
International Nonproprietary Names for Pharmaceutical Substances (INN)

RECOMMENDED International Nonproprietary Names: List 74

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 (1–109) and Recommended (1–70) International Nonproprietary Names can be found in *Cumulative List No. 15, 2013* (available in CD-ROM only).

Dénominations communes internationales des Substances pharmaceutiques (DCI)

Dénominations communes internationales RECOMMANDÉES: Liste 74

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 (1–109) et recommandées (1–70) dans la *Liste récapitulative No. 15, 2013* (disponible sur CD-ROM seulement).

Denominaciones Comunes Internacionales para las Sustancias Farmacéuticas (DCI)

Denominaciones Comunes Internacionales RECOMENDADAS: Lista 74

De conformidad con lo que dispone el párrafo 7 del Procedimiento de Selección de Denominaciones Comunes Internacionales Recomendadas para las Sustancias Farmacéuticas [*Act. Of. Mund. Salud*, 1955, **60**, 3 (Resolución EB15.R7); 1969, **173**, 10 (Resolución EB43.R9); Résolution EB115.R4 (EB115/2005/REC/1) EB115.R4 (EB115/2005/REC/1)], se comunica por el presente anuncio que las denominaciones que a continuación se expresan han sido seleccionadas como Denominaciones Comunes Internacionales Recomendadas. La inclusión de una denominación en las listas de las Denominaciones Comunes Recomendadas no supone recomendación alguna en favor del empleo de la sustancia respectiva en medicina o en farmacia.

Las listas de Denominaciones Comunes Internacionales Propuestas (1–109) y Recomendadas (1–70) se encuentran reunidas en *Cumulative List No. 15, 2013* (disponible sólo en CD-ROM).

Latin , English, French, Spanish: <i>Recommended INN</i>	<i>Chemical name or description; Molecular formula; Graphic formula</i>
<i>DCI Recommandée</i>	<i>Nom chimique ou description; Formule brute; Formule développée</i>
<i>DCI Recomendada</i>	<i>Nombre químico o descripción; Fórmula molecular; Fórmula desarrollada</i>

abemaciclibum

abemaciclib

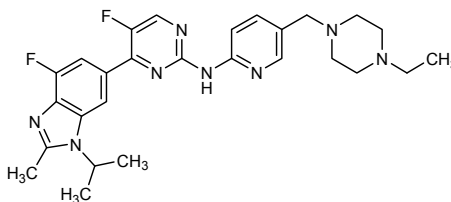
N-{5-[(4-ethylpiperazin-1-yl)methyl]pyridin-2-yl}-5-fluoro-4-[4-fluoro-2-methyl-1-(propan-2-yl)-1*H*-benzimidazol-6-yl]pyrimidin-2-amine

abémaciclib

N-{5-[(4-éthylpipérazin-1-yl)méthyl]pyridin-2-yl}-5-fluoro-4-[4-fluoro-2-méthyl-1-(propan-2-yl)-1*H*-benzimidazol-6-yl]pyrimidin-2-amine

abemaciclib

N-{5-[(4-etilpiperazin-1-il)metil]piridin-2-il}-5-fluoro-4-[4-fluoro-2-metil-1-(propan-2-il)-1*H*-benzoimidazol-6-il]pirimidin-2-amina

C₂₇H₃₂F₂N₈**amiselimodum**

amiselimod

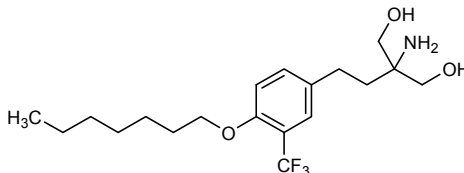
2-amino-2-{2-[4-(heptyloxy)-3-(trifluoromethyl)phenyl]ethyl}propane-1,3-diol

amiséli-mod

2-amino-2-{2-[4-(heptyloxy)-3-(trifluorométhyl)phényl]éthyl}propane-1,3-diol

amiselimod

2-amino-2-{2-[4-(heptiloxi)-3-(trifluorometil)fenil]etil}propano-1,3-diol

C₁₉H₃₀F₃NO₃

atezolizumabum #

atezolizumab

immunoglobulin G1-kappa, anti-[*Homo sapiens* CD274 (programmed death ligand 1, PDL1, PD-L1, B7 homolog 1, B7H1)], humanized monoclonal antibody; gamma1 heavy chain (1-448) [humanized VH (*Homo sapiens* IGHV3-23*04 (86.70%) -(IGHD)-IGHJ4*01) [8.8.11] (1-118) -*Homo sapiens* IGHG1*03 (CH1 R120>K (215) (119-216), hinge (217-231), CH2 N84.4>A (298) (232-341), CH3 (342-446), CHS (447-448)) (119-448)], (221-214')-disulfide with kappa light chain (1'-214') [humanized V-KAPPA (*Homo sapiens* IGKV1-5*01 (87.90%) -IGKJ1*01) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01(108'-214')]; dimer (227-227":230-230")-bisdisulfide

atézolizumab

immunoglobuline G1-kappa, anti-[*Homo sapiens* CD274 (ligand 1 de mort programmée, PDL1, PD-L1, homologue 1 de B7, B7H1)], anticorps monoclonal humanisé; chaîne lourde gamma1 (1-448) [VH humanisé (*Homo sapiens* IGHV3-23*04 (86.70%) -(IGHD)-IGHJ4*01) [8.8.11] (1-118) -*Homo sapiens* IGHG1*03 (CH1 R120>K (215) (119-216), charnière (217-231), CH2 N84.4>A (298) (232-341), CH3 (342-446), CHS (447-448)) (119-448)], (221-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA humanisé (*Homo sapiens* IGKV1-5*01 (87.90%) -IGKJ1*01) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (108'-214')]; dimère (227-227":230-230")-bisdisulfure

atezolizumab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CD274 (ligando 1 de muerte programada, PDL1, PD-L1, homólogo 1 de B7, B7H1)], anticuerpo monoclonal humanizado; cadena pesada gamma1 (1-448) [VH humanizado (*Homo sapiens* IGHV3-23*04 (86.70%) -(IGHD)-IGHJ4*01) [8.8.11] (1-118) -*Homo sapiens* IGHG1*03 (CH1 R120>K (215) (119-216), bisagra (217-231), CH2 N84.4>A (298) (232-341), CH3 (342-446), CHS (447-448)) (119-448)], (221-214')-disulfuro com la cadena ligera kappa (1'-214') [V-KAPPA humanizado (*Homo sapiens* IGKV1-5*01 (87.90%) -IGKJ1*01) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (108'-214')]; dímero (227-227":230-230")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAASGPTFS DSWIHWVRQA PGRGLEWVAV 50
ISPYGGSTYY ADSVKGGRFTI SADTSKNITAY LQMNSLRAED TAVYYCARRH 100
WFGGFDYWGQ GTLVTVSSAS TKGPSVFPLA PSSKSTSGGT AALGCLVKDY 150
FFEPVTVSWN SGALTSGVHT FFAVLQSSGL YSLSSVTVTF SSSLGTQTYI 200
CIVNKHFSNT KVDKVEPKS CDKTHITCFPC PARELLGGPS VFLPFRKDK 250
TLMISRTPEV TCVVVVDSHE DDEVKFNWVY DGEVHNNAKT KRFREQYAST 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPVVY 350
TLPFSSREEMT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTFPVLD 400
SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSFGK 448
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Light chain / Chaîne légère / Cadena ligera

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DIQMTQSPSS LSASVGDRTV ITCRASQDVS TAVAWYQQKPK GKAPKLLIYS 50
ASFLYSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YLYHPATFGQ 100
GTRKVEIKRTV AAPSVEFIFPP SDEQLKSGTA SVVCLLNHFY PREAKVQWVK 150
DNALQSGNSQ ESVTEQDSKD STYLSLSTLT LSKADYERHK VYACEVTHQG 200
LSSPVTKSFN RGECC 214
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Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

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

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

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

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

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

H CH2 N84.4>A (298, 298)';

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

avoralstatum
avoralstat

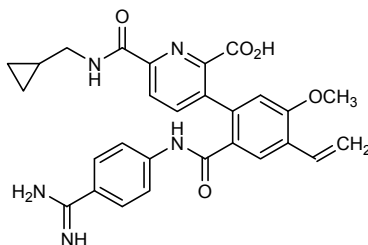
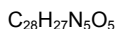
3-{2-[(4-carbamimidoylphenyl)carbamoyl]-4-ethenyl-5-methoxyphenyl}-6-[(cyclopropylmethyl)carbamoyl]pyridine-2-carboxylic acid

avoralstat

acide 3-{2-[(4-carbamimidoylphenyl)carbamoyl]-4-éthényl-5-méthoxyphényl}-6-[(cyclopropylméthyl)carbamoyl]pyridine-2-carboxylique

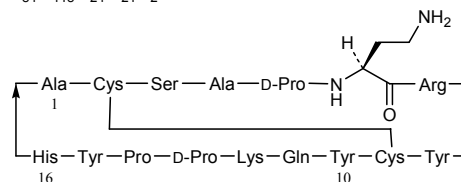
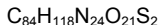
avoralstat

ácido 3-{2-[(4-carbamimidóilfenil)carbamóil]-4-etenil-5-metoxifenil}-6-[(ciclopropilmetil)carbamóil]piridina-2-carboxílico

**axalimogenum filolisbacum #**
axalimogene filolisbac

A live attenuated recombinant strain of *Listeria monocytogenes* (*Lm*) bacterium bioengineered to secrete an antigen-adjuvant fusion (tLLO-E7) protein consisting of non-hemolytic listeriolysin O (truncated LLO, tLLO) fused to the human papilloma virus-16 (HPV-16) E7 protein, contained within the multi-copy plasmid pGG-55. The bacterial strain used, XFL-7, had been attenuated by excision of the essential transcription activator gene for virulence gene expression *prfA* (10403S Δ *prfA*) and complemented with a mutated, less active *prfA* to maintain *in vivo* retention. In plasmid pGG-55, the *Lm hly* promoter drives the expression of fusion protein tLLO-E7, an approximately 67-kDa protein. The tLLO fragment of the fusion gene codes for the first 440 amino acids of full-length listeriolysin and is genetically fused to the E7 gene using the restriction site *Xho*I. The plasmid pGG55 is retained in XFL-7 *in vivo* due to the expression of the mutated PrfA protein.

axalimogène filolisbac	souche bactérienne vivante atténuée de <i>Listeria monocytogenes</i> (<i>Lm</i>) recombinante sécrétant une protéine de fusion antigène-adjuvant (tLLO-E7) qui comprend une listériolysine O non-hémolytique (LLO tronquée, tLLO), fusionnée à la protéine E7 du papillomavirus humain de type 16 (HPV-16), contenue dans le plasmide à copies multiples pGC-55. La souche bactérienne utilisée, XFL-7, a été atténuée par excision du gène <i>prfA</i> essentiel à l'activation de la transcription des gènes de virulence (10403S Δ <i>prfA</i>) et complété par un gène <i>prfA</i> muté, moins actif, afin de maintenir une rétention <i>in vivo</i> . Dans le plasmide pGC-55, le promoteur <i>Lm hly</i> contrôle l'expression de la protéine de fusion tLLO-E7, une protéine d'approximativement 67 kDa. Le fragment tLLO du gène de fusion code les premiers 440 acides aminés de la listériolysine et est génétiquement fusionné au gène E7 en utilisant le site de restriction <i>XhoI</i> . Le plasmide pGG55 est retenu dans XFL-7 <i>in vivo</i> par l'expression de la protéine PrfA mutée.
axalimogén filolisbac	Cepa bacteriana viva atenuada de <i>Listeria monocytogenes</i> (<i>Lm</i>) recombinante secretando una proteína de fusión antigéno-adyuvante (tLLO-E7) que consiste en una listeriolisina O no-hemolítica (LLO truncada, tLLO), fusionada con la proteína E7 del papilomavirus humano de tipo 16 (HPV-16) contenida en el plásmido multicopia pGC-55. La cepa bacteriana utilizada, XFL-7, se ha atenuado por escisión del gen <i>prfA</i> esencial a la activación de la transcripción de los genes de virulencia (10403S Δ <i>prfA</i>) y completada por un gen <i>prfA</i> mutado, menos activo, con el fin de mantener la retención <i>in vivo</i> . En el plásmido pGC-55, el promotor <i>Lm hly</i> controla la expresión de la proteína de fusión tLLO-E7, una proteína de aproximadamente 67 kDa. El fragmento tLLO del gen de fusión codifica los primeros 440 aminoácidos de la listeriolisina y se fusiona genéticamente con el gen E7 utilizando el sitio de restricción <i>XhoI</i> . El plásmido pGG55 es retenido en XFL-7 <i>in vivo</i> por la expresión de la proteína PrfA mutada.
balixafortidum balixafortide	cyclo[L-alanyl-L-cysteinyl-L-seryl-L-alanyl-D-prolyl-(2S)-2,4-diaminobutanoyl-L-arginyl-L-tyrosyl-L-cysteinyl-L-tyrosyl-L-glutaminyll-L-lysyl-D-prolyl-L-prolyl-L-tyrosyl-L-histidyl] (2-9)-disulfide
balixafortide	(2-9)-disulfure de cyclo[L-alanyl-L-cystéinyl-L-séryl-L-alanyl-D-prolyl-(2S)-2,4-diaminobutanoyl-L-arginyl-L-tyrosyl-L-cystéinyl-L-tyrosyl-L-glutaminyll-L-lysyl-D-prolyl-L-prolyl-L-tyrosyl-L-histidyl]
balixafortida	(2-9)-disulfuro de ciclo[L-alanyl-L-cisteinil-L-seril-L-alanyl-D-prolil-(2S)-2,4-diaminobutanoyl-L-arginil-L-tirosil-L-cisteinil-L-tirosil-L-glutaminil-L-lisil-D-prolil-L-prolil-L-tirosil-L-histidil]



bovhyaluronidasum azoximerum #

bovhyaluronidase azoximer

hyaluronidase-2 bovine (hyaluronoglucosaminidase-2, Hyal-2, EC 3.2.1.35) *Bos taurus* precursor protein linked to poly[[1-(carboxymethyl)piperazin-1-ium-1,4-diyl bromide]ethylene-co-[(piperazine-1,4-diyl 1-oxide)ethylene]] by an amido covalent bond

bovhyaluronidase azoximère

précurseur de la hyaluronidase-2 bovine (hyaluronoglucosaminidase-2, Hyal-2, EC 3.2.1.35) *Bos taurus* lié au poly{[bromure de 1-(carboxyméthyl)pipérazin-1-ium-1,4-diyl]éthylène-co-[(1-oxyle de pipérazin-1,4-diyl)éthylène]} par une liaison covalente amide

bovhyaluronidasa azoxímero

precursor de la hialuronidasa-2 bovina (hialuronoglucosaminidasa-2, Hyal-2, EC 3.2.1.35) *Bos taurus* unido al poli{[bromuro de 1-(carboximetil)piperazin-1-io-1,4-diil]etileno-co-[(1-óxido de piperazin-1,4-diil)etileno]} por un enlace covalente amida

Hyal-2 *Bos taurus* seq. (H₂N-Enz) / Hyal-2 *Bos taurus* seq. (H₂N-Enz) / Hyal-2 *Bos taurus* seq. (H₂N-Enz)

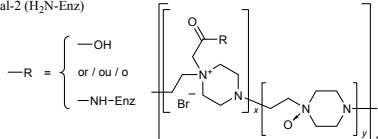
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MWTGLGPAVT LALVLVVAVA TELKPTAPPI FTGRPFVVAW DVPTQDCGPR 50
HKMPLDPKDM KAFDVQASPN EGFVNQNTI FYRDLGMYP HFNVSVGRSVH 100
GGVYPQNGSLW VHLEMLKGVH EHYIRTQEP AGLAVLDWEDW RPYVVRNWQD 150
KDVYRRLSRH LVAIRHPDWP PERVAKEAQY EFEFAARQFM LETLRFVKAF 200
RPRHLWGFYL FPDCCYNHDYV QNWETYTGRC PDVEVSRNDQ LAWLWAESTA 250
LFPVLYLEET LASSTHGRNF VSFVQEQALR VADVHHANHA LPVYVTFRPT 300
YSRGLTGLSE MDLISTIGES AALGAAGVIL WGDAGFTTSN ETCRRLKDYL 350
TRSLVPYVVN VSWAAQYCSW AQCHGHGRCV RRDPAHTFL HLSASSFRLV 400
PSHAPDEPRL RPEGELSWAD RNHLQMHFRC QCYLGGWGEQ CQWDRRRAAG 450
GASGAWAGSH LTGLLAVAVL AET
    
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Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
47-343 214-230 368-379 373-430 432-441

Glycosylation sites (N) / Sites de glycosylation (N) / Posiciones de glicosilación (N)
Asn-77 Asn-106 Asn-340 Asn-360

Carrier & Hyal-2 (H₂N-Enz) / Transporteur & Hyal-2 (H₂N-Enz) / Transportador & Hyal-2 (H₂N-Enz)



brolocizumabum #

brolocizumab

immunoglobulin scFv, anti-[*Homo sapiens* VEGFA (vascular endothelial growth factor A, VEGF-A, VEGF)], humanized monoclonal antibody single chain; scFv (1-252) [methionyl (1) -humanized V-KAPPA (*Homo sapiens* IGKV1-5*01 (87.60%)-IGKJ2*01 E125>T (108), I126>V (109), K127>L (110) [6.3.12] (2-111) -21-mer (glycyl-tetrakis(tetraglycyl-seryl)) linker (112-132) -humanized VH (*Homo sapiens* IGHV3-66*01 (80.40%)- (IGHD)-IGHJ1*01 [9.7.13] (133-252)

brolocizumab immunoglobuline scFv, anti-[*Homo sapiens* VEGFA (facteur de croissance A de l'endothélium vasculaire, VEGF-A, VEGF)], anticorps monoclonal humanisé à chaîne unique;
scFv (1-252) [méthionyl (1) -V-KAPPA humanisé (*Homo sapiens* IGKV1-5*01 (87.60%)- IGKJ2*01 E125>T (108), I126>V (109), K127>L (110) [6.3.12] (2-111) -21-mer (glycyl-tétrakis(tétraglycyl-séryl)) linker (112-132) -VH humanisé (*Homo sapiens* IGHV3-66*01 (80.40%)-(IGHD)-IGHJ1*01 [9.7.13] (133-252)

brolocizumab inmunoglobulina scFv, anti-[VEGFA de *Homo sapiens* (factor de crecimiento A del endotelio vascular, VEGF-A, VEGF)], anticuerpo monoclonal humanizado monocatenario;
scFv (1-252) [metionil (1) -V-KAPPA humanizado (*Homo sapiens* IGKV1-5*01 (87.60%)- IGKJ2*01E125>T (108), I126>V (109), K127>L (110) [6.3.12] (2-111) -21-mer (glicil-tetrakis(tetráglicil-seril)) conector (112-132) -VH humanizado (*Homo sapiens* IGHV3-66*01 (80.40%)-(IGHD)-IGHJ1*01 [9.7.13] (133-252)

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MEIVMTQSPF TLSASVGRV IITCASEII HSWLAWYQK FGKAPKLLIY 50
LASTLASGVP SRFSGSGSGA EFTLTISLQ PDDFATYYCQ NRYLASTNGA 100
NFGQGTRLTV LGGGGSGGGG GSGGGSGGG GSEVQLVESG GGLVQPGSL 150
RLSCTASGFS LTYDYYMTWV RQAPGKLEW VGFIDPDDP YYATWAKGRF 200
TISRDNKNT LYLQMNLSRA EDTAVYYCAG GDHNSGWGLD IWGQGLTVV 250
SS 252
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Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-chain C23 C104 24-89 154-228

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
None

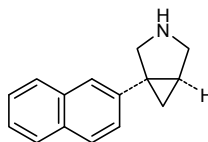
centanafadinum

centanafadine (1*R*,5*S*)-1-(naphthalen-2-yl)-3-azabicyclo[3.1.0]hexane

centanafadine (1*R*,5*S*)-1-(naphtalén-2-yl)-3-azabicyclo[3.1.0]hexane

centanafadina (1*R*,5*S*)-1-(naftalen-2-il)-3-azabicyclo[3.1.0]hexane

C₁₅H₁₅N



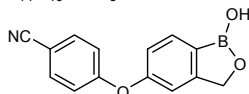
crisaborolum

crisaborole 4-[(1-hydroxy-1,3-dihydro-2,1-benzoxaborol-5-yl)oxy]benzonitrile

crisaborole 4-[(1-hydroxy-1,3-dihydro-2,1-benzoxaborol-5-yl)oxy]benzonitrile

crisaborol 4-[(1-hidroxi-1,3-dihidro-2,1-benzoxaborol-5-il)oxil]benzonitrilo

C₁₄H₁₀BNO₃



dectrekumabum #
dectrekumab

immunoglobulin G1-kappa, anti-[*Homo sapiens* IL13 (interleukin 13, IL-13)], *Homo sapiens* monoclonal antibody;
gamma1 heavy chain (1-450) [*Homo sapiens* VH (IGHV3-33*01 (98.00%) -(IGHD)-IGHJ3*02) [8.8.13] (1-120) -IGHG1*03 (CH1 (121-218), hinge (219-233), CH2 (234-343), CH3 (344-448), CHS (449-450)) (121-450)], (223-216')-disulfide with kappa light chain (1'-216')] [*Homo sapiens* V-KAPPA (IGKV3-11*01 (95.80%) -IGKJ2*01) [6.3.11] (1'-109') -IGKC*01 (110'-216')]]; dimer (229-229":232-232")-bisdisulfide

dectrékumab

immunoglobuline G1-kappa, anti-[*Homo sapiens* IL13 (interleukine 13, IL-13)], *Homo sapiens* anticorps monoclonal;
chaîne lourde gamma1 (1-450) [*Homo sapiens* VH (IGHV3-33*01 (98.00%) -(IGHD)-IGHJ3*02) [8.8.13] (1-120) -IGHG1*03 (CH1 (121-218), charnière (219-233), CH2 (234-343), CH3 (344-448), CHS (449-450)) (121-450)], (223-216')-disulfure avec la chaîne légère kappa (1'-216')] [*Homo sapiens* V-KAPPA (IGKV3-11*01 (95.80%) -IGKJ2*01) [6.3.11] (1'-109') -IGKC*01 (110'-216')]]; dimère (229-229":232-232")-bisdisulfure

dectrekumab

immunoglobulina G1-kappa, anti-[IL13 de *Homo sapiens* (interleukina 13, IL-13)], anticuerpo monoclonal de *Homo sapiens*;
cadena pesada gamma1 (1-450) [VH de *Homo sapiens* (IGHV3-33*01 (98.00%) -(IGHD)-IGHJ3*02) [8.8.13] (1-120) -IGHG1*03 (CH1 (121-218), bisagra (219-233), CH2 (234-343), CH3 (344-448), CHS (449-450)) (121-450)], (223-216')-disulfuro con la cadena ligera kappa (1'-216')] [V-KAPPA de *Homo sapiens* (IGKV3-11*01 (95.80%) -IGKJ2*01) [6.3.11] (1'-109') -IGKC*01 (110'-216')]]; dímero (229-229":232-232")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada
EVQLVESGGG VVQPGRSLRL SCAASGTFPS SYGMHWVRQA PGKLEWVAI 50
IWYDGSNKYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARLW 100
FGDLDAFDIW GQGTMTVTVSS ASTRGPVSPFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHPKS NTKVDKRVPEP KSCDKTHTCP PCPAPELLGG PSVFLFPPPK 250
KDTLMIKSRTP EIVTCVVVDVSD HEDPEVKFNW YVDGVEVHNA RTKPREPEQYN 300
STYRVVSVLT VLNQDNLNGK EYKCKVSNKA LPAPIEKTIS KARGQPREPQ 350
VYTLPPSREE MTKNQVSLTC LVKGFVPSDI AVEVESNGQP ENNYKTTPEV 400
LDSGSPFFLY SKLTVDKSRW QQGNVPSV MHEALHNHYT QKSLSLSPGK 450

Light chain / Chaîne légère / Cadena ligera
EIVLTQSPAT LSLSPGERAI LSCRAGQSVS SYLVWVYQQKP QQAPRLLIYD 50
ASNRATGIPA RPSGSGSGTD FTLTISLSLEP EDFAVYYCQQ RSSWPPVYTF 100
GQGTKLEIKR TVAAPSDFIF PPSDEQLKSG TASVCLLNN FYPREAKVQW 150
KVDNALQSGN SQESVTEQDS KDSTYLSLST LTLKADYEK HKVYACEVTH 200
QGLSSPVTKS FNRGEC 216

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" 136"-196"
23"-88" 136"-196"
Inter-H-L (h 5-CL 126) 223-216' 223"-216"
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'

Other post-translational modifications / Autres modifications post-traduccionnelles / Otras modificaciones post-traduccionales
H CHS K2 C-terminal lysine clipping:
450, 450'

desfesoterodinium

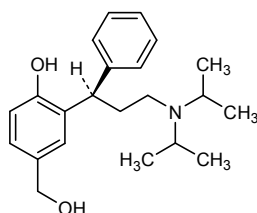
desfesoterodine

2-((1*R*)-3-[bis(propan-2-yl)amino]-1-phenylpropyl)-4-(hydroxymethyl)phenol

desfésotérodine

2-((1*R*)-3-[bis(propan-2-yl)amino]-1-phénylpropyl)-4-(hydroxyméthyl)phenol

desfesoterodina

2-((1*R*)-3-[bis(propan-2-il)amino]-1-fenilpropil)-4-(hidroximetil)fenolC₂₂H₃₁NO₂**deutetrabenazinum**

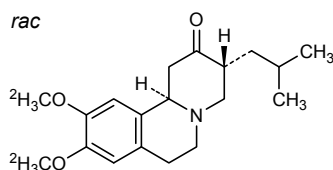
deutetrabenazine

rac-(3*R*,11*bR*)-9,10-di[(²H₃)methoxy]-3-(2-methylpropyl)-1,3,4,6,7,11*b*-hexahydro-2*H*-pyrido[2,1-*a*]isoquinolin-2-one

deutétrabénazine

rac-(3*R*,11*bR*)-9,10-di[(²H₃)méthoxy]-3-(2-méthylpropyl)-1,3,4,6,7,11*b*-hexahydro-2*H*-pyrido[2,1-*a*]isoquinoléin-2-one

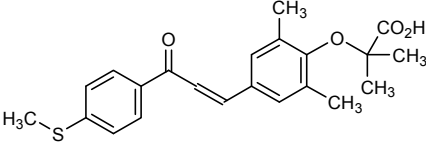
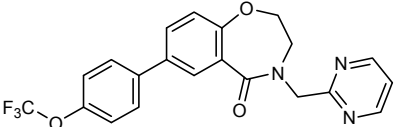
deutetrabenazina

rac-(3*R*,11*bR*)-3-(2-metilpropi)-9,10-di[(²H₃)metoxi]-1,3,4,6,7,11*b*-hexahidro-2*H*-pirido[2,1-*a*]isoquinolein-2-onaC₁₉H₂₁(²H₆)NO₃**durvalumabum #**

durvalumab

immunoglobulin G1-kappa, anti-[*Homo sapiens* CD274 (programmed death ligand 1, PDL1, PD-L1, B7 homolog 1, B7H1)], *Homo sapiens* monoclonal antibody; gamma1 heavy chain (1-451) [*Homo sapiens* VH (IGHV3-7*01 (99.00%) -(IGHD)-IGHJ4*01 [8.8.14] (1-121) -IGHG1*03 (CH1 (122-219), hinge (220-234), CH2 (235-344) L1.3>F (238), L1.2>E (239), P116>S (335), CH3 (345-449), CHS (450-451)) (122-451)], (224-215')-disulfide with kappa light chain (1'-215')] [*Homo sapiens* V-KAPPA (IGKV3-20*01 (96.90%) -IGKJ1*01 [7.3.9] (1'-108') -IGKC*01 (109'-215'))]; dimer (230-230":233-233")-bisdisulfide

durvalumab	<p>immunoglobuline G1-kappa, anti-[<i>Homo sapiens</i> CD274 (ligand 1 de mort programmée, PDL1, PD-L1, homologue 1 de B7, B7H1)], <i>Homo sapiens</i> anticorps monoclonal; chaîne lourde gamma1 (1-451) [<i>Homo sapiens</i> VH (IGHV3-7*01 (99.00%) -(IGHD)-IGHJ4*01) [8.8.14] (1-121) -IGHG1*03 (CH1 (122-219), charnière (220-234), CH2 (235-344) L1.3>F (238), L1.2>E (239), P116>S (335), CH3 (345-449), CHS (450-451)) (122-451)], (224-215')-disulfure avec la chaîne légère kappa (1'-215') [<i>Homo sapiens</i> V-KAPPA (IGKV3-20*01 (96.90%) -IGKJ1*01) [7.3.9] (1'-108') -IGKC*01 (109'-215')]; dimère (230-230":233-233")-bisdisulfure</p>
durvalumab	<p>inmunoglobulina G1-kappa, anti-[<i>Homo sapiens</i> CD274 (ligando 1 de muerte programada, PDL1, PD-L1, homólogo 1 de B7, B7H1)], anticuerpo monoclonal de <i>Homo sapiens</i>; cadena pesada gamma1 (1-451) [<i>Homo sapiens</i> VH (IGHV3-7*01 (99.00%) -(IGHD)-IGHJ4*01) [8.8.14] (1-121) -IGHG1*03 (CH1 (122-219), bisagra (220-234), CH2 (235-344) L1.3>F (238), L1.2>E (239), P116>S (335), CH3 (345-449), CHS (450-451)) (122-451)], (224-215')-disulfuro con la cadena ligera kappa (1'-215') [<i>Homo sapiens</i> V-KAPPA (IGKV3-20*01 (96.90%) -IGKJ1*01) [7.3.9] (1'-108') -IGKC*01 (109'-215')]; dímero (230-230":233-233")-bisdisulfuro</p>
	<p>Heavy chain / Chaîne lourde / Cadena pesada</p> <pre> EVQLVESGGG LVQPGGSLRL SCAASGFTFS RYWMSWVRQA PGKGLEWVAN 50 IKQDGESEKYY VDSVKGRFTI SRDNKNSLY LQMNSLRAED TAVYYCAREG 100 GWFGELAFDY WQQGLTIVTS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150 KDYFPEPFTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200 TYICNVNHKP SNTKVKDRVE PKSCDKTHTC PPCPAPEFEG GPSVFLFPFK 250 PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY 300 NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPASIEKTI SKAKGQPREP 350 QVYTLPPSRE EMTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKPTTP 400 VLDSDGSFFL YSKLTVDKSR WQQGNVFCSS VMHEALHNHY TQKLSLSLSPG 450 K </pre>
	<p>Light chain / Chaîne légère / Cadena ligera</p> <pre> EIVLTQSPGT LSLSPGERAT LSCRASQRVS SSYLAWYQQK PGQAPRLLIY 50 DASSRATGIP DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QYGSLLPWF 100 QGTRKVEIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNPF YPREAKVQWK 150 VDNALQSGNS QESVTEQDSK DSTYLSSTL TLSKADYEKH KVYACEVTHQ 200 GLSSPVTKSF NRGEC 215 </pre>
	<p>Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disul</p> <p>Intra-H (C23-C104) 22"-96" 148"-204" 265"-325" 371"-429" 22"-96" 148"-204" 265"-325" 371"-429"</p> <p>Intra-L (C23-C104) 23"-89" 135"-195" 23"-89" 135"-195"</p> <p>Inter-H-L (h 5-CL 126) 224"-215" 224"-215" Inter-H-H (h 11, h 14) 230"-230" 233"-233"</p>
	<p>N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación H CH2 N84.4: 301, 301"</p>
elafibranorum elafibranor	<p>2-(2,6-dimethyl-4-{3-[4-(methylsulfonyl)phenyl]-3-oxoprop-1-en-1-yl}phenoxy)-2-methylpropanoic acid</p>
elafibranor	<p>acide 2-(2,6-diméthyl-4-{3-[4-(méthylsulfonyl)phényl]-3-oxoprop-1-én-1-yl}phénoxy)-2-méthylpropanoïque</p>

elafibranor	<p>ácido 2-(2,6-dimetil-4-[3-[4-(metilsulfanil)fenil]-3-oxoprop-1-en-1-il]fenoxi)-2-metilpropanoico</p> <p>$C_{22}H_{24}O_4S$</p> 
eleclazinum eleclazine	4-[(pyrimidin-2-yl)methyl]-7-[4-(trifluoromethoxy)phenyl]-3,4-dihydro-1,4-benzoxazepin-5(2 <i>H</i>)-one
éléclazine	4-[(pyrimidin-2-yl)méthyl]-7-[4-(trifluorométhoxy)phényl]-3,4-dihydro-1,4-benzoxazépin-5(2 <i>H</i>)-one
eleclazina	<p>4-[(pirimidin-2-il)metil]-7-[4-(trifluorometoxi)fenil]-3,4-dihidro-1,4-benzoxazepin-5(2<i>H</i>)-ona</p> <p>$C_{21}H_{16}F_3N_3O_3$</p> 
elgantumabum # elgantumab	<p>immunoglobulin G1-kappa, anti-[<i>Homo sapiens</i> ERBB3 (receptor tyrosine-protein kinase erbB-3, HER3)], <i>Homo sapiens</i> monoclonal antibody;</p> <p>gamma1 heavy chain (1-447) [<i>Homo sapiens</i> VH (IGHV3-23*01 (94.90%) -(IGHD)-IGHJ4*01) [8.8.10] (1-117) -IGHG1*03 (CH1 (118-215), hinge (216-230), CH2 (231-340), CH3 (341-445), CHS (446-447)) (118-447)], (220-214')-disulfide with kappa light chain (1'-214') [<i>Homo sapiens</i> V-KAPPA (IGKV1-12*01 (94.70%) -IGKJ1*01) [6.3.9] (1'-107') -IGKC*01 (108'-214')]; dimer (226-226'':229-229'')-bisdisulfide</p>
elgantumab	<p>immunoglobuline G1-kappa, anti-[<i>Homo sapiens</i> ERBB3 (récepteur à activité tyrosine kinase erbB-3, HER3)], <i>Homo sapiens</i> anticorps monoclonal;</p> <p>chaîne lourde gamma1 (1-447) [<i>Homo sapiens</i> VH (IGHV3-23*01 (94.90%) -(IGHD)-IGHJ4*01) [8.8.10] (1-117) -IGHG1*03 (CH1 (118-215), charnière (216-230), CH2 (231-340), CH3 (341-445), CHS (446-447)) (118-447)], (220-214')-disulfure avec la chaîne légère kappa (1'-214') [<i>Homo sapiens</i> V-KAPPA (IGKV1-12*01 (94.70%) -IGKJ1*01) [6.3.9] (1'-107') -IGKC*01 (108'-214')]; dimère (226-226'':229-229'')-bisdisulfure</p>

elgemtumab

inmunoglobulina G1-kappa, anti-[ERBB3 de *Homo sapiens* (receptor tirosina-proteína kinasa erbB-3, HER3)], anticuerpo monoclonal de *Homo sapiens*; cadena pesada gamma1 (1-447) [*Homo sapiens* VH (IGHV3-23*01 (94.90%) -(IGHD)-IGHJ4*01) [8.8.10] (1-117) -IGHG1*03 (CH1 (118-215), bisagra (216-230), CH2 (231-340), CH3 (341-445), CHS (446-447)) (118-447)], (220-214')-disulfuro con la cadena ligera kappa (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-12*01 (94.70%) -IGKJ1*01) [6.3.9] (1'-107') -IGKC*01 (108'-214')]; dímero (226-226":229-229")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada
 EVQLLESGGG LVQPGGSLRL SCAASGFTFS SYAMSWVRQA PGKGLEWVSA 50
 INSGQKSTYY ADSVKGRFTI SRDANSKNTLY LQMNSLRAED TAVYYCARWG 100
 DEGFDIWQGG TLVTVSSAST KGPSVFPLAP SSRSTSGGTA ALGCLVKDYF 150
 PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVTVVPS SSLGTQTYIC 200
 NVNHRKPSNTK VDKRVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT 250
 LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNARTK PREEQYNSTY 300
 RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTIKAK GQPREPQVYV 350
 LPPSREEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTTPVPLDS 400
 DGSFFLYSKL TVDKSRWQGG NVFSCSVMHE ALHNYTQKS LSLSPGK 447

Light chain / Chaîne légère / Cadena ligera
 DIQMTQSPFSS LSASVGRVPT ITCRASQGIS NWLAWYQQKP GKAPKLLIYG 50
 ASSLQSGVPS RFGSGSGTD FTLTISSLQP EDFATYVQQ YSSFPFTFGQ 100
 CTKVEIKRTV AAPSVEIFPP SDEQLKSGTA SVVCLLNIFY PREAKVQNKV 150
 DNALQSGNSQ ESVTEQDSKD STYSLSSLT LSKADYEKHK VYACEVTHQG 200
 LSSPVTKSFN RGEC 214

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
 Intra-H (C23-C104) 22"-96" 144"-200" 261"-321" 367"-425"
 22"-96" 144"-200" 261"-321" 367"-425"
 Intra-L (C23-C104) 23"-88" 134"-194"
 23"-88" 134"-194"
 Inter-H-L (h 5-CL 126) 220-214' 220"-214"
 Inter-H-H (h 11, h 14) 226-226" 229-229"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
 H CH2 N84.4:
 297, 297"

Other post-translational modifications / Autres modifications post-traductionnelles / Otras modificaciones post-traduccionales
 H CHS K2 C-terminal lysine clipping:
 447, 447"

emeramidum
 emeramide

*N*¹,*N*³-bis(2-sulfanylethyl)benzene-1,3-dicarboxamide

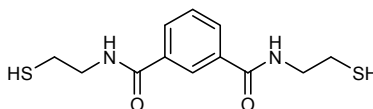
éméramide

*N*¹,*N*³-bis(2-sulfanyléthyl)benzène-1,3-dicarboxamide

emeramida

*N*¹,*N*³-bis(2-sulfaniletíl)bencono-1,3-dicarboxamida

C₁₂H₁₆N₂O₂S₂

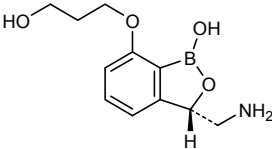
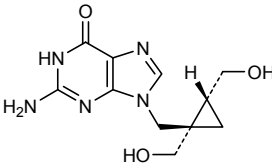


epetraborolum
 petraborole

(3*S*)-3-(aminomethyl)-7-(3-hydroxypropoxy)-2,1-benzoxaborol-1(3*H*)-ol

épétraborole

(3*S*)-3-(aminométhyl)-7-(3-hydroxypropoxy)-2,1-benzoxaborol-1(3*H*)-ol

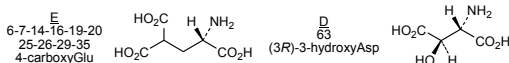
epetaborol	(3 <i>S</i>)-3-(aminometil)-7-(3-hidroxiopropoxi)-2,1-benzoxaborol-1(3 <i>H</i>)-ol C ₁₁ H ₁₆ BNO ₄ 
eprociclovirum eprociclovir	2-amino-9-[[[(1 <i>S</i> ,2 <i>R</i>)-1,2-bis(hydroxymethyl)cyclopropyl]methyl]-1,9-dihydro-6 <i>H</i> -purin-6-one
éprociclovir	2-amino-9-[[[(1 <i>S</i> ,2 <i>R</i>)-1,2-bis(hydroxyméthyl)cyclopropyl]méthyl]-1,9-dihydro-6 <i>H</i> -purin-6-one
eprociclovir	2-amino-9-[[[(1 <i>S</i> ,2 <i>R</i>)-1,2-bis(hidroxi)metil]ciclopropil]metil]-1,9-dihidro-6 <i>H</i> -purin-6-ona C ₁₁ H ₁₅ N ₅ O ₃ 
eptacogum beta (activatum) # eptacog beta (activated)	recombinant DNA derived blood-coagulation factor VII (activated), extracted from transgenic rabbits' milk: blood-coagulation factor VII (EC 3.4.21.21, proconvertin, serum prothrombin conversion accelerator), human factor VII light chain (135-262)-disulfide with human factor VII heavy chain
eptacog bêta (activé)	facteur VII de la coagulation sanguine (activé) à partir d'ADN recombinant, extrait du lait de lapins transgéniques: facteur VII de la coagulation sanguine (EC3.4.21.21, proconvertine, accélérateur de conversion de la prothrombine sérique), (135-262) disulfure entre la chaîne légère et la chaîne lourde du facteur VII humain, glycoforme beta
eptacog beta (activado)	factor VII de la coagulación sanguínea (activado) a partir de ADN recombinante, extraído de leche de conejas transgénicas: factor VII de la coagulación sanguínea (EC 3.4.21.21, proconvertina, acelerador de conversión de la protrombina sérica), (135-262) disulfuro entre la cadena ligera y la cadena pesada del factor VII humano, glicoforma beta

Light chain / Chaîne légère / Cadena ligera
 ANAFLEELRP GSELECKEE QCSFEAREI FKAERTKLF WISYSDGDQC 50
 ASGPCNGGS CKDQLQSYIC FCLPAFEGRN CETHRDDQLI CVNENGGCEQ 100
 YCSDHTGTRK SCRCHEGYSL LADGVSCTPT VEYPCGKIPI LEKRNASKPQ 150
 GR 152

Heavy chain / Chaîne lourde / Cadena pesada
 IVGGKVCV KGECPWQVLL LVNGAQLCGG TLINTIWWVS AAHCFDKIKN 200
 WRNLI AVLGE HDLSEHDGDE QSRRAQVII PSTYVPGTTN HDIALLRLHQ 250
 PVVLT DHHVP LCLPERTFSE RTLAFVRFSL VSWGQQLLDR GATALEMLVL 300
 NVPRMLTQDC LQQSRKVGDS PNI TEYMFCA GYSDGSKDSC KGDSGGPHAT 350
 HYRGTWYLTG IVSWGQGCAT VGHFVYTRV SQYIEWLQKL MRSEPRPGVL 400
 LRAPFF 406

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
 17-22 50-61 55-70 72-81 91-102 98-112
 114-127 135-262 159-164 178-194 310-329 340-368

Modified residues / Résidus modifiés / Restos modificados



Glycosylation sites (S, N) / Sites de glycosylation (S, N) / Posiciones de glicosilación (S, N)
 Ser-52 Ser-60 Asn-145 Asn-322

etelcalcetidium

etelcalcetide

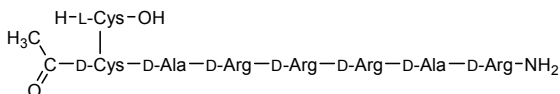
N-acetyl-D-cysteinyl-D-alanyl-D-arginyl-D-arginyl-D-arginyl-D-alanyl-D-argininamide disulfide with L-cystein

ételcalcétide

disulfure entre le *N*-acétyl-D-cystéinyl-D-alanyl-D-arginyl-D-arginyl-D-arginyl-D-alanyl-D-argininamide et la L-cystéine

etelcalcetida

disulfuro entre el *N*-acetil-D-cisteinil-D-alanil-D-arginil-D-arginil-D-arginil-D-alanil-D-argininamida y la L-cisteina



evinacumabum #

evinacumab

immunoglobulin G4-kappa, anti-[*Homo sapiens* ANGPTL3 (angiopoietin-like 3)], human monoclonal antibody; gamma4 heavy chain (1-453) [*Homo sapiens* VH (IGHV3-43*02 (92.90%) -(IGHD)-IGHJ3*02) [8.8.19](1-126) -IGHG4*01 (CH1(127-224), hinge S10>P(234) (225-236), CH2 (237-346), CH3(347-451), CHS (452-453)) (127-453)], (140-214')-disulfide with kappa light chain (1'-214') [*Homo sapiens* (V-KAPPA (IGKV1-5*03 (98.90%) -IGKJ2*01) [6.3.9] (1'-107') -IGKC*01 (108'-214'))]; dimer (232-232":235-235")-bisdisulfide

évinacumab

immunoglobuline G4-kappa, anti-[*Homo sapiens* ANGPTL3 (angiopoïétine-like 3)], anticorps monoclonal humain; chaîne lourde gamma4 (1-453) [*Homo sapiens* VH (IGHV3-43*02 (92.90%) -(IGHD)-IGHJ3*02) [8.8.19] (1-126) -IGHG4*01 (CH1 (127-224), charnière S10>P (234) (225-236), CH2 (237-346), CH3 (347-451), CHS (452-453)) (127-453)], (140-214')-disulfure avec la chaîne légère kappa (1'-214') [*Homo sapiens* (V-KAPPA (IGKV1-5*03 (98.90%) -IGKJ2*01) [6.3.9] (1'-107') -IGKC*01 (108'-214'))]; dimère (232-232":235-235")-bisdisulfure

evinacumab

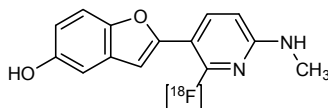
inmunoglobulina G4-kappa, anti-[ANGPTL3 (angiopoyetina-like 3) *de Homo sapiens*], anticuerpo monoclonal humano; cadena pesada gamma4 (1-453) [VH de *Homo sapiens* (IGHV3-43*02 (92.90%) -(IGHD)-IGHJ3*02) [8.8.19] (1-126) -IGHG4*01 (CH1 (127-224), bisagra S10>P (234) (225-236), CH2 (237-346), CH3 (347-451), CHS (452-453) (127-453)], (140-214')-disulfuro con la cadena ligera kappa (1'-214') [*Homo sapiens* (V-KAPPA (IGKV1-5*03 (98.90%) -IGKJ2*01) [6.3.9] (1'-107') -IGKC*01 (108'-214'))]; dímero (232-232":235-235")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada
 EVQLVESGGG VIQPGGSLRL SCAASGFTFD DYAMNWVRQG PGKGLEWVSA 50
 ISGDGGSTYY ADSVKGRTI SRDYSKNSLY LQMSLRAED TAFYCAKDL 100
 RNTIFGVVLP DAFDIWQGT MVTSSASTK GPSVFFLAPC SRSTSESTAA 150
 LGCLVKDYFP EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVTVTPSS 200
 SLGKTYTCN VDHKPSNTKV DKRVESRYGF PCPPCPAPEF LGGPSVFLFP 250
 PKPKDTLMIS RTPEVTCVVV DVSQEDPEVQ FNWYVDGVEV HNAKTKPREE 300
 QFNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKGLPSSIEK TISKAKGQPR 350
 EPQVYTLPPS QEEMTKNQS LTCLVKGYFP SDIAVESWESN GQPENNYKTT 400
 PFLVDSGDSF FLYSRLTVDK SRWQEGNVFS CSMHEALHN HYTQKSLSL 450
 LGK 453

Light chain / Chaîne légère / Cadena ligera
 DIQMTQSPST LSASVGRDRT ITCRASQSR SWLAWYQQKPK GKAPKLLIYK 50
 ASSLESGVPS RFGSGSGSTE FTLTISLQPD DDFATYYCQQ YNSYSYTFGQ 100
 GTKLEIKRIV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWVK 150
 DNALQSGNSQ ESVTEQDSKD STYLSSTLT LSKADYKHKK VYACEVTHQG 200
 LSSPVTKSFN RGEK 214

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
 Intra-H (C23-C104) 22-96 153-209 267-327 373-431
 22"-96" 153"-209" 267"-327" 373"-431"
 Intra-L (C23-C104) 23'-88' 134'-194'
 23"'-88"' 134"'-194"
 Inter-H-L (CH1 10-CL 126) 140-214' 140"-214"
 Inter-H-H (h 8, h 11) 232-232" 235-235"

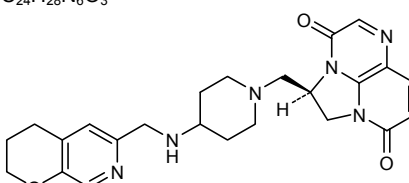
N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
 H CH2 N84.4:
 303, 303"

flutafuranolum (¹⁸F)flutafuranol (¹⁸F)2-{2-[¹⁸F]fluoro-6-(methylamino)pyridin-3-yl}-1-benzofuran-5-olflutafuranol (¹⁸F)2-{2-[¹⁸F]fluoro-6-(méthylamino)pyridin-3-yl}-1-benzofuran-5-olflutafuranol (¹⁸F)2-{2-[¹⁸F]fluoro-6-(metilamino)piridin-3-il}-1-benzofuran-5-olC₁₄H₁₁¹⁸FN₂O₂

follitropinum delta

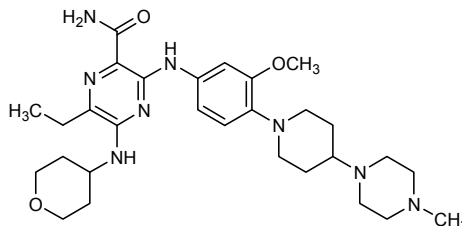
follitropin delta

recombinant DNA derived heterodimer of human glycoprotein hormones alpha chain and follitropin subunit beta (FSH-beta) follicle-stimulating hormone, expressed in PER.C6 cells, glycoform delta

follitropine delta	hétérodimère constitué de la chaîne alpha des hormones glycoprotéiques et de la sous-unité bêta de la follitropine (HFS-bêta) humaines, hormone folliculostimulante, exprimée dans les cellules PER.C6 à partir d'ADN recombinant, forme glycosylée delta
folitropina delta	heterodímero constituido por la cadena alfa de las hormonas glicoproteicas y la subunidad beta de la follitropina (HFS-beta) humanas, hormona estimulante del foliculo, expresada en células PER.C6 a partir de ADN recombinante, forma glicosilada delta
	<p>alpha chain / chaîne alpha / cadena alfa APDVQDCPEC TLQENPFFSQ PGAPILQCMG CCFSRAYPTF LRSKKTMLVQ 50 KNVTSESTCC VAKSYNRVTV MGGFKVENHT ACHCSTCYH KS 92</p> <p>beta chain / chaîne bêta / cadena beta NSCELTNITI AIEKEECRFC ISINTTWCAG YCYTRDLVYK DPARPKIQKT 50' CTFKELVYET VRVPGCAHHA DSLTYFPVAT QCHCGKCDSD STDCTVRGLG 100' PSYCSFGEMK E 111'</p> <p>Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro 7-31 10-60 28-82 32-84 59-87 3'-51' 17'-66' 20'-104' 28'-82' 32'-84' 87'-94'</p> <p>Glycosylation sites (N) / Sites de glycosylation (N) / Posiciones de glicosilación (N) Asn-52 Asn-78 Asn-7' Asn-24'</p>
gepotidacinum gepotidacin	(2 <i>R</i>)-2-[(4-[(3,4-dihydro-2 <i>H</i> -pyrano[2,3- <i>c</i>]pyridin-6-yl)methyl]amino)piperidin-1-yl)methyl]-1,2-dihydro-3 <i>H</i> ,8 <i>H</i> -2a,5,8a-triazaacenaphthylene-3,8-dione
gépotidacine	(2 <i>R</i>)-2-[(4-[(3,4-dihydro-2 <i>H</i> -pyrano[2,3- <i>c</i>]pyridin-6-yl)méthyl]amino)pipéridin-1-yl)méthyl]-1,2-dihydro-3 <i>H</i> ,8 <i>H</i> -2a,5,8a-triazaacénaphthylène-3,8-dione
gepotidacina	(2 <i>R</i>)-2-[(4-[(3,4-dihidro-2 <i>H</i> -pirano[2,3- <i>c</i>]piridin-6-il)metil]amino)piperidin-1-il)metil]-1,2-dihidro-3 <i>H</i> ,8 <i>H</i> -2a,5,8a-triazaacenaftileno-3,8-diona
	<p>$C_{24}H_{28}N_6O_3$</p> 
gilteritinibum gilteritinib	6-ethyl-3-{3-methoxy-4-[4-(4-methylpiperazin-1-yl)piperidin-1-yl]anilino}-5-[(oxan-4-yl)amino]pyrazine-2-carboxamide
giltéritinib	6-éthyl-3-{3-méthoxy-4-[4-(4-méthylpipérazin-1-yl)pipéridin-1-yl]anilino}-5-[(oxan-4-yl)amino]pyrazine-2-carboxamide

gilteritinib

6-etil-3-{4-[4-(4-metilpiperazin-1-il)piperidin-1-il]-3-metoxianilino}-5-[[oxan-4-il)amino]pirazina-2-carboxamida

 $C_{29}H_{44}N_8O_3$ 

indimilastum

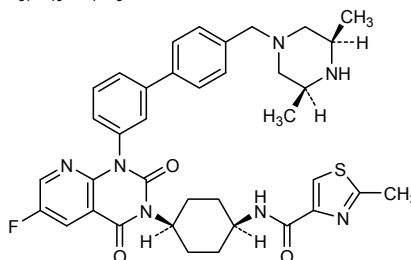
indimilast

N-{*cis*-4-[1-(4'-[[[(3*R*,5*S*)-3,5-dimetilpiperazin-1-yl]metil]}[1,1'-bifenil]-3-yl]-6-fluoro-2,4-dioxo-1,4-dihidropirido[2,3-*d*]pirimidin-3(2*H*)-yl]ciclohexil)-2-metil-1,3-tiazol-4-carboxamida

indimilast

N-{*cis*-4-[1-(4'-[[[(3*R*,5*S*)-3,5-diméthylpipérazin-1-yl]méthyl]}[1,1'-biphényl]-3-yl]-6-fluoro-2,4-dioxo-1,4-dihidropirido[2,3-*d*]pirimidin-3(2*H*)-yl]ciclohexil)-2-méthyl-1,3-tiazol-4-carboxamida

indimilast

N-{*cis*-4-[1-(4'-[[[(3*R*,5*S*)-3,5-dimetilpiperazin-1-il]metil]}[1,1'-bifenil]-3-il)-6-fluoro-2,4-dioxo-1,4-dihidropirido[2,3-*d*]pirimidin-3(2*H*)-il]ciclohexil)-2-metil-1,3-tiazol-4-carboxamida $C_{37}H_{40}FN_7O_3S$ 

indusatumabum #

indusatumab

immunoglobulin G1-kappa, anti-[*Homo sapiens* GUCY2C (guanylate cyclase 2C, guanylyl cyclase C, GCC, guanylate cyclase C, GC-C, heat-stable enterotoxin receptor, hSTAR, intestinal guanylate cyclase)], *Homo sapiens* monoclonal antibody; gamma1 heavy chain (1-449) [*Homo sapiens* VH (IGHV4-34*01 (94.80%) -(IGHD)-IGHJ1*01) [8.7.13] (1-119)-IGHG1*01 (CH1 (120-217), hinge (218-232), CH2 (233-342), CH3 (343-447), CHS (448-449)) (120-449)], (222-214')-disulfide with kappa light chain (1'-214') [*Homo sapiens* V-KAPPA (IGKV3-15*01 (95.80%) -IGKJ1*01 K123>N (103) [6.3.9] (1'-107') -IGKC*01 (108'-214')]; dimer (228-228":231-231")-bisdisulfide

indusatumab

immunoglobuline G1-kappa, anti-[*Homo sapiens* GUCY2C (guanylate cyclase 2C, guanylyl cyclase C, GCC, guanylate cyclase C, GC-C, récepteur d'entérotoxine résistante à la chaleur, hSTAR, guanylate cyclase intestinale)], *Homo sapiens* anticorps monoclonal;
chaîne lourde gamma1 (1-449) [*Homo sapiens* VH (IGHV4-34*01 (94.80%) -(IGHD)-IGHJ1*01) [8.7.13] (1-119)-IGHG1*01 (CH1 (120-217), charnière (218-232), CH2 (233-342), CH3 (343-447), CHS (448-449))] (120-449)], (222-214')-disulfure avec la chaîne légère kappa (1'-214') [*Homo sapiens* V-KAPPA (IGKV3-15*01 (95.80%) -IGKJ1*01 K123>N (103) [6.3.9] (1'-107') -IGKC*01 (108'-214'))]; dimère (228-228":231-231")-bisdisulfure

indusatumab

immunoglobulina G1-kappa, anti-[GUCY2C de *Homo sapiens* (guanilato ciclase 2C, guanilil ciclase C, GCC, guanilato ciclase C, GC-C, receptor de enterotoxina resistente al calor, hSTAR, guanilato ciclase intestinal)], anticuerpo monoclonal de *Homo sapiens*;
cadena pesada gamma1 (1-449) [VH de *Homo sapiens* (IGHV4-34*01 (94.80%) -(IGHD)-IGHJ1*01) [8.7.13] (1-119) -IGHG1*01 (CH1 (120-217), bisagra (218-232), CH2 (233-342), CH3 (343-447), CHS (448-449))] (120-449)], (222-214')-disulfuro con la cadena ligera kappa (1'-214') [V-KAPPA de *Homo sapiens* (IGKV3-15*01 (95.80%) -IGKJ1*01 K123>N (103) [6.3.9] (1'-107') -IGKC*01 (108'-214'))]; dímero (228-228":231-231")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada
QVQLQQWAG LLKPSETLSL TCAVFGGSFS GYYSWIRQP PGKGLEWIGE 50
INHRGNTNDN PSLKSRVTIS VDTSRNQFAL KLSSTVAADT AVYGCARERG 100
YTYGNFDHWG QGTLVIVSSA STKGPSVFPL APSSKSTSGG TAALGCLVKD 150
YFPEPVTYSW NSGALTSGVH TTPAVLQSSG LYSLSVVTY FSSSLGTQTY 200
ICMVAHFKSN TKVDKVEPK SCOKTHTCP CPAPPELLGG SVFLPFRPK 250
DTLMSRTPE VTCVVDVSH EDPEVKFNMY VDGVEVHNAK YKPREEQNS 300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV 350
YTLPPSRDEL TKNQVSLTCL VKGFYPSDIA VEVESNGQPE NNYKTTTPVL 400
DSDGSEFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK 449

Light chain / Chaîne légère / Cadena ligera
EIVMTQSPAT LSVSPGERAT LSCRASQSVS RNLAWYQQKPK QGAPRLLIYG 50
ASTRATGIPA RFGSGSGSTE FTLTIGSLQS EDFAVYYCQQ YKTPRTFGQ 100
GTNVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNIFY PREAKVQWKV 150
DNLQALGNSGQ ESVTEQDSKD STYLSLSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEK 214

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-95 146-202 263-323 369-427
22"-95" 146"-202" 263"-323" 369"-427"
Intra-L (C23-C104) 23'-88' 134'-194'
23"'-88"' 134"'-194"
Inter-H-L (h 5-CL 126) 222-214' 222"-214"
Inter-H-H (h 11, h 14) 228-228" 231-231"

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

indusatumabum vedotinum #
indusatumab vedotin

immunoglobulin G1-kappa, anti-[*Homo sapiens* GUCY2C (guanylate cyclase 2C, guanylyl cyclase C, GCC, guanylate cyclase C, GC-C, heat-stable enterotoxin receptor, hSTAR, intestinal guanylate cyclase)], *Homo sapiens* monoclonal antibody;
gamma1 heavy chain (1-449) [*Homo sapiens* VH (IGHV4-34*01 (94.80%) -(IGHD)-IGHJ1*01) [8.7.13] (1-119)-IGHG1*01 (CH1 (120-217), hinge (218-232), CH2 (233-342), CH3 (343-447), CHS (448-449))] (120-449)], (222-214')-disulfide with kappa light chain (1'-214') [*Homo sapiens* V-KAPPA (IGKV3-15*01 (95.80%) -IGKJ1*01 K123>N (103) [6.3.9] (1'-107') -IGKC*01 (108'-214'))]; dimer (228-228":231-231")-bisdisulfide; conjugated, on an average of 3 to 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*".

indusatumab védotine

immunoglobuline G1-kappa, anti-[*Homo sapiens* GUCY2C (guanylate cyclase 2C, guanylyl cyclase C, GCC, guanylate cyclase C, GC-C, récepteur d'entérotoxine résistante à la chaleur, hSTAR, guanylate cyclase intestinale)], *Homo sapiens* anticorps monoclonal;
chaîne lourde gamma1 (1-449) [*Homo sapiens* VH (IGHV4-34*01 (94.80%) -(IGHD)-IGHJ1*01) [8.7.13] (1-119)-IGHG1*01 (CH1 (120-217), charnière (218-232), CH2 (233-342), CH3 (343-447), CHS (448-449)) (120-449)], (222-214')-disulfure avec la chaîne légère kappa (1'-214') [*Homo sapiens* V-KAPPA (IGKV3-15*01 (95.80%) -IGKJ1*01 K123>N (103) [6.3.9] (1'-107') -IGKC*01 (108'-214'))]; dimère (228-228'':231-231'')-bisdisulfure; conjugué, sur 3 à 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".

indusatumab vedotina

inmunoglobulina G1-kappa, anti-[GUCY2C de *Homo sapiens* (guailato ciclaza 2C, guanilil ciclaza C, GCC, guanilato ciclaza C, GC-C, receptor de enterotoxina resistente al calor, hSTAR, guanilato ciclase intestinal), *Homo sapiens* anticuerpo monoclonal;
cadena pesada gamma1 (1-449) [*Homo sapiens* VH (IGHV4-34*01 (94.80%) -(IGHD)-IGHJ1*01) [8.7.13] (1-119) -IGHG1*01 (CH1 (120-217), bisagra (218-232), CH2 (233-342), CH3 (343-447), CHS (448-449)) (120-449)], (222-214')-disulfuro con la cadena ligera kappa (1'-214') [*Homo sapiens* V-KAPPA (IGKV3-15*01 (95.80%) -IGKJ1*01 K123>N (103) [6.3.9] (1'-107') -IGKC*01 (108'-214'))]; dímero (228-228'':231-231'')-bisdisulfuro; conjugada, en una media de 3 a 4 cisteinil, con monometilauristatina E (MMAE), mediante un conector escindible de tipo maleimidocaproyl-valil-citrulinil-*p*-aminobenciloxicarbonil (mc-val-cit-PABC)
La fracción vedotina, pueden encontrarla en el documento "INN for pharmaceutical substances: Names for radicals, groups and others".

Heavy chain / Chaîne lourde / Cadena pesada

QVQLQIQGAG LLKPSSETLSL TCAVFGGSF GYYWSWIRQP PGKGLEWIGE 50
INHRGNTNDN PSLKSRVTIS VDTSKNQFAL KLSVTAADT AVYICARERG 100
YTYGNDFHWG QGTLVTVSSA STKGPSVFPL APSSKSTSGG TAALGLCVKD 150
YFPEPVTVSW NSGALTSVGH TFFAVLQSSG LYSLSVVTV PSSSLGTQTY 200
ICNVNHKPSN TKVDKKEPK SCDKTHCTCP CPAPPELLGGP SVFLFPPKPK 250
DTLMSRTPTE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREQKNS 300
TYRVVSVLTV LHQDVLNGKE YKCKVSNKAL PAPIERTISK AKGQPREPQV 350
YTLPPSRDEL TKNQVSLTCL VKGIFYPSDIA VEWESNGQPE NNYKTPPPVL 400
DSDGSEFLYS KLTVDKSRWQ QGNVFCSVM HEALHNYHTQ KSLSLSPGK 449

Light chain / Chaîne légère / Cadena ligera

EIVMTQSPAT LSVSPGERAT LSCRASQSVS RNLAWYQQKPK GQAPRLLIYG 50
ASTRATGIPA RFGSGSGSTE FTLTIGSLQS EDFAVVYCCQ YKTPRFTFGQ 100
GTNVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNIFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYLSSTLT LSKADYERHK VYACEVTHQG 200
LSSPVTKSFN RGEK 214

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

Intra-H (C23-C104) 22-95 146-202 263-323 369-427
22"-95" 146"-202" 263"-323" 369"-427"

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

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

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

*Two or three of the inter-chain disulfide bridges are not present, an average of 3 to 4 cysteinyl being conjugated each via a thioether bond to a drug linker.

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

*Faltan dos o tres puentes disulfuro inter-catenarios, una media de 3 a 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"

infigratinibum

infigratinib

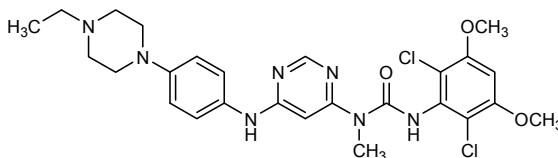
N'-(2,6-dichloro-3,5-dimethoxyphenyl)-*N*-{6-[4-(4-ethylpiperazin-1-yl)anilino]pyrimidin-4-yl}-*N*-methylurea

infigratinib

N'-(2,6-dichloro-3,5-diméthoxyphényl)-*N*-{6-[4-(4-éthylpipérazin-1-yl)anilino]pyrimidin-4-yl}-*N*-méthylurée

infigratinib

N'-(2,6-dicloro-3,5-dimetoxifenil)-*N*-{6-[4-(4-etilpiperazin-1-il)anilino]pirimidin-4-il}-*N*-metilurea

 $C_{26}H_{31}Cl_2N_7O_3$
**isatuximabum #**

isatuximab

immunoglobulin G1-kappa, anti-[*Homo sapiens* CD38 (ADP-ribosyl cyclase 1, cyclic ADP-ribose hydrolase 1, cADPr hydrolase 1, T10)], chimeric monoclonal antibody; gamma1 heavy chain (1-450) [*Mus musculus* VH (IGHV1-7*01 (80.60%) -(IGHD)-IGHJ4*01) [8.8.13] (1-120) -*Homo sapiens* IGHG1*01 (CH1 (121-218), hinge (219-233), CH2 (234-343), CH3 (344-448), CHS (449-450)) (121-450)], (223-214')-disulfide with kappa light chain (1'-214') [*Mus musculus* V-KAPPA (IGKV6-17*01 (89.50%) -IGKJ2*01) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (108'-214')]; dimer (229-229":232-232")-bisdisulfide

isatuximab

immunoglobuline G1-kappa, anti-[*Homo sapiens* CD38 (ADP-ribosyl cyclase 1, ADP-ribose cyclique hydrolase 1, cADPr hydrolase 1, T10)], anticorps monoclonal chimérique; chaîne lourde gamma1 (1-450) [*Mus musculus* VH (IGHV1-7*01 (80.60%) -(IGHD)-IGHJ4*01) [8.8.13] (1-120) -*Homo sapiens* IGHG1*01 (CH1 (121-218), charnière (219-233), CH2 (234-343), CH3 (344-448), CHS (449-450)) (121-450)], (223-214')-disulfure avec la chaîne légère kappa (1'-214') [*Mus musculus* V-KAPPA (IGKV6-17*01 (89.50%) -IGKJ2*01) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (108'-214')]; dimère (229-229":232-232")-bisdisulfure

isatuximab

immunoglobulina G1-kappa, anti-[CD38 de *Homo sapiens* (ADP-ribosil ciclaza 1, hidrolasa 1 de ADP-ribosa cíclica, cADPr hidrolasa 1, T10)], anticuerpo monoclonal quimérico; cadena pesada gamma1 (1-450) [*Mus musculus* VH (IGHV1-7*01 (80.60%) -(IGHD)-IGHJ4*01) [8.8.13] (1-120) -*Homo sapiens* IGHG1*01 (CH1 (121-218), bisagra (219-233), CH2 (234-343), CH3 (344-448), CHS (449-450)) (121-450)], (223-214')-disulfuro con la cadena ligera kappa (1'-214') [*Mus musculus* V-KAPPA (IGKV6-17*01 (89.50%) -IGKJ2*01) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (108'-214')]; dímero (229-229":232-232")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada
 QQVLVQSGAE VAKPGTSVKL SCKASGYTFT DYWMQWVKQR PGQGLEWIGT 50
 IYPPGDGTGY AQKFGKATL TADKSSKTVY MHLSSLASED SAVYYCARGD 100
 YYGNSLDYW QGQTSVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
 DYFPEPVTVS WNSGALTSVG HTFPAVLQSS GLYLSLSVVT VPSSSLGTQT 200
 YICNVNHKPS NTKVDKVEP KSCDKHTPCP PCPAPPELLGG PSVFLFPPKP 250
 KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYN 300
 STYRVVSVLT VHLQDNLNGK EYKCKVSNKA LPAPIEKTIS KARGQPREQP 350
 VYTLPPSRDE LTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTTPV 400
 LDDSGSFPLY SKLTVDKSRW QQGNVFCSCV MHEALHNHYT QKSLSLSPGK 450

Light chain / Chaîne légère / Cadena ligera
 DIVMTQSHLS MSTSLGDPVS ITCKASQDVS TVVAVYQQKPK GQSPRRLIYS 50
 ASYRYIGVDP RFTGSGAGTD FTFTISSVQA EDLAVYYCQQ HYSPPYTFGG 100
 GTKLEIKRTV AAPSVEIFPP SDEQLKSGTA SVVCLLNFFY PREAKVQWKV 150
 DNALQSGNSQ ESVTEQDSKD STYLSLSTLT LSKADYEKHK VYACEVTHQG 200
 LSSPVTKSFN RGECL

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"

lanopepdenum

lanopepden

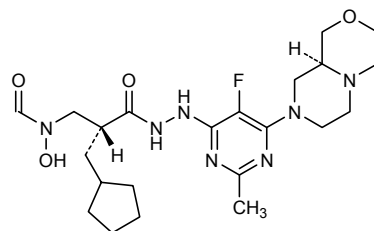
N-[(2*R*)-2-(cyclopentylmethyl)-3-(2-{5-fluoro-6-[(9*aS*)-hexahydropyrazino[2,1-*c*][1,4]oxazin-8(1*H*)-yl]-2-methylpyrimidin-4-yl}hydrazin-1-yl)-3-oxopropyl]-*N*-hydroxyformamide

lanopepdeène

N-[(2*R*)-2-(cyclopentylméthyl)-3-(2-{5-fluoro-6-[(9*aS*)-hexahydropyrazino[2,1-*c*][1,4]oxazin-8(1*H*)-yl]-2-méthylpyrimidin-4-yl}hydrazin-1-yl)-3-oxopropyl]-*N*-hydroxyformamide

lanopepdeén

N-[(2*R*)-2-(ciclopentilmetil)-3-(2-{5-fluoro-6-[(9*aS*)-hexahidropirazino[2,1-*c*][1,4]oxazin-8(1*H*)-il]-2-metilpirimidin-4-il}hidrazin-1-il)-3-oxopropil]-*N*-hidroxiformamida

C₂₂H₃₄FN₇O₄**lascufloxacinum**

lascufloxacin

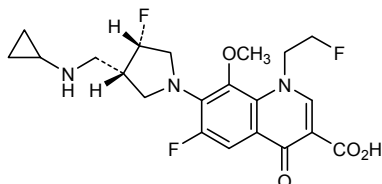
7-[(3*S*,4*S*)-3-[(cyclopropylamino)methyl]-4-fluoropyrrolidin-1-yl]-6-fluoro-1-(2-fluoroethyl)-8-methoxy-4-oxo-1,4-dihydroquinoline-3-carboxylic acid

lascufloxacine

acide 7-[(3*S*,4*S*)-3-[(cyclopropylamino)méthyl]-4-fluoropyrrolidin-1-yl]-6-fluoro-1-(2-fluoroéthyl)-8-méthoxy-4-oxo-1,4-dihydroquinoléine-3-carboxylique

lascufloxacino

ácido 7-[(3*S*,4*S*)-3-[(ciclopropilamino)metil]-4-fluoropirrolidin-1-il]-6-fluoro-1-(2-fluoroetil)-8-metoxi-4-oxo-1,4-dihidroquinoleína-3-carboxílico

 $C_{21}H_{24}F_3N_3O_4$
lavamilastum
lavamilast

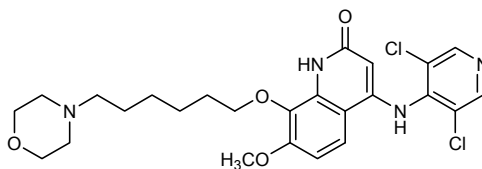
4-[(3,5-dichloropyridin-4-yl)amino]-7-metoxi-8-[[6-(morpholin-4-yl)hexil]oxy]quinolin-2(1*H*)-one

lavamilast

4-[(3,5-dichloropyridin-4-yl)amino]-7-méthoxy-8-[[6-(morpholin-4-yl)hexil]oxy]quinoléin-2(1*H*)-one

lavamilast

4-[(3,5-dicloropiridin-4-il)amino]-7-metoxi-8-[[6-(morfolin-4-il)hexil]oxi]quinolein-2(1*H*)-ona

 $C_{25}H_{30}Cl_2N_4O_4$
lilotomabum #
lilotomab

immunoglobulin G1-kappa, anti-[*Homo sapiens* CD37(TSPAN26, tetraspanin-26)], *Mus musculus* monoclonal antibody;
gamma1 heavy chain (1-443) [*Mus musculus* VH (IGHV1S135*01 (96.90%) -(IGHD)-IGHJ4*01) [8.8.12] (1-119) -IGHG1*01 (CH1 E84>Q (177), P95>T (193), R96>W (194) (120-216), hinge (217-229), CH2 (230-336), CH3 N84.2>D (395), N84.4>D (397) (337-441), CHS (442-443)) (120-443)], (221-214')-disulfide with kappa light chain (1'-214') [*Mus musculus* V-KAPPA (IGKV6-25*01 (93.70%) -IGKJ4*01) [6.3.9] (1'-107') -IGKC*01 (108'-214')]; dimer (223-223":226-226":228-228")-trisulfide

lilotomab

immunoglobuline G1-kappa, anti-[*Homo sapiens* CD37 (TSPAN26, tétraspanine-26)], *Mus musculus* anticorps monoclonal;
chaîne lourde gamma1 (1-443) [*Mus musculus* VH (IGHV1S135*01 (96.90%) -(IGHD)-IGHJ4*01) [8.8.12] (1-119) -IGHG1*01 (CH1 E84>Q (177), P95>T (193), R96>W (194) (120-216), charnière (217-229), CH2 (230-336), CH3 N84.2>D (395), N84.4>D (397) (337-441), CHS (442-443)) (120-443)], (221-214')-disulfure avec la chaîne légère kappa (1'-214') [*Mus musculus* V-KAPPA (IGKV6-25*01 (93.70%) -IGKJ4*01) [6.3.9] (1'-107') -IGKC*01 (108'-214')]; dimère (223-223":226-226":228-228")-trisulfure

lilotomab

inmunoglobulina G1-kappa, anti-[CD37 de *Homo sapiens* (TSPAN26, tetraspanina-26)], anticuerpo monoclonal de *Mus musculus*;
cadena pesada gamma1 (1-443) [VH de *Mus musculus* (IGHV1S135*01 (96.90%) -(IGHD)-IGHJ4*01) [8.8.12] (1-119) -IGHG1*01 (CH1 E84>Q (177), P95>T (193), R96>W (194) (120-216), bisagra (217-229), CH2 (230-336), CH3 N84.2>D (395), N84.4>D (397) (337-441), CHS (442-443)) (120-443)], (221-214')-disulfuro con la cadena ligera kappa (1'-214') [*Mus musculus* V-KAPPA (IGKV6-25*01 (93.70%) -IGKJ4*01) [6.3.9] (1'-107') -IGKC*01 (108'-214')]; dímero (223-223":226-226":228-228")-trisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

EIQLQQSGPE LVKPGASVKV SCASGYSEFT DYNMYWVKQS HGKSLIEWIGY 50
IDPYNGDTTY NQKFKGKATL TVDKSSSTAF IHLNSLTSED SAVYYCARSP 100
YGHYAMDYWG QGTSVTVSSA KTFPPSVYPL APGSAQTNS MVTLGCLVKG 150
YFPEPVTVTW NSGSLSSGVH TFFPAVLQSDL YTLSSSVTVF SSTWPSSETV 200
CNVAHPASST KVDKKLVPRD CGCKPCICTV PEVSSVFIFP PKFKDVLIT 250
LTPKVTGVV DISKDDPEVQ FSWFVDDVEV HTAQIQREE QFNSTFRSVS 300
ELPFMBQDWL NGKFKKRVN SNAFPPIEK TSKTKGRPK APQVYVTFPF 350
KEQMAKDKVS LTCMITDFEF EDITVENQWN GQPAENYKNT QPIMDTDGSY 400
FVYSKLNQK SNWEAGNTFT CSVLHEGLHN HRTKSLSHS PGK 443

Light chain / Chaîne légère / Cadena ligera

DIVMTQSHKL LSTSVGDRVS ITCKASQDVS TAVDWYQKQP GQSPKLLINW 50
ASTRHTGVDP RFTGSGSGTD YTLTISMQA EDLALYCRQ HYSTPFTFGS 100
GTKLEIKRAD AAPTVSIFFP SSEQLTSGGA SVVCFLNIFY PKDINVKWKI 150
DGSERQNGVL NSWTDQDSKD STYSMSSTLT LTKDEYERHN SYTCEATHKT 200
STSPIVKSFN RNEC 214

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

Intra-H (C23-C104) 22-96 146-201 257-317 363-421
22"-96" 146"-201" 257"-317" 363"-421"
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 7, h 10, h 12) 223-223" 226-226" 228-228"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
293, 293"

lokivetmabum

lokivetmab

immunoglobulin G2-kappa, anti-[*Canis lupus familiaris* IL31 (interleukin 31)], caninized monoclonal antibody;
gamma2 heavy chain (1-452) [caninized VH (*Canis lupus familiaris* IGHV-E2RCC8 (85.90%) -(IGHD)-IGHJ) [8.8.11] (1-118) -*Canis lupus familiaris* IGHG2*01 (CH1 (119-216), hinge (217-234), CH2 (235-344), CH3 (345-451), CHS (452)) (119-452)], (133-217')-disulfide with kappa light chain (1'-217') [caninized V-KAPPA (*Canis lupus familiaris* IGKV-F1PNY2 (56.00%) -IGKJ) [10.3.9] (1'-111') -*Canis lupus familiaris* IGKC*01 (112'-217')]; dimer (230-230":233-233")-bisulfide

lokivetmab immunoglobuline G2-kappa, anti-[*Canis lupus familiaris* IL31 (interleukine 31)], anticorps monoclonal caninisé; chaîne lourde gamma2 (1-452) [VH caninisé (*Canis lupus familiaris* IGHV-E2RCC8 (85.90%) -(IGHD)-IGHJ) [8.8.11] (1-118) -*Canis lupus familiaris* IGHG2*01 (CH1 (119-216), charnière (217-234), CH2 (235-344), CH3 (345-451), CHS (452)) (119-452)], (133-217')-disulfure avec la chaîne légère kappa (1'-217') [V-KAPPA caninisé (*Canis lupus familiaris* IGKV-F1PNY2 (56.00%) -IGKJ) [10.3.9] (1'-111') -*Canis lupus familiaris* IGKC*01 (112'-217')]; dimère (230-230":233-233")-bisdisulfure

lokivetmab inmunoglobulina G2-kappa, anti-[*Canis lupus familiaris* IL31 (interleukina 31)], anticuerpo monoclonal caninizado; cadena pesada gamma2 (1-452) [VH caninizado (*Canis lupus familiaris* IGHV-E2RCC8 (85.90%) -(IGHD)-IGHJ) [8.8.11] (1-118) -*Canis lupus familiaris* IGHG2*01 (CH1 (119-216), bisagra (217-234), CH2 (235-344), CH3 (345-451), CHS (452)) (119-452)], (133-217')-disulfuro con la cadena ligera kappa (1'-217') [V-KAPPA caninizado (*Canis lupus familiaris* IGKV-F1PNY2 (56.00%) -IGKJ) [10.3.9] (1'-111') -*Canis lupus familiaris* IGKC*01 (112'-217')]; dímero (230-230":233-233")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada
 EVQLVESGGD LVKPGGSLRL SCVASGFTFS NYGMSWVRQA PGKGLQWVAT 50
 ISYGGSYTY PDNIKGRFTI SRDNAKNTLY LQMNSLRAD TAMYYCVRGY 100
 GYDTMDYWGQ GTLVTYSSAS TTAPSVFPLA FSGGTSVSGT VALACLVSQY 150
 FPEPVTYWSN SGLTSGVHT PFSVLQSSGL YSLSSMVTVF SSRWSESTFT 200
 CNVAHPASKT KVDKVPFKRE NGRVRFPPDC PKCPAPEMLG GPSVFIFPFK 250
 PKDTLLIART PEVTCVVVDL DPEDFEVQLS WFDVGGKMQQT AKTQPREEQF 300
 NGTYRVSIVL PIGHQDWLKG KQFTCKVNNK ALPSPFIERTI SKARGQAHPQ 350
 SVYVLPESRE ELSKNFVSLT CLIKDFPFEP IDVEWQSNQG QEPESKRYRT 400
 PFLDEDEGSY FLYSKLSVDR SRWQRGDTFI CAVMHEALHN HYTQESLSHS 450
 PG 452

Light chain / Chaîne légère / Cadena ligera
 EIVMTQSPAS LSLSQEEKVT ITCKASQSVS FAGTGLMHWY QQKPGQAPKL 50
 LIYRASNLEA GVPFRFSGSG SGTDFSFSTIS SLEPEDVAVY YCQQSREYFW 100
 TFGQGTKLEI KRNDAPQAVY LFQFSPDQLH TGSASVCLL NSFYPKDINV 150
 KWKVDGVIQD TGIQESVTEQ DKDSTYSLSL TLTMSSTEYL SHELVSCEIT 200
 HKSLFSLIK SPQRSEK 217

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"-92" 138"-197"
 23"-92" 138"-197"

Inter-H-L (CH1 11-CL 126) 133-217 133"-217"
 Inter-H-H (h 14, h 17) 230-230" 233-233"

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

Other post-translational modifications / Autres modifications post-traductionnelles / Otras modificaciones post-traduccionales
 Lacking H chain C-terminal lysine (CHS K2>del)

lutetium (¹⁷⁷Lu) lilotomabum satetraxetanum #
 lutetium (¹⁷⁷Lu) lilotomab satetraxetan

immunoglobulin G1-kappa, anti-[*Homo sapiens* CD37 (SPAN26, tetraspanin-26)], *Mus musculus* monoclonal antibody, lutetium (Lu 177) radiolabelled satetraxetan (DOTA derivative) conjugate;
 gamma1 heavy chain (1-443) [*Mus musculus* VH (IGHV1S135*01 (96.90%) -(IGHD)-IGHJ4*01) [8.8.12] (1-119) -IGHG1*01 (CH1 E84>Q (177), P95>T (193), R96>W (194) (120-216), hinge (217-229), CH2 (230-336), CH3 N84.2>D (395), N84.4>D (397) (337-441), CHS (442-443)) (120-443)], (221-214')-disulfide with kappa light chain (1'-214') [*Mus musculus* V-KAPPA (IGKV6-25*01 (93.70%) -IGKJ4*01) [6.3.9] (1'-107') -IGKC*01 (108'-214')]; dimer (223-223":226-226":228-228")-trisdisulfide, an average of 1 to 2 amino groups (N^δ of lysines) are substituted:
 N-[rac-(4-[[[(2R)-1,4,7,10-tetrakis(carboxymethyl)-1,4,7,10-tetraazacyclododecan-2-yl]methyl]phenyl]carbamoithoyl] (¹⁷⁷Lu)lutetium(3+) chelate

lutécium (¹⁷⁷Lu) lilotomab satétraxétan

immunoglobuline G1-kappa, anti-[*Homo sapiens* CD37 (TSPAN26, tétraspanine-26)], *Mus musculus* anticorps monoclonal; conjugué au satétraxétan (dérivé DOTA) radiomarqué au lutécium (Lu 177); chaîne lourde gamma1 (1-443) [*Mus musculus* VH (IGHV1S135*01 (96.90%) -(IGHD)-IGHJ4*01) [8.8.12] (1-119) -IGHG1*01 (CH1 E84>Q (177), P95>T (193), R96>W (194) (120-216), charnière (217-229), CH2 (230-336), CH3 N84.2>D (395), N84.4>D (397) (337-441), CHS (442-443)) (120-443)], (221-214')-disulfure avec la chaîne légère kappa (1'-214') [*Mus musculus* V-KAPPA (IGKV6-25*01 (93.70%) -IGKJ4*01) [6.3.9] (1'-107') -IGKC*01 (108'-214')]; dimère (223-223":226-226":228-228")-trisdisulfure, une moyenne de 1 à 2 groupes amino (N^o de lysines) sont substitués: *N*-[*rac*-(4-(((2*R*)-1,4,7,10-tétrakis(carboxyméthyl)-1,4,7,10-tétrazaacyclododécan-2-yl)méthyl)phényl)carbamothioyl] chélate de (¹⁷⁷Lu)lutécium(3+)

lutecio (¹⁷⁷Lu) lilotomab satetraxetán

inmunoglobulina G1-kappa, anti-[CD37 de *Homo sapiens* (TSPAN26, tetraspanina-26)], anticuerpo monoclonal de *Mus musculus*, conjugada al satetraxetán (derivado DOTA) radiomarcado con lutecio (Lu 177); cadena pesada gamma1 (1-443) [VH de *Mus musculus* (IGHV1S135*01 (96.90%) -(IGHD)-IGHJ4*01) [8.8.12] (1-119) -IGHG1*01 (CH1 E84>Q (177), P95>T (193), R96>W (194) (120-216), bisagra (217-229), CH2 (230-336), CH3 N84.2>D (395), N84.4>D (397) (337-441), CHS (442-443)) (120-443)], (221-214')-disulfuro con la cadena ligera kappa (1'-214') [*Mus musculus* V-KAPPA (IGKV6-25*01 (93.70%) -IGKJ4*01) [6.3.9] (1'-107') -IGKC*01 (108'-214')]; dímero (223-223":226-226":228-228")-trisdisulfuro; pro termino medio, 1 a 2 grupos amino (N^o de lisinas) están sustituidos: *N*-[*rac*-(4-(((2*R*)-1,4,7,10-tetrakis(carboximetil)-1,4,7,10-tetraazacyclododecan-2-il]metil)fenil)carbamotioil] quelato de (¹⁷⁷Lu)lutecio(3+)

Heavy chain / Chaîne lourde / Cadena pesada
 EIQLQQSGPE LVKPGASVKV SCRASGYSFT DYNMYWVKQS HGKSLIEWIGY 50
 IDPFGNDTTY NQKFRGKATL TVDKSSSTAF IHLNSLTSFD SAVIYCARSF 100
 YGHYAMDYWG QGTSVTVSSA RTTFPSVYPL AFGSAAQTNS MVTGLCLVKG 150
 YFPEPVTYTW NSGSLSSGVH TFFAVLQSDL YTLSSSVYFP STFWSEVTV 200
 CNVAHPASST KVDKKTIVERD CGCKPCICITV PEVSSVIFFP PKPKDVLIT 250
 LTPKVTQVVV DISKDDPEVQ FSWFVDVDEV HTAQTPREE QFNSTFRSVS 300
 ELPIMHQDWL NGKEFKCRVN SAAFPAPIEK TISKTKGRPK APQVYTIPPP 350
 KEQMAKDQVS LTCMITDFFP EDITVEQWVN GQPAENYKNT QPIMDTGGSY 400
 FVYSKLNQVK SNWEAGNTFT CSVLHEGLHN HHTEKLSLHS PGK 443

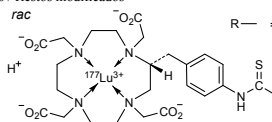
Light chain / Chaîne légère / Cadena ligera
 DIVMTQSHKL LSTSVGDRVS ITCKASQDVS TAVDWYQQPK GQSPKLLINW 50
 ASTRHTGVPD RFTGSGSGTD YTLTISSMQA EDLALYCRQ HYSTPPTFGS 100
 GTKLEIKRAD AAPTVISIFPP SSEQLTSGGA SVVCFLNFFY PKDINVKWKI 150
 DGSERQNGVL NSWTDQDSKD STYMSSTLT LTKDEYERHN SYTCEATHKT 200
 STSPIVKSFN RNEC 214

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
 Intra-H (C23-C104) 22-96 146-201 257-317 363-421
 22"-96" 146"-201" 257"-317" 363"-421"
 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 7, h 10, h 12) 223-223" 226-226" 228-228"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
 H CH2 N84.4:
 293, 293"

Modified residues / Résidus modifiés / Restos modificados

An average of 1 to 2 are N-substituted by R
 Environ 1 à 2 sont N-substitués par R
 Una media de 1 a 2 están N-substituidos por R



motolimodum

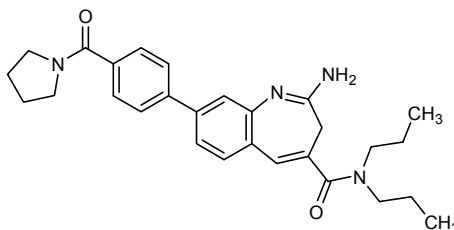
motolimod

2-amino-*N,N*-dipropyl-8-[4-(pyrrolidine-1-carbonyl)phenyl]-3*H*-1-benzazepine-4-carboxamide

motolimod

2-amino-*N,N*-dipropyl-8-[4-(pyrrolidine-1-carbonyl)phényl]-3*H*-1-benzazépine-4-carboxamide

motolimod

2-amino-*N,N*-dipropil-8-[4-(pirrolidina-1-carbonil)fenil]-3*H*-1-benzazepina-4-carboxamidaC₂₈H₃₄N₄O₂**necuparanibum**

necuparanib

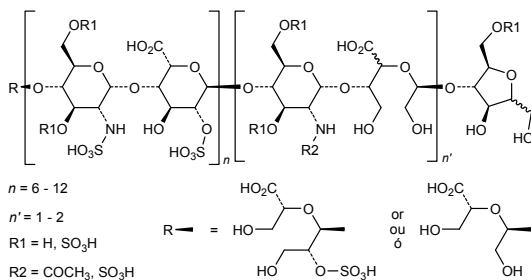
low molecular mass heparan sulfate mimetic compound that is obtained by nitrous sodium depolymerization of heparin from porcine intestinal mucosa, sodium periodate glycol split oxidation of uronic acids elements and sodium borohydride reduction of aldehydes produced during oxidation; the majority of the components have a split uronic acid structure at the non-reducing end and a 2,5-anhydromannitol structure at the reducing end of their chain; the average molecular weight range is 5000 to 8000 Da; the degree of sulfatation is about 2 per disaccharidic unit

nécuparanib

dérivé de basse masse moléculaire à action mimétique du sulfate d'héparane, obtenu par dépolymérisation d'héparine de muqueuse intestinale de porc, catalysée par du nitrite de sodium, puis dégradation oxydative des glycols des unités uroniques par le périodate de sodium et réduction, par le borohydrure de sodium, des aldéhydes produits ; la majorité des composants ont, une structure éclatée d'acide uronique à leur extrémité non-réductrice et une structure 2,5-anhydromannitol à leur extrémité réductrice, une masse molaire comprise entre 4500 et 7200 daltons et un degré de sulfatation d'environ de 2 par unité disaccharide

necuparanib

derivado de baja masa molecular de acción mimética de la del sulfato de heparán, obtenido por despolimerización de heparina de mucosa intestinal de cerdo, catalizada por nitrito de sodio, seguida de degradación oxidativa, con peryodato de sodio, de los glicoles de las unidades urónicas y reducción, con borohidruro de sodio, de los aldehídos producidos; la mayoría de los componentes tienen una estructura abierta de ácido urónico en su extremo no-reductor y una estructura 2,5-anhidromanitol en el reductor, el peso molecular medio está comprendido entre 4500 y 7200 daltons y el grado de sulfatación es aproximadamente de 2 por unidad de disacárido



neloniclinum

nelonicline

(3*R*,4*s*,5*S*)-4-[(5-phenyl-1,3,4-thiadiazol-2-yl)oxy]-1-azaadamantane

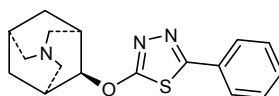
nélonicline

(3*R*,4*s*,5*S*)-4-[(5-phényl-1,3,4-thiadiazol-2-yl)oxy]-1-azaadamantane

neloniclina

(3*R*,4*s*,5*S*)-4-[(5-fenil-1,3,4-tiadiazol-2-il)oxi]-1-azaadamantano

C₁₇H₁₉N₃OS



nemolizumabum #

nemolizumab

immunoglobulin G2-kappa, anti-[*Homo sapiens* IL31RA (interleukin 31 receptor subunit alpha)], humanized monoclonal antibody;
 gamma2 heavy chain (1-445) [humanized VH (*Homo sapiens* IGHV1-2*02 (83.70%) -(IGHD)-IGHJ5*01) [8.8.14] (1-121) -*Homo sapiens* IGHG2*01 (CH1 C10>S (135), R12>K (137), E16>G (141), S17>G (142) (122-219), hinge C4>S (223) (220-231), CH2 H30>Q (268) (232-340), CH3 R11>Q (355), Q98>E (419) (341-445)) (122-445)], (224-214')-disulfide with kappa light chain (1'-214') [humanized V-KAPPA (*Homo sapiens* IGKV1-39*01 (82.10%) - IGKJ4*01) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 (108'-214')]; dimer (227-227'':230-230'')-bisdisulfide

némolizumab	<p>immunoglobuline G2-kappa, anti-[<i>Homo sapiens</i> IL31RA (sous-unité alpha du récepteur de l'interleukine 31)], anticorps monoclonal humanisé;</p> <p>chaîne lourde gamma2 (1-445) [VH humanisé (<i>Homo sapiens</i> IGHV1-2*02 (83.70%) -(IGHD)-IGHJ5*01) [8.8.14] (1-121) -<i>Homo sapiens</i> IGHG2*01 (CH1 C10>S (135), R12>K (137), E16>G (141), S17>G (142) (122-219), charnière C4>S (223) (220-231), CH2 H30>Q (268) (232-340), CH3 R11>Q (355), Q98>E (419) (341-445)) (122-445)], (224-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA humanisé (<i>Homo sapiens</i> IGKV1-39*01 (82.10%) -IGKJ4*01) [6.3.9] (1'-107') -<i>Homo sapiens</i> IGKC*01 (108'-214')]; dimère (227-227":230-230")-bisdisulfure</p>
nemolizumab	<p>inmunoglobulina G2-kappa, anti-[IL31RA de <i>Homo sapiens</i> (subunidad alfa del receptor de la interleukina 31)], anticuerpo monoclonal humanizado;</p> <p>cadena pesada gamma2 (1-445) [VH humanizado (<i>Homo sapiens</i> IGHV1-2*02 (83.70%) -(IGHD)-IGHJ5*01) [8.8.14] (1-121) -<i>Homo sapiens</i> IGHG2*01 (CH1 C10>S (135), R12>K (137), E16>G (141), S17>G (142) (122-219), bisagra C4>S (223) (220-231), CH2 H30>Q (268) (232-340), CH3 R11>Q (355), Q98>E (419) (341-445)) (122-445)], (224-214')-disulfuro con la cadena ligera kappa (1'-214') [V-KAPPA humanizado (<i>Homo sapiens</i> IGKV1-39*01 (82.10%) -IGKJ4*01) [6.3.9] (1'-107') -<i>Homo sapiens</i> IGKC*01 (108'-214')]; dímero (227-227":230-230")-bisdisulfuro</p>
	<p>Heavy chain / Chaîne lourde / Cadena pesada</p> <pre> QVQLVQSGAE VKKPGASVKV SCKASGYTFT GYIMNWRQA PGQGLEWMGL 50 INPYNGGTDY NPFQQRVTI TADKSTSTAY MELSSLRSRD TAVYYCARDG 100 YDDGPTLET WGQGTLLVTSV SASTKGPSVF PLAPSSKSTS GGTAAALGCLV 150 KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSV TVPSSNFGTQ 200 TYTCNVDHKP SNTKVDKTVS RKSCVECPFC PAPPVAGPSV FLFPFKKDT 250 LMSRTEPVT CVVVDVSDQD FEVQFNWYVD GVEVHNAKTK PREEQENSTF 300 RVVSVLTVVH QDMLNGKEYK CKVSNKGLPA FIEKTIKTK GPREFQVYT 350 LPFSQEEMTK NQVSLTCLVK GYFSPDAVE WESNGQPEMN YKTTPEMLDS 400 DGSFFLYSKL TVDKSRWQEG NVFSCSVMH EALHNHYTQKS LSLSP 445 </pre>
	<p>Light chain / Chaîne légère / Cadena ligera</p> <pre> DIQMTQSPSS LSASVGRVIT ITCQASEDIY SFVAVYQQKP GKAPKLLIYN 50 AQTEAQGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQH HYDSPLTFGG 100 GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNIFY PREAKVQWKV 150 DNALQSGNSQ ESVTEQDSKD STYLSLSTLT LSKADYEKHK VYACEVTHQG 200 LSSPVTKSFN RGEK 214 </pre>
	<p>Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro</p> <p>Intra-H (C23-C104) 22-96 148-204 261-321 367-425 22"-96" 148"-204" 261"-321" 367"-425"</p> <p>Intra-L (C23-C104) 23'-88' 134'-194' 23"'-88"' 134"'-194"</p> <p>Inter-H-L (h 5-CL 126) 224-214' 224"-214" Inter-H-H (h 8, h 11) 227-227" 230-230"</p>
	<p>N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación</p> <p>H CH2 N84.4: 297, 297"</p>
	<p>Other post-translational modifications / Autres modifications post-traductionnelles / Otras modificaciones post-traduccionales</p> <p>Lacking H chain C-terminal glycine and lysine (CHS G1>del, K2>del)</p>

nusinersenum

nusinersen

all-P-ambo-2'-O-(2-methoxyethyl)-5-methyl-P-thiouridylyl-(3'→5')-2'-O-(2-methoxyethyl)-5-methyl-P-thiocytidylyl-(3'→5')-2'-O-(2-methoxyethyl)-P-thioadenylyl-(3'→5')-2'-O-(2-methoxyethyl)-5-methyl-P-thiocytidylyl-(3'→5')-2'-O-(2-methoxyethyl)-5-methyl-P-thiouridylyl-(3'→5')-2'-O-(2-methoxyethyl)-5-methyl-P-thiouridylyl-(3'→5')-2'-O-(2-methoxyethyl)-5-methyl-P-thiouridylyl-(3'→5')-2'-O-(2-methoxyethyl)-5-methyl-P-thiocytidylyl-(3'→5')-2'-O-(2-methoxyethyl)-P-thioadenylyl-(3'→5')-2'-O-(2-methoxyethyl)-5-methyl-P-thiouridylyl-(3'→5')-2'-O-(2-methoxyethyl)-P-thioadenylyl-(3'→5')-2'-O-(2-methoxyethyl)-P-thioadenylyl-(3'→5')-2'-O-(2-methoxyethyl)-5-methyl-P-thiouridylyl-(3'→5')-2'-O-(2-methoxyethyl)-P-thioguanilyl-(3'→5')-2'-O-(2-methoxyethyl)-5-methyl-P-thiocytidylyl-(3'→5')-2'-O-(2-methoxyethyl)-5-methyl-P-thiouridylyl-(3'→5')-2'-O-(2-methoxyethyl)-P-thioguanilyl-(3'→5')-2'-O-(2-methoxyethyl)guanosine

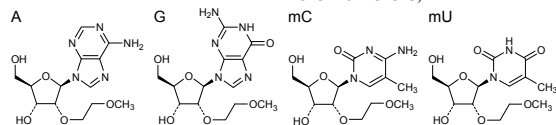
nusinersen

tout-P-ambo-2'-O-(2-méthoxyéthyl)-5-méthyl-P-thiouridylyl-(3'→5')-2'-O-(2-méthoxyéthyl)-5-méthyl-P-thiocytidylyl-(3'→5')-2'-O-(2-méthoxyéthyl)-P-thioadénylyl-(3'→5')-2'-O-(2-méthoxyéthyl)-5-méthyl-P-thiocytidylyl-(3'→5')-2'-O-(2-méthoxyéthyl)-5-méthyl-P-thiouridylyl-(3'→5')-2'-O-(2-méthoxyéthyl)-5-méthyl-P-thiouridylyl-(3'→5')-2'-O-(2-méthoxyéthyl)-5-méthyl-P-thiouridylyl-(3'→5')-2'-O-(2-méthoxyéthyl)-5-méthyl-P-thiocytidylyl-(3'→5')-2'-O-(2-méthoxyéthyl)-P-thioadénylyl-(3'→5')-2'-O-(2-méthoxyéthyl)-5-méthyl-P-thiouridylyl-(3'→5')-2'-O-(2-méthoxyéthyl)-P-thioadénylyl-(3'→5')-2'-O-(2-méthoxyéthyl)-P-thioadénylyl-(3'→5')-2'-O-(2-méthoxyéthyl)-5-méthyl-P-thiouridylyl-(3'→5')-2'-O-(2-méthoxyéthyl)-P-thioadénylyl-(3'→5')-2'-O-(2-méthoxyéthyl)-5-méthyl-P-thiouridylyl-(3'→5')-2'-O-(2-méthoxyéthyl)-P-thioguanilyl-(3'→5')-2'-O-(2-méthoxyéthyl)-5-méthyl-P-thiocytidylyl-(3'→5')-2'-O-(2-méthoxyéthyl)-5-méthyl-P-thiouridylyl-(3'→5')-2'-O-(2-méthoxyéthyl)-P-thioguanilyl-(3'→5')-2'-O-(2-méthoxyéthyl)guanosine

nusinersén

todo-P-ambo-2'-O-(2-metoxietil)-5-metil-P-tiouridilil-(3'→5')-2'-O-(2-metoxietil)-5-metil-P-tiocitidilil-(3'→5')-2'-O-(2-metoxietil)-P-tioadenilil-(3'→5')-2'-O-(2-metoxietil)-5-metil-P-tiocitidilil-(3'→5')-2'-O-(2-metoxietil)-5-metil-P-tiouridilil-(3'→5')-2'-O-(2-metoxietil)-5-metil-P-tiouridilil-(3'→5')-2'-O-(2-metoxietil)-5-metil-P-tiouridilil-(3'→5')-2'-O-(2-metoxietil)-5-metil-P-tiocitidilil-(3'→5')-2'-O-(2-metoxietil)-P-tioadenilil-(3'→5')-2'-O-(2-metoxietil)-P-tioadenilil-(3'→5')-2'-O-(2-metoxietil)-5-metil-P-tiouridilil-(3'→5')-2'-O-(2-metoxietil)-P-tioguanilil-(3'→5')-2'-O-(2-metoxietil)-5-metil-P-tiocitidilil-(3'→5')-2'-O-(2-metoxietil)-5-metil-P-tiouridilil-(3'→5')-2'-O-(2-metoxietil)-P-tioguanilil-(3'→5')-2'-O-(2-metoxietil)guanosina

$C_{234}H_{340}N_{61}O_{128}P_{17}S_{17}$
 [2'-O-(2-methoxyethyl)](3'-5')(P-thio)(mU-mC-A-mC-mU-mU-mU-mC-A-mU-A-A-mU-G-mC-mU-G-G)



onalespibum

onalespib

[2,4-dihydroxy-5-(propan-2-yl)phenyl]{5-[(4-methylpiperazin-1-yl)methyl]-1,3-dihydro-2*H*-isoindol-2-yl}methanone

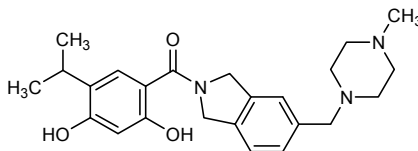
onalespib

[2,4-dihydroxy-5-(propan-2-yl)phényl]{5-[(4-méthylpipérazin-1-yl)méthyl]-1,3-dihydro-2*H*-isoindol-2-yl}méthanone

onalespib

[2,4-dihidroxi-5-(propan-2-il)fenil]{5-[(4-metilpiperazin-1-il)metil]-1,3-dihidro-2*H*-isoindol-2-il}metanona

$C_{24}H_{31}N_3O_3$



ozanimodum

ozanimod

5-(3-((1*S*)-1-[(2-hydroxyethyl)amino]-2,3-dihydro-1*H*-inden-4-yl)-1,2,4-oxadiazol-5-yl)-2-[(propan-2-yl)oxy]benzonitrile

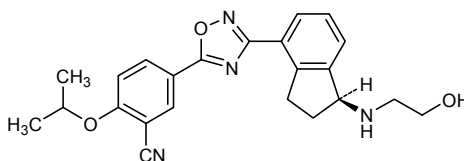
ozanimod

5-(3-((1*S*)-1-[(2-hydroxyéthyl)amino]-2,3-dihydro-1*H*-indén-4-yl)-1,2,4-oxadiazol-5-yl)-2-[(propan-2-yl)oxy]benzonitrile

ozanimod

5-(3-((1*S*)-1-[(2-hidroxietil)amino]-2,3-dihidro-1*H*-inden-4-il)-1,2,4-oxadiazol-5-il)-2-[(propan-2-il)oxi]benzonitrilo

$C_{23}H_{24}N_4O_3$



pegpleranibum

pegpleranib

5'-O-[(6-{N², N⁶-bis[α-carbonyl-ω-methoxypoly(oxyethane-1,2-diy)]-DL-lysylamido}hexyl)oxy]hydroxyphosphoryl-2'-deoxycytidyl-(3'→5')-2'-deoxyadenyl-(3'→5')-2'-deoxyguanylyl-(3'→5')-2'-deoxyguanylyl-(3'→5')-2'-deoxycytidyl-(3'→5')-2'-deoxy-2'-fluorouridyl-(3'→5')-2'-deoxyadenyl-(3'→5')-2'-deoxy-2'-fluorocytidyl-(3'→5')-2'-O-methylguanylyl-(3'→17)-hydroxy[(17-hydroxy-3,6,9,12,15-pentaoxaheptadecyl)oxy]phosphoryl-(1→5')-2'-deoxycytidyl-(3'→5')-2'-deoxyguanylyl-(3'→5')-thymidyl-(3'→5')-2'-deoxyadenyl-(3'→5')-2'-O-methylguanylyl-(3'→5')-2'-deoxyadenyl-(3'→5')-2'-O-methylguanylyl-(3'→5')-2'-deoxycytidyl-(3'→5')-2'-deoxyadenyl-(3'→5')-2'-deoxy-2'-fluorouridyl-(3'→5')-2'-deoxy-2'-fluorocytidyl-(3'→5')-2'-O-methyladenyl-(3'→17)-hydroxy[(17-hydroxy-3,6,9,12,15-pentaoxaheptadecyl)oxy]phosphoryl-(1→5')-thymidyl-(3'→5')-2'-deoxyguanylyl-(3'→5')-2'-deoxyadenyl-(3'→5')-thymidyl-(3'→5')-2'-deoxy-2'-fluorocytidyl-(3'→5')-2'-deoxy-2'-fluorocytidyl-(3'→5')-2'-deoxy-2'-fluorouridyl-(3'→5')-2'-O-methylguanylyl-(3'→3')-thymidine

pegpléranib

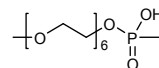
5'-O-[(6-{N², N⁶-bis[α-carbonyl-ω-méthoxypoly(oxyéthane-1,2-diy)]-DL-lysylamido}hexyl)oxy]hydroxyphosphoryl-2'-déoxycytidyl-(3'→5')-2'-déoxyadényl-(3'→5')-2'-déoxyguanylyl-(3'→5')-2'-déoxyguanylyl-(3'→5')-2'-déoxycytidyl-(3'→5')-2'-déoxy-2'-fluorouridyl-(3'→5')-2'-déoxyadényl-(3'→5')-2'-déoxy-2'-fluorocytidyl-(3'→5')-2'-O-méthylguanylyl-(3'→17)-hydroxy[(17-hydroxy-3,6,9,12,15-pentaoxaheptadécy]oxy]phosphoryl-(1→5')-2'-déoxycytidyl-(3'→5')-2'-déoxyguanylyl-(3'→5')-thymidyl-(3'→5')-2'-déoxyadényl-(3'→5')-2'-O-méthylguanylyl-(3'→5')-2'-déoxyadényl-(3'→5')-2'-O-méthylguanylyl-(3'→5')-2'-déoxycytidyl-(3'→5')-2'-déoxyadényl-(3'→5')-2'-déoxy-2'-fluorouridyl-(3'→5')-2'-déoxy-2'-fluorocytidyl-(3'→5')-2'-O-méthyladényl-(3'→17)-hydroxy[(17-hydroxy-3,6,9,12,15-pentaoxaheptadécy]oxy]phosphoryl-(1→5')-thymidyl-(3'→5')-2'-déoxyguanylyl-(3'→5')-2'-déoxyadényl-(3'→5')-thymidyl-(3'→5')-2'-déoxy-2'-fluorocytidyl-(3'→5')-2'-déoxy-2'-fluorocytidyl-(3'→5')-2'-déoxy-2'-fluorouridyl-(3'→5')-2'-O-méthylguanylyl-(3'→3')-thymidine

pegpleranib

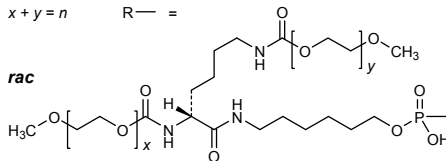
5'-O-[(6-{N², N⁶-bis[α-carbonil-ω-metoxipoli(oxietano-1,2-diil)]-DL-lisilamido}hexil)oxi]hidroxifosforil-2'-desoxicidilil-(3'→5')-2'-desoxiadenilil-(3'→5')-2'-desoxiguanilil-(3'→5')-2'-desoxiguanilil-(3'→5')-2'-desoxi-2'-fluorouridilil-(3'→5')-2'-desoxiadenilil-(3'→5')-2'-desoxi-2'-fluorocitidilil-(3'→5')-2'-O-metilguanilil-(3'→17)-hidroxi[(17-hidroxi-3,6,9,12,15-pentaoxaheptadecil)oxi]fosforil-(1→5')-2'-desoxicidilil-(3'→5')-2'-desoxiguanilil-(3'→5')-timidilil-(3'→5')-2'-desoxiadenilil-(3'→5')-2'-O-metilguanilil-(3'→5')-2'-desoxiadenilil-(3'→5')-2'-O-metilguanilil-(3'→5')-2'-desoxicidilil-(3'→5')-2'-desoxiadenilil-(3'→5')-2'-desoxi-2'-fluorouridilil-(3'→5')-2'-desoxi-2'-fluorocitidilil-(3'→5')-2'-O-metiladenilil-(3'→17)-hidroxi[(17-hidroxi-3,6,9,12,15-pentaoxaheptadecil)oxi]fosforil-(1→5')-timidilil-(3'→5')-2'-desoxiguanilil-(3'→5')-2'-desoxiadenilil-(3'→5')-timidilil-(3'→5')-2'-desoxi-2'-fluorocitidilil-(3'→5')-2'-desoxi-2'-fluorocitidilil-(3'→5')-2'-desoxi-2'-fluorouridilil-(3'→5')-2'-O-metilguanilil-(3'→3')-timidina

(3'-5')-R-dC-dA-dG-dG-dC-dUfl-dA-dCfl-Gm3'-17Xp1-
5'dC-dG-dT-dA-Gm-dA-Gm-dC-dA-dUfl-dCfl-Am3'-
17Xp1-5'dT-dG-dA-dT-dCfl-dCfl-dUfl-Gm3'-3'dT
—Xp—

d (as prefix) = 2'-deoxy
fl (as suffix) = 2'-fluoro
m (as suffix) = 2'-O-methyl



$x + y = n$ R — =



pexidartinibum

pexidartinib

5-[(5-chloro-1*H*-pyrrolo[2,3-*b*]pyridin-3-yl)methyl]-
N-[[6-(trifluoromethyl)pyridin-3-yl]methyl]pyridin-2-amine

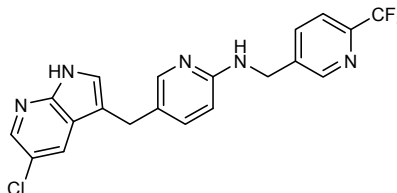
pexidartinib

5-[(5-chloro-1*H*-pyrrolo[2,3-*b*]pyridin-3-yl)méthyl]-
N-[[6-(trifluorométhyl)pyridin-3-yl]méthyl]pyridin-2-amine

pexidartinib

5-[(5-cloro-1*H*-pirrolo[2,3-*b*]piridin-3-il) metil]-
N-[[6-(trifluorometil)piridin-3-il]metil]piridin-2-amina

C₂₀H₁₅ClF₃N₅



pinometostatam

pinometostat

9-[5-deoxy-5-[[*cis*-3-[2-(5-*tert*-butyl-1*H*-benzimidazol-
2-yl)ethyl]cyclobutyl](propan-2-yl)amino]-
β-D-ribofuranosyl]-9*H*-purin-6-amine

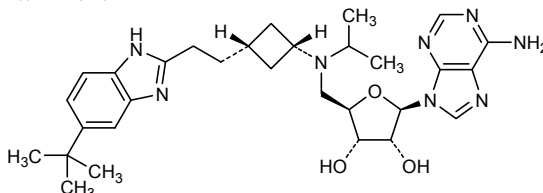
pinométoestat

9-[5-déoxy-5-[[*cis*-3-[2-(5-*tert*-butyl-1*H*-benzimidazol-
2-yl)éthyl]cyclobutyl](propan-2-yl)amino]-
β-D-ribofuranosyl]-9*H*-purin-6-amine

pinometostat

9-[5-desoxi-5-[[*cis*-3-[2-(5-*terc*-butil-1*H*-benzoimidazol-
2-il)etil]ciclobutil](propan-2-il)amino]-β-D-ribofuranosil]-
9*H*-purin-6-amina

C₃₀H₄₂N₈O₃



radalbuvirum

radalbuvir

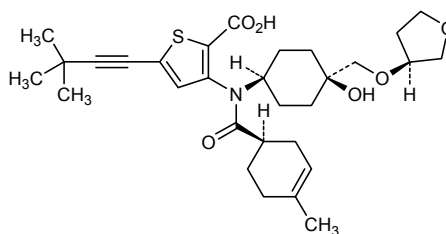
5-(3,3-dimethylbut-1-yn-1-yl)-3-((1*R*)-*N*-[(1*s*,4*s*)-4-hydroxy-4-(((3*S*)-oxolan-3-yl]oxy)methyl)cyclohexyl]-4-methylcyclohex-3-ene-1-carboxamido}thiophene-2-carboxylic acid

radalbuvir

acide 5-(3,3-diméthylbut-1-yn-1-yl)-3-((1*R*)-*N*-[(1*s*,4*s*)-4-hydroxy-4-(((3*S*)-oxolan-3-yl]oxy)méthyl)cyclohexyl]-4-méthylcyclohex-3-ène-1-carboxamido}thiophène-2-carboxylique

radalbuvir

ácido 5-(3,3-dimetilbut-1-in-1-il)-3-((1*R*)-*N*-[(1*s*,4*s*)-4-hidroxi-4-(((3*S*)-oxolan-3-il]oxi)metil)ciclohexil]-4-metilciclohex-3-eno-1-carboxamido}tiofeno-2-carboxílico

C₃₀H₄₁NO₆S**ralinepagum**

ralinepag

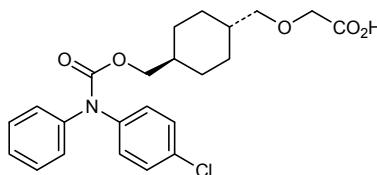
{{*trans*-4-(((4-chlorophenyl)(phenyl)carbamoyl)oxy)methyl)cyclohexyl}methoxy}acetic acid

ralinépag

acide {{*trans*-4-(((4-chlorophényl)(phényl)carbamoyl)oxy)méthyl)cyclohex-yl}methoxy}acétique

ralinepag

ácido {{*trans*-4-(((4-clorofenil)(fenil)carbamoil)oxi)metil)ciclohexil}metoxi}acético

C₂₃H₂₆ClNO₅**relebactamum**

relebactam

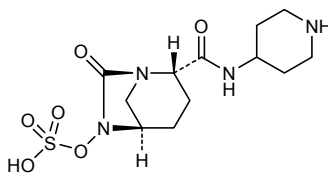
(1*R*,2*S*,5*R*)-7-oxo-2-[(piperidin-4-yl)carbamoyl]-1,6-diazabicyclo[3.2.1]octan-6-yl hydrogen sulfate

rélebactam

hydrogénosulfate de (1*R*,2*S*,5*R*)-7-oxo-2-[(pipéridin-4-yl)carbamoyl]-1,6-diazabicyclo[3.2.1]octan-6-yle

relebactam

hidrógenosulfato de (1*R*,2*S*,5*R*)-7-oxo-2-[(piperidin-4-il)carbamoil]-7-oxo-1,6-diazabicyclo[3.2.1]octan-6-ilo

**ridinilazolium**

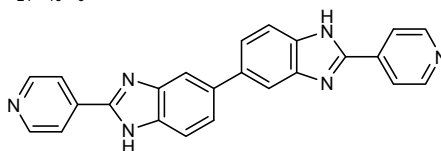
ridinilazole

2,2'-di(pyridin-4-yl)-1*H*,1'*H*-5,5'-bi(benzimidazole)

ridinilazole

2,2'-di(pyridin-4-yl)-1*H*,1'*H*-5,5'-bi(benzimidazole)

ridinilazol

2,2'-di(piridin-4-il)-1*H*,1'*H*-5,5'-bi(benzoimidazol)**roneparstatum**

roneparstat

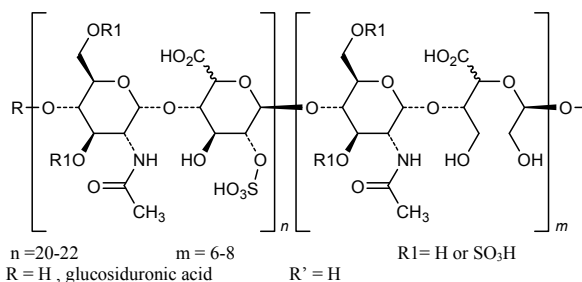
heparan sulfate mimetic compound that is obtained by *N*-des-sulfo and *N*-acetyl reactions on heparin from porcine intestinal mucosa, sodium periodate glycol split oxidation of uronic acids elements and sodium borohydride reduction of aldehydes produced during oxidation; the majority of the components have a glucuronic acid (coming from the heparin starting material) and glucosamine (formed via decomposition of the glucuronic acid) structure at the non-reducing end and iduronic acid 2-sulphate or glycol split structure at the reducing end of their chain; the average molecular weight range is 15000 to 25000 Da; the degree of glycol split is about 25% [m/(n+m)] and the degree of sulfatation is about 1.2 per disaccharidic unit

ronéparstat

dérivé à action mimétique du sulfate d'héparane, obtenu par des réactions conduisant à la *N*-acétyl-*N*-désulfohéparine de muqueuse intestinale de porc, puis dégradation oxydative des glycols des unités uroniques par le périodate de sodium et réduction, par le borohydrure de sodium, des aldéhydes produits ; la majorité des composants ont, une structure acide glucuronique (présente dans l'héparine de départ) et glucosamine (formé par décomposition de l'acide glucuronique) à leur extrémité non-réductrice et une structure dérivée de l'acide iduronique soit l'ester sulfurique soit sa forme acyclique à leur extrémité réductrice, une masse molaire comprise entre 15000 et 25000 daltons, la proportion d'acide uronique ouvert [m/(n+m)] est d'environ 25% et un degré de sulfatation d'environ de 1.2 par unité disaccharide

roneparstat

derivado de acción mimética de la del sulfato de heparán, obtenido por reacciones que producen *N*-acetil-*N*-desulfoheparina de mucosa intestinal de cerdo, que se somete a degradación oxidativa con peryodato de sodio de los glicoles de las unidades urónicas y a reducción, por borohidruro de sodio de los aldehídos producidos; la mayoría de cuyos componentes tienen una estructura de ácido glucurónico (presente en la heparina de partida) y glucosamina (formado por descomposición del ácido glucurónico) en su extremo no-reductor y una estructura derivada del ácido idurónico que puede ser su éster sulfúrico o su forma acíclica en su extremo reductor, masa molar comprendida entre 15000 y 25000 daltons, la proporción de ácido urónico abierto [$m/(n+m)$] es de alrededor de 25% y el grado de sulfatación de alrededor de 1.2 par unidad de disacárido



sacrosidasum #
sacrosidase

invertase 2 (beta-fructofuranosidase 2, saccharase, EC=3.2.1.26) from *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c, Baker's yeast)

sacrosidase

invertase 2 (bêta-fructofuranosidase 2, saccharase, EC=3.2.1.26) de *Saccharomyces cerevisiae* (souche ATCC 204508 / S288c, levure de boulanger)

sacrosidasa

invertasa 2 (beta-fructofuranosidasea 2, sacarasa, EC=3.2.1.26) de *Saccharomyces cerevisiae* (cepa ATCC 204508 / S288c, levadura de cerveza)

Sequence / Séquence / Secuencia

```

SMTNETSDRP LVHFTPNKGW MNDPNGLWYD EKDAKWHLYF QYNPNDTVWG 50
TFLFWGHATS DDLTNWEDQP IAIAPKRNDG GAFSGSMVVD YNNTSGFND 100
TIDPRQRCVA IWTYNTPESE EQYISYSLDG GYTTFTEYQKN PVLAANSTQF 150
RDPKRVWYEP SQKWIMTAAK SQDYKIEIYS SDDLKSWKLE SAFANEGFLG 200
YQYECPLIE VPTEQDPSKS YWVMFISINP GAPAGGSFNQ YFVGSFNGTH 250
FEAFDNQSRV VDFGKDYAL QTFFNTPDPT GSALGIANAS NWEYSAFVPT 300
NFWRSSMSLV RKFSLNTEYQ ANPETELINL KAEPILNIN AGPWSRFATN 350
TTLTKANSYN VDLNSNTGTL EPELVYAVNT TQTISKSVFA DLSLWFKGLE 400
DPEEYLRMGF EVSASSFFLD RGNKVKFKV ENPYFTNRMS VNNQPFKSEN 450
DLSYKRVYGL LDQNILEYF NDGDVVSTNT YFMTTGNALG SVNMTTGVND 500
LFYIDKFQVR EVK 513

```

Glycosylation sites (potential) / Sites potentiels de glycosylation / Posiciones potenciales de glicosilación

Asn-4 Asn-45 Asn-78 Asn-92 Asn-99 Asn-146 Asn-247
Asn-256 Asn-337 Asn-350 Asn-365 Asn-379 Asn-493

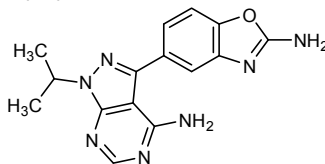
sapanisertibum
sapanisertib

3-(2-amino-1,3-benzoxazol-5-yl)-1-(propan-2-yl)-
1*H*-pyrazolo[3,4-*d*]pyrimidin-4-amine

sapanisertib 3-(2-amino-1,3-benzoxazol-5-yl)-1-(propan-2-yl)-1*H*-pyrazolo[3,4-*d*]pyrimidin-4-amine

sapanisertib 3-(2-amino-1,3-benzoxazol-5-il)-1-(propan-2-il)-1*H*-pirazolo[3,4-*d*]pirimidin-4-amina

C₁₅H₁₅N₇O



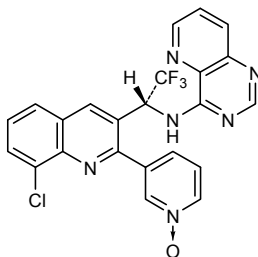
seletalisibum

seletalisib 3-(8-chloro-3-((1*R*)-1-[(pyrido[3,2-*d*]pyrimidin-4-yl)amino]-2,2,2-trifluoroethyl)quinolin-2-yl)pyridine *N*-oxide

sélétalisib *N*-oxyde de 3-(8-chloro-3-((1*R*)-1-[(pyrido[3,2-*d*]pyrimidin-4-yl)amino]-2,2,2-trifluoroéthyl)quinoléin-2-yl)pyridine

seletalisib *N*-óxido de 3-(8-cloro-3-((1*R*)-1-[(pirido[3,2-*d*]pirimidin-4-il)amino]-2,2,2-trifluoroetil)quinolein-2-il)piridina

C₂₃H₁₄ClF₃N₆O



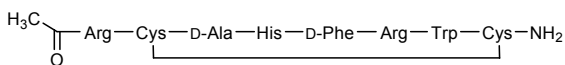
setmelanotidum

setmelanotide *N*²-acetyl-L-arginyl-L-cysteinyl-D-alanyl-L-histidyl-D-phenylalanyl-L-arginyl-L-tryptophyl-L-cysteinamide, cyclic (2-8)-disulfide

setmélanotide (2-8)-disulfure cyclique du *N*²-acétyl-L-arginyl-L-cystéinyl-D-alanyl-L-histidyl-D-phénylalanil-L-arginil-L-tryptophyl-L-cystéinamide

setmelanotida (2-8)-disulfuro cíclico del *N*²-acetyl-L-arginil-L-cisteinil-D-alanil-L-histidil-D-fenilalanil-L-arginil-L-triptofil-L-cisteinamida

C₄₉H₆₈N₁₈O₉S₂



solcitinibum

solcitinib

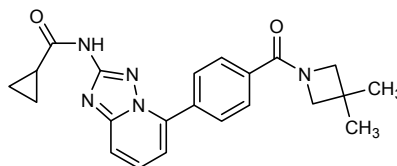
N-[5-[4-(3,3-dimethylazetidino-1-carbonyl)phenyl][1,2,4]triazolo[1,5-*a*]pyridin-2-yl]cyclopropanecarboxamide

solcitinib

N-[5-[4-(3,3-diméthylazétidine-1-carbonyl)phényl][1,2,4]triazolo[1,5-*a*]pyridin-2-yl]cyclopropanecarboxamide

solcitinib

N-[5-[4-(3,3-dimetilazetidina-1-carbonil)fenil][1,2,4]triazolo[1,5-*a*]piridin-2-il]ciclopropanocarboxamida

C₂₂H₂₃N₅O₂**somapacitanum #**

somapacitan

[101-{S-[(8*S*,22*S*,27*S*)-8-carbamoyl-22,27-dicarboxy-2,10,19,24,29,38,42,42,44-nonaoxo-59-(1*H*-tetrazol-5-yl)-12,15,31,34-tetraoxa-42-λ⁶-thia-3,9,18,23,28,37,43-heptaazanapentacontyl]-L-cysteine}]human somatropin

somapacitan

[101-{S-[(8*S*,22*S*,27*S*)-8-carbamoyl-22,27-dicarboxy-2,10,19,24,29,38,42,42,44-nonaoxo-59-(1*H*-tétrazol-5-yl)-12,15,31,34-tétraoxa-42-λ⁶-thia-3,9,18,23,28,37,43-heptaazanapentacontyl]-L-cystéine}]somatropine humaine

somapacitán

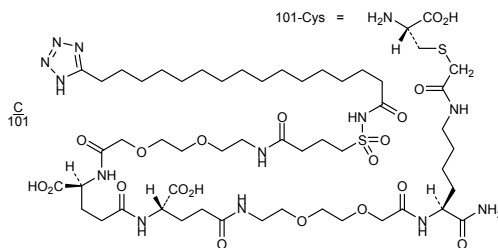
[101-{S-[(8*S*,22*S*,27*S*)-8-carbamoiil-22,27-dicarboxi-2,10,19,24,29,38,42,42,44-nonaoxo-59-(1*H*-tetrazol-5-il)-12,15,31,34-tetraoxa-42-λ⁶-tia-3,9,18,23,28,37,43-heptaazanapentacontil]-L-cisteina}]somatropina humana

Sequence / Séquence / Secuencia

FFTIPLSRLEF DNAMLRARHL HQLAFDTYQE FEEAYIPKEQ KYSFLQNPQT 50
 SLCFSESIPT PSNREETQOK SNLELLRISL LLIQSWLEPV QFLRSVFANS 100
 CVYGASDSNV YDLLKDLLEEG IQTLMGRLED GSPRTGQIFK QTYSKFDTNS 150
 HNDALLKNY GLLYCFRKM DKVETFLRIV QCRSVEGSCG F 191

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

Modified residue / Résidu modifié / Resto modificado



somavaratanum #

somavaratan

rDNA derived human somatotropin (growth hormone of 191 residues) fusion protein with a hydrophilic amino acid sequence* (913 residues) at the N-terminus and another** (146 residues) at the C-terminus, produced in *Escherichia coli*.

*starting with alanine plus 76 dodecapeptides: EPAGSPTSTEEG (AE₃G₂P₂S₂T₂), three different sequences of AG₃P₂S₄T₂ and 72 of 4 different sequences of AE₂G₂P₂S₃T₂

** starting with glycylglycine plus 12 dodecapeptides of 4 different sequences of AE₂G₂P₂S₃T₂

somavaratan

Protéine de fusion entre la somatotropine humaine (facteur de croissance de 191 résidus) et deux protéines hydrophiles, l'une*, de 913 résidus, sur son acide aminé N-terminal, et l'autre**, de 146 résidus, sur son acide aminé C-terminal, obtenue par la technique de l'ADN recombinant à partir de culture d'*Escherichia coli*.

*constituée d'alanine suivie de 76 dodécapeptides, EPAGSPTSTEEG (AE₃G₂P₂S₂T₂) puis trois différentes séquences de AG₃P₂S₄T₂ et 72 de 4 différentes séquences de AE₂G₂P₂S₃T₂

**constituée de glycylglycine suivie de 12 dodécapeptides de 4 différentes séquences de AE₂G₂P₂S₃T₂

somavaratán

proteína de fusión entre la somatotropina humana (factor de crecimiento 191 restos) y dos proteínas hidrófilas, una*, de 913 restos, en el extremo N-terminal, y otra**, de 146 restos, en el extremo C-terminal, obtenida por técnicas de ADN recombinante en cultivos d'*Escherichia coli*.

*constituída por alanina seguida de 76 dodecapéptidos, EPAGSPTSTEEG (AE₃G₂P₂S₂T₂) tres secuencias diferentes de AG₃P₂S₄T₂ y 72 de 4 secuencias diferentes de AE₂G₂P₂S₃T₂

**constituída por glicilglicina seguida de 12 dodecapéptidos de 4 secuencias diferentes de AE₂G₂P₂S₃T₂

Sequence / Sequence / Secuencia
 AEPAGSPTST EEGTPGSGTA SSSPGSSTPS GATGSPGASP GTSSTGSPGS 50
 PAGSPTSTEE GTSSEATPES GPGTSTPESE GSAPGSPAGS PTSTEEGTST 100
 EPSEGSAPGT STEPSEGSAP GTSSEATPES GPGSEPATSG SETPGSEPAT 150
 SGSETPGSPA GSPTSIEEGT SESATPESGP GTSTPESEGS APGTSTPESE 200
 GSAPGSPAGS PTSTEEGTST EPSEGSAPGT STEPEGSAP GTSSEATPES 250
 GPGTSTPESE GSAPGTSESA TPESGPGSEP ATSGSETPGT STEPEGSAP 300
 GTSTPESEGS APGTSESATP ESGPGTSESA TPESGPGSPA GSPTSIEEGT 350
 SESATPESGP GSEPATSGSE TPGTSESATP ESGPGTSTEP SEGSAPGTST 400
 EPSEGSAPGT STEPSEGSAP GTSTPESEGS APGTSTPESE GSAPGTSTEP 450
 SEGSAPGSPA GSPTSIEEGT STEPSEGSAP GTSSEATPES GPGSEPATSG 500
 SETPGTSESA TPESGPGSEP ATSGSETPGT SESATPESGP GTSTPESEGS 550
 APGTSESATP ESGPGSPAGS PTSTEEGSPA GSPTSIEEGS PAGSPTSTEE 600
 GTSSEATPES GPGTSTPESE GSAPGTSESA TPESGPGSEP ATSGSETPGT 650
 SESATPESGP GSEPATSGSE TPGTSESATP ESGPGTSTEP SEGSAPGSPA 700
 GSPTSIEEGT SESATPESGP GSEPATSGSE TPGTSESATP ESGPGSPAGS 750
 PTSTEEGSPA GSPTSIEEGT STEPSEGSAP GTSSEATPES GPGTSESATP 800
 ESGPGTSESA TPESGPGSEP ATSGSETPGS EPATSGSETP GSPAGSPTST 850
 EEGTSTPESE GSAPGTSTEP SEGSAPGSEP ATSGSETPGT SESATPESGP 900
 GTSTPESEGS APGFPITPLS RLFNAMLRA HRLHQLAFDT YQEFEEAYIP 950
 KEQKYSFLQN PQTSLCFSES IPTFSNREET QOKSNLELLR ISLLLIQSWL 1000
 EFPVQFLRSVF ANSLVYGASD SNVYDLLKDL EEGIQLMGR LEDGSPRTGQ 1050
 IFKQTYSKFD TNSHNDALL KNYGLLYCFR KMDKVVETFL RIVQCRSVEG 1100
 SCGFGGTSES ATPESGPGTS TEPSEGSAPG TSTPESEGSA PGTSESATPE 1150
 SGPGTSTEPS EGSAPGTSTE PSEGSAPGTS ESATPESGPG TSTPESEGSA 1200
 FGTSTPESEG SAPGTSTEPS EGSAPGSPAG SPTSIEEGTS TEPSEGSAPG 1250

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
 966-1078 1095-1102

spanlecortemlocelum

spanlecortemlocel

Consists of human expanded CD34+ haematopoietic stem cells that have been isolated from umbilical cord blood and cultured *in vitro* in media supplemented with THPO (thrombopoietin), KITLG (KIT ligand, stem cell factor, SCF), IL6 (interleukin 6), FLT3LG (fms-related tyrosine kinase 3 (FLT3) ligand), and an antagonist of AHR (aryl hydrocarbon receptor); typically contains >10% of cells expressing CD34

spanlécortemlocel

cellules souches hématopoïétiques humaines exprimant CD34+ isolées du sang de cordon ombilical et mises en culture *in vitro* en milieu enrichi en THPO (thrombopoïétine), KITLG (ligand de KIT, facteur de cellules souches, SCF), IL6 (interleukine 6), FLT3LG (ligand de tyrosine kinase 3 fms-like (FLT3)) et un antagoniste d'AHR (récepteur des hydrocarbures aromatiques); typiquement, contient >10% de cellules exprimant CD34

espanlecortemlocel

células madre hematopoyéticas humanas que expresan CD34+ aisladas de sangre de cordón umbilical y cultivadas *in vitro* en un medio enriquecido en THPO (trombopoyetina), KITLG (ligante de KIT, factor de células madre, SCF), IL6 (interleukina 6), FLT3LG (ligando de tirosina kinasa 3 fms-like (FLT3)) y un antagonista de AHR (receptor de hidrocarburos arílicos); normalmente, contiene >10% de células que expresan CD34

spebrutinibum

spebrutinib

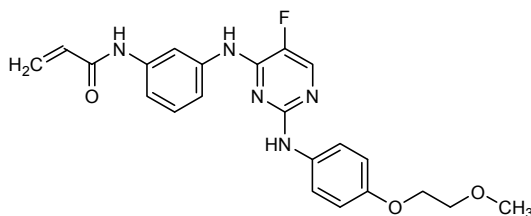
N-[3-((5-fluoro-2-[4-(2-methoxyethoxy)anilino]pyrimidin-4-yl)amino)phenyl]prop-2-enamide

spébrutinib

N-[3-((5-fluoro-2-[4-(2-méthoxyéthoxy)anilino]pyrimidin-4-yl)amino)phényl]prop-2-énamide

espebrutinib

N-[3-((5-fluoro-2-[4-(2-metoxietoxi)anilino]pirimidin-4-il)amino)fenil]prop-2-enamida

$$C_{22}H_{22}FN_5O_3$$
**susoctocogum alfa #**

susoctocog alfa

recombinant DNA derived B-domain deleted porcine blood-coagulation factor VIII analogue, produced in BHK21 cells: des-(753-1418)-blood-coagulation factor VIII (procoagulant component) *Sus scrofa*, glycosylated

susoctocog alfa

analogue du facteur de coagulation VIII porcine dont le domaine B a été supprimé, produit dans des cellules BHK21, à partir d'ADN recombinant: dès-(753-1418)-facteur VIII de coagulation (composant procoagulant) de *Sus scrofa* (porc), glycosylé

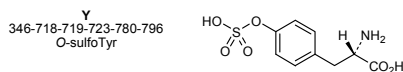
susoctocog alfa

análogo del factor de coagulación VIII porcino del cual se ha suprimido el dominio B, producido en células BHK21, a partir de ADN recombinante: des-(753-1418)-factor VIII de coagulación (componente procoagulante) de *Sus scrofa* (cerdo) glicosilado

Sequene / Séquence / Secuencia
 AIRRYVLEAV ELSNDYRQSE LLRELHVDTR FPATAPGALP LGPSVLYKKT 50
 VFVEFTDQLF SVARPRPMM GLLGPTIQAE VYDTVVVTLK NMA5HPVSLH 100
 AVGV5FWKSS EGAEYEDHTS QREKEDDKVL PCKSQTYVWQ VLKENGPTAS 150
 DPPCLTYSYL SHVDLVKDLN SGLIGALLVC REGSLTRERT QNLHEFVLLF 200
 AVFDEGKSWH SARND5WTRA MDPAPARAQP AMHTVNGYVN RSLPGLIGCH 250
 KKSVMYWHVIG MGT5PEVHSI FLEGHFTLVR HHRQASLEI5 PLTFLTAQTF 300
 LMDLQGLLFF CHISSHHHGG MEAHVVRVESC AEEPQLRKA DEEEDYDDNL 350
 YDSDMDVVRLL DGDDVSPFIQ IRSVAKHKPK TWVHYISAE EDWDYAPAVP 400
 SP5DR5YKSL YLNSGPPRIQ RKYKARFVA YTDVTFKTRK AIPY5ESGLL 450
 PLLYGEVGDY LLIIFKNKAS RPYNIYPHGI TDV5ALHPGR LLKGWKHLKD 500
 MPILPGETFK YKWTVTVEDG PTKSDPRCLT RY5SSINLE KDLASGLIGP 550
 LLICYKESVD QRGNO5MSDK RNVILFSVFD ENQ5WYLAEN IQRFLNPDG 600
 LQPDPPEFQA SNIMHSINGY VFD5LQLSVC LHEVAYWYIL SVGAQTFDPLS 650
 VVFSGYTFKH KMYVEDTLTL FPF5GETVFM SMENPGLWVL GCHNSDLRNR 700
 GMTALLKVYS CDRDIGDYD NTYEDIPGFL LSGKNVIEPR SFAQNSRP5S 750
 ASAPKPPVLR RHQRDISLPT FQPEEDKMDY DDIFSTETKG E5DFDIYGEDE 800
 N5DPR5FQKR TRHYFIAAV5 QLWDYGMSES PRALNRNAQN GEVPRFKKV 850
 FREFADGSFT QPSYRGELNK HLG5LGPYIR A5VEDNIMVT FKNQASRP5S 900
 FY5SL5Y5PD DQEQGAEPRH NFVQPNETRT YFWK5QH5MA PTEDEFDCKA 950
 WAYFSDVDLE KDVH5GLIGP LLI5CRANTLN AAH5RQVTVQ EFALFFTFIF 1000
 ETK5WYFTEN VERNCRAPCH LQMEDPTLKE NYRFHAINGY VMDTLPG5VM 1050
 AQNRIRWYL L5MGSNENIH SIHF5GHVFS VRK5E5YKMA VYNLYPGVFE 1100
 TVEM5LPSKVG IWR5ECLIGE HLQAGM5TF L5V5KECQAP LGM5AGRI5D 1150
 FQITASGQYG QWAPKLARLH Y5GSINAW5T KDP5HWIKVD LLAPMI5HGI 1200
 MTQGARQKFS SLYISQFIIM Y5LDGRNWQ5 YRGN5TG5TLM V5F5GNVDASG 1250
 IKHNI5NPPI VARYIRLHPT H5YIR5TLRM ELM5GCDLNSC S5MPLGMQ5NKA 1300
 ISDSQITASS H5L5NI5FAT5S P5QARLHLQ5G RTN5AWR5PRV5 S5AE5EWLQ5VDL 1350
 QKTVKVTGIT TQGVK5LL5S MYVKEFLV5S5 SQDGR5RWTLF LQDGH5TKV5FQ 1400
 GNQD5STPVV NALDP5L5FTR YLR5IHPT5WA QH5ALR5LEVL GCEAQ5DLY 1448

Disulfide bridges location / Positions des ponts disulfure / Posiciones de los puentes disulfuro
 154-180 249-330 528-554 630-711 948-974 1015-1019 1137-1285 1290-1442

Modified residues / Résidus modifiés / Restos modificados



Glycosylation sites (N,S,T) / Sites de glycosylation (N,S,T) / Posiciones de glicosilación (N,S,T)

Ser-44 Asn-214 Asn-240 Ser-353 Asn-582
 Ser-741 Ser-752 Thr-770 Asn-926 Asn-1234

tazemetostatam
 tazemetostat

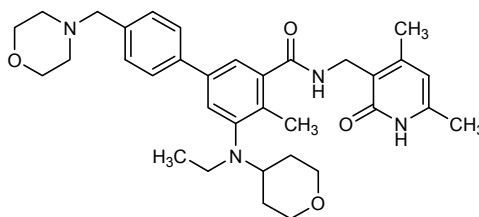
N-[[4,6-dimethyl-2-oxo-1,2-dihydropyridin-3-yl)methyl]-5-[ethyl(oxan-4-yl)amino]-4-methyl-4'-[(morpholin-4-yl)methyl][1,1'-biphenyl]-3-carboxamide

tazéméstostat

N-[[4,6-diméthyl-2-oxo-1,2-dihydropyridin-3-yl)méthyl]-5-[éthyl(oxan-4-yl)amino]-4-méthyl-4'-[(morpholin-4-yl)méthyl][1,1'-biphényl]-3-carboxamide

tazemetostat

N-[[4,6-dimetil-2-oxo-1,2-dihidropiridin-3-il)metil]-5-[etil(oxan-4-il)amino]-4-metil-4'-[(morfolin-4-il)metil][1,1'-bifenil]-3-carboxamida

C₃₄H₄₄N₄O₄**temsavirum**

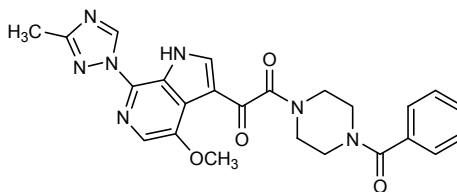
temsavir

1-(4-benzoylpiperazin-1-yl)-2-[4-methoxy-7-(3-methyl-1*H*-1,2,4-triazol-1-yl)-1*H*-pyrrolo[2,3-*c*]pyridin-3-yl]ethane-1,2-dione

temsavir

1-(4-benzoylpipérazin-1-yl)-2-[4-méthoxy-7-(3-méthyl-1*H*-1,2,4-triazol-1-yl)-1*H*-pyrrolo[2,3-*c*]pyridin-3-yl]éthane-1,2-dione

temsavir

1-(4-benzoilpiperazin-1-il)-2-[4-metoxi-7-(3-metil-1*H*-1,2,4-triazol-1-il)-4-metoxi-1*H*-pirrolo[2,3-*c*]piridin-3-il]etano-1,2-dionaC₂₄H₂₃N₇O₄**tesidolumabum #**

tesidolumab

immunoglobulin G1-lambda2, anti-[*Homo sapiens* C5 (complement C5)], *Homo sapiens* monoclonal antibody; gamma1 heavy chain (1-446) [*Homo sapiens* VH (IGHV1-69*01 (96.90%) -(IGHD)-IGHJ4*01) [8.8.9] (1-116) -IGHG1*03 (CH1 (117-214), hinge (215-229), CH2 (230-339) L1.3>A (233), L1.2>A (234), CH3 (340-444), CHS (445-446) (117-446)], (219-213')-disulfide with lambda2 light chain (1'-214') [*Homo sapiens* V-LAMBDA (IGLV3-9*01 (88.20%) -IGLJ2*01) [6.3.11] (1'-108') -IGLC2*01 (109'-214')]; dimer (225-225":228-228")-bisdisulfide

tésidolumab

immunoglobuline G1-lambda2, anti-[*Homo sapiens* C5 (complément C5)], *Homo sapiens* anticorps monoclonal; chaîne lourde gamma1 (1-446) [*Homo sapiens* VH (IGHV1-69*01 (96.90%) -(IGHD)-IGHJ4*01) [8.8.9] (1-116) -IGHG1*03 (CH1 (117-214), charnière (215-229), CH2 (230-339) L1.3>A (233), L1.2>A (234), CH3 (340-444), CHS (445-446) (117-446)], (219-213')-disulfure avec la chaîne légère lambda2 (1'-214') [*Homo sapiens* V-LAMBDA (IGLV3-9*01 (88.20%) -IGLJ2*01) [6.3.11] (1'-108') -IGLC2*01 (109'-214')]; dimère (225-225":228-228")-bisdisulfure

tesidolumab

immunoglobulina G1-lambda2, anti-[C5 (complemento C5) de *Homo sapiens*], anticuerpo monoclonal de *Homo sapiens*;
 cadena pesada gamma1 (1-446) [*Homo sapiens* VH (IGHV1-69*01 (96.90%) -(IGHD)-IGHJ4*01) [8.8.9] (1-116) -IGHG1*03 (CH1 (117-214), bisagra (215-229), CH2 (230-339) L1.3>A (233), L1.2>A (234), CH3 (340-444), CHS (445-446) (117-446)], (219-213')-disulfuro con la cadena ligera lambda2 (1'-214') [*Homo sapiens* V-LAMBDA (IGLV3-9*01 (88.20%) -IGLJ2*01) [6.3.11] (1'-108') -IGLC2*01 (109'-214')]; dímero (225-225":228-228")-bisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVQSGAE VKKFGSSVKV SCKASGGTFS SYAISWVRQA PGQGLEWMGG 50
IGPFFGTANY AQKFQGRVTI TADESTSTAY MELSSLRSED TAVYVCARDT 100
PYFDYWGQGT LVTVSSASTK GPSVFPLAPS SKSTSGGTA LGCLVKDYFP 150
EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVTVVPS SLGTQTYICN 200
VNHKPSNTKV DKRVEPKSCD KTHTCPPCPA PEAAGGVSFV LFPPKPKDTL 250
MISRTFEVTC VVVDVSHEDP EVKFNWYVDG VEVHNAKTKF REEQYNSTYR 300
VVSVLTVLHQ DWLNGKEYKC KVSNKALPAP IEKTIKAKG QPREPQVYTL 350
PPSREEMTKN QVSLTCLVKG FYPSSDIAVEW ESNQGPENNY KTTTPVLDS 400
GSFFLYSKLT VDKSRWQQGN VFSCSVMHEA LHNHYTQKSL SLSPGK 446
```

Light chain / Chaîne légère / Cadena ligera

```
SYELTQPLSV SVALGQTARI TCSGDSIPNY YVYVYQQKPG QAPVLVIYDD 50
SNRPSGIPER FSGNSNGNTA TLTISRAQAG DEADYCYQSF DSSLNAEVFG 100
GGTKLTVLQG PKAAPSVTLF PPSSEELQAN KATLVCLISD FYPGAVTVAV 150
KADSSPVKAG VETTTPSKQS NNKYAASSYL SLTPEQWKSH RSYSCQVTHE 200
GSTVEKTVAP TECS 214
```

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

```
Intra-H (C23-C104) 22"-96" 143"-199" 260"-320" 366"-424"
22"-96" 143"-199" 260"-320" 366"-424"
Intra-L (C23-C104) 22"-87" 136"-195"
22"-87" 136"-195"
Inter-H-L (h 5-CL 126) 219"-213" 219"-213"
Inter-H-H (h 11, h 14) 225"-225" 228"-228"
```

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

toreforantum

toreforant

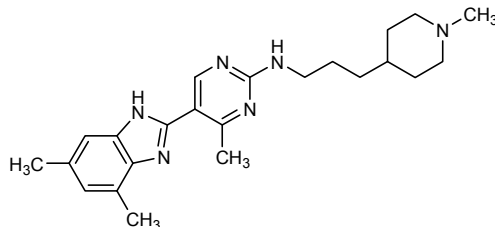
5-(4,6-dimethyl-1*H*-benzimidazol-2-yl)-4-methyl-*N*-[3-(1-methylpiperidin-4-yl)propyl]pyrimidin-2-amine

toréforant

5-(4,6-diméthyl-1*H*-benzimidazol-2-yl)-4-méthyl-*N*-[3-(1-méthylpipéridin-4-yl)propyl]pyrimidin-2-amine

toreforant

5-(4,6-dimetil-1*H*-benzoimidazol-2-il)-4-metil-*N*-[3-(1-metilpiperidin-4-il)propil]pirimidin-2-amina

C₂₃H₃₂N₆

trofinetidum

trofinetide

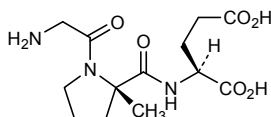
glycyl-2-methyl-L-prolyl-L-glutamic acid

trofinétide

acide glycyl-2-méthyl-L-prolyl-L-glutamique

trofinetida

ácido glicil-2-metil-L-prolil-L-glutámico

C₁₃H₂₁N₃O₆**vandortuzumabum vedotinum #**

vandortuzumab vedotin

immunoglobulin G1-kappa, anti-[*Homo sapiens* STEAP1 (six-transmembrane epithelial antigen of the prostate 1, PRSS24, STEAP)], humanized monoclonal antibody; gamma1 heavy chain (1-454) [humanized VH (*Homo sapiens* IGHV3-48*03 (80.80%) -(IGHD)-IGHJ4*01) [9.7.17] (1-124) -*Homo sapiens* IGHG1*03 (CH1 R120>K (221) (125-222), hinge (223-237), CH2 (238-347), CH3 (348-452), CHS (453-454)) (125-454)], (227-220')-disulfide with kappa light chain (1'-220') [humanized V-KAPPA (*Homo sapiens* IGKV1-16*01 (81.20%) -IGKJ1*01) [12.3.9] (1'-113') -*Homo sapiens* IGKC*01 (114'-220')]; dimer (233-233":236-236")-bisdisulfide; conjugated, on an average of 3 to 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*".

vandortuzumab védotine

immunoglobuline G1-kappa, anti-[*Homo sapiens* STEAP1 (antigène épithélial 1 à six-transmembrane de la prostate, PRSS24, STEAP)], anticorps monoclonal humanisé; chaîne lourde gamma1(1-454) [VH humanisé (*Homo sapiens* IGHV3-48*03 (80.80%) -(IGHD)-IGHJ4*01) [9.7.17] (1-124) -*Homo sapiens* IGHG1*03 (CH1 R120>K (221) (125-222), charnière (223-237), CH2 (238-347), CH3 (348-452), CHS (453-454)) (125-454)], (227-220')-disulfure avec la chaîne légère kappa (1'-220') [V-KAPPA humanisé (*Homo sapiens* IGKV1-16*01 (81.20%) -IGKJ1*01) [12.3.9] (1'-113') -*Homo sapiens* IGKC*01 (114'-220')]; dimère (233-233":236-236")-bisdisulfure; conjugué, sur 3 à 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*".

vandortuzumab vedotina

inmunoglobulina G1-kappa, anti-[STEAP1 de *Homo sapiens* (antígeno epitelial 1 seis-transmembrana de la próstata, PRSS24, STEAP)], anticuerpo monoclonal humanizado;
 cadena pesada gamma1 (1-454) [VH humanizada (*Homo sapiens* IGHV3-48*03 (80.80%) -(IGHD)-IGHJ4*01) [9.7.17] (1-124) -*Homo sapiens* IGHG1*03 (CH1 R120>K (221) (125-222), bisagra (223-237), CH2 (238-347), CH3 (348-452), CHS (453-454)) (125-454)], (227-220')-disulfuro con la cadena ligera kappa (1'-220') [V-KAPPA humanizado (*Homo sapiens* IGKV1-16*01 (81.20%) -IGKJ1*01) [12.3.9] (1'-113') -*Homo sapiens* IGKC*01 (114'-220')]; dímero (233-233":236-236")-bisdisulfuro;
 conjugado, en 3 – 4 restos cisteinil por término medio, con monometilauristatina E (MMAE), mediante una secuencia de conexión escindible de tipo maleimidocaproil-valil-citrulinil-*p*-aminobenciloxicarbonil (mc-val-cit-PABC)
 La fracción vedotina pueden encontrarla en el documento "INN for pharmaceutical substances: Names for radicals, groups and others".

Heavy chain / Chaîne lourde / Cadena pesada
 EVQLVDSGGG LVQPGGSLRL SCAVSGYSIT SDYAWNVRQ AFGKLEWVG 50
 YISNSGTSY NPSLKSRTI SRDTSKNTLY LQMNSLRAED TAVYICARER 100
 NYDYDDIYYA MDYWCQGTIV TVSSASTKGP SVFLAPLPSK STSGGTAALG 150
 CLVKDYFPEP VTVSWNSGAL TSGVHTFPAV LQSSGLYSLV SVVTVPSSSL 200
 GTQYICNVN HKPSNTRKVK KVEPKSCDKT HTPCPCPAPE LLLGSPSVFLF 250
 PPKPKDTLMI SRTPEVTCVV VDVSHEDPEV KFNWYVDGVE VHNAKTKPRE 300
 EQYNSTYRVV SVLTVLHQDW LNKKEYKCKV SNKALPAPIE KTISKAKGQP 350
 REPQVYTLPP SREEMTKNQV SLTCLVKGFI PSDIAVEWES NGQPENNYKT 400
 TTPVLDSDGS FFLYSKLTVD KSRWQQGNVF SCSVMHEALH NHYTQKLSL 450
 SPGK 454
 Light chain / Chaîne légère / Cadena ligera
 DIQMTQSPSS LSASVGRVT ITCRSSQSLI YRSNOKNYLA WYQQKPGKAP 50
 RLLTITWASTR ESGVPSRFSG SGSGTDFTL ISSLQPEDFA TYICQQYNY 100
 PRFPGQTKV EIKRTVAAPS VPIPPPSDEQ LKSGTASVVC LLNNFYPREA 150
 KVQWKVDNAL QSGNSQESVT EQDSKDSYIS LSSITLPSKA DYERHKVYAC 200
 EVTHQGLSSP VTKSFNRGEC 220

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
 Intra-H (C23-C104) 22-96 151-207 268-328 374-432
 22"-96" 151"-207" 268"-328" 374"-432"
 Intra-L (C23-C104) 23-94" 140"-200"
 23"-94" 140"-200"
 Inter-H-L* (h 5-CL 126) 227-220" 227"-220"
 Inter-H-H* (h 11, h 14) 233-233" 236-236"
 *Two or three of the inter-chain disulfide bridges are not present, an average of 3 to 4 cysteinyl being conjugated each via a thioether bond to a drug linker.
 *Deux ou trois des ponts disulfures inter-chaînes ne sont pas présents, 3 à 4 cystéinyl en moyenne étant chacun conjugué via une liaison thioéther à un linker-principe actif.
 *Faltan dos o tres puentes disulfuro inter-catenarios, una media de 3 a 4 cisteinil está conjugada a conectores de principio activo.

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
 H CH2 N84.4:
 304, 304

verosudilum

verosudil

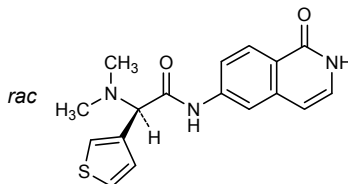
rac-(2*R*)-2-(dimethylamino)-*N*-(1-oxo-1,2-dihydroisoquinolin-6-yl)-2-(thiophen-3-yl)acetamide

vérosudil

rac-(2*R*)-2-(diméthylamino)-*N*-(1-oxo-1,2-dihydroisoquinoléin-6-yl)-2-(thiophén-3-yl)acétamide

verosudil

rac-(2*R*)-2-(dimetilamino)-*N*-(1-oxo-1,2-dihidroisoquinolein-6-il)-2-(tiofen-3-il)acetamida

C₁₇H₁₇N₃O₂S**verubecestatum**

verubecestat

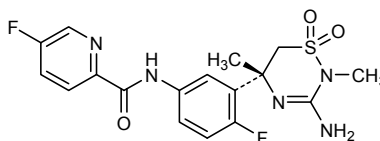
N-{3-[(5*R*)-3-amino-2,5-dimethyl-1,1-dioxo-1,2,5,6-tetrahydro-1λ⁶,2,4-thiadiazin-5-yl]-4-fluorophenyl}-5-fluoropyridine-2-carboxamide

vérubécestat

N-{3-[(5*R*)-3-amino-2,5-diméthyl-1,1-dioxo-1,2,5,6-tétrahydro-1λ⁶,2,4-thiadiazin-5-yl]-4-fluorophényl}-5-fluoropyridine-2-carboxamide

verubecestat

N-{3-[(5*R*)-3-amino-2,5-dimetil-1,1-dioxo-1,2,5,6-tetrahydro-1λ⁶,2,4-tiadiazin-5-il]-4-fluorofenil}-5-fluoropiridina-2-carboxamida
C₁₇H₁₇F₂N₅O₃S

**vosoritidum**

vosoritide

A modified recombinant human C-type natriuretic peptide (CNP) consisting of 39 amino acids comprised of the 37 C-terminal amino acids of the human CNP sequence plus the addition of 2 amino acids (Pro-Gly) on the *N*-terminus, produced in *Escherichia coli*:
L-prolylglycyl-(human C-type natriuretic peptide-(17-53)-peptide (CNP-37)), cyclic-(23-39)-disulfide

vosoritide

peptide natriurétique de type C humain modifié consistant en une séquence de 39 acides aminés comprenant les 37 acides aminés C-terminaux du peptide humain CNP plus deux acides aminés (Pro-Gly) *N*-terminaux, produit par *Escherichia coli*:
L-prolylglycyl-(peptide natriurétique de type C humain-(17-53)-peptide (CNP-37)), (23-39)-disulfure cyclique

vosoritida

péptido natriurético de tipo C humano modificado consistente en una secuencia de 39 aminoácidos que comprende los 37 aminoácidos C-terminales del péptido humano CNP más dos aminoácidos (Pro-Gly) *N*-terminales, producido por *Escherichia coli*:
L-prolilglicil-(péptido natriurético de tipo C humano-(17-53)-péptido (CNP-37)), (23-39)-disulfuro cíclico

C₁₇₆H₂₉₀N₅₆O₅₁S₃

Sequence / Séquence / Secuencia

PGQEHFNARK YKGANKKGLS KGCFGLKLDLDR IGSM9GLGC 39

Disulfide bridge location / Position du pont disulfure / Posición del puente disulfuro
23-39**zuretinoli acetas**

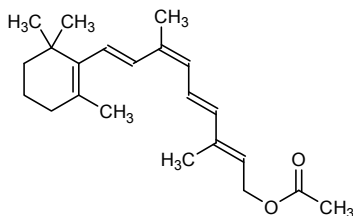
zuretinol acetate

(2*E*,4*E*,6*Z*,8*E*)-3,7-dimethyl-9-(2,6,6-trimethylcyclohex-1-en-1-yl)nona-2,4,6,8-tetraen-1-yl acetate

acétate de zurétinol

acétate de (2*E*,4*E*,6*Z*,8*E*)-3,7-diméthyl-9-(2,6,6-triméthylcyclohex-1-én-1-yl)nona-2,4,6,8-tétraén-1-yle

acetato de zuretinol

acetato de (2*E*,4*E*,6*Z*,8*E*)-3,7-dimetil-9-(2,6,6-trimetilciclohex-1-en-1-il)nona-2,4,6,8-tetraen-1-iloC₂₂H₃₂O₂# Electronic structure available on Mednet: <http://mednet.who.int/># Structure électronique disponible sur Mednet: <http://mednet.who.int/># Estructura electrónica disponible en Mednet: <http://mednet.who.int/>* <http://www.who.int/medicines/services/inn/publication/en/>

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

Recommended International Nonproprietary Names (Rec. INN): List 29
Dénominations communes internationales recommandées (DCI Rec.): Liste 29
Denominaciones Comunes Internacionales recomendadas (DCI Rec.): Lista 29
(WHO Drug Information, Vol. 3, No. 3, 1989)

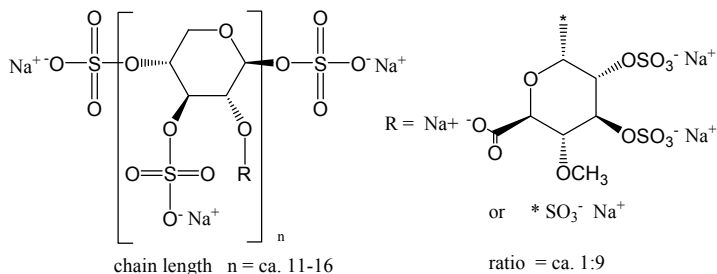
- p. 7 **natrii pentosani polysulfas**
 pentosan polysulfate sodium *replace the chemical name, the molecular formula by the following ones and insert the following structure*
 pentosane polysulfate sodique *remplacer le nom chimique, la formule moléculaire par les suivants et insérer la structure suivante*
 pentosano polisulfato de sodio *sustitúyase el nombre químico, la fórmula molecular por los siguientes y insértese la estructura siguiente*

a mixture of the sodium salts of linear polymers of (1→4)-β-D-xylopyranan usually sulfated at the 2-and 3-positions and occasionally (approximately 1 in every 10 residues) substituted at the 2-position with a (4-O-methyl-2,3-di-O-sulfo-α-D-glucopyranosyluronic acid) group; the average molecular weight lies between 4000 and 6000 with a total molecular weight range of 1000 to 40000

un mélange de sels de sodium de polymères linéaires de (1→4)-β-D-xylopyranane habituellement sulfatés en positions 2 et 3 et parfois (approximativement 1 résidu sur 10) substitué en position 2 avec un groupe acide 4-O-méthyl-2,3-di-O-sulfo-α-D-glucopyranosyluronique; le poids moléculaire moyen est compris entre 4000 et 6000 avec un poids moléculaire total compris entre 1000 et 40000

una mezcla de sales sódicas de polímeros lineales de (1→4)-β-D-xilopiranoano generalmente sulfatados en posiciones 2 y 3 y ocasionalmente (aproximadamente 1 resto cada 10) sustituido en posición 2 por un grupo ácido 4-O-metil-2,3-di-O-sulfo-α-D-glucopiranosilurónico; el peso molecular medio está comprendido entre 4000 y 6000 con un peso molecular total comprendido entre 1000 y 40000

$(C_5H_6Na_2O_{10}S_2)_n (C_7H_8Na_2O_9S)_0.1n (Na_2O_7S_2)$, average $n = ca$ 11 to 16



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.