

International Nonproprietary Names for Pharmaceutical Substances (INN)

RECOMMENDED International Nonproprietary Names: List 88

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 88

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 88

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

abimtrevirum

abimtrevir

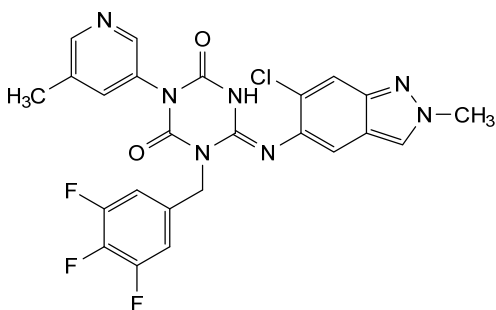
(6E)-6-[(6-chloro-2-methyl-2H-indazol-5-yl)imino]-3-(5-methylpyridin-3-yl)-1-[(3,4,5-trifluorophenyl)methyl]-1,3,5-triazinane-2,4-dione

abimtrevir

(6E)-6-[(6-chloro-2-méthyl-2H-indazol-5-yl)imino]-3-(5-méthylpyridin-3-yl)-1-[(3,4,5-trifluorophényl)méthyl]-1,3,5-triazinane-2,4-dione

abimtrevir

(6E)-6-[(6-cloro-2-metil-2H-indazol-5-il)imino]-3-(5-metilpiridin-3-il)-1-[(3,4,5-trifluorofenil)metil]-1,3,5-triazinano-2,4-diona

 $C_{24}H_{17}ClF_3N_7O_2$ **acidum icomidocholicum**

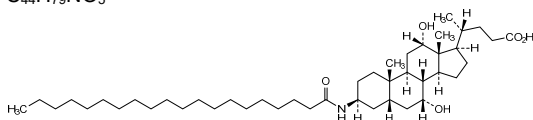
icomidocholic acid

7 α ,12 α -dihydroxy-3 β -icosanamido-5 β -cholan-24-oic acid

acide icomidocholique

acide 7 α ,12 α -dihydroxy-3 β -icosanamido-5 β -cholan-24-oïque

ácido icomidocólico

ácido 7 α ,12 α -dihidroxi-3 β -icosanamido-5 β -colan-24-oico $C_{44}H_{79}NO_5$ 

acrixolimabum #

acrixolimab

immunoglobulin G4-kappa, anti-[*Homo sapiens* PDCD1 (programmed cell death 1, PD-1, PD1, CD279)], *Homo sapiens* monoclonal antibody; gamma4 heavy chain *Homo sapiens* (1-441) [VH (*Homo sapiens* IGHV3-30*01 (95.8%) -(IGHD) - IGHJ5*01 (100%), CDR-IMGT [8.8.7] (26-33.51-58.97-103)) (1-114)-*Homo sapiens* IGHG4*01, G4v5 h P10 (CH1 (115-212), hinge 1-12 S10>P (222) (213-224), CH2 (225-334), CH3 (335-439), CHS (440-441)) (115-441)], (128-220')-disulfide with kappa light chain *Homo sapiens* (1'-220') [V-KAPPA (*Homo sapiens* IGKV2-40*01 (94.1%) -IGKJ3*01 (91.7%) P120>Q (106), CDR-IMGT [12.3.9] (27-38.56-58.95-103)) (1'-113') - *Homo sapiens* IGKC*01 (100%), Km3 A45.1 (159), V101 (197) (114'-220')]; dimer (220-220":223-223")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-DG44, glycoform alfa

acrixolimab

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* (1-441) [VH (*Homo sapiens* IGHV3-30*01 (95.8%) -(IGHD) - IGHJ5*01 (100%), CDR-IMGT [8.8.7] (26-33.51-58.97-103)) (1-114)-*Homo sapiens* IGHG4*01, G4v5 h P10 (CH1 (115-212), charnière 1-12 S10>P (222) (213-224), CH2 (225-334), CH3 (335-439), CHS (440-441)) (115-441)], (128-220')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-220') [V-KAPPA (*Homo sapiens* IGKV2-40*01 (94.1%) -IGKJ3*01 (91.7%) P120>Q (106), CDR-IMGT [12.3.9] (27-38.56-58.95-103)) (1'-113') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (159), V101 (197) (114'-220')]; dimère (220-220":223-223")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-DG44, glycoforme alfa

acrixolimab

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* (1-441) [VH (*Homo sapiens* IGHV3-30*01 (95.8%) -(IGHD) - IGHJ5*01 (100%), CDR-IMGT [8.8.7] (26-33.51-58.97-103)) (1-114)-*Homo sapiens* IGHG4*01, G4v5 h P10 (CH1 (115-212), bisagra 1-12 S10>P (222) (213-224), CH2 (225-334), CH3 (335-439), CHS (440-441)) (115-441)], (128-220')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-220') [V-KAPPA (*Homo sapiens* IGKV2-40*01 (94.1%) -IGKJ3*01 (91.7%) P120>Q (106), CDR-IMGT [12.3.9] (27-38.56-58.95-103)) (1'-113') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (159), V101 (197) (114'-220')]; dímero (220-220":223-223")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-DG44, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada
 QVQLVESGGG VVQPGRSLRL SCAASGFTFL RYAMHWVRQA PGKGLEWVAV 50
 ISYDGRYKYY ADSVKGRFTI SRDNSKNTLY LQMSLRAED TAVYYCTTTT 100
 FDSWQGGTLV TVSSASTKGP SVFPLAPCSR STSESTAALG CLVKDYFPEP 150
 VTVSWNSGAL TSGVHTFFAV LQSSGLYSLS SVVTVFSSSL GKTYTCNVD 200
 HKPSNTKVDK RVESKYGPPC PCCPAPEFLG GPSVLEFPFK PKDTLMSRT 250
 FEVTCVVVDV SQEDPEVQFN WYWDGVEVHN AKTKFREEQF NSTYRVVSVL 300
 TVLHQDWLNG KEYKCKVSNK GLPFSIEKTI SKAKGQPREP QVYTLPPSQE 350
 EMTKQVSLT CLVKGFYPSD IAVWEESNGQ PENNYKTTFP VLDSDDGFFL 400
 YSRLTVDKSR WQEGNVFSCS VMHEALHNHY TQKSLSLSLG K 441

Light chain / Chaîne légère / Cadena ligera
 DIVMTQTPLS LPVTPGEAAS ISCRSSQSLD DSEGDNTYLD WYLQKPGQSP 50
 QLLIYTLNHR ASGVPRDFSG SGGSTDFMLE ISRVEAEDVG VYVCMQRRDF 100
 PFTFGQGTKV DIKRTVAAPS VFIFPPSDEQ LKSGTASVVC LLNNFYPREA 150
 KVQWKVDNAL QSGNSQESVT EQDSKDSSTYS LSSTLTLNSA DYEKHKVYAC 200
 EVTHQGLSSP VTRKSNRGEK 220

Post-translational modifications
 Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
 Intra-H (C23-C104) 22-96 141-197 255-315 361-419
 22"-96" 141"-197" 255"-315" 361"-419"
 Intra-L (C23-C104) 23"-94" 140"-200"
 23"-94" 140"-200"
 Inter-H-L (CH1 10-CL 126) 128-220" 128"-220"
 Inter-H-H (h 8, h 11) 220-220" 223-223"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutamínilo N-terminal
 H VH Q1> pyroglutamyl (pE, 5-oxopropyl): 1, 1"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
 H CH2 N84.4: 291, 291"

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

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
 H CHS K2: 441, 441"

aguracingenum cadoparovecum #
 aguracingene cadoparovec

recombinant, non-replicating adeno-associated virus serotype 8 (rAAV8) vector encoding codon-optimized human retinal cone cyclic nucleotide-gated cation channel $\alpha 3$ (CNGA3), under control of a synthetic promoter, derived from the human opsin locus control region and the human green-sensitive opsin gene promoter, terminated with the simian virus 40 (SV40) polyadenylation (polyA) sequence, and flanked by AAV2 inverted terminal repeats (ITRs).

aguracingène cadoparovec

vecteur recombinant, non répliquant, du virus adéno-associé de sérotype 8 (rAAV8) codant le canal cationique $\alpha 3$ des cônes de la rétine humaine dépendant des nucléotides cycliques (CNGA3), sous le contrôle d'un promoteur synthétique, dérivé de la région de contrôle du locus de l'opsine humaine et du promoteur du gène de l'opsine humaine sensible au vert, terminé par la séquence polyadénylation (polyA) du virus simien 40 (SV40), et flanqué de répétitions terminales inversées (ITR) de l'AAV2.

aguracingén cadoparovec

vector de virus adenoasociado recombinante de serotipo 8 (rAAV8) no replicativo que codifica para el canal catiónico modulado por nucleótidos cíclicos $\alpha 3$ (CNGA3) de los conos retinales humanos, bajo el control de un promotor sintético derivado de la región de control del locus de la opsina humana y del promotor del gen de la opsina sensible al verde humana, terminado con la secuencia poliadenilación (polyA) del virus simio 40 (SV40), y flanqueado por las repeticiones terminales invertidas (ITRs) del AAV2.

amredobresibum

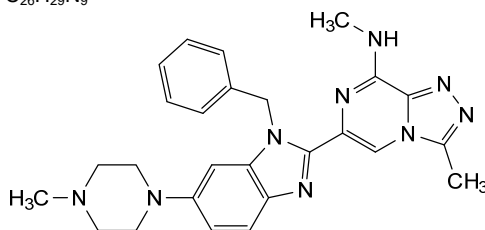
amredobresib

6-[1-benzyl-6-(4-methylpiperazin-1-yl)-1*H*-benzimidazol-2-yl]-*N*,3-diméthyl[1,2,4]triazolo[4,3-*a*]pyrazin-8-amine

amrédobrésib

6-[1-benzyl-6-(4-méthylpipérazin-1-yl)-1*H*-benzimidazol-2-yl]-*N*,3-diméthyl[1,2,4]triazolo[4,3-*a*]pyrazin-8-amine

amredobresib

6-[1-bencil-6-(4-metilpiperazin-1-il)-1*H*-benzimidazol-2-il]-*N*,3-dimetil[1,2,4]triazolo[4,3-*a*]pirazin-8-aminaC₂₆H₂₉N₉**anivovetmabum #**

anivovetmab

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 (93.7%) -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

anivovetmab

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 (93.7%) -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

anivovetmab

inmunoglobulina 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 (93.7%) -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 hámster chino (CHO), línea celular CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

QVQLKESGPG LVAPSQTLSL TCTVSGFSL S YHVMVVRQP PGKLEWLVG 50
 MWNDGDTSYN LALNSRLSIS RDTSKSQVFF KMSSIQTEDT ATYYCARPEL 100
 PGLTYGVWFP YWQCTLVTV SAASTTAPSV FPLAPSCGST SGSTVALACL 150
 VSGYFPEPVT VSWNSGSLTS GVHTFPFVLQ SSGLYLSLSSM VTFPSSRWPS 200
 EFTFCNVAHP ASKTKVDKVF FKRENGRVRP PFDPCPCFAP EMLGGPSVFI 250
 FFPKPKDTLL IARTPEVTCV VVDLDPEDPE VQISWFFVGG QMQTAKTQPR 300
 EEQFNGTYRV VSVLPIGHQD WLKGRQFTCK VNNKALFSP I ERTISKARGQ 350
 AHQFSVYVLP PSREELSKNT VSLTCLIKDF FPPDIDVWVQ SNGQQEPESK 400
 YRTTFFQLDE DGSYFLYSKL SVDKSRWQRG DTFICAVMHE ALHNHYTQES 450
 LSHSPGK 457

Light chain / Chaîne légère / Cadena ligera

DIVMTQTFAS MSISVGRDVT MNCASQNV D SNVDWYQKQT GQSPNLLIYK 50
 ASNRNRTGVPD RFTGSGSGTD FTFTISNMQA EDLAVVYCMQ STSYPLTFGS 100
 GTKLEIKRND AQPAVLYLQFP SPDQLHTGSA SVVCLLNSFY PKDINVKWKV 150
 DGVLIQDTGIQ ESVTEQDKDS TYSLSSTLTM SSTEYLSHEL YSCEITHKSL 200
 PSTLIKSFQR SECQRVD 217

Post-translational modifications

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

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

H VH Q1 > pyroglutamyl (pE, 5-oxoprolyl): 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 biantenarijos complejos fucosilados.

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

H CHS K2: 457, 457"

atinvicitinibum

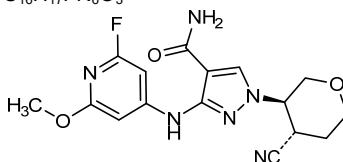
atinvicitinib

1-[(3R,4S)-4-cyanooxan-3-yl]-3-[(2-fluoro-6-methoxy-pyridin-4-yl)amino]-1H-pyrazole-4-carboxamide

atinvicitinib

1-[(3R,4S)-4-cyanooxan-3-yl]-3-[(2-fluoro-6-méthoxy-pyridin-4-yl)amino]-1H-pyrazole-4-carboxamide

atinvicitinib

1-[(3*R*,4*S*)-4-cianooxan-3-il]-3-[(2-fluoro-6-metoxipiridin-4-il)amino]-1*H*-pirazol-4-carboxamidaC₁₆H₁₇FN₆O₃

avutometinibum

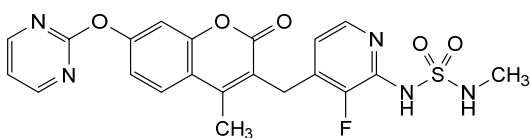
avutometinib

N-[3-fluoro-4-({4-methyl-2-oxo-7-[(pyrimidin-2-yl)oxy]-2*H*-1-benzopyran-3-yl)methyl}pyridin-2-yl]-*N'*-methylsulfuric diamide

avutométinib

N-[3-fluoro-4-({4-méthyl-2-oxo-7-[(pyrimidin-2-yl)oxy]-2*H*-1-benzopyran-3-yl)méthyl}pyridin-2-yl]-*N'*-méthyldiamide sulfurique

avutometinib

N-[3-fluoro-4-({4-metil-2-oxo-7-[(pirimidin-2-il)oxi]-2*H*-1-benzopiran-3-il)metil}piridin-2-il]-*N'*-metildiamida sulfúricaC₂₁H₁₈FN₅O₅S

azilsartanum mepixetilum

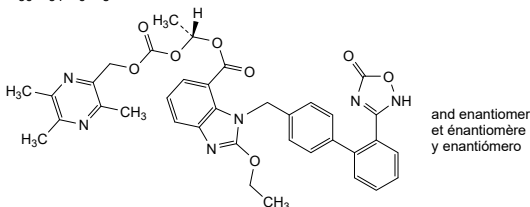
azilsartan mepixetil

rac-(1*R*)-1-({(3,5,6-trimethylpyrazin-2-yl)methoxy}carbonyl)oxyethyl 2-ethoxy-1-[[2'-(5-oxo-2,5-dihydro-1,2,4-oxadiazol-3-yl)[1,1'-biphenyl]-4-yl)methyl]-1*H*-benzimidazole-7-carboxylate

azilsartan mépixétíl

rac-2-éthoxy-1-[[2'-(5-oxo-2,5-dihydro-1,2,4-oxadiazol-3-yl)[1,1'-biphényl]-4-yl)méthyl]-1*H*-benzimidazole-7-carboxylate de (1*R*)-1-({(3,5,6-triméthylpyrazin-2-yl)méthoxy}carbonyl)oxyéthyle

azilsartán mepixetil

rac-2-etoxi-1-[[2'-(5-oxo-2,5-dihidro-1,2,4-oxadiazol-3-il)[1,1'-bifenil]-4-il)metil]-1*H*-benzimidazol-7-carboxilato de (1*R*)-1-({(3,5,6-trimetilpirazin-2-il)metoxi}carbonyl)oxi)etiloC₃₆H₃₄N₆O₈and enantiomer
et énantiomère
y enantiómero

azilsartanum mopivabilum

azilsartan mopivabil

{4-[(2,2-dimethylpropanoyl)oxy]-3-methoxyphenyl)methyl 2-ethoxy-1-[[2'-(5-oxo-2,5-dihydro-1,2,4-oxadiazol-3-yl)[1,1'-biphenyl]-4-yl]methyl]-1*H*-benzimidazole-7-carboxylate

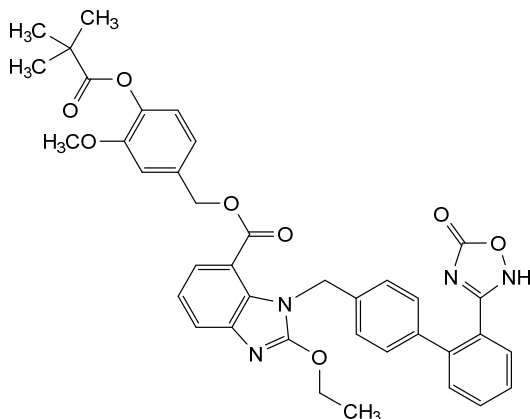
azilsartan mopivabil

2-éthoxy-1-[[2'-(5-oxo-2,5-dihydro-1,2,4-oxadiazol-3-yl)[1,1'-biphényl]-4-yl]méthyl]-1*H*-benzimidazole-7-carboxylate de {4-[(2,2-diméthylpropanoyl)oxy]-3-méthoxyphényl}méthyle

azilsartán mopivabilo

2-etoxi-1-[[2'-(5-oxo-2,5-dihidro-1,2,4-oxadiazol-3-il)[1,1'-bifenil]-4-il]metil]-1*H*-benzimidazol-7-carboxilato de {4-[(2,2-dimetilpropanoil)oxil]-3-metoxifenil}metilo

C₃₈H₃₆N₄O₈



bafrekalantum

bafrekalant

(3-chloro-6-methoxypyridin-2-yl)[3-({2-[4-(propan-2-yl)phenyl]imidazo[1,2-*a*]pyrimidin-3-yl)methyl}-3,8-diazabicyclo[3.2.1]octan-8-yl]methanone

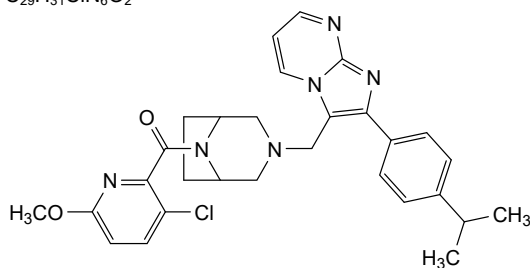
bafrékalant

(3-chloro-6-méthoxypyridin-2-yl)[3-({2-[4-(propan-2-yl)phényl]imidazo[1,2-*a*]pyrimidin-3-yl]méthyl)-3,8-diazabicyclo[3.2.1]octan-8-yl]méthanone

bafrekalant

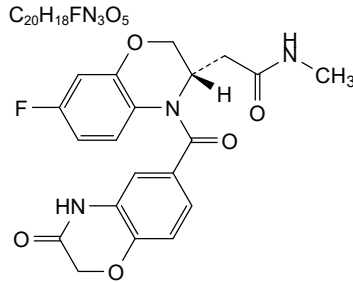
(3-cloro-6-metoxipiridin-2-il)[3-({2-[4-(propan-2-il)fenil]imidazo[1,2-*a*]pirimidin-3-il]metil)-3,8-diazabicyclo[3.2.1]octan-8-il]metanona

C₂₉H₃₁ClN₆O₂



balcinrenonum

balcinrenone	2-[(3S)-7-fluoro-4-(3-oxo-3,4-dihydro-2H-1,4-benzoxazine-6-carbonyl)-3,4-dihydro-2H-1,4-benzoxazin-3-yl]-N-methylacetamide
balcinrénone	2-[(3S)-7-fluoro-4-(3-oxo-3,4-dihydro-2H-1,4-benzoxazine-6-carbonyl)-3,4-dihydro-2H-1,4-benzoxazin-3-yl]-N-méthylacétamide
balcinrenona	2-[(3S)-7-fluoro-4-(3-oxo-3,4-dihydro-2H-1,4-benzoxazina-6-carbonil)-3,4-dihidro-2H-1,4-benzoxazin-3-il]-N-metilacetamida

**bebtelovimabum #**

bebtelovimab	immunoglobulin G1-lambda2, anti-[severe acute respiratory syndrome (human) coronavirus 2 (SARS-CoV-2) spike (S) glycoprotein, receptor binding domain (RBD)], <i>Homo sapiens</i> monoclonal antibody; gamma1 heavy chain <i>Homo sapiens</i> (1-449) [VH (<i>Homo sapiens</i> IGHV2-5*02 (94.9%) -(IGHD) -IGHJ1*01 (92.9%), CDR-IMGT [10.7.11] (26-35.53-59.98-108)) (1-119) - <i>Homo sapiens</i> IGHG1*03 (100%), G1m3, nG1m1 (CH1 R120 (216) (120-217), hinge 1-15 (218-232), CH2 (233-342), CH3 E12 (358), M14 (360) (343-447), CHS (448-449)) (120-449)], (222-214')-disulfide with lambda2 light chain <i>Homo sapiens</i> (1'-215') [V-LAMBDA (<i>Homo sapiens</i> IGLV2-14*01 (91.9%) -IGLJ2*01 (100%), CDR-IMGT [9.3.9] (26-34.52-54.91-99)) (1'-109') - <i>Homo sapiens</i> IGLC2*01 (100%) (110'-215')]; dimer (228-228'':231-231'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1SV lacking the glutamine synthetase (GS-KO) gene, glycoform alfa
bebtélovimab	immunoglobuline G1-lambda2, anti-[domaine de liaison au récepteur (RBD) de la glycoprotéine spike (S) du coronavirus 2 (humain) du syndrome respiratoire aigu sévère (SARS-CoV-2)], anticorps monoclonal <i>Homo sapiens</i> ; chaîne lourde gamma1 <i>Homo sapiens</i> (1-449) [VH (<i>Homo sapiens</i> IGHV2-5*02 (94.9%) -(IGHD) -IGHJ1*01 (92.9%), CDR-IMGT [10.7.11] (26-35.53-59.98-108)) (1-119) - <i>Homo sapiens</i> IGHG1*03 (100%), G1m3, nG1m1 (CH1 R120 (216) (120-217), charnière 1-15 (218-232), CH2 (233-342), CH3 E12 (358), M14 (360) (343-447), CHS (448-449)) (120-449)], (222-214')-disulfure avec la chaîne légère lambda2 <i>Homo sapiens</i> (1'-215') [V-LAMBDA (<i>Homo sapiens</i> IGLV2-14*01 (91.9%) -IGLJ2*01 (100%), CDR-IMGT [9.3.9] (26-34.52-54.91-99)) (1'-109') - <i>Homo sapiens</i> IGLC2*01 (100%) (110'-215')]; dimère (228-228'':231-231'')-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

bebtelovimab

inmunoglobulina G1-lambda2, anti-[dominio de unión al receptor (RBD) de la glicoproteína spike (S) del coronavirus 2 (humano) del síndrome respiratorio agudo severo (SARS-CoV-2)], anticuerpo monoclonal *Homo sapiens*;
 cadena pesada gamma1 *Homo sapiens* (1-449) [VH (*Homo sapiens* IGHV2-5*02 (94.9%) -(IGHD) - IGHJ1*01 (92.9%), CDR-IMGT [10.7.11] (26-35.53-59.98-108)) (1-119) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 (CH1 R120 (216) (120-217), bisagra 1-15 (218-232), CH2 (233-342), CH3 E12 (358), M14 (360) (343-447), CHS (448-449)) (120-449)], (222-214')-disulfuro con la cadena ligera lambda2 *Homo sapiens* (1'-215') [V-LAMBDA (*Homo sapiens* IGLV2-14*01 (91.9%) -IGLJ2*01 (100%), CDR-IMGT [9.3.9] (26-34.52-54.91-99)) (1'-109') -*Homo sapiens* IGLC2*01 (100%) (110'-215')]; dímero (228-228":231-231")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1SV en ausencia del gen glutamina sintetasa (GS-KO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada
 QITLKRESGPT LVKPTQTLTL TCTFSGFSL S ISGVGVGWL R QPPGKALEWL 50
 ALIYWD DDKR YSPSLKSR L T ISK DTSR NQV VLKMTNIDPV DTATYYCAHH 100
 SISTIFDHWG QGTLVTVSSA STKGPSVFP L APSSKSTSGG TAALGCLVKD 150
 YFPEPVTWSW NSGALTSQVH TFPVAVLQSSG LYSLSVVTV PSSSLGTQTY 200
 IGVNHNKPSN TKVDRKVEPK SCDKHTCCP CPAPPELLGGP SVFLFPKPK 250
 DTLMISRTP E VTCVVVDVSH EDPEVKFNW Y VDGVEVHNK TKPREQYNS 300
 TYRVS SVLTV LHQVDLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV 350
 YTLFPPSREEM TKNQVSLTCL VGGFYPSDIA VEWESNGQPE NNYKTTTPVL 400
 DSDGSFFLYS KLTVDKSRWQ QGNVFCSCVM HEALHNHYTQ KSLSLSPGK 449

Light chain / Chaîne légère / Cadena ligera
 QSALTPASV S GSPGQSITI SCTATSSDVG DYNVVS WYQQ HPGKAPKIMI 50
 FEVSDRPSGI SNRFSGSKSG NTASLTISGL QAED EADYYC SSYTTSSAVF 100
 GGGTKLTVLG QPKAAPSVTL FPPSSEELQA NKATLIVCLIS DFYPGA V TVA 150
 WKADSSPVKA GVETTTPSKQ SNNKYAASSY LSLTPEQWKS HRSYSCQVTH 200
 EGSTVEK TVA PTECS 215

Post-translational modifications
 Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
 Intra-H (C23-C104) 22-97 146-202 263-323 369-427
 22"-97" 146"-202" 263"-323" 369"-427"
 Intra-L (C23-C104) 22"-90' 137"-196'
 22"-90'" 137"-196'"
 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 glutamínilo N-terminal
 Q > pyroglutamyl (pE, 5-oxoprolyl)
 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 biantenarios complejos fucosilados.

benzgalantaminum
 benzgalantamine

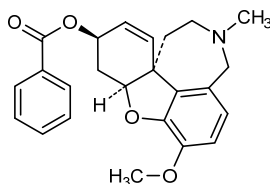
(4aS,6R,8aS)-3-methoxy-11-methyl-4a,5,9,10,11,12-hexahydro-6H-[1]benzofuro[3a,3,2-ef][2]benzazepin-6-yl benzoate;
 3-O-benzoylgalanthamine

benzgalantamine

benzoate de (4aS,6R,8aS)-3-méthoxy-11-méthyl-4a,5,9,10,11,12-hexahydro-6H-[1]benzofuro[3a,3,2-ef][2]benzazépin-6-yle;
 3-O-benzoylgalanthamine

benzgalantamina

benzoato de (4a*S*,6*R*,8a*S*)-11-metil-3-metoxi-4a,5,9,10,11,12-hexahidro-6*H*-[1]benzofuro[3a,3,2-*ef*][2]benzazepin-6-ilo;
3-*O*-benzoilgalantamina

C₂₄H₂₅NO₄

bersiporocinum

bersiporocin

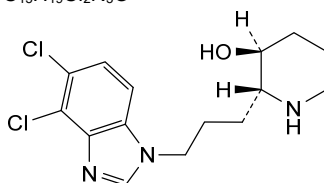
(2*R*,3*S*)-2-[3-(4,5-dichloro-1*H*-benzimidazol-1-yl)propyl]piperidin-3-ol

bersiporocine

(2*R*,3*S*)-2-[3-(4,5-dichloro-1*H*-benzimidazol-1-yl)propyl]pipéridin-3-ol

bersiporocina

(2*R*,3*S*)-2-[3-(4,5-dicloro-1*H*-benzimidazol-1-il)propil]piperidin-3-ol

C₁₅H₁₉Cl₂N₃O

betifisolimabum #

betifisolimab

immunoglobulin G1-kappa, anti-[*Homo sapiens* CD274 (programmed death ligand 1, PDL1, PD-L1, B7 homolog 1, B7H1)], monoclonal antibody;
gamma1 heavy chain (1-449) [VH Musmus/Homsap (*Mus musculus* IGHV1-64*01 (84.7%) -(IGHD) -IGHJ2*01 (93.3%) T122>S (113)/*Homo sapiens* IGHV1-2*02 (79.6%) -(IGHD) -IGHJ4*01 (80.0%) T122>S (113), L123>T (114), V124>L (115), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1*01, G1m17,1, G1v29 CH2 N84.4>A (CH1 K120 (216) (120-217), hinge 1-15 (218-232), CH2 N84.4>A (299) (233-342), CH3 D12 (358), L14 (360) (343-447), CHS (448-449)) (120-449)], (222-218')-disulfide with kappa light chain (1'-218') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV3-5*01 (93.9%) -IGKJ2*01 (100%)/*Homo sapiens* IGKV4-1*01 (65.3%) -IGKJ2*01 (91.7%) Q120>G (104), 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, cell line CHO-K1, non-glycosylated

bétifisolimab

immunoglobuline G1-kappa, anti-[*Homo sapiens* CD274 (ligand 1 de mort programmée, PDL1, PD-L1, homologue 1 de B7, B7H1)], anticorps monoclonal;

chaîne lourde gamma1 (1-449) [VH Musmus/Homsap (*Mus musculus* IGHV1-64*01 (84.7%) -(IGHD) -IGHJ2*01 (93.3%) T122>S (113)/*Homo sapiens* IGHV1-2*02 (79.6%) -(IGHD) -IGHJ4*01 (80.0%) T122>S (113), L123>T (114), V124>L (115), CDR-IMGT [8.8.12] (26-33.51-58.97-108))] (1-119) -*Homo sapiens* IGHG1*01, G1m17,1, G1v29 CH2 N84.4>A (CH1 K120 (216) (120-217), charnière 1-15 (218-232), CH2 N84.4>A (299) (233-342), CH3 D12 (358), L14 (360) (343-447), CHS (448-449)) (120-449)], (222-218')-disulfure avec la chaîne légère kappa (1'-218') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV3-5*01 (93.9%) -IGKJ2*01 (100%)/*Homo sapiens* IGKV4-1*01 (65.3%) -IGKJ2*01 (91.7%) Q120>G (104), 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), lignée cellulaire CHO-K1, non-glycosylé

betifisolimab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CD274 (ligando 1 de muerte programada, PDL1, PD-L1, homólogo 1 de B7, B7H1)], anticuerpo monoclonal;

cadena pesada gamma1 (1-449) [VH Musmus/Homsap (*Mus musculus* IGHV1-64*01 (84.7%) -(IGHD) -IGHJ2*01 (93.3%) T122>S (113)/*Homo sapiens* IGHV1-2*02 (79.6%) -(IGHD) -IGHJ4*01 (80.0%) T122>S (113), L123>T (114), V124>L (115), CDR-IMGT [8.8.12] (26-33.51-58.97-108))] (1-119) -*Homo sapiens* IGHG1*01, G1m17,1, G1v29 CH2 N84.4>A (CH1 K120 (216) (120-217), bisagra 1-15 (218-232), CH2 N84.4>A (299) (233-342), CH3 D12 (358), L14 (360) (343-447), CHS (448-449)) (120-449)], (222-218')-disulfuro con la cadena ligera kappa (1'-218') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV3-5*01 (93.9%) -IGKJ2*01 (100%)/*Homo sapiens* IGKV4-1*01 (65.3%) -IGKJ2*01 (91.7%) Q120>G (104), 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), línea celular CHO-K1, no glicosilado

Heavy chain / Chaîne lourde / Cadena pesada

QVQLVQSGAE	VKKPGASVKL	SCKASGYIFT	TYMHWVKQR	PGQGLEWIGM	50
IQPNSSGTTY	NEKFKKKATL	TVDKSISTAY	MELSRLLTSD	TAVYICARGA	100
GTVDYFDYWG	QGSTLTVSSA	STKGPSVFP	APSSKSTSGG	TAALGCLVKD	150
YFPEPVTYSW	NSGALTSQVH	TFFAVLQSSG	LYSLSSVTV	PSSSLGTQTY	200
ICNVNHHKPSN	TKVDKKEVPEK	SCDKTHTCCP	CPAPELLGGP	SVFLFPPPKK	250
DTLMISRTP	VTCVVVDVSH	EDPEVKFNWY	VDGVEVHNAK	TKPREEQYAS	300
TYRVVSVLTV	LHQDNLNGKE	YKCKVSNKAL	PAPIEKTIISK	AKGQPREPQV	350
YTLFPPSRDEL	TKNQVSLTCL	VKGIFYPSDIA	VEWESNGQPE	NNYKTPFPVL	400
DSGDSFFLYS	KLTVDKSRWQ	QGNVFCSVM	HEALHNHYTQ	KLSLSLSPGK	449

Light chain / Chaîne légère / Cadena ligera

DIVLTQSPAS	LAVSVGQRAT	ITCRASEVD	IYGNFMHWY	QQKPGQPPK	50
LIYRASNL	ESGIPARFSSG	SRTDFTLTIN	PVEAQDTATY	YCOQSTEDPY	100
TFGGGKLEI	KRTVAAPSVF	IFPPSDEQLK	SGTASVVCLL	NNFYPREAKV	150
QWKVDNALQS	GNSQESVTEQ	DSKSTYSLS	STLTLSKADY	EKHVKYACEV	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	263-323	369-427
	22"-96"	146"-202"	263"-323"	369"-427"
Intra-L (C23-C104)	23-92"	138"-198"		
	23"-92"	138"-198"		
Inter-H-L (h 5-CL 126)	222-218'	222"-218"		
Inter-H-H (h 11, h 14)	228-228"	231-231"		

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

H VH Q1 > pyroglutamy (pE, 5-oxopropyl): 1, 1"

No N-glycosylation site / pas de site de N-glycosylation / ningún posición de N-glicosilación
H CH2 N84.4>A (G1v29): 299, 299"

Aglycosylated / aglycosylé / aglicosilado

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

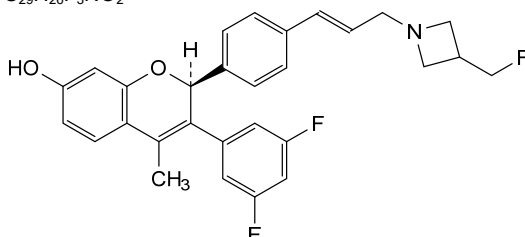
bexirestrant

bexirestrant (2²S,4E)-1³,1⁵-difluoro-7³-(fluoromethyl)-2⁴-methyl-2²H-7(1)-azetidina-2(3,2)-[1]benzopyrana-1(1),3(1,4)-dibenzenaheptaphan-4-en-2⁷-ol

béxirestrant (2²S,4E)-1³,1⁵-difluoro-7³-(fluorométhyl)-2⁴-méthyl-2²H-7(1)-azétidina-2(3,2)-[1]benzopyrana-1(1),3(1,4)-dibenzénaheptaphan-4-én-2⁷-ol

bexirestrant (2²S,4E)-1³,1⁵-difluoro-7³-(fluorometil)-2⁴-metil-2²H-7(1)-azetidina-2(3,2)-[1]benzopirana-1(1),3(1,4)-dibencenaheptafan-4-en-2⁷-ol

C₂₉H₂₆F₃NO₂

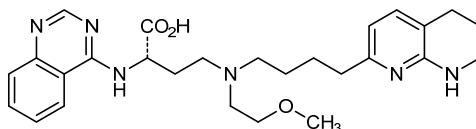
**bexotegrast**

bexotegrast (2S)-4-((2-methoxyethyl)[4-(5,6,7,8-tetrahydro-1,8-naphthyridin-2-yl)butyl]amino)-2-[(quinazolin-4-yl)amino]butanoic acid

béxotégrast acide (2S)-4-((2-méthoxyéthyl)[4-(5,6,7,8-tétrahydro-1,8-naphtyridin-2-yl)butyl]amino)-2-[(quinazolin-4-yl)amino]butanoïque

bexotegrast ácido (2S)-4-((2-metoxietil)[4-(5,6,7,8-tetrahidro-1,8-naftiridin-2-il)butil]amino)-2-[(quinazolin-4-il)amino]butanoico

C₂₇H₃₆N₆O₃

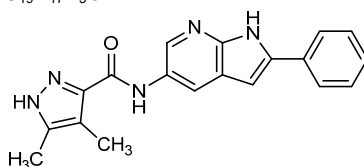
**bezuclastinib**

bezuclastinib 4,5-dimethyl-N-(2-phenyl-1H-pyrrolo[2,3-b]pyridin-5-yl)-1H-pyrazole-3-carboxamide

bézuclastinib 4,5-diméthyl-N-(2-phényl-1H-pyrrolo[2,3-b]pyridin-5-yl)-1H-pyrazole-3-carboxamide

bezuclastinib N-(2-fenil-1H-pirrolo[2,3-b]piridin-5-il)-4,5-dimetil-1H-pirazol-3-carboxamida

C₁₉H₁₇N₅O



bliretriginum

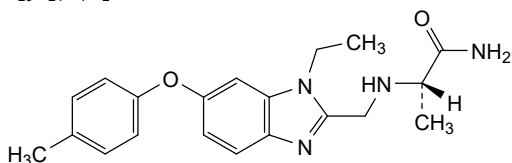
bliretrigine

(2*S*)-2-({[1-ethyl-6-(4-methylphenoxy)-1*H*-benzimidazol-2-yl]méthyl}amino)propénamide

blirétrigine

(2*S*)-2-({[1-éthyl-6-(4-méthylphénoxy)-1*H*-benzimidazol-2-yl]méthyl}amino)propénamide

bliretrigina

(2*S*)-2-({[1-etil-6-(4-metilfenoksi)-1*H*-benzimidazol-2-il]metil}amino)propanamidaC₂₀H₂₄N₄O₂**bocidelparum**

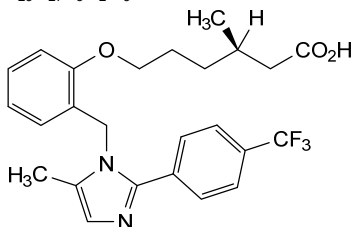
bocidelpar

(3*R*)-3-méthyl-6-[2-({5-méthyl-2-[4-(trifluorométhyl)phényl]-1*H*-imidazol-1-yl]méthyl}phénoxy)]hexanoïque

bocidelpar

acide (3*R*)-3-méthyl-6-[2-({5-méthyl-2-[4-(trifluorométhyl)phényl]-1*H*-imidazol-1-yl]méthyl)phénoxy)]hexanoïque

bocidelpar

ácido (3*R*)-3-metil-6-[2-({5-metil-2-[4-(trifluorometil)fenil]-1*H*-imidazol-1-il]metil)fenoksi]hexanoicoC₂₅H₂₇F₃N₂O₃**botaretigenum sparoparovecum #**

botaretigène sparoparovec

recombinant, non-replicating adeno-associated virus serotype 5 (rAAV5) vector, encoding a truncated form of human retinitis pigmentosa GTPase regulator (RPGR) isoform 6 (RPGR-ORF15), containing an in-frame deletion of 378 base pairs (bp) in the highly repetitive purine-rich region, preceded by a simian virus 40 (SV40) intron, under control of a human rhodopsin kinase (RK) promoter and terminated with a polyadenylation signal; flanked by AAV2 inverted terminal repeats (ITRs).

botarétigène sparoparovec

vecteur recombinant et non répliquant du virus adéno-associé de sérotype 5 (rAAV5) codant une forme tronquée de l'isoforme 6 (RPGR-ORF15) du régulateur de la GTPase de la rétinite pigmentaire humaine

- (RPGR), contenant une délétion de 378 paires de bases (pb) sans décalage du cadre de lecture dans la région riche en purines très répétitive, précédée d'un intron du virus simien 40 (SV40), sous le contrôle du promoteur de la rhodopsine kinase (RK) humaine et terminée par un signal de polyadénylation; flanquée de répétitions terminales inversées (ITRs) d'AAV2.
- botaretigén sparoparovec vector de virus adenoasociado recombinante de serotipo 5 (rAAV5) no replicativo que codifica para una forma truncada de la isoforma 6 del regulador GTPasa de la retinitis pigmentosa humana (RPGR-ORF15), que contiene una deleción sin cambio del marco de lectura de 378 pares de bases (bp) en la región altamente repetitiva rica en purinas, precedido por un intrón del virus simio 40 (SV40), bajo el control de un promotor de la rodopsina quinasa (RK) humana y terminado con una señal de poliadenilación; flanqueado por repeticiones terminales invertidas (ITRs) del AAV2.
- briquilimabum #**
briquilimab immunoglobulin G1-kappa, anti-[*Homo sapiens* KIT (KIT proto-oncogene, receptor tyrosine kinase, C-Kit, c-kit, SCFR, CD117)], monoclonal antibody;
gamma1 heavy chain (1-447) [VH (*Homo sapiens*IGHV1-3*01 (87.8%) -IGHD) -IGHJ6*01 (90.9%) T123>L (112), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens*IGHG1*01, G1m17,1, G1v36 CH2 N84.4>Q (CH1 K120 (214) (118-215), hinge 1-15 (216-230), CH2 N84.4>Q (297) (231-340), CH3 D12 (356), L14 (358) (341-445), CHS (446-447)) (118-447)], (220-218')-disulfide with kappa light chain (1'-218') [V-KAPPA Musmus/Homsap (*Mus musculus*IGKV3-10*01 (84.8%) -IGKJ2*01 (91.7%) L124>V (108))/*Homo sapiens*IGKV4-1*01 (80.2%) -IGKJ4*01 (100%), CDR-IMGT [10.3.9] (27-36.54-56.93-101)) (1'-111') -*Homo sapiens*IGKC*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218')]; dimer (226-226":229-229")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, non-glycosylated
- briquilimab immunoglobuline G1-kappa, anti-[*Homo sapiens* KIT (proto-oncogène KIT, récepteur tyrosine kinase, CD117, SCFR, C-Kit)], anticorps monoclonal;
chaîne lourde gamma1 (1-447) [VH (*Homo sapiens*IGHV1-3*01 (87.8%) -IGHD) -IGHJ6*01 (90.9%) T123>L (112), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens*IGHG1*01, G1m17,1, G1v36 CH2 N84.4>Q (CH1 K120 (214) (118-215), charnière 1-15 (216-230), CH2 N84.4>Q (297) (231-340), CH3 D12 (356), L14 (358) (341-445), CHS (446-447)) (118-447)], (220-218')-disulfure avec la chaîne légère kappa (1'-218') [V-KAPPA Musmus/Homsap (*Mus musculus*IGKV3-10*01 (84.8%) -IGKJ2*01 (91.7%) L124>V (108))/*Homo sapiens*IGKV4-1*01 (80.2%) -IGKJ4*01 (100%), CDR-IMGT [10.3.9] (27-36.54-56.93-101)) (1'-111') -*Homo sapiens*IGKC*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218')]; dimère (226-226":229-229")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), non-glycosylé
- briquilimab immunoglobulina G1-kappa, anti-[*Homo sapiens* KIT (proto-oncogén KIT, receptor tirosina kinasa, CD117, SCFR, C-Kit)], anticuerpo monoclonal;

cadena pesada gamma1 (1-447) [VH (*Homo sapiens* IGHV1-3*01 (87.8%) -(IGHD) -IGHJ6*01 (90.9%) T123>L (112), CDR-IMGT [8.8.10] (26-33.51-58.97-106))] (1-117) - *Homo sapiens* IGHG1*01, G1m17,1, G1v36 CH2 N84.4>Q (CH1 K120 (214) (118-215), bisagra 1-15 (216-230), CH2 N84.4>Q (297) (231-340), CH3 D12 (356), L14 (358) (341-445), CHS (446-447)) (118-447)], (220-218')-disulfuro con la cadena ligera kappa (1'-218') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV3-10*01 (84.8%) -IGKJ2*01 (91.7%) L124>V (108)/*Homo sapiens* IGKV4-1*01 (80.2%) -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 (226-226":229-229")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), no glicosilado

Heavy chain / Chaîne lourde / Cadena pesada

QQLVQSGAE VKKPGASVKV SCASGYTFT SYNMHWVRQA PGQGLEWMGV 50
 IYSGNGDTSY NQKFKGRVTI TADKSTSTAY MELSSLRSED TAVYYCARER 100
 DTRFGNWGQG TLVTVSSAST KGPSVFP LAP SSKSTSGGTA ALGCLVKDYF 150
 PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVTVVPS SSLGTQTYIC 200
 NVNHKFSTNK VDKRVEPKSK DKHTCTPPCP APELLGGPSV FLFPPKPKDT 250
 LMSRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNARTK PREPEQYQSTY 300
 RVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTIKAK GQPREPQVYV 350
 LPSPSDELTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTTPPVLD 400
 DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPGK 447

Light chain / Chaîne légère / Cadena ligera

DIVMTQSPDS LAVSLGERAT INCREASEVD IYNSFMHWY QKPKGPPKFL 50
 LIYLASNLES GVPDRFSGSG SGTDFLTIS SLQAEDVAVY YCQQNEDPY 100
 TFGGGTKVEI KRTVAAPSVF IFPPSDEQLK SGTASVCLL NNFYPREAKV 150
 QWKVDNALQS GNSQESVTEQ DSKDSTYSLS 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" 144"-200" 261"-321" 367"-425"
 22"-96" 144"-200" 261"-321" 367"-425"

Intra-L (C23-C104) 23"-92" 138"-198"
 23"-92" 138"-198"

Inter-H-L (h 5-CL 126) 220-218" 220"-218"

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

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

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

No N-glycosylation site / pas de site de N-glycosylation / ningún posición de N-glicosilación
 H CH2 N84.4>Q (G1v36): 297, 297"

Aglycosylated / aglycosylé / aglicósilado

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

burfiralimab #
 burfiralimab

immunoglobulin G4-kappa, anti-[*Homo sapiens* VIM (vimentin)], humanized monoclonal antibody; gamma4 heavy chain humanized (1-445) [VH (*Homo sapiens* IGHV1-2*06 (86.7%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.11] (26-33.51-58.97-107))] (1-118)-*Homo sapiens* IGHG4*01 (100%) (CH1 (119-216), hinge 1-12 (217-228), CH2 (229-338), CH3 (339-443), CHS (444-445)) (119-445)], (132-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (85.3%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (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

burfiralimab

immunoglobuline G4-kappa, anti-[*Homo sapiens* VIM (vimentine)], anticorps monoclonal humanisé; chaîne lourde gamma4 humanisée (1-445) [VH (*Homo sapiens* IGHV1-2*06 (86.7%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118)-*Homo sapiens* IGHG4*01 (100%) (CH1 (119-216), charnière 1-12 (217-228), CH2 (229-338), CH3 (339-443), CHS (444-445)) (119-445)], (132-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (85.3%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (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

burfiralimab

immunoglobulina G4-kappa, anti-[*Homo sapiens* VIM (vimentina)], anticuerpo monoclonal humanizado; cadena pesada gamma4 humanizada (1-445) [VH (*Homo sapiens* IGHV1-2*06 (86.7%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118)-*Homo sapiens* IGHG4*01 (100%) (CH1 (119-216), bisagra 1-12 (217-228), CH2 (229-338), CH3 (339-443), CHS (444-445)) (119-445)], (132-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (85.3%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (224-224'':227-227'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1SV en ausencia del gen glutamina sintetasa (GS-KO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVQSGAE VKKPGASVKV SCKASGYTFT GYNMNVVRQA PGKGLEWMGN 50
IDPFGYSDTY AQKFKQGRVTM TVDKSISTAY MELSRLRSDD TAVYVCARET 100
GTRAMDYWGQ GTLVTVSSAS TKGPSVFFLA PCSRSTSEST AALGLVKVDY 150
FFEPVTVSWN SGALTSVGHV FFAVLQSSGL YSLSSVVTVP SSSLGKTYT 200
CNVDHKFSNT KVDKRVESKY GPCPCSCPAP EFLGGPVSFL FFPKPKDTLM 250
ISRTPEVTCV VVDVQEDPE VQFNWYVDGV EVHNAKTKPR EEQFNSTYRV 300
VSVLTVLHQD WLNKKEYCKK VSNKGLPSSI EKTISKARGQ PREPQVYITLP 350
PSQEEMTKNQ VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG 400
SFFLYSRLTV DKSRWQEGNV FSCVSMHEAL HNHYTQKSL SLSLGLK 445
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Light chain / Chaîne légère / Cadena ligera

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DIQMTQSPSS LSASVGDRTV ITCRASENIY SNLAWYQQKP GKAPKLLIYV 50
ADNLADGVPS RFSGSGSGTD FTLTISLQPE EDFATYYCQH FYGSPRTFGG 100
GTRKVEIKRTV AAPSVEIFPP SDEQLKSGTA SVVCLLNIFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYLSLSTLT LSKADYEKHK VYACEVTHQG 200
LSSEFVTKSFN RGECL 214
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Post-translational modifications

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

Intra-H (C23-C104) 22-96 145-201 259-319 365-423
22"-96" 145"-201" 259"-319" 365"-423"

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

Inter-H-L (CH1 10-CL 126) 132-214' 132"-214"

Inter-H-H (h 8, h 11) 224-224" 227-227"

N-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 biantennarios complejos fucosilados.

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

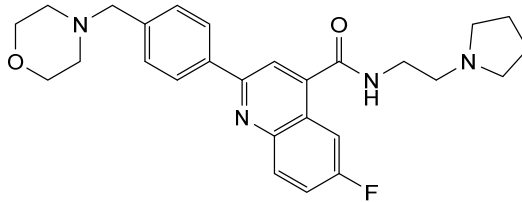
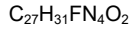
H CHS K2: 445, 445"

cabamiquinum

cabamiquine 6-fluoro-2-{4-[(morpholin-4-yl)méthyl]phényl}-N-[2-(pyrrolidin-1-yl)éthyl]quinoline-4-carboxamide

cabamiquine 6-fluoro-2-{4-[(morpholin-4-yl)méthyl]phényl}-N-[2-(pyrrolidin-1-yl)éthyl]quinoléine-4-carboxamide

cabamiquina 6-fluoro-2-{4-[(morfolin-4-il)metil]fenil}-N-[2-(pirrolidin-1-il)etil]quinoléina-4-carboxamida



camoteskimabum #

camoteskimab immunoglobulin G1-kappa, anti-[*Homo sapiens* IL18 (interleukin 18, IL-18, interferon gamma-inducing factor, IGIF, interleukin-1 gamma, IL-1 γ , IL1F4)], *Homo sapiens* monoclonal antibody; gamma1 heavy chain *Homo sapiens* (1-455) [VH (*Homo sapiens*IGHV4-39*01 (91.9%) -(IGHD) -IGHJ2*01 (86.7%), CDR-IMGT [10.7.17] (26-35.53-59.98-114)) (1-125) -*Homo sapiens*IGHG1*03, G1m3, nG1m1, G1v39 CH2 F1.3, E1.2, S116 (CH1 A1.4>S (127), S1.3>T (128), T1.2>K (129), K1.1>C (130), G1>L (131), R120 (222) (126-223), hinge 1-15 (224-238), CH2 L1.3>F (242), L1.2>E (243), P116>S (339) (239-348), CH3 E12 (364), M14 (366) (349-453), CHS (454-455)) (126-455)], (228-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens*IGKV1-5*03 (96.7%) -IGKJ2*02 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens*IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (234-234":237-237")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1SV, glycoform alfa

camoteskimab immunoglobuline G1-kappa, anti-[*Homo sapiens* IL18 (interleukine 18, IL-18, facteur induisant l'interféron gamma, IGIF, interleukine-1 gamma, IL-1 γ , IL1F4)], anticorps monoclonal *Homo sapiens*; chaîne lourde gamma1 *Homo sapiens* (1-455) [VH (*Homo sapiens*IGHV4-39*01 (91.9%) -(IGHD) -IGHJ2*01 (86.7%), CDR-IMGT [10.7.17] (26-35.53-59.98-114)) (1-125) -*Homo sapiens*IGHG1*03, G1m3, nG1m1, G1v39 CH2 F1.3, E1.2, S116 (CH1 A1.4>S (127), S1.3>T (128), T1.2>K (129), K1.1>C (130), G1>L (131), R120 (222) (126-223), charnière 1-15 (224-238), CH2 L1.3>F (242), L1.2>E (243), P116>S (339) (239-348), CH3 E12 (364), M14 (366) (349-453), CHS (454-455)) (126-455)], (228-214')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens*IGKV1-5*03 (96.7%) -IGKJ2*02 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens*IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (234-234":237-237")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1SV, glycoform alfa

camoteskimab

immunoglobulina G1-kappa, anti-[*Homo sapiens* IL18 (interleukina 18, IL-18, factor inductor del interferón gamma, IGIF, interleukina-1 gamma, IL-1γ, IL1F4)], anticuerpo monoclonal *Homo sapiens*; cadena pesada gamma1 *Homo sapiens* (1-455) [VH (*Homo sapiens* IGHV4-39*01 (91.9%) -(IGHD) -IGHJ2*01 (86.7%), CDR-IMGT [10.7.17] (26-35.53-59.98-114)) (1-125) -*Homo sapiens* IGHG1*03, G1m3, nG1m1, G1v39 CH2 F1.3, E1.2, S116 (CH1 A1.4>S (127), S1.3>T (128), T1.2>K (129), K1.1>C (130), G1>L (131), R120 (222) (126-223), bisagra 1-15 (224-238), CH2 L1.3>F (242), L1.2>E (243), P116>S (339) (239-348), CH3 E12 (364), M14 (366) (349-453), CHS (454-455)) (126-455)], (228-214')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5*03 (96.7%) -IGKJ2*02 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214''); dímero (234-234':237-237'')-bisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1SV, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

QVQLQESGPG	LVKPSETLSL	TCTVSGGIS	ADGYYSWIR	QPPGKLEWI	50
GSLYYSGSTY	YNPSLGRVIT	ISGDTSKNQF	SLKLSVTA	DTAVYICART	100
PAYFGQDRD	FFDVWGRGLT	VTVSSASTKG	PSVFFLAPSS	KSTSGGTAAL	150
GCLVKDYFPE	PVTVSWNSGA	LTSGVHTFPA	VLQSSGLYSL	SSVTVVPSSS	200
LGTQTYICNV	NHKPSTNKVD	KRVEPKSCDK	THTCPPCPAP	EFEGGSPVFL	250
FPPKPKDTLM	ISRTPPEVTCV	VVDVSHEDPE	VKFNWYVDG	EVHNAKTKPR	300
EEQYNSTYRV	VSVLTVLHQD	WLNKKEYCK	VSNKALPASI	EKTISKARGQ	350
PREPQVYTLF	PSREEMTKNQ	VSLTCLVKG	YPSDIAVEWE	SNGQPENNYK	400
TTPFVLDSDG	SFFLYSKLTV	DKSRWQQGNV	FSCSVMHEAL	HNHYTQKSLS	450
LSPGK					455

Light chain / Chaîne légère / Cadena ligera

DIQMTQSPFST	LSASVGDRTV	ITCRASQGIS	SWLAWYQQK	GKAPKVLIIK	50
ASTLVSGVPS	RFGSGSGSTE	FTLTISLQF	DDFATYYCQ	SHHPPTWFGQ	100
GTKLEIKRTV	AAPSVFIFPP	SDEQLKSGTA	SUVCLLNIFY	PREAKVQMKV	150
DNALQSGNSQ	ESVTEQDSKD	STYSLSSLT	LSKADYEKHK	VYACEVTHQG	200
LSSPVTKSFN	RGEC				214

Post-translational modifications

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

Intra-H (C23-C104)	22-97	152-208	269-329	375-433
	22"-97"	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 glutamínulo N-terminal

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

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

H CH2 N84.4: 305, 305"

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

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

cemdomespibum

cemdomespib

N-(2-{5-[(6-deoxy-5-*C*-methyl-4-*O*-methyl- α -*L*-lyxo-hexopyranosyl)oxy]-3'-fluoro[1,1'-biphenyl]-2-yl)ethyl)acetamide

cemdomespib

N-(2-{5-[(6-désoxy-5-*C*-méthyl-4-*O*-méthyl- α -*L*-lyxo-hexopyranosyl)oxy]-3'-fluoro[1,1'-biphényl]-2-yl)éthyl)acétamide

cemdomespib

N-(2-{5-[(6-desoxi-5-*C*-metil-4-*O*-metil- α -*L*-lixo-hexopiranosil)oxi]-3'-fluoro[1,1'-bifenil]-2-il)etil)acetamida

C₂₄H₃₀FNO₆



cifurtilimabum #
cifurtilimab

immunoglobulin G1-kappa, anti-[*Homo sapiens* CD40 (tumor necrosis factor receptor superfamily member 5, TNFRSF5)], monoclonal antibody;
gamma1 heavy chain (1-444) [VH (*Homo sapiens* IGHV3-66*01 (77.6%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.8.7] (26-33.51-58.97-103)) (1-114) - *Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (211) (115-212), hinge 1-15 (213-227), CH2 (228-337), CH3 E12 (353), M14 (355) (338-442), CHS (443-444)) (115-444)], (217-219')-disulfide with kappa light chain (1'-219') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (78.0%) -IGKJ1*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 (223-223":226-226")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-DXB11, glycoform alfa

cifurtilimab

immunoglobuline G1-kappa, anti-[*Homo sapiens* CD40 (membre 5 de la superfamille des récepteurs du TNF, TNFRSF5)], anticorps monoclonal;
chaîne lourde gamma1 (1-444) [VH (*Homo sapiens* IGHV3-66*01 (77.6%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.8.7] (26-33.51-58.97-103)) (1-114) - *Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (211) (115-212), charnière 1-15 (213-227), CH2 (228-337), CH3 E12 (353), M14 (355) (338-442), CHS (443-444)) (115-444)], (217-219')-disulfure avec la chaîne légère kappa (1'-219') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (78.0%) -IGKJ1*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 (223-223":226-226")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-DXB11, glycoforme alfa

cifurtilimab

immunoglobulina G1-kappa, anti-[*Homo sapiens* CD40 (miembro 5 de la superfamilia de los receptores del TNF, TNFRSF5)], anticuerpo monoclonal;

cadena pesada gamma1 (1-444) [VH (*Homo sapiens* IGHV3-66*01 (77.6%) -(IGHD)-IGHJ1*01 (100%), CDR-IMGT [8.8.7] (26-33.51-58.97-103)) (1-114) - *Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (211) (115-212), bisagra 1-15 (213-227), CH2 (228-337), CH3 E12 (353), M14 (355) (338-442), CHS (443-444)) (115-444)], (217-219')-disulfuro con la cadena ligera kappa (1'-219') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (78.0%) -IGKJ1*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 (223-223":226-226")-bisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-DXB11, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAASGYSFT GYYIHWVRQA PGKLEHWVAR 50
VIPNAGGTSY NQRFKGRFTL SVDNSKNTAY LQMNSLRAED TAVYYCAREG 100
IYWWGQQTIV TVSSASTKGP SVFPLAPSSK STSGGTAALG CLVKDYFPEP 150
VTVSWNSGAL TSGVHTFPVA LQSSGLISLS SVVTVPSSSL GTQTYICNVN 200
HKFSNTKVDK KVEPKSCDKT HTPFPCFAPE LLGGPSVFLF PPKFKDTLMI 250
SRTPEVTCV VDVSHEDPEV KFNWYVDGVE VHNAKTKPRE EQYNSTYRVV 300
SVLTVLHQDW LNKKEYRCKV SNKALPAPLE KTISKAKGQP REPQVYTLFP 350
SREEMTKMQV SLTCLVKGFY PSDIAVEWES NGQPENNYKT TFPVLDSDGS 400
FFLYSKLTVD KSRWQQGNVF SCSVMHEALH NHYTQKLSL SPGK 444
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Light chain / Chaîne légère / Cadena ligera

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DIQMTQSPSS LSASVGRDVT ITCRSSQSLV HSGNNTFLHW YQQKPKRAPP 50
LLIYTVSNRF SGVPSRFSGS GSGTDFTLTI SSLQPEDFAT YFCSQTHIVE 100
WTFGQGTKVE IKRTVAAPSV FIFPPSDEQL KSGTASVCL LNNFYPREAK 150
VQWKVDNALQ SGNISQESVTE QDSKDSYSL SSTLTLSKAD YERHKVYACE 200
VTHQGLSSPV TKSFNREGC 219
```

Post-translational modifications

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

Intra-H (C23-C104) 22-96 141-197 258-318 364-422
 22"-96" 141"-197" 258"-318" 364"-422"

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

Inter-H-L (h 5-CL 126) 217-219' 217"-219"

Inter-H-H (h 11, h 14) 223-223" 226-226"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
 HCH2 N84.4; 294, 294"

Afucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes afucosylés / glicanos de tipo CHO biantenaricos complejos afucosilados

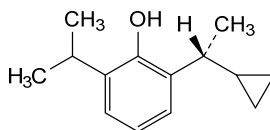
C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
 HCHSK2: 444, 444"

cipepofolum

cipepofol

cipépofof

cipepofol

2-[(1*R*)-1-cyclopropylethyl]-6-(propan-2-yl)phenol2-[(1*R*)-1-cyclopropyléthyl]-6-(propan-2-yl)phénol2-[(1*R*)-1-ciclopropiletil]-6-(propan-2-il)fenolC₁₄H₂₀O

cirevetmabum

cirevetmab

immunoglobulin G2-kappa, anti-[*Canis lupus familiaris* TGFB1 (transforming growth factor beta1, TGF beta)], caninized monoclonal antibody; gamma2 heavy chain caninized (1-452) [VH (*Canis lupus familiaris* IGHV1-30*01 (88.8%) -(IGHD) - IGHJ4*01 (100%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Canis lupus familiaris* IGHG2*01, G2v1 A1.3, A1.2, A1 (CH1 (118-214), hinge 1-19 (215-233), CH2 M1.3>A (237), L1.2>A (238), G1>A (240) (234-343), CH3 (344-450), CHS (451-452)) (118-452)], (132-213')-disulfide with kappa light chain caninized (1'-213') [V-KAPPA (*Canis lupus familiaris* IGKV3-18*02 (83.5%) -IGKJ3*01 (91.7%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Canis lupus familiaris* IGKC*01 (100%) (108'-213')]; dimer (229-229":232-232")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1SV lacking the glutamine synthetase (GS-KO) gene, glycoform alfa

civévetmab

immunoglobuline G2-kappa, anti-[*Canis lupus familiaris* TGFB1 (facteur de croissance transformant bêta1, TGF bêta)], anticorps monoclonal caninisé; chaîne lourde gamma2 caninisée (1-452) [VH (*Canis lupus familiaris* IGHV1-30*01 (88.8%) -(IGHD) - IGHJ4*01 (100%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Canis lupus familiaris* IGHG2*01, G2v1 A1.3, A1.2, A1(CH1 (118-214), charnière 1-19 (215-233), CH2 M1.3>A (237), L1.2>A (238), G1>A (240) (234-343), CH3 (344-450), CHS (451-452)) (118-452)], (132-213')-disulfure avec la chaîne légère kappa caninisée (1'-213') [V-KAPPA (*Canis lupus familiaris* IGKV3-18*02 (83.5%) -IGKJ3*01 (91.7%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Canis lupus familiaris* IGKC*01 (100%) (108'-213')]; 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), glycoforme alfa

cirevetmab

immunoglobulina G2-kappa, anti-[*Canis lupus familiaris* TGFB1 (factor de crecimiento transformante beta1, TGF beta)], anticuerpo monoclonal caninizado; cadena pesada gamma2 caninizada (1-452) [VH (*Canis lupus familiaris* IGHV1-30*01 (88.8%) -(IGHD) - IGHJ4*01 (100%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Canis lupus familiaris* IGHG2*01, G2v1 A1.3, A1.2, A1 (CH1 (118-214), bisagra 1-19 (215-233), CH2 M1.3>A (237), L1.2>A (238), G1>A (240) (234-343), CH3 (344-450), CHS (451-452)) (118-452)], (132-213')-disulfuro con la cadena ligera kappa caninizada (1'-213') [V-KAPPA (*Canis lupus familiaris* IGKV3-18*02 (83.5%) -IGKJ3*01 (91.7%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Canis lupus familiaris* IGKC*01 (100%) (108'-213')]; 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), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada
 EVQLVQSGAE VKKPGASVKV SCKTSGYTFI SSWMNWVRQA PGAGLDWMGQ 50
 IYPGDGDTNY NGKFKGRVTL TADTSTSTAY MELSSLRAGD IAVYYCARHY 100
 DGSTDYWGQG TLVTVSSAST TAPSVFPLAP SCGSTSGSTV ALACLVSGYF 150
 PEPVTVVWNS GSLTSGVHTF PSQLQSSGLY SLSMVTVPFS SRWPSETPTC 200
 NVAHPASKTK VDKFVPKREN GRVPRPPDCP KCPAPEAAGA PSVFIFFPKP 250
 KDTLLIARTP EVTCVVVDLD FEDPEVQISW FVDGKQMQTA KTQPREEQFN 300
 GTYRIVSVLP IGHQDWLKGK QFTCKVNNKA LPSFIERTIS KARGQAHQFS 350
 VYVLPFSREE LSKNTVSLTC LIKDFPFPII DVEWQSNQQ EFESKYRTTP 400
 PQLDEGDSYF LYSKLSVDKS RWQRGDTFIC AVMEALHNNH YTQESLSHSP 452
 GK

Light chain / Chaîne légère / Cadena ligera
 EIVMTQSPAS LSLSQGEKVT ITCRASENIY SNLAWYQQRG GQAPKLLIYA 50
 ATNLADGVPS RFGSGSGTD FSLTISSELP EDVAVYYCQH FWGTPYTFGQ 100
 GTKLEIKRND AQPAVYLFQP SPDQLHTGSA SVVCLLNSFY PKDINVKWV 150
 DGVIQDTGIQ ESVTEQDKDS TYSLSLTLM 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) 22-96 144-200 264-324 370-430
 22"-96" 144"-200" 264"-324" 370"-430"

Intra-L (C23-C104) 23"-88" 134"-193"
 23"-88" 134"-193"

Inter-H-L (CH1 I1-CL 126) 132-213' 132"-213"

Inter-H-H (h 15, h 19) 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: 452, 452"

claficapavirum

claficapavir

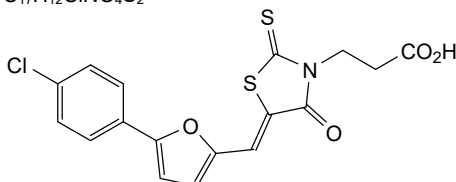
3-[(5Z)-5-[[5-(4-chlorophenyl)furan-2-yl]methylidene]-4-oxo-2-sulfanylidene-1,3-thiazolidin-3-yl]propanoic acid

claficapavir

acide 3-[(5Z)-5-[[5-(4-chlorophényl)furan-2-yl]méthylidène]-4-oxo-2-sulfanylidène-1,3-thiazolidin-3-yl]propanoïque

claficapavir

ácido 3-[(5Z)-5-[[5-(4-clorofenil)furan-2-il]metilideno]-4-oxo-2-sulfanilideno-1,3-tiazolidin-3-il]propanoico

C₁₇H₁₂ClNO₄S₂**clesrovimabum #**

clesrovimab

immunoglobulin G1-kappa, anti-[human respiratory virus (RSV) fusion glycoprotein F site IV], monoclonal antibody;
 gamma1 heavy chain (1-457) [VH (*Homo sapiens* IGHV3-49*04 (89.0%) -(IGHD) -IGHJ6*01 (94.4%), CDR-IMGT [8.10.18] (26-33.51-60.99-116))] (1-127) -*Homo sapiens* IGHG1*01 G1m17.1, G1v21 CH2 Y15.1, T16, E18 (CH1 K120 (224) (128-225), hinge 1-15 (226-240), CH2 M15.1>Y (262), S16>T (264), T18>E (266) (241-350), CH3 D12 (366), L14 (368) (351-455), CHS (456-457)) (128-457)], (230-214')-disulfide with kappa light chain (1'-214') [V-KAPPA (*Homo sapiens* IGKV1D-13*01 (86.2%) -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 (236-236"::239-239")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1SV, glycoform alfa

clesrovimab immunoglobuline G1-kappa, anti-[site IV de la glycoprotéine de fusion F du virus respiratoire syncytial (VRS) humain], anticorps monoclonal; chaîne lourde gamma1 (1-457) [VH (*Homo sapiens* IGHV3-49*04 (89.0%) -(IGHD) -IGHJ6*01 (94.4%), CDR-IMGT [8.10.18] (26-33.51-60.99-116)) (1-127) -*Homo sapiens* IGHG1*01 G1m17,1, G1v21 CH2 Y15.1, T16, E18 (CH1 K120 (224) (128-225), charnière 1-15 (226-240), CH2 M15.1>Y (262), S16>T (264), T18>E (266) (241-350), CH3 D12 (366), L14 (368) (351-455), CHS (456-457)) (128-457)], (230-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA (*Homo sapiens* IGKV1D-13*01 (86.2%) -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 (236-236'':239-239'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1SV, glycoforme alfa

clesrovimab inmunoglobulina G1-kappa, anti-[lugar IV de la glicoproteína de fusión F del virus respiratorio sincitial (VRS) humano], anticuerpo monoclonal; cadena pesada gamma1 (1-457) [VH (*Homo sapiens* IGHV3-49*04 (89.0%) -(IGHD) -IGHJ6*01 (94.4%), CDR-IMGT [8.10.18] (26-33.51-60.99-116)) (1-127) -*Homo sapiens* IGHG1*01 G1m17,1, G1v21 CH2 Y15.1, T16, E18 (CH1 K120 (224) (128-225), bisagra 1-15 (226-240), CH2 M15.1>Y (262), S16>T (264), T18>E (266) (241-350), CH3 D12 (366), L14 (368) (351-455), CHS (456-457)) (128-457)], (230-214')-disulfuro con la cadena ligera kappa (1'-214') [V-KAPPA (*Homo sapiens* IGKV1D-13*01 (86.2%) -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 (236-236'':239-239'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1SV, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada
 EVQLVESGGG LVPGRGSLRL SCTVSGFSFD DSAMSWVRQA PGKGLEWISF 50
 IKSKTYGGTK EYAASVKGRF TISRDDSKNI AYLQMNLSKT EDTAVYYCTR 100
 GAPPYGGNSDY YGGLDVWGQG TTVTVSSAST KGPSVFLAP SRKSTSGGTA 150
 ALGLCLVDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTGPS 200
 SSSLGTYTIC NVNHKPSNTK VDKKVEPKSC DKHTCCPPCP APELLGGVPS 250
 FLFPPKPKDT LYITREPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK 300
 FREQEYNSTY RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTIKSAK 350
 GQPREPQVYT LPFSRDELTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN 400
 YKTTTPPLVDS DGSFFLYSKL TVDKSRWQQG NVFSCSVHME ALHNYHTQKS 450
 LSLSPGK 457

Light chain / Chaîne légère / Cadena ligera
 DIQMTQSPSS LSASVGRDRT ITCRTSQDVR GALAWYQQKPK GKAPKLLIFD 50
 ASSLETGVPS RFGSGSGSTV FTLTISLSLPQ EDFAAAYCQQ FLDFPPTFGQ 100
 GTRLEIKRTV AAFSVFIFFP SDEQLKSGTA SVVCLLNIFY PREAKVQNKV 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) 22-98 154-210 271-331 377-435
 22"-98" 154"-210" 271"-331" 377"-435"
 Intra-L (C23-C104) 23'-88" 134'-194"
 23"'-88"' 134"'-194"
 Inter-H-L (h 5-CL 126) 230-214' 230"-214"
 Inter-H-H (h 11, h 14) 236-236" 239-239"

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

C-terminal lysine clipping / Coupeure de la lysine C-terminale / Recorte de lisina C-terminal
 H CHS K2: 457, 457"

crefmirlimabum

crefmirlimab

immunoglobulin scFv-kappa-heavy-G1h-CH3-CHS dimer, anti-[*Homo sapiens* CD8A (CD8a molecule, CD8)], monoclonal antibody;
 scFv-kappa-heavy-G1-h-linker-CH3-CHS chain (1-376) [V-KAPPA (*Homo sapiens* IGKV1-27*01 (87.4%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1-107) -18-mer glycyL-seryl-threonyL-tris(seryl-triglycyL)-glycyL-diseryl linker (108-125) -VH Musmus/Homsap (*Mus musculus* IGHV14-3*02 (73.5%) -(IGHD) -IGHJ3*01 (84.6%)/*Homo sapiens* IGHV3-66*01 (71.4%) -(IGHD) -IGHJ1*01 (92.3%), CDR-IMGT [8.8.11] (151-158.176-183.222-232)) (126-243) -*Homo sapiens* IGHG1*03 hinge 1-17 (244-260), 10-mer triglycyL-diseryl-triglycyL-seryl-glycyL linker (261-270), *Homo sapiens* IGHG1*03 nG1m1 CH3-CHS (CH3 E12 (286), M14 (288) (271-375), CHS K2>del (376)) (271-376)]; dimer (254-254":257-257":260-260")-trisdisulfide, produced in Chinese hamster ovary (CHO) cells, non-glycosylated

crefmirlimab

immunoglobuline scFv-kappa-heavy-G1h-CH3-CHS dimère, anti-[*Homo sapiens* CD8A (molécule CD8a, CD8)], anticorps monoclonal;
 chaîne scFv-kappa-heavy-G1-h-linker-CH3-CHS (1-376) [V-KAPPA (*Homo sapiens* IGKV1-27*01 (87.4%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1-107) -18-mer glycyL-séryL-thréonyL-tris(séryL-triglycyL)-glycyL-diséryL linker (108-125) -VH Musmus/Homsap (*Mus musculus* IGHV14-3*02 (73.5%) -(IGHD) -IGHJ3*01 (84.6%)/*Homo sapiens* IGHV3-66*01 (71.4%) -(IGHD) -IGHJ1*01 (92.3%), CDR-IMGT [8.8.11] (151-158.176-183.222-232)) (126-243) -*Homo sapiens* IGHG1*03 charnière 1-17 (244-260), 10-mer triglycyL-diséryL-triglycyL-séryL-glycyL linker (261-270), *Homo sapiens* IGHG1*03 nG1m1 CH3-CHS (CH3 E12 (286), M14 (288) (271-375), CHS K2>del (376)) (271-376)]; dimère (254-254":257-257":260-260")-trisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), non-glycosylé

crefmirlimab

immunoglobulina scFv-kappa-pesada-G1h-CH3-CHS dímero, anti-[*Homo sapiens* CD8A (molécula CD8a, CD8)], anticuerpo monoclonal;
 cadena scFv-kappa-pesada-G1-h-linker-CH3-CHS (1-376) [V-KAPPA (*Homo sapiens* IGKV1-27*01 (87.4%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1-107) -18-mer glicil-seril-treonil-tris(seril-triglicil)-glicil-diseril linker (108-125) -VH Musmus/Homsap (*Mus musculus* IGHV14-3*02 (73.5%) -(IGHD) -IGHJ3*01 (84.6%)/*Homo sapiens* IGHV3-66*01 (71.4%) -(IGHD) -IGHJ1*01 (92.3%), CDR-IMGT [8.8.11] (151-158.176-183.222-232)) (126-243) -*Homo sapiens* IGHG1*03 bisagra 1-17 (244-260), 10-mer triglicil-diseril-triglicil-seril-glicil linker (261-270), *Homo sapiens* IGHG1*03 nG1m1 CH3-CHS (CH3 E12 (286), M14 (288) (271-375), CHS K2>del (376)) (271-376)]; dímero (254-254":257-257":260-260")-trisdisulfuro, producido en las células ováricas de hámster chino (CHO), no glicosilado

Sequence / Séquence / Secuencia

DVQITQSPSS LSASVGDRTV ITCRTSRSSIS QYLAWYQQKPK GKVPKLLIYS 50
 GSTLQSGVPS RFGSGSGSDT FTLTISLQPE EDVATVYCCQ HNNPLTFGG 100
 GTKVEIKGST SGGSGGGSG GGSSEVQLV EGGGLVQPG GSLRLSCAAS 150
 GENIKDTYIH FVRQAPGRGL ENIGRIDPAN DNTLYASKFQ GKATISADTS 200
 KNTAVLQMS LRAEDTAVY CGRCYGYVF DHWQQTIVT VSSEPKSSDK 250
 THTCFPCPC GGGSSGGSG GQPREQVYV LPPSREEMTK NQVSLTCLVK 300
 GFYFSDIAVE WESNGQFENN YKTTFPVLDS DGSFFLYSKL TVDKSRWQQG 350
 NVFSCVMHE ALHNHYTQKS LSLSPG 376

Post-translational modifications

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

Intra-H (C23-C104) 23-88 147-221 297-355
 23^o-88^o 147^o-221^o 297^o-355^o

Inter-H-H (h 11, h 14, h 17) 254-254^o 257-257^o 260-260^o

No N-glycosylation site / pas de site de N-glycosylation / ningún posición de N-glicosilación
 Aglycosylated / aglycosylé / aglicosilado

crexavibartum #

crexavibart

immunoglobulin G1-lambda2, anti-[severe acute respiratory syndrome (human) coronavirus 2 (SARS-CoV-2) spike (S) glycoprotein, receptor binding domain (RBD)], *Homo sapiens* monoclonal antibody;
 gamma1 heavy chain *Homo sapiens* (1-460) [VH (*Homo sapiens*IGHV3-53*01 (97.9 %) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.7.25] (26-33.51-57.96-120)) (1-131) -*Homo sapiens*IGHG1*03, G1m3, nG1m1, G1v24 CH3 L107, S114 (CH1 R120 (228) (132-229), hinge 1-15 (230-244), CH2 (245-354), CH3 E12 (370), M14 (372), M107>L (442), N114>S (448) (355-459), CHS K2>del (460)) (132-460)], (234-215')-disulfide with lambda2 light chain *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV2-14*03 (100%) - IGLJ1*01 (100%), CDR-IMGT [9.3.10] (26-34.52-54.91-100)) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')]; dimer (240-240":243-243")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

crexavibart

immunoglobuline G1-lambda2, anti-[domaine de liaison au récepteur (RBD) de la glycoprotéine spike (S) du coronavirus 2 (humain) du syndrome respiratoire aigu sévère (SARS-CoV-2)], anticorps monoclonal *Homo sapiens*;
 chaîne lourde gamma1 *Homo sapiens* (1-460) [VH (*Homo sapiens*IGHV3-53*01 (97.9 %) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.7.25] (26-33.51-57.96-120)) (1-131) -*Homo sapiens*IGHG1*03, G1m3, nG1m1, G1v24 CH3 L107, S114 (CH1 R120 (228) (132-229), charnière 1-15 (230-244), CH2 (245-354), CH3 E12 (370), M14 (372), M107>L (442), N114>S (448) (355-459), CHS K2>del (460)) (132-460)], (234-215')-disulfure avec la chaîne légère lambda2 *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV2-14*03 (100%) - IGLJ1*01 (100%), CDR-IMGT [9.3.10] (26-34.52-54.91-100)) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')]; dimère (240-240":243-243")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

crexavibart

inmunoglobulina G1-lambda2, anti-[dominio de unión al receptor (RBD) de la glicoproteína spike (S) del coronavirus 2 (humano) del síndrome respiratorio agudo severo (SARS-CoV-2)], anticuerpo monoclonal *Homo sapiens*;

cadena pesada gamma1 *Homo sapiens* (1-460) [VH (*Homo sapiens* IGHV3-53*01 (97.9 %) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.7.25] (26-33.51-57.96-120)) (1-131) -*Homo sapiens* IGHG1*03, G1m3, nG1m1, G1v24 CH3 L107, S114 (CH1 R120 (228) (132-229), bisagra 1-15 (230-244), CH2 (245-354), CH3 E12 (370), M14 (372), M107>L (442), N114>S (448) (355-459), CHS K2>del (460)) (132-460)], (234-215')-disulfuro con la cadena ligera lambda2 *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV2-14*03 (100%) -IGLJ1*01 (100%), CDR-IMGT [9.3.10] (26-34.52-54.91-100)) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')]; dímero (240-240":243-243")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LIQPGGSLRL SCAASGFTVS NNYMSWVRQA PGKGLEWVSV 50
IYSGGSTYYA DSVKGRFTIS RDKSKNTLYL QMNSLRAEDT AVYICAREGE 100
VEGYNDFWSG YSRDRYFDY WQGTLVTVS SASTKGPSVF PLAPSSKSTS 150
GGTAALGCLV KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV 200
TVPSSSLGTQ TYICNVNHPK SNTKVDKRVK PKSCDKTHTC PPCPAPELLG 250
GPSVFLFPPK PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN 300
AKTKPREEQY NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI 350
SKAKGQPREP QVYTLPPSRE EMTKNQVSLT CLVKGFFPSD IAVWEWSNGQ 400
PENNYKTPFP VLDSGSGFFL YSKLTVDKSR WQQGNVFCSS VLHEALHSHY 450
TQKSLSLSPG 460
```

Light chain / Chaîne légère / Cadena ligera

```
QSALTPQASV SGSPGQSITI SCTGTSSDVG GYNYVSNVYQQ HPGKAPKLM 50
YDVSNRPSGV SNRFSGSKSG NTASLTIISGL QAEDEADYYC SSYTSSSTRV 100
FGTGTKVTVL GQPKAAPSVT LFPPSSEELQ ANKATLVCLI SDFYPGAVTV 150
ANKADSSPVK AGVETTTSPK QSNNKYAASS YLSLTFPEQWK SHRSYSCQVT 200
HEGSTVEKTV APTECS 216
```

Post-translational modifications

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

Intra-H (C23-C104) 22-95 158-214 275-335 381-439
 22"-95" 158"-214" 275"-335" 381"-439"

Intra-L (C23-C104) 22'-90' 138'-197"
 22"-90" 138"-197"

Inter-H-L (h 5-CL 126) 234-215" 234"-215"

Inter-H-H (h 11, h 14) 240-240" 243-243"

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

L VL Q1 > pyroglutamyl (pE, 5-oxopropyl): 1', 1"

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

H CH2 N84.4: 311, 311"

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

cudetaxestatum

cudetaxestat

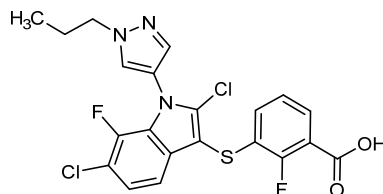
3-[[2,6-dichloro-7-fluoro-1-(1-propyl-1*H*-pyrazol-4-yl)-1*H*-indol-3-yl]sulfanyl]-2-fluorobenzoic acid

cudétaxestat

acide 3-[[2,6-dichloro-7-fluoro-1-(1-propyl-1*H*-pyrazol-4-yl)-1*H*-indol-3-yl]sulfanyl]-2-fluorobenzoïque

cudetaxestat

ácido 3-[[2,6-dicloro-7-fluoro-1-(1-propil-1*H*-pirazol-4-il)-1*H*-indol-3-il]sulfanil]-2-fluorobenzoico

$$C_{21}H_{15}Cl_2F_2N_3O_2S$$


dalucabtagenium autoleucelum #

dalucabtagene autoleucel

autologous T cells obtained from peripheral blood mononuclear cells by leukapheresis, transduced with a replication incompetent Moloney murine leukemia virus (MoMLV)-based retroviral vector, encoding two T cell chimeric antigen receptors (CARs) targeting CD19 and CD22, separated by a 2A self-cleaving peptide derived from the *Thosea asigna* virus capsid protein, under control of a MoMLV-based promoter. The construct is flanked by 5' and 3' long terminal repeats (LTRs), and contains a ψ packaging signal and the scaffold/matrix attachment region (S/MAR) from the human β interferon gene.

The cells are activated using an anti-CD3/CD28 reagent in medium supplemented with human AB serum, interleukin 7 (IL-7) and 15 (IL-15). Activated cells are incubated with the vector before further culture expansion. The CAR positive T cells are predominantly CD4/CD8, and secrete granzyme B, interferon gamma, tumour necrosis factor alpha (TNF- α) and interleukin-2 (IL-2) after co-culture with a cell line expressing the CD19 and CD22 antigen.

dalucabtagène autoleucel

lymphocytes T autologues obtenus à partir de cellules mononucléaires de sang périphérique par leucaphérèse, transduits avec un vecteur rétroviral incompetent à la réplication basé sur le virus de la leucémie murine de Moloney (MoMLV), codant deux récepteurs antigéniques chimériques (CAR) des lymphocytes T ciblant CD19 et CD22, séparés par un peptide 2A auto-clivant dérivé de la protéine de capsid du virus *Thosea asigna*, sous le contrôle d'un promoteur basé sur MoMLV. La construction est flanquée de longues répétitions terminales (LTR) en 5' et 3', et contient un signal d'encapsidation ψ et la région structure/matrice d'attachement (S/MAR) du gène de l'interféron β humain.

Les cellules sont activées à l'aide d'un réactif anti-CD3/CD28 dans un milieu complété de sérum AB humain, d'interleukine 7 (IL-7) et 15 (IL-15). Les cellules activées sont incubées avec le vecteur avant une nouvelle expansion de la culture. Les lymphocytes T CAR-positifs sont principalement CD4/CD8, et sécrètent du granzyme B, de l'interféron gamma, du facteur de nécrose tumorale alpha (TNF- α) et de l'interleukine-2 (IL-2) après co-culture avec une lignée cellulaire exprimant les antigènes CD19 et CD22.

dalucabtagén autoleucel

linfocitos T autólogos obtenidos a partir de células mononucleares de sangre periférica por leucoaféresis, transducidos con un vector retroviral incompetente de replicación basado en el virus de la leucemia murina de Moloney (MoMLV) que codifica para dos receptores de antígeno quiméricos (CARs) de linfocitos T dirigidos a CD19 y CD22, separados por un péptido 2A de autoescisión derivado de la proteína de la cápsida del virus *Thosea asigna*, bajo el control de un promotor basado en el MoMLV. El constructo está flanqueado por repeticiones terminales largas (LTRs) en 5' y 3' y contiene una señal de empaquetamiento ψ y la región de andamiaje/fijación de la matriz (S/MAR) del gen del interferon β humano.

Las células se activan usando un reactivo anti-CD3/CD28 en medio suplementado con suero AB humano e interleukinas 7 (IL-7) y 15 (IL-15). Las células activadas se incuban con el vector antes de una expansión adicional en cultivo. Los linfocitos T positivos para el CAR son predominantemente CD4/CD8 y secretan granzima B, interferon gamma, factor de necrosis tumoral alfa (TNF- α) e interleukina 2 (IL-2) tras el cocultivo con una línea celular que expresa los antígenos CD19 y CD22.

deucricitabantum

deucricitabant

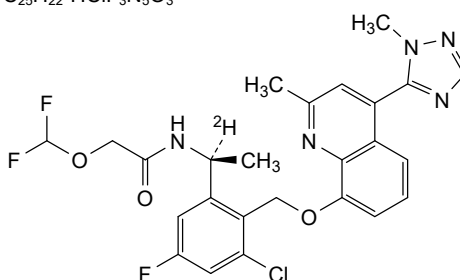
N-{(1*S*)-1-[3-chloro-5-fluoro-2-({[2-méthyl-4-(1-méthyl-1*H*-1,2,4-triazol-5-yl)quinolin-8-yl]oxy)méthyl]phényl](1-²H)éthyl}-2-(difluorométhoxy)acétamide

deucricitabant

N-{(1*S*)-1-[3-chloro-5-fluoro-2-({[2-méthyl-4-(1-méthyl-1*H*-1,2,4-triazol-5-yl)quinoléin-8-yl]oxy)méthyl]phényl](1-²H)éthyl}-2-(difluorométhoxy)acétamide

deucricitabant

N-{(1*S*)-1-[3-cloro-5-fluoro-2-({[2-metil-4-(1-metil-1*H*-1,2,4-triazol-5-il)quinolein-8-il]oxi)metil]fenil](1-²H)etil}-2-(difluorometoxi)acetamida

$$C_{25}H_{22}^2HCIF_3N_5O_3$$
**deutenzalutamidum**

deutenzalutamide

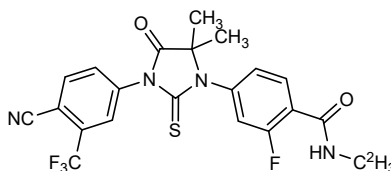
4-{3-[4-cyano-3-(trifluorométhyl)phényl]-5,5-diméthyl-4-oxo-2-sulfanylidèneimidazolidin-1-yl}-2-fluoro-*N*-(²H₃)méthylbenzamide

deutenzalutamide

4-{3-[4-cyano-3-(trifluorométhyl)phényl]-5,5-diméthyl-4-oxo-2-sulfanylidèneimidazolidin-1-yl}-2-fluoro-*N*-(²H₃)méthylbenzamide

deutenzalutamida

4-{3-[4-ciano-3-(trifluorometil)fenil]-5,5-dimetil-4-oxo-2-sulfanilidenoimidazolidin-1-il}-2-fluoro-*N*-(²H₃)metilbenzamida

$$C_{21}H_{13}^2H_3F_4N_4O_2S$$
**dexfadrostatum**

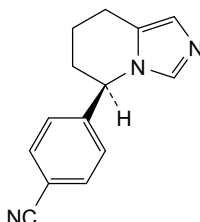
dexfadrostat

4-[(5*R*)-5,6,7,8-tetrahydroimidazo[1,5-*a*]pyridin-5-yl]benzonitrile

dexfadrostat 4-[(5*R*)-5,6,7,8-tétrahydroimidazo[1,5-*a*]pyridin-5-yl]benzonnitrile

dexfadrostat 4-[(5*R*)-5,6,7,8-tetrahydroimidazo[1,5-*a*]piridin-5-il]benzonnitrilo

$C_{14}H_{13}N_3$



eciruciclibum

eciruciclib

N-[5-[(4-éthylpiperazin-1-yl)méthyl]pyridin-2-yl]-5-fluoro-4-[2-méthyl-3-(propan-2-yl)-2*H*-indazol-5-yl]pyrimidin-2-amine

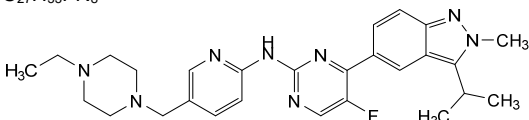
éciruciclib

N-[5-[(4-éthylpipérazin-1-yl)méthyl]pyridin-2-yl]-5-fluoro-4-[2-méthyl-3-(propan-2-yl)-2*H*-indazol-5-yl]pyrimidin-2-amine

eciruciclib

N-[5-[(4-etilpiperazin-1-il)metil]piridin-2-il]-5-fluoro-4-[2-metil-3-(propan-2-il)-2*H*-indazol-5-il]pirimidin-2-amina

$C_{27}H_{33}FN_8$



ecnoglutidum

ecnoglutide

$N^{6,24}$ -[(2*S*)-22,40-dicarboxy-10,19,24-trioxo-3,6,12,15-tétraoxa-9,18,23-triazatetracontan-1-oyl]-[Ala⁸>Val², Gly²²>Glu¹⁶, Lys²⁶>Arg²⁰, Ala³⁰>Lys²⁴, Lys³⁴>Arg²⁸]-human glucagon-like peptide 1 (GLP-1) (7-37)-peptide (1-31);

L-histidyl-L-valyl-L- α -glutamylglycyl-L-threonyl-L-phenylalanyl-L-threonyl-L-seryl-L- α -aspartyl-L-valyl-L-seryl-L-seryl-L-tyrosyl-L-leucyl-L- α -glutamyl-L- α -glutamyl-L-glutaminy-L-alanyl-L-alanyl-L-arginyl-L- α -glutamyl-L-phenylalanyl-L-isoleucyl- N^6 -[(2*S*)-22,40-dicarboxy-10,19,24-trioxo-3,6,12,15-tétraoxa-9,18,23-triazatetracontan-1-oyl]-L-lysyl-L-tryptophyl-L-leucyl-L-valyl-L-arginylglycyl-L-arginylglycine

ecnoglutide

$N^{6,24}$ -[(2*S*)-22,40-dicarboxy-10,19,24-trioxo-3,6,12,15-tétraoxa-9,18,23-triazatetracontan-1-oyl]-[Ala⁸>Val², Gly²²>Glu¹⁶, Lys²⁶>Arg²⁰, Ala³⁰>Lys²⁴, Lys³⁴>Arg²⁸]-peptide-1 semblable au glucagon humain (GLP-1) (7-37)-peptide (1-31);

ecnoglutida

L-histidyl-L-valyl-L- α -glutamylglycyl-L-thréonyl-L-phénylalanil-L-thréonyl-L-séryl-L- α -aspartyl-L-valyl-L-séryl-L-séryl-L-tyrosyl-L-leucyl-L- α -glutamyl-L- α -glutamyl-L-glutaminy-L-alanyl-L-alanyl-L-arginyl-L- α -glutamyl-L-phénylalanil-L-isoleucyl-*N*⁶-[(22S)-22,40-dicarboxy-10,19,24-trioxo-3,6,12,15-tétraoxa-9,18,23-triazatétracontan-1-oyl]-L-lysyl-L-tryptophyl-L-leucyl-L-valyl-L-arginylglycyl-L-arginylglycine

N^{6,24}-[(22S)-22,40-dicarboxy-10,19,24-trioxo-3,6,12,15-tétraoxa-9,18,23-triazatétracontan-1-oyl]-[Ala⁸>Val², Gli²²>Glu¹⁶, Lis²⁶>Arg²⁰, Ala³⁰>Lis²⁴, Lis³⁴>Arg²⁸]-péptido similar al glucagón tipo 1 humano (GLP-1) (7-37)-péptido (1-31);

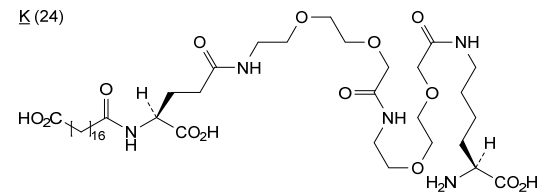
L-histidil-L-valil-L- α -glutamilglicil-L-treonil-L-fenilalanil-L-treonil-L-seril-L- α -aspartil-L-valil-L-seril-L-seril-L-tirosil-L-leucil-L- α -glutamil-L- α -glutamil-L-glutamini-L-alanil-L-alanil-L-arginil-L- α -glutamil-L-fenilalanil-L-isoleucil-*N*⁶-[(22S)-22,40-dicarboxy-10,19,24-trioxo-3,6,12,15-tétraoxa-9,18,23-triazatétracontan-1-oyl]-L-lisil-L-triptofil-L-leucil-L-valil-L-arginilglicil-L-arginilglicina

C₁₉₄H₃₀₄N₄₈O₆₁

HVEGTFTSDV SSYLEEQAAR EFIKWLVRGR G 31

Modified residues / Résidus modifiés / Restos modificados

K (24)



efocipegrutridum #
efocipegrutride

chimeric triple receptor agonist peptide (1"-40"), sharing balanced sequence homology with glucagon, glucagon-like peptide 1 (GLP1) and gastric inhibitory polypeptide (GIP, glucose-dependent insulinotropic polypeptide, incretin hormone), produced by chemical synthesis, conjugated at the S atom of the C-terminal cysteinamide 40" via a polyethylene glycol linker (~10 kDa) to the N atom of one N-terminal proline residue of the dimer (3-3')-disulfide of an immunoglobulin G4 (IgG4) heavy chain constant fragment (Fc, C-terminal 221-peptide, produced in *Escherichia coli*, not glycosylated): *N*^{1,1}-(3- α -[3-(3-((3*RS*)-3-[16,20-anhydro(L-tyrosyl-2-methylalanyl-L-glutaminyglycyl-L-thréonyl-L-phénylalanil-L-thréonyl-L-séryl-L- α -aspartyl-L-tyrosyl-L-séryl-L-lysyl-L-tyrosyl-L-leucyl-L- α -aspartyl-L- α -glutamyl-L-lysyl-L-arginyl-L-alanyl-L-lysyl-L- α -glutamyl-L-phénylalanil-L-valyl-L-glutaminy-L-tryptophyl-L-leucyl-L-leucyl-L- α -aspartyl-L-histidyl-L-histidyl-L-prolyl-L-séryl-L-serylglycyl-L-glutaminy-L-prolyl-L-prolyl-L-prolyl-L-séryl-L-cysteinamide)-S^{3,40}-yl]-2,5-dioxopyrrolidin-1-yl]propanamido)propyl]poly(oxyethylene)- ω -oxy}propyl)(IgG4 Fc (*Homo sapiens* IGHG4*01 (hinge (1-4, N-terminal hinge residues ESKYGPPC deleted), CH2 (5-114), CH3 (115-219), CHS (220-221))(1-221) dimer (3-3')-disulfide)

éfocipégrutride

peptide chimérique agoniste de trois récepteurs (1^{''}-40''), partageant une homologie équilibrée de séquence avec le glucagon, le glucagon-like peptide 1 (GLP1) et le polypeptide inhibiteur gastrique (GIP, polypeptide insulino-trope glucose-dépendant, hormone incré-tine), produit par synthèse chimique, conjugué à l'atome S du cystéinamide C-terminal 40'' via un lieu polyéthylène glycol (~10 kDa) à l'atome N d'un résidu proline N-terminal du dimère (3-3')-disulfure d'un fragment constant de la chaîne lourde d'immunoglobuline G4 (IgG4) (Fc, 221-peptide C-terminal, produit par *Escherichia coli*, non glycosylé):

N^{1:1}-(3-{α-[3-(3-((3RS)-3-[16,20-anhydro(L-tyrosyl-2-méthylalanyl-L-glutaminyglycyl-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-lysyl-L-arginyl-L-alanyl-L-lysyl-L-α-glutamyl-L-phénylalanyl-L-valyl-L-glutamyl-L-tryptophyl-L-leucyl-L-leucyl-L-α-aspartyl-L-histidyl-L-histidyl-L-prolyl-L-séryl-L-sérylglycyl-L-glutamyl-L-prolyl-L-prolyl-L-prolyl-L-séryl-L-cystéinamide)-S^{3,40}-yl]-2,5-dioxopyrrolidin-1-yl}propanamido)propyl]poly(oxyéthylène)-ω-oxy}propyl)(IgG4 Fc (*Homo sapiens* IGHG4*01 (charnière (1-4, résidus ESKYGPPC N-terminaux de la charnière supprimés), CH2 (5-114), CH3 (115-219), CHS (220-221))(1-221) dimère (3-3')-disulfure)

efocipegtrutrida

péptido quimérico agonista de tres receptores (1^{''}-40''), que comparte homología equilibrada de secuencia con glucagón, péptido similar al glucagón tipo 1 (GLP1) y polipéptido inhibidor gástrico (GIP, polipéptido insulino-trópico dependiente de glucosa, hormona incretina), producido por síntesis química, conjugado en el átomo S de la cisteinamida C-terminal 40'' a través de un enlace de polietilenglicol (~10 kDa) al átomo N de un residuo de prolina N-terminal del dímero (3-3')-disulfuro de un fragmento constante de la cadena pesada de inmunoglobulina G4 (IgG4) (Fc, 221-péptido C-terminal, producido en *Escherichia coli*, no glicosilado):

N^{1:1}-(3-{α-[3-(3-((3RS)-3-[16,20-anhydro(L-tirosil-2-metilalanil-L-glutaminyglycyl-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-glutamyl-L-lisil-L-arginil-L-alanil-L-lisil-L-α-glutamyl-L-fenilalanil-L-valil-L-glutamyl-L-triptofil-L-leucil-L-leucil-L-α-aspartil-L-histidil-L-histidil-L-prolil-L-seril-L-serilglycyl-L-glutamyl-L-prolil-L-prolil-L-prolil-L-seril-L-cisteinamida)-S^{3,40}-il]-2,5-dioxopirrolidin-1-il}propanamido)propil]poli(oxiétileno)-ω-oxi}propil)(IgG4 Fc (*Homo sapiens* IGHG4*01 (bisagra (1-4, residuos ESKYGPPC N-terminales de la bisagra suprimidos), CH2 (5-114), CH3 (115-219), CHS (220-221))(1-221) dímero (3-3')-disulfuro)

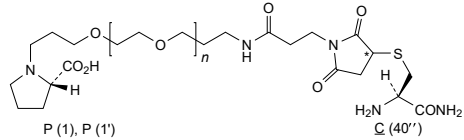
Conjugated peptide / peptide conjugué / péptido conjugado

YXQGTFTSDY SKYLDEKRAK EFVQWLLDHH PSSGQPPESC 40''

Monomer / Monomère / Monómero IgG4 Fc

PSCFAPEFLG GPSVFLFPPK PKDTLMISRT PEVTCVVVDV SQEDPEVQFN 50
 WYVDGVEVHN AKTKPREEQF NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK 100
 GLPSSIEKTI SKAKGQPREP QVYTLPPSQE EMTKNQVSLT CLVKGFPYSD 150
 IAVEWESNGQ PENNYKTTTP VLDSGDGSFFL YSRLTVDKSR WQEGNVFSCS 200
 VMHEALHNNHY TQKSLSLSLG K 221

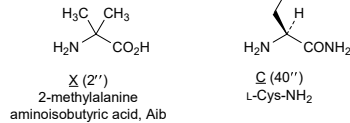
Linker / Linker / Conector



Conjugation sites / Sites de conjugaison / Posiciones de conjugación

1-40'' (Pro^{1,1}-Cys^{3,40'}) 1'-40'' (Pro^{1,1}-Cys^{3,40'})

Modified residues / Résidus modifiés / Restos modificados



Amide bridge location / Position du pont amide / Posición del puente amido

16''-20'' (Glu^{5,16''}-Lys^{6,20''})

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
 intra-chain: 35-95 141-199 35'-95' 141'-199'
 inter-chain: 3-3'

efrilacedasum alfa # efrilacedase alfa

human angiotensin-converting enzyme 2 (ACE2, angiotensin-converting enzyme homolog, ACEH, ACE-related carboxypeptidase, metalloprotease MPROT15) fragment (1-715, containing soluble extracellular domains), fused to a human immunoglobulin G4 Fc fragment (716-944), covalent disulfide bridged dimer, produced in Chinese hamster ovary (CHO) cells, glycoform alfa;

human angiotensin-converting enzyme 2 (ACE2, angiotensin-converting enzyme homolog, ACEH, ACE-related carboxypeptidase, metalloprotease MPROT15, EC:3.4.17.23), [PPNQPPVS (716-723)>del]-soluble extracellular domains (1-715), fused with a C-terminal Fc fragment (229-peptide) of *Homo sapiens* immunoglobulin G4 [*Homo sapiens* IGHG4*01 (hinge S⁷²⁵>P (716-727), CH2 (728-837), CH3 (838-942), CHS (943-944))] (716-944), dimer (723-723':726-726')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

efrilacédase alfa

fragment (1-715, contenant des domaines extracellulaires solubles) de l'enzyme humaine de conversion de l'angiotensine 2 (ACE2, homologue de l'enzyme de conversion de l'angiotensine, ACEH, carboxypeptidase de type ACE, métalloprotéase MPROT15), fusionné à un fragment Fc de l'immunoglobuline humaine G4 (716-944), dimère covalent à pont disulfure, produit dans des cellules d'ovaire de hamster chinois (CHO), glycoforme alpha;

enzyme humaine de conversion de l'angiotensine 2 (ACE2, homologue de l'enzyme de conversion de l'angiotensine, ACEH, carboxypeptidase de type ACE, métalloprotéase MPROT15, EC:3.4.17.23), [PPNQPPVS (716-723)>del] domaines extracellulaires solubles (1-715), fusionné avec un fragment Fc C-terminal (229-peptide) de l'immunoglobuline G4 d'*Homo sapiens* [*Homo sapiens* IGHG4*01 (charnière S725>P (716-727), CH2 (728-837), CH3 (838-942), CHS (943-944))] (716-944), dimère (723-723':726-726')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

efrilacedasa alfa

enzima convertidora de angiotensina humana 2 (ACE2, homólogo de la enzima convertidora de angiotensina, ACEH, carboxipeptidasa relacionada con ACE, metaloproteasa MPROT15) fragmento (1-715, que contiene dominios extracelulares solubles), fusionado al fragmento Fc de la inmunoglobulina humana G4 (716-944), dímero covalente unido al disulfuro, producido en células ováricas de hámster chino (CHO), glicofoma alfa;
enzima convertidora de angiotensina humana 2 (ACE2, homólogo de la enzima convertidora de angiotensina, ACEH, carboxipeptidasa relacionada con ACE, metaloproteasa MPROT15, EC:3.4.17.23), [PPNQPPVS (716-723)>del] dominios extracelulares solubles (1-715), fusionado con un fragmento Fc C-terminal (229-péptido) de inmunoglobulina G4 de *Homo sapiens* [*Homo sapiens* IGHG4*01 (bisagra S725>P (716-727), CH2 (728-837), CH3 (838-942), CHS (943-944))] (716-944), dímero (723-723':726-726')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), glicofoma alfa

Sequence / Séquence / Secuencia	
QSTIEEQAKT	FLDKFNHEAE DLFYQSSLAS WNYNTNITEE NVQNMMNAGD 50
KWSAFLKEQS	TLAQMYPLQE IQNLTVKLQL QALQQNGSSV LSEDKSKRLN 100
TILNTMSTIY	STGKVCNPDN PQECLLLEPG LNEIMANSLD YNERLWAWES 150
WRSEVQKQLR	PLYEYVVLK NEMARANHYE DYGDYWRG DY EVNGVDGYDY 200
SRGQLIEDVE	HTFEEIKFLY EHLHAYVRAK LMNAYPSYIS PIGCLPAHLL 250
GDMWGRFWTN	LYSLTVFPGG KPNIDVTDAM VDQAWDAQRI FKEAEKFFVS 300
VGLPNTQGF	WENSMLTFPG NVQKAVCHPT AWDLKGDFR ILMCTKVITMD 350
DFLTAHHMGG	HIQYDMAYAA QPFLRNGAN EGFHEAVGEI MSLSAATPKH 400
LKSIIGLLSPD	FQEDNETEIN FLLKQALTIV GTLFPTYMLE KWRMNVFKGE 450
IPKQDQMKKW	WEMKREIVGV VEPVPHDETY CDPASLFHVS NDYSEFIYYT 500
RTLYQFQFQE	ALCQAQHEG FLHKCDISNS TEAGQKLFNM LRLGKSEFWT 550
LALENVGAK	NMNVRELLNY FEPLETWLKD QNKNSFVGSW TDWSPYADQS 600
IKVRI SLKSA	LGDKAYEWNDD NEMYLFRSSV AYAMROYFLK VRNQMILFGE 650
EDVRVANLKP	RISFNFFVTA PKWVSDIIPR TEVEKAIRMS RSRINDAFLR 700
NDNSLEFLGI	QPTLGESEKYG FPFCPE PAPE FLGGPESVFLF FPKPKDTLMI 750
SRTPFVTCVV	VVVSQEDPEV QFNWYVDGVE VHNAKTKPRE EQFNSTYRVV 800
SVLTVLHQDW	LNGKEYRCKV SNRGLPSSIE KTIISKARQGP REFQVYTLFP 850
SQEMTKNQV	SLTCLVKGFY PSDIAVEWES NGQPENNYKT TFPVLDSDGS 900
FFLYSRLTVD	KSRWQEGNVF SCSVMHEALH NHYTQKLSL SLGK 944

Mutation / Mutation / Mutación
S725, S725>P

Post-translational modifications

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

Intra-chain: 116-124, 327-344, 513-525, 758-818, 864-922;
116'-124', 327'-344', 513'-525', 758'-818', 864'-922';
(Cys-SH: C244, C481, C244', C481')

Inter-chain: 723-723', 726-726'

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

N36, N73, N86, N305, N415, N529, N673, N794;
N36', N73', N86', N305', N415', N529', N673', N794'

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

T713, T713' (very low level)

elapomestrocelum

elapomestrocel

autologous mesenchymal progenitor cells derived from bone marrow fluid. The cells are culture expanded in standard culture media supplemented with autologous serum. The cells express mesenchymal progenitor cell marker CD73, CD90, and CD105 (>90%) and do not express CD34 and CD45 (<5%). The cells secrete neurotrophic factors (brain-derived neurotrophic factor (BDNF), vascular endothelial growth factor (VEGF), placental growth factor (PGF), and hepatocyte growth factor (HGF)). The cells are capable to differentiate into osteoblasts, adipocytes and chondrocytes under standard *in vitro* tissue culture-differentiating conditions.

élapomestrocel

cellules progénitrices mésenchymateuses autologues dérivées du liquide de la moelle osseuse. Les cellules sont mises en culture dans un milieu de culture standard complété avec du sérum autologue. Les cellules expriment les marqueurs de cellules progénitrices mésenchymateuses CD73, CD90 et CD105 (>90%) et n'expriment pas les marqueurs CD34 et CD45 (<5%). Les cellules sécrètent des facteurs neurotrophiques (facteur neurotrophique dérivé du cerveau (BDNF), facteur de croissance endothélial vasculaire (VEGF), facteur de croissance placentaire (PGF) et facteur de croissance hépatocytaire (HGF)). Les cellules sont capables de se différencier en ostéoblastes, en adipocytes et en chondrocytes dans des conditions standard de différenciation de culture tissulaire *in vitro*.

elapomestrocel

células progenitoras mesenquimales autólogas derivadas del fluido de médula ósea. Las células se expanden en medio de cultivo estándar suplementado con suero autólogo. Las células expresan los marcadores de células progenitoras mesenquimales CD73, CD90 y CD105 (>90%) y no expresan CD34 ni CD45 (<5%). Las células secretan factores neurotróficos (factor neurotrófico derivado de cerebro (BDNF), factor de crecimiento del endotelio vascular (VEGF), factor de crecimiento placentario (PGF) y factor de crecimiento de hepatocitos (HGF)). Las células son capaces de diferenciarse a osteoblastos, adipocitos y condrocitos bajo condiciones de diferenciación estándar en cultivo *in vitro*.

elarekibepum #

elarekibep

engineered human lipocalin-1 binding protein (tear lipocalin, tear prealbumin, von Ebner gland protein) (1-154) variant (REF²²SRC²⁴, EMNLE²⁶RAVYN³⁰, V⁴⁹F⁴⁹, MLIS⁵¹AQRK⁵⁴, C⁵⁷W⁵⁷, EV⁵⁹KY⁶⁰, A⁶²L⁶², D⁷⁶S⁷⁶, K⁷⁹R⁷⁹, YC⁹⁶HS⁹⁷, ELH¹⁰⁰LCP¹⁰², K¹⁰⁴Q¹⁰⁴, R¹⁰⁷P¹⁰⁷, K¹¹⁰W¹¹⁰, C¹⁴⁹S¹⁴⁹) anti-(human interleukin 4 receptor subunit alpha (IL4R α)), non-glycosylated, produced in *Corynebacterium glutamicum*;
human lipocalin-1 (LCN1, tear lipocalin, Tlc, von Ebner gland protein, vEG protein, VEGP, tear prealbumin, TP), des-(1-22) pre-protein (1-154), [²²REF²⁴SRC, ²⁶EMNLE³⁰RAVYN, V⁴⁹F⁴⁹, ⁵¹MLIS⁵⁴AQRK, C⁵⁷W⁵⁷, ⁵⁹EV⁶⁰KY, A⁶²L⁶², D⁷⁶S⁷⁶, K⁷⁹R⁷⁹, ⁹⁶YC⁹⁷HS, ¹⁰⁰ELH¹⁰²LCP, K¹⁰⁴Q¹⁰⁴, R¹⁰⁷P¹⁰⁷, K¹¹⁰W¹¹⁰, C¹⁴⁹S¹⁴⁹] mutant engineered for binding to the human interleukin 4 receptor subunit alpha (IL4R α), non-glycosylated, produced in *Corynebacterium glutamicum*

élarékibep

protéine de liaison de la lipocaline-1 humaine modifiée (lipocaline lacrymale, préalbumine lacrymale, protéine de la glande de von Ebner) (1-154) variant (REF>²²SRC²⁴, EMNLE>²⁶RAVYN³⁰, V>F⁴⁹, MLIS>⁵¹AQRK⁵⁴, C>W⁵⁷, EV>⁵⁹KY⁶⁰, A>L⁶², D>S⁷⁶, K>R⁷⁹, YC>⁹⁶HS⁹⁷, ELH>¹⁰⁰LCP¹⁰², K>Q¹⁰⁴, R>P¹⁰⁷, K>W¹¹⁰, C>S¹⁴⁹) anti-(sous-unité alpha du récepteur humain de l'interleukine 4 (IL4Rα)), non glycosylée, produite dans *Corynebacterium glutamicum*;
lipocaline-1 humaine (LCN1, lipocaline lacrymale, Tlc, protéine de la glande de von Ebner, protéine vEG, VEGP, préalbumine lacrymale humaine, TP), des-(1-22) pré-protéine (1-154), mutant [²²REF²⁴>SRC, ²⁶EMNLE³⁰>RAVYN, V⁴⁹>F, ⁵¹MLIS⁵⁴>AQRK, C⁵⁷>W, ⁵⁹EV⁶⁰>KY, A⁶²>L, D⁷⁶>S, K⁷⁹>R, ⁹⁶YC⁹⁷>HS, ¹⁰⁰ELH¹⁰²>LCP, K¹⁰⁴>Q, R¹⁰⁷>P, K¹¹⁰>W, C¹⁴⁹>S] conçue pour se lier à la sous-unité alpha du récepteur de l'interleukine 4 (IL4Rα), non glycosylée, produite dans *Corynebacterium glutamicum*

elarekibep

proteína humana modificada de unión a la lipocalina-1 (lipocalina lagrimal, prealbúmina lagrimal, proteína de la glándula von Ebner) (1-154) variante (REF>²²SRC²⁴, EMNLE>²⁶RAVYN³⁰, V>F⁴⁹, MLIS>⁵¹AQRK⁵⁴, C>W⁵⁷, EV>⁵⁹KY⁶⁰, A>L⁶², D>S⁷⁶, K>R⁷⁹, YC>⁹⁶HS⁹⁷, ELH>¹⁰⁰LCP¹⁰², K>Q¹⁰⁴, R>P¹⁰⁷, K>W¹¹⁰, C>S¹⁴⁹) anti-(interleukina humana 4 receptor subunidad alfa (IL4Rα)), no glicosilada, producida en *Corynebacterium glutamicum*;
lipocalina-1 humana (LCN1, lipocalina lagrimal, Tlc, proteína de la glándula de von Ebner, proteína vEG, VEGP, prealbúmina lagrimal humana, TP), des-(1-22) pre-proteína (1-154), mutante [²²REF²⁴>SRC, ²⁶EMNLE³⁰>RAVYN, V⁴⁹>F, ⁵¹MLIS⁵⁴>AQRK, C⁵⁷>W, ⁵⁹EV⁶⁰>KY, A⁶²>L, D⁷⁶>S, K⁷⁹>R, ⁹⁶YC⁹⁷>HS, ¹⁰⁰ELH¹⁰²>LCP, K¹⁰⁴>Q, R¹⁰⁷>P, K¹¹⁰>W, C¹⁴⁹>S] diseñada para unirse a la subunidad alfa del receptor de interleukina 4 humano (IL4Rα), no glicosilada, producida en *Corynebacterium glutamicum*

Sequence / Séquence / Secuencia

ASDEEIQDVS GTWYLKAMTV <u>LSRCFRAVYN</u> SVTPMTLTTL EGGNLEAK <u>FT</u>	50
<u>AQRKGF</u> <u>WKY</u> KLWLEKTDEP GK ^Y TA <u>SGGRH</u> VAYIIRSHVK DHYI <u>FHSEGL</u>	100
<u>CP</u> <u>CP</u> <u>VP</u> <u>PGVW</u> LVGRDPKNNL EALED ^F E ^K AA GARGLSTESI LIPRQSET <u>SS</u>	150
PGSD	154

Mutation / Mutation / Mutación

R22> **S**, E23> **R**, F24> **C**, E26> **R**, M27> **A**, N28> **V**, L29> **Y**, E30> **N**, V49> **F**, M51> **A**, L52> **Q**, I53> **R**, S54> **K**, C57> **W**, E59> **K**, V60> **Y**, A62> **L**, D76> **S**, K79> **R**, Y96> **H**, C97> **S**, E100> **L**, L101> **C**, H102> **E**, K104> **Q**, R107> **P**, K110> **W**, C149> **S**

Post-translational modifications

Disulfide bridge location / Position du pont disulfure / Posición del puente disulfuro
24-101

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

elcubragistatum

elcubragistat

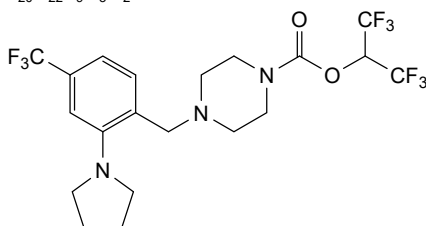
1,1,1,3,3,3-hexafluoropropan-2-yl 4-[[2-(pyrrolidin-1-yl)-4-(trifluoromethyl)phenyl]methyl]piperazine-1-carboxylate

elcubragistat

4-[[2-(pyrrolidin-1-yl)-4-(trifluorométhyl)phényl]méthyl]pipérazine-1-carboxylate de 1,1,1,3,3,3-hexafluoropropan-2-yle

elcubragistat

4-[[2-(pirrolidin-1-il)-4-(trifluorometil)fenil]metil]piperazina-1-carboxilato de 1,1,1,3,3,3-hexafluoropropan-2-ilo

 $C_{20}H_{22}F_9N_3O_2$ 

elzovantinibum

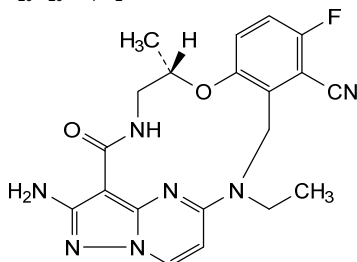
elzovantinib

(6S)-1²-amino-2-ethyl-4⁵-fluoro-6-methyl-9-oxo-5-oxa-2,8-diaza-1(5,3)-pirazolo[1,5-a]pirimidina-4(1,2)-benzenacyclononaphane-4⁶-carbonitrile

elzovantinib

(6S)-1²-amino-2-éthyl-4⁵-fluoro-6-méthyl-9-oxo-5-oxa-2,8-diaza-1(5,3)-pirazolo[1,5-a]pirimidina-4(1,2)-benzénacyclononaphane-4⁶-carbonitrile

elzovantinib

(6S)-1²-amino-2-etil-4⁵-fluoro-6-metil-9-oxo-5-oxa-2,8-diaza-1(5,3)-pirazolo[1,5-a]pirimidina-4(1,2)-benzenacyclononafano-4⁶-carbonitrilo $C_{20}H_{20}FN_7O_2$ 

emfizatamabum #

emfizatamab

immunoglobulin scFv-G1-scFv-scFv_L-kappa, anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], anti-[*Homo sapiens* CD19 (B lymphocyte surface antigen B4, Leu-12)], anti-[*Homo sapiens* CD274 (programmed death ligand 1, PDL1, PD-L1, B7 homolog 1, B7H1)] and anti-[*Homo sapiens* TNFRSF9 (tumor necrosis factor receptor (TNFR) superfamily member 9, 4-1BB, CD137)], *Homo sapiens* and humanized monoclonal antibody, tetraspecific;

scFv-G1-scFv-scFv fused heavy chain *Homo sapiens* and humanized (1-1230) [scFv kappa-heavy anti-CD3E humanized (1-252) [V-KAPPA (*Homo sapiens* IGKV1-5*01 (90.1%) -IGKJ4*01 (90.9%), CDR-IMGT [6.3.14] (27-32.50-52.89-102)) (1-112) -20-mer tetrakis(tetraglycyl-seryl) linker (113-132) -VH (*Homo sapiens*IGHV3-66*01 (86.6%) - (IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.7.14] (158-165.183-189.228-241)) (133-252)] -10-mer bis(tetraglycyl-seryl) linker (253-262) - gamma-1 heavy chain anti-CD19 *Homo sapiens* (263-712) [VH (*Homo sapiens* IGHV5-51*01 (94.9%) - (IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.8.14] (288-295.313-320.359-372)) (263-383) -*Homo sapiens*

1-15 (482-496), CH2 L1.3>A (500), L1.2>A (501), G1>A (503), K105>A (588) (497-606), CH3 D12 (622), L14 (624) (607-711), CHS K2>del (712)] (384-712)] -10-mer bis(tétraglycyl-séryl) linker (713-722) -scFv heavy-kappa anti-CD274 humanized (723-974) [VH (*Homo sapiens*IGHV3-23*01 (84.0%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [9.8.13] (748-756.774-781.821-833)) (723-844) -20-mer tétrakis(tétraglycyl-séryl) linker (845-864) -V-KAPPA (*Homo sapiens* IGKV1-5*03 (91.5%) -IGKJ4*01 (100%), CDR-IMGT [6.3.12] (891-896.914-916.953-964)) (865-974)] -10-mer bis(tétraglycyl-séryl) linker (975-984) -scFv heavy-kappa anti-TNFRSF9 humanized (985-1230) [VH (*Homo sapiens* IGHV3-64*04 (82.1%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.7.10] (1009-1016.1034-1040.1079-1088)) (985-1099) -20-mer tétrakis(tétraglycyl-séryl) linker (1100-1119) -V-KAPPA (*Homo sapiens* IGKV1-12*01 (83.1%) -IGKJ4*01 (100%), CDR-IMGT [6.3.13] (1146-1151.1169-1171.1208-1220)) (1120-1230)]; (486-214')-disulfide with kappa light chain anti-CD19 *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-13*02 (100%) -IGKJ3*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (492-492":495-495")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

emfizatamab

immunoglobuline scFv-G1-scFv-scFv_L-kappa, anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], anti-[*Homo sapiens* CD19 (antigène de surface B4 des lymphocytes B, Leu-12)], anti-[*Homo sapiens* CD274 (ligand 1 de mort programmée, PDL1, PD-L1, homologue 1 de B7, B7H1)] et anti-[*Homo sapiens* TNFRSF9 (membre 9 de la superfamille des récepteurs du facteur de nécrose tumorale, 4-1BB, CD137)], anticorps monoclonal *Homo sapiens* et humanisé, tétraspécifique; chaîne lourde fusionnée scFv-G1-scFv-scFv *Homo sapiens* et humanisée (1-1230) [scFv kappa-lourd anti-CD3E humanisé (1-252) [V-KAPPA (*Homo sapiens* IGKV1-5*01 (90.1%) -IGKJ4*01 (90.9%), CDR-IMGT [6.3.14] (27-32.50-52.89-102)) (1-112) -20-mer tétrakis(tétraglycyl-séryl) linker (113-132) -VH (*Homo sapiens* IGHV3-66*01 (86.6%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.7.14] (158-165.183-189.228-241)) (133-252)] -10-mer bis(tétraglycyl-séryl) linker (253-262) -chaîne lourde gamma-1 anti-CD19 *Homo sapiens* (263-712) [VH (*Homo sapiens* IGHV5-51*01 (94.9%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.8.14] (288-295.313-320.359-372)) (263-383) -*Homo sapiens* IGHG1*03, G1m3, nG1m1, G1v14 CH2 A1.3, A1.2, G1v20 CH2 A105 (CH1 R120 (480) (384-481), charnière 1-15 (482-496), CH2 L1.3>A (500), L1.2>A (501), G1>A (503), K105>A (588) (497-606), CH3 D12 (622), L14 (624) (607-711), CHS K2>del (712)] (384-712)] -10-mer bis(tétraglycyl-séryl) linker (713-722) -scFv lourd-kappa anti-CD274 humanisé (723-974) [VH (*Homo sapiens* IGHV3-23*01 (84.0%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [9.8.13] (748-756.774-781.821-833)) (723-844) -20-mer tétrakis(tétraglycyl-séryl) linker (845-864) -V-KAPPA (*Homo sapiens* IGKV1-5*03 (91.5%) -IGKJ4*01 (100%), CDR-IMGT [6.3.12] (891-896.914-916.953-964)) (865-974)] -10-mer bis(tétraglycyl-séryl) linker (975-984) -

- scFv lourd-kappa anti-TNFRSF9 humanisé (985-1230) [VH (*Homo sapiens*IGHV3-64*04 (82.1%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.7.10] (1009-1016.1034-1040.1079-1088)) (985-1099) -20-mer tétrakis(tétraglycyl-séryl) linker (1100-1119) -V-KAPPA (*Homo sapiens*IGKV1-12*01 (83.1%) -IGKJ4*01 (100%), CDR-IMGT [6.3.13] (1146-1151.1169-1171.1208-1220)) (1120-1230)]; (486-214')-disulfure avec la chaîne légère kappa anti-CD19 *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens*IGKV1-13*02 (100%) -IGKJ3*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens*IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (492-492":495-495")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa
- emfizata^mab
- immunoglobulina scFv-G1-scFv-scFv_L-kappa, anti-[*Homo sapiens* CD3E (CD3 épsilon, Leu-4)], anti-[*Homo sapiens* CD19 (antígeno de superficie B4 de los linfocitos B, Leu-12)], anti-[*Homo sapiens* CD274 (ligando 1 de muerte programada, PDL1, PD-L1, homólogo 1 de B7, B7H1)] y anti-[*Homo sapiens* TNFRSF9 (miembro 9 de la superfamilia de los receptores del factor de necrosis tumoral, 4-1BB, CD137)], anticuerpo monoclonal *Homo sapiens* y humanizado, tetraespecífico;
- cadena pesada fusionada scFv-G1-scFv-scFv *Homo sapiens* y humanizada (1-1230) [scFv kappa-pesado anti-CD3E humanizado (1-252) [V-KAPPA (*Homo sapiens*IGKV1-5*01 (90.1%) -IGKJ4*01 (90.9%), CDR-IMGT [6.3.14] (27-32.50-52.89-102)) (1-112) -20-mer tetrakis(tetraglicil-seril) linker (113-132) -VH (*Homo sapiens*IGHV3-66*01 (86.6%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.7.14] (158-165.183-189.228-241)) (133-252)] -10-mer bis(tetraglicil-seril) linker (253-262) -cadena pesada gamma-1 anti-CD19 *Homo sapiens* (263-712) [VH (*Homo sapiens*IGHV5-51*01 (94.9%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.8.14] (288-295.313-320.359-372)) (263-383) -*Homo sapiens*IGHG1*03, G1m3, nG1m1, G1v14 CH2 A1.3, A1.2, G1v20 CH2 A105 (CH1 R120 (480) (384-481), bisagra 1-15 (482-496), CH2 L1.3>A (500), L1.2>A (501), G1>A (503), K105>A (588) (497-606), CH3 D12 (622), L14 (624) (607-711), CHS K2>del (712)) (384-712)] -10-mer bis(tetraglicil-seril) linker (713-722) -scFv pesado-kappa anti-CD274 humanizado (723-974) [VH (*Homo sapiens*IGHV3-23*01 (84.0%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [9.8.13] (748-756.774-781.821-833)) (723-844) -20-mer tetrakis(tetraglicil-seril) linker (845-864) -V-KAPPA (*Homo sapiens*IGKV1-5*03 (91.5%) -IGKJ4*01 (100%), CDR-IMGT [6.3.12] (891-896.914-916.953-964)) (865-974)] -10-mer bis(tetraglicil-seril) linker (975-984) -scFv pesado-kappa anti-TNFRSF9 humanizado (985-1230) [VH (*Homo sapiens*IGHV3-64*04 (82.1%) -(IGHD) -IGHJ1*01 (100%), CDR-IMGT [8.7.10] (1009-1016.1034-1040.1079-1088)) (985-1099) -20-mer tetrakis(tetraglicil-seril) linker (1100-1119) -V-KAPPA (*Homo sapiens*IGKV1-12*01 (83.1%) -IGKJ4*01 (100%), CDR-IMGT [6.3.13] (1146-1151.1169-1171.1208-1220)) (1120-1230)]; (486-214')-disulfuro con la cadena ligera kappa anti-CD19 *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens*IGKV1-13*02 (100%) -IGKJ3*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens*IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (492-492":495-495")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada [scFv (anti-CD3E)-G1 (anti-CD19)-scFv (anti-CD274)-scFv (anti-TNFRSF9)]

DVVMTQSPST	LSASVGDRTV	INCQASESIS	SWLAWYQQKP	GKAPKLLIYE	50
ASKLASGVPS	RFSGSGSGTE	FTLTISLQF	DDFATYYCQG	YFYFISRLTYV	100
NSFGGGTKVE	IKGGGGSGGG	GSGGGGGGG	GSEVQLVESG	GGLVQPGGSL	150
RLSCAASGFT	ISTNAMSWVR	QAPKGLEWI	GUITGRDITY	YASWAKGRFT	200
ISRDNSKNTL	YLQMNLSRAE	DTAVVYCARD	GGSSAITSMN	IWGQGTLVTV	250
SSGGGGSGGG	GSEVQLVQSG	AEVKKPGESL	KISCKGSGYS	FSSSWIGWVR	300
QAPGKGLEWM	GILYPDDSDT	RYSFSPGQGV	TISADKSIRT	AYLQWSSLKA	350
SDTAMYICAR	HVTMIWGVII	DFWGGTTLVT	VSSASTKGPS	VFPLAPSSKS	400
TSGGTAALGC	LVRDYFPEPV	TVSWNSGALT	SGVHTFFPAVL	QSSGLYSLSS	450
VVTVPSSSLG	TQTYICNVNH	KPSNTRVDKR	VEPKSCDKTH	TCPPCPAPEA	500
AGAPSVFLFP	PKPKDTLMIS	RTPEVTCVVV	DVSHEDPEVK	FNWYVDGVEV	550
HNAKTKPREE	QYNSTYRVVS	VLTVLHQDWL	NGKEYKCAVS	NKALPAPIEK	600
TISKAKGQPR	EPQVYTLPPS	RDELTKNQVS	LTCLVKGFYFP	SDIAVEWESN	650
GQPENNYKTT	PPVLDSDGFS	FLYSKLTVDK	SRWQQGNVFS	CSVMHEALHN	700
HYTQKSLSL	PGGGGGSGGG	GSEVQLLESG	GGLVQPGGSL	RLSCAASGHN	750
FSSGYDMCWV	RQAPGKGLEW	IACIAAGSAG	ITYDANWAKG	RFTISRDNKSK	800
NTLYLQMNLS	RAEDTAVVYC	ARSAFSFDYA	MDLWQQGTLV	TVSSGGGGSG	850
GGSGGGGGSG	GGGSDIQTMT	SPSTLSASVQ	DRVTITCQAS	QSISSHLNMY	900
QQKFGKAPKL	LIYKASTLAS	GVPSRFSGSG	SGTEFTLTIS	SLQPDFPATY	950
YQQQGYSWG	VDNVFGGTTK	VEIKGGGGSG	GGGSRSLVES	GGGLVQPGGS	1000
LRLSCTASGF	TISSYHMQWV	RQAPGKGLEW	IGTISGGGNV	YYASSARGRF	1050
TISRPFSSKNT	VDLQMNLSRA	EDTAVVYCAR	DSGYSDEPMG	QGTLLVTVSSG	1100
GGSGGGGGSG	GGSGGGGGSD	VVMTQSPSSV	SASVGDRTVI	TCQASQNIPT	1150
YLSWYQQKPG	KAPKLLIYAA	ANLASGVPSR	FSGSGSGTDF	TLTISDLPEP	1200
DAATYYCQST	YLGTDYVGGG	FGGGTKVEIK			1230

Light chain / Chaîne légère / Cadena ligera (anti-CD19)

AIQLTQSPSS	LSASVGDRTV	ITCRASQGIS	SALAWYQQKP	GKAPKLLIYD	50
ASSLESQVPS	RFSGSGSGTD	FTLTISLQF	EDFATYYCQG	FNSYPFTFGP	100
GTKVDIKRTV	AAPSVFIPTP	SDEQLKSGTA	SUVCLLNNEY	PREAKVQWKV	150
DNALQSGSNQ	ESVTEQDSKD	STYLSLSTLT	LSKADYEKHK	VYACEVTHQG	200
LSSPVTWYKFN	RGEC				214

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

Intra-H (C23-C104)	23-88	154-227	284-358	410-466	527-587
	23"-88"	154"-227"	284"-358"	410"-466"	527"-587"
	633-691	744-820	887-952	1005-1078	1142-1207
	633"-691"	744"-820"	887"-952"	1005"-1078"	1142"-1207"
Intra-H (VH 40-55)	758-773	758"-773"			
Intra-L (C23-C104)	23"-88"	134"-194"			
	23"-88"	134"-194"			
Inter-H-L (h 5-CL 126)	486-214"	486"-214"			
Inter-H-H (h 11, h 14)	492-492"	495-495"			

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
 H CH2 N84.4: 563, 563"
 Fucosylated complex bi-antennary CHO-type glycans / glicanos de tipo CHO bi-antennarios complejos fucosilados.

emilimogenum sigulactibacum #
 emilimogene sigulactibac

émilimogène sigulactibac

recombinant live *Limosilactobacillus reuteri* bacteria (previously known as *Lactobacillus reuteri*), strain R2LC, transformed with a plasmid expressing a codon-optimised human C-X-C motif chemokine ligand 12 isoform alpha (CXCL12-1 α ; also known as stromal cell-derived factor 1 isoform alpha) with the native secretion signal replaced with the secretion signal of the *L. reuteri* collagen-binding protein, under control of the inducible promoter P_{orfX} (part of a peptide-based quorum-sensing system).

bactéries vivantes recombinantes *Limosilactobacillus reuteri* (précédemment connues sous le nom de *Lactobacillus reuteri*), souche R2LC, transformées avec un plasmide exprimant l'isoforme alpha du ligand 12 de la chimiokine humaine à motif C-X-C (CXCL12-1 α ; également connue sous le nom d'isoforme alpha du facteur 1 dérivé des cellules stromales) aux codons optimisés, le signal de sécrétion natif remplacé par le signal de sécrétion de la protéine de liaison au collagène de *L. reuteri*, sous le contrôle du promoteur inducible P_{orfX} (qui fait partie d'un système peptidique de détection du quorum).

emilimogén sigulactibac

bacteria viva recombinante *Limosilactobacillus reuteri* (antes conocida como *Lactobacillus reuteri*), cepa R2LC, transformada con un plásmido que expresa la isoforma alfa del ligando 12 de la quimoquina con motivo C-X-C humana (CXCL12-1 α ; también conocida como isoforma alfa del factor derivado de células estromales 1), con codones optimizados, con la señal de secreción nativa reemplazada con la señal de secreción de la proteína de unión a colágeno de *L. reuteri*, bajo el control del promotor inducible P_{orfX} (parte del sistema de percepción de cuórum (quorum sensing) basado en péptidos).

emirotatamabum #

emirotatamab

immunoglobulin scFv-scFv-scFc, anti-[*Homo sapiens* FLT3 (fms related receptor tyrosine kinase 3, STK1, FLK2, CD135)] and anti-[*Homo sapiens* CD3E (CD3e, CD3 epsilon)], single chain monoclonal antibody, bispecific;

scFv-scFv-scFc fused single chain (1-989) [scFv heavy-kappa anti-FLT3 (1-246) [VH (*Homo sapiens* IGHV2-26*03 (92.0%) -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [10.7.16] (26-35.53-59.98-113)) (1-124) -15-mer tris(tetraglycyl-seryl) linker (125-139) -V-KAPPA (*Homo sapiens* IGKV1-17*01 (98.9%) -IGKJ4*01 (91.7%) G120>C (239), CDR-IMGT [6.3.9] (166-171.189-191.228-236)) (140-246)] -6-mer seryl-tetraglycyl-seryl linker (247-252) -scFv heavy-lambda anti-CD3E (253-501) [VH Musmus/Homsap (*Mus musculus* IGHV10-1*02 (91.9%) -(IGHD) -IGHJ3*01 (92.9%)/*Homo sapiens* IGHV3-73*01 (87.0%) -(IGHD) -IGHJ5*01 (100%), CDR-IMGT [8.10.16] (278-285.303-312.351-366)) (253-377) -15-mer tris(tetraglycyl-seryl) linker (378-392) -V-LAMBDA (*Homo sapiens* IGLV7-43*01 (85.1%) -IGLJ3*02 (100%), CDR-IMGT [9.3.9] (418-426.444-446.483-491)) (393-501)] -4-mer tetraglycyl linker (502-505) -scFc gamma1 (h-CH2-CH3)-(h-CH2-CH3) (506-989) [*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1, G1v30 CH2 N84.4>G (hinge 6-15 (506-515), CH2 R83>C (577), N84.4>G (582), V85>C (587) (516-625), CH3 E12 (641), M14 (643) (626-730), CHS (731-732) (506-732)] -30-mer hexakis(tetraglycyl-seryl) linker (733-762) -*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1, G1v30 CH2 N84.4>G (hinge 6-15 (763-772), CH2 R83>C (834), N84.4>G (839), V85>C (844) (773-882), CH3 E12 (898), M14 (900) (883-987), CHS (988-989)], produced in Chinese hamster ovary (CHO) cells, non-glycosylated

émirotatamab

immunoglobuline scFv-scFv-scFc, anti-[*Homo sapiens* FLT3 (récepteur tyrosine kinase 3 lié à fms, STK1, FLK2, CD135)] et anti-[*Homo sapiens* CD3E (CD3e, CD3 epsilon)], anticorps monoclonal à chaîne unique, bispécifique;

chaîne unique fusionnée scFv-scFv-scFc (1-989) [scFv heavy-kappa anti-FLT3 (1-246) [VH (*Homo sapiens*IGHV2-26*03 (92.0%) -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [10.7.16] (26-35.53-59.98-113)) (1-124) -15-mer tris(tétraglycyl-séryl) linker (125-139) -V-KAPPA (*Homo sapiens* IGKV1-17*01 (98.9%) -IGKJ4*01 (91.7%) G120>C (239), CDR-IMGT [6.3.9] (166-171.189-191.228-236)) (140-246)] -6-mer séryl-tétraglycyl-séryl linker (247-252) -scFv heavy-lambda anti-CD3E (253-501) [VH Musmus/Homsap (*Mus musculus* IGHV10-1*02 (91.9%) -(IGHD) -IGHJ3*01 (92.9%)/*Homo sapiens* IGHV3-73*01 (87.0%) -(IGHD) -IGHJ5*01 (100%), CDR-IMGT [8.10.16] (278-285.303-312.351-366)) (253-377) -15-mer tris(tétraglycyl-séryl) linker (378-392) -V-LAMBDA (*Homo sapiens* IGLV7-43*01 (85.1%) -IGLJ3*02 (100%), CDR-IMGT [9.3.9] (418-426.444-446.483-491)) (393-501)] -4-mer tétraglycyl linker (502-505) -scFc gamma1 (h-CH2-CH3)-(h-CH2-CH3) (506-989) [*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1, G1v30 CH2 N84.4>G (charnière 6-15 (506-515), CH2 R83>C (577), N84.4>G (582), V85>C (587) (516-625), CH3 E12 (641), M14 (643) (626-730), CHS (731-732)) (506-732)] -30-mer hexakis(tétraglycyl-séryl) linker (733-762) -*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1, G1v30 CH2 N84.4>G (charnière 6-15 (763-772), CH2 R83>C (834), N84.4>G (839), V85>C (844) (773-882), CH3 E12 (898), M14 (900) (883-987), CHS (988-989)]], produit dans des cellules ovariennes de hamster chinois (CHO), non-glycosylé

emirodatamab

immunoglobulina scFv-scFv-scFc, anti-[*Homo sapiens* FLT3 (receptor tirosina kinasa 3 relacionado con fms, STK1, FLK2, CD135)] y anti-[*Homo sapiens* CD3E (CD3e, CD3 épsilon)], anticuerpo monoclonal con cadena única, biespecífico;

cadena única fusionada scFv-scFv-scFc (1-989) [scFv pesada-kappa anti-FLT3 (1-246) [VH (*Homo sapiens* IGHV2-26*03 (92.0%) -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [10.7.16] (26-35.53-59.98-113)) (1-124) -15-mer tris(tetraglicil-seril) linker (125-139) -V-KAPPA (*Homo sapiens* IGKV1-17*01 (98.9%) -IGKJ4*01 (91.7%) G120>C (239), CDR-IMGT [6.3.9] (166-171.189-191.228-236)) (140-246)] -6-mer seril-tetraglicil-seril linker (247-252) -scFv pesado-lambda anti-CD3E (253-501) [VH Musmus/Homsap (*Mus musculus* IGHV10-1*02 (91.9%) -(IGHD) -IGHJ3*01 (92.9%)/*Homo sapiens* IGHV3-73*01 (87.0%) -(IGHD) -IGHJ5*01 (100%), CDR-IMGT [8.10.16] (278-285.303-312.351-366)) (253-377) -15-mer tris(tetraglicil-seril) linker (378-392) -V-LAMBDA (*Homo sapiens* IGLV7-43*01 (85.1%) -IGLJ3*02 (100%), CDR-IMGT [9.3.9] (418-426.444-446.483-491)) (393-501)] -4-mer tetraglicil linker (502-505) -scFc gamma1 (h-CH2-CH3)-(h-CH2-CH3) (506-989) [*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1, G1v30 CH2 N84.4>G (bisagra 6-15 (506-515), CH2 R83>C (577), N84.4>G (582), V85>C (587) (516-625), CH3 E12 (641), M14 (643) (626-730), CHS (731-732)) (506-732)] -30-mer hexakis(tetraglicil-seril) linker (733-762) -*Homo sapiens* IGHG1*03 h-CH2-CH3, nG1m1, G1v30 CH2 N84.4>G (bisagra 6-15 (763-772), CH2 R83>C (834), N84.4>G (839), V85>C (844) (773-882), CH3 E12 (898), M14 (900) (883-987), CHS (988-989)]], producido en las células ováricas de hámster chino (CHO), no glicosilado

Sequence / Séquence / Secuencia

QVTLKESGPT LVKPTETLTL TCTLSGFSLN NARMGVSIR QPPGKCLEWL 50
 AHIFSNDKES YSTSLKNRLT ISKDSKTKQV VLTMTNVDPV DTATYYCARI 100
 VGYGSGWYGF FDYWGQGLTV TVSSGGGSGG GGGSGGGGSD IQMTQSPSSL 150
 SASVGDRTVI TCRASGIRN DLGWYQKQPG KAPKRLIYAA STLQSGVPSR 200
 FSGSGSGTFF TLTISLQPE DFTYYCLQH NSYPLTFGGG TKVEIKSGGG 250
 GSEVQLVESG GGLVQPGSSL KLSCAASGFT FNKYAMNWR QAPKGLEWV 300
 ARIRSKYNY ATYYADSVKD RFTISRDDSK NTAFLQMNLL KTEDTAVYYC 350
 VRHGNFGNSY ISYWAYNGQG TLTVYSSGGG GSGGGSGGGG GSQTVVYQEP 400
 SLTVSPFGTV TLTGSSSTA VTSNGYFNWV QQKPGQAPRG LIGGTFKFLAP 450
 CTPARFSGSL LGGKAALTLG GVQPEDEABY YCVLWYSNRW VFGGKTLTV 500
 LGGGDKTHT CPPCPAPPELL GGPSVFLPPP KPKDTLMSR TPEVTCVVVD 550
 VSHEDPEVKF NWYVDGVEVH NAKTKPCEEQ YGSTRCVSV LTVLHQDNLN 600
 GKPYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR EEMTKNQVSL 650
 TCLVRGFPVS DIAVEWESNG QPENNYKTTT PVLDSGGSFF LYSKLTVDKS 700
 RWQQGNVFC SVMHEALHWH YTKSLSLSP GKGGGGSGGG GSGGGSGGG 750
 GSGGGSGGG GSDKTHTCP CPAPPELLGGP SVFLFPKPK DTLMISRTPE 800
 VTCVVVDVSH EDPEVKFNWY VDGVEVHNK TKPCEEQYGS TYRCVSVLT 850
 LHQDNLNGKE YRCKVSNKAL PAPIEKTIK AKGQPREPQV YTLPPSREEM 900
 TKNQVSLTCL VKGFPYSDIA VEWESNGQPE NNYKTTFPVL DSDGSFFLYS 950
 KLTVDKSRWQ QGNVFCSCVM HEALHNYTQ KSLSLSPGK 989

Post-translational modifications

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
 Intra-domain (C23 C104) 22-97 162-227 274-350 414-482
 546-606 652-710 803-863 909-967

Inter-V (49-120) 46-239
 Inter-h (h11), (h14) 511-768 514-771
 Inter-CH2 (83), (85) 577-587 834-844

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutamino N-terminal
 H VH Q1 > pyroglutamyl (pE, 5-oxopropyl): 1

No N-glycosylation sites / pas de sites de N-glycosylation / ningún posición de N-glicosilación
 CH2 N84.4-G (G1v30): 582, 839
 Aglycosylated / aglycosylé / aglycosilado

C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
 H CHS K2: 989

emprumapimodum

emprumapimod

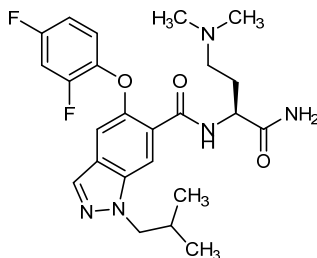
N-[(2*S*)-1-amino-4-(dimethylamino)-1-oxobutan-2-yl]-5-(2,4-difluorophenoxy)-1-(2-methylpropyl)-1*H*-indazole-6-carboxamide

emprumapimod

N-[(2*S*)-1-amino-4-(diméthylamino)-1-oxobutan-2-yl]-5-(2,4-difluorophénoxy)-1-(2-méthylpropyl)-1*H*-indazole-6-carboxamide

emprumapimod

N-[(2*S*)-1-amino-4-(dimetilamino)-1-oxobutan-2-il]-5-(2,4-difluorofenoxi)-1-(2-metilpropil)-1*H*-indazol-6-carboxamida

 $C_{24}H_{29}F_2N_5O_3$


enbezotininibum

enbezotininib

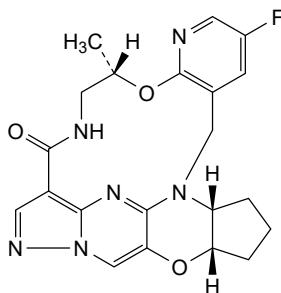
(1^{5a}*R*, 1^{8a}*S*, 5*S*)-3⁵-fluoro-5-methyl-1^{5a}, 1⁷, 1⁸, 1^{8a}-tetrahydro-1⁶*H*-4-oxa-7-aza-1(5,3)-cyclopenta[*b*]pyrazolo[1',5':1,2]pyrimido[4,5-*e*][1,4]oxazina-3(3,2)-pyridinacyclooctaphan-8-one

enbézotininib

(1^{5a}R,1^{8a}S,5S)-3⁵-fluoro-5-méthyl-1^{5a},1⁷,1⁸,1^{8a}-
tétrahydro-1⁶H-4-oxa-7-aza-1(5,3)-
cyclopenta[*b*]pyrazolo[1',5':1,2]pyrimido[4,5-
e][1,4]oxazina-3(3,2)-pyridinacyclooctaphan-8-one

enbezotininib

(1^{5a}R,1^{8a}S,5S)-3⁵-fluoro-5-metil-1^{5a},1⁷,1⁸,1^{8a}-tetrahydro-
1⁶H-4-oxa-7-aza-1(5,3)-
ciclopenta[*b*]pirazolo[1',5':1,2]pirimido[4,5-
e][1,4]oxazina-3(3,2)-piridinaciclooctafan-8-ona

C₂₁H₂₁FN₆O₃**engabexagenum cincesparvovecum #**

engabexagene cincesparvovec

recombinant, non-replicating adeno-associated virus serotype 9 (rAAV9) vector, encoding codon-optimised human β -hexosaminidase subunits β and α , joined by a porcine teschovirus 2A peptide linker, under control of a synthetic promoter (cytomegalovirus (CMV) enhancer, chicken β -actin promoter and β -actin intron) and terminated with the simian virus 40 (SV40) polyadenylation (polyA) signal, flanked by adeno-associated virus serotype 2 (AAV2) inverted terminal repeats (ITRs).

engabexagène cincesparvovec

vecteur recombinant et non répliquant du virus adéno-associé de sérotype 9 (rAAV9) codant les sous-unités β et α de la β -hexosaminidase humaine aux codons optimisés, reliées par une liaison peptidique du teschovirus 2A porcin, sous le contrôle d'un promoteur synthétique (amplificateur du cytomégalo virus (CMV), promoteur et intron de la β -actine de poulet) et terminé par le signal de polyadénylation (polyA) du virus simien 40 (SV40), flanqué de répétitions terminales inversées (ITR) du virus adéno-associé de sérotype 2 (AAV2).

engabexagén cincesparvovec

vector de virus adenoasociado recombinante de serotipo 9 (rAAV9) no replicativo que codifica para las subunidades β y α de la β -hexosaminidasa humana, con codones optimizados, unidas por un péptido conector 2A del teschovirus porcino, bajo el control de un promotor sintético (potenciador de citomegalovirus (CMV), promotor de la β -actina de pollo y un intrón de la β -actina) y terminado con la señal de poliadenilación (polyA) del virus simio 40 (SV40), flanqueado por las repeticiones terminales invertidas (ITRs) del virus adenoasociado de serotipo 2 (AAV2).

enitociclibum

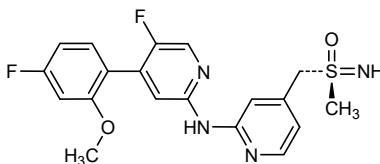
enitociclib

(S)-[(2-[[5-fluoro-4-(4-fluoro-2-methoxyphenyl)pyridin-2-yl]amino]pyridin-4-yl)methyl](imino)(methyl)-λ⁶-sulfanone

énitociclib

(S)-[(2-[[5-fluoro-4-(4-fluoro-2-méthoxyphényl)pyridin-2-yl]amino]pyridin-4-yl)méthyl](imino)(méthyl)-λ⁶-sulfanone

enitociclib

(S)-[(2-[[5-fluoro-4-(4-fluoro-2-metoxifenil)piridin-2-il]amino]piridin-4-il)metil](imino)(metil)-λ⁶-sulfanonaC₁₉H₁₈F₂N₄O₂S**ensitrelvirum**

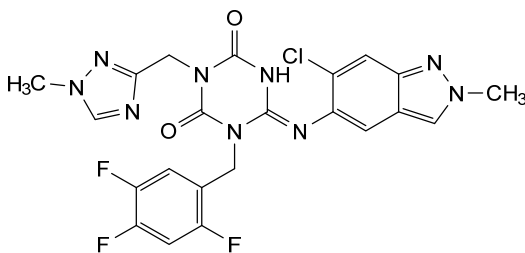
ensitrelvir

(6*E*)-6-[(6-chloro-2-methyl-2*H*-indazol-5-yl)imino]-3-[(1-methyl-1*H*-1,2,4-triazol-3-yl)methyl]-1-[(2,4,5-trifluorophenyl)methyl]-1,3,5-triazinane-2,4-dione

ensitrelvir

(6*E*)-6-[(6-chloro-2-méthyl-2*H*-indazol-5-yl)imino]-3-[(1-méthyl-1*H*-1,2,4-triazol-3-yl)méthyl]-1-[(2,4,5-trifluorophényl)méthyl]-1,3,5-triazinane-2,4-dione

ensitrelvir

(6*E*)-6-[(6-cloro-2-metil-2*H*-indazol-5-il)imino]-3-[(1-metil-1*H*-1,2,4-triazol-3-il)metil]-1-[(2,4,5-trifluorofenil)metil]-1,3,5-triazinano-2,4-dionaC₂₂H₁₇ClF₃N₉O₂**envonalkibum**

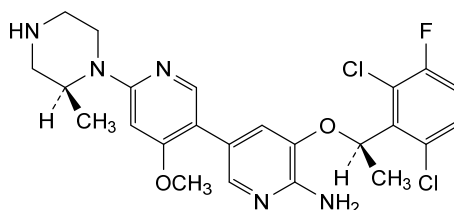
envonalkib

5-[(1*R*)-1-(2,6-dichloro-3-fluorophenyl)ethoxy]-4'-methoxy-6'-[(2*S*)-2-methylpiperazin-1-yl][3,3'-bipyridin]-6-amine

envonalkib

5-[(1*R*)-1-(2,6-dichloro-3-fluorophényl)éthoxy]-4'-méthoxy-6'-[(2*S*)-2-méthylpipérazin-1-yl][3,3'-bipyridin]-6-amine

envonalkib

5-[(1*R*)-1-(2,6-dichloro-3-fluorophenyl)etoxi]-6'-[(2*S*)-2-méthylpiperazin-1-il]-4'-métoxi[3,3'-bipiridin]-6-amina $C_{24}H_{26}Cl_2FN_5O_2$ 

esmethadonum

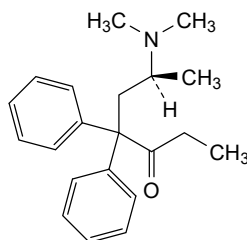
esmethadone

(6*S*)-6-(diméthylamino)-4,4-diphénylheptan-3-one

esméthadone

(6*S*)-6-(diméthylamino)-4,4-diphénylheptan-3-one

esmetadona

(6*S*)-6-(diméthilamino)-4,4-difenilheptan-3-ona $C_{21}H_{27}NO$ 

evencaleucelum

evencaleucel

autologous lymphocytes enriched in activated natural killer cells (NK), derived from peripheral blood mononuclear cells (PBMCs). The cells are cultured in medium supplemented with human serum and interleukin 2 (IL-2), and activated by addition of the anti-CD3 antibody *muromonab-CD3*. At least 10% of the cells are NK cells (CD3-CD56+), but the substance also contains T cells (CD3+CD56-) and NK-like T cells (CD3+CD56+). At least 30% of the NK cells show cytotoxic activity and respond in a functional test against the leukemia cell line K562 with surface expression of lysosomal-associated membrane protein 1 (LAMP-1, CD107a).

évencaleucel

lymphocytes autologues enrichis en cellules tueuses naturelles (NK) activées, dérivés de cellules mononucléaires de sang périphérique (PBMC). Les cellules sont cultivées dans un milieu complétement de sérum humain et d'interleukine 2 (IL-2), et activées par l'ajout d'anticorps anti-CD3 *muromonab-CD3*. Au moins 10% des cellules sont des cellules NK (CD3-CD56+), mais la substance contient également des lymphocytes T (CD3+CD56-) et des lymphocytes T de type NK (CD3+CD56+). Au moins 30% des cellules NK présentent une activité cytotoxique et répondent, dans un test fonctionnel, contre la lignée cellulaire leucémique K562 avec une expression de surface de protéines de membrane associées aux lysosomes 1 (LAMP-1, CD107a).

evencaleucel

linfocitos autólogos enriquecidos en células natural killer (NK) activadas, derivados de células mononucleares de sangre periférica (PBMCs). Las células se cultivan en medio suplementado con suero humano e interleukina 2 (IL-2), y se activan añadiendo el anticuerpo anti-CD3 *muromonab-CD3*. Al menos el 10% de las células son células NK (CD3-CD56+), pero la substancia también contiene linfocitos T (CD3+CD56-) y linfocitos T similares a NK (CD3+CD56+). Al menos el 30% de las células NK muestran actividad citotóxica y responden en un test funcional contra la línea celular leucémica K562 con la expresión en la superficie de la proteína de membrana asociada al lisosoma 1 (LAMP-1, CD107a).

evorpaceptum #
evorpacept

human signal-regulatory protein alpha (Sirp- α , tyrosine-protein phosphatase non-receptor type substrate 1, inhibitory receptor SHPS-1) N-terminal fragment (1-119) variant (V>I⁶, A>I²⁷, I>F³¹, K>R⁵³, H>P⁵⁶, L>T⁶⁶, N>A⁸⁰) fused to a human immunoglobulin G1 C-terminal Fc fragment (120-345) (L>A¹³³, L>A¹³⁴, G>A¹³⁶, N>A¹⁹⁶, C-terminal K³⁴⁶ deleted), covalent disulfide bridged dimer, produced in Chinese hamster ovary (CHO) cells, glycoform alfa;

human signal-regulatory protein alpha (SIRP α , tyrosine-protein phosphatase non-receptor type substrate 1, inhibitory receptor SHPS-1) [V⁶>I, A²⁷>I, I³¹>F, K⁵³>R, H⁵⁶>P, L⁶⁶>T, N⁸⁰>A]-mutant, N-terminal (1-119)-fragment [binding domain for CD47 (inhibitor of phagocytosis by macrophages)], fused to a human immunoglobulin G1 C-terminal Fc fragment (CH2-CH3-CHS domains) [*Homo sapiens* IGHG1*03 (hinge (120-129, N-terminal hinge residues EPKSC deleted), CH2 L¹³³>A, L¹³⁴>A, G¹³⁶>A, N¹⁹⁶>A (130-239), CH3 (240-344), CHS K³⁴⁶>del (345))] (120-345), dimer (125-125':128-128')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

évorpacept

fragment N-terminal (1-119) de la protéine humaine de régulation du signal alpha (Sirp- α , substrat 1 de la tyrosine-protéine-phosphatase de type non-récepteur, récepteur inhibiteur SHPS-1) variant (V>I⁶, A>I²⁷, I>F³¹, K>R⁵³, H>P⁵⁶, L>T⁶⁶, N>A⁸⁰) fusionné à un fragment Fc C-terminal de l'immunoglobuline G1 humaine (120-345) (L>A¹³³, L>A¹³⁴, G>A¹³⁶, N>A¹⁹⁶, C-terminal K³⁴⁶ supprimé), dimère covalent à pont disulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa;

protéine humaine de régulation de signal alpha (SIRP α , substrat 1 de type non-récepteur de la tyrosine-protéine phosphatase, récepteur inhibiteur SHPS-1), [V⁶>I, A²⁷>I, I³¹>F, K⁵³>R, H⁵⁶>P, L⁶⁶>T, N⁸⁰>A]-mutant, fragment N-terminal (1-119) [domaine se liant au CD47 (inhibiteur de la phagocytose par les macrophages)], fusionnée au fragment Fc C-terminal de l'immunoglobuline G1 (domaines CH2-CH3-CHS) [*Homo sapiens* IGHG1*03 (charnière (120-129, sans les résidus N-terminaux EPKSC), CH2 L¹³³>A, L¹³⁴>A, G¹³⁶>A, N¹⁹⁶>A (130-239), CH3 (240-344), CHS K³⁴⁶>del (345))] (120-345), dimère (125-125':128-128')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

evorpacept

proteína reguladora de señal alfa humana (Sirp- α , sustrato 1 de tipo no-receptor de la tirosina-proteína fosfatasa, receptor inhibidor SHPS-1) fragmento terminal N (1-119) variante (V>I6, A>I27, I>F31, K>R53, H>P56, L>T66, N>A80) fusionada con el fragment Fc del terminal C de la inmunoglobulina humana G1 (120-345) (L>A¹³³, L>A¹³⁴, G>A¹³⁶, N>A¹⁹⁶, terminal C K³⁴⁶ eliminado), dímero covalente acortado disulfuro, producido en células ováricas de hámster chino (CHO), glicofoma alfa;

proteína reguladora de señal alfa, humana (SIRP α , sustrato 1 de tipo no-receptor de la tirosina-proteína fosfatasa, receptor inhibidor SHPS-1), [V⁶>I, A²⁷>I, I³¹>F, K⁵³>R, H⁵⁶>P, L⁶⁶>T, N⁸⁰>A]-mutante, fragmento N-terminal (1-119) [dominio unido al CD47 (inhibidor de la fagocitosis por los macrófagos)], fusionada con el fragmento Fc C-terminal de la inmunoglobulina G1 (dominios CH2-CH3-CHS) [*Homo sapiens* IGHG1*03 (bisagra (120-129, sin residuos N-terminales EPKSC), CH2 L¹³³>A, L¹³⁴>A, G¹³⁶>A, N¹⁹⁶>A (130-239), CH3 (240-344), CHS K³⁴⁶>del (345))] (120-345), dímero (125-125':128-128')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), glicofoma alfa

Sequence / Séquence / Secuencia	
EEELQIIQPD KSVLVAAGET ATLRCTITSL F VPVGIQWFR GAGPGRRELIY	50
NQ R EC F FRPV TTVSD T TKRN NMDFSI R IG A ITPADAGTYI CVKFRKGSFD	100
DVEFKSGAGT ELSVRAK F SD K THTC P PC P A F E A A C A P SV F L FP P K P K D T L	150
M IS R T F EV T C V VVDV S HED F E VKFNW I VD G V EVH N AK T K P R EEQ F A S T Y R	200
V VS V LT V L H Q D WLN G K E Y K C K VS N KAL P AP I E K T I S K A G K Q PRE F Q V Y T L	250
P FS R EEM T KN Q VSL T CL V KG F Y F SD I AVE A E SN G Q P EN N Y K T T PF V L D SD	300
G S F FL Y SK L T V DK S R W Q G GN V F S CS V M H EA L HN H Y T Q K SL S LS P G	345

Mutation / Mutation / Mutación
V6, 6'>**I**, A27, 27'>**I**, I31, 31'>**E**, K53, 53'>**R**, H56, 56'>**P**, L66, 66'>**T**, N80, 80'>**A**; L133, 133'>**A**, L134, 134'>**A**, G136, 136'>**A**, N196, 196'>**A**, K346, 346'>del

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-chain 25-91' 160-220' 266-324'
25-91' 160'-220' 266'-324'
Inter-chain 125-125' 128-128'
N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
none / aucun / ninguna (N196,196'>A)
O-glycosylation sites / Sites de O-glycosylation / Posiciones de O-glicosilación
S119, S119' (GalNAc, HexNAc-Hex-NeuAc)

fasedienolum

fasedienol

fasédiénol

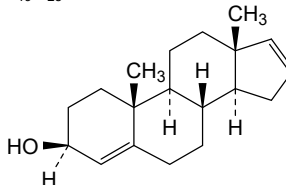
fasedienol

androsta-4,16-dien-3 β -ol

androsta-4,16-dién-3 β -ol

androsta-4,16-dien-3 β -ol

C₁₉H₂₈O



- gamma1 heavy chain anti-FGFR1 (1"-446") [VH (*Homo sapiens* IGHV3-66*01 (86.6%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.9] (26-33.51-58.97-105)) (1"-116") -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, G1v30 CH2 N84.4>G, G1v32 CH3 W22 (CH1 R120>K (213) (117"-214"), hinge 1-15 (215"-229"), CH2 N84.4>G (296) (230"-339"), CH3 E12 (355), M14 (357), T22>W (365) (340"-444"), CHS (445"-446")) (117"-446")), (219"-214")-disulfide with kappa light chain anti-FGFR1 (1"-214") [V-KAPPA (*Homo sapiens* IGKV1-39*01 (89.5%) -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 (229-225":232-228")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, non-glycosylated
- fazpilodémab immunoglobuline G1-kappa, anti-[*Homo sapiens* KLB (klotho bêta, b-Klotho)] et anti-[*Homo sapiens* FGFR1 (récepteur 1 du facteur de croissance des fibroblastes, FLT2, KAL2)], anticorps monoclonal, bispécifique;
chaîne lourde gamma1 anti-KLB (1-450) [VH (*Homo sapiens* IGHV3-66*01 (77.3%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.14] (26-33.51-58.96-109)) (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, G1v30 CH2 N84.4>G, G1v33 CH3 S22, A24, V86 (CH1 R120>K (217) (121-218), charnière 1-15 (219-233), CH2 N84.4>G (300) (234-343), CH3 E12 (359), M14 (361), T22>S (369), L24>A (371), Y86>V (410) (344-448), CHS (449-450)) (121-450)], (223-218')-disulfure avec la chaîne légère kappa anti-KLB (1'-218') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV3-5*01 (81.8%) -IGKJ1*01 (83.3%) G120>Q (104), L124>V (108))/*Homo sapiens* IGKV4-1*01 (79.2%) -IGKJ1*01 (100%), CDR-IMGT [10.3.9] (27-36.54-56.93-101)) (1'-111') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218')];
chaîne lourde gamma1 anti-FGFR1 (1"-446") [VH (*Homo sapiens* IGHV3-66*01 (86.6%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.9] (26-33.51-58.97-105)) (1"-116") -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, G1v30 CH2 N84.4>G, G1v32 CH3 W22 (CH1 R120>K (213) (117"-214"), charnière 1-15 (215"-229"), CH2 N84.4>G (296) (230"-339"), CH3 E12 (355), M14 (357), T22>W (365) (340"-444"), CHS (445"-446")) (117"-446")), (219"-214")-disulfure avec la chaîne légère kappa anti-FGFR1 (1"-214") [V-KAPPA (*Homo sapiens* IGKV1-39*01 (89.5%) -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 (229-225":232-228")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, non-glycosylé
- fazpilodemab inmunoglobulina G1-kappa, anti-[*Homo sapiens* KLB (klotho beta, b-Klotho)] y anti-[*Homo sapiens* FGFR1 (receptor 1 del factor de crecimiento de los fibroblastos, FLT2, KAL2)], anticuerpo monoclonal, biespecifico;
cadena pesada gamma1 anti-KLB (1-450) [VH (*Homo sapiens* IGHV3-66*01 (77.3%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.14] (26-33.51-58.96-109)) (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, G1v30 CH2 N84.4>G, G1v33 CH3 S22, A24, V86 (CH1 R120>K (217) (121-218), bisagra 1-15 (219-233), CH2 N84.4>G (300) (234-343), CH3 E12 (359), M14 (361), T22>S (369), L24>A (371), Y86>V (410) (344-448), CHS (449-450)) (121-450)], (223-218')-disulfuro con la cadena ligera kappa anti-KLB (1'-218') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV3-5*01 (81.8%) -IGKJ1*01 (83.3%) G120>Q (104), L124>V (108))/*Homo sapiens* IGKV4-1*01 (79.2%) -IGKJ1*01 (100%), CDR-IMGT [10.3.9] (27-36.54-56.93-101)) (1'-111') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218')];

cadena pesada gamma1 anti-FGFR1 (1^o-446^o) [VH (*Homo sapiens* IGHV3-66*01 (86.6%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.9] (26-33.51-58.97-105))] (1^o-116^o) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, G1v30 CH2 N84.4>G, G1v32 CH3 W22 (CH1 R120>K (213) (117^o-214^o), bisagra 1-15 (215^o-229^o), CH2 N84.4>G (296) (230^o-339^o), CH3 E12 (355), M14 (357), T22>W (365) (340^o-444^o), CHS (445^o-446^o))] (117^o-446^o); (219^o-214^o)-disulfuro con la cadena ligera kappa anti-FGFR1 (1^o-214^o) [V-KAPPA (*Homo sapiens* IGKV1-39*01 (89.5%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97))] (1^o-107^o) -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108^o-214^o)]; dimère (229-225^o:232-228^o)-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, no glicosilado

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

```
EVQLVESGGG LVQPGGSLRL SCAASDFSLT TYGVHWVRQA PGKGLEWLVG 50
IWSGGSTDYN AAFISRLTIS KDNSKNTVYL QMNSLRAEDT AVYICARDYG 100
STYVDAIDYW GQGTLVTVSS ASTKGPSVFP LAFSSKSTSG GTAALGCLVK 150
DYFPEFVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKRVFP KSCDKHTCP PCFAPPELLGG PSVFLFPPKP 250
KDTLMISRTF EIVTCVVVDVH HEDPEVKFNW YVDGVEVHNA KTKPREEQYG 300
STYRVVSVLT VLGQDQLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSREE MTKNQVSLSC AVKGFYPSDI AVEWESNGQP ENNYKTTTTPV 400
LSDSGSFFLV SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK 450
```

Heavy chain / Chaîne lourde / Cadena pesada (anti-FGFR1)

```
EVQLVESGGG LVQPGGSLRL SCAASGFTFT SNIYSWVRQA PGKGLEWVGE 50
IDPYDGDITY ADSVKGRFTI SADTSKNTAY LQMNSLRAED TAVYVCATGT 100
DMVDYWGQGT LVTVSSASTK GPSVFFPLAS SKSTSGGTA LGCLVKDYFP 150
EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVVTVPSS SLGTQTYICN 200
VNHKPSNTKV DKKVEPKSCD KHTCPCCPA BELLGGPSVF LFPPKPKDTL 250
MISRTPEVTC VVVDVSHEDP EVKFNWYVDG VEVHNAKTKP REEQYGSTYR 300
VSVSLTVLHQ DMLNGKEYKC KVSNKALPAP IEKTIKSKAQ QPREPQVYTL 350
PPSREEMTKN QVSLWCLVKG FYPDSIAVEW ESNQGPENNY KTTTPVLDS 400
GSFFLYSKLT VDKSRWQQGN VFSCSVHMEA LHNHYTQKSL SLSPGK 446
```

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

```
DIVLTQSPDS LAVSLGERAT INCREASESVE SYGNRYMTWY QQKFGQPPKL 50
LIYRAANLQS GVPDRFSGSG SGTDFTLTIS SLQAEDVAVY YCQQSNEDPW 100
TFGQGTGKVEI KRTVAAPSVF IFPPSDEQLK SGTASVCLL NNFYPREAKV 150
QWKVDNALQS GNSQESVTEQ DSKDSTYLSL STLTLSKADY ERHKVYACEV 200
THQGLSSFPV KSFNRGEC 218
```

Light chain / Chaîne légère / Cadena ligera (anti-FGFR1)

```
DIQMTQSPSS LSASVGDRTV ITCRASQDVS TAVAWYQQKPK GKAPKLLIYS 50
ASFLYSGVPS RFSGSGSGTD FTLTISLQEP EDFATYTCQQ SYTTPPTFGQ 100
GTKVEIKRVT AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYLSLSTLT LSKADYEKHK VYACEVTHQG 200
LSSPFTKSFN RGEC 214
```

Post-translational modifications

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

Intra-H (C23-C104) 22-95 147-203 264-324 370-428

22^o-96^o 143^o-199^o 260^o-320^o 366^o-424^o

Intra-L (C23-C104) 23^o-92^o 138^o-198^o

23^o-88^o 134^o-194^o

Inter-H-L (h 5-CL 126) 223-218^o 219^o-214^o

Inter-H-H (h 11, h 14) 229-225^o 232-228^o

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

H CH2 N84.4>G (G1v30): 300, 296^o

Aglycosylated / aglycosylé / aglicosilado

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

H CHS K2: 450, 446^o

feniralstatum

feniralstat

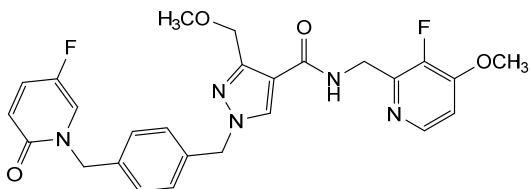
N-[(3-fluoro-4-methoxypyridin-2-yl)methyl]-1-({4-[(5-fluoro-2-oxopyridin-1(2H)-yl)methyl]phenyl)methyl)-3-(methoxymethyl)-1H-pyrazole-4-carboxamide

féniralstat

N-[(3-fluoro-4-méthoxypyridin-2-yl)méthyl]-1-({4-[(5-fluoro-2-oxopyridin-1(2H)-yl)méthyl]phényl)méthyl)-3-(méthoxyméthyl)-1H-pyrazole-4-carboxamide

feniralstat

N-[(3-fluoro-4-metoxipiridin-2-il)metil]-1-({4-[(5-fluoro-2-oxopiridin-1(2*H*)-il)metil]fenil}metil)-3-(metoximetil)-1*H*-pirazol-4-carboxamida

 $C_{26}H_{25}F_2N_5O_4$


fidrisertibum

fidrisertib

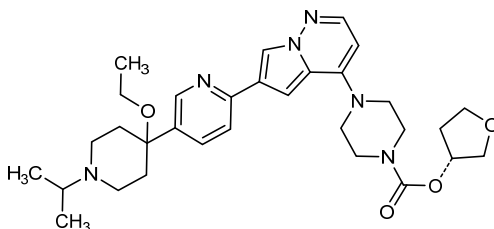
(3*R*)-oxolan-3-yl 4-(6-{5-[4-ethoxy-1-(propan-2-yl)piperidin-4-yl]pyridin-2-yl}pyrrolo[1,2-*b*]pyridazin-4-yl)piperazine-1-carboxylate

fidrisertib

4-(6-{5-[4-éthoxy-1-(propan-2-yl)pipéridin-4-yl]pyridin-2-yl}pyrrolo[1,2-*b*]pyridazin-4-yl)pipérazine-1-carboxylate de (3*R*)-oxolan-3-yle

fidrisertib

4-(6-{5-[4-etoxi-1-(propan-2-il)piperidin-4-il]piridin-2-il}pirrolo[1,2-*b*]pidridazin-4-il)piperazina-1-carboxilato de (3*R*)-oxolan-3-ilo

 $C_{31}H_{42}N_6O_4$


fipaxalparantum

fipaxalparant

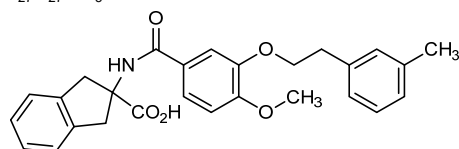
2-[4-methoxy-3-[2-(3-methylphenyl)ethoxy]benzamido]-2,3-dihydro-1*H*-indene-2-carboxylic acid

fipaxalparant

acide 2-[4-méthoxy-3-[2-(3-méthylphényl)éthoxy]benzamido]-2,3-dihydro-1*H*-indène-2-carboxylique

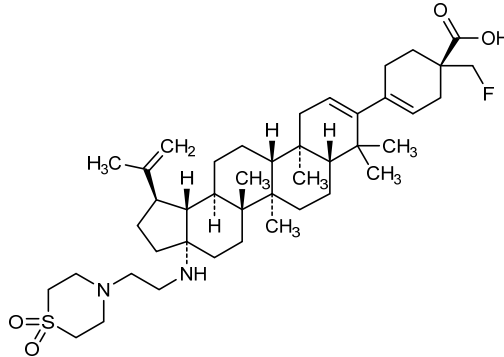
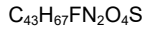
fipaxalparant

ácido 2-[3-[2-(3-metilfenil)etoxi]-4-metoxibenzamido]-2,3-dihidro-1*H*-indeno-2-carboxílico

 $C_{27}H_{27}NO_5$


fipravirimum

- fipravirimat (1*R*)-4-[17-[[2-(1,1-dioxo-1λ⁶-thiomorpholin-4-yl)éthyl]amino]-28-norlupa-2,20(29)-dién-3-yl]-1-(fluorométhyl)cyclohex-3-ène-1-carboxylique acid
- fipravirimat acide (1*R*)-4-[17-[[2-(1,1-dioxo-1λ⁶-thiomorpholin-4-yl)éthyl]amino]-28-norlupa-2,20(29)-dién-3-yl]-1-(fluorométhyl)cyclohex-3-ène-1-carboxylique
- fipravirimat ácido (1*R*)-4-[17-[[2-(1,1-dioxo-1λ⁶-tiomorfolin-4-il)etil]amino]-28-norlupa-2,20(29)-dién-3-il]-1-(fluorometil)ciclohex-3-eno-1-carboxílico



fiztasovimabum #

- fiztasovimab immunoglobulin G1-lambda2, anti-[human betaherpesvirus 5 (HHV-5, human cytomegalovirus, HCMV) envelope glycoprotein B (gB) domain 1 (AD-1)], *Homo sapiens* monoclonal antibody; gamma1 heavy chain *Homo sapiens* (1-454) [VH (*Homo sapiens* IGHV4-34*01 (93.8%) -(IGHD) -IGHJ6*04 (93.8%), CDR-IMGT [8.7.18] (26-33.51-57.96-113)) (1-124) -*Homo sapiens* IGHG1*07p (100%), G1m17,1,2 (CH1 K120 (221) (125-222), hinge 1-15 (223-237), CH2 (238-347), CH3 D12 (363), L14 (365), G110 (438) (348-452), CHS (453-454)) (125-454)], (227-215')-disulfide with lambda2 light chain *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV1-47*01 (93.9%) -IGLJ1*01 (100%), CDR-IMGT [8.3.11] (26-33.51-53.90-100)) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')]; dimer (233-233":236-236")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1SV, glycoform alfa
- fiztasovimab immunoglobuline G1-lambda2, anti-[domaine 1 (AD-1) de la glycoprotéine d'enveloppe B (gB) du bêtaherpèsvirus humain 5 (HHV-5, cytomégalovirus humain, HCMV)], anticorps monoclonal *Homo sapiens*; chaîne lourde gamma1 *Homo sapiens* (1-454) [VH (*Homo sapiens* IGHV4-34*01 (93.8%) -(IGHD) -IGHJ6*04 (93.8%), CDR-IMGT [8.7.18] (26-33.51-57.96-113)) (1-124) -*Homo sapiens* IGHG1*07p (100%), G1m17,1,2 (CH1 K120 (221) (125-222), charnière 1-15 (223-237), CH2 (238-347), CH3 D12 (363), L14 (365), G110 (438) (348-452), CHS (453-454)) (125-454)], (227-215')-disulfure avec la chaîne légère lambda2 *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV1-47*01 (93.9%) -IGLJ1*01 (100%), CDR-IMGT [8.3.11] (26-33.51-53.90-100)) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')]; dimère (233-233":236-236")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1SV, glycoforme alfa

fiztasovimab

inmunoglobulina G1-lambda2, anti-[dominio 1 (AD-1) de la glicoproteína de cubierta B (gB) del betaherpesvirus humano 5 (HHV-5, citomegalovirus humano, HCMV)], anticuerpo monoclonal *Homo sapiens*;

cadena pesada gamma1 *Homo sapiens* (1-454) [VH (*Homo sapiens* IGHV4-34*01 (93.8%) -(IGHD) -IGHJ6*04 (93.8%), CDR-IMGT [8.7.18] (26-33.51-57.96-113)) (1-124) -*Homo sapiens* IGHG1*07p (100%), G1m17,1,2 (CH1 K120 (221) (125-222), bisagra 1-15 (223-237), CH2 (238-347), CH3 D12 (363), L14 (365), G110 (438) (348-452), CHS (453-454)) (125-454)], (227-215')-disulfuro con la cadena ligera lambda2 *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV1-47*01 (93.9%) -IGLJ1*01 (100%), CDR-IMGT [8.3.11] (26-33.51-53.90-100)) (1'-110') -*Homo sapiens* IGLC2*01 (100%) (111'-216')]; dímero (233-233":236-236")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1SV, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

QVQLQWAGG LLKPSSETLSL TCAVYGGSFY GYYWGWIQQP PCKGLEWIGE 50
 INHSGSANSN PSLKSRVTMS VDTSKNQFSL KVSSVTAADT AVYFCARVTR 100
 DLEWIPGDVY MDVWKGKTTV TVSSASTKGP SVFFPLAPSSK STSGGTAALG 150
 CLVKDYFPEP VTVSWNSGAL TSGVHTFFAV LQSSGLYSLV SVVTVFSSSL 200
 GTQTYICNVN HKPSNTRKVDK KVEPKSCDKT HTPCPCPAPE LLGGPSVFLF 250
 PPKPKDTLMI SRTPEVTCVV VDVSHEDPEV KFNWYVDGVE VHNKTKFRE 300
 EQYNSTYRVV SVLTVLHQDW LNKKEYKCKV SNKALPAPIE KTISKAKGQP 350
 REPQVYTLPP SRDELTKNQV SLTCLVKGFY PSDIAEVNES NGQPENNYKT 400
 TTPVLDSDGS FFLYSKLTVD KSRWQQGNVF SCVMEHGLH NHYTQKSLSL 450
 SPGK 454

Light chain / Chaîne légère / Cadena ligera

QSVLTQPPSA SGTPGQRVSI SCSGSLSNIG TNYVYVYQQL PGTAPKLLIF 50
 KNNQRPSGVF DRFSGSKSGT SASLAISGLR SEDEADYCA AWDDSLNGYV 100
 FGGTKVTVL GQPKANPTVT LFPPSSEELQ ANKATLVCLI SDFYGAVTY 150
 AWKADGSPVK AGVETTRPSK QSNNKYAASS YLSLTPQWK SHRSYSCQVT 200
 HEGSTVEKTV APTECS 216

Post-translational modifications

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

Intra-H (C23-C104) 22-95 151-207 268-328 374-432

22"-95" 151"-207" 268"-328" 374"-432"

Intra-L (C23-C104) 22-89" 138"-197"

22"-89" 138"-197"

Inter-H-L (h 5-CL 126) 227-215' 227"-215"

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

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

Q > pyroglutamyl (pE, 5-oxoprolyl)

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

H CHS K2: 454, 454"

florquinitaum (¹⁸F)

florquinitau (¹⁸F)

6-(¹⁸F)fluoro-3-(1*H*-pirrolo[2,3-*c*]piridin-1-yl)isoquinolin-5-amina

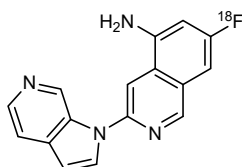
florquinitau (¹⁸F)

6-(¹⁸F)fluoro-3-(1*H*-pirrolo[2,3-*c*]piridin-1-yl)isoquinoléin-5-amina

florquinitau (¹⁸F)

6-(¹⁸F)fluoro-3-(1*H*-pirrolo[2,3-*c*]piridin-1-il)isoquinolein-5-amina

C₁₆H₁₁¹⁸FN₄



frexalimabum

frexalimab

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)], monoclonal antibody; gamma1 heavy chain (1-450) [VH Musmus/Homsap (*Mus musculus* IGHV3-8*02 (82.3%) -(IGHD) -IGHJ2*01 (100%)/*Homo sapiens* IGHV4-59*11 (81.2%) -(IGHD) -IGHJ4*01 (86.7%) L123>T (115), V124>L (116), CDR-IMGT [8.7.14] (26-33.51-57.96-109)) (1-120) -*Homo sapiens* IGHG1*01, G1m17.1, G1v20 CH2 A105 (CH1 K120 (217) (121-218), hinge 1-15 (219-233), CH2 E31>R (272), K105>A (325) (234-343), CH3 D12 (359), L14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfide with kappa light chain (1'-214') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV6-13*01 (83.2%) -IGKJ2*01 (100%)/*Homo sapiens* IGKV1-33*01 (76.8%) -IGKJ2*01 (91.7%) Q120>G (100), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (229-229'':232-232'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, derived from the cell line CHO-DXB11, glycoform alfa

frexalimab

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; chaîne lourde gamma1 (1-450) [VH Musmus/Homsap (*Mus musculus* IGHV3-8*02 (82.3%) -(IGHD) -IGHJ2*01 (100%)/*Homo sapiens* IGHV4-59*11 (81.2%) -(IGHD) -IGHJ4*01 (86.7%) L123>T (115), V124>L (116), CDR-IMGT [8.7.14] (26-33.51-57.96-109)) (1-120) -*Homo sapiens* IGHG1*01, G1m17.1, G1v20 CH2 A105 (CH1 K120 (217) (121-218), charnière 1-15 (219-233), CH2 E31>R (272), K105>A (325) (234-343), CH3 D12 (359), L14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV6-13*01 (83.2%) -IGKJ2*01 (100%)/*Homo sapiens* IGKV1-33*01 (76.8%) -IGKJ2*01 (91.7%) Q120>G (100), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (229-229'':232-232'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), dérivant de la lignée cellulaire CHO-DXB11, glycoforme alfa

frexalimab

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 relacionada con el factor de necrosis tumoral, TRAP, CD154)], anticuerpo monoclonal; cadena pesada gamma1 (1-450) [VH Musmus/Homsap (*Mus musculus* IGHV3-8*02 (82.3%) -(IGHD) -IGHJ2*01 (100%)/*Homo sapiens* IGHV4-59*11 (81.2%) -(IGHD) -IGHJ4*01 (86.7%) L123>T (115), V124>L (116), CDR-IMGT [8.7.14] (26-33.51-57.96-109)) (1-120) -*Homo sapiens* IGHG1*01, G1m17.1, G1v20 CH2 A105 (CH1 K120 (217) (121-218), bisagra 1-15 (219-233), CH2 E31>R (272), K105>A (325) (234-343), CH3 D12 (359), L14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfuro con la cadena ligera kappa (1'-214') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV6-13*01 (83.2%) -IGKJ2*01 (100%)/*Homo sapiens* IGKV1-33*01 (76.8%) -IGKJ2*01 (91.7%) Q120>G (100), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (229-229'':232-232'')-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular derivada de CHO-DXB11, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada
 EVQLQESGGPG LVKPSSETLSL TCTVSGDSIT NGFWIWRKP PGNKLEYMGY 50
 ISYSGSTYYN PSLKSRISIS RDTSKNQFSL KLSVSTAADT GVVYCAIRSY 100
 GRTPYYFDYW GQGTTLTVSS ASTKGPSVFP LAPSSKSTSG GTAALGLVK 150
 DYFPEPVTVS WNSGALTSVG HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
 YICNVNHPKS NTKVDKKAEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP 250
 KDTLMSRTP EVTCTVVVDVS HRDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
 STYRVVSVLT VLHQDWLNGK EYKCAVSNKA LPAPIETKIS KAKGQPREPQ 350
 VYTLPPSRDE LTRKQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTFPV 400
 LDDSGSFFLY SKLTVDKSRW QQGNVFSVSV MHEALHNHYT QKSLSLSPGK 450

Light chain / Chaîne légère / Cadena ligera
 DIVMTQSPSF LSASVGDRTV ITCKASSNLG HAVAWYQQKPK GKSPKLLIYS 50
 ASNRYTQVDP RFGSGSGSDT FTLTISSLPQ EDFADYFCQQ YDDYPTTFGG 100
 GTKLEIKRTV AAPSVEIFPP SDEQLKSGTA SVVCLLNIFY PREAKVQWKV 150
 DNALQSGNSQ ESVTEQDSKD STYLSLSTLT LSKADYEKHK VYACEVTHQG 200
 LSSFPVTKSFN RGEK 214

Post-translational modifications

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

22"-95" 147"-203" 264"-324" 370"-428"

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"

gallium (⁶⁸Ga) boclatixafortidumgallium (⁶⁸Ga) boclatixafortide

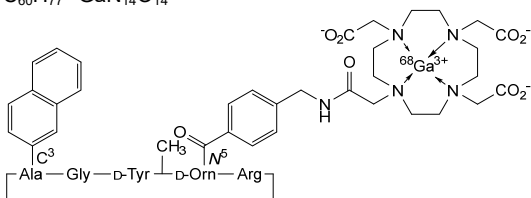
(1,5-anhydro{3-(naphthalen-2-yl)-L-alanylglycyl-D-tyrosyl-N²-methyl-N⁵-[4-((2-[4,7,10-tris(carboxylato-κ-O-methyl)-1,4,7,10-tetraazacyclododecan-1-yl-κ⁴N¹,N⁴,N⁷,N¹⁰]acetamido-κO)methyl)benzoyl]-D-ornithyl-L-arginine)})(⁶⁸Ga)gallium

gallium (⁶⁸Ga) boclatixafortide

(1,5-anhydro{3-(naphtalén-2-yl)-L-alanylglycyl-D-tyrosyl-N²-méthyl-N⁵-[4-((2-[4,7,10-tris(carboxylato-κ-O-méthyl)-1,4,7,10-tétraazacyclododécane-1-yl-κ⁴N¹,N⁴,N⁷,N¹⁰]acétamido-κO)méthyl)benzoyl]-D-ornithyl-L-arginine)})(⁶⁸Ga)gallium

galio (⁶⁸Ga) boclatixafortida

(1,5-anhidro{3-(naftalen-2-il)-L-alanilglicil-D-tirosil-N²-metil-N⁵-[4-((2-[4,7,10-tris(carboxilato-κO-metil)-1,4,7,10-tetraazaciclododecan-1-il-κ⁴N¹,N⁴,N⁷,N¹⁰]acetamido-κO)metil)benzoil]-D-ornitil-L-arginina)})(⁶⁸Ga)galio

**garsorasibum**

garsorasib

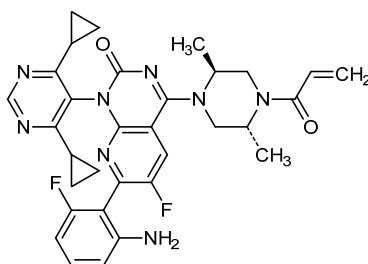
7-(2-amino-6-fluorophenyl)-1-(4,6-dicyclopropylpyrimidin-5-yl)-4-[(2*S*,5*R*)-2,5-dimethyl-4-(prop-2-enoyl)piperazin-1-yl]-6-fluoropyrido[2,3-*d*]pyrimidin-2(1*H*)-one

garsorasib

7-(2-amino-6-fluorophényl)-1-(4,6-dicyclopropylpyrimidin-5-yl)-4-[(2*S*,5*R*)-2,5-diméthyl-4-(prop-2-énoyl)pipérazin-1-yl]-6-fluoropyrido[2,3-*d*]pyrimidin-2(1*H*)-one

garsorasib

7-(2-amino-6-fluorofenil)-1-(4,6-diciclopropilpirimidin-5-il)-4-[(2*S*,5*R*)-2,5-dimetil-4-(prop-2-enoil)piperazin-1-il]-6-fluoropirido[2,3-*d*]pirimidin-2(1*H*)-ona

$$C_{32}H_{32}F_2N_8O_2$$


gebasaxturevum

gebasaxturev

oncolytic genetically unmodified human
Coxsackievirus A21 (CVA21)

gébasaxturev

virus Coxsackie A21 (CVA21) humain oncolytique
génétiquement non modifié

gebasaxturev

virus Coxsackie A21 (CVA21) oncolítico humano sin
ninguna modificación genética.

gefurulimabum #

gefurulimab

immunoglobulin single chain VH-VH', anti-[*Homo sapiens* C5 (complement C5, CPAMD4, C5a, C5b)] and anti-[*Homo sapiens* ALB (albumin, human serum albumin, HAS)], humanized monoclonal antibody single chain, bispecific;
IG single chain VH-VH' anti-ALB and anti-C5 chimeric (1-264) [VH anti-ALB Vicpac/Homsap (*Vicugna pacos* IGHV3-3*01 (80.6%) -(IGHD) -IGHJ3*01 (92.3%)/*Homo sapiens* IGHV3-23*04 (79.4%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.8.17] (26-33.51-58.96-112)) (1-123) -15-mer bis(tetraglycyl-alanyl)-tetraglycyl-seryl linker (124-138) -VH' anti-C5 Vicpac/Homsap (*Vicugna pacos* IGHV3-3*01 (82.7%) -(IGHD) -IGHJ4*01 (92.9%) Q123>L (259)/*Homo sapiens* IGHV3-23*04 (81.4%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.8.19] (164-171.189-196.235-253)) (139-264)], produced in Chinese hamster ovary (CHO) cells, non-glycosylated

géfurulimab

immunoglobuline à chaîne unique VH-VH', anti-[*Homo sapiens* C5 (C5 complément, CPAMD4, C5a, C5b)] et anti-[*Homo sapiens* ALB (albumine, sérum albumine humaine, SAH)], anticorps monoclonal à chaîne unique humanisé, bispécifique;

	<p>IG à chaîne unique VH-VH' anti-ALB et anti-C5 chimérique (1-264) [VH anti-ALB Vicpac/Homsap (<i>Vicugna pacos</i> IGHV3-3*01 (80.6%) -(IGHD) -IGHJ3*01 (92.3%)/<i>Homo sapiens</i> IGHV3-23*04 (79.4%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.8.17] (26-33.51-58.96-112)) (1-123) -15-mer bis(tétraglycyl-alanyl)-tétraglycyl-séryl linker (124-138) -VH' anti-C5 Vicpac/Homsap (<i>Vicugna pacos</i> IGHV3-3*01 (82.7%) -(IGHD) -IGHJ4*01 (92.9%) Q123>L (259)/<i>Homo sapiens</i> IGHV3-23*04 (81.4%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.8.19] (164-171.189-196.235-253)) (139-264)], produit dans des cellules ovariennes de hamster chinois (CHO), non-glycosylé</p>																																				
<p>gefurulimab</p>	<p>immunoglobulina con una cadena única VH-VH', anti-[<i>Homo sapiens</i> C5 (C5 complemento, CPAMD4, C5a, C5b)] y anti-[<i>Homo sapiens</i> ALB (albúmina, albúmina sérica humana, SAH)], anticuerpo monoclonal con cadena única humanizada, biespecífica ; IG con cadena única VH-VH' anti-ALB y anti-C5 quimérica (1-264) [VH anti-ALB Vicpac/Homsap (<i>Vicugna pacos</i> IGHV3-3*01 (80.6%) -(IGHD) -IGHJ3*01 (92.3%)/<i>Homo sapiens</i> IGHV3-23*04 (79.4%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.8.17] (26-33.51-58.96-112)) (1-123) -15-mer bis(tetraglicil-alanyl)-tetraglicil-seril linker (124-138) -VH' anti-C5 Vicpac/Homsap (<i>Vicugna pacos</i> IGHV3-3*01 (82.7%) -(IGHD) -IGHJ4*01 (92.9%) Q123>L (259)/<i>Homo sapiens</i> IGHV3-23*04 (81.4%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.8.19] (164-171.189-196.235-253)) (139-264)], producido en las células ováricas de hámster chino (CHO), no glicosilado</p> <p>Sequence / Séquence / Secuencia</p> <table border="0"> <tr> <td>EVQLVESGGG</td> <td>LVKPGGSLRL</td> <td>SCAASGRPVV</td> <td>NYAAAWFRQA</td> <td>PKEREFVSA</td> <td>50</td> </tr> <tr> <td>INWQRTATYA</td> <td>DSVKGRTIS</td> <td>RDNAKNSLYL</td> <td>QMNSLRAEDT</td> <td>AVVYCAAVFR</td> <td>100</td> </tr> <tr> <td>VVAPKTKQYDY</td> <td>DYWGQGLTLV</td> <td>VSSGGGGAGG</td> <td>GGAGGGGSEV</td> <td>QLVESGGGLV</td> <td>150</td> </tr> <tr> <td>QPGGSLRLSC</td> <td>AASGRAHSDY</td> <td>AMAWFRQAPG</td> <td>QEREFVAVIG</td> <td>WSGGDTLYAD</td> <td>200</td> </tr> <tr> <td>SVRGRFTNSR</td> <td>DNSKNTLYLQ</td> <td>MNSLRAEDTA</td> <td>VVYCAARQGG</td> <td>YIYSSMRSDS</td> <td>250</td> </tr> <tr> <td>YDYWGQGLTV</td> <td>TVSS</td> <td></td> <td></td> <td></td> <td>264</td> </tr> </table> <p>Post-translational modifications</p> <p>Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro Intra-chain (C23 C104) 22-95 160-234</p> <p>No N-glycosylation sites / pas de sites de N-glycosylation / ninguna posición de N-glicosilación Aglycosylated / aglycosylé / aglicosilado</p>	EVQLVESGGG	LVKPGGSLRL	SCAASGRPVV	NYAAAWFRQA	PKEREFVSA	50	INWQRTATYA	DSVKGRTIS	RDNAKNSLYL	QMNSLRAEDT	AVVYCAAVFR	100	VVAPKTKQYDY	DYWGQGLTLV	VSSGGGGAGG	GGAGGGGSEV	QLVESGGGLV	150	QPGGSLRLSC	AASGRAHSDY	AMAWFRQAPG	QEREFVAVIG	WSGGDTLYAD	200	SVRGRFTNSR	DNSKNTLYLQ	MNSLRAEDTA	VVYCAARQGG	YIYSSMRSDS	250	YDYWGQGLTV	TVSS				264
EVQLVESGGG	LVKPGGSLRL	SCAASGRPVV	NYAAAWFRQA	PKEREFVSA	50																																
INWQRTATYA	DSVKGRTIS	RDNAKNSLYL	QMNSLRAEDT	AVVYCAAVFR	100																																
VVAPKTKQYDY	DYWGQGLTLV	VSSGGGGAGG	GGAGGGGSEV	QLVESGGGLV	150																																
QPGGSLRLSC	AASGRAHSDY	AMAWFRQAPG	QEREFVAVIG	WSGGDTLYAD	200																																
SVRGRFTNSR	DNSKNTLYLQ	MNSLRAEDTA	VVYCAARQGG	YIYSSMRSDS	250																																
YDYWGQGLTV	TVSS				264																																
<p>gersizangitidum gersizangitide</p>	<p>collagen alpha-5(IV) chain (human collagen IV α-5 chain, COL4A5) (1484-1503)-peptide (1-20), [M¹⁴⁹⁰>A⁷, M¹⁴⁹³>A¹⁰, C¹⁴⁹⁵>I¹², N¹⁴⁹⁶>D¹³, N¹⁴⁹⁹>D¹⁶, C¹⁵⁰¹>I¹⁸]-modified, 20-amide; L-leucyl-L-arginyl-L-arginyl-L-phenylalanyl-L-seryl-L-threonyl-L-alanyl-L-prolyl-L-phenylalanyl-L-alanyl-L-phenylalanyl-L-isoleucyl-L-α-aspartyl-L-isoleucyl-L-asparaginyll-L-α-aspartyl-L-valyl-L-isoleucyl-L-asparaginyll-L-phenylalaninamide</p>																																				
<p>gersizangitide</p>	<p>chaîne alpha-5(IV) de collagène (chaîne α-5 de collagène IV humain, COL4A5), peptide 1484-1503 (1-20), [M¹⁴⁹⁰>A⁷, M¹⁴⁹³>A¹⁰, C¹⁴⁹⁵>I¹², N¹⁴⁹⁶>D¹³, N¹⁴⁹⁹>D¹⁶, C¹⁵⁰¹>I¹⁸]-modifié, 20-amide;</p>																																				

gersizangitida

L-leucyl-L-arginyl-L-arginyl-L-phénylalanil-L-seryl-L-thréonyl-L-alanyl-L-prolyl-L-phénylalanil-L-alanyl-L-phénylalanil-L-isoleucyl-L- α -aspartyl-L-isoleucyl-L-asparaginyL-L- α -aspartyl-L-valyl-L-isoleucyl-L-asparaginyL-L-phénylalaninamide

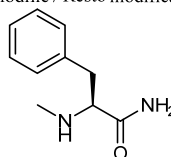
cadena alfa-5(IV) de colágeno (cadena α -5 de colágeno IV humano, COL4A5), péptido 1484-1503 (1-20), [M¹⁴⁹⁰>A⁷, M¹⁴⁹³>A¹⁰, C¹⁴⁹⁵>I¹², N¹⁴⁹⁶>D¹³, N¹⁴⁹⁹>D¹⁶, C¹⁵⁰¹>I¹⁸]-modificado, 20-amida; L-leucil-L-arginil-L-arginil-L-fenilalanil-L-seril-L-treonil-L-alanil-L-prolil-L-fenilalanil-L-alanil-L-fenilalanil-L-isoleucil-L- α -aspartil-L-isoleucil-L-asparaginyL-L- α -aspartil-L-valil-L-isoleucil-L-asparaginyL-L-fenilalaninamida

$$C_{111}H_{167}N_{29}O_{28}$$

Sequence / Séquence / Secuencia
LRRFSTAPFA FIDINDVINF 20

Modified residue / Résidu modifié / Resto modificado

$\frac{E}{20}$
L-Phenylalaninamide



gilmelisibum
gilmelisib

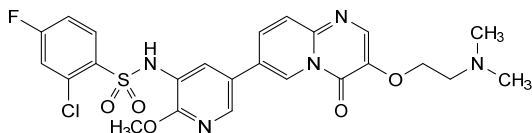
2-chloro-*N*-(5-{3-[2-(dimethylamino)ethoxy]-4-oxo-4*H*-pyrido[1,2-*a*]pyrimidin-7-yl]-2-methoxy-pyridin-3-yl)-4-fluorobenzene-1-sulfonamide

gilmélisib

2-chloro-*N*-(5-{3-[2-(diméthylamino)éthoxy]-4-oxo-4*H*-pyrido[1,2-*a*]pyrimidin-7-yl]-2-méthoxy-pyridin-3-yl)-4-fluorobenzène-1-sulfonamide

gilmelisib

2-cloro-*N*-(5-{3-[2-(dimetilamino)etoxi]-4-oxo-4*H*-pirido[1,2-*a*]pirimidin-7-il]-2-metoxipiridin-3-il)-4-fluorobenceno-1-sulfonamida

$$C_{24}H_{23}ClFN_5O_5S$$


golocdacimabum #
golocdacimab

immunoglobulin G1-lambda2, anti-[*Homo sapiens* OLR1 (oxidized low density lipoprotein receptor 1, LOX-1, SCARE1, CLEC8A)], *Homo sapiens* monoclonal antibody;

- gamma1 heavy chain *Homo sapiens* (1-459) [VH (*Homo sapiens* IGHV1-24*01 (93.8%) -(IGHD) - IGHJ6*01 (100%), CDR-IMGT [8.8.22] (26-33.51-58.97-118)) (1-129) -*Homo sapiens* IGHG1*03, G1m3, nG1m1, G1v39 CH2 F1.3, E1.2, S116 (CH1 R120 (226) (130-227), hinge 1-15 (228-242), CH2 L1.3>F (246), L1.2>E (247), P116>S (343) (243-352), CH3 E12 (368), M14 (370) (353-457), CHS (458-459)) (130-459)], (232-216')-disulfide with lambda2 light chain *Homo sapiens* (1'-217')] [V-LAMBDA (*Homo sapiens* IGLV1-40*02 (100%) -IGLJ3*02 (100%), CDR-IMGT [9.3.11] (26-34.52-54.91-101)) (1'-111') -*Homo sapiens* IGLC2*01 (100%) (112'-217')]; dimer (238-238":241-241")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa
- golocdacimab immunoglobuline G1-lambda2, anti-[*Homo sapiens* OLR1 (récepteur 1 de lipoprotéines de basse densité oxydées, LOX-1, SCARE1, CLEC8A)], anticorps monoclonal *Homo sapiens*;
chaîne lourde gamma1 *Homo sapiens* (1-459) [VH (*Homo sapiens* IGHV1-24*01 (93.8%) -(IGHD) - IGHJ6*01 (100%), CDR-IMGT [8.8.22] (26-33.51-58.97-118)) (1-129) -*Homo sapiens* IGHG1*03, G1m3, nG1m1, G1v39 CH2 F1.3, E1.2, S116 (CH1 R120 (226) (130-227), charnière 1-15 (228-242), CH2 L1.3>F (246), L1.2>E (247), P116>S (343) (243-352), CH3 E12 (368), M14 (370) (353-457), CHS (458-459)) (130-459)], (232-216')-disulfure avec la chaîne légère lambda2 *Homo sapiens* (1'-217')] [V-LAMBDA (*Homo sapiens* IGLV1-40*02 (100%) -IGLJ3*02 (100%), CDR-IMGT [9.3.11] (26-34.52-54.91-101)) (1'-111') -*Homo sapiens* IGLC2*01 (100%) (112'-217')]; dimère (238-238":241-241")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa
- golocdacimab inmunoglobulina G1-lambda2, anti-[*Homo sapiens* OLR1 (receptor 1 de lipoproteínas de baja densidad oxidadas, LOX-1, SCARE1, CLEC8A)], anticuerpo monoclonal *Homo sapiens*;
cadena pesada gamma1 *Homo sapiens* (1-459) [VH (*Homo sapiens* IGHV1-24*01 (93.8%) -(IGHD) - IGHJ6*01 (100%), CDR-IMGT [8.8.22] (26-33.51-58.97-118)) (1-129) -*Homo sapiens* IGHG1*03, G1m3, nG1m1, G1v39 CH2 F1.3, E1.2, S116 (CH1 R120 (226) (130-227), bisagra 1-15 (228-242), CH2 L1.3>F (246), L1.2>E (247), P116>S (343) (243-352), CH3 E12 (368), M14 (370) (353-457), CHS (458-459)) (130-459)], (232-216')-disulfuro con la cadena ligera lambda2 *Homo sapiens* (1'-217')] [V-LAMBDA (*Homo sapiens* IGLV1-40*02 (100%) -IGLJ3*02 (100%), CDR-IMGT [9.3.11] (26-34.52-54.91-101)) (1'-111') -*Homo sapiens* IGLC2*01 (100%) (112'-217')]; dímero (238-238":241-241")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada
 QVQLVQSGAE VKKPGASVKV SCKVSGYTLT ELSMHWVRQA PGKGLEWMGG 50
 FDPEDFKYHT HQKFGQGRVTM TEDITSTDTAY MELSSLRSED TAVYYCALVW 100
 GTQCGKGRGW DYYFGMDWVG QGTTVTVSSA STKGFVSFPL APSSKSTSGG 150
 TAAALGCLVKD YFPEPVTWSW NSGALTSGVH TFFAVLQSSG LYSLSVVTV 200
 PSSSLGTQTY IGVNHNKFSN TKVDRKVEPK SCDKTHTCPF CPAPEFEGGP 250
 SVFLFPPKPK DTLMIISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK 300
 TKPREEQYNS TYRVVSVLTV LHQDNLNGKE YCKKVSINKAL PASIEKTISK 350
 AKGQPREPQV YTLPPSREEM TKMQVSLTCL VKGFYPSDIA VEWESNGQPE 400
 NNYKTTTTPVL DSDGSFFLYS KLTVDKSRWQ QGNVFCSCVM HEALHNHYTQ 450
 KSLSLSPGK 459

Light chain / Chaîne légère / Cadena ligera
 QSVVTQPPSV SGAPGQRVTI SCTGSSSNIG AGYDVHWYQQ LFGTAPKLLI 50
 YGNSNRPSGV PDRFSGSKSG TSASLAITGL QAEDEADYYC QSYDSSLGSG 100
 VFGGGTKLTV LGQPKAAPSV TLFPPSSEEL QANKATLVCL ISDFYPGAFT 150
 VAWKADSSPV KAGVETTTPS KQSNNKYAAS SYLSLTPEQW KSHRSYSCQV 200
 THEGSTVEKT VAPTECS 217

Post-translational modifications
 Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
 Intra-H (C23-C104) 22"-96" 156"-212" 273"-333" 379"-437"
 22"-96" 156"-212" 273"-333" 379"-437"
 Intra-L (C23-C104) 22"-90" 139"-198"
 22"-90" 139"-198"
 Inter-H-L (h 5-CL 126) 232"-216" 232"-216"
 Inter-H-H (h 11, h 14) 238"-238" 241"-241"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutamilo N-terminal
 Q > pyroglutamyl (pE, 5-oxoprolyl)
 HVHQI: 1, 1"
 L VLQI: 1, 1"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
 H CH2 N84.4: 309, 309"
 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: 459, 459"

hemoglobinum sucistilum (bovinum) #

hemoglobin sucistil (bovine)

hemoglobin (*Bos taurus*)($\alpha_2\beta_2$ tetramer) with about 95% of the β subunits covalently linked via L-cystein-S-ylsuccinyl bridges connecting either $N M\beta_1^{1-} - N^6 K\beta_2^{81}$ or $N^6 K\beta_1^{81} - N M\beta_2^{1-}$ or $N^6 K\beta_1^{81} - N^6 K\beta_2^{81}$; $N^{\beta 1}, N^{6,\beta 81-}, N^{6,\beta 81}, N^{\beta 1-}$ and $N^{6,\beta 81}, N^{6,\beta 81}-[(2RS)-2-(L-cystein-S-yl)butanedioyl]$ hemoglobin (*Bos taurus*, $\alpha_2\beta_2$ tetramer)

hémoglobine sucistil (bovine)

hémoglobine (*Bos taurus*) ($\alpha_2\beta_2$ tétramère) avec environ 95% des sous-unités β liées de manière covalente par des ponts L-cystéine-S-ylsuccinyle connectant soit $N M\beta_1^{1-} - N^6 K\beta_2^{81}$ ou $N^6 K\beta_1^{81} - N M\beta_2^{1-}$ ou $N^6 K\beta_1^{81} - N^6 K\beta_2^{81}$; $N^{\beta 1}, N^{6,\beta 81-}, N^{6,\beta 81}, N^{\beta 1-}$ et $N^{6,\beta 81}, N^{6,\beta 81}-[(2RS)-2-(L-cystéin-S-yl)butanedioyl]$ hémoglobine (*Bos taurus*, tétramère $\alpha_2\beta_2$)

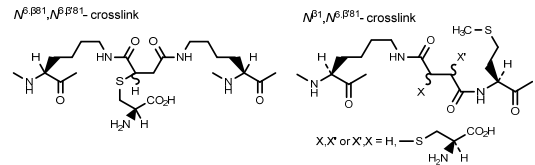
hemoglobina sucistilo (bovina)

hemoglobina (*Bos taurus*) ($\alpha_2\beta_2$ tetrámero) con un 95% de subunidades β covalentemente unidas a través de puentes de L-cisteína-S-ilsuccinil conectando cualquier $N M\beta_1^{1-} - N^6 K\beta_2^{81}$ o $N^6 K\beta_1^{81} - N M\beta_2^{1-}$ o $N^6 K\beta_1^{81} - N^6 K\beta_2^{81}$; $N^{\beta 1}, N^{6,\beta 81-}, N^{6,\beta 81}, N^{\beta 1-}$ y $N^{6,\beta 81}, N^{6,\beta 81}-[(2RS)-2-(L-cistein-S-il)butanedioil]$ hemoglobina (*Bos taurus*, tetrámero $\alpha_2\beta_2$)

alpha and alpha' chains / chaînes alpha et alpha' / cadenas alfa y alfa'
 VLSAADKGNV KAAWGKVGGH AAEYGAEALE RMFLSFTPTK TYFPHFDSLH 50
 GSAQVKHGHA KVAALTKAV EHLDDLPGAL SELSDLHAHK LRVDPVNFKL 100
 LSHSLLVTLA SHLPSDFTPA VHASLQKFLA NVSTVLTISKY R 150

beta and beta' chains / chaînes bêta et bêta' / cadenas beta y beta'
~~M~~LTAEEKAAV TAFWGKVKVD EVGGEALGRL LVVYPWTQRF FESFGDLSTA 50
 DAYMNNPKYK AHGKVLDSF SNGMKHLDDI ~~K~~GTFAALSEL HCDKLHVDEPE 100
 NFKLLGNVLV VVLARNFGKE FTFVLQADFQ KVVAGVANAL AHRYH 150

Crosslinks: ~95% of the $\alpha_2\beta_2$ tetramers with one crosslink each, mainly either $N^6(K\beta 81)-N^6(K\beta' 81)$ or $N^2(M\beta 1)-N^6(K\beta' 81)$



ifinatumabum #
 ifinatumab

immunoglobulin G1-kappa, anti-[*Homo sapiens* CD276 (B7H3, B7-H3, B7-related protein 2, B7RP2, B7RP-2, B7 homolog 3, B7 homologue 3)], humanized monoclonal antibody; gamma1 heavy chain humanized (1-452) [VH (*Homo sapiens* IGHV1-3*01 (83.7%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 (CH1 R120 (219) (123-220), hinge 1-15 (221-235), CH2 (236-345), CH3 E12 (361), M14 (363) (346-450), CHS (451-452)) (123-452)], (225-213')-disulfide with kappa light chain humanized (1'-213') [V-KAPPA (*Homo sapiens* IGKV3D-11*02 (85.6%) -IGKJ1*01 (100%), CDR-IMGT [5.3.9] (27-31.49-51.88-96)) (1'-106') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (152), V101 (190) (107'-213')]; dimer (231-231":234-234")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1SV, glycoform alfa

ifinatumab

immunoglobuline G1-kappa, anti-[*Homo sapiens* CD276 (B7H3, B7-H3, protéine 2 liée à B7, B7RP2, B7RP-2, B7 homologue 3, B7 homologue 3)], anticorps monoclonal humanisé; chaîne lourde gamma1 humanisée (1-452) [VH (*Homo sapiens* IGHV1-3*01 (83.7%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 (CH1 R120 (219) (123-220), charnière 1-15 (221-235), CH2 (236-345), CH3 E12 (361), M14 (363) (346-450), CHS (451-452)) (123-452)], (225-213')-disulfure avec la chaîne légère kappa humanisée (1'-213') [V-KAPPA (*Homo sapiens* IGKV3D-11*02 (85.6%) -IGKJ1*01 (100%), CDR-IMGT [5.3.9] (27-31.49-51.88-96)) (1'-106') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (152), V101 (190) (107'-213')]; dimère (231-231":234-234")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1SV, glycoforme alfa

ifinatumab

immunoglobulina G1-kappa, anti-[*Homo sapiens* CD276 (B7H3, B7-H3, proteína 2 relacionada con B7, B7RP2, B7RP-2, B7 homólogo 3, B7 homólogo 3)], anticuerpo monoclonal humanizado; cadena pesada gamma1 humanizada (1-452) [VH (*Homo sapiens* IGHV1-3*01 (83.7%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 (CH1 R120 (219) (123-220), bisagra 1-15 (221-235), CH2 (236-345), CH3 E12 (361), M14 (363) (346-450), CHS (451-452)) (123-452)], (225-213')-disulfuro con la cadena ligera kappa humanizada (1'-213') [V-KAPPA (*Homo sapiens* IGKV3D-11*02 (85.6%) -IGKJ1*01 (100%), CDR-IMGT [5.3.9] (27-31.49-51.88-96)) (1'-106') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (152), V101 (190) (107'-213')]; dímero (231-231":234-234")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1SV, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

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QVQLVQSGAE VKKPGSSVKV SCKASGYTFT NYVMHWVRQA FGGLEWMGY 50
INPYNDVVKY NEKFKGRVITF TADESTSTAY MELSSLASED TAVYYCARWG 100
YYGSPLYYFD YWGQGLTWTV SSASTKGPSV FPLAPSSKST SGGTAAAGCL 150
VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ SGLYLSLSSV VTPSSSLGT 200
QTYLGNVNHK PSNTKVDKRV EPKSCDKTHT CPPCPAPELL GGPSVFLFPP 250
KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NMYVDGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE 350
PQVYTLPPSR EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTPP 400
PVLDSGDSFF LYSKLTVDKRS RWQGNVFSC SVMHEALHNN YTKQSLSLSP 450
GK
    
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Light chain / Chaîne légère / Cadena ligera

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EIVLTQSPAT LSLSPGERAT LSCRASSRLI YMHWYQQKPG QAPRPLIYAT 50
SNLASGIFAR FSGSGSGTDF TLTISLSLEPE DFAVYVYQQW NSNPTFGQG 100
TKVEIKRTVA APSVFI FPPS DEQLKSGTAS VVCLLNFFYP REAKVQWKVD 150
NALQSGNSQE SVTEQDSKDS TYSLSSTLTL SKADYERHKV YACEVTHQGL 200
SSPVTKSFNR GEC
    
```

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"-87" 133"-193"
 23""-87"" 133""-193""
 Inter-H-L (h5-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 glutamínilo N-terminal

H V H Q I > pyroglutamyl (pE, 5-oxopropyl): 1, 1"

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

HCH2 N84.4: 302, 302"

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

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

ifinatumabum deruxtecanum #
 ifinatumab deruxtecan

immunoglobulin G1-kappa, anti-[*Homo sapiens* CD276 (B7H3, B7-H3, B7-related protein 2, B7RP2, B7RP-2, B7 homolog 3, B7 homologue 3)], humanized monoclonal antibody, conjugated to *deruxtecan*, comprising a linker and a camptothecin derivative;

- gamma1 heavy chain humanized (1-452) [VH (*Homo sapiens*IGHV1-3*01 (83.7%) -(IGHD)-IGHJ4*01 (100%), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens*IGHG1*03 (100%), G1m3, nG1m1 (CH1 R120 (219) (123-220), hinge 1-15 (221-235), CH2 (236-345), CH3 E12 (361), M14 (363) (346-450), CHS (451-452)) (123-452)], (225-213')-disulfide with kappa light chain humanized (1'-213') [V-KAPPA (*Homo sapiens*IGKV3D-11*02 (85.6%) -IGKJ1*01 (100%), CDR-IMGT [5.3.9] (27-31.49-51.88-96)) (1'-106') -*Homo sapiens*IGKC*01 (100%), Km3 A45.1 (152), V101 (190) (107'-213')]; dimer (231-231":234-234")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1SV, glycoform alfa, conjugated, on an average of 4 cysteinyl, each via a thioether bond, to *deruxtecan*, comprising a linker and a camptothecin derivative.
For the deruxtecan part, please refer to the Proposed INN List 116, published in the WHO Drug Information, Vol.30, No.4, 2016.
- ifinatamab déruxtécán immunoglobuline G1-kappa, anti-[*Homo sapiens* CD276 (B7H3, B7-H3, protéine 2 liée à B7, B7RP2, B7RP-2, B7 homolog 3, B7 homologue 3)], anticorps monoclonal humanisé, conjugué au *déruxtécán*, qui comprend un linker et un dérivé de la camptothécine;
chaîne lourde gamma1 humanisée (1-452) [VH (*Homo sapiens*IGHV1-3*01 (83.7%) -(IGHD)-IGHJ4*01 (100%), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens*IGHG1*03 (100%), G1m3, nG1m1 (CH1 R120 (219) (123-220), charnière 1-15 (221-235), CH2 (236-345), CH3 E12 (361), M14 (363) (346-450), CHS (451-452)) (123-452)], (225-213')-disulfure avec la chaîne légère kappa humanisée (1'-213') [V-KAPPA (*Homo sapiens*IGKV3D-11*02 (85.6%) -IGKJ1*01 (100%), CDR-IMGT [5.3.9] (27-31.49-51.88-96)) (1'-106') -*Homo sapiens*IGKC*01 (100%), Km3 A45.1 (152), V101 (190) (107'-213')]; dimère (231-231":234-234")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1SV, glycoforme alfa, conjugué, sur une moyenne de 4 cystéinyl, chacune via une liaison thioéther, au *déruxtécán*, qui comprend un linker et un dérivé de la camptothécine.
Pour la partie déruxtécán, veuillez-vous référer à la Liste 116 des DCI proposées, publiée dans le WHO Drug Information, Vol.30, No.4, 2016.
- ifinatamab deruxtecán inmunoglobulina G1-kappa, anti-[*Homo sapiens* CD276 (B7H3, B7-H3, proteína 2 relacionada con B7, B7RP2, B7RP-2, B7 homólogo 3, B7 homólogo 3)], anticuerpo monoclonal humanizado, conjugado con *deruxtecán*, que consta de un enlace y un derivado de la camptotecina;
cadena pesada gamma1 humanizada (1-452) [VH (*Homo sapiens*IGHV1-3*01 (83.7%) -(IGHD)-IGHJ4*01 (100%), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens*IGHG1*03 (100%), G1m3, nG1m1 (CH1 R120 (219) (123-220), bisagra 1-15 (221-235), CH2 (236-345), CH3 E12 (361), M14 (363) (346-450), CHS (451-452)) (123-452)], (225-213')-disulfuro con la cadena ligera kappa humanizada (1'-213') [V-KAPPA (*Homo sapiens*IGKV3D-11*02 (85.6%) -IGKJ1*01 (100%), CDR-IMGT [5.3.9] (27-31.49-51.88-96)) (1'-106') -*Homo sapiens*IGKC*01 (100%), Km3 A45.1 (152), V101 (190) (107'-213')]; dímero (231-231":234-234")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1SV, forma glicosilada alfa, conjugado, en 4 restos cisteinil por término medio, cada uno a través de un enlace tioéther, al *deruxtecán*, que consta de un enlace y un derivado de la camptotecina.
Para la parte deruxtecán, por favor vaya a la Lista 116 de los DCI propuestas, publicada en el WHO Drug Information, Vol.30, No.4, 2016.

Heavy chain / Chaîne lourde / Cadena pesada
 QVQLVQSGAE VKKPGSSVKV SCKASGYFT NYVMHWVRQA PGQGLEWMGY 50
 INFYNDVVKY NEKFKGRVTI TADESTSTAY MELSSLSRSED TAVYYCARWG 100
 YYGSPLYYFD YWGQGTLLVTV SSASTKGPSV FFLAPSSKST SGGTAAALGCL 150
 VKDYFPEPVT VSWNSGALTS GVHTFPVAVLQ SSGLYLSLSSV VTFPSSSLGT 200
 QTYICNVNHH PSNTKVDKRV EPKSCDKTHT CPFCPAPELL GGPVSFLFPP 250
 KPKDTLMI SR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ 300
 YNSTYRVVSV LTVLHQDWLN GREYKCKVSN KALPAFIEKT ISKAKGQPRE 350
 PQVYTLFPPSR EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QFENNYKTFP 400
 PVLDSGDSFF LYSKLTVDKS RWQQGNVFC SVMHEALHNN YTKSLSLSP 450
 GK 452

Light chain / Chaîne légère / Cadena ligera
 EIVLTQSPAT LSLSPGERAT LSCRASSRLI YMHVYQQKPG QAPRPLIYAT 50
 SNLASGIPAR FSGSGSGTDF TLTISSELEPE DPAVYYCQWV NSNPPTFGQG 100
 TKVEIKRTVA APSVFIPTPS DEQLKSGTAS VVCLLNNFYP REAKVQWKVD 150
 NALQSGNSQE SVTEQDSKDS TYSLSSITLTL SKADYERHKV YACEVTHQGL 200
 SSPVTKSFNR GEC 213

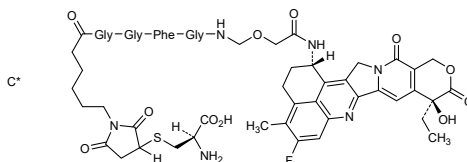
Post-translational modifications
 Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
 Intra-H (C23-C104) 22"-96" 149"-205" 266"-326" 372"-430"
 22"-96" 149"-205" 266"-326" 372"-430"
 Intra-L (C23-C104) 23"-87" 133"-193"
 23"-87" 133"-193"
 Inter-H-L (h 5-CL 126)* 225"-213' 225"-213"
 Inter-H-H (h 11, h 14)* 231"-231" 234"-234"
 *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.
 *Les 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.
 *Faltan los cuatro puentes disulfuro inter-catenarios, una media de 4 cisteinil está conjugada a conectores de principio activo.

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

Potential modified residues / résidus modifiés potentiels / restos modificados potenciales



imlunestrant
 imlunestrant

(5*R*)-5-(4-{2-[3-(fluorométhyl)azetidín-1-yl]étoxy}phényl)-8-(trifluorométhyl)-5*H*-[1]benzopyrano[4,3-*c*]quinolin-2-ol

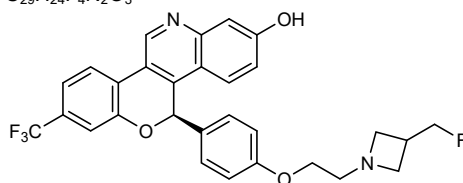
imlunestrant

(5*R*)-5-(4-{2-[3-(fluorométhyl)azetidín-1-yl]étoxy}phényl)-8-(trifluorométhyl)-5*H*-[1]benzopyrano[4,3-*c*]quinoléin-2-ol

imlunestrant

(5*R*)-5-(4-{2-[3-(fluorometil)azetidín-1-il]etoxi}fenil)-8-(trifluorometil)-5*H*-[1]benzopirano[4,3-*c*]quinolein-2-ol

C₂₉H₂₄F₄N₂O₃



imvotamabum

imvotamab

immunoglobulin M-kappa cyclic pentamer bisdisulfide with a fused scFv -JCHAIN (joining chain of multimeric IgA and IgM) -ALB (albumin) chain, anti-[*Homo sapiens* MS4A1 (membrane-spanning 4-domains subfamily A member 1, CD20)] (decavalent) and anti-[*Homo sapiens* CD3E (CD3e, CD3 epsilon)] (monovalent), monoclonal antibody, bispecific;

mu heavy chain anti-MS4A1 (1-575) [VH (*Homo sapiens*IGHV5-51*01 (99.0%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens*IGHM*03 (CH1 (123-226), CH2 (227-338), CH3 (339-444), CH4 (445-555), CH5 (556-575)) (123-575)], (136-219')-disulfide with kappa light chain anti-MS4A1 (1'-219') [V-KAPPA (*Homo sapiens*IGKV2-24*01 (98.0%) -IGKJ4*01 (100%), CDR-IMGT [11.3.9] (27-37.55-57.94-102)) (1'-112') -*Homo sapiens*IGKC*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; dimer (336-336":413-413")-bisdisulfide, 5 [mu_kappa]2 dimers forming a cyclic pentamer, disulfide 4 x (574"-574), and 1x (574"-271""-325""-574)-bisdisulfide with scFv-JCHAIN-ALB (1""-993""") [scFv heavy-kappa anti-CD3E (1""-241""") [VH Musmus/Homsap (*Mus musculus*IGHV1-4*01 (83.7%) -(IGHD) -IGHJ3*01 (92.9%) A128>S (120)/*Homo sapiens*IGHV1-46*04 (82.7%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1""-120""") -15-mer tris(tetraglycyl-seryl) linker (121""-135""") -V-KAPPA (*Homo sapiens*IGKV1-39*01 (86.3%) -IGKJ4*01 (100%), CDR-IMGT [5.3.9] (162-166.184-186.223-231)) (136""-241""") -15-mer tris(tetraglycyl-seryl) linker (242""-256""") -JCHAIN (257""-393""") -15-mer tris(tetraglycyl-seryl) linker (394""-408""") -*Homo sapiens*ALB (albumin) (409""-993""")], produced in Chinese hamster ovary (CHO) cells, derived from CHO-K1 cell line, lacking the glutamine synthetase (GS-KO) gene, glycoform alfa

imvotamab

immunoglobuline M-kappa pentamère cyclique bisdisulfure avec une chaîne fusionnée scFv - JCHAIN (chaîne de jonction des IgA et IgM multimériques) -ALB (albumine), anti-[*Homo sapiens* MS4A1 (membre 1 de la sous-famille A à 4 domaines transmembranaires, CD20)] (décavalent) et anti-[*Homo sapiens* CD3E (CD3e, CD3 epsilon)] (monovalent), anticorps monoclonal, bispécifique; chaîne lourde mu anti-MS4A1 (1-575) [VH (*Homo sapiens*IGHV5-51*01 (99.0%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens*IGHM*03 (CH1 (123-226), CH2 (227-338), CH3 (339-444), CH4 (445-555), CH5 (556-575)) (123-575)], (136-219')-disulfure avec la chaîne légère kappa anti-MS4A1 (1'-219')

[V-KAPPA (*Homo sapiens* IGKV2-24*01 (98.0%) - IGKJ4*01 (100%), CDR-IMGT [11.3.9] (27-37.55-57.94-102)) (1'-112') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; dimère (336-336":.413-413")-bisdisulfure, 5 dimères [mu_kappa]2 formant un pentamère cyclique disulfure 4x (574"-574) et 1x (574-271""-.325""-.574")-bisdisulfure avec la protéine de fusion scFv-JCHAIN-ALB (1""-993"")) [scFv heavy-kappa anti-CD3E (1""-241"")) [VH Musmus/Homsap (*Mus musculus* IGHV1-4*01 (83.7%) -(IGHD) -IGHJ3*01 (92.9%) A128>S (120)/*Homo sapiens* IGHV1-46*04 (82.7%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1""-120"")) -15-mer tris(tétraglycyl-séryl) linker (121""-135"")) -V-KAPPA (*Homo sapiens* IGKV1-39*01 (86.3%) -IGKJ4*01 (100%), CDR-IMGT [5.3.9] (162-166.184-186.223-231)) (136""-241"")) -15-mer tris(tétraglycyl-séryl) linker (242""-256"")) -JCHAIN (257""-393"")) -15-mer tris(tétraglycyl-séryl) linker (394""-408"")) -*Homo sapiens* ALB (albumine) (409""-993"")), 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

imvotamab

immunoglobulina M-kappa pentámero cíclico bisdisulfuro con una cadena fusionada scFv -JCHAIN (cadena de unión de las IgA e IgM multiméricas) -ALB (albúmina), anti-[*Homo sapiens* MS4A1 (miembro 1 de la subfamilia A con 4 dominios transmembranarios, CD20)] (decaivalente) y anti-[*Homo sapiens* CD3E (CD3e, CD3 épsilon)] (monovalente), anticuerpo monoclonal, biespecífico; cadena pesada mu anti-MS4A1 (1-575) [VH (*Homo sapiens* IGHV5-51*01 (99.0%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.15] (26-33.51-58.97-111)) (1-122) -*Homo sapiens* IGHM*03 (CH1 (123-226), CH2 (227-338), CH3 (339-444), CH4 (445-555), CH5 (556-575)) (123-575)], (136-219')-disulfuro con la cadena ligera kappa anti-MS4A1 (1'-219') [V-KAPPA (*Homo sapiens* IGKV2-24*01 (98.0%) -IGKJ4*01 (100%), CDR-IMGT [11.3.9] (27-37.55-57.94-102)) (1'-112') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (158), V101 (196) (113'-219')]; dímero (336-336":.413-413")-bisdisulfuro, 5 dímeros [mu_kappa]2 formando un pentámero cíclico disulfuro 4x (574"-574) et 1x (574-271""-.325""-.574")-bisdisulfuro con la proteína de fusión scFv-JCHAIN-ALB (1""-993"")) [scFv pesado-kappa anti-CD3E (1""-241"")) [VH Musmus/Homsap (*Mus musculus* IGHV1-4*01 (83.7%) -(IGHD) -IGHJ3*01 (92.9%) A128>S (120)/*Homo sapiens* IGHV1-46*04 (82.7%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1""-120"")) -15-mer tris(tetraglicil-seril) linker (121""-135"")) -V-KAPPA (*Homo sapiens* IGKV1-39*01 (86.3%) -IGKJ4*01 (100%), CDR-IMGT [5.3.9] (162-166.184-186.223-231)) (136""-241"")) -15-mer tris(tetraglicil-seril) linker (242""-256"")) -JCHAIN (257""-393"")) -15-mer tris(tetraglicil-seril) linker (394""-408"")) -*Homo sapiens* ALB (albúmina) (409""-993"")), 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 (anti-MS4A1) (x10)
 EVQLVQSGAE VKKPGESLKI SCKGSGYSFT SYWIGWVRQM PGKGLEWMMGI 50
 IYPGDSSTRY SPSFQGGVTTI SADKSIITAY LQWSSLKASD TAMYICARHP 100
 SYGSGSPNFD YWGGQTLVTV SSGSASAPTL FPLVSCENSF SDTSSVAVGC 150
 LAQDFLPDSI TFSWKYKMSN DISSTRGFPS VLRGGKYAAT SQVLLPSKDV 200
 MQGTDDEHVVC KVQHPNNGKE KNVPLPVIAE LPPKVSFVFP PRDGFEGNPR 250
 KSKLICQATG FSPRQIQVSW LREGKQVGSV VTTDQVQAEA KESGPTTYKV 300
 TSLTIKESD WLSQSMFTCR VDRHGLTFQQ NASSMCVPDQ DTAIRVFAIP 350
 PSFASIFLTR STKLTCLVTD LTTYDSVTIS WTRQNGEAVK THTNISESHP 400
 NATFSAVGEA SICEDDWNSS ERFCTCVTHT DLPSPLKQTI SRPKGVALHR 450
 PDVYLLPPAR EQLNLRRESAT ITCLVTGFSP ADVFVQWMMQR GQPLSPEKYV 500
 TSAPMPPEPQA PGRYFAHSIL TVSEEEWNTG ETYTCVVAHE ALPNRVVERT 550
 VDKSTGKPTL YNVSLVMSDT AGTCY 575

Light chain / Chaîne légère / Cadena ligera (anti-MS4A1) (x10)
 DIVMTQTPLS SPVTLGQPAS ISCRSSQSLV YSDGNTYLSV LQQRPGQPPR 50
 LLIYKISNRF SGVPRDFSGS GAGTDFTLKI SRVEAEDVGV YYCVQATQFP 100
 LTFGGGTKEV IKRTVAAPSV FIFPPSDEQL KSGTASVCL LNNFYPREAK 150
 VQWKVDNALQ SGNSQESVTE QDSKDSITYSL SSTLTLSKAD YEKHKVYACE 200
 VTHQGLSSPV TKSFNRGEC 219

Joining chain / Chaîne de jonction / Cadena de unión scFv (anti-CD3E)-JCHAIN-ALB (x1)
 VQQLVQSGAE VKKPGASVKV SCKASGYTFI SYTMHWVRQA PGQGLEWMMGY 50
 INPRSGYTHY NQKLRKDKATL TADKASASTAY MELSSLRSED TAVYICARSA 100
 YYDYDGFAYW GGGTLVTVSS GGGSGGGGS GGGSDIQMT QSPSSLSASV 150
 GDRVITITCSA SSSVSVMNYY QQKPKGAPKR LIYDTSKLAS GVPSPRFSGG 200
 SGTDFTLTIS SLQPEDFATY YCQWNSNPP TFGGGTKVEI KGGGSGGGG 250
 SGGGGSQDEE RIVLVDNCKC CARITSRIRI SSEDPNEDIV ERNIRI IVPL 300
 NNRENISDPT SFLRTRFVYH LSDLCKKCPD TEVELDNQIV TATQSNICDE 350
 DSATETCTYV DRNKCYTAVV PLYVGGETKM VETALTDPAC YPDGGGSGG 400
 GSGGGGSDA HKSEVAHREF DLGEBENFKAL VLIAFAQYQL QCFEDHVKL 450
 VNEVTEFAKT CVADESAENC DKSLLHTLFGD KLCTVATLRE TYGEMADCCA 500
 KQEFPERNECF LQHKDDPNPL FRLVRPEVDV MCTAFHDNEE TFLKKYLYEI 550
 ARRHPIFYAP ELLFFAKRYK AAFTECCQAA DKAACLPLKL DELRDEGKAS 600
 SAKQRLKCAS LQKFGERAFK AWAVARLSQR FPKAEFAEVS KLVTDLTKVH 650
 TECCHGDLEL CADDRADLAK YICENQDSIS SKLKECCERK LLEKSHCIAE 700
 VENDEMPADL PSLAADFVES KDVCNKYAEA KDVLGFMFLY EYARRHPDYS 750
 VVLLRLAKT YETTLKCCA AADPHCEYAK VFDEFKPLVE EPQNLIKQNC 800
 ELFKQLGEYK FQNALLVRYT KKVQVQSTPT LVEVSRNLGK VGSCKCKHPE 850
 AKRMPCAEYD LSVVLLNQLCV LHEKTPVSDR VTKCCTESLV NRRPCFSALE 900
 VDETVVPKEF NAETPTFHAD ICTLSEKERQ IKKQATALVEL VKHKPKATKE 950
 QLKAVMDDFA AFVEKCKCAD DKETCFAEEG KKLVAASQAA LGL 993

Post-translational modifications

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
 Intra-H (C23-C104) (10x5=50) 22-96 150-210 256-319 366-425 473-535
 22"-96" 150"-210" 256"-319" 366"-425" 473"-535"
 Intra-L (C23-C104) (4x5=20) 23"-93" 139"-199"
 23"-93" 139"-199"
 Intra-J (C23-C104) (2) 22"-96" 158"-222"
 Intra-J (JCHAIN) (3) 269"-357" 328"-348" 365"-390"
 Intra-J (ALB) (17) 461"-470" 483"-499" 498"-509" 532"-577" 576"-585"
 608"-654" 653"-661" 673"-687" 686"-697" 724"-769"
 768"-777" 800"-846" 845"-856" 869"-885" 884"-895"
 922"-967" 966"-975"
 Inter-H-L (CH1 10-CL 126) (2x5=10) 136-219" 136-219"
 Inter-H-H (CH2 125, CH3 92) (2x5=10) 336-336" 413-413"
 Inter-H-H (CHS 147) (4) 574"-574
 Inter-H-J (CHS 147-J) (J-CHS 147) (2) 574"-271" 325"-574
 Total: 118 S-S

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

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

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
 H CH1 N45, CH2 N120, CH3 N81 (6 per dimer): 168, 331, 394, 168", 331", 394"
 J JCHAIN (1x): 305"

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

H CH3 N84.4, CHS N135 (4 per dimer): 401, 562, 401", 562"

High mannose glycans / glycanes riche en mannose / glicanos ricos en manosa

inezetamabum #
 inezetamab

immunoglobulin G1-scFv_L-lambda2 dimer, anti-[*Homo sapiens* CD40 (tumor necrosis factor receptor superfamily member 5, TNFRSF5)] and anti-[*Homo sapiens* MSLN (mesothelin, pre-pro-megakaryocyte-potentiating factor, megakaryocyte-potentiating factor, MPF, CAK1)], *Homo sapiens* monoclonal antibody, tetravalent, bispecific;

- G1-scFv fused chain *Homo sapiens* (1-698) [gamma1 heavy chain anti-CD40 *Homo sapiens* (1-448) [VH (*Homo sapiens* IGHV3-23*01 (93.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, G1v30 CH2 N84.4>G (CH1 R120>K (217) (121-218), hinge 1-15 (219-233), CH2 R83>C (295), N84.4>G (300), V85>C (305) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS>del)] (121-448)] -10-mer bis(tetraglycyl-seryl) linker (449-458) -scFv heavy-kappa anti-MSLN *Homo sapiens* (459-698) [VH (*Homo sapiens* IGHV3-11*01 (93.9%) G49>C -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [8.8.10] (484-491.509-516.555-564)) (459-575) -15-mer tris(tetraglycyl-seryl) linker (576-590) -V-KAPPA (*Homo sapiens* IGKV1-12*01 (93.7%) -IGKJ1*01 (90.9%) Q120>C (690), CDR-IMGT [6.3.9] (617-622.640-642.679-687)) (591-698)], (223-216')-disulfide with lambda2 light chain anti-CD40 *Homo sapiens* (1'-217') [V-LAMBDA (*Homo sapiens* IGLV2-14*01 (90.8%) -IGLJ2*01 (91.7%), CDR-IMGT [9.3.11] (26-34.52-54.91-101)) (1'-111') -*Homo sapiens* IGLC2*01 (100%) (112'-217')]; dimer (229-229":232-232")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, non-glycosylated
- inézétamab immunoglobuline G1-scFv_L-lambda2 dimère, anti-[*Homo sapiens* CD40 (membre 5 de la superfamille des récepteurs du TNF, TNFRSF5)] and anti-[*Homo sapiens* MSLN (mésotéline, facteur de potentialisation du pré-pro-mégacaryocyte, facteur de potentialisation des mégacaryocytes, MPF, CAK1)], anticorps monoclonal *Homo sapiens*, tétravalent, bispécifique; chaîne lourde fusionnée G1-scFv *Homo sapiens* (1-698) [gamma1 anti-CD40 *Homo sapiens* (1-448) [VH (*Homo sapiens* IGHV3-23*01 (93.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, G1v30 CH2 N84.4>G (CH1 R120>K (217) (121-218), charnière 1-15 (219-233), CH2 R83>C (295), N84.4>G (300), V85>C (305) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS>del)] (121-448)] -10-mer bis(tétraglycyl-séryl) linker (449-458) -scFv heavy-kappa anti-MSLN *Homo sapiens* (459-698) [VH (*Homo sapiens* IGHV3-11*01 (93.9%) G49>C -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [8.8.10] (484-491.509-516.555-564)) (459-575) -15-mer tris(tétraglycyl-séryl) linker (576-590) -V-KAPPA (*Homo sapiens* IGKV1-12*01 (93.7%) -IGKJ1*01 (90.9%) Q120>C (690), CDR-IMGT [6.3.9] (617-622.640-642.679-687)) (591-698)], (223-216')-disulfure avec la chaîne légère lambda2 anti-CD40 *Homo sapiens* (1'-217') [V-LAMBDA (*Homo sapiens* IGLV2-14*01 (90.8%) -IGLJ2*01 (91.7%), CDR-IMGT [9.3.11] (26-34.52-54.91-101)) (1'-111') -*Homo sapiens* IGLC2*01 (100%) (112'-217')]; dimère (229-229":232-232")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), non-glycosylé
- inezetamab inmunoglobulina G1-scFv_L-lambda2 dímero, anti-[*Homo sapiens* CD40 (miembro 5 de la superfamilia de los receptores del TNF, TNFRSF5)] y anti-[*Homo sapiens* MSLN (mesotelina, factor de potenciación del pre-pro-megacariocito, factor de potenciación de los megacariocitos, MPF, CAK1)], anticuerpo monoclonal *Homo sapiens*, tetraivalente, biespecífico; cadena pesada fusionada G1-scFv *Homo sapiens* (1-698) [gamma1 anti-CD40 *Homo sapiens* (1-448) [VH (*Homo sapiens* IGHV3-23*01 (93.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, G1v30 CH2 N84.4>G (CH1 R120>K (217) (121-218), bisagra 1-15 (219-233), CH2 R83>C (295), N84.4>G (300), V85>C (305) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS>del)] (121-448)] -10-mer bis(tetraglicil-seril) linker (449-458) -scFv pesada-kappa anti-MSLN *Homo sapiens* (459-698) [VH (*Homo sapiens* IGHV3-11*01 (93.9%) G49>C -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [8.8.10] (484-491.509-516.555-564)) (459-575) -15-mer tris(tetraglicil-seril) linker (576-590) -V-KAPPA (*Homo sapiens* IGKV1-12*01 (93.7%) -IGKJ1*01 (90.9%) Q120>C (690), CDR-IMGT [6.3.9] (617-622.640-642.679-687)) (591-698)], (223-216')-disulfuro con la cadena ligera lambda2 anti-CD40 *Homo sapiens* (1'-217') [V-LAMBDA (*Homo sapiens* IGLV2-14*01 (90.8%) -IGLJ2*01 (91.7%), CDR-IMGT [9.3.11] (26-34.52-54.91-101)) (1'-111') -*Homo sapiens* IGLC2*01 (100%) (112'-217')]; dímero (229-229":232-232")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), no glicosilado

Heavy chain / Chaîne lourde / Cadena pesada (anti-CD40, anti-MSLN)
 EVQLLESGGG LVQPGGSLRL SCAASGFTFS RNAMSWVRQA PGKGLEWVSA 50
 TGGSGISTYY ADSVKGRFTI SRDNKNTLY LQMNSLRAED TAVYYCARGY 100
 SNSWYFDYW GQGTLVTVSS ASTKGPSVFF LAPSSKSTSG GTALGCLVK 150
 DYFPEPVTS WNSGALTSGV HTPFAVLQSS GLYSLSSVVT VPSSSLGTQT 200
 YICNVNHKPS NTKVDKKEVEP KSCDKTHTCP PCPAPPELLGG PSVFLFPPPK 250
 KDTLMISRTP EVTCTVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPCCEEQYG 300
 STYRCVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIK KAKGQPPREPQ 350
 VYTLPPSREE MTRNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTTPV 400
 LDSDGSFFLY SKLTVDKSRW QQGNVFCSSV MHEALHNHYT QKSLSLSPGG 450
 GSGGGGGSQV QLVESGGGLV KPGGSLRLSC AASGFTFSYD YMSWIRQAPG 500
 KCLEWISYIS SSESIIYYVD AVKGRFTISR DNAKNSLYLQ MNSLRAEDTA 550
 VYYCARDVGS HFDYWGQGTL VTVSSGGGGS GGGGSGGGGS DIQMTQSPSS 600
 VASVSGDRVT ITCRASQDIS RWLAWYQQKPK GKAPKLLISA ASRLQSGVPS 650
 RFSGSGSGTD FTLTISSLQP EDFAIYYCQQ AKSFRPTFGC GTKVEIKR 698

Light chain / Chaîne légère / Cadena ligera (anti-CD40)
 QSALTQPASV SGGSPGQSITI SCTGTSDDVG NYNLVSWYQQ HPGKAPKLM 50
 FEVNRPSGV SNRFSGSKSG TTSALTSISGL QAADAEADYFC SSYTTSSTYV 100
 IFGGGKTLTV LGQPAAAFV TLFPPSSEEL QANKATLVCL ISDFYPGAVT 150
 VAWKADSPV KAGVETTTFS KQSNKYAAS SYLSLTPEQW KSHRSYSCQV 200
 THEGSTVEKT VAPTECS 217

Post-translational modifications
 Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
 Intra-H (C23-C104) 22°-96' 147°-203' 264°-324' 370°-428' 480°-554' 613°-678'
 22°-96" 147°-203" 264°-324" 370°-428" 480°-554" 613°-678"
 CH2 C83-C85 295-305 295°-305"
 scFv VH C49-VL C120 502-690 502°-690"
 Intra-L (C23-C104) 22°-90' 139°-198'
 22°-90" 139°-198"
 Inter-H-L (h 5-CL 126) 223°-216' 223°-216"
 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
 L VL Q1 > pyroglutamyl (pE, 5-oxopropyl): 1', 1"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
 H CH2 N84.4>G (G1V30): 300, 300"
 Aglycosylated / aglycosylé / aglicosilado

iofoposinum ^(131I)
 iofoposine ^(131I)

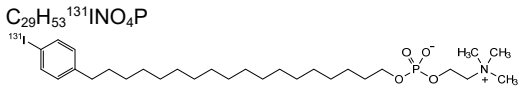
18-[4-(^{131I})iodophenyl]octadecyl 2-
 (trimethylazaniumyl)ethyl

iofoposine ^(131I)

phosphate de 18-[4-(^{131I})iodophényl]octadécyle et de
 2-(triméthylazaniumyl)éthyle

iofoposina ^(131I)

fosfato de 18-[4-(^{131I})iodofenil]octadecilo y de 2-
 (trimetilazaniumil)etilo



iruplinalkibum
 iruplinalkib

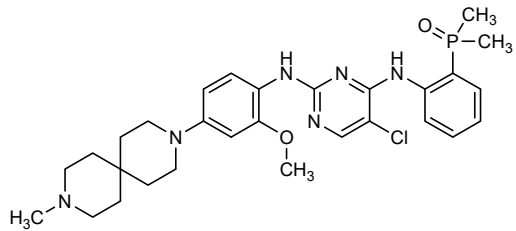
[2-({5-chloro-2-[2-methoxy-4-(9-methyl-3,9-diazaspiro[5.5]undecan-3-yl)anilino]pyrimidin-4-yl)amino)phenyl]dimethyl-λ⁵-phosphanone

iruplinalkib

[2-({5-chloro-2-[2-méthoxy-4-(9-méthyl-3,9-diazaspiro[5.5]undécán-3-yl)anilino]pyrimidin-4-yl)amino)phényl]diméthyl-λ⁵-phosphanone

iruplinalkib

[2-({5-cloro-2-[4-(9-metil-3,9-diazaspiro[5.5]undecan-3-il)-2-metoxianilino]pirimidin-4-il}amino)fenil]dimetil-λ⁵-fosfanona



ispectamabum debotansinum #
ispectamab debotansine

immunoglobulin G1-kappa, anti-[*Homo sapiens* TNFRSF17 (TNF receptor superfamily member 17, tumor necrosis factor receptor superfamily, member 17, B cell maturation antigen, BCMA, BCM, TNFRSF13A, CD269)], humanized monoclonal antibody, conjugated at C-4 of four specific phenylalanine residues with *N*²-deacetylmaytansine via a noncleavable linker; gamma1 heavy chain humanized (1-453) [VH (*Homo sapiens* IGHV3-66*01 (82.7%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.8.15] (27-34.52-59.98-112)) (1-123) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 Y85.2>F (pAMF) (186), R120>K (220) (124-221), hinge 1-15 (222-236), CH2 (237-346), CH3 E12 (362), M14 (364), F85.2>F (pAMF) (410) (347-451), CHS (452-453)) (124-453)], (226-215'-disulfide with kappa light chain humanized (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (84.2%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (28-33.51-53.90-98)) (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')]; dimer (232-232":235-235")-bisdisulfide, produced by a cell-free protein synthesis system based on *Escherichia coli* lysate, non-glycosylated, substituted at C-4 of the L-phenylalanyl residues 186, 410, 186" and 410" with {8-[(2*S*)-1-[[[(1⁴*S*,1⁶*S*,2*R*,3²*S*,3³*S*,4*S*,10*E*,12*E*,14*R*)-8⁶-chloro-1⁴-hydroxy-8⁵,14-dimethoxy-2,3³,7,10-tetramethyl-1²,6-dioxo-7-aza-1(6,4)-[1,3]oxazinana-3(2,3)-oxirana-8(1,3)-benzenacyclotetradecaphane-10,12-dien-4-yl]oxy]-2,3,9-trimethyl-1,4,8,24-tetraoxo-12,15,18,21-tetraoxa-3,9,25-triazaoctacosan-28-oyl]-8,9-dihydro-1*H*(or 3*H*)-dibenzo[*b*,*f*][1,2,3]triazolo[4,5-*d*]azocin-1(or 3)-yl]methyl (*debotansine*) groups

ispectamab débotansine

immunoglobuline G1-kappa, anti-[*Homo sapiens* TNFRSF17 (membre 17 de la superfamille des récepteurs du TNF, membre 17 de la superfamille des récepteurs du facteur de nécrose tumorale, antigène de maturation de cellule B, BCMA, BCM, TNFRSF13A, CD269)], anticorps monoclonal humanisé, conjugué en C-4 de quatre résidus phénylalanine spécifiques avec *N*²-déacétylmaytansine via un linker non-clivable;

cadena pesada gamma1 humanizada (1-453) [VH (*Homo sapiens* IGHV3-66*01 (82.7%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.8.15] (27-34.52-59.98-112)) (1-123) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 Y85.2>F (pAMF) (186), R120>K (220) (124-221), charnière 1-15 (222-236), CH2 (237-346), CH3 E12 (362), M14 (364), F85.2>F (pAMF) (410) (347-451), CHS (452-453)) (124-453)], (226-215')-disulfuro avec la chaîne légère kappa humanisée (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (84.2%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (28-33.51-53.90-98)) (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')]; dimère (232-232":235-235")-bisdisulfuro, produit par un système acellulaire de synthèse de protéines à base de lysat d'*Escherichia coli*, non-glycosylé, substitué en C-4 des résidus L-phénylalanyle 186, 410, 186" et 410" par des groupes {8-[(2S)-1-{{[(1⁴S,1⁶S,2R,3²S,3³S,4S,10E,12E,14R)-8⁶-chloro-1⁴-hydroxy-8⁵,14-diméthoxy-2,3³,7,10-tétraméthyl-1²,6-dioxo-7-aza-1(6,4)-[1,3]oxazinana-3(2,3)-oxirana-8(1,3)-benzénacyclotétradécaphane-10,12-diène-4-yl]oxy)-2,3,9-triméthyl-1,4,8,24-tétraoxo-12,15,18,21-tétraoxa-3,9,25-triazaoctacosan-28-oyl]-8,9-dihydro-1H(ou 3H)-dibenzo[b,f][1,2,3]triazolo[4,5-d]azocin-1(ou 3)-yl}méthyle (*débotansine*)

ispectamab debotansina

inmunoglobulina G1-kappa, anti-[*Homo sapiens* TNFRSF17 (miembro 17 de la superfamilia de los receptores del TNF, miembro 17 de la superfamilia de los receptores del factor de necrosis tumoral, antígeno de maduración de célula B, BCMA, BCM, TNFRSF13A, CD269)], anticuerpo monoclonal humanizado, conjugado en C-4 de cuatro residuos fenilalanina específicos con N²-deacetilmaitansina a través de un enlace no escindible; cadena pesada gamma1 humanizada (1-453) [VH (*Homo sapiens* IGHV3-66*01 (82.7%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.8.15] (27-34.52-59.98-112)) (1-123) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 Y85.2>F (pAMF) (186), R120>K (220) (124-221), bisagra 1-15 (222-236), CH2 (237-346), CH3 E12 (362), M14 (364), F85.2>F (pAMF) (410) (347-451), CHS (452-453)) (124-453)], (226-215')-disulfuro con la cadena ligera kappa humanizada (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (84.2%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (28-33.51-53.90-98)) (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')]; dímero (232-232":235-235")-bisdisulfuro, producido por un sistema de síntesis de proteínas sin células basado en lisado de *Escherichia coli*, no glicosilado, sustituido en C-4 de los residuos de L-fenilalanilo 186, 410, 186" y 410" con grupos {8-[(2S)-1-{{[(1⁴S,1⁶S,2R,3²S,3³S,4S,10E,12E,14R)-8⁶-cloro-1⁴-hidroxi-2,3³,7,10-tetrametil-8⁵,14-dimetoxi-1²,6-dioxo-7-aza-1(6,4)-[1,3]oxazinana-3(2,3)-oxirana-8(1,3)-benzenacyclotetradecafano-10,12-dien-4-yl]oxi)-2,3,9-trimetil-1,4,8,24-tetraoxo-12,15,18,21-tetraoxa-3,9,25-triazaoctacosan-28-oyl]-8,9-dihydro-1H(o 3H)-dibenzo[b,f][1,2,3]triazolo[4,5-d]azocin-1(o 3)-yl}metil (*debotansina*)

Heavy chain / Chaîne lourde / Cadena pesada

MEVQLVESGG GLVQPGGSLR LSCAASGFNI SAPGIHWVRQ APGKGLEWVG 50
 FINPAGGYTD YADSVKGRFT ISADTSKNTA YLQMNLSRAE DTAVYYCARD 100
 YIRQYWTYVL DYWGQGTLLVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC 150
 LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLFSLSS VVTVPSSSLG 200
 TQTYICNVNH KPSNTKVDKK VEPKSCDKTH TCPPCPAPEL LGGPSVFLFP 250
 PKPKDTLMIS RTPETCVVVV DVSHEDEPKV FNWYVDGVEV HNAKTKPREE 300
 QYNSTYRVVVS VLTVLHQDML NGKEYKCKVVS NKALPAPIEK TISKARQQR 350
 EPQVYTLPPS REEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT 400
 PPFVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMEALHN HYTQKSLSL 450
 PGK 453

Light chain / Chaîne légère / Cadena ligera

MDIQMTQSPS SLSASVGRDV TITCRASQDV NTAVAWYQQK PGKAPKLLIY 50
 SASFLYSGVP SRFSGSRSGT DFTLTITSSQL PEDFATYYCQ QHYTTPPTFG 100
 QGTKEIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK 150
 VDNALQSGNS QESVTEQDSK DSTYLSSTL TLSKADYERK KRYACEVTHQ 200
 GLSSPVTKSF NRGEC 215

E indicates non-natural amino acid *p*-azidomethyl-L-phenylalanine (pAMF)

Post-translational modifications

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

Intra-H (C23-C104) 23-97 150-206 267-327 373-431
 23"-97" 150"-206" 267"-327" 373"-431"

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

Inter-H-L (h 5-CL 126) 226-215" 226"-215"

Inter-H-H (h 11, h 14) 232-232" 235-235"

N-terminal methionine / Méthionine N-terminale / Metionina N-terminal

H VH M1.1: 1, 1"

L V-KAPPA M1.1: 1, 1"

No N-terminal methionine clipping (expressed in a cell-free expression system) / Pas de coupure de la méthionine N-terminale (exprimé dans un système d'expression acellulaire)
 Sin recorte de metionina N-terminal (expresado en un sistema de expresión libre de célula)

Conjugation sites / Sites de conjugation / Posiciones de conjugación

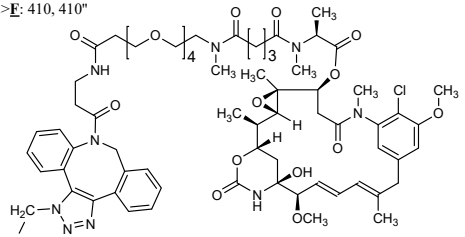
E: *p*-azidomethyl-L-phenylalanine (pAMF) used as conjugation specific site /

E: *p*-azidométhyl-L-phénylalanine (pAMF) utilisé comme site spécifique de conjugaison

E: *p*-azidometil-L-fenilalanina (pAMF) utilizada como sitio específico de conjugación

H CH1 Y85.2>**E**: 186, 186"

H CH3 F85.2>**E**: 410, 410"



itruvonum

itruvone

itruvone

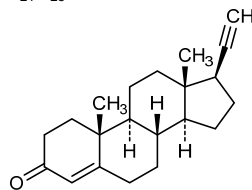
itruvona

pregn-4-en-20-yn-3-one

prégn-4-én-20-yn-3-one

pregn-4-en-20-in-3-ona

C₂₁H₂₈O



ivarmacitinibum

ivarmacitinib

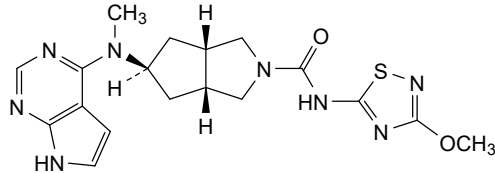
(3*aR*,5*s*,6*aS*)-*N*-(3-methoxy-1,2,4-thiadiazol-5-yl)-5-[methyl(*7H*-pyrrolo[2,3-*d*]pyrimidin-4-yl)amino]hexahydrocyclopenta[*c*]pyrrole-2(*1H*)-carboxamide

ivarmacitinib

(3*aR*,5*s*,6*aS*)-*N*-(3-méthoxy-1,2,4-thiadiazol-5-yl)-5-[méthyl(*7H*-pyrrolo[2,3-*d*]pyrimidin-4-yl)amino]hexahydrocyclopenta[*c*]pyrrole-2(*1H*)-carboxamide

ivarmacitinib

(3*aR*,5*s*,6*aS*)-5-[metil(*7H*-pirrolo[2,3-*d*]pirimidin-4-il)amino]-*N*-(3-metoxi-1,2,4-tiadiazol-5-il)hexahidrociopenta[*c*]pirrol-2(*1H*)-carboxamida

C₁₈H₂₂N₈O₂S**izalontamabum #**

izalontamab

immunoglobulin G1-scFv_L-kappa dimer, anti-[*Homo sapiens* EGFR (epidermal growth factor receptor, receptor tyrosine-protein kinase erbB-1, ERBB1, HER1, HER-1, ERBB)] and anti-[*Homo sapiens* ERBB3 (receptor tyrosine-protein kinase erbB-3, HER3)], monoclonal antibody, tetravalent, bispecific;
G1-scFv fused chain (1-702) [gamma1 heavy chain anti-EGFR (1-448) [VH (*Mus musculus* IGHV2-2*03 (93.8%) - (IGHD) -IGHJ3*01 (92.9%) A128>S (119), CDR-IMGT [8.7.13] (26-33.51-57.96-108))] (1-119) -*Homo sapiens* IGHG1*08p (100%), G1m3,1 (CH1 I103 (201), R120 (216) (120-217), hinge 1-15 (218-232), CH2 (233-342), CH3 D12 (358), L14 (360) (343-447), CHS K2>del (448)) (120-448)] -10-mer bis(tetraglycyl-seryl) linker (449-458) -scFv heavy-lambda anti-ERBB3 (459-702) [VH (*Homo sapiens* IGHV3-7*01 (91.8%) -(IGHD) -IGHJ2*01 (100%), CDR-IMGT [8.8.11] (484-491.509-516.555-565)) (459-576) -15-mer tris(tetraglycyl-seryl) linker (577-591) -V-LAMBDA (*Homo sapiens* IGLV2-14*03 (93.9%) -IGLJ2*01 (83.3%) L124>V (699), CDR-IMGT [9.3.11] (617-625.643-645.682-692)) (592-702)], (222-214')-disulfide with kappa light chain anti-EGFR (1'-214') [V-KAPPA (*Mus musculus* IGKV5-48*01 (95.8%) -IGKJ5*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (228-228":231-231")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

izalontamab

immunoglobuline G1-scFv_L-kappa dimère, anti-[*Homo sapiens* EGFR (récepteur du facteur de croissance épidermique, récepteur tyrosine-protéine kinase erb-1, ERBB1, HER1, HER-1, ERBB)], et anti-[*Homo sapiens* ERBB3 (récepteur à activité tyrosine kinase erbB-3, HER3)], anticorps monoclonal, tétravalent, bispécifique;

chaîne lourde fusionnée G1-scFv (1-702) [gamma1 anti-EGFR chimérique (1-448) [VH (*Mus musculus* IGHV2-2*03 (93.8%) -(IGHD) -IGHJ3*01 (92.9%) A128>S (119), CDR-IMGT [8.7.13] (26-33.51-57.96-108)) (1-119) -*Homo sapiens* IGHG1*08p (100%), G1m3,1 (CH1 I103 (201), R120 (216) (120-217), charnière 1-15 (218-232), CH2 (233-342), CH3 D12 (358), L14 (360) (343-447), CHS K2>del (448)) (120-448)] -10-mer bis(tétraglycyl-séryl) linker (449-458) -scFv lourde-lambda anti-ERBB3 (459-702) [VH (*Homo sapiens* IGHV3-7*01 (91.8%) -(IGHD) -IGHJ2*01 (100%), CDR-IMGT [8.8.11] (484-491.509-516.555-565)) (459-576) -15-mer tris(tétraglycyl-séryl) linker (577-591) -V-LAMBDA (*Homo sapiens* IGLV2-14*03 (93.9%) -IGLJ2*01 (83.3%) L124>V (699), CDR-IMGT [9.3.11] (617-625.643-645.682-692)) (592-702)]]; (222-214')-disulfure avec la chaîne légère kappa anti-EGFR (1'-214') [V-KAPPA (*Mus musculus* IGKV5-48*01 (95.8%) -IGKJ5*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]]; dimère (228-228":231-231")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

izalontamab

immunoglobulina G1-scFv_L-kappa dímero, anti-[*Homo sapiens* EGFR (receptor del factor de crecimiento epidérmico, receptor tirosina-proteína quinasa erb-1, ERBB1, HER1, HER-1, ERBB)], y anti-[*Homo sapiens* ERBB3 (receptor con actividad tirosina quinasa erbB-3, HER3)], anticuerpo monoclonal, tetravalente, biespecífico;

cadena pesada fusionada G1-scFv (1-702) [gamma1 anti-EGFR (1-448) [VH (*Mus musculus* IGHV2-2*03 (93.8%) -(IGHD) -IGHJ3*01 (92.9%) A128>S (119), CDR-IMGT [8.7.13] (26-33.51-57.96-108)) (1-119) -*Homo sapiens* IGHG1*08p (100%), G1m3,1 (CH1 I103 (201), R120 (216) (120-217), bisagra 1-15 (218-232), CH2 (233-342), CH3 D12 (358), L14 (360) (343-447), CHS K2>del (448)) (120-448)] -10-mer bis(tetraglicil-seril) linker (449-458) -scFv pesado-lambda anti-ERBB3 (459-702) [VH (*Homo sapiens* IGHV3-7*01 (91.8%) -(IGHD) -IGHJ2*01 (100%), CDR-IMGT [8.8.11] (484-491.509-516.555-565)) (459-576) -15-mer tris(tetraglicil-seril) linker (577-591) -V-LAMBDA (*Homo sapiens* IGLV2-14*03 (93.9%) -IGLJ2*01 (83.3%) L124>V (699), CDR-IMGT [9.3.11] (617-625.643-645.682-692)) (592-702)]]; (222-214')-disulfuro con la cadena ligera kappa anti-EGFR (1'-214') [V-KAPPA (*Mus musculus* IGKV5-48*01 (95.8%) -IGKJ5*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]]; dímero (228-228":231-231")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada (anti-EGFR, anti-ERBB3)

QVQLKQSGPG LVQPSQSLSI TCTVSGFSLT NYGVHWRVRS PGKGLEWLVG 50
 IWSGGNTDYN TPTFRLSIN KDNKSKQVFF KMNSLQSDNT AIYYCARALT 100
 YYDFEFAYWG QGTLVTVSSA STKGFVSVPL APSSKSTSGG TAALGLCVKD 150
 YFPEPVTWSV NSGALTSGVH TFFAVLQSSG LYSLSVVTV PSSSLGTQT 200
 ICNVNHNKPSN TKVDKRVEPK SCDKTHTCP CPAPPELLGPG SVFLFPPKPK 250
 DTLMISRTPF VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKFREEQYNS 300
 TYRVVSVLTV LHQDVLNGKE YKCKVSKNAL PAPIEKTIISK AKGQPREPQV 350
 YTLFPPRDEL TKNQVSLTCL VGFYFSDIA VEWESNGQFE NNYKTFPPVL 400
 DSDGFFFLYS KLTVDKSRWQ QGNVFSVSM HEALHNHYTQ KSLSLSPGGG 450
 GSGGGGGSQV QLQESGGGLV KPGGSLRLSC AASGFTFSSY WMSWVRQAPG 500
 KGLEWVANIN RDGSASYVDV SVKGRFTISR DDAKNSLYLQ MNSLRAEDTA 550
 VYYCARDRQV GYFDLWGRGT LVTVSSGGGG SGGGGSGGGG SQSALTQPAS 600
 VSGSPGQSIT ISCTGTSDDV GGYNFVSWYQ QHPGKAPKLM IYDVSDRPSG 650
 VSDRFRSGSKS GNTASLIISG LQADDEADYY CSSYSSSSTH VIFGGGTRVT 700
 VL 702

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

DILLTQSFVI LSVSPGERVS FSCRASQSIG TNIHWYQQRT NGSPRLLIKY 50
 ASESISGIPR RFSGGSGSDT FTLSINSVSE EDIADYCCQG NNNWPTTFFGA 100
 GTKLELRKRV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
 DNALQSGNSQ ESVTEQDQSKD STYLSLSTLT LSKADYKHKH VYACEVTHQG 200
 LSSPVTKSFN RGEV 214

Post-translational modifications

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
 Intra-H (C23-C104) 22°-95' 146°-202' 263°-323' 369°-427' 480°-554' 613°-681'
 22°-95' 146°-202' 263°-323' 369°-427' 480°-554' 613°-681"
 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 glutamínilo N-terminal
 H VH QI > pyroglutamyl (pE, 5-oxoprolyl): 1, 1"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
 H VH N97: 88, 88"
 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.

izenivetmabum #
izenivetmab

immunoglobulin G2-kappa, anti-[*Canis lupus familiaris* NGF (nerve growth factor beta polypeptide, NGFB)], caninized monoclonal antibody; gamma2 heavy chain caninized (1-453) [VH (*Canis lupus familiaris* IGHV3-67*01 (82.7%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Canis lupus familiaris* IGHG2*02 (CH1 (119-215), hinge 1-19 (216-234), CH2 M1.3>A (238), L1.2>A (239), G1>A (241) (235-344), CH3 (345-451), CHS (452-453)) (119-453)], (133-213')-disulfide with kappa light chain caninized (1'-213') [V-KAPPA (*Canis lupus familiaris* IGKV3-18*02 (85.7%) -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 (230-230":233-233")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1SV lacking the glutamine synthetase (GS-KO) gene, glycoform alfa

izénivetmab

immunoglobuline G2-kappa, anti-[*Canis lupus familiaris* NGF (facteur de croissance du nerf polypeptide bêta, NGFB)], anticorps monoclonal caninisé; chaîne lourde gamma2 caninisée (1-453) [VH (*Canis lupus familiaris* IGHV3-67*01 (82.7%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Canis lupus familiaris* IGHG2*02 (CH1 (119-215), charnière 1-19 (216-234), CH2 M1.3>A (238), L1.2>A (239), G1>A (241) (235-344), CH3 (345-451), CHS (452-453)) (119-453)], (133-213')-disulfure avec la chaîne légère kappa caninisée (1'-213') [V-KAPPA (*Canis lupus familiaris* IGKV3-18*02 (85.7%) -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 (230-230":233-233")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1SV ne présentant pas le gène de la glutamine synthétase (GS-KO), glycoforme alfa

izenivetmab

immunoglobulina G2-kappa, anti-[*Canis lupus familiaris* NGF (factor de crecimiento del nervio polipéptido beta, NGFB)], anticuerpo monoclonal caninizado; cadena pesada gamma2 caninizada (1-453) [VH (*Canis lupus familiaris* IGHV3-67*01 (82.7%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [8.8.11] (26-33.51-58.97-107))] (1-118) -*Canis lupus familiaris* IGHG2*02 (CH1 (119-215), bisagra 1-19 (216-234), CH2 M1.3>A (238), L1.2>A (239), G1>A (241) (235-344), CH3 (345-451), CHS (452-453)) (119-453)], (133-213')-disulfuro con la cadena ligera kappa caninizada (1'-213') [V-KAPPA (*Canis lupus familiaris* IGKV3-18*02 (85.7%) -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 (230-230":233-233")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1SV en ausencia del gen glutamina sintetasa (GS-KO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGD LVKPGGSLRL SCVASGFTFS NYWMHWVRQA PGKGLQWAR 50
IDPYGGGTKH NEKFKRRFTI SRDNAKNTLY LQMNSLRAED TAMYYCVRSR 100
YDYFYFDVWGQ GTLVTVSSAS TTAFTSVEFLA PSCGSTSGST VALACLVSGY 150
FPEFVTVSWN SGLSLTSGVHT PPSVLQSSGL YSLSSMVTVP SSRWPESETT 200
CNVAHFASKT KVDKPYPKRE NGRVPRPPDC PKCPAPEAAG AFSVFIFFPK 250
PKDTLLIART PEVTCVVDL DPEDPEVQIS WFDGKQMQT AKTQPREEQF 300
NGTYRVVSVL PIGHQDMLKG KQFTCKVNNK ALFSPFIERTI SKARGQAHP 350
SVYYLPPSR ELSKNTVSLT CLIKDFEPPD IDVERQSNQG QEPESKYRTT 400
FPQLDEGDSY FLYSKLSVDK SRWQRGDTFI CAVMHEALHN HYTQESLSHS 450
PGK 453
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Light chain / Chaîne légère / Cadena ligera

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EIVMTQSPAS LLSLQEEKVT ITCRASENIY SFLAWYQQKQ GQAPKLLIYN 50
ANTLAEGVPS RFSGGSGSDT FSFTISSLEP EDVAVYYCQH HFGTPTFPQG 100
GTKLEIKRND AQPAVYLFQP SPDQLHTGSA SVVCLNSFY PKDINVKWKV 150
DGVIQDTGIQ ESVTEQDKDS TYSLSLTLM 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) 22-96 145-201 265-325 371-431
22"-96" 145"-201" 265"-325" 371"-431"

Intra-L (C23-C104) 23"-88" 134"-193"
23"-88" 134"-193"

Inter-H-L (CH1 11-CL 126) 133-213' 133"-213"

Inter-H-H (h 15, h 19) 230-230" 233-233"

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

HCH2 N84.4; 301, 301"

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

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

izilendustatum

izilendustat

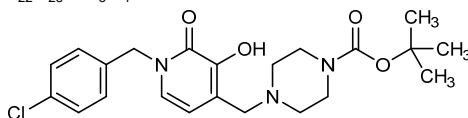
tert-butyl 4-({1-[(4-chlorophenyl)methyl]-3-hydroxy-2-oxo-1,2-dihydropyridin-4-yl)methyl}piperazine-1-carboxylate

izilendustat

4-({1-[(4-clorofénil)méthyl]-3-hydroxy-2-oxo-1,2-dihydropyridin-4-yl)méthyl}pipérazine-1-carboxylate de *tert*-butyle

izilendustat

4-({1-[(4-clorofenil)metil]-3-hidroxi-2-oxo-1,2-dihidropiridin-4-il}metil)piperazina-1-carboxilato de *terc*-butilo

**izorlisibum**

izorlisib

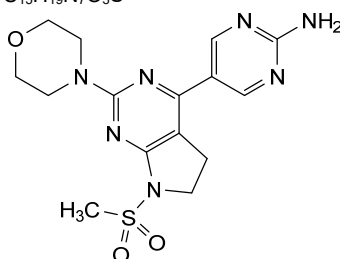
5-[7-(methanesulfonyl)-2-(morpholin-4-yl)-6,7-dihydro-5H-pyrrolo[2,3-d]pyrimidin-4-yl]pyrimidin-2-amine

izorlisib

5-[7-(méthanesulfonyl)-2-(morpholin-4-yl)-6,7-dihydro-5H-pyrrolo[2,3-d]pyrimidin-4-yl]pyrimidin-2-amine

izorlisib

5-[7-(metanosulfonyl)-2-(morfolin-4-il)-6,7-dihidro-5H-pirrolo[2,3-d]pirimidin-4-il]pirimidin-2-amina

**lafadofensinum**

lafadofensine

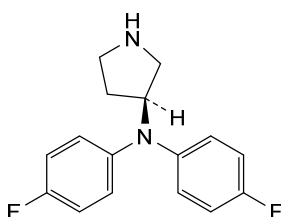
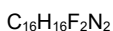
(3S)-N,N-bis(4-fluorophenyl)pyrrolidin-3-amine

lafadofensine

(3S)-N,N-bis(4-fluorophényl)pyrrolidin-3-amine

lafadofensina

(3S)-N,N-bis(4-fluorofenil)pirrolidin-3-amina

**laruparetigenum zovaparvovecum #**

laruparetigene zovaparvovec

recombinant, non-replicating adeno-associated virus serotype 2 (AAV2) vector, in which the capsid contains three tyrosine (Y) to phenylalanine (F) mutations (AAV2tYF), encoding codon-optimised human retinitis pigmentosa GTPase regulator (RPGR) isoform 6 (RPGR-ORF15), under control of the human G protein-coupled receptor kinase 1 promoter, preceded by a synthetic splice donor/splice acceptor, terminated with the simian virus 40 (SV40) polyadenylation (polyA) sequence, and flanked by AAV2 inverted terminal repeats (ITRs).

laruparétigène zovaparvec

vecteur recombinant et non répliquant du virus adéno-associé de sérotype 2 (AAV2), dont la capside présente trois mutations de la tyrosine (Y) à la phénylalanine (F) (AAV2tYF), codant pour l'isoforme 6 du régulateur de la GTPase de la rétinite pigmentaire humaine (RPGR) aux codons optimisés (RPGR-ORF15), sous le contrôle du promoteur du récepteur de la kinase 1 humain couplé à la protéine G, précédé d'un site synthétique donneur/accepteur d'épissage, terminé par la séquence polyadénylation (polyA) du virus simien 40 (SV40), et flanqué de répétitions terminales inversées (ITR) d'AAV2.

laruparetigén zovaparvec

vector de virus adenoasociado recombinante de serotipo 2 (AAV2) no replicativo, en el que la cápsida contiene tres mutaciones de tirosina (Y) a fenilalanina (F) (AAV2tYF), que codifica para la isoforma 6 del regulador GTPasa de la retinitis pigmentosa (RPGR) humana (RPGR-ORF15), con codones optimizados, bajo el control del promotor del receptor acoplado a proteína G quinasa 1 humano, precedido por un donante/aceptor de procesamiento sintéticos, terminado con la secuencia poliadenilación (polyA) del virus simio 40 (SV40) y flanqueado por las repeticiones terminales invertidas (ITRs) del AAV2.

latikafuspum #
latikafusp

human immunoglobulin G1-lambda, anti-(human programmed cell death protein 1), with one gamma1 heavy chain (1-450, variant R>C²⁹⁶, N>G³⁰¹, V>C³⁰⁶, E>K³⁶⁰, D>K⁴⁰³, C-terminal K⁴⁵¹ deleted) fused at the C-terminus to a human interleukin 21 fragment (1-133, 451-583 in the current sequence) variant (R⁹>E⁴⁵⁹, R⁷⁶>A⁵²⁶), disulfide bridged to gamma1 heavy chain (1-451, variant R>C²⁹⁶, N>G³⁰¹, V>C³⁰⁶, K>D³⁹⁶, K>D⁴¹³), with each gamma1 chain disulfide bridged to the same lambda light chain, non-glycosylated, produced in Chinese hamster ovary (CHO) cells; immunoglobulin G1-lambda, anti-[*Homo sapiens* PDCD1 (programmed cell death protein 1, PD1, PD-1, CD279)], *Homo sapiens* monoclonal antibody derived from a transgenic mouse, fused at the C-terminus of one of the heavy chains to a human interleukin 21 fragment; gamma1 heavy chain *Homo sapiens* (1-451) [VH (*Homo sapiens* IGHV3-20*04 (90.8%) -(IGHD) -IGHJ5*02 (100%), CDR-Kabat [5.17.12] (31-35.50-66.99-110)), (1-121) -*Homo sapiens* IGHG1*03 (CH1 R²¹⁸>K (122-219), hinge (220-234), CH2 R²⁹⁶>C, N³⁰¹>G, V³⁰⁶>C (235-344), CH3 E³⁶⁰>K, D⁴⁰³>K (345-449), CHS K⁴⁵¹>del (450)) (122-450)], fused to interleukin-21 (IL-21) (451-583) [R⁹>E⁴⁵⁹, R⁷⁶>A⁵²⁶]-mutant, (224-213')-disulfide with lambda light chain *Homo sapiens* (1'-214') [V-LAMBDA (*Homo sapiens* IGLV3-10*01 (95.8%) -IGLJ2*01 (100%), CDR-Kabat [11.7.11] (23-33.49-55.88-98)) (1'-108') -*Homo sapiens* IGLC2*01 (100%) (109'-214')]; gamma1 heavy chain *Homo sapiens* (1''-451'') [VH (*Homo sapiens* IGHV3-20*04 (90.8%) -(IGHD) -IGHJ5*02 (100%), CDR-Kabat [5.17.12] (31-35.50-66.99-110)) (1''-121'') -*Homo sapiens* IGHG1*03 (CH1 R²¹⁸>K (122''-219''), hinge (220''-234''), CH2 R²⁹⁶>C, N³⁰¹>G, V³⁰⁶>C (235''-344''), CH3 K³⁹⁶>D, K⁴¹³>D (345''-449''), CHS (450''-451'')) (122''-451'')], (224''-213'')-disulfide with lambda light chain *Homo sapiens* (1'''-214''') [V-LAMBDA (*Homo sapiens* IGLV3-10*01 (95.8%) -IGLJ2*01 (100%) CDR-Kabat [11.7.11] (23-33.49-55.88-98)) (1'''-108''') -*Homo sapiens* IGLC2*01 (100%) (109'''-214''')]; (230-230'':233-233'')-bisdisulfide, non-glycosylated, produced in Chinese hamster ovary (CHO) cells

- latikafusp immunoglobuline G1-lambda humaine, anti-(protéine 1 de mort cellulaire programmée humaine), une chaîne lourde $\gamma 1$ (1-450, variant R>C²⁹⁶, N>G³⁰¹, V>C³⁰⁶, E>K³⁶⁰, D>K⁴⁰³, K⁴⁵¹ C-terminal supprimé) fusionnée au C-terminal avec un fragment d'interleukine 21 humaine (1-133, 451-583 dans la séquence actuelle) variant (R⁹>E⁴⁵⁹, R⁷⁶>A⁵²⁶), attachée à la chaîne lourde $\gamma 1$ par ponts disulfure (1-451, variant R>C²⁹⁶, N>G³⁰¹, V>C³⁰⁶, K>D³⁹⁶, K>D⁴¹³), avec chaque chaîne $\gamma 1$ attachée à la même chaîne légère λ par des ponts disulfure, non glycosylée, produite dans des cellules d'ovaire de hamster chinois (CHO); immunoglobuline G1-lambda, anti-[*Homo sapiens* PDCD1 (mort cellulaire programmée 1, PD1, PD-1, CD279)], anticorps monoclonal d'*Homo sapiens* dérivé d'une souris transgénique, fusionné à l'extrémité C-terminale de l'une des chaînes lourdes à un fragment d'interleukine 21 humaine; chaîne lourde gamma1 d'*Homo sapiens* (1-451) [VH (*Homo sapiens*IGHV3-20*04 (90,8%) -(IGHD) -IGHJ5*02 (100%), CDR-Kabat [5.17.12] (31-35.50-66.99-110)), (1-121) -*Homo sapiens*IGHG1*03 (CH1 R²¹⁸>K (122-219), charnière (220-234), CH2 R²⁹⁶>C, N³⁰¹>G, V³⁰⁶>C (235-344), CH3 E³⁶⁰>K, D⁴⁰³>K (345-449), CHS K⁴⁵¹>del (450)) (122-450)], fusionné à l'interleukine-21 (IL-21) (451-583) [R⁹>E⁴⁵⁹, R⁷⁶>A⁵²⁶] -mutant, (224-213')-disulfure avec la chaîne légère lambda d'*Homo sapiens* (1'-214') [V-LAMBDA (*Homo sapiens*IGLV3-10*01 (95,8%) -IGLJ2*01 (100%), CDR-Kabat [11.7.11] (23-33.49-55.88-98)) (1'-108') -*Homo sapiens*IGLC2*01 (100%) (109'-214')]; chaîne lourde gamma1 d'*Homo sapiens* (1''-451'') [VH (*Homo sapiens*IGHV3-20*04 (90,8%) -(IGHD) -IGHJ5*02 (100%), CDR-Kabat [5.17.12] (31-35.50-66.99-110)) (1''-121'') -*Homo sapiens*IGHG1*03 (CH1 R²¹⁸>K (122''-219''), charnière (220''-234''), CH2 R²⁹⁶>C, N³⁰¹>G, V³⁰⁶>C (235''-344''), CH3 K³⁹⁶>D, K⁴¹³>D (345''-449''), CHS (450''-451'')) (122''-451'')], (224''-213'')-disulfure avec la chaîne légère lambda d'*Homo sapiens* (1'''-214''') [V-LAMBDA (*Homo sapiens*IGLV3-10*01 (95,8%) -IGLJ2*01 (100%) CDR-Kabat [11.7.11] (23-33.49-55.88-98)) (1'''-108''') -*Homo sapiens*IGLC2*01 (100%) (109'''-214''')]; (230-230''':233-233'')-bis-disulfure, non glycosylé, produite dans des cellules d'ovaire de hamster chinois (CHO)
- latikafusp inmunoglobulina humana G1-lambda, anti-(proteína humana 1 de muerte celular programada), una cadena pesada $\gamma 1$ (1-450, variante R>C²⁹⁶, N>G³⁰¹, V>C³⁰⁶, E>K³⁶⁰, D>K⁴⁰³, terminal C K⁴⁵¹ eliminada) fusionada con el terminal C con el fragmento de una interleukina 21 (1-133, 451-583 en la secuencia actual) variante (R⁹>E⁴⁵⁹, R⁷⁶>A⁵²⁶), unida al disulfuro a una cadena pesada $\gamma 1$ (1-451, variante R>C²⁹⁶, N>G³⁰¹, V>C³⁰⁶, K>D³⁹⁶, K>D⁴¹³), con cada cadena $\gamma 1$ unida al disulfuro a la misma cadena ligera λ , no glicosilada, producida en células ováricas de hámster chino (CHO); inmunoglobulina G1-lambda, anti-[*Homo sapiens* PDCD1 (muerte celular programada 1, PD1, PD-1, CD279)], *Homo sapiens* anticuerpo monoclonal derivado de un ratón transgénico, fusionado en el terminal de una de las cadenas pesada al fragmento humano de la interleukina 21; cadena pesada gamma1 *Homo sapiens* (1-451) [VH (*Homo sapiens*IGHV3-20*04 (90,8%) -(IGHD) -IGHJ5*02 (100%), CDR-Kabat [5.17.12] (31-35.50-66.99-110)), (1-121) -*Homo sapiens*IGHG1*03 (CH1 R²¹⁸>K (122-219), bisagra (220-234), CH2 R²⁹⁶>C, N³⁰¹>G, V³⁰⁶>C (235-344), CH3 E³⁶⁰>K, D⁴⁰³>K (345-449), CHS K⁴⁵¹>del (450)) (122-450)], fusionada a la interleukina-21 (IL-21) (451-583) [R⁹>E⁴⁵⁹, R⁷⁶>A⁵²⁶] -mutante, (224-213')-disulfuro con la cadena ligera lambda *Homo sapiens* (1'-214') [V-LAMBDA (*Homo sapiens*IGLV3-10*01 (95,8%) -IGLJ2*01 (100%), CDR-Kabat [11.7.11] (23-33.49-55.88-98)) (1'-108') -*Homo sapiens*IGLC2*01 (100%) (109'-214')]; cadena pesada gamma1 *Homo sapiens* (1''-451'') [VH (*Homo sapiens*IGHV3-20*04 (90,8%) -(IGHD) -IGHJ5*02 (100%), CDR-Kabat [5.17.12] (31-35.50-66.99-110)) (1''-121'') -*Homo sapiens*IGHG1*03 (CH1 R²¹⁸>K (122''-219''), bisagra (220''-234''), CH2 R²⁹⁶>C, N³⁰¹>G, V³⁰⁶>C (235''-344''), CH3 K³⁹⁶>D, K⁴¹³>D (345''-449''), CHS (450''-451'')) (122''-451'')], (224''-213'')-disulfuro con la cadena ligera lambda *Homo sapiens* (1'''-214''') [V-LAMBDA (*Homo sapiens*IGLV3-10*01 (95,8%) -IGLJ2*01 (100%) CDR-Kabat [11.7.11] (23-33.49-55.88-98)) (1'''-108''') -*Homo sapiens*IGLC2*01 (100%) (109'''-214''')]; (230-230''':233-233'')-bisdisulfuro, no glicosilada, producida en células ováricas de hámster chino (CHO)

Heavy chain × IL21 / Chaîne lourde × IL21 / Cadena pesada × IL21
 EVQLVESGGS VVRPGGSLRL SCAASGFTVD DYMSWVRQV PGKLEWVSG 50
 INWNAGRTRY ADAVKGRTFI SRDSAKNSLY LQMNSLRAED TALYYCAREF 100
 NNFESNWFDV WGQGTLVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150
 KDYFPEPVTV SWNSGALTSV VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200
 TYICNVNHKP SNTKVDK**K**VE PKSCDKTHTC PPCPAPELLG GPSVFLFPPK 250
 PKDTLMISRT FEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKP**C**EEQY 300
GSTYR**C**VSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP 350
 QVYTLPPSR**K** EMTKNQVSLT CLVKGIFYSD IAVWEWSNGQ PENNYKTTTP 400
 VL**K**SDGSFFL YSKLTVDKSR WQQGNVFSVS VMHEALHNHY TQKSLSLSPG 450
CGQDRHMI**E**M RQLIDIVDQL KNYVNDLVPE FLPAPEDEVET NCEWSAFSCF 500
QKAQLKSANT GNNERI INVS IKKLR**A**KPPS TNAGRRQRKR LTCFSCDSYE 550
KKPPKEFLER FKSLQKMIH QHLSSRTHGS EDS 583

Heavy chain / Chaîne lourde / Cadena pesada (*)
 EVQLVESGGS VVRPGGSLRL SCAASGFTVD DYMSWVRQV PGKLEWVSG 50
 INWNAGRTRY ADAVKGRTFI SRDSAKNSLY LQMNSLRAED TALYYCAREF 100
 NNFESNWFDV WGQGTLVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150
 KDYFPEPVTV SWNSGALTSV VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200
 TYICNVNHKP SNTKVDK**K**VE PKSCDKTHTC PPCPAPELLG GPSVFLFPPK 250
 PKDTLMISRT FEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKP**C**EEQY 300
GSTYR**C**VSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP 350
 QVYTLPPSR**E** EMTKNQVSLT CLVKGIFYSD IAVWEWSNGQ PENNY**D**TTTP 400
 VLSDGSFFL YS**D**LTVDKSR WQQGNVFSVS VMHEALHNHY TQKSLSLSPG 450
 K 451

Light chain / Chaîne légère / Cadena ligera
 SYELTQPPSV SVSPGQTARI TCSGDALPKK YAYWYQQ**K**P**G** QAPVLVISED 50
AKRPSGIPER FSGSSSGTMA IRLTISGAQVE DEADYYCYST **D**ASGNHRVFG 100
 GGTKLTVLGQ PKAAPSVTLF PPSSEELQAN KATLVCLISD FYPGAVTVAW 150
 KADSSPVKAG VETTTPSKQS NNKYAASSYL SLTPEQWKSH RYSYCSQVTHE 200
 GSTVEKTVAP TECS 214

Mutation / Mutation / Mutación
 R218, R218"**>K**", R296, R296"**>C**", N301, N301"**>G**", V306, V306"**>C**;
 E360 **>K**, D403 **>K**, K451 **>deL**, **R459****>E**, **R526****>A**;
 K396"**>D**", K413"**>D**;
 S39', 39"**>E**, S51', 51"**>A**, S92', 92"**>A**

Post-translational modifications
 Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
 Intra-H 22-96 148-204 265-325 296-306 371-429
 22"-96" 148"-204" 265"-325" 296"-306" 371"-429"
 Intra-IL21 492-543 499-546 (predicted)
 Intra-L 22-87' 136-195'
 22"-87" 136"-195"
 Inter-H-L 224-213' 224"-213"
 Inter-H-H 230-230" 233-233"
 N-glycosylation sites / Sites de N-glicosylation / Posiciones de N-glicosilación
 none / aucun / ninguna (N301, N301"**>G**; N518 not glycosylated)
 C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
 H CHS K2: K451"

Icelimogenum autotemcelum #
 icelimogene autotemcel

autologous CD34+ cells obtained by apheresis from mobilised peripheral blood of patients who received a prior hematopoietic stem cell transplant, transduced *ex vivo* with a self-inactivating lentiviral vector, encoding codon-optimized human interleukin-2 receptor subunit gamma (IL2RG) also known as common gamma chain (γ_c), driven by a short version of the EF1 α promoter. The vector contains human immunodeficiency virus (HIV) central polyurine tract sequences, the HIV Rev response element (RRE) and is flanked by HIV long terminal repeats. The vector also contains a 400 bp insulator fragment from the chicken β -globin locus inserted into the deleted U3 region of the HIV long terminal repeat followed by a polyadenylation sequence derived from the rabbit β -globin gene. The vector is pseudotyped with the envelope glycoprotein (G) of vesicular stomatitis virus (VSV). The suspension is enriched for CD34+ cells using magnetic bead separation. The cells are overnight cultured in media containing human serum albumin (1%), human stem cell factor (SCF), human thrombopoietin protein (TPO), and human Flt3 ligand (Flt3L) prior to vector transduction.

lécilimogène autotemcel

cellules CD34+ autologues obtenues par aphérèse à partir de sang périphérique mobilisé de patients ayant déjà reçu une greffe de cellules souches hématopoïétiques, transduites *ex vivo* avec un vecteur lentiviral auto-inactivant, codant la sous-unité gamma du récepteur de l'interleukine-2 (IL2RG) humaine aux codons optimisés, également connue sous le nom de chaîne gamma commune (γ_c), dirigée par une version courte du promoteur EF1 α . Le vecteur contient des séquences du tractus polypurine central du virus de l'immunodéficience humaine (VIH), l'élément de réponse Rev (RRE) du VIH et est flanqué de longues répétitions terminales du VIH. Le vecteur contient également un fragment isolateur de 400 pb du locus de la β -globine de poulet inséré à la place de la région U3 supprimée de la longue répétition terminale du VIH, suivi d'une séquence de polyadénylation dérivée du gène de la β -globine de lapin. Le vecteur est pseudotypé avec la glycoprotéine de l'enveloppe (G) du virus de la stomatite vésiculaire (VSV). La suspension est enrichie en cellules CD34+ utilisant la séparation par billes magnétiques. Les cellules sont cultivées pendant une nuit dans du milieu contenant de l'albumine sérique humaine (1 %), du facteur de cellules souches humain (SCF), de la protéine thrombopoïétine humaine (TPO) et du ligand Flt3 humain (Flt3L) avant la transduction du vecteur.

leclimogén autotemcel

células CD34+ autólogas obtenidas a partir de células movilizadas en sangre periférica mediante aféresis de pacientes que recibieron previamente un trasplante de células madre hematopoyéticas, transducidas *ex vivo* con un vector lentiviral auto inactivante, que codifica para la subunidad gamma del receptor de interleuquina 2 (IL2RG) humano, también conocido como la cadena gamma común (γ_c), con codones optimizados, dirigido por una versión corta del promotor EF1 α . El vector contiene secuencias del tracto de poli-purina central del virus de la inmunodeficiencia humana (VIH), el elemento de respuesta Rev (RRE) del VIH y está flanqueado por repeticiones terminales largas del VIH. El vector también contiene un fragmento aislante de 400 pares de bases del locus de la β -globina de pollo insertado en la región delecionada U3 de la repetición terminal larga del VIH seguido de una secuencia de poliadenilación derivada del gen de la β -globina de conejo. El vector está seudotipado con la glicoproteína de la envuelta (G) del virus de la estomatitis vesicular (VSV). La suspensión se enriquece en células CD34+ mediante separación con bolas magnéticas. Las células se incuban una noche en medio que contiene albúmina sérica humana (1%), factor de células madre humano (SCF), proteína trombopoyetina humana (TPO) y ligando Flt3 humano (Flt3L) antes de la transducción con el vector.

lesabelimabum

lesabelimab

immunoglobulin G1-kappa, anti-[*Homo sapiens* CD274 (programmed death ligand 1, PDL1, PD-L1, B7 homolog 1, B7H1)], monoclonal antibody; gamma1 heavy chain (1-448) [VH (*Homo sapiens* IGHV3-66*01 (79.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.7.10] (26-33.51-57.98-107)) (1-118) - *Homo sapiens* IGHG1*01 (100%), G1m17,1 (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)], (221-216')-disulfide with kappa light chain (1'-216') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (92.6%) -IGKJ1*01 (91.7%), 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 (227-227":230-230")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa

lésabélimab

immunoglobuline G1-kappa, anti-[*Homo sapiens* CD274 (ligand 1 de mort programmée, PDL1, PD-L1, homologue 1 de B7, B7H1)], anticorps monoclonal; chaîne lourde gamma1 (1-448) [VH (*Homo sapiens* IGHV3-66*01 (79.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.7.10] (26-33.51-57.98-107)) (1-118) - *Homo sapiens* IGHG1*01 (100%), G1m17,1 (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)], (221-216')-disulfure avec la chaîne légère kappa (1'-216') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (92.6%) -IGKJ1*01 (91.7%), 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 (227-227":230-230")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa

lesabelimab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CD274 (ligando 1 de muerte programada, PDL1, PD-L1, homólogo 1 de B7, B7H1)], anticuerpo monoclonal; cadena pesada gamma1 (1-448) [VH (*Homo sapiens* IGHV3-66*01 (79.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.7.10] (26-33.51-57.98-107)) (1-118) - *Homo sapiens* IGHG1*01 (100%), G1m17,1 (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)], (221-216')-disulfuro con la cadena ligera kappa (1'-216') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (92.6%) -IGKJ1*01 (91.7%), 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 (227-227":230-230")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

EVQLVESGGG	LVQPGGSLRL	SCAASGYSIS	SGYYWGWIQK	APGKGLEWIG	50
I IYFSGGGTN	YAQFQGRVT	ISRDNKNTL	YLQLNLSRAE	DTAVVYCARG	100
GGLGFDYWGQ	GTLVTVSSAS	TKGPSVFPLA	PSKSTSGGT	AALGCLVKDY	150
FFEPVTVSWN	SGALTSGVHT	FPAVLQSSGL	YLSL SVVTVP	SSSLGTQTYI	200
CNVNHKPSNT	KVDKKVEPKS	CDKTHCTCPP	PAPELLGGPS	VFLFPKPKD	250
TLMISRTPEV	TCVVVDVSH	DPEVKFNWYV	DGVEVHNAKT	KPREEQYNST	300
YRVVSVLTVL	HQDWLNGKEY	KCKVSNKALP	APIEKTIISKA	KGQPREPQVY	350
TLPPSRDEL	KNQVSLTCLV	KGFYPSDIAV	EWESNGQFEN	NYKTTTTPVLD	400
SDGSFFLYSK	LTVDKSRWQQ	GNVFSCSVHM	EALHNHYTQK	SLSLSPGK	448

Light chain / Chaîne légère / Cadena ligera

DIQLTQSPSS	LSASVGDVRT	ITCRASQSQIP	SFLNWIYQQK	GKAPKLLIYA	50
ASLSQSGVPS	RFGSGSGSDT	FTLTISSLQP	EDFATYYCQH	YISWPRQPTF	100
QGQTKVEIKR	TVAAPSFIIF	PPSDEQLKSG	TASVVCLLNN	FYPREAKVQW	150
KVDNALQSGN	SQESVTEQDS	KDSTYSLSST	LTLSKADYEK	HKVYACEVTH	200
QGSSSFVTKS	FNRGEC				216

Post-translational modifications

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

Intra-H (C23-C104)	22-97	145-201	262-322	368-426
	22"-97"	145"-201"	262"-322"	368"-426"

Intra-L (C23-C104)	23"-88"	136"-196"
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Inter-H-L (h 5-CL 126)	221"-216"	221"-216"
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Inter-H-H (h 11, h 14)	227"-227"	230"-230"
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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.

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

linaprazan glurate

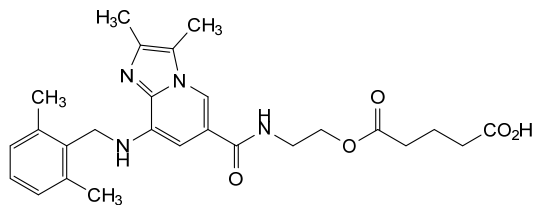
5-[2-(8-[[2,6-dimethylphenyl)methyl]amino]-2,3-dimethylimidazo[1,2-a]pyridine-6-carboxamido)ethoxy]-5-oxopentanoic acid

glurate de linaprazan

acide 5-[2-(8-[[2,6-diméthylphényl)méthyl]amino)-2,3-diméthylimidazo[1,2-a]pyridine-6-carboxamido)éthoxy]-5-oxopentanoïque

glurato de linaprazán

ácido 5-[2-(8-[[2,6-dimetilfenil)metil]amino)-2,3-dimetilimidazo[1,2-a]piridina-6-carboxamido)etoxi]-5-oxopentanoico

C₂₆H₃₂N₄O₅**linvencorvirum**

linvencorvir

3-[(8aS)-7-[[[(6S)-5-(ethoxycarbonyl)-6-(3-fluoro-2-methylphenyl)-2-(1,3-thiazol-2-yl)-1,6-dihydropyrimidin-4-yl]methyl]-3-oxohexahydroimidazo[1,5-a]pyrazin-2(3H)-yl]-2,2-dimethylpropanoic acid

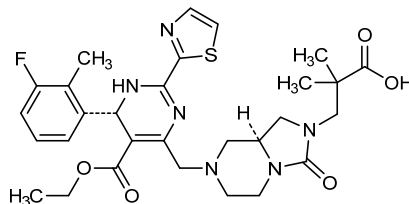
linvencorvir

acide 3-[(8aS)-7-[[[(6S)-5-(éthoxycarbonyl)-6-(3-fluoro-2-méthylphényl)-2-(1,3-thiazol-2-yl)-1,6-dihydropyrimidin-4-yl]méthyl]-3-oxohexahydroimidazo[1,5-a]pyrazin-2(3H)-yl]-2,2-diméthylpropanoïque

linvencorvir

ácido 3-[(8aS)-7-[[[(6S)-5-(etoxicarbonil)-6-(3-fluoro-2-metilfenil)-2-(1,3-tiazol-2-il)-1,6-dihidropirimidin-4-il]metil]-3-oxohexahidroimidazo[1,5-a]pirazin-2(3H)-il]-2,2-dimetilpropanoico

C₂₉H₃₅FN₆O₅S



linvoseltamabum #

linvoseltamab

immunoglobulin G4-kappa, anti-[*Homo sapiens* TNFRSF17 (TNF receptor superfamily member 17, tumor necrosis factor receptor superfamily, member 17, B cell maturation antigen, BCMA, BCM, TNFRSF13A, CD269)] and anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], *Homo sapiens* monoclonal antibody; 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, G4v7 CH2 del 1.4, P1.3, V1.2, A1.1 (G2-like) (CH1 (126-223), hinge 1-12 S10>P (233) (224-235), CH2 'E1.4,F1.3'>P1.3 (238), L1.2>V (239), G1.1>A (240) (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 (98.0%) -(IGHD) - IGHJ1*01 (90.9%) L123>T (119), CDR-IMGT [8.8.17] (26-33.51-58.97-113)) (1''-124'') -*Homo sapiens* IGHG4*01, G4v5 h P10, G4v8 CH3 R115, F116, P125 (CH1 (125''-222''), hinge 1-12 S10>P (232) (223''-239''), CH2 (240''-343''), CH3 H115>R (438), Y116>F (439), L125>P (448) (G3-like) (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, glycoform alfa

linvoseltamab

immunoglobuline G4-kappa, anti-[*Homo sapiens* TNFRSF17 (membre 17 de la superfamille des récepteurs du TNF, membre 17 de la superfamille des récepteurs du facteur de nécrose tumorale, antigène de maturation de cellule B, BCMA, BCM, TNFRSF13A, CD269)] et anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], anticorps monoclonal *Homo sapiens*;

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, G4v7 CH2 del 1.4, P1.3, V1.2, A1.1 (G2-like) (CH1 (126-223), charnière 1-12 S10>P (233) (224-235), CH2 'E1.4,F1.3'>P1.3 (238), L1.2>V (239), G1.1>A (240) (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 (98.0%) -(IGHD) -IGHJ1*01 (90.9%) L123>T (119), CDR-IMGT [8.8.17] (26-33.51-58.97-113)) (1"-124") -*Homo sapiens* IGHG4*01, G4v5 h P10, G4v8 CH3 R115, F116, P125 (CH1 (125"-222"), charnière 1-17 S10>P (232) (223"-239"), CH2 (240"-343"), CH3 H115>R (438), Y116>F (439), L125>P (448) (G3-like) (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")-bisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

linvoseltamab

immunoglobulina G4-kappa, anti-[*Homo sapiens* TNFRSF17 (miembro 17 de la superfamilia de los receptores del TNF, miembro 17 de la superfamilia de los receptores del factor de necrosis tumoral, antígeno de maduración de célula B, BCMA, BCM, TNFRSF13A, CD269)] y anti-[*Homo sapiens* CD3E (CD3 épsilon, Leu-4)], anticuerpo monoclonal *Homo sapiens*;

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, G4v7 CH2 del 1.4, P1.3, V1.2, A1.1 (G2-like) (CH1 (126-223), bisagra 1-12 S10>P (233) (224-235), CH2 'E1.4,F1.3'>P1.3 (238), L1.2>V (239), G1.1>A (240) (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 (98.0%) -(IGHD) -IGHJ1*01 (90.9%) L123>T (119), CDR-IMGT [8.8.17] (26-33.51-58.97-113)) (1"-124") -*Homo sapiens* IGHG4*01, G4v5 h P10, G4v8 CH3 R115, F116, P125 (CH1 (125"-222"), bisagra 1-17 S10>P (232) (223"-239"), CH2 (240"-343"), CH3 H115>R (438), Y116>F (439), L125>P (448) (G3-like) (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")-bisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada (anti-TNFRSF17)
 EVQLVDSGGG LVQPGGSLRL SCAASGFTFS NFWMTWVRQA PGKGLEWVAN 50
 MQQDGSSEKYY VDSVKGRFTI SRDIAKNSLY LQMNSLRAED TAVYYCARDR 100
 EYCIISTSCYD DFDYWGQGTLL TVVSSASTKG PSVFPLAFCR RSTSESTAAL 150
 GCLVKDYFPEP FVTVSWNSGA LTSQVHTFPA VLQSSGLYSL SSVTVFPPSS 200
 LGTRKTYTCNV DHKPSNTKVD KRVESKYGPP CFCPCAPPVA GPSVFLFPPK 250
 PKDTLMISTR PEVTCVVDV SQEDPEVQFN WYVDGVEVHN AKTKPREEQF 300
 NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK GLPSSIEKTI SKAKGQPREP 350
 QVYTLPPSQE EMTKNQVSLT CLVKGFPYSD IAVEWESNGQ PENNYKTPFP 400
 LVDSDGSFFL YSRLTVDKSR WQEGNVFSCS VMHEALHNNY TQKSLSLSLG 450
 K 451

Heavy chain / Chaîne lourde / Cadena pesada (anti-CD3E)
 EVQLVDSGGG LVQPGGSLRL SCAASGFTFD DYSMHVVRQA PGKGLEWVSG 50
 ISWNSGSKGY ADSVKGRFTI SRDIAKNSLY LQMNSLRAED TALYYCAKYG 100
 SGYKGFYHYG LDVWGQGTTV TVVSSASTKGP SVFPLAPCSR STSESTAALG 150
 CLVKDYFPEP FVTVSWNSGAL TSGVHTFPAV LQSSGLYSL SSVTVFPPSS 200
 GTKTYTCNV DHKPSNTKVD KRVESKYGPP CFCPCAPPVA GPSVFLFPPK 250
 KDTLMISTRP EVTCVVDVDS QEDPEVQFNW YVDGVEVHNA KTKPREEQFN 300
 STYRVVSVLT VLHQDWLNGK EYKCKVSNK GLPSSIEKTI SKAKGQPREP 350
 VYTLPPSQEE MTKNQVSLT CLVKGFPYSDI AVEWESNGQ ENNYKTPFP 400
 LVDSDGSFFL YSRLTVDKSRW WQEGNVFSCSV MHEALHNNRF TQKSLSLSPGK 450

Light chain / Chaîne légère / Cadena ligera
 DIQMTQSPSS LSASVGRDVT ITCRASQSI SYLNWYQKPK GKAPKLLIYA 50
 ASSLQSGVPS RFGSGSGTD FTLTISSLQP EDFATYYCQQ SYSTPPIITFG 100
 QGTRLEIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNFP YPREAKVQWK 150
 VDNALQSGNS QESVTEQDSK DSTYISLSTL TSLKADYEKH KVAACEVTHQ 200
 GLSSPVTKSF NRGEC 215

Post-translational modifications
 Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
 Intra-H (C23-C104) 22-96 152-208 265-325 371-429
 22^o-96^o 151^o-207^o 264^o-324^o 370^o-428^o
 (intra CDR3 111-112.1) 103-108 103^o-108^o
 Intra-L (C23-C104) 23^o-88^o 135^o-195^o
 23^o-88^o 135^o-195^o
 Inter-H-L (CH1 10-CL 126) 139-215^o 138^o-215^o
 Inter-H-H (h 8, h 11) 231-230^o 234-233^o

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
 HCH2 N84.4: 301, 300^o
 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
 HCHS K2: 451, 450^o

litifilimumab #

litifilimumab

immunoglobulin G1-kappa, anti-[*Homo sapiens* CLEC4C (C-type lectin domain family 4 member C, CLECSF11, CLECSF7, CD303)], humanized monoclonal antibody;
 gamma1 heavy chain humanized (1-451) [VH (*Homo sapiens* IGHV3-21*01 (85.7%) -(IGHD) -IGHJ5*01 (86.7%), CDR-IMGT [8.8.14] (26-33.51-58.98-111)) (1-122) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 (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)], (225-218')-disulfide with kappa light chain humanized (1'-218') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (84.8%) -IGKJ1*01 (100%), CDR-IMGT [10.3.9] (27-36.54-56.93-101)) (1'-111') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218')]; dimer (231-231^o:234-234^o)-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-DG44, glycoform alfa

litifilimumab

immunoglobuline G1-kappa, anti-[*Homo sapiens* CLEC4C (membre C du domaine de la famille 4 lectine de type C, CLECSF11, CLECSF7, CD303)], anticorps monoclonal humanisé;
 chaîne lourde gamma1 humanisée (1-451) [VH (*Homo sapiens* IGHV3-21*01 (85.7%) -(IGHD) -IGHJ5*01 (86.7%), CDR-IMGT [8.8.14] (26-33.51-58.98-111)) (1-122) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 (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)], (225-218')-disulfure avec la chaîne légère kappa humanisée (1'-218') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (84.8%) -IGKJ1*01 (100%), CDR-IMGT [10.3.9] (27-36.54-56.93-101)) (1'-111') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218')]; dimère (231-231^o:234-234^o)-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-DG44, glycoforme alfa

litifilimab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CLEC4C (miembro C del dominio de la familia 4 lectina de tipo C, CLECSF11, CLECSF7, CD303)], anticuerpo monoclonal humanizado; cadena pesada gamma1 humanizada (1-451) [VH (*Homo sapiens* IGHV3-21*01 (85.7%) -(IGHD) -IGHJ5*01 (86.7%), CDR-IMGT [8.8.14] (26-33.51-58.98-111)) (1-122) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 (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)], (225-218')-disulfuro con la cadena ligera kappa humanizada (1'-218') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (84.8%) -IGKJ1*01 (100%), CDR-IMGT [10.3.9] (27-36.54-56.93-101)) (1'-111') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (157), V101 (195) (112'-218')]; dímero (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
 DVQLVESGGG LVKPGGSLRL SCAASGFTFS TYTMSWVRQA FKGLEWVAT 50
 ISPGDSFGYY YPDSVQGRFT ISRDNAKNSL YLQMNSLRAE DTAVYYCTRD 100
 IYYNYGAWFA YWGQGLVTV SSASTKGPSV FPLAPFSKST SGGTAAAGCL 150
 VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ SSGLYSLSSV VTPVSSSLGT 200
 QTYICNVNHK PSNTRKVDKVK EPKSCDKTHT CPPCPAPELL GGPSVFLPPP 250
 KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ 300
 YNSTYRVVSV LTVLHQDWLW GKEYKCKVSN KALPAPIEKT ISKAKGQPRE 350
 PQVYTLPPSR DELTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTPP 400
 PVLDSGDSFF LYSKLTVDKRS RWQQGNVFSC SVMHEALHNN YTQKSLSLSP 450
 G 451

Light chain / Chaîne légère / Cadena ligera
 DIQLTQSPSS LSASVGDRTV ITCASQSVSD YDGDSYMNWY QQKPGKAPKL 50
 LIYAASTLES GVPSRFSGSG SGTDFLTLSL SLQPEDFATY YCQQANEDPR 100
 FFGQGTKEVI KRTVAAPSVE IFPPSDEQLK SGTASVVCLL NNFYPREAKV 150
 QWKVDNALQS GNSQESVTEQ DSKDSTYSLY STLTLSKADY EKHKVYACEV 200
 THQGLSSPVT KSPNRGEC 218

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"
 Intra-L (C23-C104) 23"-92" 138"-198"
 23"-92" 138"-198"
 Inter-H-L (h 5-CL 126) 225"-218" 225"-218"
 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.

lixmabegagenum relduparvovecum #
 lixmabegagenum relduparvovec

a recombinant, non-replicating adeno-associated virus serotype rh.10 (rAAVrh.10) vector encoding human β-galactosidase (GLB1), under control of the synthetic CAG promoter (CMV immediate-early enhancer/chicken β-actin (CB) promoter, chicken β-actin exon, chicken β-actin intron, rabbit β-globin intron, rabbit β-globin exon), terminated with a human growth hormone 1 (GH1) polyadenylation (polyA) sequence, and flanked by adeno-associated virus serotype 2 (AAV2) inverted terminal repeats (ITRs).

lixmabégagène relduparvec

un vecteur recombinant et non répliquant du virus adéno-associé de sérotype rh.10 (rAAVrh.10) codant la β-galactosidase humaine (GLB1), sous le contrôle du promoteur synthétique CAG (activateur immédiat précoce du CMV/promoteur de la β-actine de poulet (CB), exon de la β-actine de poulet, intron de la β-actine de poulet, intron de la β-globine de lapin, exon de la β-globine de lapin), terminé par une séquence polyadénylation (polyA) de l'hormone de croissance humaine 1 (GH1), et flanqué de répétitions terminales inversées (ITRs) du virus adéno-associé de sérotype 2 (AAV2).

lixmabegagén relduparvec

un vector de virus adenoasociado recombinante de serotipo rh.10 (rAAVrh.10) no replicativo, que codifica para la β-galactosidasa (GLB1) humana bajo el control del promotor sintético CAG (potenciador inmediato-temprano de CMV/promotor de la β-actina (CB) de pollo, exón de la β-actina de pollo, intrón de la β-actina de pollo, intrón de la β-globina de conejo, exón de la β-globina de conejo), terminado con una secuencia poliadenilación (polyA) de la hormona de crecimiento 1 (GH1) humana y flanqueado por las secuencias terminales invertidas (ITRs) del virus adenoasociado de serotipo 2 (AAV2).

luveltamabum tazevibulinum #
luveltamab tazevibulin

immunoglobulin G1-kappa, anti-[*Homo sapiens* FOLR1 (folate receptor 1, folate receptor alpha, FR-alpha, adult folate-binding protein, FBP, ovarian tumor-associated antigen MOV18)], humanized monoclonal antibody, conjugated on four modified phenylalanine residues via a cleavable valyl-citrullyl linker with a hemiassterlin analogue;
gamma1 heavy chain humanized (1-455) [VH (*Homo sapiens* IGHV3-66*01 (79.6%) -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [8.8.17] (27-34.52-59.98-114)) (1-125) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 Y85.2>F (pAMF) (188), R120>K (222) (126-223), hinge 1-15 (224-238), CH2 (239-348), CH3 E12 (364), M14 (366), F85.2> F (pAMF) (412) (349-453), CHS (454-455)) (126-455)], (228-215')-disulfide with kappa light chain humanized (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (86.3%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (28-33.51-53.90-98)) (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109-215)]; dimer (234-234":237-237")-bisdisulfide, produced by a cell-free protein synthesis system based on *Escherichia coli* lysate, non-glycosylated, conjugated at C-4 of the four L-phenylalanyl residues 188, 412, 188" and 412" with [8-(4-{{(2S)-1-{{(2S)-5-(carbamoylamino)-1-(4-{{[[3-[[3S)-4-{{(2S)-1-{{(3S,4E)-5-carboxy-2-methylhex-4-en-3-yl}}(methyl)amino}-3,3-dimethyl-1-oxobutan-2-yl]amino}-2-methyl-3-(methylamino)-4-oxobutan-2-yl]phenyl}carbamoyl}oxy)methyl}anilino)-1-oxopentan-2-yl]amino)-3-methyl-1-oxobutan-2-yl]amino}-4-oxobutanoyl)-8,9-dihydro-1*H*(or 3*H*)-dibenzo[*b,f*][1,2,3]triazolo[4,5-*d*]azocin-1(or 3)-yl]methyl (tazevibulin) groups

luveltamab tazéviluline	<p>immunoglobuline G1-kappa, anti-[<i>Homo sapiens</i> FOLR1 (récepteur 1 du folate, récepteur alpha du folate, FR-alpha, protéine de l'adulte liant le folate, FBP, antigène MOV18 associé à des tumeurs ovariennes)], anticorps monoclonal humanisé, conjugué à quatre résidus pénnylalanine modifiés via un linker valyl-citrullyle clivable avec un analogue de l'hémiasterline; chaîne lourde gamma1 humanisée (1-455) [VH (<i>Homo sapiens</i> IGHV3-66*01 (79.6%) -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [8.8.17] (27-34.52-59.98-114)) (1-125) -<i>Homo sapiens</i> IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 Y85.2>F (pAMF) (188), R120>K (222) (126-223), charnière 1-15 (224-238), CH2 (239-348), CH3 E12 (364), M14 (366), F85.2>F (pAMF) (412) (349-453), CHS (454-455)) (126-455)], (228-215')-disulfure avec la chaîne légère kappa humanisée (1'-215') [V-KAPPA (<i>Homo sapiens</i> IGKV1-39*01 (86.3%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (28-33.51-53.90-98)) (1'-108') -<i>Homo sapiens</i> IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')]; dimère (234-234":237-237")-bisdisulfure, produit par un système acellulaire de synthèse de protéines à base de lysat d'<i>Escherichia coli</i>, non-glycosylé, conjugué en C-4 des quatre résidus L-phénylalanyle 188, 412, 188" et 412" avec des groupes [8-(4-(((2S)-1-(((2S)-5-(carbamoylamino)-1-(4-(((3-((3S)-4-(((2S)-1-(((3S,4E)-5-carboxy-2-méthylhex-4-én-3-yl)](méthyl)amino)-3,3-diméthyl-1-oxobutan-2-yl]amino)-2-méthyl-3-(méthylamino)-4-oxobutan-2-yl]phényl)carbamoyl)oxy)méthyl]anilino)-1-oxopentan-2-yl]amino)-3-méthyl-1-oxobutan-2-yl]amino)-4-oxobutanoyl)-8,9-dihydro-1H(ou 3H)-dibenzo[b,f][1,2,3]triazolo[4,5-d]azocin-1(ou 3)-yl]méthyle (<i>tazéviluline</i>)</p>
luveltamab tazevilulina	<p>inmunoglobulina G1-kappa, anti-[<i>Homo sapiens</i> FOLR1 (receptor 1 del folato, receptor alfa del folato, FR-alfa, proteína del adulto de unión al folato, FBP, antígeno MOV18 asociado con los tumores ováricos)], anticuerpo monoclonal humanizado, conjugado en cuatro residuos de fenilalanina modificados a través de un enlace escindible valil-citruilil con un análogo de la hemiasterlina; cadena pesada gamma1 humanizada (1-455) [VH (<i>Homo sapiens</i> IGHV3-66*01 (79.6%) -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [8.8.17] (27-34.52-59.98-114)) (1-125) -<i>Homo sapiens</i> IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 Y85.2>F (pAMF) (188), R120>K (222) (126-223), bisagra 1-15 (224-238), CH2 (239-348), CH3 E12 (364), M14 (366), F85.2>F (pAMF) (412) (349-453), CHS (454-455)) (126-455)], (228-215')-disulfuro con la cadena ligera kappa humanizada (1'-215') [V-KAPPA (<i>Homo sapiens</i> IGKV1-39*01 (86.3%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (28-33.51-53.90-98)) (1'-108') -<i>Homo sapiens</i> IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')]; dímero (234-234":237-237")-bisdisulfuro, producido por un sistema de síntesis de proteínas sin células basado en lisado de <i>Escherichia coli</i>, no glicosilado, conjugado en C-4 de los cuatro residuos de L-fenilalanilo 188, 412, 188" y 412" con grupos [8-(4-(((2S)-1-(((2S)-5-(carbamoilamino)-1-(4-(((3-((3S)-4-(((2S)-1-(((3S,4E)-5-carboxi-2-metilhex-4-en-3-il)](metil)amino)-3,3-dimetil-1-oxobutan-2-il]amino)-2-metil-3-(metilamino)-4-oxobutan-2-il]fenil)carbamoil)oxi]metil]anilino)-1-oxopentan-2-il]amino)-3-metil-1-oxobutan-2-il]amino)-4-oxobutanoyl)-8,9-dihidro-1H(o 3H)-dibenzo[b,f][1,2,3]triazolo[4,5-d]azocin-1(o 3)-il]metilo (<i>tazevilulina</i>)</p>

Heavy chain / Chaîne lourde / Cadena pesada
 MEVLVESGG GLVQPGGSLR LSCAASGFNI RTQSIHWVRQ APGKGLEWIG 50
 DIFPIDGITD YADSVKGRFT ISADTSKNTA YLQMNSLRAE DTAVVYVYARG 100
 SWSVSGMDY YLDYWGQGTI VTVSSASTKG PSVFPFLAPSS KSTSGGTAAL 150
 GCLVLDYFPE PVTVSWNSGA LTVSGVHTFPA VLQSSGLFSL SSVVTVPSSS 200
 LGTQTYICNV NHRKPSNTKVD KKVPEKSCDK THTCPPCPAP ELLGGPSVFL 250
 FPFKPKDTLM ISRTPEVTCV VVDVSHEDPE VKFNWYVDGV EVHNAKTKPR 300
 EEQYNSTYRV VSVLTVLHQD WLVGKEVKCK VSNKALPAPI ERTISKARQG 350
 PREPQVYTLF PSREEMTKNQ VSLTCLVKGF YPSDIAVEWE SNGQPENNYK 400
 TTPPVLDSDG **S**EFLYSKLTV DKSRWQQGNV FSCSVMEAL HNHYTQKSL 450
 LSPGK 455

Light chain / Chaîne légère / Cadena ligera
 MDIQMTQSPS SLSASVGDV TITCRASQDV NTAVAWYQQK PGKAPKLLIY 50
 SASFLYSGVP SRFSGSRSGT DFTLTISLQ PEDFATYYCQ QHYTTPPTFG 100
 QGKVELIKRT VAAPSVFIFP PSDEQLKSGT ASVCLLNFF YPREAKVQWK 150
 VDNALQSGNS QESVTEQDSK DSTYLSSTL TLSKADYEKH KVIACEVTHQ 200
 GLSSPVTKSF NRGEK 215

E indicates non-natural amino acid *p*-azidomethyl-L-phenylalanine (pAMF)

Post-translational modifications

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

Intra-H (C23-C104) 23-97 152-208 269-329 375-433
 23"-97" 152"-208" 269"-329" 375"-433"

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

Inter-H-L (h 5-CL 126) 228-215' 228"-215"

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

N-terminal methionine / Méthionine N-terminale / Metionina N-terminal

H VH M1.1: 1, 1"

L V-KAPPA M1.1: 1', 1"

No N-terminal methionine clipping (expressed in a cell-free expression system) / Pas de coupure de la méthionine N-terminale (exprimé dans un système d'expression acellulaire) / Sin recorte de metionina N-terminal (expresado en un sistema de expresión libre de células)

Conjugation sites / Sites de conjugation / Posiciones de conjugación

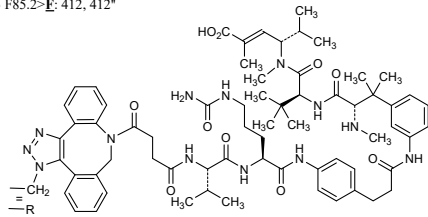
E: *p*-azidomethyl-L-phenylalanine (pAMF) used as conjugation specific site /

E: *p*-azidométhyl-L-phénylalanine (pAMF) utilisé comme site spécifique de conjugaison /

E: *p*-azidometil-L-fenilalanina (pAMF) utilizada como sitio específico de conjugación

H CH1 Y85.2>**E**: 188, 188"

H CH3 F85.2>**E**: 412, 412"



luveltamabum tazidum #
 luveltamab tazide

immunoglobulin G1-kappa, anti-[*Homo sapiens* FOLR1 (folate receptor 1, folate receptor alpha, FR-alpha, adult folate-binding protein, FBP, ovarian tumor-associated antigen MOV18)], humanized monoclonal antibody, genetically modified at four specific positions with reactive 4-(azidomethyl)-L-phenylalanine residues;

gamma1 heavy chain humanized (1-455) [VH (*Homo sapiens*IGHV3-66*01 (79.6%) -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [8.8.17] (27-34.52-59.98-114)) (1-125) -*Homo sapiens*IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 Y85.2>F (pAMF) (188), R120>K (222) (126-223), hinge 1-15 (224-238), CH2 (239-348), CH3 E12 (364), M14 (366), F85.2>F (pAMF) (412) (349-453), CHS (454-455)) (126-455)], (228-215')-disulfide with kappa light chain humanized (1'-215') [V-KAPPA (*Homo sapiens*IGKV1-39*01 (86.3%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (28-33.51-53.90-98)) (1'-108') -*Homo sapiens*IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')]; dimer (234-234":237'-237")-bisdisulfide, produced by a cell-free protein synthesis system based on *Escherichia coli* lysate, non-glycosylated; conjugated at C-4 of the four L-phenylalananyl residues 188, 412, 188" and 412" with azidomethyl (*tazide*) groups

luveltamab tazide

immunoglobuline G1-kappa, anti-[*Homo sapiens* FOLR1 (récepteur 1 du folate, récepteur alpha du folate, FR-alpha, protéine de l'adulte liant le folate, FBP, antigène MOv18 associé à des tumeurs ovariennes)], anticorps monoclonal humanisé, génétiquement modifié sur quatre positions spécifiques avec des résidus 4-(azidométhyl)-L-phénylalanine réactifs; chaîne lourde gamma1 humanisée (1-455) [VH (*Homo sapiens* IGHV3-66*01 (79.6%) -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [8.8.17] (27-34.52-59.98-114))] (1-125) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 Y85.2>F (pAMF) (188), R120>K (222) (126-223), charnière 1-15 (224-238), CH2 (239-348), CH3 E12 (364), M14 (366), F85.2>F (pAMF) (412) (349-453), CHS (454-455)) (126-455)], (228-215')-disulfure avec la chaîne légère kappa humanisée (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (86.3%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (28-33.51-53.90-98))] (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215'); dimère (234-234":237-237")-bisdisulfure, produit par un système acellulaire de synthèse de protéines à base de lysat d'*Escherichia coli*, non-glycosylé; conjugué en C-4 des quatre résidus L-phénylalanyle 188, 412, 188" et 412" avec des groupes azidométhyle (*tazide*)

luveltamab tazida

immunoglobulina G1-kappa, anti-[*Homo sapiens* FOLR1 (receptor 1 del folato, receptor alfa del folato, FR-alfa, proteina del adulto de unión al folato, FBP, antígeno MOv18 asociado con los tumores ováricos)], anticuerpo monoclonal humanizado, genéticamente modificado en cuatro posiciones específicas con residuos 4-(azidometil)-L-fenilalanina reactivos; cadena pesada gamma1 humanizada (1-455) [VH (*Homo sapiens* IGHV3-66*01 (79.6%) -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [8.8.17] (27-34.52-59.98-114))] (1-125) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 Y85.2>F (pAMF) (188), R120>K (222) (126-223), bisagra 1-15 (224-238), CH2 (239-348), CH3 E12 (364), M14 (366), F85.2>F (pAMF) (412) (349-453), CHS (454-455)) (126-455)], (228-215')-disulfuro con la cadena ligera kappa humanizada (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (86.3%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (28-33.51-53.90-98))] (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215'); dímero (234-234":237-237")-bisdisulfuro, producido por un sistema de síntesis de proteínas sin células basado en lisado de *Escherichia coli*, no glicosilado; conjugado en C-4 de los cuatro residuos de L-fenilalanilo 188, 412, 188" y 412" con grupos azidometilo (*tazida*)

Heavy chain / Chaîne lourde / Cadena pesada
 MEVQLVESGG GLVQPGGSLR LSCAASGFNI RTQSIHWVRQ APGKLEWIG 50
 DIFPIDGITD YADSVKGRFT ISADTSKNTA YLQMNLSRAE DTAVVYVYCAR 100
 SWSNPSGMDY YLDYWGQCTL VTSSASTKG PSVFPLAPSS KSTSGGTAAL 150
 GCLVKDYFPE PUTVSWNSGA LTSGVHTFPA VLQSSGLFSL SSVVTVPSSS 200
 LGTQTYICNV NHKPSNTKVD KKVEPKSCDK THTCPPCPAP ELLGGPVSFL 250
 FFPKPKDTLM ISRTPEVTCV VVDVSHEDPE VKFNWYVDGV EVHNAKTKPR 300
 EEQYINSTRYR VSVLTVLHQD WLNKGEYKCK VSNKALPAPI EKTISKAKGQ 350
 PREPQVYTLF PSREEMTKNQ VSLTCLVKGK YPSDIAVEWE SNGQPENNYK 400
 TTPFVLDSDG SFLYSLKLTV DKSRWQGGNV FSCSVMHEAL HNHYYQKSL 450
 LSPGK 455

Light chain / Chaîne légère / Cadena ligera
 MDIQMTQSPS SLSASVGRDV TITCRASQDV NTAVAWYQQK PGKAPKLLIY 50
 SASFLYSGVP SRFGSGRSGT DFTLTISLQ PEDFATYYCQ QHYTTPPTFG 100
 QGQTKVEIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNFF YPREAKVQWK 150
 VDNALQSGNS QESVTEQDSK DSTYLSLSTL TLSKADYEKH KVVACEVTHQ 200
 GLSSPVTKSF NRGEC 215

F indicates non-natural amino acid *p*-azidomethyl-L-phenylalanine (pAMF)

Post-translational modifications

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
 Intra-H (C23-C104) 23-97 152-208 269-329 375-433
 23"-97" 152"-208" 269"-329" 375"-433"
 Intra-L (C23-C104) 24'-89' 135'-195'
 24"-89" 135"-195"
 Inter-H-L (h 5-CL 126) 228-215' 228"-215"
 Inter-H-H (h 11, h 14) 234-234" 237-237"

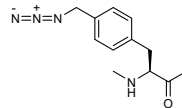
N-terminal methionine / Méthionine N-terminale / Metionina N-terminal

H VH M1.1: 1, 1"
 L V-KAPPA M1.1: 1', 1"

No N-terminal methionine clipping (expressed in a cell-free expression system) / Pas de coupure de la méthionine N-terminale (exprimé dans un système d'expression acellulaire / Sin recorte de metionina N-terminal (expresado en un sistema de expresión libre de células)

Conjugation sites / Sites de conjugation / Posiciones de conjugación

F: *p*-azidomethyl-L-phenylalanine (pAMF) used as conjugation specific site /
F: *p*-azidometil-L-fenilalanina (pAMF) utilisé comme site spécifique de conjugaison /
F: *p*-azidometil-L-fenilalanina (pAMF) utilizada como sitio específico de conjugación
 H CH1 Y85.2>**F**: 188, 188"
 H CH3 F85.2>**F**: 412, 412"



masavibartum #
 masavibart

immunoglobulin G1-lambda, anti-[severe acute respiratory syndrome (human) coronavirus 2 (SARS-CoV-2) spike (S) glycoprotein, receptor binding domain (RBD)], *Homo sapiens* monoclonal antibody; gamma1 heavy chain *Homo sapiens* (1-450) [VH (*Homo sapiens*IGHV3-30*01 (96.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens*IGHG1*03v, G1m3>G1m17, nG1m1, G1v14 CH2 A1.3, A1.2, G1v24 CH3 L107, S114 (CH1 R120>K (217) (121-218), hinge 1-15 (219-233), CH2 L1.3>A (237), L1.2>A (238), P114>G (332) (234-343), CH3 E12 (359), M14 (361), M107>L (431), N114>S (437) (344-448), CHS (449-450)) (121-450)], (223-215')-disulfide with lambda light chain *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV2-14*03 (94.9%) -IGLJ3*02 (100%), CDR-IMGT [9.3.10] (26-34.52-54.91-100)) (1'-110') -*Homo sapiens* IGLC1*02 (100%) (111'-216')]; dimer (229-229":232-232")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1SV lacking the glutamine synthetase (GS-KO) gene, glycoform alfa

masavibart immunoglobuline G1-lambda, anti-[domaine de liaison au récepteur (RBD) de la glycoprotéine spike (S) du coronavirus 2 (humain) du syndrome respiratoire aigu sévère (SARS-CoV-2)], anticorps monoclonal *Homo sapiens*; chaîne lourde gamma1 *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV3-30*01 (96.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, G1v14 CH2 A1.3, A1.2, G1v24 CH3 L107, S114 (CH1 R120>K (217) (121-218), charnière 1-15 (219-233), CH2 L1.3>A (237), L1.2>A (238), P114>G (332) (234-343), CH3 E12 (359), M14 (361), M107>L (431), N114>S (437) (344-448), CHS (449-450)) (121-450)], (223-215')-disulfure avec la chaîne légère lambda *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV2-14*03 (94.9%) -IGLJ3*02 (100%), CDR-IMGT [9.3.10] (26-34.52-54.91-100)) (1'-110') -*Homo sapiens* IGLC1*02 (100%) (111'-216'')]; 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), glycoforme alfa

masavibart inmunoglobulina G1-lambda, anti-[dominio de unión al receptor (RBD) de la glicoproteína spike (S) del coronavirus 2 (humano) del síndrome respiratorio agudo severo (SARS-CoV-2)], anticuerpo monoclonal *Homo sapiens*; cadena pesada gamma1 *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV3-30*01 (96.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, G1v14 CH2 A1.3, A1.2, G1v24 CH3 L107, S114 (CH1 R120>K (217) (121-218), bisagra 1-15 (219-233), CH2 L1.3>A (237), L1.2>A (238), P114>G (332) (234-343), CH3 E12 (359), M14 (361), M107>L (431), N114>S (437) (344-448), CHS (449-450)) (121-450)], (223-215')-disulfuro con la cadena ligera lambda *Homo sapiens* (1'-216') [V-LAMBDA (*Homo sapiens* IGLV2-14*03 (94.9%) -IGLJ3*02 (100%), CDR-IMGT [9.3.10] (26-34.52-54.91-100)) (1'-110') -*Homo sapiens* IGLC1*02 (100%) (111'-216'')]; dímero (229-229":232-232")-bisdisulfuro, producido en las células ováricas de hamster chino (CHO), línea celular CHO-K1SV en ausencia del gen glutamina sintetasa (GS-KO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

QVQLVESGGG VVQPGKSLRL SCAASGFTFS NYAMYVWRQA PGKGLEWVAV	50
ISYDGSNKY ADSVKGRFTI SRDNSKNTLY LQMNSLRTE TAVYYCASGS	100
DYGDYLLVYV GQGLTIVTSS ASTKGPSVFP LAPSSKSTSG TAAALGCLVK	150
DYFPEPVTVS WNSGALTSVQ HTFFPAVLQSS GLYSLSSVVT VPSSSLGTTQ	200
YICNVNHKPS NTKVDKRVKVP KSCDKTHTCP PCPAPEAAGG PSVFLFPPK	250
KDTLMISRTPEVTQCVVDVDS HEDPEVKFNW YVDGVEVHNA RTKPREEQYN	300
STYRVSVVLT VLGQDNLNGK EYKCKVSNKA LGAPIEKTIS KAKGQPREPQ	350
VYVLPFSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTTPV	400
LDSGDSFFLY SKLTVDKSRW QQGNVFSCSV LHEALHSHYT QKSLSLSPGK	450

Light chain / Chaîne légère / Cadena ligera

QSALTQPASV SGSPGQSITI SCTGTSSDVG GYNYVSWYQQ HPGKAPKLM	50
YDVKRPSGV SNRFSGSKSG NTASLTISGL QSEDEADYYC NSLTSISTW	100
FGGGTKLTVL GQPKANPTVT LFPPSSEELQ ANKATLVCLI SDFYPGAVT	150
AWKADGSPVK AGVETTKPKS QSNNKYAASS YLSLTPQWQK 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	147-203	264-324	370-428
	22"-96"	147"-203"	264"-324"	370"-428"
Intra-L (C23-C104)	22'-90'	138'-197'		
	22"-90"	138"-197"		
Inter-H-L (h 5-CL 126)	223-215'	223"-215"		
Inter-H-H (h 11, h 14)	229-229"	232-232"		

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutamínilo N-terminal
 Q > pyroglutamyl (pE, 5-oxopropyl)
 H VH Q1: 1, 1"
 L VL Q1: 1, 1"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
 H CH2 N84:4:300, 300"
 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: 450, 450"

mazdutidum

mazdutide

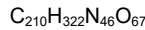
L-histidyl-2-methylalanyl-L-glutaminyglycyl-L-threonyl-L-phenylalanyl-L-threonyl-L-seryl-L- α -aspartyl-L-tyrosyl-L-seryl-L-lysyl-L-tyrosyl-L-leucyl-L- α -aspartyl-L- α -glutamyl-L-lysyl-L-lysyl-L-alanyl-L- N^{β} -[(22S)-22,42-dicarboxy-10,19,24-trioxo-3,6,12,15-tetraoxa-9,18,23-triazadotetracontan-1-oyl]-L-lysyl-L- α -glutamyl-L-phenylalanyl-L-valyl-L- α -glutamyl-L-tryptophyl-L-leucyl-L-leucyl-L- α -glutamylglycylglycyl-L-prolyl-L-seryl-L-serylglycinamide

mazdutide

L-histidyl-2-méthylalanyl-L-glutaminyglycyl-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-lysyl-L-lysyl-L-alanyl-L- N^{β} -[(22S)-22,42-dicarboxy-10,19,24-trioxo-3,6,12,15-tétraoxa-9,18,23-triazadotétracontan-1-oyl]-L-lysyl-L- α -glutamyl-L-phénylalanyl-L-valyl-L- α -glutamyl-L-tryptophyl-L-leucyl-L-leucyl-L- α -glutamylglycylglycyl-L-prolyl-L-séryl-L-sérylglycinamide

mazdutida

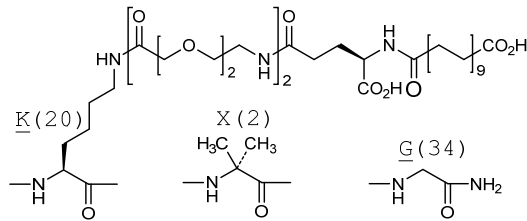
L-histidil-2-metilalanil-L-glutaminilglicil-L-treonil-L-fenilalanil-L-treonil-L-seril-L- α -aspartil-L-tirosil-L-seril-L-lisil-L-tirosil-L-leucil-L- α -aspartil-L- α -glutamil-L-lisil-L-lisil-L-alanil-L- N^{β} -[(22S)-22,42-dicarboxi-10,19,24-trioxo-3,6,12,15-tetraoxa-9,18,23-triazadotetracontan-1-oil]-L-lisil-L- α -glutamil-L-fenilalanil-L-valil-L- α -glutamil-L-triptofil-L-leucil-L-leucil-L- α -glutamilglicilglicil-L-proilil-L-seril-L-serilglicinamida



Sequence / séquence / secuencia

HXQGTFTSDY SKYLDEKKAK EFVEWLLEGG PSSG 34

Modified residues / résidus modifiés / restos modificados



mecbotamabum #

mecbotamab

immunoglobulin G1-kappa, anti-[*Homo sapiens* AXL (AXL receptor tyrosine kinase, tyrosine-protein kinase receptor UFO)], humanized monoclonal antibody; gamma1 heavy chain humanized (1-449) [VH (*Homo sapiens* IGHV5-51*01 (74.2%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 (CH1 K120 (217) (121-218), hinge 1-15 (219-233), CH2 (234-343), CH3 D12 (359), L14 (361) (344-448), CHS K2 > del (449)) (121-449)], (223-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5*03 (79.6%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (229-229'':232-232'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-S, glycoform alfa

mecbotamab

immunoglobuline G1-kappa, anti-[*Homo sapiens* AXL (récepteur tyrosine kinase AXL, récepteur tyrosine-protéine kinase UFO)], anticorps monoclonal humanisé; chaîne lourde gamma1 humanisée (1-449) [VH (*Homo sapiens* IGHV5-51*01 (74.2%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 (CH1 K120 (217) (121-218), charnière 1-15 (219-233), CH2 (234-343), CH3 D12 (359), L14 (361) (344-448), CHS K2 < del (449)) (121-449)], (223-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5*03 (79.6%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (229-229":232-232")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-S, glycoforme alfa

mecbotamab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* AXL (receptor tirosina kinasa AXL, receptor tirosina-protéina kinasa UFO)], anticuerpo monoclonal humanizado; cadena pesada gamma1 humanizada (1-449) [VH (*Homo sapiens* IGHV5-51*01 (74.2%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 (CH1 K120 (217) (121-218), bisagra 1-15 (219-233), CH2 (234-343), CH3 D12 (359), L14 (361) (344-448), CHS K2 < del (449)) (121-449)], (223-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5*03 (79.6%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (229-229":232-232")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-S, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

EVQLVQSGAE	VKKFGATVKI	SCRVSGYSEW	GATMNNIRQP	PGKLEWIGL	50
IKPSNGGTSY	NQRFKGRVTI	SADKSIISTAY	LQWSSLKASD	TAMYYCARHG	100
YESYEAMDYW	QGGLTLTVSS	ASTKGPSVFP	LAPSSKSTSG	GTAALGCLVK	150
DYFPEPVTVS	WNSGALTSGV	HTFPAVLQSS	GLYLSVSVT	VFSSSLGTQT	200
YICNVNHKPS	NTKVDKRVPE	KSCDKTHTCP	PCPAPELLGG	PSVFLFPPKP	250
KDTLMISRTF	EVTCTVVDVS	HEDPEVKFNW	YVDGVEVHNA	KTKFPEEQYN	300
STYRVVSVLT	VLHQDWLNGK	EYKCKVSNKA	LPAPIEKTIIS	KAKGQPREPK	350
VYTLPPSRDE	LTKNQVSLTC	LVKGFYPSDI	AVEVESNGQP	ENNYKTTTPPV	400
LDSGGSFFLY	SKLTVDKSRW	QQGNVFPSCSV	MHEALHNHYT	QKSLSLSPG	449

Light chain / Chaîne légère / Cadena ligera

DIQMTQSPSS	LSASVGDRTV	ITCKASQDVV	SAVAWYQQKP	GQAPRLLIYW	50
QDTRHTGVPS	RFSGSGSGTE	FTLTISLLQP	DDFATYYCQE	HFSFPLTFGQ	100
GTKVEIKRTV	AAPSVFIFFP	SDEQLKSGTA	SVVCLLNIFY	PREAKVQWKV	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" 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.

mecbotamabum vedotinum

mecbotamab vedotin

immunoglobulin G1-kappa, anti-[*Homo sapiens* AXL (AXL receptor tyrosine kinase, tyrosine-protein kinase receptor UFO)], humanized monoclonal antibody, conjugated to auristatin E; gamma1 heavy chain humanized (1-449) [VH (*Homo sapiens* IGHV5-51*01 (74.2%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 (CH1 K120 (217) (121-218), hinge 1-15 (219-233), CH2 (234-343), CH3 D12 (359), L14 (361) (344-448), CHS K2>del (449)) (121-449)], (223-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5*03 (79.6%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (229-229":232-232")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-S, glycoform alfa, conjugated, on an average of 4 cysteinyl, to monomethylauristatin E (MMAE), via a cleavable maleimidocaproyl-valyl-citrullinyl-*p*-aminobenzyloxycarbonyl (mc-val-cit-PABC) type linker

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

mecbotamab védotine

immunoglobuline G1-kappa, anti-[*Homo sapiens* AXL (récepteur tyrosine kinase AXL, récepteur tyrosine-protéine kinase UFO)], anticorps monoclonal humanisé, conjugué à l'auristatine E; chaîne lourde gamma1 humanisée (1-449) [VH (*Homo sapiens* IGHV5-51*01 (74.2%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 (CH1 K120 (217) (121-218), charnière 1-15 (219-233), CH2 (234-343), CH3 D12 (359), L14 (361) (344-448), CHS K2>del (449)) (121-449)], (223-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5*03 (79.6%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (229-229":232-232")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-S, glycoforme alfa, conjugué, sur 4 cystéinyl en moyenne, au monométhylauristatine E (MMAE), via un linker clivable de type maléimidocaproyl-valyl-citrullinyl-*p*-aminobenzyloxycarbonyl (mc-val-cit-PABC)

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

mecbotamab vedotina

immunoglobulina G1-kappa, anti-[*Homo sapiens* AXL (receptor tirosina kinasa AXL, receptor tirosina-proteína kinasa UFO)], anticuerpo monoclonal humanizado, conjugado con la auristatina E; cadena pesada gamma1 humanizada (1-449) [VH (*Homo sapiens* IGHV5-51*01 (74.2%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 (CH1 K120 (217) (121-218), bisagra 1-15 (219-233), CH2 (234-343), CH3 D12 (359), L14 (361) (344-448), CHS K2>del (449)) (121-449)], (223-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5*03 (79.6%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (229-229":232-232")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-S, forma glicosilada alfa, conjugado, en 4 restos cisteinil por término medio, con monometilauristatina E (MMAE), a través de un enlace escindible de tipo maleimidocaproyl-valil-citrulinil-*p*-aminobenciloxicarbonil (mc-val-cit-PABC)

Para la parte vedotina, por favor vaya al documento "INN for pharmaceutical substances: Names for radicals, groups and others".

Heavy chain / Chaîne lourde / Cadena pesada

EVQLVQSGAE	VKKPGATVKI	SCKVSGYSEF	GATMNIWIRQP	PGKGLEWIGL	50
IKPNSGGTSY	NQKFKGRVTI	SADKISITAY	LQWSSLKASD	TAMYCAHGH	100
YESYEAMDYW	GQGTLVTVSS	ASTKGPSVFP	LAFSSKSTSG	GTAALGCLVK	150
DYFPEPVTVS	WNSGALTSGV	HTFFPAVLQSS	GLYSLSSVVT	VPSSSLGTQT	200
YICNVNHKPS	NTKVDKKEVEP	KSCDKTHTCP	PCPAPELLGG	PSVFLFPPKP	250
KDTLMISRTP	EVTCVVVDVS	HEDPEVKFHW	YVDGVEVHNA	KTKPREEQYN	300
STRVIVSVLT	VLHGDWLNK	EYKCKVSNKA	LPAPIEKTIS	KAKGQPREPQ	350
VYTLPPSRDE	LTRKQVSLTC	LVKGFYPSDI	AVEWESNGQP	ENNYKTTFPV	400
LDSGGSFFLY	SKLTVDKSRW	QQGNVFCSCV	MHEALHNYHT	QKSLSLSPG	449

Light chain / Chaîne légère / Cadena ligera

DIQMTQSPSS	LSASVGDRTV	ITCKASQDVV	SAVAWYQQKP	GQAPRLLIYW	50
QDTRHTGVPS	RFSGSGSGTE	FTLTISSLPQ	DDFATYYCQE	HFSPLTTPGQ	100
GTRKVEIKRTV	AAPSVFIFPP	SDEQLKSGTA	SVVCLLNNFY	PREAKVQWKV	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) 22-96 147-203 264-324 370-428

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.

minzasolminum

minzasolmin

N-[(2*R*)-1-(1*H*-indol-3-yl)hexan-2-yl]-2-(4-methylpiperazin-1-yl)-1,3-thiazole-5-carboxamide

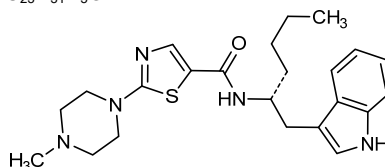
minzasolmine

N-[(2*R*)-1-(1*H*-indol-3-yl)hexan-2-yl]-2-(4-méthylpipérazin-1-yl)-1,3-thiazole-5-carboxamide

minzasolmina

N-[(2*R*)-1-(1*H*-indol-3-il)hexan-2-il]-2-(4-metilpiperazin-1-il)-1,3-tiazol-5-carboxamida

C₂₃H₃₁N₅OS

**mitiperstatum**

mitiperstat

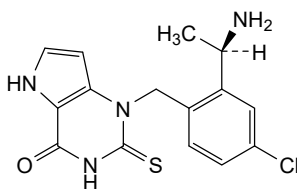
1-({2-[(1*R*)-1-aminoethyl]-4-chlorophenyl}methyl)-2-sulfanylidene-1,2,3,5-tetrahydro-4*H*-pyrrolo[3,2-*d*]pyrimidin-4-one

mitiperstat

1-({2-[(1*R*)-1-aminoéthyl]-4-chlorophényl}méthyl)-2-sulfanylidène-1,2,3,5-tétrahydro-4*H*-pyrrolo[3,2-*d*]pyrimidin-4-one

mitiperstat

1-({2-[(1*R*)-1-aminoetil]-4-clorofenil}metil)-2-sulfanilideno-1,2,3,5-tetrahidro-4*H*-pirrolo[3,2-*d*]pirimidin-4-ona

C₁₅H₁₅ClN₄OS**motugivatrepum**

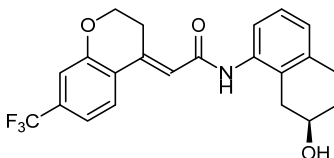
motugivatrep

(2*E*)-*N*-[(7*R*)-7-hydroxy-5,6,7,8-tetrahydronaphthalen-1-yl]-2-[7-(trifluoromethyl)-2,3-dihydro-4*H*-1-benzopyran-4-ylidene]acetamide

motugivatrep

(2*E*)-*N*-[(7*R*)-7-hydroxy-5,6,7,8-tétrahydronaphthalén-1-yl]-2-[7-(trifluorométhyl)-2,3-dihydro-4*H*-1-benzopyran-4-ylidène]acetamide

motugivatrep

(2*E*)-*N*-[(7*R*)-7-hidroxi-5,6,7,8-tetrahidronaftalen-1-il]-2-[7-(trifluorometil)-2,3-dihidro-4*H*-1-benzopiran-4-ilideno]acetamidaC₂₂H₂₀F₃NO₃**mufemilastum**

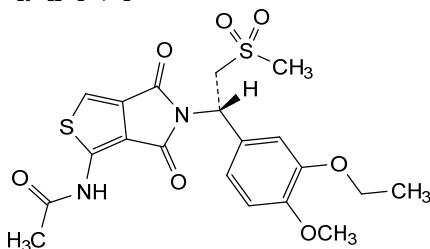
mufemilast

N-{5-[(1*S*)-1-(3-ethoxy-4-methoxyphenyl)-2-(methanesulfonyl)ethyl]-4,6-dioxo-5,6-dihydro-4*H*-thieno[3,4-*c*]pyrrol-1-yl}acetamide

mufémilast

N-{5-[(1*S*)-1-(3-éthoxy-4-méthoxyphényl)-2-(méthanesulfonyl)éthyl]-4,6-dioxo-5,6-dihydro-4*H*-thiéno[3,4-*c*]pyrrol-1-yl}acetamide

mufemilast

N-{5-[(1*S*)-1-(3-etoxi-4-metoxifenil)-2-(metanosulfonyl)etil]-4,6-dioxo-5,6-dihidro-4*H*-tieno[3,4-*c*]pirrol-1-il}acetamidaC₂₀H₂₂N₂O₇S₂

nanrilkéfusp alfa

fragment alpha de la sous-unité du récepteur de l'interleukine-15 humaine (IL15R α) (31-108, 1-78 dans la séquence actuelle) fusionné via une liaison peptidique ⁷⁹GSGGGGGSGGGSGGGSGG⁹⁷ à l'interleukine 15 humaine (98-211 dans la séquence actuelle), produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa;

sous-unité alpha du récepteur de l'interleukine-15 (humaine) (IL15R α , IL15RA), peptide 31-108 (domaine sushi 31-95 plus extension 96-108) (1-78) fusionné via la liaison peptidique G₂SG₄SG₃SG₄SG₂ (79-97) avec l'interleukine humaine 15 (98-211), produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

nanrilkefusp alfa

receptor subunidad alfa del receptor de interleukina-15 humana (IL15R α) fragmento (31-108, 1-78 en la actual secuencia) fusionado a través del enlace peptidil ⁷⁹GSGGGGGSGGGSGGGSGG⁹⁷ a la interleukina 15 humana (98-211 en la secuencia actual), producida en células ováricas de hamster chino (CHO), glicofoma alfa;

subunidad alfa del receptor de interleukina-15 (humano) (IL15R α , IL15RA), péptido 31-108 (dominio sushi 31-95 más extensión 96-108) (1-78) fusionado a través de un enlace peptídico G₂SG₄SG₃SG₄SG₂ (79-97) con la interleucina 15 humana (98-211), producido en células ováricas de hámster chino (CHO), glicofoma alfa

Sequence / Séquence / Secuencia

ITCPPMMSVE HADIWVKYSY LYSRERYICN SGFKRKAGTS SLTECVLNKA	50
TNVAHWTTPS LKCIKDPALV HQRPAAPPSSG <u>SGGGGGGGG</u> <u>GGGGGG</u> NWV	100
NVISDLKKIE DLIQSMHIDA TLYTESDVHP SCKVTAMKCF LLELQVISLE	150
SGDASIHDTV ENLILANNSS LSSNGNVTES GCKECEELKE KNIKEFLQSF	200
VHIVQMFINT S	211

Peptide linker / Peptide liant / Péptido de unión

79 SGGGGGGGGGGGGGGGG 97 (1-19)

Post-translational modifications / Modifications post-translationnelles / Modificaciones post-translacionales

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-chain 3-45, 29-63, 132-182, 139-185

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
N168, N176

narazaciliclibum

narazaciliclib

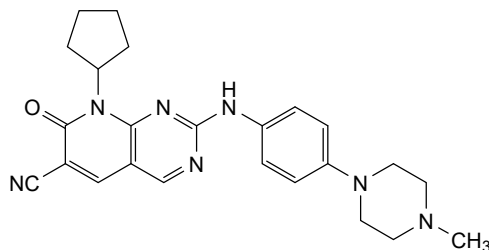
8-cyclopentyl-2-[4-(4-methylpiperazin-1-yl)anilino]-7-oxo-7,8-dihydropyrido[2,3-*d*]pyrimidine-6-carbonitrile

narazaciliclib

8-cyclopentyl-2-[4-(4-méthylpipérazin-1-yl)anilino]-7-oxo-7,8-dihydropyrido[2,3-*d*]pyrimidine-6-carbonitrile

narazaciliclib

8-ciclopentil-2-[4-(4-metilpiperazin-1-il)anilino]-7-oxo-7,8-dihidropirido[2,3-*d*]pirimidina-6-carbonitrilo

C₂₄H₂₇N₇O

nepuvibartum

nepuvibart

immunoglobulin G1-kappa, anti-[severe acute respiratory syndrome (human) coronavirus 2 (SARS-CoV-2) spike (S) glycoprotein, receptor binding domain (RBD)], *Homo sapiens* monoclonal antibody;

gamma1 heavy chain *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV3-11*01 (96.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, G1v14 CH2 A1.3, A1.2, G1v24 CH3 L107, S114 (CH1 R120>K (217) (121-218), hinge 1-15 (219-233), CH2 L1.3>A (237), L1.2>A (238), P114>G (332) (234-343), CH3 E12 (359), M14 (361), M107>L (431), N114>S (437) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (96.8%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (229-229":232-232")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1SV lacking the glutamine synthetase (GS-KO) gene, glycoform alfa

népuvibart

immunoglobuline G1-kappa, anti-[domaine de liaison au récepteur (RBD) de la glycoprotéine spike (S) du coronavirus 2 (humain) du syndrome respiratoire aigu sévère (SARS-CoV-2)], anticorps monoclonal *Homo sapiens*;

chaîne lourde gamma1 *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV3-11*01 (96.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, G1v14 CH2 A1.3, A1.2, G1v24 CH3 L107, S114 (CH1 R120>K (217) (121-218), charnière 1-15 (219-233), CH2 L1.3>A (237), L1.2>A (238), P114>G (332) (234-343), CH3 E12 (359), M14 (361), M107>L (431), N114>S (437) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (96.8%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (229-229":232-232")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1SV ne présentant pas le gène de la glutamine synthétase (GS-KO), glycoforme alfa

nepuvibart

inmunoglobulina G1-kappa, anti-[dominio de unión al receptor (RBD) de la glicoproteína spike (S) del coronavirus 2 (humano) del síndrome respiratorio agudo severo (SARS-CoV-2)], anticuerpo monoclonal *Homo sapiens*;

cadena pesada gamma1 *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV3-11*01 (96.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1, G1v14 CH2 A1.3, A1.2, G1v24 CH3 L107, S114 (CH1 R120>K (217) (121-218), bisagra 1-15 (219-233), CH2 L1.3>A (237), L1.2>A (238), P114>G (332) (234-343), CH3 E12 (359), M14 (361), M107>L (431), N114>S (437) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-33*01 (96.8%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (229-229":232-232")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1SV en ausencia del gen glutamina sintetasa (GS-KO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada
 QVQLVESGGG LVKPGGSLRL SCAASGFTFS DYYMSWIRQA PGKLEWVSY 50
 ITYSGSTIYY ADSVKGRFTI SRDNAKSSLY LQMNSLRAED TAVYYCARDR 100
 GTTMVFPFDYW GQGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
 DYFPEFVTVS WNSGALTSGV HTPFAVLQSS GLYSLSSVVT VPSSSLGTQT 200
 YICNVNHPKS NTKVDKRVPE KSCDKTHTCP PCPAPFAEAGG PSVFLFPPKP 250
 RDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
 STYRVVSVLT VLNQDNLNGK EYKCKVSNKA LGAPTEKTIK KAKGQPREPQ 350
 VYTLPPSREE MTRKQVSLTLC LVKGFYPSDI AVEWESNGQP ENNYKTTTPPV 400
 LDDSGSFFLY SKLTVDKSRW QQGNVFSCSV LHEALHSHYT QKSLSLSPGK 450

Light chain / Chaîne légère / Cadena ligera
 DIQMTQSPSS LSASVGRDRTVITCQASQDITNYLNWYQQKPKGAPKLLIYA 50
 ASNLEIGVPS RFGSGSGTDFTFTISGLQPEDIATYYCQQYDNLPLTFFG 100
 GTRVEIKRTV AAPSVFIFPPSDEQLKSGTASVCLLNNFYPRKAVQWVK 150
 DNALQSGNSQESVTEQDSKDTSTYLSSTLTLSKADYERHKVYACEVTHQG 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-L (C23-C104) 23"-88" 134"-194"
 23"-88"" 134"-194"
 Inter-H-L (h5-CL126) 223-214" 223"-214"
 Inter-H-H (h11, h14) 229-229" 232-232"

N-terminal glutaminy cyclization / Cyclisation du glutaminy N-terminal / Ciclación del glutaminy N-terminal
 HVHQ1 > pyroglutamy (pE, 5-oxopropyl): 1, 1"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
 HCH2N84.4: 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 / Coupeure de la lysine C-terminale / Recorte de lisina C-terminal
 HCHSK2: 450, 450"

nesuparibum

nesuparib

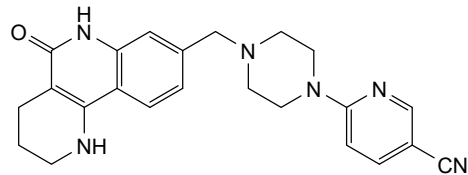
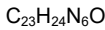
6-{4-[(5-oxo-1,2,3,4,5,6-hexahydrobenzo[h][1,6]naphthyridin-8-yl)methyl]piperazin-1-yl}pyridine-3-carbonitrile

nésuparib

6-{4-[(5-oxo-1,2,3,4,5,6-hexahydrobenzo[h][1,6]naphtyridin-8-yl)méthyl]pipérazin-1-yl}pyridine-3-carbonitrile

nesuparib

6-{4-[(5-oxo-1,2,3,4,5,6-hexahydrobenzo[h][1,6]naftiridin-8-il)metil]piperazin-1-il}piridina-3-carbonitrilo



nirmatrelvirum

nirmatrelvir

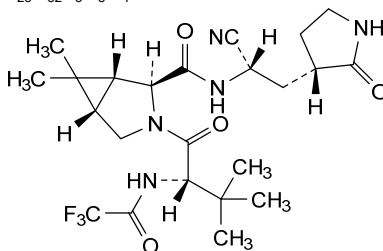
(1R,2S,5S)-N-((1S)-1-cyano-2-[(3S)-2-oxopyrrolidin-3-yl]ethyl)-3-[(2S)-3,3-dimethyl-2-(2,2,2-trifluoroacetamido)butanoyl]-6,6-dimethyl-3-azabicyclo[3.1.0]hexane-2-carboxamide

nirmatrelvir

(1R,2S,5S)-N-((1S)-1-cyano-2-[(3S)-2-oxopyrrolidin-3-yl]éthyl)-3-[(2S)-3,3-diméthyl-2-(2,2,2-trifluoroacétamido)butanoyl]-6,6-diméthyl-3-azabicyclo[3.1.0]hexane-2-carboxamide

nirmatrelvir

(1R,2S,5S)-N-((1S)-1-ciano-2-[(3S)-2-oxopirrolidin-3-yl]etil)-3-[(2S)-3,3-dimetil-2-(2,2,2-trifluoroacetamido)butanoil]-6,6-dimetil-3-azabicyclo[3.1.0]hexane-2-carboxamida

 $C_{23}H_{32}F_3N_5O_4$


nomlabofuspum #

nomlabofusp

cell-penetrating peptide TAT-cpp (1-12), derived from the human immunodeficiency virus 1 (HIV-1) HIV-TAT nuclear trans-activator, fused via peptidyl linker $^{13}GG^{14}$ to the human isoform 1 precursor of mitochondrial frataxin (Friedreich ataxia protein) (15-224), non-glycosylated, produced in *Escherichia coli*;
cell-penetrating peptide TAT-cpp (1-12), derived from the trans-activator of transcription HIV-TAT of the human immunodeficiency virus 1 (HIV-1), fused via a glycyglycyl linker (13-14) with the human isoform 1 precursor of mitochondrial frataxin (Friedreich ataxia protein, FXN, EC:1.16.3.1) (15-224), non-glycosylated, produced in *Escherichia coli*

nomlabofusp

peptide de pénétration cellulaire TAT-cpp (1-12), dérivé du transactivateur nucléaire du virus de l'immunodéficience humaine 1 (VIH-1) VIH-TAT, fusionné par l'intermédiaire de la liaison peptidique $^{13}GG^{14}$ au précurseur de l'isoforme 1 humaine de la frataxine mitochondriale (protéine de l'ataxie de Friedreich) (15-224), non glycosylé, produit dans *Escherichia coli*;
peptide de pénétration cellulaire TAT-cpp (1-12), dérivé du trans-activateur de transcription VIH-TAT du virus de l'immunodéficience humaine 1 (VIH-1), fusionné via une liaison peptidique glycyglycyle (13-14) avec l'isoforme 1 humaine du précurseur de la frataxine mitochondriale (protéine d'ataxie de Friedreich, FXN, EC:1.16.3.1) (15-224), non glycosylé, produit dans *Escherichia coli*

nomlabofusp

peptido de penetración celular TAT-cpp (1-12), derivado del virus de la inmunodeficiencia humana 1 (VIH-1) VIH-TAT nuclear trans-activador, fusionado a través de un enlace peptídico $^{13}GG^{14}$ a la isoforma humana 1 precursor de la frataxina mitocondrial (proteína de ataxia de Friedreich) (15-224), no glicosilado, producido en *Escherichia coli*;
peptido de penetración celular TAT-cpp (1-12), derivado del trans-activador de la transcripción genética VIH-TAT del virus de inmunodeficiencia

humana 1 (VIH-1), fusionado a través de un enlace de glicilglicilo (13-14) con la isoforma 1 humana del precursor de la frataxina mitocondrial (proteína de ataxia de Friedreich, FXN, EC:1.16.3.1) (15-224), no glicosilado, producido en *Escherichia coli*

Sequence / Séquence / Secuencia	
MYGKKRRQR RRG ^{GG} WTLGR FAVAGLLASP SPAQAQTLTR VFRPAELAPL	50
CGRRLRTDI DATCTPRRAS SNQRGLNQIW NVKQSVYLM NLRKSGTLGH	100
FGSLDETTYE FLAETLDSL AEFEDLADK PYTFEDYDVS FSGVLTVKL	150
GGDLGTYVIN KQTPNKQIWL SSPSSGPKRY DWTGKNWVYS HDGVSHELL	200
AELTKALKT KLDLSSLAYS GKDA	224

Peptide linker / Peptide liant / Péptide de unión : 13 ^{GG} 14 (1-2)

Post-translational modifications / Modifications post-translationnelles / Modificaciones post-translacionales

Disulfide bridge location / Position du pont disulfure / Posición del puente disulfuro
51-64

nulabeglogenum autogedtemcelum #

nulabeglogene autogedtemcel

autologous CD34+ hematopoietic stem and progenitor cells (HSPCs) obtained by apheresis from sickle cell patients, genetically modified *ex vivo* by CRISPR/Cas9 (clustered regularly interspaced short palindromic repeats/CRISPR-associated protein 9) mediated gene editing consisting of a single guide RNA (sgRNA) targeting the first exon of the human β -globin (HBB) gene, and using a homology-directed repair mechanism to correct the nucleic acid sequence encoding the glutamic acid to valine mutation at position 6 in the HBB protein via an adeno-associated virus serotype 6 (AAV6) vector in which the sgRNA targeting sequence is located between two HBB homology arms. Following genetic modification, each cell can have one of six combinations of HBB allele (WT/WT, INDEL/WT, INDEL/INDEL, INDEL/HR, WT/HR, HR/HR, where WT refers to the wild type sickle cell disease allele, INDEL refers to an insertion/deletion event but no correction of the HBB gene, and HR refers to a corrected HBB allele). On average 56% of the cells have at least one corrected HBB allele (HR).

The cell suspension is enriched for CD34+ cells using magnetic bead separation. The substance consists of cells with the CD45+ and CD34+ phenotype, with $\geq 70\%$ CD34 purity. The functional characterization of the cells is based on the ability to form erythroid and myeloid colonies on semisolid methylcellulose-based medium.

nulabéglogène autogedtemcel

cellules souches et progénitrices hématopoïétiques CD34+ autologues (HSPC) obtenues par aphérese à partir de patients atteints de drépanocytose, génétiquement modifiées *ex vivo* par édition génique médiée par CRISPR/Cas9 (courtes répétitions palindromiques groupées et régulièrement espacées / protéine 9 associée à CRISPR) consistant d'un ARN guide unique (sgRNA) ciblant le premier exon du gène de la β -globine humaine (HBB), et l'utilisation d'un mécanisme de réparation dirigé par homologie pour corriger la mutation de la séquence d'acide nucléique codant l'acide glutamique en valine en position 6 dans la protéine HBB via un vecteur du virus adéno-associé de sérotype 6 (AAV6) dans lequel la séquence de ciblage de l'ARNg est située entre deux bras d'homologie HBB. Après modification génétique, chaque cellule peut présenter l'une des six combinaisons de l'allèle HBB (WT/WT, INDEL/WT,

obéversen

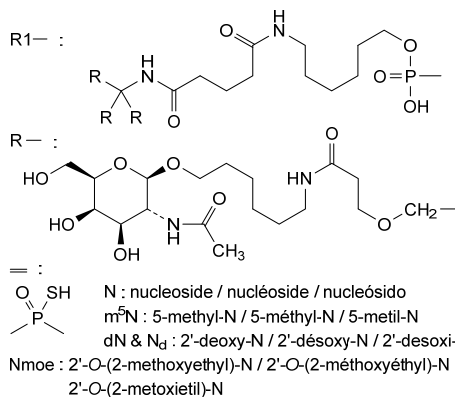
tout-P-ambo-5'-O-(28-[(2-acétamido-2-désoxy-β-D-galactopyranosyl)oxy]-16,16-bis[3-((6-[(2-acétamido-2-désoxy-β-D-galactopyranosyl)oxy]hexyl)amino)-3-oxopropoxy]méthyl)-1-hydroxy-1,10,14,21-tétraoxo-2,18-dioxa-9,15,22-triaza-1λ⁵-phosphaoctacosan-1-yl)-2'-O-(2-méthoxyéthyl)-5-méthyl-P-thiouridylyl-(3'→5')-2'-O-(2-méthoxyéthyl)guanylyl-(3'→5')-2'-O-(2-méthoxyéthyl)-5-méthylcytidylyl-(3'→5')-2'-O-(2-méthoxyéthyl)-5-méthylcytidylyl-(3'→5')-2'-O-(2-méthoxyéthyl)adénylyl-(3'→5')-P-thiothymidylyl-(3'→5')-P-thiothymidylyl-(3'→5')-P-thiothymidylyl-(3'→5')-2'-désoxy-P-thioadénylyl-(3'→5')-2'-désoxy-P-thioadénylyl-(3'→5')-P-thiothymidylyl-(3'→5')-2'-désoxy-P-thioguanilyl-(3'→5')-2'-désoxy-P-thioadénylyl-(3'→5')-2'-désoxy-P-thioguanilyl-(3'→5')-2'-désoxy-5-méthyl-P-thiocytidylyl-(3'→5')-2'-O-(2-méthoxyéthyl)-5-méthyluridylyl-(3'→5')-2'-O-(2-méthoxyéthyl)-5-méthyluridylyl-(3'→5')-2'-O-(2-méthoxyéthyl)-5-méthyl-P-thiocytidylyl-(3'→5')-2'-O-(2-méthoxyéthyl)-P-thioadénylyl-(3'→5')-2'-O-(2-méthoxyéthyl)-5-méthylcytidine

obeversén

todo-P-ambo-5'-O-(28-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]-16,16-bis[3-((6-[(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]hexil)amino)-3-oxopropoxi]metil)-1-hidroxi-1,10,14,21-tetraoxo-2,18-dioxa-9,15,22-triaza-1λ⁵-fosfaoctacosan-1-il)-5-metil-2'-O-(2-metoxietil)-P-tiouridilil-(3'→5')-2'-O-(2-metoxietil)guanilil-(3'→5')-5-metil-2'-O-(2-metoxietil)citidilil-(3'→5')-5-metil-2'-O-(2-metoxietil)citidilil-(3'→5')-2'-O-(2-metoxietil)adenilil-(3'→5')-P-tiotimidilil-(3'→5')-P-tiotimidilil-(3'→5')-2'-desoxi-P-tioadenilil-(3'→5')-P-tiotimidilil-(3'→5')-2'-desoxi-P-tioguanilil-(3'→5')-2'-desoxi-P-tioadenilil-(3'→5')-2'-desoxi-P-tioguanilil-(3'→5')-2'-desoxi-5-metil-P-tiocitidilil-(3'→5')-5-metil-2'-O-(2-metoxietil)uridilil-(3'→5')-5-metil-2'-O-(2-metoxietil)uridilil-(3'→5')-5-metil-2'-O-(2-metoxietil)-P-tiocitidilil-(3'→5')-2'-O-(2-metoxietil)-P-tioadenilil-(3'→5')-5-metil-2'-O-(2-metoxietil)citidina

C₂₉₆H₄₃₇N₇₇O₁₅₆P₂₀S₁₃

R1-m⁵Umoe=Gmoe-m⁵Cmoe-m⁵Cmoe-Amoe-dT=dT=dA=dA=dT=dG=dA=dG=m⁵C_d=m⁵Umoe-m⁵Umoe-m⁵Cmoe=Amoe=m⁵Cmoe



ogalvibartum #
ogalvibart

immunoglobulin G1-kappa, anti-[severe acute respiratory syndrome (human) coronavirus 2 (SARS-CoV-2) spike (S) glycoprotein, receptor binding domain (RBD)], *Homo sapiens* monoclonal antibody; gamma1 heavy chain *Homo sapiens* (1-448) [VH (*Homo sapiens* IGHV3-30*01 (95.9%) -(IGHD) - IGHJ4*01 (100%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1*03, G1m3, nG1m1, G1v24 CH3 L107, S114 (CH1 R120 (216) (120-217), hinge 1-15 (218-232), CH2 (233-342), CH3 E12 (360), M14 (362), M107>L (430), N114>S (436) (343-447), CHS K2>del (448)) (120-448)], (222-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5*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 (228-228":231-231")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

ogalvibart

immunoglobuline G1-kappa, anti-[domaine de liaison au récepteur (RBD) de la glycoprotéine spike (S) du coronavirus 2 (humain) du syndrome respiratoire aigu sévère (SARS-CoV-2)], anticorps monoclonal *Homo sapiens*; chaîne lourde gamma1 *Homo sapiens* (1-448) [VH (*Homo sapiens* IGHV3-30*01 (95.9%) -(IGHD) - IGHJ4*01 (100%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1*03, G1m3, nG1m1, G1v24 CH3 L107, S114 (CH1 R120 (216) (120-217), charnière 1-15 (218-232), CH2 (233-342), CH3 E12 (360), M14 (362), M107>L (430), N114>S (436) (343-447), CHS K2>del (448)) (120-448)], (222-214')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5*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 (228-228":231-231")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

ogalvibart

immunoglobulina G1-kappa, anti-[dominio de unión al receptor (RBD) de la glicoproteína spike (S) del coronavirus 2 (humano) del síndrome respiratorio agudo severo (SARS-CoV-2)], anticuerpo monoclonal *Homo sapiens*; cadena pesada gamma1 *Homo sapiens* (1-448) [VH (*Homo sapiens* IGHV3-30*01 (95.9%) -(IGHD) - IGHJ4*01 (100%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1*03, G1m3, nG1m1, G1v24 CH3 L107, S114 (CH1 R120 (216) (120-217), bisagra 1-15 (218-232), CH2 (233-342), CH3 E12 (360), M14 (362), M107>L (430), N114>S (436) (343-447), CHS K2>del (448)) (120-448)], (222-214')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-5*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 (228-228":231-231")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

QVQLVESGGG VVQPGRSLRL SCAASGTFES SYAMHWVRQA PGKGLEWVAV 50
 IPFDGRNKYV ADSVTGRFTI SRDNSKNTLY LQMNSLRAED TAVYVCASSS 100
 GYLFDSDYWG QGTLVTVSSA STKGPSVFLP APSSKSTSGG TAALGCLVKD 150
 YFPEPVTVSW NSGALTSGVH TTPAVLQSSG LYSLSVVTV PSSLGQTQY 200
 ICNWNHKFNS TKYDKRVEPK SCDKTHCPP CPAPELLGGF SVFLFPPPKK 250
 DTLMISRTPV VTCVVVDVSH EDPEVKFNMY VDGVEVHNAK TKPREEQYNS 300
 TYRIVSVLTV LHQDWLNGKE YKCKVSKNAL PAFIEKTIKSK ARGQPREFQV 350
 YTLFPSREEM TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTFPVL 400
 DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVL HEALHSHYDQ KSLSLSPG 448

Light chain / Chaîne légère / Cadena ligera

DIQMTQSPST LSASVGRDRTV ITCRASQGIS NWLAWFQQRP GKAPKLLIYE 50
 ASSLESQVPS RFSGSGSGTE FTLTISLQPD DDFATYYCQQ YNSYPWTFGQ 100
 GTKVEIKRTV AAPSVEFIFPP SDEQLKSGTA SVVCLLNIFY PREAKVQWKV 150
 DNALQSGNSQ ESVTEQDSKD STYLSLSTLT LSKADYEKHK VYACEVTHQG 200
 LSSFPVTKSFN RGECL 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

H VHQ1 > pyroglutamyl (pE, 5-oxoprolyl): 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 biantenaríos complejos fucosilados.

oligtalintum

oligtalintin

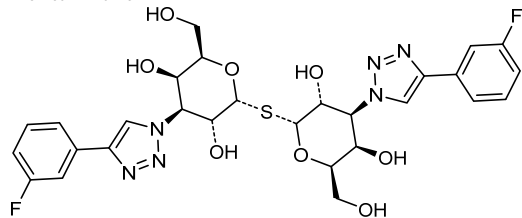
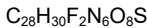
3-deoxy-3-[4-(3-fluorophenyl)-1H-1,2,3-triazol-1-yl]-β-D-galactopyranosyl 3-deoxy-3-[4-(3-fluorophenyl)-1H-1,2,3-triazol-1-yl]-1-thio-β-D-galactopyranoside

oligtalintine

3-désoxy-3-[4-(3-fluorophényl)-1H-1,2,3-triazol-1-yl]-1-thio-β-D-galactopyranoside de 3-désoxy-3-[4-(3-fluorophényl)-1H-1,2,3-triazol-1-yl]-β-D-galactopyranosyle

oligtalintina

3-desoxi-3-[4-(3-fluorofenil)-1H-1,2,3-triazol-1-il]-1-thio-β-D-galactopiranosido de 3-desoxi-3-[4-(3-fluorofenil)-1H-1,2,3-triazol-1-il]-β-D-galactopiranosilo



onfasprodilum

onfasprodil

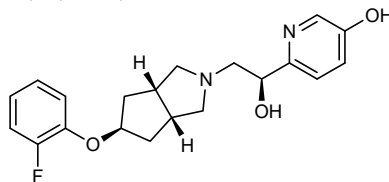
6-((1S)-2-[(3aR,5R,6aS)-5-(2-fluorophenoxy)hexahydrocyclopenta[c]pyrrol-2(1H)-yl]-1-hydroxyethyl)pyridin-3-ol

onfasprodil

6-((1S)-2-[(3aR,5R,6aS)-5-(2-fluorophénoxy)hexahydrocyclopenta[c]pyrrol-2(1H)-yl]-1-hydroxyéthyl)pyridin-3-ol

onfasprodil

6-{{(1*S*)-2-[(3*aR*,5*R*,6*aS*)-5-(2-fluorofenoxy)hexahidrociclopenta[*c*]pirrol-2(1*H*)-il]-1-hidroxietyl}piridin-3-ol

C₂₀H₂₃FN₂O₃**onradivirum**

onradivir

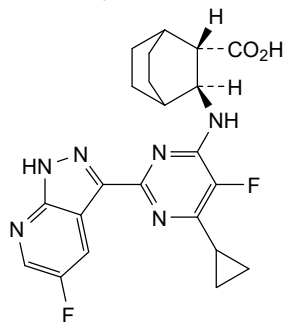
(2*S*,3*S*)-3-[[6-cyclopropyl-5-fluoro-2-(5-fluoro-1*H*-pyrazolo[3,4-*b*]pyridin-3-yl)pyrimidin-4-yl]amino]bicyclo[2.2.2]octane-2-carboxylic acid

onradivir

acide (2*S*,3*S*)-3-[[6-cyclopropyl-5-fluoro-2-(5-fluoro-1*H*-pyrazolo[3,4-*b*]pyridin-3-yl)pyrimidin-4-yl]amino]bicyclo[2.2.2]octane-2-carboxylique

onradivir

ácido (2*S*,3*S*)-3-[[6-ciclopropil-5-fluoro-2-(5-fluoro-1*H*-pirazolo[3,4-*b*]piridin-3-il)pirimidin-4-il]amino]biciclo[2.2.2]octano-2-carboxílico

C₂₂H₂₂F₂N₆O₂**opilrelagenum atradenorepvecum #**

opilrelagene atradenorepvec

recombinant replication-competent oncolytic adenovirus type 5 (Ad5), with the original promoter of E1A replaced with two consecutive human telomerase reverse transcriptase (TERT) promoters, with E1B-19kDa inactivated (by deletion of the start codon and the adjacent insertion of a stop codon), and with E3 deleted and replaced with the human relaxin 1 gene whose expression is under control of a cytomegalovirus (CMV) promoter.

opilrelágène atradénorepvec

adénovirus de type 5 (Ad5) recombinant oncolytique, capable de réplication, dont le promoteur original E1A a été remplacé par deux promoteurs consécutifs de la transcriptase inverse de la télomérase humaine (TERT), dont E1B-19kDa a été inactivé (par délétion du codon d'initiation et insertion adjacente d'un codon stop), et dont E3 a été supprimé et remplacé par le gène de la relaxine 1 humaine dont l'expression est sous le contrôle du promoteur du cytomégalovirus (CMV).

opilrelagén atradenorepvec

adenovirus tipo 5 (Ad5) oncolítico, recombinante y competente para replicación, con el promotor original de E1A reemplazado por dos promotores consecutivos de la telomerasa transcriptasa inversa (TERT) humana, con el gen E1B-19kDa inactivado (mediante deleción del codón de iniciación y la inserción adyacente de un codón de terminación) y con el gen E3 delecionado y reemplazado por el gen de la relaxina 1 humana cuya expresión está bajo el control de un promotor de citomegalovirus (CMV).

osemitamabum #
osemitamab

immunoglobulin G1-kappa, anti-[*Homo sapiens* CLDN18 (SFTPJ, surfactant associated protein J) isoform 2, extracellular domain 1 (EC1)], humanized monoclonal antibody;
gamma1 heavy chain humanized (1-448) [VH (*Homo sapiens* IGHV1-46*01 (87.8%) -(IGHD) -IGHJ4*01 (92.9%) L123>T (113), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 (CH1 K120 (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* IGKV4-1*01 (91.1%) -IGKJ4*01 (100%), CDR-IMGT [12.3.9] (27-38.56-58.95-103)) (1'-113') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (159), V101 (197) (114'-220')]; dimer (227-227":230-230")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1 lacking the glutamine synthetase (GS-KO) gene, glycoform alfa

osémitamab

immunoglobuline G1-kappa, anti-[*Homo sapiens* CLDN18 (SFTPJ, surfactant associé à la protéine J) isoforme 2, domaine extracellulaire 1 (EC1)], anticorps monoclonal humanisé;
chaîne lourde gamma1 humanisée (1-448) [VH (*Homo sapiens* IGHV1-46*01 (87.8%) -(IGHD) -IGHJ4*01 (92.9%) L123>T (113), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 (CH1 K120 (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* IGKV4-1*01 (91.1%) -IGKJ4*01 (100%), CDR-IMGT [12.3.9] (27-38.56-58.95-103)) (1'-113') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (159), V101 (197) (114'-220')]; dimère (227-227":230-230")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1 ne présentant pas le gène de la glutamine synthétase (GS-KO), glycoforme alfa

osemitamab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CLDN18 (SFTPJ, surfactante asociado a la proteína J) isoforma 2, dominio extracelular 1 (EC1)], anticuerpo monoclonal humanizado;

cadena pesada gamma1 humanizada (1-448) [VH (*Homo sapiens* IGHV1-46*01 (87.8%) -(IGHD) -IGHJ4*01 (92.9%) L123>T (113), CDR-IMGT [8.8.11] (26-33.51-58.97-107))] (1-118) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 (CH1 K120 (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* IGKV4-1*01 (91.1%) -IGKJ4*01 (100%), CDR-IMGT [12.3.9] (27-38.56-58.95-103)) (1'-113') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (159), V101 (197) (114'-220')]; dímero (227-227":230-230")-bisulfuro, 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 VKKFGASVKV SCKASGYTFT GYNMNVWRQA PGQGLEWMGN 50
IDPYYGGTYS NQKFKGRVTM TIDKSTSTVY MELSSLRSED TAVYVCARMY 100
HGNAFDYWGQ GTTIVTSSAS TKGPSVFPLA PSSKSTSGGT AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVTVTP SSSLGTQTYI 200
CNVNHKPSNT KVDKVEPKS CDKTHTCPPC PAPELLGPPS VFLFPPKPKD 250
TLMISRTPPEV TCVVVDVSHS DPEVKFNWYV DGEVHNAKT KPREEQYNST 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY 350
TLPPSRDELDT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPEPVL 400
SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPGK 448

Light chain / Chaîne légère / Cadena ligera

DIIVMTQSPDS LAVSLGERAT INCKSSQSLN NSGNLKNYLT WYQQKPGQPFP 50
KLLIYNASTR KSGVDFRFSG SSGSTDFTLT ISSLQAEDVA VYYQNDYSY 100
PLTFGGGTTKV EIKRTVAAPS VFIFPPSDEQ LKSGTASVVC LLNMFYPREA 150
VQWVKVDNAL QSGNSQESVT EQDSKDYSTY LSSTLTLSKA DYEKHKVYAC 200
EVTHQGLSSP VTKSFNRGEC 220

Post-translational modifications

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

Intra-H (C23-C104) 22-96 145-201 262-322 368-426
22"-96" 145"-201" 262"-322" 368"-426"
Intra-L (C23-C104) 23"-94" 140"-200"
23"-94" 140"-200"
Inter-H-L (h 5-CL 126) 221-220" 221"-220"
Inter-H-H (h 11, h 14) 227-227" 230-230"

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

H VH Q1 > pyroglutamyl (pE, 5-oxoprolyl): 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 biantenararios complejos fucosilados.

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

H CHS K2: 448, 448"

ozuriftamabum #
ozuriftamab

immunoglobulin G1-kappa, anti-[*Homo sapiens* ROR2 (receptor tyrosine kinase like orphan receptor 2, NTRKR2)], monoclonal antibody;

gamma1 heavy chain (1-451) [VH (*Homo sapiens* IGHV5-10-1*04 (79.4%) -(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 (219) (123-220), hinge 1-15 (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS K2>del (451)) (123-451)], (225-213')-disulfide with kappa light chain (1'-213') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV4-57*01 (75.3%) -IGKJ4*01 (83.3%) S120>Q (99), L124>V (103)/*Homo sapiens* IGKV1-13*02 (70.5%) -IGKJ1*01 (91.7%), 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 (231-231":234-234")-bisulfuro, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa

ozuriftamab

immunoglobuline G1-kappa, anti-[*Homo sapiens* ROR2 (récepteur orphelin 2 de type récepteur tyrosine kinase, NTRKR2), anticorps monoclonal; chaîne lourde gamma1 (1-451) [VH (*Homo sapiens* IGHV5-10-1*04 (79.4%) -(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 (219) (123-220), charnière 1-15 (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS K2>del (451)) (123-451)], (225-213')-disulfure avec la chaîne légère kappa (1'-213') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV4-57*01 (75.3%) -IGKJ4*01 (83.3%) S120>Q (99), L124>V (103)/*Homo sapiens* IGKV1-13*02 (70.5%) -IGKJ1*01 (91.7%), 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 (231-231":234-234")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa

ozuriftamab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* ROR2 (receptor huérfano 2 de tipo receptor tirosina kinasa, NTRKR2), anticuerpo monoclonal; cadena pesada gamma 1 (1-451) [VH (*Homo sapiens* IGHV5-10-1*04 (79.4%) -(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 (219) (123-220), bisagra 1-15 (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS K2>del (451)) (123-451)], (225-213')-disulfuro con la cadena ligera kappa (1'-213') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV4-57*01 (75.3%) -IGKJ4*01 (83.3%) S120>Q (99), L124>V (103)/*Homo sapiens* IGKV1-13*02 (70.5%) -IGKJ1*01 (91.7%), 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 (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

```
EVQLVQSGAE VKKPGESLRI SCKGSGYTFE EYTMHWVRQA PGQGLEWVGG 50
INTNNGGTGY NQKFKGRVTI SADKSISTAY LQWSSLKASD TAMYCAHGS 100
LYSYGNSYFD YWGQGLTIVT SSASTRGPVS FFLAPSSKST SGGTAALGCL 150
VKDYFPEPVT VSWNSGALTS GVHTFFPAVLQ SSGLYSLSSV VTFVSSSLGT 200
QTYICNVNHK PSNTRKVDKVK EPKSCDKTHT CPCCPAPELL GGPVFLFPP 250
KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NNYVDGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLW GKEYYCKVSN KALPAPIEKT ISKAKGQPRE 350
PQVYTLPPSR DELTKNQVSL TCLVKGFPYS DIAVEWESNG QPENNYKTFP 400
PVLDSGSPFF LYSKLTVDKRS RQQGNVFC SVMHEALHNH YTKRSLSLSP 450
G 451
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Light chain / Chaîne légère / Cadena ligera

```
AIQLTQSPSS LSASVGRDRT ITCSATSSVS YMHNYLQKPG QSPQLLIYGT 50
SNLASGVFDR FSGSGSGTDF TLKISRVEAE DVGYYCQQR SYPFFTFQGG 100
TKVEIKRTVA AFSVFIPPPS DEQLKSGTAS VVCLLNNEFP REAKVQWVKD 150
NALQSGNSQE SVTEQDSKDS TYSLSSTLTL SKADYEKHKV YACEVTHQGL 200
SSPVTKSFNR GEC 213
```

Post-translational modifications

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

Intra-H (C23-C104) 22^o-96^o 149^o-205^o 266^o-326^o 372^o-430^o
 22^o-96^o 149^o-205^o 266^o-326^o 372^o-430^o
 Intra-L (C23-C104) 23^o-87^o 133^o-193^o
 23^o-87^o 133^o-193^o
 Inter-H-L (h 5-CL 126) 225-213' 225'-213"
 Inter-H-H (h 11, h 14) 231-231" 234-234"

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

H CH2 N84.4:302, 302"

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

ozuriftamabum vedotinum

ozuriftamab vedotin

immunoglobulin G1-kappa, anti-[*Homo sapiens* ROR2 (receptor tyrosine kinase-like orphan receptor 2, NTRKR2)], monoclonal antibody, conjugated to auristatin E;

gamma1 heavy chain (1-451) [VH (*Homo sapiens* IGHV5-10-1*04 (79.4%) -(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 (219) (123-220), hinge 1-15 (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS K2>del (451)) (123-451)], (225-213')-disulfide with kappa light chain (1'-213') [V-KAPPA *Mus musculus*/Homsap (*Mus musculus* IGKV4-57*01 (75.3%) -IGKJ4*01 (83.3%) S120>Q (99), L124>V (103)/*Homo sapiens* IGKV1-13*02 (70.5%) -IGKJ1*01 (91.7%), 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 (231-231":234-234")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa, conjugated, on an average of 4 cysteinyl, to monomethylauristatin E (MMAE), via a cleavable maleimidocaproyl-valyl-citrullinyl-*p*-aminobenzoyloxycarbonyl (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".

ozuriftamab védotine

immunoglobuline G1-kappa, anti-[*Homo sapiens* ROR2 (récepteur orphelin 2 de type récepteur tyrosine kinase, NTRKR2)], anticorps monoclonal, conjugué à l'auristatine E;

chaîne lourde gamma1 (1-451) [VH (*Homo sapiens* IGHV5-10-1*04 (79.4%) -(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 (219) (123-220), charnière 1-15 (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS K2>del (451)) (123-451)], (225-213')-disulfure avec la chaîne légère kappa (1'-213') [V-KAPPA *Mus musculus*/Homsap (*Mus musculus* IGKV4-57*01 (75.3%) -IGKJ4*01 (83.3%) S120>Q (99), L124>V (103)/*Homo sapiens* IGKV1-13*02 (70.5%) -IGKJ1*01 (91.7%), 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 (231-231":234-234")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa, conjugué, sur 4 cystéinyl en moyenne, au monométhylauristatine E (MMAE), via un linker clivable de type maléimidocaproyl-valyl-citrullinyl-*p*-aminobenzoyloxycarbonyl (mc-val-cit-PABC)

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

ozuriftamab vedotina

immunoglobulina G1-kappa, anti-[*Homo sapiens* ROR2 (receptor huérfano 2 de tipo receptor tirosina kinasa, NTRKR2)], anticuerpo monoclonal, conjugado con la auristatina E;

cadena pesada gamma1 (1-451) [VH (*Homo sapiens* IGHV5-10-1*04 (79.4%) -(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 (219) (123-220), bisagra 1-15 (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS K2>del (451)) (123-451)], (225-213')-disulfuro con la cadena ligera kappa (1'-213') [V-KAPPA Musmus/Homsap (*Mus musculus* IGV4-57*01 (75.3%) -IGKJ4*01 (83.3%) S120>Q (99), L124>V (103)/*Homo sapiens* IGKV1-13*02 (70.5%) -IGKJ1*01 (91.7%), 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 (231-231":234-234")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, forma glicosilada alfa, conjugado, en 4 restos cisteinil por término medio, con monometilauristatina E (MMAE), a través de un enlace escindible de tipo maleimidocaproil-valil-citrulinil-p-aminobenciloxicarbonil (mc-val-cit-PABC)
 Para la parte vedotina, por favor vaya al documento "INN for pharmaceutical substances: Names for radicals, groups and others".

Heavy chain / Chaîne lourde / Cadena pesada
 EVQLVQSGAE VKKPGESLRI SCKGSGYTF EYTMHWVRQA PGQGLEWMGG 50
 INTNNGGTFY NQKFKGRVTI SADKISITAY LQWSSLKASD TAMYYCAHGS 100
 LYSYGNSTYFD YWQGGTLVTV SSASTKGPVS FPLAPSSKST SGGTAALGCL 150
 VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ SSGLYLSSV VTPVSSSLGT 200
 QTYICNVNHK PSNTKVDKVK EPKSCDKTHT CPPCPAPELL GGPSVFLFPP 250
 RPKDTLMISR TPEVTCVVVD VSHEDPEVKF NNYVDGVEVH NAKTKPREEQ 300
 YNSTYRVVSV LTVLHQDWLNL GKEYKCKVSN KALPAPIEKT ISKAKGQPRE 350
 PQVYTLPPSR DELTKNQVSL TCLVKGFEYPS DIAVEWESNG QPENNYKTTT 400
 PVLDSDDGSFF LYSKLTVDKLS RWQQGNVFPSC SVMHEALHNNH YTKQSLSLSP 450
 G 451

Light chain / Chaîne légère / Cadena ligera
 AIQLTQSPSS LSASVGDRTV ITCSATSSVS YMHWYLQKPG QSPQLLIYGT 50
 SNLASGVFDR FSGSGSGTDF TLKISRVEAE DVGVIYCCQR SSYPFTFGQG 100
 TKVEIKRTVA APSVFIPTPS DEQLKSGTAS VVCLLNHFYP REAKVQWQVD 150
 NALQSGNSQSE SVTTEQDSKDS TYSLSSTLT 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) 22-96 149-205 266-326 372-430
 22"-96" 149"-205" 266"-326" 372"-430"
 Intra-L (C23-C104) 23'-87' 133'-193'
 23"-87'" 133"-193'"
 Inter-H-L* (h 5-CL 126) 225-213' 225"-213"
 Inter-H-H* (h 11, h 14) 231-231" 234-234"

*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 están 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: 302, 302"

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

paclitaxeli obaluronas
 paclitaxel obaluronate

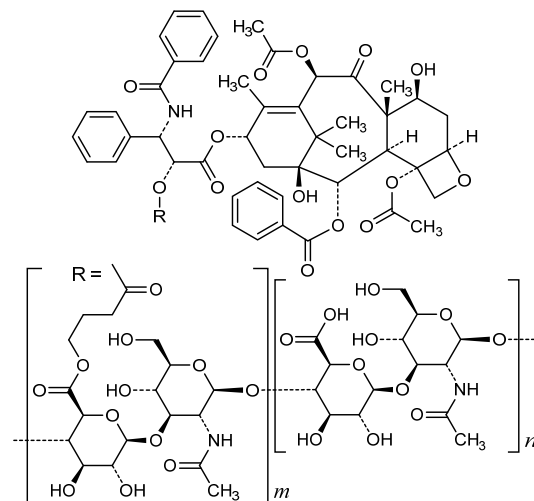
hyaluronic acid partly esterified (0.08-0.12) with 4-
 {{{(1S,2R)-1-benzamido-3-[[4,10β-bis(acetyloxy)-2α-(benzoyloxy)-5β,20-epoxy-1,7β-dihydroxy-9-oxotax-11-en-13α-yl]oxy}-3-oxo-1-phenylpropan-2-yl]oxy}-4-oxobutyl groups

obaluronate de paclitaxel

acide hyaluronique estérifié partiellement (0.08-0.12) avec des groupes 4-[[[(1*S*,2*R*)-1-benzamido-3-[[4,10β-bis(acétyloxy)-2α-(benzoyloxy)-5β,20-époxy-1,7β-dihydroxy-9-oxotax-11-én-13α-yl]oxy]-3-oxo-1-phénylpropan-2-yl]oxy]-4-oxobutyle

obaluronato de paclitaxel

ácido hialurónico esterificado parcialmente (0.08-0.12) con grupos 4-[[[(1*S*,2*R*)-1-benzamido-3-[[4,10β-bis(acetiloxi)-2α-(benzoihoxi)-5β,20-epoxi-1,7β-dihidroxi-9-oxotax-11-en-13α-il]oxi]-3-oxo-1-fenilpropan-2-il]oxi]-4-oxobutilo

**padnarsertibum**

padnarsertib

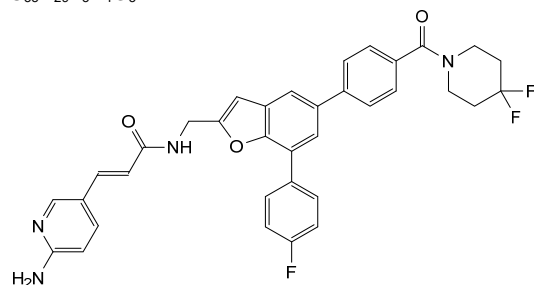
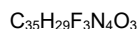
(2*E*)-3-(6-aminopyridin-3-yl)-*N*-({5-[4-(4,4-difluoropiperidine-1-carbonyl)phényl]-7-(4-fluorophényl)-1-benzofuran-2-yl)méthyl}prop-2-énamide

padnarsertib

(2*E*)-3-(6-aminopyridin-3-yl)-*N*-({5-[4-(4,4-difluoropiperidina-1-carbonil)fenil]-7-(4-fluorofenil)-1-benzofuran-2-yl)méthyl}prop-2-énamide

padnarsertib

(2*E*)-3-(6-aminopiridin-3-il)-*N*-({5-[4-(4,4-difluoropiperidina-1-carbonil)fenil]-7-(4-fluorofenil)-1-benzofuran-2-il}metil}prop-2-énamida



palsucibepum pegolium #
palsucibep pegol

engineered human lipocalin-2 binding protein (LCN2, neutrophil gelatinase-associated lipocalin, NGAL, siderocalin, oncogene 24p3) variant (N-terminal M added, Q>H²⁸, A>E⁴⁰, I>V⁴¹, Q>M⁴⁹, Y>W⁵², K>E⁵⁹, S>I⁶⁸, L>M⁷⁰, F>P⁷¹, R>L⁷², K>A⁷³, K>E⁷⁴, D>E⁷⁷, W>L⁷⁹, I>F⁸⁰, R>Q⁸¹, N>G⁹⁶, Y>G¹⁰⁰, L>R¹⁰³, Y>G¹⁰⁶, K>V¹²⁵, S>I¹²⁷W, Y>V¹³², K>W¹³⁴, I>V¹³⁵), anti-[human hepcidin (human liver-expressed antimicrobial peptide 1, LEAP-1, HAMP, putative liver tumor regressor, PLTR)], non-glycosylated, produced by *Escherichia coli*, conjugated at the S atom of C87 with PEG (~30 kDa);

artificial recombinant protein, derived from human lipocalin-2 (LCN2, neutrophil gelatinase-associated lipocalin, NGAL, siderocalin, oncogene 24p3), designed for binding to hepcidin (human liver-expressed antimicrobial peptide 1, LEAP-1, HAMP, putative liver tumor regressor, PLTR) by exchanging 25 residues; L-methionyl-[Q²⁸H, A⁴⁰E, I⁴¹V, Q⁴⁹M, Y⁵²W, K⁵⁹E, S⁶⁸I, L⁷⁰M, F⁷¹P, R⁷²L, K⁷³A, K⁷⁴E, D⁷⁷E, W⁷⁹L, I⁸⁰F, R⁸¹Q, N⁹⁶G, Y¹⁰⁰G, L¹⁰³R, Y¹⁰⁶G, K¹²⁵V, S¹²⁷W, Y¹³²V, K¹³⁴W, I¹³⁵V]-lipocalin-2, non-glycosylated, produced by *Escherichia coli*, conjugated at the S atom of Cys87 with a (3RS)-1-(3-{3-[α -methylpoly(oxyethylene)- ω -amino]propyl}-3-oxopropyl)-2,5-dioxopyrrolidin-3-yl group (~30 kDa)

palsucibep pégol

protéine de liaison de la lipocaline-2 humaine modifiée (LCN2, lipocaline associée à la gélatinase des neutrophiles, NGAL, sidérocaldine, oncogène 24p3) variant (addition M au N-terminal, Q>H²⁸, A>E⁴⁰, I>V⁴¹, Q>M⁴⁹, Y>W⁵², K>E⁵⁹, S>I⁶⁸, L>M⁷⁰, F>P⁷¹, R>L⁷², K>A⁷³, K>E⁷⁴, D>E⁷⁷, W>L⁷⁹, I>F⁸⁰, R>Q⁸¹, N>G⁹⁶, Y>G¹⁰⁰, L>R¹⁰³, Y>G¹⁰⁶, K>V¹²⁵, S>I¹²⁷W, Y>V¹³², K>W¹³⁴, I>V¹³⁵), anti-[hepcidine humaine (peptide antimicrobien exprimé par le foie humain 1, LEAP-1, HAMP, régresseur de tumeur hépatique putatif, PLTR)], non glycosylée, produite dans *Escherichia coli*, conjuguée à l'atome S de C87 avec PEG (~30 kDa);

protéine artificielle recombinante, dérivée de la lipocaline-2 humaine (LCN2, lipocaline associée à la gélatinase des neutrophiles, NGAL, sidérocaldine, oncogène 24p3), conçue pour se lier à l'hepcidine (peptide antimicrobien 1 exprimé dans le foie humain, LEAP-1, HAMP, régresseur de tumeur hépatique putatif, PLTR) grâce à l'échange de 25 résidus d'acides aminés; L-méthionyl-[Q²⁸H, A⁴⁰E, I⁴¹V, Q⁴⁹M, Y⁵²W, K⁵⁹E, S⁶⁸I, L⁷⁰M, F⁷¹P, R⁷²L, K⁷³A, K⁷⁴E, D⁷⁷E, W⁷⁹L, I⁸⁰F, R⁸¹Q, N⁹⁶G, Y¹⁰⁰G, L¹⁰³R, Y¹⁰⁶G, K¹²⁵V, S¹²⁷W, Y¹³²V, K¹³⁴W, I¹³⁵V]-lipocaline-2, non glycosylée, produite dans *Escherichia coli*, conjuguée à l'atome S de Cys87 avec un groupe (3RS)-1-(3-{3-[α -méthylpoly(oxyéthylène)- ω -amino]propyl}-3-oxopropyl)-2,5-dioxopyrrolidine-3-yle (~30 kDa)

palsucibep pegol

proteína diseñada de unión a la lipocalina-2 humana (LCN2, lipocalina asociada a la gelatinasa de neutrófilos, NGAL, siderocalina, oncogén 24p3) variante (terminal N añadido M, Q>H²⁸, A>E⁴⁰, I>V⁴¹, Q>M⁴⁹, Y>W⁵², K>E⁵⁹, S>I⁶⁸, L>M⁷⁰, F>P⁷¹, R>L⁷², K>A⁷³, K>E⁷⁴, D>E⁷⁷, W>L⁷⁹, I>F⁸⁰, R>Q⁸¹, N>G⁹⁶, Y>G¹⁰⁰, L>R¹⁰³, Y>G¹⁰⁶, K>V¹²⁵, S>I¹²⁷W, Y>V¹³², K>W¹³⁴, I>V¹³⁵), anti-[hepcidina humana (péptido antimicrobiano 1 expresado en hígado humano, LEAP-1, HAMP, regresor de tumor hepático putativo, PLTR)], no glicosilada, producida por *Escherichia coli*, conjugada en el átomo de S de C87 con PEG (~30 kDa); proteína artificial recombinante, derivada de la lipocalina-2 humana (LCN2, lipocalina asociada a la gelatinasa de neutrófilos, NGAL, siderocalina, oncogén 24p3), diseñada para unirse a la hepcidina (péptido antimicrobiano 1 expresado en hígado humano, LEAP-1, HAMP, regresor de tumor hepático putativo, PLTR) por intercambio de 25 residuos de aminoácidos; L-metionil-[Q²⁸H, A⁴⁰E, I⁴¹V, Q⁴⁹M, Y⁵²W, K⁵⁹E, S⁶⁸I, L⁷⁰M, F⁷¹P, R⁷²L, K⁷³A, K⁷⁴E, D⁷⁷E, W⁷⁹L, I⁸⁰F, R⁸¹Q, N⁹⁶G, Y¹⁰⁰G, L¹⁰³R, Y¹⁰⁶G, K¹²⁵V, S¹²⁷W, Y¹³²V, K¹³⁴W, I¹³⁵V]-lipocalina-2, no glicosilada, producida por *Escherichia coli*, conjugada en el átomo de S de Cys87 con un grupo (3RS)-1-(3-{3-[α-metilpoli(oxietileno)-ω-amino]propil}-3-oxopropil)-2,5-dioxopirrolidin-3-ilo (~30 kDa)

Sequence / Séquence / Secuencia	
M	0
QDSTSDLIFA PPLSKVPLQQ NFQDNQFHGK WYVVGLAGNE VLREDKDPMK	50
MWATIVLEEE DKSYNVIVM PLAEKCEVLF QTFVPGQPG EFTLGGIKSG	100
PGRTSGLVRV VSTNYNQHAM VFFKVVQNR EVFVWTLYGR TKELTSSELKE	150
NFRFSKSLG LPENHIVFPV PIDQCIDG	178

Mutation / Mutation / Mutación

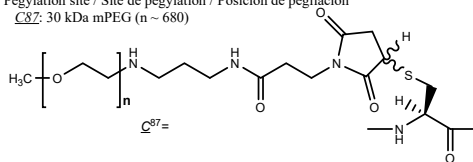
Q28> H, A40> E, I41> V, Q49> M, Y52> W, K59> E, S68> I, L70> M, F71> P, R72> L, K73> A, K74> E, D77> E, W79> L, I80> F, R81> Q, N96> G, Y100> G, L103> R, Y106> G, K125> V, S127> W, Y132> V, K134> W, I135> V

Post-translational modifications / modifications post-traductionnelles / modificaciones postraduccionales

Disulfide bridge location / Position du pont disulfure / Posición del puente disulfuro 76-175

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

Pegylation site / Site de pégylation / Posición de pegilación C87: 30 kDa mPEG (n ~ 680)



paltimatrectinibum

paltimatrectinib

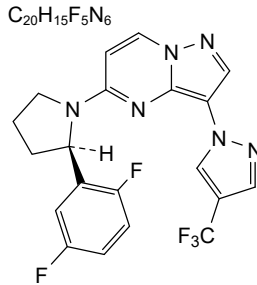
5-[(2R)-2-(2,5-difluorophenyl)pyrrolidin-1-yl]-3-[4-(trifluoromethyl)-1H-pyrazol-1-yl]pyrazolo[1,5-a]pyrimidine

paltimatrectinib

5-[(2R)-2-(2,5-difluorophényl)pyrrolidin-1-yl]-3-[4-(trifluorométhy)-1H-pyrazol-1-yl]pyrazolo[1,5-a]pyrimidine

paltimatrectinib

5-[(2R)-2-(2,5-difluorofenil)pirrolidin-1-il]-3-[4-(trifluorometil)-1H-pirazol-1-il]pirazolo[1,5-a]pirimidina



palupiprantum

palupiprant

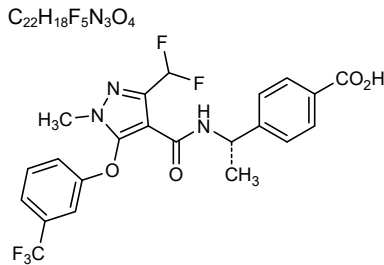
4-[(1*S*)-1-{3-(difluorométhyl)-1-méthyl-5-[3-(trifluorométhyl)phénoxy]-1*H*-pyrazole-4-carboxamido]éthyl]benzoïque acid

palupiprant

acide 4-[(1*S*)-1-{3-(difluorométhyl)-1-méthyl-5-[3-(trifluorométhyl)phénoxy]-1*H*-pyrazole-4-carboxamido]éthyl]benzoïque

palupiprant

ácido 4-[(1*S*)-1-{3-(difluorometil)-1-metil-5-[3-(trifluorometil)fenoxi]-1*H*-pirazol-4-carboxamido]etil]benzoico



paridiprubartum #

paridiprubart

immunoglobulin G1-kappa, anti-[*Homo sapiens* TLR4 (toll like receptor 4, toll-like receptor 4, CD284)], humanized monoclonal antibody; gamma1 heavy chain humanized (1-448) [VH (*Homo sapiens* IGHV4-30-4*07 (85.7%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [9.7.11] (26-34.52-58.97-107)) (1-118) -*Homo sapiens* IGHG1*03, G1m3, nG1m1, G1v38 CH2 S108, F113 (CH1 R120 (215) (119-216), hinge 1-15 (217-231), CH2 N108>S (326), L113>F (329) (232-341), CH3 E12 (357), M14 (359) (342-446), CHS (447-448)) (119-448)), (221-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV6-21*02 (90.5%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (227-227'':230-230'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1SV, glycoform alfa

paridiprubart

immunoglobuline G1-kappa, anti-[*Homo sapiens* TLR4 (récepteur 4 de type Toll, récepteur 4 toll-like, CD284)], anticorps monoclonal humanisé;

paridiprubart

chaîne lourde gamma1 humanisée (1-448) [VH (*Homo sapiens* IGHV4-30-4*07 (85.7%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [9.7.11] (26-34.52-58.97-107)) (1-118) -*Homo sapiens* IGHG1*03, G1m3, nG1m1, G1v38 CH2 S108, F113 (CH1 R120 (215) (119-216), charnière 1-15 (217-231), CH2 N108>S (326), L113>F (329) (232-341), CH3 E12 (357), M14 (359) (342-446), CHS (447-448)) (119-448)], (221-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV6-21*02 (90.5%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (227-227":230-230")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1SV, glycoforme alfa

immunoglobulina G1-kappa, anti-[*Homo sapiens* TLR4 (receptor 4 de tipo Toll, receptor 4 toll-like, CD284)], anticuerpo monoclonal humanizado; cadena pesada gamma1 humanizada (1-448) [VH (*Homo sapiens* IGHV4-30-4*07 (85.7%) -(IGHD) -IGHJ4*01 (92.9%), CDR-IMGT [9.7.11] (26-34.52-58.97-107)) (1-118) -*Homo sapiens* IGHG1*03, G1m3, nG1m1, G1v38 CH2 S108, F113 (CH1 R120 (215) (119-216), bisagra 1-15 (217-231), CH2 N108>S (326), L113>F (329) (232-341), CH3 E12 (357), M14 (359) (342-446), CHS (447-448)) (119-448)], (221-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV6-21*02 (90.5%) -IGKJ4*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (227-227":230-230")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1SV, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

QVQLQESGPG LVKPSDTLSL TCAVSGYSIT GGYSWHWIRQ PPGKLEWMMG 50
YIHYSYGTDF NPSLKRTRIT SRDTSKNQFS LKLSSTVAVD TAVYICARKD 100
PSDAFPYWGQ GTLTVTSSAS TKGPSVFLPA PSKSTSGGT AALGCLVKDY 150
FPEFVTVSWN SGALTSVGHV FPAVLQSSGL YSLSSVTVTF SSSLGTQTYI 200
CNVNHKPSNT KVDKRVEPKS CDKTHCTPCP PAFELLGGPS VLFEPKPKD 250
TLMISRTPEV TCVVVDVSHS DPEVKFNWYV DGEVHNNAKT KPREEQYNS 300
YRVVSVLTVL HQDWLNGKEY KCKVSSKAFP APIEKTISKA KGQPREPQVY 350
TLPPSREEMT KNQVSLTCLV KGFYPSDIAV EWESNGQFEN NYKTTTPEVLD 400
SDGSFFLYSK LTVDKSRWQQ GNVFSCSWMH EALHNHYTQK SLSLSPGK 448

Light chain / Chaîne légère / Cadena ligera

EIVLTQSPDF QSVTPKKEVT ITCRASQGIS DHLHWYQQKQ DQSPKLLIKY 50
ASHAISGVFS RFGSGSGTD FTLTINSLEA EDAATYYCQQ GHSFPLTFGG 100
GTRVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNIFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYLSLSTLT LSKADYERKH VYACEVTHQG 200
LSSPVTKSFN RGEC 214

Post-translational modifications

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

Intra-H (C23-C104) 22-96 145-201 262-322 368-426
22"-96" 145"-201" 262"-322" 368"-426"

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

Inter-H-L (h 5-CL 126) 221-214' 221"-214"

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

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

H V H Q I > pyroglutamyl (pE, 5-oxoprolyl); 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 CHS K2: 448, 448"

peceleganum

peceleganan

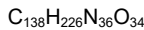
artificial antimicrobial cecropin A (1-10) × melittin B (3-18) hybrid (10+16)-peptide analogue; *N*⁶-acetyl-L-lysyl-L-tryptophyl-L-lysyl-L-seryl-L-phenylalanyl-L-leucyl-L-lysyl-L-threonyl-L-phenylalanyl-L-lysyl-L-seryl-L-alanyl-L-alanyl-L-lysyl-L-threonyl-L-valyl-L-leucyl-L-histidyl-L-threonyl-L-alanyl-L-leucyl-L-lysyl-L-alanyl-L-isoleucyl-L-seryl-L-serinamide

pécéleganan

analogue d'un peptide artificiel antimicrobien hybride (10+16) de cécropine A (1-10) × mélittine B (3-18); *N*⁶-acétyl-L-lysyl-L-tryptophyl-L-lysyl-L-séryl-L-phénylalanyl-L-leucyl-L-lysyl-L-thréonyl-L-phénylalanyl-L-lysyl-L-séryl-L-alanyl-L-alanyl-L-lysyl-L-thréonyl-L-valyl-L-leucyl-L-histidyl-L-thréonyl-L-alanyl-L-leucyl-L-lysyl-L-alanyl-L-isoleucyl-L-séryl-L-sérinamide

peceleganán

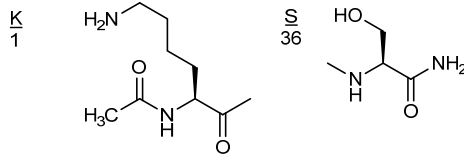
análogo de un péptido artificial antimicrobiano híbrido (10+16) de cecropina A (1-10) × melitina B (3-18); *N*⁶-acétil-L-lisil-L-triptofil-L-lisil-L-seril-L-fenilalanil-L-leucil-L-lisil-L-treonil-L-fenilalanil-L-lisil-L-seril-L-alanil-L-alanil-L-lisil-L-treonil-L-valil-L-leucil-L-histidil-L-treonil-L-alanil-L-leucil-L-lisil-L-alanil-L-isoleucil-L-seril-L-serinamida



Sequence / Séquence / Secuencia

KWKSFLKTFK SAAKTVLHTA LKAISS S 36

Modified residues / Résidus modifiés / Restos modificados



pegenzileukinum #

pegenzileukin

human interleukin 2 (IL2, T-cell growth factor, TCGF) (2-133) variant (A¹ deleted, Pro⁶⁵>Lys, Cys¹²⁵>Ser), non-glycosylated, produced in *Escherichia coli*, conjugated at N⁶ of K65 with a PEG derivative (30 kDa); [Ala¹>del, Pro⁶⁵>Lys, Cys¹²⁵>Ser]-human interleukin 2 (IL2, T-cell growth factor, TCGF), non-glycosylated, produced in *Escherichia coli*, N^{6,65}-({2-[8-{4-[α-methylpoly(oxyethylene)-ω-amino]-4-oxobutanoyl}-8,9-dihydro-1(or 3)*H*-dibenzo[*b,f*][1,2,3]triazolo[4,5-*d*]azocin-1(or 3)-yl]ethoxy}carbonyl)-derivative

pégenzileukine

interleukine 2 humaine (IL-2, facteur de croissance des cellules T, TCGF) (2-133) variant (A¹ supprimé, Pro⁶⁵>Lys, Cys¹²⁵>Ser), non glycosylée, produite dans *Escherichia coli*, conjuguée en N⁶ de K65 avec un dérivé PEG (30 kDa);

pegenzileukina

[Ala¹>del, Pro⁶⁵>Lys, Cys¹²⁵>Ser]-interleukine 2 humaine (IL-2, facteur de croissance des cellules T, TCGF), non glycosylée, produite dans *Escherichia coli*, conjuguée en N^{6,65}-({2-[β-4-[α-méthylpoly(oxyéthylène)-ω-amino]-4-oxobutanoyl]-8,9-dihydro-1(ou 3)H-dibenzo[b, f][1,2,3]triazolo[4,5-d]azocin-1(ou 3)-yl]éthoxy}carbonyle)

interleukina 2 humana (IL-2, factor de crecimiento de células T, TCGF) (2-133) variante (A¹ eliminada, Pro⁶⁵>Lys, Cys¹²⁵>Ser), no glicosilada, producida en *Escherichia coli*, conjugada en N⁶ del K65 con un derivado PEG (30 kDa);
Ala¹>del, Pro⁶⁵>Lis, Cis¹²⁵>Ser]-interleukina 2 humana (IL-2, factor de crecimiento de células T, TCGF), no glicosilada, producida en *Escherichia coli*, conjugada en N^{6,65}-({2-[8-{4-[α-metilpoli(oxi-etileno)-ω-amino]-4-oxobutanoyl]-8,9-dihidro-1(o 3)H-dibenzo[b, f][1,2,3]triazolo[4,5-d]azocin-1(o 3)-il]etoxi}carbonilo)

Sequence / Séquence / Secuencia

```
-PTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA 50
TELKHLQCLE EELKLEEVV NLAQSKNFHL RPRDLISNIN VIVLELKGSE 100
TTFMCEYADE TATIVEFLNR WITFSQSIIS TLT 133
```

Mutation / Mutation / Mutación

A1>del, P65>K, C125>S

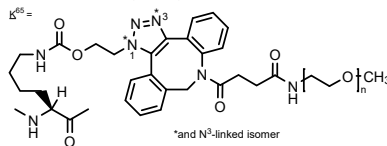
Post-translational modifications

Disulfide bridge location / Position du pont disulfure / Posición del puente disulfuro
58-105

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

Pegylation site / Site de pégylation / Posición de pegilación

K⁶⁵: 30 kDa mPEG (n ~ 680)



pelgifatamabum #
pelgifatamab

immunoglobulin G1-kappa, anti-[*Homo sapiens* FOLH1 (folate hydrolase, prostate specific membrane antigen, PSMA)], *Homo sapiens* monoclonal antibody; gamma1 heavy chain *Homo sapiens* (1-453) [VH (*Homo sapiens* IGHV3-33*01 (96.9%) -(IGHD) - IGHJ6*01 (100%), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 (CH1 R120 (220) (124-221), hinge 1-15 (222-236), CH2 (237-346), CH3 E12 (362), M14 (364) (347-451), CHS (452-453)) (124-453)], (226-214')-disulfide with kappa light chain *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-27*01 (94.7%) - IGKJ3*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (232-232':235-235'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa

pelgifatamab

immunoglobuline G1-kappa, anti-[*Homo sapiens* FOLH1 (folate hydrolase, antigène membranaire spécifique de la prostate, PSMA)], anticorps monoclonal *Homo sapiens*; chaîne lourde gamma1 *Homo sapiens* (1-453) [VH (*Homo sapiens* IGHV3-33*01 (96.9%) -(IGHD) -IGHJ6*01 (100%), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 (CH1 R120 (220) (124-221), charnière 1-15 (222-236), CH2 (237-346), CH3 E12 (362), M14 (364) (347-451), CHS (452-453)) (124-453)], (226-214')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-27*01 (94.7%) -IGKJ3*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (232-232":235-235")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa

pelgifatamab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* FOLH1 (folato hidrolasa, antígeno membranario específico de la próstata, PSMA)], anticuerpo monoclonal *Homo sapiens*; cadena pesada gamma1 *Homo sapiens* (1-453) [VH (*Homo sapiens* IGHV3-33*01 (96.9%) -(IGHD) -IGHJ6*01 (100%), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 (CH1 R120 (220) (124-221), bisagra 1-15 (222-236), CH2 (237-346), CH3 E12 (362), M14 (364) (347-451), CHS (452-453)) (124-453)], (226-214')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-27*01 (94.7%) -IGKJ3*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (232-232":235-235")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

QVQLVESGGG VVQPGRSRLR SCAASGFAPS RYGMHWVRQA PGKGLEWVAV 50
 IWDGSKNYK ADSVGRFRFTI SRDNSKNTQY LQMNSLRAED TAVYICARGG 100
 DFLYYYYYGM DVWGGQTTVT VSSASTKGPS VFPLAPSSKS TSGGTAALCG 150
 LVKDYFFPEPV TVSWNSGALT SGVHTFFAVL QSSGLYSLSS VVTVPSSSLG 200
 TQTYICNVNH KPSNTKVDKR VEPKSCDKTH TCPPCPAPEL LGGSPVFLFP 250
 PKPKDILMIS RTPEVTCVVV DVSHEDEVK FNWVVDGVEV HNAKTKPREE 300
 QYNSTRYRVVS VLTVLHQDWL NGKEYCKKVS NKALPAPIEK TISKARQQPR 350
 EFPQVTLFPPS REEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT 400
 PFLVDSGDSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTKSLSLS 450
 PGK 453

Light chain / Chaîne légère / Cadena ligera

DIQMTQSPSS LSASVGRDRTV ITCRASQGIS NYLAWYQQKT GKVPKFLIYE 50
 ASTLQSGVPS RFSGGGSGTD FTLTISLQEP EDVATYYCQN YNSAPFTFGP 100
 GTKVDIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNIFY PREAKVQWVK 150
 DNALQSGNSQ ESVTEQDSKD STYLSSTLT LSKADYEKHK VVACEVTHQG 200
 LSSPVTKSFN RGEK 214

Post-translational modifications

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

Intra-H (C23-C104) 22-96 150-206 267-327 373-431
 22"-96" 150"-206" 267"-327" 373"-431"
 Intra-L (C23-C104) 23-88" 134"-194"
 23"-88" 134"-194"
 Inter-H-L (h 5-CL 126) 226-214" 226"-214"
 Inter-H-H (h 11, h 14) 232-232" 235-235"

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

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

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

H CH2 N84.4: 303, 303"

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

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

H CHS K2: 453, 453"

pemvidutidum

pemvidutide

C^{5.16}, N^{6.20}-anhydro{L-histidyl-2-methylalanyl-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-N⁶-[1-O-(17-carboxyheptadecyl)-β-D-glucopyranuronoyl]-L-lysyl-L-alanyl-L-alanyl-L-lysyl-L-α-glutamyl-L-phenylalanyl-L-isoleucyl-L-glutaminy-L-tryptophyl-L-leucyl-L-leucyl-L-glutaminy-L-threoninamide}

pemvidutide

C^{5.16}, N^{6.20}-anhydro{L-histidyl-2-méthylalanyl-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-N⁶-[1-O-(17-carboxyheptadécyl)-β-D-glucopyranuronoyl]-L-lysyl-L-alanyl-L-alanyl-L-lysyl-L-α-glutamyl-L-phénylalanyl-L-isoleucyl-L-glutaminy-L-tryptophyl-L-leucyl-L-leucyl-L-glutaminy-L-thréoninamide}

pemvidutida

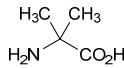
C^{5.16}, N^{6.20}-anhidro{L-histidil-2-metilalanyl-L-glutaminilglicil-L-treonil-L-fenilalanil-L-treonil-L-seril-L-α-aspartil-L-tirosil-L-seril-L-lisil-L-tirosil-L-leucil-L-α-aspartil-L-α-glutamil-N⁶-[1-O-(17-carboxiheptadecil)-β-D-glucopirranuronoi]-L-lisil-L-alanil-L-alanil-L-lisil-L-α-glutamil-L-fenilalanil-L-isoleucil-L-glutaminil-L-triptofil-L-leucil-L-leucil-L-glutaminil-L-treoninamida}

C₁₈₂H₂₇₅N₃₉O₅₄

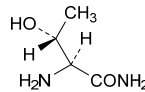
HXQGTFTSDY SKYLDEKAAK EFIQWLLQT 29

Amide bridge location / Position du pont amide / Posición del puente amido
16-20 (Glu^{5.16}-Lys^{6.20})

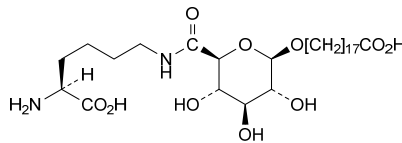
Modified residues / Résidus modifiés / Restos modificados



X (2)
2-methylalanine



T (29)
L-Thr-NH₂



K (17)
N⁶-[1-O-(17-carboxyheptadecyl)-D-glucopyranuronoyl]-L-Lys

peresolimabum #

peresolimab

immunoglobulin G1-kappa, anti-[*Homo sapiens* PDCD1 (programmed cell death 1, PD-1, PD1, CD279)], humanized monoclonal antibody; gamma1 heavy chain humanized (1-449) [VH (*Homo sapiens* IGHV1-24*01 (85.7%) -(IGHD) -IGHJ5*01 (87.5%), CDR-IMGT [8.8.13] (26-33.50-57.96-108))] (1-119) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 (CH1 K120 (216) (120-217), hinge 1-15 (218-232), CH2 (233-342), CH3 D12 (358), L14 (360) (343-447), CHS (448-449)) (120-449)], (222-217')-disulfide with kappa light chain humanized (1'-217') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (88.8%) -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 (228-228''-231-231'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1SV, glycoform alfa

péresolimab

immunoglobuline G1-kappa, anti-[*Homo sapiens* PDCD1 (protéine 1 de mort cellulaire programmée, PD-1, PD1, CD279)], anticorps monoclonal humanisé; chaîne lourde gamma1 humanisée (1-449) [VH (*Homo sapiens* IGHV1-24*01 (85.7%)-(IGHD)-IGHJ5*01 (87.5%), CDR-IMGT [8.8.13] (26-33.50-57.96-108)) (1-119) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 (CH1 K120 (216) (120-217), charnière 1-15 (218-232), CH2 (233-342), CH3 D12 (358), L14 (360) (343-447), CHS (448-449)) (120-449)], (222-217')-disulfure avec la chaîne légère kappa humanisée (1'-217') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (88.8%) -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 (228-228":231-231")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1SV, glycoforme alfa

peresolimab

immunoglobulina G1-kappa, anti-[*Homo sapiens* PDCD1 (proteína 1 de muerte celular programada, PD-1, PD1, CD279)], anticuerpo monoclonal humanizado; cadena pesada gamma1 humanizada (1-449) [VH (*Homo sapiens* IGHV1-24*01 (85.7%)-(IGHD)-IGHJ5*01 (87.5%), CDR-IMGT [8.8.13] (26-33.50-57.96-108)) (1-119) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 (CH1 K120 (216) (120-217), bisagra 1-15 (218-232), CH2 (233-342), CH3 D12 (358), L14 (360) (343-447), CHS (448-449)) (120-449)], (222-217')-disulfuro con la cadena ligera kappa humanizada (1'-217') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (88.8%) -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 (228-228":231-231")-bisdisulfuro, producido en las células ováricas de hamster chino (CHO), línea celular CHO-K1SV, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada
 QVQLVQSGAE VKKPGASVKV SCRVSGYSLK KYDMSWVRQA PGRGLEWMMGI 50
 IYTSGYTDYA QKFQGRVTMT EDTSTDTAYM ELSSLRSEDT AVVYCATGNP 100
 YYTNGFNSWG QGTLVTVSSA STKGPSVFPFL APSSKSTSGG TAALGCLVKD 150
 YFPEPVTWSV NSGALTSGVH TFPFVLSQSSG LYSLSSVTVV PSSSLGTQTY 200
 ICNVNHPKPSN TKVDKVKVEPK SCDKTHTCPP CPAPELLGGP SVFLFPPKPK 250
 DTLMISRTPF VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS 300
 TYRVVSVLTV LHQDWLNGKE YKCVSNKAL PAPIEKTISK AKGQPREPQV 350
 YTLPPSRDEL TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTTPVL 400
 DSDGFFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK 449

Light chain / Chaîne légère / Cadena ligera
 DIQMTQSPSS LSASVGRVRT ITCCQASQSPN NLLAWYQQKP GKAPKLLIYG 50
 ASDLPSSGVPV RFGSGSGSGTD FTLTISSLQP EDFATYVYCN NYVYGPVSYA 100
 FGGGTKEVEIK RTVAAPSVEFI FPPSDEQLKS GTASVYCLLN NFYPREAKVQ 150
 WKVDNALQSG NSQESVTEQD SKDSTYLSLS TLTLSKADYE KHKVYACEVT 200
 HQGLSSPVTK SFNRGEC 217

Post-translational modifications
 Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
 Intra-H (C23-C104) 22-95 146-202 263-323 369-427
 22"-95" 146"-202" 263"-323" 369"-427"
 Intra-L (C23-C104) 23'-88" 137"-197"
 23"'-88"' 137"'-197"
 Inter-H-L (h 5-CL 126) 222-217' 222"-217"
 Inter-H-H (h 11, h 14) 228-228" 231-231"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutamínilo N-terminal
 H VH Q1> pyroglutamyl (pE, 5-oxoprolyl): 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.

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

pertuzumabum zuvotolimodum #

pertuzumab zuvotolimod

immunoglobulin G1-kappa, anti-[*Homo sapiens* ERBB2 (epidermal growth factor receptor 2, receptor tyrosine-protein kinase erbB-2, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], humanized monoclonal antibody, conjugated via a cleavable linker to an analogue of *motolimod* (an agonist for the toll-like receptor 8, TLR8);
 gamma1 heavy chain humanized (1-448) [VH (*Homo sapiens* IGHV3-66*01 (78.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (216) (120-217), hinge 1-15 (218-232), CH2 (233-342), CH3 E12 (358), M14 (360) (343-447), CHS K2>del (448)) (120-448)], (222-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-NL1*01 (84.2%) -IGKJ2*01 (91.7%) L124>V (104), CDR-IMGT [6.3.9] (27-32.50-52.89-97))] (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (228-228":231-231")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa, substituted at S of an average of 4 cysteinyl residues of reduced inter-chain disulfide bridges with (11S,14S,22³RS)-1²-amino-11-[3-(carbamoylamino)propyl]-1⁴-(dipropylcarbamoyl)-2,5,10,13,16,22²,22⁵-heptaoxo-14-(propan-2-yl)-4⁷,4⁸-dihydro-1³H,4⁵H-6-oxa-3,9,12,15-tetraaza-1(8)-[1]benzazepina-4(3,6)-[1,6]naphthyridina-22(1)-pyrrolidina-8(1,4)-benzenadocosaphan-22³-yl (*zuvotolimod*) groups

pertuzumab zuvotolimod

immunoglobuline G1-kappa, anti-[*Homo sapiens* ERBB2 (récepteur 2 du facteur de croissance épidermique, récepteur tyrosine-protéine kinase erbB-2, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], anticorps monoclonal humanisé, conjugué à un analogue du *motolimod* (un agoniste du récepteur de type toll 8, TLR8), via un linker clivable;
 chaîne lourde gamma1 humanisée (1-448) [VH (*Homo sapiens* IGHV3-66*01 (78.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (216) (120-217), charnière 1-15 (218-232), CH2 (233-342), CH3 E12 (358), M14 (360) (343-447), CHS K2>del (448)) (120-448)], (222-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-NL1*01 (84.2%) -IGKJ2*01 (91.7%) L124>V (104), CDR-IMGT [6.3.9] (27-32.50-52.89-97))] (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (228-228":231-231")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa, substitué en S sur un moyenne de 4 résidus cystéinyl de ponts disulfure inter-chaînes réduits par des groupes (11S,14S,22³RS)-1²-amino-11-[3-(carbamoylamino)propyl]-1⁴-(dipropylcarbamoyl)-2,5,10,13,16,22²,22⁵-heptaoxo-14-(propan-2-yl)-4⁷,4⁸-dihydro-1³H,4⁵H-6-oxa-3,9,12,15-tétraaza-1(8)-[1]benzazépine-4(3,6)-[1,6]naphthyridina-22(1)-pyrrolidina-8(1,4)-benzénadocosaphan-22³-yle (*zuvotolimod*)

pertuzumab zuvotolimod

immunoglobulina G1-kappa, anti-[*Homo sapiens* ERBB2 (receptor 2 del factor de crecimiento epidérmico, receptor tirosina-proteína kinasa erbB-2, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], anticuerpo monoclonal humanizado, conjugado con un análogo de *motolimod* (un agonista del receptor de tipo toll 8, TLR8), mediante un conector escindible;

cadena pesada gamma1 humanizada (1-448) [VH (*Homo sapiens* IGHV3-66*01 (78.8%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.12] (26-33.51-58.97-108)) (1-119) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (216) (120-217), bisagra 1-15 (218-232), CH2 (233-342), CH3 E12 (358), M14 (360) (343-447), CHS K2>del (448)) (120-448)], (222-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-NL1*01 (84.2%) -IGKJ2*01 (91.7%) L124>V (104), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (228-228":231-231")-bisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, forma glicosilada alfa, sustituido en S de un promedio de 4 residuos de cisteinilo de puentes disulfuro intercatenarios reducidos con grupos de (11S,14S,22³RS)-1²-amino-11-[3-(carbamoilamino)propil]-1⁴-(dipropilcarbamoil)-2,5,10,13,16,22⁵-heptaoxo-14-(propan-2-il)-4⁷,4⁸-dihidro-1³H,4⁵H-6-oxa-3,9,12,15-tetraaza-1(8)-[1]benzazepina-4(3,6)-[1,6]naftiridina-22(1)-pirrolidina-8(1,4)-bencenadocosafan-22³-ilo (*zuvotolimod*)

Heavy chain / Chaîne lourde / Cadena pesada

EVQLVESGGG	LVQPGGSLRL	SCAASGFTFT	DYTMDFVRQA	PGKGLEWVAD	50
VNPNSGGSIY	NQRFKGRFTL	SVDRSKNTLY	LQMNLSRAED	TAVVYCARNL	100
GPSFYFDYWG	QGTLVTVSSA	STKGPSVFFL	APSKSTSGG	TAALGCLVKD	150
YFPEPVTVSW	NSGALTSGVH	TFPAVLQSSG	LYLSLSSVTV	PSSSLGTQTY	200
ICNVNHKFSN	TKVDKKEVPEK	SCDKTHTCPP	CPAPELGGP	SVFLFPPPKK	250
DTLMSIRTP	ETCVCVVDVSH	EDPEVKFNWY	VDGVEVHNAK	TKPREQYNS	300
TYRVVSVLTV	LHQDNLNGKE	YKCKVSNKAL	PAPIEKTISK	AKGQPREPQV	350
YTLPPSREEM	TKNQVSLTCL	VKGFYPSDIA	VEWESNGQPE	NNYKTTPPVL	400
DSDGSFFLYS	KLTVDKSRWQ	QGNVFSCVM	HEALHNHYTQ	KSLSLSPG	448

Light chain / Chaîne légère / Cadena ligera

DIQMTQSPSS	LSASVGDRLT	ITCKASQDVS	IGVAWYQQPK	GKAPKLLIYS	50
ASRYRTGVPF	SFSGSGSGTD	FTLTISLQP	EDFATYYCQQ	YYIYPYTFGQ	100
GTKVEIKRTV	AAPSVFIFPP	SDEQLKSGTA	SVVCLLNIFY	PREAKVQWVK	150
DNALQSGNSQ	ESVTEQDSKD	STYLSLSTLT	LSKADYEKHK	VYACEVTHQG	200
LSSPVTKFSN	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"

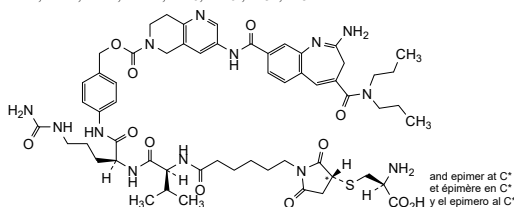
*At least two of the four inter-chain disulfide bridges are not present, an average of 4 cysteinyl being conjugated each via a thioether bond to a drug linker.

*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 están presentes, una media de 4 cisteinil está conjugada a conectores de principio activo.

Potential modified residues / résidus modifiés potentiels / restos modificados potenciales

C222, C214', C222', C214"', C228, C228"', C231, C231'"



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

H CH2 N84.4; 299, 299"

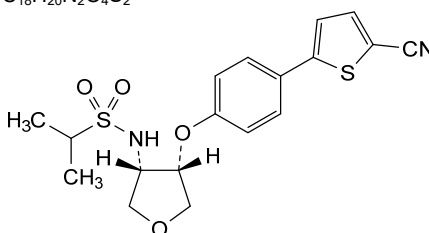
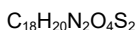
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantennarios complejos fucosilados

pesampatorum

pesampator *N*-{(3*S*,4*S*)-4-[4-(5-cyanothiophen-2-yl)phenoxy]oxolan-3-yl}propane-2-sulfonamide

pésampator *N*-{(3*S*,4*S*)-4-[4-(5-cyanothiophén-2-yl)phénoxy]oxolan-3-yl}propane-2-sulfonamide

pesampator *N*-{(3*S*,4*S*)-4-[4-(5-cianotiofen-2-il)fenoksi]oxolan-3-il}propano-2-sulfonamida

**pezadeftidum**

pezadeftide

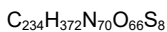
antifungal peptide derived from the mature N-terminal domain of a plant defensin of *Picramnia pentandra* (Florida bitterbush); L-alanyl-L-lysyl-L-valyl-L-cysteinyl-L-threonyl-L-lysyl-L-prolyl-L-seryl-L-lysyl-L-phenylalanyl-L-phenylalanyl-L-lysylglycyl-L-leucyl-L-cysteinylglycyl-L-threonyl-L- α -aspartylglycyl-L-alanyl-L-cysteinyl-L-threonyl-L-threonyl-L-alanyl-L-cysteinyl-L-arginyl-L-lysyl-L- α -glutamylglycyl-L-leucyl-L-histidyl-L-serylglycyl-L-tyrosyl-L-cysteinyl-L-glutaminyl-L-leucyl-L-lysylglycyl-L-phenylalanyl-L-leucyl-L-asparaginyl-L-seryl-L-valyl-L-cysteinyl-L-valyl-L-cysteinyl-L-arginyl-L-lysyl-L-histidyl-L-cysteine, non-glycosylated, produced in *Pichia pastoris* (*Komagataella phaffii*) yeast cells

pézadeftide

peptide antifongique dérivé du domaine N-terminal mature d'une défensine végétale de *Picramnia pentandra* (buisson amer de Floride); L-alanyl-L-lysyl-L-valyl-L-cystéinyl-L-thréonyl-L-lysyl-L-prolyl-L-séryl-L-lysyl-L-phénylalanyl-L-phénylalanyl-L-lysylglycyl-L-leucyl-L-cystéinylglycyl-L-thréonyl-L- α -aspartylglycyl-L-alanyl-L-cystéinyl-L-thréonyl-L-thréonyl-L-alanyl-L-cystéinyl-L-arginyl-L-lysyl-L- α -glutamylglycyl-L-leucyl-L-histidyl-L-sérylglycyl-L-tyrosyl-L-cystéinyl-L-glutaminyl-L-leucyl-L-lysylglycyl-L-phénylalanyl-L-leucyl-L-asparaginyl-L-séryl-L-valyl-L-cystéinyl-L-valyl-L-cystéinyl-L-arginyl-L-lysyl-L-histidyl-L-cystéine, non glycosylé, produit dans des cellules de levure *Pichia pastoris* (*Komagataella phaffii*)

pezadeftida

péptido antifúngico derivado del dominio N-terminal maduro de una defensiva vegetal de *Picramnia pentandra* (arbusto amargo de Florida); L-alanil-L-lisil-L-valil-L-cisteinil-L-treonil-L-lisil-L-prolil-L-seril-L-lisil-L-fenilalanil-L-fenilalanil-L-lisilglicil-L-leucil-L-cisteinilglicil-L-treonil-L- α -aspartilglicil-L-alanil-L-cisteinil-L-treonil-L-treonil-L-alanil-L-cisteinil-L-arginil-L-lisil-L- α -glutamilglicil-L-leucil-L-histidil-L-serilglicil-L-tirosil-L-cisteinil-L-glutaminiil-L-leucil-L-lisilglicil-L-fenilalanil-L-leucil-L-asparaginil-L-seril-L-valil-L-cisteinil-L-valil-L-cisteinil-L-arginil-L-lisil-L-histidil-L-cisteina, no glicosilada, producido en células de levadura de *Pichia pastoris* (*Komagataella phaffii*)



Sequence / Séquence / Secuencia:

AKVCTKPSKF FKGLCGTDGA CTTACRKEGL HSGYCQLKGF LNSVCVCRKH 50
C 51

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

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
4-51, 15-35, 21-45, 25-47

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

piflufolastatum (¹⁸F)

piflufolastat (¹⁸F)

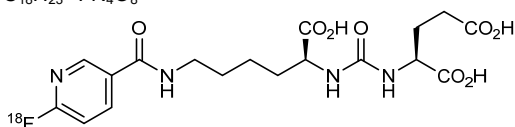
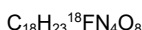
N-({*N*⁶-[6-(¹⁸F)fluoropyridine-3-carbonyl]-L-lysine-*N*²-yl}carbonyl)-L-glutamic acid

piflufolastat (¹⁸F)

acide *N*-({*N*⁶-[6-(¹⁸F)fluoropyridine-3-carbonyl]-L-lysine-*N*²-yl}carbonyl)-L-glutamique

piflufolastat (¹⁸F)

ácido *N*-({*N*⁶-[6-(¹⁸F)fluoropiridina-3-carbonil]-L-lisina-*N*²-il}carbonil)-L-glutámico



pirmitegravirum

pirmitegravir

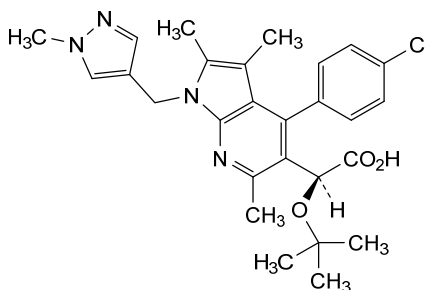
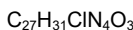
(*S*)-*tert*-butoxy{4-(4-chlorophenyl)-2,3,6-trimethyl-1-[(1-methyl-1*H*-pyrazol-4-yl)methyl]-1*H*-pyrrolo[2,3-*b*]pyridin-5-yl}acetic acid

pirmitégravir

acide (*S*)-*tert*-butoxy{4-(4-clorophényl)-2,3,6-triméthyl-1-[(1-méthyl-1*H*-pyrazol-4-yl)méthyl]-1*H*-pyrrolo[2,3-*b*]pyridin-5-yl}acétique

pirmitegravir

ácido (*S*)-*terc*-butoxi{4-(4-clorofenil)-2,3,6-trimetil-1-[(1-metil-1*H*-pirazol-4-il)metil]-1*H*-pirrolo[2,3-*b*]piridin-5-il}acético



plixacabtagenum autoleucelum #

plixacabtagene autoleucel

autologous T cells obtained from peripheral blood mononuclear cells by leukapheresis, transduced with a self-inactivating, non-replicating lentiviral vector, encoding a chimeric antigen receptor (CAR) targeting CD19. The expressed transgene comprises a

granulocyte-macrophage colony stimulating factor receptor subunit alpha (CSF2RA) signal peptide, a murine anti-CD19 single chain variable fragment (scFv) derived from mouse hybridoma FMC63, consisting of a variable light chain (VL), a 15 amino acid flexible glycine/serine spacer (G4S)₃, and a variable heavy-chain (VH), followed by a short linker sequence and the invariant human CD3ε TCR subunit coding sequence, and is under control of the elongation factor 1 alpha (EF1α) 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 an optimized Woodchuck hepatitis virus posttranscriptional regulatory element (WPRE).

The leukapheresis material is enriched for CD4/CD8 T cells by positive immunoselection and then activated and expanded through CD3 and CD28 receptor stimulation. Following activation, the T cells are transduced with the vector and expanded in media supplemented with human male AB serum and cytokines. The cells comprise of >80% CD3+ cells, >70% viable total cells, >5% viable CD3+/transgene+ cells and a mixture of CD4+ and CD8+ cells.

plixacabtagène 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) ciblant CD19. Le transgène exprimé comprend un peptide signal de la sous-unité alpha du récepteur du facteur de stimulation des colonies de granulocytes-macrophages (CSF2RA), un fragment variable à chaîne unique (scFv) anti-CD19 murin dérivé de l'hybridome de souris FMC63, consistant en une chaîne légère variable (VL), d'un espaceur glycine/sérine flexible de 15 acides aminés (G4S)₃, et d'une chaîne lourde variable (VH), suivie d'une courte séquence de liaison et de la séquence codante invariante humaine de la sous-unité TCR CD3ε, et est sous le contrôle du promoteur du facteur d'élongation 1 alpha (EF1α). La construction est flanquée de longues répétitions 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 optimisé du virus de l'hépatite de marmotte (WPRE).

Le matériel de leucaphérèse est enrichi en lymphocytes T CD4/CD8 par immunosélection positive, puis activé et amplifié par stimulation des récepteurs CD3 et CD28. Après l'activation, les lymphocytes T sont transduits avec le vecteur et amplifiés avec du milieu complété par du sérum AB masculin humain et des cytokines. Les cellules sont constituées de >80% de cellules CD3+, >70% de cellules totales viables, >5% de cellules CD3+/transgène+ viables et un mélange de cellules CD4+ et CD8+.

plixacabtagén autoleucel

linfocitos T autólogos obtenidos a partir de células mononucleares de sangre periférica mediante leucoaféresis, transducidos con un vector lentiviral auto inactivante y no replicativo, que codifica para un receptor de antígenos quimérico (CAR) dirigido a CD19. El transgén expresado consta de un péptido señal de la subunidad alfa del receptor del factor estimulante de colonias de granulocitos-macrófagos (CSF2RA), un fragmento sencillo de cadena variable (scFv) murina anti-CD19 derivado del hibridoma

de ratón FMC63, que consiste en linfocitos T autólogos obtenidos a partir de células mononucleares de sangre periférica mediante leucoaféresis, transducidos con un vector lentiviral auto inactivante y no replicativo, que codifica para un receptor de antígenos quimérico (CAR) dirigido a CD19. El transgén expresado consta de un péptido señal de la subunidad alfa del receptor del factor estimulante de colonias de granulocitos-macrófagos (CSF2RA), un fragmento sencillo de cadena variable (scFv) murina anti-CD19 derivado del hibridoma de ratón FMC63, que consiste en una cadena ligera variable (VL), un espaciador glicina/serina (G4S)₃ flexible de 15 amino ácidos y una cadena pesada variable (VH), seguido de una secuencia conectora corta y la secuencia que codifica para la subunidad no variable CD3ε del TCR humano, y está bajo el control del promotor del factor de elongación 1 alfa (EF1a). El constructo está flanqueado por repeticiones terminales largas (LTRs) en 5' y 3', y contiene también una señal de empaquetamiento ψ, un elemento de respuesta Rev (RRE), una secuencia del tracto de poli-purina central (cPPT) y un elemento regulador post-transcripcional del virus de la hepatitis de marmota (WPRE) optimizado.

El material de leucoaféresis se enriquece para linfocitos T CD4/CD8 mediante inmunoselección positiva y después se activan y expanden por estimulación a través de los receptores CD3 y CD28. Tras la activación, los linfocitos T se transducen con el vector y se expanden en medio suplementado con suero AB humano de varones y citoquinas. Las células consisten en >80% de células CD3+, >70% de células viables totales, >5% de células viables CD3+/transgén+ y una mezcla de células CD4+ y CD8+.

plutavimabum #
plutavimab

immunoglobulin G1-kappa, anti-[severe acute respiratory syndrome (human) coronavirus 2 (SARS-CoV-2) spike (S) glycoprotein, receptor binding domain (RBD)], *Homo sapiens* monoclonal antibody; gamma1 heavy chain *Homo sapiens* (1-447) [VH (*Homo sapiens*IGHV3-53*01 (95.9%) -(IGHD) -IGHJ6*01 (100%), CDR-IMGT [8.7.11] (26-33.51-57.96-106)) (1-117) -*Homo sapiens*IGHG1*03 (100%), G1m3, nG1m1, G1v14 CH2 A1.3, A1.2(CH1 R120 (214) (118-215), hinge 1-15 (216-230), CH2 L1.3>A (234), L1.2>A (235) (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*IGKV1-12*01 (93.7%) -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 (226-226":229-229")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa

plutavimab
 immunoglobuline G1-kappa, anti-[domaine de liaison au récepteur (RBD) de la glycoprotéine spike (S) du coronavirus 2 (humain) du syndrome respiratoire aigu sévère (SARS-CoV-2)], anticorps monoclonal *Homo sapiens*;
 chaîne lourde gamma1 *Homo sapiens* (1-447) [VH (*Homo sapiens*IGHV3-53*01 (95.9%) -(IGHD)-IGHJ6*01 (100%), CDR-IMGT [8.7.11] (26-33.51-57.96-106)) (1-117) -*Homo sapiens*IGHG1*03 (100%), G1m3, nG1m1, G1v14 CH2 A1.3, A1.2 (CH1 R120 (214) (118-215), charnière 1-15 (216-230), CH2 L1.3>A (234), L1.2>A (235) (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*IGKV1-12*01 (93.7%) -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 (226-226'':229-229'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa

plutavimab
 inmunoglobulina G1-kappa, anti-[dominio de unión al receptor (RBD) de la glicoproteína spike (S) del coronavirus 2 (humano) del síndrome respiratorio agudo severo (SARS-CoV-2)], anticuerpo monoclonal *Homo sapiens*;
 cadena pesada gamma1 *Homo sapiens* (1-447) [VH (*Homo sapiens*IGHV3-53*01 (95.9%) -(IGHD)-IGHJ6*01 (100%), CDR-IMGT [8.7.11] (26-33.51-57.96-106)) (1-117) -*Homo sapiens*IGHG1*03 (100%), G1m3, nG1m1, G1v14 CH2 A1.3, A1.2(CH1 R120 (214) (118-215), bisagra 1-15 (216-230), CH2 L1.3>A (234), L1.2>A (235) (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*IGKV1-12*01 (93.7%) -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 (226-226'':229-229'')-bisdisulfuro, producido en las células ováricas de hamster chino (CHO), línea celular CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LIQPGGSLRL SCAASGFTVS SNYMSWRQA PGKGLEWVSI 50
IYPGGSTEYA DSVKGRFTIS RDNRSRNTLYL QMNSLRAEDT AVYYCARELG 100
YYGMDVWGQG TTVTVSSAST KGPSVFFLAP SSKTSGGTA ALGCLVKDYF 150
PEPVTWSWNS GALTSGVHTF PAVLQSSGLY SLSSVTVPS SSLGTQTYIC 200
NVNHKPSNTK VDKRVEPKSC DKHTCTPCP APEAAGGSPV FLFPKPKDT 250
LMISRTPPEVT CVVVDVSHED PEVKFNWYVD GVEVHNKTK PREEQYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALFA PIEKTISKAK GQPREPQVYT 350
LPPSREEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPEVLDS 400
DGSFFLYSKL TVDKSRWQQG NVFSCSVME ALHNHYTQKS LSLSPGK 447
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS VSASVGDRTV ITCRASQGIS TWLVWYQQKPK GKAPNLLIYG 50
ASSLQSGVPS RFGSGSGTD FTLTISSLQP EDFATYYCQQ ANAYPYTFGQ 100
GTRKLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNFFV PREAKVQWVK 150
DNALQSGNSQ ESVTEQDSKD STYLSLSTLT LSKADYKHKH VYACEVTHQG 200
LSSPVTKSFN RGEC 214
```

Post-translational modifications

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

Intra-H (C23-C104) 22-95 144-200 261-321 367-425
 22"-95" 144"-200" 261"-321" 367"-425"

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

23"-88" 134"-194"

Inter-H-L (h 5-CL 126) 220-214' 220'-214"

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

N-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 biantennarios complejos fucosilados.

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

H CHS K2: 447, 447"

polvitolimodum

polvitolimod

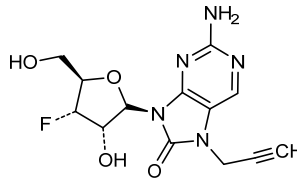
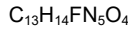
2-amino-9-(3-deoxy-3-fluoro-β-D-ribofuranosyl)-7-(prop-2-yn-1-yl)-7,9-dihydro-8H-purin-8-one

polvitolimod

2-amino-9-(3-désoxy-3-fluoro-β-D-ribofuranosyl)-7-(prop-2-yn-1-yl)-7,9-dihydro-8H-purin-8-one

polvitolimod

2-amino-9-(3-desoxi-3-fluoro-β-D-ribofuranosil)-7-(prop-2-in-1-il)-7,9-dihidro-8H-purin-8-ona



posdinemabum #

posdinemab

immunoglobulin G1-kappa, anti-[*Homo sapiens* MAPT (microtubule associated protein tau, tau), phosphorylated], humanized monoclonal antibody; gamma1 heavy chain humanized (1-448) [VH (*Homo sapiens* IGHV3-30*01 (93.9%) -(IGHD) -IGHJ5*01 (80.0%) G121>V (111), CDR-IMGT [8.7.12] (26-33.51-57.96-107)) (1-118) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (215) (119-216), hinge 1-15 (217-231), CH2 (232-341), CH3 E12 (357), M14 (359) (342-446), CHS (447-448)) (119-448)], (221-214')-disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-16*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 (227-227'' :230-230'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

posdinémab

immunoglobuline G1-kappa, anti-[*Homo sapiens* MAPT (protéine tau associée aux microtubules, tau), phosphorylée], anticorps monoclonal humanisé; chaîne lourde gamma1 humanisée (1-448) [VH (*Homo sapiens* IGHV3-30*01 (93.9%) -(IGHD) -IGHJ5*01 (80.0%) G121>V (111), CDR-IMGT [8.7.12] (26-33.51-57.96-107)) (1-118) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (215) (119-216), charnière 1-15 (217-231), CH2 (232-341), CH3 E12 (357), M14 (359) (342-446), CHS (447-448)) (119-448)], (221-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-16*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 (227-227'' :230-230'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

posdinemab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* MAPT (proteína tau asociada con los microtúbulos, tau), fosforilada], anticuerpo monoclonal humanizado; cadena pesada gamma1 humanizada (1-448) [VH (*Homo sapiens* IGHV3-30*01 (93.9%) -(IGHD) -IGHJ5*01 (80.0%) G121>V (111), CDR-IMGT [8.7.12] (26-33.51-57.96-107)) (1-118) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (215) (119-216), bisagra 1-15 (217-231), CH2 (232-341), CH3 E12 (357), M14 (359) (342-446), CHS (447-448)) (119-448)], (221-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-16*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 (227-227":230-230")-bisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

QVQLVESGGG VVQPGKSLRL SCAASGFTFS SYAMSWVRQA PGKGLEWVAS 50
 ISKGGNTYYA DSVKGRFTIS RDNSKNTLYL QMNSLRAEDT AVYVCARGWG 100
 DYGFAYWQV VTLVTVSSAS TKGPSVFLPA PSSKSTSGGT AALGCLVKDY 150
 FPEFVTVSWN SGALTSGVHT FPAVLQSSGL YLSSVVTVP SSSLGQTYYI 200
 CNVNHKPSNT KVDKKEPKS CDKTHCTPCP PAPELLGGPS VLFPPKPKD 250
 TLMISRTPEV TCVVVDVSH E DPEVKFNWYV DGEVHNAKT KPREEQYNST 300
 YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY 350
 TLPFPREEMT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTTPVLD 400
 SDGSFFLYSK LTVDKSRWQ GNVFSCSVMH EALHNNHYTQK SLSLSPGK 448

Light chain / Chaîne légère / Cadena ligera

DIQMTQSPSS LSASVGDRTV ITCKASQDIN RYLNWFQQKP GKAPKSLIYR 50
 ANRLLDGVPS RFGSGSGTD FTLTISLQP EDFATYYCLQ YDFPFLTFGQ 100
 GTKLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNIFY PREAKVQWKV 150
 DNALQSGNSQ ESVTEQDSKD STYLSSTLT LSKADYEKHK VYACEVTHQG 200
 LSSFVTKSFN RGEK 214

Post-translational modifications

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
 Intra-H (C23-C104) 22-95 145-201 262-322 368-426
 22"-95" 145"-201" 262"-322" 368"-426"
 Intra-L (C23-C104) 23"-88" 134"-194"
 23""-88"" 134""-194""
 Inter-H-L (h 5-CL 126) 221-214' 221"-214"
 Inter-H-H (h 11, h 14) 227-227" 230-230"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
 H VH Q1 > pyroglutamyI (pE, 5-oxopropyl): 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"

posovolonum

posovolone

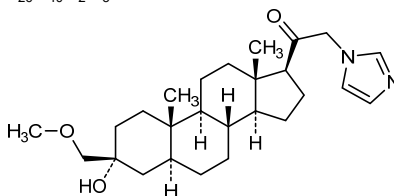
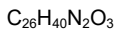
3α-hydroxy-21-(1*H*-imidazol-1-yl)-3β-(methoxymethyl)-5α-pregnan-20-one

posovolone

3α-hydroxy-21-(1*H*-imidazol-1-yl)-3β-(méthoxyméthyl)-5α-prégnan-20-one

posovolona

3α-hidroxi-21-(1*H*-imidazol-1-il)-3β-(metoximetil)-5α-pregnan-20-ona



povorcitinibum

povorcitinib

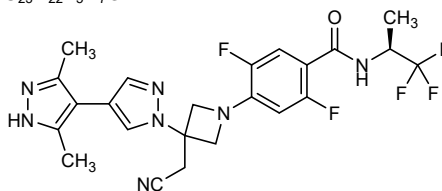
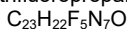
4-[3-(cyanomethyl)-3-(3',5'-dimethyl-1*H*,1'*H*-[4,4'-bipyrazol]-1-yl)azetidín-1-yl]-2,5-difluoro-*N*-[(2*S*)-1,1,1-trifluoropropan-2-yl]benzamida

povorcitinib

4-[3-(cyanométhy)-3-(3',5'-diméthyl-1*H*,1'*H*-[4,4'-bipyrázol]-1-yl)azétidín-1-yl]-2,5-difluoro-*N*-[(2*S*)-1,1,1-trifluoropropan-2-yl]benzamida

povorcitinib

4-[3-(cianometil)-3-(3',5'-dimetil-1*H*,1'*H*-[4,4'-bipirazol]-1-il)azetidín-il]-2,5-difluoro-*N*-[(2*S*)-1,1,1-trifluoropropan-2-il]benzamida



quabodepistatum

quabodepistat

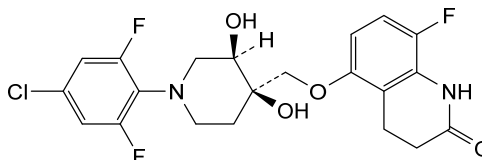
5-[[*(3R,4R)*-1-(4-chloro-2,6-difluorophenyl)-3,4-dihydroxypiperidin-4-yl]metoxy]-8-fluoro-3,4-dihydroquinolin-2(1*H*)-one

quabodépistat

5-[[*(3R,4R)*-1-(4-chloro-2,6-difluorophényl)-3,4-dihydroxypipéridin-4-yl]méthoxy]-8-fluoro-3,4-dihydroquinoléin-2(1*H*)-one

quabodepistat

5-[[*(3R,4R)*-1-(4-cloro-2,6-difluorofenil)-3,4-dihroxipiperidin-4-il]metoxi]-8-fluoro-3,4-dihidroquinolein-2(1*H*)-ona



rafutrombopagum

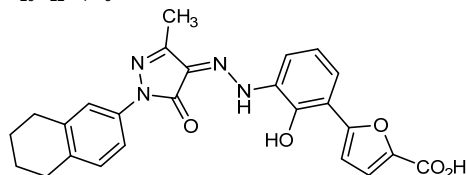
rafutrombopag

5-(2-hydroxy-3-((*Z*)-[3-methyl-5-oxo-1-(5,6,7,8-tetrahydronaphthalen-2-yl)-1,5-dihydro-4*H*-pyrazol-4-ylidene]hydrazinyl)phenyl)furan-2-carboxylic acid

rafutrombopag acide 5-(2-hydroxy-3-((Z)-[3-méthyl-5-oxo-1-(5,6,7,8-tétrahydronaphtalén-2-yl)-1,5-dihydro-4H-pyrazol-4-ylidène]hydrazinyl)phényl)furane-2-carboxylique

rafutrombopag ácido 5-(2-hidroxi-3-((Z)-[3-metil-5-oxo-1-(5,6,7,8-tetrahidronaftalen-2-il)-1,5-dihidro-4H-pirazol-4-ilideno]hidrazinil)fenil)furano-2-carboxílico

$C_{25}H_{22}N_4O_5$



rapcabtagemum autoleucelum

rapcabtogene autoleucel

autologous T cells obtained from peripheral blood mononuclear cells by leukapheresis, transduced with a self-inactivating, non-replicating lentiviral vector, encoding a T cell chimeric antigen receptor targeting CD19. The expressed transgene comprises a CD8 α leader sequence, a murine anti-CD19 single chain variable fragment (scFv) derived from the mouse hybridoma FMC63, a CD8 α hinge and transmembrane region, and a 4-1BB (CD137) and CD3 ζ (TCR ζ) signaling 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 an optimized Woodchuck hepatitis virus posttranscriptional regulatory element (WPRE).

The leukapheresis material is enriched for CD4/CD8 T cells by positive immunoselection, activated by CD3 and CD28 agonists and transduced with the vector. Without further cell propagation, the T cells are washed, formulated for infusion, and cryopreserved. The substance is composed of $\geq 80\%$ T cells and $\leq 1\%$ B cells, with a mixture of transgene positive ($>3.4\%$) and negative T cells. The CD4 $^+$ and CD8 $^+$ naïve T cell subsets (CD45RA $^+$ CCR7 $^+$) present in the leukapheresis material are largely retained.

rapcabtagène autoleucel

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 des lymphocytes T ciblant CD19. Le transgène exprimé comprend une séquence de tête CD8 α , un fragment variable à chaîne unique (scFv) anti-CD19 murin dérivé de l'hybridome de souris FMC63, une région transmembranaire et charnière CD8 α , et un domaine de signalisation 4-1BB (CD137) et CD3 ζ (TCR ζ) et est sous le contrôle du promoteur du facteur d'élongation 1 alpha (EF1 α). La construction est flanquée de longues répétitions 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 optimisé du virus de l'hépatite de marmotte (WPRE).

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. Sans propagation cellulaire supplémentaire, les lymphocytes T sont lavés, formulés pour une perfusion et cryoconservés. La substance est composée de ≥80% de lymphocytes T et ≤1% de lymphocytes B, avec un mélange de lymphocytes T positifs (>3,4%) et négatifs au transgène. Les sous-types de lymphocytes T naïfs CD4+ et CD8+ (CD45RA+CCR7+) présents dans le matériel de leucaphérèse sont largement conservés.

rapcabtagén autoleucel

linfocitos T autólogos obtenidos a partir de células mononucleares de sangre periférica mediante leucoaféresis, transducidos con un vector lentiviral auto inactivante y no replicativo, que codifica para un receptor de antígenos de linfocitos T quimérico (CAR) dirigido a CD19. El transgén expresado consta de una secuencia líder de CD8α, un fragmento sencillo de cadena variable (scFv) murina anti-CD19 derivado del hibridoma de ratón FMC63, una bisagra y una región transmembrana de CD8α y los dominios de señalización de 4-1BB (CD137) y CD3ζ (TCRζ) y está 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 contiene también una señal de empaquetamiento ψ, un elemento de respuesta Rev (RRE), una secuencia del tracto de poli-purina central (cPPT) y un elemento regulador post-transcripcional del virus de la hepatitis de marmota (WPRE) optimizado.

El material de leucoaféresis se enriquece para linfocitos T CD4/CD8 mediante inmunoselección positiva, y después se activan con agonistas de CD3 y CD28 y se transducen con el vector. Sin más expansión, los linfocitos T se lavan, se formulan para infusión y se criopreservan. La substancia está compuesta por ≥80% de linfocitos T y ≤1% de linfocitos B, con una mezcla de linfocitos T positivos (>3.4%) y negativos para el transgén. Se mantienen bastante las subpoblaciones naïve de linfocitos T CD4+ y CD8+ (CD45RA+CCR7+) presentes en el material de leucoaféresis.

reozalimabum #
reozalimab

immunoglobulin G1-kappa_G1-lambda2, anti-[*Homo sapiens* PDCD1 (programmed cell death 1, PD1, PD-1, CD279)] and anti-[*Homo sapiens* CD274 (programmed death ligand 1, PDL1, PD-L1, B7 homolog 1, B7H1)], *Homo sapiens* monoclonal antibody, bispecific;

gamma1 heavy chain anti-PDCD1 *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV1-69*15 (93.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1*08p, G1m3,1, G1v44 CH1 E7, T26, E84.2, G1v14 CH2 A1.3, A1.2, G1v46 CH3 V6, L22, L79, W81 (CH1 L7>E (131), K26>T (150), Q84.2>E (178), I103 (202), R120 (217) (121-218), hinge 1-15 (219-233), CH2 L1.3>A (237), L1.2>A (238), D27>S (268) (234-343), CH3 T6>V (353), D12 (359), L14 (361), T22>L (369), K79>L (395), T81>W (397) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfide with kappa light chain anti-PDCD1 *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (96.8%) -IGKJ4*01 (91.7%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01, Km3 S20>R (131), V22>G (133), A45.1 (153), S86>R (176), V101 (191) (108'-214')]; gamma1 heavy chain anti-CD274 *Homo sapiens* (1''-453'') [VH (*Homo sapiens* IGHV1-69*06 (100%) -(IGHD) -IGHJ6*01 (100%), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1''-123'') -*Homo*

sapiens IGHG1*08p, G1m3.1, G1v45 CH1 K86, G1v14 CH2 A1.3, A1.2, G1v47 CH3 V6, Y7, A85.1, V86 (CH1 S86>K (189), I103 (205), R120 (220) (124"-221"), hinge 1-15 (222"-236"), CH2 L1.3>A (240), L1.2>A (241), D27>S (271) (237"-346"), CH3 T6>V (356), L7>Y (357), D12 (362), L14 (364), F85.1>A (411), Y86>V (413) (347"-451"), CHS (452"-453") (124"-453")), (226"-215")-disulfide with lambda2 light chain anti-CD274 *Homo sapiens* (1"-216") [V-LAMBDA (*Homo sapiens* IGLV1-44*01 (91.8%) - IGLJ2*01 (90.9%) T122>I (105), CDR-IMGT [8.3.11] (26-33.51-53.90-100)) (1"-110") -*Homo sapiens* IGLC2*01, S86>E (179), Y88>E (181), T124>A (213) (111"-216")]; dimer (229-232":232-235")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1SV lacking the glutamine synthetase (GS-KO) gene, glycoform alfa

réozalimab

immunoglobuline G1-kappa/lambda, anti-[*Homo sapiens* PDCD1 (protéine 1 de mort cellulaire programmée, PD1, PD-1, CD279)] et anti-[*Homo sapiens* CD274 (ligand 1 de mort programmée, PDL1, PD-L1, homologue 1 de B7, B7H1)], anticorps monoclonal *Homo sapiens*, bispécifique; chaîne lourde gamma1 anti-PDCD1 *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV1-69*15 (93.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1*08p, G1m3.1, G1v44 CH1 E7, T26, E84.2, G1v14 CH2 A1.3, A1.2, G1v46 CH3 V6, L22, L79, W81 (CH1 L7>E (131), K26>T (150), Q84.2>E (178), I103 (202), R120 (217) (121-218), charnière 1-15 (219-233), CH2 L1.3>A (237), L1.2>A (238), D27>S (268) (234-343), CH3 T6>V (353), D12 (359), L14 (361), T22>L (369), K79>L (395), T81>W (397) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfure avec la chaîne légère kappa anti-PDCD1 *Homo sapiens* (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-12*01 (96.8%) -IGKJ4*01 (91.7%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01, Km3 S20>R (131), V22>G (133), A45.1 (153), S86>R (176), V101 (191) (108'-214')]; chaîne lourde gamma1 anti-CD274 *Homo sapiens* (1"-453") [VH (*Homo sapiens* IGHV1-69*06 (100%) -(IGHD) -IGHJ6*01 (100%), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1"-123") -*Homo sapiens* IGHG1*08p, G1m3.1, G1v45 CH1 K86, G1v14 CH2 A1.3, A1.2, G1v47 CH3 V6, Y7, A85.1, V86 (CH1 S86>K (189), I103 (205), R120 (220) (124"-221"), charnière 1-15 (222"-236"), CH2 L1.3>A (240), L1.2>A (241), D27>S (271) (237"-346"), CH3 T6>V (356), L7>Y (357), D12 (362), L14 (364), F85.1>A (411), Y86>V (413) (347"-451"), CHS (452"-453") (124"-453")), (226"-215")-disulfure avec la chaîne légère lambda2 anti-CD274 *Homo sapiens* (1"-216") [V-LAMBDA (*Homo sapiens* IGLV1-44*01 (91.8%) - IGLJ2*01 (90.9%) T122>I (105), CDR-IMGT [8.3.11] (26-33.51-53.90-100)) (1"-110") -*Homo sapiens* IGLC2*01, S86>E (179), Y88>E (181), T124>A (213) (111"-216")]; dimère (229-232":232-235")-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

reozalimab

immunoglobulina G1-kappa/lambda, anti-[*Homo sapiens* PDCD1 (proteína 1 de muerte celular programada, PD1, PD-1, CD279)] y anti-[*Homo sapiens* CD274 (ligando 1 de muerte programada, PDL1, PD-L1, homólogo 1 de B7, B7H1)], anticuerpo monoclonal *Homo sapiens*, biespecífico; cadena pesada gamma1 anti-PDCD1 *Homo sapiens* (1-450) [VH (*Homo sapiens* IGHV1-69*15 (93.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [8.8.13] (26-33.51-58.97-109)) (1-120) -*Homo sapiens* IGHG1*08p, G1m3.1, G1v44 CH1 E7, T26, E84.2, G1v14 CH2 A1.3, A1.2, G1v46 CH3 V6, L22, L79, W81 (CH1 L7>E (131), K26>T (150), Q84.2>E (178), I103 (202), R120 (217) (121-218), bisagra 1-15 (219-233), CH2 L1.3>A (237), L1.2>A (238), D27>S (268) (234-343), CH3 T6>V (353), D12 (359), L14 (361), T22>L (369), K79>L (395), T81>W (397) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfuro con la cadena ligera kappa anti-PDCD1 *Homo sapiens* (1'-214')

[V-KAPPA (*Homo sapiens* IGKV1-12*01 (96.8%) -IGKJ4*01 (91.7%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01, Km3 S20>R (131), V22>G (133), A45.1 (153), S86>R (176), V101 (191) (108'-214')];

cadena pesada gamma1 anti-CD274 *Homo sapiens* (1"-453") [VH (*Homo sapiens* IGHV1-69*06 (100%) -(IGHD) -IGHJ6*01 (100%), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1"-123") -*Homo sapiens* IGHG1*08p, G1m3.1, G1v45 CH1 K86, G1v14 CH2 A1.3, A1.2, G1v47 CH3 V6, Y7, A85.1, V86 (CH1 S86>K (189), I103 (205), R120 (220) (124"-221"), bisagra 1-15 (222"-236"), CH2 L1.3>A (240), L1.2>A (241), D27>S (271) (237"-346"), CH3 T6>V (356), L7>Y (357), D12 (362), L14 (364), F85.1>A (411), Y86>V (413) (347"-451"), CHS (452"-453")) (124"-453")], (226"-215")-disulfuro con la cadena ligera lambda2 anti-CD274 *Homo sapiens* (1"-216") [V-LAMBDA (*Homo sapiens* IGLV1-44*01 (91.8%) -IGLJ2*01 (90.9%) T122>I (105), CDR-IMGT [8.3.11] (26-33.51-53.90-100)) (1"-110") -*Homo sapiens* IGLC2*01, S86>E (179), Y88>E (181), T124>A (213) (111"-216")]; dímero (229-232":232-235")-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

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

QVQLVQSGAE VKKPGSSVKV SCKASGGTFS SYAISWVRQA PGQGLEWMGL 50
 IIPSFDTAGY AQKFGGRVAI TVDESTSTAY MELSSLRSED TAVYYCARAE 100
 HSSGTGTFDYW GQGTTLTVSS ASTKGPSVFP EAPSSKSTSG GTAALGCLVT 150
 DYFPEFVTVS WNSGALTSKV HTFFAVLESS GLYSLSSVVT VPSSSLGTQT 200
 YICNVNHPKS NTKVDRKVEP KSCDKHTCP PCPAPAEAGG PVSFLFPKPK 250
 KDTLMISRTP EVTCVVSVS HEDPEVFNW YVDGVEVHNA KTKPREQYN 300
 STYRVSVLT VLHQDNLNGK EYKCKVSNKA LPALIEKTI S KAKGQPREPQ 350
 VYVLPFSRDE LTKNQVSLLC LVKGFYPSDI AVEWESNGQP ENNYLTWPFV 400
 LSDSGSFFLY SKLTVDKSRW QQGNVFCSV MHEALHNHYT QKSLSLSPGK 450

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

QVQLVQSGAE VKKPGSSVKV SCKASGGTFS SYAISWVRQA PGQGLEWMGG 50
 IIPFIFGTANY AQKFGGRVTI TADKSTSTAY MELSSLRSED TAVYYCARSP 100
 DYSPPYYYGDM DWVGGQTTVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC 150
 LVKDYFFPEV TVSNNGALTSKV SGVHTFPAVL QSSGLYSLKS VVTVPSSSLG 200
 TQTYICNVNH KPSNNTKVDKR VEPKSCDKTH TCPPCPAPEA AGGFSVFLFP 250
 PKPKDTLMIS RTPEVTCVVV SVSHEDPEVK FNWYVDGVEV HNAKTKPREE 300
 QYNSTYRVVS VLTVLHQDNL NGEKYKCKVS NKALPAPIEK TISKAKGQPR 350
 EPQYVYVPPS RDELTKNQVS LTLCLVKGFYP SDIAVEWESN GQPENNYKTT 400
 PPVLDSDGSF ALVSKLTVDK SRWQQGNVFS CVMHEALHN HYTKSLSLSL 450
 PGK 453

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

DIQMTQSPSS VSASVGRDVT ITCRASQGIS SWLAWYQQKPK GKAPKLLISA 50
 ASSLQSGVPS RFSGSGSGTD FLTISSLQP EDFATYYCQQ ANHLPTFTFGG 100
 GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA RVGCLLNIFY PREAKVQWKV 150
 DNALQSGNSQ ESVTEQDSKD STYSLRSLTL LSKADYKHK VYACEVTHQG 200
 LSSPVTKSFN RGEK 214

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

QSVLTQPPSA SGTTPGQRVTI SCSGSSNIG SNTVNWYQQP PGTAPKLLIY 50
 GNSNRPSGVP DRFSGSKSGT SASLAISGLQ SEDEADYYCQ SYDSSLGSSV 100
 FGGGKILTVL GQPKAAPSVT LFPSSSEELQ ANKATLVCLIS SDFYPGAATV 150
 AMKADSSPVK AGVETTTPSK QSNNKVAEAS ELSLTPPEQWK SHRSYSCQVT 200
 HEGSTVEKTV APAECS 216

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

Intra-L (C23-C104) 23-88 134-194
 22"-89" 138"-197"

Inter-H-L (h 5-CL 126) 223-214 226"-215"

Inter-H-H (h 11, h 14) 229-232" 232-235"

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

Q > pyroglutamyl (pE, 5-oxopropyl)

H VH Q1: 1, 1"

L VL Q1: 1"

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

H CH2 N84.4: 300, 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 CHS K2: 450, 453"

retezorogantum

retezorogant

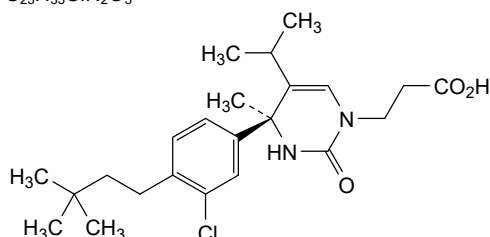
3-{(4S)-4-[3-chloro-4-(3,3-dimethylbutyl)phenyl]-4-methyl-2-oxo-5-(propan-2-yl)-3,4-dihydropyrimidin-1(2H)-yl}propanoic acid

rétézorogant

acide 3-{(4S)-4-[3-chloro-4-(3,3-diméthylbutyl)phényl]-4-méthyl-2-oxo-5-(propan-2-yl)-3,4-dihydropyrimidin-1(2H)-yl}propanoïque

retezorogant

ácido 3-{(4S)-4-[3-cloro-4-(3,3-dimetilbutil)fenil]-4-metil-2-oxo-5-(propan-2-il)-3,4-dihidropirimidin-1(2H)-il}propanoico

C₂₃H₃₃ClN₂O₃**revumenibum**

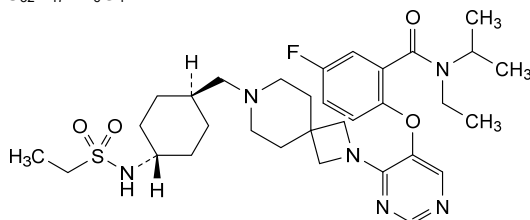
revumenib

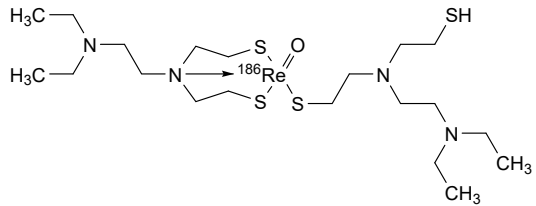
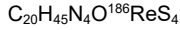
2-{{[4-(7-{{*trans*-4-(ethanesulfonamido)cyclohexyl]methyl}-2,7-diazaspiro[3.5]nonan-2-yl)pyrimidin-5-yl]oxy}-*N*-ethyl-5-fluoro-*N*-(propan-2-yl)benzamide

révuménib

2-{{[4-(7-{{*trans*-4-(éthanesulfonamido)cyclohexyl]méthyl}-2,7-diazaspiro[3.5]nonan-2-yl)pyrimidin-5-yl]oxy}-*N*-éthyl-5-fluoro-*N*-(propan-2-yl)benzamide

revumenib

2-{{[4-(7-{{*trans*-4-(etanosulfonamido)ciclohexil]metil}-2,7-diazaspiro[3.5]nonan-2-il)pirimidin-5-il]oxi}-*N*-etil-5-fluoro-*N*-(propan-2-il)benzamideC₃₂H₄₇FN₆O₄S**rhenium (¹⁸⁶Re) obisbemedum**rhenium (¹⁸⁶Re) obisbameda[2,2'-[[2-(diethylamino)ethyl]azanediyl-*κN*]bis(ethane-1-thiolato-*κS*)](2-{[2-(diethylamino)ethyl](2-sulfanyléthyl)amino}éthane-1-thiolato-*κS*)oxido(¹⁸⁶Re)rheniumrhénium (¹⁸⁶Re) obisbéméda[2,2'-[[2-(diéthylamino)éthyl]azanediyl-*κN*]bis(éthane-1-thiolato-*κS*)](2-{[2-(diéthylamino)éthyl](2-sulfanyléthyl)amino}éthane-1-thiolato-*κS*)oxido(¹⁸⁶Re)rheniumrenio (¹⁸⁶Re) obisbameda[2,2'-[[2-(diethylamino)etil]azanodiil-*κN*]bis(etano-1-tiolato-*κS*)](2-{[2-(diethylamino)etil](2-sulfaniletil)amino}etano-1-tiolato-*κS*)óxico(¹⁸⁶Re)renio



rilunerminum alfa #
rilunermin alfa

human tumor necrosis factor ligand superfamily member 10 (TNFSF10, TNF-related apoptosis-inducing ligand, TRAIL, apo-2 ligand, apo-2L, CD253), extracellular fragment (111-281, 1-171 in the current sequence) variant (S¹¹¹>L¹, P¹¹²>K²), fused via the peptidyl linker ¹⁷²GS¹⁷³ to human collagen α-1(I) chain (α-1 type I collagen, COL1A1) C-terminal fragment (1156-1464, 174-482 in the current sequence) variant (D¹²¹⁹>N²³⁷), covalent disulfide bridged trimer, produced in Chinese hamster ovary (CHO) cells, glycoform alfa;

human tumor necrosis factor ligand superfamily member 10 (TNFSF10, TNF-related apoptosis-inducing ligand, TRAIL, apo-2 ligand, apo-2L, CD253), extracellular (111-281)-peptide (1-171), [S¹¹¹>L¹, P¹¹²>K²]-variant, fused via a glycylyseryl dipeptide linker (172-173) with the C-terminal (1156-1464)-peptide (174-482) [D¹²¹⁹>N²³⁷]-variant of the human collagen α-1(I) chain (α-1 type I collagen, COL1A1), trimer (283-300':283'-300":283"-300)-trisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

rilunermine alfa

membre 10 de la superfamille des ligands du facteur de nécrose tumorale humain (TNFSF10, ligand induisant l'apoptose apparenté au TNF, TRAIL, ligand apo-2, apo-2L, CD253), fragment extracellulaire (S¹¹¹>L¹, P¹¹²>K²), fusionné via une liaison peptidique ¹⁷²GS¹⁷³ au fragment terminal C (1156-1464, 174-482 dans la séquence actuelle) de la chaîne α-1(I) du collagène humain (collagène α-1 de type I, COL1A1) variant (D¹²¹⁹>N²³⁷), trimère à pont disulfure covalent, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa;

membre 10 de la superfamille des ligands du facteur de nécrose tumorale (humain) (TNFSF10, ligand induisant l'apoptose apparenté au TNF, TRAIL, ligand de apo-2, apo-2L, CD253), peptide 111-281 extracellulaire (1-171), variant [S¹¹¹>L¹, P¹¹²>K²], fusionné via un une liaison dipeptidique glycylyséryle (172-173) avec le peptide 1156-1464 C-terminal (174-482) variant [D¹²¹⁹>N²³⁷] de la chaîne α-1(I) du collagène humain (collagène α-1 de type I, COL1A1), trimère (283-300':283'-300":283"-300)-trisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

rilunermina alfa

miembro 10 de la superfamilia de ligandos del factor de necrosis tumoral humano (TNFSF10, ligando inductor de apoptosis relacionado con TNF, TRAIL, ligando del apo-2, apo-2L, CD253), fragmento extracelular (111-281, 1-171 en la secuencia actual) variante (S¹¹¹>L¹, P¹¹²>K²), fusionada a través de un enlace peptidil ¹⁷²GS¹⁷³ a la cadena α-1(I) del colágeno humano (colágeno α-1 tipo I, COL1A1) fragmento terminal C (1156-1464, 174-482 en la secuencia actual) variante (D¹²¹⁹>N²³⁷), trímero covalente acortado disulfuro, producido en células ováricas de hámster chino (CHO), glicofoma alfa; miembro 10 de la superfamilia de ligandos del factor de necrosis tumoral (humano) (TNFSF10, ligando inductor de apoptosis relacionado con TNF, TRAIL, ligando del apo-2, apo-2L, CD253), péptido 111-281 extracelular (1-171), variante [S¹¹¹>L¹, P¹¹²>K²], fusionado a través de un conector dipeptidil de glicilserilo (172-173) con el péptido C-terminal 1156-1464 (174-482) variante [D¹²¹⁹>N²³⁷] de la cadena α-1(I) del colágeno humano (colágeno α-1 tipo I, COL1A1), trímero (283-300":283'-300":283"-300)-trisdifuro, producida en las células ováricas de hámster chino (CHO), glicofoma alfa

Sequence / Séquence / Secuencia

L KLVREGRPQ	RVAAHITGTR	GRSNTLSSPN	SKNEKALGRK	INSWESSRSG	50
HSFLSNLHLR	NGELVIEHKG	FYIYSQTYF	RFQEI KENT	KNDKQMVQYI	100
YKYTSYPDPI	LLMKSARNSC	WSKDAEYGLY	SIYQGGIFEL	KENDRIFVSV	150
TNEHLIDMDH	EASFFGAFLV	G SNLPGPI	GPPGPRGRTG	DAGPVGPPGP	200
PGPPGPPGPF	SAGDFSFPLP	QPFQEKANDG	GRYRAN	VVRDRDLEVD	250
TTLKSLSQI	ENIRSEPSR	KNPARTCRDL	KMCHSDWKS	EYVIDPNQGC	300
NLDAIKVFCN	METGETCVYP	TQPSVAQKNW	YISKNDKDKR	HWVFGESMTD	350
GFQFEYGGQG	SDPADVAIQI	TFRLMSTEA	SQNIYHCKN	SVAYMDQQTG	400
NLKKALLLQG	SNEIIRAEQ	NSRFTYSVTV	DGCTSHTGAW	GKTVIEYKTT	450
KTSRLPIIDV	APLDVGPDPQ	EPGFDVGPVC	FL		482

Peptide linker / Peptide liant / Péptido de unión

172 **GS** 173 (1-2)

Mutation / Mutation / Mutación

S1>**L**, P2>**K**, D237>**N**

Post-translational modifications

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

Intra-chain 277-309, 317-480, 388-433
 277'-309', 317'-480', 388'-433'
 277"-309", 317"-480", 388"-433"

Inter-chain 283-300', 283'-300", 283"-300

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
 N383, N383', N383"

Hydroxyproline (Hyp) sites / Sites de hydroxyproline (Hyp) / Posiciones de hidroxiprolina (Hip)
 up to 9 undetermined P>Hyp positions within the 174-224 region in the collagen fragment

riminkefonom

riminkefon

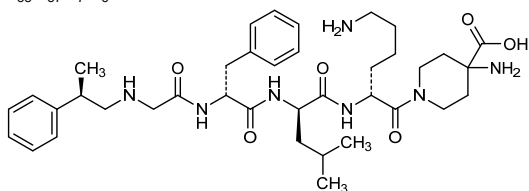
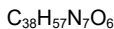
4-amino-1-*N*-[(2*R*)-2-fenilpropil]glicil-D-fenilalanil-D-leucil-D-lisil]piperidina-4-carboxílico acid

riminkéfon

acide 4-amino-1-*N*-[(2*R*)-2-phénylpropil]glicil-D-phénylalanil-D-leucyl-D-lisyl]pipéridine-4-carboxylique

riminkefón

ácido 4-amino-1-*N*-[(2*R*)-2-fenilpropil]glicil-D-fenilalanil-D-leucil-D-lisil]piperidina-4-carboxílico



rimegepant

rimegepant

*N*¹-acetyl-(104-118)-peptide (1-15) of the human regenerating islet-derived protein 3- α (Reg3 α , RegIII α , hepato-intestinal pancreatic protein, HIP, human proislet peptide, pancreatitis-associated protein 1, PAP) pre-pro-protein, [T¹¹⁰>S⁷, Q¹¹¹>H⁸, E¹¹⁴>L¹¹, N¹¹⁶>A¹³, E¹¹⁸>S¹⁵]-variant:

N-acetyl-L-isoleucylglycyl-L-leucyl-L-histidyl-L- α -aspartyl-L-prolyl-L-seryl-L-histidylglycyl-L-threonyl-L-leucyl-L-prolyl-L-alanylglycyl-L-serine

rimegepant

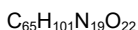
*N*¹-acétyl-peptide 104-118 (1-15) de la pré-pro-protéine humaine de la protéine 3- α dérivée des îlots en régénération (Rég3 α , RégIII α , protéine pancréatique hépato-intestinale, HIP, peptide pro-îlot humain, protéine 1 associée à la pancréatite, PAP), variante [T¹¹⁰>S⁷, Q¹¹¹>H⁸, E¹¹⁴>L¹¹, N¹¹⁶>A¹³, E¹¹⁸>S¹⁵]:

N-acétyl-L-isoleucylglycyl-L-leucyl-L-histidyl-L- α -aspartyl-L-prolyl-L-séryl-L-histidylglycyl-L-thréonyl-L-leucyl-L-prolyl-L-alanylglycyl-L-sérine

rimegepant

*N*¹-acetyl-peptide 104-118 (1-15) de la pre-pro-proteína humana de la proteína 3- α derivada de islotes en regeneración (Reg3 α , RegIII α , proteína pancreática hepato-intestinal, HIP, péptido pro-islole humano, proteína 1 asociada a pancreatitis, PAP), [T¹¹⁰>S⁷, Q¹¹¹>H⁸, E¹¹⁴>L¹¹, N¹¹⁶>A¹³, E¹¹⁸>S¹⁵]:

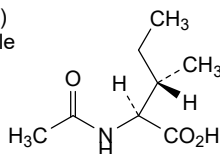
N-acetyl-L-isoleucylglycyl-L-leucyl-L-histidyl-L- α -aspartyl-L-prolyl-L-seryl-L-histidylglycyl-L-threonyl-L-leucyl-L-prolyl-L-alanylglycyl-L-serine



IGLHDP SHGT LPAGS 15

Modified residues / Résidus modifiés / Restos modificados

↓ (1)
Ac-Ile



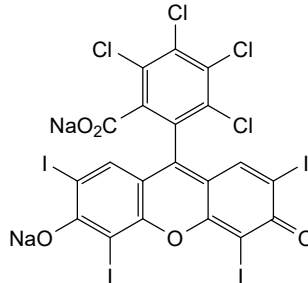
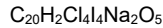
rose bengal sodium

rose bengal sodium

disodium 2,3,4,5-tetrachloro-6-(2,4,5,7-tetraiodo-6-oxido-3-oxo-3*H*-xanthen-9-yl)benzoate

rose bengale sodique 2,3,4,5-tétrachloro-6-(2,4,5,7-tétraiodo-6-oxido-3-oxo-3*H*-xanthén-9-yl)benzoate de disodium

rosa de bengala de sodio 2,3,4,5-tetracloro-6-(2,4,5,7-tetraiodo-6-oxido-3-oxo-3*H*-xanten-9-il)benzoato de sodio



rosnilimabum

rosnilimab

immunoglobulin G1-kappa, anti-[*Homo sapiens* PDCD1 (programmed cell death 1, PD-1, PD1, CD279)], humanized monoclonal antibody;

gamma1 heavy chain humanized (1-451) [VH (*Homo sapiens* IGHV7-4-1*02 (87.8%) -(IGHD) -IGHJ4*01 (92.3%) L123>T (116), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1-121) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 (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)], (224-215')-disulfide with kappa light chain humanized (1'-215') [V-KAPPA (*Homo sapiens* IGKV3D-11*02 (86.8%) -IGKJ4*01 (100%), CDR-IMGT [7.3.9] (27-33.51-53.90-98)) (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')]; dimer (230-230":233-233")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa

rosnilimab

immunoglobuline G1-kappa, anti-[*Homo sapiens* PDCD1 (protéine 1 de mort cellulaire programmée, PD-1, PD1, CD279)], anticorps monoclonal humanisé; chaîne lourde gamma1 humanisée (1-451) [VH (*Homo sapiens* IGHV7-4-1*02 (87.8%) -(IGHD) -IGHJ4*01 (92.3%) L123>T (116), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1-121) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 (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)], (224-215')-disulfure avec la chaîne légère kappa humanisée (1'-215') [V-KAPPA (*Homo sapiens* IGKV3D-11*02 (86.8%) -IGKJ4*01 (100%), CDR-IMGT [7.3.9] (27-33.51-53.90-98)) (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')]; dimère (230-230":233-233")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1, glycoforme alfa

rosnilimab

immunoglobulina G1-kappa, anti-[*Homo sapiens* PDCD1 (proteína 1 de muerte celular programada, PD-1, PD1, CD279)], anticuerpo monoclonal humanizado;

cadena pesada gamma1 humanizada (1-451) [VH (*Homo sapiens* IGHV7-4-1*02 (87.8%) -(IGHD) -IGHJ4*01 (92.3%) L123>T (116), CDR-IMGT [8.8.14] (26-33.51-58.97-110)) (1-121) -*Homo sapiens* IGHG1*01 (100%), G1m17,1 (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)], (224-215')-disulfuro con la cadena ligera kappa humanizada (1'-215') [V-KAPPA (*Homo sapiens* IGKV3D-11*02 (86.8%) -IGKJ4*01 (100%), CDR-IMGT [7.3.9] (27-33.51-53.90-98)) (1'-108') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (154), V101 (192) (109'-215')]; dímero (230-230":233-233")-bisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

QVQLVQSGSE LKPKGASVKV SCKASNYTFT DYSMHVVRQA PGQGLEWMGW 50
 INIETIYPTV ADQFKGRFAF SLDTSVSTAY LQISSLKAED TAVYYCARDY 100
 YGRFYIYAMDY WQQGTTVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150
 KDYFPEPVTV SWNSGALTSV VHTFFAVLQS SGLYSLSSV TVPSSSLGTQ 200
 TYICNVNHKP SNTKVDKKEV FKSCDKTHTC PPCPAPELLG GPSVFLFPPK 250
 PKDTLMSIRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY 300
 NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP 350
 QVYTLPPSRD ELTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTPP 400
 VLDSDDGSFFL YSKLTVDKSR WQQGNVFSKS VMHEALHNHY TQKSLSLSPG 450
 K 451

Light chain / Chaîne légère / Cadena ligera

EIVLTQSPAT LSLSPGERAT LSCASSSVS SYPFHYYQQK PGQAPRLLIY 50
 STSNLAGSIP ARFSGSGSGT DFTLTISRLE PEDFAVYYCH QYRHSPLTFG 100
 GGTKVIEIKRT VAAPSVFIFP FSDEQLKSGT ASVVCLLNMF YPREAKVQWK 150
 VDNALQSGNS QESVTEQDSK DSTYLSLSTL TSKADYERH KYVACEVTHQ 200
 GLSSPVTKSF NRGEC 215

Post-translational modifications

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

Intra-H (C23-C104) 22-96 148-204 265-325 371-429
 22"-96" 148"-204" 265"-325" 371"-429"
 Intra-L (C23-C104) 23"-89" 135"-195"
 23"-89" 135"-195"
 Inter-H-L (h 5-CL 126) 224-215" 224"-215"
 Inter-H-H (h 11, h 14) 230-230" 233-233"

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

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

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

H VH N26: 26, 26"
 Glycosylated / glycosylé / glicosilado
 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"

ruzotolimodum

ruzotolimod

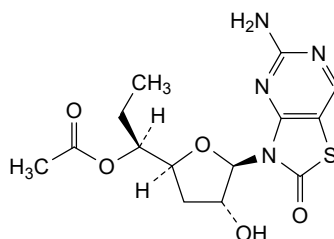
3-(5-O-acetyl-3,6,7-trideoxy- α -L-lyxo-heptofuranosyl)-5-amino[1,3]thiazolo[4,5-d]pyrimidin-2(3H)-one; (1S)-1-[(2S,4R,5R)-5-(5-amino-2-oxo[1,3]thiazolo[4,5-d]pyrimidin-3(2H)-yl)-4-hydroxyoxolan-2-yl]propyl acetate

ruzotolimod

3-(5-O-acétyl-3,6,7-tridésoxy- α -L-lyxo-heptofuranosyl)-5-amino[1,3]thiazolo[4,5-d]pyrimidin-2(3H)-one; acétate de (1S)-1-[(2S,4R,5R)-5-(5-amino-2-oxo[1,3]thiazolo[4,5-d]pyrimidin-3(2H)-yl)-4-hydroxyoxolan-2-yl]propyle

ruzotolimod

3-(5-O-acetil-3,6,7-tridesoxi- α -L-lyxo-heptofuranosil)-5-amino[1,3]thiazolo[4,5-d]pirimidin-2(3H)-ona; acetato de (1S)-1-[(2S,4R,5R)-5-(5-amino-2-oxo[1,3]thiazolo[4,5-d]pirimidin-3(2H)-il)-4-hidroxi oxolan-2-il]propilo

C₁₄H₁₈N₄O₅S**safimaltibum**

safimaltib

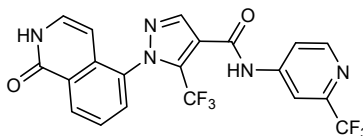
1-(1-oxo-1,2-dihydroisoquinolin-5-yl)-5-(trifluoromethyl)-N-[2-(trifluoromethyl)pyridin-4-yl]-1H-pyrazole-4-carboxamide

safimaltib

1-(1-oxo-1,2-dihydroisoquinoléin-5-yl)-5-(trifluorométhyl)-N-[2-(trifluorométhyl)pyridin-4-yl]-1H-pyrazole-4-carboxamide

safimaltib

1-(1-oxo-1,2-dihidroisoquinolein-5-il)-5-(trifluorometil)-N-[2-(trifluorometil)piridin-4-il]-1H-pirazol-4-carboxamida

C₂₀H₁₁F₆N₅O₂**safusidenibum**

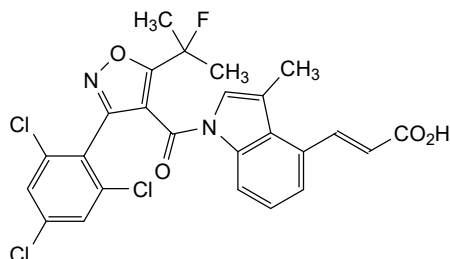
safusidenib

(2*E*)-3-{1-[5-(2-fluoropropan-2-yl)-3-(2,4,6-trichlorophenyl)-1,2-oxazole-4-carbonyl]-3-methyl-1*H*-indol-4-yl}prop-2-enoic acid

safusidénib

acide (2*E*)-3-{1-[5-(2-fluoropropan-2-yl)-3-(2,4,6-trichlorophényl)-1,2-oxazole-4-carbonyl]-3-méthyl-1*H*-indol-4-yl}prop-2-énoïque

safusidenib

ácido (2*E*)-3-{1-[5-(2-fluoropropan-2-il)-3-(2,4,6-triclorofenil)-1,2-oxazol-4-carbonil]-3-metil-1*H*-indol-4-il}prop-2-enoicoC₂₅H₁₈Cl₃FN₂O₄

selcopintidum

selcopintide

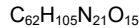
(344-353)-peptide (1-10) of human copine 7 (copine VII, CPNE7, epithelium-derived calcium-dependent phospholipid-binding protein);
L-lysyl-L-tyrosyl-L-lysyl-L-glutaminy-L-lysyl-L-arginyl-L-arginyl-L-seryl-L-tyrosyl-L-lysine

selcopintide

peptide 344-353 (1-10) de la copine 7 humaine (copine VII, CPNE7, protéine de liaison aux phospholipides dépendante du calcium dérivée de l'épithélium);
L-lysyl-L-tyrosyl-L-lysyl-L-glutaminy-L-lysyl-L-arginyl-L-arginyl-L-seryl-L-tyrosyl-L-lysine

selcopintida

péptido 344-353 (1-10) de la copina 7 humana (copina VII, CPNE7, proteína de unión a fosfolípidos dependiente de calcio derivada del epitelio);
L-lisil-L-tirosil-L-lisil-L-glutamini-L-lisil-L-arginil-L-arginil-L-seril-L-tirosil-L-lisina



Lys – Tyr – Lys – Gln – Lys – Arg – Arg – Ser – Tyr – Lys

semzuvolimabum #

semzuvolimab

immunoglobulin G1-kappa, anti-[*Homo sapiens* CD4 (p55, T cell surface antigen T4/Leu-3)], monoclonal antibody; gamma1 heavy chain (1-448) [VH Musmus/Homsap (*Mus musculus*IGHV1-75*01 (78.6%) -(IGHD) -IGHJ3*01 (100%)/*Homo sapiens* IGHV1-2*06 (73.5%) -(IGHD) -IGHJ4*01 (92.3%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG1*01, G1m17,1, G1v48 H84.4 (CH1 K120 (215) (119-216), hinge 1-15 (217-231), CH2 N84.4>H (298) (232-341), CH3 D12 (357), L14 (359) (342-446), CHS (447-448)) (119-448)], (221-218')-disulfide with kappa light chain (1'-218') [V-KAPPA Musmus/Homsap (*Mus musculus*IGKV3-4*01 (93.9%) -IGKJ2*03 (90.9%) S120>Q (104)/*Homo sapiens* IGKV4-1*01 (68.3%) -IGKJ2*01 (100%), CDR-IMGT [10.3.9] (27-36.54-56.93-101)) (1'-111') -*Homo sapiens* IGKC*04 (100%), Km1,2 A45.1 (158), L101 (195) (112'-218'')]; dimer (227-227'':230-230'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

semzuvolimab

immunoglobuline G1-kappa, anti-[*Homo sapiens* CD4 (p55, antigène de surface des cellules T T4/Leu-3)], anticorps monoclonal; chaîne lourde gamma1 (1-448) [VH Musmus/Homsap (*Mus musculus*IGHV1-75*01 (78.6%) -(IGHD) -IGHJ3*01 (100%)/*Homo sapiens* IGHV1-2*06 (73.5%) -(IGHD) -IGHJ4*01 (92.3%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) -*Homo sapiens* IGHG1*01, G1m17,1, G1v48 H84.4 (CH1 K120 (215) (119-216), charnière 1-15 (217-231), CH2 N84.4>H (298) (232-341), CH3 D12 (357), L14 (359) (342-446), CHS (447-448)) (119-448)], (221-218')-disulfure avec la chaîne légère kappa (1'-218') [V-KAPPA Musmus/Homsap (*Mus musculus*IGKV3-4*01 (93.9%) -IGKJ2*03 (90.9%) S120>Q (104)/*Homo sapiens* IGKV4-1*01 (68.3%) -IGKJ2*01 (100%), CDR-IMGT [10.3.9] (27-36.54-56.93-101)) (1'-111') -*Homo sapiens* IGKC*04 (100%), Km1,2 A45.1 (158), L101 (195) (112'-218'')]; dimère (227-227'':230-230'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

semzuvolimab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CD4 (p55, antígeno de superficie de las células T T4/Leu-3)], anticuerpo monoclonal; cadena pesada gamma1 (1-448) [VH Musmus/Homsap (*Mus musculus* IGHV1-75*01 (78.6%) -(IGHD) -IGHJ3*01 (100%)/*Homo sapiens* IGHV1-2*06 (73.5%) -(IGHD) -IGHJ4*01 (92.3%), CDR-IMGT [8.8.11] (26-33.51-58.97-107)) (1-118) - *Homo sapiens* IGHG1*01, G1m17,1, G1v48 H84.4 (CH1 K120 (215) (119-216), bisagra 1-15 (217-231), CH2 N84.4>H (298) (232-341), CH3 D12 (357), L14 (359) (342-446), CHS (447-448)) (119-448)], (221-218')-disulfuro con la cadena ligera kappa (1'-218') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV3-4*01 (93.9%) -IGKJ2*03 (90.9%) S120>Q (104)/*Homo sapiens* IGKV4-1*01 (68.3%) -IGKJ2*01 (100%), CDR-IMGT [10.3.9] (27-36.54-56.93-101)) (1'-111') -*Homo sapiens* IGKC*04 (100%), Km1,2 A45.1 (158), L101 (195) (112'-218')]; dímero (227-227''-230-230''')-bisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada
 QVQLVQSGPE LKPKGASVKV SCKASGYTFT DYVIHWVKQA TGGLEWIGE 50
 IYFGSGSAYS NAKFKDRVTM TADKSSNTAY MELSSLTSD TAVYFCARRG 100
 NGTGFAYWQO GTLVTVSSAS TKGPSVEFLA PSKSTSGT AALGCLVKDY 150
 FFEPTVTSWN SGALTSQVHT FPAVLQSSGL YLSLSTVTPV SSSLGQTYYI 200
 CNVNHKPSNT KVDKVEPKS CDKTHTCPCP PARELLGGPS VLFPPKPKD 250
 TLMISRTPEV TCVVVDVSHD DPEVFNWYV DGEVFNNAKT KPREEQYHST 300
 YRVVSLTVL HQDWLNGKEY KKVSNKALP APIEKTISKA KGQPREPQVY 350
 TLPSPDELT KNQVSLTCLV KGFYPSDIAV EWESNGQPN NYKTTTPVLD 400
 SDGSPFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPGK 448

Light chain / Chaîne légère / Cadena ligera
 DIVLTQSPAS LAVSLGQRAT ITCKAGQSDV YDGDSYMNVY QKPGQPPKL 50
 LIYVASNLSE GIPARFSGSG SGTDFTLNIH PVEENDAATY YCQQSYKDPL 100
 TFGQGTLEI KRTVAAPSVF IFPPSDEQLK SGTASVCLL NNFYPREAKV 150
 QWRVDNALQS GNSQESVTEQ DSKDSTYLSL STLTLKADY EKHKLYACEV 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) 221-218" 221"-218"
 Inter-H-H (h 11, h 14) 227-227" 230-230"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutamínilo N-terminal
 Q > pyroglutamy (pE, 5-oxoprolyl)
 H VH Q1:
 I, I"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
 H VH CDR3 109
 101, 101"

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

H CH2 N84.4>H (G1v48):
 298, 298"

Aglycosylated / aglycosylé / aglicosilado

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

sepiapterinum
 sepiapterin

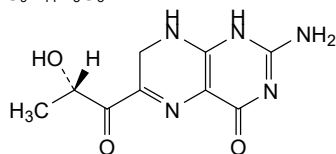
2-amino-6-[(2S)-2-hydroxypropanoyl]-7,8-dihydropteridin-4(1H)-one

sépiaptérine

2-amino-6-[(2S)-2-hydroxypropanoyl]-7,8-dihydroptéridin-4(1H)-one

sepiapterina 2-amino-6-[(2*S*)-2-hidroxiopropanoil]-7,8-dihidropteridin-4(1*H*)-ona

C₉H₁₁N₅O₃



sirpefenicolum

sirpefenicol

2,2-difluoro-*N*-[(1*R*,2*S*)-3-fluoro-1-hidroxi-1-(4-{6-[(*R**S*)-metanesulfonimidoyl]piridin-3-yl}fenil)propan-2-yl]acetamide

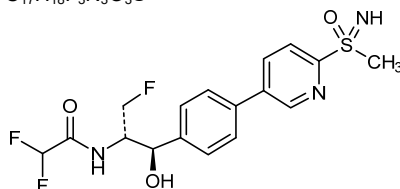
sirpéfénicol

2,2-difluoro-*N*-[(1*R*,2*S*)-3-fluoro-1-hidroxi-1-(4-{6-[(*R**S*)-méthanesulfonimidoyl]piridin-3-yl}phényl)propan-2-yl]acetamide

sirpefenicol

2,2-difluoro-*N*-[(1*R*,2*S*)-3-fluoro-1-hidroxi-1-(4-{6-[(*R**S*)-metanosulfonimidoil]piridin-3-il}fenil)propan-2-il]acetamida

C₁₇H₁₈F₃N₃O₃S



sovleplenibum

sovleplenib

7-{4-[1-(methanesulfonyl)piperidin-4-yl]fenil}-*N*-{[(2*S*)-morpholin-2-yl]metil}pirido[3,4-*b*]pirazin-5-amina

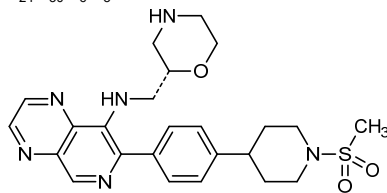
sovléplénib

7-{4-[1-(méthanesulfonyl)pipéridin-4-yl]phényl}-*N*-{[(2*S*)-morpholin-2-yl]méthyl}pyrido[3,4-*b*]pirazin-5-amina

sovleplenib

7-{4-[1-(metanosulfonil)piperidin-4-il]fenil}-*N*-{[(2*S*)-morfolin-2-il]metil}pirido[3,4-*b*]pirazin-5-amina

C₂₄H₃₀N₆O₃S



soziniberceptum

sozinibercept

human vascular endothelial growth factor receptor 3 (VEGFR3, Fms-like tyrosine kinase 4, tyrosine-protein kinase receptor FLT4) fragment (1-305, containing the immunoglobulin-like C2-type domains 1, 2 and 3) variant (N>Q⁸⁰), fused to human immunoglobulin G1 C-terminal Fc fragment (306-537), disulfide bridged dimer, produced in Chinese hamster ovary (CHO) cells, glycoform alfa;

[N⁸⁰>Q]-human vascular endothelial growth factor receptor 3 (VEGFR3, Fms-like tyrosine kinase 4, FLT-4, tyrosine-protein kinase receptor FLT4, EC:2.7.10.1) (1-305)-peptide fragment (containing the immunoglobulin-like C2-type domains 1, 2 and 3), fused with a human immunoglobulin G1 C-terminal 232-peptide Fc fragment (CH2-CH3-CHS domains) [*Homo sapiens* IGHG1*01 (hinge (306-320), CH2 (321-430), CH3 (431-535), CHS (536-537))] (306-537), dimer (310-310':316-316':319-319')-trisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

sozinibercept

fragment du récepteur 3 du facteur de croissance de l'endothélium vasculaire humain (VEGFR3, tyrosine kinase 4 de type Fms, récepteur tyrosine-protéine kinase FLT4) (1-305, contenant les domaines 1, 2 et 3 de type immunoglobuline C2) variant (N>Q⁸⁰), fusionné au fragment Fc C-terminal de l'immunoglobuline G1 humaine (306-537), dimère à pont disulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa;

[N⁸⁰>Q]-récepteur 3 humain du facteur de croissance de l'endothélium vasculaire (VEGFR3, tyrosine kinase 4 de type Fms, FLT-4, récepteur tyrosine-protéine kinase FLT4, EC:2.7.10.1), fragment du peptide 1-305 (contenant les domaines 1, 2 et 3 de type C2 similaires aux immunoglobulines), fusionné avec un fragment Fc de peptide-232 C-terminal d'immunoglobuline G1 humaine (domaines CH2-CH3-CHS) [*Homo sapiens* IGHG1*01 (charnière (306-320), CH2 (321-430), CH3 (431-535), CHS (536-537))] (306-537), dimère (310-310':316-316':319-319')-trisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

sozinibercept

receptor 3 humano del factor de crecimiento endotelial vascular (VEGFR3, tirosina kinasa 4 similar a Fms, receptor tirosina-proteína kinasa FLT4) fragmento (1-305, que contiene los dominios 1, 2 y 3 de tipo C2 similares a inmunoglobulinas) variante (N>Q⁸⁰), fusionado con un fragmento Fc (306-537) terminal C de inmunoglobulina G1 humana, dímero acortado disulfuro, producido en células ováricas de hámster chino (CHO), glicoforma alfa; [N⁸⁰>Q]-receptor 3 humano del factor de crecimiento endotelial vascular (VEGFR3, tirosina kinasa 4 similar a Fms, FLT-4, receptor tirosina-proteína kinasa FLT4, EC:2.7.10.1) fragmento de péptido 1-305 (que contiene los dominios 1, 2 y 3 de tipo C2 similares a inmunoglobulinas), fusionado con un fragmento Fc de 232-péptido C-terminal de inmunoglobulina G1 humana (dominios CH2-CH3-CHS) [*Homo sapiens* IGHG1*01 (bisagra (306-320), CH2 (321-430), CH3 (431-535), CHS (536-537))] (306-537), dímero (310-310':316-316':319-319')-trisulfuro, producida en las células ováricas de hámster chino (CHO), glicoforma alfa

Sequence / Séquence / Secuencia

YSMTPTTIANI	TEESHVIDTG	DSLISISCRGQ	HPLEWAWPGA	QEAPATGDKD	50
SEDTGVVRDC	EGTDARFYCK	VLLLHEVHAQ	DTGSYVCYK	YIKARIEGTT	100
AASSYVFRD	FEQPFINKPD	TLLVNRKAMD	WVPCLVSIIPG	LNVTLSRQSS	150
VLWPDGQEVV	WDDRRGMLVS	TPLLHDALYL	QCETTWGDQD	FLSNPFLVHI	200
TGNELYDIQL	LPRKSLLELL	GEKLVNCTV	WAEFNSGVTF	DWDYPGKQAE	250
RGKWPERRS	QQTHTELSST	LTIHNVSHQD	LGSYVCKANN	GIQRFRESTE	300
VIVHEEPKSC	DKTHTCPPCP	APELLGGPSV	FLFPPKPKDT	LMISRTPEVT	350
CVVVDVSHED	PEVKFNWYVD	GVEVHNAKTK	PREEQYNSTY	RVVSVLTVLH	400
QDWLNGKEYK	CKVSKALPA	PIEKTISKAK	GQPREPQVYT	LPSPRDELTK	450
NQVSLTCLVK	GFYPSDIAVE	WESNGQPENN	YKTTTPVLDL	DGSFFLYSKL	500
TVDKSRWQQG	NVFCSCVMHE	ALHNNHYTKS	LSLSPGK		537

Mutation / Mutation / Mutación

N80>Q, N80'>Q

Post-translational modifications

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

Intra-chain 27-87 60-69 134-182 228-286 351-411 457-515
27-87' 60'-69' 134'-182' 228'-286' 351'-411' 457'-515'

Inter-chain 310-310' 316-316' 319-319'

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

N9, N142, N227, N275, N387;

N9', N142', N227', N275', N387'

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

H CHS K2: K537, K537'

sudocetaxelum zendusortidum

sudocetaxel zendusortide

$N^{6,5}, N^{6,13}$ -bis[4-(((2*R*,3*S*)-1-[[4-(acetyloxy)-2α-(benzoyloxy)-5β,20-epoxy-1,7β,10β-trihydroxy-9-oxotax-11-en-13α-yl]oxy)-3-[(*tert*-butoxycarbonyl)amino]-1-oxo-3-phenylpropan-2-yl]oxy)-4-oxobutanoyl][*N*-acetylglucyl-L-valyl-L-arginyl-L-alanyl-L-lysyl-L-alanylglucyl-L-valyl-L-arginyl-L-asparaginy-(2*S*)-2-aminohexanoyl-L-phenylalanyl-L-lysyl-L-seryl-L-α-glutamyl-L-seryl-L-tyrosine]

sudocétaxel zendusortide

$N^{6,5}, N^{6,13}$ -bis[4-(((2*R*,3*S*)-1-[[4-(acétyloxy)-2α-(benzoyloxy)-5β,20-époxy-1,7β,10β-trihydroxy-9-oxotax-11-én-13α-yl]oxy)-3-[(*tert*-butoxycarbonyl)amino]-1-oxo-3-phénylpropan-2-yl]oxy)-4-oxobutanoyl][*N*-acétylglucyl-L-valyl-L-arginyl-L-alanyl-L-lysyl-L-alanylglucyl-L-valyl-L-arginyl-L-asparaginy-(2*S*)-2-aminohexanoyl-L-phénylalanyl-L-lysyl-L-séryl-L-α-glutamyl-L-séryl-L-tyrosine]

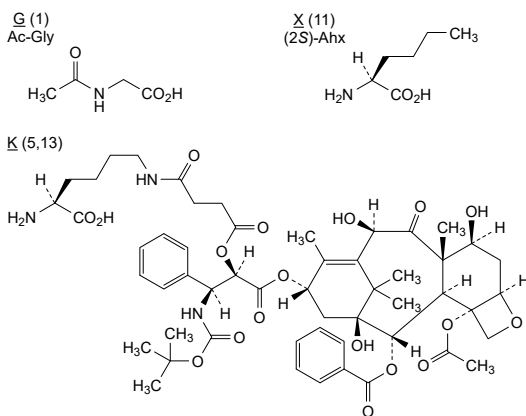
sudocetaxel zendusortida

$N^{6,5}, N^{6,13}$ -bis[4-(((2*R*,3*S*)-1-[[4-(acetiloxi)-2α-(benzoiłoxi)-5β,20-epoxi-1,7β,10β-trihidroxi-9-oxotax-11-en-13α-il]oxi)-3-[(*terc*-butoxicarbonil)amino]-3-fenil-1-oxopropan-2-il]oxi)-4-oxobutanoil][*N*-acetilglucil-L-valil-L-arginil-L-alanil-L-lisil-L-alanilglucil-L-valil-L-arginil-L-asparaginil-(2*S*)-2-aminohexanoil-L-fenilalanil-L-lisil-L-seril-L-α-glutamil-L-seril-L-tirosina]

$C_{176}H_{248}N_{28}O_{57}$

GVRAKAGVRN XFKSESY 17

Modified residues / Résidus modifiés / Restos modificados



tanoxiciclibum

tanoxiciclib

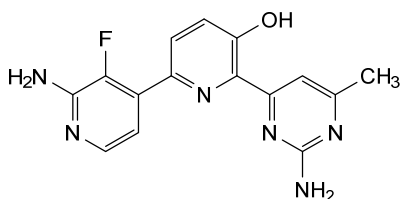
2'-amino-6-(2-amino-6-methylpyrimidin-4-yl)-3'-fluoro[2,4'-bipyridin]-5-ol

tanoxiciclib

2'-amino-6-(2-amino-6-méthylpyrimidin-4-yl)-3'-fluoro[2,4'-bipyridin]-5-ol

tanoxiciclib

2'-amino-6-(2-amino-6-metilpirimidin-4-il)-3'-fluoro[2,4'-bipiridin]-5-ol

C₁₅H₁₃FN₆O

tarcocimabum tedromerum #
tarcocimab tedromer

immunoglobulin G1-kappa, anti-[*Homo sapiens* VEGFA (vascular endothelial growth factor A, VEGF-A, VEGF)], humanized monoclonal antibody, conjugated via a linker to a nona-antennary dendrimer 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-diy])ω-y])]-2-methylpropanoyl)oxy]methyl)ethoxy]acetamido]propanamido)methyl)-16,32-dioxo-3,6,9,12,19,22,25,28-octaoxa-15,31-diazatetracontan-34-yl]-2,5-dioxopyrrolidin-1-yl (*tedromer*) group

tarcocimab tédomère

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 dendrimère nonaantennaire 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

	<p>avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA (<i>Homo sapiens</i> IGKV1-16*01 (87.4%) - 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 (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-6λ⁵-phosphaundécan-10-ium-1-oyl)-1-méthyléthane-1,2-diy]-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 (<i>tédromère</i>)</p>
<p>tarcocimab tetrómero</p>	<p>inmunoglobulina G1-kappa, anti-[<i>Homo sapiens</i> VEGFA (factor de crecimiento A del endotelio vascular, VEGF-A, VEGF)], anticuerpo monoclonal humanizado, conjugado a través de un enlace a un dendrímero con nueve antenas con grupos terminales de polímero fosforilcolina ; cadena pesada gamma1 humanizada (1-453) [VH (<i>Homo sapiens</i> IGHV3-30*02 (75.8%) -(IGHD) - IGHJ4*01 (93.3%), CDR-IMGT [8.8.16] (26-33.51-58.97-112)) (1-123) -<i>Homo sapiens</i> 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 (<i>Homo sapiens</i> IGKV1-16*01 (87.4%) -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 (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-6λ⁵-fosfaundecan-10-io-1-oil)-1-metiletano-1,2-dii]-ω-il)-2-metilpropanoil]oxi]metil]etoxi]acetamido]propanamido]metil]-16,32-dioxo-3,6,9,12,19,22,25,28-octaoxa-15,31-diazatétratriacontan-34-il]-2,5-dioxopyrrolidin-1-ilo (<i>tetrómero</i>)</p>

Heavy chain / Chaîne lourde / Cadena pesada

EVQLVESGGG LVQPFGSLRL SCAASGYDFT HYGMNWRVQA PGKLEWVWG 50
 INTYTGPEY AADFKRRFTF SLDTSKSTAY LQMNSLRAED TAVYYCAKYP 100
 YYGTSHWYF DVWGQGTLLV VSSASTKGPS VFPLAPSSKS TSGGTAALGC 150
 LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSL VVTVPSSSLG 200
 TQTYICNVNH KPSNTKVDK VEPKSCDKTH TCPCPAPEA AGAPSVFLFP 250
 PKPKDLMIS RTPVTCVVV DVSHEDEPKV FNVYVDGVEV HNAKTKPREE 300
 QYNSTYRVVS VLTVLHQDWL NGKEYCKVS NKALFAPIEK TISKAKQPR 350
 EFQVYTLPPS REEMTKNQVS LTCVKGFPY SDIAVEWESN GQPENNYKTT 400
 PAVLDSGGSF FLYSKLTVDK SRWQQGNVFS CSMVHEALHN HYTKSLSCS 450
 PGK 453

Light chain / Chaîne légère / Cadena ligera

DIQLTQSPSS LSASVGDRTV ITCSASQDIS NYLNWYQQKPK GKAPKVLIIYF 50
 TSSLHSGVPS RFGSGSGSDT FTLLTISSLQP EDFATYYCQQ YSTVPWTFGQ 100
 GTKVEIKRTV AAPSVEIFPP SDEQLKSGTA SUVCLLNIFY PREAKVQMKV 150
 DNALQSGNSQ ESVTEQDSK STYSLSSITL 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) 22-96 150-206 267-327 373-431
 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"

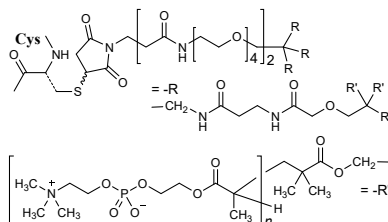
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenaríos complejos fucosilados

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

H CHS K2: 453, 453"

Conjugation sites / Sites de conjugation / Posiciones de conjugación:

H CH3 L123>C: 449, 449"



tegileridinum

tegileridine

(1*S*,4*S*)-4-ethoxy-*N*-{2-[(9*R*)-9-(pyridin-2-yl)-6-oxaspiro[4.5]decan-9-yl]ethyl}-1,2,3,4-tetrahydronaphthalen-1-amine

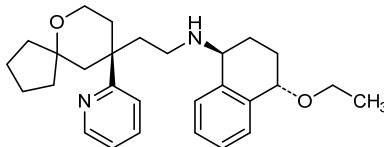
tégileridine

(1*S*,4*S*)-4-éthoxy-*N*-{2-[(9*R*)-9-(pyridin-2-yl)-6-oxaspiro[4.5]décan-9-yl]éthyl}-1,2,3,4-tétrahydronaphtalén-1-amine

tegileridina

(1*S*,4*S*)-4-etoxi-*N*-{2-[(9*R*)-9-(piridin-2-il)-6-oxaspiro[4.5]decan-9-il]etil}-1,2,3,4-tetrahidronaftalen-1-amina

C₂₈H₃₈N₂O₂



tinengotinibum

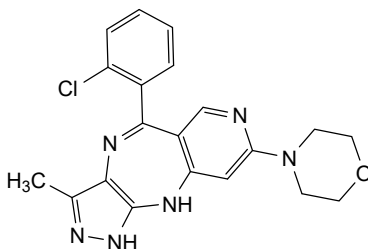
tinengotinib

5-(2-chlorophenyl)-3-methyl-8-(morpholin-4-yl)-1,10-dihydropyrazolo[4,3-*b*]pyrido[4,3-*e*][1,4]diazepine

tinengotinib

5-(2-chlorophényl)-3-méthyl-8-(morpholin-4-yl)-1,10-dihydropyrazolo[4,3-*b*]pyrido[4,3-*e*][1,4]diazépine

tinengotinib

5-(2-clorofenil)-3-metil-8-(morfolin-4-il)-1,10-dihidropirazolo[4,3-*b*]pirido[4,3-*e*][1,4]diazepinaC₂₀H₁₉ClN₆O**tovorafenibum**

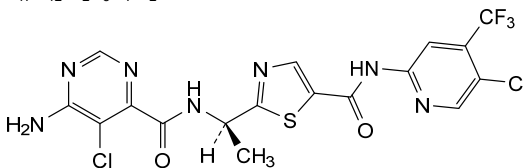
tovorafenib

6-amino-5-chloro-*N*-[(1*R*)-1-(5-[[5-chloro-4-(trifluoromethyl)pyridin-2-yl]carbamoyl]-1,3-thiazol-2-yl)ethyl]pyrimidine-4-carboxamide

tovorafénib

6-amino-5-chloro-*N*-[(1*R*)-1-(5-[[5-chloro-4-(trifluorométyl)pyridin-2-yl]carbamoyl]-1,3-thiazol-2-yl)éthyl]pyrimidine-4-carboxamide

tovorafenib

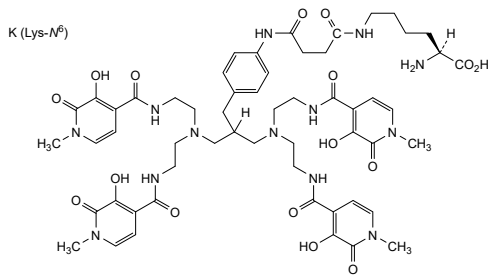
6-amino-5-cloro-*N*-[(1*R*)-1-(5-[[5-cloro-4-(trifluorometil)piridin-2-il]carbamoil]-1,3-tiazol-2-il)etil]pirimidina-4-carboxamidaC₁₇H₁₂Cl₂F₃N₇O₂S**trastuzumabum corixetanum #**

trastuzumab corixetan

immunoglobulin G1-kappa, anti-[*Homo sapiens* ERBB2 (epidermal growth factor receptor 2, receptor tyrosine-protein kinase erbB-2, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], humanized monoclonal antibody, conjugated to *corixetan*, comprising a linker and an octadentate chelator;
 gamma1 heavy chain humanized (1-449) [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 R120>K (217) (121-218), hinge 1-15 (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS K2>del (449)) (121-449)], (223-214')-

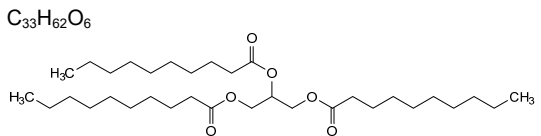
- disulfide with kappa light chain humanized (1'-214') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (86.3%) -IGKJ1*01 (100%), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (229-229":232-232")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1, glycoform alfa, conjugated to the chelator group *corixetan* on an average of 0.5 lysyl per antibody
For the corixetan part, please refer to the Proposed INN List 121, published in the WHO Drug Information, Vol.33, No.2, 2019.
- trastuzumab corixétan immunoglobuline G1-kappa, anti-[*Homo sapiens* ERBB2 (récepteur 2 du facteur de croissance épidermique, récepteur tyrosine-protéine kinase erbB-2, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], anticorps monoclonal humanisé, conjugué au *corixétan*, qui comprend un linker et un chélateur octadenté; chaîne lourde gamma1 humanisée (1-449) [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 R120>K (217) (121-218), charnière 1-15 (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS K2>del (449)) (121-449)], (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-K1, glycoforme alfa, conjugué au groupe chélateur *corixétan* sur une moyenne de 0.5 lysyles par anticorps
Pour la partie corixétan, veuillez-vous référer à la Liste 121 des DCI proposées, publiée dans le WHO Drug Information, Vol.33, No.2, 2019.
- trastuzumab corixétán inmunoglobulina G1-kappa, anti-[*Homo sapiens* ERBB2 (receptor 2 del factor de crecimiento epidérmico, receptor tirosina-proteína kinasa erbB-2, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], anticuerpo monoclonal humanizado, conjugado con *corixétán*, que consta de un enlace y un quelante octadentado; cadena pesada gamma1 humanizada (1-449) [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 R120>K (217) (121-218), bisagra 1-15 (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS K2>del (449)) (121-449)], (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-K1, forma glicosilada alfa, conjugado en 0.5 lisilos, por término medio, con el grupo quelante *corixétán*
Para la parte corixétán, por favor vaya a la Lista 121 de los DCI propuestas, publicada en el WHO Drug Information, Vol.33, No.2, 2019.

Heavy chain / Chaîne lourde / Cadena pesada
 EVQLVESGGG LVQPGGSLRL SCAASGFNIK DTYIHWVRQA PGKGLEWVAR 50
 IYPTNGYTRY ADSVKGRFTI SADTSKNTAY LQMNSLRAED TAVVYCSRWG 100
 GDGFYAMDYW GQGTLVTVSS ASTKGPSVFP LAPSSKSTGS GTPAALGLVK 150
 DYFPEFVTVS WNSGALTSGV HTPFAVLQSS GLYSLSSVVT VPSSSLGTQT 200
 YICNVNHKPS NTKVKDKVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP 250
 KDTLMI SRTPEVTVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
 STYRVVSVLT VLHQDNLNGK EYKCKVSNKA LPAPIEKTI S KAKGQPREPQ 350
 VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVESWGNGP ENNYKTTTPV 400
 LDSDGSFFLY SKLTVDKSRW QGQNVFCSV MHEALHNHYT QKSLSLSPG 449
 Light chain / Chaîne légère / Cadena ligera
 DIQMTQSPFSS LSASVGRVIT ITCRASQDVN TAVAWYQQKPK GKAPKLLIYS 50
 ASFLYSGVPS RFGSRSRGTD FTLTISLQPE EDFATYYCQQ HYTPPTFGQ 100
 GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNFIY FREAKVQWKV 150
 DNALQSGNSQ ESVTEQDSK D STYSLSSLT LSKADYEKHK VYACEVTHQG 200
 LSSVPEKSFN RQEC 214
 Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
 Intra-H 22-96 147-203 264-324 370-428
 22"-96" 147"-203" 264"-324" 370"-428"
 Intra-L 23"-88" 134"-194" 233"-214"
 23"-88" 134"-194"
 Inter-H-L 223-214" 223"-214"
 Inter-H-H 229-229" 232-232"
 N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
 300, 300"
 Potential modified residues / résidus modifiés potentiels / restos modificados potenciales



trisdecanoinum

- trisdecanoïn propane-1,2,3-triyl tri(decanoate)
- trisdécanoïne tri(décanoate) de propane-1,2,3-triyle
- trisdecanoína tri(decanoato) de propano-1,2,3-triilo



trontinemabum #

trontinemab

immunoglobulin [G1-VH-Ckappa_Vkappa-CH1]_[G1_kappa] with domain crossover, anti-[*Homo sapiens* APP (amyloid beta, A4 precursor protein) Abeta, conformational epitope 1-40/42]] and anti-[*Homo sapiens* TFRC (transferrin receptor, p90, CD71)], humanized monoclonal antibody, bispecific;
 fused chain G1-VH-Ckappa bispecific, anti-APP A beta and anti-TFRC (1-702) [gamma1 heavy chain anti-APP Abeta (1-455) humanized [VH (*Homo sapiens* IGHV3-23*04 (92.9%) -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [8.8.19] (26-33.51-58.97-115))] (1-126) -*Homo sapiens* IGHG1*01, G1m17,1, G1v32 CH3 W22 (CH1 K26>E (156), K119>E (222), K120 (223) (127-224), hinge 1-15 (225-239), CH2 (240-349), CH3 S10>C (363), D12 (365), L14 (367), T22>W (375) (350-454), CHS K2>del (455)) (127-455))] -18-mer diglycyl-seryl-tris(tetraglycyl-seryl) linker (456-473) -VH-C kappa chain anti-TFRC (474-702)

humanized [VH (*Homo sapiens* IGHV4-31*02 (76.0%) -(IGHD) -IGHJ5*02 (100%), CDR-IMGT [8.7.19] (498-505.523-529.566-584)) (474-595) -alanyl-seryl (596-597) -C-KAPPA (*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (641), V101 (679) (598-702)], (229-215')-disulfide with kappa light chain anti-APP Abeta (1'-215') humanized [V-KAPPA (*Homo sapiens* IGKV3D-7*01 (89.6%) -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), E12>R (124), Q13>K (125) (109'-215')], (702-215''''')-disulfide with Vkappa-CH1 chain anti-TFRC (1''''-215''''') humanized [V-KAPPA (*Homo sapiens* IGKV1-13*02 (94.4%) -IGKJ4*01 (100%), CDR-IMGT [6.3.12] (27-32.50-52.89-100)) (1''''-110''''') -diseryl (111''''-112''''') -CH1-hinge (*Homo sapiens* IGHG1*01 CH1-h, G1m17 (CH1 K120 (209) (113''''-210'''''), hinge 1-5 (211''''-215''''')) (113''''-215''''')], gamma1 heavy chain anti-APP Abeta (1''-456'') humanized [VH (*Homo sapiens* IGHV3-23*04 (92.9%) -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [8.8.19] (26-33.51-58.97-115)) (1''-126'') -*Homo sapiens* IGHG1*01, G1m17,1, G1v33 CH3 S22, A24, V86 (CH1 K26>E (156), K119>E (222), K120 (223) (127''-224''), hinge 1-15 (225''-239''), CH2 (240''-349''), CH3 Y5>C (358), D12 (365), L14 (367), T22>S (375), L24>A (377), Y86>V (416) (350''-454''), CHS (455''-456'') (127''-456'')], (229''-215''''')-disulfide with kappa light chain anti-APP Abeta (1''-215''') humanized [V-KAPPA (*Homo sapiens* IGKV3D-7*01 (89.6%) -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) E12>R (124), Q13>K (125)(109''-215''')], dimer (235-235'':238-238'':363-358'')-trisulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

trontinémab

immunoglobuline [G1-VH-Ckappa_Vkappa-CH1]_[G1_kappa], anti-[*Homo sapiens* APP (amyloïde bêta, protéine précurseur A4) Abêta, épitope conformationnel 1-40/42] et anti-[*Homo sapiens* TFRC (récepteur de la transferrine, p90, CD71)], anticorps monoclonal humanisé, bispécifique; chaîne lourde fusionnée G1-VH-Ckappa bispécifique, anti-APP A bêta et anti-TFRC (1-702) [gamma1 anti-APP Abêta (1-455) humanisée [VH (*Homo sapiens* IGHV3-23*04 (92.9%) -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [8.8.19] (26-33.51-58.97-115)) (1-126) -*Homo sapiens* IGHG1*01, G1m17,1, G1v32 CH3 W22 (CH1 K26>E (156), K119>E (222), K120 (223) (127-224), charnière 1-15 (225-239), CH2 (240-349), CH3 S10>C (363), D12 (365), L14 (367), T22>W (375) (350-454), CHS K2>del (455)) (127-455)] -18-mer diglycyl-séryl-tris(tétraglycyl-séryl) linker (456-473) -VH-Ckappa anti-TFRC (474-702) humanisé [VH (*Homo sapiens* IGHV4-31*02 (76.0%) -(IGHD) -IGHJ5*02 (100%), CDR-IMGT [8.7.19] (498-505.523-529.566-584)) (474-595) -alanyl-séryl (596-597) -C-KAPPA (*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (641), V101 (679) (598-702)]], (229-215')-disulfure avec la chaîne légère kappa anti-APP Abêta(1'-215') [V-KAPPA (*Homo sapiens* IGKV3D-7*01 (89.6%) -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), E12>R (124), Q13>K (125) (109'-215')], (702-215''''')-disulfure avec Vkappa-CH1 chain anti-TFRC (1''''-215''''') humanisée [V-KAPPA (*Homo sapiens* IGKV1-13*02 (94.4%) -IGKJ4*01 (100%), CDR-IMGT [6.3.12] (27-32.50-52.89-100)) (1''''-110''''') -diseryl (111''''-112''''') -CH1-charnière (*Homo sapiens* IGHG1*01 CH1-h, G1m17 (CH1 K120 (209) (113''''-210''), charnière 1-5 (211''''-215''''')) (113''''-215''''')],

chaîne lourde gamma1 anti-APP Abêta(1"-456") humanisée [VH (*Homo sapiens* IGHV3-23*04 (92.9%) -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [8.8.19] (26-33.51-58.97-115)) (1"-126") -*Homo sapiens* IGHG1*01, G1m17,1, G1v33 CH3 S22, A24, V86 (CH1 K26>E (156), K119>E (222), K120 (223) (127"-224"), charnière 1-15 (225"-239"), CH2 (240"-349"), CH3 Y5>C (358), D12 (365), L14 (367), T22>S (375), L24>A (377), Y86>V (416) (350"-454"), CHS (455"-456")) (127"-456")], (229"-215")-disulfure avec la chaîne légère kappa anti-APP Abêta(1"-215") humanisée [V-KAPPA (*Homo sapiens* IGKV3D-7*01 (89.6%) -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), E12>R (124), Q13>K (125) (109"-215")]; dimère (235-235":238-238":363-358")-trisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), glycoforme alfa

trontinemab

immunoglobulina [G1-VH-Ckappa_Vkappa-CH1]_[G1_kappa], anti-[*Homo sapiens* APP (amieloide beta, proteina precursora A4) Abêta, epitopo conformacional 1-40/42] y anti-[*Homo sapiens* TFRC (receptor de la transferrina, p90, CD71)], anticuerpo monoclonal humanizado, biespecifico;

cadena pesada fusionada G1-VH-Ckappa biespecifica, anti-APP A bêta y anti-TFRC (1-702) [gamma1 anti-APP Abêta (1-455) humanizada [VH (*Homo sapiens* IGHV3-23*04 (92.9%) -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [8.8.19] (26-33.51-58.97-115)) (1-126) -*Homo sapiens* IGHG1*01, G1m17,1, G1v32 CH3 W22 (CH1 K26>E (156), K119>E (222), K120 (223) (127-224), bisagra 1-15 (225-239), CH2 (240-349), CH3 S10>C (363), D12 (365), L14 (367), T22>W (375) (350-454), CHS K2>del (455)) (127-455)] -18-mer diglicil-seril-tris(tetraglicil-seril) linker (456-473) -VH-Ckappa anti-TFRC (474-702) humanizado [VH (*Homo sapiens* IGHV4-31*02 (76.0%) -(IGHD) -IGHJ5*02 (100%), CDR-IMGT [8.7.19] (498-505.523-529.566-584)) (474-595) -alanil-seril (596-597) -C-KAPPA (*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (641), V101 (679) (598-702))], (229-215')-disulfuro con la cadena ligera kappa anti-APP Abêta(1'-215') [V-KAPPA (*Homo sapiens* IGKV3D-7*01 (89.6%) -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), E12>R (124), Q13>K (125) (109'-215')], (702-215''')-disulfuro con cadena Vkappa-CH1 anti-TFRC (1''''-215''''') humanizada [V-KAPPA (*Homo sapiens* IGKV1-13*02 (94.4%) -IGKJ4*01 (100%), CDR-IMGT [6.3.12] (27-32.50-52.89-100)) (1''''-110''''') -diseril (111''''-112''''') -CH1-bisagra (*Homo sapiens* IGHG1*01 CH1-h, G1m17 (CH1 K120 (209) (113''''-210'), bisagra 1-5 (211''''-215''''')) (113''''-215''''')], Cadena pesada gamma1 anti-APP Abêta(1"-456") humanizada [VH (*Homo sapiens* IGHV3-23*04 (92.9%) -(IGHD) -IGHJ4*01 (93.3%), CDR-IMGT [8.8.19] (26-33.51-58.97-115)) (1"-126") -*Homo sapiens* IGHG1*01, G1m17,1, G1v33 CH3 S22, A24, V86 (CH1 K26>E (156), K119>E (222), K120 (223) (127"-224"), bisagra 1-15 (225"-239"), CH2 (240"-349"), CH3 Y5>C (358), D12 (365), L14 (367), T22>S (375), L24>A (377), Y86>V (416) (350"-454"), CHS (455"-456")) (127"-456")], (229"-215")-disulfuro con la cadena ligera kappa anti-APP Abêta(1"-215") humanizada [V-KAPPA (*Homo sapiens* IGKV3D-7*01 (89.6%) -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), E12>R (124), Q13>K (125) (109"-215")]; dímero (235-235":238-238":363-358")-trisdisulfuro, producido en las células ováricas de hámster chino (CHO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada: anti-APP beta 1-40/42, anti-TFRC (H)
 QVELVESGGG LVQPGGSLRL SCAASGFTFS SYAMSWVRQA PGKGLEWVSA 50
 INASGTRTYI ADSVKGRTFI SRDNSKNTLY LQMSLRAED TAVYYCARGK 100
 GNTHKPYGYV RYFDVWGQGT LVTVSSASTK GPSVFPLAPS SKSTSGGTAA 150
 LGCLVEDYFP EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVTVTPSS 200
 SLGTQTYICN VNHKPSNTKV DEKVEPKSCD KTHCTPCPCA PELLGGPSVF 250
 LFPFKPKDTL MISRTPEVTC VVVDVSHEDP EVKFNWYVDG VEVHNAKTKP 300
 REEQYNSTYR VVSVLTVLHQ DWLNGKEYKC KVSNKALPAP IEKTIKAKG 350
 QPREPQVYTL PFCRDELTRN QVSLWCLVKG FYPSDIAVEW ESNQGPENNY 400
 KTFPFLVDSG GSFFLYSKLT VDKSRWQQGN VFSCSVMHEA LHNHYTQKSL 450
 SLSFPGGSGG GSGGGGSGG GGSQSMQESG PGLVKPSQTL SLTCTVSGFS 500
 LSSYAMSWIR QHPKGLLEWI GYIWSGGSTD YASWAKSRVT ISKTSTTVSL 550
 KLSSVTAADT AVYVCARRYG TSYPDYGDAS GFDPWQGQTL VTVSSASVAA 600
 PSVFIFFPSD EQLKSGTASV VCLLNNEYFR EAKVQWKVDN ALQSGNSQES 650
 VTEQDSKSDT YLSLSTLTLS KADYKHKVY ACEVTHQGLS SPVTKSFNRG 700
 EC 702

Heavy chain / Chaîne lourde / Cadena pesada: anti-APP A beta 1-40/42 (H¹)
 QVELVESGGG LVQPGGSLRL SCAASGFTFS SYAMSWVRQA PGKGLEWVSA 50
 INASGTRTYI ADSVKGRTFI SRDNSKNTLY LQMSLRAED TAVYYCARGK 100
 GNTHKPYGYV RYFDVWGQGT LVTVSSASTK GPSVFPLAPS SKSTSGGTAA 150
 LGCLVEDYFP EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVTVTPSS 200
 SLGTQTYICN VNHKPSNTKV DEKVEPKSCD KTHCTPCPCA PELLGGPSVF 250
 LFPFKPKDTL MISRTPEVTC VVVDVSHEDP EVKFNWYVDG VEVHNAKTKP 300
 REEQYNSTYR VVSVLTVLHQ DWLNGKEYKC KVSNKALPAP IEKTIKAKG 350
 QPREPQVYTL PFCRDELTRN QVSLWCLVKG FYPSDIAVEW ESNQGPENNY 400
 KTFPFLVDSG GSFFLYSKLT VDKSRWQQGN VFSCSVMHEA LHNHYTQKSL 450
 SLSFPGK 456

Light chain / Chaîne légère / Cadena ligera: kappa, anti-APP Abeta 140/42 (L, L¹)
 DIVLTQSPAT LSLSPGERAT LSCRASQSVS SSYLAWYQQK PGQAPRLLIY 50
 GASSRATGVP ARFSGSGSGT DFTLTISLSE PEDFATYYCL QIYNMPTFG 100
 QGTKVEIKRT VAAPSVFIFP FSDRKLKSGT ASVVCLLNFF YPREAKVQWK 150
 VDNALQSGNS QESVTEQDSK DSTYSLSTL TLSKADYKHK VYACEVTHQ 200
 GLSSPVTKSF NRGEC 215

Light chain / Chaîne légère / Cadena ligera: V kappa-CH1, anti-TFRC (L¹)
 AIQLTQSPSS LSASVGDRTV ITCRASQSVS SYLAWYQQK GKAPKLLIYR 50
 ASTLASGVPS RFSGSGSGTD FTLTISLQPE EDFATYYCQQ NYASSNVNDT 100
 FGGGKVEIK SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT 150
 VSWNSGALTS GVHTFPVAVLQ SSGLYLSSV VTVPSSSLGT QTYICNVNHK 200
 PSNTKVDKVV EPKSC 215

Post-translational modifications

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
 Intra-H (C23-C104) 22-96 153-209 270-330 376-434 494-565 622-682
 22"-96" 153"-209" 270"-330" 376"-434"
 Intra-L (C23-C104) 23"-89" 135"-195"
 23"-89" 135"-195"
 23"-88" 139"-195"
 Inter-H-L (h 5-CL 126) 229-215" 229"-215" (CL126-h 5) 702-215"
 Inter-H-H (h 11, h 14) 235-235" 238-238" (CH3 S10>C- CH3 Y5>C) 363-358"

N-terminal glutaminyl cyclization / Cyclisation du glutaminyle N-terminal / Ciclación del glutaminilo N-terminal
 H VH Q1 > pyroglutamyl (pE, 5-oxopropyl): 1, 1"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
 H VH N57: 52, 52"
 Glycosylated / glycosylé / glicosilado
 H CH2 N84.4: 306, 306"

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

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

tulmimetostatum

tulmimetostat

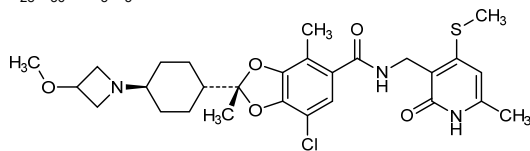
(2*R*)-7-chloro-2-[*trans*-4-(3-methoxyazetidín-1-yl)cyclohexyl]-2,4-diméthyl-*N*-{[6-méthyl-4-(méthylsulfanyl)-2-oxo-1,2-dihydropyridín-3-yl]méthyl}-2*H*-1,3-benzodioxole-5-carboxamide

tulmimétostat

(2*R*)-7-chloro-2-[*trans*-4-(3-méthoxyazétidín-1-yl)cyclohexyl]-2,4-diméthyl-*N*-{[6-méthyl-4-(méthylsulfanyl)-2-oxo-1,2-dihydropyridín-3-yl]méthyl}-2*H*-1,3-benzodioxole-5-carboxamide

tulmimetostat

(2*R*)-7-cloro-2,4-dimetil-*N*-{[6-metil-4-(metilsulfanil)-2-oxo-1,2-dihidropiridin-3-il]metil}-2-[*trans*-4-(3-metoxiazetidín-1-il)ciclohexil]-2*H*-1,3-benzodioxol-5-carboxamida

**ulixacaltamidum**

ulixacaltamide

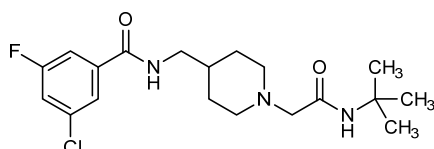
N-({1-[2-(*tert*-butylamino)-2-oxoethyl]piperidin-4-yl)methyl}-3-chloro-5-fluorobenzamide

ulixacaltamide

N-({1-[2-(*tert*-butylamino)-2-oxoéthyl]pipéridin-4-yl)méthyl}-3-chloro-5-fluorobenzamide

ulixacaltamida

N-({1-[2-(*terc*-butilamino)-2-oxoetil]piperidin-4-il}metil)-3-cloro-5-fluorobenzamida

**utatrectinibum**

utatrectinib

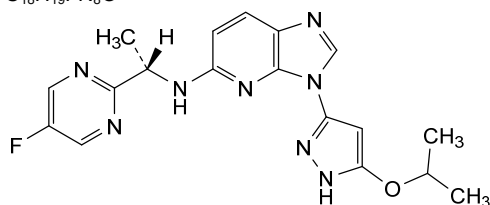
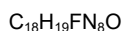
N-[(1*S*)-1-(5-fluoropyrimidin-2-yl)ethyl]-3-{5-[(propan-2-yl)oxy]-1*H*-pyrazol-3-yl}-3*H*-imidazo[4,5-*b*]pyridin-5-amine

utatrectinib

N-[(1*S*)-1-(5-fluoropyrimidin-2-yl)éthyl]-3-{5-[(propan-2-yl)oxy]-1*H*-pyrazol-3-yl}-3*H*-imidazo[4,5-*b*]pyridin-5-amine

utatrectinib

N-[(1*S*)-1-(5-fluoropirimidin-2-il)etil]-3-{5-[(propan-2-il)oxi]-1*H*-pirazol-3-il}-3*H*-imidazo[4,5-*b*]piridin-5-amina

**utreglutidum**

utreglutide

$N^{6,20}$ -[(16*S*)-16,34-dicarboxy-11,11-dimethyl-10,13,18-trioxo-3,6-dioxo-9,12,17-triazatetraatriacontan-1-oyl]-[Ala⁸>Aib², Lys³⁴>Arg²⁸]-glucagon-like peptide 1 (GLP-1, human) (7-37)-peptidyl-L-leucine; L-histidyl-2-methylalanyl-L-α-glutamylglycyl-L-threonyl-L-phenylalanyl-L-threonyl-L-seryl-L-α-aspartyl-L-valyl-L-seryl-L-seryl-L-tyrosyl-L-leucyl-L-α-glutamylglycyl-L-glutaminy-L-alanyl-L-alanyl- N^6 -{*N*-(17-carboxyheptadecanoyl)-L-γ-glutamyl-2-methylalanyl-2-[2-(2-aminoethoxy)ethoxy]acetyl}-L-lysyl-L-α-glutamyl-L-phenylalanyl-L-isoleucyl-L-alanyl-L-tryptophyl-L-leucyl-L-valyl-L-arginylglycyl-L-arginylglycyl-L-leucine

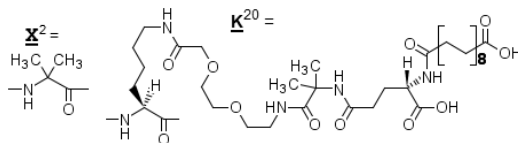
utréglutide $N^{6,20}$ -[[16S]-16,34-dicarboxy-11,11-diméthyl-10,13,18-trioxo-3,6-dioxa-9,12,17-triazatétratriacontan-1-oil]-[Ala⁶>Aib², Lys³⁴>Arg²⁸]-peptide 1 semblable au glucagon (GLP-1, humain) (7-37)-peptidyl-L-leucine;
L-histidyl-2-méthylalanyl-L- α -glutamylglycyl-L-thréonyl-L-phénylalanyl-L-thréonyl-L-séryl-L- α -aspartyl-L-valyl-L-séryl-L-séryl-L-tyrosyl-L-leucyl-L- α -glutamylglycyl-L-glutamyl-L-alanyl-L-alanyl- N^6 -{N-(17-carboxyheptadécanoil)-L- γ -glutamyl-2-méthylalanyl-2-[2-(2-aminoéthoxy)éthoxy]acétyl)-L-lysyl-L- α -glutamyl-L-phénylalanyl-L-isoleucyl-L-alanyl-L-tryptophyl-L-leucyl-L-valyl-L-arginylglycyl-L-arginylglycyl-L-leucine

utreglutida $N^{6,20}$ -[[16S]-16,34-dicarboxi-11,11-dimetil-10,13,18-trioxo-3,6-dioxa-9,12,17-triazatétratriacontan-1-oil]-[Ala⁶>Aib², Lis³⁴>Arg²⁸]-péptido 1 semejante al glucagón (GLP-1, humano) (7-37)-peptidil-L-leucina;
L-histidil-2-metilalanyl-L- α -glutamilglicil-L-treonil-L-fenilalanyl-L-treonil-L-seril-L- α -aspartil-L-valil-L-seril-L-seril-L-tirosil-L-leucil-L- α -glutamilglicil-L-glutamini-L-alanyl-L-alanyl- N^6 -{N-(17-carboxiheptadecanoil)-L- γ -glutamil-2-metilalanyl-2-[2-(2-aminoetoxi)etoxi]acetil)-L-lisil-L- α -glutamil-L-fenilalanyl-L-isoleucil-L-alanyl-L-triptofil-L-leucil-L-valil-L-arginilglicil-L-arginilglicil-L-leucina



Sequence / Séquence / Secuencia:

H^XEGTFTSDV SSYLEGQAA^K EPIAWLVRGR GL 32



valiltramiprosatum

valiltramiprosate

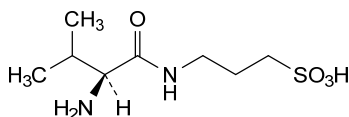
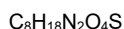
3-[(2S)-2-amino-3-methylbutanamido]propane-1-sulfonic acid

valiltramiprosate

acide 3-[(2S)-2-amino-3-méthylbutanamido]propane-1-sulfonique

valiltramiprosato

ácido 3-[(2S)-2-amino-3-metilbutanamido]propano-1-sulfónico



vanzacافتور

vanzacافتور

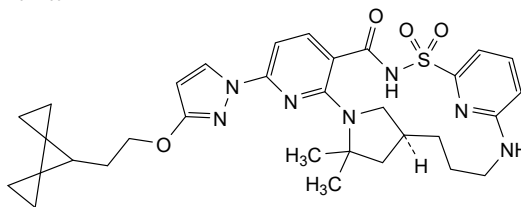
(1³S)-2⁶-{3-[2-(dispiro[2.0.2.1]heptan-7-yl)ethoxy]-1H-pyrazol-1-yl]-1⁵,1⁵-diméthyl-5 λ^6 -thia-4,7-diaza-2(2,3),6(2,6)-dipyridina-1(1,3)-pyrrolidinacyclodécaphane-3,5,5-trione

vanzacافتور

(1³S)-2⁶-{3-[2-(dispiro[2.0.2.1]heptan-7-yl)éthoxy]-1H-pyrazol-1-yl]-1⁵,1⁵-diméthyl-5 λ^6 -thia-4,7-diaza-2(2,3),6(2,6)-dipyridina-1(1,3)-pyrrolidinacyclodécaphane-3,5,5-trione

vanzacaftor

(1³S)-2⁶-[3-[2-(dispiro[2.0.2.1]heptan-7-il)etoxil]-1*H*-pirazol-1-il]-1⁵,1⁵-dimetil-5λ⁶-tia-4,7-diaza-2(2,3),6(2,6)-dipiridina-1(1,3)-pirrolidinaciclodecafan-3,5,5-triona

C₃₂H₃₉N₇O₄S**vicasinabinum**

vicasinabin

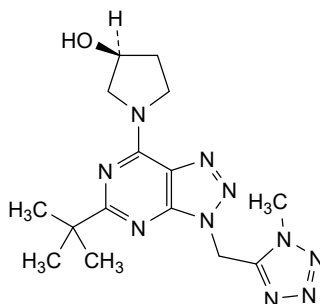
(3*S*)-1-[5-*tert*-butyl-3-[(1-metil-1*H*-tetrazol-5-yl)methyl]-3*H*-[1,2,3]triazolo[4,5-*d*]pirimidin-7-yl]pyrrolidin-3-ol

vicasinabine

(3*S*)-1-[5-*tert*-butyl-3-[(1-méthyl-1*H*-tétrazol-5-yl)méthyl]-3*H*-[1,2,3]triazolo[4,5-*d*]pyrimidin-7-yl]pyrrolidin-3-ol

vicasinabina

(3*S*)-1-[5-*terc*-butil-3-[(1-metil-1*H*-tetrazol-5-il)metil]-3*H*-[1,2,3]triazolo[4,5-*d*]pirimidin-7-il]pirrolidin-3-ol

C₁₅H₂₂N₁₀O**visugromabum #**

visugromab

immunoglobulin G4-kappa, anti-[*Homo sapiens* GDF15 (growth differentiation factor 15, PLAB, MIC-1, PDF, MIC1, NAG-1, PTGFB)], monoclonal antibody; gamma4 heavy chain (1-444) [VH (*Homo sapiens* IGHV2-5*02 (92.9%) -(IGHD)-IGHJ4*01 (100%), CDR-IMGT [10.7.10] (26-35.53-59.98-107)) (1-118)-*Homo sapiens* IGHG4*01, G4v5 h P10 (CH1 (119-216), hinge 1-12 S10>P (226) (217-228), CH2 (229-338), CH3 (339-443), CHS K2>del (444)) (119-444)], (201-214')-disulfide with kappa light chain (1'-214') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV6-15*01 (82.1%) -IGKJ2*01 (100%)/*Homo sapiens* IGKV1-9*01 (76.8%) -IGKJ2*01 (91.7%) Q120>G (100), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (224-224":227-227")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1SV lacking the glutamine synthetase (GS-KO) gene, glycoform alfa

visugromab

immunoglobuline G4-kappa, anti-[*Homo sapiens* GDF15 (facteur 15 de croissance et de différenciation, PLAB, MIC-1, PDF, MIC1, NAG-1, PTGFB)], anticorps monoclonal; chaîne lourde gamma4 (1-444) [VH (*Homo sapiens* IGHV2-5*02 (92.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [10.7.10] (26-35.53-59.98-107)) (1-118)-*Homo sapiens* IGHG4*01, G4v5 h P10 (CH1 (119-216), charnière 1-12 S10>P (226) (217-228), CH2 (229-338), CH3 (339-443), CHS K2>del (444)) (119-444)], (201-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV6-15*01 (82.1%) -IGKJ2*01 (100%)/*Homo sapiens* IGKV1-9*01 (76.8%) -IGKJ2*01 (91.7%) Q120>G (100), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (224-224":227-227")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1SV ne présentant pas le gène de la glutamine synthétase (GS-KO), glycoforme alfa

visugromab

inmunoglobulina G4-kappa, anti-[*Homo sapiens* GDF15 (factor 15 de crecimiento y de diferenciación, PLAB, MIC-1, PDF, MIC1, NAG-1, PTGFB)], anticuerpo monoclonal; cadena pesada gamma4 (1-444) [VH (*Homo sapiens* IGHV2-5*02 (92.9%) -(IGHD) -IGHJ4*01 (100%), CDR-IMGT [10.7.10] (26-35.53-59.98-107)) (1-118) -*Homo sapiens* IGHG4*01, G4v5 h P10 (CH1 (119-216), bisagra 1-12 S10>P (226) (217-228), CH2 (229-338), CH3 (339-443), CHS K2>del (444)) (119-444)], (201-214')-disulfuro con la cadena ligera kappa (1'-214') [V-KAPPA Musmus/Homsap (*Mus musculus* IGKV6-15*01 (82.1%) -IGKJ2*01 (100%)/*Homo sapiens* IGKV1-9*01 (76.8%) -IGKJ2*01 (91.7%) Q120>G (100), CDR-IMGT [6.3.9] (27-32.50-52.89-97)) (1'-107') -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (224-224":227-227")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1SV en ausencia del gen glutamina sintetasa (GS-KO), forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

```

QITLKESGPT LVKPTQTLTL TCTFSGFSL S TSGMGVSWIR QPPGKGLEWL 50
AHLYWDDDKR YNPTLKSRLT ITKDPSKNQV VLTMTNMDPV DTATYYCARS 100
SYGAMDYWGQ GTLVTVSSAS TRGPFVFLA PCSRSTSEST AALGCLVKDY 150
FPFPTVSWN SGALTSVGHV FPAVLQSSGL YSLSSVTVTP SSSLGKTYT 200
CNVDHKFSNT KVDRKVESKY GPCCPPCPAP EFLGGSPVFL FPPKPKDTLM 250
ISRTPEVTCV VVDVSDQEDPE VQFNWYVDGV EVHNAKTFR EEQFNSTYRV 300
VSLTVLHQD WLNKKEYKCK VSNKGLPSSI EKTISKARGQ PREPQVYTLF 350
PSQEEMTKNQ VSLTCLVKGF YPSDIAWEVE SNGQPENNYK TTPPELSDG 400
SFFLYSRLTV DKSRWQEGNV FSCSVMHEAL HNHYTEKQSL LSLG 444
    
```

Light chain / Chaîne légère / Cadena ligera

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DIVLTQSPSF LSASVGRVIT ITCKASQNWG TNVAWFQKPK GKSPKALIYS 50
ASYRYSQVDP RFTGSGSGTE FTLTISLQF EDFAAVFCQQ YNNFPYTFGG 100
GKTLKIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNIFY PREAKVQKVK 150
DNALQSGNSQ ESVTEQDSKD STYLSLSTLT LSKADYERKH VYACEVTHQG 200
LSSPFTKSFN RGEC 214
    
```

Post-translational modifications

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

Intra-H (C23-C104) 22-97 145-201 259-319 365-423
 22"-97" 145"-201" 259"-319" 365"-423"
 Intra-L (C23-C104) 23'-88" 134'-194"
 23"'-88"' 134"'-194"
 Inter-H-L (CH1 10-CL 126) 132-214' 132"-214"
 Inter-H-H (h 8, h 11) 224-224" 227-227"

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

HVH Q1 > pyroglutamyl (pE, 5-oxoprollyl): 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 biantennarios complejos fucosilados.

vixicovtogenum oboplasmidum #

vixicovtogene oboplasmid DNA plasmid encoding a codon-optimized full-length SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2) spike (S) glycoprotein (sequence based upon the SARS-CoV-2 isolate Wuhan-Hu-1 complete genome, GenBank: MN908947.3), including the S glycoprotein signal peptide, under control of the cytomegalovirus (CMV) immediate early promoter and bovine growth hormone polyadenylation (bGH polyA) signal. The plasmid also contains a pUC origin of replication and a *neomycin/kanamycin* antibiotic resistance gene.

vixicovtogène oboplasmide plasmide d'ADN codant la séquence entière aux codons optimisés de la glycoprotéine du spicule (S) SRAS-CoV-2 (coronavirus 2 du syndrome respiratoire aigu sévère) (séquence basée sur le génome complet de l'isolat Wuhan-Hu-1 de SARS-CoV-2, GenBank: MN908947.3), y compris le peptide signal de la glycoprotéine S, sous le contrôle du promoteur précoce immédiat du cytomégalovirus (CMV) et du signal de polyadénylation de l'hormone de croissance bovine (bGH polyA). Le plasmide contient également une origine de réplication pUC et un gène de résistance aux antibiotiques *néomycine/kanamycine*.

vixicovtogen oboplasmida plásmido de DNA que codifica para la glicoproteína de la espícula (S) completa del SRAS-CoV-2 (coronavirus del síndrome respiratorio agudo severo 2), con codones optimizados (secuencia basada en el genoma completo del aislado de SARS-CoV-2 Wuhan-Hu-1, GenBank: MN908947.3), incluyendo el péptido señal de la glicoproteína S, bajo el control del promotor inmediato temprano del citomegalovirus (CMV) y la señal de poliadenilación de la hormona de crecimiento bovina (bGH poli A). El plásmido también contiene un origen de replicación pUC y un gen de resistencia a los antibióticos *neomicina/kanamicina*.

vobramitamabum #

vobramitamab immunoglobulin G1-kappa, anti-[*Homo sapiens* CD276 (B7H3, B7-H3, B7-related protein 2, B7RP2, B7RP-2, B7 homolog 3, B7 homologue 3)], humanized monoclonal antibody; gamma1 heavy chain humanized (1-447) [VH (*Homo sapiens* IGHV3-7*01 (89.8%) -(IGHD) -IGHJ6*01 (92.9%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 (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)], (220-215)-disulfide with kappa light chain humanized (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (86.3%) -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 (226-226":229-229")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-S, glycoform alfa

vobramitamab immunoglobuline G1-kappa, anti-[*Homo sapiens* CD276 (B7H3, B7-H3, protéine 2 liée à B7, B7RP2, B7RP-2, B7 homolog 3, B7 homologue 3)], anticorps monoclonal humanisé;

vobramitamab

chaîne lourde gamma1 humanisée (1-447) [VH (*Homo sapiens* IGHV3-7*01 (89.8%) -(IGHD) -IGHJ6*01 (92.9%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 (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)], (220-215')-disulfure avec la chaîne légère kappa humanisée (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (86.3%) -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 (226-226":229-229")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-S, glycoforme alfa

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CD276 (B7H3, B7-H3, proteína 2 de unión al B7, B7RP2, B7RP-2, B7 homólogo 3, B7 homólogo 3)], anticuerpo monoclonal humanizado; cadena pesada gamma1 humanizada (1-447) [VH (*Homo sapiens* IGHV3-7*01 (89.8%) -(IGHD) -IGHJ6*01 (92.9%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 (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)], (220-215')-disulfuro con la cadena ligera kappa humanizada (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (86.3%) -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 (226-226":229-229")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-S, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada

EVQLVESGGG	LVKPGGSLRL	SCAASGFTFS	SYGMSWVRQA	PGKLEWVAT	50
INSGGSNTYY	PDSLKGRFTI	SRDNAKNSLY	LQMSLRAED	TAVYICARHD	100
GGAMDYWGQG	TTVTYSSAST	KGPSVFPLAP	SSKSTSSGTA	ALGCLVKDYF	150
PEPFTVSWNS	GALTSGVHTF	PAVLQSSGLY	SLSSVTVTPS	SSLGTQTYIC	200
NVNHKPSNTR	VDRKRVKPKS	DKTHTCPPCP	APELLGGPFS	FLFPPKPKDT	250
LMISRTPEVT	CVVVDVSHED	FEVKENWYVD	GVEVHNAKTK	FREEQINSTY	300
RVVSVLTVLH	QDWLNGKEYK	CKVSNKALPA	PIEKTIKAK	GQPREPQVYT	350
LPPSREEMTK	NQVSLTCLVK	GFYPSDIAVE	WESNGQPENN	YKTPPVLDS	400
DGSFFLYSKL	TVDKSRWQGG	NVFSCSVMEH	ALHNHYTQKS	LSSLSPGK	447

Light chain / Chaîne légère / Cadena ligera

DIQMTQSPSS	LSASVGRDRT	ITCRASESIY	SYLAWYQQKQ	GKAPKLLVYN	50
TKTLPEGVPS	RFGSGSGSDT	FTLTISLQOP	EDFATYYCQH	HYGTPPWFQ	100
QGTRLEIKRT	VAAPSVFIFP	PSDEQLKSGT	ASVVCCLNFF	YPREAKVQWK	150
VDNALQSGNS	QESVTEQDSK	DSTYLSSTLT	TLSKADYEKH	KVYACEVTHQ	200
GLSSPVTKSF	NRGEC				215

Post-translational modifications

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

Intra-H (C23-C104) 22-96 144-200 261-321 367-425
 22"-96" 144"-200" 261"-321" 367"-425"

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

Inter-H-L (h 5-CL 126) 220-215' 220"-215"

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

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 biantennarios complejos fucosilados.

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

vobramitamabum duocarmazinum

vobramitamab duocarmazine

immunoglobulin G1-kappa, anti-[*Homo sapiens* CD276 (B7H3, B7-H3, B7-related protein 2, B7RP2, B7RP-2, B7 homolog 3, B7 homologue 3)], humanized monoclonal antibody, conjugated to the pro-drug seco-duocarmycin-*p*-hydroxybenzamide-azaindole (seco-DUBA) via a linker; gamma1 heavy chain humanized (1-447) [VH (*Homo sapiens* IGHV3-7*01 (89.8%) -(IGHD) -IGHJ6*01 (92.9%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 (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)], (220-215')-disulfide with kappa light chain humanized (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (86.3%) -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 (226-226''-229-229'')-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-S, glycoform alfa, conjugated on an average of 2.7 cysteines, to seco-DUBA via the cleavable linker *N*-[2-(2-maleimidoethoxy)ethoxy-carbonyl]-L-valyl-L-citrullyl-*p*-aminobenzoyloxycarbonyl-*N*-[2-(2-hydroxyethoxy)ethyl]-*N*-[2-(methylamino)ethyl]carbamoil
 For the duocarmazine part, please refer to the Proposed INN List 115, published in the WHO Drug Information, Vol.30, No.2, 2016.

vobramitamab duocarmazine

immunoglobuline G1-kappa, anti-[*Homo* CD276 (B7H3, B7-H3, protéine 2 liée à B7, B7RP2, B7RP-2, B7 homolog 3, B7 homologue 3)], anticorps monoclonal humanisé, conjugué à la pro-drogue séco-duocarmycine-*p*-hydroxybenzamide-azaindole (séco-DUBA) via un linker; chaîne lourde gamma1 humanisée (1-447) [VH (*Homo sapiens* IGHV3-7*01 (89.8%) -(IGHD) -IGHJ6*01 (92.9%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)) (1-117) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 (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)], (220-215')-disulfure avec la chaîne légère kappa humanisée (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (86.3%) -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 (226-226''-229-229'')-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-S, glycoforme alfa, conjugué sur une moyenne de 2,7 cystéines au séco-DUBA via le linker clivable *N*-[2-(2-maléimidoéthoxy)éthoxy-carbonyl]-L-valyl-L-citrullyl-*p*-aminobenzoyloxycarbonyl-*N*-[2-(2-hydroxyéthoxy)éthyl]-*N*-[2-(méthylamino)éthyl]carbamoyle
 Pour la partie duocarmazine, veuillez-vous référer à la Liste 115 des DCI proposées, publiée dans le WHO Drug Information, Vol.30, No.2, 2016.

vobramitamab duocarmazina

immunoglobulina G1-kappa, anti-[*Homo* CD276 (B7H3, B7-H3, proteína 2 de unión con B7, B7RP2, B7RP-2, B7 homólogo 3, B7 homólogo 3)], anticuerpo monoclonal humanizado, conjugado con el profármaco seco-duocarmicina-*p*-hidroxibenzamida-azaindol (seco-DUBA) a través de un enlace;

cadena pesada gamma1 humanizada (1-447) [VH (*Homo sapiens* IGHV3-7*01 (89.8%) -(IGHD) -IGHJ6*01 (92.9%), CDR-IMGT [8.8.10] (26-33.51-58.97-106)] (1-117) -*Homo sapiens* IGHG1*03 (100%), G1m3, nG1m1 (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)], (220-215')-disulfuro con la cadena ligera kappa humanizada (1'-215') [V-KAPPA (*Homo sapiens* IGKV1-39*01 (86.3%) -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 (226-226":229-229")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-S, forma glicosilada alfa, conjugado en 2.7 cisteínas, por término medio, con seco-DUBA mediante el enlace escindible *N*-[2-(2-maleimidoetoxi)etoxicarbonil]-L-valil-L-citrulil-*p*-aminobenciloicarbonyl-*N*-[2-(2-hidroxi)etil]-*N*-[2-(metilamino)etil]carbamoilo

Para la parte duocarmazina, por favor vaya a la Lista 115 de los DCI propuestas, publicada en el WHO Drug Information, Vol.30, No.2, 2016.

Heavy chain / Chaîne lourde / Cadena pesada

EVQLVESGGG	LVPKGGSLRL	SCAASGFFFS	SYGMSWVRQA	PGKLEWVAT	50
INSGGSNTYY	PDSLKGRFTI	SRDNAKNSLY	LQMNLSRAED	TAVYYCARHD	100
GGAMDYWGQG	TVTIVSSAST	KGPSVFFLAP	SSKSTSGGTA	ALGCLVKDYF	150
PEPVTIVSWNS	GALTSVGHTE	PAVLQSSGLY	SLSSVVTVPS	SSLGTQTYIC	200
NVNHKPSNTK	VDRKVEPKSC	DKTHTCPCCP	APELLGGGFSV	FLFPPKPKDT	250
LMISRTPEVT	CVVVDVSHED	PEVKFNWYVD	GVEVHNAKTK	PREEQYNSTY	300
RVVSVLTVLH	QDWLNGKEYK	CKVSNKALPA	PIEKTIKAKK	GQPREPQVYV	350
LPPSREEMTK	NQVSLTCLVK	GFYPDIAVE	WESNGQPENN	YKTTTPVLDS	400
DGSFFLYSKL	TVDKSRWQQG	NVFSCSVHME	ALHNHYTQKS	LSSLSPGK	447

Light chain / Chaîne légère / Cadena ligera

DIQMTQSPSS	LSASVGRDRT	ITCRASESIY	SYLAWYQQKFL	GKAPKLLVYN	50
TKTLPEGVFS	RFGSGSGTD	FLFTISLLQP	EDFATYYCQH	HYGTPPWTFG	100
QGTRLEIKRT	VAAPSVFIFF	PSDEQLKSGT	ASVVCLLNFE	YPREAKVQWK	150
VDNALQSGNS	QESVTEQDSK	DSTYLSSTL	TLSKADYEKH	KVYACEVTHQ	200
GLSSEFVTKSF	NRGEC				215

Post-translational modifications

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

Intra-H (C23-C104) 22"-96" 144"-200" 261"-321" 367"-425"
22"-96" 144"-200" 261"-321" 367"-425"

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

Inter-H-L* (h 5-CL 126) 220-215' 220"-215"

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

*At least two of the four inter-chain disulfide bridges are not present, an average of 2.7 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, 2,7 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 están presentes, una media de 2.7 cisteinil está conjugada a conectores de principio activo.

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

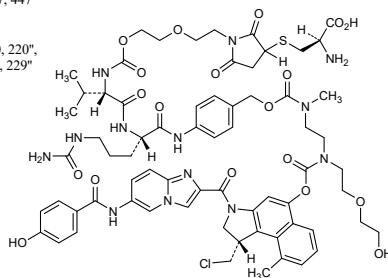
H CH2 N84.4: 297, 297"

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

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

H CHS K2: 447, 447"

C*
215', 215", 220, 220",
226, 226", 229, 229"



volamcabtagenum durzigedleucelum

volamcabtagene durzigedleucel

allogeneic T cells obtained from peripheral blood by leukapheresis, genetically modified by CRISPR/Cas9 (clustered regularly interspaced short palindromic repeats/CRISPR-associated protein 9) mediated gene editing consisting of three guide RNAs (gRNAs) introduced transiently as Cas9-gRNA ribonucleoprotein (RNP) complex for the targeted disruption of the T cell receptor alpha chain constant (TRAC), β_2 microglobulin (B2M) and the cluster of differentiation 70 (CD70) loci and insertion of an anti-CD70 chimeric antigen receptor (CAR) transgene into the TRAC locus via an adeno-associated virus serotype 6 (AAV6) vector. The CAR is composed of a signal peptide sequence from human CD8a, an anti-CD70 single-chain variable fragment (scFv) derived from anti-CD70 hybridoma 1F6, a CD8 hinge and transmembrane domain, and the 4-1BB and CD3 ζ co-stimulatory domains. Expression of the CAR is driven by the elongation factor 1 alpha (EF-1 α) promoter and is terminated by a synthetic polyadenylation (polyA) sequence. The anti-CD70 CAR expression cassette is flanked by two TRAC homology arms guiding the expression cassette to the TRAC locus.

The leukapheresis material is enriched for T cells using CD4/CD8 selection and activated with anti-CD3/CD28 antibody-coated beads. T cells are cultured in the presence of growth media containing human serum, interleukin 2 (IL-2) and 7 (IL-7). The final T cells are $\geq 30\%$ CAR+ T cells, $\leq 0.4\%$ TCR+, $\leq 2\%$ CD70+, and $\leq 30\%$ B2M+ and secrete interferon gamma (IFN γ) and IL-2 when co-cultured with CD70 expressing cells.

volamcabtagène durzigedleucel

lymphocytes T allogéniques obtenus à partir de sang périphérique par leucaphérèse, génétiquement modifiés par édition génique médiée par CRISPR/Cas9 (courtes répétitions palindromiques groupées et régulièrement espacées / protéine 9 associée à CRISPR) consistant en trois ARN guides (ARNg) introduits de manière transitoire sous forme de complexe ribonucléoprotéique (RNP) Cas9-ARNg pour la rupture ciblée des loci de la partie constante de la chaîne alpha du récepteur des lymphocytes T (TRAC), de la β_2 microglobuline (B2M) et le cluster de différenciation 70 (CD70), et l'insertion d'un transgène du récepteur antigénique chimérique (CAR) anti-CD70 dans le locus TRAC via un vecteur du virus adéno-associé de sérotype 6 (AAV6). Le CAR est composé d'une séquence peptidique signal provenant du CD8a humain, d'un fragment variable à chaîne unique (scFv) anti-CD70 dérivé de l'hybridome 1F6 anti-CD70, d'un domaine transmembranaire et charnière CD8, ainsi que les domaines costimulateurs 4-1BB et CD3 ζ . L'expression du CAR est dirigée par le promoteur du facteur d'élongation 1 alpha (EF-1 α) et est terminée par une séquence synthétique de polyadénylation (polyA). La cassette d'expression du CAR anti-CD70 est flanquée de deux bras d'homologie TRAC guidant la cassette d'expression vers le locus TRAC.

Le matériel de leucophérèse est enrichi en lymphocytes T par sélection CD4/CD8 et activé par des billes recouvertes d'anticorps anti-CD3/CD28. Les lymphocytes T sont cultivés en présence de milieu de croissance contenant du sérum humain, de l'interleukine 2 (IL-2) et 7 (IL-7). Les lymphocytes T finaux sont $\geq 30\%$ de lymphocytes T CAR+, $\leq 0,4\%$ de TCR+, $\leq 2\%$ de CD70+ et $\leq 30\%$ de B2M+ et sécrètent de l'interféron gamma (IFN γ) et de l'IL-2 lorsqu'ils sont co-cultivés avec des cellules exprimant CD70.

volamcabtágén durzigeleucel

linfocitos T alogénicos obtenidos de sangre periférica por leucoaféresis, modificados genéticamente mediante edición génica mediada por CRISPR/Cas9 (repeticiones palindrómicas cortas agrupadas y espaciadas regularmente /proteína asociada a CRISPR 9) consistente en tres RNAs guía (sgRNA) introducidos transitoriamente como un complejo de ribonucleoproteína (RNP) Cas9-gRNA para la ruptura dirigida del locus de la cadena constante alfa del receptor de linfocitos T (TRAC), el locus de la β_2 microglobulina (B2M) y el locus del grupo de diferenciación 70 (CD70) y la inserción de un transgén de receptor de antígenos quimérico (CAR) anti-CD70 en el locus TRAC mediante un vector de virus adenoasociado de serotipo 6 (AAV6). El CAR está compuesto por una secuencia de péptido señal del CD8a humano, un fragmento variable de cadena sencilla (scFv) anti-CD70 derivado del hibridoma anti-CD70 1F6, una bisagra y un dominio transmembrana de CD8 y los dominios coestimuladores de 4-1BB y CD3 ζ . La expresión del CAR está dirigida por el promotor del factor de elongación 1 alfa (EF-1 α) y terminada por una secuencia de poliadenilación (polyA) sintética. El casete de expresión del CAR anti-CD70 está flanqueado por dos brazos de homología TRAC que guían al casete de expresión al locus TRAC.

El material de leucoaféresis se enriquece para linfocitos T usando selección de CD4/CD8 y se activan con bolas forradas de anticuerpos anti-CD3/CD28. Las linfocitos T se cultivan en presencia de medio de crecimiento que contiene suero humano e interleuquinas 2 (IL-2) y 7 (IL-7). Las linfocitos T finales son $\geq 30\%$ linfocitos T CAR+, $\leq 0.4\%$ TCR+, $\leq 2\%$ CD70+ y $\leq 30\%$ B2M+, y secretan interferon gamma (IFN γ) e IL-2 cuando se cocultivan con células que expresan CD70.

voxxogananum

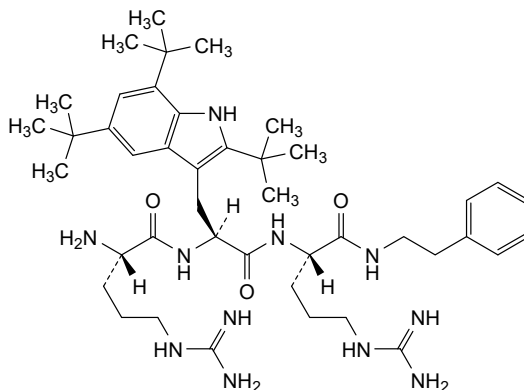
voxxoganan

L-arginyl-2,5,7-tri-*tert*-butyl-L-tryptophyl-*N*¹-(2-phenylethyl)-L-argininamide

voxxoganan

L-arginyl-2,5,7-tri-*tert*-butyl-L-tryptophyl-*N*¹-(2-phényléthyl)-L-argininamide

voxxoganáń

L-arginil-2,5,7-tri-*tert*-butil-L-triptofil-*N*¹-(2-feniletíl)-L-argininamidaC₄₃H₆₉N₁₁O₃

vurolenatidium

vurolenatide

exendin 4 (*Heloderma suspectum*, Gila monster lizard) (1-39) fused via a Gly-Gly dipeptide linker (40-41) to an artificial hydrophilic protein (864-peptide, 42-905) comprising 72 randomly repeating dodecapeptides (4 types of A₁E₂G₂P₂S₃T₂), produced in *Escherichia coli*

vurolénatide

exendine 4 (*Heloderma suspectum*, lézard monstre de Gila) (1-39), fusionnée via un dipeptide Gly-Gly liant (40-41) à une protéine hydrophile artificielle (864-peptide, 42-905) comprenant 72 dodécapeptides à répétition aléatoire (4 types d'A₁E₂G₂P₂S₃T₂), produite dans *Escherichia coli*

vurolenatida

exendina 4 (*Heloderma suspectum*, lagarto monstruo de Gila) (1-39), fusionada a través de un dipéptido de unión (40-41) a una proteína hidrófila artificial (864-péptido, 42-905) que comprende 72 dodecapéptidos que se repiten aleatoriamente (4 tipos de A₁E₂G₂P₂S₃T₂), producida en *Escherichia coli*

Sequence / Séquence / Secuencia

```
HGEGTFTSDL SKQMEEEAVR LFIEWLKNKG PSSGAPPPSG GSPAGSPTST 50
EEGTSESATP ESGPGTSTEP SEGSAFSGPA GSPTSTEEGT STEPSEGSAP 100
GTSTEPSEGS APGTSESATP ESGPGSEPAT SGSETPGSEP ATSGSETPGS 150
PAGSPTSTEE GTSESATPES GPGTSTEPSE GSAPGTSTEP SEGSAFSGPA 200
GSPTSTEEGT STEPSEGSAP GTSTEPSEGS APGTSESATP ESGPGTSTEP 250
SEGSAFPTSE SATPESGPGS EPATSGSETP GTSTEPSEGS APGTSTEPSE 300
GSAPGTSESA TPESGPGTSE SATPESGPGS PAGSPTSTEE GTSESATPES 350
GPGSEPATSG SETPGTSESA TPESGPGTST EPSEGSAPGT STEPSEGSAP 400
GTSTEPSEGS APGTSTEPSE GSAPGTSTEP SEGSAFPTST EPSEGSAPGS 450
PAGSPTSTEE GTSTEPSEGS APGTSESATP ESGPGSEPAT SGSETPGTSE 500
SATPESGPGS EPATSGSETP GTSESATPES GPGTSTEPSE GSAPGTSESA 550
TPESGPGSPA GSPTSTEEGS PAGSPTSTEE GSPAGSPTST EEGTSESATP 600
ESGPGTSTEP SEGSAFPTSE SATPESGPGS EPATSGSETP GTSESATPES 650
GPGSEPATSG SETPGTSESA TPESGPGTST EPSEGSAPGS PAGSPTSTEE 700
GTSESATPES GPGSEPATSG SETPGTSESA TPESGPGSPA GSPTSTEEGS 750
PAGSPTSTEE GTSTEPSEGS APGTSESATP ESGPGTSESA TPESGPGTSE 800
SATPESGPGS EPATSGSETP GSEPATSGSE TPGSPAGSPT STEEGTSTEP 850
SEGSAFPTST EPSEGSAPGS EPATSGSETP GTSESATPES GPGTSTEPSE 900
GSAPG 905
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vutigliabridinum

vutigliabridin

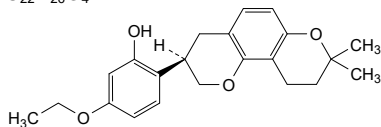
rac-2-[(3*R*)-8,8-dimethyl-3,4,9,10-tetrahydro-2*H*,8*H*-benzo[1,2-*b*:3,4-*b'*]dipyran-3-yl]-5-ethoxyphenol

vutigliabridine

rac-2-[(3*R*)-8,8-diméthyl-3,4,9,10-tétrahydro-2*H*,8*H*-benzo[1,2-*b*:3,4-*b'*]dipyran-3-yl]-5-éthoxyphénol

vutigliabridina

rac-2-[(3*R*)-8,8-dimetil-3,4,9,10-tetrahidro-2*H*,8*H*-benzo[1,2-*b*:3,4-*b'*]dipiran-3-il]-5-etoxifenol

C₂₂H₂₆O₄

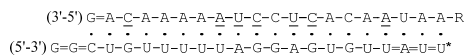
and enantiomer
et énantiomère
y enantiómero

xalnesirán

todo-P-ambo-2'-O-metil-P-tioguanilil-(3'→5')-2'-O-metiladenilil-(3'→5')-2'-desoxi-2'-fluorocitidilil-(3'→5')-2'-O-metiladenilil-(3'→5')-2'-O-metiladenilil-(3'→5')-2'-O-metiladenilil-(3'→5')-2'-O-metiladenilil-(3'→5')-2'-desoxi-2'-fluoroadenilil-(3'→5')-2'-desoxi-2'-fluorouridilil-(3'→5')-2'-desoxi-2'-fluorocitidilil-(3'→5')-2'-O-metilcitidilil-(3'→5')-2'-O-metiladenilil-(3'→5')-2'-desoxi-2'-fluoroadenilil-(3'→5')-2'-O-metiluridilil-(3'→5')-2'-O-metiladenilil-(3'→5')-2'-O-metiladenilil-(3'→5')-2'-O-metilguanilil-(3'→5')-2'-O-metilcitidilil-(3'→5')-2'-O-metilguanilil-(3'→5')-2'-O-metilcitidilil-(3'→5')-2'-O-metilcitidilil-(3'→5')-2'-O-[[2-(2-{5-[[2-(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]pentanamido)etoxi]etoxi]metil]guanilil-(3'→5')-2'-O-[[2-(2-{5-[[2-(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]pentanamido)etoxi]etoxi]metil]adenilil-(3'→5')-2'-O-[[2-(2-{5-[[2-(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]pentanamido)etoxi]etoxi]metil]adenilil-(3'→5')-2'-O-[[2-(2-{5-[[2-(2-acetamido-2-desoxi-β-D-galactopiranosil)oxi]pentanamido)etoxi]etoxi]metil]adenilil-(3'→5')-2'-O-metilguanilil-(3'→5')-2'-O-metilguanilil-(3'→5')-2'-O-metilcitidilil-(3'→5')-2'-O-metiluridilil-(3'→5')-2'-O-metilguanilil-(3'→5')-2'-O-metilcitidina,

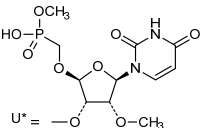
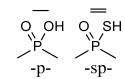
duplex con *todo-P-ambo-2'-O-metil-P-tioguanilil-(5'→3')-2'-O-metil-P-tioguanilil-(5'→3')-2'-O-metilcitidilil-(5'→3')-2'-desoxi-2'-fluorouridilil-(5'→3')-2'-O-metilguanilil-(5'→3')-2'-O-metiluridilil-(5'→3')-2'-desoxi-2'-fluorouridilil-(5'→3')-2'-O-metiluridilil-(5'→3')-2'-desoxi-2'-fluoroadenilil-(5'→3')-2'-O-metilguanilil-(5'→3')-2'-desoxi-2'-fluoroguanilil-(5'→3')-2'-O-metiladenilil-(5'→3')-2'-desoxi-2'-fluoroguanilil-(5'→3')-2'-desoxi-2'-fluorouridilil-(5'→3')-2'-O-metil-P-tiouridilil-(5'→3')-2'-desoxi-2'-fluoro-P-tioadenilil-(5'→3')-2'-desoxi-2'-fluoro-P-tiouridilil-(5'→3')-hidrógeno-2'-O-metil-5'-oxa-O-5'-carba-5'-uridilato de metilo*

C₆₆₄H₈₇₁F₁₇N₂₃₁O₄₁₅P₅₇S₆

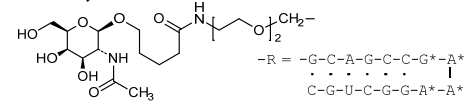


Legend

X̄ : 2'-deoxy-2'-fluoronucleotide / 2'-désoxy-2'-fluoronucléotide / 2'-desoxi-2'-fluoronucleotide
 X : 2'-O-methylnucleotide / 2'-O-méthylnucléotide / 2'-O-metilnucléotide



2'-O-substituent of nucleotides A* & G* / 2'-O-substituant des nucléotides A* & G* / 2'-O-sustituente de nucléotides A* & G*



yttrium (⁹⁰Y) anditixafortidum

yttrium (⁹⁰Y) anditixafortide

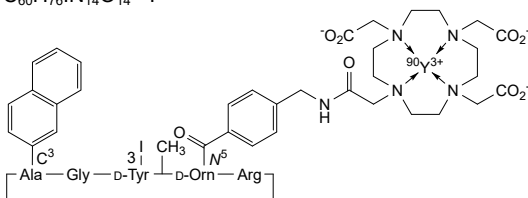
(1,5-anhydro{3-(naphthalen-2-yl)-L-alanylglycyl-3-iodo-D-tyrosyl-N²-methyl-N⁵-[4-({2-[4,7,10-tris(carboxylato-κO-methyl)-1,4,7,10-tetraazadodecan-1-yl-κ^N1,N⁴,N⁷,N¹⁰]acetamido-κO)methyl]benzoyl]-D-ornithyl-L-arginine})(⁹⁰Y)yttrium

yttrium (⁹⁰Y) anditixafortide

(1,5-anhydro{3-(naphtalén-2-yl)-L-alanylglycyl-3-iodo-D-tyrosyl-*N*²-méthyl-*N*⁶-[4-({2-[4,7,10-tris(carboxylato-κO-méthyl)-1,4,7,10-tétrazaadodécane-1-yl-κ⁴*N*¹,*N*⁴,*N*⁷,*N*¹⁰]acétamido-κO)méthyl)benzoyl]-D-ornithyl-L-arginine)})(⁹⁰Y)yttrium

ytrio (⁹⁰Y) anditixafortida

(1,5-anhidro{3-(naftalen-2-il)-L-alanilglicil-3-iodo-D-tirosil-*N*²-metil-*N*⁶-[4-({2-[4,7,10-tris(carboxilato-κO-metil)-1,4,7,10-tetraazadodecane-1-il-κ⁴*N*¹,*N*⁴,*N*⁷,*N*¹⁰]acetamido-κO)metil)benzoi]l]-D-ornitil-L-arginin)})(⁹⁰Y)ytrio

C₆₀H₇₆IN₁₄O₁₄⁹⁰Y**zaftuclenegenum piruparvovecum #**

zaftuclenegene piruparvovec

recombinant, self-complementary (dimeric), non-replicating adeno-associated virus serotype 9 (scAAV9) vector, encoding codon-optimised human palmitoyl-protein thioesterase 1 (PPT1, CLN1), under the control of a synthetic promoter consisting of a cytomegalovirus (CMV) enhancer/chicken β-actin (CBA) promoter and a hybrid intron derived from chicken β-actin and minute virus of mice (MVM) introns, followed by a Kozak sequence, and terminated by a bovine growth hormone (bGH) polyadenylation (polyA) signal; the vector genome contains a mutated adeno-associated virus serotype 2 (AAV2) inverted terminal repeat (mtTR) and is flanked by AAV2 wild-type inverted terminal repeats (wtITRs).

zaftuclénégène piruparvovec

vecteur recombinant, auto-complémentaire (dimère) et non répliquant du virus adéno-associé de sérotype 9 (scAAV9) codant la palmitoyl-protéine thioestérase 1 (PPT1, CLN1) humaine aux codons optimisés, sous le contrôle d'un promoteur synthétique constitué d'un amplificateur du cytomégalovirus (CMV)/promoteur de la β-actin de poulet (CBA) et d'un intron hybride dérivé des introns de la β-actine de poulet et du virus minute de la souris (MVM), suivi d'une séquence Kozak, et terminé par le signal de polyadénylation (polyA) de l'hormone de croissance bovine (bGH); le génome du vecteur contient une répétition terminale inversée mutée (mtTR) du virus adéno-associé de sérotype 2 (AAV2) et est flanqué de répétitions terminales inversées de type sauvage (wtITR) d'AAV2.

zaftuclenegén piruparvovec

vector de virus adenoasociado recombinante, auto complementario (dimérico) de serotipo 9 (scAAV9) no replicativo que codifica para la palmitoil-proteína tioesterasa 1 (PPT1, CLN1) humana, bajo el control de

un promotor sintético consistente en un potenciador del citomegalovirus (CMV)/promotor de la β-actina (CBA) de pollo y un intrón híbrido derivado de intrones de la β-actina de pollo y del virus diminuto de ratones (MMV), seguido de una secuencia Kozak y terminado con una señal de poliadenilación (polyA) de la hormona de crecimiento bovina (bGH); el genoma del vector contiene una repetición terminal invertida mutada (mlTR) del virus adenoasociado de serotipo 2 (AAV2) y está flanqueado por repeticiones terminales invertidas de tipo silvestre (wtITRs) del AAV2.

zagociguatum

zagociguat

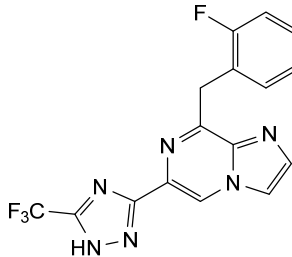
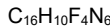
8-[(2-fluorophenyl)methyl]-6-[5-(trifluoromethyl)-1H-1,2,4-triazol-3-yl]imidazo[1,2-a]pyrazine

zagociguat

8-[(2-fluorophényl)méthyl]-6-[5-(trifluorométhyl)-1H-1,2,4-triazol-3-yl]imidazo[1,2-a]pyrazine

zagociguat

8-[(2-fluorofenil)metil]-6-[5-(trifluorometil)-1H-1,2,4-triazol-3-il]imidazo[1,2-a]pirazina



zamaglutenasum #

zamaglutenasase

Alicyclobacillus sendaiensis gliadin peptidase (kumamolysin-A.s. serine endopeptidase, UniProt Q8GB88, EC:3.4.21.B48) engineered variant (N-terminal M removed, V>D¹¹⁸, P>R¹⁷⁰, H>R¹⁷¹, S>E²⁶¹, E>T²⁶⁸, N>D²⁹⁰, D>T²⁹², G>S³¹⁸, G>M³¹⁹, S>Q³⁵³, D>S³⁵⁷, D>H³⁶⁷, D>Q³⁹⁸, A>Q⁴⁴⁸, I>T⁴⁶²), non-glycosylated, produced in *Escherichia coli*;
gliadin peptidase (*Alicyclobacillus sendaiensis*) (kumamolysin-A.s. serine endopeptidase, UniProt Q8GB88, EC:3.4.21.B48) [M⁰>del, V>D¹¹⁸, P>R¹⁷⁰, H>R¹⁷¹, S>E²⁶¹, E>T²⁶⁸, N>D²⁹⁰, D>T²⁹², G>S³¹⁸, G>M³¹⁹, S>Q³⁵³, D>S³⁵⁷, D>H³⁶⁷, D>Q³⁹⁸, A>Q⁴⁴⁸, I>T⁴⁶²]-mutant, non-glycosylated, produced in *Escherichia coli*

zamagluténase

Alicyclobacillus sendaiensis gliadine peptidase (kumamolysine-A.s. endopeptidase à sérine, UniProt Q8GB88, EC:3.4.21.B48) variant modifié (suppression M au N-terminal, V>D¹¹⁸, P>R¹⁷⁰, H>R¹⁷¹, S>E²⁶¹, E>T²⁶⁸, N>D²⁹⁰, D>T²⁹², G>S³¹⁸, G>M³¹⁹, S>Q³⁵³, D>S³⁵⁷, D>H³⁶⁷, D>Q³⁹⁸, A>Q⁴⁴⁸, I>T⁴⁶²), produite dans *Escherichia coli*;

gliadine peptidase (*Alicyclobacillus sendaiensis*) (kumamolysine-A.s. endopeptidase à sérine, UniProt Q8GB88, EC:3.4.21.B48), mutant [M⁰>del, V>D¹¹⁸, P>R¹⁷⁰, H>R¹⁷¹, S>E²⁶¹, E>T²⁶⁸, N>D²⁹⁰, D>T²⁹², G>S³¹⁸, G>M³¹⁹, S>Q³⁵³, D>S³⁵⁷, D>H³⁶⁷, D>Q³⁹⁸, A>Q⁴⁴⁸, I>T⁴⁶²], non glycosylée, produite dans *Escherichia coli*

zamaglutenasas

Alicyclobacillus sendaiensis gliadina peptidasa (kumamolisin-A.s. serina endopeptidasa, UniProt Q8GB88, EC:3.4.21.B48) variant diseñado (N-terminal M eliminado, V>D¹¹⁸, P>R¹⁷⁰, H>R¹⁷¹, S>E²⁶¹, E>T²⁶⁸, N>D²⁹⁰, D>T²⁹², G>S³¹⁸, G>M³¹⁹, S>Q³⁵³, D>S³⁵⁷, D>H³⁶⁷, D>Q³⁹⁸, A>Q⁴⁴⁸, I>T⁴⁶²), no glicosilada, producida en *Escherichia coli*;

gliadina peptidasa (*Alicyclobacillus sendaiensis*) (kumamolisin-A.s. serina endopeptidasa, UniProt Q8GB88, EC:3.4.21.B48), mutante [M⁰>del, V>D¹¹⁸, P>R¹⁷⁰, H>R¹⁷¹, S>E²⁶¹, E>T²⁶⁸, N>D²⁹⁰, D>T²⁹², G>S³¹⁸, G>M³¹⁹, S>Q³⁵³, D>S³⁵⁷, D>H³⁶⁷, D>Q³⁹⁸, A>Q⁴⁴⁸, I>T⁴⁶²], no glicosilada, producida en *Escherichia coli*

Sequence / Séquence / Secuencia

SDMEKFWKEG	EEARAVLQGH	ARAQAPQAVD	KGPVAGDERM	AVTVVLRQR	50
AGELAAHVER	QAATAFHARE	HLKREAFPAAS	HGASLDDFAE	LRRFADAHGL	100
ALDRANVAAG	TAVLSGPDDA	INRAFGVELR	HFDHPDGSYR	SYLGEVTVPA	150
SIAPMIEAVL	GLDTRFPVARE	EFRMQRRAEG	GFEARSAQAA	PTAYTPLDVA	200
QAYQPFEGLD	GQGCCIATIE	LGGGYDEASL	AQYFASLGVP	APQVVSVSVD	250
GASNQPTGDP	ESPDGEVTLD	IEVAGALAPG	AKFAVYFAED	TTAGFLDAIT	300
TAIHDFTLKP	SVVSIWSPMP	EDSWTSAATA	AMNRAFLDAA	ALGVTVLAAA	350
GDQGSSTSGEQ	DGLYHVHPPA	ASPYVLACGG	TRLVASGGRI	AQETVWVNGCP	400
DGGATGGGVS	RIFPLPAWQE	HANVPPSANP	GASSGRGVPE	LAGNADEQDTG	450
YEVVIDGEAT	VTTGGTSAVAP	LFAALVARIN	QKLGKAVGYL	NPTLYQLPAD	500
VEHDITEGNN	DIANRAQIYQ	AGPGWDPCPT	LGSPIGVRL	QALLPSASQP	550
QP					552

Mutation / Mutation / Mutación

M⁰>del, V118>D, P170>R, H171>R, S261>E, E268>T, N290>D, D292>T, G318>S, G319>M, S353>Q, D357>S, D367>H, D398>Q, A448>Q, I462>T

Post-translational modifications

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
none / aucune / ninguna
Glycosylation sites / Sites de glycosylation / Posiciones de glicosilación
none / aucun / ninguna

zelpultidum alfa #
zelpultide alfa

human pulmonary surfactant-associated protein D (PSPD, surfactant protein D, SP-D, collectin-7, surfactant protein D), non-covalent quadruple trimer, produced in human myelogenous leukemia K562 cells, glycoforme alfa;
human pulmonary surfactant protein D (PSPD, pulmonary surfactant-associated protein D, SP-D, lung surfactant protein D, collectin-7, COLEC7, SFTPD, SFTP4), non-covalent quadruple trimer, produced by recombinant human myelogenous leukemia K562 cells engineered for optimized glycosylation, glycoform alfa

zelpultide alfa

protéine D humaine associée au surfactant pulmonaire (PSPD, protéine D du surfactant, SP-D, collectine-7, protéine D du surfactant), quadruple trimère non covalent, produite dans des cellules K562 de leucémie myéloïde humaine, glycoforme alfa;

protéine D humaine du surfactant pulmonaire (PSPD, protéine D associée au surfactant pulmonaire, SP-D, protéine D du surfactant pulmonaire, collectine-7, COLEC7, SFTPD, SFTP4), trimère quadruple non covalent, produite par des cellules humaines recombinantes K562 de leucémie myéloïde conçues pour une glycosylation optimisée, glycoforme alfa

zelpultida alfa

proteína D humana asociada a los surfactantes pulmonares (PSPD, proteína surfactante D, SP-D, colectina-7, surfactante proteína D), trímero no covalente cuádruple, producida en células humanas K562 de la leucemia mielógena, glicoforma alfa; proteína surfactante D humana (PSPD, proteína D asociada con surfactantes pulmonares, SP-D, proteína D del surfactante pulmonar, colectina-7, COLEC7, SFTPD, SFTP4), trímero cuádruple no covalente, producida por células humanas recombinantes K562 de la leucemia mielógena diseñadas para una glicosilación optimizada, glicoforma alfa

Sequence / Séquence / Secuencia

AEMKTYSHRT MPSACTLVMC SSVESGLPGR DGRDREGREP GEKGDPLPG	50
AAGQAGMPGQ AGPVGPKGDN GSVGEPGPKG DTGPGSGPPG PGVPGFAGRE	100
GPLGKQGNIG PQGKPGPKGE AGPKGEVGAP GMQGSAGARG LAGPKGERGV	150
PGERGVPGNT GAAGSAGAMG PQGSPGARGP PGLKGDGIP GDRGAKGESG	200
LPDVASLRQQ VEALQGQVQH LQAAFSQYKK VELFPNGQSV GEKIFKTAGF	250
VKPFTEAQLL CTQAGGQLAS PRSAAENAAL QQLVVAKNEA AFLSMTDSKT	300
EKGFTYPTGE SLVYSNWAPE EPNDGGSED CVELFTNGKW NDRACGEKRL	350
VVCEF	355

Post-translational modifications

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
261-353, 331-345

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
N70

Hydroxylation (Lys→5Hyl, Pro→4Hyp) and O-glycosylation
complete: P28, K145, K184;

partial: K43, P46, P49, P58, K67, P76, K79, P88, P91, P94, P115, K118, K124, P130, P151, P157, P175, P181, P190, K193, K196, P202
(highly sialylated and core-fucosylated complex glycans)

zendusortidum

zendusortide

N-acetylglcyl-L-valyl-L-arginyl-L-alanyl-L-lysyl-L-alanylglcyl-L-valyl-L-arginyl-L-asparaginy-(2S)-2-aminohexanoyl-L-phenylalanyl-L-lysyl-L-seryl-L-α-glutamyl-L-seryl-L-tyrosine

zendusortide

N-acétylglycyl-L-valyl-L-arginyl-L-alanyl-L-lysyl-L-alanylglcyl-L-valyl-L-arginyl-L-asparaginy-(2S)-2-aminohexanoyl-L-phénylalanyl-L-lysyl-L-séryl-L-α-glutamyl-L-séryl-L-tyrosine

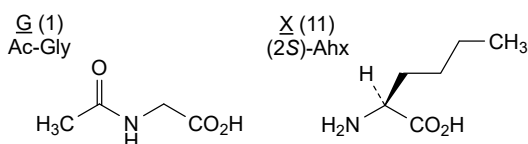
zendusortida

N-acetilglicil-L-valil-L-arginil-L-alanil-L-lisil-L-alanilglicil-L-valil-L-arginil-L-asparaginil-(2S)-2-aminohexanoil-L-fenilalanil-L-lisil-L-seril-L-α-glutamil-L-seril-L-tirosina

C₈₅H₁₃₈N₂₆O₂₅

GVRAKAGVRN XFKSESY 17

Modified residues / Résidus modifiés / Restos modificados



zevaquenabantum

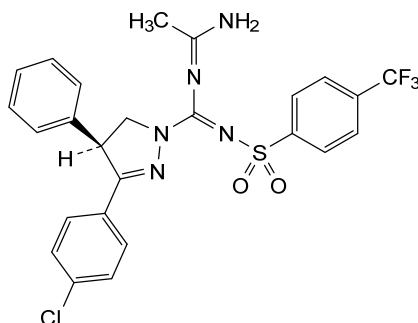
zevaquenabant

(4*S*)-*N*-(1-aminoethylidene)-3-(4-chlorophenyl)-4-phenyl-*N'*[4-(trifluoromethyl)benzene-1-sulfonyl]-4,5-dihydro-1*H*-pyrazole-1-carboximidamide

zévaquéabant

(4*S*)-*N*-(1-aminoéthylidène)-3-(4-chlorophényl)-4-phényl-*N'*[4-(trifluorométhyl)benzène-1-sulfonyl]-4,5-dihydro-1*H*-pyrazole-1-carboximidamide

zevaquenabant

(4*S*)-*N*-(1-aminoetilideno)-3-(4-clorofenil)-4-fenil-*N'*[4-(trifluorometil)bencono-1-sulfonyl]-4,5-dihidro-1*H*-pirazol-1-carboximidamidaC₂₅H₂₁ClF₃N₅O₂S**zilganersenum**

zilganersen

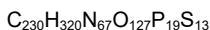
all-P-ambo-2'-O-(2-methoxyethyl)-5-methyl-*P*-thiocytidylyl-(3'→5')-2'-*O*-(2-methoxyethyl)adenylyl-(3'→5')-2'-*O*-(2-methoxyethyl)guanylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyluridylyl-(3'→5')-2'-*O*-(2-methoxyethyl)adenylyl-(3'→5')-2'-*O*-(2-methoxyethyl)-5-methyluridylyl-(3'→5')-*P*-thiothymidylyl-(3'→5')-2'-deoxy-*P*-thioadenylyl-(3'→5')-2'-deoxy-5-methyl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

zilganersen

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

zilganersén

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



$m^FCmoe=Amoe-Gmoe-m^5Umoe-Amoe-m^5Umoe-dT=dA=m^5C_d=m^5C_d=dT=m^5C_d=dT=dA=m^5C_d=dT=Amoe-Gmoe=m^5Umoe=m^5Cmoe$

= :



N : nucleoside / nucléoside / nucleósido

m^5N : 5-methyl-N / 5-méthyl-N / 5-metil-N

dN & N_d : 2'-deoxy-N / 2'-désoxy-N / 2'-desoxi-N

Nmoe : 2'-O-(2-methoxyethyl)-N / 2'-O-(2-méthoxyéthyl)-N / 2'-O-(2-metoxietil)-N

zilurgisertibum

zilurgisertib

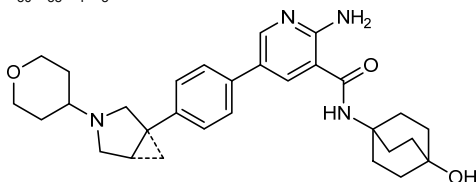
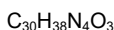
2-amino-*N*-(4-hydroxybicyclo[2.2.2]octan-1-yl)-5-{4-[(1*R*,5*S*)-3-(oxan-4-yl)-3-azabicyclo[3.1.0]hexan-1-yl]phenyl}pyridine-3-carboxamide

zilurgisertib

2-amino-*N*-(4-hydroxybicyclo[2.2.2]octan-1-yl)-5-{4-[(1*R*,5*S*)-3-(oxan-4-yl)-3-azabicyclo[3.1.0]hexan-1-yl]phényl}pyridine-3-carboxamide

zilurgisertib

2-amino-*N*-(4-hidroxibiciclo[2.2.2]octan-1-il)-5-{4-[(1*R*,5*S*)-3-(oxan-4-il)-3-azabiciclo[3.1.0]hexan-1-il]fenil}piridina-3-carboxamida



zinlirvimabum #

zinlirvimab

immunoglobulin G1-lambda2, anti-[human immunodeficiency virus type 1 (HIV-1) gp120 envelope glycoprotein N-glycan V3 region], *Homo sapiens* monoclonal antibody;

- gamma1 heavy chain *Homo sapiens* (1-461) [VH (*Homo sapiens* IGHV4-4*08 (79.2%) -(IGHD) -IGHJ6*04 (85.0%), CDR-IMGT [8.7.26] (26-33.51-57.96-121)) (1-132) -*Homo sapiens* IGHG1*01, G1m17,1, G1v24 CH3 L107, S114 (CH1 K120 (229) (133-230), hinge 1-15 (231-245), CH2 (246-355), CH3 D12 (371), L14 (373), M107>L (443), N114>S (449) (356-460), CHS K2>del (461)) (133-461)], (235-213')-disulfide with lambda2 light chain *Homo sapiens* (1'-214') [V-LAMBDA (*Homo sapiens* IGLV3-21*01 (64.9%) -IGLJ2*01 (80.0%) G121>A (102), K123>R (104), CDR-IMGT [6.3.12] (22-27.45-47.87-98)) (1'-108') -*Homo sapiens* IGLC2*01 (100%) (109'-214')]; dimer (241-241":244-244")-bisdisulfide, produced in Chinese hamster ovary (CHO) cells, cell line CHO-K1SV, glycoform alfa
- zinlirvimab immunoglobuline G1-lambda2, anti-[région V3 N-glycosylée 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* (1-461) [VH (*Homo sapiens* IGHV4-4*08 (79.2%) -(IGHD) -IGHJ6*04 (85.0%), CDR-IMGT [8.7.26] (26-33.51-57.96-121)) (1-132) -*Homo sapiens* IGHG1*01, G1m17,1, G1v24 CH3 L107, S114 (CH1 K120 (229) (133-230), charnière 1-15 (231-245), CH2 (246-355), CH3 D12 (371), L14 (373), M107>L (443), N114>S (449) (356-460), CHS K2>del (461)) (133-461)], (235-213')-disulfure avec la chaîne légère lambda2 *Homo sapiens* (1'-214') [V-LAMBDA (*Homo sapiens* IGLV3-21*01 (64.9%) -IGLJ2*01 (80.0%) G121>A (102), K123>R (104), CDR-IMGT [6.3.12] (22-27.45-47.87-98)) (1'-108') -*Homo sapiens* IGLC2*01 (100%) (109'-214')]; dimère (241-241":244-244")-bisdisulfure, produit dans des cellules ovariennes de hamster chinois (CHO), lignée cellulaire CHO-K1SV, glycoforme alfa
- zinlirvimab inmunoglobulina G1-lambda2, anti-[región V3 N-glicosilada de la proteína de envoltura gp120 del virus de la inmunodeficiencia humana de tipo 1 (HIV-1)], anticuerpo monoclonal *Homo sapiens*; cadena pesada gamma1 *Homo sapiens* (1-461) [VH (*Homo sapiens* IGHV4-4*08 (79.2%) -(IGHD) -IGHJ6*04 (85.0%), CDR-IMGT [8.7.26] (26-33.51-57.96-121)) (1-132) -*Homo sapiens* IGHG1*01, G1m17,1, G1v24 CH3 L107, S114 (CH1 K120 (229) (133-230), bisagra 1-15 (231-245), CH2 (246-355), CH3 D12 (371), L14 (373), M107>L (443), N114>S (449) (356-460), CHS K2>del (461)) (133-461)], (235-213')-disulfuro con la cadena ligera lambda2 *Homo sapiens* (1'-214') [V-LAMBDA (*Homo sapiens* IGLV3-21*01 (64.9%) -IGLJ2*01 (80.0%) G121>A (102), K123>R (104), CDR-IMGT [6.3.12] (22-27.45-47.87-98)) (1'-108') -*Homo sapiens* IGLC2*01 (100%) (109'-214')]; dímero (241-241":244-244")-bisdisulfuro, producido en las células ováricas de hámster chino (CHO), línea celular CHO-K1SV, forma glicosilada alfa

Heavy chain / Chaîne lourde / Cadena pesada
 QVQLQESGPG LVPKSETLSV TCSVSGDSMN NYYWTWIRQS PGKGLEWIGY 50
 ISDRSATYN PSLNRSRVVIS RDTSKNQSL KLSVTPADT AVYVCATARR 100
 GQRIYGVVVF GEFVYYSMD VWGKGTTVTV SSASTKGPSV FPLAPSSKST 150
 SGGTAALGCL VKDYFPEPVT VSMNSGALTS GVHTFPAVLQ SSGLYSLSSV 200
 VTVFSSSLGT QTYICNVNHR PSNTKVDKVK EPKSCDKTHT CPPCPAPELL 250
 GGFSPVLEFP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH 300
 NAKTKFREQ YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT 350
 ISKAKGQFRE PQVYTLPPSR DELTHNQVSL TCLVKGFYPS DIAVEVESNG 400
 QFENNYKTFP FVLDSGGSFF LYSKLTVDKS RWQGNVFSK SVLHEALHSH 450
 YTQKSLSLSP G 461

Light chain / Chaîne légère / Cadena ligera
 SYVRLPSVAL GETARISGR QALGSRVAVQ YQHRPGQAPI LLIYNNQDRP 50
 SGIPERFSGT PDINFGTRAT LTISGVEAGD EADYCHMWD SRSGFSWSFG 100
 GATRLTLVIG PKAAPSVTLF PPSSEELQAN KATLVCLISD FYPGAFTVAW 150
 KADSSPVKAG VETTTPSKQS NNKYAASSYL SLTPEQWKSH RSYSCQVTHE 200
 GSTVEKTVAP TECS 214

Post-translational modifications

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

Intra-H (C23-C104) 22-95 159-215 276-336 382-440
 22"-95" 159"-215" 276"-336" 382"-440"

Intra-L (C23-C104) 18"-86" 136"-195"
 18"-86" 136"-195"

Inter-H-L (h 5-CL 126) 235-213' 235"-213"

Inter-H-H (h 11, h 14) 241-241" 244-244"

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

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

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

H CH2 N84.4: 312, 312"

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

zipalertinibum

zipalertinib

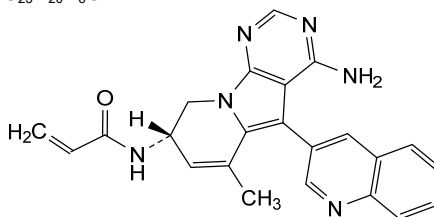
N-[(8*S*)-4-amino-6-methyl-5-(quinolin-3-yl)-8,9-dihydropyrimido[5,4-*b*]indolizin-8-yl]prop-2-enamide

zipalertinib

N-[(8*S*)-4-amino-6-méthyl-5-(quinoléin-3-yl)-8,9-dihydropyrimido[5,4-*b*]indolizin-8-yl]prop-2-énamide

zipalertinib

N-[(8*S*)-4-amino-6-metil-5-(quinolin-3-il)-8,9-dihidropirimido[5,4-*b*]indolizin-8-il]prop-2-enamida

C₂₃H₂₀N₆O# Electronic structure available on Mednet: <https://extranet.who.int/soinn/># Structure électronique disponible sur Mednet: <https://extranet.who.int/soinn/># Estructura electrónica disponible en Mednet: <https://extranet.who.int/soinn/>

RECOMMENDED International Nonproprietary Names:**List 88 – COVID-19 (special edition)****Dénominations communes internationales RECOMMANDÉES:****Liste 88 - COVID-19 (édition spéciale)****Denominaciones Comunes Internacionales RECOMENDADAS:****Lista 88 - COVID-19 (edición especial)****davesomeranum #**

davesomeran

messenger RNA (mRNA), 5'-capped, encoding a full-length, codon-optimised pre-fusion stabilised conformation variant (K981P and V982P) of the SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2) spike (S) glycoprotein (Omicron variants B.1.1.529.4 and B.1.1.529.5; also known as BA.4 and BA.5; based upon GISAID No. EPI_ISL_12548717) 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' poly(A) tail; contains *N*¹-methylpseudouridine instead of uridine (*all-U*>*m*¹Ψ).

davésoméran

ARN messenger (ARNm), protégé d'une coiffe en 5', codant la séquence entière optimisée au niveau des codons d'un variant de conformation stabilisée avant fusion (K981P et V982P) de la glycoprotéine de spicule (S) du SARS-CoV-2 (coronavirus 2 du syndrome respiratoire aigu sévère) (variants Omicron B.1.1.529.4 et B.1.1.529.5; également connus sous les noms de BA.4 et BA.5; basé sur le numéro GISAID EPI_ISL_12548717), dont l'optimisation a été renforcée par deux codons stop supplémentaires, flanqué 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 terminé par une queue poly(A) en 3'; contient de la *N*¹-méthylpseudouridine à la place de l'uridine (*tout-U*>*m*¹Ψ).

davesomerán

ARN mensajero (ARNm), protegido en 5', que codifica para la secuencia completa, con codones optimizados, de una variante estabilizada en conformación pre-fusión (K981P y V982P) de la glicoproteína de la espícula (S) del SARS-Cov-2 (coronavirus 2 del síndrome respiratorio agudo severo (variantes Omicron B.1.1.529.4 y B.1.1.529.5; también conocidas como BA.4 y BA.5; basadas en GISAID No. EPI_ISL_12548717) con dos codones de terminación adicionales, flanqueado por una región 5' no traducida (UTR) artificial y una UTR en 3' derivada del gen de la globina alfa humana (HBA1) modificada para incluir una secuencia de identificación y ratio (IDR) para permitir la identificación y la determinación el ratio relativo de los componentes individuales de ARN en una vacuna de ARNm multivalente, y terminado por una cola poli(A) en 3'; contiene *N*¹-metilpseudouridina en lugar de uridina (*todo-U*>*m*¹Ψ).

famtozinameranum

famtozinameran messenger RNA (mRNA), 5'-capped, encoding a full-length, codon-optimised pre-fusion stabilised conformation variant (K981P and V982P) of the SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2) spike (S) glycoprotein (Omicron sub-lineages B.1.1.529.4 and B.1.1.529.5 also referred to as BA.4 and BA.5; based upon GISAID: EPI_ISL_13017830), flanked by 5' and 3' untranslated regions and a 3' poly(A) tail; contains *N*¹-methylpseudouridine instead of uridine (*all-U*>*m*¹Ψ).

famtozinaméran 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 (K981P et V982P) de la glycoprotéine de spicule (S) du SARS-CoV-2 (coronavirus 2 du syndrome respiratoire aigu sévère) (sous-lignées Omicron B.1.1.529.4 et B.1.1.529.5; également connues sous les noms de BA.4 et BA.5; d'après GISAID : EPI_ISL_13017830), flanqué de régions non traduites en 5' et 3' et d'une queue poly(A) en 3'; contient de la *N*¹-méthylpseudouridine à la place de l'uridine (*tout-U*>*m*¹Ψ).

famtozinamerán ARN mensajero (ARNm), protegido en 5', que codifica para la secuencia completa, con codones optimizados, de una variante estabilizada en conformación pre-fusión (K981P y V982P) de la glicoproteína de la espícula (S) del SARS-Cov-2 (coronavirus 2 del síndrome respiratorio agudo severo) (sublinajes B.1.1.529.4 and B.1.1.529.5 de Omicron, también conocidas como BA.4 y BA.5; basadas en GISAID: EPI_ISL_13017830), flanqueada por regiones 5' y 3' no traducidas y una cola poli(A) en 3'; contiene *N*¹-metilpseudouridina en lugar de uridina (*todo-U*>*m*¹Ψ).

imelasomeranum

imelasomeran messenger RNA (mRNA), 5'-capped, encoding a full-length, codon-optimised pre-fusion stabilised conformation variant (K983P and V984P) of the SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2) spike (S) glycoprotein (Omicron variant, B.1.1.529; based upon GISAID No. EPI_ISL_6640919), further optimized by two additional stop codons, flanked by an artificial 5' untranslated region (UTR) and a 3' UTR derived from the human alpha globin gene (HBA1) and terminated by a 3' poly(A) tail; contains *N*¹-methylpseudouridine instead of uridine (*all-U*>*m*¹Ψ).

imélasoméran ARN messenger (ARNm), protégé d'une coiffe en 5', codant la séquence entière d'un variant de la glycoprotéine de spicule (S) du SARS-CoV-2 (coronavirus 2 du syndrome respiratoire aigu sévère; Omicron variant, B.1.1.529; basé sur GISAID No. EPI_ISL_6640919) à la conformation stabilisée par pré-fusion (K983P et V984P) et aux codons optimisés, optimisation renforcée par l'ajout de deux codons stop, flanqué d'une région non traduite (UTR) en 5' artificielle et d'une UTR en 3' dérivée du gène de l'alpha-globine humaine (HBA1) et terminé par une queue poly(A) en 3'; contient de la *N*¹-méthylpseudouridine au lieu de l'uridine (*tout-U*>*m*¹Ψ).

imelasomerán ARN mensajero (ARNm), protegido en 5', que codifica para una variante estabilizada en conformación pre-fusión (K983P and V984P) de la glicoproteína de la espícula (S) del SARS-Cov-2 (coronavirus 2 del síndrome respiratorio agudo severo; Omicron variant, B.1.1.529; basada en GISAID No. EPI_ISL_6640919) completa, con codones optimizados

y dos codones de terminación adicionales, flanqueado por una región 5' no traducida (UTR) artificial y una UTR en 3' derivada del gen de la globina alfa humana (HBA1) y terminado por una cola poly(A) en 3'; contiene *N*¹-metilpseudouridina en lugar de uridina (*todo-U>m*¹Ψ).

secelasomeranum

secelasomeran

messenger RNA (mRNA), 5'-capped, encoding a full-length, codon-optimised pre-fusion stabilised conformation variant (K983P and V984P) of the SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2) spike (S) glycoprotein (Beta variant, B.1.351; based upon GISAID No. EPI_ISL_2689878), further optimized by two additional stop codons, flanked by an artificial 5' untranslated region (UTR) and a 3' UTR derived from the human alpha globin gene (HBA1) and terminated by a 3' poly(A) tail; contains *N*¹-methylpseudouridine instead of uridine (*all-U>m*¹Ψ).

sécélasoméran

ARN messenger (ARNm), protégé d'une coiffe en 5', codant la séquence entière d'un variant de la glycoprotéine de spicule (S) du SARS-CoV-2 (coronavirus 2 du syndrome respiratoire aigu sévère; Bêta variant, B.1.351; basé sur GISAID No. EPI_ISL_2689878) à la conformation stabilisée par pré-fusion (K983P et V984P) et aux codons optimisés, optimisation renforcée par l'ajout de deux codons stop, flanqué d'une région non traduite (UTR) en 5' artificielle et d'une UTR en 3' dérivée du gène de l'alpha-globine humaine (HBA1) et terminé par une queue poly(A) en 3'; contient de la *N*¹-méthylpseudouridine au lieu de l'uridine (*tout-U>m*¹Ψ).

secelasomerán

ARN mensajero (ARNm), protegido en 5', que codifica para una variante estabilizada en conformación pre-fusión (K983P and V984P) de la glicoproteína de la espícula (S) del SARS-Cov-2 (coronavirus 2 del síndrome respiratorio agudo severo; Beta variant, B.1.351; basada en GISAID No. EPI_ISL_2689878) completa, con codones optimizados y dos codones de terminación adicionales, flanqueado por una región 5' no traducida (UTR) artificial y una UTR en 3' derivada del gen de la globina alfa humana (HBA1) y terminado por una cola poly(A) en 3'; contiene *N*¹-metilpseudouridina en lugar de uridina (*todo-U>m*¹Ψ).

The procedure "INN for Variant COVID-19 Vaccine Active Substances" can be found at <https://www.who.int/publications/i/item/inn-21-520>.

La procédure "INN for Variant COVID-19 Vaccine Active Substances" peut être trouvée à <https://www.who.int/publications/i/item/inn-21-520>.

Se puede encontrar la procedura "INN for Variant COVID-19 Vaccine Active Substances" en nuestro sitio web <https://www.who.int/publications/i/item/inn-21-520>.

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

Recommended International Non Proprietary Names (Rec. INN): List 40
Dénominations communes internationales proposées (DCI Rec.): Liste 40
Denominaciones Comunes Internacionales Propuestas (DCI Rec.): Lista 40
(WHO Drug Information, Vol. 12, No. 2, 1998)

p.172 **aviptadilum**

aviptadil	<i>replace the chemical names and structure by the following ones</i>
aviptadil	<i>remplacer les noms chimiques et la structure par les suivants</i>
aviptadil	<i>sustitúyase los nombres químicos y la estructura por los siguientes</i>

L-histidyl-L-seryl-L- α -aspartyl-L-alanyl-L-valyl-L-phenylalanyl-L-threonyl-L- α -aspartyl-L-asparaginyL-L-tyrosyl-L-threonyl-L-arginyl-L-leucyl-L-arginyl-L-lysyl-L-glutaminyL-L-methionyl-L-alanyl-L-valyl-L-lysyl-L-lysyl-L-tyrosyl-L-leucyl-L-asparaginyL-L-seryl-L-isoleucyl-L-leucyl-L-aspartamide

L-histidyl-L-séryl-L- α -aspartyl-L-alanyl-L-valyl-L-phénylalanyl-L-thréonyl-L- α -aspartyl-L-asparaginyL-L-tyrosyl-L-thréonyl-L-arginyl-L-leucyl-L-arginyl-L-lysyl-L-glutaminyL-L-méthionyl-L-alanyl-L-valyl-L-lysyl-L-lysyl-L-tyrosyl-L-leucyl-L-asparaginyL-L-séryl-L-isoleucyl-L-leucyl-L-aspartamide

L-histidil-L-seril-L- α -aspartil-L-alanil-L-valil-L-fenilalanil-L-treonil-L- α -aspartil-L-asparaginil-L-tirosil-L-treonil-L-arginil-L-leucil-L-arginil-L-lisil-L-glutaminil-L-metionil-L-alanil-L-valil-L-lisil-L-lisil-L-tirosil-L-leucil-L-asparaginil-L-seril-L-isoleucil-L-leucil-L-aspartamida

H His - Ser - Asp - Ala - Val - Phe - Thr - Asp - Asn - Tyr - Thr - Arg - Leu - Arg - Lys - Gln -
10

Met - Ala - Val - Lys - Lys - Tyr - Leu - Asn - Ser - Ile - Leu - Asn - NH₂
20

Recommended International Non Proprietary Names (Rec. INN): List 44
Dénominations communes internationales proposées (DCI Rec.): Liste 44
Denominaciones Comunes Internacionales Propuestas (DCI Rec.): Lista 44
(WHO Drug Information, Vol. 14, No. 3, 2000)

p. 206	suprimáse vardenafil	insértese vardenafilo
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Recommended International Non Proprietary Names (Rec. INN): List 61
Dénominations communes internationales proposées (DCI Rec.): Liste 61
Denominaciones Comunes Internacionales Propuestas (DCI Rec.): Lista 61
(WHO Drug Information, Vol. 23, No. 1, 2009)

p. 81 **velneperitum**

velneperit	replace and the chemical name by the following ones remplacer et le nom chimique par les suivantes sustitúyase y el nombre químico por las siguientes
velnépérit	
velneperit	

trans-4-(2-methylpropane-2-sulfonamido)-N-[5-(trifluoromethyl)pyridin-2-yl]cyclohexanecarboxamide

trans-4-(2-méthylpropane-2-sulfonamido)-*N*-[5-(trifluorométhyl)pyridin-2-yl]cyclohexanecarboxamide

trans-4-(2-metilpropano-2-sulfonamido)-*N*-[5-(trifluorometil)piridin-2-il]ciclohexanocarboxamida

Recommended International Non Proprietary Names (Rec. INN): List 75
Dénominations communes internationales proposées (DCI Rec.): Liste 75
Denominaciones Comunes Internacionales Propuestas (DCI Rec.): Lista 75
(WHO Drug Information, Vol. 30, No. 1, 2016)

p. 152 supprimer insérer
 sacituzumab govitecan sacituzumab govitécan

Recommended International Non Proprietary Names (Rec. INN): List 79
Dénominations communes internationales proposées (DCI Rec.): Liste 79
Denominaciones Comunes Internacionales Propuestas (DCI Rec.): Lista 79
(WHO Drug Information, Vol. 32, No. 1, 2018)

p.132 **lonapegsomatropinum#**
 lonapegsomatropin
 lonapegsomatropine
 lonapegsomatropina

replace the structure by the following one
remplacer la structure par la suivante
sustitúyase la estructura por la siguiente

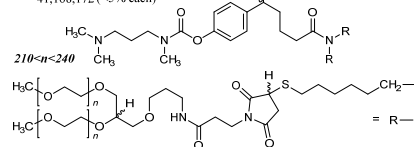
Sequence / Séquence / Secuencia

FPTIPLSRLF DNAMLRARHL HQLAFDTYQE FEEAYIPEEQ KYSFLQNPQT 50
 SLCFSES IPT PSNREETQOK SNLELLRISL LLIQSWLEPV QFLRSVFNAS 100
 LVIYGASDSNV YDLLKDLLEEG IQTLMGRLED GSPRTGQIKK QTYSKFDTNS 150
 HNDALLKNY GLLYCFRQDM DKVETFLRIV QCRSVEGSGG F 191

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

Potential modified residues / Résidus modifiés potentiels / Restos modificados potenciales

158 (~50%)
 K 38,70,140,145 (~10% each)
 41,168,172 (<5% each)

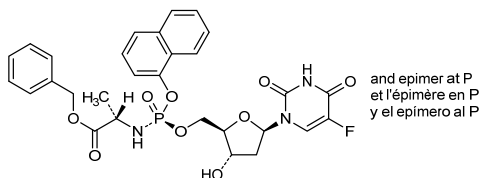


Recommended International Non Proprietary Names (Rec. INN): List 81
Dénominations communes internationales proposées (DCI Rec.): Liste 81
Denominaciones Comunes Internacionales Propuestas (DCI Rec.): Lista 81
(WHO Drug Information, Vol. 33, No. 1, 2019)

p.72 **fosifloxadinum nafalbenamidum**

fosifloxadinum nafalbenamide
 fosifloxadine nafalbénamide
 fosifloxadina nafalbenamida

replace the structure by the following one
remplacer la structure par la suivante
sustitúyase la estructura por la siguiente



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

p. 47 **epcoritamabum #**

epcoritamab
 épcoritamab
 epcoritamab

replace the description by the following one
remplacer la description par la suivante
sustitúyase la descripción por la siguiente

immunoglobulin G1-lambda/kappa, anti-[*Homo sapiens* CD3E (CD3 epsilon)] and anti-[*Homo sapiens* MS4A1 (membrane-spanning 4-domains subfamily A member 1, CD20)], monoclonal antibody, bispecific;
 gamma1 heavy chain chimeric anti-CD3E (1-454) [VH (*Mus musculus* IGHV10-1*02 (93.9%) -(IGHD) -IGHJ3*01 (93.3%)/*Homo sapiens* IGHV3-72*01 (81.0%) -(IGHD) -IGHJ6*01 (67.0%)) [8.10.16] (1-125) -*Homo sapiens* IGHG1*03G1m3, nG1m1 (CH1 R120 (222) (126-223), hinge 1-15 (224-238), CH2L1.3>F (242), L1.2>E (243), D27>A (273) (239-348), CH3 E12 (364), M14(366), F85.1>L (413) (349-453), CHS K2>del (454)) (126-454)], (228-214')-disulfide with lambda light chain chimeric (1'-215') [V-LAMBDA (*Mus musculus* IGLV1*01 (83.3%) -IGLJ1*01 (100%)/*Homo sapiens* IGLV8-61*01 (70.8%) -IGLJ3*02 (100%)] [9.3.9] (1'-109') -*Homo sapiens* IGLC2*01 (100%) (110'-215')];
 gamma1 heavy chain *Homo sapiens* anti-MS4A1 (1"-451") [VH (*Homo sapiens* IGHV3-9*01 (96.0%) -(IGHD) -IGHJ6*01 (100%)) [8.8.15] (1"-122") -*Homo sapiens* IGHG1*03 G1m3, G1m1 (CH1 R120 (219) (123-220), hinge 1-15 (221-235), CH2 L1.3>F (239), L1.2>E (240), D27>A (270) (236-345), CH3E12 (361), M14 (363), K88>R (414) (346-450), CHS K2>del (451)) (123"-451"), (225"-214"")-disulfide with kappa light chain *Homo sapiens* (1""-214"" [V-KAPPA (*Homo sapiens* IGKV3-11*01 (100%) -IGKJ5*01 (100%)] [6.3.9] (1""-107"" -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108""-214"")]; dimer (234-231":237-234")-bisdisulfide, produced in Chinese hamster ovary (CHO)-S cell line, glycoform alfa

immunoglobuline G1-lambda/kappa, anti-[*Homo sapiens* CD3E (CD3 epsilon)] et anti-[*Homo sapiens* MS4A1 (membre 1 de la sous-famille A à 4 domaines transmembranaires, CD20)], anticorps monoclonal bispécifique;
 chaîne lourde gamma1 chimérique anti-CD3E (1-454) [VH (*Mus musculus* IGHV10-1*02 (93.9%) -(IGHD) -IGHJ3*01 (93.3%)/*Homo sapiens* IGHV3-72*01 (81.0%) -(IGHD) -IGHJ6*01 (67.0%)) [8.10.16] (1-125) -*Homo sapiens* IGHG1*03G1m3, nG1m1 (CH1 R120 (222) (126-223), charnière 1-15 (224-238), CH2 L1.3>F (242), L1.2>E (243), D27>A (273) (239-348), CH3 E12 (364), M14(366), F85.1>L (413) (349-453), CHS K2>del (454)) (126-454)], (228-214')-disulfure avec la chaîne légère lambda chimérique (1'-215') [V-LAMBDA (*Mus musculus* IGLV1*01 (83.3%) -IGLJ1*01 (100%)/*Homo sapiens* IGLV8-61*01 (70.8%) -IGLJ3*02 (100%)] [9.3.9] (1'-109') -*Homo sapiens* IGLC2*01 (100%) (110'-215')];
 chaîne lourde gamma1 *Homo sapiens* anti-MS4A1 (1"-451") [VH (*Homo sapiens* IGHV3-9*01 (96.0%) -(IGHD) -IGHJ6*01 (100%)) [8.8.15] (1"-122") -*Homo sapiens* IGHG1*03G1m3, nG1m1 (CH1 R120 (219) (123-220), charnière 1-15 (221-235), CH2 L1.3>F (239), L1.2>E (240), D27>A (270) (236-345), CH3 E12 (361),

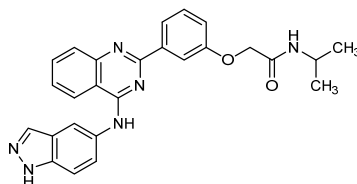
M14 (363), K88>R (414) (346-450), CHS K2>del (451)) (123"-451"), (225"-214")-disulfure avec la chaîne légère kappa *Homo sapiens* (1"-214") [V-KAPPA (*Homo sapiens* IGKV3-11*01 (100%) -IGKJ5*01 (100%)) [6.3.9] (1"-107") -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108"-214")]; dimère (234-231":237-234")-bisdisulfure, produit dans des cellules ovariennes de hamsters chinois (CHO) lignée cellulaire CHO-S, glycoforme alfa

immunoglobulina G1-lambda/kappa, anti-[*Homo sapiens* CD3E (CD3 épsilon)] y anti-[*Homo sapiens* MS4A1 (miembro 1 de la sub-familia A de 4 dominios transmembranarios, CD20)], anticuerpo monoclonal biespecifico;
cadena pesada gamma1 quimérica anti-CD3E (1-454) [VH (*Mus musculus* IGHV10-1*02 (93.9%) -(IGHD) -IGHJ3*01 (93.3%)/*Homo sapiens* IGHV3-72*01 (81.0%) -(IGHD) -IGHJ6*01 (67.0%)] [8.10.16] (1-125) -*Homo sapiens* IGHG1*03G1m3, nG1m1 (CH1 R120 (222) (126-223), bisagra 1-15 (224-238), CH2 L1.3>F (242), L1.2>E (243), D27>A (273) (239-348), CH3 E12 (364), M14(366), F85.1>L (413) (349-453), CHS K2>del (454)) (126-454)], (228-214')-disulfuro con la cadena ligera lambda quimérica (1'-215') [V-LAMBDA (*Mus musculus* IGLV1*01 (83.3%) -IGLJ1*01 (100%)/*Homo sapiens* IGLV8-61*01 (70.8%) -IGLJ3*02 (100%)] [9.3.9] (1'-109') -*Homo sapiens* IGLC2*01 (100%) (110'-215')];
cadena pesada gamma1 *Homo sapiens* anti-MS4A1 (1"-451") [VH (*Homo sapiens* IGHV3-9*01 (96.0%) -(IGHD) -IGHJ6*01 (100%)] [8.8.15] (1"-122") -*Homo sapiens* IGHG1*03G1m3, nG1m1 (CH1 R120 (219) (123-220), bisagra 1-15 (221-235), CH2 L1.3>F (239), L1.2>E (240), D27>A (270) (236-345), CH3 E12 (361), M14 (363), K88>R (414) (346-450), CHS K2>del (451)) (123"-451"), (225"-214")-disulfuro con la cadena ligera kappa *Homo sapiens* (1"-214") [V-KAPPA (*Homo sapiens* IGKV3-11*01 (100%) -IGKJ5*01 (100%)) [6.3.9] (1"-107") -*Homo sapiens* IGKC*01 (100%), Km3 A45.1 (153), V101 (191) (108"-214")]; dímero (234-231":237-234")-bisdisulfuro, producido en las células ováricas de hamsters chinos (CHO) línea celular CHO-S, glicoforma alfa

p.89 *supprimer* *insérer*
patritumab déruxtecan patritumab déruxtécan

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

p.111 **belumosudilum**
belumosudil *replace the structure by the following one*
bélumosudil *remplacer la structure par la suivante*
belumosudil *sustitúyase la estructura por la siguiente*



p.170 *supprimer* lutécium (¹⁷⁷Lu) vipivotide tétraxétan *insérer* lutécium (¹⁷⁷Lu) vipivotide tétraxétan

p. 213 **taniraleucelum #**

taniraleucel *replace the description by the following one*
 taniraleucel *remplacer la description par la suivante*
 taniraleucel *sustitúyase la descripción por la siguiente*

Allogeneic natural killer (NK) cells derived from CD34+ **human placental** stem/progenitor cells.

The cells are expanded and differentiated in the presence of cytokines including thrombopoietin, SCF, Flt3 ligand, IL-7, IL-15 and IL-2 (~~average population doublings 15~~) to generate the NK cell population. Cells (on average >95% of the cells) are CD56+/CD3- and have detectable levels of CD94, NKG2D and CD16. The cells secrete IFN- γ , perforin and granzyme B, and have cytolytic activity against human tumour cell lines.

Cellules tueuses naturelles (NK) allogéniques dérivées de cellules souches/progénitrices hématopoïétiques CD34+ **humaines placentaires** du sang de cordon ombilical (UCB).

Les cellules sont amplifiées et différenciées en présence de cytokines, notamment la thrombopoïétine, le SCF, le ligand de Flt3, l'IL-7, l'IL-15 et l'IL-2 (~~la population double en moyenne 15 fois~~) pour générer la population de cellules NK.

Les cellules (en moyenne >95% des cellules) sont CD56+/CD3- et ont des niveaux détectables de CD94, NKG2D et CD16. Les cellules sécrètent l'IFN- γ , la perforine et la granzyme B, et ont une activité cytolytique contre les lignées de cellules tumorales humaines.

Células natural killer (NK) alogénicas derivadas de células madre/progenitoras hematopoyéticas **CD34+ placentarias humanas** de sangre de cordón umbilical (UCB).

Las células se expanden y diferencian en presencia de citoquinas incluyendo trombopoyetina, SCF, ligando de Flt3, IL-7, IL-15 e IL-2 (~~la media de duplicaciones de la población es 15 veces~~) hasta generar la población de células NK. Las células (como media >95% de las células) son CD56+/CD3- y tienen niveles detectables de CD94, NKG2D y CD16. Las células secretan IFN- γ , perforina y granzima B, y tienen actividad citolítica frente a líneas celulares tumorales humanas.

p.232 *supprimer* zalsénertant tétraxétan *insérer* zalsénertant tétraxétan

Recommended International Non Proprietary Names (Rec. INN): List 86

Dénominations communes internationales proposées (DCI Rec.): Liste 86

Denominaciones Comunes Internacionales Propuestas (DCI Rec.): Lista 86

(WHO Drug Information, Vol. 36, No. 3, 2021)

p. 739 **efruxiferminum #**

-740 efruxifermin *replace the description by the following one*

human L-methionyl immunoglobulin G1 Fc fragment (1-228) fused via peptidyl linker ²²⁹GGGGSGGGSGGGGS²⁴³ to human fibroblast growth factor 21 (FGF-21) fragment (29-209, 244-424 in the current sequence) variant (L⁹⁸>R³⁴¹, P¹⁷¹>G⁴¹⁴, A¹⁸⁰>E⁴²³), dimer, produced in *Escherichia coli*;

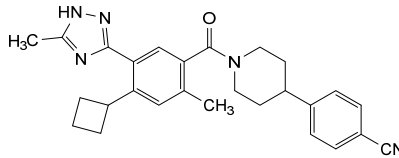
L-methionyl-immunoglobulin G1 (*Homo sapiens*)

33γ1-chain C-terminal 227-peptide Fc fragment (1-228) [*Homo sapiens* IGHG1*1; hinge 1-11; CH2 12-121; CH3 122-226; CHS 227-228] fused with the peptide linker (G₄S)₃ (229-243) and [L⁹⁸>R³⁴¹, P¹⁷¹>G⁴¹⁴, A¹⁸⁰>E⁴²³]-fibroblast growth factor 21 (*Homo sapiens* FGF-21) (244-424), dimer (7-7':10-10')-bisdisulfide, non-glycosylated, produced in *Escherichia coli*

Recommended International Non Proprietary Names (Rec. INN): List 87
Dénominations communes internationales proposées (DCI Rec.): Liste 87
Denominaciones Comunes Internacionales Propuestas (DCI Rec.): Lista 87
(WHO Drug Information, Vol. 36, No. 1, 2022)

p.90 **denifanstatum**
denifanstat
dénifanstat
denifanstat

replace the structure by the following one
remplacer la structure par la suivante
sustitúyase la estructura por la siguiente



p.116 **farletuzumabum ecteribulinum #**
farletuzumab ecteribulin
farlétuzumab ectéribuline
farletuzumab ecteribulina

replace the structure by the following one
remplacer la structure par la suivante
sustitúyase la estructura por la siguiente

Heavy chain / Chaîne lourde / Cadena pesada
EVQLVESGGG VQPGKSLK LSCASGFPS LYGSLWVFGA PGRGLEWVM 50
TSGGSTTY ADYWGDFLI ERDNRNTEF LQDSELRER TGYFCRRH 100
DPAWFAWYG QCFEVTSSA STKGPVEFPL AFSSKSTSGG TAALGLVKD 150
YFPEPTVSW NSGALTSVH TFAVLQSGG LYSLSSVTV PSSSLGTQTV 200
ICNVHKSFN TRVORVVEK SCRTHTCFP CPAPELGGP SVFLFPPRF 250
DPLASRPEK YTCVTVVGH EDRVDFRWY VQGVHNRK TPFRERQNS 300
TRVVSVLTV LHQDNLNGE YKCKVSNKAL PARIKTIKSK AKGQPREPQV 350
YTLFPRDEL TRNQVSLTCL VGGFYFSDIA VEHESNGQPE NNYKTPFVL 400
DSDGSFFLY KLTVDKSRWQ QGVFSCVYM HEALNHYTQ KSLSLSPGK 449

Light chain / Chaîne légère / Cadena ligera
DIQLTQSPFS LSASVGRVT ITCSVSSIS SNLHWYQQK PKRAPPFIWY 50
GSMNLASGP SRFSGGGDT DITFFISLQ PEDIATYICQ QWSYFPMIT 100
PQCFYFTEK RTVAARVFI PFRDRQLQS GKASVCLLN NFRFERAQV 150
WKVDNALQSG NSQESVTEGD SKDSTYSLS TLTSLKADYE KHKVYACEV 200
HQLLSPTFK SFNRGEC 217

Post-translational modifications

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

Intra-H (C23-C104) 22-96 146-202 263-323 369-427
22-96* 146-202* 263-323* 369-427*
Intra-L (C23-C104) 23-89 137-197
23-89* 137-197*

Inter-H-L (h 5-CL 126)* 222-217* 222-217*

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

*At least two of the four inter-chain disulfide bridges are not present, an average of 4 cysteinyl being conjugated each via a thioether bond to a drug linker. *Au moins deux des quatre ponts disulfures inter-chaînes ne sont pas présents. 4 cystéinyl en moyenne étant chacun conjugué via une liaison thioéther à un linker-principe actif. *Al menos dos de los cuatro puentes disulfuro inter-catenarios no están presentes, una media de 4 cisteinil está conjugada a conectores de principio activo.

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

H CH2 N84.4, 299, 299*

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

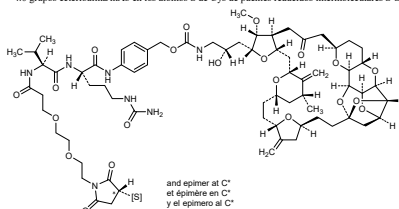
C-terminal lysine clipping / Coupure de la lysine C-terminale / Recorte de lisina C-terminal
H CHS K2: 449, 449*

Conjugation sites / Sites de conjugaison / Posiciones de conjugación

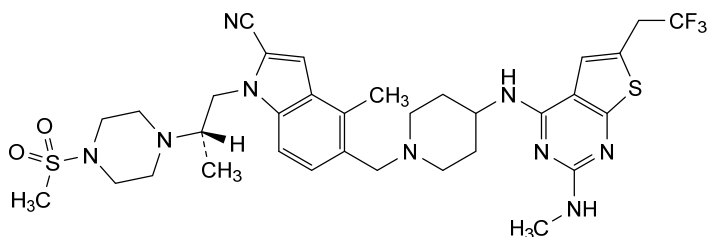
-4.0 ecteribulin groups/mAb at the S atoms of Cys of reduced intermolecular S-S bonds /

-4.0 ecteribulin groups/mAb at the S atoms of Cys of reduced intermolecular S-S bonds /

-4.0 grupos ecteribulina/mAb en los átomos S de Cys de puentes reducidos intermoleculares S-S:



p.252 **ziftomenibum**
ziftomenib *replace the structure by the following one*
ziftoménib *remplacer la structure par la suivante*
ziftomenib *sustitúyase la estructura por la siguiente*



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.