQ DSKDSTYLSL STLTLKADY EKHKVYACEV 200
 THQGLSSPVT KSFNRGEC 218

Post-translational modifications

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

Intra-H (C23-C104) 22-96 149-205 262-322 368-426
 22"-96" 149"-205" 262"-322" 368"-426"
 Intra-L (C23-C104) 23"-92" 138"-198"
 23"-92" 138"-198"
 Inter-H-L (CH1 10-CL 126) 136-218" 136"-218"
 Inter-H-H (h 4, h 5, h 8, h11) 224-224" 225-225" 228-228" 231-231"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal

Q > pyroglutaminyl (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 biantenaricos complejos fucosilados

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

H CHS K2: 448, 448"

veligrotugum #
 veligrotug

immunoglobulin G1-kappa , anti-[*Homo sapiens* IGF1R (insulin-like growth factor 1 receptor, IGF1-R, IGF-1R, CD221)], chimeric monoclonal antibody;
 gamma1 heavy chain chimeric (1-454) [VH (*Mus musculus* IGHV1S81*02 (91.8%) -(IGHD) -IGHJ1*01 (93.8%), CDR-IMGT [8.8.17] (26-33.51-58.97-113))] (1-124) -*Homo sapiens* IGHG1*01 (100%), G1m17, 1 CH1 K120, D12, L14 (CH1 K120 (221) (125-222), hinge 1-15 (223-237), CH2 (238-347), CH3 D12 (363), L14 (365) (348-452), CHS (453-454)) (125-454)], (227-219')-disulfide with kappa light chain chimeric (1'-219') [V-KAPPA (*Mus musculus* IGKV1-117*01 (93.0%) -IGKJ1*02 (100%), CDR-IMGT [11.3.9] (27-37.55-57.94-102))] (1'-112') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; dimer (233-233":236-236")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, glycoform alfa

véligrotug

immunoglobuline G1-kappa, anti-[*Homo sapiens* IGF1R (récepteur du facteur de croissance 1 analogue à l'insuline, IGF1-R, IGF-1R, CD221)], anticorps monoclonal chimérique; chaîne lourde gamma1 chimérique (1-454) [VH (*Mus musculus* IGHV1S81*02 (91.8%) -(IGHD) -IGHJ1*01 (93.8%), CDR-IMGT [8.8.17] (26-33.51-58.97-113)) (1-124) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, D12, L14 (CH1 K120 (221) (125-222), charnière 1-15 (223-237), CH2 (238-347), CH3 D12 (363), L14 (365) (348-452), CHS (453-454)) (125-454)], (227-219')-disulfure avec la chaîne légère kappa chimérique (1'-219') [V-KAPPA (*Mus musculus* IGKV1-117*01 (93.0%) -IGKJ1*02 (100%), CDR-IMGT [11.3.9] (27-37.55-57.94-102)) (1'-112') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; dimère (233-233":236-236")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1, glycoforme alfa

veligrotug

inmunoglobulina G1-kappa, anti-[*Homo sapiens* IGF1R (receptor del factor de crecimiento 1 análogo a la insulina, IGF1-R, IGF-1R, CD221)], anticuerpo monoclonal quimérico; cadena pesada gamma1 quimérica (1-454) [VH (*Mus musculus* IGHV1S81*02 (91.8%) -(IGHD) -IGHJ1*01 (93.8%), CDR-IMGT [8.8.17] (26-33.51-58.97-113)) (1-124) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, D12, L14 (CH1 K120 (221) (125-222), bisagra 1-15 (223-237), CH2 (238-347), CH3 D12 (363), L14 (365) (348-452), CHS (453-454)) (125-454)], (227-219')-disulfuro con la cadena ligera kappa quimérica (1'-219') [V-KAPPA (*Mus musculus* IGKV1-117*01 (93.0%) -IGKJ1*02 (100%), CDR-IMGT [11.3.9] (27-37.55-57.94-102)) (1'-112') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; dímero (233-233":236-236")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular derivada de CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

QVQLVQSGAE	VVKPGASVKL	SKCASGYTFT	SYWMHWVKQR	PGQGLEWIGE	50
INFSNGRNTY	NQKFGQKATL	TVDRKSSSTAY	MQLSSLTSED	SAVYFFARGR	100
PDYYSKSKWY	FDWVGQGTIV	TVSSASTKGP	SVFPLAPSPK	STSGGTAALG	150
CLVKDYFPEP	VTVSWNSGAL	TSGVHTFPAV	LQSSGLYSLS	SVVTVPSSSL	200
GTQTYICNVN	HKPSNTKVDK	KVEPKSCDKT	HTCPCCPAPE	LLGGPSVFLF	250
PPKPKDTLMI	SRTPEVTCVQ	VDVSHEDPEV	KFNWYVDGVE	VHNAKTKPRE	300
EQYNSTYRVV	SVLTVLHQDW	LNGKEYKCKV	SNKALPAPIE	KTISKAKGQP	350
REPQVYTLPP	SRDELTKNQV	SLTCLVKGFY	PSDIAVEWES	NGQPENNYKT	400
TPPVLDSGGS	FFLYSKLTVD	KSRWQQGNVF	SCSVMHREALH	NHYTQKSLSL	450
SPGK					454

Light chain / Chaîne légère / Cadena ligera

DVYMTQTPLS	LPVSLGDPAS	ISCRSSQSIIV	HSNVNTYLEW	YLQKFGQSPR	50
LLIYKVSNRF	SGVPDRFSGS	GAGTDFTLRI	SRVEAEDLGI	YYCFQGSHPV	100
PTFGGGTKLE	IKRTVAAPSV	FIFPPSDEQL	KSGTASVVCL	LNNFYPREAK	150
VQWKVDNALQ	SGNSQESVTE	QDSKSTYSYL	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, F96 151-207 268-328 374-432
22", F96" 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"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal

Q > pyroglutamyl (pE, 5-oxopropyl) / pyroglutamyle (pE, 5-oxopropyle) / piroglutamilo (pE, 5-oxopropililo)
H VH Q1: I, I"

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 biantenaricos complejos fucosilados

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

H CHS K2: 454, 454"

ventoberantum

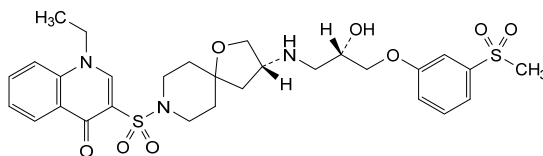
ventoberant

1-ethyl-3-[(3*R*)-3-((2*S*)-2-hydroxy-3-[3-(methanesulfonyl)phenoxy]propyl)amino]-1-oxa-8-azaspiro[4.5]decane-8-sulfonyl]quinolin-4(1*H*)-one

ventobérant

1-éthyl-3-[(3*R*)-3-((2*S*)-2-hydroxy-3-[3-(méthanesulfonyl)phénoxy]propyl)amino]-1-oxa-8-azaspiro[4.5]décane-8-sulfonyl]quinoléin-4(1*H*)-one

ventoberant

1-etil-3-[(3*R*)-3-((2*S*)-2-hidroxi-3-[3-(metanosulfonyl)fenoksi]propil)amino]-1-oxa-8-azaspiro[4.5]decano-8-sulfonyl]quinolein-4(1*H*)-onaC₂₉H₃₇N₃O₈S₂**vensobafuspum alfa #**

vensobafusp alfa

humanized immunoglobulin G4-kappa, anti-(human complement factor C5) engineered heavy chain variant (S²³³>P, M⁴³³>L, N⁴³⁹>A), fused at the C-terminus of the heavy chain (1-452) to a human complement factor H (CFH, H factor 1, HF1) functional domain fragment (1-306, 453-758 in the current sequence), variant (V⁴⁴⁴>⁴⁹⁶), disulfide bridged dimer, produced in Chinese hamster ovary (CHO) cells, glycoform alfa; humanized monoclonal antibody fusion with human complement factor H; type: IgG4-kappa; antigen: human complement C5, CPAMD4 (C5); CDR source: *Mus musculus* (humanized by CDR grafting); heavy chain class: gamma 4; HV germline: *Homo sapiens* IGHV1-18*01; HJ germline: *Homo sapiens* IGHJ3*01; HC germline: *Homo sapiens* IGHG4*01; VH: 1-125; CH1: 126-223; hinge: 224-235 (S233P hinge stabilization); CH2: 236-345; CH3: 346-450 (M433L, N439A; enhance FcRn binding); CHS: 451-452; LV germline: *Homo sapiens* IGKV1-9*01; LJ germline: *Homo sapiens* IGKJ2*01; LC germline: *Homo sapiens* IGKC*01; VL: 1-107; CL: 108-214; CDR Kabat H1: DYHFD (31-35); CDR Kabat H2: DISMNYGYHIYNQKFKD (50-66); CDR Kabat H3: RDIRYSGNSYKWFYFDE (99-114); CDR Kabat L1: RTSKSIKHLA (24-34); CDR Kabat L2: SGSTLQS (50-56); CDR Kabat L3: QQHNEYPYT (89-97); fusion protein heavy: 453-758; human complement factor H residues 1-306 (CFH)

vensobafusp alfa

immunoglobuline G4-kappa humanisée, anti-(facteur du complément humain C5), variant modifié de la chaîne lourde (S²³³>P, M⁴³³>L, N⁴³⁹>A), fusionné à l'extrémité C-terminale de la chaîne lourde (1-452) à un fragment du domaine fonctionnel du facteur du complément humain H (CFH, factor 1 H, HF1) (1-306, 453-758 dans la séquence actuelle), variant (V⁴⁴>I⁴⁹⁶), dimère à pont disulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa; fusion d'un anticorps monoclonal humanisé avec le facteur H du complément humain; type: IgG4-kappa; antigène: complément humain C5, CPAMD4 (C5); Source CDR: *Mus musculus* (humanisé par greffe de CDR); classe de la chaîne lourde: gamma 4; HV lignée germinale: *Homo sapiens* IGHV1-18*01; HJ lignée germinale: *Homo sapiens* IGHJ3*01; HC lignée germinale: *Homo sapiens* IGHG4*01; VH: 1-125; CH1: 126-223; charnière: 224-235 (stabilisation de la charnière S233P); CH2: 236-345; CH3: 346-450 (M433L, N439A; améliorant la liaison FcRn); CHS: 451-452; LV lignée germinale: *Homo sapiens* IGKV1-9*01; LJ lignée germinale: *Homo sapiens* IGKJ2*01; LC lignée germinale: *Homo sapiens* IGKC*01; VL: 1-107; CL: 108-214; CDR Kabat H1: DYHFD (31-35); CDR Kabat H2: DISMNYGYHIYNQKFKD (50-66); CDR Kabat H3: RDIRYSGNSYKWFDE (99-114); CDR Kabat L1: RTSKSISKHLA (24-34); CDR Kabat L2: SGSTLQS (50-56); CDR Kabat L3: QQHNEYPYT (89-97); protéine de fusion lourde: 453-758; résidus 1-306 du facteur du complément H humain (CFH)

vensobafusp alfa

inmoglobulina humanizada G4-kappa, anti-(factor de complemento humano C5) diseñado con la variante de cadena pesada (S²³³>P, M⁴³³>L, N⁴³⁹>A), fusionado en la terminal C de la cadena pesada (1-452) a un factor H de complemento humano (CFH, H factor 1, HF1) fragmento de dominio funcional (1-306, 453-758 en la secuencia actual), variante (V⁴⁴>I⁴⁹⁶), dímero con puente disulfuro, producido en células ováricas de hámster Chino (CHO), forma glicosilada alfa; anticuerpo monoclonal humanizado de fusion con factor H del complemento humano; tipo: IgG4-kappa; antígeno: complemento humano C5, CPAMD4 (C5); fuente CDR: *Mus musculus* (humanizado por injerto CDR); clase cadena pesada: gamma 4; línea germinal HV: *Homo sapiens* IGHV1-18*01; línea germinal HJ: *Homo sapiens* IGHJ3*01; línea germinal HC: *Homo sapiens* IGHG4*01; VH: 1-125; CH1: 126-223; bisagra: 224-235 (S233P estabilización de bisagra); CH2: 236-345; CH3: 346-450 (M433L, N439A; promover union FcRn); CHS: 451-452; línea germinal LV: *Homo sapiens* IGKV1-9*01; línea germinal LJ: *Homo sapiens* IGKJ2*01; línea germinal LC: *Homo sapiens* IGKC*01; VL: 1-107; CL: 108-214; CDR Kabat H1: DYHFD (31-35); CDR Kabat H2: DISMNYGYHIYNQKFKD (50-66); CDR Kabat H3: RDIRYSGNSYKWFDE (99-114); CDR Kabat L1: RTSKSISKHLA (24-34); CDR Kabat L2: SGSTLQS (50-56); CDR Kabat L3: QQHNEYPYT (89-97); proteína de fusión pesada: 453-758; residuos del factor H del complemento humano 1-306 (CFH)

Sequence / Séquence / Secuencia

Heavy chain / Chaîne lourde / Cadena pesada: IgG4-CFH
 VQQLVQSGAE VKKPGASVKV SCKASGYTIT DYHFDWVRQA PGQGLEWMD 50
 ISMNYGHIY NQKFKDRVT TTDTSSTAY MELRSLRSD TAVYYCARRD 100
 IRYSNSYKWK YFDEWGGQGM VTVSSASTKG PSVFLAPCS RSTSESTAAL 150
 GCLVKDYFPE PVTVSWNSGA LTVSGVHTFPA VLQSSGLYSL SSVVTPSSS 200
 LGTKTYTCNV DHKPSNPKVD KRVESKYGPP CPCCPAPEFL GGPSVFLFPP 250
 KPKDLMISR TPEVTCVVDV VQEDPEVQF NNYVDGVEVH NAKTKPREEQ 300
 FNSTYRVVSV LTVLHQDNLN GKEYCKVSN KGLPSSIEKT ISKAKGQPRE 350
 PQVYTLPPSQ EEMTKNQVSL TCLVKGFPYS DIAVWEWSNG QPENNYKTP 400
 PVLDSGDSFF LYSRLTVDKS RWQEGNVFSC SVLHEALHAAH YTQKSLSLSL 450
 GKEDCNELPP RRNTEILLTGS WSDQTYPEGT QAIYKCRPGY RSLGNIIMVC 500
 RKGEVALNP LRKQCQRKPC HPGDTPFGTF TLTGGNVFEY GVKAVYTCNE 550
 GYQLLGEINY RECDTDGWTN DIPICEVVKC LPTVAPENGG IVSSAMEPDR 600
 EYHFQAVRF VCNISGYKIEG DEEMHCSDDG FWSKERPKCV EISCKSPDVI 650
 NGSPISQKII YKENERFQYK CNMGYEYSER GDAVCTESGW RPLPSCEEK 700
 CDNPIYPNGD YSPLRIKHRT GDEITYQCRN GFYPATRGNT AKCTSTGWIP 750
 APRCTLKP 758

Light chains / Chaînes légères / Cadenas ligeras
 DIQLTQSPSF LSASVGDVRT ITCRTSKSIS KHLAWYQQKP GKAPKLLIYS 50
 GSTLQSGVPS RFSGSGSGTE FTLTISLQP EDFATYYCQQ HNEYPTFGQ 100
 GTKLEIKRVT AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
 DNALQSGNSQ ESVTEQDSKD STYSLSSLT LSKADYERKHK VYACEVTHQG 200
 LSSPVTKSFN RGEK 214

Mutation / Mutation / Mutación

IgG1 Heavy chain: S²³³>P, M⁴³³>L, N⁴³⁹>A, S²³³>P, M⁴³³>L, N⁴³⁹>A

Natural variant / Variante naturelle / Variante natural

CHF: V⁴⁴-I^{49b}, V⁴⁴-I^{49b}

Post-translational modifications

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

Intra-H: 22-96, 152-208, 226-326, 372-430
 22"-96", 152"-208", 226"-326", 372"-430"
 Intra-CFH: 455-500, 486-514, 519-563, 548-575, 580-626, 612-639, 644-685,
 671-696, 701-743, 728-754
 455"-500", 486"-514", 519"-563", 548"-575", 580"-626", 612"-639", 644"-685",
 671"-696", 701"-743", 728"-754"
 Intra-L: 23'-88', 134'-194'
 23"-88'", 134"-194"'
 Inter-H-L: 139-214', 139"-214"
 Inter-H-H: 231-231", 234-234"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
 N302, N302"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal

H VH Q1> pyroglutamyl (pE, 5-oxoprolyl): I, I"

verzistobartum #
 verzistobart

immunoglobulin G1- kappa, anti-[*Homo sapiens* HAVCR2 (hepatitis A virus cellular receptor 2, T cell immunoglobulin and mucin domains family member 3, TIM3, TIM-3, TIMD3, CD366)], *Homo sapiens* monoclonal antibody; gamma1 heavy chain *Homo sapiens* (1-449) [VH (*Homo sapiens* IGHV3-23*04 (94.9%) -(IGHD)-IGHJ4*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, IGHG1v29 CH2 A84.4 (CH1 R120 (217) (121-218), hinge 1-15 (219-233), CH2 N84.4>A (300) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS K2>del (449)) (121-449)], (223-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V- KAPPA (*Homo sapiens* IGKV3D-11*02 (96.7%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (229-229":232-232")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1SV lacking the glutamine synthetase (GS-KO) gene, non-glycosylated

verzistobart immunoglobuline G1-kappa, anti-[*Homo sapiens* HAVCR2 (récepteur cellulaire 2 du virus de l'hépatite A, membre 3 de la famille à domaines immunoglobuline et mucine des cellules T, TIM3, TIM-3, TIMD3, CD366)], anticorps monoclonal *Homo sapiens*; chaîne lourde gamma1 *Homo sapiens* (1-449) [VH (*Homo sapiens* IGHV3-23*04 (94.9%) -(IGHD) - IGHJ4*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, IGHG1v29 CH2 A84.4 (CH1 R120 (217) (121-218), charnière 1-15 (219-233), CH2 N84.4>A (300) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS K2>del (449)) (121-449)], (223-214')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3D-11*02 (96.7%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (229-229":232-232")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1SV ne présentant pas le gène de la glutamine synthétase (GS-KO), non-glycosylé

verzistobart inmunoglobulina G1-kappa, anti-[*Homo sapiens* HAVCR2 (receptor celular 2 del virus de la hepatitis A, miembro 3 de la familia con dominios inmunoglobulina y mucina de las células T, TIM3, TIM-3, TIMD3, CD366)], anticuerpo monoclonal *Homo sapiens*; cadena pesada gamma1 *Homo sapiens* (1-449) [VH (*Homo sapiens* IGHV3-23*04 (94.9%) -(IGHD) - IGHJ4*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 CH1 R120, CH3 E12, M14, IGHG1v29 CH2 A84.4 (CH1 R120 (217) (121-218), bisagra 1-15 (219-233), CH2 N84.4>A (300) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS K2>del (449)) (121-449)], (223-214')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV3D-11*02 (96.7%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (229-229":232-232")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1SV en ausencia del gen glutamina sintetasa (GS-KO), no glicosilado

Heavy chain / Chaîne lourde / Cadena pesada

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EVQLVESGGG LVQPGGSLRL SCAASGFTFR QNAWSWVRRR PGKGLEWVSA 50
ISGSGGSTYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARGG 100
DYGGNYFDYW QGGILVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSVG HTPFAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHPKS NTKVDKRVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYA 300
STYRVVSVLT VLNQDNLNGK EYKCKVSNKA LPAPIEKTTIS KAKGQPREPQ 350
VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEVESNGQP ENNYKTTTPV 400
LDSGGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPG 449
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Light chain / Chaîne légère / Cadena ligera

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EIVLTQSPAT LSLSPGERAT LSCRASQSVS SYLAWYQQKP GQAPRLLIYD 50
ASNRATGIPA SFGSGSGTD FTLTISRLEP EDFAVYYCQQ YGSSPLTFGG 100
GTKVEIKRTV AAPSVFIAPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYLSLSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEK 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"
 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"

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

HCH2 N84.4>A (G1v29): 300, 300"

vididencelum

vididencel

cell-cycle arrested dendritic cells (DCs) derived from the cell line DCOne, which originated from MUTZ-3 cells that arose from mononuclear blasts isolated from a patient with acute myelomonocytic leukaemia. The cells are initially grown in media containing granulocyte-macrophage colony-stimulating factor (GM-CSF), followed by differentiation in the presence of granulocyte-macrophage colony-stimulating factor (GM-CSF), tumour necrosis factor alpha (TNF- α), interleukin 4 (IL-4) and *mitoxantrone*. Finally, the cells are matured in the presence of media containing prostaglandin-E2 (PGE2), TNF- α , and IL-1 β . After cryopreservation the cells are irradiated to induce cell-cycle arrest. The final cell suspension contains >70% viable cells, of which >70% HLA-DR/DP/DQ-positive, >70% HLA-ABC-positive, >30% CD1a (DC differentiation marker)-positive, >30% CD83 (DC maturation marker)-positive, and which express co-stimulatory molecules highly expressed by mature DCs, i.e., CD40 (>60%), CD80 (>50%) and CD86 (>70%). The preparation also stimulates T lymphocytes in a mixed lymphocyte reaction (MLR).

vididencel

cellules dendritiques (CD) au cycle cellulaire arrêté, dérivées de la lignée cellulaire DCOne, qui provient de cellules MUTZ-3 issues de blastes mononucléaires isolés d'un patient atteint de leucémie myélomonocytaire aiguë. Les cellules sont initialement cultivées dans un milieu contenant le facteur de stimulation des colonies de granulocytes-macrophages (GM-CSF), puis elles sont différenciées en présence du facteur de stimulation des colonies de granulocytes-macrophages (GM-CSF), du facteur de nécrose tumorale alpha (TNF- α), de l'interleukine 4 (IL-4) et de la *mitoxantrone*. Enfin, les cellules sont maturées en présence d'un milieu contenant de la prostaglandine-E2 (PGE2), du TNF- α et de l'IL-1 β . Après la cryoconservation, les cellules sont irradiées pour induire un arrêt du cycle cellulaire. La suspension cellulaire finale contient >70% de cellules viables, dont >70% sont positives au HLA-DR/DP/DQ, > 70% positives au HLA-ABC, >30% positives au CD1a (marqueur de différenciation des CD), >30% positives au CD83 (marqueur de maturation des CD), et qui expriment des molécules de co-stimulation hautement exprimées par ces CD matures, par ex. CD40 (>60%), CD80 (>50%) et CD86 (>70%). La préparation stimule également les lymphocytes T dans une réaction lymphocytaire mixte (MLR).

vididencel

células dendríticas (DCs) con el ciclo celular detenido derivadas de la línea celular DCOne, que se originaron a partir de células MUTZ-3 que a su vez surgieron de blastos mononucleares aislados de un paciente con leucemia mielomonocítica aguda. Las células se crecen inicialmente en medio que contiene factor estimulador de colonias de monocitos-macrófagos (GM-CSF), seguido de diferenciación en presencia de factor estimulador de colonias de monocitos-macrófagos (GM-CSF), factor de necrosis tumoral alfa (TNF- α), interleuquina 4 (IL-4) y *mitoxantrona*. Finalmente, las células se maduran en presencia de medio que contiene prostaglandina E2 (PGE2), TNF- α e IL-1 β . Después de la criopreservación, las células se someten a radiación para inducir la detención del ciclo celular. La suspensión celular final contiene >70% de células viables, donde >70% son positivas a HLA-DR/DP/DQ, > 70% positivas a HLA-ABC, >30% positivas a CD1a (marcador de diferenciación de DC), >30% positivas a CD83 (marcador de maduración de DC), y qui expresan moléculas de co-stimulación altamente expresadas por estas Dc maduras, por ej. CD40 (>60%), CD80 (>50%) y CD86 (>70%). La preparación también estimula a los linfocitos T en una reacción mixta de linfocitos (MLR).

vintesomeranum #

vintesomeran

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 variant XBB.1.16; based upon GISAID: EPI_ISL_16835403) further optimized by two additional stop codons, flanked by an artificial 5' untranslated region (UTR) and a 3' UTR derived from the human alpha globin gene (HBA1) modified to contain an identification and ratio (IDR) sequence to enable identification and relative ratio determination of individual RNA components in a multivalent mRNA vaccine, and terminated by a 3' polyadenylation (polyA) tail; contains *N*¹-methylpseudouridine instead of uridine (*all-U>m¹Ψ*)

vintésoméran

ARN messenger (ARNm), protégé d'une coiffe en 5', codant la séquence entière aux codons optimisés d'un variant de conformation stabilisée avant fusion (K982P et V983P) de la glycoprotéine de spicule (S) du SARS-CoV-2 (coronavirus 2 du syndrome respiratoire aigu sévère) (variant Omicron XBB.1.16; d'après GISAID: EPI_ISL_16835403) dont l'optimisation a été renforcée par l'addition de deux codons stop supplémentaires, flanquée d'une région non traduite (UTR) artificielle en 5' et d'une UTR en 3' dérivée du gène de l'alpha-globine humaine (HBA1) modifiée pour contenir une séquence d'identification et de ratio (IDR) afin de permettre l'identification et la détermination du ratio relatif de chaque composant d'ARN dans un vaccin ARNm multivalent, et terminée par une queue polyadénylation (polyA) en 3'; contient de la *N*¹-méthylpseudouridine en lieu de l'uridine (*tout-U>m¹Ψ*)

vintesomerán

ARN mensajero (ARNm), protegido en 5', que codifica, para la secuencia completa con codones optimizados, de una variante (K982P y V983P) estabilizada en la conformación pre-fusión de la glicoproteína de la espícula (S) del SARS-Cov-2 (coronavirus 2 del síndrome respiratorio agudo severo) (variante XBB.1.16 de Omicron; basado en GISAID: EPI_ISL_16835403), optimizada mediante dos codones de terminación adicionales, flanqueado por una región artificial no traducida (UTR) en 5' y una 3' UTR derivada del gen de la alfa globina humana (HBA1), modificada para que contenga una secuencia de identificación y ratio (IDR) para permitir la identificación y la determinación del ratio relativo de los componentes individuales de ARN en una vacuna de ARNm multivalente, y terminado por una cola poliadenilación (poliA) en 3'; contiene *N*¹-metilpseudouridina en lugar de uridina (*todo-U>m¹Ψ*)

vonifimodum

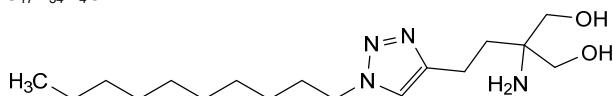
vonifimod

2-amino-2-[2-(1-decyl-1*H*-1,2,3-triazol-4-yl)ethyl]propane-1,3-diol

vonifimod

2-amino-2-[2-(1-décyl-1*H*-1,2,3-triazol-4-yl)éthyl]propane-1,3-diol

vonifimod

2-amino-2-[2-(1-decil-1*H*-1,2,3-triazol-4-il)etil]propano-1,3-diolC₁₇H₃₄N₄O₂

vonsetamigum

vonsetamig

immunoglobulin G4-kappa, anti-[*Homo sapiens* TNFRSF17 (TNF receptor superfamily member 17, BCMA, TNFRSF13A, CD269) and CD3E (CD3 epsilon)], *Homo sapiens* monoclonal antibody, bispecific, bivalent;

gamma4 heavy chain anti-TNFRSF17 *Homo sapiens* (1-451) [VH (*Homo sapiens* IGHV3-7*01 (93.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.18] (26-33.51-58.97-114)) (1-125) -*Homo sapiens* IGHG4*01, G4v5 h P10, nG4m(a) CH2 L92, IGHG4v7 CH2 delE1.4, P1.3, V1.2, A1.1 (CH1 (126-223), hinge 1-12 S10>P (233) (224-235), CH2 E1.4>del, F1.3>P (238), L1.2>V (239), G1.1>A (240), L92 (313) (236-344), CH3 (345-449), CHS (450-451)) (126-451)], (139-215')-disulfide with 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 (154), V101 (192) (109'-215')];

gamma4 heavy chain anti-CD3E *Homo sapiens* (1"-450") [VH (*Homo sapiens* IGHV3-9*01 (99.0%) -(IGHD) -IGHJ6*01 (94.7%), CDR-IMGT [8.8.17] (26-33.51-58.96-113)) (1"-124") -*Homo sapiens* IGHG4*01, G4v5 h P10, nG4m(a) CH2 L92, IGHG4v7 CH2 delE1.4, P1.3, V1.2, A1.1, IGHG4v8 CH3 R115, F116, P125 (CH1 (125"-222"), hinge 1-12 S10>P (232) (223"-234"), CH2 E1.4>del, F1.3>P (237), L1.2>V (238), G1.1>A (239), L92 (312) (235"-343"), CH3 H115>R (438), Y116>F (439), L125>P (448) (344"-448"), CHS (449"-450")) (125"-450")], (138"-215'")-disulfide with 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 (154), V101 (192) (109'"-215'")]; dimer (231-230":234-233")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, glycoform alfa

vonsétamig

immunoglobuline G4-kappa, anti-[*Homo sapiens* TNFRSF17 (membre 17 de la superfamille des récepteurs du TNF, BCMA, TNFRSF13A, CD269) and CD3E (CD3 epsilon)], anticorps monoclonal *Homo sapiens*, bispécifique, bivalent;

chaîne lourde gamma4 anti-TNFRSF17 *Homo sapiens* (1-451) [VH (*Homo sapiens* IGHV3-7*01 (93.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.18] (26-33.51-58.97-114)) (1-125) -*Homo sapiens* IGHG4*01, G4v5 h P10, nG4m(a) CH2 L92, IGHG4v7 CH2 delE1.4, P1.3, V1.2, A1.1 (CH1 (126-223), charnière 1-12 S10>P (233) (224-235), CH2 E1.4>del, F1.3>P (237), L1.2>V (238), G1.1>A (239), L92 (313) (236-344), CH3 (345-449), CHS (450-451)) (126-451)], (139-215')-disulfure avec la chaîne légère 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 (154), V101 (192) (109'-215')];

chaîne lourde gamma4 anti-CD3E *Homo sapiens* (1"-450") [VH (*Homo sapiens* IGHV3-9*01 (99.0%) -(IGHD) -IGHJ6*01 (94.7%), CDR-IMGT [8.8.17] (26-33.51-58.96-113)) (1"-124") -*Homo sapiens* IGHG4*01, G4v5 h P10, nG4m(a) CH2 L92, IGHG4v7 CH2 delE1.4, P1.3, V1.2, A1.1, IGHG4v8 CH3 R115, F116, P125 (CH1 (125"-222"), charnière 1-12 S10>P (232) (223"-234"), CH2 E1.4>del, F1.3>P (237), L1.2>V (238), G1.1>A (239), L92 (312) (235"-343"), CH3 H115>R (438), Y116>F (439), L125>P (448) (344"-448"), CHS (449"-450")) (125"-450")], (138"-215'")-disulfure avec la chaîne légère 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 (154), V101 (192) (109'"-215'")]; dimère (231-230":234-233")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1, glycoforme alfa

vonsetamig immunoglobulina G4-kappa, anti-[*Homo sapiens* TNFRSF17 (miembro 17 de la superfamilia de los receptores del TNF, BCMA, TNFRSF13A, CD269) y CD3E (CD3 épsilon)], anticuerpo monoclonal *Homo sapiens*, biespecifico, bivalente; cadena pesada gamma4 anti-TNFRSF17 *Homo sapiens* (1-451) [VH (*Homo sapiens* IGHV3-7*01 (93.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.18] (26-33.51-58.97-114)) (1-125) -*Homo sapiens* IGHG4*01, G4v5 h P10, nG4m(a) CH2 L92, IGHG4v7 CH2 delE1.4, P1.3, V1.2, A1.1 (CH1 (126-223), bisagra 1-12 S10>P (233) (224-235), CH2 E1.4>del, F1.3>P (237), L1.2>V (238), G1.1>A (239), L92 (313) (236-344), CH3 (345-449), CHS (450-451)) (126-451)], (139-215')-disulfuro con la cadena ligera 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 (154), V101 (192) (109'-215')]; cadena pesada gamma4 anti-CD3E *Homo sapiens* (1"-450") [VH (*Homo sapiens* IGHV3-9*01 (99.0%) -(IGHD) -IGHJ6*01 (94.7%), CDR-IMGT [8.8.17] (26-33.51-58.96-113)) (1"-124") -*Homo sapiens* IGHG4*01, G4v5 h P10, nG4m(a) CH2 L92, IGHG4v7 CH2 delE1.4, P1.3, V1.2, A1.1, IGHG4v8 CH3 R115, F116, P125 (CH1 (125"-222"), bisagra 1-12 S10>P (232) (223"-234"), CH2 E1.4>del, F1.3>P (237), L1.2>V (238), G1.1>A (239), L92 (312) (235"-343"), CH3 H115>R (438), Y116>F (439), L125>P (448) (344"-448"), CHS (449"-450")) (125"-450")], (138"-215")-disulfuro con la cadena ligera 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 (154), V101 (192) (109'"-215'")]; dímero (231"-230":234-233")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular derivada de CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada: anti-TNFRSF17 (H)
 EVQLVESGGG LVQPGGSLRL SCAASGFTFS NFWMTWVRQA PGKGLEWVAN 50
 MNQDQSEKYY VDSVKGGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARDR 100
 EYCIISTSCYD DFDYWGQGTLL VTSASASTKG PSVFPLAPCS RSTSESTAAL 150
 GCLVKDYFPE PVTVSNWSGA LTVSGVHTFAV VLQSSGLYSL SSVTVFSSS 200
 LGTKTYTCNV DHKFSNTKVD KRVESKYGPP CPCCPAPPVA GPSVFLFPFK 250
 PKDTLMISRT PEVTCVVVDV SQEDPEVQFNW YVDGVEVHNA AKTKPREEQF 300
 NSTYRVVSVL TVLHQDWLNG KEYCKVSNK GLPSSIEKTI SKAKGQPREP 350
 QVYTLPPSQE EMTKNQVSLT CLVKGYFPESD IAEWESNGQ PENNYKTTPE 400
 VLDSGSGFFL YSRLLTVDKSR WQEGNVFSCS VMHEALHNHY TQKLSLSLGG 450
 K 451

Heavy chain / Chaîne lourde / Cadena pesada: anti-CD3E (H")
 EVQLVESGGG LVQPGRSLRL SCAASGPTFD DYSMHWVRQA PGKGLEWVSG 50
 ISWNSGSGIG ADSVKGGRFTI SRDNAKNSLY LQMNSLRAED TALYYCAKYG 100
 SGYKGFYYG MDVWVGQGTIV TVSSASTKGP SVFFPLAPCSR STSESTAALG 150
 CLVKDYFPEP VTVSNWSGAL TSGVHTFPAV LQSSGLYSLS SVTVFSSSL 200
 GTKTYTCNV DHKFSNTKVD KRVESKYGPP CPCCPAPPVAG PSVFLFPFKP 250
 KDTLMISRT PEVTCVVVDV SQEDPEVQFNW YVDGVEVHNA AKTKPREEQFN 300
 STYRVVSVLT VLNHQDWLNGK EYCKVSNKGLPSSIEKTI SKAKGQPREPQ 350
 VLTPLPPSQEE MTKNQVSLTCLVKGYFPESDIAEWESNGQP ENNYKTTPEV 400
 LDSGSGFFLY SRLTVDKSRW QEGNVFSCSV MHEALHNRF TQKLSLSLSPK 450

Light chain / Chaîne légère / Cadena ligera (L', L")
 DIQMTQSPFS LSASVGRVITITCRASQGIS SYLNWYQQKPK GKAPKLLIYA 50
 ASSLQSGVPS RFGSGSGTDFTLTISSLQP EDFATYYCQQ SYSTPPPTFG 100
 QCTRLEIKRTVAAPSFYFIPPSDEQLKSGTASVVCLLNHF YPREAKVQWK 150
 VDNALQSGNS QESVTEQDSK DSTYISLSTL TLSKADYERKH KVVACEVTHQ 200
 GLSSPVTKSFNRGEC 215

Post-translational modifications
 Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
 Intra-H (C23-C104) 22-96 152-208 265-325 371-429
 22"-96" 151"-207" 264"-324" 370"-428"
 Intra-H CDR3 (C111-C112.1) 103-108
 Intra-L (C23-C104) 23"-88" 135"-195"
 23'"-88'" 135'"-195'"
 Inter-H-L (CH1 10-CL 126) 139-215' 138"-215"
 Inter-H-H (h 8, h 11) 231-230" 234-233"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
 H CH2N84.4: 301, 300"
 Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantennarios complejos fucosilados.

C-terminal lysine clipping / Coupeure de la lysine C-terminale / Recorte de lisina C-terminal
 H CHS K2: 451, 450"

vopikitungum #
vopikitung

immunoglobulin G1-kappa , anti-[*Homo sapiens* IL2RA (interleukin 2 receptor alpha subunit, IL-2RA, TAC, p55, CD25)], *Homo sapiens* monoclonal antibody; gamma1 heavy chain *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV1-69*01 (99.0%) -(IGHD) -IGHJ3*02 (100%), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, D12, L14 (CH1 K120 (219) (123-220), hinge 1-15 (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS (451-452)) (123-452)], (225-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5*03 (98.9%) -IGKJ4*01 (91.7%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (231-231":234-234")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa

vopikitung

immunoglobuline G1-kappa, anti-[*Homo sapiens* IL2RA (sous-unité alpha du récepteur de l'interleukine 2, IL-2RA, TAC, p55, CD25)], anticorps monoclonal *Homo sapiens*; chaîne lourde gamma1 *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV1-69*01 (99.0%) -(IGHD) -IGHJ3*02 (100%), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens* IGHG1*01 (100%), G1m17,1CH1 K120, D12, L14 (CH1 K120 (219) (123-220), charnière 1-15 (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS (451-452)) (123-452)], (225-214')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5*03 (98.9%) -IGKJ4*01 (91.7%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (231-231":234-234")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa

vopikitung

inmunoglobulina G1-kappa, anti-[*Homo sapiens* IL2RA (subunidad alfa del receptor de la interleukina 2, IL-2RA, TAC, p55, CD25)], anticuerpo monoclonal *Homo sapiens*; cadena pesada gamma1 *Homo sapiens* (1-452) [VH (*Homo sapiens* IGHV1-69*01 (99.0%) -(IGHD) -IGHJ3*02 (100%), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 CH1 K120, D12, L14 (CH1 K120 (219) (123-220), bisagra 1-15 (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS (451-452)) (123-452)], (225-214')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5*03 (98.9%) -IGKJ4*01 (91.7%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (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				
QVQLVQSGAE	VKFKPGSSVKV	SCKASGGTFS	SLAISWVRQA	PGQGLEWMGG 50
IIPFIPTANY	AQKFQGRVTI	TADESTSTAY	MELSSLSRSED	TAVYYCARGG 100
SVSGTLDVDF	IWQGQTMVTV	SSASTKGPSV	FPLAPSSKST	SGGTAALGCL 150
VKDYFPEPVT	VSWNSGALTS	GVHTFPAVLQ	SSGLYSLSSV	VTPVSSSLGT 200
QTYICNVNHK	PSNTKVDKVK	EPKSCDKTHT	CPPCPAPELL	GGPSVFLPPP 250
KPKDTLMISR	TPEVTCVVVD	VSHEDPEVKF	NWYVDGVEVH	NAKTKPREEQ 300
YNSTYRVVSV	LTVLHQDQDLN	GKEYKCKVSN	KALPAPIEKT	ISKAKGQPRE 350
PQVYTLPPSR	DELTKNQVSL	TCLVKGFPYS	DIAVEWESNG	QPENNYKTTT 400
PVLDSDGSFF	LYSKLTVDKS	RWQQGNVFC	SVMHEALHNN	YTQKSLSLSP 450
GK				452

Light chain / Chaîne légère / Cadena ligera				
DIQMTQSPST	LSASVGDRTV	ITCRASQGIS	SWLAWYQQKP	GKAPKLLIYK 50
ASSLESGVPS	RFGSGSGSTE	FTLTITSSLQP	DDFATYYCQQ	YNIYPIITFGG 100
GTKVEIKRTV	AAPSVFIFPP	SDEQLKSGTA	SVVCLLNNFY	PREAKVQKWV 150
DNALQSGNSQ	ESVTEQDSKD	STYLSLSTLT	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-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal

Q > pyroglutamyl (pE, 5-oxopropyl) / pyroglutamyle (pE, 5-oxopropyle) / piroglutamilo (pE, 5-oxoprolilo)

H VH Q1: 1, 1"

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

H CH2 N84.4: 302, 302"

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

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

vorumotide

human Wilms tumor protein (WT33)-(328-349)-peptide;

L-prolylglycyl-L-cysteinyl-L-asparaginyll-L-lysyl-L-arginyl-L-tyrosyl-L-phenylalanyl-L-lysyl-L-leucyl-L-seryl-L-histidyl-L-leucyl-L-glutaminyll-L-methionyl-L-histidyl-L-seryl-L-arginyl-L-lysyl-L-histidyl-L-threonylglycine

vorumotide

protéine humaine de la tumeur de Wilms (WT33)-(328-349)-peptide;

L-prolylglycyl-L-cystéinyl-L-asparaginyll-L-lysyl-L-arginyl-L-tyrosyl-L-phénylalanyl-L-lysyl-L-leucyl-L-séryl-L-histidyl-L-leucyl-L-glutaminyll-L-méthionyl-L-histidyl-L-séryl-L-arginyl-L-lysyl-L-histidyl-L-thréonylglycine

vorumotida

proteína humana del tumor de Wilms (WT33)-(328-349)-péptido;

L-proliliglicil-L-cisteinil-L-asparaginil-L-lisil-L-arginil-L-tirosil-L-fenilalanil-L-lisil-L-leucil-L-seril-L-histidil-L-leucil-L-glutamínil-L-metionil-L-histidil-L-seril-L-arginil-L-lisil-L-histidil-L-treonilglicina

C₁₁₄H₁₈₁N₃₉O₂₉S₂

PGCNKRYFKL SHLQMHSRKH TG 22

zasocitinibum

zasocitinib

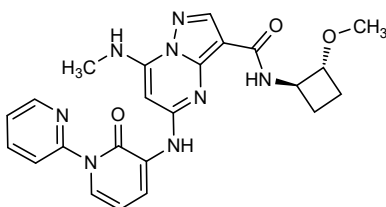
N-[(1*R*,2*R*)-2-methoxycyclobutyl]-7-(methylamino)-5-[(2-oxo[1(2*H*),2'-bipyridin]-3-yl)amino]-pyrazolo[1,5-*a*]pyrimidine-3-carboxamide

zasocitinib

N-[(1*R*,2*R*)-2-méthoxycyclobutyl]-7-(méthylamino)-5-[(2-oxo[1(2*H*),2'-bipyridin]-3-yl)amino]-pyrazolo[1,5-*a*]pyrimidine-3-carboxamide

zasocitinib

N-[(1*R*,2*R*)-2-metoxiciclobutil]-7-(metilamino)-5-[(2-oxo[1(2*H*),2'-bipiridin]-3-il)amino]-pirazolo[1,5-*a*]pirimidina-3-carboxamida

 $C_{23}H_{24}N_8O_3$
**zatonacaftorum**

zatonacaftor

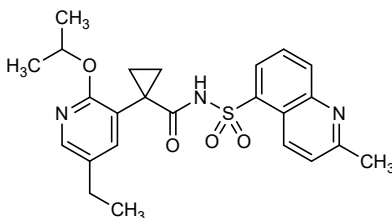
1-[5-ethyl-2-(propan-2-yloxy)pyridin-3-yl]-*N*-[(2-methylquinolin-5-yl)sulfonyl]-cyclopropanecarboxamide

zatonacaftor

1-[5-éthyl-2-(propan-2-yloxy)pyridin-3-yl]-*N*-[(2-méthylquinolin-5-yl)sulfonyl]-cyclopropanecarboxamide

zatonacaftor

1-[5-etil-2-(propan-2-iloxi)piridin-3-il]-*N*-[(2-metilquinolin-5-il)sulfonyl]-ciclopropanecarboxamida

 $C_{24}H_{27}N_3O_4S$
**zelasudilum**

zelasudil

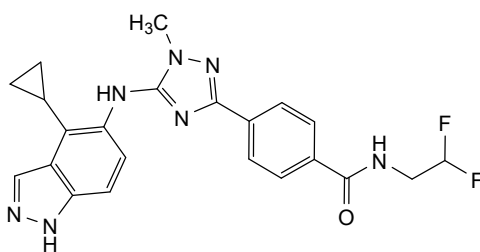
4-{5-[(4-cyclopropyl-1*H*-indazol-5-yl)amino]-1-methyl-1*H*-1,2,4-triazol-3-yl}-*N*-(2,2-difluoroethyl)benzamide

zélasudil

4-{5-[(4-cyclopropil-1*H*-indazol-5-yl)amino]-1-méthyl-1*H*-1,2,4-triazol-3-yl}-*N*-(2,2-difluoroéthyl)benzamide

zelasudil

4-{5-[(4-ciclopropil-1*H*-indazol-5-il)amino]-1-metil-1*H*-1,2,4-triazol-3-il}-*N*-(2,2-difluoroetil)benzamida

$C_{22}H_{21}F_2N_7O$ **zelnicirnonum**

zelnicirnon

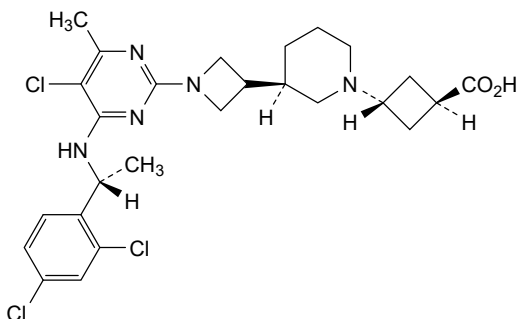
(1^{1r},1^{3r},2^{3R},6^R)-4⁵,7²,7⁴-trichloro-4⁶,6-diméthyl-5-aza-4(2,4)-pyrimidina-2(1,3)-piperidina-3(3,1)-azetidina-7(1)-benzena-1(1)-cyclobutanaheptaphane-3-carboxylic acid

zelnécirnon

acide (1^{1r},1^{3r},2^{3R},6^R)-4⁵,7²,7⁴-trichloro-4⁶,6-diméthyl-5-aza-4(2,4)-pyrimidina-2(1,3)-pipéridina-3(3,1)-azétidina-7(1)-benzéna-1(1)-cyclobutanaheptaphane-3-carboxylique

zelnicirnón

ácido (1^{1r},1^{3r},2^{3R},6^R)-4⁵,7²,7⁴-triclóro-4⁶,6-dimetil-5-aza-4(2,4)-pirimidina-2(1,3)-piperidina-3(3,1)-azetidina-7(1)-bencena-1(1)-ciclobutanaheptafano-3-carboxílico

 $C_{27}H_{34}Cl_3N_5O_2$ **zenidololum**

zenidolol

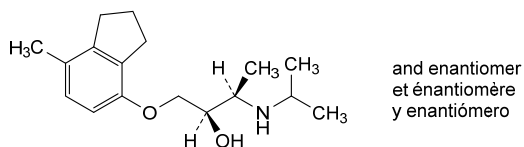
rac-(2*R*,3*R*)-1-[(7-méthyl-2,3-dihydro-1*H*-inden-4-yl)oxy]-3-[(propan-2-yl)amino]butan-2-ol

zénidolol

rac-(2*R*,3*R*)-1-[(7-méthyl-2,3-dihydro-1*H*-indén-4-yl)oxy]-3-[(propan-2-yl)amino]butan-2-ol

zenidolol

rac-(2*R*,3*R*)-1-[(7-metil-2,3-dihidro-1*H*-inden-4-il)oxi]-3-[(propan-2-il)amino]butan-2-ol

C₁₇H₂₇NO₂.**zidesamintinibum**

zidesamintinib

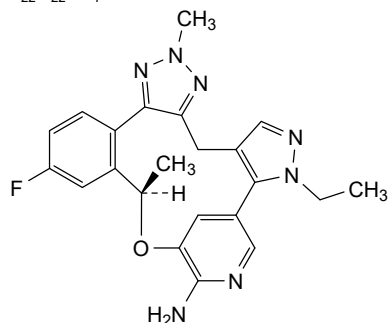
(6*R*)-2²-ethyl-5⁴-fluoro-4²,6-dimethyl-2²*H*,4²*H*-7-oxa-1(3,5)-pyridina-2(3,4)-pyrazola-4(4,5)-[1,2,3]triazola-5(1,2)-benzenacycloheptaphan-1⁶-amine

zidésamintinib

(6*R*)-2²-éthyl-5⁴-fluoro-4²,6-diméthyl-2²*H*,4²*H*-7-oxa-1(3,5)-pyridina-2(3,4)-pyrazola-4(4,5)-[1,2,3]triazola-5(1,2)-benzénacycloheptaphan-1⁶-amine

zidesamintinib

(6*R*)-2²-etil-5⁴-fluoro-4²,6-dimetil-2²*H*,4²*H*-7-oxa-1(3,5)-piridina-2(3,4)-pirazola-4(4,5)-[1,2,3]triazola-5(1,2)-benzenacicloheptafan-1⁶-amina

C₂₂H₂₂FN₇O**zongertinibum**

zongertinib

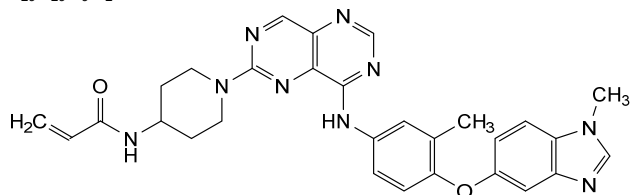
N-[1-(8-{3-methyl-4-[(1-methyl-1*H*-1,3-benzimidazol-5-yl)oxy]anilino}pyrimido[5,4-*d*]pyrimidin-2-yl)piperidin-4-yl]prop-2-enamide

zongertinib

N-[1-(8-{3-méthyl-4-[(1-méthyl-1*H*-1,3-benzimidazol-5-yl)oxy]anilino}pyrimido[5,4-*d*]pyrimidin-2-yl)pipéridin-4-yl]prop-2-énamide

zongertinib

N-[1-(8-{3-metil-4-[(1-metil-1*H*-1,3-benzimidazol-5-il)oxi]anilino}pirimido[5,4-*d*]pirimidin-2-il)piperidin-4-il]prop-2-enamida

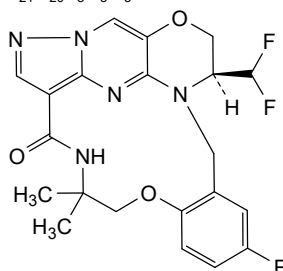
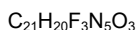
C₂₉H₂₉N₉O₂

zotizalkibum

zotizalkib (1³S)-1³-(difluorométhyl)-3⁵-fluoro-6,6-diméthyl-1²,1³-dihydro-4-oxa-7-aza-1(4,6)-pyrazolo[1',5':1,2]pyrimido[5,4-b][1,4]oxazina-3(1,2)-benzenacyclooctaphan-8-one

zotizalkib (1³S)-1³-(difluorométhyl)-3⁵-fluoro-6,6-diméthyl-1²,1³-dihydro-4-oxa-7-aza-1(4,6)-pyrazolo[1',5':1,2]pyrimido[5,4-b][1,4]oxazina-3(1,2)-benzénacyclooctaphan-8-one

zotizalkib (1³S)-1³-(difluorometil)-3⁵-fluoro-6,6-dimetil-1²,1³-dihidro-4-oxa-7-aza-1(4,6)-pirazolo[1',5':1,2]pirimido[5,4-b][1,4]oxazina-3(1,2)-bencenaciclooctafan-8-ona



zovostotugum

zovostotug

immunoglobulin G1-kappa, anti-[*Homo sapiens* CD163 (scavenger receptor cysteine-rich (SRCR) type 1 M130)], *Homo sapiens* monoclonal antibody;

gamma1 heavy chain *Homo sapiens* (1-463) [VH (*Homo sapiens* IGHV3-30*01 (99.0%) -(IGHD) -IGHJ6*01 (100%), CDR-IMGT [8.8.26] (26-33.51-58.97-122)) (1-133) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (230) (134-231), hinge 1-15 (232-246), CH2 (247-356), CH3 E12 (372), M14 (374) (357-461), CHS (462-463)) (134-463)], (236-215')-disulfide with kappa light chain *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (100%) -IGKJ1*01 (100%), CDR-IMGT [6.3.10] (27-32.50-52.89-98)) (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')]; dimer (242-242''-245-245''-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1 lacking the glutamine synthetase (GS-KO) gene, glycoform alfa

zovostotug

immunoglobuline G1-kappa, anti-[*Homo sapiens* CD163 (récepteur éboueur riche en cystéines (SRCR) de type 1 M130)], anticorps monoclonal *Homo sapiens*;

chaîne lourde gamma1 *Homo sapiens* (1-463) [VH (*Homo sapiens* IGHV3-30*01 (99.0%) -(IGHD) -IGHJ6*01 (100%), CDR-IMGT [8.8.26] (26-33.51-58.97-122)) (1-133) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (230) (134-231), charnière 1-15 (232-246), CH2 (247-356), CH3 E12 (372), M14 (374) (357-461), CHS (462-463)) (134-463)], (236-215')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (100%) -IGKJ4*01 (91.7%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')]; dimère (242-242''-245-245''-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1 ne présentant pas le gène de la glutamine synthétase (GS-KO), glycoforme alfa

zovostotug

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CD163 (receptor desactivador rico en cisteina (SRCR) de tipo 1 M130)], anticuerpo monoclonal *Homo sapiens*; cadena pesada gamma1 *Homo sapiens* (1-463) [VH (*Homo sapiens* IGHV3-30*01 (99.0%) -(IGHD) -IGHJ6*01 (100%), CDR-IMGT [8.8.26] (26-33.51-58.97-122)) (1-133) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 CH1 R120, CH3 E12, M14 (CH1 R120 (230) (134-231), bisagra 1-15 (232-246), CH2 (247-356), CH3 E12 (372), M14 (374) (357-461), CHS (462-463)) (134-463)], (236-215')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (100%) -IGKJ4*01 (91.7%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107')] -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')]; dímero (242-242":245-245")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1 en ausencia del gen glutamina sintetasa (GS-KO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG VVQPGRSLRL SCAASGFTFS SYAMHWVRQA PGKGLEWVAV 50
ISYDGSNKYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAREN 100
VRPYYDFWSG YYSEYYYGM DWVWQQTTVT VSSASTKGPS VFPLAPSSKS 150
TSGGTAALGC LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS 200
VVTVPSSSLG TQTYICNVNH KPSNTKVDKR VEPKSCDKTH TCPPCPAPEL 250
LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV DVSHEDEPKV FNWYVDGVEV 300
HNAKTKPREE QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALPAPIEK 350
TISKARGQPR EPQVYTLPPS REEMTKNQVS LTCLVKGFYP SDIAVEWESN 400
GQPENNYKTT PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSMVHEALHN 450
HYTQKSLSLG PGK 463
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGRDVT ITCRASQSIG SYLNWYQQKPK GKAPKLLIYA 50
ASSLQSGVPS RFGSGSGSTD FTLTISSLQP EDFATYYCQQ SYSTPRGTFG 100
QGKTKVEIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNPF YPREAKVQWK 150
VDNALQSGNS QESVTEQDSK DSTYSLSTL TLSKADYEKH KVAACEVTHQ 200
GLSSPVTKSF NRGEC 215
```

Post-translational modifications

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

Intra-H (C23-C104) 22-96 160-216 277-337 383-441
22"-96" 160"-216" 277"-337" 383"-441"

Intra-L (C23-C104) 23'-88" 135'-195"
23"'-88"' 135"'-195'"

Inter-H-L (h 5-CL 126) 236-215' 236"-215"

Inter-H-H (h 11, h 14) 242-242" 245-245"

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

H CH2 N84.4: 313, 313"

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

N-terminal L-kappa end clipping at serine S9 / Coupure de l'extrémité N-terminale de L-kappa

à la sérine S9 / Recorte del extremo N de L-kappa en la serina S9

1'-9', 1"'-9'" (1%)

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

H CHS K2: 463, 463"

zurletrectinibum

zurletrectinib

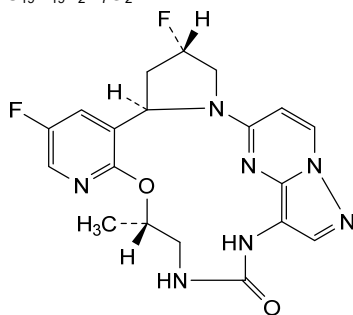
(2^R,2⁴S,5S)-3⁵,2⁴-difluoro-5-methyl-4-oxa-7,9-diaza-1(5,3)-pyrazolo[1,5-a]pyrimidina-3(3,2)-pyridina-2(1,2)-pyrrolidinacyclonaphan-8-one

zurletrectinib

(2^R,2⁴S,5S)-3⁵,2⁴-difluoro-5-méthyl-4-oxa-7,9-diaza-1(5,3)-pyrazolo[1,5-a]pyrimidina-3(3,2)-pyridina-2(1,2)-pyrrolidinacyclonaphan-8-one

zurletrectinib

(2²R,2⁴S,5S)-3⁵,2⁴-difluoro-5-metil-4-oxa-7,9-diaza-1(5,3)-
pirazolo[1,5-a]pirimidina-3(3,2)-piridina-2(1,2)-
pirrolidinaciclonoanfan-8-ona

C₁₉H₁₉F₂N₇O₂

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

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.133 loncastuximabum tesirinum #

-134

loncastuximab tesirine
loncastuximab tésirine
loncastuximab tesirina

*replace the description and structure by the following ones
remplacer la description et la structure par les suivantes
sustitúyase la descripción y la estructura por las siguientes*

immunoglobulin G1-kappa, anti-[*Homo sapiens* CD19 (B lymphocyte surface antigen B4, Leu-12)], chimeric monoclonal antibody conjugated to the pyrrolobenzodiazepine (PBD) dimer SCX;

gamma1 heavy chain (1-449) [*Mus musculus* VH (IGHV1-69*02 (85.70%) -(IGHD) -IGHJ4*01) [8.8.13] (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (217) (121-218), hinge (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS K2>del (449)) (121-449)], (223-211')-disulfide with kappa light chain (1'-211') [*Mus musculus* V-KAPPA (IGKV4-70*01 (91.40%) -IGKJ1*01) [5.3.7] (1'-104') -*Homo sapiens* IGKC*01, Km3 A45.1 (150), V101 (188) (105'-211')]; dimer (229-229":232-232")-bisdisulfide; conjugated, on an average of 2 to 3 cysteines, to the pyrrolobenzodiazepine (PBD) dimer SCX, via a cleavable (valine-alanine dipeptide as cathepsine B cleavage site) maleimide type linker containing a spacer PEG (n=8)

For the tesirine part, please refer to the prop.INN List 113, published in the WHO Drug Information, Vol.29, No.2, 2015.

immunoglobuline G1-kappa, anti-[*Homo sapiens* CD19 (antigène de surface B4 des lymphocytes B, Leu-12)], anticorps monoclonal chimérique conjugué au dimère de pyrrolobenzodiazépine (PDB) SCX;

chaîne lourde gamma1 (1-449) [*Mus musculus* VH (IGHV1-69*02 (85.70%) -(IGHD) -IGHJ4*01) [8.8.13] (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (217) (121-218), charnière (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS K2>del (449)) (121-449)], (223-211')-disulfure avec la chaîne légère kappa (1'-211') [*Mus musculus* V-KAPPA (IGKV4-70*01 (91.40%) -IGKJ1*01) [5.3.7] (1'-104') -*Homo sapiens* IGKC*01, Km3(105'-211')]; dimère (229-229":232-232")-bisdisulfure; conjugué, sur 2 à 3 cystéines en moyenne, au dimère de pyrrolobenzodiazépine (PBD) SCX, via un linker clivable (dipeptide valine-alanine clivable par la cathepsine B) de type maléimide et comprenant un espaceur PEG (n=8)

Pour la partie tésirine, veuillez-vous référer à la Liste 113 des DCI prop, publiée dans le WHO Drug Information, Vol.29, No.2, 2015.

immunoglobulina G1-kappa, anti-[*Homo sapiens* CD19 (antígeno de superficie B4 de los linfocitos B, Leu-12)], anticuerpo monoclonal quimérico conjugado con el dímero de pirrolobenzodiazepina (PDB) SCX;
cadena pesada gamma1 (1-449) [*Mus musculus* VH (IGHV1-

69*02 (85.70%) -(IGHD) -IGHJ4*01 [8.8.13] (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (217) (121-218), bisagra (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS K2>del (449)) (121-449)], (223-211')-disulfuro con la cadena ligera kappa (1'-211') [*Mus musculus* V-KAPPA (IGKV4-70*01 (91.40%) -IGKJ1*01 [5.3.7] (1'-104') -*Homo sapiens* IGKC*01, Km3(105'-211'))]; dímero (229-229":232-232")-bisulfuro; conjugado, en una media de 2 a 3 cisteinil, con el dímero de pirrolbenzodiazepina (PBD) SCX, mediante un conector escindible (dipéptido valina-alanina escindible por la catepsina B) de tipo maleimida y comprende un espaciador PEG (n=8)

Para la fracción *tesirina* se puede referir a la Lista 113 de DCI prop., publicada en el *WHO Drug Information*, Vol.29, No.2, 2015.

Heavy chain / Chaîne lourde / Cadena pesada

QVQLVQPGAE VVKPGASVKL SCKTSGYTFE SNMHWVKQA PGQGLEWIGE	50
IDPDSYNTY NQNFQGGKAKL TVDKSTSTAY MEVSSLSRDD TAVYVCARGS	100
NFYFYAMDYV GQGTSTVTSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK	150
DYFPEPTVS WNSGALTSV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT	200
YICNVNHRKPS NTKVDRKKEP KSCDRKHTCP PCPAPELLGG PSVFLFPPKP	250
KDTLMSRTP EVTCTVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN	300
STYRVVSVLT VLHQDNLNGK EYKCKVSNKA LPAPIEKTIS KARKGPREPQ	350
VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTTPV	400
LDSDGSEFFLY SKLTVDKSRW QQGNVFCVSV MHEALHNHYT QKSLSLSPG	449

Light chain / Chaîne légère / Cadena ligera

EIVLTQSPAI MSASPGERVV MTCSSASSGVN YMHVYQQKPG TSPRRWIYDT	50
SKLASGVPAR FSGSGSTSY SLTISSMEPE DAATYCHQR GSYTFGGGTK	100
LEIKRTVAAP SVFIKPPSDE QLKSGTASVV CLLNFFYPRE AKVQKVDNA	150
LQSGNSQESV TEQDSKDYT SLSSTLTLSK ADYKHKVYA CEVTHQGLSS	200
PVTKSFNRGE C	211

Post-translational modifications

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

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

Intra-L (C23-C104) 23"-87" 131"-191"
 23"-87" 131"-191"

Inter-H-L (h 5-CL 126) * 223-211' 223"-211"

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

*One, two or three of the inter-chain disulfide bridges are not present, an average of 2 to 3 cysteinyl being conjugated each via a thioether bond to a drug linker.

*Un, deux ou trois des ponts disulfures inter-chaînes ne sont pas présents, 2 à 3 cystéinyl en moyenne étant chacun conjugué via une liaison thioéther à un linker-principe actif.

*Faltan uno, dos o tres puentes disulfuro inter-catenarios, una media de 2 a 3 cisteinil conjugados con sendos enlaces tioéther, 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 biantennarios complejos fucosilados

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.728 **inavolisibum**

inavolisib

inavolisib

replace the chemical name by the following one

remplacer le nom chimique par le suivant

(2S)-2-({2-[(4S)-4-(difluoromethyl)-2-oxo-1,3-oxazolidin-3-yl]-5,6-dihydroimidazo[1,2-d][1,4]benzoxazepin-9-yl)amino}propanamide

(2S)-2-({2-[(4S)-4-(difluorométil)-2-oxo-1,3-oxazolidin-3-yl]-5,6-dihydroimidazo[1,2-d][1,4]benzoxazépin-9-yl)amino}propanamide

p.782 -783	<i>delete/supprimer/suprimáse</i> upifitamabum upifitamab upifitamab upifitamab	<i>insert/insérer/insertese</i> upinitatugum upinitatug upinitatug upinitatug
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Recommended International Nonproprietary Names (Rec. INN): List 85
Dénominations communes internationales recommandées (DCI Rec.): Liste 85
Denominaciones Comunes Internacionales recomendadas (DCI Rec.): Lista 85
(WHO Drug Information, Vol. 35, No. 1, 2021)

p.221 -222	<i>delete/supprimer/suprimáse</i> upifitamabum rilsodotinum upifitamab rilsodotin upifitamab rilsodotine upifitamab rilsodotina	<i>insert/insérer/insertese</i> upinitatugum rilsodotinum upinitatug rilsodotin upinitatug rilsodotine upinitatug rilsodotina
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Recommended International Nonproprietary Names (Rec. INN): List 87
Dénominations communes internationales recommandées (DCI Rec.): Liste 87
Denominaciones Comunes Internacionales recomendadas (DCI Rec.): Lista 87
(WHO Drug Information, Vol. 36, No. 1, 2022)

p.121	<i>delete/supprimer/suprimáse</i> flumatinib	<i>insert/insérer/insertese</i> flumatinibum
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p.218 -219	tarcocimabum # tarcocimab tarcocimab tarcocimab
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replace the description by the following one
remplacer la description par la suivante
sustitúyase la descripción por la siguiente

immunoglobulin G1-kappa, anti-[*Homo sapiens* VEGFA (vascular endothelial growth factor A, VEGF-A, VEGF)], humanized monoclonal antibody;
 gamma1 heavy chain humanized (1-453) [VH (*Homo sapiens* IGHV3-30*02 (75.8%) -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, G1v14 CH2 A1.3, A1.2 (CH1 R120>K (220) (124-221), hinge 1-15 (222-236), CH2 **L1.3**>A (240), L1.2>A (241), G1>A (243) (237-346), CH3 E12 (362), M14 (364), L123>C (449) (347-451), CHS (452-453)) (124-453)], (226-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-16*01 (87.4%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (232-232":235-235")-bisdisulfide, produced in Chinese hamster ovary (CHO)-K1SV cell line lacking the glutamine synthetase gene (GS-KO), glycoform alfa

immunoglobuline G1-kappa, anti-[*Homo sapiens* VEGFA (facteur de croissance A de l'endothélium vasculaire, VEGF-A, VEGF)], anticorps monoclonal humanisé;
 chaîne lourde gamma1 humanisée (1-453) [VH (*Homo sapiens* IGHV3-30*02 (75.8%) -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, G1v14 CH2 A1.3, A1.2 (CH1 R120>K (220) (124-221), charnière 1-15 (222-236), CH2 **L1.3**>A (240), L1.2>A (241), G1>A (243) (237-346), CH3 E12 (362), M14 (364), L123>C (449) (347-451), CHS (452-453))

(124-453)], (226-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-16*01 (87.4%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (232-232":235-235")-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

immunoglobulina G1-kappa, anti-[*Homo sapiens* VEGFA (factor de crecimiento A del endotelio vascular, VEGF-A, VEGF)], anticuerpo monoclonal humanizado; cadena pesada gamma1 humanizada (1-453) [VH (*Homo sapiens* IGHV3-30*02 (75.8%) -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, G1v14 CH2 A1.3, A1.2 (CH1 R120>K (220) (124-221), bisagra 1-15 (222-236), CH2 L1.3>A (240), L1.2>A (241), G1>A (243) (237-346), CH3 E12 (362), M14 (364), L123>C (449) (347-451), CHS (452-453)) (124-453)], (226-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-16*01 (87.4%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (232-232":235-235")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO) línea celular CHO-K1SV en ausencia del gen glutamina sintetasa (GS-KO), forma glicosilada alfa

Recommended International Nonproprietary Names (Rec. INN): List 88

Dénominations communes internationales recommandées (DCI Rec.): Liste 88

Denominaciones Comunes Internacionales recomendadas (DCI Rec.): Lista 88

(WHO Drug Information, Vol. 36, No. 3, 2022)

p.699 **anivovetmabum #**

-700 anivovetmab
anivovetmab
anivovetmab

*replace the description and structure by the following ones
remplacer la description et la structure par les suivantes
sustitúyase la descripción y la estructura por las siguientes*

immunoglobulin G2-kappa, anti-[canine (*Canis lupus familiaris*) parvovirus major capsid protein VP2)], chimeric monoclonal antibody; gamma2 heavy chain chimeric (1-457) [VH Ratnor/Canlupfam (*Rattus norvegicus* IGHV2-32*01 (92.8%) -(IGHD) -IGHJ3*01 (92.9%)/*Canis lupus familiaris* IGHV4-1*01 (60.2%) -(IGHD) -IGHJ5*01 (92.9%), CDR-IMGT [8.7.16] (26-33.51-57.96-111)) (1-122) -*Canis lupus familiaris* IGHG2*02 (100%) (CH1 (123-219), hinge 1-19 (220-238), CH2 (239-348), CH3 (349-455), CHS (456-457)) (123-457)], (137-213')-disulfide with kappa light chain chimeric (1'-217') [V-KAPPA Ratnor/Canlupfam (*Rattus norvegicus* IGKV6S10*01 (95.8%) -IGKJ5*01 (100%)/*Canis lupus familiaris* IGKV3-18*01 (65.6%) -IGKJ3*01 (83.3%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Canis lupus familiaris* IGKC*01 (100%) (108'-217')]; dimer (234-234":237-237")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa

immunoglobuline G2-kappa, anti-[protéine de capsid majeure VP2 du parvovirus canin (*Canis lupus familiaris*)], anticorps monoclonal chimérique;

chaîne lourde gamma2 chimérique (1-457) [VH Ratnor/Canlupfam (*Rattus norvegicus* IGHV2-32*01 (92.8%) -(IGHD) -IGHJ3*01 (92.9%)/*Canis lupus familiaris* IGHV4-1*01 (60.2%) -(IGHD) -IGHJ5*01 (92.9%), CDR-IMGT [8.7.16] (26-33.51-57.96-111)) (1-122) -*Canis lupus familiaris* IGHG2*02 (100%) (CH1 (123-219), charnière 1-19 (220-238), CH2 (239-348), CH3 (349-455), CHS (456-457)) (123-457)], (137-213')-disulfure avec la chaîne légère kappa chimérique (1'-217') [V-KAPPA Ratnor/Canlupfam (*Rattus norvegicus* IGKV6S10*01 (95.8%) -IGKJ5*01 (100%)/*Canis lupus familiaris* IGKV3-18*01 (65.6%) -IGKJ3*01 (83.3%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Canis lupus familiaris* IGKC*01 (100%) (108'-217')]; dimère (234-234'':237-237'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa

immunoglobulina G2-kappa, anti-[proteína de cápsida mayor VP2 del parvovirus canino (*Canis lupus familiaris*)], anticuerpo monoclonal quimérico;

cadena pesada gamma2 quimérica (1-457) [VH Ratnor/Canlupfam (*Rattus norvegicus* IGHV2-32*01 (92.8%) -(IGHD) -IGHJ3*01 (92.9%)/*Canis lupus familiaris* IGHV4-1*01 (60.2%) -(IGHD) -IGHJ5*01 (92.9%), CDR-IMGT [8.7.16] (26-33.51-57.96-111)) (1-122) -*Canis lupus familiaris* IGHG2*02 (100%) (CH1 (123-219), bisagra 1-19 (220-238), CH2 (239-348), CH3 (349-455), CHS (456-457)) (123-457)], (137-213')-disulfuro con la cadena ligera kappa quimérica (1'-217') [V-KAPPA Ratnor/Canlupfam (*Rattus norvegicus* IGKV6S10*01 (95.8%) -IGKJ5*01 (100%)/*Canis lupus familiaris* IGKV3-18*01 (65.6%) -IGKJ3*01 (83.3%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Canis lupus familiaris* IGKC*01 (100%) (108'-217')]; dímero (234-234'':237-237'')-bisdisulfuro, producido en las células ováricas de hamster chino (CHO), línea celular CHO-K1, forma glicosilada alfa

Heavy chain:

```

QVQLKESGPG LVAPSQTLST TCTVSGFSLT SYHWVWRQP PGKLEWLVG 50
MWNQDGTSYN LALNSRLSIS RDTSKSQVFF KMSSLQTEDT ATYYCARPEL 100
PGLTYGWFVP YWGQGLVTV SAASTTAPSV FPLAPSCGST SGSTVALACL 150
VSGYFPEPVT VSWNSGSLTS GVHTFPPVLQ SSGLYSLSSM VTPVSSRWP 200
ETFTCNVAHP ASKTKVDPKV PKRENGRVRP PDPCKCPAP EMLGGPSVFT 250
FPPKPKDTLL IARTPEVTCV VVDLDPEDPE VQISWFDGK QMQTAKTQPR 300
EEQFNGTYRV VSVLPIGHQD WLKKGQFTCK VMNKALPSP IERTISKARGQ 350
AHQPSVYVLP PSREELSKNT VSLTCLIKDF FPPDIDVEWQ SNGQQEPESK 400
YRTTTPQLDE DGSYFLYSKL SVDKSRWQRG DTFICAVMRE ALHNHYTQES 450
LSHSPGK 457
    
```

Light chain:

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DIVMTQSPTS MSISVGDVRT MNCKASQNV DSNVDWYQQT GQSPKLLIYK 50
ASNRNTGVPD RFTSGSGSTD FTLTISNMQA EDLAVVYCMQ STSYPLTFGS 100
GKLEIKRND AQPAVYLFQP SPDQLHTGSA SVVCLLNSFY PKDINVKWKV 150
DGVIQDTGIQ ESVTEQDKDS TYLSSTLTM SSTEYLSHEL YSCEITHKSL 200
PSTLIKSFQR SECQRVD 227
    
```

Post-translational modifications

Disulfide bridges location

Intra-H (C23-C104) 22-95 149-205 269-329 375-435
 22"-95" 149"-205" 269"-329" 375"-435"
 Intra-L (C23-C104) 23'-88' 134'-193'
 23"'-88"' 134"'-193"
 Inter-H-L (CH1 11-CL 126) 137-213' 137"-213"
 Inter-H-H (h 15, h 19) 234-234* 237-237*

N-terminal glutaminy cyclization

Q > pyroglutamyl (pE, 5-oxoprolyl)
 H VH Q1: 1, 1"

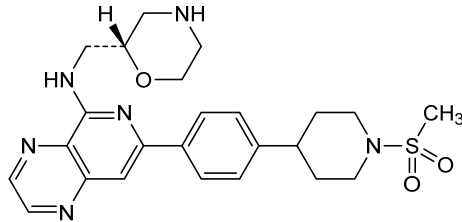
N-glycosylation sites

H CH2 N84.4: 305, 305"

Fucosylated complex bi-antennary CHO-type glycans

C-terminal lysine clipping

H CHS K2: 457, 457"

p.844 **sovleplenibum**sovleplenib
sovleplénib
sovleplenib*replace the structure by the following one
remplacer la structure par la suivante
sustitúyase la estructura por la siguiente*p.1088 **tarcoicimabum tedromerum #**

-1090

tarcoicimab tedromer
tarcoicimab tédomère
tarcoicimab tedrómero*replace the description and structure by the following ones
remplacer la description et la structure par les suivantes
sustitúyase la descripción y la estructura por las siguientes*

immunoglobulin G1-kappa, anti-[*Homo sapiens* VEGFA (vascular endothelial growth factor A, VEGF-A, VEGF)], humanized monoclonal antibody, conjugated via a linker to a **nine-armed star polymer** with phosphorylcholine polymer end groups; gamma1 heavy chain humanized (1-453) [VH (*Homo sapiens*IGHV3-30*02 (75.8%) -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens*IGHG1*03v, G1m3>G1m17, nG1m1, G1v14 CH2 A1.3, A1.2 (CH1 R120>K (220) (124-221), hinge 1-15 (222-236), CH2 L1.3>A (240), L1.2>A (241), G1>A (243) (237-346), CH3 E12 (362), M14 (364), L123>C (449) (347-451), CHS (452-453)) (124-453)], (226-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens*IGKV1-16*01 (87.4%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens*IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (232-232":235-235")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1SV lacking the glutamine synthetase (GS-KO) gene, glycoform alfa, substituted at an average of one S atom of cysteine residues 449 and 449" with the (3RS)-1-[1,1,1-tris({3-[2-(2,2,2-tris{[(2-{alpha-(bromo / ethoxy / hydro / hydroxy)poly[1-(10,10-dimethyl-6-oxido-6-oxo-2,5,7-trioxa-10-aza-6λ⁵-phosphaundecan-10-ium-1-oyl)-1-methylethane-1,2-diyl]-ω-yl)-2-methylpropanoyl]oxy)methyl]ethoxy)acetamido]propanamido)methyl]-16,32-dioxo-3,6,9,12,19,22,25,28-octaooxa-15,31-diazatetracontan-34-yl]-2,5-dioxopyrrolidin-1-yl (*tedromer*)

immunoglobuline G1-kappa, anti-[*Homo sapiens* VEGFA (facteur de croissance A de l'endothélium vasculaire, VEGF-A, VEGF)], anticorps monoclonal humanisé, conjugué via un linker à un **polymère en étoile à neuf branches** avec groupes terminaux de polymère phosphorylcholine; chaîne lourde gamma1 humanisée (1-453) [VH (*Homo sapiens*IGHV3-30*02 (75.8%) -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens*IGHG1*03v, G1m3>G1m17, nG1m1, G1v14 CH2 A1.3, A1.2 (CH1 R120>K (220) (124-221), charnière 1-15 (222-236), CH2 L1.3>A (240), L1.2>A (241), G1>A (243) (237-346), CH3 E12 (362), M14 (364), L123>C (449) (347-451), CHS (452-453)) (124-453)], (226-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens*IGKV1-16*01 (87.4%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens*IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (232-232":235-235")-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, substitué à une moyenne d'un atome S des résidus cystéine 449 et 449" par le groupe (3RS)-1-[1,1,1-tris({3-[2-(2,2,2-tris({2- α -(bromo / éthoxy / hydro / hydroxy)poly[1-(10,10-diméthyl-6-oxido-6-oxo-2,5,7-trioxa-10-aza-6 λ^5 -phosphaundécane-10-ium-1-oyl)-1-méthyléthane-1,2-diyl]- ω -yl)]-2-méthylpropanoyl)oxy)méthyl]éthoxy)acétamido]propanamido)méthyl]-16,32-dioxo-3,6,9,12,19,22,25,28-octaoxa-15,31-diazatétratriacontan-34-yl]-2,5-dioxopyrrolidin-1-yle (*tédromère*)

inmunoglobulina G1-kappa, anti-[*Homo sapiens* VEGFA (factor de crecimiento A del endotelio vascular, VEGF-A, VEGF)], anticuerpo monoclonal humanizado, conjugado a través de un enlace a un **polímero estrellado con nueve ramas** con grupos terminales de polímero fosforilcolina ;

cadena pesada gamma1 humanizada (1-453) [VH (*Homo sapiens* IGHV3-30*02 (75.8%) -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, G1v14 CH2 A1.3, A1.2 (CH1 R120>K (220) (124-221), bisagra 1-15 (222-236), CH2 L1.3>A (240), L1.2>A (241), G1>A (243) (237-346), CH3 E12 (362), M14 (364), L123>C (449) (347-451), CHS (452-453)) (124-453)], (226-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-16*01 (87.4%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (232-232':235-235')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1SV en ausencia del gen glutamina sintetasa (GS-KO), forma glicosilada alfa, sustituido en un promedio de un átomo de S de residuos de cisteína 449 y 449" con el grupo (3RS)-1-[1,1,1-tris({3-[2-(2,2,2-tris({2- α -(bromo / etoxi / hidro / hidroxi)poli[1-(10,10-dimetil-6-oxido-6-oxo-2,5,7-trioxa-10-aza-6 λ^5 -fosfaundecan-10-io-1-oil)-1-metiletano-1,2-diiil]- ω -il)]-2-metilpropanoil)oxi]metil)etoxi)acetamido]propanamido)metil]-16,32-dioxo-3,6,9,12,19,22,25,28-octaoxa-15,31-diazatetraatriacontan-34-il]-2,5-dioxopirrolidin-1-ilo (*tédromero*)

Heavy chain / Chaîne lourde / Cadena pesada
 EVGLVESGGG LVQFGGSLRL SCAASGYDFT HYGMNVVRQA PGKGLVWGW 50
 INTYTGEPY AAEFKRRFTF SLDTSKSTAY LQMSLRAED TAVYYCAKYP 100
 YYYGTSHWY DWVGGQLT VSSASTKGPS VFPLAFSSKS TSGGTAALGQ 150
 LKVDYFPEPV TVSWNSGALT SGVHTFFAVL QSSGLVSLSS VTFVSSSLG 200
 TQTIICWNH KFSMTKVDK VEPKSCDATH TQPCFAPFA AGAPSVLFLP 250
 EKIKTILMS RFEFTVGVY DVSHDEVE FHWYDGVGV HNAKTRREE 300
 QYNSTRVVS VLTVLHQDL NGKEYKCKVS NRALAEPIK TISKAGQQR 350
 EFGVYTLFPS REEMTKQVS LTCLKGFYF SDIAVEWESN GQPENNYKT 400
 FVPLDSDGFS FLYSKLTVDK SRWQGNVFS CSMVHEALHN HYTEKLSLCS 450
 FGK 453

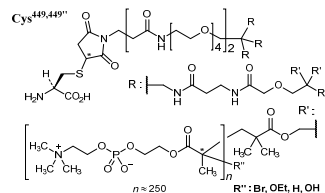
Light chain / Chaîne légère / Cadena ligera
 DIGLTQSPS LSAISGDRVT ITCSASDIS NYLNVQQKPK GKAPKVLVIF 50
 TSSLHGVPS RFGSGSGTDT PTLTISLSLP EDFATYVQQQ YSTVFWTFGQ 100
 GTKLVEIKRV AAPSVFIFPP SDEQLKSGTA SVVCLLNIFY PREAKVQWKV 150
 DNALQSGNSQ ESVTEQDSKD STYLSLSLT LSKADYKHKH YVACEVTHGQ 200
 LSSPVTKSN RGEK 214

Post-translational modifications
 Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
 Intra-H (C23-C104) 22-96 150-206 267-327 373-431
 22'-96' 150'-206' 267'-327' 373'-431'
 Intra-L (C23-C104) 23'-88" 134"-194"
 23"-88" 134"-194"
 Inter-H-L (h 5-CL 126) 226-214' 226"-214"
 Inter-H-H (h 11, h 14) 232-232' 235-235"

N-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 biantennarios complejos fucosilados

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
 H CHSK2:453,453"

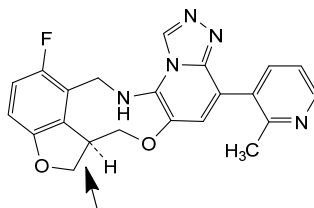
Conjugation sites / Sites de conjugation / Posiciones de conjugación:
 H CH3 L123>C:449,449"



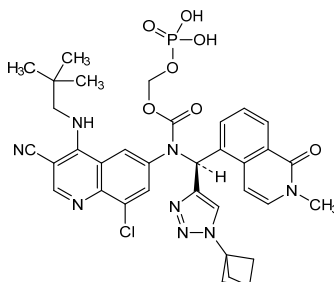
Recommended International Nonproprietary Names (Rec. INN): List 89
Dénominations communes internationales recommandées (DCI Rec.): Liste 89
Denominaciones Comunes Internacionales recomendadas (DCI Rec.): Lista 89
(WHO Drug Information, Vol. 37, No. 1, 2023)

p.61 *delete/supprimer/suprimáse* *insert/insérer/insertese*
casdozokitug **casdozokitugum**

p.168 **pociredirum**
 pociredir
 pocirédír
 pociredir
replace the structure by the following one
remplacer la structure par la suivante
sustitúyase la estructura por la siguiente



p.203 **tilpisertibum fosmecarbilum**
 tilpisertib fosmecarbil
 tilpisertib fosmécarbil
 tilpisertib fosmecarbil
replace the structure by the following one
remplacer la structure par la suivante
sustitúyase la estructura por la siguiente



p.203 **tobemstomigum #**
 -205 tobemstomig
 tobemstomig
 tobemstomig
replace the description by the following one
remplacer la description par la suivante
sustitúyase la descripción por la siguiente

immunoglobulin G1-kappa with crossed domains, anti-[*Homo sapiens* PDCD1 (programmed cell death 1, PD1, PD-1, CD279)] and anti-[*Homo sapiens* LAG3 (lymphocyte activating 3, lymphocyte-activation 3, CD223)], humanized monoclonal antibody, bispecific;
 gamma1 heavy chain with crossed V-kappa anti-PDCD1 (1-443) [V-KAPPA humanized (*Homo sapiens* IGKV4-1*01 (82.2%) - IGKJ1*01 (100%), CDR-IMGT) [10.3.9] (27-36.54-56.93-101) (1-111) -2-mer biseryl linker (112-113) -*Homo sapiens* IGHG1*01, G1m17.1, G1v14-49 CH2 A1.3, A1.2, G114, G1v32 CH3 W22 (knob) (CH1 K120 (210) (114-211), hinge 1-15 (212-226), CH2 L1.3>A (230), L1.2>A (231), P114>G (325) (227- 336), CH3 D12 (352), L14 (354), S10>C (350), T22>W (362) (337- 441), CHS (442-443)) (112-443)], (216-227')-disulfide with kappa light chain with crossed VH anti-PDCD1 (1'-227') [VH humanized (*Homo*

sapiens IGHV3-23*01 (90.6%) -(IGHD) -IGHJ5*01 (92.9%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1'-120') -*Homo sapiens* IGKC*01 (99.1%), R1.4>A (121), T1.3>S (122), Km3 A45.1 (166), V101 (204) (121'-227)]; gamma1 heavy chain anti-LAG3 (1"-451") [VH humanized (*Homo sapiens* IGHV3-23*01 (86.7%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1"-121") -*Homo sapiens* IGHG1*01, G1m17,1, G1v14-49 CH2 A1.3, A1.2, G114, G1v33 CH3 S22, A24, V86 (hole) (CH1 K26>E (151), K119>E (217), K120 (218) (122"-219")), hinge 1-15 (220"-234"), CH2 L1.3>A (238), L1.2>A (239), P114>G (333) (235"-344"), CH3 D12 (360), L14 (362), Y5>C (353), T22>S (370), L24>A (372), Y86>V (411) (345"-449"), CHS (450"-451")) (122"-451")), (224"-214")-disulfide with kappa light chain anti-LAG3 (1""-214"" [*Homo sapiens* V-KAPPA (IGKV1D-39*01 (96.8%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1""-107"") -*Homo sapiens* IGKC*01 (98.1%), E12>R (123), Q13>K (124) (108""-214"")]; dimer (222-230":225-233":350-353")-trisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from the cell line CHO-K1, glycoform alfa

immunoglobuline G1-kappa avec domaines croisés, anti-[*Homo sapiens* PDCD1 (protéine 1 de mort cellulaire programmée, PD-1, PD1, CD279)] and anti-[*Homo sapiens* LAG3 (activateur 3 des lymphocytes, lymphocyte-activation 3, CD223)], anticorps monoclonal humanisé, bispécifique; chaîne lourde gamma1 à V-kappa croisé anti-PDCD1 (1-443) [V-KAPPA humanisé (*Homo sapiens* IGKV4-1*01 (82.2%) -IGKJ1*01 (100%), CDR-IMGT [10.3.9] (27-36.54-56.93-101)) (1-111) -2-mer biséryl linker (112-113) -*Homo sapiens* IGHG1*01, G1m17,1, G1v14-49 CH2 A1.3, A1.2, G114, CH2 G1v32 CH3 W22 (knob) (CH1 K120 (210) (114-211), charnière 1-15 (212-226), CH2 L1.3>A (230), L1.2>A (231), P114>G (325) (227- 336), CH3 D12 (352), L14 (354), S10>C (350), T22>W (362))] (337- 441), CHS (442-443)) (112-443)], (216-227')-disulfure avec la chaîne légère kappa à VH croisé anti-PDCD1 (1'-227') [VH humanisé (*Homo sapiens* IGHV3-23*01 (90.6%) -(IGHD) -IGHJ5*01 (92.9%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1'-120') -*Homo sapiens* IGKC*01 (99.1%), R1.4>A (121), T1.3>S (122), Km3 A45.1 (166), V101 (204) (121'-227)]; chaîne lourde gamma1 anti-LAG3 (1"-451") [VH humanisé (*Homo sapiens* IGHV3-23*01 (86.7%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1"-121") -*Homo sapiens* IGHG1*01, G1m17,1, G1v14-49 CH2 A1.3, A1.2, G114, G1v33 CH3 S22, A24, V86 (hole) (CH1 K26>E (151), K119>E (217), K120 (218) (122"-219")), charnière 1-15 (220"-234"), CH2 L1.3>A (238), L1.2>A (239), P114>G (333) (235"-344"), CH3 D12 (360), L14 (362), Y5>C (353), T22>S (370), L24>A (372), Y86>V (411)] (345"-449"), CHS (450"-451")) (122"-451")), (224"-214")-disulfure avec la chaîne légère kappa anti-LAG3 (1""-214"" [*Homo sapiens* V-KAPPA (IGKV1D-39*01 (96.8%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1""-107"") -*Homo sapiens* IGKC*01 (98.1%), E12>R (123), Q13>K (124) (108""-214"")]; dimère (222-230":225-233":350-353")-trisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-K1, glycoforme alfa

immunoglobulina G1-kappa con dominios cruzados, anti-[*Homo sapiens* PDCD1 (proteína 1 de muerte celular programada, PD-1, PD1, CD279)] y anti-[*Homo sapiens* LAG3 (activador 3 de los linfocitos, linfocito-activación 3, CD223)], anticuerpo monoclonal humanizado, biespecífico;

cadena pesada gamma1 con V-kappa cruzada anti-PDCD1 (1-443) [V-KAPPA humanizado (*Homo sapiens* IGKV4-1*01 (82.2%) -IGKJ1*01 (100%), CDR-IMGT [10.3.9] (27-36.54-56.93-101))] (1-111) -2-mer biserial linker (112-113) -*Homo sapiens* IGHG1*01, G1m17.1, G1v14-49 CH2 A1.3, A1.2, G114, CH2 G1v32 CH3 W22 (knob) (CH1 K120 (210) (114-211), bisagra 1-15 (212-226), CH2 L1.3>A (230), L1.2>A (231), P114>G (325) (227-336), CH3 D12 (352), L14 (354), S10>C (350), T22>W (362)) (337-441), CHS (442-443)) (112-443)], (216-227')-disulfuro con la cadena ligera kappa con VH cruzado anti-PDCD1 (1'-227') [VH humanizado (*Homo sapiens* IGHV3-23*01 (90.6%) -(IGHD) -IGHJ5*01 (92.9%), CDR-IMGT [8.8.13] (26-33.51-58.97-109))] (1'-120') -*Homo sapiens* IGKC*01 (99.1%), R1.4>A (121), T1.3>S (122), Km3 A45.1 (166), V101 (204) (121'-227'); cadena pesada gamma1 anti-LAG3 (1"-451") [VH humanizado (*Homo sapiens* IGHV3-23*01 (86.7%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.14] (26-33.51-58.97-110))] (1"-121") -*Homo sapiens* IGHG1*01, G1m17.1, G1v14-49 CH2 A1.3, A1.2, G114, G1v33 CH3 S22, A24, V86 (hole) (CH1 K26>E (151), K119>E (217), K120 (218) (122"-219"), bisagra 1-15 (220"-234"), CH2 L1.3>A (238), L1.2>A (239), P114>G (333) (235"-344"), CH3 D12 (360), L14 (362), Y5>C (353), T22>S (370), L24>A (372), Y86>V (411)) (345"-449"), CHS (450"-451")) (122"-451"), (224"-214'")-disulfuro con la cadena ligera kappa anti-LAG3 (1'"-214'") [*Homo sapiens* V-KAPPA (IGKV1D-39*01 (96.8%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97) (1'"-107'") -*Homo sapiens* IGKC*01 (98.1%), E12>R (123), Q13>K (124) (108'"-214'")); dímero (222-230":225-233":350-353")-trisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular derivada de CHO-K1, forma glicosilada alta

p.253 **zifibancimig #**
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immunoglobulin Fab G1-kappa, anti-[*Homo sapiens* ANGPT2 (angiopoietin 2, Ang2)] and anti-[*Homo sapiens* VEGFA (vascular endothelial growth factor A, VEGF-A, VEGF)], monoclonal antibody, bispecific, biparatope monovalent; VH-(CH1-hinge) gamma1 heavy chain (1-223) [VH (*Homo sapiens* IGHV3-31*07 (74.0%) -(IGHD) -IGHJ4*01 (86.7%), CDR-IMGT [7.8.9] (26-32.50-57.96-104)) (1-115) -CH1-hinge (*Homo sapiens* IGHG1*01 (100%), G1m17 (CH1 K120 (212) (116-213), hinge 1-10 (214-223)) (116-223)], (218-214')-disulfide with kappa light chain (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5*01 (72.2%) -IGKJ4*01 (90.9%), 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')]; bispecific, biparatope monovalent: anti-ANG2 paratope (VH CDR1 and CDR3, V-KAPPA CDR2) and anti-VEGFA paratope (V-KAPPA CDR1 and CDR3, VH CDR2), produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, non-glycosylated

immunoglobuline Fab G1-kappa, anti-[*Homo sapiens* VEGFA (facteur A de croissance de l'endothélium vasculaire humain) et *Homo sapiens* ANGPT2 (angiopoïétine 2, Ang2)], anticorps monoclonal, bispécifique, biparatope monovalent; VH-(CH1-charnière) chaîne lourde gamma1 (1-223) [VH (*Homo*

sapiens IGHV3-31*07 (74.0%) -(IGHD) -IGHJ4*01 (86.7%), CDR-IMGT [7.8.9] (26-32.50-57.96-104)) (1-115) -CH1-charnière (*Homo sapiens* IGHG1*01 (100%), G1m17 (CH1 K120 (212) (116-213), charnière 1-10 (214-223)) (116-223)], (218-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5*01 (72.2%) -IGKJ4*01 (90.9%), 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'-213')]; bispécifique, bivalent: anti-ANG2 paratope (VH CDR1 et CDR3, V-KAPPA CDR2) et anti-VEGFA paratope (V-KAPPA CDR1 et CDR3, VH CDR2), produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, non-glycosylé

immunoglobulina Fab G1-kappa, anti-[*Homo sapiens* VEGFA (factor A de crecimiento del endotelio vascular humano) y *Homo sapiens* ANGPT2 (angiopoetina 2, Ang2)], anticuerpo monoclonal, biespecífico, bivalente; VH-(CH1-bisagra) cadena pesada gamma1 (1-223) [VH (*Homo sapiens* IGHV3-31*07 (74.0%) -(IGHD) -IGHJ4*01 (86.7%), CDR-IMGT [7.8.9] (26-32.50-57.96-104)) (1-115) -CH1-bisagra (*Homo sapiens* IGHG1*01 (100%), G1m17 (CH1 K120 (212) (116-213), bisagra 1-10 (214-223)) (116-223)], (218-214')-disulfuro con la cadena ligera kappa (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5*01 (72.2%) -IGKJ4*01 (90.9%), 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'-213')]; biespecífico, bivalente: anti-ANG2 paratope (VH CDR1 et CDR3, V-KAPPA CDR2) y anti-VEGFA paratope (V-KAPPA CDR1 et CDR3, VH CDR2), producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, no glicosilado

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.